

# Supplementary File 1

## *S1.1 Obligatory criteria*

Our differential expression analyses required non-normalised RNA-seq data for the hybrid and both parental species in each allopolyploid or homoploid hybrid complex. Only datasets that included at least two biological replicates of each species were considered. A genome or gene sequences for at least one of the parental species was needed to use the *HyLiTE* pipeline (Duchemin et al., 2015) in the differential expression analyses. The implementation of GO for functional analyses required genome annotations for at least one parental species, but both a genome *and* genome annotation were not required, so a dataset was still considered if only gene annotations were available. The RNA-seq data for the parents species and hybrid had to be extracted from the same tissue, or from cells grown in the same medium, where applicable, and extracted under the same conditions.

## *S1.2 Preferential criteria*

We gave preference to datasets where the hybrid species from which RNA-seq data was obtained were naturally occurring to mitigate the influence of synthetic formation on any observed gene expression patterns. (It is common in the literature to see synthetic hybrids, commonly formed via artificial crosses for homoploid hybrids or colchicine treatment to obtain allopolyploids). We also gave preference to allopolyploid and homoploid hybrids that were as taxonomically close as possible, to minimise taxon-specific differences in observed gene expression patterns. Moreover, we preferred that both parental species were extant, where possible, as opposed to only being relatives of extinct parents.

A broad search of the literature and online databases was performed with the above criteria. The following are the resulting options and their justifications for use, or omission, in differential gene expression analysis.

### ***S1.3 Animals***

#### *Achondrostoma oligolepis* x *Pseudochondrostoma polylepis*

Naturally-occurring homoploid hybrid of two Iberian Leuciscinae fish (Pereira et al., 2014). No comparative transcriptomic studies are available of this parent-hybrid complex.

#### *Ambystoma*

McElroy et al. (2017) studied an allotriploid *Ambystoma* (mole salamander) with three parental species. This would have complicated our analyses as the classes used in the categorisation of differential gene expression are based on a two parent system (Cox et al., 2014).

Also, in other publications, it was unclear exactly how many species were parents of a given hybrid (it seems that parental species can potentially range from 2-4), or if the hybrid had a duplicated genome (Schmid et al., 2015, Bogart et al., 2007).

We additionally searched NCBI BioProjects for *Ambystoma*. While some hybrids were among the results, they did not specify polyploidy/homoploidy, and because no papers have given specific hybrid/parent pairs other than McElroy et al, *Ambystoma* were not used in the analyses.

#### *Bacillus*

44 Stick insect genus purportedly containing allopolyploid species (Mallet, 2007). Subsequent  
45 searches of Google to identify specific species were unsuccessful and no data could be found  
46 on NCBI SRA.

47 *Bufo viridis*

48 The *B. viridis* subgroup contains a complex of diploid, triploid and tetraploid green toad  
49 species from Central Asia. The parental species of the triploid and tetraploid species are  
50 unclear (Betto-Colliard et al., 2015, Stöck et al., 2005).

51 *Bulinus truncates*

52 Allopolyploid freshwater snail briefly mentioned in (Mallet, 2007). Searches of NCBI SRA  
53 found no data.

54 *Carassius auratus* x *Cyprinus carpio*

55 Both parental species of this allopolyploid fish (carp) had genome sequences and annotations;  
56 the issue was a lack of homoploid hybrid species from within the carp or carp-like fishes.  
57 Due to the lack of an accompanying publication, it was also unclear if this allopolyploid  
58 (NCBI BioProject PRJNA86641) was naturally formed.

59 *Carassius auratus gibelio*

60 Naturally-occurring allopolyploid fish (carp) formed from *Carassius auratus* x *Cyprinus*  
61 *carpio* pairing (Li et al., 2014). Only an mtDNA genome was available and limited gene  
62 models (n=13), however, there were extensive genome annotations available for the parental  
63 species. The issue was a lack of a homoploid hybrid species from within the carp fishes.

64 *Carassius auratus red var.* × *Cyprinus carpio*

65 Allopolyploid fish (carp) formed via artificial cross (Wang et al., 2015).

66 *Carassius auratus red var.* × *Megalobrama amblycephala*

67 Allopolyploid fish (carp) with genome sequence, but only transcriptome data for one  
68 biological replicate (Qin et al., 2016).

69 Cichlids

70 Within the literature, there exist a number of studies on cichlids (fish, family Cichlidae, e.g.  
71 (Selz et al., 2014, Santos et al., 2016, Stelkens et al., 2009, Genner & Turner, 2011), but none  
72 produced RNA-seq data from a comparative analysis of both the hybrid and the parents.

73 *Cobitis taenia* × *Colbitis elongatoides*

74 These two diploid fish hybridised to form both diploid and polyploid lineages (Juchno &  
75 Boroń, 2018, Juchno et al., 2007). Transcriptomic data was only available for one parental  
76 species, *C. taenia* (NCBI BioProject PRJNA436080).

77 *Cottus gobio*

78 Homoploid hybrid fish derived from *C. perifretum* × *C. rhenanum* (Mallet, 2007, Stemshorn  
79 et al., 2011). No RNA-seq data was available for the hybrid.

80 *Ctenopharyngodon idellus* × *Megalobrama amblycephala*

81 This interspecific diploid fish pairing can form both diploid and triploid hybrids (He et al.,  
82 2013), but there is no transcriptomic study that encompasses both parental species and the  
83 hybrids in the literature.

84 Two transcriptome accessions for triploid *Ctenopharyngodon idellus* × *Megalobrama*  
85 *amblycephala* hybrids are available (NCBI BioProject PRJNA240314).

86 *Danio rerio* × *Danio nigrofasciatus*

A homoploid hybrid zebrafish complex (Spiewak et al., 2018). Although extensive genomic information is available for *D. rerio*, there are no comparative transcriptomic data available for this complex.

Artificial triploid *D. rerio* can be generated, but these are not allopolyploids (Mizgireuv et al., 2004).

## *Daphnia*

The water flea genus *Daphnia* does contain hybrid species, such as *D. galeata* × *D. hyalina* (Wolinska et al., 2006) and some allopolyploids within the *D. pulex* complex (Dufresne, 2011). Comparative RNA-seq data could not be found for either complex.

## *Drosophila*

Interspecific homoploid hybrids are common in the fruit fly genus *Drosophila* (Landry et al., 2005, Kelleher et al., 2012, Goulielmos & Alahiotis, 1989). Some *Drosophila* species do exhibit mosaic polyploidy (Fox et al., 2010), but there are no entirely allopolyploid species.

## *Epinephelus coioides* x *Epinephelus lanceolatus*

There are transcriptome accessions for diploid and triploid hybrids from the *Epinephelus coioides* x *Epinephelus lanceolatus* (grouper fish) pairing (NCBI BioProject PRJNA431058). However, there are no accompanying parental transcriptomes, and only one biological replicate at each ploidy level with two different tissues sampled.

NCBI BioProject PRJNA497240 has transcriptomic sequences for *E. coioides*, but there is only one replicate subjected to each different treatment condition. Likewise, NCBI BioProject PRJNA413272 has transcriptomic sequences for a single replicate of *E. lanceolatus*, sampled over a time series, post-hatch.

109 *Gasterosteus nipponicus* x *Gasterosteus aculeatus*

110 Parent-hybrid fish complex with 6 or 7 RNA-seq runs available for each species (NCBI  
111 BioProject PRJDB7242). A genome with gene models is also available for *G. aculeatus*  
112 (three-spined stickleback fish). However, as data was unpublished, it was unclear if the  
113 hybrid was homoploid and if it was naturally or synthetically formed.

114 *Gila seminuda*

115 Homoploid hybrid fish formed from the hybridisation of *Gila robusta* x *Gila elegans*  
116 (Mavárez & Linares, 2008, Mallet, 2007). Only an organellar genome is available for *G.*  
117 *robusta* on NCBI, in addition to 13 gene models. Further, no comparative RNA-seq data is  
118 available for this hybrid complex.

119 *Megalobrama amblycephala* x *Cyprinus carpio*

120 RNA-seq data for the hybrid was unavailable (Wang et al., 2017). The research group was  
121 contacted but no response was obtained.

122 *Morone chrysops* x *Morone saxatilis*

123 Six transcriptome accessions of homoploid hybrid striped bass are available (NCBI  
124 BioProject PRJNA382266). There were no accompanying parental transcriptome accessions.  
125 A single transcriptomic replicate for *M. chrysops* and *M. saxatilis* was found under  
126 BioSamples SRR1187194 and SRR1187193, respectively.

127 *Oncorhynchus*

128 This genus in the Salmonidae family contains a number of hybrid species, including  
129 *Oncorhynchus keta* x *Oncorhynchus gorbuscha* (Zhivotovsky et al., 2016), and diploid and

triploid *Oncorhynchus kisutch* (Withler et al., 1995). No comparative transcriptomic analyses were found for either an allopolyploid or homoploid *Oncorhynchus* complex.

#### *Pelophylax esculentus*

This hybrid water frog is *Pelophylax lessonae* x *Pelophylax ridibundus* (Doležálková-Kaštánková et al., 2018). Searches of NCBI databases and <https://amphibiaweb.org> did not find any genome sequences or comparative RNA-seq analyses.

#### *Poecilia formosa*

Naturally-occurring diploid clonal fish (molly) that originated from a *Poecilia mexicana* x *Poecilia latipinna* interspecific hybrid (Warren et al., 2018). Only single replicate RNA-seq data is available for the hybrid and both parental species from a comparative study (NCBI BioProject PRJNA385580), in addition to assembled and annotated genomic data. Rare cases of naturally-occurring allotriploids have been found in the wild (Matos et al., 2016).

#### *Salmo salar*

Atlantic salmon can occur as natural diploid and artificial triploid hybrids (Refstie & Gjerdem, 1975, Murray et al., 2018, Vera et al., 2017). However, there are no comparative transcriptomic analyses of parental species and hybrids in the literature.

#### *Squalius*

A genus of Cyprinidae fish with allopolyploid and homoploid hybrids produced from the same parental pairing. *Sq. alburnoides* exists as natural populations of hybrid allotriploid PAA, homodiploid hybrid PA, and the parental-like diploid AA genotypes. The parental species of *Sq. alburnoides* are *Sq. pyrenaicus* (PP) and an extinct species related to *Anaecypris hispanica* (Pala et al., 2010, Matos et al., 2015).

There are genome sequences and annotations for *Sq. pyrenaicus* available at [ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/403/095/GCA\\_001403095.1\\_pp\\_cds\\_nonRedundant](ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/403/095/GCA_001403095.1_pp_cds_nonRedundant). There is also a GenBank record (accession CVRK000000000) for the *Sq. pyrenaicus* whole genome shotgun sequencing project, but it contains no sequence data.

Pala et al. (2008) performed cDNA sequencing of allotriploid *Sq. alburnoides*, but only for 6 genes.

There is comparative small RNA data available for this complex under GEO Series GSE38691 (Inácio et al., 2012).

Comparative RNA-seq data for allopolyploid and homoploid *Squalius* complexes can be found under ArrayExpress E-MTAB-3174 (Matos et al., 2015, Matos et al., 2019). For all of these reasons, this genus was a strong candidate for our homoploid and allopolyploid animal representatives.

#### *Takifugu rubripes* x *Takifugu flavidus*

An artificially formed homoploid hybrid fish (pufferfish), with transcriptome accessions only available for one replicate each of the parental species and hybrid (Gao et al., 2013).

#### *Tigriopus californicus*

Copepod species whose hybridisations are limited to being inter-population only (Barreto et al., 2014, Pritchard et al., 2013).

#### *Xenopus laevis*

Allopolyploid African clawed frog with unknown parental species (Session et al., 2016).



#### 173 **SI.4 Fungi**

##### 174 *Aspergillus flavus* x *Aspergillus parasiticus*

175 These Ascomycete moulds form interspecific hybrid strains through artificial crosses, some  
176 with evidence of allopolyploidisation (Olarite et al., 2015). Genome sequences and  
177 annotations for both parental species are available through the NCBI database. No  
178 comparative transcriptomic studies are available.

##### 179 *Blumeria graminis* f. sp. *triticales*

180 A homoploid species of powdery mildew formed from the hybridisation of *B. g. f. sp. tritici*  
181 and *B. g. f. sp. secalis*. There is an annotated genome available for *B. g. tritici* and RNA-seq  
182 data for all members of this complex are available. However, these transcriptomic data did  
183 not originate from a single study, so the conditions around RNA extraction could not be  
184 guaranteed as controlled across all samples. Therefore, we chose not to use this dataset (Praz  
185 et al., 2018, Menardo et al., 2016).

186 Additional comparative transcriptomic analyses relating to this complex involve only *B. g.*  
187 *tritici* (Hu et al., 2018).

##### 188 *Epichloë canadensis*

189 Allopolyploid endophyte hybrid of *E. elymi* x *E. amarillans* with RNA-seq data with  
190 replicates for all members of the complex, in addition to genomes and gene sequences for  
191 both parental species (data unpublished). A strong candidate for our allopolyploid fungal  
192 complex.

##### 193 *Neotyphodium lolii* x *Epichloë typhina* Lp1

194 Allopolyploid endophyte. RNA-seq data with replicates available for all members of the  
195 complex, in addition to gene sequences for both the parental species (Cox et al., 2014,  
196 Campbell et al., 2017). Broadly similar to the *E. canadensis* option.

197 *Ophiostoma ulmi* x *Ophiostoma novo-ulmi*

198 Transient hybrids of *Ophiostoma ulmi* x *Ophiostoma novo-ulmi* occur in nature (Brasier,  
199 2001). No comparative transcriptomic analyses of this homoploid hybrid complex are  
200 available; only a single study in which the *O. novo-ulmi* transcriptome was compared with  
201 that of *Candida albicans* and *Histoplasma capsulatum* (Nigg et al., 2015).

202 *Saccharomyces cerevisiae* x *Saccharomyces bayanus*

203 Homoploid hybrid yeast. Genome annotations for both parental species are available at  
204 [http://www.saccharomycessensustricto.org/cgi-](http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current)  
205 [bin/s3.cgi?data=Annotations&version=current](http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current), in addition to RNA-seq reads from a  
206 comparative transcriptomic analysis of this complex. The hybrids were generated  
207 synthetically through mating a single haploid individual of each parental species, growing a  
208 clonal population of the diploid, and checking it by PCR (Schraiber et al., 2013).

209 *Saccharomyces cerevisiae* x *Saccharomyces kudriavzevii*

210 There is a comparative transcriptomic study available that used two biological replicates of  
211 this homoploid hybrid yeast, but it used a microarray, not RNA-seq, and compared only the  
212 hybrids at varying temperatures (Tronchoni et al., 2017).

213 *Saccharomyces cerevisiae* x *Saccharomyces paradoxus*

214 Homoploid hybrid yeast. RNA-seq-based transcriptomic analyses of multiple replicates are  
215 available. The hybrids were generated synthetically through mating a single haploid

individual of each parental species, growing a clonal population of the diploid, and checking it by PCR (Schraiber et al., 2013). Genome annotations for both parental species available at <http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current>. This was a strong candidate for our homoploid fungal complex.

Swain Lenz et al. (2014) also did a comparative transcriptomic analysis of this complex, but due to the genetic manipulations performed during their synthetic crossing of the parental species, we have opted to use the data from Schraiber et al. (2013) instead.

#### *Saccharomyces cerevisiae* x *Saccharomyces uvarum*

Synthetically formed homoploid hybrids (Pfliegler et al., 2012). Although genome annotations are available for both parental species on <http://www.saccharomycessensustricto.org/cgi-bin/s3.cgi?data=Annotations&version=current>, the only comparative transcriptomic studies available relating to this complex are of a single hybrid replicate grown at varying temperatures (NCBI BioProject PRJNA505697).

#### *Saccharomyces pastorianus* (syn. *Saccharomyces carlsbergensis*)

This allopolyploid yeast is formed from the mating of *S. cerevisiae* and *S. eubayanus*. The allopolyploid does not have a genome sequence or annotations available, but both parental species are available through the NCBI database. A comparative transcriptomic analysis of this complex was performed by (Gibson et al., 2010), but they used a microarray, not RNA-seq. It was unclear whether the *S. pastorianus* they used was a naturally occurring allopolyploid, so the authors were emailed to clarify. Their response was that their experimental procedure involved an industrial strain that had been in use for decades, thus its

ancestry is not entirely certain. However, the author did not think it had originated from a synthetic protocol. The literature also suggests that *S. pastorianus* arose through instantaneous speciation during an interspecific hybridisation event (Dunn & Sherlock, 2008).

#### *Zygosaccharomyces parabailii*

A homoploid hybrid species of *Z. bailii sensu stricto* and an unidentified *Zygosaccharomyces* species. There is an RNA-seq study of the response to lactic acid stress in *Z. parabailii*, but it does not involve comparisons to its parental species (Ortiz-Merino et al., 2018).

#### *Zygosaccharomyces rouxii*

Yeast with allopolyploid strains. A *Zygosaccharomyces rouxii* NBRC 1876 draft genome sequence is available (Sato et al., 2017). RNA-seq data for this species is also available (NCBI BioProject PRJNA437612). However, no comparative transcriptomic studies for the parent species were found through NCBI SRA.

#### *Zymoseptoria pseudotritici*

*Zymoseptoria pseudotritici* is a fungal homoploid hybrid grass pathogen with unknown parental species (Stukenbrock et al., 2012). No RNA-seq data is available.

### ***S1.5 Plants***

#### *Arabidopsis suecica*

Natural allopolyploid of *A. thaliana* x *A. arenosa* (Chen et al., 2004). Comparative RNA-seq data of this complex is available (NCBI BioProject PRJNA393427) with two biological

260 replicates for each member, in addition to genome annotations available through NCBI SRA.

261 The main issue was no suitable *Arabidopsis* homoploid hybrid complex.

262 *Arabidopsis thaliana* x *Arabidopsis lyrata*

263 Artificial homoploid hybrid with two RNA-seq replicates available for the hybrid and *A.*

264 *lyrata* (Zhu *et al.*, 2017). The issue was that this study did not perform RNA-seq for *A.*

265 *thaliana*, so there was no guarantee that the conditions under which extraction was performed

266 were held constant across all species.

267 *Arachis hypogaea*

268 Peanut is an allopolyploid of *A. ipaensis* and *A. duranensis*. RNA-seq data, genomes and

269 genome annotations for the parental species and the allopolyploid are available (Bertioli *et*

270 *al.*, 2019).

271 Further RNA-seq data for allopolyploid *A. hypogaea* is also available, but without biological

272 replicates (Han *et al.*, 2017).

273 The major issue was a lack on a homoploid hybrid complex from within this genus.

274 *Brassica juncea*

275 Allotetraploid hybrid of *B. rapa* and *B. nigra*. (Yang *et al.*, 2016) did RNA-seq analysis of *B.*

276 *juncea* only, in addition to a genome annotation of *B. juncea*. The genome annotation of *B.*

277 *rapa* is available through NCBI SRA.

278 *Brassica napus*

279 An allotetraploid hybrid of *B. rapa* x *B. oleracea*. RNA-seq data with three biological

280 replicates for each member of the complex is available under NCBI BioProject

281 PRJNA449400 (Wu et al., 2018). All members have genes and genomes available through  
282 NCBI SRA. This is a possible option for an allopolyploid complex.

283 *Brassica napus* x *Brassica carinata*

284 Homoploid hybrid artificially produced via hand pollination and embryo rescue. Comparative  
285 RNA-seq analysis of this homoploid hybrid complex with three biological replicates for each  
286 member, and functional gene annotations is available (Chu et al., 2014). Extensive genome  
287 annotations are available for *B. napus* through NCBI SRA. Limited gene models are available  
288 for *B. carinata* through NCBI SRA and <http://brassicadb.org>. This is a possible option for a  
289 homoploid hybrid plant complex.

290 *Brassica napus* x *Brassica rapa*

291 Comparative RNA-seq analysis of this homoploid hybrid complex (Zhang et al., 2015), with  
292 no biological replicates.

293 *Camellia*

294 *Camellia reticulata* can exist as an allopolyploid (Gu & Xiao, 2003), but there are no  
295 comparative transcriptomic studies on the allopolyploid complex. The only related RNA-seq  
296 data on NCBI SRA is of five different *C. reticulata* tissues (Yao et al., 2016).

297 A homoploid hybrid complex exists in *Camellia azalea* x *Camellia amplexicaulis*, with  
298 RNA-seq data on each member available. There are no biological replicates; the RNA  
299 libraries were formed from pooled RNA of three individuals (Zhang et al., 2018).

300 *Capsella bursa-pastoris*

301 Natural allopolyploid of *C. orientalis* and *C. grandiflora*. Multiple replicates of RNA-seq data  
302 are available for the allopolyploid and parental species (Kryvokhyzha et al., 2019).

303 *Capsella rubella* x *Capsella grandiflora*

304 Reciprocal homoploid hybrids with RNA-seq data, but no accompanying RNA-seq data is  
305 available for the parental species (Rebernig et al., 2015).

306 *Chrysanthemum nankingense* x *Tanacetum vulgare*

307 Homoploid hybrid with comparative RNA-seq data available for hybrid and parental species  
308 (Wang et al., 2013, Qi et al., 2018). Qi et al. also generated allopolyploids through colchicine  
309 treatment of homoploid hybrids in addition to performing functional annotations of genes,  
310 making this a possible option for our analyses.

311 *Coffea arabica*

312 Natural allopolyploid of *C. eugenioides* and *C. canephora*. Data from a microarray-based  
313 comparative analysis of this complex are available (Bardil et al., 2011), as well as an RNA-  
314 seq-based comparative analysis of *C. arabica* grown under different temperatures (Combes et  
315 al., 2013).

316 *Glycine*

317 No records of an RNA-seq-based study of *Glycine* homoploid hybrids. However, an  
318 intraspecific comparative transcriptome analysis of homoploid *G. max* hybrids has been done  
319 (Zhang et al., 2017).

320 *Glycine dolichocarpa*

321 A naturally formed recent allopolyploid of *G. syndetika* and *G. tomentella*. Only RNA-seq  
322 data for the allopolyploid is available (Coate et al., 2014).

323 A comparative transcriptomic study of the allopolyploid and its parents was found, with 3  
324 biological replicates per member (Ilut et al., 2012). <https://soybase.org> only has *G. max* and

325 *G. soja* genome and gene sequences. NCBI SRA has 127 gene models available for each of  
326 *G. syndetika*, *G. tomentella* and *G. dolichocarpa*.

327 Transcriptomic analyses of this complex can also be found here (Coate et al., 2012).

### 328 *Gossypium*

329 Microarray-based analysis of natural allopolyploid cotton (*G. hirsutum*) and synthetic  
330 homoploid hybrid progeny of *G. arboreum* and *G. raimondii* (Flagel et al., 2008).

331 RNA-seq based analysis of natural allopolyploid (*G. hirsutum*) and synthetic homoploid  
332 hybrid progeny of *G. arboreum* and *G. raimondii* (Yoo et al., 2013). There are 3 biological  
333 replicates of RNA-seq data available for each member (NCBI BioProject PRJNA171342).

334 The synthetic hybrid was formed by emasculation of the A2 parent in the evening and  
335 subsequent cross-pollination the following morning. They are a strong option for our  
336 homoploid and allopolyploid plant representatives.

### 337 *Helianthus*

338 The sunflower genus *Helianthus* contains several homoploid hybrid species (Ungerer et al.,  
339 2006). RNA-seq data is available (Renaut et al., 2014), in addition to a reference genome for  
340 the parental species *H. annuus* (Badouin et al., 2017).

341 There are some purportedly allopolyploid *Helianthus* species (Espinasse et al., 1995), but  
342 data on these are very limited, especially RNA-seq.

### 343 *Mimulus*

344 *Mimulus peregrinus* is a naturally formed recent allopolyploid of *M. luteus* x *M. guttatus*.  
345 Genomes and genome annotations for both parents can be found at  
346 <https://datadryad.org/resource/doi:10.5061/dryad.d4vr0>. Edger et al. (2017) performed a



comparative RNA-seq analysis of this complex, in addition to an artificially formed *M. x robertsii* of the same parent pairing. *Mimulus x robertsii* was formed by hand pollination via diallel cross. They also did GO and KEGG. The issue was that there were no biological replicates for any of the RNA-seq data.

#### *Oryza*

Comparative RNA-seq analysis of intraspecific rice hybrids and their derived allopolyploids (Xu et al., 2014).

Comparative RNA-seq analysis of a synthetic interspecific rice hybrid and its two parental species (Wu et al., 2016). However, the hybrid is a triploid produced from a diploid and tetraploid, so its genome size relative to one parent has increased and to the other, decreased, and thus it would confound the interpretation of our analyses.

#### *Saccharum*

Modern allopolyploid and homoploid sugarcane cultivars are commonly formed from pairings between domesticated *S. officinarum* and wild *S. spontaneum* (Song et al., 2016). RNA-seq data for *S. officinarum*, *S. spontaneum*, and their F<sub>1</sub> hybrid are available (NCBI BioProject PRJNA335885). *Saccharum intermedium*, an allopolyploid of *S. angustifolium* and *S. villosum*, has recently been described (Welker et al., 2017), but the complex lacks accompanying RNA-seq data.

#### *Senecio*

Comparative transcriptomic analyses of both an allopolyploid (*S. cambrensis* = *S. vulgaris* x *S. squalidus*) and homoploid hybrid (*S. x baxteri* = *S. vulgaris* x *S. squalidus*) of this ragwort genus are available (Hegarty et al., 2006), but they are microarray-based. Further microarray-

369 based transcriptomic analyses of this genus are also available (Hegarty et al., 2005, Hegarty  
370 et al., 2009, Hegarty et al., 2008).

### 371 *Spartina*

372 The cordgrass genus contains a recently formed natural allopolyploid, *S. anglica* (Ainouche  
373 et al., 2004), two interspecific hybrids *S. x neyrautii* and *S. x townsendii*, and the parental  
374 species *S. maritima* and *S. alterniflora*. Non-normalised Illumina data is available for these  
375 complexes as assembled reference transcriptomes (Boutte et al., 2016), but comparative  
376 RNA-seq data is as yet unavailable.

377 Microarray data for allopolyploid, homoploid hybrid and parental *Spartina* are also available  
378 (Chelaifa et al., 2010).

### 379 *Tragopogon*

380 RNA-seq data with biological replicates for the allopolyploid species *T. mirus* and *T.*  
381 *miscellus* and their diploid parents is available (NCBI BioProject PRJNA210897).

382 A study of *T. miscellus*, its parental species, and their synthetically produced homoploid  
383 hybrid has been done, but it was not RNA-seq based, rather surveying expression of 144  
384 duplicated gene pairs derived from the parental species (Buggs et al., 2011).

### 385 Triticeae

386 Synthetic allopolyploid of *Aegilops sharonensis* and *Triticum monococcum* ssp. *aegilopoides*  
387 obtained through colchicine treatment of F<sub>1</sub> hybrids. Gene expression was analysed through  
388 cDNA-AFLP (Kashkush et al., 2002).

389 Synthetic allopolyploid of *Aegilops longissimi* and *Triticum urartu*. Gene expression of the  
390 allopolyploid and its diploid parental species was analysed through RNA-seq (Wang et al.,

391 2016). The main issue was that the allopolyploid was synthetic, as well as the lack of RNA-  
392 seq data for a homoploid hybrid complex within these genera.

393 *Vigna reflexo-pilosa* var. *glabra*

394 Allopolyploid mungbean species with hypothetical parental species, one of which is thought  
395 to be extinct. RNA-seq assemblies are available for the allopolyploid (Kang et al., 2014).

396 *Zea mays*

397 Maize is purportedly of allotetraploid origin that has subsequently undergone rediploidisation  
398 (Gaut et al., 2000). Thus, it would not be suitable for investigating the impact of genome  
399 doubling on gene expression.

400 *Zea mays* x *Tripsacum dactyloides*

401 Interspecific hybrid of maize and gamagrass (Shavrukov & Sokolov, 2015) with  
402 transcriptomic studies of each parent available (Gault et al., 2018, Wu et al., 2017), but none  
403 for the entire complex including the parent species.

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## SI.6 References

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