

Supplementary Tables

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.

	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. Allo: allopolyploid; HH: homoploid hybrid.

	Median Parental log ₂ FC	Median Hybrid log ₂ 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. 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