**S2 Table. Comparison between evolved and ancestral host phenotypes1**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Trait** | **Treatment** | **Transfer2** | ***F*** | **df** | ***P*** |
| Survival rate | Coevolution | 12 | 7.72 | 1,12 | **0.0167** |
|  |  | 20 | 10.79 | 1,14 | **0.0054** |
|  |  | 28 | 3.63 | 1,13 | 0.0788 |
|  | Adaptation | 12 | 0.25 | 1,15 | 0.6210 |
|  |  | 20 | 4.28 | 1,15 | 0.0562 |
|  |  | 28 | 0.26 | 1,15 | 0.6118 |
|  | Control | 12 | 0.19 | 1,14 | 0.6657 |
|  |  | 20 | 2.52 | 1,16 | 0.1315 |
|  |  | 28 | 2.08 | 1,14 | 0.1703 |
| Host pop.  | Coevolution | 12 | 2.26 | 1,10 | 0.1633 |
| growth |  | 20 | 0.54 | 1,7 | 0.4841 |
|  |  | 28 | 4.78 | 1,8 | 0.0602 |
|  | Adaptation | 12 | 0.99 | 1,9 | 0.3445 |
|  |  | 20 | 0.47 | 1.10 | 0.5047 |
|  |  | 28 | 0.32 | 1,11 | 0.5782 |
|  | Control | 12 | 0.00 | 1,9 | 0.9372 |
|  |  | 20 | 1.49 | 1,10 | 0.2497 |
|  |  | 28 | 0.25 | 1,10 | 0.6229 |
| Host body  | Coevolution | 12 | 0.29 | 1,11 | 0.5952 |
| size |  | 20 | 0.26 | 1,14 | 0.6142 |
|  |  | 28 | 0.04 | 1,12 | 0.8380 |
|  | Adaptation | 12 | 0.42 | 1,13 | 0.5242 |
|  |  | 20 | 0.00 | 1,14 | 0.9963 |
|  |  | 28 | 0.19 | 1,13 | 0.6638 |
|  | Control | 12 | 0.18 | 1,12 | 0.6739 |
|  |  | 20 | 0.00 | 1,15 | 0.9535 |
|  |  | 28 | 0.02 | 1,12 | 0.8752 |
| Host infection  | Coevolution | 12 | 1.12 | 1,12 | 0.3113 |
| load3 |  | 20 | 3.37 | 1,14 | 0.0877 |
|  |  | 28 | 0.09 | 1,12 | 0.7733 |
|  | Adaptation | 12 | 3.84 | 1,12 | 0.0737 |
|  |  | 20 | 2.39 | 1,14 | 0.1447 |
|  |  | 28 | 0.08 | 1,12 | 0.7801 |
|  | Control | 12 | 1.06 | 1,11 | 0.3246 |
|  |  | 20 | 2.23 | 1,15 | 0.1562 |
|  |  | 28 | 0.03 | 1,12 | 0.8588 |

1 Comparison between evolved (host coevolution, host one-sided adaptation and host control) and ancestral hosts both exposed to ancestral pathogens using an analysis of variance. Degrees of freedom (df) are given for the comparison and the error (before and after comma, respectively). Significant values after FDR adjustment are given in bold. The data is shown in S1 Data.

2 Time point is given as host transfer number.

3 Infection load is adjusted by body size.