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	74.8%	0.3%	24.9%
Pea aphid v2.3	31,391	21.0%	0.0%	79.0%
Bed bug v1.1	41,503	83.4%	0.3%	16.3%
White fly v1.1	19,761	77.9%	0.0%	22.1%

Table 1b: Gene sets and transcriptome

Data	Sequences	Complete	Fragmented	Missing
OGS v1.0	21,026	74.5%	0.3%	25.2%
MCOT v1.0	30,562	92.9%	0.1%	7.0%
NCBI v100	20,996	74.7%	0.3%	25.0%
Maker v1.1	18,242	72.3%	0.4%	27.3%
Egg	76,467	71.5%	0.2%	28.3%
Nymph	69,175	71.6%	0.1%	28.3%
Adult	62,412	60.6%	0.2%	39.2%

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