

Table S2. Genome assembly completeness assessment by BUSCO versus the Euarchontoglires unique single-copy ortholog database version 9. The high percentage of BUSCOs detected (C+F = 98.5%) indicates near complete capture of the expected single copy ortholog genes in this gerbil assembly and annotation, while the number of fragmented BUSCOs (F=4.9%) is consistent with the current somewhat fragmented state of the assembly.

Species	Size	BUSCO notation assessment results versus Euarchontoglires
<i>M. unguiculatus</i>	2523 Mbp 38,750 CDS	C:93.6% [S:53.5%, D:40.1%], F:4.9%, M:1.5%, n:6192