

## Description of Additional Supplementary Files

**Supplementary Data 1.** Description of the 25 Old World camel samples used in this study.

**Supplementary Data 2.** Summary of the raw and cleaned sequencing data, and the mapping results for each camel individual. MQ = Phred-scaled mapping quality score.

**Supplementary Data 3.** Summary of the positively selected genes identified in dromedaries using a combination of the homogeneity and HKA tests. Transcript = GenBank accession number; A = number of polymorphic sites in the dromedary samples; B = number of polymorphic sites in the wild camel samples; C = number of fixed differences between dromedaries and both wild camels and the alpaca genome sequence; D = number of fixed differences between wild camels and both dromedaries and the alpaca genome sequence; Homo\_P = p-value from the Fisher exact test for 2x2 contingency table; HKA\_Drom\_P = p-value from the HKA test within the dromedaries; HKA\_WC\_P = p-value from the HKA test within the wild camel; OMIA = domestic species disease or disorder [accession ID number] associated with this gene according to the Online Mendelian Inheritance in Animals database (<https://www.omia.org>); OMIM = Name [accession ID number] of diseases or disorders associated with this gene according to the Online Mendelian Inheritance in Man database (<https://www.omim.org>); GO\_Terms = Gene Ontology (GO) terms annotated to the gene using Blast2GO; Entrez = gene description from the NCBI Entrez database; Uniprot = gene description from the Uniprot database.

**Supplementary Data 4.** Results of the Gene Ontology (GO) enrichment analysis using TopGO for the positively selected genes from Table S1 in dromedaries. P values (P) were corrected using the false discovery rate (FDR).

**Supplementary Data 5.** Summary of the positively selected regions identified in dromedaries from a comparison of nucleotide diversity ( $\pi$ ; 0.5 percentile) and divergence (Dxy; 99.5 percentile). Scaffold = GenBank accession number of the scaffold from the *C. ferus* genome; OMIM = Name [accession ID number] of diseases or disorders associated with this gene according to the Online Mendelian Inheritance in Man database (<https://www.omim.org>); GO\_Terms = Gene Ontology (GO) terms annotated to the gene using Blast2GO; Entrez = gene description from the NCBI Entrez database; Uniprot = gene description from the Uniprot database.

**Supplementary Data 6.** Results of the Gene Ontology (GO) enrichment analysis using TopGO for the positively selected genes from Table S3 in dromedaries. P values (P) were corrected using the false discovery rate (FDR).

**Supplementary Data 7.** Summary of the positively selected regions identified in domestic Bactrian camels using the population branch statistic. Scaffold = GenBank accession number of the scaffold from the *C. ferus* genome; OMIM = Name [accession ID number] of diseases or disorders associated with this gene according to the Online Mendelian Inheritance in Man database (<https://www.omim.org>); GO\_Terms = Gene Ontology (GO) terms annotated to the gene using Blast2GO; Entrez = gene description from the NCBI Entrez database; Uniprot = gene description from the Uniprot database.

**Supplementary Data 8.** Results of the Gene Ontology (GO) enrichment analysis using TopGO for the positively selected genes from Table S5 in domestic Bactrian camels. P values (P) were corrected using the false discovery rate (FDR).

**Supplementary Data 9.** Summary of the positively selected regions identified in wild camels. Scaffold = GenBank accession number of the scaffold from the *C. ferus* genome; OMIM = Name [accession ID number] of diseases or disorders associated with this gene according to the Online Mendelian Inheritance in Man database (<https://www.omim.org>); GO\_Terms = Gene Ontology (GO) terms annotated to the gene using Blast2GO; Entrez = gene description from the NCBI Entrez database; Uniprot = gene description from the Uniprot database.

**Supplementary Data 10.** Complete list of the 17,912 canonical (longest isoforms) genes annotated in *C. ferus* and used in this study and their associated annotations. Transcript = GenBank accession number; GO\_Terms = Gene Ontology (GO) terms annotated to the gene using Blast2GO.