Supplementary Table 1

Hemiptera BUSCO markers were selected from 9 species in OTHODBv9.1 and included 3350 genes. The ana

Table 1a: Genome

Data	Sequences	Complete	Fragmented	Missing
Diaci1.1 genome	**161,988**	74.80%	0.30%	24.90%
Pea aphid v2.3	**31,391**	21.00%	0.00%	79.00%
Bed bug v1.1	**41,503**	83.40%	0.30%	16.30%
White fly v1.1	**19,761**	77.90%	0.00%	22.10%

Table 1b: Gene sets and transcriptome

Data	Sequences	Complete	Fragmented	Missing
OGS v1.0	**21,026**	74.50%	0.30%	25.20%
MCOT v1.0	**30,562**	92.90%	0.10%	7.00%
NCBI v100	**20,996**	74.70%	0.30%	25.00%
Maker v1.1	**18,242**	72.30%	0.40%	27.30%
Egg	**76,467**	71.50%	0.20%	28.30%
Nymph	**69,175**	71.60%	0.10%	28.30%
Adult	**62,412**	60.60%	0.20%	39.20%

alysis shows the number of markers present full-length, in fragments and missing from a given dataset.