**Supplementary Table 1: Phases of gene filtering.** ‘Full’ refers to the number of genes in the raw gene sets, ‘CD-HIT’ refers to the number of representative sequences following CD-HIT clustering with a 0.95 similarity threshold, ‘Final’ refers to the number of genes that gained an expression category classification after excluding genes with very low coverage. Phases of gene filtering occurred successively, from left to right. The ‘Final’ gene set was used in analyses.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Full** | **CD-HIT** | **Final** |
| **Allo Fungi** | 6223 | 6223 | 5818 |
| **HH Fungi** | 6106 | 5872 | 4274 |
| **Allo Plants** | 47568 | 34825 | 9578 |
| **HH Plants** | 47568 | 34825 | 9542 |
| **Allo Animals** | 40926 | 39759 | 3632 |
| **HH Animals** | 40926 | 39759 | 3628 |

**Supplementary Table 2: Representative system transcriptomes do not exhibit subgenome dominance.** Median parental and hybrid log2 fold change (to 3 decimal places) in expression across all systems.

|  |  |  |
| --- | --- | --- |
|  | **Med. Parental log2 FC** | **Med. Hybrid log2 FC** |
| **Allo Fungi** | 0.007 | -0.020 |
| **HH Fungi** | -0.214 | -0.020 |
| **Allo Plants** | -0.055 | 0.104 |
| **HH Plants** | -0.050 | 0.040 |
| **Allo Animals** | -0.939 | -0.014 |
| **HH Animals** | -0.891 | -0.039 |

**Supplementary Table 3: Parental and hybrid extremely differentially expressed genes are not correlated.** Percentage (to 2 decimal places) of extremely differentially expressed (EDE) orthologs that are also EDE homeologs.

|  |  |  |
| --- | --- | --- |
|  | **EDE Orthologs** | **% also EDE Homeologs** |
| **Allo Fungi** | 15 | 26.67 |
| **HH Fungi** | 1 | 0.00 |
| **Allo Plants** | 0 | - |
| **HH Plants** | 1 | 0.00 |
| **Allo Animals** | 33 | 6.06 |
| **HH Animals** | 30 | 6.67 |