**Supplementary Tables**

**Supplementary Table 1: Read mapping by system.** Number of reads (millions) mapped to each biological replicate in each representative system. The number of reads mapped against the *Epichloë* species is substantially lower than the total number of RNA-seq reads as the *Epichloë* endophytes were grown *in planta* to measure expression in their natural state, thus the majority of reads in the RNA-seq libraries were from their grass host.

| Replicate                  | Replicate | n Reads (millions) | n Reads Mapped (millions) | % Reads Mapped |
|----------------------------|-----------|-------------------|---------------------------|----------------|
| *Epichloë elymi*           | 1         | 313               | 1.4                       | 0.4            |
| *E. elymi*                 | 2         | 309               | 0.6                       | 0.2            |
| *E. amarillans*            | 1         | 318               | 1.2                       | 0.4            |
| *E. amarillans*            | 2         | 315               | 1.2                       | 0.4            |
| *E. canadensis*            | 1         | 304               | 2.7                       | 0.9            |
| *E. canadensis*            | 2         | 311               | 8.1                       | 2.6            |
| *Saccharomyces cerevisiae* | 1         | 35.3              | 13.4                      | 38.0           |
| *S. cerevisiae*            | 2         | 32.1              | 12.1                      | 37.7           |
| *S. paradoxus*             | 1         | 35.1              | 11.1                      | 31.6           |
| *S. paradoxus*             | 2         | 35.8              | 11.5                      | 32.1           |
| *S. cerevisiae x paradoxus*| 1         | 31.9              | 11.4                      | 35.7           |
| *S. cerevisiae x paradoxus*| 2         | 30.7              | 10.6                      | 34.5           |
| *Gossypium arboreum*       | 1         | 9.0               | 5.8                       | 64.4           |
| *G. arboreum*              | 2         | 5.4               | 3.8                       | 70.3           |
| *G. raimondii*             | 1         | 8.2               | 5.5                       | 67.1           |
| Species                        | Sample | Length | Width | Height |
|-------------------------------|--------|--------|-------|--------|
| *G. raimondii*                | 2      | 5.8    | 3.8   | 65.5   |
| *G. hirsutum* TX2094          | 1      | 7.5    | 5.1   | 68.0   |
| *G. hirsutum* TX2094          | 2      | 8.4    | 5.3   | 63.1   |
| *G. arboreum* x *raimondii*   | 1      | 7.1    | 4.8   | 67.6   |
| *G. arboreum* x *raimondii*   | 2      | 6.2    | 4.0   | 64.5   |
| *Squalius pyrenaicus*         | 1      | 22.7   | 10.1  | 44.5   |
| *Sq. alburnoides*             | 1      | 27.8   | 14.2  | 51.1   |
| *Sq. alburnoides* (PAA)       | 1      | 28.1   | 15.6  | 55.5   |
| *Sq. alburnoides* (PA)        | 1      | 20.9   | 10.5  | 50.2   |
Supplementary Table 2: 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. Genes with low coverage were identified as those with zero reads in at least one hybrid replicate and in at least one parental replicate. 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  | 3576   |
| HH Animals    | 40926  | 39759  | 3586   |
Supplementary Table 3: Representative system transcriptomes do not exhibit subgenome dominance. Median parental and hybrid log$_2$ 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** | 0.116                       | 0.055                    |
| **HH Fungi**   | -1.319                      | -0.312                   |
| **Allo Plants**| -0.011                      | 0.199                    |
| **HH Plants**  | -0.018                      | 0.118                    |
| **Allo Animals**| -0.208                      | 0.170                    |
| **HH Animals** | -0.260                      | 0.087                    |
Supplementary Table 4: 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. Extreme differential expression was defined as fold change > 50 in either the parental or hybrid differential expression analysis, $p < 0.05$. Allo: allopolyploid; HH: homoploid hybrid.

| EDE Orthologs       | % also EDE Homeologs |
|---------------------|----------------------|
| **Allo Fungi**      | 29.41                |
| **HH Fungi**        | 11.11                |
| **Allo Plants**     | –                    |
| **HH Plants**       | 0.00                 |
| **Allo Animals**    | 8.00                 |
| **HH Animals**      | 12.50                |
Supplementary Table 5: Extreme differential gene expression is more prevalent among homeologs (in the hybrid) than orthologs (in the parent species). Numbers of extremely differentially expressed (EDE) orthologs and homeologs in each representative system. Extreme differential expression was defined as fold change > 50 in either the parental or hybrid differential expression analysis, \( p < 0.05 \). Allo: allopolyploid; HH: homoploid hybrid.

| System       | EDE Orthologs | EDE Homeologs |
|--------------|---------------|---------------|
| Allo Fungi   | 17            | 49            |
| HH Fungi     | 9             | 10            |
| Allo Plants  | 0             | 929           |
| HH Plants    | 1             | 228           |
| Allo Animals | 25            | 150           |
| HH Animals   | 24            | 225           |