

**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. Allo: allopolyploid; HH: homoploid hybrid.

	<b>Full</b>	<b>CD-HIT</b>	<b>Final</b>
<b>Allo Fungi</b>	6223	6223	5818
<b>HH Fungi</b>	6106	5872	4274
<b>Allo Plants</b>	47568	34825	9578
<b>HH Plants</b>	47568	34825	9542
<b>Allo Animals</b>	40926	39759	3632
<b>HH Animals</b>	40926	39759	3628

**Supplementary Table 2: Representative system transcriptomes do not exhibit subgenome dominance.** Median parental and hybrid log<sub>2</sub> fold change (to 3 decimal places) in expression across all systems. Allo: allopolyploid; HH: homoploid hybrid.

	Median Parental log <sub>2</sub> FC	Median Hybrid log <sub>2</sub> FC
<b>Allo Fungi</b>	0.007	-0.020
<b>HH Fungi</b>	-0.214	-0.020
<b>Allo Plants</b>	-0.055	0.104
<b>HH Plants</b>	-0.050	0.040
<b>Allo Animals</b>	-0.939	-0.014
<b>HH Animals</b>	-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. Allo: allopolyploid; HH: homoploid hybrid.

	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