



Figure S5. Genome wide diversity, Tajima D and ROH analysis of the sampled *Hermetia illucens* EVE population. Tajima D (A), nucleotide diversity (B) and Runs of Homozygosity (ROH) values for each of the seven assembled chromosomes. Contigs < 1 Mb (n=13) not included.

Supplementary Table 7. Genomic diversity and inbreeding of the sampled *Hermetia illucens* EVE population. Statistics describing mean *H. illucens* sequence diversity, Tajima D values, ROH counts, ROH mean lengths and inbreeding coefficients of the sampled population. Reported statistics generated on a per chromosome basis and genome wide. ^a Final genome wide F_{ROH} excludes identified sex chromosome seven (S7).

Query sequence	Pi (π)	Tajima D	ROH (#)	ROH mean length (kb)	F_{ROH}
S1	0.017	2.1	68	415.43	0.011
S2	0.018	1.802	37	282.13	0.005
S3	0.019	2.170	21	299.14	0.003
S4	0.018	1.019	38	270.68	0.005
S5	0.010	-0.066	193	439.10	0.060
S6	0.016	1.586	85	396.49	0.027
S7	0.072	0.428	2	573.86	0.040
Genome Wide	0.017	1.576	444	393.81	0.019