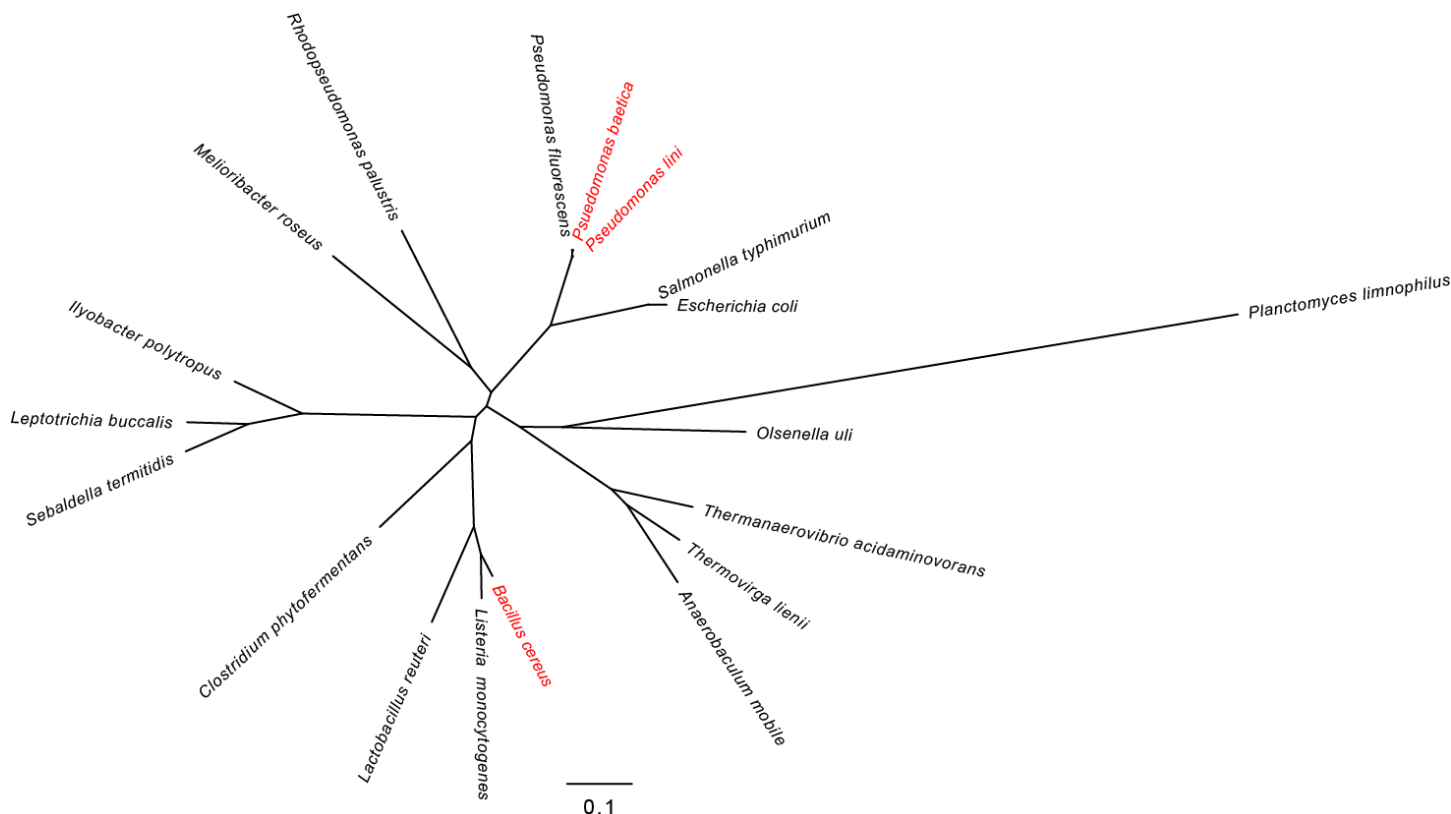
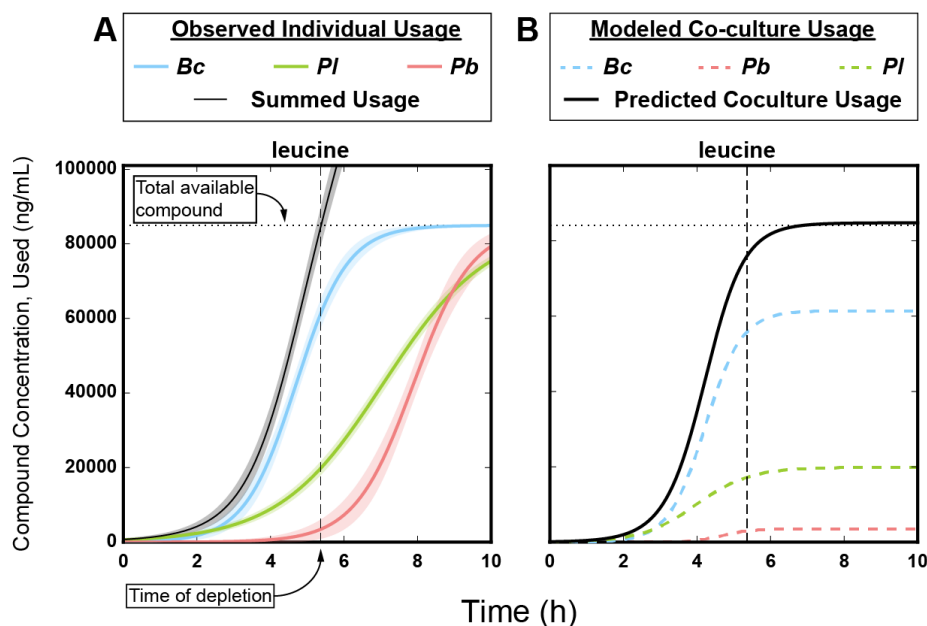


**Table S2.** Dynamic Multiple Reaction Monitoring (dMRM) data acquisition table.

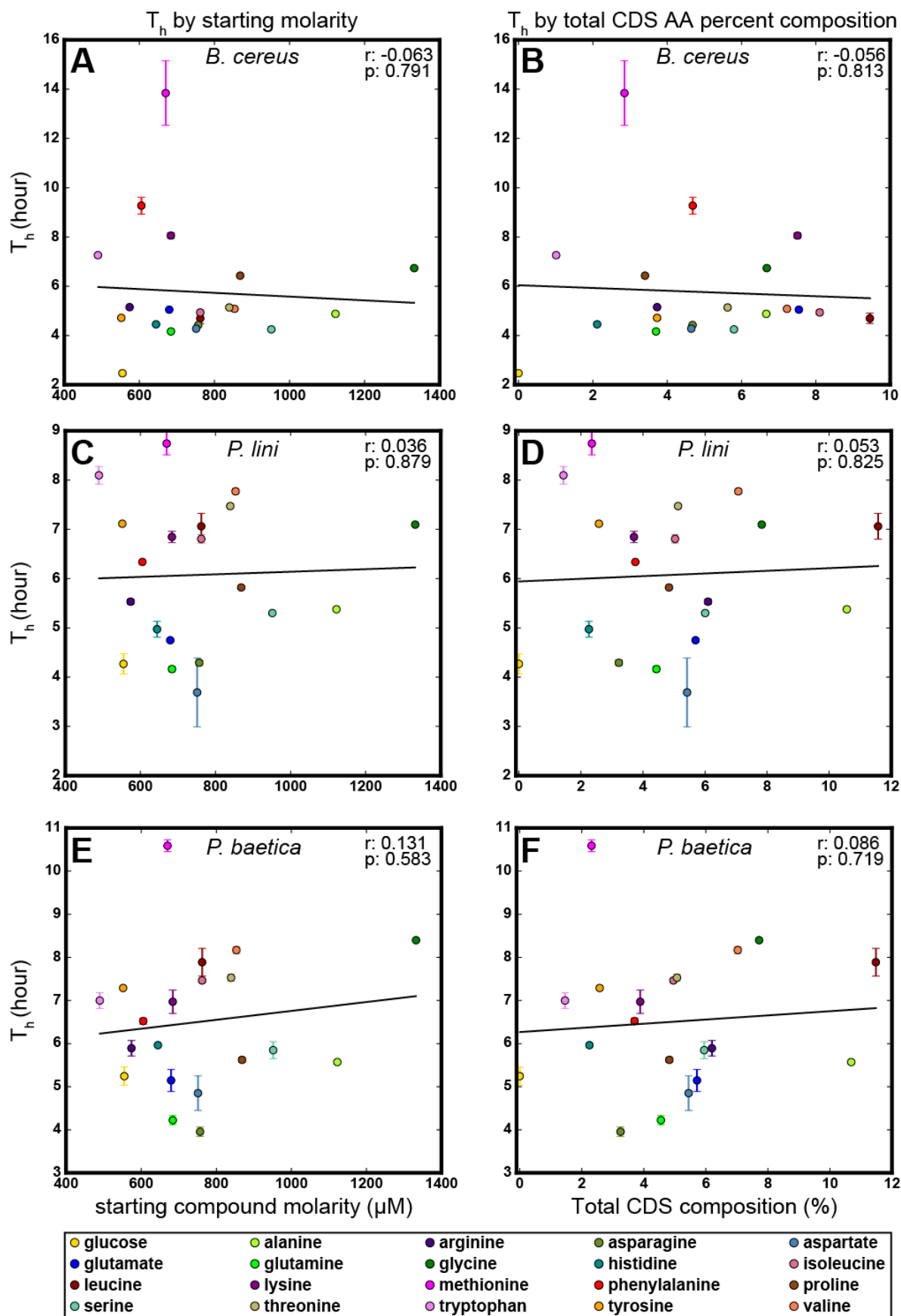
| Compound Name | Precursor Ion | Product Ion | Ret Time (min) | Fragmentor | Collision Energy | Cell Accelerator Voltage | Polarity | ion type   |
|---------------|---------------|-------------|----------------|------------|------------------|--------------------------|----------|------------|
| alanine       | 90.1          | 45.2        | 11.523         | 45         | 39               | 4                        | Positive | quantifier |
| alanine       | 90.1          | 44.3        | 11.523         | 45         | 19               | 4                        | Positive | qualifier  |
| arginine      | 175.1         | 70.2        | 23.36          | 99         | 23               | 4                        | Positive | quantifier |
| arginine      | 175.1         | 60.2        | 23.36          | 99         | 19               | 4                        | Positive | qualifier  |
| asparagine    | 133.1         | 74.2        | 13.292         | 89         | 19               | 4                        | Positive | quantifier |
| asparagine    | 133.1         | 46.2        | 13.292         | 89         | 19               | 4                        | Positive | qualifier  |
| aspartate     | 134           | 88.1        | 14.653         | 84         | 15               | 4                        | Positive | quantifier |
| aspartate     | 134           | 74.2        | 14.653         | 84         | 15               | 4                        | Positive | qualifier  |
| aspartate     | 134           | 74.1        | 14.653         | 89         | 19               | 4                        | Positive | qualifier  |
| glucose       | 203.1         | 203.1       | 11.082         | 0          | 0                | 4                        | Positive | quantifier |
| glucose       | 203.1         | 143         | 11.082         | 147        | 15               | 4                        | Positive | qualifier  |
| glucose       | 203.1         | 101         | 11.082         | 147        | 19               | 4                        | Positive | qualifier  |
| glucose       | 203.1         | 83          | 11.082         | 147        | 23               | 4                        | Positive | qualifier  |
| glutamate     | 148.1         | 102         | 14.087         | 89         | 15               | 4                        | Positive | quantifier |
| glutamate     | 148.1         | 84.2        | 14.087         | 89         | 19               | 4                        | Positive | qualifier  |
| glutamate     | 148.1         | 56.2        | 14.087         | 89         | 31               | 4                        | Positive | qualifier  |
| glutamine     | 147.1         | 130         | 12.797         | 94         | 15               | 4                        | Positive | qualifier  |
| glutamine     | 147.1         | 84.2        | 12.797         | 94         | 19               | 4                        | Positive | quantifier |
| glycine       | 76            | 31          | 12.77          | 50         | 35               | 4                        | Positive | quantifier |
| glycine       | 76            | 30.3        | 12.77          | 50         | 15               | 4                        | Positive | qualifier  |
| heavy-phe     | 176.1         | 129         | 7.967          | 94         | 19               | 4                        | Positive | quantifier |
| heavy-phe     | 176.1         | 83          | 7.967          | 94         | 47               | 4                        | Positive | qualifier  |
| histidine     | 156.1         | 110         | 13.222         | 104        | 15               | 4                        | Positive | quantifier |
| histidine     | 156.1         | 83.2        | 13.222         | 104        | 27               | 4                        | Positive | qualifier  |
| isoleucine    | 132.1         | 86.2        | 8.361          | 59         | 15               | 4                        | Positive | quantifier |
| isoleucine    | 132.1         | 69.2        | 8.361          | 59         | 19               | 4                        | Positive | qualifier  |
| leucine       | 132.1         | 86.2        | 7.952          | 70         | 15               | 4                        | Positive | quantifier |
| leucine       | 132.1         | 44.3        | 7.952          | 70         | 23               | 4                        | Positive | qualifier  |
| lysine        | 147.1         | 84.2        | 22.928         | 104        | 19               | 4                        | Positive | quantifier |
| lysine        | 147.1         | 56.2        | 22.928         | 104        | 35               | 4                        | Positive | qualifier  |
| methionine    | 150.1         | 61.2        | 9.124          | 94         | 27               | 4                        | Positive | quantifier |
| methionine    | 150.1         | 56.2        | 9.124          | 94         | 19               | 4                        | Positive | qualifier  |
| phenylalanine | 166.1         | 120         | 7.967          | 94         | 19               | 4                        | Positive | quantifier |
| phenylalanine | 166.1         | 77.2        | 7.967          | 94         | 43               | 4                        | Positive | qualifier  |
| proline       | 116.1         | 70.2        | 9.234          | 99         | 19               | 4                        | Positive | quantifier |
| proline       | 116.1         | 43.3        | 9.234          | 99         | 35               | 4                        | Positive | qualifier  |
| serine        | 106           | 60.2        | 13.368         | 55         | 15               | 4                        | Positive | quantifier |
| serine        | 106           | 42.2        | 13.368         | 55         | 23               | 4                        | Positive | qualifier  |
| threonine     | 120.1         | 74.2        | 11.992         | 89         | 15               | 4                        | Positive | quantifier |
| threonine     | 120.1         | 56.2        | 11.992         | 89         | 19               | 4                        | Positive | qualifier  |
| tryptophan    | 103.1         | 77.2        | 9.077          | 191        | 19               | 4                        | Positive | quantifier |
| tryptophan    | 103.1         | 50.2        | 9.077          | 191        | 55               | 4                        | Positive | Qualifier  |
| tyrosine      | 182.1         | 136         | 10.595         | 94         | 19               | 4                        | Positive | Quantifier |
| tyrosine      | 182.1         | 123         | 10.595         | 94         | 15               | 4                        | Positive | Qualifier  |
| valine        | 118.1         | 72.2        | 9.454          | 65         | 15               | 4                        | Positive | quantifier |
| valine        | 118.1         | 55.2        | 9.454          | 65         | 23               | 4                        | Positive | qualifier  |



**Figure S1. 16S rRNA tree.** Species used in this study are highlighted in red.



**Figure S2. Example prediction development for leucine.** A) Colored lines represent the use of the compound over time by each strain. The solid black line is the addition of all three curves. The horizontal dashed line represents the highest amount of compound available to the strains, and the vertical dashed line is the time at which the additive usage reaches this amount, predicting the time of depletion: when all available resource has been consumed. This time was used to approximate the amount of compound that each strain consumed up to that point, which was used to model the dashed lines in (B). B) Dashed colored lines represent the predicted usage curve of individual strains when grown in coculture, the sum of which is depicted by the solid black line; the predicted overall usage of the co-culture.



**Figure S3.** Correlation tests between  $T_h$  and starting molarity of compounds (A, C, E) and percent amino acid composition of all predicted genes in the closes sequenced genome (B, D, F) for *Bc* (A, B), *Pl* (C, D), and *Pb* (E, F). Pearson correlation coefficients ( $r$ ) and p-values ( $p$ ) are shown in the upper right-hand corner of each plot.

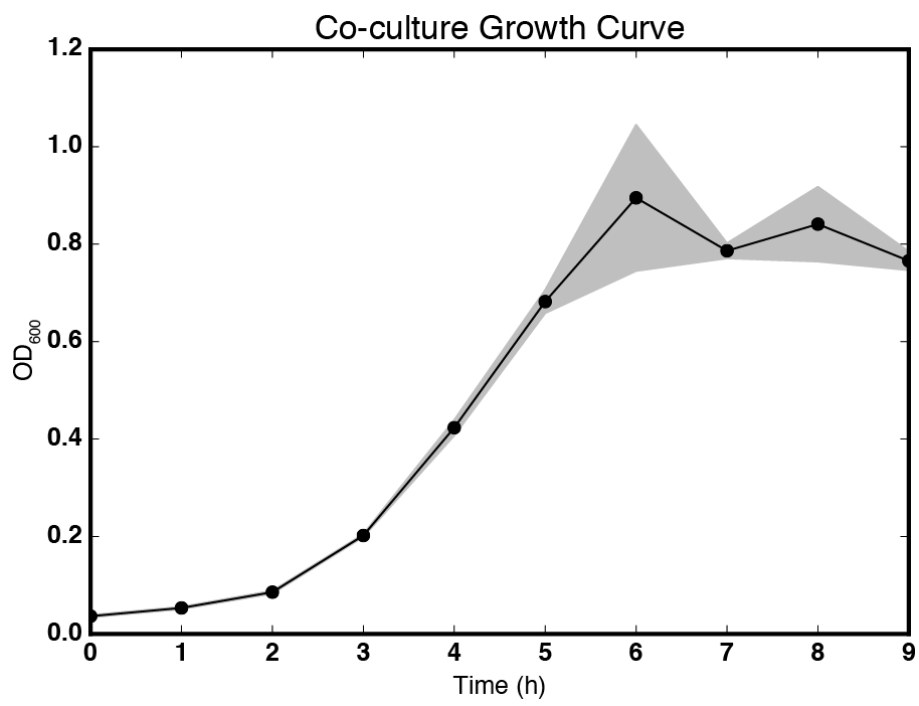


Figure S4. Growth curve of co-culture. Shaded region represents standard deviation (n=3)

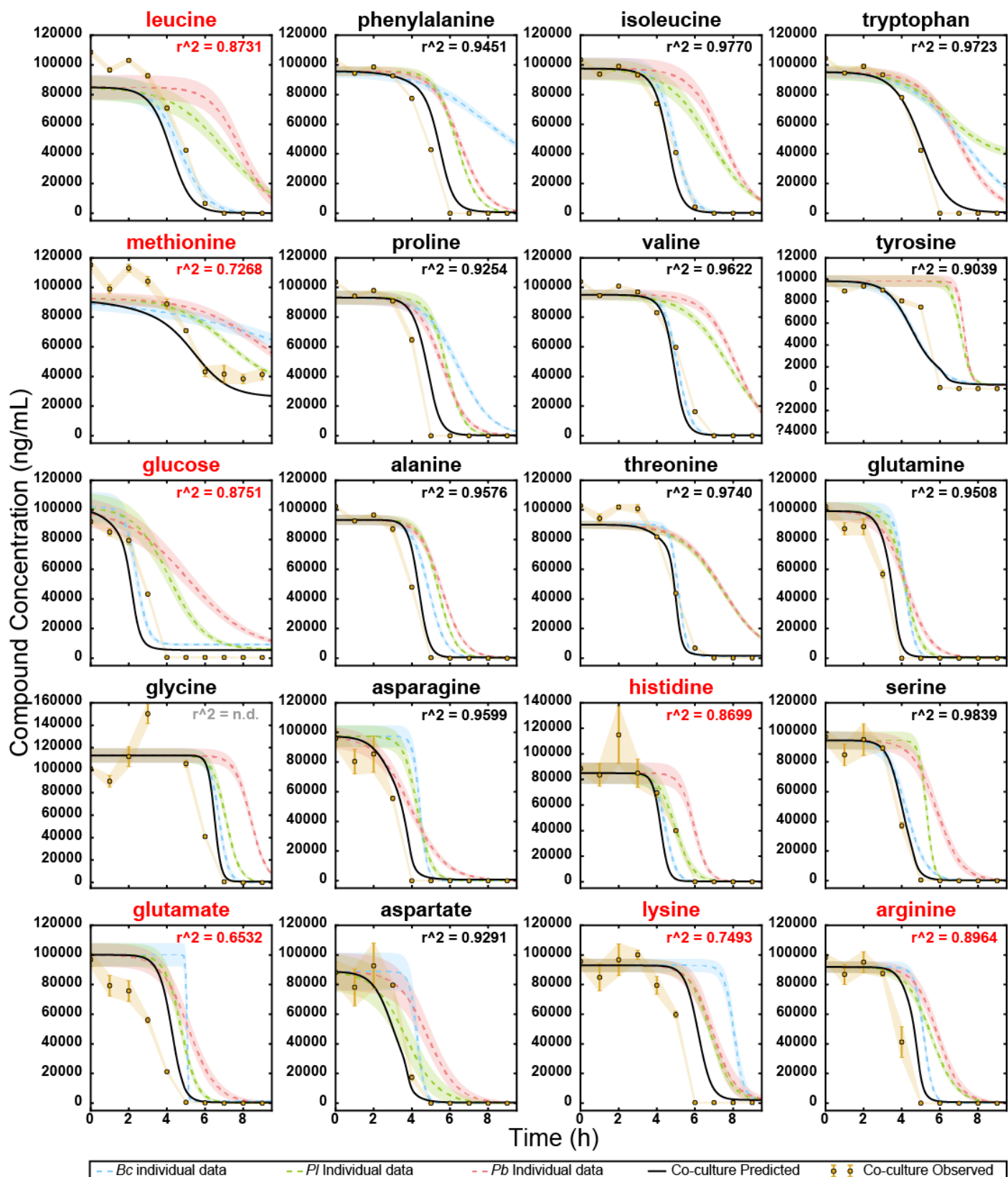


Figure S5. Co-culture observations compared to individuals' data and coculture prediction, not normalized to starting conditions.