



Artificial Selection on Microbiomes To Breed Microbiomes That Confer Salt Tolerance to Plants

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ABSTRACT We develop a method to artificially select for rhizosphere microbiomes that confer salt tolerance to the model grass *Brachypodium distachyon* grown under sodium salt stress or aluminum salt stress. In a controlled greenhouse environment, we differentially propagated rhizosphere microbiomes between plants of a nonevolving, highly inbred plant population; therefore, only microbiomes evolved in our experiment, but the plants did not evolve in parallel. To maximize microbiome perpetuation when transplanting microbiomes between plants and, thus, maximize response to microbiome selection, we improved earlier methods by (i) controlling microbiome assembly when inoculating seeds at the beginning of each selection cycle; (ii) fractionating microbiomes before transfer between plants to harvest, perpetuate, and select on only bacterial and viral microbiome components; (iii) ramping of salt stress gradually from minor to extreme salt stress with each selection cycle to minimize the chance of overstressing plants; (iv) using two nonselection control treatments (e.g., nonselection microbial enrichment and null inoculation) that permit comparison to the improving fitness benefits that selected microbiomes impart on plants. Unlike previous methods, our selection protocol generated microbiomes that enhance plant fitness after only 1 to 3 rounds of microbiome selection. After nine rounds of microbiome selection, the effect of microbiomes selected to confer tolerance to aluminum salt stress was nonspecific (these artificially selected microbiomes equally ameliorate sodium and aluminum salt stresses), but the effect of microbiomes selected to confer tolerance to sodium salt stress was specific (these artificially selected microbiomes do not confer tolerance to aluminum salt stress). Plants with artificially selected microbiomes had 55 to 205% greater seed production than plants with unselected control microbiomes.

IMPORTANCE We developed an experimental protocol that improves earlier methods of artificial selection on microbiomes and then tested the efficacy of our protocol to breed root-associated bacterial microbiomes that confer salt tolerance to a plant. Salt stress limits growth and seed production of crop plants, and artificially selected microbiomes conferring salt tolerance may ultimately help improve agricultural productivity. Unlike previous experiments of microbiome selection, our selection protocol generated microbiomes that enhance plant productivity after only 1 to 3 rounds of artificial selection on root-associated microbiomes, increasing seed production under extreme salt stress by 55 to 205% after nine rounds of microbiome selection. Although we artificially selected microbiomes under controlled greenhouse conditions that differ from outdoor conditions, increasing seed production by 55 to 205% under extreme salt stress is a remarkable enhancement of plant productivity compared to traditional plant breeding. We describe a series of additional experimental protocols that will advance insights into key parameters that determine efficacy and response to microbiome selection.

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A challenge in plant-microbiome research is engineering of microbiomes with specific and lasting beneficial effects on plants. These difficulties of microbiome engineering derive from several interrelated factors, including transitions in microbiome function during plant ontogeny and the complexity of microbiome communities, such as hyperdiverse rhizosphere or phyllosphere microbiomes containing countless fungal, bacterial, and viral components (1–3). Even when beneficial microbiomes can be assembled experimentally to generate specific microbiome functions that benefit a plant, microbiomes are often ecologically unstable and undergo turnover (i.e., microbiome communities change dynamically over time), for example, when new microbes immigrate into microbiomes, when beneficial microbes are lost from microbiomes, or when beneficial microbes evolve new properties under microbe-microbe competition that are detrimental to a host plant.

One strategy to engineer sustainable beneficial microbiome function uses repeated cycles of differential microbiome propagation to perpetuate between hosts only those microbiomes that have the most desired fitness effects on a host (Fig. 1). Such differential propagation of microbiomes between hosts can therefore artificially select for microbiome components that best mediate stresses that impact host fitness (4–7). Only three experimental studies have used this approach so far for plants. Two studies selected on rhizosphere microbiomes of the plant *Arabidopsis thaliana* (4, 8), and both studies needed more than 10 cycles of microbiome selection to generate a modest and highly variable phenotypic response in plant phenotypes (e.g., increase in above-ground biomass by ~10%) (4). A third study (9) used seven cycles of microbiome selection to generate microbiomes that significantly delayed the onset of drought symptoms of water-stressed wheat plants. Here, we expand on these studies to artificially select for bacterial rhizosphere microbiomes that confer salt tolerance to the model grass *Brachypodium distachyon* (Fig. 1). Our methods specifically aim to improve microbiome perpetuation between plants and to optimize response to artificial microbiome selection by controlling microbiome assembly when inoculating seeds, using low-carbon soil to enhance host control exerted by seedlings during initial microbiome assembly and early plant growth, harvesting and perpetuating microbiomes that are in close physical contact with plants, short cycling of microbiome generations to select for microbiomes that benefit seedling growth, and ramping of salt stress between selection cycles to minimize the chance of either understressing or overstressing plants.

To optimize microbiome selection experiments, we found it useful to conceptualize the process of microbiome selection within a host-focused quantitative genetic framework (6) rather than within a multilevel selection framework preferred by Swenson et al. (4) (artificial ecosystem selection; see also reference 10). Both frameworks capture the same processes (i.e., neither framework is wrong), but a host-focused quantitative genetic framework is more useful to identify factors that can be manipulated to increase efficacy of microbiome selection. First, because microbiome selection aims to shape a fitness component of the host plant (e.g., stress tolerance) and because it is typically easier to measure plant phenotypes rather than measure microbiome properties, selection is indirect. Microbiomes are not measured directly, but microbiomes are evaluated indirectly by measuring host performance. Indirect selection is an established breeding technique that can be used when the target trait is difficult or costly to measure (11), as is the case for microbiome traits compared to the ease of measuring a host phenotype that is dependent on microbiome properties. The efficacy of indirect selection depends on strong correlations between microbiome and host traits; therefore, indirect microbiome selection should be more efficient if such correlations can be maximized experimentally, for example, by controlling ecological priority effects during initial microbiome assembly (12–15) or by increasing host control over microbiome assembly and persistence (14, 16). Second, because a typical host likely experienced a long history of evolution to monitor and manipulate its microbiomes (a process called host control) (16–19), indirect microbiome

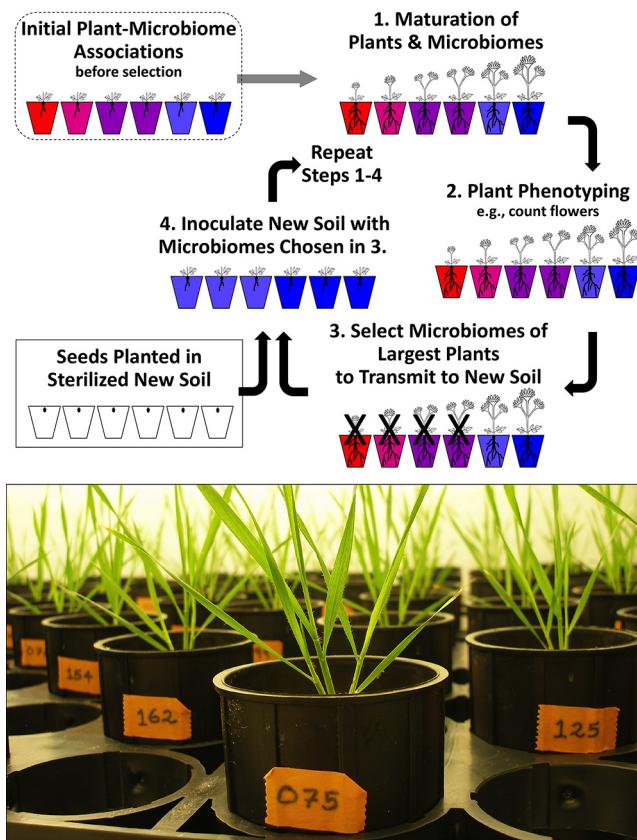


FIG 1 Host-mediated artificial selection on microbiomes. (Top) Method of differential microbiome propagation to impose artificial selection on rhizosphere microbiomes (modified from reference 6 with permission of the publisher). The host plant does not evolve because this method harvests microbiomes from mature plants and propagates these microbiomes to sterilized seeds planted in sterilized soil (step 4), but seeds are taken each cycle from a nonevolving source (stored seeds). The method imposes indirect selection on microbiomes because microbiome properties are not measured directly; instead, microbiome effects are estimated indirectly by measuring host fitness (e.g., plant biomass); therefore, host fitness is used as an indicator to infer association with rhizosphere microbiomes that benefit a plant. Both evolutionary and ecological processes can alter microbiomes at each step in the cycle (see the text), but at steps 3 and 4 in each cycle, experimental protocols aim to maximize evolutionary changes stemming from differential microbiome propagation. (Bottom) Experimental plants of the model grass *Brachypodium distachyon* shortly before harvesting of rhizosphere microbiomes for differential microbiome propagation. Photo by U.G.M.

selection uses the host as a kind of thermostat to help gauge and adjust the temperature of its microbiomes, and then propagate desired microbiomes between hosts (Fig. 1). Based on previous theories (5, 6, 20), such host-mediated indirect selection on microbiomes can be easier than direct selection on microbiomes, particularly with host species that exert strong host control over assembly and stability of their microbiomes (6, 13, 14, 21).

Microbiome engineering by means of differential microbiome propagation (Fig. 1) alters microbiomes through both ecological and evolutionary processes. Ecological processes include changes in community diversity, relative species abundances, or structure of microbe-microbe or microbe-plant interaction networks. Evolutionary processes include extinction of specific microbiome members; allele frequency changes, mutation, or gene transfer between microbes; and differential persistence of microbiome components when differentially propagating microbiomes at each selection cycle. These processes can be interdependent (e.g., in the case of ecoevolutionary feedback [22, 23]), and some processes can be called either ecological or evolutionary (e.g., loss of a microbe from a microbiome can be viewed as evolutionary extinction or as an outcome of ecological competition), but for the design of a microbiome selection protocol, it is useful to think about ecological processes separately from evolutionary processes. Microbiome selection protocols aim to maximize changes in the genetic makeup of microbiomes through differential microbiome propagation (steps 3

and 4 in Fig. 1), for example, by optimizing microbiome transmission during microbiome transplanting between hosts or by optimizing microbiome reassembly after such transfers (e.g., by facilitating ecological priority effects at host inoculation). Although both evolutionary and ecological processes alter genetic makeup of microbiomes during each propagation cycle (Fig. 1), as shorthand, we refer to the changes resulting from host-mediated indirect selection on microbiomes as microbiome response due to microbiome selection.

RESULTS

Artificially selected microbiomes confer increased salt tolerance to plants. Figure 2 shows the changes in relative plant fitness (aboveground dry biomass) during eight rounds of differential microbiome propagation. Relative to fallow-soil control (nonselection enrichment) treatment and null control treatment, selected microbiomes confer increased salt tolerance to plants after only 1 to 3 selection cycles for both the sodium stress (Fig. 2a and c) and the aluminum stress treatments (Fig. 2b and d). Relative to fallow-soil control plants, artificially selected microbiomes increase plant fitness by 75% under sodium sulfate stress ($P < 0.001$) and by 38% under aluminum sulfate stress ($P < 0.001$). Relative to null control plants, selected microbiomes increase plant fitness by 13% under sodium sulfate stress and by 12% under aluminum sulfate stress. Although repeated rounds of differential microbiome propagation improved plant fitness between successive microbiome generations (particularly relative to the null controls; Fig. 2c and d), interactions between treatment and generation were not statistically significant (see Text S3 in the supplemental material). This implies that fitness-enhancing effects of microbiomes from selection lines were realized after one or a few rounds of microbiome selection (e.g., Fig. 2c and d), and there was insufficient statistical support that, under the gradually increasing salt stress, any additional rounds further resulted in greater plant biomass of selection lines relative to control lines. However, because plants were exposed to increasingly greater salt stresses in later generations (Fig. 2e and f, Text S1), selected microbiomes of later generations helped plants tolerate more extreme salt stresses.

The phenotypic effect on plants due to the evolving microbiomes fluctuated during the eight rounds of differential microbiome propagation (Fig. 2a to d). Such fluctuations can occur in typical artificial selection experiments (24), but fluctuations may be more pronounced when artificially selecting on microbiomes (25) because additional factors can contribute to between-generation fluctuations. Specifically, across the eight selection cycles in our experiment, the observed fluctuations could have been due to (i) uncontrolled humidity changes and correlated humidity-dependent water needs of plants (humidity was not controlled in our growth chamber), consequently changing the effective salt stresses; (ii) the strong ramping of salt stress during the first five selection cycles, possibly resulting in excessively stressed plants in generations 4 and 5 (see discussion in Text S1); (iii) random microbiome changes (microbiome drift) and consequent random microbe-microbe interactions; or (iv) other such uncontrolled factors. The fluctuations in plant fitness are most prominent during the first five selection cycles (Fig. 2a to d) when we increased salt stress 2- to 5-fold between generations and when humidity varied most in our growth chamber (Text S1), whereas fluctuations were less pronounced during the last three generations when we changed salt stress only minimally and humidity was relatively stable. These observations are consistent with known responses of *B. distachyon* to environmental stresses (26), predicting that artificial selection on microbiomes conferring salt tolerance to plants should be most efficient under experimental conditions that rigorously control soil moisture, salt stress, humidity, and plant transpiration.

Effect of artificially selected microbiomes on seed production. In the last microbiome generation after a ninth microbiome selection cycle (generation 9), we grew plants for 68 days to quantify the effect of our artificially selected microbiomes on seed production. We also added one control treatment, solute transfer control (solute control), to help elucidate some of the mechanisms underlying the salt tolerance-conferring effects of selected microbiomes on seed production (Fig. 3). In solute control

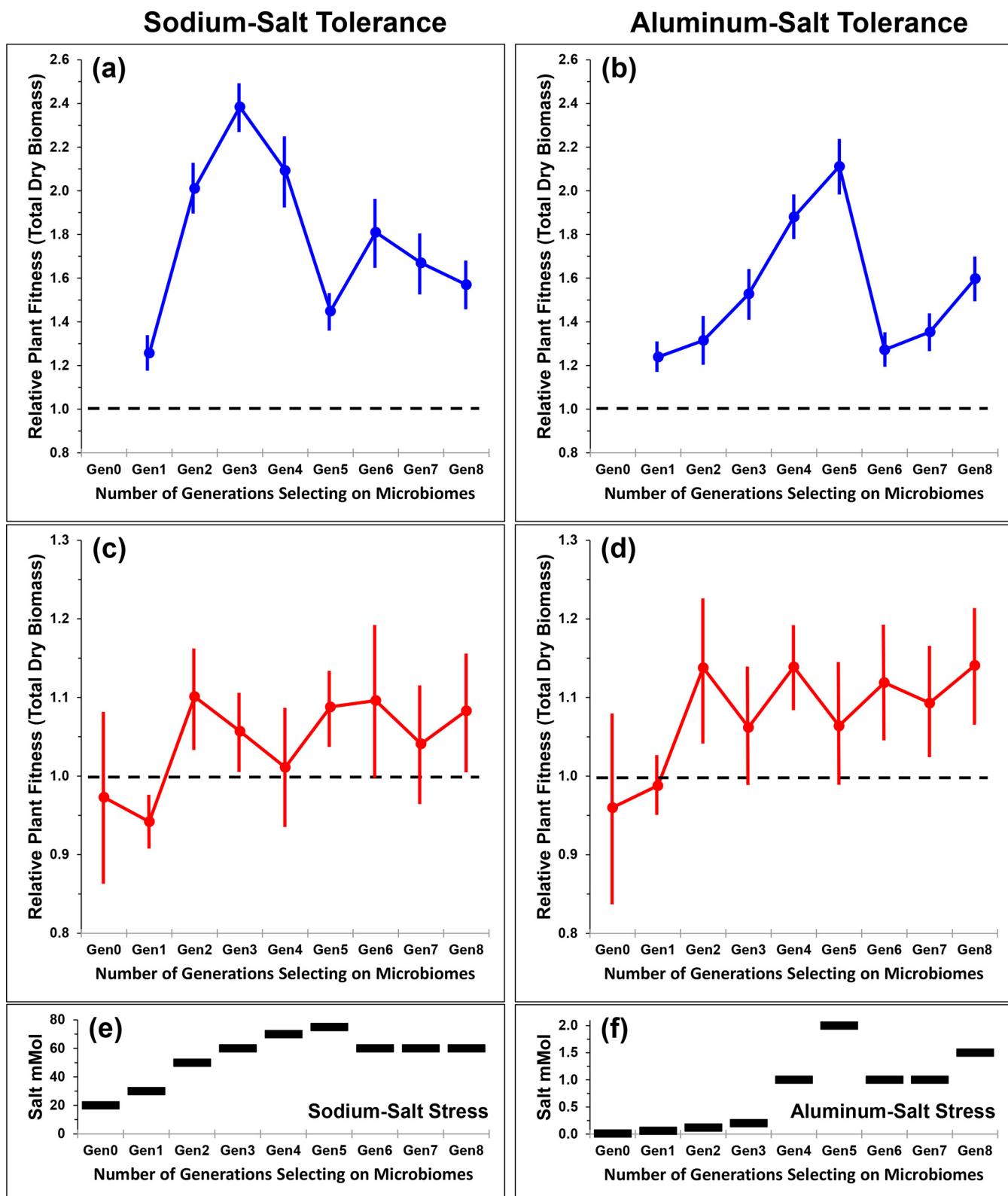


FIG 2 Artificial selection on microbiomes to generate microbiomes that confer salt tolerance to plants. Microbiomes were artificially selected in two concurrent experiments under either sodium salt stress (left column) or aluminum salt stress (right column). After microbiome inoculation of plants in the baseline generation (Gen0), microbiomes were propagated differentially for 8 selection cycles (generations, Gen), using the microbiome propagation scheme in Fig. 1. Two salt stresses, sodium sulfate stress (a, c, and e) and aluminum sulfate stress (b, d, and f), were imposed in parallel in different lines of microbiome selection. Fitness of plants receiving artificially selected microbiomes is shown in panels a to d relative to two nonselected control treatments. In fallow-soil microbiome propagation control, microbiomes were harvested from fallow soil (soil in pot with no plant) and then propagated to sterile

(Continued on next page)

treatments, we eliminated with 0.2- μm filters live cells from the harvested microbiomes in the selection lines to test the growth-enhancing effects of root exudates and viruses that may be copropagated with bacterial microbiomes in the selection lines. Plants receiving these bacterium-free, filtered solutes had (i) significantly poorer seed production than plants that received these same solutes together with the live bacterial microbiomes ($P < 0.02$ for sodium stress treatment; $P < 0.05$ for aluminum stress treatment; Text S3) and (ii) seed production that was comparable to that of plants from null control treatments ($P > 0.7$ for sodium stress treatment; $P > 0.25$ for aluminum stress treatment; Text S3). These findings indicate that no plant exudates or viruses copropagated with bacterial microbiomes accounted for the salt tolerance-conferring effects of selected microbiomes and that any cotransplanted solutes (e.g., root exudates) and any copropagated viruses affected plant growth like the null control treatments (i.e., no exudates, no viruses).

Specificity test by crossing evolved SOD and ALU microbiomes with SOD and ALU stress. In the cross-fostering control of the last microbiome generation, we crossed harvested microbiomes from the sodium stress (SOD) and aluminum stress (ALU) selection lines with the two types of salt stress in soil to test specificity of the salt-ameliorating effects of the microbiomes (Fig. 4, Table S2). The effect of microbiomes selected to confer tolerance to aluminum sulfate appears nonspecific (aluminum-selected microbiomes appear to confer equal tolerance to both sodium and aluminum sulfate stress; $P > 0.5$; Fig. 4), but the effect of bacterial microbiomes selected to confer tolerance to sodium sulfate appears specific (sodium-selected microbiomes confer less tolerance to aluminum sulfate stress; $P < 0.002$; Fig. 4).

DISCUSSION

Our study aimed to improve the differential microbiome propagation scheme that was originally developed by Swenson et al. (4) and then test the utility of our improved methods by artificially selecting on microbiomes to confer salt stress tolerance to plants. Swenson et al.'s original whole-soil community propagation scheme failed to generate consistent benefits for plant growth, and growth enhancement due to putatively selected communities was overall minor when averaged across all propagation cycles (average of ~10% growth enhancement). To address these problems, we adopted in our experiment ideas from quantitative genetics, microbial ecology, and host-microbiome evolution to optimize steps in our microbiome propagation protocol (Fig. 1), with the aim to improve perpetuation of beneficial microbiomes. Specifically, our methods aimed to (i) facilitate ecological priority effects during initial microbiome assembly (13, 14, 21), increasing microbiome inheritance by steering the initial recruitment of symbiotic bacteria into rhizosphere microbiomes of seedlings; (ii) propagate microbiomes harvested from within the sphere of host control (i.e., microbiomes in close physical proximity to roots), whereas Swenson et al. (4) and Panke-Buisse et al. (8) harvested microbes from outside the sphere of host control; (iii) enhance carbon-dependent host control of microbiome assembly and of microbiome persistence by using low-carbon soil (1, 6, 27, 28); and (iv) gradually increase salt stress between selection cycles to minimize the chance of either understressing or overstressing plant. Without additional experiments, it is not possible to say which of these experimental steps was most important to increase response to microbiome selection. Because Jochum et al. (9) succeeded at artificially selecting for microbiomes that confer

FIG 2 Legend (Continued)

fallow soil of the next microbiome generation. In the null control, plants did not receive microbiome inocula, but microbes could "rain in" from air, as in all treatments. Horizontal dashed lines in panels a to d indicate the threshold above which plants given selected microbiomes had higher relative fitness than control plants relative to fallow-soil control plants (a and b) and relative to null control plants (c and d). Each selection treatment had 5 selection lines (8 plants/line), and the error bars show the standard deviation from the 5 averages of these 5 selection lines. (e and f) Salt stresses were increased between selection cycles, starting with minor salt stresses, increasing gradually to minimize the chance of overstressing the plants but decreasing salt stress if plants seemed overstressed (details in the supplemental material). Because of the increasing salt stresses (e and f), selected microbiomes enabled plants to cope with more severe stresses and, therefore, had stronger fitness-enhancing effects on plants in later generations. Relative to fallow-soil control treatments, selected microbiomes increase plant fitness by 75% under sodium sulfate stress (a) and by 38% under aluminum sulfate stress (b). Relative to null control treatments, selected microbiomes increase plant fitness by 13% under sodium sulfate stress (c) and by 12% under aluminum sulfate stress (d).

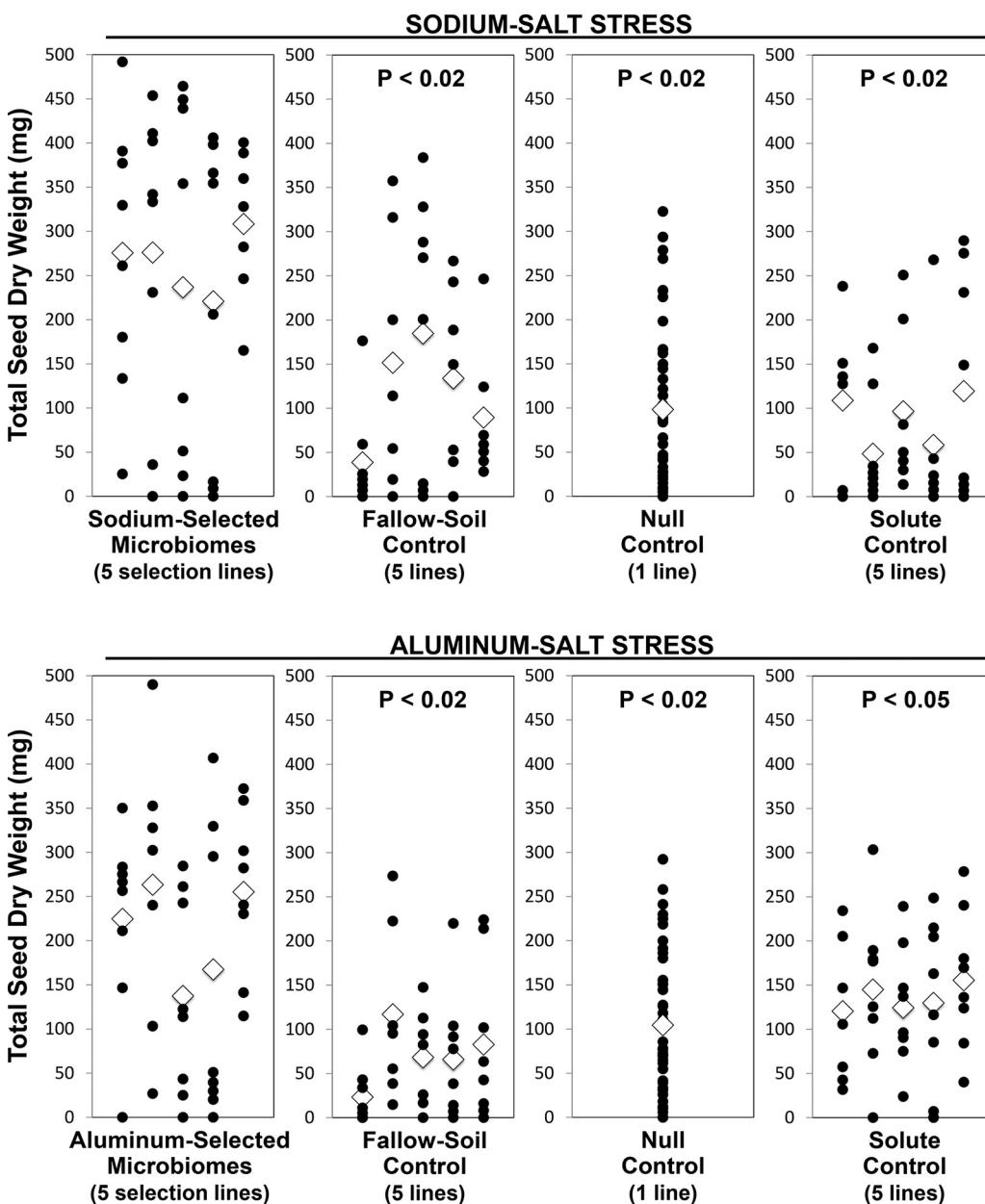


FIG 3 Artificially selected microbiomes increase seed production under salt stress. At the end of our experiment after a ninth selection cycle (generation 9), plants were grown to seed for 68 days to test whether rhizosphere microbiomes selected to increase aboveground biomass of preflowering plants generated microbiomes that also enhance seed production. Total seed dry weight is plotted as a black dot for each plant; plants of the same selection line are plotted vertically above each other; and the average for each line is plotted as a diamond. Overlapping data points are adjusted here minimally to separate such data points and visualize all data points. In addition to fallow-soil control and null control used in generations 1 to 8 (Fig. 2), solute control was added in generation 9. In solute control, selected bacterial microbiomes harvested from rhizospheres were filtered to remove all bacterial components to test for any growth-enhancing effects of viruses and solutes (e.g., plant hormones exuded into soil) that are unavoidably copropagated with any harvested rhizosphere microbiome. All controls are significantly different from the corresponding selection treatment (leftmost panel); P values are shown above each control, and P values are corrected using the false discovery rate for *post hoc* comparisons (Text S3). Plants were salt stressed because many plants never produced seeds (or few seeds; see also Fig. S5, top left), whereas essentially all plants would produce many seeds under stress-free conditions. Artificially selected microbiomes helped plants cope with these salt stresses, because plants that received selected microbiomes outperformed plants of all three control treatments, including solute control plants (indicating that selected bacterial microbiomes conferred salt tolerance to plants rather than any copropagated viruses). Seed production of solute control plants is indistinguishable from the corresponding null control plants ($P = 0.71$, sodium salt stress; $P = 0.29$, aluminum salt stress; Text S3), indicating that plants receiving bacterium-free filtrate performed as if they had received a null control treatment. Although microbiomes were selected to increase aboveground biomass of preflowering plants (20 to 30 days old), selected microbiomes also enhanced seed production of older plants (68 days old).

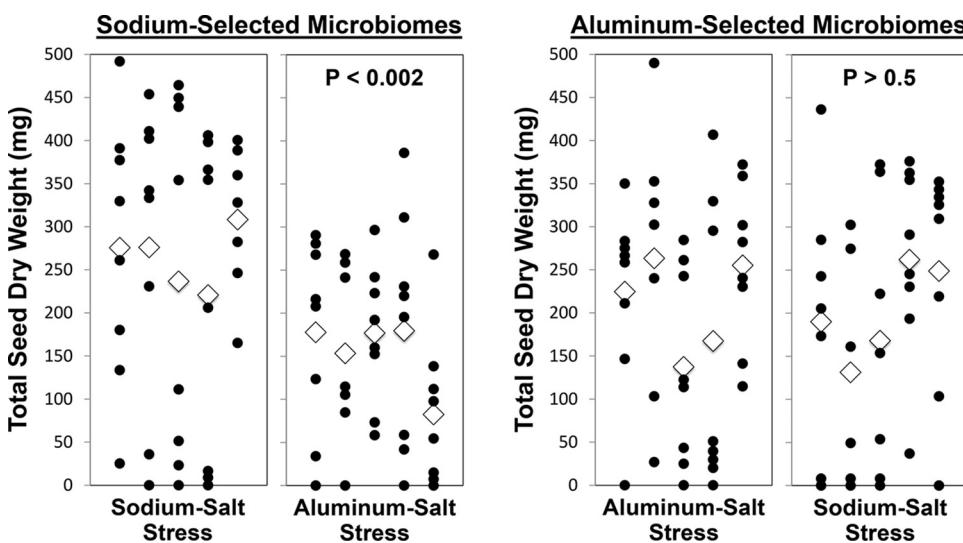


FIG 4 Specific and nonspecific growth-enhancing effects of artificially selected microbiomes. In generation 9, a 2 by 2 cross-fostering experiment tested whether microbiomes selected under sodium salt stress conferred greater salt tolerance to plants stressed with sodium salt compared to plants stressed with aluminum salt and, conversely, whether microbiomes selected under aluminum salt stress conferred greater salt tolerance to plants stressed with aluminum salt compared to plants stressed with sodium salt. P values are shown for each comparison, and P values are corrected using the false discovery rate for post hoc comparisons (Text S3). The effect of microbiomes selected to confer tolerance to aluminum salt appears to be nonspecific because these microbiomes confer equal tolerance to plants stressed with either sodium salt or aluminum salt ($P > 0.5$; two rightmost panels), whereas the effect of bacterial microbiomes selected to confer tolerance to sodium salt appears specific, because these sodium-selected microbiomes confer less salt tolerance, or confer no salt tolerance, to plants under aluminum salt stress ($P < 0.002$; two leftmost panels).

drought tolerance to wheat grown in high-carbon soil, either low-carbon soil may not be essential for plant-mediated microbiome selection, contrary to our assumption, or high-carbon soil may facilitate microbiome selection of fungal components, because Jochum et al. (9) propagated between generations both bacterial and eukaryote rhizosphere components.

Compared to two earlier experiments of host-mediated microbiome selection by Swenson et al. (4) and Panke-Buisse et al. (8), our selection scheme appears to generate more pronounced and more stable effects on plant phenotype as a result of host-mediated microbiome selection. Except for the initial two selection cycles (Fig. 2a to d), our selected microbiomes consistently outperformed in subsequent selection cycles of the nonselected microbiomes of the control conditions. In contrast, for example, Swenson et al.'s (4) experiments sometimes resulted in selected microbiomes that were outperformed by control microbiomes. Our methods may have generated more stable microbiome effects because (i) only bacteria but no fungi were propagated between generations (Swenson et al. suspected fungal disease as a cause of occasional devastation of plant populations); (ii) we conducted our experiment in a more stable growth environment; and (iii) we selected for microbiomes conferring specific benefits (salt tolerance) rather than the nonspecific, general-purpose beneficial microbiomes selected by Swenson et al. (4) and Panke-Buisse et al. (8). After only 1 to 3 selection cycles, our selected microbiomes consistently outperformed the control microbiomes, with averages of 75% (SOD) and 38% (ALU) growth improvement relative to fallow-soil controls and 13% (SOD) and 12% (ALU) growth improvement relative to null controls (Fig. 2a to d). Most importantly, when quantifying plant fitness by total seed production in the final generation 9, plants with selected microbiomes outperformed fallow-soil controls, null controls, and solute controls by 120 to 205% (SOD) and 55 to 195% (ALU) (Fig. 3). Although we achieved these results under controlled greenhouse conditions that are very different from outdoor conditions, this seems a remarkable enhancement of plant productivity compared to traditional plant breeding.

An interesting result is that microbiomes selected to benefit growth of plants during the early vegetative phase (biomass of ~4-week-old plants, well before flowering; Fig. 1)

generated microbiomes that enhanced plant fitness during the reproductive phase by increasing the seed set of 10-week-old plants (Fig. 3). Rhizosphere microbiomes of grasses can change significantly during plant ontogeny (29); therefore, microbiomes selected to serve one function, such as early growth, may not necessarily optimize other functions, such as seed set. Therefore, the finding that microbiome selection to promote early growth (Fig. 2) also promotes increased seed set (Fig. 3) implies that (i) seed set is intrinsically tied to optimal early growth in *B. distachyon*, possibly by accelerating the timing of flowering; (ii) some of the same bacteria benefitting plants during the early vegetative phase also benefit plants during the reproductive phase, despite overall microbiome changes during plant ontogeny; and (iii) microbiome selection experiments aiming to increase seed productivity do not necessarily have to select on seed set as a measured phenotype but can shorten each selection cycle by selecting other phenotypes measurable during early vegetative growth.

Because Jochum et al.'s (9) and our experiments were the first systematic attempts to improve the methods of Swenson et al. (4), we predict that it should be possible to further optimize protocols of differential microbiome propagation. Microbiome selection therefore could emerge as a novel tool to elucidate microbiome functions in controlled laboratory environments and possibly also in those natural environments that allow control of key parameters affecting microbiome harvest, microbiome transfer, and microbiome inheritance. Such optimization of microbiome selection should ideally be informed by metagenomic analyses of experimental contrasts (e.g., comparison of microbiomes selected to confer tolerance to either sodium stress or aluminum stress) and by time-series analyses across microbiome propagation cycles to identify candidate microbes and microbial consortia important in mediating stresses.

Additional experiments to improve methods of microbiome selection. To expand on our methods of artificial microbiome selection, we outline here a series of additional experiments that should generate insights into key parameters that determine efficacy of microbiome selection. Arias-Sánchez et al. (7), Xie et al. (30), Chang et al. (31, 32), and Sánchez et al. (33) recently summarized criteria for microbiome selection experiments that are not host mediated (e.g., selection on CO₂ emission by a microbiome in the absence of a plant host); Lawson et al. (34) summarized protocols for engineering any kind of microbiome (e.g., using bottom-up and top-down design criteria); Henry et al. (35), Arora et al. (36), and Henry and Ayroles (37) developed methods for host-mediated microbiome selection using *Drosophila* as a host; and we focus below on methods of host-mediated microbiome selection to improve performance of a plant host. Because host-mediated microbiome selection leverages traits that evolved to recruit and control microbiomes (so-called host control [6, 19, 38]), the first four experiments outlined below explore whether factors promoting strong microbiome control by a plant host could improve efficacy of microbiome selection.

(i) Artificial microbiome selection on endophytic versus rhizosphere microbiomes. Microbiomes internal to a host (e.g., endophytic microbes of plants) require some form of host infection and, therefore, could be under greater host control than external microbiomes, such as rhizoplane or rhizosphere microbiomes. Consequently, under stresses that are mediated by host-controlled microbes, it may be easier to obtain a response to microbiome selection when targeting selection on endophytic microbiomes. This prediction can be tested in an experiment that compares, in separate selection lines, the responses to microbiome selection when harvesting and propagating only endophytic microbiomes versus only rhizosphere microbiomes. This prediction may not hold for stresses that require stress mediation by microbes in the external microbiome compartment of roots (e.g., microbes that detoxify toxins, such as aluminum, before they enter the root and then affect the plant negatively, for example, microbes that chelate toxins external to the plant in the rhizosphere [39]); however, this prediction about a key role of host control for the efficacy of microbiome selection should hold for many other stresses that are mediated by microbes that a plant permits to enter into the endophytic compartment.

(ii) Microbiome selection in two genetic backgrounds differing in host control. A second approach to test for the role of host control is to compare microbiome selection in two different host genotypes, such as two inbred strains of the same plant species. For example, different host genotypes may recruit different kinds of microbes into symbiosis

(40). Such differences in host-controlled microbiome recruitment could result in differences in microbiome selection, and a microbiome artificially selected within one host genotype to improve one particular host trait may produce a different phenotypic effect when tested in a different host genotype.

(iii) Varying host control by varying carbon content in soil. A third approach to test host control is to compare the efficacy of microbiome selection in low- versus high-carbon soil. Microbial growth in some soils is limited by carbon, and many plants therefore regulate their soil microbiomes by carbon exudates (41). We therefore hypothesized that a low-carbon soil (like the carbon-free soil in our experiment) facilitates host control and consequently also microbiome selection. This hypothesis remains to be tested in, for example, a microbiome selection experiment contrasting response to selection when using soils with different carbon contents. Because Jochum et al. (9) recently showed that it is possible to artificially select for microbiomes that confer drought tolerance to wheat grown in high-carbon soil, low-carbon soil may not be essential for plant-mediated microbiome selection, but low-carbon soil could be a facilitating condition.

(iv) Manipulating resource-limited host control by varying seed size. A fourth approach to test host control could be to compare the efficacy of microbiome selection between plant species with large seeds versus small seeds (e.g., *Brachypodium* versus *Arabidopsis*) or between seedlings of the same species grown from small versus large seeds. A germinating seed has to allocate resources to aboveground growth to fix carbon and to belowground growth to access nutrients and water, and seedlings growing from resource-rich large seeds therefore may be better able to allocate resources to manipulate microbiomes effectively, for example, by root exudates. If such resource allocation constraints exist for young seedlings, this could explain why our microbiome selection experiment with *B. distachyon* appears to have generated stronger and faster response to microbiome selection than other such experiments with *Arabidopsis thaliana* (4, 8).

(v) Propagation of fractionated versus whole microbiomes. Experimental microbiome propagation between host generations can be complete (all soil community members are propagated between hosts, as in Swenson et al. [4], Panke-Buisse et al. [8], and Jochum et al. [9]), or microbiomes can be fractionated by excluding specific microbial components, as in our protocol where we propagated only organisms of bacterial or smaller sizes. We used fractionated microbiome propagation because (i) we were more interested in elucidating contributions to host fitness of the understudied bacterial components than the fungal components (e.g., mycorrhizal fungi) and (ii) fractionation simplifies analyses of the microbiome responses to selection (e.g., bacterial microbiome components, but not necessarily fungal components, need to be analyzed with metagenomic techniques). However, because fungal components and possible synergistic fungal-bacterial interactions cannot be selected on when using our fractionated microbiome propagation scheme, we hypothesized previously (6) that selection on fractionated microbiomes shows attenuated selection responses compared to selection on whole microbiomes. This can be tested in an experiment comparing the response to microbiome selection when propagating fractionated versus whole microbiomes, for example, by using different size-selecting filters.

(vi) Propagation of mixed versus unmixed microbiomes. When propagating microbiomes to new hosts, it is possible to propagate mixed microbiomes harvested from different hosts or only unmixed microbiomes. Therefore, mixed versus unmixed propagation schemes represent two principal methods of microbiome selection (4–6, 42, 43). Compared to unmixed propagation, mixed propagation generated a faster response to microbiome selection for microbiomes propagated *in vitro* in the absence of a host (43), but the respective advantages of mixed versus unmixed propagation have yet to be tested for host-associated microbiomes, such as the rhizosphere microbiomes studied here. Mixed propagation may be superior to unmixed propagation if, for example, mixing generates novel combinations of microbes with novel beneficial effects on a host (6), may merge separate networks of microbes into a superior compound network (so-called community network coalescence; 42, 44), or may generate novel microbial interactions that increase microbiome stability (13).

(vii) Microbiome diversity of the starter inoculum. In our salt stress experiment, we aimed for a highly diverse starter microbiome to inoculate all pots of generation 0, but

we did not specifically try to include bacteria from sources that are most likely to include microbes that confer salt tolerance to plants. Could inclusion of microbiomes harvested from grasses growing naturally in salty soil have improved the diversity of bacteria in the starter inoculum and, thus, increased the response to microbiome selection in our experiment? Comparison of starter inocula harvested from plants growing naturally in salty versus nonsalty soils may be able to address this question.

MATERIALS AND METHODS

We developed our microbiome selection protocol between 2011 and 2014 in a series of pilot experiments, conducted the microbiome selection experiment reported here between January and October 2015, and then disseminated our protocol via *bioRxiv* in 2016 (45) to facilitate teaching of workshops on microbiome selection. We describe here our experimental protocols, and a separate report (unpublished data) will describe the metagenomic analyses complementing the protocols and phenotypic results reported here.

Maximizing microbiome perpetuation. To select for microbiomes that confer salt tolerance to plants, we used a differential host-microbiome copropagation scheme as described in Swenson et al. (4), Mueller et al. (46), and Mueller and Sachs (6) but improved on these earlier selection schemes by (i) maximizing evolutionary microbiome changes stemming from differential propagation of whole microbiomes at step 3 in Fig. 1 while (ii) minimizing some, but not all, ecological microbiome changes that can occur at any of the steps in a selection cycle (e.g., we tried to minimize uncontrolled microbe-community turnover). In essence, our protocol aimed to maximize microbiome perpetuation (i.e., maximize inheritance of key microbes). To increase microbiome inheritance, we added protocol steps of known techniques, most importantly (i) facilitation of ecological priority effects during initial microbiome assembly (21), increasing microbiome inheritance by controlling in each selection cycle the initial recruitment of symbiotic bacteria into rhizosphere microbiomes of seedlings, and (ii) low-carbon soil to enhance carbon-dependent host control of microbiome assembly and microbiome persistence (1, 6, 27, 28). Theory predicts that any experimental steps increasing fidelity of microbiome perpetuation from mother microbiome to offspring microbiome should increase the efficacy of microbiome selection (6, 30, 35, 47).

Maximizing microbiome heritability. In each microbiome propagation cycle (microbiome generation), we inoculated surface-sterilized seeds taken from nonevolving stock (inbred strain Bd3-1 of the grass *Brachypodium distachyon*) (48), using rhizosphere bacteria harvested from roots of those plants within each selection line that exhibited the greatest aboveground biomass (Fig. 1). Microbiome selection within the genetic background of an invariant (i.e., highly inbred) plant genotype increases microbiome heritability, defined as the proportion of overall variation in the plant phenotype that can be attributed to differences in microbiome-encoded genetic effects on plants. By keeping plant genotype invariant, microbiome heritability increases because a greater proportion of the overall plant-phenotypic variation in a selection line can be attributed to differences in microbiomes. This increases an experimenter's ability to identify association with a desired microbiome (4), enhancing reliability of the plant phenotype as an indicator of microbiome effects and, thus, increasing efficacy of indirect selection on microbiomes.

Harvesting rhizosphere microbiomes and selection scheme. Each selection line consisted of a population of eight replicate plants, and each selection treatment had five replicate selection lines (i.e., 40 plants total per treatment). To determine phenotypes of plants on the day of microbiome harvesting, we judged aboveground growth visually by placing all eight plants of the same selection line in ascending order next to each other (see Fig. S3 in the supplemental material) and then choosing the two largest plants for microbiome harvest. For all plants, we cut plants at the soil level and then stored the aboveground portion in an envelope for drying and weighing. For each plant chosen for microbiome harvest, we extracted the entire root system from the soil and then harvested rhizosphere microbiomes immediately to minimize microbiome changes in the absence of a plant control. Root structures could be extracted whole because of a granular soil texture (profile porous ceramic soil), with some loss of fine roots. Because we were interested in harvesting microbiomes that were in close association with roots, we discarded any soil adhering loosely to roots, leaving a root system with few firmly attached soil particles. We combined the root systems from the two best-growing plants of the same selection line and harvested their mixed rhizosphere microbiomes by immersing and gently shaking the roots in the same salt nutrient buffer that we used to hydrate soils (details are in Text S1). Combining root systems from the two best-growing plants generated a so-called mixed microbiome harvested from two mother rhizospheres, which we then transferred within the same selection line to all eight offspring plants (i.e., germinating seeds) of the next microbiome generation (Fig. 1).

Microbiome fractionation with size-selecting filters before microbiome propagation. To simplify future metagenomic analyses from propagated microbiomes, we used 2-μm filters (details are in Text S1) to filter microbiomes harvested from rhizospheres of mother plants, thereby capturing only bacteria (and possibly also viruses) for microbiome propagation to the next microbiome generation but eliminating from propagation any larger-celled soil organisms (i.e., we excluded all eukaryote organisms in soil, including fungi). This fractionation step distinguishes our methods from those of Swenson et al. (4), Panke-Buisse et al. (8), and Jochum et al. (9), all of whom transferred between pots all organisms living in soil (including algae, nematodes, protozoans, fungi, etc.). Plant phenotypic changes in these previous experiments therefore were not necessarily due to changing microbiomes but possibly to eukaryotes that were copropagated with microbiomes, whereas we transferred only bacteria and viruses between microbiome generations to rule out any confounding effects of copropagated eukaryotes.

Salt stress treatments and experimental contrasts. Using different selection lines, we selected for beneficial microbiomes conferring salt tolerance to either sodium sulfate, Na₂SO₄, or aluminum sulfate,

$\text{Al}_2(\text{SO}_4)_3$. Such an experimental contrast of two treatments (here, two salt stresses) enables an experimenter to (i) compare evolving microbiomes using metagenomic time-series analyses, (ii) identify candidate microbes (indicator taxa) that differ between salt treatments and that may therefore confer salt tolerance to plants, and (iii) test the specificity of beneficial effects of evolved microbiomes in a cross-fostering experiment (described below).

Control treatments. To evaluate the effects of selection treatments, we included two nonselection control treatments. In the null control, we did not inoculate germinating seeds with any microbiomes, but microbes could enter soil from air, as was also the case for all other treatments. In the fallow-soil microbiome propagation control, we harvested microbiomes from fallow soil (no plant growing in a pot; microbiomes were harvested from root-free soil) and then propagated the harvested microbiomes to a pot with sterile fallow soil of the next microbiome generation. Specifically, each microbiome harvested from fallow soil was split, one part was propagated to sterile fallow soil to start the next microbiome generation, and another part of the same microbiome was applied to seeds planted in sterile soil to test the effect of such fallow-soil microbiomes on the growth of plants (details are in Text S1). Fallow-soil control is a nonselection treatment because a microbiome is transferred from exactly one pot in the previous generation to one pot in the next generation, resulting in enrichment (49) of microbes that proliferate under the specific salt conditions in soil but in the absence of higher-level microbiome selection that, in the selection treatment, selectively perpetuate growth-promoting microbiomes while discarding inferior microbiomes (i.e., there is no such discarding of inferior microbiomes in the fallow-soil control treatment).

Number of selection cycles. Our complete experiment involved one baseline generation (generation 0; Table S1) to establish initial microbiomes in replicate pots; eight rounds of differential microbiome propagation (generations 1 to 8; Table S1); and one final round (generation 9; Table S2) to evaluate the effects of the artificially selected microbiomes on seed set, for a total of 10 microbiome generations.

Ramping of salt stress. We increased salt stresses gradually during the selection experiment by (i) increasing between generations the molarity of the water used to hydrate dry soil before soil sterilization and planting (Text S1) and (ii) increasing correspondingly the molarity of the water that was added regularly to pots of growing plants to keep soils hydrated (Text S1). Over the 10 generations, sodium sulfate molarity in sodium stress treatments increased from 20 mM to 60 mM, and aluminum sulfate molarity in aluminum stress treatments increased from 0.02 mM to 1.5 mM (Text S1). The salt stresses of the baseline generation were chosen because, in pilot experiments, these stresses caused minimal delays in germination and growth compared to unstressed plants (Text S1). We did not preplan any maximum salt stresses that we wanted to reach via ramping within the 10 generations of microbiome propagation, because the salt stresses were increased judiciously each generation such that the plants would not be overstressed (because then beneficial microbiomes would not be able to ameliorate severe salt stresses) or understressed (and plants would then not need the help of beneficial microbiomes). The logic of increasing salt stresses stepwise between generations and decreasing salt stresses once between generations 5 and 6 when plants seemed overstressed (Fig. 2) is explained in the Text S1 under the sub-heading Soil Hydration and Salt Stress Treatments.

Diversity of starter microbiome for baseline generation 0. We prepared a single, well-mixed bacterial microbiome batch to inoculate all pots of the initial baseline generation 0, combining bacterial microbiomes from several rhizosphere sources to maximize the bacterial diversity of this starter inoculum. We used 2- μm Whatman filters to filter bacterial communities from root systems of three local grass species (*Bromus* sp., *Andropogon* sp., and *Eragrostis* sp.) and from root-systems of *B. distachyon* Bd3-1 plants used in earlier experiments (Text S1). We combined microbiomes from several sources in the hope of capturing a great diversity of bacteria, and we included microbiomes harvested from Bd3-1 roots to capture bacterial taxa that may be readily recruited by *B. distachyon* into its rhizosphere. This diverse starter microbiome changed during generation 0 through the aforementioned ecological processes once associated with a plant. The resulting variation in microbiomes between experimental replicates contributed to the variation in plant growth that we used for indirect selection on microbiome properties.

Statistical analyses: plant biomass, generations 1 to 8. We performed all analyses in R v3.3.1. We assessed differences in aboveground plant biomass (dry weight) among treatments of generations 1 to 8 by fitting the data to a generalized linear mixed model with a gamma error distribution. Statistical significance in the generalized linear mixed models was assessed with likelihood ratio tests and Tukey tests employed for posthoc comparisons of treatment means (more details are in Text S2).

Statistical analyses: total seed weight, generation 9. Because plants were severely salt stressed in generation 9 and many plants therefore did not flower or produced very few seeds, the distribution of data was not normal (Fig. S5, top left). We attempted several data transformations to achieve approximate normality, but none of these transformations generated a distribution that approximated normality (Fig. S5b to d). We therefore used Kruskal-Wallis tests for nonparametric evaluation of differences between treatments in generation 9, and we used Mann-Whitney U tests for nonparametric *post hoc* comparisons between treatment means, correcting *P* values using the false discovery rate. All tests were two-tailed with alpha of 0.05 (more details are in Text S2).

Data availability. All data are available in Tables S1 and S2. All methods are described in detail in Text S1.

SUPPLEMENTAL MATERIAL

Supplemental material is available online only.

TEXT S1, PDF file, 0.7 MB.

TEXT S2, PDF file, 0.2 MB.

TEXT S3, PDF file, 0.1 MB.

TABLE S1, PDF file, 0.7 MB.**TABLE S2**, PDF file, 0.1 MB.**ACKNOWLEDGMENTS**

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U.G.M., D.L.D., K.B., and T.E.J. developed the plant methods; U.G.M. developed the microbial and microbiome selection methods; T.E.J. contributed equipment and Bd3-1 seeds; U.G.M., M.R.K., and A.L.C. conducted experiments; A.L.C. and M.R.K. recorded all data (dry weights) blindly; J.A.E., C.C.S., and C.C.F. analyzed the data and designed figures; U.G.M. led the writing of the manuscript.

REFERENCES

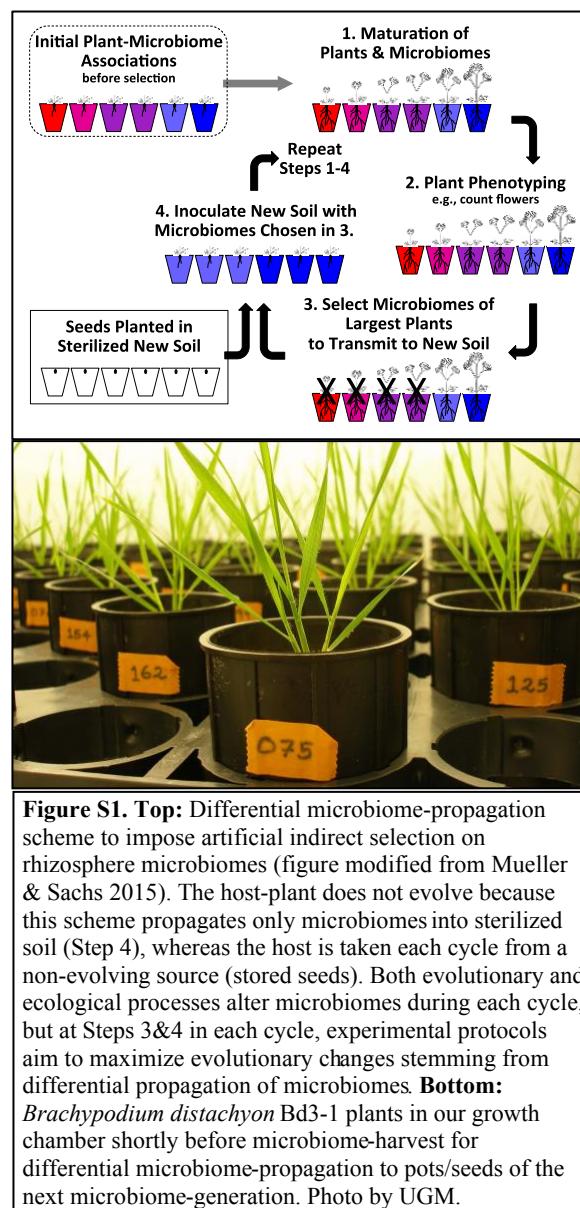
- Bulgarelli D, Schlaepff K, Spaepen S, van Themaat EVL, Schulze-Lefert P. 2013. Structure, and functions of the bacterial microbiota of plants. *Annu Rev Plant Biol* 64:807–838. <https://doi.org/10.1146/annurev-arplant-050312-121016>.
- Peiffer JA, Spor A, Koren O, Jin Z, Tringe SG, Dangl JL, Buckler ES, Ley RE. 2013. Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proc Natl Acad Sci U S A* 110:6548–6553. <https://doi.org/10.1073/pnas.1302837110>.
- Roossinck MJ. 2015. Plants, viruses and the environment: ecology and mutualism. *Virology* 479–480:271–277. <https://doi.org/10.1016/j.virol.2015.03.041>.
- Swenson W, Wilson DS, Elias R. 2000. Artificial ecosystem selection. *Proc Natl Acad Sci U S A* 97:9110–9114. <https://doi.org/10.1073/pnas.150237597>.
- Williams HTP, Lenton TM. 2007. Artificial selection of simulated microbial ecosystems. *Proc Natl Acad Sci U S A* 104:8918–8923. <https://doi.org/10.1073/pnas.0610038104>.
- Mueller UG, Sachs JL. 2015. Engineering microbiomes to improve plant and animal health. *Trends Microbiol* 23:606–617. <https://doi.org/10.1016/j.tim.2015.07.009>.
- Arias-Sánchez FI, Vessman B, Mitri S. 2019. Artificially selecting microbial communities: if we can breed dogs, why not microbiomes? *PLoS Biol* 17: e3000356. <https://doi.org/10.1371/journal.pbio.3000356>.
- Panke-Buisse K, Poole AC, Goodrich JK, Ley RE, Kao-Kniffin J. 2015. Selection on soil microbiomes reveals reproducible impacts on plant function. *ISME J* 9:980–989. <https://doi.org/10.1038/ismej.2014.196>.
- Jochum MD, McWilliams KL, Pierson EA, Jo Y-K. 2019. Host-mediated microbiome engineering (HMME) of drought tolerance in the wheat rhizosphere. *PLoS One* 14:e0225933. <https://doi.org/10.1371/journal.pone.0225933>.
- Garcia J, Kao-Kniffin J. 2018. Microbial group dynamics in plant rhizospheres and their implications on nutrient cycling. *Front Microbiol* 9: 1516. <https://doi.org/10.3389/fmicb.2018.01516>.
- Falconer DS, Mackay TFC. 1996. An introduction to quantitative genetics. Addison Wesley Longman, Hoboken, NJ.
- Goldford JE, Lu N, Bajic D, Estrela S, Tikhonov M, Sanchez-Gorostiaga A, Segre D, Mehta P, Sanchez A. 2018. Emergent simplicity in microbial community assembly. *Science* 361:469–474. <https://doi.org/10.1126/science.aat1168>.
- Coyte KZ, Schluter J, Foster KR. 2015. The ecology of the microbiome: networks, competition, and stability. *Science* 350:663–666. <https://doi.org/10.1126/science.aad2602>.
- Coyte KZ, Rao C, Rakoff-Nahoum S, Foster KR. 2021. Ecological rules for the assembly of microbiome communities. *PLoS Biol* 19:e3001116. <https://doi.org/10.1371/journal.pbio.3001116>.
- Estrela S, Sánchez Á, Rebolleda-Gómez M. 2021. Multi-replicated enrichment communities as a model system in microbial ecology. *Front Microbiol* 12:657467. <https://doi.org/10.3389/fmicb.2021.657467>.
- Sachs JL, Mueller UG, Wilcox TP, Bull JJ. 2004. The evolution of cooperation. *Q Rev Biol* 79:135–160. <https://doi.org/10.1086/383541>.
- Friesen M, Porter SS, Stark SC, von Wettberg EJ, Sachs JL, Martinez-Romero E. 2011. Microbially mediated plant functional traits. *Annu Rev Ecol Evol Syst* 42: 23–46. <https://doi.org/10.1146/annurev-ecolsys-102710-145039>.
- Larrea A, Burton F, Schäfer P. 2016. Plant root-microbe communication in shaping root microbiomes. *Plant Mol Biol* 90:575–587. <https://doi.org/10.1007/s11103-015-0417-8>.
- Foster KR, Schlüter J, Coyte KZ, Rakoff-Nahoum S. 2017. The evolution of the host microbiome as an ecosystem on a leash. *Nature* 548:43–51. <https://doi.org/10.1038/nature23292>.
- Fitzpatrick BM. 2014. Symbiote transmission and maintenance of extra-genomic associations. *Front Microbiol* 5:46.
- Scheuring I, Yu DW. 2012. How to assemble a beneficial microbiome in three easy steps. *Ecol Lett* 15:1300–1307. <https://doi.org/10.1111/j.1462-0248.2012.01853.x>.
- Strauss S. 2014. Ecological and evolutionary responses in complex communities: implications for invasions and eco-evolutionary feedbacks. *Oikos* 123:257–266. <https://doi.org/10.1111/j.1600-0706.2013.01093.x>.
- Theis KR, Dheilly NM, Klassen JL, Brucker RM, Baines JF, Bosch TCG, Cryan JF, Gilbert SF, Goodnight CJ, Lloyd EA, Sapp J, Vandenkoornhuyse P, Zilberman-Rosenberg I, Rosenberg E, Bordenstein SR. 2016. Getting the hologenome concept right. *mSystems* 1:e00028-16. <https://doi.org/10.1128/mSystems.00028-16>.
- Garland T, Rose MR. 2009. Experimental evolution. University of California Press, Berkeley, CA.
- Blouin M, Karimi B, Mathieu J, Lerch TZ. 2015. Levels and limits in artificial selection of communities. *Ecol Lett* 18:1040–1048. <https://doi.org/10.1111/ele.12486>.
- Des Marais DL, Juenger TE. 2016. *Brachypodium* and the abiotic environment, p 291–311. In Vogel JP (ed), *Genetics and genomics of Brachypodium*. Springer, Berlin, Germany.
- Bais HP, Weir TL, Perry LG, Gilroy S, Vivanco JM. 2006. The role of root exudates in rhizosphere interactions with plants and other organisms. *Annu Rev Plant Biol* 57:233–266. <https://doi.org/10.1146/annurev.arplant.57.032905.105159>.

28. Tkacz A, Poole P. 2015. Role of root microbiota in plant productivity. *J Exp Bot* 66:2167–2175. <https://doi.org/10.1093/jxb/erv157>.
29. Edwards JA, Santos-Medellín CM, Liechty ZS, Nguyen B, Lurie E, Eason S, Phillips G, Sundaresan V. 2018. Compositional shifts in root-associated bacterial and archaeal microbiota track the plant life cycle in field-grown rice. *PLoS Biol* 16:e2003862. <https://doi.org/10.1371/journal.pbio.2003862>.
30. Xie L, Yuan AE, Shou W. 2019. Simulations reveal challenges to artificial community selection and possible strategies for success. *PLoS Biol* 17: e3000295. <https://doi.org/10.1371/journal.pbio.3000295>.
31. Chang CY, Osborne ML, Bajic D, Sanchez A. 2020. Artificially selecting microbial communities using propagule strategies. *bioRxiv* <https://doi.org/10.1101/2020.05.01.066282>.
32. Chang C-Y, Vila JCC, Bender M, Li R, Mankowski MC, Bassette M, Borden J, Golfiger S, Sanchez PGL, Waymack R, Zhu X, Diaz-Colunga J, Estrela S, Rebolleda-Gomez M, Sanchez A. 2021. Engineering complex communities by directed evolution. *Nat Ecol Evol* 5:1011–1023. <https://doi.org/10.1038/s41559-021-01457-5>.
33. Sánchez Á, Vila JCC, Chang C-Y, Diaz-Colunga J, Estrela S, Rebolleda-Gomez M. 2021. Directed evolution of microbial communities. *Annu Rev Biophys* 50:323–341. <https://doi.org/10.1146/annurev-biophys-10120-072829>.
34. Lawson CE, Harcombe WR, Hatzepichler R, Lindemann SR, Löffler FE, O'Malley MA, García Martín H, Pfleger BF, Raskin L, Venturelli OS, Weissbrodt DG, Noguera DR, McMahon KD. 2019. Common principles and best practices for engineering microbiomes. *Nat Rev Microbiol* 17: 725–741. <https://doi.org/10.1038/s41579-019-0255-9>.
35. Henry LP, Bruijning M, Forsberg SKG, Ayroles JF. 2021. The microbiome extends evolutionary potential. *Nat Commun* 12:5141. <https://doi.org/10.1038/s41467-021-25315-x>.
36. Arora J, Brisbin MAM, Mikheyev AS. 2020. Effects of microbial evolution dominate those of experimental host-mediated indirect selection. *Peer J* 8:e9350. <https://doi.org/10.7717/peerj.9350>.
37. Henry LP, Ayroles JF. 2021. Meta-analysis suggests the microbiome responds to evolve and resequence experiments in *Drosophila melanogaster*. *BMC Microbiol* 21:108. <https://doi.org/10.1186/s12866-021-02168-4>.
38. Porter SS, Sachs JL. 2020. Agriculture and the disruption of plant-microbial symbiosis. *Trends Ecol Evol* 35:426–439. <https://doi.org/10.1016/j.tree.2020.01.006>.
39. Aggarwal A, Ezaki B, Munjal A, Tripathi BN. 2015. Physiology and biochemistry of aluminum toxicity and tolerance in crops, p 35–57. In Tripathi BN, Müller M (ed), *Stress responses in plants*. Springer, Berlin, Germany.
40. Morella NM, Weng FCH, Joubert PM, Metcalf CJE, Lindow S, Koskella B. 2020. Successive passaging of a plant-associated microbiome reveals robust habitat and host genotype-dependent selection. *Proc Natl Acad Sci U S A* 117:1148–1159. <https://doi.org/10.1073/pnas.1908600116>.
41. Sasse J, Martinho E, Northen T. 2018. Feed your friends: do plant exudates shape the root microbiome? *Trends Plant Sci* 23:25–41. <https://doi.org/10.1016/j.tplants.2017.09.003>.
42. Rillig MC, Tsang A, Roy J. 2016. Microbial community coalescence for microbiome engineering. *Front Microbiol* 7:1967.
43. Raynaud T, Devers M, Spor A, Blouin M. 2019. Effect of the reproduction method in an artificial selection experiment at the community level. *Front Ecol Evol* 7:416. <https://doi.org/10.3389/fevo.2019.00416>.
44. Castledine M, Sierociński P, Padfield D, Buckling A. 2020. Community coalescence: an eco-evolutionary perspective. *Philos Trans R Soc Lond B Biol Sci* 375:20190252. <https://doi.org/10.1098/rstb.2019.0252>.
45. Mueller UG, Juenger TE, Kardish MR, Carlson AL, Burns K, Edwards JA, Smith CC, Fang C-C, Des Marais DL. 2016. Artificial microbiome-selection to engineer microbiomes that confer salt-tolerance to plants. *bioRxiv* <https://doi.org/10.1101/081521>.
46. Mueller UG, Gerardo NM, Aanen DK, Six DL, Schultz TR. 2005. The evolution of agriculture in insects. *Annu Rev Ecol Evol Syst* 36:563–595. <https://doi.org/10.1146/annurev.ecolsys.36.102003.152626>.
47. Zeng Q, Wu S, Sukumaran J, Rodrigo A. 2017. Models of microbiome evolution incorporating host and microbial selection. *Microbiome* 5:127–130. <https://doi.org/10.1186/s40168-017-0343-x>.
48. Brkljacic J, Grotewold E, Scholl R, Mockler T, Garvin DF, Vain P, Brutnell T, Sibout R, Bevan M, Budak H, Caicedo AL, Gao C, Gu Y, Hazen SP, Holt BF, Hong S-Y, Jordan M, Manzaneda AJ, Mitchell-Olds T, Mochida K, Mur LAJ, Park C-M, Sedbrook J, Watt M, Zheng SJ, Vogel JP. 2011. *Brachypodium* as a model for the grasses: today and the future. *Plant Physiol* 157:3–13. <https://doi.org/10.1104/pp.111.179531>.
49. Day MD, Beck D, Foster JA. 2011. Microbial communities as experimental units. *Bioscience* 61:398–406. <https://doi.org/10.1525/bio.2011.61.5.9>.

SUPPLEMENTAL MATERIAL: METHODS

Protocol Outline: We used a differential host-microbiome co-propagation scheme as described in Swenson *et al* (2000) and in Mueller *et al* (2005) (Figure S1), but we added to this scheme steps to enhance microbiome transmission and thus response to selection, including (a) microbiome-fractionation using size-selecting filters (Bakken & Olsen 1987; Mueller & Sachs 2015); (b) ramping of stress in successive selection cycles (Garland & Rose 2009); (c) facilitation of priority effects during microbiome assembly (Fierer *et al* 2012; Scheuring & Yu 2012) by capping pots for the first 4 days of the germination stage (i.e., we used a so-called *semi-open system*; Mueller & Sachs 2015), thus controlling in each selection cycle the initial recruitment of symbiotic bacteria into rhizosphere microbiomes of seedlings; and (d) low-carbon soil to enhance carbon-dependent host-control of microbiome assembly and persistence (Bais *et al* 2006; Bulgarelli *et al* 2013; Mueller & Sachs 2015; Coyte *et al* 2015). In each microbiome-propagation cycle ('Microbiome Generation' = Gen), we inoculated surface-sterilized seeds taken from non-evolving stock (inbred strain Bd3-1 of the grass *Brachypodium distachyon*, derived via single-seed-descent inbreeding from the source accession; Vogel *et al* 2006; Garvin *et al* 2008; Vogel & Bragg 2009; Brkljacic *et al* 2011). We chose to conduct the experiment with *B. distachyon* because it is a model for biofuel and cereal crops, including research on salt stresses and water-use efficiency (Des Marais & Juenger 2016; Des Marais *et al* 2016).

We inoculated seeds with rhizosphere bacteria harvested from roots of those plants of the previous selection cycle that exhibited the greatest above-ground biomass (Figure S1). Because the plant-host could not evolve between selection-cycles (seeds were taken from non-evolving stock), whereas microbiomes could potentially evolve due to differential microbiome propagation, our selection-scheme was *one-sided selection* (Mueller & Sachs 2015). Both evolutionary and ecological processes alter microbiomes during and between selection-cycles, but our protocol aimed to maximize evolutionary changes stemming from differential microbiome-propagation at Steps 3 & 4 (Figure S1). To focus indirect selection on bacterial communities, we filtered the microbiomes harvested from rhizospheres, perpetuating only bacteria (and possibly also viruses) to the next generation, but eliminating from propagation between microbiome-generations any larger-celled soil-organisms with filters (i.e., we excluded fungi, protozoa, algae, mites, nematodes, etc. from between-plant transfers). This fractionation step distinguishes our methods from those of Swenson *et al* (2000) and from a replication of that study by Panke-Buisse *et al* (2015), both of which used differential 'whole-community' propagation to transfer between generations all organism living in soil, including the larger-celled fungi, protozoa, algae, mites, and nematodes that were excluded through size-selecting filtering in our experiment. Our complete experiment involved one baseline Generation (Generation 0, Table S1) to establish initial microbiomes in replicate pots; eight rounds of microbiome selection (i.e.,



differential microbiome-propagation) (Generations 1-8, Table S1); and one final ninth round of selection (Generation 9, Table S2) to evaluate the effects of the engineered (i.e., evolved) microbiomes on flower-production and seed-set, for a total of 10 Generations. Our entire selection experiment lasted 300 days from 3. January -29. October 2015.

Logic of Salt-Stress Ramping: We used ramping of salt-stress (Mueller & Sachs 2015) to ensure that (a) plants were neither under-stressed nor excessively over-stressed during any selection-cycle of our microbiome-selection experiment, and thus (b) facilitate that microbiomes can gradually improve under differential microbiome-propagation to confer increasingly greater salt-tolerance to plants under increasingly greater salt-stress. The experimental rationale of stress-ramping is as follows: if salt-stress is too weak, plants grow well, any salt-stress-mediating microbiomes will make little or no difference to plants, and no microbiome-mediated variation in plant-phenotype may emerge that could be used as direct target for indirect selection on microbiomes; in contrast, if salt-stress is excessive, plants suffer severely, and any observed variation in plant-phenotype may be due to microbiome-unrelated effects emerging under excessive stress, such that possible beneficial effects of salt-stress-mediating microbiomes are dwarfed and masked by the excessive stress. Stress-ramping is therefore an experimental trick that permits an experimenter to continuously adjust stress during a selection experiment, particularly in experimental evolution where the evolving effect sizes cannot be known *a priori* (i.e., in our experiment, it was not possible to predict *a priori* the approximate effect sizes attributable to beneficial microbiomes that could emerge as a result of multiple rounds of differential microbiome propagation).

Table S3 lists the ramped salt-concentrations for the two salt treatments of soils in our experiment, Na₂SO₄ (sodium-sulfate, henceforth *SOD-soil treatment*) and Al₂(SO₄)₃ (aluminum-sulfate, *ALU-soil treatment*). We chose the particular two salt stresses because sodium-cations are a problem in saline and sodic soils (e.g., Lodeyro & Carrillo 2015), and aluminum-cations are a problem because aluminum inhibits, at even minimum concentrations, plant growth in low-pH soils (Delhazie *et al* 1995; Aggarwal *et al* 2015). Our maximum sodium-salt stress of 75 mMolar salt-concentration sodium-sulfate of water used to hydrate soil and water plants during the experiment is not quite comparable to the salt stress of 500 mMolar sodium-chloride used by Priest *et al* (2014) because (a) the two experiments used different kinds of salts and (b) Priest *et al* spiked salt stress after initial growth of unstressed plants, whereas in our experiment the plants were salt-stressed already at the germination stage and at all times during each selection cycle.

Table S3. Salt concentrations (Millimolar = mMolar) of salt-nutrient solutions used to hydrate soil for each selection cycle (= Microbiome-Generation = Gen); the recipes to mix these solutions; and growth parameters for each Generation. In the short-cycled Generations 0-8, time was too short for plants to flower, and we quantified plant-performance by visually estimating above-ground biomass (see *Phenotyping of Plants*). In Generation 9, plants were grown for 68 days to produce seeds, and we quantified plant-performance as total seed weight per plant.

	Microbiome-Generation (Selection Cycle)									
	Gen 0	Gen 1	Gen 2	Gen 3	Gen 4	Gen 5	Gen 6	Gen 7	Gen 8	Gen 9
Sodium-Sulfate Concentration	20 mMolar	30 mMolar	50 mMolar	60 mMolar	70 mMolar	75 mMolar	60 mMolar	60 mMolar	60 mMolar	60 mMolar
1-molar sodium-sulfate	240 mL	360 mL	600 mL	720 mL	840 mL	900 mL	720 mL	720 mL	720 mL	1200 mL
Dyna-Gro fertilizer	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	400 mL
e-pure water	12 L	12 L	12 L	12 L	12 L	12 L	12 L	12 L	12 L	20 L
number of pots (plants)	100	100	100	100	100	100	100	100	100	200
Aluminum-Sulfate Concentration	0.02 mMolar	0.04 mMolar	0.08 mMolar	0.20 mMolar	1.0 mMolar	2.0 mMolar	1.0 mMolar	1.0 mMolar	1.5 mMolar	1.5 mMolar
1-molar aluminum-sulfate	240 µL	480 µL	960 µL	2.4 mL	12 mL	24 mL	12 mL	12 mL	18 mL	30 mL
Dyna-Gro fertilizer	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	240 mL	400 mL
e-pure water	12 L	12 L	12 L	12 L	12 L	12 L	12 L	12 L	12 L	20 L
number of pots (plants)	100	100	100	100	100	100	100	100	100	200

Start date (= microbiome transfer/inoculation date)	03. Jan 2015	25. Jan 2015	14. Feb 2015	07. Mar 2015	31. Mar 2015	25. Apr 2015	27. May 2015	22. Jun 2015	20. Jul 2015	20. Aug 2015
Number of days plants allowed to grow until microbiome harvest & transfer to next generation	22	20	21	24	25	32	26	28	31	68
Number of leaves of well-growing plants at day of microbiome harvest & transfer	9-11	9-11	9-11	10-13	8-10	11-13	11-14	17-22	25-30	plants allowed to grow to seed
Number of plants	200	200	200	200	200	200	200	200	200	400
Weight bin of seed weights used for planting	5.8-5.9 mg	5.7-5.8 mg	5.5-5.6 mg	5.4-5.5 mg	5.3-5.4 mg	5.2-5.3 mg	5.1 mg	5.0 mg	4.9 mg	4.6-4.8 mg

A second pre-planned feature of our experimental design was to use ‘short-cycling’ in the initial selection-cycles (cycling at about 20-day intervals; plants grew to about the 9-13 leaf stage to grow sufficiently large root systems for microbiome harvest, but plants did not have sufficient time to flower), and then to increase lengths of selection-cycles gradually as plants became more stressed under the ramped salt-concentrations and plants needed more time to grow to the 9-13 leaf stage. Although we planned lengthening the duration of selection-cycles during our multi-generation experiment, we did not pre-plan at the beginning of our experiment the exact length of each selection-cycle, because the exact transfer dates were dependent also on time-constraints of the main experimenter (UGM) performing the microbiome-transfers. Because we increased salt-stress during the 10-Generation experiment (Table S3), plant growth was expectedly slower in later generations.

Preparation of *Brachypodium distachyon* Seeds: Prior to the start of the microbiome-selection experiment, we harvested about 6000 seeds from 36 plants (*B. distachyon* strain Bd3-1; Garvin *et al* 2008; Vogel & Bragg 2009) grown simultaneously at room temperature under constant light-cycle (14h light, 10h dark) in well-homogenized, well-watered and well-fertilized greenhouse potting soil. Seeds were air-dried at room temperature for 4 months, mixed well, then weighed individually to the nearest 0.1mg to generate groups of seeds of equal weight (binned to within 0.1mg). To reduce within-generation phenotypic variation due to differences in seed-weight-dependent maternal effects, we used seeds of only one or two adjacent weight-bins for each generation (see last row in Table S3). We used seeds of 5.9&5.8mg weight for the initial baseline Generation 0, then we used up seeds of bins of gradually decreasing seed-weight (5.9&5.8mg, 5.8&5.7mg, 5.6&5.5mg, ...), as shown in the last row of Table S3 for each microbiome-generation. All microbiome selection-cycles used seeds from this stored (non-evolving) seed-stock of Bd3-1 plants, and microbiomes were therefore selected under a so-called *one-sided selection* scheme (Mueller & Sachs 2015) in the single plant-genotype background Bd3-1, such that only microbiomes can change between selection-cycles but the plant host cannot evolve.

Growth Chamber: For the multi-generation selection experiment, we grew plants under constant temperature (24°C) and constant light-cycle (20h light 4AM-midnight, 4h dark) in a walk-in growth chamber (model MTPS72; Conviron, Winnipeg, Canada) at the Welch Greenhouse Facility of the University of Texas at Austin. The chamber was not humidity-controlled, and chamber humidity therefore varied with outdoor humidity/rainfall and with any heating (in winter) affecting humidity of the air circulating in the Greenhouse Facility. Because of unusual rainfall in spring 2015, humidity was highest in the growth chamber during Generations 4 & 5, and lowest during selection-cycles 0-2 and 7-9. Unfortunately, we did not monitor exact humidity with a hygrometer in the chamber, but we recorded in a journal any days of high humidity. We grew plants on two shelves (each 120cm x 100cm) in the Conviron chamber, under fluorescent lights (Sylvania T8 fluorescent tubes spaced at 10cm, plus a center row of T2 fluorescent spiral-bulbs) generating a light-intensity of 192 $\mu\text{mol}/\text{m}^2/\text{s}$ at soil level. Except for preparation of pots and planting of seeds, we performed all experimental steps for artificial microbiome selection in this chamber, including microbiome-harvesting from rhizospheres, microbiome-fractionation (filtering), and microbiome-transfers to surface-sterilized seeds planted in sterile soil (details below).

Soil & Pot Preparation: We grew plants from surface-sterilized seeds, each planted individually in the center of its own D50-Deepot (5cm pot diameter, 17.8cm depth, total volume 262ml; model D16H; Stewe & Sons, Tangent, Oregon, USA) filled with autoclaved PPC soil (Profile Porous Ceramic soil, Greens-Grade™ Emerald, Natural Color; PROFILE Products LLC, Buffalo Grove, IL, USA). To permit autoclaving of soil in the Deepots prior to planting, we pressed heat-tolerant fiberglass-fill into the bottom of each pot to plug bottom-drainage holes, then compacted dry PPC soil into each pot until the soil level reached 15mm below the pot margin. Each plug consisted of a fiberglass square (9.5cm x 9.5cm) cut from an insulation-sheet (R-13 EcoTouch Insulation Roll; 38cm width; GreenGuard-certified, formaldehyde-free), then pressed firmly into the bottom of a pot. After compacting soil in all pots used for a given selection-cycle (200 pots in Generations 0-8; 400 pots in the final Generation 9) we carefully equalized soil levels between all pots.

According to the manufacturer's website (www.profileevs.com/products/soil-amendments/profile-porous-ceramic-ppc), PPC soil is a calcined, non-swelling illite, non-crystalline opal mineral; it has 74% pore space, with 39% capillary (water) pores and 35% non-capillary (air) pores; pH = 5.5; cation-exchange-capacity of 33.6 mEq/100g; and a chemical composition of 74% SiO₂, 11% Al₂O₃, 5% Fe₂O₃, and less than 5% of the remainder combining all other chemicals (e.g., CaO, MgO, K₂O, Na₂O, TiO₂). We chose PPC soil for three reasons: First, PPC has a very homogeneous consistency because of its uniform particle size; soil-quantity and soil-quality are therefore easy to standardize between pots. Second, whole root systems can be easily extracted from hydrated soil with little rupture of roots. Third, because the manufacturer exposes PPC soil to high temperature (heated in a rotary kiln at 1200 degrees Fahrenheit, then de-dusted), the soil contains minimum carbon, and we believed that such low- or no-carbon soil could facilitate a plant's ability for carbon-mediated host-control (via carbon exudates by roots; see above *Protocol Outline*) (Bais *et al* 2006; Bulgarelli *et al* 2013; Mueller & Sachs 2015; Coyte *et al* 2015) of microbiome-assembly and microbiome-stability.

Soil Hydration & Salt-Stress Treatments: After compacting soil into each pot with a wooden dowel and equalizing soil levels between all pots used in a selection-cycle, we hydrated each pot with 94ml of a fertilizer-salt solution (recipes for solutions are listed in Table S3, and are described also below). The fertilizer concentrations in this solution was identical in each selection-cycle (i.e., we added the same amount of fertilizer to soil of each microbiome generation), but we increased salt-concentrations gradually between successive selection-cycles in order to ramp salt-stress, as shown in Table S3 for the two salt-stress treatments, Na₂S0₄ (decahydrate sodium-sulfate, MW=322.2g; *SOD-soil*) and Al₂(S0₄)₃ (anhydrous aluminum-sulfate, MW=342.15; *ALU-soil*). We chose the particular two salt stresses because sodium is a problem in saline soils (e.g., Lodeyro & Carrillo 2015), and aluminum is a problem because it inhibits, at even minimum concentrations, plant growth in low-pH soils (Delhazie *et al* 1995; Aggarwal *et al* 2015). Because of this pH-dependent growth-attenuating effect of aluminum in soil, we suspected that it may be easier to select for a microbiome conferring tolerance to aluminum salt, for example by selecting for a microbiome that increases soil pH (i.e., artificial microbiome selection could perhaps select against acidifying bacteria in microbiomes). We therefore were able to formulate this *a priori* hypothesis on a possible pH-based mechanistic basis of a microbiome-conferred tolerance to aluminum-salt. In contrast, we did not formulate a similarly specific mechanistic hypothesis for why a microbiome could confer tolerance to sodium-salt, although a number of hypotheses have been suggested in the literature, such as changes in phytohormone concentrations influencing plant physiology, or indirect physiological effects on transpiration rates (Dodd & Pérez-Alfocea 2012). We selected for microbiomes conferring sodium-salt-tolerance and in parallel for microbiomes conferring aluminum-salt-tolerance because such a dual experimental design of two soil-treatments in the same experiment offered two advantages: (i) we could contrast evolving microbiomes between aluminum- versus sodium-treatments to identify candidate bacterial taxa or candidate consortia that may be important in mediating microbiome-conferred salt-tolerance to plants; and (ii) we could cross selection history with selection stress in the last Generation 9 to test for possible specificities of evolved microbiomes, as explained further below in *Crossing Evolved SOD- and ALU-Microbiomes with SOD- and ALU-Stress*.

The salt-concentration of the baseline Generation 0 (Table S3) was determined in a salt-gradient pilot experiment as that salt-concentration that caused a minimal, but just noticeable, delay in germination and a minimal growth-rate reduction. Because aluminum-sulfate delays germination and attenuates growth at far lower concentrations than sodium-sulfate, concentrations in the ALU-treatment (Table S3) were lower by several orders of magnitude than the concentrations of sodium-sulfate in the SOD-treatment. For ramping of salt-stress, pre-planned step-increments in salt-concentration between selection-cycles were likewise informed by our pilot experiments, which suggested increments for aluminum-sulfate concentrations of about two- to five-fold for the first few microbiome-generations, and less than two-fold increments for sodium-sulfate concentrations, with gradual decrease in step-increments in later microbiome-generations so as not to over-stress plants (Table S3). Because we had to prepare hydrated soil for the next selection-cycle about 1-2 weeks before the end of a given Generation, we had to decide salt-stress increments for the next selection-cycle well in advance, using information from relative growth of younger plants in the sodium-sulfate and the aluminum-sulfate treatments. Decisions on salt-increments between Generations therefore typically involved some informed guessing, to adjust salt concentrations for the next cycle such that plants in either treatment were projected to germinate and grow at about the same rate (i.e., we aimed for plants in either salt treatment to grow to comparable sizes in the same time during a selection cycle). With such projected equal growth between sodium- and aluminum-treatments, microbiomes could be harvested at the end of a selection cycle from plants of comparable sizes (typically 9-15 leaves at the time of microbiome harvesting) regardless of whether a plant was stressed with aluminum-sulfate or sodium-sulfate (i.e., sodium-treated plants were not behind in growth compared to aluminum-treated plants, or vice versa). A second pre-planned feature of our salt-ramping design was to increase salt-stress in successive selection-cycles as long as differences in effect-sizes seemed to increase between salt- and control-treatments, but to reduce the salt-stress if differences in effect-sizes diminished or disappeared, possibly because of over-stressing the plants (see above *Logic of Salt-Stress Ramping*). This seemed to happen in Generations 4 & 5 (see Figure 1 in main text), and salt-stress was therefore reduced somewhat in the subsequent four Generations 6-9 (Table S3).

For hydration of 100 pots, we mixed, in a large carboy, 12 liter double-distilled e-pure water at a 50:1-ratio with 240ml Dyna-Gro 9-7-5 (Nutrient Solutions, Richmond, CA; www.dyna-gro.com/795.htm), plus an aliquot of 1-Molar salt solution (Table S3 lists salt-aliquots in recipes for salt-nutrient mixes) to generate the specific salt-stress planned for a particular selection cycle. [To prepare 1-Molar ALU-salt stock, we dissolved 307.94g anhydrous aluminum-sulfate in 900ml e-pure water in a 1-liter bottle; to prepare 1-Molar SOD-salt stock, we dissolved 289.98g decahydrous sodium-sulfate in 900ml e-pure water in a 1-liter bottle; then filter-sterilized each salt solution to prepare sterile stock.] We used different carboys to prepare salt-nutrient mixes for the different salt treatments (SOD, ALU). The nutrient concentration in each mix (Table S3) was sufficient such that plants did not need additional fertilization during each selection-cycle of 20-30 days during Generations 0-8 when we quantified plant fitness as above-ground biomass production, and plants even had sufficient nutrients to flower and grow seed during the 68 days of Generation 9 when we quantified plant fitness as seed production. For both salt treatments, fertilizer-salt solutions had a pH = 3.75 before addition to soil, but because of the buffering capacity of PPC soil (natural pH = 5.5, see above), the hydrated soil had a pH of about 5.0-5.5 after autoclaving soils, using the pH-measurement protocol in ISO/FDIS 10390 (2005). After hydration of all pots, we immediately autoclaved all pots (to minimize the time that any live microbes in the soil could consume any nutrients), and we autoclaved in separate 1-liter flasks at the same time 800ml of each of the unused salt-nutrient solutions; these autoclaved salt-nutrient solutions were used later during planting, and as buffer (at half-concentration) to suspend microbiomes harvested from rhizospheres for microbiome-transfers (see *Planting & Microbiome-Harvest* below).

Autoclaving of Soil: After hydration of soil by carefully pouring exactly 94ml of fertilizer-salt solution into a pot, we leveled and smoothed the soil-surface in a pot with the bottom of a glass (same size as interior diameter of a pot); taped to each pot a label of autoclavable label-tape (FisherbrandTM) with a pre-written pot-number (#001-100 for pots of SOD-treatment; #101-200 for pots of ALU-treatment) to the top side of

each pot (Figure S1); then used pre-cut pieces of aluminum foil to cap the top and wrap the bottom of each pot to prevent microbial contamination during seed-stratification (see below *Planting & Stratification*). Wrapped pots were arranged vertically in large autoclave trays (67 pots per tray, 3 trays total), the trays were covered with sheets of aluminum foil, then all pots in these 3 trays were sterilized simultaneously in a large autoclave. Hydration, labeling and capping of a set of 200 pots needed typically 5-6 hours. The subsequent autoclaving procedure lasted about 10 hours overnight, starting in the evening with a first cycle of 35 minutes autoclaving (121C° temperature, 20 atm pressure) with a slow-exhaust phase lasting 90 minutes; followed by overnight exposure to high temperature in the unpressurized autoclave, followed in the morning by a second cycle of 35 minutes autoclaving with a 90-minute slow-exhaust phase. This stringent autoclaving regime was sufficient to sterilize PPC soil, because plating on PDA-medium of about 0.5g soil ($n=2$ SOD pots, $n=2$ ALU pots) taken with a sterile spatula from the interior of such autoclaved pots produced no visible microbial growth within a month of incubation of these plates at room temperature. After cooling of autoclaved pots in the foil-covered trays at room temperature for at least 16 hours, we planted seeds into the sterilized soil (one seed per pot; see below *Planting*).

Seeds Preparation & Binning of Seeds by Weight: To have enough seeds for our 10-generation selection experiment, we first grew *Brachypodium distachyon* Bd3-1 plants under standardized light conditions (14h light, 10h dark) and room temperature in well-fertilized and well-watered greenhouse soil, harvested about 6000 seeds from these plants, then dried and stored seeds at room temperature (see above *Preparation of Brachypodium distachyon Seeds*). For our experiment, we used only long-awn seeds; that is, we discarded any short-awn seeds positioned peripherally in inflorescences (spikelet), and we discarded also any misshapen or discolored seeds. We used only long-awn seeds because these kind of seeds grow in more standardized central positions in a spikelet, because we could grasp an awn with a forceps during weighing and planting without risk of injuring a seed, and because we could plant seeds vertically into soil with only the awn protruding above the soil to reveal the exact location of a seed during later microbiome inoculation (see below *Seed Inoculation*). To weigh each seed accurately, we first removed any attached glumes to weigh only the seed with its awn. One experimenter pre-weighed each seed to bin seeds by weight to the nearest 0.1mg, then a second experimenter re-weighed all seeds in bins 4.5mg – 6.0mg again (i.e., each seed was weighed twice). To help reduce within-treatment variation in plant-phenotype (specifically here, reduce seed-weight-dependent maternal effects on plant-phenotypes, as illustrated in Figure S2), we used seeds of only a narrow weight-window for each microbiome-selection cycle. We used seeds of 5.9&5.8mg weight for the initial baseline Generation 0, then we used up seeds of bins of gradually decreasing seed-weight (5.9&5.8mg, 5.8&5.7mg, 5.6&5.5mg, ...), as shown in Table S3 for each microbiome-generation.

Planting & Stratification: For planting of seeds in sterile soil, we first surface-sterilized Bd3-1 seeds in a laminar flow-hood by gently shaking the seeds for 8 minutes in 10% bleach [Chlorox®, 4ml bleach added to 36ml autoclaved e-pure water in a 50ml Falcon tube; plus 4µl Tween80-surfactant (Sigma-Aldrich, Saint Louis, MO, USA) to promote wetting of seeds], then rinsing the seeds three times to wash off bleach (three successive 1-minute gentle shaking, each in fresh 40ml e-pure autoclaved water in a 50-ml Falcon tube). In pilot tests, such surface-sterilized seeds placed on PDA-medium did not lead to bacterial or fungal growth. After rinsing, we blotted seeds on autoclaved filter paper, then air-dried the seeds in an open Petri dish in the flow-hood while preparing the flow-hood for planting inside the hood. To plant one seed into the center

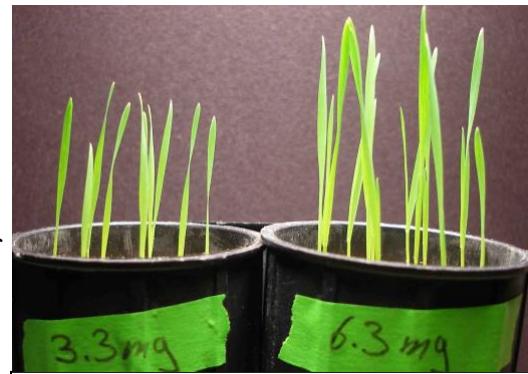


Figure S2. Pilot experiment illustrating growth variation of *B. distachyon* Bd3-1 plants growing under identical conditions from seeds weighing either 3.3mg or 6.3mg. The seed-weight range tested here includes about 90% of the 6000 seeds that we bulked before start of our microbiome-selection experiment. We used seeds of a narrow weight-window of only 0.1mg or 0.2mg for each microbiome-selection cycle (see Table S3), to help reduce within-generation and within-treatment variation in plant-phenotype (specifically here, reduce seed-weight-dependent maternal effects on plant phenotypes). Photo by UGM.

of a pot, we removed the aluminum-foil lid from a pot inside the flow-hood, pushed a narrow hole into the center of the soil with a flame-sterilized fine-tipped forceps (#5 forceps), then inserted a seed into that hole such that the seed was positioned vertically in the soil and only the awn was protruding above the soil (i.e., the pointed tip of a seed was just below the soil surface). Because seeds used for a selection cycle had been binned to within 0.1mg weight (i.e., all seeds were of same size for each Generation), seeds were therefore planted at the same depth (to within about 0.5-1.0 mm identical depth), and any differences in initial germination rate (i.e., appearance of the shoot at soil surface) was unlikely due to differences in planting depth between seeds. To solidify the soil around each seed, we applied 4ml autoclaved salt-nutrient solution (same concentration that was used to hydrate soil in a given selection-cycle; Table S3) with a 5ml pipette to flush soil into the hole and completely cover each seed (excepting the awn protruding vertically above the soil surface). We covered each pot with a translucent, ethanol-sterilized lid (inverted Mini Clear Plastic Bowl 40ct; Party City, Rockaway, NJ, USA). The lids prevented entry of airborne microbes into each pot, but did not seal pots completely and permitted some gas exchange at the bottom of each lid overlapping the top of a pot. Each lid measured 5.7cm diameter x 3.8cm height, and fit snugly on each pot such that a series of 50 capped pots could be kept in a rack (D50T rack, see above) without the lids interfering with each other. We placed each rack of 50 capped pots into its own ethanol-sterilized plastic tub (Jumbo Box; Container Store, Coppell, TX), covered the tub with the tub's lid, then sealed the spaces at the side of each lid by wrapping lid & tub with a 2-meter-long strip of 10-cm-wide Parafilm to prevent entry of contaminants during subsequent cold-storage for stratification of seeds. We moved each tub into cold-storage immediately after completing the planting of 50 pots (= one full rack). For stratification, we stored the tubs with planted seeds in a 5°C cold-room for about 5 days (range 4-10 days, the duration differing slightly between Generations because of scheduling-constraints affecting planting). Planting of a set of 200 seeds (4 racks of 50 pots each) using the above methods needed typically 4.5-5.5 hours.

Preparations for Microbiome-Harvesting: To prepare salt-nutrient buffer-solution for microbiome harvesting, we used the autoclaved salt-nutrient solution that we had prepared for hydration of soil for a particular selection-cycle (see *Soil Hydration* above; Table S3), then diluted the solution to half-concentration by addition of an equal volume of autoclaved e-pure water. We decided to use for microbiome-harvesting the salt-nutrient solution at half-concentration, because we were concerned that the full-concentration may have too high osmolarity compared to the osmolarity that may exist in the soil after weeks of root- and microbiome-growth in the soil; this dilution precaution may not have been necessary, and it may be possible to harvest and propagate microbiomes even with the full-concentration of salt-nutrient buffer. Aliquots of 45ml of the sterile, half-concentration salt-nutrient buffer were added to 50ml Falcon tubes in a laminar-flow hood, and these tubes were then pre-labeled with relevant information (SOD vs ALU treatment; Generation #; date of microbiome-harvest) to save time on the actual day of microbiome-harvest. To sterilize microfilters needed for fractionation of harvested microbiomes (2µm WhatmanTM filters; model Puradisc 25 GD2 Syringe Filter, 25mm diameter; Whatman PLC, United Kingdom), we wrapped filters individually in aluminum-foil, then autoclaved these in a 15min-exposure fast-exhaust cycle. On the evening before the day of microbiome-harvest, we set up a custom-made flow-hood on a bench in our Conviron growth-chamber, sterilized the inside of the hood by spraying liberally with 100% ethanol, then allowed the flow of clean air to purify the inside of the hood overnight. Our custom-made hood was constructed of a large plastic tub placed on its side, with the lid cut half so that a lid-portion affixed to the tub could shield the inside of the hood from above (like a sash on a regular flow-hood), whereas the bottom half was kept open to permit access to the inside of the hood. To generate a flow of clean air through the hood, we cut a large hole into the top of the hood (i.e., one of the original sides of the tub now resting on its side) to fit into that hole the top portion of an air purifier (model HPA104 Honeywell HEPA Allergen Remover, with HEPA filter of 0.3 microns; Honeywell International Inc., Morris Plains, NJ, USA). We operated the purifier at medium flow-setting, which generated an even flow through the hood and minimized any air-vortices that could draw impure air into the hood at high flow-setting. In a pilot test, Petri-plates with PDA-medium, exposed overnight to the flow inside our hood, revealed no visible growth within seven days of incubation of these plates at room temperature. Early on a day of a between-

generation microbiome-transfer, we moved the tubs with racks of planted, cold-stratified seeds from the cold-room into our growth-chamber, to have sufficient time for completion of all microbiome-harvests and -transfers (the total time needed on the day of microbiome harvest for completion of harvests/transfers of all lines was 8-10 hours, plus an additional 2 hours for distribution of pots in pre-determined randomized arrangements across 8 racks used to support pots in the growth-chamber). We began microbiome-harvests and -transfers immediately after moving pots with vernalized seeds into the growth chamber, so transferred microbiomes would interact with seeds at the very early stages of germination.

Phenotyping of Plants; Quantification of Above-Ground Biomass: To select the two best-growing plants from a particular selection line on the day of microbiome-harvest and -transfer, we moved all eight pots from a selection line into a separate, ethanol-sterilized rack, recorded the number of leaves of each plant, and arranged plants visually by apparent above-ground biomass into a size-ranked series (Figure S3). We chose visual sizing rather than weighing for phenotyping of plants, because visual evaluation of all eight plants in a selection-line needed only about 5-10 minutes (including recording the number of leaves for all eight plants), and because microbiomes could be harvested immediately after visually identifying a particular plant for microbiome harvest without first having to cut and weigh above-ground biomass of all plants in a selection line. We harvested rhizosphere microbiomes from only those two plants within a selection line that we visually judged to have grown the largest and second-largest above-ground biomass (Figure S3).



Figure S3. Plants of the same selection-line ranked by visually estimating above-ground biomass. The 8 plants were grown in 8 different racks (one plant per rack) in randomized positions in each rack, and the 8 plants were moved to a separate ethanol-sterilized rack for visual comparison immediately before microbiome harvesting from the two largest plants. See text for further details on *Phenotyping of Plants; Quantification of Above-Ground Biomass*. Photo by UGM.

To test the accuracy of our visual rankings, we later compared these rankings with dry above-ground (shoot) biomass of each plant in a selection line. To weigh shoot-biomass, we cut each plant at soil-level at the time of microbiome harvesting, stored above-ground biomass for drying in an individual paper envelope (Coin Envelope 8cm x 14cm), dried these envelopes/plants for at least two weeks at 60°C in a drying oven, then weighed dry biomass for each plant to the nearest 0.1mg. Although we judged above-ground plant-biomass visually on the day of microbiome harvesting, of the 80 lines judged during our entire experiment (5 SOD-lines + 5 ALU-lines judged each Generation, times 8 Generations; Table S1), we picked for microbiome harvest the combination of largest (#1) and second-largest (#2) plants in 56.25% of the cases; the largest (#1) and third-largest (#3) plants in 27.50%; the largest (#1) and fourth-largest (#4) plants in 6.25%; the second-largest (#2) and third-largest (#3) plants in 5.00%; the second-largest (#2) and fourth-largest (#4) plants in 5.00%; and never any lower-ranked combination. In cases where we did not identify visually the combination of #1 and #2 plants as determined later by dry weight, the slightly lighter #3 or #4 plants were typically within 0.2-4mg (0.5-9% of total dry-weight) of the two best-growing plants in the same selection-line. Moreover, because harvested microbiomes of the two chosen plants were mixed for propagation to the next microbiome-generation (see below *Microbiome Mixing*), we harvested in 100% of the cases the microbiomes from either the best-growing or second-best growing plant into the mixed microbiome that we then propagated to the next microbiome generation (i.e., a microbiome of one of the two best-growing plants was always included in the propagated microbiome mix). In sum, therefore, our method to visually judge plant size was both time-efficient (about 5-10 minutes to visually size all plants in a selection-line

and record number of leaves for each plant), and our method was also accurate to identify those plants that had grown biomass well above-average within any given selection-line (i.e., our methods were accurate to visually identify plants that were likely associated with microbiomes that conferred salt-tolerance to plants).

In some cases, on the day of microbiome-harvest, more than two plants of the same selection line appeared to have the largest above-ground biomass. To decide between those plants for microbiome-harvest, we considered as a second criterion also the growth trajectory recorded from the day of germination to the day of microbiome-harvest, choosing then the plant with the best growth-trajectory. We quantified growth trajectory of plants during each generation with three methods: (i) measuring the length of the first leaf on Days 2-5; (ii) after Day 5, recording the number of leaves grown by a plant every other day up to a time when plants had grown about 10 leaves; and (iii) once plants had grown about 10 leaves, visual ranking of relative plant size (visual appearance of overall biomass) on a 10-point scale from 1-9, using the protocol below.

Length of first leaf: After moving pots from the cold-room into the growth-chamber, the fastest-growing shoots became visible, as they pushed through the soil, after about 44 hours in the early, low-salt Generations, but growth rate was somewhat slower in the later, high-salt Generations when the first shoots became visible after 55-70 hours. To quantify this early growth each selection-cycle, we estimated length of the first leaf during Days 2 & 3 visually without lifting the translucent lids from pots, but measured leaf-length on Days 4 & 5 to the nearest millimeter with an ethanol-sterilized ruler (millimeter scale printed on paper strip; Figure S4) held next to the growing leaf, using a different sterile paper-ruler for each plant so as not to transfer microbes between pots. In blind, repeat evaluations, the visual sizing on Days 2 & 3 is accurate to about ± 0.5 mm for leaves less than 15mm tall, and accurate to about ± 2 mm for plants larger than 25mm. Despite the somewhat lower accuracy of the visual leaf-length estimation compared to the precise measurement with a ruler, we chose to visually size plants on Days 2 & 3 because that method allowed us to leave the pots covered with the translucent lids, thus preventing any influx of microbes when lifting a lid; plants therefore interacted only with the experimentally-transferred microbiomes for the first 4 days of growth without any influx of additional microbes, thus facilitating priority effects in microbiome recruitment into the initial microbiome assembled by a plant.

Counting leaf number: The fastest-growing plants showed growth of a second leaf typically late on Day 5 (in the early low-salt Generations) or on Day 6 (in the later high-salt Generations). We counted the number of leaves regularly after Day 6, typically every other day.

Above-ground biomass estimated on a 10-point scale ranging from 0-9: This third method gave the most precise estimate of above-ground biomass once plant had grown more than 10 leaves, and we used this method therefore every generation to obtain a relative measure of above-ground biomass a few days before microbiome harvesting. An experimenter first looked over all plants to gain an impression of the largest plants, of the appearance of average-sized plants, and of the smallest plants, then subdivided the entire range on a subjective 0-9 point-scale, with plants of average size to be scored as 4.5 on the 0-9 point-scale. Evaluating all plants rack-by rack, the experimenter scored and recorded sizes of all 200 plants in a Generation, then blindly re-scored all plants again rack-by-rack, then calculated an average between the 1st & 2nd size-values for each plant. Comparison of the 1st & 2nd size-values for each plant showed that about 70% of the blind re-scoring were identical between 1st & 2nd size-values; and in most of the remaining 30% cases, 1st & 2nd size-values of the same plant differed by only a 1-point-value, and only in very exceptional cases (<2%) the size-values differed by 2-points on our scale. Because of this high repeatability of this scoring method, we used this method every generation to obtain estimates of the relative above-ground biomass of each plant 1-3 days before each day of microbiome harvesting.



Figure S4. Measuring length of the first leaf on Day 3, using an ethanol-sterilized dry paper-strip with printed millimeter-scale. Photo by UGM.

Microbiome-Harvesting from a Rhizosphere & Microbiome Mixing: We performed all steps of microbiome harvest and microbiome transfer in a clean-air flow-hood (see above) set up on a bench inside our growth-chamber (i.e., we did not have to move microbiomes/pots of selection lines outside the growth chamber), and we sterilized hands and work-surfaces regularly with 100% ethanol to prevent contamination of samples. After choosing the two plants with the greatest above-ground biomass (see above *Phenotyping of Plants*), we cut each plant at soil level with ethanol-sterilized scissors, stored the above-ground portion in an envelope for drying, and harvested rhizosphere microbiomes immediately to minimize microbiome changes in the absence of plant-control in the rhizosphere. To extract the root-system from a pot (Deepot) with minimal contamination, we held the shoot-stub at the soil surface with ethanol-sterilized forceps, tilted the pot such that PPC-soil would gradually loosen and fall out when squeezing the plastic pot, until the root-structure could be extracted as a whole by gentle pulling at the main root with the forceps. In most cases, the entire root structure could be extracted whole, with some loss of fine roots embedded in spilled soil. Because we were interested in harvesting microbiomes that were in close physical association with a plant (i.e., we were interested in rhizoplane bacteria, plus any endophytic bacteria if they were released during root processing as a result of any root damage), we discarded any soil adhering loosely to the roots. We dislodged loosely adhering soil by knocking the root-system gently against the wall of an autoclaved aluminum-pan (e.g., Hefty EZ Foil Roaster Pan; 32cm length x 26cm width, vertical depth 11cm) such that any dislodged soil would fall into the pan without the roots contacting any discarded soil. We then cut off the top 2 cm of the root-system (i.e., roots close to the soil surface), then transferred the remaining root-system into a 50 ml Falcon tube filled with 45 ml of salt-nutrient buffer (the same buffer used also to hydrate soils of the subsequent microbiome-generation, but diluted to half-concentration to suspend harvested microbiomes; see above *Preparations for Microbiome-Harvesting*). We repeated this process with the second plant chosen for microbiome-harvest from the same selection line, and added this second root-system to the same Falcon tube as the first root-system. Combining both root-systems for microbiome-harvesting generated a so-called mixed-microbiome collected from two ‘mother’ rhizospheres (see *Mixed Microbiome Propagation*; and Box 3 in Mueller & Sachs 2015), which we then transferred within the same selection line to all eight ‘offspring’ plants/seeds of the next microbiome-generation.

Microbiome-Fractionation with Microfilters: To dislodge microbes from roots and from soil-particles adhering to roots, we turned a closed Falcon tube upside-down 50 times, then permitted soil-particles to settle in the bottom of the tube for 1 minute. A 1cm-deep sediment of PPC-soil particles typically accumulated in the bottom cone of a Falcon tube, with the roots settling on top of this sediment, and small particles and colloids remaining suspended in the salt-nutrient buffer. We aspirated 20 ml of this suspension with a sterile 20 ml syringe (external syringe diameter fitting into a 50 ml Falcon tube), then attached to the syringe’s Luer-lock a 2 μm Whatman microfilter (model Puradisc 25 GD2 Syringe Filter, 25 mm diameter; Whatman PLC, United Kingdom), then filtered the aspirated suspension into an empty sterile 50 ml Falcon tube. Making sure that the exterior of the syringe did not become contaminated during this first filtering, we repeating this step with the same syringe to filter another 15-20 ml of the suspension, then mixed the combined filtrates by inverting the Falcon tube several times. The total volume of 35-40 ml filtrate was sufficient to inoculate 8 ‘offspring’ plants/seeds each with 4 ml filtrate (total of 8 x 4 ml = 32 ml needed). In pilot tests, plating on PDA-medium 10 μL of this filtrate (2 μm filter) yielded thousands of bacterial colony-forming-units (CFUs) but no fungal CFUs within 24 hours growth; whereas plating on PDA-medium 50 μL of this same filtrate that had been filtered a second time with a 0.2 μm filter (VWR Sterile Syringe Filter, 0.2 μm polyethersulfone membrane, 25mm diameter; Catalog #28145-501; retains even the very-small-sized bacteria, such as *Brevundimonas diminuta*) did not yield any visible microbial growth on these PDA plates kept for 7 days at room temperature. These results justified addition of a third control-treatment in Generation 9 (0.2 μm filtration of suspension; *Solvent Control*) to test growth-promoting effects of root exudates, soil nutrients, and viruses that are unavoidably co-harvested with harvested bacterial microbiomes. Although a 0.2 μm filter may not eliminate ultra-small bacteria (e.g., Luef *et al* 2015; we did not use filters of smaller pore size because it was too difficult to press liquid through such filters), our control comparison between 2.0 μm -filtered and 0.2 μm -filtered bacterial microbiomes can still test whether

the bulk of the bacterial microbiome (in size range 0.2-2.0 μm) or alternatively any smaller-sized organisms (viruses, ultra-small bacteria) are responsible for conferring salt-tolerance to plants.

Inoculation of Seeds; Transfer of Microbiomes to Plants of the Next Microbiome-Generation: During planting, the 200 pots of each microbiome generation had been ordered numerically in the 4 racks used for stratification in the cold-room, so it was easy to locate in these racks a pot with a particular number that had been assigned to a specific selection-line and needed to be inoculated with a microbiome. To inoculate a seed planted in a particular pot, we moved the pot into our clean-hood in our growth chamber, opened the pot's translucent cap inside the hood (using one hand to hold the pot while opening the cap with thumb and index finger of that same hand), then used a 5 ml pipetter to transfer 4 ml of the microbiome-filtrate to the center soil in a pot where a seed had been planted before vernalization/stratification. We spread the 4 ml filtrate across an area with a radius of about 5mm around a seed, applying some of the filtrate directly onto the seed (the exact location of the seed was indicated by its awn protruding above the soil; see *Planting* above), and we spread some of the filtrate also in a circle onto the surrounding soil within 5 mm distance of a seed. To keep the filtrate well-mixed during the time needed to inoculate all 8 'offspring' soils of the same selection-line, we repeatedly mixed the filtrate in the Falcon tube with the pipette-tip before aspirating a 4 ml-aliquot to inoculate the next pot. We then taped a small tag of labeling-tape to the lid of each pot that had received an inoculum (as a check to verify later that all pots had received an inoculate, no pot/seed was accidentally skipped, and no pot/seed was accidentally inoculated twice), then we returned the pot to its appropriate position in one of the four racks. After inoculation of all 200 plants within a Generation, all pots were distributed among the 8 racks used to support plants in the growth chamber (see below *Randomization of Pot-Positions in Racks*).

Each pot was capped for the first 4 days to promote priority effects during microbiome establishment (i.e., capping prevented immigration of extrinsic microbes into the soils/microbiomes for the first 4 days; see above *Planting*), but all caps were removed on Day4 because the tallest plants (35-40mm tall on Day4) were close to reaching the cap-ceiling. We monitored growth during the first 5 days (see above *Phenotyping*) by recording length of the first leaf on Days 2-5, and recording day of appearance of the second leaf (typically on Days 6 or 7). Seeds that did not germinate or that germinated very late (i.e., no above-ground growth visible by Day 4) were extracted from pots with forceps and inspected. Most of these seeds had failed to grow both a rootlet and shoot by Day4, but some seeds had grown a rootlet but no shoot. In a typical microbiome generation, about 88-100% of the plants showed a visible shoot within the first 3 days. Germination rates were therefore good overall, and most lines had the planned 8 replicates (sometimes 7 replicates, rarely 6 replicates, if some seeds failed to germinate; see Tables S1 & S2). Germination-rates were often minimally higher in the Null-Control treatments compared to other treatments of the same soil-stress (slightly fewer non-germinating seeds in Null-Controls); and, across all plants, germination-rates were minimally higher in ALU-soil than in SOD-soil (Tables S1 & S2); we did not analyze these trends for statistical significance because differences seemed minimal, but we simply note here these general patterns that became apparent only when pooling information across all 10 Generations.

Randomization of Pot-Positions in Racks in Growth-Chamber: Deepots were supported in D50T racks (Stewe & Sons, Tangent, Oregon, USA). Each rack can hold a total of 50 pots (5 rows of 10 pots each), but to prevent contact of leaves from different plants and to reduce accidental between-pot transfer of microbes during watering (see below *Watering*), we used only 25 rack-positions (25 pots per rack, total of 8 racks, for a total number of 200 pots per selection cycle). Pots within a selection line were first assigned by blocking to a particular rack (e.g., of the 8 replicates within a selection line, one replicate was assigned to each of the 8 racks. Within each rack, however, we randomly assigned pot positions, using the *Random Sequence Generator* option at Random.Org (www.random.org/sequences/). For Generations 0-8 (growth cycles 0-8), Table S1 lists pot positions (#1-#25) from different treatments within each rack (Rack #1-8), corresponding to the following pot arrangement:

#1		#2		#3		#4		#5	
	#6		#7		#8		#9		#10
#11		#12		#13		#14		#15	
	#16		#17		#18		#19		#20
#21		#22		#23		#24		#25	

For the final Generation 9 when we added two more control-treatments (details below), we randomized 400 pot-positions by first assigning a pot to one of the 8 racks, then randomizing position within each of the 8 racks (50 pots/rack; the position-numbering of pots shown for Generation 9 in Table S2 for each rack is numbered consecutively, starting in left top corner, without leaving empty spacer-slots between pots).

The 8 racks were positioned in two groups of 4 racks each on two comparable shelves at either side of the growth chamber. Within each selection cycle, we rotated these 8 racks in clockwise rotation each day (moving one rack from right shelf to left shelf, and one rack from left to right shelf), and at the same time we also turned each rack (such that the rack-side facing the chamber wall one day faced the chamber center the next day). This rotation-turning scheme aimed to minimize possible environmental influences dependent on location of a rack on the two shelves, and to reduce any minimal differences in light-level, air-circulation, or any such uncontrolled environmental factors that may exist between different positions on the two shelves in our growth chamber. Despite our effort to minimize rack effects through daily rack-rotation and rack-turning, as well as randomization of processing order (e.g., watering, phenotyping, microbiome-harvesting), we had occasionally racks of poorer or better plant growth (e.g., Rack 7 of Generation 9 had lower average seed production compared to other racks, because many plants in that rack did not flower, or flowered late). We do not know the exact causes for occasional small rack-effects.

Starter Inoculum for Microbiomes at Beginning of the Experiment for Baseline Generation 0: We used a single microbiome-batch to inoculate all replicate pots of the initial baseline Generation 0. To prepare that inoculum, we filtered bacterial communities from a mix of roots and adhering soil taken from three principal sources: (a) root-systems with adhering soil of three local grass species (*Bromus* sp., *Andropogon* sp., *Eragrostis* sp.) collected into individual plastic bags on 3. Jan. 2015 (about 90 minutes before microbiome harvesting) at restored native habitat at Brackenridge Field Lab of the University of Texas at Austin (www.bfl.utexas.edu/); (b) root-systems with adhering soil of 40 16-day-old *B.distachyon* Bd3-1 plants grown in PPC-soil Deepots as part of a pilot experiment quantifying the effect of salt in soil on the growth rate of *B. distachyon* (see below *Salt Treatments*); and (c) old root-systems with adhering soil of 15 Bd3-1 plants grown in PPC-soil Deepots, but that had been stored in the soil/Deepots in a cold-room (6°C) for 7 months after completion of a previous low-nutrient microbiome-selection experiment. We combined roots and rhizosphere soils from these three sources in order to capture a diversity of microbes into our starter inoculum, and we included Bd3-1 rhizospheres in order to capture specific microbial taxa that may be readily recruited by *B. distachyon* into its rhizosphere microbiomes. We suspended this mix of roots and rhizosphere soil in 200 ml e-pure water, blended the mix for 30 seconds in an autoclaved Waring blender to generate a liquid slurry, allowed the solids to settle in the blender for 1 minute, then decanted the supernatant into a separate autoclaved beaker. Adding each time 200 ml e-pure water, we repeated this blending/decanting with the remaining slurry three more times to collect a total of about 600 ml supernatant. Using vacuum filtration, we pre-filtered this supernatant in a Buchner funnel through filter paper (Ahlstrom filter paper S02-007-42), eliminating larger particles suspended in the supernatant. To harvest only bacterial microbiome components (and viruses) from this pre-filtrate, we filtered the supernatant a second time in a laminar-flow hood, using a sterile 60 ml syringe fitted with a sterile 2 µm Whatman™ microfilter (Puradisc 25 GD2 Syringe Filter, 25 mm diameter; Whatman PLC, United Kingdom) to generate the bacterial mix for inoculation of replicate pots of our initial baseline Generation 0. Because the Puradisc filters became clogged after filtration of about 70-100 ml supernatant, we used 8 Puradisc filters to process about 600 ml of filtrate. We reserved 500 ml of this filtrate for inoculation of 160 randomly-assigned pots in a Bacterial-

Inoculate treatment (80 Bacterial-Inoculate with SOD soil, 80 Bacterial-Inoculate with ALU soil), and filtered the remaining 100 ml with 0.2 μm filters (VWR Sterile Syringe Filter, 0.2 μm polyethersulfone membrane, 25 mm diameter; Catalog #28145-501) for inoculation of 40 pots in Null-Control treatments (20 Null-Control with SOD soil, 20 Null-Control with ALU soil). The Null-Control treatments controlled for, after elimination of bacteria, the effect of any chemicals and viruses that may have been co-harvested from rhizosphere roots and soils. Seeds in the Bacterial-Inoculum and the Null-Control treatments were inoculated following the procedure described above (see *Inoculation of Seeds*), except that each seed of Generation 0 received 2 ml inoculate, whereas each seed of subsequent Generations 1-9 received 4 ml inoculate transferred between generations. During inoculation of seeds, we mixed the stock filtrates regularly to prevent bacterial sedimentation and to insure standardized inoculation of all replicates across all treatments. We needed about 3 hours to complete the entire process from root collection to conclusion of all filtration steps, and another 2 hours to apply inoculate-aliquots of the filtrates to each of the assigned pots. We then moved all pots immediately into our growth chamber, and set out all 200 pots of Generation 0 into randomized positions in 8 racks (see above *Randomization of Pot Positions*; Tables S1 & S2).

To test for live bacteria in our 2 μm filtrate used as the Starter Inoculum, we plated on PDA-medium (2 replicate plates) 10 μL each of the 2 μm filtrate and maintained plates at room temperature; the plates showed thousands of bacterial colony-forming-units (CFUs) within 24 hours, but no fungal growth within 7 days. To test for absence of live bacteria in our 0.2 μm filtrate, we plated on PDA-medium (3 replicate plates) 50 μL each of the 0.2 μm -filtrate; these platings did not yield any visible growth on the PDA plates kept for 7 days at room temperature. These results indicate (i) a great abundance of live bacteria (and apparently no live fungi) in our initial inoculum, and (ii) elimination by the 0.2 μm filters of live bacteria that would be apparent when plating out such filtrate on PDA plates. The latter justified our use of a third control-treatment in Generation 9 (0.2 μm filtration of suspension to test growth-promoting effects of chemicals and viruses co-propagated with the harvested bacterial microbiomes; see *Solute-Control* below).

Selection of Microbiomes from Generation 0 to Inoculate Plants from Generation 1: At the start of our experiment, we did not assign microbiomes (i.e., pot numbers) from Generation 0 to specific selection lines, to permit selecting the best-growing plants from Generation 0 to contribute microbiomes to the selection-lines starting with Generation 1. We chose this particular assignment rule because random assignment to selection lines would result in some cases for a poorly-growing plant to contribute microbiomes to Generation 1, and we wanted to increase the chance of obtaining a response to microbiome selection in the fewest rounds of selection. To select plants for harvesting and propagation of rhizosphere microbiomes, we ranked, separately for plants in the SOD and ALU treatments, the plants in the Bacterial-Inoculate treatments of Generation 0 by relative size, then picked the 10 best-growing plants of each salt-treatment to contribute microbiomes to the selection-lines that we started with Generation 1 (Table S1). On Day 22 of Generation 0 (day of microbiome harvest and microbiome transfer, we first ranked plants by relative size-scores (i.e., average size-score averaged across three scores received by a plant on Days 18, 19, 20; see protocol *Above-Ground Biomass Estimated on a 10-Point Scale*), then used number of leaves recorded on Day 21 as a second criterion to differentiate between plants of equal size-score. Among the 10 best-growing plants within each of the SOD and ALU salt-treatments, we paired plants randomly to generate 5 combinations (2 plants each) for mixing of harvested microbiomes within each pair (i.e., harvested root-systems were combined from the two plants to harvest a mixed microbiome from both plants, as described above for *Microbiome Mixing*). Within each of the SOD and ALU treatments, the 5 mixed microbiomes from Generation 0 were assigned randomly to 5 SOD and 5 ALU selection lines (each with 8 'offspring' microbiome replicates per line) that started with Generation 1. Microbiomes were harvested and processed from chosen rhizospheres as described above. At the end of Generation 0, as well as at the end of each subsequent Generation, we cut all plants at soil level to preserve above-ground growth for later weighing of dry biomass for each plant (Tables S1 & S2; see also above *Phenotyping*).

Salt- and Control-Treatments in Generation 0-9; Sample Sizes Per Treatment: Starting with Generation 1 and continuing until the last Generation 9, we included the two aforementioned salt-treatments

(SOD and ALU soil) with 5 *SOD Microbiome-Selection* Lines (8 replicates each, for a total of 40 replicates) and with 5 *ALU Microbiome-Selection* Lines (8 replicates each, for a total of 40 replicates). Also starting with Generation 1 and continuing until the last Generation 9, we included two control treatments for each of the SOD and ALU treatments, *Null-Control* (on SOD- and on ALU-soils) and *Fallow-Soil Microbiome Propagation* (on SOD- and on ALU-soils). **Control 1, Fallow-Soil Microbiome Propagation:** For this control, we harvested microbiomes from fallow soil (from pots without a plant), then propagated the harvested microbiome to sterile fallow soil to perpetuate ‘Fallow-Soil Microbiomes’ in the absence of plant influences (e.g., absence of plant exudates into the soil). Fallow-soil pots were treated throughout each selection-cycle exactly like pots with plants; for example, these fallow-soil pots received the same amount of water whenever all other pots were watered. Each Fallow-Soil-Line had only one replicate pot, so a microbiome harvested from fallow-soil was propagated to a single pot of the next selection-cycle to continue a particular Fallow-Soil-Line; a portion of the same microbiome from the same pot was also transferred to pots with plants of the next cycle, to evaluate the effect of a harvested fallow-soil-microbiome on plant growth (but those microbiomes were later not propagated to subsequent Generations; i.e., these inoculations of control plants aimed at assaying the effect of un-selected fallow-soil-microbiomes on plant growth under the increasing salt stress that we increased stepwise between Generations; see above *Logic of Salt-Stress Ramping*). We chose a control of fallow-soil microbiome-propagation because this treatment resembles the kind of microbiome conditions that many plants encounter in horticulture and agriculture (soils are left fallow for some time before planting). Changes in fallow-soil microbiomes between Generations reflect ecological changes as microbe communities change over time, as well as any microbial immigration from external sources (e.g., airborne microbes raining into the soil; perhaps also unintended accidental cross-contamination between soils from different pots). We initially allocated 8 control-replicate test-plants per Fallow-Soil-Line to test the effect of each harvested fallow-soil microbiomes on plant growth (total of $5 \times 8 = 40$ replicates for SOD, $5 \times 8 = 40$ replicates for ALU), but we reduced the number of control-replicate test-plants for each of the 5 Fallow-Soil-Control replicates per line in later Generations (first reducing the number to 6 control-replicate test-plants per line in Generation 4; then reducing the number to 4 control-replicate test-plants per line in Generation 5-9), because it became clear during the first few Generations that plants receiving fallow-soil-microbiomes grew poorly under the salt stresses, far inferior to plants in the corresponding selection-lines where plants received artificially selected microbiomes (i.e., we could differentiate averages between fallow-soil and microbiome-selection lines even with the smaller number of control-replicate test-plants in the fallow-soil controls). **Control 2, Null-Control:** For this control, plants received no experimental microbial inoculation; instead, these control plants received on the day of microbiome transfer an aliquot of the same sterile salt-nutrient buffer that we used to harvest microbiomes and then transfer to seeds of the next Generation. Because our pots were capped for the first 4 days of seed germination, Null-Control-plants grow initially under sterile conditions (before caps are lifted on Day4), but airborne microbes could enter the sterile soil and rhizospheres of Null plants from the air after Day4 once caps are lifted from pots. In pilot experiments, Null-Control plants invariably grew better during the first 10-20 days than any plant inoculated with microbiomes, possibly because Null-Control plants do not need to expend resources to mediate interactions with microbes, or because Null-Control plants do not have to compete with microbes for nutrients in the soil. Despite the microbially unusual soils of Null-Control plants, we included this control treatment because it was easy to set up (no microbiomes needed to be harvested to inoculate Null-Control soils), because Null-Control conditions were easy to standardize within Generations, and because Null-control Conditions may even be standardized between Generations if microbial immigration (i.e., rain of airborne microbes) into Null-Control soils can be assumed to be relatively constant over time. We initially allocated 10 replicates of SOD pots and 10 replicates of ALU pots to Null-Controls, but we increased the number of replicates in later Generations for the Null-Control treatments (first we increased to 20 replicates in Generation 4, then to 30 replicates in subsequent Generations) in order to improve the estimates (reduce confidence intervals) of the average growth of plants in Null-Control treatments. Tables S1 & S2 list sample sizes for all treatments for each of Generations 0-9.

Watering During Each Selection Cycle: We watered pots such that the total weight (pot plus hydrated soil) per pot remained between 200-250g and did not exceed 260g. We found in pilot experiments that a pot would be over-hydrated if the total weight reached 260-270g or more, which would result in dripping of excess water from the bottom of the pot, thus leaching nutrients and salts. Keeping pot weights below 260g at all times therefore prevented leaching of nutrients and salt. To prevent cross-contamination (microbe-exchange) between pots, we did not use bottom-hydration by immersing racks in a waterbath, but we watered pots individually, only from above, and always with autoclaved water that we dispensed with a Seripettor Dispenser (adjustable to dispense volumes of 2.5-25ml; BrandTech Scientific Inc; Essex, CT, USA) mounted on a 6-liter carboy. Because we kept pots capped during the first 4 days of plant growth (we removed caps during the afternoon of Day 4), soils remained well-hydrated during germination (little water evaporated from soil, humidity inside the cap was near 100%). We watered for the first time on Day 5 of each selection-cycle, and thereafter approximately every 2 days (sometimes also at 1-day or 3-day intervals, depending on humidity in the growth chamber and on experimenter time-constraints), but we did not pre-plan to follow a rigorous 2-day watering schedule (see Table S4). We typically watered 15-25 ml per pot depending on water loss, which depended on humidity in the growth chamber and on the size of plants (humidity was greatest during Generations 4&5 because of unusually high rainfall in spring 2015). To determine the volume to be watered on a given day, we selected six pots haphazardly from 4 racks, and weighed these on a scale (sterilizing the surface of the scale with 100% ethanol before placing a pot onto the scale). The difference between the average weight of these six pots and 255mg was the maximum quantity of water to be added to each pot. The amount to be watered could be varied to the nearest 0.5 milliliter with the carboy-mounted Seripettor Dispenser. To prepare carboys, we filled each with 6 liter of e-pure water, and autoclaved the water to ensure sterile watering. Immediately before watering, we quickly opened a carboy to add a specific volume of 1-Molar salt solution to generate a desired salt-concentration in the water (recipes listed in Table S3), mixed the contents by vigorous shaking of the carboy, mounted the ethanol-sterilized Seripettor Dispenser onto the carboy, flushed the dispenser five times to eliminate any ethanol in the dispenser, then began the watering. During the days when the Seripettor Dispenser was not used, we mounted it on a 1-Liter bottle with 100% ethanol, and kept the entire dispenser filled with ethanol to prevent growth of microbial biofilms inside the dispenser. We used different carboys dedicated to watering of SOD-salt and ALU-salt, to minimize cross-contamination of salts between treatments. In each round of watering, we first watered all pots of the SOD-treatment, then rinsed the dispenser with 100% ethanol, then watering all pots of the ALU-treatment. To minimize the chance of accidentally adding the wrong salt-water to a pot (e.g., accidentally watering ALU-soil with SOD-water, or vice versa), we labeled pots of the different salt treatments with different colors (white-label for pots ##001-100 to indicate SOD-treatment, and green-label for pots ##101-200 to indicate ALU-treatment). Table S4 summarizes the exact watering schedules, volumes of water added, and salt concentrations of the water added.

Flowering: Because we short-cycled plants in Generations 0-8 and harvested microbiomes when plants were relatively young (20-30 days old; the largest plants had typically 10-15 leaves, Table S3), only few plants bolted and developed flowers during the short-cycled Generations 0-8; these few cases of flowering were in Generations 1 & 8, whereas no plants flowered in Generation 0 and in Generations 2-7. The long light-phase (20h light, 4h dark) stimulated flowering uniformly in each Generation, but our short-cycling scheme aimed to harvest microbiomes well before plants began to flower in Generations 0-8. Because of scheduling-constraints, Generation 8 was grown for slightly longer (31 days) than earlier Generations, which could explain the flowering in some of these plants, but it is unclear why some plants began to flower in the far shorter Generation 1 (20 days). Plants in Generation 9 were grown for 68 days (see above) to permit seeds to ripen, and most of these plants produced at least some seeds (Table S1). The fact that not all plants flowered in Generation 9, and the observation that onset of flowering was delayed in the control-treatments, indicate that plants were indeed stressed by the salts, because in salt-free soils virtually all plants would have flowered.

Table S4. Ramping Salt-Stress Between and Within Microbiome-Generations. Soil in each pot was initially hydrated with 102 ml salt-solution [94 ml added to soil prior to autoclaving; 4 ml during planting; and 4 ml during microbiome inoculation in Generations 1-9 (2 ml in Generation 0); see *Planting and Inoculation of Seeds*]. In the baseline Generation 0, plants were watered only with unsalted water, but starting with Generation 1, we increased salt-stress *within* each Generation by watering with salted water (details in Table S3). Because we capped pots for the first 4 days to control initial microbiome assembly, we started watering each Generation on Days 5 or 6. Pots of Generations 0-3 were watered more because of low humidity (because of heating of our Greenhouse Facility in winter) and pots of Generations 4&5 were watered less because of high humidity (unusual rainfall in spring, increasing general humidity; see *Growth Chamber*). Pots were watered more in the second half of Generation 9 because plants grew large and transpired more water. Plants of Generations 0-8 were short-cycled to grow only for 20-30 days before microbiome transfer (to about 10-15 leaves for the largest plants); plants in Generation 9 were grown for 68 days to permit ripening of seeds. SOD = sodium-sulfate; ALU = aluminum-sulfate.

		Microbiome-Generation (Selection-Cycle)																			
		Gen 0		Gen 1		Gen 2		Gen 3		Gen 4		Gen 5		Gen 6		Gen 7		Gen 8		Gen 9	
Initial Soil Hydration (see also Table S3)		SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU	SOD	ALU		
100 ml 20 mM	100 ml 0.02 mM	102 ml 30 mM	102 ml 0.04 mM	102 ml 50 mM	102 ml 0.08 mM	102 ml 60 mM	102 ml 0.2 mM	102 ml 70 mM	102 ml 1.0 mM	102 ml 75 mM	102 ml 2.0 mM	102 ml 60 mM	102 ml 1.0 mM	102 ml 60 mM	102 ml 1.0 mM	102 ml 60 mM	102 ml 1.5 mM	102 ml 60 mM	102 ml 1.5 mM		
Watering Schedule																					
Day 5	15ml 0 mM	15ml 0 mM	15ml 0 mM	15ml 15 mM	15ml 0.16 mM	15ml 15 mM	15ml 0.20 mM	10ml 15 mM	10ml 3.0 mM	-	-	-	-	-	-	15ml 15 mM	15ml 2.0 mM	20ml 15 mM	20ml 2.0 mM	20ml 15 mM	
Day 6	23ml 0 mM	23ml 0 mM	20ml 0 mM	25ml 15 mM	25ml 0.16 mM	-	-	-	-	5ml 15 mM	5ml 5.0 mM	15ml 15 mM	15ml 4.0 mM	-	-	-	-	-	-	-	
Day 7	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.60 mM	25ml 15 mM	25ml 3.0 mM	-	-	-	-	15ml 15 mM	15ml 2.0 mM	25ml 15 mM	25ml 2.0 mM	-	
Day 8	17ml 0 mM	17ml 0 mM	20ml 15 mM	20ml 0.02 mM	25ml 15 mM	25ml 0.16 mM	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	
Day 9	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.90 mM	-	-	10ml 15 mM	10ml 10.0 mM	25ml 15 mM	25ml 4.0 mM	15ml 15 mM	15ml 2.0 mM	25ml 15 mM	25ml 2.0 mM	-	-
Day 10	25ml 0 mM	25ml 0 mM	20ml 0 mM	25ml 15 mM	25ml 0.24 mM	-	-	-	-	-	-	-	-	-	-	-	-	-	15ml 15 mM	15ml 2.0 mM	
Day 11	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.90 mM	25ml 15 mM	25ml 5.0 mM	-	-	-	-	15ml 15 mM	15ml 4.0 mM	-	-	15ml 15 mM	15ml 2.0 mM
Day 12	25ml 0 mM	25ml 0 mM	25ml 15 mM	25ml 0.02 mM	25ml 15 mM	25ml 0.32 mM	-	-	-	-	-	-	-	-	-	15ml 15 mM	15ml 2.0 mM	-	-	-	-
Day 13	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.32 mM	25ml 15 mM	25ml 1.20 mM	-	-	20ml 15 mM	20ml 15.0 mM	25ml 15 mM	25ml 5.0 mM	-	-	15ml 15 mM	15ml 2.0 mM
Day 14	25ml 0 mM	25ml 0 mM	25ml 15 mM	25ml 0.04 mM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	15ml 15 mM	15ml 2.0 mM	
Day 15	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.40 mM	25ml 15 mM	25ml 1.50 mM	-	-	-	-	-	-	-	15ml 15 mM	15ml 2.0 mM	
Day 16	25ml 0 mM	25ml 0 mM	25ml 15 mM	25ml 0.08 mM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 17	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.60 mM	-	-	20ml 15 mM	20ml 15.0 mM	15ml 15 mM	15ml 5.0 mM	20ml 15 mM	20ml 5.0 mM	-	-	15ml 15 mM	15ml 2.0 mM
Day 18	25ml 0 mM	25ml 0 mM	25ml 15 mM	25ml 0.08 mM	-	-	-	25ml 15 mM	25ml 1.80 mM	15ml 15 mM	15ml 5.0 mM	-	-	-	-	-	-	-	-	-	-
Day 19	-	-	-	-	-	-	-	25ml 15 mM	25ml 0.90 mM	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-	-	-
Day 20	25ml 0 mM	25ml 0 mM	Transfer to Gen2	Transfer to Gen2	-	-	-	25ml 15 mM	25ml 1.80 mM	-	-	-	-	25ml 15 mM	25ml 3.0 mM	-	-	20ml 15 mM	20ml 2.0 mM	18ml 15 mM	18ml 2.0 mM
Day 21	-	-	-	-	-	-	-	Transfer to Gen3	Transfer to Gen3	-	-	20ml 15 mM	20ml 5.0 mM	25ml 15 mM	25ml 15.0 mM	-	-	15ml 15 mM	15ml 2.0 mM	-	-
Day 22	Transfer to Gen1	Transfer to Gen1	-	-	-	-	-	10ml 15 mM	10ml 1.80 mM	-	-	-	-	-	-	-	-	-	-	-	-
Day 23	-	-	-	-	-	-	-	Transfer to Gen4	Transfer to Gen4	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	25ml 15 mM	25ml 2.0 mM	20ml 15 mM	20ml 2.0 mM
Day 24	-	-	-	-	-	-	-	10ml 15 mM	10ml 5.0 mM	-	-	20ml 15 mM	20ml 3.0 mM	-	-	-	-	-	-	-	-
Day 25	-	-	-	-	-	-	-	Transfer to Gen5	Transfer to Gen5	-	-	20ml 15 mM	20ml 15.0 mM	-	-	20ml 15 mM	20ml 2.0 mM	-	-	-	-
Day 26	-	-	-	-	-	-	-	Transfer to Gen6	Transfer to Gen6	-	-	Transfer to Gen7	Transfer to Gen7	-	-	25ml 15 mM	25ml 2.0 mM	18ml 15 mM	18ml 2.0 mM	-	-
Day 27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-	-	-	
Day 28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Transfer to Gen8	Transfer to Gen8	20ml 15 mM	20ml 2.0 mM	20ml 15 mM	20ml 2.0 mM	
Day 29	-	-	-	-	-	-	-	20ml 15 mM	20ml 15.0 mM	-	-	-	-	-	-	10ml 15 mM	10ml 2.0 mM	-	-	-	-
Day 30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10ml 15 mM	10ml 2.0 mM	-	-	-	-
Day 31	-	-	-	-	-	-	-	10ml 15 mM	10ml 18.0 mM	-	-	-	-	-	-	Transfer to Gen9	Transfer to Gen9	20ml 15 mM	20ml 2.0 mM	-	-
Day 32	-	-	-	-	-	-	-	Transfer to Gen6	Transfer to Gen6	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 33	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 34	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 35	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 36	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 39	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 41	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 42	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 44	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Day 46	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-
Day 47	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20ml 15 mM	20ml 2.0 mM	-	-

Visualization of Relative Plant Performance (Figure 2): Because successive generations were not grown under precisely identical conditions (e.g., we had to increase the duration of selection-cycles in later generations because plant-growth decelerated under the increasing salt-stress; we had to adjust watering schedules because of uncontrolled humidity in our growth chamber), we plot in Figure 2 (main article) plant-performance as relative above-ground biomass (rather than absolute biomass), relative to control plants of the same salt treatment. Because we had for each salt treatment (SOD, ALU) two control treatments (Fallow-Soil Control, Null Control), we calculated relative performance of plants with selected microbiomes in two ways for each salt treatment, relative to the average performance (dry above-ground biomass) of Fallow-Soil-Control plants (Figure 2a&b) and relative to average performance (dry above-ground biomass) of Null-Control plants (Figure 2c&d). To calculate average performance of Fallow-Soil-Control plants, we first averaged within each of the 5 Fallow-Soil lines, then averaged across these 5 averages. To calculate average performance of Null-Control plants, because there was only one line of Null-Control plants, average performance could be calculated directly for these plants. The calculations of relative plant-performance for Generations 0-8 appear in Columns V-AE of Table S1. In Generation 9, we allowed plants to grow for 68 days to permit flowering and ripening of seeds; plants and microbiomes of Generation 9 are therefore not comparable to those of Generations 0-8, and we analyzed data from Generation 9 therefore separately (see next; Table S2, Figures 3 & 4).

Crossing Evolved SOD- and ALU-Microbiomes with SOD- and ALU-Stress in Generation 9; Solute Control in Generation 9: At the end of the experiment in Generation 9, we modified protocols in three important ways: (a) we grew plants for 68 days to permit flowering and ripening of seeds, because seed production seemed a more informative estimator of plant fitness than the proxy of above-ground biomass used in Generations 0-8; and (b) we doubled the total number of pots to 400 (i.e., 400 plants) to permit addition of two control treatments (in addition to Fallow-Soil-Control and Null-Control treatments already used in earlier Generations). We added these two control treatments to understand the mechanistic basis of the salt-tolerance-conferring effects of microbiomes in the SOD and ALU selection lines. The first additional control was *Solute Control* (Figure 3, main text), where we filtered out all live cells from the harvested microbiomes in the selection lines (using a $0.2\mu\text{m}$ filter; see above *Microbiome-Fractionation with Microfilters*), to test the growth-enhancing effect of viruses and plant-exuded solutes that may be co-harvested from rhizosphere soil together with the bacterial rhizosphere microbiomes propagated in the selection-lines. The second control was *2x2 Cross-Fostering Control* (Figure 4, main text), where we crossed harvested microbiomes from the SOD and ALU selection lines with the two types of salt stress in

soil (i.e., microbiomes harvested from SOD-selection-lines were tested in both SOD-soil and in ALU-soil; microbiomes harvested from ALU-selection-lines were tested in both SOD-soil and in ALU-soil) to test specificity of the salt-tolerance-conferring effects of the microbiomes. This Cross-Fostering treatment allowed us to address the question whether the salt-tolerance-conferring effects of the *SOD-selected* microbiomes confer these effects only under SOD-stress, or also in ALU-stress; and vice versa the additional question whether the salt-tolerance-conferring effects of the *ALU-selected* microbiomes confer these effects only under SOD-stress, or also in ALU-stress. This basic cross-fostering design was inspired by the experimental methods developed by Lau & Lennon (2012), except that, in contrast to Lau & Lennon (2012), our plant-populations did not evolve because we used seeds from non-evolving stock, and that we artificially selected on microbiomes (whereas in Lau & Lennon the plants evolved under artificial selection on plants, and microbiomes were *not* propagated *differentially* as in Steps 3 & 4 of Figure 1S).

Phenotyping of Plants and Microbiome-Harvesting in the Last Generation 9: In contrast to Generations 0-8 when we used early growth of plants (above-ground biomass during first 3-4 weeks) as host phenotype to select indirectly on microbiomes, in the last Generation 9, we allowed plants to mature for 68 days (10 weeks), such that plants could flower and seeds could ripen. Because of the longer growth, some plants started to senesce towards the end of Generation 9 and some individual flower stalks of some plants started to dry (no plant dried completely by the end of Generation 9). We decided to grow plants to seed in this last Generation because we were interested in understanding how short-cycle microbiome-selection to increase above-ground biomass of young, pre-flowing plants (20-30 days old, when we harvested and transplanted microbiomes in Generations 0-8) would affect flowering and seed-set if plants were allowed to grow older (68 days). Apart from the longer duration of Generation 9 to permit flowering, a second important difference is likely the gradually increasing salt-concentration in soils of Generation 9 that were watered 34 times with salted water over 68 days (Table S4), in contrast to watering with salted water fewer times over the shorter 20-30 days in Generations 0-8 (9-12 waterings, depending on the Generation; see Table S4). At the end of Generation 9, all plants were cut at soil level, above-ground biomass was preserved for each plant in individual envelopes (for drying and later weighing of seeds and overall biomass; see above), and each root system was extracted from its pot and placed into an autoclaved aluminum-tub for further processing. Root-systems of plants from Generations 0-8 were comparatively small (filling about 30-60% of the soil-volume in each pot), but root-systems at the end of Generation 9 were large and extended through the entire soil-volume in each pot. We shook-off most of the adhering soil from each root system of Generation 9, cut off and discarded the top-most 2cm portion with sterile scissors, then cut the remaining root-system lengthwise (top to bottom) to preserve half of the root-system in 100% ethanol (for metagenomic screens of bacterial communities), whereas we flash-froze (in liquid nitrogen) the other half of the root-system for possible later transcriptomics analyses. For some of the best-growing plants in the SOD- and ALU-selection-lines, we also preserved a representative portion of the root-system in sterile 20% glycerol (for storage at -80°C for possible later isolation of microbes). Processing all root-systems (nearly 400 plants) took considerable time over three successive days (Days 68-70 of Generation 9). Although we processed plants from 3 racks on Day 68 (Racks #3, #8, #7), 3 racks on Day 69 (Racks #6, #2, #4), and 2 racks on Day 70 (Racks #1, #5), to simplify, we label all weight-data of these plants as if collected on Day 68.

References

- Aggarwal A, Ezaki B, Munjal A, Tripathi BN. 2015. Physiology and biochemistry of aluminum toxicity and tolerance in crops. Pp 35-57 in *Stress Responses in Plants* (Tripathi BN & Müller M, eds), Springer International Publishing.
- Bais HP, Weir TL, Perry LG, Gilroy S, Vivanco JM. 2006. The role of root exudates in rhizosphere interactions with plants and other organisms. *Annu Rev Plant Biol* 57: 233-66.
DOI: 10.1146/annurev.arplant.57.032905.105159
- Bakken LR, Olsen RA. 1987. The relationship between cell size and viability of soil bacteria. *Microb Ecol* 13: 103-114. DOI: 10.1007/BF02011247

- Brkljacic J, Grotewold E, Scholl R, Mockler T, Garvin DF, Vain P, Brutnell T, Sibout R, Bevan M, Budak H, Caicedo A, Gao C, Gu Y, Hazen S, Holt BF, Hong S, Jordan M, Manzaneda AJ, Mitchell-Olds T, Mochida K, Mur LAJ, Park C-M, Sedbrook J, Watt M, Zheng S, Vogel JP. 2011. *Brachypodium* as a model for the grasses: today and the future. *Plant Physiol* 157: 3–13. DOI: 10.1104/pp.111.179531
- Bulgarelli D, Schlaepi K, Spaepen S, van Themaat EVL, Schulze-Lefert P. 2013. Structure and functions of the bacterial microbiota of plants. *Annu Rev Plant Biol* 64: 807–838. DOI: 10.1146/annurev-arplant-050312-120106
- Coyte KZ, Schluter J, Foster KR. 2015. The ecology of the microbiome: Networks, competition, and stability. *Science* 350: 663–666. DOI: 10.1126/science.aad2602
- Delhaize E, Ryan PR. 1995. Aluminum toxicity and tolerance in plants. *Plant Physiology* 107: 315–321. DOI: 10.1104/pp.107.2.315
- Des Marais DL, Juenger TE. 2016. *Brachypodium* and the abiotic environment. Pages 291–311 in *Genetics and Genomics of Brachypodium* (Vogel JP, ed). Springer International Publishing. DOI: 10.1007/7397_2015_13
- Des Marais DL, Razzaque S, Hernandez KM, Garvin DF, Juenger TE. 2016. Quantitative trait loci associated with natural diversity in water-use efficiency and response to soil drying in *Brachypodium distachyon*. *Plant Science* 251: 2–11. DOI: 10.1016/j.plantsci.2016.03.010
- Dodd IC1, Pérez-Alfocea F. 2012. Microbial amelioration of crop salinity stress. *J Exp Bot* 63: 3415–3428. DOI: 10.1093/jxb/ers033.
- Fierer N, Ferrenberg S, Flores GE, González A, Kueneman J, Legg T, Lynch RC, McDonald D, Mihaljevic JR, O'Neill SP, Rhodes ME, Song SJ, Walters WA. 2012. From animalcules to an ecosystem: Application of ecological concepts to the human microbiome. *Annu Rev Ecol Evol Syst* 43: 137–155. DOI: 10.1146/annurev-ecolsys-110411–160307
- Garland T, Rose MR. 2009. *Experimental Evolution*. University of California Press.
- Garvin DF, Gu YQ, Hasterok R, Hazen SP, Jenkins G, Mockler TC, Mur LAJ, Vogel JP. 2008. Development of genetic and genomic research resources for *Brachypodium distachyon*, a new model system for grass crop research. *Crop Science* 48: S69–S84. DOI: 10.2135/cropsci2007.06.0332tpg
- ISO/CDIS 10390 (2005) Soil quality – Determination of pH. International Organization for Standardization, 2005. www.iso.org/iso/catalogue_detail.htm?csnumber=40879
www.ecn.nl/docs/society/horizontal/pH_standard_for_validation.pdf
- Lau JA, Lennon JT. 2012. Rapid responses of soil microorganisms improve plant fitness in novel environments. *Proc Natl Acad Sci USA* 109: 14058–14062. DOI: 10.1073/pnas.1202319109
- Lodeyro AF, Carrillo N. 2015. Salt stress in higher plants: mechanisms of toxicity and defensive responses. Pp 1–33 in *Stress Responses in Plants* (Tripathi BN & Müller M, eds), Springer International Publishing.
- Luef B, Frischkorn KR, Wrighton KC, Holman HY, Birarda G, Thomas BC, Singh A, Williams KH, Siegerist CE, Tringe SG, Downing KH, Comolli LR, Banfield JF. 2015. Diverse uncultivated ultra-small bacterial cells in groundwater. *Nat Commun* 6: 6372. DOI: 10.1038/ncomms7372
- Mueller, U.G. Gerardo NM, Aanen DK, Six DL, Schultz TR. 2005. The evolution of agriculture in insects. *Annu Rev Ecol Evol Syst* 36: 563–595. DOI: 10.1146/annurev.ecolsys.36.102003.152626
- Mueller UG, Sachs JL. 2015. Engineering microbiomes to improve plant and animal health. *Trends Microbiol* 23: 606–617. DOI: 10.1016/j.tim.2015.07.009
- Panke-Buisse K, Poole AC, Goodrich JK, Ley RE, Kao-Kniffin J. 2015. Selection on soil microbiomes reveals reproducible impacts on plant function. *ISME J* 9: 980–989. DOI: 10.1038/ismej.2014.196
- Priest HD, Fox SE, Rowley ER, Murray JR, Michael TP, Mockler TC. 2014. Analysis of global gene expression in *Brachypodium distachyon* reveals extensive network plasticity in response to abiotic stress. *PLoS One* 9: e87499. DOI: 10.1371/journal.pone.0087499

- Scheuring I, Yu DW. 2012. How to assemble a beneficial microbiome in three easy steps. *Ecol Lett* 15: 1300–1307. DOI: 10.1111/j.1461-0248.2012.01853.x
- Swenson W, Wilson DS, Elias R. 2000. Artificial ecosystem selection. *Proc Natl Acad Sci USA* 97: 9110–9114. DOI: 10.1073/pnas.150237597
- Vogel JP, Garvin DF, Leong O, Hayden DM 2006. *Agrobacterium*-mediated transformation and inbred line development in the model grass *Brachypodium distachyon*. *Plant Cell, Tissue & Organ Culture* 84: 199–211. DOI: 10.1007/s11240-005-9023-9
- Vogel J, Bragg J. 2009. *Brachypodium distachyon*, a new model for the Triticeae. In *Genetics and Genomics of the Triticeae*, pp. 427–449. Edited by GJ Muehlbauer & C Feuillet. New York: Springer.

SUPPLEMENTAL MATERIAL: RESULTS

Generations 1-8: Effects of differential microbiome propagation under sodium-sulfate (SOD) stress:

We found a significant main effect of treatment on plant biomass over 8 generations of microbiome selection under sodium-sulfate stress (LRT: Treatment, Chisq=27.8, p<0.001; Generation, Chisq=381.8, p<0.001; Treatment x Generation, Chisq=15.2, p=0.37; Figure 2 left). Plant biomass was 75% higher in the plant-present Microbiome-Selection lines ($\beta=0.57 \pm 0.06$, $z=10.0$, p<0.001) than in the Fallow-Soil Control lines, and 66% higher than in the Null-Control line ($\beta=0.50 \pm 0.07$, $z=7.4$, p<0.001). There was no significant difference in biomass between the fallow-soil and the null-control treatments ($\beta=0.07 \pm 0.06$, $z=1.1$, p=0.29). The lack of a significant interaction between treatment and generation (Chisq=15.2, p=0.37) indicates that gains in plant biomass were realized quickly in the first few selection cycles, and that the advantage of the plant-present Microbiome-Selection treatment over the Fallow-Soil treatment was maintained as the concentration of sodium-sulfate was ramped up over the course of the experiment.

Generation 9, SOD-treatments: We measured total seed weight in the final Generation 9 of the experiment and found significant difference among treatments (Kruskal-Wallis Chisq=10.6, p=0.01; Figure 2 right). Total seed weight in the plant-present Microbiome-Selection lines were 168% greater compared to the null-control line, 120% greater than the Fallow-Soil-Control lines, and 205% greater than plants grown in soil that was inoculated with filtrate (0.2 μ m filter) from the soil of plant-present Microbiome-Selection lines (Figure 2 right; Table S5).

Table S5. Mann-Whitney pairwise comparisons of total seed weight in the sodium-sulfate (SOD) treatments. Values represent the test statistics (p-value in parentheses) for each comparison. Significant comparisons are indicated in bold. Np = Fallow-Soil microbiome-propagation control, Null=Null-Control line, Pp=Plant-present Microbiome-Selection line, PpFilt=Plant-present Microbiome-Selection line filtrate.

	Np	Null	Pp
Null	100 (0.50)		
Pp	0 (0.02)	20 (0.02)	
PpFilt	20 (0.50)	90 (0.71)	20 (0.02)

Generations 1-8: Effects of microbiome propagation under aluminum-sulfate (ALU) stress: Unlike the sodium-sulfate experiment, we found a significant interaction between treatment and generation under aluminum-sulfate stress (LRT: Treatment, Chisq=25.7, p<0.001; Generation, Chisq=753.7, p<0.001; Treatment x Generation, Chisq=26.6, p=0.02). The interaction was due to a drop in plant biomass in the Fallow-Soil treatment in Generations 4 and 5 (Figure 2). To calculate a conservative estimate of the effect size of our treatments on plant biomass, we re-ran the analysis excluding Generations 4 and 5, which eliminated the significant interaction between treatment and generation (LRT: Treatment, Chisq=17.8, p<0.001; Generation, Chisq=614.5, p<0.001, Treatment x Generation, Chisq=7.67, p=0.66). In the reduced dataset, we found that plant biomass in plant-present Microbiome-Selection lines were 38% larger than in fallow-soil lines ($\beta=0.32 \pm 0.04$, $z=8.9$, p<0.001), but not significantly different from the Null-Control line ($\beta=0.09 \pm 0.4$, $z=2.3$, p=0.06). Null-Control plants generated 26% greater biomass than Fallow-Soil-Control plants ($\beta=0.23 \pm 0.04$, $z=5.1$, p<0.001).

Generation 9, ALU-treatments: As in the sodium sulfate experiment, total seed weight in the final Generation 9 was significantly different among treatments (Kruskal-Wallis: Chisq=9, p=0.02; Figure 2 right). Total seeds weight in the plant-present Microbiome-Selection lines were 194% greater than in the fallow-soil lines, 101% greater than in the Null-Control line, and 55.4% greater than in the filtrate lines (Table S6). Plants with filtrate-inoculated soil produced total seed weights that were 89.2% greater than plants grown in the Fallow-Soil Control (Figure 2 right; Table S6).

Table S6. Mann-Whitney pairwise comparisons of total seed weight in the aluminum-sulfate (ALU) treatments. Values represent the test statistics (p-value in parentheses) for each comparison. Significant comparisons are indicated in bold. Np = Fallow-Soil microbiome-propagation control, Null=Null-Control line, Pp=Plant-present Microbiome-Selection line, PpFilt=Plant-present Microbiome-Selection line filtrate.

	Np	Null	Pp
Null	80 (0.55)		
Pp	0 (0.02)	30 (0.03)	
PpFilt	0 (0.02)	70 (0.29)	20 (0.05)

Interactions between selection history and salt stress on plant fitness: By growing plants with microbiomes from selection lines under both sodium- and aluminum-sulfate stress (*Cross-Fostering Control*), we examined whether microbiome selection produced microbiomes that conferred a salt-specific effect on plants (e.g., whether microbiomes selected to confer tolerance to SOD conferred such tolerance only under SOD stress, but not under ALU stress), or alternatively whether selected microbiomes produced a generalized improvement in plant fitness under both SOD and ALU stresses. There was a significant interaction between selection history and the type of salt stress to which plants were exposed in the last generation on seed mass (Analysis of deviance: Selection history, $F_{1,8}=<0.01$, $p=0.99$; Salt exposure, $F_{1,141}=5.82$, $p=0.017$; Selection history x Salt exposure, $F_{1,141}=6.42$, $p=0.012$; Figure 2 right), indicating that performance under SOD-stress or ALU-stress in Generation 9 depended upon which salt the microbiome was selected on during Generations 0-8.

We conducted post-hoc comparisons of the treatment means and found that plants grown with microbiomes selected under sodium-sulfate stress had total seed weights that were 70.1% greater when exposed to sodium-sulfate stress compared to exposure of aluminum-sulfate stress in Generation 9 ($\beta=108 \pm 31.0$, $z=3.5$, $p=0.002$). In contrast, plants grown in microbiomes selected under aluminum-sulfate stress did not differ in total seed weight, regardless of whether they were stressed with sodium- or aluminum-sulfate in Generation 9 ($\beta=4.2 \pm 31.8$, $z=0.13$, $p=0.99$). The effect of exposure to different kinds of salt stress on plant fitness thus depends upon the selection history of the soil microbiome.

Unlike total seed weight, there was no interaction between selection history and the type of salt stress on total plant biomass, however there was a trend toward plants growing larger under ALU-stress compared to SOD-stress irrespective of the selection history (Analysis of deviance: Selection history, $F=0.14$, $p=0.72$; Salt exposure, $F=3.71$, $p=0.056$; Selection history x Salt exposure, $F=1.38$, $p=0.24$).

SUPPLEMENTAL MATERIAL: STATISTICAL ANALYSES

Statistical Analyses: Plant Biomass, Generations 1-8: We performed all analyses in R v3.3.1. We assessed differences in above-ground plant biomass (dry weight) among treatments of Generations 1-8 by fitting the data to a generalized linear mixed model with a gamma error distribution. Line was entered as a random effect; generation, treatment, and their interaction were entered as fixed effects. Statistical significance of fixed effects in the GLMMs were assessed with likelihood ratio tests and Tukey tests employed for post-hoc comparisons of treatment means. Selection of the appropriate error distribution for the GLMMs was evaluated by visual inspection of Q-Q plots, and homoscedasticity was assessed using plots of the residuals of the model against the fitted values. Because plants were short-cycled in Generations 1-8 (i.e., grown long enough so plants produce typically 9-15 leaves, too short to develop flowers), plants did not produce any seeds, and therefore only above-ground plant biomass (dry weight) could be compared between treatments of Generations 1-8.

Statistical Analyses: Total Seed Weight, Generation 9: Because plants were grown long enough to flower in Generation 9, we compared total seed weight per plant among microbiome-selection treatments (plant present; microbiomes were differentially transplanted from plants of Generation 8 to seeds of Generation 9), Fallow-Soil Control (no plant present; microbiomes were harvested from fallow soil of

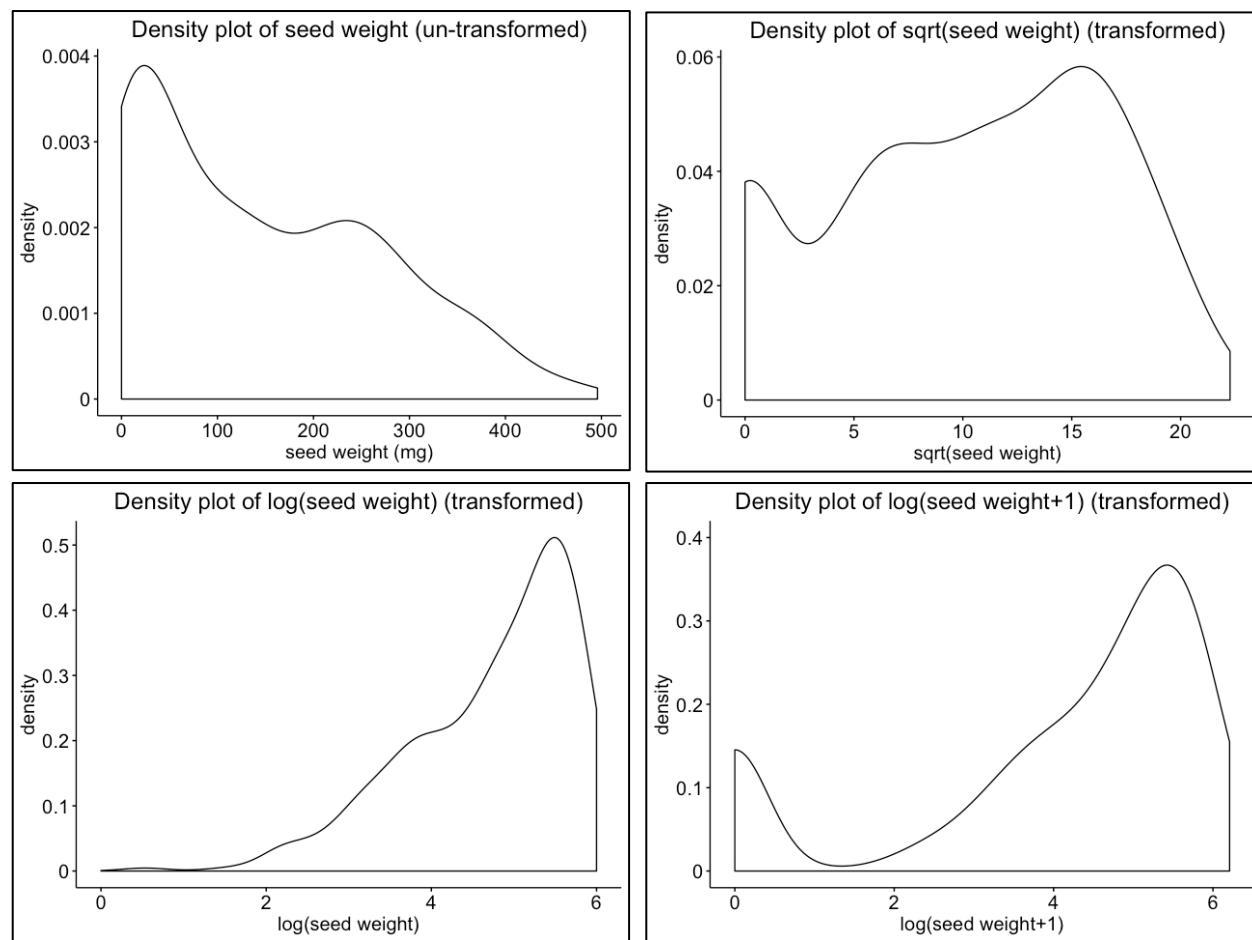


Figure S5. Top-left: untransformed seed-weight data in milligram (mg), indicating a skewed distribution, with many plants producing no or few seeds because of the extreme salt stress during Generation 9. **Top-right:** square-root transformed seed-weight data. **Bottom-left:** log-transformed seed-weight data, excluding seed-weights of zero because $\log(0)$ is not defined.

Bottom-right: log-transformed seed-weight+1 data. None of the three transformations generated a distribution that approximated normality, and we therefore used non-parametric tests to evaluate differences in seed production between treatments.

Generation 8 for transfer to seeds of Generation 9), and Null-Control (no initial microbiome inoculation, microbes establish in microbiomes when microbes "rain in" from the air). Because plants were strongly salt-stressed in Generation 9 and many plants therefore did not flower or only produced very few seeds, the distribution of data was not normal (Figure S5 top-left). We therefore attempted several data-transformations to achieve approximate normality, including *square-root(seed weight)* transformation (Figure S5 top-right), *log(seed weight)* transformation [excluding the plants that generated zero seeds because $\log(0)$ is undefined; Figure S5 bottom-left], and *log(seed weight +1)* transformation (making it possible to retain the plants that produced zero seeds, because seed-weight values of all plants was increased by 1mg; Figure S5 bottom-right). None of these transformations generated a distribution that approximated normality (Figures S5b-d), and we therefore used Kruskal-Wallis tests for non-parametric evaluation of differences between treatments in Generation 9; and we used Mann-Whitney U-tests for non-parametric post-hoc comparisons between treatment means, correcting p-values using the false discovery rate. All tests were two-tailed with alpha=0.05.

Supplemental Table S1

Table S1 (Data Generations 0-8)																
sent to co-authors for analyses 5. Sep. 2016																
Abbreviations used in this Table:																
"NA" denotes empty cell (e.g., seed that failed to germinate)																
"SOD" denotes sodium-sulfate stress, "ALU" denotes aluminum-sulfate stress																
"Bact" denotes inoculation of soil&seed with the initial bacterial inoculum at the beginning of the experiment (i.e., inoculation of seeds of Generation 0)																
"Null" denotes no microbiome-inoculation of a seed, but microbes can accumulate from aerial microbial rain																
Explanation of Columns:																
Column B	selection cycle (Microbiome Generation); Generation "0" is baseline Generation prior to first round of selection; plants were not yet assigned to selection lines in Generation 0															
Column C	salt treatment of soil (and water used to water plants); SOD denotes sodium-sulfate stress, ALU denotes aluminum-sulfate stress															
Column D	Pp is "plant present", a microbiome is harvested from rhizosphere and propagated to germinating seeds of next microbiome-generation;															
"	Np is "no plant", a microbiome is harvested from fallow soil with no plant in pot, then propagated to (a) germinating seeds to test microbiome effects, and to (b) soil in pot with no seed planted in it (i.e., Fallow-Soil Microbiome Propagation)															
"	Null is "no microbiome-inoculation of seed", plants acquire microbiomes from aerial microbial rain; number of replicates in Null-treatment increases in later Generations															
Column E	selection lines in Pp and Np treatments; for each salt-treatment, there are 5 selection-lines for Pp, and 5 lines for Np															
"	number of replicates in Pp-lines is always 8 replicates (minus a few seeds that did not germinate, or seeds that germinated very late and were then removed);															
"	number of replicates in Np-lines is 8 replicates per line in Gen1-3, then was reduced to 6 replicates per line in Gen4, then to 4 replicates per line in subsequent Generations															
Column F	plant number used to identify individual plants (i.e., pots);															
"	each Generation had 200 pots, but 10+10 pots/soils were "parents" for the fallow-microbiome-propagation treatments, and															
"	these fallow-microbiome "parents" are not included in this sheet and are moved to the second sheet in this Excel file															
Column G	rack number; for each selection-line, replicates were blocked evenly between racks; there were 8 racks total, each with 25 pots (total 200 pots)															
Column H	position of pot in rack; pots assigned to a particular rack were randomly assigned to the 25 pot-positions in each rack															
Column I	dry weight (above-ground biomass in mg) of plant harvested at end of microbiome-generation; biomass was weighed blindly with respect to plant treatment															
"	THESE ARE THE ABSOLUTE VALUES OF THE DEPENDENT VARIABLE "DRY WEIGHT"															
"	"NA" in this column denotes that a seed did not germinate, or seed was removed because of very late germination, and therefore no DryWeight is available for this plant															
Column J	"LineAverage" is the average calculated across all replicates in that line															
Column K	"TreatmentAverage" is the average of the treatment (averaged across the 5 line-averages of the 5 lines in each treatment)															
Column L	column to calculate "AverageDryWeight" for all observations in same SaltTreatment in same Generation															
Column M	"AverageDryWeight" for all observations in same SaltTreatment in same Generation															
Column N	"RelativeDryWeight" is calculated as observed DryWeight divided by "AverageDryWeight" (calculated in Column L, then copied into Column M) for all observations in same SaltTreatment in same Generation															
"	THESE ARE THE RELATIVIZED VALUES OF THE DEPENDENT VARIABLE "DRY WEIGHT"															
Column O	"Relative LineAverage" is the average of a line calculated across all relativized replicates in that line															
Column P	"Relative TreatmentAverage" is the average of treatment (averaged across the 5 relativized averages of the 5 lines in each treatment)															
Column W	Relative Fitness 1: Fitness (dry weight) of plant with selected microbiome, relative to average dry weight of Fallow-Soil plants															
Column AE	Relative Fitness 2: Fitness (dry weight) of plant with selected microbiome, relative to average dry weight of Null plants															
###	Generation	Salt	Microbiome	Selection	Plant #	Rack #	Position in Rack	Dry Weight	Line Average	Treatment Average	Average Dry Weight for Salt Treatment of same Generation	Average Dry Weight for Salt Treatment of same Generation	Relative Dry Weight	Relative Line Average	Relative Treatment Average	Treatment Average Ignoring Line-Nesting
0	SOD	Bact	NA	90	1	14	29.5				31.9	0.92			0	Bact SOD
0	SOD	Bact	NA	78	6	23	31.2				31.9	0.98			0	Bact SOD
0	SOD	Bact	NA	41	7	17	33.8				31.9	1.06			0	Bact SOD
0	SOD	Bact	NA	19	8	15	30.4				31.9	0.95			0	Bact SOD
0	SOD	Bact	NA	64	1	1	33.6				31.9	1.05			0	Bact SOD
0	SOD	Bact	NA	29	2	4	26.8				31.9	0.84			0	Bact SOD
0	SOD	Bact	NA	16	3	5	NA				NA	NA			0	Bact SOD
0	SOD	Bact	NA	95	5	7	28.3				31.9	0.89			0	Bact SOD
0	SOD	Bact	NA	69	2	10	30.1				31.9	0.94			0	Bact SOD
0	SOD	Bact	NA	23	3	19	29.7				31.9	0.93			0	Bact SOD
0	SOD	Bact	NA	50	4	7	35.6				31.9	1.12			0	Bact SOD

Supplemental Table S1

Fallow-Soil-Control Relativization of Fitness Data, Averages & StDev										Null-Control Relativization of Fitness Data, Averages & StDev		
Average Dry Weight of Fallow-Soil Plant	Fitness Relative to Average Fallow-Soil Plant	Line-Averages	Averages	St.Dev.	Average Dry Weight of NullPlant	Fitness Relative to Average Null Plant	Line-Averages	Averages	St.Dev.			
NA	NA	NA	NA	NA	32.59	0.91			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.96			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	1.04			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.93			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	1.03			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.82			0	Bact	SOD	
NA	NA	NA	NA	NA	NA	NA			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.87			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.92			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	0.91			0	Bact	SOD	
NA	NA	NA	NA	NA	32.59	1.09			0	Bact	SOD	

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0	SOD	Bact	NA	82	2	18	32.9			31.9	1.03			0	Bact	SOD	
0	SOD	Bact	NA	2	5	25	29.0			31.9	0.91			0	Bact	SOD	
0	SOD	Bact	NA	35	8	19	28.0			31.9	0.88			0	Bact	SOD	
0	SOD	Bact	NA	53	2	5	38.4			31.9	1.20			0	Bact	SOD	
0	SOD	Bact	NA	93	3	23	27.0			31.9	0.85			0	Bact	SOD	
0	SOD	Bact	NA	62	6	3	32.3			31.9	1.01			0	Bact	SOD	
0	SOD	Bact	NA	71	1	16	29.5			31.9	0.92			0	Bact	SOD	
0	SOD	Bact	NA	18	3	20	25.5			31.9	0.80			0	Bact	SOD	
0	SOD	Bact	NA	1	4	19	32.5			31.9	1.02			0	Bact	SOD	
0	SOD	Bact	NA	24	5	5	32.9			31.9	1.03			0	Bact	SOD	
0	SOD	Bact	NA	12	6	9	31.6			31.9	0.99			0	Bact	SOD	
0	SOD	Bact	NA	88	3	14	34.9			31.9	1.09			0	Bact	SOD	
0	SOD	Bact	NA	31	5	9	33.5			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	32	6	14	36.2			31.9	1.13			0	Bact	SOD	
0	SOD	Bact	NA	48	8	4	35.9			31.9	1.13			0	Bact	SOD	
0	SOD	Bact	NA	61	3	9	31.1			31.9	0.97			0	Bact	SOD	
0	SOD	Bact	NA	89	4	11	26.3			31.9	0.82			0	Bact	SOD	
0	SOD	Bact	NA	17	8	11	26.1			31.9	0.82			0	Bact	SOD	
0	SOD	Bact	NA	37	5	22	35.2			31.9	1.10			0	Bact	SOD	
0	SOD	Bact	NA	22	8	22	35.8			31.9	1.12			0	Bact	SOD	
0	SOD	Bact	NA	99	1	4	34.5			31.9	1.08			0	Bact	SOD	
0	SOD	Bact	NA	45	6	19	30.8			31.9	0.97			0	Bact	SOD	
0	SOD	Bact	NA	38	3	12	33.0			31.9	1.03			0	Bact	SOD	
0	SOD	Bact	NA	25	4	6	33.1			31.9	1.04			0	Bact	SOD	
0	SOD	Bact	NA	15	5	18	29.3			31.9	0.92			0	Bact	SOD	
0	SOD	Bact	NA	14	2	11	33.4			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	26	5	8	34.2			31.9	1.07			0	Bact	SOD	
0	SOD	Bact	NA	79	8	12	NA			NA	NA			0	Bact	SOD	
0	SOD	Bact	NA	47	2	24	33.4			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	40	6	24	33.3			31.9	1.04			0	Bact	SOD	
0	SOD	Bact	NA	7	7	25	33.5			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	13	1	10	27.3			31.9	0.86			0	Bact	SOD	
0	SOD	Bact	NA	36	6	10	29.5			31.9	0.92			0	Bact	SOD	
0	SOD	Bact	NA	85	2	9	29.9			31.9	0.94			0	Bact	SOD	
0	SOD	Bact	NA	92	4	24	27.0			31.9	0.85			0	Bact	SOD	
0	SOD	Bact	NA	55	7	12	35.0			31.9	1.10			0	Bact	SOD	
0	SOD	Bact	NA	21	1	6	28.1			31.9	0.88			0	Bact	SOD	
0	SOD	Bact	NA	27	6	20	32.4			31.9	1.02			0	Bact	SOD	
0	SOD	Bact	NA	57	8	6	32.4			31.9	1.02			0	Bact	SOD	
0	SOD	Bact	NA	67	1	25	32.8			31.9	1.03			0	Bact	SOD	
0	SOD	Bact	NA	81	2	7	34.8			31.9	1.09			0	Bact	SOD	
0	SOD	Bact	NA	20	3	7	33.6			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	74	5	16	25.7			31.9	0.81			0	Bact	SOD	
0	SOD	Bact	NA	65	6	4	26.8			31.9	0.84			0	Bact	SOD	
0	SOD	Bact	NA	6	7	15	31.2			31.9	0.98			0	Bact	SOD	
0	SOD	Bact	NA	94	2	8	36.3			31.9	1.14			0	Bact	SOD	
0	SOD	Bact	NA	84	3	17	32.5			31.9	1.02			0	Bact	SOD	
0	SOD	Bact	NA	9	8	13	33.9			31.9	1.06			0	Bact	SOD	
0	SOD	Bact	NA	66	2	12	33.5			31.9	1.05			0	Bact	SOD	
0	SOD	Bact	NA	60	7	7	31.4			31.9	0.98			0	Bact	SOD	
0	SOD	Bact	NA	43	8	7	38.0			31.9	1.19			0	Bact	SOD	
0	SOD	Bact	NA	98	2	15	25.8			31.9	0.81			0	Bact	SOD	
0	SOD	Bact	NA	72	4	12	33.4			31.9	1.05			0	Bact	SOD	

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NA	NA	NA	NA	NA	32.59	1.01				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.89				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.86				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.18				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.83				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.99				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.91				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.78				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.00				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.01				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.97				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.07				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.03				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.11				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.10				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.95				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.81				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.80				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.08				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.10				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.06				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.95				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.01				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.02				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.90				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.02				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.05				0	Bact	SOD
NA	NA	NA	NA	NA	NA	NA				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.02				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.02				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.03				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.84				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.91				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.92				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.83				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.07				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.86				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.99				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.99				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.01				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.07				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.03				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.79				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.82				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.11				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.00				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.04				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.03				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.17				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.79				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.02				0	Bact	SOD

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0	SOD	Bact	NA	91	4	23	32.2			31.9	1.01			0	Bact	SOD	
0	SOD	Bact	NA	49	5	19	30.5			31.9	0.96			0	Bact	SOD	
0	SOD	Bact	NA	46	7	9	32.8			31.9	1.03			0	Bact	SOD	
0	SOD	Bact	NA	44	1	21	26.0			31.9	0.82			0	Bact	SOD	
0	SOD	Bact	NA	30	2	19	37.2			31.9	1.17			0	Bact	SOD	
0	SOD	Bact	NA	34	4	2	34.4			31.9	1.08			0	Bact	SOD	
0	SOD	Bact	NA	51	7	8	NA			NA	NA			0	Bact	SOD	
0	SOD	Bact	NA	96	2	23	35.6			31.9	1.12			0	Bact	SOD	
0	SOD	Bact	NA	8	5	14	30.5			31.9	0.96			0	Bact	SOD	
0	SOD	Bact	NA	33	8	18	31.6			31.9	0.99			0	Bact	SOD	
0	SOD	Bact	NA	5	1	24	40.0			31.9	1.25			0	Bact	SOD	
0	SOD	Bact	NA	73	4	3	29.3			31.9	0.92			0	Bact	SOD	
0	SOD	Bact	NA	86	1	2	30.2			31.9	0.95			0	Bact	SOD	
0	SOD	Bact	NA	56	2	13	22.2			31.9	0.70			0	Bact	SOD	
0	SOD	Bact	NA	97	3	22	30.7			31.9	0.96			0	Bact	SOD	
0	SOD	Bact	NA	54	7	13	36.0	31.72		31.9	1.13	0.994		0	Bact	SOD	31.7
0	SOD	Null	NA	42	4	4	30.6			31.9	0.96			0	Null	SOD	
0	SOD	Null	NA	68	6	15	32.2			31.9	1.01			0	Null	SOD	
0	SOD	Null	NA	76	1	7	31.3			31.9	0.98			0	Null	SOD	
0	SOD	Null	NA	39	3	24	31.3			31.9	0.98			0	Null	SOD	
0	SOD	Null	NA	77	7	19	30.6			31.9	0.96			0	Null	SOD	
0	SOD	Null	NA	70	4	22	31.8			31.9	1.00			0	Null	SOD	
0	SOD	Null	NA	11	3	11	40.3			31.9	1.26			0	Null	SOD	
0	SOD	Null	NA	59	2	6	33.9			31.9	1.06			0	Null	SOD	
0	SOD	Null	NA	100	6	25	31.3			31.9	0.98			0	Null	SOD	
0	SOD	Null	NA	63	6	5	32.5			31.9	1.02			0	Null	SOD	
0	SOD	Null	NA	3	5	11	32.0			31.9	1.00			0	Null	SOD	
0	SOD	Null	NA	10	5	1	30.3			31.9	0.95			0	Null	SOD	
0	SOD	Null	NA	75	1	23	35.6			31.9	1.12			0	Null	SOD	
0	SOD	Null	NA	80	3	18	28.1			31.9	0.88			0	Null	SOD	
0	SOD	Null	NA	4	5	15	34.0			31.9	1.07			0	Null	SOD	
0	SOD	Null	NA	58	7	23	32.0			31.9	1.00			0	Null	SOD	
0	SOD	Null	NA	28	2	20	32.6			31.9	1.02			0	Null	SOD	
0	SOD	Null	NA	87	8	2	34.7			31.9	1.09			0	Null	SOD	
0	SOD	Null	NA	52	2	22	31.3		Grand Average	31.9	0.98			0	Null	SOD	
0	SOD	Null	NA	83	6	21	35.4	32.59		31.9	1.11	1.022		0	Null	SOD	32.59
0	ALU	Bact	NA	144	2	25	37.0			33.1	1.12			0	Bact	ALU	
0	ALU	Bact	NA	177	3	1	26.1			33.1	0.79			0	Bact	ALU	
0	ALU	Bact	NA	151	5	17	30.1			33.1	0.91			0	Bact	ALU	
0	ALU	Bact	NA	156	7	3	40.0			33.1	1.21			0	Bact	ALU	
0	ALU	Bact	NA	133	8	21	36.2			33.1	1.09			0	Bact	ALU	
0	ALU	Bact	NA	170	5	2	31.4			33.1	0.95			0	Bact	ALU	
0	ALU	Bact	NA	146	6	18	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	186	7	2	36.0			33.1	1.09			0	Bact	ALU	
0	ALU	Bact	NA	169	8	10	38.5			33.1	1.16			0	Bact	ALU	
0	ALU	Bact	NA	132	4	18	34.7			33.1	1.05			0	Bact	ALU	
0	ALU	Bact	NA	116	6	2	33.9			33.1	1.02			0	Bact	ALU	
0	ALU	Bact	NA	145	1	5	25.6			33.1	0.77			0	Bact	ALU	
0	ALU	Bact	NA	111	4	9	31.9			33.1	0.96			0	Bact	ALU	
0	ALU	Bact	NA	193	7	11	31.6			33.1	0.95			0	Bact	ALU	
0	ALU	Bact	NA	149	2	1	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	153	7	20	34.4			33.1	1.04			0	Bact	ALU	
0	ALU	Bact	NA	147	8	17	31.5			33.1	0.95			0	Bact	ALU	

Supplemental Table S1

NA	NA	NA	NA	NA	32.59	0.99				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.94				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.01				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.80				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.14				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.06				0	Bact	SOD
NA	NA	NA	NA	NA	NA	NA				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.09				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.94				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.97				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.23				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.90				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.93				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.68				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.94				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	1.10				0	Bact	SOD
NA	NA	NA	NA	NA	32.59	0.94				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.99				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.94				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.98				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.24				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.04				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.00				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.98				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.93				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.09				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.86				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.04				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.98				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.00				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.06				0	Null	SOD
NA	NA	NA	NA	NA	32.59	0.96				0	Null	SOD
NA	NA	NA	NA	NA	32.59	1.09				0	Null	SOD
NA	NA	NA	NA	NA	34.21	1.08				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.76				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.88				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.17				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.06				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.05				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.13				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.99				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.75				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.93				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU

Supplemental Table S1

0	ALU	Bact	NA	148	1	20	33.6			33.1	1.02			0	Bact	ALU	
0	ALU	Bact	NA	172	2	16	29.5			33.1	0.89			0	Bact	ALU	
0	ALU	Bact	NA	103	5	24	34.2			33.1	1.03			0	Bact	ALU	
0	ALU	Bact	NA	197	6	6	33.6			33.1	1.02			0	Bact	ALU	
0	ALU	Bact	NA	122	7	4	31.4			33.1	0.95			0	Bact	ALU	
0	ALU	Bact	NA	139	1	17	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	188	2	3	37.5			33.1	1.13			0	Bact	ALU	
0	ALU	Bact	NA	129	4	15	30.4			33.1	0.92			0	Bact	ALU	
0	ALU	Bact	NA	180	2	21	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	123	3	6	34.3			33.1	1.04			0	Bact	ALU	
0	ALU	Bact	NA	112	4	20	34.8			33.1	1.05			0	Bact	ALU	
0	ALU	Bact	NA	159	5	23	34.6			33.1	1.05			0	Bact	ALU	
0	ALU	Bact	NA	114	7	22	21.0			33.1	0.63			0	Bact	ALU	
0	ALU	Bact	NA	162	1	18	34.3			33.1	1.04			0	Bact	ALU	
0	ALU	Bact	NA	195	7	1	35.9			33.1	1.08			0	Bact	ALU	
0	ALU	Bact	NA	124	8	23	39.6			33.1	1.20			0	Bact	ALU	
0	ALU	Bact	NA	189	1	22	31.0			33.1	0.94			0	Bact	ALU	
0	ALU	Bact	NA	137	3	25	27.6			33.1	0.83			0	Bact	ALU	
0	ALU	Bact	NA	131	4	5	28.3			33.1	0.86			0	Bact	ALU	
0	ALU	Bact	NA	198	7	21	29.7			33.1	0.90			0	Bact	ALU	
0	ALU	Bact	NA	173	3	4	31.5			33.1	0.95			0	Bact	ALU	
0	ALU	Bact	NA	175	4	25	32.7			33.1	0.99			0	Bact	ALU	
0	ALU	Bact	NA	187	8	25	29.2			33.1	0.88			0	Bact	ALU	
0	ALU	Bact	NA	140	3	15	27.7			33.1	0.84			0	Bact	ALU	
0	ALU	Bact	NA	200	4	1	36.0			33.1	1.09			0	Bact	ALU	
0	ALU	Bact	NA	135	5	13	26.4			33.1	0.80			0	Bact	ALU	
0	ALU	Bact	NA	199	1	8	38.3			33.1	1.16			0	Bact	ALU	
0	ALU	Bact	NA	127	3	3	37.1			33.1	1.12			0	Bact	ALU	
0	ALU	Bact	NA	105	6	7	33.5			33.1	1.01			0	Bact	ALU	
0	ALU	Bact	NA	181	8	16	30.7			33.1	0.93			0	Bact	ALU	
0	ALU	Bact	NA	196	2	17	39.7			33.1	1.20			0	Bact	ALU	
0	ALU	Bact	NA	110	3	10	29.3			33.1	0.89			0	Bact	ALU	
0	ALU	Bact	NA	171	7	16	33.1			33.1	1.00			0	Bact	ALU	
0	ALU	Bact	NA	163	4	16	30.3			33.1	0.92			0	Bact	ALU	
0	ALU	Bact	NA	125	1	19	41.0			33.1	1.24			0	Bact	ALU	
0	ALU	Bact	NA	138	4	13	42.2			33.1	1.28			0	Bact	ALU	
0	ALU	Bact	NA	160	5	10	28.3			33.1	0.86			0	Bact	ALU	
0	ALU	Bact	NA	119	6	1	29.2			33.1	0.88			0	Bact	ALU	
0	ALU	Bact	NA	104	7	5	33.4			33.1	1.01			0	Bact	ALU	
0	ALU	Bact	NA	191	4	10	34.0			33.1	1.03			0	Bact	ALU	
0	ALU	Bact	NA	141	5	21	32.0			33.1	0.97			0	Bact	ALU	
0	ALU	Bact	NA	161	1	15	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	126	5	6	28.6			33.1	0.86			0	Bact	ALU	
0	ALU	Bact	NA	107	6	16	32.4			33.1	0.98			0	Bact	ALU	
0	ALU	Bact	NA	178	7	14	34.6			33.1	1.05			0	Bact	ALU	
0	ALU	Bact	NA	101	8	1	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	194	1	11	22.9			33.1	0.69			0	Bact	ALU	
0	ALU	Bact	NA	190	2	2	38.6			33.1	1.17			0	Bact	ALU	
0	ALU	Bact	NA	109	3	21	33.3			33.1	1.01			0	Bact	ALU	
0	ALU	Bact	NA	174	6	8	27.8			33.1	0.84			0	Bact	ALU	
0	ALU	Bact	NA	167	8	8	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	143	6	11	31.6			33.1	0.95			0	Bact	ALU	
0	ALU	Bact	NA	182	8	20	33.6			33.1	1.02			0	Bact	ALU	

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NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.86				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.00				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.10				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.89				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.00				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.02				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.61				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.00				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.05				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.16				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.91				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.81				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.83				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.87				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.96				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.85				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.81				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.05				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.77				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.12				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.08				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.90				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.16				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.86				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.97				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.89				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.20				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.23				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.83				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.85				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.99				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.94				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.84				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.95				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.67				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.13				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.97				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.81				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.92				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU

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0	ALU	Bact	NA	183	1	13	35.0			33.1	1.06			0	Bact	ALU	
0	ALU	Bact	NA	158	3	13	29.5			33.1	0.89			0	Bact	ALU	
0	ALU	Bact	NA	155	6	12	36.0			33.1	1.09			0	Bact	ALU	
0	ALU	Bact	NA	184	3	8	39.6			33.1	1.20			0	Bact	ALU	
0	ALU	Bact	NA	113	5	3	33.0			33.1	1.00			0	Bact	ALU	
0	ALU	Bact	NA	176	6	22	NA			NA	NA			0	Bact	ALU	
0	ALU	Bact	NA	166	7	24	29.4			33.1	0.89			0	Bact	ALU	
0	ALU	Bact	NA	136	4	14	34.4			33.1	1.04			0	Bact	ALU	
0	ALU	Bact	NA	150	5	20	34.1			33.1	1.03			0	Bact	ALU	
0	ALU	Bact	NA	134	8	5	33.6	32.83		33.1	1.02	0.992		0	Bact	ALU	32.83
0	ALU	Null	NA	157	4	21	NA			NA	NA			0	Null	ALU	
0	ALU	Null	NA	142	1	9	31.0			33.1	0.94			0	Null	ALU	
0	ALU	Null	NA	152	5	12	NA			NA	NA			0	Null	ALU	
0	ALU	Null	NA	120	8	3	40.7			33.1	1.23			0	Null	ALU	
0	ALU	Null	NA	154	1	12	35.2			33.1	1.06			0	Null	ALU	
0	ALU	Null	NA	128	2	14	NA			NA	NA			0	Null	ALU	
0	ALU	Null	NA	121	7	6	36.2			33.1	1.09			0	Null	ALU	
0	ALU	Null	NA	102	6	17	38.2			33.1	1.15			0	Null	ALU	
0	ALU	Null	NA	164	7	10	34.4			33.1	1.04			0	Null	ALU	
0	ALU	Null	NA	106	8	24	35.6			33.1	1.08			0	Null	ALU	
0	ALU	Null	NA	130	1	3	37.4			33.1	1.13			0	Null	ALU	
0	ALU	Null	NA	117	7	18	34.9			33.1	1.05			0	Null	ALU	
0	ALU	Null	NA	108	8	14	31.8			33.1	0.96			0	Null	ALU	
0	ALU	Null	NA	185	4	17	28.6			33.1	0.86			0	Null	ALU	
0	ALU	Null	NA	165	5	4	25.7			33.1	0.78			0	Null	ALU	
0	ALU	Null	NA	115	8	9	38.2			33.1	1.15			0	Null	ALU	
0	ALU	Null	NA	118	6	13	37.6			33.1	1.14			0	Null	ALU	
0	ALU	Null	NA	179	3	16	31.2			33.1	0.94			0	Null	ALU	
0	ALU	Null	NA	192	3	2	28.0		Grand Average	33.1	0.85			0	Null	ALU	
0	ALU	Null	NA	168	4	8	36.8	34.21		33.1	1.11	1.034		0	Null	ALU	34.21
1	SOD	Pp	1	65	1	24	24.1			18.98	1.27			1	Pp	SOD	
2	SOD	Pp	1	53	2	7	10.1			18.98	0.53			1	Pp	SOD	
3	SOD	Pp	1	75	3	8	19.3			18.98	1.02			1	Pp	SOD	
4	SOD	Pp	1	89	4	6	25.4			18.98	1.34			1	Pp	SOD	
5	SOD	Pp	1	71	5	21	NA			NA	NA			1	Pp	SOD	
6	SOD	Pp	1	88	6	22	17.8			18.98	0.94			1	Pp	SOD	
7	SOD	Pp	1	70	7	24	25.6			18.98	1.35			1	Pp	SOD	
8	SOD	Pp	1	86	8	19	NA	20.38		NA	NA	1.074		1	Pp	SOD	
9	SOD	Pp	2	97	1	7	21.5			18.98	1.13			1	Pp	SOD	
10	SOD	Pp	2	69	2	14	20.2			18.98	1.06			1	Pp	SOD	
11	SOD	Pp	2	31	3	14	19.5			18.98	1.03			1	Pp	SOD	
12	SOD	Pp	2	61	4	25	19.6			18.98	1.03			1	Pp	SOD	
13	SOD	Pp	2	49	5	5	21.7			18.98	1.14			1	Pp	SOD	
14	SOD	Pp	2	11	6	25	19.7			18.98	1.04			1	Pp	SOD	
15	SOD	Pp	2	66	7	13	19.7			18.98	1.04			1	Pp	SOD	
16	SOD	Pp	2	67	8	3	16.0	19.74		18.98	0.84	1.040		1	Pp	SOD	
17	SOD	Pp	3	3	1	3	21.1			18.98	1.11			1	Pp	SOD	
18	SOD	Pp	3	72	2	21	21.4			18.98	1.13			1	Pp	SOD	
19	SOD	Pp	3	8	3	17	21.7			18.98	1.14			1	Pp	SOD	
20	SOD	Pp	3	2	4	7	22.1			18.98	1.16			1	Pp	SOD	
21	SOD	Pp	3	54	5	12	15.3			18.98	0.81			1	Pp	SOD	
22	SOD	Pp	3	40	6	17	26.5			18.98	1.40			1	Pp	SOD	
23	SOD	Pp	3	42	7	7	22.1			18.98	1.16			1	Pp	SOD	

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NA	NA	NA	NA	NA	34.21	1.02				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.86				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.05				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.16				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.96				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.86				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	1.00				0	Bact	ALU
NA	NA	NA	NA	NA	34.21	0.98				0	Bact	ALU
NA	NA	NA	NA	NA	NA	NA				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.91				0	Null	ALU
NA	NA	NA	NA	NA	NA	NA				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.19				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.03				0	Null	ALU
NA	NA	NA	NA	NA	NA	NA				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.06				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.12				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.01				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.04				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.09				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.02				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.93				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.84				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.75				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.12				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.10				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.91				0	Null	ALU
NA	NA	NA	NA	NA	34.21	0.82				0	Null	ALU
NA	NA	NA	NA	NA	34.21	1.08				0	Null	ALU
16.54	1.46				22.07	1.09				1	Pp	SOD
16.54	0.61				22.07	0.46				1	Pp	SOD
16.54	1.17				22.07	0.87				1	Pp	SOD
16.54	1.54				22.07	1.15				1	Pp	SOD
NA	NA				NA	NA				1	Pp	SOD
16.54	1.08				22.07	0.81				1	Pp	SOD
16.54	1.55				22.07	1.16				1	Pp	SOD
NA	NA	1.232			NA	NA	0.924			1	Pp	SOD
16.54	1.30				22.07	0.97				1	Pp	SOD
16.54	1.22				22.07	0.92				1	Pp	SOD
16.54	1.18				22.07	0.88				1	Pp	SOD
16.54	1.18				22.07	0.89				1	Pp	SOD
16.54	1.31				22.07	0.98				1	Pp	SOD
16.54	1.19				22.07	0.89				1	Pp	SOD
16.54	1.19				22.07	0.89				1	Pp	SOD
16.54	0.97	1.193			22.07	0.72	0.894			1	Pp	SOD
16.54	1.28				22.07	0.96				1	Pp	SOD
16.54	1.29				22.07	0.97				1	Pp	SOD
16.54	1.31				22.07	0.98				1	Pp	SOD
16.54	1.34				22.07	1.00				1	Pp	SOD
16.54	0.92				22.07	0.69				1	Pp	SOD
16.54	1.60				22.07	1.20				1	Pp	SOD
16.54	1.34				22.07	1.00				1	Pp	SOD

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24	1	SOD	Pp	3	45	8	11	23.8	21.75			18.98	1.25	1.146		1	Pp	SOD	
25	1	SOD	Pp	4	34	1	14	24.5				18.98	1.29			1	Pp	SOD	
26	1	SOD	Pp	4	41	2	22	21.5				18.98	1.13			1	Pp	SOD	
27	1	SOD	Pp	4	26	3	20	22.3				18.98	1.18			1	Pp	SOD	
28	1	SOD	Pp	4	7	4	23	NA				NA	NA			1	Pp	SOD	
29	1	SOD	Pp	4	87	5	7	20.0				18.98	1.05			1	Pp	SOD	
30	1	SOD	Pp	4	33	6	1	19.4				18.98	1.02			1	Pp	SOD	
31	1	SOD	Pp	4	50	7	14	18.6				18.98	0.98			1	Pp	SOD	
32	1	SOD	Pp	4	51	8	5	22.7	21.29			18.98	1.20	1.122		1	Pp	SOD	
33	1	SOD	Pp	5	56	1	15	22.1				18.98	1.16			1	Pp	SOD	
34	1	SOD	Pp	5	48	2	20	NA				NA	NA			1	Pp	SOD	
35	1	SOD	Pp	5	78	3	25	18.0				18.98	0.95			1	Pp	SOD	
36	1	SOD	Pp	5	57	4	4	19.5				18.98	1.03			1	Pp	SOD	
37	1	SOD	Pp	5	81	5	8	20.9				18.98	1.10			1	Pp	SOD	
38	1	SOD	Pp	5	24	6	16	20.2				18.98	1.06			1	Pp	SOD	
39	1	SOD	Pp	5	35	7	2	24.3				18.98	1.28			1	Pp	SOD	
40	1	SOD	Pp	5	64	8	13	NA	20.83	20.80		NA	NA	1.098	1.096	1	Pp	SOD	20.81
41	1	SOD	Np	1	6	1	16	16.7				18.98	0.88			1	Np	SOD	
42	1	SOD	Np	1	29	2	23	16.4				18.98	0.86			1	Np	SOD	
43	1	SOD	Np	1	68	3	6	10.7				18.98	0.56			1	Np	SOD	
44	1	SOD	Np	1	93	4	17	NA				NA	NA			1	Np	SOD	
45	1	SOD	Np	1	9	5	1	15.5				18.98	0.82			1	Np	SOD	
46	1	SOD	Np	1	59	6	2	16.6				18.98	0.87			1	Np	SOD	
47	1	SOD	Np	1	38	7	1	8.7				18.98	0.46			1	Np	SOD	
48	1	SOD	Np	1	4	8	22	16.0	14.37			18.98	0.84	0.757		1	Np	SOD	
49	1	SOD	Np	2	98	1	18	17.0				18.98	0.90			1	Np	SOD	
50	1	SOD	Np	2	84	2	16	17.4				18.98	0.92			1	Np	SOD	
51	1	SOD	Np	2	18	3	11	20.9				18.98	1.10			1	Np	SOD	
52	1	SOD	Np	2	99	4	18	16.0				18.98	0.84			1	Np	SOD	
53	1	SOD	Np	2	46	5	4	18.8				18.98	0.99			1	Np	SOD	
54	1	SOD	Np	2	90	6	5	20.1				18.98	1.06			1	Np	SOD	
55	1	SOD	Np	2	94	7	25	13.8				18.98	0.73			1	Np	SOD	
56	1	SOD	Np	2	91	8	7	16.9	17.61			18.98	0.89	0.928		1	Np	SOD	
57	1	SOD	Np	3	5	1	10	12.4				18.98	0.65			1	Np	SOD	
58	1	SOD	Np	3	100	2	1	11.2				18.98	0.59			1	Np	SOD	
59	1	SOD	Np	3	1	3	12	22.4				18.98	1.18			1	Np	SOD	
60	1	SOD	Np	3	25	4	11	17.2				18.98	0.91			1	Np	SOD	
61	1	SOD	Np	3	39	5	18	18.9				18.98	1.00			1	Np	SOD	
62	1	SOD	Np	3	13	6	3	14.4				18.98	0.76			1	Np	SOD	
63	1	SOD	Np	3	44	7	9	17.8				18.98	0.94			1	Np	SOD	
64	1	SOD	Np	3	28	8	20	13.4	15.96			18.98	0.71	0.841		1	Np	SOD	
65	1	SOD	Np	4	32	1	2	19.7				18.98	1.04			1	Np	SOD	
66	1	SOD	Np	4	52	2	25	17.9				18.98	0.94			1	Np	SOD	
67	1	SOD	Np	4	10	3	10	17.3				18.98	0.91			1	Np	SOD	
68	1	SOD	Np	4	77	4	3	17.1				18.98	0.90			1	Np	SOD	
69	1	SOD	Np	4	83	5	9	10.4				18.98	0.55			1	Np	SOD	
70	1	SOD	Np	4	23	6	11	17.0				18.98	0.90			1	Np	SOD	
71	1	SOD	Np	4	30	7	3	17.5				18.98	0.92			1	Np	SOD	
72	1	SOD	Np	4	37	8	9	20.0	17.11			18.98	1.05	0.902		1	Np	SOD	
73	1	SOD	Np	5	79	1	4	18.8				18.98	0.99			1	Np	SOD	
74	1	SOD	Np	5	82	2	12	15.7				18.98	0.83			1	Np	SOD	
75	1	SOD	Np	5	76	3	7	11.2				18.98	0.59			1	Np	SOD	
76	1	SOD	Np	5	17	4	5	12.4				18.98	0.65			1	Np	SOD	

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77	1	SOD	Np	5	62	5	19	23.2				18.98	1.22				1	Np	SOD	
78	1	SOD	Np	5	58	6	13	21.7				18.98	1.14				1	Np	SOD	
79	1	SOD	Np	5	55	7	23	19.5				18.98	1.03				1	Np	SOD	
80	1	SOD	Np	5	12	8	2	16.5	17.38	16.49		18.98	0.87	0.916	0.869		1	Np	SOD	16.54
91	1	SOD	Null	NA	96	1	21	21.6				18.98	1.14				1	Null	SOD	
92	1	SOD	Null	NA	22	2	15	24.5				18.98	1.29				1	Null	SOD	
93	1	SOD	Null	NA	95	3	4	22.9				18.98	1.21				1	Null	SOD	
94	1	SOD	Null	NA	85	4	12	20.8				18.98	1.10				1	Null	SOD	
95	1	SOD	Null	NA	15	5	17	18.6				18.98	0.98				1	Null	SOD	
96	1	SOD	Null	NA	16	6	19	24.6				18.98	1.30				1	Null	SOD	
97	1	SOD	Null	NA	73	7	11	17.3				18.98	0.91				1	Null	SOD	
98	1	SOD	Null	NA	60	8	12	24.6				18.98	1.30				1	Null	SOD	
99	1	SOD	Null	NA	74	3	16	25.2		Grand Average		18.98	1.33				1	Null	SOD	
100	1	SOD	Null	NA	14	8	23	20.6	22.07		18.98	18.98	1.09	1.163		1	Null	SOD	22.07	
101	1	ALU	Pp	1	183	1	6	9.0				20.16	0.45				1	Pp	ALU	
102	1	ALU	Pp	1	190	2	17	19.5				20.16	0.97				1	Pp	ALU	
103	1	ALU	Pp	1	139	3	18	24.6				20.16	1.22				1	Pp	ALU	
104	1	ALU	Pp	1	149	4	24	28.1				20.16	1.39				1	Pp	ALU	
105	1	ALU	Pp	1	152	5	10	21.6				20.16	1.07				1	Pp	ALU	
106	1	ALU	Pp	1	146	6	4	18.6				20.16	0.92				1	Pp	ALU	
107	1	ALU	Pp	1	192	7	22	NA				NA	NA				1	Pp	ALU	
108	1	ALU	Pp	1	188	8	24	25.1	20.93			20.16	1.24	1.038			1	Pp	ALU	
109	1	ALU	Pp	2	131	1	12	24.7				20.16	1.23				1	Pp	ALU	
110	1	ALU	Pp	2	128	2	6	27.7				20.16	1.37				1	Pp	ALU	
111	1	ALU	Pp	2	122	3	19	20.6				20.16	1.02				1	Pp	ALU	
112	1	ALU	Pp	2	159	4	22	19.7				20.16	0.98				1	Pp	ALU	
113	1	ALU	Pp	2	196	5	20	NA				NA	NA				1	Pp	ALU	
114	1	ALU	Pp	2	123	6	9	NA				NA	NA				1	Pp	ALU	
115	1	ALU	Pp	2	127	7	5	22.3				20.16	1.11				1	Pp	ALU	
116	1	ALU	Pp	2	138	8	15	19.3	22.38			20.16	0.96	1.110			1	Pp	ALU	
117	1	ALU	Pp	3	160	1	23	11.2				20.16	0.56				1	Pp	ALU	
118	1	ALU	Pp	3	187	2	4	14.3				20.16	0.71				1	Pp	ALU	
119	1	ALU	Pp	3	162	3	22	25.7				20.16	1.27				1	Pp	ALU	
120	1	ALU	Pp	3	110	4	15	27.5				20.16	1.36				1	Pp	ALU	
121	1	ALU	Pp	3	125	5	11	22.1				20.16	1.10				1	Pp	ALU	
122	1	ALU	Pp	3	191	6	21	23.8				20.16	1.18				1	Pp	ALU	
123	1	ALU	Pp	3	165	7	4	21.0				20.16	1.04				1	Pp	ALU	
124	1	ALU	Pp	3	151	8	8	25.4	21.38			20.16	1.26	1.060			1	Pp	ALU	
125	1	ALU	Pp	4	120	1	19	24.0				20.16	1.19				1	Pp	ALU	
126	1	ALU	Pp	4	129	2	9	25.2				20.16	1.25				1	Pp	ALU	
127	1	ALU	Pp	4	168	3	2	23.5				20.16	1.17				1	Pp	ALU	
128	1	ALU	Pp	4	142	4	10	17.1				20.16	0.85				1	Pp	ALU	
129	1	ALU	Pp	4	137	5	24	19.6				20.16	0.97				1	Pp	ALU	
130	1	ALU	Pp	4	181	6	8	NA				NA	NA				1	Pp	ALU	
131	1	ALU	Pp	4	166	7	19	23.8				20.16	1.18				1	Pp	ALU	
132	1	ALU	Pp	4	194	8	18	26.0	22.74			20.16	1.29	1.128			1	Pp	ALU	
133	1	ALU	Pp	5	150	1	22	25.9				20.16	1.28				1	Pp	ALU	
134	1	ALU	Pp	5	174	2	13	24.4				20.16	1.21				1	Pp	ALU	
135	1	ALU	Pp	5	133	3	5	22.0				20.16	1.09				1	Pp	ALU	
136	1	ALU	Pp	5	154	4	19	23.4				20.16	1.16				1	Pp	ALU	
137	1	ALU	Pp	5	126	5	14	17.1				20.16	0.85				1	Pp	ALU	
138	1	ALU	Pp	5	161	6	7	NA				NA	NA				1	Pp	ALU	
139	1	ALU	Pp	5	167	7	6	21.0				20.16	1.04				1	Pp	ALU	

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140	1	ALU	Pp	5	147	8	25	26.4	22.89	22.06			20.16	1.31	1.135	1.094	1	Pp	ALU	22.03
141	1	ALU	Np	1	169	1	17	18.1					20.16	0.90			1	Np	ALU	
142	1	ALU	Np	1	105	2	3	15.4					20.16	0.76			1	Np	ALU	
143	1	ALU	Np	1	113	3	3	NA					NA	NA			1	Np	ALU	
144	1	ALU	Np	1	104	4	14	19.5					20.16	0.97			1	Np	ALU	
145	1	ALU	Np	1	134	5	2	18.6					20.16	0.92			1	Np	ALU	
146	1	ALU	Np	1	182	6	20	16.2					20.16	0.80			1	Np	ALU	
147	1	ALU	Np	1	144	7	15	21.6					20.16	1.07			1	Np	ALU	
148	1	ALU	Np	1	141	8	16	7.0	16.63				20.16	0.35	0.825		1	Np	ALU	
149	1	ALU	Np	2	115	1	9	19.6					20.16	0.97			1	Np	ALU	
150	1	ALU	Np	2	163	2	11	20.5					20.16	1.02			1	Np	ALU	
151	1	ALU	Np	2	106	3	15	17.1					20.16	0.85			1	Np	ALU	
152	1	ALU	Np	2	177	4	1	20.0					20.16	0.99			1	Np	ALU	
153	1	ALU	Np	2	197	5	15	14.5					20.16	0.72			1	Np	ALU	
154	1	ALU	Np	2	136	6	14	18.3					20.16	0.91			1	Np	ALU	
155	1	ALU	Np	2	155	7	12	18.6					20.16	0.92			1	Np	ALU	
156	1	ALU	Np	2	170	8	21	22.2	18.85				20.16	1.10	0.935		1	Np	ALU	
157	1	ALU	Np	3	112	1	13	NA					NA	NA			1	Np	ALU	
158	1	ALU	Np	3	200	2	10	20.4					20.16	1.01			1	Np	ALU	
159	1	ALU	Np	3	101	3	21	19.1					20.16	0.95			1	Np	ALU	
160	1	ALU	Np	3	178	4	21	19.5					20.16	0.97			1	Np	ALU	
161	1	ALU	Np	3	102	5	6	18.7					20.16	0.93			1	Np	ALU	
162	1	ALU	Np	3	140	6	23	17.3					20.16	0.86			1	Np	ALU	
163	1	ALU	Np	3	153	7	8	19.1					20.16	0.95			1	Np	ALU	
164	1	ALU	Np	3	158	8	4	20.2	19.19				20.16	1.00	0.952		1	Np	ALU	
165	1	ALU	Np	4	184	1	25	16.1					20.16	0.80			1	Np	ALU	
166	1	ALU	Np	4	107	2	2	19.1					20.16	0.95			1	Np	ALU	
167	1	ALU	Np	4	109	3	24	14.0					20.16	0.69			1	Np	ALU	
168	1	ALU	Np	4	180	4	2	17.9					20.16	0.89			1	Np	ALU	
169	1	ALU	Np	4	118	5	25	12.2					20.16	0.61			1	Np	ALU	
170	1	ALU	Np	4	114	6	12	17.1					20.16	0.85			1	Np	ALU	
171	1	ALU	Np	4	124	7	17	21.0					20.16	1.04			1	Np	ALU	
172	1	ALU	Np	4	185	8	17	20.7	17.26				20.16	1.03	0.856		1	Np	ALU	
173	1	ALU	Np	5	189	1	8	NA					NA	NA			1	Np	ALU	
174	1	ALU	Np	5	148	2	5	15.9					20.16	0.79			1	Np	ALU	
175	1	ALU	Np	5	176	3	9	15.9					20.16	0.79			1	Np	ALU	
176	1	ALU	Np	5	117	4	16	14.9					20.16	0.74			1	Np	ALU	
177	1	ALU	Np	5	199	5	13	13.5					20.16	0.67			1	Np	ALU	
178	1	ALU	Np	5	111	6	10	22.1					20.16	1.10			1	Np	ALU	
179	1	ALU	Np	5	172	7	16	18.8					20.16	0.93			1	Np	ALU	
180	1	ALU	Np	5	143	8	6	18.1	17.03	17.79			20.16	0.90	0.845	0.882	1	Np	ALU	17.81
191	1	ALU	Null	NA	119	1	5	21.1					20.16	1.05			1	Null	ALU	
192	1	ALU	Null	NA	145	2	18	27.9					20.16	1.38			1	Null	ALU	
193	1	ALU	Null	NA	130	3	23	22.2					20.16	1.10			1	Null	ALU	
194	1	ALU	Null	NA	108	4	20	18.1					20.16	0.90			1	Null	ALU	
195	1	ALU	Null	NA	156	5	22	21.6					20.16	1.07			1	Null	ALU	
196	1	ALU	Null	NA	195	6	6	20.5					20.16	1.02			1	Null	ALU	
197	1	ALU	Null	NA	164	7	21	20.2					20.16	1.00			1	Null	ALU	
198	1	ALU	Null	NA	121	8	10	23.0					20.16	1.14			1	Null	ALU	
199	1	ALU	Null	NA	186	2	19	26.0		Grand Average			20.16	1.29			1	Null	ALU	
200	1	ALU	Null	NA	103	5	23	22.6	22.32		20.16		20.16	1.12	1.107		1	Null	ALU	22.32
1	2	SOD	Pp	1	79	1	24	27.5					19.25	1.43			2	Pp	SOD	
2	2	SOD	Pp	1	100	2	22	23.2					19.25	1.21			2	Pp	SOD	

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3	2	SOD	Pp	1	26	3	17	NA				NA	NA			2	Pp	SOD	
4	2	SOD	Pp	1	6	4	10	23.3				19.25	1.21			2	Pp	SOD	
5	2	SOD	Pp	1	29	5	16	22.1				19.25	1.15			2	Pp	SOD	
6	2	SOD	Pp	1	98	6	7	25.5				19.25	1.32			2	Pp	SOD	
7	2	SOD	Pp	1	46	7	21	23.9				19.25	1.24			2	Pp	SOD	
8	2	SOD	Pp	1	5	8	3	27.2	24.67			19.25	1.41	1.282		2	Pp	SOD	
9	2	SOD	Pp	2	96	1	20	25.5				19.25	1.32			2	Pp	SOD	
10	2	SOD	Pp	2	22	2	11	21.5				19.25	1.12			2	Pp	SOD	
11	2	SOD	Pp	2	14	3	19	27.6				19.25	1.43			2	Pp	SOD	
12	2	SOD	Pp	2	49	4	11	NA				NA	NA			2	Pp	SOD	
13	2	SOD	Pp	2	38	5	2	25.7				19.25	1.34			2	Pp	SOD	
14	2	SOD	Pp	2	78	6	3	26.7				19.25	1.39			2	Pp	SOD	
15	2	SOD	Pp	2	30	7	20	21.9				19.25	1.14			2	Pp	SOD	
16	2	SOD	Pp	2	11	8	19	23.3	24.60			19.25	1.21	1.278		2	Pp	SOD	
17	2	SOD	Pp	3	54	1	1	26.5				19.25	1.38			2	Pp	SOD	
18	2	SOD	Pp	3	13	2	10	NA				NA	NA			2	Pp	SOD	
19	2	SOD	Pp	3	80	3	8	29.1				19.25	1.51			2	Pp	SOD	
20	2	SOD	Pp	3	92	4	4	25.7				19.25	1.34			2	Pp	SOD	
21	2	SOD	Pp	3	39	5	5	27.5				19.25	1.43			2	Pp	SOD	
22	2	SOD	Pp	3	88	6	21	25.3				19.25	1.31			2	Pp	SOD	
23	2	SOD	Pp	3	18	7	4	26.3				19.25	1.37			2	Pp	SOD	
24	2	SOD	Pp	3	9	8	7	25.0	26.49			19.25	1.30	1.376		2	Pp	SOD	
25	2	SOD	Pp	4	21	1	10	25.9				19.25	1.35			2	Pp	SOD	
26	2	SOD	Pp	4	60	2	25	30.5				19.25	1.58			2	Pp	SOD	
27	2	SOD	Pp	4	47	3	2	25.4				19.25	1.32			2	Pp	SOD	
28	2	SOD	Pp	4	43	4	8	28.9				19.25	1.50			2	Pp	SOD	
29	2	SOD	Pp	4	12	5	7	21.7				19.25	1.13			2	Pp	SOD	
30	2	SOD	Pp	4	42	6	16	23.3				19.25	1.21			2	Pp	SOD	
31	2	SOD	Pp	4	99	7	23	25.7				19.25	1.34			2	Pp	SOD	
32	2	SOD	Pp	4	25	8	11	25.7	25.89			19.25	1.34	1.345		2	Pp	SOD	
33	2	SOD	Pp	5	69	1	15	25.1				19.25	1.30			2	Pp	SOD	
34	2	SOD	Pp	5	95	2	6	19.8				19.25	1.03			2	Pp	SOD	
35	2	SOD	Pp	5	36	3	15	20.5				19.25	1.07			2	Pp	SOD	
36	2	SOD	Pp	5	66	4	3	23.2				19.25	1.21			2	Pp	SOD	
37	2	SOD	Pp	5	89	5	23	24.6				19.25	1.28			2	Pp	SOD	
38	2	SOD	Pp	5	97	6	17	22.2				19.25	1.15			2	Pp	SOD	
39	2	SOD	Pp	5	59	7	2	25.5				19.25	1.32			2	Pp	SOD	
40	2	SOD	Pp	5	63	8	20	21.0	22.74	24.88		19.25	1.09	1.181	1.292	2	Pp	SOD	24.85
41	2	SOD	Np	1	81	1	18	17.6				19.25	0.91			2	Np	SOD	
42	2	SOD	Np	1	61	2	18	NA				NA	NA			2	Np	SOD	
43	2	SOD	Np	1	76	3	21	0.8				19.25	0.04			2	Np	SOD	
44	2	SOD	Np	1	48	4	16	15.9				19.25	0.83			2	Np	SOD	
45	2	SOD	Np	1	57	5	14	16.8				19.25	0.87			2	Np	SOD	
46	2	SOD	Np	1	24	6	15	14.9				19.25	0.77			2	Np	SOD	
47	2	SOD	Np	1	90	7	11	18.4				19.25	0.96			2	Np	SOD	
48	2	SOD	Np	1	34	8	22	1.4	12.26			19.25	0.07	0.637		2	Np	SOD	
49	2	SOD	Np	2	94	1	8	1.1				19.25	0.06			2	Np	SOD	
50	2	SOD	Np	2	56	2	23	17.3				19.25	0.90			2	Np	SOD	
51	2	SOD	Np	2	31	3	24	21.6				19.25	1.12			2	Np	SOD	
52	2	SOD	Np	2	87	4	17	19.3				19.25	1.00			2	Np	SOD	
53	2	SOD	Np	2	20	5	15	3.0				19.25	0.16			2	Np	SOD	
54	2	SOD	Np	2	23	6	14	0.5				19.25	0.03			2	Np	SOD	
55	2	SOD	Np	2	41	7	5	19.2				19.25	1.00			2	Np	SOD	

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56	2	SOD	Np	2	72	8	2	9.4	11.43			19.25	0.49	0.594		2	Np	SOD	
57	2	SOD	Np	3	28	1	4	22.2				19.25	1.15			2	Np	SOD	
58	2	SOD	Np	3	73	2	8	17.3				19.25	0.90			2	Np	SOD	
59	2	SOD	Np	3	17	3	1	3.0				19.25	0.16			2	Np	SOD	
60	2	SOD	Np	3	82	4	1	NA				NA	NA			2	Np	SOD	
61	2	SOD	Np	3	15	5	25	NA				NA	NA			2	Np	SOD	
62	2	SOD	Np	3	93	6	5	19.2				19.25	1.00			2	Np	SOD	
63	2	SOD	Np	3	8	7	19	NA				NA	NA			2	Np	SOD	
64	2	SOD	Np	3	1	8	16	15.8	15.50			19.25	0.82	0.805		2	Np	SOD	
65	2	SOD	Np	4	75	1	21	11.6				19.25	0.60			2	Np	SOD	
66	2	SOD	Np	4	86	2	15	15.2				19.25	0.79			2	Np	SOD	
67	2	SOD	Np	4	37	3	13	18.4				19.25	0.96			2	Np	SOD	
68	2	SOD	Np	4	53	4	12	21.1				19.25	1.10			2	Np	SOD	
69	2	SOD	Np	4	74	5	13	15.8				19.25	0.82			2	Np	SOD	
70	2	SOD	Np	4	2	6	12	3.0				19.25	0.16			2	Np	SOD	
71	2	SOD	Np	4	40	7	6	0.8				19.25	0.04			2	Np	SOD	
72	2	SOD	Np	4	4	8	14	10.5	12.05			19.25	0.55	0.626		2	Np	SOD	
73	2	SOD	Np	5	83	1	13	14.7				19.25	0.76			2	Np	SOD	
74	2	SOD	Np	5	64	2	7	16.2				19.25	0.84			2	Np	SOD	
75	2	SOD	Np	5	62	3	3	0.6				19.25	0.03			2	Np	SOD	
76	2	SOD	Np	5	33	4	14	NA				NA	NA			2	Np	SOD	
77	2	SOD	Np	5	10	5	20	16.3				19.25	0.85			2	Np	SOD	
78	2	SOD	Np	5	71	6	1	3.7				19.25	0.19			2	Np	SOD	
79	2	SOD	Np	5	45	7	15	17.6				19.25	0.91			2	Np	SOD	
80	2	SOD	Np	5	91	8	5	12.8	11.70	12.59		19.25	0.67	0.608	0.654	2	Np	SOD	12.37
91	2	SOD	Null	NA	77	1	7	27.8				19.25	1.44			2	Null	SOD	
92	2	SOD	Null	NA	51	2	16	23.6				19.25	1.23			2	Null	SOD	
93	2	SOD	Null	NA	68	3	5	23.0				19.25	1.19			2	Null	SOD	
94	2	SOD	Null	NA	16	4	25	22.8				19.25	1.18			2	Null	SOD	
95	2	SOD	Null	NA	84	5	1	17.7				19.25	0.92			2	Null	SOD	
96	2	SOD	Null	NA	65	6	8	23.5				19.25	1.22			2	Null	SOD	
97	2	SOD	Null	NA	50	7	14	22.7				19.25	1.18			2	Null	SOD	
98	2	SOD	Null	NA	7	8	8	23.4				19.25	1.22			2	Null	SOD	
99	2	SOD	Null	NA	32	3	22	22.0		Grand Average		19.25	1.14			2	Null	SOD	
100	2	SOD	Null	NA	70	6	20	19.5	22.60		19.25	19.25	1.01	1.174		2	Null	SOD	22.60
101	2	ALU	Pp	1	143	1	19	28.2				25.64	1.10			2	Pp	ALU	
102	2	ALU	Pp	1	117	2	12	NA				NA	NA			2	Pp	ALU	
103	2	ALU	Pp	1	125	3	16	21.4				25.64	0.83			2	Pp	ALU	
104	2	ALU	Pp	1	103	4	13	22.6				25.64	0.88			2	Pp	ALU	
105	2	ALU	Pp	1	174	5	8	26.7				25.64	1.04			2	Pp	ALU	
106	2	ALU	Pp	1	190	6	10	25.5				25.64	0.99			2	Pp	ALU	
107	2	ALU	Pp	1	196	7	18	33.8				25.64	1.32			2	Pp	ALU	
108	2	ALU	Pp	1	105	8	25	28.8	26.71			25.64	1.12	1.042		2	Pp	ALU	
109	2	ALU	Pp	2	186	1	23	31.3				25.64	1.22			2	Pp	ALU	
110	2	ALU	Pp	2	162	2	5	15.2				25.64	0.59			2	Pp	ALU	
111	2	ALU	Pp	2	185	3	20	33.1				25.64	1.29			2	Pp	ALU	
112	2	ALU	Pp	2	126	4	9	28.6				25.64	1.12			2	Pp	ALU	
113	2	ALU	Pp	2	179	5	10	28.6				25.64	1.12			2	Pp	ALU	
114	2	ALU	Pp	2	176	6	6	32.1				25.64	1.25			2	Pp	ALU	
115	2	ALU	Pp	2	107	7	1	28.9				25.64	1.13			2	Pp	ALU	
116	2	ALU	Pp	2	131	8	10	29.9	28.46			25.64	1.17	1.110		2	Pp	ALU	
117	2	ALU	Pp	3	121	1	25	29.6				25.64	1.15			2	Pp	ALU	
118	2	ALU	Pp	3	130	2	20	20.7				25.64	0.81			2	Pp	ALU	

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									2	Np	SOD
									2	Np	SOD
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									2	Null	SOD
									2	Null	SOD
22.13	1.27				25.58	1.10			2	Pp	ALU
NA	NA				NA	NA			2	Pp	ALU
22.13	0.97				25.58	0.84			2	Pp	ALU
22.13	1.02				25.58	0.88			2	Pp	ALU
22.13	1.21				25.58	1.04			2	Pp	ALU
22.13	1.15				25.58	1.00			2	Pp	ALU
22.13	1.53				25.58	1.32			2	Pp	ALU
22.13	1.30	1.21			25.58	1.13	1.044		2	Pp	ALU
22.13	1.41				25.58	1.22			2	Pp	ALU
22.13	0.69				25.58	0.59			2	Pp	ALU
22.13	1.50				25.58	1.29			2	Pp	ALU
22.13	1.29				25.58	1.12			2	Pp	ALU
22.13	1.29				25.58	1.12			2	Pp	ALU
22.13	1.45				25.58	1.25			2	Pp	ALU
22.13	1.31				25.58	1.13			2	Pp	ALU
22.13	1.35	1.29			25.58	1.17	1.113		2	Pp	ALU
22.13	1.34				25.58	1.16			2	Pp	ALU
22.13	0.94				25.58	0.81			2	Pp	ALU

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119	2	ALU	Pp	3	110	3	14	30.3				25.64	1.18			2	Pp	ALU	
120	2	ALU	Pp	3	128	4	20	32.6				25.64	1.27			2	Pp	ALU	
121	2	ALU	Pp	3	173	5	17	32.4				25.64	1.26			2	Pp	ALU	
122	2	ALU	Pp	3	153	6	19	31.0				25.64	1.21			2	Pp	ALU	
123	2	ALU	Pp	3	194	7	9	28.9				25.64	1.13			2	Pp	ALU	
124	2	ALU	Pp	3	184	8	21	24.5	28.75			25.64	0.96	1.121		2	Pp	ALU	
125	2	ALU	Pp	4	109	1	12	30.1				25.64	1.17			2	Pp	ALU	
126	2	ALU	Pp	4	104	2	9	26.3				25.64	1.03			2	Pp	ALU	
127	2	ALU	Pp	4	139	3	4	34.2				25.64	1.33			2	Pp	ALU	
128	2	ALU	Pp	4	175	4	6	36.3				25.64	1.42			2	Pp	ALU	
129	2	ALU	Pp	4	116	5	24	38.6				25.64	1.51			2	Pp	ALU	
130	2	ALU	Pp	4	182	6	22	41.1				25.64	1.60			2	Pp	ALU	
131	2	ALU	Pp	4	192	7	24	33.9				25.64	1.32			2	Pp	ALU	
132	2	ALU	Pp	4	198	8	17	25.2	33.21			25.64	0.98	1.295		2	Pp	ALU	
133	2	ALU	Pp	5	137	1	16	31.5				25.64	1.23			2	Pp	ALU	
134	2	ALU	Pp	5	200	2	4	28.1				25.64	1.10			2	Pp	ALU	
135	2	ALU	Pp	5	132	3	6	27.4				25.64	1.07			2	Pp	ALU	
136	2	ALU	Pp	5	141	4	19	30.6				25.64	1.19			2	Pp	ALU	
137	2	ALU	Pp	5	177	5	6	30.7				25.64	1.20			2	Pp	ALU	
138	2	ALU	Pp	5	102	6	11	26.8				25.64	1.05			2	Pp	ALU	
139	2	ALU	Pp	5	154	7	25	24.7				25.64	0.96			2	Pp	ALU	
140	2	ALU	Pp	5	161	8	1	27.4	28.40	29.11		25.64	1.07	1.107	1.135	2	Pp	ALU	29.17
141	2	ALU	Np	1	188	1	2	26.7				25.64	1.04			2	Np	ALU	
142	2	ALU	Np	1	101	2	21	11.0				25.64	0.43			2	Np	ALU	
143	2	ALU	Np	1	181	3	9	21.0				25.64	0.82			2	Np	ALU	
144	2	ALU	Np	1	140	4	18	25.9				25.64	1.01			2	Np	ALU	
145	2	ALU	Np	1	197	5	12	20.6				25.64	0.80			2	Np	ALU	
146	2	ALU	Np	1	155	6	18	24.4				25.64	0.95			2	Np	ALU	
147	2	ALU	Np	1	157	7	7	23.7				25.64	0.92			2	Np	ALU	
148	2	ALU	Np	1	166	8	13	32.4	23.21			25.64	1.26	0.905		2	Np	ALU	
149	2	ALU	Np	2	170	1	11	26.1				25.64	1.02			2	Np	ALU	
150	2	ALU	Np	2	147	2	1	19.6				25.64	0.76			2	Np	ALU	
151	2	ALU	Np	2	150	3	11	20.6				25.64	0.80			2	Np	ALU	
152	2	ALU	Np	2	165	4	21	22.0				25.64	0.86			2	Np	ALU	
153	2	ALU	Np	2	171	5	19	28.2				25.64	1.10			2	Np	ALU	
154	2	ALU	Np	2	191	6	25	22.9				25.64	0.89			2	Np	ALU	
155	2	ALU	Np	2	112	7	13	25.7				25.64	1.00			2	Np	ALU	
156	2	ALU	Np	2	114	8	4	22.2	23.41			25.64	0.87	0.913		2	Np	ALU	
157	2	ALU	Np	3	187	1	9	27.6				25.64	1.08			2	Np	ALU	
158	2	ALU	Np	3	118	2	13	27.0				25.64	1.05			2	Np	ALU	
159	2	ALU	Np	3	146	3	23	25.3				25.64	0.99			2	Np	ALU	
160	2	ALU	Np	3	136	4	7	26.3				25.64	1.03			2	Np	ALU	
161	2	ALU	Np	3	124	5	4	24.0				25.64	0.94			2	Np	ALU	
162	2	ALU	Np	3	163	6	23	26.4				25.64	1.03			2	Np	ALU	
163	2	ALU	Np	3	142	7	10	25.8				25.64	1.01			2	Np	ALU	
164	2	ALU	Np	3	180	8	6	2.1	23.06			25.64	0.08	0.899		2	Np	ALU	
165	2	ALU	Np	4	183	1	22	33.0				25.64	1.29			2	Np	ALU	
166	2	ALU	Np	4	134	2	17	15.7				25.64	0.61			2	Np	ALU	
167	2	ALU	Np	4	156	3	12	27.0				25.64	1.05			2	Np	ALU	
168	2	ALU	Np	4	122	4	2	29.5				25.64	1.15			2	Np	ALU	
169	2	ALU	Np	4	199	5	22	23.0				25.64	0.90			2	Np	ALU	
170	2	ALU	Np	4	111	6	13	0.6				25.64	0.02			2	Np	ALU	
171	2	ALU	Np	4	113	7	3	11.1				25.64	0.43			2	Np	ALU	

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172	2	ALU	Np	4	106	8	23	6.6	18.31			25.64	0.26	0.714		2	Np	ALU	
173	2	ALU	Np	5	129	1	6	26.2				25.64	1.02			2	Np	ALU	
174	2	ALU	Np	5	148	2	24	25.8				25.64	1.01			2	Np	ALU	
175	2	ALU	Np	5	149	3	10	NA				NA	NA			2	Np	ALU	
176	2	ALU	Np	5	168	4	22	32.7				25.64	1.28			2	Np	ALU	
177	2	ALU	Np	5	127	5	9	12.4				25.64	0.48			2	Np	ALU	
178	2	ALU	Np	5	123	6	4	24.9				25.64	0.97			2	Np	ALU	
179	2	ALU	Np	5	160	7	17	9.5				25.64	0.37			2	Np	ALU	
180	2	ALU	Np	5	120	8	18	27.7	22.74	22.15		25.64	1.08	0.887	0.864	2	Np	ALU	22.13
191	2	ALU	Null	NA	145	1	3	26.8				25.64	1.05			2	Null	ALU	
192	2	ALU	Null	NA	164	2	19	NA				NA	NA			2	Null	ALU	
193	2	ALU	Null	NA	151	3	25	23.6				25.64	0.92			2	Null	ALU	
194	2	ALU	Null	NA	108	4	5	23.9				25.64	0.93			2	Null	ALU	
195	2	ALU	Null	NA	158	5	11	23.4				25.64	0.91			2	Null	ALU	
196	2	ALU	Null	NA	152	6	9	25.6				25.64	1.00			2	Null	ALU	
197	2	ALU	Null	NA	178	7	22	23.2				25.64	0.90			2	Null	ALU	
198	2	ALU	Null	NA	133	8	24	25.6				25.64	1.00			2	Null	ALU	
199	2	ALU	Null	NA	172	4	15	29.0		Grand Average		25.64	1.13			2	Null	ALU	
200	2	ALU	Null	NA	195	7	8	29.1	25.58		25.64	25.64	1.13	0.997		2	Null	ALU	25.58
1	3	SOD	Pp	1	62	1	2	NA				NA	NA			3	Pp	SOD	
2	3	SOD	Pp	1	43	2	5	33.4				24.66	1.35			3	Pp	SOD	
3	3	SOD	Pp	1	27	3	9	33.8				24.66	1.37			3	Pp	SOD	
4	3	SOD	Pp	1	44	4	13	41.3				24.66	1.67			3	Pp	SOD	
5	3	SOD	Pp	1	75	5	10	31.7				24.66	1.29			3	Pp	SOD	
6	3	SOD	Pp	1	19	6	20	31.2				24.66	1.27			3	Pp	SOD	
7	3	SOD	Pp	1	50	7	16	NA				NA	NA			3	Pp	SOD	
8	3	SOD	Pp	1	96	8	2	31.0	33.73			24.66	1.26	1.368		3	Pp	SOD	
9	3	SOD	Pp	2	76	1	3	37.6				24.66	1.52			3	Pp	SOD	
10	3	SOD	Pp	2	54	2	4	35.2				24.66	1.43			3	Pp	SOD	
11	3	SOD	Pp	2	81	3	5	40.2				24.66	1.63			3	Pp	SOD	
12	3	SOD	Pp	2	36	4	25	37.3				24.66	1.51			3	Pp	SOD	
13	3	SOD	Pp	2	87	5	21	32.7				24.66	1.33			3	Pp	SOD	
14	3	SOD	Pp	2	39	6	16	37.3				24.66	1.51			3	Pp	SOD	
15	3	SOD	Pp	2	24	7	18	36.7				24.66	1.49			3	Pp	SOD	
16	3	SOD	Pp	2	51	8	10	31.3	36.04			24.66	1.27	1.461		3	Pp	SOD	
17	3	SOD	Pp	3	64	1	14	37.8				24.66	1.53			3	Pp	SOD	
18	3	SOD	Pp	3	94	2	21	34.0				24.66	1.38			3	Pp	SOD	
19	3	SOD	Pp	3	90	3	24	31.5				24.66	1.28			3	Pp	SOD	
20	3	SOD	Pp	3	58	4	2	30.3				24.66	1.23			3	Pp	SOD	
21	3	SOD	Pp	3	42	5	6	26.5				24.66	1.07			3	Pp	SOD	
22	3	SOD	Pp	3	88	6	23	32.9				24.66	1.33			3	Pp	SOD	
23	3	SOD	Pp	3	66	7	2	32.8				24.66	1.33			3	Pp	SOD	
24	3	SOD	Pp	3	17	8	20	27.0	31.60			24.66	1.09	1.282		3	Pp	SOD	
25	3	SOD	Pp	4	16	1	24	33.3				24.66	1.35			3	Pp	SOD	
26	3	SOD	Pp	4	69	2	10	35.8				24.66	1.45			3	Pp	SOD	
27	3	SOD	Pp	4	57	3	21	32.1				24.66	1.30			3	Pp	SOD	
28	3	SOD	Pp	4	91	4	16	32.8				24.66	1.33			3	Pp	SOD	
29	3	SOD	Pp	4	72	5	3	31.4				24.66	1.27			3	Pp	SOD	
30	3	SOD	Pp	4	30	6	10	31.2				24.66	1.27			3	Pp	SOD	
31	3	SOD	Pp	4	55	7	22	37.6				24.66	1.52			3	Pp	SOD	
32	3	SOD	Pp	4	53	8	1	35.5	33.71			24.66	1.44	1.367		3	Pp	SOD	
33	3	SOD	Pp	5	82	1	13	NA				NA	NA			3	Pp	SOD	
34	3	SOD	Pp	5	59	2	18	42.6				24.66	1.73			3	Pp	SOD	

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										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Np	ALU
										2	Null	ALU
										2	Null	ALU
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										2	Null	ALU
										2	Null	ALU
										2	Null	ALU
										2	Null	ALU
										2	Null	ALU
NA	NA				NA					3	Pp	SOD
14.15	2.36				31.92	1.05				3	Pp	SOD
14.15	2.39				31.92	1.06				3	Pp	SOD
14.15	2.92				31.92	1.29				3	Pp	SOD
14.15	2.24				31.92	0.99				3	Pp	SOD
14.15	2.21				31.92	0.98				3	Pp	SOD
NA	NA				NA	NA				3	Pp	SOD
14.15	2.19	2.38			31.92	0.97	1.057			3	Pp	SOD
14.15	2.66				31.92	1.18				3	Pp	SOD
14.15	2.49				31.92	1.10				3	Pp	SOD
14.15	2.84				31.92	1.26				3	Pp	SOD
14.15	2.64				31.92	1.17				3	Pp	SOD
14.15	2.31				31.92	1.02				3	Pp	SOD
14.15	2.64				31.92	1.17				3	Pp	SOD
14.15	2.59				31.92	1.15				3	Pp	SOD
14.15	2.21	2.55			31.92	0.98	1.129			3	Pp	SOD
14.15	2.67				31.92	1.18				3	Pp	SOD
14.15	2.40				31.92	1.07				3	Pp	SOD
14.15	2.23				31.92	0.99				3	Pp	SOD
14.15	2.14				31.92	0.95				3	Pp	SOD
14.15	1.87				31.92	0.83				3	Pp	SOD
14.15	2.33				31.92	1.03				3	Pp	SOD
14.15	2.32				31.92	1.03				3	Pp	SOD
14.15	1.91	2.23			31.92	0.85	0.990			3	Pp	SOD
14.15	2.35				31.92	1.04				3	Pp	SOD
14.15	2.53				31.92	1.12				3	Pp	SOD
14.15	2.27				31.92	1.01				3	Pp	SOD
14.15	2.32				31.92	1.03				3	Pp	SOD
14.15	2.22				31.92	0.98				3	Pp	SOD
14.15	2.21				31.92	0.98				3	Pp	SOD
14.15	2.66				31.92	1.18				3	Pp	SOD
14.15	2.51	2.38			31.92	1.11	1.056			3	Pp	SOD
NA	NA				NA	NA				3	Pp	SOD
14.15	3.01				31.92	1.33				3	Pp	SOD

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35	3	SOD	Pp	5	14	3	13	31.5				24.66	1.28			3	Pp	SOD	
36	3	SOD	Pp	5	34	4	23	35.0				24.66	1.42			3	Pp	SOD	
37	3	SOD	Pp	5	79	5	18	25.7				24.66	1.04			3	Pp	SOD	
38	3	SOD	Pp	5	40	6	1	30.0				24.66	1.22			3	Pp	SOD	
39	3	SOD	Pp	5	29	7	3	NA				NA	NA			3	Pp	SOD	
40	3	SOD	Pp	5	20	8	18	36.5	33.55	33.73		24.66	1.48	1.361	1.368	3	Pp	SOD	33.74
41	3	SOD	Np	1	100	1	23	NA				NA	NA			3	Np	SOD	
42	3	SOD	Np	1	67	2	1	0.2				24.66	0.01			3	Np	SOD	
43	3	SOD	Np	1	28	3	7	1.4				24.66	0.06			3	Np	SOD	
44	3	SOD	Np	1	70	4	24	6.3				24.66	0.26			3	Np	SOD	
45	3	SOD	Np	1	8	5	16	26.7				24.66	1.08			3	Np	SOD	
46	3	SOD	Np	1	2	6	14	27.8				24.66	1.13			3	Np	SOD	
47	3	SOD	Np	1	93	7	4	0.4				24.66	0.02			3	Np	SOD	
48	3	SOD	Np	1	13	8	19	29.7	13.21			24.66	1.20	0.536		3	Np	SOD	
49	3	SOD	Np	2	92	1	15	0.2				24.66	0.01			3	Np	SOD	
50	3	SOD	Np	2	23	2	15	0.6				24.66	0.02			3	Np	SOD	
51	3	SOD	Np	2	41	3	23	33.0				24.66	1.34			3	Np	SOD	
52	3	SOD	Np	2	22	4	15	13.5				24.66	0.55			3	Np	SOD	
53	3	SOD	Np	2	83	5	11	0.3				24.66	0.01			3	Np	SOD	
54	3	SOD	Np	2	4	6	11	20.7				24.66	0.84			3	Np	SOD	
55	3	SOD	Np	2	6	7	5	18.8				24.66	0.76			3	Np	SOD	
56	3	SOD	Np	2	12	8	13	22.1	13.65			24.66	0.90	0.554		3	Np	SOD	
57	3	SOD	Np	3	32	1	1	28.9				24.66	1.17			3	Np	SOD	
58	3	SOD	Np	3	85	2	16	20.9				24.66	0.85			3	Np	SOD	
59	3	SOD	Np	3	7	3	22	13.0				24.66	0.53			3	Np	SOD	
60	3	SOD	Np	3	1	4	18	0.9				24.66	0.04			3	Np	SOD	
61	3	SOD	Np	3	73	5	20	0.2				24.66	0.01			3	Np	SOD	
62	3	SOD	Np	3	5	6	4	1.3				24.66	0.05			3	Np	SOD	
63	3	SOD	Np	3	15	7	23	0.4				24.66	0.02			3	Np	SOD	
64	3	SOD	Np	3	46	8	5	27.5	11.64			24.66	1.12	0.472		3	Np	SOD	
65	3	SOD	Np	4	78	1	5	0.7				24.66	0.03			3	Np	SOD	
66	3	SOD	Np	4	97	2	6	34.1				24.66	1.38			3	Np	SOD	
67	3	SOD	Np	4	47	3	3	1.0				24.66	0.04			3	Np	SOD	
68	3	SOD	Np	4	80	4	20	0.8				24.66	0.03			3	Np	SOD	
69	3	SOD	Np	4	26	5	15	28.9				24.66	1.17			3	Np	SOD	
70	3	SOD	Np	4	25	6	9	4.8				24.66	0.19			3	Np	SOD	
71	3	SOD	Np	4	68	7	24	30.2				24.66	1.22			3	Np	SOD	
72	3	SOD	Np	4	65	8	11	NA	14.36			NA	NA	0.582		3	Np	SOD	
73	3	SOD	Np	5	74	1	20	27.2				24.66	1.10			3	Np	SOD	
74	3	SOD	Np	5	11	2	9	29.2				24.66	1.18			3	Np	SOD	
75	3	SOD	Np	5	21	3	19	30.8				24.66	1.25			3	Np	SOD	
76	3	SOD	Np	5	98	4	9	0.9				24.66	0.04			3	Np	SOD	
77	3	SOD	Np	5	33	5	25	31.0				24.66	1.26			3	Np	SOD	
78	3	SOD	Np	5	84	6	17	0.5				24.66	0.02			3	Np	SOD	
79	3	SOD	Np	5	52	7	17	0.2				24.66	0.01			3	Np	SOD	
80	3	SOD	Np	5	10	8	24	22.5	17.79	14.13		24.66	0.91	0.721	0.573	3	Np	SOD	14.15
91	3	SOD	Null	NA	49	1	19	32.6				24.66	1.32			3	Null	SOD	
92	3	SOD	Null	NA	60	2	7	40.0				24.66	1.62			3	Null	SOD	
93	3	SOD	Null	NA	86	3	17	37.2				24.66	1.51			3	Null	SOD	
94	3	SOD	Null	NA	89	4	7	28.8				24.66	1.17			3	Null	SOD	
95	3	SOD	Null	NA	95	5	2	30.7				24.66	1.25			3	Null	SOD	
96	3	SOD	Null	NA	77	6	15	31.2				24.66	1.27			3	Null	SOD	
97	3	SOD	Null	NA	45	7	19	25.5				24.66	1.03			3	Null	SOD	

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98	3	SOD	Null	NA	56	8	4	32.5			24.66	1.32			3	Null	SOD		
99	3	SOD	Null	NA	38	1	12	32.9			Grand Average	24.66	1.33			3	Null	SOD	
100	3	SOD	Null	NA	35	7	1	27.8	31.92		24.66	24.66	1.13	1.294	3	Null	SOD	31.92	
101	3	ALU	Pp	1	133	1	22	50.1				36.81	1.36			3	Pp	ALU	
102	3	ALU	Pp	1	108	2	22	42.2				36.81	1.15			3	Pp	ALU	
103	3	ALU	Pp	1	143	3	20	45.0				36.81	1.22			3	Pp	ALU	
104	3	ALU	Pp	1	122	4	6	48.3				36.81	1.31			3	Pp	ALU	
105	3	ALU	Pp	1	132	5	8	50.0				36.81	1.36			3	Pp	ALU	
106	3	ALU	Pp	1	158	6	7	44.4				36.81	1.21			3	Pp	ALU	
107	3	ALU	Pp	1	172	7	20	51.3				36.81	1.39			3	Pp	ALU	
108	3	ALU	Pp	1	181	8	21	50.5	47.73			36.81	1.37	1.296		3	Pp	ALU	
109	3	ALU	Pp	2	170	1	9	47.2				36.81	1.28			3	Pp	ALU	
110	3	ALU	Pp	2	144	2	8	54.6				36.81	1.48			3	Pp	ALU	
111	3	ALU	Pp	2	120	3	15	46.2				36.81	1.25			3	Pp	ALU	
112	3	ALU	Pp	2	116	4	12	49.1				36.81	1.33			3	Pp	ALU	
113	3	ALU	Pp	2	167	5	19	49.1				36.81	1.33			3	Pp	ALU	
114	3	ALU	Pp	2	150	6	19	45.1				36.81	1.23			3	Pp	ALU	
115	3	ALU	Pp	2	105	7	9	35.1				36.81	0.95			3	Pp	ALU	
116	3	ALU	Pp	2	168	8	3	46.6	46.63			36.81	1.27	1.267		3	Pp	ALU	
117	3	ALU	Pp	3	163	1	17	29.1				36.81	0.79			3	Pp	ALU	
118	3	ALU	Pp	3	184	2	14	40.9				36.81	1.11			3	Pp	ALU	
119	3	ALU	Pp	3	110	3	2	52.2				36.81	1.42			3	Pp	ALU	
120	3	ALU	Pp	3	175	4	3	39.8				36.81	1.08			3	Pp	ALU	
121	3	ALU	Pp	3	199	5	23	36.9				36.81	1.00			3	Pp	ALU	
122	3	ALU	Pp	3	180	6	6	40.5				36.81	1.10			3	Pp	ALU	
123	3	ALU	Pp	3	142	7	6	35.2				36.81	0.96			3	Pp	ALU	
124	3	ALU	Pp	3	126	8	16	45.7	40.04			36.81	1.24	1.088		3	Pp	ALU	
125	3	ALU	Pp	4	178	1	11	39.7				36.81	1.08			3	Pp	ALU	
126	3	ALU	Pp	4	140	2	17	47.6				36.81	1.29			3	Pp	ALU	
127	3	ALU	Pp	4	164	3	25	46.6				36.81	1.27			3	Pp	ALU	
128	3	ALU	Pp	4	129	4	21	44.7				36.81	1.21			3	Pp	ALU	
129	3	ALU	Pp	4	191	5	1	38.4				36.81	1.04			3	Pp	ALU	
130	3	ALU	Pp	4	174	6	25	40.2				36.81	1.09			3	Pp	ALU	
131	3	ALU	Pp	4	165	7	21	40.8				36.81	1.11			3	Pp	ALU	
132	3	ALU	Pp	4	187	8	7	43.3	42.66			36.81	1.18	1.159		3	Pp	ALU	
133	3	ALU	Pp	5	188	1	4	55.0				36.81	1.49			3	Pp	ALU	
134	3	ALU	Pp	5	145	2	2	24.0				36.81	0.65			3	Pp	ALU	
135	3	ALU	Pp	5	119	3	18	52.0				36.81	1.41			3	Pp	ALU	
136	3	ALU	Pp	5	183	4	11	40.8				36.81	1.11			3	Pp	ALU	
137	3	ALU	Pp	5	179	5	14	48.6				36.81	1.32			3	Pp	ALU	
138	3	ALU	Pp	5	200	6	22	42.3				36.81	1.15			3	Pp	ALU	
139	3	ALU	Pp	5	148	7	10	42.6				36.81	1.16			3	Pp	ALU	
140	3	ALU	Pp	5	130	8	15	32.0	42.16	43.84		36.81	0.87	1.145	1.191	3	Pp	ALU	43.84
141	3	ALU	Np	1	198	1	16	27.0				36.81	0.73			3	Np	ALU	
142	3	ALU	Np	1	134	2	25	41.1				36.81	1.12			3	Np	ALU	
143	3	ALU	Np	1	111	3	10	26.5				36.81	0.72			3	Np	ALU	
144	3	ALU	Np	1	173	4	8	32.0				36.81	0.87			3	Np	ALU	
145	3	ALU	Np	1	124	5	24	34.4				36.81	0.93			3	Np	ALU	
146	3	ALU	Np	1	152	6	24	1.2				36.81	0.03			3	Np	ALU	
147	3	ALU	Np	1	141	7	15	0.9				36.81	0.02			3	Np	ALU	
148	3	ALU	Np	1	194	8	22	0.6	20.46			36.81	0.02	0.556		3	Np	ALU	
149	3	ALU	Np	2	192	1	25	30.6				36.81	0.83			3	Np	ALU	
150	3	ALU	Np	2	154	2	19	35.4				36.81	0.96			3	Np	ALU	

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151	3	ALU	Np	2	137	3	8	NA				NA	NA			3	Np	ALU	
152	3	ALU	Np	2	197	4	17	41.8				36.81	1.14			3	Np	ALU	
153	3	ALU	Np	2	117	5	9	27.3				36.81	0.74			3	Np	ALU	
154	3	ALU	Np	2	135	6	18	31.1				36.81	0.84			3	Np	ALU	
155	3	ALU	Np	2	131	7	13	43.3				36.81	1.18			3	Np	ALU	
156	3	ALU	Np	2	182	8	17	41.0	35.79			36.81	1.11	0.972		3	Np	ALU	
157	3	ALU	Np	3	190	1	21	9.4				36.81	0.26			3	Np	ALU	
158	3	ALU	Np	3	138	2	13	37.5				36.81	1.02			3	Np	ALU	
159	3	ALU	Np	3	196	3	16	46.4				36.81	1.26			3	Np	ALU	
160	3	ALU	Np	3	101	4	1	42.6				36.81	1.16			3	Np	ALU	
161	3	ALU	Np	3	153	5	22	42.0				36.81	1.14			3	Np	ALU	
162	3	ALU	Np	3	149	6	12	41.8				36.81	1.14			3	Np	ALU	
163	3	ALU	Np	3	161	7	11	32.8				36.81	0.89			3	Np	ALU	
164	3	ALU	Np	3	193	8	8	0.2	31.59			36.81	0.01	0.858		3	Np	ALU	
165	3	ALU	Np	4	195	1	10	36.5				36.81	0.99			3	Np	ALU	
166	3	ALU	Np	4	106	2	3	8.3				36.81	0.23			3	Np	ALU	
167	3	ALU	Np	4	159	3	12	19.3				36.81	0.52			3	Np	ALU	
168	3	ALU	Np	4	169	4	14	41.7				36.81	1.13			3	Np	ALU	
169	3	ALU	Np	4	171	5	17	37.9				36.81	1.03			3	Np	ALU	
170	3	ALU	Np	4	109	6	2	27.4				36.81	0.74			3	Np	ALU	
171	3	ALU	Np	4	123	7	7	32.0				36.81	0.87			3	Np	ALU	
172	3	ALU	Np	4	118	8	12	31.6	29.34			36.81	0.86	0.797		3	Np	ALU	
173	3	ALU	Np	5	128	1	7	40.5				36.81	1.10			3	Np	ALU	
174	3	ALU	Np	5	136	2	20	38.1				36.81	1.03			3	Np	ALU	
175	3	ALU	Np	5	185	3	1	0.3				36.81	0.01			3	Np	ALU	
176	3	ALU	Np	5	127	4	4	32.7				36.81	0.89			3	Np	ALU	
177	3	ALU	Np	5	151	5	13	0.7				36.81	0.02			3	Np	ALU	
178	3	ALU	Np	5	177	6	21	29.7				36.81	0.81			3	Np	ALU	
179	3	ALU	Np	5	189	7	12	40.5				36.81	1.10			3	Np	ALU	
180	3	ALU	Np	5	102	8	14	34.7	27.15	28.86		36.81	0.94	0.737	0.784	3	Np	ALU	28.69
191	3	ALU	Null	NA	147	1	18	47.2				36.81	1.28			3	Null	ALU	
192	3	ALU	Null	NA	186	2	12	NA				NA	NA			3	Null	ALU	
193	3	ALU	Null	NA	176	3	4	NA				NA	NA			3	Null	ALU	
194	3	ALU	Null	NA	162	4	10	39.7				36.81	1.08			3	Null	ALU	
195	3	ALU	Null	NA	146	5	7	41.4				36.81	1.12			3	Null	ALU	
196	3	ALU	Null	NA	107	6	8	36.4				36.81	0.99			3	Null	ALU	
197	3	ALU	Null	NA	103	7	25	45.1				36.81	1.23			3	Null	ALU	
198	3	ALU	Null	NA	157	8	9	31.5				36.81	0.86			3	Null	ALU	
199	3	ALU	Null	NA	113	2	23	41.8	Grand Average			36.81	1.14			3	Null	ALU	
200	3	ALU	Null	NA	166	6	3	47.2	41.29		36.81	36.81	1.28	1.122		3	Null	ALU	41.29
1	4	SOD	Pp	1	2	1	21	16.7				16.14	1.03			4	Pp	SOD	
2	4	SOD	Pp	1	21	2	19	20.7				16.14	1.28			4	Pp	SOD	
3	4	SOD	Pp	1	27	3	25	20.8				16.14	1.29			4	Pp	SOD	
4	4	SOD	Pp	1	77	4	14	20.7				16.14	1.28			4	Pp	SOD	
5	4	SOD	Pp	1	82	5	20	13.3				16.14	0.82			4	Pp	SOD	
6	4	SOD	Pp	1	61	6	13	22.5				16.14	1.39			4	Pp	SOD	
7	4	SOD	Pp	1	76	7	8	21.6				16.14	1.34			4	Pp	SOD	
8	4	SOD	Pp	1	58	8	5	22.2	19.81			16.14	1.38	1.228		4	Pp	SOD	
9	4	SOD	Pp	2	92	1	6	16.0				16.14	0.99			4	Pp	SOD	
10	4	SOD	Pp	2	72	2	5	15.9				16.14	0.99			4	Pp	SOD	
11	4	SOD	Pp	2	33	3	1	16.8				16.14	1.04			4	Pp	SOD	
12	4	SOD	Pp	2	38	4	2	20.3				16.14	1.26			4	Pp	SOD	
13	4	SOD	Pp	2	54	5	23	18.3				16.14	1.13			4	Pp	SOD	

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14	4	SOD	Pp	2	5	6	24	16.2				16.14	1.00			4	Pp	SOD	
15	4	SOD	Pp	2	80	7	16	18.9				16.14	1.17			4	Pp	SOD	
16	4	SOD	Pp	2	89	8	14	19.7	17.76			16.14	1.22	1.101		4	Pp	SOD	
17	4	SOD	Pp	3	32	1	18	19.4				16.14	1.20			4	Pp	SOD	
18	4	SOD	Pp	3	67	2	4	22.6				16.14	1.40			4	Pp	SOD	
19	4	SOD	Pp	3	26	3	7	21.9				16.14	1.36			4	Pp	SOD	
20	4	SOD	Pp	3	87	4	9	19.5				16.14	1.21			4	Pp	SOD	
21	4	SOD	Pp	3	41	5	9	19.7				16.14	1.22			4	Pp	SOD	
22	4	SOD	Pp	3	35	6	16	19.3				16.14	1.20			4	Pp	SOD	
23	4	SOD	Pp	3	85	7	17	22.4				16.14	1.39			4	Pp	SOD	
24	4	SOD	Pp	3	84	8	15	20.6	20.68			16.14	1.28	1.281		4	Pp	SOD	
25	4	SOD	Pp	4	23	1	2	19.2				16.14	1.19			4	Pp	SOD	
26	4	SOD	Pp	4	16	2	17	19.0				16.14	1.18			4	Pp	SOD	
27	4	SOD	Pp	4	95	3	15	18.6				16.14	1.15			4	Pp	SOD	
28	4	SOD	Pp	4	36	4	4	19.1				16.14	1.18			4	Pp	SOD	
29	4	SOD	Pp	4	24	5	19	19.6				16.14	1.21			4	Pp	SOD	
30	4	SOD	Pp	4	60	6	17	16.2				16.14	1.00			4	Pp	SOD	
31	4	SOD	Pp	4	96	7	12	NA				NA	NA			4	Pp	SOD	
32	4	SOD	Pp	4	28	8	8	19.2	18.70			16.14	1.19	1.159		4	Pp	SOD	
33	4	SOD	Pp	5	6	1	11	18.2				16.14	1.13			4	Pp	SOD	
34	4	SOD	Pp	5	12	2	18	19.8				16.14	1.23			4	Pp	SOD	
35	4	SOD	Pp	5	98	3	23	21.4				16.14	1.33			4	Pp	SOD	
36	4	SOD	Pp	5	46	4	5	18.1				16.14	1.12			4	Pp	SOD	
37	4	SOD	Pp	5	86	5	2	22.2				16.14	1.38			4	Pp	SOD	
38	4	SOD	Pp	5	19	6	8	23.2				16.14	1.44			4	Pp	SOD	
39	4	SOD	Pp	5	9	7	13	25.6				16.14	1.59			4	Pp	SOD	
40	4	SOD	Pp	5	42	8	4	23.0	21.44	19.68		16.14	1.43	1.328	1.219	4	Pp	SOD	19.70
41	4	SOD	Np	1	71	3	13	0.4				16.14	0.02			4	Np	SOD	
42	4	SOD	Np	1	39	4	22	13.8				16.14	0.86			4	Np	SOD	
43	4	SOD	Np	1	31	5	14	15.9				16.14	0.99			4	Np	SOD	
44	4	SOD	Np	1	55	6	4	0.5				16.14	0.03			4	Np	SOD	
45	4	SOD	Np	1	34	7	19	0.8				16.14	0.05			4	Np	SOD	
46	4	SOD	Np	1	90	8	9	12.0	7.23			16.14	0.74	0.448		4	Np	SOD	
47	4	SOD	Np	2	15	1	7	14.4				16.14	0.89			4	Np	SOD	
48	4	SOD	Np	2	37	2	14	12.3				16.14	0.76			4	Np	SOD	
49	4	SOD	Np	2	52	5	11	16.8				16.14	1.04			4	Np	SOD	
50	4	SOD	Np	2	45	6	2	2.0				16.14	0.12			4	Np	SOD	
51	4	SOD	Np	2	69	7	20	13.3				16.14	0.82			4	Np	SOD	
52	4	SOD	Np	2	49	8	10	13.1	11.98			16.14	0.81	0.743		4	Np	SOD	
53	4	SOD	Np	3	3	1	10	12.8				16.14	0.79			4	Np	SOD	
54	4	SOD	Np	3	40	2	2	12.2				16.14	0.76			4	Np	SOD	
55	4	SOD	Np	3	59	3	6	8.7				16.14	0.54			4	Np	SOD	
56	4	SOD	Np	3	74	4	21	0.8				16.14	0.05			4	Np	SOD	
57	4	SOD	Np	3	50	7	18	0.4				16.14	0.02			4	Np	SOD	
58	4	SOD	Np	3	51	8	2	20.7	9.27			16.14	1.28	0.574		4	Np	SOD	
59	4	SOD	Np	4	18	1	16	0.6				16.14	0.04			4	Np	SOD	
60	4	SOD	Np	4	79	2	21	11.4				16.14	0.71			4	Np	SOD	
61	4	SOD	Np	4	47	3	24	17.7				16.14	1.10			4	Np	SOD	
62	4	SOD	Np	4	29	4	8	20.1				16.14	1.25			4	Np	SOD	
63	4	SOD	Np	4	94	5	3	24.1				16.14	1.49			4	Np	SOD	
64	4	SOD	Np	4	20	6	11	2.5	12.73			16.14	0.15	0.789		4	Np	SOD	
65	4	SOD	Np	5	81	1	25	NA				NA	NA			4	Np	SOD	
66	4	SOD	Np	5	93	3	21	7.4				16.14	0.46			4	Np	SOD	

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67	4	SOD	Np	5	4	4	15	0.7				16.14	0.04			4	Np	SOD	
68	4	SOD	Np	5	91	5	22	0.4				16.14	0.02			4	Np	SOD	
69	4	SOD	Np	5	44	6	5	1.0				16.14	0.06			4	Np	SOD	
70	4	SOD	Np	5	88	7	2	15.8	5.06	9.26		16.14	0.98	0.314	0.573	4	Np	SOD	9.40
81	4	SOD	Null	NA	1	1	14	18.1				16.14	1.12			4	Null	SOD	
82	4	SOD	Null	NA	63	2	12	NA				NA	NA			4	Null	SOD	
83	4	SOD	Null	NA	73	3	16	18.7				16.14	1.16			4	Null	SOD	
84	4	SOD	Null	NA	70	4	7	21.6				16.14	1.34			4	Null	SOD	
85	4	SOD	Null	NA	100	5	7	NA				NA	NA			4	Null	SOD	
86	4	SOD	Null	NA	53	6	6	NA				NA	NA			4	Null	SOD	
87	4	SOD	Null	NA	57	7	21	16.3				16.14	1.01			4	Null	SOD	
88	4	SOD	Null	NA	43	8	7	17.3				16.14	1.07			4	Null	SOD	
89	4	SOD	Null	NA	56	1	24	17.0				16.14	1.05			4	Null	SOD	
90	4	SOD	Null	NA	10	2	16	20.4				16.14	1.26			4	Null	SOD	
91	4	SOD	Null	NA	62	3	4	24.8				16.14	1.54			4	Null	SOD	
92	4	SOD	Null	NA	8	4	1	17.2				16.14	1.07			4	Null	SOD	
93	4	SOD	Null	NA	75	5	10	15.3				16.14	0.95			4	Null	SOD	
94	4	SOD	Null	NA	22	6	14	23.0				16.14	1.43			4	Null	SOD	
95	4	SOD	Null	NA	17	7	24	19.9				16.14	1.23			4	Null	SOD	
96	4	SOD	Null	NA	66	8	18	24.4				16.14	1.51			4	Null	SOD	
97	4	SOD	Null	NA	25	1	3	21.2				16.14	1.31			4	Null	SOD	
98	4	SOD	Null	NA	48	3	10	17.9				16.14	1.11			4	Null	SOD	
99	4	SOD	Null	NA	65	5	21	15.9			Grand Average	16.14	0.99			4	Null	SOD	
100	4	SOD	Null	NA	11	7	5	21.8	19.46		16.14	16.14	1.35	1.206		4	Null	SOD	19.46
101	4	ALU	Pp	1	120	1	15	NA				NA	NA			4	Pp	ALU	
102	4	ALU	Pp	1	126	2	11	29.3				22.10	1.33			4	Pp	ALU	
103	4	ALU	Pp	1	198	3	8	29.6				22.10	1.34			4	Pp	ALU	
104	4	ALU	Pp	1	169	4	17	26.9				22.10	1.22			4	Pp	ALU	
105	4	ALU	Pp	1	130	5	15	23.8				22.10	1.08			4	Pp	ALU	
106	4	ALU	Pp	1	195	6	19	32.6				22.10	1.47			4	Pp	ALU	
107	4	ALU	Pp	1	165	7	6	31.0				22.10	1.40			4	Pp	ALU	
108	4	ALU	Pp	1	105	8	24	31.3	29.21			22.10	1.42	1.322		4	Pp	ALU	
109	4	ALU	Pp	2	175	1	9	26.4				22.10	1.19			4	Pp	ALU	
110	4	ALU	Pp	2	184	2	8	24.2				22.10	1.09			4	Pp	ALU	
111	4	ALU	Pp	2	147	3	20	26.1				22.10	1.18			4	Pp	ALU	
112	4	ALU	Pp	2	167	4	23	26.0				22.10	1.18			4	Pp	ALU	
113	4	ALU	Pp	2	103	5	6	33.2				22.10	1.50			4	Pp	ALU	
114	4	ALU	Pp	2	172	6	10	24.1				22.10	1.09			4	Pp	ALU	
115	4	ALU	Pp	2	196	7	14	30.0				22.10	1.36			4	Pp	ALU	
116	4	ALU	Pp	2	152	8	21	24.2	26.78			22.10	1.09	1.211		4	Pp	ALU	
117	4	ALU	Pp	3	161	1	17	26.7				22.10	1.21			4	Pp	ALU	
118	4	ALU	Pp	3	104	2	25	27.2				22.10	1.23			4	Pp	ALU	
119	4	ALU	Pp	3	157	3	18	26.3				22.10	1.19			4	Pp	ALU	
120	4	ALU	Pp	3	199	4	12	28.6				22.10	1.29			4	Pp	ALU	
121	4	ALU	Pp	3	189	5	16	26.9				22.10	1.22			4	Pp	ALU	
122	4	ALU	Pp	3	148	6	12	32.1				22.10	1.45			4	Pp	ALU	
123	4	ALU	Pp	3	155	7	9	30.4				22.10	1.38			4	Pp	ALU	
124	4	ALU	Pp	3	150	8	6	24.9	27.89			22.10	1.13	1.262		4	Pp	ALU	
125	4	ALU	Pp	4	197	1	8	32.7				22.10	1.48			4	Pp	ALU	
126	4	ALU	Pp	4	160	2	20	22.2				22.10	1.00			4	Pp	ALU	
127	4	ALU	Pp	4	176	3	12	20.5				22.10	0.93			4	Pp	ALU	
128	4	ALU	Pp	4	131	4	25	18.1				22.10	0.82			4	Pp	ALU	
129	4	ALU	Pp	4	200	5	17	27.4				22.10	1.24			4	Pp	ALU	

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										4	Np	SOD
										4	Np	SOD
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										4	Null	SOD
										4	Null	SOD
NA	NA				NA	NA				4	Pp	ALU
14.44	2.03				23.84	1.23				4	Pp	ALU
14.44	2.05				23.84	1.24				4	Pp	ALU
14.44	1.86				23.84	1.13				4	Pp	ALU
14.44	1.65				23.84	1.00				4	Pp	ALU
14.44	2.26				23.84	1.37				4	Pp	ALU
14.44	2.15				23.84	1.30				4	Pp	ALU
14.44	2.17	2.02			23.84	1.31	1.225			4	Pp	ALU
14.44	1.83				23.84	1.11				4	Pp	ALU
14.44	1.68				23.84	1.02				4	Pp	ALU
14.44	1.81				23.84	1.09				4	Pp	ALU
14.44	1.80				23.84	1.09				4	Pp	ALU
14.44	2.30				23.84	1.39				4	Pp	ALU
14.44	1.67				23.84	1.01				4	Pp	ALU
14.44	2.08				23.84	1.26				4	Pp	ALU
14.44	1.68	1.85			23.84	1.02	1.123			4	Pp	ALU
14.44	1.85				23.84	1.12				4	Pp	ALU
14.44	1.88				23.84	1.14				4	Pp	ALU
14.44	1.82				23.84	1.10				4	Pp	ALU
14.44	1.98				23.84	1.20				4	Pp	ALU
14.44	1.86				23.84	1.13				4	Pp	ALU
14.44	2.22				23.84	1.35				4	Pp	ALU
14.44	2.11				23.84	1.28				4	Pp	ALU
14.44	1.72	1.93			23.84	1.04	1.170			4	Pp	ALU
14.44	2.26				23.84	1.37				4	Pp	ALU
14.44	1.54				23.84	0.93				4	Pp	ALU
14.44	1.42				23.84	0.86				4	Pp	ALU
14.44	1.25				23.84	0.76				4	Pp	ALU
14.44	1.90				23.84	1.15				4	Pp	ALU

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130	4	ALU	Pp	4	171	6	7	28.6				22.10	1.29			4	Pp	ALU	
131	4	ALU	Pp	4	180	7	3	29.5				22.10	1.33			4	Pp	ALU	
132	4	ALU	Pp	4	115	8	19	29.2	26.03			22.10	1.32	1.177		4	Pp	ALU	
133	4	ALU	Pp	5	159	1	12	25.8				22.10	1.17			4	Pp	ALU	
134	4	ALU	Pp	5	121	2	7	27.2				22.10	1.23			4	Pp	ALU	
135	4	ALU	Pp	5	111	3	5	17.0				22.10	0.77			4	Pp	ALU	
136	4	ALU	Pp	5	154	4	10	27.6				22.10	1.25			4	Pp	ALU	
137	4	ALU	Pp	5	108	5	4	27.8				22.10	1.26			4	Pp	ALU	
138	4	ALU	Pp	5	101	6	18	23.0				22.10	1.04			4	Pp	ALU	
139	4	ALU	Pp	5	177	7	7	31.6				22.10	1.43			4	Pp	ALU	
140	4	ALU	Pp	5	168	8	17	27.3	25.91	27.16		22.10	1.24	1.172	1.229	4	Pp	ALU	27.11
141	4	ALU	Np	1	173	3	9	15.2				22.10	0.69			4	Np	ALU	
142	4	ALU	Np	1	149	4	20	7.6				22.10	0.34			4	Np	ALU	
143	4	ALU	Np	1	128	5	13	20.0				22.10	0.90			4	Np	ALU	
144	4	ALU	Np	1	106	6	25	18.4				22.10	0.83			4	Np	ALU	
145	4	ALU	Np	1	143	7	25	16.5				22.10	0.75			4	Np	ALU	
146	4	ALU	Np	1	107	8	22	19.2	16.15			22.10	0.87	0.731		4	Np	ALU	
147	4	ALU	Np	2	185	1	1	5.7				22.10	0.26			4	Np	ALU	
148	4	ALU	Np	2	145	2	3	3.5				22.10	0.16			4	Np	ALU	
149	4	ALU	Np	2	129	5	12	11.1				22.10	0.50			4	Np	ALU	
150	4	ALU	Np	2	164	6	21	13.5				22.10	0.61			4	Np	ALU	
151	4	ALU	Np	2	139	7	4	10.7				22.10	0.48			4	Np	ALU	
152	4	ALU	Np	2	190	8	13	8.6	8.85			22.10	0.39	0.400		4	Np	ALU	
153	4	ALU	Np	3	109	1	22	12.7				22.10	0.57			4	Np	ALU	
154	4	ALU	Np	3	134	2	24	14.6				22.10	0.66			4	Np	ALU	
155	4	ALU	Np	3	133	3	3	16.7				22.10	0.76			4	Np	ALU	
156	4	ALU	Np	3	188	4	6	1.4				22.10	0.06			4	Np	ALU	
157	4	ALU	Np	3	183	7	10	13.0				22.10	0.59			4	Np	ALU	
158	4	ALU	Np	3	124	8	25	12.4	11.80			22.10	0.56	0.534		4	Np	ALU	
159	4	ALU	Np	4	127	1	19	19.5				22.10	0.88			4	Np	ALU	
160	4	ALU	Np	4	114	2	1	19.0				22.10	0.86			4	Np	ALU	
161	4	ALU	Np	4	122	3	19	21.0				22.10	0.95			4	Np	ALU	
162	4	ALU	Np	4	102	4	13	17.4				22.10	0.79			4	Np	ALU	
163	4	ALU	Np	4	141	5	8	20.2				22.10	0.91			4	Np	ALU	
164	4	ALU	Np	4	156	6	23	8.9	17.67			22.10	0.40	0.799		4	Np	ALU	
165	4	ALU	Np	5	151	2	23	17.3				22.10	0.78			4	Np	ALU	
166	4	ALU	Np	5	163	3	11	18.3				22.10	0.83			4	Np	ALU	
167	4	ALU	Np	5	140	4	16	17.6				22.10	0.80			4	Np	ALU	
168	4	ALU	Np	5	174	6	22	17.8				22.10	0.81			4	Np	ALU	
169	4	ALU	Np	5	178	7	1	13.0				22.10	0.59			4	Np	ALU	
170	4	ALU	Np	5	144	8	23	22.4	17.73	14.4		22.10	1.01	0.802	0.653	4	Np	ALU	14.44
181	4	ALU	Null	NA	110	1	13	26.0				22.10	1.18			4	Null	ALU	
182	4	ALU	Null	NA	119	2	13	22.5				22.10	1.02			4	Null	ALU	
183	4	ALU	Null	NA	153	3	2	22.6				22.10	1.02			4	Null	ALU	
184	4	ALU	Null	NA	191	4	11	20.9				22.10	0.95			4	Null	ALU	
185	4	ALU	Null	NA	136	5	5	22.8				22.10	1.03			4	Null	ALU	
186	4	ALU	Null	NA	123	6	20	25.5				22.10	1.15			4	Null	ALU	
187	4	ALU	Null	NA	117	7	23	25.8				22.10	1.17			4	Null	ALU	
188	4	ALU	Null	NA	116	8	3	27.7				22.10	1.25			4	Null	ALU	
189	4	ALU	Null	NA	118	1	4	9.0				22.10	0.41			4	Null	ALU	
190	4	ALU	Null	NA	166	2	6	19.3				22.10	0.87			4	Null	ALU	
191	4	ALU	Null	NA	142	3	14	23.0				22.10	1.04			4	Null	ALU	
192	4	ALU	Null	NA	137	4	3	23.0				22.10	1.04			4	Null	ALU	

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193	4	ALU	Null	NA	146	5	18	25.0				22.10	1.13			4	Null	ALU	
194	4	ALU	Null	NA	181	6	15	24.9				22.10	1.13			4	Null	ALU	
195	4	ALU	Null	NA	193	7	22	25.3				22.10	1.14			4	Null	ALU	
196	4	ALU	Null	NA	194	8	20	25.6				22.10	1.16			4	Null	ALU	
197	4	ALU	Null	NA	170	2	22	28.2				22.10	1.28			4	Null	ALU	
198	4	ALU	Null	NA	162	4	18	24.4				22.10	1.10			4	Null	ALU	
199	4	ALU	Null	NA	138	6	9	25.8			Grand Average	22.10	1.17			4	Null	ALU	
200	4	ALU	Null	NA	132	8	1	29.5	23.84		22.1	22.10	1.33	1.079	4	Null	ALU	23.84	
1	5	SOD	Pp	1	21	1	13	35.5				31.72	1.12			5	Pp	SOD	
2	5	SOD	Pp	1	96	2	3	36.1				31.72	1.14			5	Pp	SOD	
3	5	SOD	Pp	1	57	3	23	40.1				31.72	1.26			5	Pp	SOD	
4	5	SOD	Pp	1	58	4	6	27.8				31.72	0.88			5	Pp	SOD	
5	5	SOD	Pp	1	48	5	11	37.2				31.72	1.17			5	Pp	SOD	
6	5	SOD	Pp	1	69	6	19	30.0				31.72	0.95			5	Pp	SOD	
7	5	SOD	Pp	1	85	7	10	27.7				31.72	0.87			5	Pp	SOD	
8	5	SOD	Pp	1	79	8	19	35.4	33.73			31.72	1.12	1.063		5	Pp	SOD	
9	5	SOD	Pp	2	50	1	14	33.8				31.72	1.07			5	Pp	SOD	
10	5	SOD	Pp	2	12	2	2	37.0				31.72	1.17			5	Pp	SOD	
11	5	SOD	Pp	2	60	3	20	37.0				31.72	1.17			5	Pp	SOD	
12	5	SOD	Pp	2	52	4	22	30.9				31.72	0.97			5	Pp	SOD	
13	5	SOD	Pp	2	87	5	23	47.4				31.72	1.49			5	Pp	SOD	
14	5	SOD	Pp	2	8	6	12	37.6				31.72	1.19			5	Pp	SOD	
15	5	SOD	Pp	2	95	7	8	39.9				31.72	1.26			5	Pp	SOD	
16	5	SOD	Pp	2	77	8	14	NA	37.66			NA	NA	1.187		5	Pp	SOD	
17	5	SOD	Pp	3	39	1	18	36.4				31.72	1.15			5	Pp	SOD	
18	5	SOD	Pp	3	92	2	16	36.6				31.72	1.15			5	Pp	SOD	
19	5	SOD	Pp	3	78	3	17	35.9				31.72	1.13			5	Pp	SOD	
20	5	SOD	Pp	3	9	4	1	28.4				31.72	0.90			5	Pp	SOD	
21	5	SOD	Pp	3	63	5	14	42.0				31.72	1.32			5	Pp	SOD	
22	5	SOD	Pp	3	15	6	23	28.7				31.72	0.90			5	Pp	SOD	
23	5	SOD	Pp	3	18	7	2	36.2				31.72	1.14			5	Pp	SOD	
24	5	SOD	Pp	3	13	8	11	34.5	34.84			31.72	1.09	1.098		5	Pp	SOD	
25	5	SOD	Pp	4	4	1	7	40.7				31.72	1.28			5	Pp	SOD	
26	5	SOD	Pp	4	36	2	7	30.3				31.72	0.96			5	Pp	SOD	
27	5	SOD	Pp	4	49	3	11	28.0				31.72	0.88			5	Pp	SOD	
28	5	SOD	Pp	4	6	4	9	31.9				31.72	1.01			5	Pp	SOD	
29	5	SOD	Pp	4	68	5	17	43.6				31.72	1.37			5	Pp	SOD	
30	5	SOD	Pp	4	43	6	22	34.4				31.72	1.08			5	Pp	SOD	
31	5	SOD	Pp	4	83	7	7	34.7				31.72	1.09			5	Pp	SOD	
32	5	SOD	Pp	4	65	8	8	NA	34.80			NA	NA	1.097		5	Pp	SOD	
33	5	SOD	Pp	5	70	1	9	34.8				31.72	1.10			5	Pp	SOD	
34	5	SOD	Pp	5	73	2	10	38.4				31.72	1.21			5	Pp	SOD	
35	5	SOD	Pp	5	93	3	5	28.3				31.72	0.89			5	Pp	SOD	
36	5	SOD	Pp	5	82	4	2	29.7				31.72	0.94			5	Pp	SOD	
37	5	SOD	Pp	5	38	5	7	43.3				31.72	1.36			5	Pp	SOD	
38	5	SOD	Pp	5	46	6	11	33.2				31.72	1.05			5	Pp	SOD	
39	5	SOD	Pp	5	67	7	16	36.5				31.72	1.15			5	Pp	SOD	
40	5	SOD	Pp	5	45	8	6	33.1	34.66	35.14		31.72	1.04	1.093	1.108	5	Pp	SOD	35.08
41	5	SOD	Np	1	99	1	24	31.7				31.72	1.00			5	Np	SOD	
42	5	SOD	Np	1	37	2	22	0.9				31.72	0.03			5	Np	SOD	
43	5	SOD	Np	1	7	5	21	34.5				31.72	1.09			5	Np	SOD	
44	5	SOD	Np	1	55	6	2	36.7	25.95			31.72	1.16	0.818		5	Np	SOD	
45	5	SOD	Np	2	47	3	14	23.6				31.72	0.74			5	Np	SOD	

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46	5	SOD	Np	2	22	4	12	39.1				31.72	1.23				5	Np	SOD	
47	5	SOD	Np	2	75	7	21	38.6				31.72	1.22				5	Np	SOD	
48	5	SOD	Np	2	44	8	4	1.3	25.65			31.72	0.04	0.809			5	Np	SOD	
49	5	SOD	Np	3	35	1	10	19.9				31.72	0.63				5	Np	SOD	
50	5	SOD	Np	3	33	2	1	5.3				31.72	0.17				5	Np	SOD	
51	5	SOD	Np	3	3	5	6	NA				NA	NA				5	Np	SOD	
52	5	SOD	Np	3	62	6	21	20.8	15.33			31.72	0.66	0.483			5	Np	SOD	
53	5	SOD	Np	4	31	3	13	0.6				31.72	0.02				5	Np	SOD	
54	5	SOD	Np	4	40	4	5	36.2				31.72	1.14				5	Np	SOD	
55	5	SOD	Np	4	94	7	5	21.5				31.72	0.68				5	Np	SOD	
56	5	SOD	Np	4	41	8	9	0.9	14.80			31.72	0.03	0.467			5	Np	SOD	
57	5	SOD	Np	5	23	1	23	41.5				31.72	1.31				5	Np	SOD	
58	5	SOD	Np	5	56	3	16	33.1				31.72	1.04				5	Np	SOD	
59	5	SOD	Np	5	81	5	1	30.5				31.72	0.96				5	Np	SOD	
60	5	SOD	Np	5	59	7	13	43.9	37.25	23.80		31.72	1.38	1.174	0.750		5	Np	SOD	24.24
71	5	SOD	Null	NA	89	1	15	38.1				31.72	1.20				5	Null	SOD	
72	5	SOD	Null	NA	14	2	5	27.0				31.72	0.85				5	Null	SOD	
73	5	SOD	Null	NA	16	3	19	28.0				31.72	0.88				5	Null	SOD	
74	5	SOD	Null	NA	5	4	23	30.6				31.72	0.96				5	Null	SOD	
75	5	SOD	Null	NA	90	5	22	32.4				31.72	1.02				5	Null	SOD	
76	5	SOD	Null	NA	2	6	7	33.2				31.72	1.05				5	Null	SOD	
77	5	SOD	Null	NA	53	7	14	31.2				31.72	0.98				5	Null	SOD	
78	5	SOD	Null	NA	27	8	21	19.5				31.72	0.61				5	Null	SOD	
79	5	SOD	Null	NA	76	1	20	38.7				31.72	1.22				5	Null	SOD	
80	5	SOD	Null	NA	91	2	21	32.1				31.72	1.01				5	Null	SOD	
81	5	SOD	Null	NA	17	3	8	29.6				31.72	0.93				5	Null	SOD	
82	5	SOD	Null	NA	72	4	18	35.2				31.72	1.11				5	Null	SOD	
83	5	SOD	Null	NA	98	5	19	30.9				31.72	0.97				5	Null	SOD	
84	5	SOD	Null	NA	11	6	20	31.3				31.72	0.99				5	Null	SOD	
85	5	SOD	Null	NA	42	7	23	NA				NA	NA				5	Null	SOD	
86	5	SOD	Null	NA	28	8	5	17.1				31.72	0.54				5	Null	SOD	
87	5	SOD	Null	NA	10	1	3	37.1				31.72	1.17				5	Null	SOD	
88	5	SOD	Null	NA	51	2	15	33.5				31.72	1.06				5	Null	SOD	
89	5	SOD	Null	NA	25	3	2	33.5				31.72	1.06				5	Null	SOD	
90	5	SOD	Null	NA	19	4	15	NA				NA	NA				5	Null	SOD	
91	5	SOD	Null	NA	100	5	15	34.6				31.72	1.09				5	Null	SOD	
92	5	SOD	Null	NA	64	6	14	NA				NA	NA				5	Null	SOD	
93	5	SOD	Null	NA	54	7	25	NA				NA	NA				5	Null	SOD	
94	5	SOD	Null	NA	61	8	7	40.5				31.72	1.28				5	Null	SOD	
95	5	SOD	Null	NA	74	1	25	34.7				31.72	1.09				5	Null	SOD	
96	5	SOD	Null	NA	30	3	6	27.0				31.72	0.85				5	Null	SOD	
97	5	SOD	Null	NA	24	4	17	36.2				31.72	1.14				5	Null	SOD	
98	5	SOD	Null	NA	66	5	8	35.5				31.72	1.12				5	Null	SOD	
99	5	SOD	Null	NA	71	6	9	38.3		Grand Average	31.72	1.21				5	Null	SOD		
100	5	SOD	Null	NA	26	8	18	33.5	32.28	31.72	31.72	1.06	1.018				5	Null	SOD	32.28
101	5	ALU	Pp	1	165	1	22	57.8				38.27	1.51				5	Pp	ALU	
102	5	ALU	Pp	1	136	2	12	42.4				38.27	1.11				5	Pp	ALU	
103	5	ALU	Pp	1	131	3	22	50.5				38.27	1.32				5	Pp	ALU	
104	5	ALU	Pp	1	103	4	4	48.2				38.27	1.26				5	Pp	ALU	
105	5	ALU	Pp	1	104	5	9	50.8				38.27	1.33				5	Pp	ALU	
106	5	ALU	Pp	1	132	6	8	49.4				38.27	1.29				5	Pp	ALU	
107	5	ALU	Pp	1	195	7	19	36.3				38.27	0.95				5	Pp	ALU	
108	5	ALU	Pp	1	145	8	12	53.5	48.61			38.27	1.40	1.270			5	Pp	ALU	

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									5	Np	SOD
									5	Np	SOD
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20.84	2.77				41.39	1.40			5	Pp	ALU
20.84	2.03				41.39	1.02			5	Pp	ALU
20.84	2.42				41.39	1.22			5	Pp	ALU
20.84	2.31				41.39	1.16			5	Pp	ALU
20.84	2.44				41.39	1.23			5	Pp	ALU
20.84	2.37				41.39	1.19			5	Pp	ALU
20.84	1.74				41.39	0.88			5	Pp	ALU
20.84	2.57	2.33			41.39	1.29	1.175		5	Pp	ALU

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109	5	ALU	Pp	2	130	1	19	38.2				38.27	1.00				5	Pp	ALU	
110	5	ALU	Pp	2	169	2	13	49.7				38.27	1.30				5	Pp	ALU	
111	5	ALU	Pp	2	178	3	21	36.2				38.27	0.95				5	Pp	ALU	
112	5	ALU	Pp	2	150	4	20	38.9				38.27	1.02				5	Pp	ALU	
113	5	ALU	Pp	2	120	5	24	NA				NA	NA				5	Pp	ALU	
114	5	ALU	Pp	2	113	6	18	36.9				38.27	0.96				5	Pp	ALU	
115	5	ALU	Pp	2	164	7	18	42.3				38.27	1.11				5	Pp	ALU	
116	5	ALU	Pp	2	134	8	25	51.3	41.93			38.27	1.34	1.096			5	Pp	ALU	
117	5	ALU	Pp	3	199	1	4	49.6				38.27	1.30				5	Pp	ALU	
118	5	ALU	Pp	3	156	2	25	36.1				38.27	0.94				5	Pp	ALU	
119	5	ALU	Pp	3	175	3	7	43.3				38.27	1.13				5	Pp	ALU	
120	5	ALU	Pp	3	196	4	19	53.4				38.27	1.40				5	Pp	ALU	
121	5	ALU	Pp	3	144	5	16	40.0				38.27	1.05				5	Pp	ALU	
122	5	ALU	Pp	3	149	6	3	36.6				38.27	0.96				5	Pp	ALU	
123	5	ALU	Pp	3	186	7	3	42.4				38.27	1.11				5	Pp	ALU	
124	5	ALU	Pp	3	121	8	3	39.2	42.58			38.27	1.02	1.113			5	Pp	ALU	
125	5	ALU	Pp	4	187	1	17	64.6				38.27	1.69				5	Pp	ALU	
126	5	ALU	Pp	4	176	2	14	46.5				38.27	1.22				5	Pp	ALU	
127	5	ALU	Pp	4	133	3	25	38.5				38.27	1.01				5	Pp	ALU	
128	5	ALU	Pp	4	114	4	21	44.7				38.27	1.17				5	Pp	ALU	
129	5	ALU	Pp	4	142	5	3	47.5				38.27	1.24				5	Pp	ALU	
130	5	ALU	Pp	4	127	6	5	43.4				38.27	1.13				5	Pp	ALU	
131	5	ALU	Pp	4	168	7	1	12.5				38.27	0.33				5	Pp	ALU	
132	5	ALU	Pp	4	111	8	17	47.8	43.19			38.27	1.25	1.129			5	Pp	ALU	
133	5	ALU	Pp	5	129	1	5	49.8				38.27	1.30				5	Pp	ALU	
134	5	ALU	Pp	5	146	2	19	48.4				38.27	1.26				5	Pp	ALU	
135	5	ALU	Pp	5	137	3	4	42.8				38.27	1.12				5	Pp	ALU	
136	5	ALU	Pp	5	135	4	8	38.3				38.27	1.00				5	Pp	ALU	
137	5	ALU	Pp	5	107	5	4	52.5				38.27	1.37				5	Pp	ALU	
138	5	ALU	Pp	5	192	6	17	41.3				38.27	1.08				5	Pp	ALU	
139	5	ALU	Pp	5	172	7	9	41.6				38.27	1.09				5	Pp	ALU	
140	5	ALU	Pp	5	154	8	2	35.5	43.78	44.02		38.27	0.93	1.144	1.150		5	Pp	ALU	44.07
141	5	ALU	Np	1	182	1	21	35.4				38.27	0.93				5	Np	ALU	
142	5	ALU	Np	1	118	2	4	1.9				38.27	0.05				5	Np	ALU	
143	5	ALU	Np	1	143	5	20	37.4				38.27	0.98				5	Np	ALU	
144	5	ALU	Np	1	112	6	10	25.8	25.13			38.27	0.67	0.657			5	Np	ALU	
145	5	ALU	Np	2	101	3	15	0.5				38.27	0.01				5	Np	ALU	
146	5	ALU	Np	2	160	4	7	0.9				38.27	0.02				5	Np	ALU	
147	5	ALU	Np	2	181	7	20	5.8				38.27	0.15				5	Np	ALU	
148	5	ALU	Np	2	198	8	22	40.2	11.85			38.27	1.05	0.310			5	Np	ALU	
149	5	ALU	Np	3	177	1	16	37.3				38.27	0.97				5	Np	ALU	
150	5	ALU	Np	3	110	2	9	25.3				38.27	0.66				5	Np	ALU	
151	5	ALU	Np	3	125	5	5	40.0				38.27	1.05				5	Np	ALU	
152	5	ALU	Np	3	166	6	25	36.7	34.83			38.27	0.96	0.910			5	Np	ALU	
153	5	ALU	Np	4	102	3	1	NA				NA	NA				5	Np	ALU	
154	5	ALU	Np	4	159	4	25	0.3				38.27	0.01				5	Np	ALU	
155	5	ALU	Np	4	188	7	15	1.6				38.27	0.04				5	Np	ALU	
156	5	ALU	Np	4	139	8	16	NA	0.95			NA	NA	0.025			5	Np	ALU	
157	5	ALU	Np	5	190	2	24	0.6				38.27	0.02				5	Np	ALU	
158	5	ALU	Np	5	171	4	24	34.2				38.27	0.89				5	Np	ALU	
159	5	ALU	Np	5	153	6	13	50.7				38.27	1.32				5	Np	ALU	
160	5	ALU	Np	5	161	8	23	0.6	21.53	18.86		38.27	0.02	0.562	0.493		5	Np	ALU	20.84
171	5	ALU	Null	NA	141	1	2	38.6				38.27	1.01				5	Null	ALU	

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172	5	ALU	Null	NA	117	2	23	41.3				38.27	1.08				5	Null	ALU	
173	5	ALU	Null	NA	108	3	24	41.0				38.27	1.07				5	Null	ALU	
174	5	ALU	Null	NA	191	4	10	37.7				38.27	0.99				5	Null	ALU	
175	5	ALU	Null	NA	162	5	10	47.8				38.27	1.25				5	Null	ALU	
176	5	ALU	Null	NA	170	6	1	40.7				38.27	1.06				5	Null	ALU	
177	5	ALU	Null	NA	185	7	11	36.4				38.27	0.95				5	Null	ALU	
178	5	ALU	Null	NA	155	8	20	NA				NA	NA				5	Null	ALU	
179	5	ALU	Null	NA	105	1	11	54.9				38.27	1.43				5	Null	ALU	
180	5	ALU	Null	NA	189	2	20	38.1				38.27	1.00				5	Null	ALU	
181	5	ALU	Null	NA	123	3	12	44.3				38.27	1.16				5	Null	ALU	
182	5	ALU	Null	NA	106	4	16	33.2				38.27	0.87				5	Null	ALU	
183	5	ALU	Null	NA	148	5	18	44.7				38.27	1.17				5	Null	ALU	
184	5	ALU	Null	NA	194	6	24	46.3				38.27	1.21				5	Null	ALU	
185	5	ALU	Null	NA	180	7	17	46.4				38.27	1.21				5	Null	ALU	
186	5	ALU	Null	NA	119	8	15	43.7				38.27	1.14				5	Null	ALU	
187	5	ALU	Null	NA	157	1	12	44.5				38.27	1.16				5	Null	ALU	
188	5	ALU	Null	NA	124	2	11	35.6				38.27	0.93				5	Null	ALU	
189	5	ALU	Null	NA	138	3	18	37.6				38.27	0.98				5	Null	ALU	
190	5	ALU	Null	NA	140	4	14	40.3				38.27	1.05				5	Null	ALU	
191	5	ALU	Null	NA	109	5	2	42.0				38.27	1.10				5	Null	ALU	
192	5	ALU	Null	NA	200	6	4	46.8				38.27	1.22				5	Null	ALU	
193	5	ALU	Null	NA	167	7	22	40.4				38.27	1.06				5	Null	ALU	
194	5	ALU	Null	NA	173	8	13	36.9				38.27	0.96				5	Null	ALU	
195	5	ALU	Null	NA	158	2	6	40.8				38.27	1.07				5	Null	ALU	
196	5	ALU	Null	NA	122	3	9	43.3				38.27	1.13				5	Null	ALU	
197	5	ALU	Null	NA	152	4	3	43.6				38.27	1.14				5	Null	ALU	
198	5	ALU	Null	NA	184	5	25	NA				NA	NA				5	Null	ALU	
199	5	ALU	Null	NA	163	7	6	39.9		Grand Average		38.27	1.04				5	Null	ALU	
200	5	ALU	Null	NA	126	8	1	32.0	41.39		38.27	38.27	0.84	1.081		5	Null	ALU	41.39	
1	6	SOD	Pp	1	4	1	25	NA				NA	NA				6	Pp	SOD	
2	6	SOD	Pp	1	71	2	4	NA				NA	NA				6	Pp	SOD	
3	6	SOD	Pp	1	58	3	16	34.8				30.05	1.16				6	Pp	SOD	
4	6	SOD	Pp	1	8	4	24	34.2				30.05	1.14				6	Pp	SOD	
5	6	SOD	Pp	1	12	5	23	30.7				30.05	1.02				6	Pp	SOD	
6	6	SOD	Pp	1	13	6	16	25.1				30.05	0.84				6	Pp	SOD	
7	6	SOD	Pp	1	68	7	7	40.4				30.05	1.34				6	Pp	SOD	
8	6	SOD	Pp	1	83	8	17	35.3	33.42			30.05	1.17	1.112			6	Pp	SOD	
9	6	SOD	Pp	2	37	1	7	39.5				30.05	1.31				6	Pp	SOD	
10	6	SOD	Pp	2	67	2	10	29.7				30.05	0.99				6	Pp	SOD	
11	6	SOD	Pp	2	54	3	22	21.4				30.05	0.71				6	Pp	SOD	
12	6	SOD	Pp	2	28	4	21	34.6				30.05	1.15				6	Pp	SOD	
13	6	SOD	Pp	2	66	5	16	30.9				30.05	1.03				6	Pp	SOD	
14	6	SOD	Pp	2	94	6	20	35.1				30.05	1.17				6	Pp	SOD	
15	6	SOD	Pp	2	89	7	4	27.6				30.05	0.92				6	Pp	SOD	
16	6	SOD	Pp	2	75	8	24	20.6	29.93			30.05	0.69	0.996			6	Pp	SOD	
17	6	SOD	Pp	3	48	1	22	36.2				30.05	1.20				6	Pp	SOD	
18	6	SOD	Pp	3	42	2	7	35.3				30.05	1.17				6	Pp	SOD	
19	6	SOD	Pp	3	23	3	13	37.8				30.05	1.26				6	Pp	SOD	
20	6	SOD	Pp	3	73	4	19	41.3				30.05	1.37				6	Pp	SOD	
21	6	SOD	Pp	3	95	5	15	NA				NA	NA				6	Pp	SOD	
22	6	SOD	Pp	3	51	6	1	38.8				30.05	1.29				6	Pp	SOD	
23	6	SOD	Pp	3	27	7	8	35.3				30.05	1.17				6	Pp	SOD	
24	6	SOD	Pp	3	59	8	10	37.4	37.44			30.05	1.24	1.246			6	Pp	SOD	

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									5	Null	ALU
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									5	Null	ALU
NA	NA				NA				6	Pp	SOD
NA	NA				NA				6	Pp	SOD
19.09	1.82				31.46	1.11			6	Pp	SOD
19.09	1.79				31.46	1.09			6	Pp	SOD
19.09	1.61				31.46	0.98			6	Pp	SOD
19.09	1.31				31.46	0.80			6	Pp	SOD
19.09	2.12				31.46	1.28			6	Pp	SOD
19.09	1.85	1.75			31.46	1.12	1.062		6	Pp	SOD
19.09	2.07				31.46	1.26			6	Pp	SOD
19.09	1.56				31.46	0.94			6	Pp	SOD
19.09	1.12				31.46	0.68			6	Pp	SOD
19.09	1.81				31.46	1.10			6	Pp	SOD
19.09	1.62				31.46	0.98			6	Pp	SOD
19.09	1.84				31.46	1.12			6	Pp	SOD
19.09	1.45				31.46	0.88			6	Pp	SOD
19.09	1.08	1.57			31.46	0.65	0.951		6	Pp	SOD
19.09	1.90				31.46	1.15			6	Pp	SOD
19.09	1.85				31.46	1.12			6	Pp	SOD
19.09	1.98				31.46	1.20			6	Pp	SOD
19.09	2.16				31.46	1.31			6	Pp	SOD
NA	NA				NA				6	Pp	SOD
19.09	2.03				31.46	1.23			6	Pp	SOD
19.09	1.85				31.46	1.12			6	Pp	SOD
19.09	1.96	1.96			31.46	1.19	1.190		6	Pp	SOD

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25	6	SOD	Pp	4	38	1	17	41.3				30.05	1.37			6	Pp	SOD	
26	6	SOD	Pp	4	35	2	25	32.1				30.05	1.07			6	Pp	SOD	
27	6	SOD	Pp	4	16	3	17	38.9				30.05	1.29			6	Pp	SOD	
28	6	SOD	Pp	4	46	4	13	29.3				30.05	0.98			6	Pp	SOD	
29	6	SOD	Pp	4	97	5	11	26.5				30.05	0.88			6	Pp	SOD	
30	6	SOD	Pp	4	52	6	22	33.1				30.05	1.10			6	Pp	SOD	
31	6	SOD	Pp	4	91	7	23	38.0				30.05	1.26			6	Pp	SOD	
32	6	SOD	Pp	4	7	8	2	37.0	34.53			30.05	1.23	1.149		6	Pp	SOD	
33	6	SOD	Pp	5	14	1	3	44.5				30.05	1.48			6	Pp	SOD	
34	6	SOD	Pp	5	86	2	12	36.3				30.05	1.21			6	Pp	SOD	
35	6	SOD	Pp	5	53	3	5	29.8				30.05	0.99			6	Pp	SOD	
36	6	SOD	Pp	5	85	4	10	33.3				30.05	1.11			6	Pp	SOD	
37	6	SOD	Pp	5	50	5	2	40.8				30.05	1.36			6	Pp	SOD	
38	6	SOD	Pp	5	79	6	4	33.2				30.05	1.10			6	Pp	SOD	
39	6	SOD	Pp	5	1	7	12	NA				NA	NA			6	Pp	SOD	
40	6	SOD	Pp	5	19	8	13	41.8	37.10	34.48		30.05	1.39	1.235	1.148	6	Pp	SOD	34.39
41	6	SOD	Np	1	64	1	6	NA				NA	NA			6	Np	SOD	
42	6	SOD	Np	1	41	2	11	0.6				30.05	0.02			6	Np	SOD	
43	6	SOD	Np	1	98	5	17	29.5				30.05	0.98			6	Np	SOD	
44	6	SOD	Np	1	72	6	17	8.1	12.73			30.05	0.27	0.424		6	Np	SOD	
45	6	SOD	Np	2	57	3	6	5.5				30.05	0.18			6	Np	SOD	
46	6	SOD	Np	2	62	4	6	23.3				30.05	0.78			6	Np	SOD	
47	6	SOD	Np	2	80	7	11	0.8				30.05	0.03			6	Np	SOD	
48	6	SOD	Np	2	31	8	5	28.5	14.53			30.05	0.95	0.483		6	Np	SOD	
49	6	SOD	Np	3	56	1	8	26.9				30.05	0.90			6	Np	SOD	
50	6	SOD	Np	3	44	2	19	30.1				30.05	1.00			6	Np	SOD	
51	6	SOD	Np	3	70	5	5	34.1				30.05	1.13			6	Np	SOD	
52	6	SOD	Np	3	34	6	7	39.7	32.70			30.05	1.32	1.088		6	Np	SOD	
53	6	SOD	Np	4	78	3	2	17.0				30.05	0.57			6	Np	SOD	
54	6	SOD	Np	4	61	4	5	19.8				30.05	0.66			6	Np	SOD	
55	6	SOD	Np	4	93	7	25	36.9				30.05	1.23			6	Np	SOD	
56	6	SOD	Np	4	74	8	8	1.0	18.68			30.05	0.03	0.622		6	Np	SOD	
57	6	SOD	Np	5	43	1	23	19.1				30.05	0.64			6	Np	SOD	
58	6	SOD	Np	5	92	3	25	22.4				30.05	0.75			6	Np	SOD	
59	6	SOD	Np	5	9	5	18	NA				NA	NA			6	Np	SOD	
60	6	SOD	Np	5	63	7	10	0.4	13.97	18.52		30.05	0.01	0.465	0.616	6	Np	SOD	19.09
71	6	SOD	Null	NA	2	1	12	23.6				30.05	0.79			6	Null	SOD	
72	6	SOD	Null	NA	90	2	24	31.9				30.05	1.06			6	Null	SOD	
73	6	SOD	Null	NA	45	3	24	34.2				30.05	1.14			6	Null	SOD	
74	6	SOD	Null	NA	39	4	16	36.0				30.05	1.20			6	Null	SOD	
75	6	SOD	Null	NA	82	5	4	33.7				30.05	1.12			6	Null	SOD	
76	6	SOD	Null	NA	69	6	23	36.4				30.05	1.21			6	Null	SOD	
77	6	SOD	Null	NA	76	7	22	31.1				30.05	1.04			6	Null	SOD	
78	6	SOD	Null	NA	77	8	6	22.6				30.05	0.75			6	Null	SOD	
79	6	SOD	Null	NA	30	1	1	32.4				30.05	1.08			6	Null	SOD	
80	6	SOD	Null	NA	29	2	22	23.3				30.05	0.78			6	Null	SOD	
81	6	SOD	Null	NA	20	3	14	31.9				30.05	1.06			6	Null	SOD	
82	6	SOD	Null	NA	65	4	7	32.2				30.05	1.07			6	Null	SOD	
83	6	SOD	Null	NA	21	5	12	33.6				30.05	1.12			6	Null	SOD	
84	6	SOD	Null	NA	18	6	25	22.6				30.05	0.75			6	Null	SOD	
85	6	SOD	Null	NA	40	7	2	35.8				30.05	1.19			6	Null	SOD	
86	6	SOD	Null	NA	100	8	4	30.4				30.05	1.01			6	Null	SOD	
87	6	SOD	Null	NA	15	1	9	32.6				30.05	1.08			6	Null	SOD	

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88	6	SOD	Null	NA	6	2	13	32.2				30.05	1.07			6	Null	SOD	
89	6	SOD	Null	NA	84	3	12	35.8				30.05	1.19			6	Null	SOD	
90	6	SOD	Null	NA	49	4	1	NA				NA	NA			6	Null	SOD	
91	6	SOD	Null	NA	33	5	3	32.9				30.05	1.09			6	Null	SOD	
92	6	SOD	Null	NA	55	6	14	36.2				30.05	1.20			6	Null	SOD	
93	6	SOD	Null	NA	25	7	16	29.2				30.05	0.97			6	Null	SOD	
94	6	SOD	Null	NA	24	8	20	33.2				30.05	1.10			6	Null	SOD	
95	6	SOD	Null	NA	81	1	15	34.8				30.05	1.16			6	Null	SOD	
96	6	SOD	Null	NA	3	3	10	31.0				30.05	1.03			6	Null	SOD	
97	6	SOD	Null	NA	5	4	8	30.5				30.05	1.02			6	Null	SOD	
98	6	SOD	Null	NA	17	5	14	29.8				30.05	0.99			6	Null	SOD	
99	6	SOD	Null	NA	60	6	10	35.4		Grand Average		30.05	1.18			6	Null	SOD	
100	6	SOD	Null	NA	96	8	11	27.0	31.46		30.05	30.05	0.90	1.047	6	Null	SOD	31.46	
101	6	ALU	Pp	1	116	1	10	38.9				39.96	0.97			6	Pp	ALU	
102	6	ALU	Pp	1	122	2	1	40.2				39.96	1.01			6	Pp	ALU	
103	6	ALU	Pp	1	102	3	7	40.5				39.96	1.01			6	Pp	ALU	
104	6	ALU	Pp	1	196	4	2	34.3				39.96	0.86			6	Pp	ALU	
105	6	ALU	Pp	1	188	5	10	43.5				39.96	1.09			6	Pp	ALU	
106	6	ALU	Pp	1	192	6	3	38.2				39.96	0.96			6	Pp	ALU	
107	6	ALU	Pp	1	131	7	6	NA				NA	NA			6	Pp	ALU	
108	6	ALU	Pp	1	158	8	3	47.4	40.43			39.96	1.19	1.012		6	Pp	ALU	
109	6	ALU	Pp	2	178	1	19	46.3				39.96	1.16			6	Pp	ALU	
110	6	ALU	Pp	2	139	2	23	47.3				39.96	1.18			6	Pp	ALU	
111	6	ALU	Pp	2	172	3	4	48.9				39.96	1.22			6	Pp	ALU	
112	6	ALU	Pp	2	169	4	9	44.4				39.96	1.11			6	Pp	ALU	
113	6	ALU	Pp	2	150	5	9	37.2				39.96	0.93			6	Pp	ALU	
114	6	ALU	Pp	2	177	6	8	NA				NA	NA			6	Pp	ALU	
115	6	ALU	Pp	2	160	7	14	40.5				39.96	1.01			6	Pp	ALU	
116	6	ALU	Pp	2	127	8	15	45.0	44.23			39.96	1.13	1.107		6	Pp	ALU	
117	6	ALU	Pp	3	140	1	20	49.3				39.96	1.23			6	Pp	ALU	
118	6	ALU	Pp	3	117	2	2	45.5				39.96	1.14			6	Pp	ALU	
119	6	ALU	Pp	3	137	3	1	38.0				39.96	0.95			6	Pp	ALU	
120	6	ALU	Pp	3	121	4	3	42.5				39.96	1.06			6	Pp	ALU	
121	6	ALU	Pp	3	171	5	1	38.9				39.96	0.97			6	Pp	ALU	
122	6	ALU	Pp	3	106	6	15	48.5				39.96	1.21			6	Pp	ALU	
123	6	ALU	Pp	3	168	7	19	40.5				39.96	1.01			6	Pp	ALU	
124	6	ALU	Pp	3	157	8	18	35.5	42.34			39.96	0.89	1.060		6	Pp	ALU	
125	6	ALU	Pp	4	163	1	14	51.8				39.96	1.30			6	Pp	ALU	
126	6	ALU	Pp	4	175	2	14	NA				NA	NA			6	Pp	ALU	
127	6	ALU	Pp	4	200	3	18	41.2				39.96	1.03			6	Pp	ALU	
128	6	ALU	Pp	4	134	4	14	47.6				39.96	1.19			6	Pp	ALU	
129	6	ALU	Pp	4	147	5	20	41.0				39.96	1.03			6	Pp	ALU	
130	6	ALU	Pp	4	189	6	9	53.2				39.96	1.33			6	Pp	ALU	
131	6	ALU	Pp	4	191	7	20	47.0				39.96	1.18			6	Pp	ALU	
132	6	ALU	Pp	4	104	8	9	43.6	46.49			39.96	1.09	1.163		6	Pp	ALU	
133	6	ALU	Pp	5	186	1	18	38.1				39.96	0.95			6	Pp	ALU	
134	6	ALU	Pp	5	133	2	3	46.6				39.96	1.17			6	Pp	ALU	
135	6	ALU	Pp	5	197	3	19	NA				NA	NA			6	Pp	ALU	
136	6	ALU	Pp	5	105	4	18	48.1				39.96	1.20			6	Pp	ALU	
137	6	ALU	Pp	5	180	5	25	42.8				39.96	1.07			6	Pp	ALU	
138	6	ALU	Pp	5	179	6	18	46.8				39.96	1.17			6	Pp	ALU	
139	6	ALU	Pp	5	136	7	17	56.4				39.96	1.41			6	Pp	ALU	
140	6	ALU	Pp	5	149	8	12	36.1	44.99	43.69		39.96	0.90	1.126	1.093	6	Pp	ALU	43.66

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34.35	1.13				39.05	1.00			6	Pp	ALU	
34.35	1.17				39.05	1.03			6	Pp	ALU	
34.35	1.18				39.05	1.04			6	Pp	ALU	
34.35	1.00				39.05	0.88			6	Pp	ALU	
34.35	1.27				39.05	1.11			6	Pp	ALU	
34.35	1.11				39.05	0.98			6	Pp	ALU	
NA	NA				NA	NA			6	Pp	ALU	
34.35	1.38	1.18			39.05	1.21	1.035		6	Pp	ALU	
34.35	1.35				39.05	1.19			6	Pp	ALU	
34.35	1.38				39.05	1.21			6	Pp	ALU	
34.35	1.42				39.05	1.25			6	Pp	ALU	
34.35	1.29				39.05	1.14			6	Pp	ALU	
34.35	1.08				39.05	0.95			6	Pp	ALU	
NA	NA				NA	NA			6	Pp	ALU	
34.35	1.18				39.05	1.04			6	Pp	ALU	
34.35	1.31	1.29			39.05	1.15	1.133		6	Pp	ALU	
34.35	1.44				39.05	1.26			6	Pp	ALU	
34.35	1.32				39.05	1.17			6	Pp	ALU	
34.35	1.11				39.05	0.97			6	Pp	ALU	
34.35	1.24				39.05	1.09			6	Pp	ALU	
34.35	1.13				39.05	1.00			6	Pp	ALU	
34.35	1.41				39.05	1.24			6	Pp	ALU	
34.35	1.18				39.05	1.04			6	Pp	ALU	
34.35	1.03	1.23			39.05	0.91	1.084		6	Pp	ALU	
34.35	1.51				39.05	1.33			6	Pp	ALU	
NA	NA				NA	NA			6	Pp	ALU	
34.35	1.20				39.05	1.06			6	Pp	ALU	
34.35	1.39				39.05	1.22			6	Pp	ALU	
34.35	1.19				39.05	1.05			6	Pp	ALU	
34.35	1.55				39.05	1.36			6	Pp	ALU	
34.35	1.37				39.05	1.20			6	Pp	ALU	
34.35	1.27	1.35			39.05	1.12	1.190		6	Pp	ALU	
34.35	1.11				39.05	0.98			6	Pp	ALU	
34.35	1.36				39.05	1.19			6	Pp	ALU	
NA	NA				NA	NA			6	Pp	ALU	
34.35	1.40				39.05	1.23			6	Pp	ALU	
34.35	1.25				39.05	1.10			6	Pp	ALU	
34.35	1.36		Generation 6		39.05	1.20		Generation 6	6	Pp	ALU	
34.35	1.64		Average	StDev	39.05	1.44		Average	6	Pp	ALU	
34.35	1.05	1.31	1.27	0.07	39.05	0.92	1.152	1.119	0.060	6	Pp	ALU

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141	6	ALU	Np	1	156	1	24	35.6				39.96	0.89				6	Np	ALU	
142	6	ALU	Np	1	132	2	8	47.3				39.96	1.18				6	Np	ALU	
143	6	ALU	Np	1	125	5	19	42.3				39.96	1.06				6	Np	ALU	
144	6	ALU	Np	1	144	6	5	29.5	38.68			39.96	0.74	0.968			6	Np	ALU	
145	6	ALU	Np	2	130	3	3	37.4				39.96	0.94				6	Np	ALU	
146	6	ALU	Np	2	193	4	4	32.2				39.96	0.81				6	Np	ALU	
147	6	ALU	Np	2	173	7	15	35.9				39.96	0.90				6	Np	ALU	
148	6	ALU	Np	2	141	8	14	33.9	34.85			39.96	0.85	0.872			6	Np	ALU	
149	6	ALU	Np	3	114	1	11	33.3				39.96	0.83				6	Np	ALU	
150	6	ALU	Np	3	164	2	17	32.4				39.96	0.81				6	Np	ALU	
151	6	ALU	Np	3	108	5	13	31.7				39.96	0.79				6	Np	ALU	
152	6	ALU	Np	3	113	6	6	26.4	30.95			39.96	0.66	0.775			6	Np	ALU	
153	6	ALU	Np	4	146	3	21	37.8				39.96	0.95				6	Np	ALU	
154	6	ALU	Np	4	112	4	22	NA				NA	NA				6	Np	ALU	
155	6	ALU	Np	4	165	7	24	36.6				39.96	0.92				6	Np	ALU	
156	6	ALU	Np	4	194	8	25	35.7	36.70			39.96	0.89	0.918			6	Np	ALU	
157	6	ALU	Np	5	190	2	16	31.3				39.96	0.78				6	Np	ALU	
158	6	ALU	Np	5	142	4	17	35.6				39.96	0.89				6	Np	ALU	
159	6	ALU	Np	5	124	6	11	30.5				39.96	0.76				6	Np	ALU	
160	6	ALU	Np	5	159	8	23	27.2	31.15	34.47		39.96	0.68	0.780	0.862		6	Np	ALU	34.35
171	6	ALU	Null	NA	199	1	21	35.3				39.96	0.88				6	Null	ALU	
172	6	ALU	Null	NA	176	2	6	35.2				39.96	0.88				6	Null	ALU	
173	6	ALU	Null	NA	185	3	9	38.9				39.96	0.97				6	Null	ALU	
174	6	ALU	Null	NA	145	4	23	37.8				39.96	0.95				6	Null	ALU	
175	6	ALU	Null	NA	184	5	22	38.0				39.96	0.95				6	Null	ALU	
176	6	ALU	Null	NA	135	6	21	42.1				39.96	1.05				6	Null	ALU	
177	6	ALU	Null	NA	128	7	13	47.0				39.96	1.18				6	Null	ALU	
178	6	ALU	Null	NA	119	8	22	36.0				39.96	0.90				6	Null	ALU	
179	6	ALU	Null	NA	198	1	4	27.6				39.96	0.69				6	Null	ALU	
180	6	ALU	Null	NA	138	2	18	37.4				39.96	0.94				6	Null	ALU	
181	6	ALU	Null	NA	107	3	15	40.4				39.96	1.01				6	Null	ALU	
182	6	ALU	Null	NA	111	4	25	34.5				39.96	0.86				6	Null	ALU	
183	6	ALU	Null	NA	151	5	7	39.7				39.96	0.99				6	Null	ALU	
184	6	ALU	Null	NA	162	6	19	NA				NA	NA				6	Null	ALU	
185	6	ALU	Null	NA	152	7	18	43.6				39.96	1.09				6	Null	ALU	
186	6	ALU	Null	NA	109	8	16	41.4				39.96	1.04				6	Null	ALU	
187	6	ALU	Null	NA	174	1	2	37.0				39.96	0.93				6	Null	ALU	
188	6	ALU	Null	NA	181	2	15	46.2				39.96	1.16				6	Null	ALU	
189	6	ALU	Null	NA	120	3	8	42.2				39.96	1.06				6	Null	ALU	
190	6	ALU	Null	NA	143	4	20	40.7				39.96	1.02				6	Null	ALU	
191	6	ALU	Null	NA	103	5	21	36.2				39.96	0.91				6	Null	ALU	
192	6	ALU	Null	NA	129	6	24	41.7				39.96	1.04				6	Null	ALU	
193	6	ALU	Null	NA	154	7	9	38.0				39.96	0.95				6	Null	ALU	
194	6	ALU	Null	NA	115	8	1	39.4				39.96	0.99				6	Null	ALU	
195	6	ALU	Null	NA	123	2	21	37.1				39.96	0.93				6	Null	ALU	
196	6	ALU	Null	NA	126	3	23	41.8				39.96	1.05				6	Null	ALU	
197	6	ALU	Null	NA	182	4	12	41.4				39.96	1.04				6	Null	ALU	
198	6	ALU	Null	NA	167	5	24	38.2				39.96	0.96				6	Null	ALU	
199	6	ALU	Null	NA	110	7	3	40.9		Grand Average		39.96	1.02				6	Null	ALU	
200	6	ALU	Null	NA	148	8	21	36.7	39.05		39.96	39.96	0.92	0.977		6	Null	ALU	39.05	
1	7	SOD	Pp	1	12	1	17	60.9				55.01	1.11				7	Pp	SOD	
2	7	SOD	Pp	1	100	2	13	65.0				55.01	1.18				7	Pp	SOD	
3	7	SOD	Pp	1	93	3	8	56.0				55.01	1.02				7	Pp	SOD	

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4	7	SOD	Pp	1	11	4	3	67.4				55.01	1.23				7	Pp	SOD	
5	7	SOD	Pp	1	5	5	11	65.0				55.01	1.18				7	Pp	SOD	
6	7	SOD	Pp	1	85	6	18	66.3				55.01	1.21				7	Pp	SOD	
7	7	SOD	Pp	1	49	7	24	76.0				55.01	1.38				7	Pp	SOD	
8	7	SOD	Pp	1	16	8	23	70.5	65.89			55.01	1.28	1.198			7	Pp	SOD	
9	7	SOD	Pp	2	69	1	14	68.3				55.01	1.24				7	Pp	SOD	
10	7	SOD	Pp	2	6	2	3	67.5				55.01	1.23				7	Pp	SOD	
11	7	SOD	Pp	2	36	3	22	60.6				55.01	1.10				7	Pp	SOD	
12	7	SOD	Pp	2	60	4	12	56.1				55.01	1.02				7	Pp	SOD	
13	7	SOD	Pp	2	97	5	20	60.5				55.01	1.10				7	Pp	SOD	
14	7	SOD	Pp	2	14	6	21	NA				NA	NA				7	Pp	SOD	
15	7	SOD	Pp	2	63	7	7	72.0				55.01	1.31				7	Pp	SOD	
16	7	SOD	Pp	2	9	8	12	73.2	65.46			55.01	1.33	1.190			7	Pp	SOD	
17	7	SOD	Pp	3	55	1	11	44.0				55.01	0.80				7	Pp	SOD	
18	7	SOD	Pp	3	89	2	25	64.1				55.01	1.17				7	Pp	SOD	
19	7	SOD	Pp	3	8	3	21	67.2				55.01	1.22				7	Pp	SOD	
20	7	SOD	Pp	3	45	4	24	56.6				55.01	1.03				7	Pp	SOD	
21	7	SOD	Pp	3	87	5	21	50.3				55.01	0.91				7	Pp	SOD	
22	7	SOD	Pp	3	7	6	22	NA				NA	NA				7	Pp	SOD	
23	7	SOD	Pp	3	46	7	13	58.2				55.01	1.06				7	Pp	SOD	
24	7	SOD	Pp	3	42	8	24	46.0	55.20			55.01	0.84	1.003			7	Pp	SOD	
25	7	SOD	Pp	4	53	1	16	61.6				55.01	1.12				7	Pp	SOD	
26	7	SOD	Pp	4	83	2	15	62.8				55.01	1.14				7	Pp	SOD	
27	7	SOD	Pp	4	76	3	3	46.6				55.01	0.85				7	Pp	SOD	
28	7	SOD	Pp	4	41	4	18	57.8				55.01	1.05				7	Pp	SOD	x
29	7	SOD	Pp	4	35	5	10	47.9				55.01	0.87				7	Pp	SOD	x
30	7	SOD	Pp	4	32	6	4	63.8				55.01	1.16				7	Pp	SOD	
31	7	SOD	Pp	4	40	7	20	52.1				55.01	0.95				7	Pp	SOD	
32	7	SOD	Pp	4	84	8	22	55.2	55.98			55.01	1.00	1.018			7	Pp	SOD	
33	7	SOD	Pp	5	58	1	10	68.2				55.01	1.24				7	Pp	SOD	
34	7	SOD	Pp	5	74	2	14	69.2				55.01	1.26				7	Pp	SOD	
35	7	SOD	Pp	5	29	3	13	70.7				55.01	1.29				7	Pp	SOD	
36	7	SOD	Pp	5	33	4	6	57.0				55.01	1.04				7	Pp	SOD	
37	7	SOD	Pp	5	96	5	3	59.3				55.01	1.08				7	Pp	SOD	
38	7	SOD	Pp	5	90	6	1	45.5				55.01	0.83				7	Pp	SOD	
39	7	SOD	Pp	5	3	7	21	71.0				55.01	1.29				7	Pp	SOD	
40	7	SOD	Pp	5	88	8	21	65.7	63.33	61.17		55.01	1.19	1.151	1.112		7	Pp	SOD	61.21
41	7	SOD	Np	1	23	1	5	0.8				55.01	0.01				7	Np	SOD	
42	7	SOD	Np	1	82	2	4	52.0				55.01	0.95				7	Np	SOD	
43	7	SOD	Np	1	15	5	18	47.1				55.01	0.86				7	Np	SOD	
44	7	SOD	Np	1	56	6	11	55.6	38.88			55.01	1.01	0.707			7	Np	SOD	
45	7	SOD	Np	2	48	3	6	47.6				55.01	0.87				7	Np	SOD	
46	7	SOD	Np	2	39	4	10	51.1				55.01	0.93				7	Np	SOD	
47	7	SOD	Np	2	26	7	4	52.6				55.01	0.96				7	Np	SOD	
48	7	SOD	Np	2	70	8	7	56.4	51.93			55.01	1.03	0.944			7	Np	SOD	
49	7	SOD	Np	3	67	1	24	67.0				55.01	1.22				7	Np	SOD	
50	7	SOD	Np	3	52	2	10	76.2				55.01	1.39				7	Np	SOD	
51	7	SOD	Np	3	81	5	13	1.6				55.01	0.03				7	Np	SOD	
52	7	SOD	Np	3	80	6	12	1.4	36.55			55.01	0.03	0.664			7	Np	SOD	
53	7	SOD	Np	4	79	3	7	NA				NA	NA				7	Np	SOD	
54	7	SOD	Np	4	59	4	15	0.8				55.01	0.01				7	Np	SOD	
55	7	SOD	Np	4	1	7	16	0.4				55.01	0.01				7	Np	SOD	
56	7	SOD	Np	4	99	8	2	46.6	15.93			55.01	0.85	0.290			7	Np	SOD	

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57	7	SOD	Np	5	19	1	19	47.9				55.01	0.87				7	Np	SOD	
58	7	SOD	Np	5	31	3	25	38.0				55.01	0.69				7	Np	SOD	
59	7	SOD	Np	5	65	5	8	53.6				55.01	0.97				7	Np	SOD	
60	7	SOD	Np	5	44	7	3	0.5	35.00	35.66		55.01	0.01	0.636	0.648		7	Np	SOD	36.69
71	7	SOD	Null	NA	13	1	3	55.8				55.01	1.01				7	Null	SOD	
72	7	SOD	Null	NA	51	2	18	52.0				55.01	0.95				7	Null	SOD	
73	7	SOD	Null	NA	22	3	11	47.1				55.01	0.86				7	Null	SOD	
74	7	SOD	Null	NA	24	4	9	55.6				55.01	1.01				7	Null	SOD	
75	7	SOD	Null	NA	38	5	4	47.6				55.01	0.87				7	Null	SOD	
76	7	SOD	Null	NA	37	6	3	51.1				55.01	0.93				7	Null	SOD	
77	7	SOD	Null	NA	54	7	12	52.6				55.01	0.96				7	Null	SOD	
78	7	SOD	Null	NA	78	8	8	56.4				55.01	1.03				7	Null	SOD	
79	7	SOD	Null	NA	86	1	6	59.1				55.01	1.07				7	Null	SOD	
80	7	SOD	Null	NA	4	2	20	57.9				55.01	1.05				7	Null	SOD	
81	7	SOD	Null	NA	43	3	17	67.7				55.01	1.23				7	Null	SOD	
82	7	SOD	Null	NA	17	4	2	55.8				55.01	1.01				7	Null	SOD	
83	7	SOD	Null	NA	73	5	12	62.3				55.01	1.13				7	Null	SOD	
84	7	SOD	Null	NA	71	6	13	74.1				55.01	1.35				7	Null	SOD	
85	7	SOD	Null	NA	21	7	22	35.5				55.01	0.65				7	Null	SOD	
86	7	SOD	Null	NA	61	8	20	59.9				55.01	1.09				7	Null	SOD	
87	7	SOD	Null	NA	34	1	4	64.9				55.01	1.18				7	Null	SOD	
88	7	SOD	Null	NA	98	2	5	59.0				55.01	1.07				7	Null	SOD	
89	7	SOD	Null	NA	91	3	5	64.0				55.01	1.16				7	Null	SOD	
90	7	SOD	Null	NA	66	4	19	58.0				55.01	1.05				7	Null	SOD	
91	7	SOD	Null	NA	95	5	2	58.2				55.01	1.06				7	Null	SOD	
92	7	SOD	Null	NA	62	6	9	71.2				55.01	1.29				7	Null	SOD	
93	7	SOD	Null	NA	75	7	25	59.5				55.01	1.08				7	Null	SOD	
94	7	SOD	Null	NA	2	8	18	70.8				55.01	1.29				7	Null	SOD	
95	7	SOD	Null	NA	30	1	22	68.2				55.01	1.24				7	Null	SOD	
96	7	SOD	Null	NA	94	3	14	56.5				55.01	1.03				7	Null	SOD	
97	7	SOD	Null	NA	72	4	25	52.8				55.01	0.96				7	Null	SOD	
98	7	SOD	Null	NA	68	5	22	67.6				55.01	1.23				7	Null	SOD	
99	7	SOD	Null	NA	57	6	7	62.7	Grand Average		55.01	1.14				7	Null	SOD		
100	7	SOD	Null	NA	47	8	17	58.5	58.75		55.01	55.01	1.06	1.068		7	Null	SOD	58.75	
101	7	ALU	Pp	1	161	1	2	88.4				80.09	1.10				7	Pp	ALU	
102	7	ALU	Pp	1	174	2	7	100.5				80.09	1.25				7	Pp	ALU	
103	7	ALU	Pp	1	137	3	24	93.9				80.09	1.17				7	Pp	ALU	
104	7	ALU	Pp	1	112	4	23	84.1				80.09	1.05				7	Pp	ALU	
105	7	ALU	Pp	1	156	5	5	80.7				80.09	1.01				7	Pp	ALU	
106	7	ALU	Pp	1	193	6	16	86.6				80.09	1.08				7	Pp	ALU	
107	7	ALU	Pp	1	149	7	14	100.1				80.09	1.25				7	Pp	ALU	
108	7	ALU	Pp	1	101	8	5	94.7	91.13			80.09	1.18	1.138			7	Pp	ALU	
109	7	ALU	Pp	2	167	1	1	63.7				80.09	0.80				7	Pp	ALU	
110	7	ALU	Pp	2	190	2	22	102.1				80.09	1.27				7	Pp	ALU	
111	7	ALU	Pp	2	154	3	9	NA				NA	NA				7	Pp	ALU	
112	7	ALU	Pp	2	148	4	16	86.9				80.09	1.08				7	Pp	ALU	
113	7	ALU	Pp	2	183	5	25	80.6				80.09	1.01				7	Pp	ALU	
114	7	ALU	Pp	2	189	6	8	120.4				80.09	1.50				7	Pp	ALU	
115	7	ALU	Pp	2	160	7	1	93.9				80.09	1.17				7	Pp	ALU	
116	7	ALU	Pp	2	110	8	25	70.3	88.27			80.09	0.88	1.102			7	Pp	ALU	
117	7	ALU	Pp	3	192	1	8	85.5				80.09	1.07				7	Pp	ALU	
118	7	ALU	Pp	3	103	2	17	86.5				80.09	1.08				7	Pp	ALU	
119	7	ALU	Pp	3	171	3	2	46.1				80.09	0.58				7	Pp	ALU	

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120	7	ALU	Pp	3	150	4	14	87.9				80.09	1.10				7	Pp	ALU	
121	7	ALU	Pp	3	186	5	6	82.8				80.09	1.03				7	Pp	ALU	
122	7	ALU	Pp	3	133	6	19	93.1				80.09	1.16				7	Pp	ALU	
123	7	ALU	Pp	3	115	7	6	69.3				80.09	0.87				7	Pp	ALU	
124	7	ALU	Pp	3	117	8	13	92.0	80.40			80.09	1.15	1.004			7	Pp	ALU	
125	7	ALU	Pp	4	119	1	7	89.0				80.09	1.11				7	Pp	ALU	
126	7	ALU	Pp	4	168	2	1	79.6				80.09	0.99				7	Pp	ALU	
127	7	ALU	Pp	4	132	3	19	98.8				80.09	1.23				7	Pp	ALU	
128	7	ALU	Pp	4	155	4	1	79.9				80.09	1.00				7	Pp	ALU	
129	7	ALU	Pp	4	172	5	15	85.2				80.09	1.06				7	Pp	ALU	
130	7	ALU	Pp	4	108	6	23	72.6				80.09	0.91				7	Pp	ALU	
131	7	ALU	Pp	4	147	7	2	84.5				80.09	1.06				7	Pp	ALU	
132	7	ALU	Pp	4	130	8	3	85.5	84.39			80.09	1.07	1.054			7	Pp	ALU	
133	7	ALU	Pp	5	143	1	12	93.0				80.09	1.16				7	Pp	ALU	
134	7	ALU	Pp	5	184	2	23	95.3				80.09	1.19				7	Pp	ALU	
135	7	ALU	Pp	5	153	3	18	83.3				80.09	1.04				7	Pp	ALU	
136	7	ALU	Pp	5	165	4	7	88.3				80.09	1.10				7	Pp	ALU	
137	7	ALU	Pp	5	134	5	7	111.2				80.09	1.39				7	Pp	ALU	
138	7	ALU	Pp	5	173	6	14	97.2				80.09	1.21				7	Pp	ALU	
139	7	ALU	Pp	5	116	7	15	91.1				80.09	1.14				7	Pp	ALU	
140	7	ALU	Pp	5	105	8	9	98.3	94.71	87.78		80.09	1.23	1.183	1.096		7	Pp	ALU	87.77
141	7	ALU	Np	1	195	1	25	79.0				80.09	0.99				7	Np	ALU	
142	7	ALU	Np	1	158	2	9	52.0				80.09	0.65				7	Np	ALU	
143	7	ALU	Np	1	164	5	24	47.1				80.09	0.59				7	Np	ALU	
144	7	ALU	Np	1	142	6	15	55.6	58.43			80.09	0.69	0.729			7	Np	ALU	
145	7	ALU	Np	2	185	3	15	47.6				80.09	0.59				7	Np	ALU	
146	7	ALU	Np	2	178	4	17	51.1				80.09	0.64				7	Np	ALU	
147	7	ALU	Np	2	125	7	5	52.6				80.09	0.66				7	Np	ALU	
148	7	ALU	Np	2	175	8	19	56.4	51.93			80.09	0.70	0.648			7	Np	ALU	
149	7	ALU	Np	3	106	1	20	70.5				80.09	0.88				7	Np	ALU	
150	7	ALU	Np	3	139	2	21	43.0				80.09	0.54				7	Np	ALU	
151	7	ALU	Np	3	191	5	16	78.5				80.09	0.98				7	Np	ALU	
152	7	ALU	Np	3	159	6	10	63.8	63.95			80.09	0.80	0.798			7	Np	ALU	
153	7	ALU	Np	4	123	3	12	77.7				80.09	0.97				7	Np	ALU	
154	7	ALU	Np	4	187	4	22	76.6				80.09	0.96				7	Np	ALU	
155	7	ALU	Np	4	157	7	23	81.5				80.09	1.02				7	Np	ALU	
156	7	ALU	Np	4	163	8	10	88.1	80.98			80.09	1.10	1.011			7	Np	ALU	
157	7	ALU	Np	5	113	2	16	59.7				80.09	0.75				7	Np	ALU	
158	7	ALU	Np	5	180	4	21	72.8				80.09	0.91				7	Np	ALU	
159	7	ALU	Np	5	198	6	5	72.8				80.09	0.91				7	Np	ALU	
160	7	ALU	Np	5	182	8	6	70.1	68.85	64.83		80.09	0.88	0.860	0.809		7	Np	ALU	64.83
171	7	ALU	Null	NA	129	1	21	66.1				80.09	0.83				7	Null	ALU	
172	7	ALU	Null	NA	152	2	6	83.0				80.09	1.04				7	Null	ALU	
173	7	ALU	Null	NA	162	3	1	86.3				80.09	1.08				7	Null	ALU	
174	7	ALU	Null	NA	145	4	5	68.1				80.09	0.85				7	Null	ALU	
175	7	ALU	Null	NA	109	5	9	83.0				80.09	1.04				7	Null	ALU	
176	7	ALU	Null	NA	196	6	25	90.6				80.09	1.13				7	Null	ALU	
177	7	ALU	Null	NA	200	7	8	58.7				80.09	0.73				7	Null	ALU	
178	7	ALU	Null	NA	120	8	4	82.6				80.09	1.03				7	Null	ALU	
179	7	ALU	Null	NA	136	1	18	59.6				80.09	0.74				7	Null	ALU	
180	7	ALU	Null	NA	131	2	8	88.4				80.09	1.10				7	Null	ALU	
181	7	ALU	Null	NA	141	3	10	83.3				80.09	1.04				7	Null	ALU	
182	7	ALU	Null	NA	102	4	13	71.3				80.09	0.89				7	Null	ALU	

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183	7	ALU	Null	NA	177	5	17	85.6				80.09	1.07			7	Null	ALU	
184	7	ALU	Null	NA	169	6	17	110.8				80.09	1.38			7	Null	ALU	
185	7	ALU	Null	NA	121	7	19	77.7				80.09	0.97			7	Null	ALU	
186	7	ALU	Null	NA	127	8	1	81.7				80.09	1.02			7	Null	ALU	
187	7	ALU	Null	NA	166	1	23	65.8				80.09	0.82			7	Null	ALU	
188	7	ALU	Null	NA	194	2	12	78.5				80.09	0.98			7	Null	ALU	
189	7	ALU	Null	NA	181	3	16	97.4				80.09	1.22			7	Null	ALU	
190	7	ALU	Null	NA	144	4	4	89.8				80.09	1.12			7	Null	ALU	
191	7	ALU	Null	NA	122	5	23	89.1				80.09	1.11			7	Null	ALU	
192	7	ALU	Null	NA	176	6	6	NA				NA	NA			7	Null	ALU	
193	7	ALU	Null	NA	111	7	17	83.4				80.09	1.04			7	Null	ALU	
194	7	ALU	Null	NA	128	8	11	55.4				80.09	0.69			7	Null	ALU	
195	7	ALU	Null	NA	197	2	2	73.3				80.09	0.92			7	Null	ALU	
196	7	ALU	Null	NA	188	3	20	75.9				80.09	0.95			7	Null	ALU	
197	7	ALU	Null	NA	151	4	8	98.8				80.09	1.23			7	Null	ALU	
198	7	ALU	Null	NA	140	5	14	61.9				80.09	0.77			7	Null	ALU	
199	7	ALU	Null	NA	135	7	9	103.4		Grand Average		80.09	1.29			7	Null	ALU	
200	7	ALU	Null	NA	179	8	14	79.3	80.30		80.09	0.99	1.003		7	Null	ALU	80.30	
1	8	SOD	Pp	1	5	1	7	35.7				96.14	0.37			8	Pp	SOD	
2	8	SOD	Pp	1	33	2	2	121.2				96.14	1.26			8	Pp	SOD	
3	8	SOD	Pp	1	100	3	5	NA				NA	NA			8	Pp	SOD	
4	8	SOD	Pp	1	75	4	15	96.0				96.14	1.00			8	Pp	SOD	
5	8	SOD	Pp	1	4	5	10	119.1				96.14	1.24			8	Pp	SOD	
6	8	SOD	Pp	1	88	6	13	NA				NA	NA			8	Pp	SOD	
7	8	SOD	Pp	1	81	7	14	122.9				96.14	1.28			8	Pp	SOD	
8	8	SOD	Pp	1	79	8	9	110.0	100.82			96.14	1.14	1.049		8	Pp	SOD	
9	8	SOD	Pp	2	92	1	21	114.7				96.14	1.19			8	Pp	SOD	
10	8	SOD	Pp	2	44	2	3	116.3				96.14	1.21			8	Pp	SOD	
11	8	SOD	Pp	2	97	3	8	72.9				96.14	0.76			8	Pp	SOD	
12	8	SOD	Pp	2	83	4	14	121.2				96.14	1.26			8	Pp	SOD	
13	8	SOD	Pp	2	8	5	6	NA				NA	NA			8	Pp	SOD	
14	8	SOD	Pp	2	55	6	9	100.8				96.14	1.05			8	Pp	SOD	
15	8	SOD	Pp	2	64	7	17	126.7				96.14	1.32			8	Pp	SOD	
16	8	SOD	Pp	2	25	8	10	99.4	107.43			96.14	1.03	1.117		8	Pp	SOD	
17	8	SOD	Pp	3	42	1	17	116.8				96.14	1.21			8	Pp	SOD	
18	8	SOD	Pp	3	96	2	16	110.6				96.14	1.15			8	Pp	SOD	
19	8	SOD	Pp	3	31	3	16	76.5				96.14	0.80			8	Pp	SOD	
20	8	SOD	Pp	3	39	4	8	110.2				96.14	1.15			8	Pp	SOD	
21	8	SOD	Pp	3	13	5	8	NA				NA	NA			8	Pp	SOD	
22	8	SOD	Pp	3	63	6	11	93.9				96.14	0.98			8	Pp	SOD	
23	8	SOD	Pp	3	12	7	11	97.4				96.14	1.01			8	Pp	SOD	
24	8	SOD	Pp	3	53	8	13	120.2	103.66			96.14	1.25	1.078		8	Pp	SOD	
25	8	SOD	Pp	4	37	1	6	106.8				96.14	1.11			8	Pp	SOD	
26	8	SOD	Pp	4	59	2	17	109.1				96.14	1.13			8	Pp	SOD	
27	8	SOD	Pp	4	45	3	18	86.9				96.14	0.90			8	Pp	SOD	
28	8	SOD	Pp	4	18	4	19	91.4				96.14	0.95			8	Pp	SOD	
29	8	SOD	Pp	4	93	5	21	105.1				96.14	1.09			8	Pp	SOD	
30	8	SOD	Pp	4	76	6	16	105.3				96.14	1.10			8	Pp	SOD	
31	8	SOD	Pp	4	10	7	24	116.4				96.14	1.21			8	Pp	SOD	
32	8	SOD	Pp	4	28	8	14	122.2	105.40			96.14	1.27	1.096		8	Pp	SOD	
33	8	SOD	Pp	5	99	1	23	119.3				96.14	1.24			8	Pp	SOD	
34	8	SOD	Pp	5	51	2	4	127.7				96.14	1.33			8	Pp	SOD	
35	8	SOD	Pp	5	98	3	22	103.4				96.14	1.08			8	Pp	SOD	

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36	8	SOD	Pp	5	67	4	3	136.0				96.14	1.41				8	Pp	SOD	
37	8	SOD	Pp	5	36	5	12	146.2				96.14	1.52				8	Pp	SOD	
38	8	SOD	Pp	5	21	6	7	116.7				96.14	1.21				8	Pp	SOD	
39	8	SOD	Pp	5	66	7	22	118.2				96.14	1.23				8	Pp	SOD	
40	8	SOD	Pp	5	70	8	5	98.2	120.71	107.60		96.14	1.02	1.256	1.119		8	Pp	SOD	108.09
41	8	SOD	Np	1	29	1	4	1.5				96.14	0.02				8	Np	SOD	
42	8	SOD	Np	1	41	2	23	75.1				96.14	0.78				8	Np	SOD	
43	8	SOD	Np	1	71	5	15	99.4				96.14	1.03				8	Np	SOD	
44	8	SOD	Np	1	52	6	3	93.8	67.45			96.14	0.98	0.702			8	Np	SOD	
45	8	SOD	Np	2	61	3	9	72.0				96.14	0.75				8	Np	SOD	
46	8	SOD	Np	2	22	4	13	98.2				96.14	1.02				8	Np	SOD	
47	8	SOD	Np	2	50	7	9	65.4				96.14	0.68				8	Np	SOD	
48	8	SOD	Np	2	16	8	18	64.4	75.00			96.14	0.67	0.780			8	Np	SOD	
49	8	SOD	Np	3	72	1	12	NA				NA	NA				8	Np	SOD	
50	8	SOD	Np	3	82	2	25	90.8				96.14	0.94				8	Np	SOD	
51	8	SOD	Np	3	1	5	20	111.1				96.14	1.16				8	Np	SOD	
52	8	SOD	Np	3	87	6	4	119.9	107.27			96.14	1.25	1.116			8	Np	SOD	
53	8	SOD	Np	4	94	3	20	69.5				96.14	0.72				8	Np	SOD	
54	8	SOD	Np	4	68	4	9	107.0				96.14	1.11				8	Np	SOD	
55	8	SOD	Np	4	62	7	10	0.8				96.14	0.01				8	Np	SOD	
56	8	SOD	Np	4	49	8	23	89.8	66.78			96.14	0.93	0.695			8	Np	SOD	
57	8	SOD	Np	5	17	1	25	1.1				96.14	0.01				8	Np	SOD	
58	8	SOD	Np	5	40	3	15	65.1				96.14	0.68				8	Np	SOD	
59	8	SOD	Np	5	24	5	9	1.1				96.14	0.01				8	Np	SOD	
60	8	SOD	Np	5	57	7	25	76.2	35.88	70.47		96.14	0.79	0.373	0.733		8	Np	SOD	68.54
71	8	SOD	Null	NA	74	1	2	81.3				96.14	0.85				8	Null	SOD	
72	8	SOD	Null	NA	60	2	22	111.9				96.14	1.16				8	Null	SOD	
73	8	SOD	Null	NA	69	3	13	82.6				96.14	0.86				8	Null	SOD	
74	8	SOD	Null	NA	11	4	6	86.1				96.14	0.90				8	Null	SOD	
75	8	SOD	Null	NA	46	5	14	70.6				96.14	0.73				8	Null	SOD	
76	8	SOD	Null	NA	48	6	23	93.2				96.14	0.97				8	Null	SOD	
77	8	SOD	Null	NA	26	7	13	108.9				96.14	1.13				8	Null	SOD	
78	8	SOD	Null	NA	6	8	21	100.3				96.14	1.04				8	Null	SOD	
79	8	SOD	Null	NA	35	1	14	119.0				96.14	1.24				8	Null	SOD	
80	8	SOD	Null	NA	90	2	15	96.6				96.14	1.00				8	Null	SOD	
81	8	SOD	Null	NA	23	3	3	92.5				96.14	0.96				8	Null	SOD	
82	8	SOD	Null	NA	65	4	20	72.5				96.14	0.75				8	Null	SOD	
83	8	SOD	Null	NA	9	5	2	86.2				96.14	0.90				8	Null	SOD	
84	8	SOD	Null	NA	77	6	10	102.1				96.14	1.06				8	Null	SOD	
85	8	SOD	Null	NA	58	7	16	108.4				96.14	1.13				8	Null	SOD	
86	8	SOD	Null	NA	38	8	25	105.1				96.14	1.09				8	Null	SOD	
87	8	SOD	Null	NA	30	1	22	NA				NA	NA				8	Null	SOD	
88	8	SOD	Null	NA	32	2	14	110.1				96.14	1.15				8	Null	SOD	
89	8	SOD	Null	NA	43	3	14	107.6				96.14	1.12				8	Null	SOD	
90	8	SOD	Null	NA	47	4	12	91.2				96.14	0.95				8	Null	SOD	
91	8	SOD	Null	NA	15	5	11	114.4				96.14	1.19				8	Null	SOD	
92	8	SOD	Null	NA	78	6	1	99.1				96.14	1.03				8	Null	SOD	
93	8	SOD	Null	NA	73	7	3	108.0				96.14	1.12				8	Null	SOD	
94	8	SOD	Null	NA	54	8	2	100.7				96.14	1.05				8	Null	SOD	
95	8	SOD	Null	NA	80	2	11	97.0				96.14	1.01				8	Null	SOD	
96	8	SOD	Null	NA	20	3	25	95.8				96.14	1.00				8	Null	SOD	
97	8	SOD	Null	NA	95	4	23	119.3				96.14	1.24				8	Null	SOD	
98	8	SOD	Null	NA	14	5	24	115.4				96.14	1.20				8	Null	SOD	

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99	8	SOD	Null	NA	3	7	15	80.6		Grand Average	96.14	0.84			8	Null	SOD		
100	8	SOD	Null	NA	86	8	7	125.3	99.37		96.14	96.14	1.30	1.034	8	Null	SOD	99.37	
101	8	ALU	Pp	1	179	1	3	164.6			125.44	1.31			8	Pp	ALU		
102	8	ALU	Pp	1	171	2	24	171.8			125.44	1.37			8	Pp	ALU		
103	8	ALU	Pp	1	166	3	11	123.7			125.44	0.99			8	Pp	ALU		
104	8	ALU	Pp	1	177	4	5	153.3			125.44	1.22			8	Pp	ALU		
105	8	ALU	Pp	1	114	5	16	NA			NA	NA			8	Pp	ALU		
106	8	ALU	Pp	1	162	6	14	162.2			125.44	1.29			8	Pp	ALU		
107	8	ALU	Pp	1	138	7	23	128.1			125.44	1.02			8	Pp	ALU		
108	8	ALU	Pp	1	144	8	11	133.0	148.10		125.44	1.06	1.181		8	Pp	ALU		
109	8	ALU	Pp	2	116	1	18	152.0			125.44	1.21			8	Pp	ALU		
110	8	ALU	Pp	2	189	2	19	143.0			125.44	1.14			8	Pp	ALU		
111	8	ALU	Pp	2	115	3	12	121.1			125.44	0.97			8	Pp	ALU		
112	8	ALU	Pp	2	174	4	22	143.1			125.44	1.14			8	Pp	ALU		
113	8	ALU	Pp	2	194	5	4	129.2			125.44	1.03			8	Pp	ALU		
114	8	ALU	Pp	2	106	6	19	145.5			125.44	1.16			8	Pp	ALU		
115	8	ALU	Pp	2	185	7	4	148.5			125.44	1.18			8	Pp	ALU		
116	8	ALU	Pp	2	196	8	16	130.1	139.06		125.44	1.04	1.109		8	Pp	ALU		
117	8	ALU	Pp	3	182	1	24	115.3			125.44	0.92			8	Pp	ALU		
118	8	ALU	Pp	3	170	2	9	149.0			125.44	1.19			8	Pp	ALU		
119	8	ALU	Pp	3	130	3	4	138.2			125.44	1.10			8	Pp	ALU		
120	8	ALU	Pp	3	186	4	16	149.9			125.44	1.20			8	Pp	ALU		
121	8	ALU	Pp	3	145	5	18	136.5			125.44	1.09			8	Pp	ALU		
122	8	ALU	Pp	3	140	6	22	138.8			125.44	1.11			8	Pp	ALU		
123	8	ALU	Pp	3	190	7	20	129.0			125.44	1.03			8	Pp	ALU		
124	8	ALU	Pp	3	118	8	12	100.7	132.18		125.44	0.80	1.054		8	Pp	ALU		
125	8	ALU	Pp	4	131	1	20	143.3			125.44	1.14			8	Pp	ALU		
126	8	ALU	Pp	4	175	2	5	121.8			125.44	0.97			8	Pp	ALU		
127	8	ALU	Pp	4	164	3	2	143.1			125.44	1.14			8	Pp	ALU		
128	8	ALU	Pp	4	111	4	4	162.5			125.44	1.30			8	Pp	ALU		
129	8	ALU	Pp	4	103	5	1	134.5			125.44	1.07			8	Pp	ALU		
130	8	ALU	Pp	4	119	6	18	170.3			125.44	1.36			8	Pp	ALU		
131	8	ALU	Pp	4	153	7	21	139.1			125.44	1.11			8	Pp	ALU		
132	8	ALU	Pp	4	133	8	15	NA	144.94		NA	NA	1.155		8	Pp	ALU		
133	8	ALU	Pp	5	135	1	10	156.8			125.44	1.25			8	Pp	ALU		
134	8	ALU	Pp	5	110	2	7	172.4			125.44	1.37			8	Pp	ALU		
135	8	ALU	Pp	5	134	3	21	162.0			125.44	1.29			8	Pp	ALU		
136	8	ALU	Pp	5	125	4	1	157.6			125.44	1.26			8	Pp	ALU		
137	8	ALU	Pp	5	143	5	17	NA			NA	NA			8	Pp	ALU		
138	8	ALU	Pp	5	122	6	24	149.1			125.44	1.19			8	Pp	ALU		
139	8	ALU	Pp	5	107	7	19	141.3			125.44	1.13			8	Pp	ALU		
140	8	ALU	Pp	5	137	8	4	NA	156.53	144.16		NA	NA	1.248	1.149	8	Pp	ALU	143.34
141	8	ALU	Np	1	188	1	15	93.4			125.44	0.74			8	Np	ALU		
142	8	ALU	Np	1	113	2	21	82.6			125.44	0.66			8	Np	ALU		
143	8	ALU	Np	1	173	5	19	90.5			125.44	0.72			8	Np	ALU		
144	8	ALU	Np	1	161	6	25	90.8	89.33		125.44	0.72	0.712		8	Np	ALU		
145	8	ALU	Np	2	124	3	6	89.5			125.44	0.71			8	Np	ALU		
146	8	ALU	Np	2	157	4	11	133.7			125.44	1.07			8	Np	ALU		
147	8	ALU	Np	2	109	7	2	138.4			125.44	1.10			8	Np	ALU		
148	8	ALU	Np	2	121	8	6	111.3	118.23		125.44	0.89	0.942		8	Np	ALU		
149	8	ALU	Np	3	148	1	8	83.3			125.44	0.66			8	Np	ALU		
150	8	ALU	Np	3	123	2	20	85.9			125.44	0.68			8	Np	ALU		
151	8	ALU	Np	3	104	5	7	84.8			125.44	0.68			8	Np	ALU		

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152	8	ALU	Np	3	158	6	17	82.3	84.08			125.44	0.66	0.670		8	Np	ALU	
153	8	ALU	Np	4	191	3	19	106.4				125.44	0.85			8	Np	ALU	
154	8	ALU	Np	4	165	4	7	61.3				125.44	0.49			8	Np	ALU	
155	8	ALU	Np	4	129	7	6	83.1				125.44	0.66			8	Np	ALU	
156	8	ALU	Np	4	167	8	1	NA	83.60			NA	NA	0.666		8	Np	ALU	
157	8	ALU	Np	5	141	2	6	77.4				125.44	0.62			8	Np	ALU	
158	8	ALU	Np	5	126	4	17	102.0				125.44	0.81			8	Np	ALU	
159	8	ALU	Np	5	151	6	5	63.0				125.44	0.50			8	Np	ALU	
160	8	ALU	Np	5	193	8	8	53.9	74.08	89.86		125.44	0.43	0.591	0.716	8	Np	ALU	90.19
171	8	ALU	Null	NA	181	1	16	119.4				125.44	0.95			8	Null	ALU	
172	8	ALU	Null	NA	105	2	13	NA				NA	NA			8	Null	ALU	
173	8	ALU	Null	NA	149	3	10	125.8				125.44	1.00			8	Null	ALU	
174	8	ALU	Null	NA	163	4	18	128.2				125.44	1.02			8	Null	ALU	
175	8	ALU	Null	NA	198	5	23	139.4				125.44	1.11			8	Null	ALU	
176	8	ALU	Null	NA	187	6	20	128.8				125.44	1.03			8	Null	ALU	
177	8	ALU	Null	NA	147	7	12	139.7				125.44	1.11			8	Null	ALU	
178	8	ALU	Null	NA	127	8	17	95.0				125.44	0.76			8	Null	ALU	
179	8	ALU	Null	NA	132	1	9	109.9				125.44	0.88			8	Null	ALU	
180	8	ALU	Null	NA	197	2	8	111.1				125.44	0.89			8	Null	ALU	
181	8	ALU	Null	NA	180	3	7	119.6				125.44	0.95			8	Null	ALU	
182	8	ALU	Null	NA	117	4	21	122.8				125.44	0.98			8	Null	ALU	
183	8	ALU	Null	NA	101	5	13	144.0				125.44	1.15			8	Null	ALU	
184	8	ALU	Null	NA	108	6	21	144.1				125.44	1.15			8	Null	ALU	
185	8	ALU	Null	NA	128	7	7	151.3				125.44	1.21			8	Null	ALU	
186	8	ALU	Null	NA	184	8	20	110.9				125.44	0.88			8	Null	ALU	
187	8	ALU	Null	NA	176	1	5	131.3				125.44	1.05			8	Null	ALU	
188	8	ALU	Null	NA	139	2	10	125.0				125.44	1.00			8	Null	ALU	
189	8	ALU	Null	NA	160	3	1	131.6				125.44	1.05			8	Null	ALU	
190	8	ALU	Null	NA	168	4	25	118.6				125.44	0.95			8	Null	ALU	
191	8	ALU	Null	NA	159	5	3	136.1				125.44	1.08			8	Null	ALU	
192	8	ALU	Null	NA	199	6	6	117.4				125.44	0.94			8	Null	ALU	
193	8	ALU	Null	NA	183	7	8	135.4				125.44	1.08			8	Null	ALU	
194	8	ALU	Null	NA	146	8	22	136.1				125.44	1.08			8	Null	ALU	
195	8	ALU	Null	NA	150	2	18	92.7				125.44	0.74			8	Null	ALU	
196	8	ALU	Null	NA	152	3	24	117.2				125.44	0.93			8	Null	ALU	
197	8	ALU	Null	NA	102	4	2	123.9				125.44	0.99			8	Null	ALU	
198	8	ALU	Null	NA	192	5	25	140.4				125.44	1.12			8	Null	ALU	
199	8	ALU	Null	NA	200	6	2	148.9	Grand Average			125.44	1.19			8	Null	ALU	
200	8	ALU	Null	NA	156	8	19	118.3	126.31		125.44	0.94	1.007		8	Null	ALU	126.31	

Supplemental Table S1

Supplemental Table S2

Table S2 (Data, Generation 9)																				
sent to co-authors for analyses 5. Sep. 2016																				
Abbreviations used in this Table:																				
"NA" denotes empty cell (e.g., seed that failed to germinate)																				
"SOD" denotes sodium-sulfate stress, "ALU" denotes aluminum-sulfate stress																				
"Null" denotes no microbiome-inoculation of a seed, but microbiomes assemble from aerial microbial-rain																				
Explanation of Columns:																				
Column B	Microbiome-Generation 9 is the final test-generation after 8 rounds of microbiome-propagation from Gen0-Gen8 (see data on Gen0-Gen8 in Tables S1) and then one additional 9th round of microbiome-propagation to plants of Gen9 tested in this spreadsheet																			
Column C	salt treatment of soil (& water used to water plants) PRIOR TO Generation 9 (i.e., selection history during Gen 0-8); this is the salt-stress under which microbiomes evolved																			
Column D	salt treatment of soil (& water used to water plants) DURING Generation 9; this is the salt-stress to test the evolved microbiomes in the final Generation 9;																			
"	selected-microbiomes (Pp) were tested under conditions under which they evolved (e.g., SOD-selected-microbiomes tested in SOD-soil), or under crossed condition (e.g., SOD-selected-microbiomes tested in ALU-soil, ALU-selected-microbiomes tested in SOD-soil)																			
Column E	Pp is "plant present", a microbiome was harvested from rhizosphere of Gen8 plant, filtered with a 2.0µm filter to retain only bacterial microbiomes, then propagated to seeds of Gen9;																			
"	PpFilt is a harvested selected microbiome of Gen8 (i.e., a Pp-microbiome) filtered a second time with a 0.2µm filter to eliminate also bacterial cells, then test on Gen9 seeds this 0.2µm-filtrate containing solutes (& any viruses) co-harvested with bacterial microbiomes																			
"	Np is "no plant", a microbiome was harvested from fallow soil with no plant in pot, then propagated to seeds of Gen9 to test microbiome effects on plants																			
"	Null is "no microbiome-inoculation of seed"; plants acquire microbiomes from aerial microbial-rain																			
Column F	selection lines in Pp, PpFilt, and Np treatments; for each salt-treatment, there are 5 selection-lines for Pp (and 5 corresponding PpFilt-lines) and 5 lines for Np																			
Column G	plant number used to identify individual plants (i.e., pots); pots were randomly allocated to treatments and replicates;																			
"	Generation 9 had 400 pots total, each planted with a single seed; 20 of these seeds showed no above-ground shoot by end of Day4 and were then removed																			
Column H	rack number; for each selection-line, replicates were blocked evenly between racks; there were 8 racks total, each with 50 pots (8x50 = 400 pots total)																			
Column I	position of pot in rack; pots assigned to a particular rack were randomly assigned to the 50 pot-positions in each rack																			
Column J	total seed dry-weight in milligram (after removing glumes from seeds) on Day 68; seeds were weighed blindly with respect to plant treatment																			
Column K	total above-ground dry-weight in milligram (leaves, stems, inflorescences, seeds) on Day 68; biomass was weighed blindly with respect to plant treatment																			
###	Generation	Salt Treatment during selection PRIOR TO Gen9	Gen9 Salt Stress	Microbiome Treatment	Selection Line	Plant #	Rack #	Position in Rack	Total Seed Weight	Total Biomass	Line-Code used in Master Spreadsheet	Plant #	Total Seed Weight	Selection Line Average	Treatment Average	Treatment StDev	Total Biomass	Selection Line Average	Treatment Average	Treatment StDev
1	9	SOD	SOD	Pp	1	106	1	12	495.9	965.7	SodPp1xSodSoil	106	495.9				965.7			
2	9	SOD	SOD	Pp	1	196	2	8	329.6	999.5	SodPp1xSodSoil	196	329.6				999.5			
3	9	SOD	SOD	Pp	1	190	3	15	272.5	1239.4	SodPp1xSodSoil	190	272.5				1239.4			
4	9	SOD	SOD	Pp	1	82	4	5	390.9	891.1	SodPp1xSodSoil	82	390.9				891.1			
5	9	SOD	SOD	Pp	1	92	5	19	133.5	1372.6	SodPp1xSodSoil	92	133.5				1372.6			
6	9	SOD	SOD	Pp	1	57	6	28	180.2	1244.5	SodPp1xSodSoil	57	180.2				1244.5			
7	9	SOD	SOD	Pp	1	194	7	20	25.2	1111.4	SodPp1xSodSoil	194	25.2				1111.4			
8	9	SOD	SOD	Pp	1	126	8	11	377.2	839.9	SodPp1xSodSoil	126	377.2	275.6			839.9	1083.0		
9	9	SOD	SOD	Pp	2	5	1	45	342.0	748.2	SodPp2xSodSoil	5	342.0				748.2			
10	9	SOD	SOD	Pp	2	87	2	28	333.5	980.2	SodPp2xSodSoil	87	333.5				980.2			
11	9	SOD	SOD	Pp	2	88	3	32	406.2	959.5	SodPp2xSodSoil	88	406.2				959.5			
12	9	SOD	SOD	Pp	2	90	4	7	0.0	1348.5	SodPp2xSodSoil	90	0.0				1348.5			
13	9	SOD	SOD	Pp	2	155	5	15	453.7	1009.8	SodPp2xSodSoil	155	453.7				1009.8			
14	9	SOD	SOD	Pp	2	135	6	13	406.8	784.2	SodPp2xSodSoil	135	406.8				784.2			
15	9	SOD	SOD	Pp	2	7	7	32	230.8	1114.3	SodPp2xSodSoil	7	230.8				1114.3			
16	9	SOD	SOD	Pp	2	176	8	48	35.9	1163.3	SodPp2xSodSoil	176	35.9	276.1			1163.3	1013.5		
17	9	SOD	SOD	Pp	3	102	1	38	111.2	1286.6	SodPp3xSodSoil	102	111.2				1286.6			
18	9	SOD	SOD	Pp	3	123	2	50	51.3	1251.2	SodPp3xSodSoil	123	51.3				1251.2			
19	9	SOD	SOD	Pp	3	58	3	19	464.3	1047.2	SodPp3xSodSoil	58	464.3				1047.2			
20	9	SOD	SOD	Pp	3	163	4	42	447.3	881.8	SodPp3xSodSoil	163	447.3				881.8			
21	9	SOD	SOD	Pp	3	170	5	24	441.2	1224.7	SodPp3xSodSoil	170	441.2				1224.7			
22	9	SOD	SOD	Pp	3	199	6	37	23.2	1202.6	SodPp3xSodSoil	199	23.2				1202.6			
23	9	SOD	SOD	Pp	3	189	7	11	354.1	944.8	SodPp3xSodSoil	189	354.1				944.8			

Supplemental Table S2

24	9	SOD	SOD	Pp	3	33	8	38	0.0	1214.6	SodPp3xSodSoil	33	0.0	236.6			1214.6	1131.7			
25	9	SOD	SOD	Pp	4	121	1	19	11.5	1322.4	SodPp4xSodSoil	121	11.5				1322.4				
26	9	SOD	SOD	Pp	4	1	2	47	219.3	1198.9	SodPp4xSodSoil	1	219.3				1198.9				
27	9	SOD	SOD	Pp	4	149	3	4	398.2	831.6	SodPp4xSodSoil	149	398.2				831.6				
28	9	SOD	SOD	Pp	4	3	4	19	9.9	1190.4	SodPp4xSodSoil	3	9.9				1190.4				
29	9	SOD	SOD	Pp	4	180	5	2	406.0	1152.8	SodPp4xSodSoil	180	406.0				1152.8				
30	9	SOD	SOD	Pp	4	65	6	10	359.4	802.5	SodPp4xSodSoil	65	359.4				802.5				
31	9	SOD	SOD	Pp	4	73	7	39	0.0	1020.9	SodPp4xSodSoil	73	0.0				1020.9				
32	9	SOD	SOD	Pp	4	130	8	29	361.1	986.3	SodPp4xSodSoil	130	361.1	220.7			986.3	1063.2			
33	9	SOD	SOD	Pp	5	161	1	4	400.5	1169.7	SodPp5xSodSoil	161	400.5				1169.7				
34	9	SOD	SOD	Pp	5	62	2	20	315.7	742.0	SodPp5xSodSoil	62	315.7				742.0				
35	9	SOD	SOD	Pp	5	195	3	42	NA	NA	SodPp5xSodSoil	195	NA				NA				
36	9	SOD	SOD	Pp	5	166	4	49	246.3	1164.5	SodPp5xSodSoil	166	246.3				1164.5				
37	9	SOD	SOD	Pp	5	100	5	34	165.1	1220.6	SodPp5xSodSoil	100	165.1				1220.6				
38	9	SOD	SOD	Pp	5	186	6	4	388.6	974.9	SodPp5xSodSoil	186	388.6				974.9				
39	9	SOD	SOD	Pp	5	69	7	24	359.7	806.6	SodPp5xSodSoil	69	359.7				806.6				
40	9	SOD	SOD	Pp	5	70	8	23	282.3	553.5	SodPp5xSodSoil	70	282.3	308.3	263.5	34.9	553.5	947.4	1047.8	70.3	
41	9	SOD	ALU	Pp	1	289	1	29	123.6	1051.5	SodPp1xAluSoil	289	123.6				1051.5				
42	9	SOD	ALU	Pp	1	330	2	16	284.8	909.9	SodPp1xAluSoil	330	284.8				909.9				
43	9	SOD	ALU	Pp	1	265	3	3	207.9	872.2	SodPp1xAluSoil	265	207.9				872.2				
44	9	SOD	ALU	Pp	1	332	4	4	216.3	1140.6	SodPp1xAluSoil	332	216.3				1140.6				
45	9	SOD	ALU	Pp	1	300	5	6	287.5	1246.3	SodPp1xAluSoil	300	287.5				1246.3				
46	9	SOD	ALU	Pp	1	264	6	19	267.9	965.7	SodPp1xAluSoil	264	267.9				965.7				
47	9	SOD	ALU	Pp	1	393	7	41	0.0	1070.1	SodPp1xAluSoil	393	0.0				1070.1				
48	9	SOD	ALU	Pp	1	266	8	31	34.0	1022.4	SodPp1xAluSoil	266	34.0	177.8			1022.4	1034.8			
49	9	SOD	ALU	Pp	2	232	1	9	266.5	1247.9	SodPp2xAluSoil	232	266.5				1247.9				
50	9	SOD	ALU	Pp	2	348	2	14	241.4	1172.5	SodPp2xAluSoil	348	241.4				1172.5				
51	9	SOD	ALU	Pp	2	378	3	36	84.9	1190.8	SodPp2xAluSoil	378	84.9				1190.8				
52	9	SOD	ALU	Pp	2	279	4	40	0.0	1138.9	SodPp2xAluSoil	279	0.0				1138.9				
53	9	SOD	ALU	Pp	2	328	5	17	112.8	1146.9	SodPp2xAluSoil	328	112.8				1146.9				
54	9	SOD	ALU	Pp	2	205	6	32	107.5	940.7	SodPp2xAluSoil	205	107.5				940.7				
55	9	SOD	ALU	Pp	2	366	7	2	NA	NA	SodPp2xAluSoil	366	NA				NA				
56	9	SOD	ALU	Pp	2	369	8	47	260.8	925.2	SodPp2xAluSoil	369	260.8	153.4			925.2	1109.0			
57	9	SOD	ALU	Pp	3	390	1	48	190.2	1232.6	SodPp3xAluSoil	390	190.2				1232.6				
58	9	SOD	ALU	Pp	3	306	2	11	223.3	1144.2	SodPp3xAluSoil	306	223.3				1144.2				
59	9	SOD	ALU	Pp	3	259	3	40	241.8	925.0	SodPp3xAluSoil	259	241.8				925.0				
60	9	SOD	ALU	Pp	3	295	4	14	58.4	1205.7	SodPp3xAluSoil	295	58.4				1205.7				
61	9	SOD	ALU	Pp	3	271	5	47	154.6	903.6	SodPp3xAluSoil	271	154.6				903.6				
62	9	SOD	ALU	Pp	3	358	6	23	296.5	1098.0	SodPp3xAluSoil	358	296.5				1098.0				
63	9	SOD	ALU	Pp	3	304	7	43	177.0	1082.5	SodPp3xAluSoil	304	177.0				1082.5				
64	9	SOD	ALU	Pp	3	247	8	35	73.3	1207.4	SodPp3xAluSoil	247	73.3	176.9			1207.4	1099.9			
65	9	SOD	ALU	Pp	4	376	1	34	231.0	1103.7	SodPp4xAluSoil	376	231.0				1103.7				
66	9	SOD	ALU	Pp	4	308	2	44	386.1	1230.1	SodPp4xAluSoil	308	386.1				1230.1				
67	9	SOD	ALU	Pp	4	234	3	49	311.2	879.8	SodPp4xAluSoil	234	311.2				879.8				
68	9	SOD	ALU	Pp	4	335	4	18	58.7	1223.2	SodPp4xAluSoil	335	58.7				1223.2				
69	9	SOD	ALU	Pp	4	303	5	36	187.5	1022.2	SodPp4xAluSoil	303	187.5				1022.2				
70	9	SOD	ALU	Pp	4	286	6	1	41.9	1121.1	SodPp4xAluSoil	286	41.9				1121.1				
71	9	SOD	ALU	Pp	4	370	7	13	0.0	995.3	SodPp4xAluSoil	370	0.0				995.3				
72	9	SOD	ALU	Pp	4	386	8	1	220.0	916.7	SodPp4xAluSoil	386	220.0	179.6			916.7	1061.5			
73	9	SOD	ALU	Pp	5	219	1	22	112.0	1171.3	SodPp5xAluSoil	219	112.0				1171.3				
74	9	SOD	ALU	Pp	5	351	2	43	0.0	1106.5	SodPp5xAluSoil	351	0.0				1106.5				
75	9	SOD	ALU	Pp	5	365	3	29	268.1	1268.7	SodPp5xAluSoil	365	268.1				1268.7				
76	9	SOD	ALU	Pp	5	346	4	31	0.0	917.0	SodPp5xAluSoil	346	0.0				917.0				

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77	9	SOD	ALU	Pp	5	254	5	50	85.9	1218.4	SodPp5xAluSoil	254	85.9				1218.4				
78	9	SOD	ALU	Pp	5	349	6	42	54.6	1189.1	SodPp5xAluSoil	349	54.6				1189.1				
79	9	SOD	ALU	Pp	5	311	7	16	0.0	730.7	SodPp5xAluSoil	311	0.0				730.7				
80	9	SOD	ALU	Pp	5	276	8	9	138.4	1142.3	SodPp5xAluSoil	276	138.4	82.4	154.0	41.4	1142.3	1093.0	1079.6	30.8	
81	9	SOD	SOD	PpFilt	1	187	1	36	151.0	978.2	SodPp1Filt2SodSoil	187	151.0				978.2				
82	9	SOD	SOD	PpFilt	1	35	2	1	238.1	560.2	SodPp1Filt2SodSoil	35	238.1				560.2				
83	9	SOD	SOD	PpFilt	1	4	3	28	131.6	1102.0	SodPp1Filt2SodSoil	4	131.6				1102.0				
84	9	SOD	SOD	PpFilt	1	2	4	45	NA	NA	SodPp1Filt2SodSoil	2	NA				NA				
85	9	SOD	SOD	PpFilt	1	174	5	44	0.0	1113.5	SodPp1Filt2SodSoil	174	0.0				1113.5				
86	9	SOD	SOD	PpFilt	1	28	6	14	0.0	913.9	SodPp1Filt2SodSoil	28	0.0				913.9				
87	9	SOD	SOD	PpFilt	1	133	7	23	NA	NA	SodPp1Filt2SodSoil	133	NA				NA				
88	9	SOD	SOD	PpFilt	1	63	8	36	131.8	355.2	SodPp1Filt2SodSoil	63	131.8	108.8			355.2	837.2			
89	9	SOD	SOD	PpFilt	2	9	1	47	168.1	1148.0	SodPp2Filt2SodSoil	9	168.1				1148.0				
90	9	SOD	SOD	PpFilt	2	78	2	49	127.7	1005.8	SodPp2Filt2SodSoil	78	127.7				1005.8				
91	9	SOD	SOD	PpFilt	2	76	3	16	0.0	952.9	SodPp2Filt2SodSoil	76	0.0				952.9				
92	9	SOD	SOD	PpFilt	2	177	4	20	0.0	958.1	SodPp2Filt2SodSoil	177	0.0				958.1				
93	9	SOD	SOD	PpFilt	2	101	5	35	41.5	1158.1	SodPp2Filt2SodSoil	101	41.5				1158.1				
94	9	SOD	SOD	PpFilt	2	129	6	48	9.0	1105.5	SodPp2Filt2SodSoil	129	9.0				1105.5				
95	9	SOD	SOD	PpFilt	2	162	7	29	16.9	910.9	SodPp2Filt2SodSoil	162	16.9				910.9				
96	9	SOD	SOD	PpFilt	2	83	8	10	24.1	992.2	SodPp2Filt2SodSoil	83	24.1	48.4			992.2	1028.9			
97	9	SOD	SOD	PpFilt	3	6	1	28	35.1	1141.2	SodPp3Filt2SodSoil	6	35.1				1141.2				
98	9	SOD	SOD	PpFilt	3	185	2	41	13.7	980.9	SodPp3Filt2SodSoil	185	13.7				980.9				
99	9	SOD	SOD	PpFilt	3	146	3	6	NA	NA	SodPp3Filt2SodSoil	146	NA				NA				
100	9	SOD	SOD	PpFilt	3	168	4	38	250.8	613.9	SodPp3Filt2SodSoil	168	250.8				613.9				
101	9	SOD	SOD	PpFilt	3	95	5	39	88.6	1130.5	SodPp3Filt2SodSoil	95	88.6				1130.5				
102	9	SOD	SOD	PpFilt	3	47	6	50	201.0	872.6	SodPp3Filt2SodSoil	47	201.0				872.6				
103	9	SOD	SOD	PpFilt	3	153	7	7	35.5	1096.4	SodPp3Filt2SodSoil	153	35.5				1096.4				
104	9	SOD	SOD	PpFilt	3	141	8	2	50.2	952.5	SodPp3Filt2SodSoil	141	50.2	96.4			952.5	969.7			
105	9	SOD	SOD	PpFilt	4	144	1	8	NA	NA	SodPp4Filt2SodSoil	144	NA				NA				
106	9	SOD	SOD	PpFilt	4	23	2	7	46.0	983.9	SodPp4Filt2SodSoil	23	46.0				983.9				
107	9	SOD	SOD	PpFilt	4	142	3	30	NA	NA	SodPp4Filt2SodSoil	142	NA				NA				
108	9	SOD	SOD	PpFilt	4	10	4	32	9.5	1021.2	SodPp4Filt2SodSoil	10	9.5				1021.2				
109	9	SOD	SOD	PpFilt	4	152	5	26	4.7	1128.9	SodPp4Filt2SodSoil	152	4.7				1128.9				
110	9	SOD	SOD	PpFilt	4	12	6	39	268.1	1074.5	SodPp4Filt2SodSoil	12	268.1				1074.5				
111	9	SOD	SOD	PpFilt	4	19	7	33	0.0	1010.2	SodPp4Filt2SodSoil	19	0.0				1010.2				
112	9	SOD	SOD	PpFilt	4	116	8	8	21.8	1037.9	SodPp4Filt2SodSoil	116	21.8	58.4			1037.9	1042.8			
113	9	SOD	SOD	PpFilt	5	40	1	49	0.0	1237.1	SodPp5Filt2SodSoil	40	0.0				1237.1				
114	9	SOD	SOD	PpFilt	5	84	2	45	231.1	659.6	SodPp5Filt2SodSoil	84	231.1				659.6				
115	9	SOD	SOD	PpFilt	5	108	3	33	149.0	923.5	SodPp5Filt2SodSoil	108	149.0				923.5				
116	9	SOD	SOD	PpFilt	5	26	4	39	284.9	813.8	SodPp5Filt2SodSoil	26	284.9				813.8				
117	9	SOD	SOD	PpFilt	5	132	5	13	279.5	905.4	SodPp5Filt2SodSoil	132	279.5				905.4				
118	9	SOD	SOD	PpFilt	5	72	6	44	1.7	1104.2	SodPp5Filt2SodSoil	72	1.7				1104.2				
119	9	SOD	SOD	PpFilt	5	80	7	45	8.4	1095.1	SodPp5Filt2SodSoil	80	8.4				1095.1				
120	9	SOD	SOD	PpFilt	5	172	8	42	0.0	1035.4	SodPp5Filt2SodSoil	172	0.0	119.3	86.3	31.3	1035.4	971.8	970.1	81.3	
121	9	SOD	SOD	Np	1	109	1	6	18.6	1328.0	SodNp1	109	18.6				1328.0				
122	9	SOD	SOD	Np	1	44	2	39	0.0	1053.3	SodNp1	44	0.0				1053.3				
123	9	SOD	SOD	Np	1	113	3	23	16.4	948.8	SodNp1	113	16.4				948.8				
124	9	SOD	SOD	Np	1	197	4	21	NA	NA	SodNp1	197	NA				NA				
125	9	SOD	SOD	Np	1	140	5	22	0.0	3.8	SodNp1	140	0.0				3.8				
126	9	SOD	SOD	Np	1	21	6	17	59.2	1179.3	SodNp1	21	59.2				1179.3				
127	9	SOD	SOD	Np	1	45	7	28	176.3	1063.2	SodNp1	45	176.3				1063.2				
128	9	SOD	SOD	Np	1	145	8	33	0.0	1162.8	SodNp1	145	0.0	38.6			1162.8	962.7			
129	9	SOD	SOD	Np	2	158	1	3	NA	NA	SodNp2	158	NA				NA				

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130	9	SOD	SOD	Np	2	25	2	13	316.0	1113.6	SodNp2	25	316.0				1113.6				
131	9	SOD	SOD	Np	2	24	3	34	19.3	1181.1	SodNp2	24	19.3				1181.1				
132	9	SOD	SOD	Np	2	49	4	36	114.0	1237.8	SodNp2	49	114.0				1237.8				
133	9	SOD	SOD	Np	2	66	5	46	54.3	1310.5	SodNp2	66	54.3				1310.5				
134	9	SOD	SOD	Np	2	75	6	18	0.0	2.0	SodNp2	75	0.0				2.0				
135	9	SOD	SOD	Np	2	193	7	17	357.3	1008.4	SodNp2	193	357.3				1008.4				
136	9	SOD	SOD	Np	2	156	8	7	200.1	715.7	SodNp2	156	200.1	151.6			715.7	938.4			
137	9	SOD	SOD	Np	3	183	1	25	383.7	942.7	SodNp3	183	383.7				942.7				
138	9	SOD	SOD	Np	3	198	2	34	8.7	1332.5	SodNp3	198	8.7				1332.5				
139	9	SOD	SOD	Np	3	148	3	27	0.0	3.3	SodNp3	148	0.0				3.3				
140	9	SOD	SOD	Np	3	182	4	9	288.0	566.5	SodNp3	182	288.0				566.5				
141	9	SOD	SOD	Np	3	64	5	37	270.5	796.3	SodNp3	64	270.5				796.3				
142	9	SOD	SOD	Np	3	192	6	6	0.0	2.5	SodNp3	192	0.0				2.5				
143	9	SOD	SOD	Np	3	120	7	21	198.7	672.4	SodNp3	120	198.7				672.4				
144	9	SOD	SOD	Np	3	188	8	25	328.0	913.6	SodNp3	188	328.0	184.7			913.6	653.7			
145	9	SOD	SOD	Np	4	16	1	23	188.5	589.1	SodNp4	16	188.5				589.1				
146	9	SOD	SOD	Np	4	13	2	27	39.4	1340.0	SodNp4	13	39.4				1340.0				
147	9	SOD	SOD	Np	4	55	3	1	0.0	1017.8	SodNp4	55	0.0				1017.8				
148	9	SOD	SOD	Np	4	37	4	12	243.0	748.9	SodNp4	37	243.0				748.9				
149	9	SOD	SOD	Np	4	137	5	49	NA	NA	SodNp4	137	NA				NA				
150	9	SOD	SOD	Np	4	128	6	21	266.7	1026.0	SodNp4	128	266.7				1026.0				
151	9	SOD	SOD	Np	4	119	7	48	52.7	1158.2	SodNp4	119	52.7				1158.2				
152	9	SOD	SOD	Np	4	53	8	50	146.6	1078.2	SodNp4	53	146.6	133.8			1078.2	994.0			
153	9	SOD	SOD	Np	5	67	1	16	53.8	1272.2	SodNp5	67	53.8				1272.2				
154	9	SOD	SOD	Np	5	79	2	6	124.2	1218.8	SodNp5	79	124.2				1218.8				
155	9	SOD	SOD	Np	5	173	3	48	49.2	869.4	SodNp5	173	49.2				869.4				
156	9	SOD	SOD	Np	5	150	4	34	NA	NA	SodNp5	150	NA				NA				
157	9	SOD	SOD	Np	5	68	5	29	28.3	1193.7	SodNp5	68	28.3				1193.7				
158	9	SOD	SOD	Np	5	122	6	22	63.4	1034.4	SodNp5	122	63.4				1034.4				
159	9	SOD	SOD	Np	5	74	7	6	61.0	1313.4	SodNp5	74	61.0				1313.4				
160	9	SOD	SOD	Np	5	112	8	13	246.3	1065.1	SodNp5	112	246.3	89.5	119.6	56.8	1065.1	1138.1	937.4	176.5	
161	9	SOD	SOD	Null	NA	127	1	21	88.5	1049.5	SodNull	127	88.5				1049.5				
162	9	SOD	SOD	Null	NA	50	2	19	293.6	797.6	SodNull	50	293.6				797.6				
163	9	SOD	SOD	Null	NA	110	3	8	47.0	1125.6	SodNull	110	47.0				1125.6				
164	9	SOD	SOD	Null	NA	86	4	50	269.1	950.2	SodNull	86	269.1				950.2				
165	9	SOD	SOD	Null	NA	30	5	21	28.2	1115.3	SodNull	30	28.2				1115.3				
166	9	SOD	SOD	Null	NA	91	6	2	44.6	1095.2	SodNull	91	44.6				1095.2				
167	9	SOD	SOD	Null	NA	11	7	44	0.0	919.0	SodNull	11	0.0				919.0				
168	9	SOD	SOD	Null	NA	115	8	16	33.0	1129.5	SodNull	115	33.0				1129.5				
169	9	SOD	SOD	Null	NA	41	1	35	0.0	1151.3	SodNull	41	0.0				1151.3				
170	9	SOD	SOD	Null	NA	96	2	26	41.7	1063.4	SodNull	96	41.7				1063.4				
171	9	SOD	SOD	Null	NA	184	3	14	0.0	970.8	SodNull	184	0.0				970.8				
172	9	SOD	SOD	Null	NA	31	4	27	149.9	1037.6	SodNull	31	149.9				1037.6				
173	9	SOD	SOD	Null	NA	103	5	42	278.8	934.6	SodNull	103	278.8				934.6				
174	9	SOD	SOD	Null	NA	107	6	11	166.5	992.4	SodNull	107	166.5				992.4				
175	9	SOD	SOD	Null	NA	124	7	3	144.7	1101.5	SodNull	124	144.7				1101.5				
176	9	SOD	SOD	Null	NA	111	8	22	232.8	947.6	SodNull	111	232.8				947.6				
177	9	SOD	SOD	Null	NA	178	1	30	0.0	1115.6	SodNull	178	0.0				1115.6				
178	9	SOD	SOD	Null	NA	32	2	12	84.0	1022.7	SodNull	32	84.0				1022.7				
179	9	SOD	SOD	Null	NA	42	3	37	66.5	1176.6	SodNull	42	66.5				1176.6				
180	9	SOD	SOD	Null	NA	71	4	22	22.9	1107.1	SodNull	71	22.9				1107.1				
181	9	SOD	SOD	Null	NA	54	5	1	27.1	1046.8	SodNull	54	27.1				1046.8				
182	9	SOD	SOD	Null	NA	147	6	47	0.0	1024.5	SodNull	147	0.0				1024.5				

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183	9	SOD	SOD	Null	NA	143	7	26	0.0	1034.6	SodNull	143	0.0				1034.6				
184	9	SOD	SOD	Null	NA	97	8	30	103.6	999.3	SodNull	97	103.6				999.3				
185	9	SOD	SOD	Null	NA	43	1	5	162.1	1032.1	SodNull	43	162.1				1032.1				
186	9	SOD	SOD	Null	NA	151	2	21	0.0	897.1	SodNull	151	0.0				897.1				
187	9	SOD	SOD	Null	NA	160	3	43	85.6	1095.1	SodNull	160	85.6				1095.1				
188	9	SOD	SOD	Null	NA	134	4	8	NA	NA	SodNull	134	NA				NA				
189	9	SOD	SOD	Null	NA	22	5	28	114.1	1047.8	SodNull	22	114.1				1047.8				
190	9	SOD	SOD	Null	NA	179	6	26	233.4	1070.1	SodNull	179	233.4				1070.1				
191	9	SOD	SOD	Null	NA	39	7	42	8.3	1074.9	SodNull	39	8.3				1074.9				
192	9	SOD	SOD	Null	NA	138	8	20	132.9	960.3	SodNull	138	132.9				960.3				
193	9	SOD	SOD	Null	NA	20	1	41	121.7	1087.0	SodNull	20	121.7				1087.0				
194	9	SOD	SOD	Null	NA	18	2	23	198.3	472.8	SodNull	18	198.3				472.8				
195	9	SOD	SOD	Null	NA	171	3	21	59.2	955.1	SodNull	171	59.2				955.1				
196	9	SOD	SOD	Null	NA	17	4	35	0.0	1062.8	SodNull	17	0.0				1062.8				
197	9	SOD	SOD	Null	NA	191	5	9	225.8	1038.1	SodNull	191	225.8				1038.1				
198	9	SOD	SOD	Null	NA	165	6	24	0.0	1084.7	SodNull	165	0.0				1084.7				
199	9	SOD	SOD	Null	NA	81	7	4	41.5	1006.9	SodNull	81	41.5				1006.9				
200	9	SOD	SOD	Null	NA	48	8	34	322.5	943.1	SodNull	48	322.5	98.2	98.2	97.1	943.1	1018.9	1018.9	119.1	
201	9	ALU	ALU	Pp	1	322	1	39	223.1	1242.5	AluPp1xAluSoil	322	223.1				1242.5				
202	9	ALU	ALU	Pp	1	297	2	18	350.1	1193.2	AluPp1xAluSoil	297	350.1				1193.2				
203	9	ALU	ALU	Pp	1	317	3	26	0.0	1069.0	AluPp1xAluSoil	317	0.0				1069.0				
204	9	ALU	ALU	Pp	1	398	4	24	272.2	1177.5	AluPp1xAluSoil	398	272.2				1177.5				
205	9	ALU	ALU	Pp	1	294	5	4	146.6	1324.4	AluPp1xAluSoil	294	146.6				1324.4				
206	9	ALU	ALU	Pp	1	241	6	31	283.3	1044.8	AluPp1xAluSoil	241	283.3				1044.8				
207	9	ALU	ALU	Pp	1	252	7	27	258.5	1040.3	AluPp1xAluSoil	252	258.5				1040.3				
208	9	ALU	ALU	Pp	1	250	8	46	263.4	1108.7	AluPp1xAluSoil	250	263.4	224.7			1108.7	1150.1			
209	9	ALU	ALU	Pp	2	212	1	50	NA	NA	AluPp2xAluSoil	212	NA				NA				
210	9	ALU	ALU	Pp	2	363	2	46	26.9	1133.0	AluPp2xAluSoil	363	26.9				1133.0				
211	9	ALU	ALU	Pp	2	272	3	9	352.6	983.6	AluPp2xAluSoil	272	352.6				983.6				
212	9	ALU	ALU	Pp	2	345	4	26	240.2	1195.2	AluPp2xAluSoil	345	240.2				1195.2				
213	9	ALU	ALU	Pp	2	261	5	10	327.7	1074.5	AluPp2xAluSoil	261	327.7				1074.5				
214	9	ALU	ALU	Pp	2	224	6	16	490.0	1075.5	AluPp2xAluSoil	224	490.0				1075.5				
215	9	ALU	ALU	Pp	2	360	7	30	302.4	946.8	AluPp2xAluSoil	360	302.4				946.8				
216	9	ALU	ALU	Pp	2	270	8	40	103.2	1089.2	AluPp2xAluSoil	270	103.2	263.3			1089.2	1071.1			
217	9	ALU	ALU	Pp	3	284	1	2	43.4	1168.6	AluPp3xAluSoil	284	43.4				1168.6				
218	9	ALU	ALU	Pp	3	269	2	17	126.4	988.1	AluPp3xAluSoil	269	126.4				988.1				
219	9	ALU	ALU	Pp	3	394	3	20	242.6	1048.9	AluPp3xAluSoil	394	242.6				1048.9				
220	9	ALU	ALU	Pp	3	395	4	28	284.6	1161.2	AluPp3xAluSoil	395	284.6				1161.2				
221	9	ALU	ALU	Pp	3	288	5	3	0.0	1132.4	AluPp3xAluSoil	288	0.0				1132.4				
222	9	ALU	ALU	Pp	3	384	6	20	25.0	1155.7	AluPp3xAluSoil	384	25.0				1155.7				
223	9	ALU	ALU	Pp	3	337	7	12	253.1	992.1	AluPp3xAluSoil	337	253.1				992.1				
224	9	ALU	ALU	Pp	3	316	8	32	122.8	1129.7	AluPp3xAluSoil	316	122.8	137.2			1129.7	1097.1			
225	9	ALU	ALU	Pp	4	290	1	7	50.9	1160.6	AluPp4xAluSoil	290	50.9				1160.6				
226	9	ALU	ALU	Pp	4	251	2	3	329.5	1071.8	AluPp4xAluSoil	251	329.5				1071.8				
227	9	ALU	ALU	Pp	4	275	3	5	406.8	1218.9	AluPp4xAluSoil	275	406.8				1218.9				
228	9	ALU	ALU	Pp	4	268	4	30	295.4	1062.5	AluPp4xAluSoil	268	295.4				1062.5				
229	9	ALU	ALU	Pp	4	201	5	11	NA	NA	AluPp4xAluSoil	201	NA				NA				
230	9	ALU	ALU	Pp	4	258	6	35	29.7	1222.3	AluPp4xAluSoil	258	29.7				1222.3				
231	9	ALU	ALU	Pp	4	218	7	35	22.1	1023.8	AluPp4xAluSoil	218	22.1				1023.8				
232	9	ALU	ALU	Pp	4	333	8	44	37.5	1142.0	AluPp4xAluSoil	333	37.5	167.4			1142.0	1128.8			
233	9	ALU	ALU	Pp	5	371	1	20	301.7	1134.4	AluPp5xAluSoil	371	301.7				1134.4				
234	9	ALU	ALU	Pp	5	326	2	4	358.9	970.3	AluPp5xAluSoil	326	358.9				970.3				
235	9	ALU	ALU	Pp	5	302	3	25	114.7	1011.2	AluPp5xAluSoil	302	114.7				1011.2				

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236	9	ALU	ALU	Pp	5	387	4	37	230.4	1184.2	AluPp5xAluSoil	387	230.4				1184.2				
237	9	ALU	ALU	Pp	5	239	5	33	240.4	1159.8	AluPp5xAluSoil	239	240.4				1159.8				
238	9	ALU	ALU	Pp	5	206	6	34	282.2	994.9	AluPp5xAluSoil	206	282.2				994.9				
239	9	ALU	ALU	Pp	5	262	7	9	141.2	1170.4	AluPp5xAluSoil	262	141.2				1170.4				
240	9	ALU	ALU	Pp	5	204	8	28	372.2	872.5	AluPp5xAluSoil	204	372.2	255.2	209.6	55.2	872.5	1062.2	1101.9	37.4	
241	9	ALU	SOD	Pp	1	52	1	40	178.5	1309.8	AluPp1xSodSoil	52	178.5				1309.8				
242	9	ALU	SOD	Pp	1	36	2	38	NA	NA	AluPp1xSodSoil	36	NA				NA				
243	9	ALU	SOD	Pp	1	117	3	50	0.0	1143.7	AluPp1xSodSoil	117	0.0				1143.7				
244	9	ALU	SOD	Pp	1	157	4	13	436.4	1026.8	AluPp1xSodSoil	157	436.4				1026.8				
245	9	ALU	SOD	Pp	1	77	5	41	285.2	1054.8	AluPp1xSodSoil	77	285.2				1054.8				
246	9	ALU	SOD	Pp	1	98	6	30	0.0	1015.0	AluPp1xSodSoil	98	0.0				1015.0				
247	9	ALU	SOD	Pp	1	15	7	49	187.5	1074.8	AluPp1xSodSoil	15	187.5				1074.8				
248	9	ALU	SOD	Pp	1	164	8	45	242.9	639.4	AluPp1xSodSoil	164	242.9	190.1			639.4	1037.8			
249	9	ALU	SOD	Pp	2	94	1	27	0.0	1156.9	AluPp2xSodSoil	94	0.0				1156.9				
250	9	ALU	SOD	Pp	2	38	2	36	NA	NA	AluPp2xSodSoil	38	NA				NA				
251	9	ALU	SOD	Pp	2	14	3	13	302.6	943.5	AluPp2xSodSoil	14	302.6				943.5				
252	9	ALU	SOD	Pp	2	181	4	16	0.0	1214.2	AluPp2xSodSoil	181	0.0				1214.2				
253	9	ALU	SOD	Pp	2	200	5	30	49.3	1251.0	AluPp2xSodSoil	200	49.3				1251.0				
254	9	ALU	SOD	Pp	2	93	6	33	274.8	1015.8	AluPp2xSodSoil	93	274.8				1015.8				
255	9	ALU	SOD	Pp	2	34	7	25	NA	NA	AluPp2xSodSoil	34	NA				NA				
256	9	ALU	SOD	Pp	2	59	8	39	161.2	1089.1	AluPp2xSodSoil	59	161.2	131.3			1089.1	1111.8			
257	9	ALU	SOD	Pp	3	136	1	42	53.8	1292.7	AluPp3xSodSoil	136	53.8				1292.7				
258	9	ALU	SOD	Pp	3	46	2	25	0.0	1152.2	AluPp3xSodSoil	46	0.0				1152.2				
259	9	ALU	SOD	Pp	3	125	3	31	162.7	940.0	AluPp3xSodSoil	125	162.7				940.0				
260	9	ALU	SOD	Pp	3	51	4	43	369.1	1073.9	AluPp3xSodSoil	51	369.1				1073.9				
261	9	ALU	SOD	Pp	3	169	5	7	NA	NA	AluPp3xSodSoil	169	NA				NA				
262	9	ALU	SOD	Pp	3	159	6	15	367.6	949.8	AluPp3xSodSoil	159	367.6				949.8				
263	9	ALU	SOD	Pp	3	105	7	8	0.0	1111.5	AluPp3xSodSoil	105	0.0				1111.5				
264	9	ALU	SOD	Pp	3	104	8	3	222.6	1103.9	AluPp3xSodSoil	104	222.6	168.0			1103.9	1089.1			
265	9	ALU	SOD	Pp	4	61	1	14	37.1	1280.2	AluPp4xSodSoil	61	37.1				1280.2				
266	9	ALU	SOD	Pp	4	114	2	15	376.3	1009.6	AluPp4xSodSoil	114	376.3				1009.6				
267	9	ALU	SOD	Pp	4	118	3	46	291.2	660.1	AluPp4xSodSoil	118	291.2				660.1				
268	9	ALU	SOD	Pp	4	8	4	1	251.4	1162.5	AluPp4xSodSoil	8	251.4				1162.5				
269	9	ALU	SOD	Pp	4	99	5	48	230.7	462.2	AluPp4xSodSoil	99	230.7				462.2				
270	9	ALU	SOD	Pp	4	89	6	41	356.8	831.8	AluPp4xSodSoil	89	356.8				831.8				
271	9	ALU	SOD	Pp	4	154	7	50	193.6	1027.6	AluPp4xSodSoil	154	193.6				1027.6				
272	9	ALU	SOD	Pp	4	85	8	18	358.9	968.2	AluPp4xSodSoil	85	358.9	262.0			968.2	925.3			
273	9	ALU	SOD	Pp	5	175	1	33	103.6	1231.6	AluPp5xSodSoil	175	103.6				1231.6				
274	9	ALU	SOD	Pp	5	27	2	5	346.6	852.8	AluPp5xSodSoil	27	346.6				852.8				
275	9	ALU	SOD	Pp	5	29	3	38	331.6	939.4	AluPp5xSodSoil	29	331.6				939.4				
276	9	ALU	SOD	Pp	5	139	4	15	309.5	778.1	AluPp5xSodSoil	139	309.5				778.1				
277	9	ALU	SOD	Pp	5	167	5	43	349.6	1026.9	AluPp5xSodSoil	167	349.6				1026.9				
278	9	ALU	SOD	Pp	5	131	6	36	330.7	1010.9	AluPp5xSodSoil	131	330.7				1010.9				
279	9	ALU	SOD	Pp	5	60	7	15	219.4	605.7	AluPp5xSodSoil	60	219.4				605.7				
280	9	ALU	SOD	Pp	5	56	8	21	0.0	964.6	AluPp5xSodSoil	56	0.0	248.9	200.0	54.9	964.6	926.3	1018.0	88.4	
281	9	ALU	ALU	PpFlt	1	209	1	44	41.6	1111.7	AluPp1Flt2AluSoil	209	41.6				1111.7				
282	9	ALU	ALU	PpFlt	1	374	2	31	120.7	989.9	AluPp1Flt2AluSoil	374	120.7				989.9				
283	9	ALU	ALU	PpFlt	1	222	3	17	234.2	446.9	AluPp1Flt2AluSoil	222	234.2				446.9				
284	9	ALU	ALU	PpFlt	1	334	4	23	205.3	499.5	AluPp1Flt2AluSoil	334	205.3				499.5				
285	9	ALU	ALU	PpFlt	1	362	5	8	146.7	1154.7	AluPp1Flt2AluSoil	362	146.7				1154.7				
286	9	ALU	ALU	PpFlt	1	400	6	46	NA	NA	AluPp1Flt2AluSoil	400	NA				NA				
287	9	ALU	ALU	PpFlt	1	359	7	40	51.3	1037.0	AluPp1Flt2AluSoil	359	51.3				1037.0				
288	9	ALU	ALU	PpFlt	1	310	8	49	42.6	943.7	AluPp1Flt2AluSoil	310	42.6	120.3			943.7	883.3			

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289	9	ALU	ALU	PpFilt	2	375	1	13	185.4	984.7	AluPp2Fit2AluSoil	375	185.4				984.7				
290	9	ALU	ALU	PpFilt	2	208	2	32	180.9	1083.8	AluPp2Fit2AluSoil	208	180.9				1083.8				
291	9	ALU	ALU	PpFilt	2	312	3	18	303.4	958.3	AluPp2Fit2AluSoil	312	303.4				958.3				
292	9	ALU	ALU	PpFilt	2	318	4	10	118.2	1136.2	AluPp2Fit2AluSoil	318	118.2				1136.2				
293	9	ALU	ALU	PpFilt	2	229	5	14	72.7	1168.9	AluPp2Fit2AluSoil	229	72.7				1168.9				
294	9	ALU	ALU	PpFilt	2	243	6	45	0.0	1027.4	AluPp2Fit2AluSoil	243	0.0				1027.4				
295	9	ALU	ALU	PpFilt	2	211	7	14	119.5	1071.5	AluPp2Fit2AluSoil	211	119.5				1071.5				
296	9	ALU	ALU	PpFilt	2	253	8	27	179.3	1107.9	AluPp2Fit2AluSoil	253	179.3	144.9			1107.9	1067.3			
297	9	ALU	ALU	PpFilt	3	307	1	1	75.0	1083.7	AluPp3Fit2AluSoil	307	75.0				1083.7				
298	9	ALU	ALU	PpFilt	3	327	2	24	96.2	1068.8	AluPp3Fit2AluSoil	327	96.2				1068.8				
299	9	ALU	ALU	PpFilt	3	321	3	7	239.1	661.3	AluPp3Fit2AluSoil	321	239.1				661.3				
300	9	ALU	ALU	PpFilt	3	255	4	46	90.5	1050.3	AluPp3Fit2AluSoil	255	90.5				1050.3				
301	9	ALU	ALU	PpFilt	3	256	5	45	128.1	938.7	AluPp3Fit2AluSoil	256	128.1				938.7				
302	9	ALU	ALU	PpFilt	3	329	6	12	23.8	954.6	AluPp3Fit2AluSoil	329	23.8				954.6				
303	9	ALU	ALU	PpFilt	3	305	7	22	143.7	1090.9	AluPp3Fit2AluSoil	305	143.7				1090.9				
304	9	ALU	ALU	PpFilt	3	223	8	15	198.0	1118.2	AluPp3Fit2AluSoil	223	198.0	124.3			1118.2	995.8			
305	9	ALU	ALU	PpFilt	4	356	1	46	210.9	928.7	AluPp4Fit2AluSoil	356	210.9				928.7				
306	9	ALU	ALU	PpFilt	4	338	2	29	163.0	1015.7	AluPp4Fit2AluSoil	338	163.0				1015.7				
307	9	ALU	ALU	PpFilt	4	203	3	45	208.7	908.6	AluPp4Fit2AluSoil	203	208.7				908.6				
308	9	ALU	ALU	PpFilt	4	215	4	33	121.4	1178.0	AluPp4Fit2AluSoil	215	121.4				1178.0				
309	9	ALU	ALU	PpFilt	4	299	5	27	85.2	1101.7	AluPp4Fit2AluSoil	299	85.2				1101.7				
310	9	ALU	ALU	PpFilt	4	361	6	27	248.6	1005.4	AluPp4Fit2AluSoil	361	248.6				1005.4				
311	9	ALU	ALU	PpFilt	4	396	7	31	0.0	792.2	AluPp4Fit2AluSoil	396	0.0				792.2				
312	9	ALU	ALU	PpFilt	4	331	8	17	0.0	1034.4	AluPp4Fit2AluSoil	331	0.0	129.7			1034.4	995.6			
313	9	ALU	ALU	PpFilt	5	291	1	17	278.6	1076.6	AluPp5Fit2AluSoil	291	278.6				1076.6				
314	9	ALU	ALU	PpFilt	5	277	2	48	84.3	1054.2	AluPp5Fit2AluSoil	277	84.3				1054.2				
315	9	ALU	ALU	PpFilt	5	240	3	39	240.3	483.1	AluPp5Fit2AluSoil	240	240.3				483.1				
316	9	ALU	ALU	PpFilt	5	399	4	2	40.2	1101.7	AluPp5Fit2AluSoil	399	40.2				1101.7				
317	9	ALU	ALU	PpFilt	5	382	5	16	165.7	530.9	AluPp5Fit2AluSoil	382	165.7				530.9				
318	9	ALU	ALU	PpFilt	5	238	6	40	123.9	945.7	AluPp5Fit2AluSoil	238	123.9				945.7				
319	9	ALU	ALU	PpFilt	5	237	7	36	174.2	345.2	AluPp5Fit2AluSoil	237	174.2				345.2				
320	9	ALU	ALU	PpFilt	5	350	8	41	136.2	912.0	AluPp5Fit2AluSoil	350	136.2	155.4	134.9	14.8	912.0	806.2	949.7	103.8	
321	9	ALU	ALU	Np	1	230	1	18	99.5	1058.4	AluNp1	230	99.5				1058.4				
322	9	ALU	ALU	Np	1	319	2	35	0.0	748.2	AluNp1	319	0.0				748.2				
323	9	ALU	ALU	Np	1	397	3	47	0.0	1119.6	AluNp1	397	0.0				1119.6				
324	9	ALU	ALU	Np	1	245	4	29	20.9	1470.8	AluNp1	245	20.9				1470.8				
325	9	ALU	ALU	Np	1	257	5	12	14.1	1133.0	AluNp1	257	14.1				1133.0				
326	9	ALU	ALU	Np	1	244	6	5	22.9	1201.0	AluNp1	244	22.9				1201.0				
327	9	ALU	ALU	Np	1	354	7	5	28.0	1141.7	AluNp1	354	28.0				1141.7				
328	9	ALU	ALU	Np	1	228	8	43	0.0	1110.3	AluNp1	228	0.0	23.2			1110.3	1122.9			
329	9	ALU	ALU	Np	2	217	1	24	38.5	1061.8	AluNp2	217	38.5				1061.8				
330	9	ALU	ALU	Np	2	355	2	42	14.8	1010.9	AluNp2	355	14.8				1010.9				
331	9	ALU	ALU	Np	2	383	3	10	100.3	1168.7	AluNp2	383	100.3				1168.7				
332	9	ALU	ALU	Np	2	202	4	17	NA	NA	AluNp2	202	NA				NA				
333	9	ALU	ALU	Np	2	301	5	32	222.6	775.8	AluNp2	301	222.6				775.8				
334	9	ALU	ALU	Np	2	248	6	8	55.3	1036.7	AluNp2	248	55.3				1036.7				
335	9	ALU	ALU	Np	2	267	7	38	113.2	1109.1	AluNp2	267	113.2				1109.1				
336	9	ALU	ALU	Np	2	314	8	6	273.7	846.5	AluNp2	314	273.7	116.9			846.5	1001.4			
337	9	ALU	ALU	Np	3	324	1	15	94.2	1098.5	AluNp3	324	94.2				1098.5				
338	9	ALU	ALU	Np	3	292	2	33	24.0	986.0	AluNp3	292	24.0				986.0				
339	9	ALU	ALU	Np	3	368	3	12	0.0	902.1	AluNp3	368	0.0				902.1				
340	9	ALU	ALU	Np	3	352	4	41	79.5	1093.9	AluNp3	352	79.5				1093.9				
341	9	ALU	ALU	Np	3	372	5	5	112.7	245.3	AluNp3	372	112.7				245.3				

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342	9	ALU	ALU	Np	3	339	6	49	18.6	1143.0	AluNp3	339	18.6				1143.0				
343	9	ALU	ALU	Np	3	274	7	19	147.5	1024.5	AluNp3	274	147.5				1024.5				
344	9	ALU	ALU	Np	3	320	8	24	NA	NA	AluNp3	320	NA	68.1			NA	927.6			
345	9	ALU	ALU	Np	4	315	1	32	103.9	1044.2	AluNp4	315	103.9				1044.2				
346	9	ALU	ALU	Np	4	380	2	22	219.9	1155.3	AluNp4	380	219.9				1155.3				
347	9	ALU	ALU	Np	4	227	3	41	38.4	984.5	AluNp4	227	38.4				984.5				
348	9	ALU	ALU	Np	4	389	4	6	0.0	1158.0	AluNp4	389	0.0				1158.0				
349	9	ALU	ALU	Np	4	341	5	20	0.0	1116.3	AluNp4	341	0.0				1116.3				
350	9	ALU	ALU	Np	4	385	6	38	0.0	941.2	AluNp4	385	0.0				941.2				
351	9	ALU	ALU	Np	4	226	7	47	72.9	1056.8	AluNp4	226	72.9				1056.8				
352	9	ALU	ALU	Np	4	225	8	12	91.5	1038.9	AluNp4	225	91.5	65.8			1038.9	1061.9			
353	9	ALU	ALU	Np	5	296	1	31	0.0	1066.0	AluNp5	296	0.0				1066.0				
354	9	ALU	ALU	Np	5	379	2	10	63.6	1133.6	AluNp5	379	63.6				1133.6				
355	9	ALU	ALU	Np	5	377	3	2	219.2	811.0	AluNp5	377	219.2				811.0				
356	9	ALU	ALU	Np	5	280	4	25	102.0	1221.6	AluNp5	280	102.0				1221.6				
357	9	ALU	ALU	Np	5	336	5	23	15.9	1128.3	AluNp5	336	15.9				1128.3				
358	9	ALU	ALU	Np	5	364	6	7	218.0	1026.1	AluNp5	364	218.0				1026.1				
359	9	ALU	ALU	Np	5	367	7	1	42.6	1146.0	AluNp5	367	42.6				1146.0				
360	9	ALU	ALU	Np	5	216	8	5	0.0	1125.0	AluNp5	216	0.0	82.7	71.3	33.8	1125.0	1082.2	1039.2	76.2	
361	9	ALU	ALU	Null	NA	249	1	26	218.5	902.8	AluNull	249	218.5				902.8				
362	9	ALU	ALU	Null	NA	260	2	30	78.0	1001.4	AluNull	260	78.0				1001.4				
363	9	ALU	ALU	Null	NA	231	3	35	54.8	1133.0	AluNull	231	54.8				1133.0				
364	9	ALU	ALU	Null	NA	285	4	48	25.9	1227.3	AluNull	285	25.9				1227.3				
365	9	ALU	ALU	Null	NA	344	5	38	10.2	1058.7	AluNull	344	10.2				1058.7				
366	9	ALU	ALU	Null	NA	282	6	25	61.5	1090.5	AluNull	282	61.5				1090.5				
367	9	ALU	ALU	Null	NA	313	7	37	70.1	1101.7	AluNull	313	70.1				1101.7				
368	9	ALU	ALU	Null	NA	278	8	4	150.9	1065.7	AluNull	278	150.9				1065.7				
369	9	ALU	ALU	Null	NA	293	1	43	39.3	1095.7	AluNull	293	39.3				1095.7				
370	9	ALU	ALU	Null	NA	263	2	9	76.8	1044.7	AluNull	263	76.8				1044.7				
371	9	ALU	ALU	Null	NA	221	3	11	106.6	937.9	AluNull	221	106.6				937.9				
372	9	ALU	ALU	Null	NA	381	4	47	144.4	1084.0	AluNull	381	144.4				1084.0				
373	9	ALU	ALU	Null	NA	340	5	31	70.1	1053.9	AluNull	340	70.1				1053.9				
374	9	ALU	ALU	Null	NA	373	6	9	258.0	941.7	AluNull	373	258.0				941.7				
375	9	ALU	ALU	Null	NA	287	7	18	229.6	505.8	AluNull	287	229.6				505.8				
376	9	ALU	ALU	Null	NA	213	8	37	0.0	907.1	AluNull	213	0.0				907.1				
377	9	ALU	ALU	Null	NA	391	1	11	69.4	974.0	AluNull	391	69.4				974.0				
378	9	ALU	ALU	Null	NA	273	2	37	0.0	961.3	AluNull	273	0.0				961.3				
379	9	ALU	ALU	Null	NA	207	3	24	115.0	1041.5	AluNull	207	115.0				1041.5				
380	9	ALU	ALU	Null	NA	343	4	3	224.7	842.3	AluNull	343	224.7				842.3				
381	9	ALU	ALU	Null	NA	353	5	18	191.3	1061.1	AluNull	353	191.3				1061.1				
382	9	ALU	ALU	Null	NA	235	6	43	125.9	1071.5	AluNull	235	125.9				1071.5				
383	9	ALU	ALU	Null	NA	347	7	10	41.5	1130.1	AluNull	347	41.5				1130.1				
384	9	ALU	ALU	Null	NA	236	8	26	0.0	833.5	AluNull	236	0.0				833.5				
385	9	ALU	ALU	Null	NA	388	1	37	115.1	1099.3	AluNull	388	115.1				1099.3				
386	9	ALU	ALU	Null	NA	242	2	40	155.4	983.5	AluNull	242	155.4				983.5				
387	9	ALU	ALU	Null	NA	357	3	22	292.2	828.9	AluNull	357	292.2				828.9				
388	9	ALU	ALU	Null	NA	298	4	11	241.2	858.6	AluNull	298	241.2				858.6				
389	9	ALU	ALU	Null	NA	214	5	25	186.2	1094.2	AluNull	214	186.2				1094.2				
390	9	ALU	ALU	Null	NA	342	6	3	85.5	1046.2	AluNull	342	85.5				1046.2				
391	9	ALU	ALU	Null	NA	210	7	34	0.0	1014.0	AluNull	210	0.0				1014.0				
392	9	ALU	ALU	Null	NA	246	8	19	150.6	944.9	AluNull	246	150.6				944.9				
393	9	ALU	ALU	Null	NA	323	1	10	30.9	1092.6	AluNull	323	30.9				1092.6				
394	9	ALU	ALU	Null	NA	283	2	2	33.1	1049.8	AluNull	283	33.1				1049.8				

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395	9	ALU	ALU	Null	NA	325	3	44	199.9	941.0	AluNull	325	199.9				941.0				
396	9	ALU	ALU	Null	NA	281	4	44	65.0	1197.0	AluNull	281	65.0				1197.0				
397	9	ALU	ALU	Null	NA	233	5	40	180.2	1047.1	AluNull	233	180.2				1047.1				
398	9	ALU	ALU	Null	NA	220	6	29	0.0	990.2	AluNull	220	0.0				990.2				
399	9	ALU	ALU	Null	NA	309	7	46	0.0	1053.2	AluNull	309	0.0				1053.2				
400	9	ALU	ALU	Null	NA	392	8	14	72.4	1108.5	AluNull	392	72.4	104.3	104.3	83.3	1108.5	1010.4	1010.4	124.9	