

**Comparative analysis of tissue-specific transcriptomes in the funnel web spider
Macrothele calpeiana (Araneae, Hexathelidae)**

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Supplementary Figures

Figure S1.

Distribution of the Gene Ontology (GO) terms associated with the complete set of *M. calpeiana* transcripts excluding singletons (transcripts formed by a single read). Panels A (for MF, molecular function) and B (for BP, Biological process) include information from the 1,734 transcripts with GO annotations over 3,467 sequences. Panels C (for MF, molecular function) and D (for BP, Biological process) include information from the 973 transcripts with GO annotations over 2,573 sequences (i.e. the 3,467 sequences after excluding HK or CEG genes).

Figure S2.

Number of *Macrothele* transcripts encoding HK or CEG genes.

Figure S3.

Venn diagrams showing the number of sequences excluding singletons expressed specifically in each tissue or in their intersections (blue, ochre and yellow indicate leg, palp and ovary, respectively). A) All transcripts ($n = 3,467$); B) Number of transcripts excluding those coding for housekeeping and CEG genes ($n = 2,589$); C) Number and percentage of transcripts coding for housekeeping genes ($n = 688$). D) Number and percentage of transcripts including in the CEG database ($n = 533$). In panels A and B, The area of each Venn diagram section is

approximately proportional to the number of transcripts (panels A and B), or to the particular fraction value (panels C and D).

Figure S4.

Differential distribution of the GO terms of the transcripts from leg or palp (Venn sections I, II and IV; in blue) and ovary (sections III, V, VI and VII; in red). Analysis comprising all transcripts with GO terms (2,619 transcripts over 6,696).

Figure S5.

Venn diagrams showing the percentage of specific interpro domains across tissues (the different Venn sections are indicated in roman numbers). Analysis conducted including HK and CEG encoding genes (3,353 transcripts with Interpro annotation over 6,696). A) Signal peptide domain. B) Transmembrane domain.

Figure S6

Phylogenetic relationships of a representative subset of arthropod iGluR (including IR8a/IR25a) and NPC2 family members. A) iGluR family tree based on “ANF_receptor” domain. Since we fail to detect the highly divergent “ANF_receptor” domain of IR8a and IR25a proteins in our HMM-search using the PF01094 profile (but see Croset et al., 2010) we did not include these sequences in the tree of this domain. B) iGluR family tree based on “Lig_chan” domain. C) NPC2 family tree, using the same protein identifiers as in Pelosi et al. (2014). NPC2 proteins expressed in the antennae of *A. melifera* and *C. japonicus* are indicated with an asterisk. Hexapods (*A. melifera*, *C. japonicum* and *D. melanogaster*), myriapods (*S. maritima*) and chelicerates (*I. scapularis*) sequences are shown in green, red and blue, respectively, while *M. calpeiana* are represented in shaded boxes. Numbers indicate node support values (percentage over 500 bootstrap replicates).

Figure S1A

ALL molecular_function Level 2

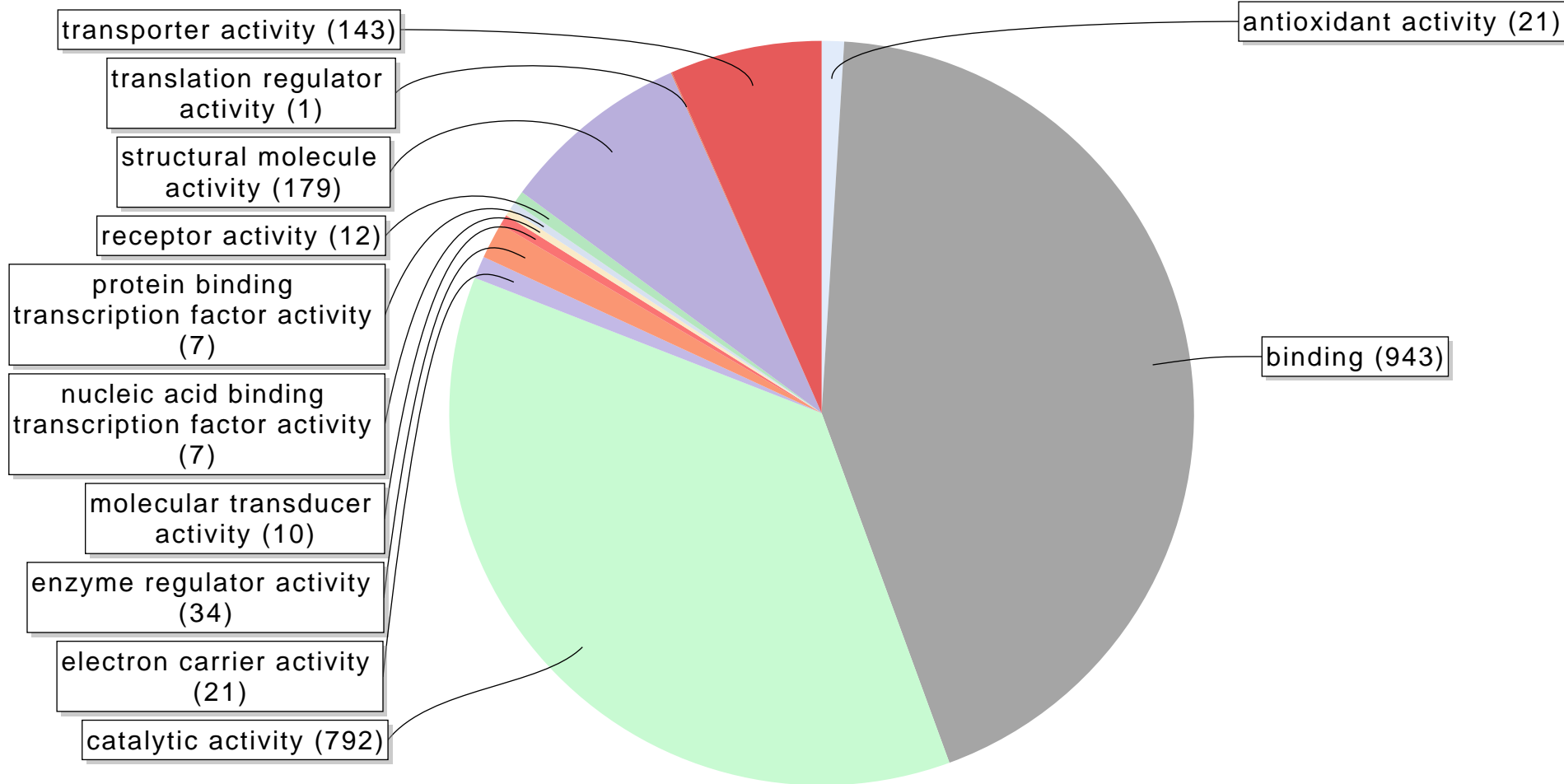


Figure S1B

ALL biological_process Level 2

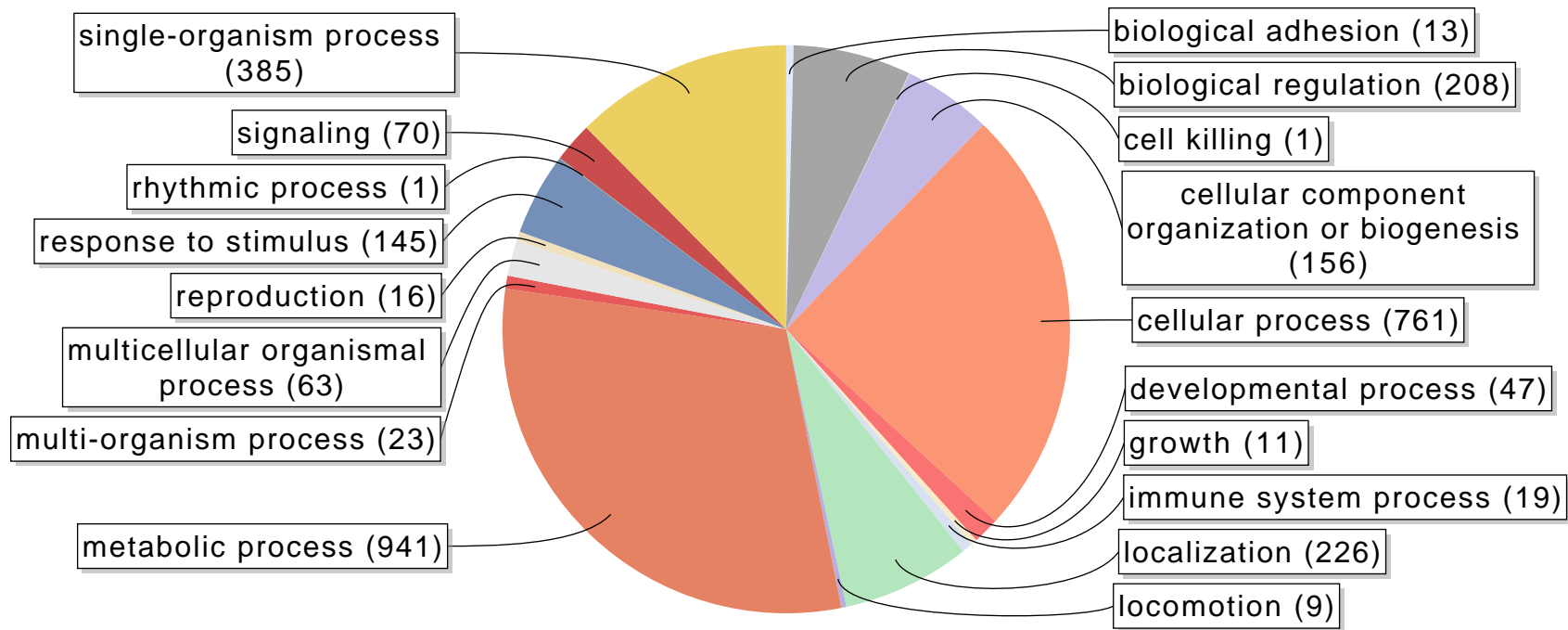


Figure S1C

NO HK/CEG molecular_function Level 2

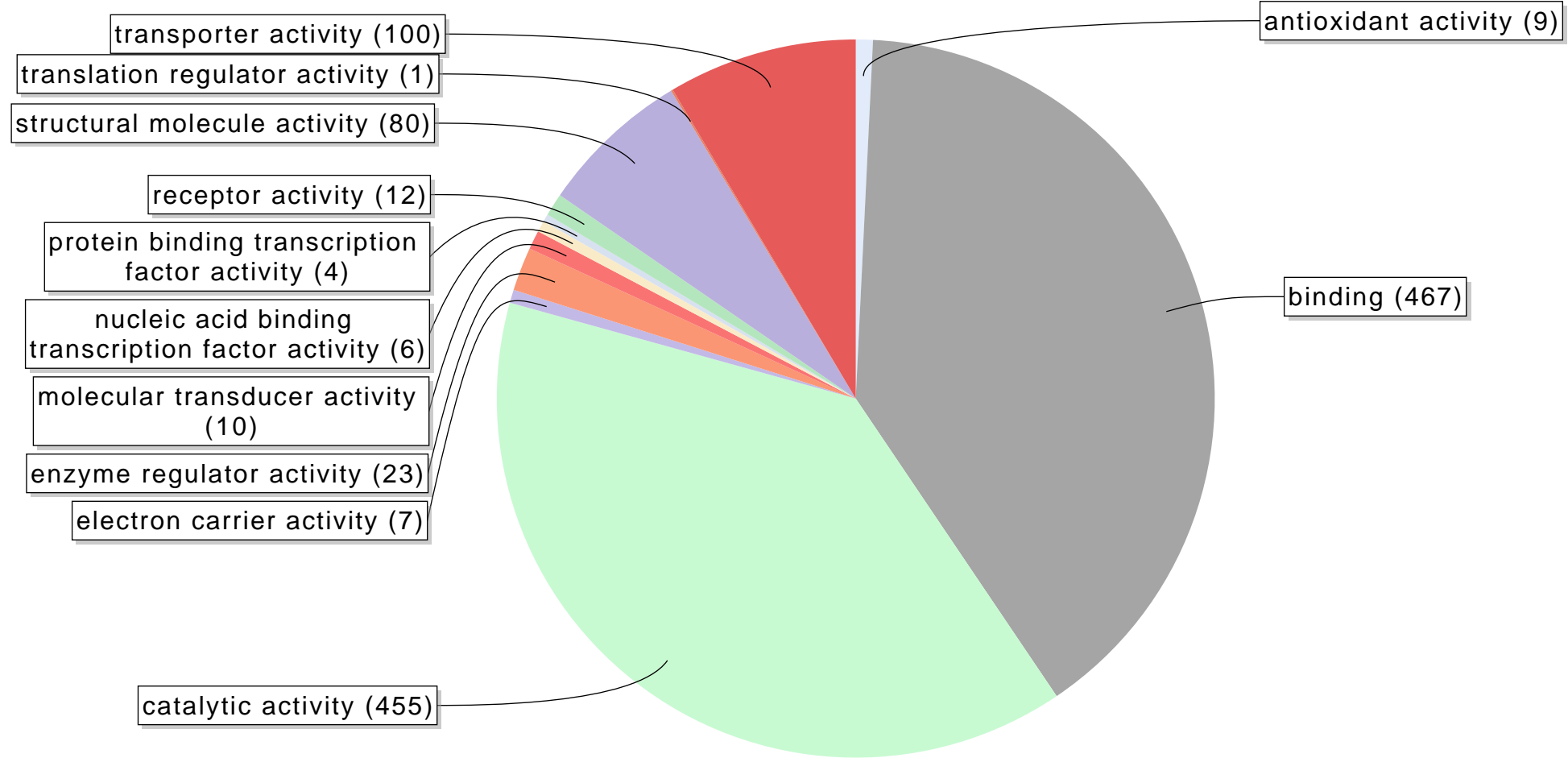


Figure S1D

NO HK/CEG biological_process Level 2

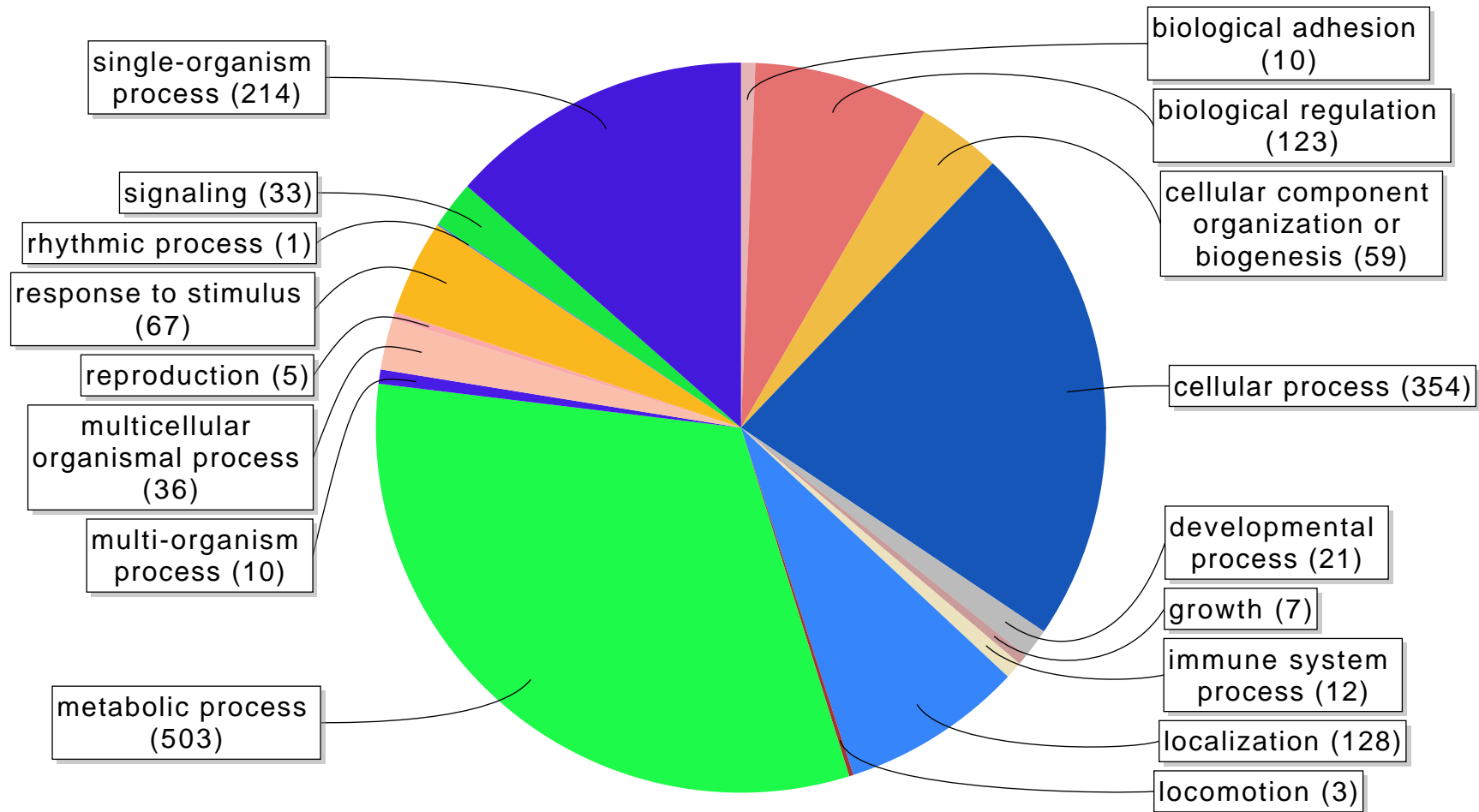


Figure S2

6696

5390

HK

CEG

517

488

301

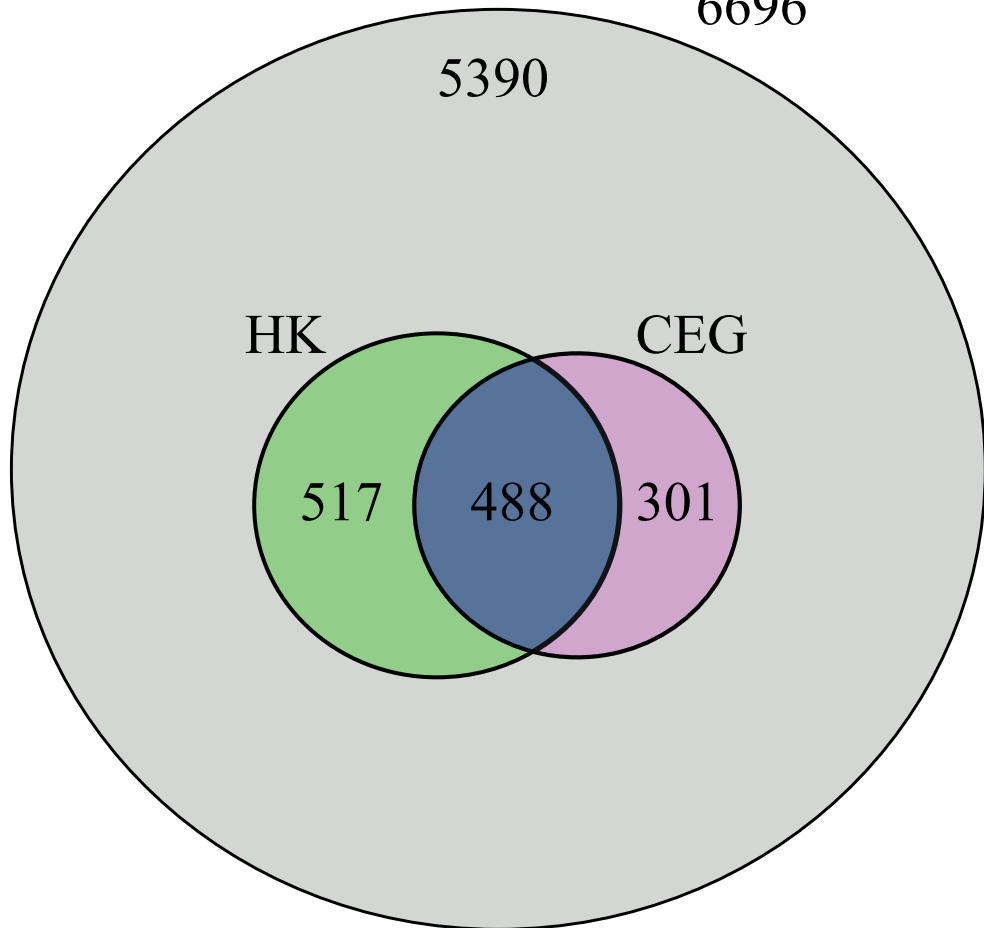


Figure S3

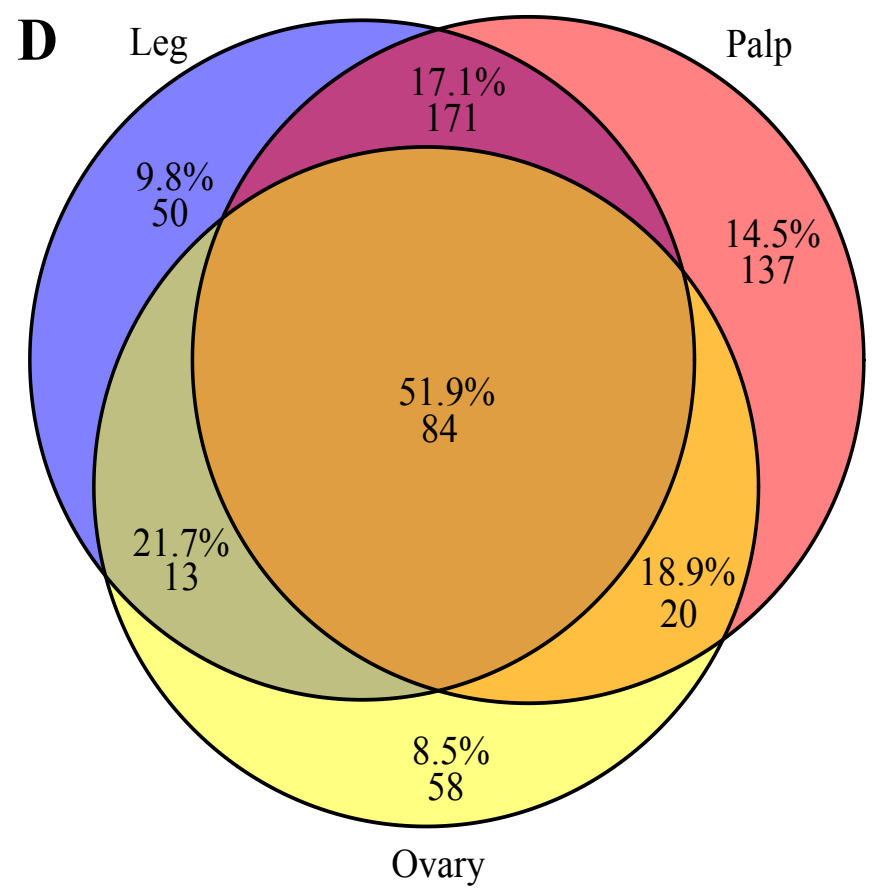
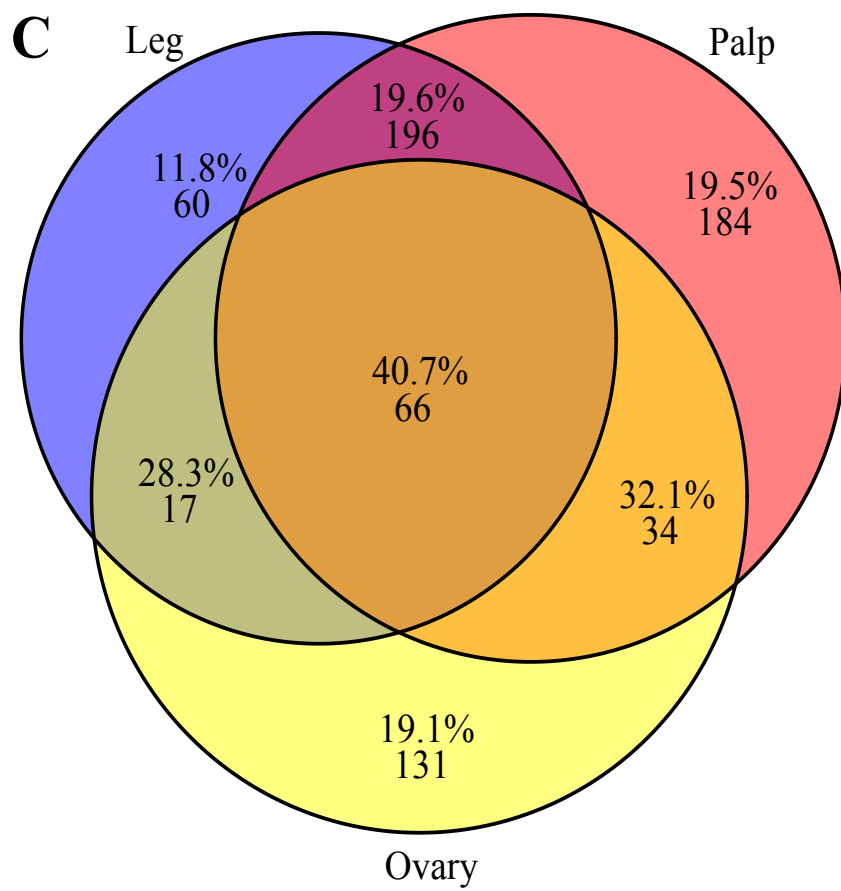
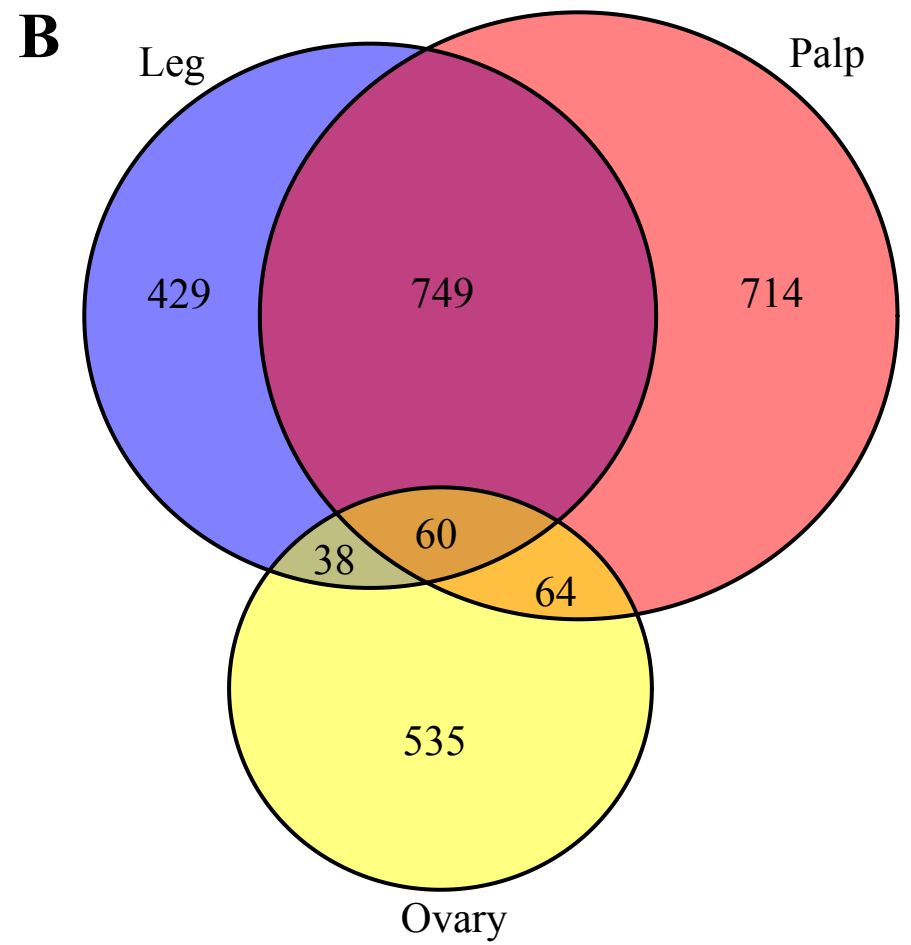
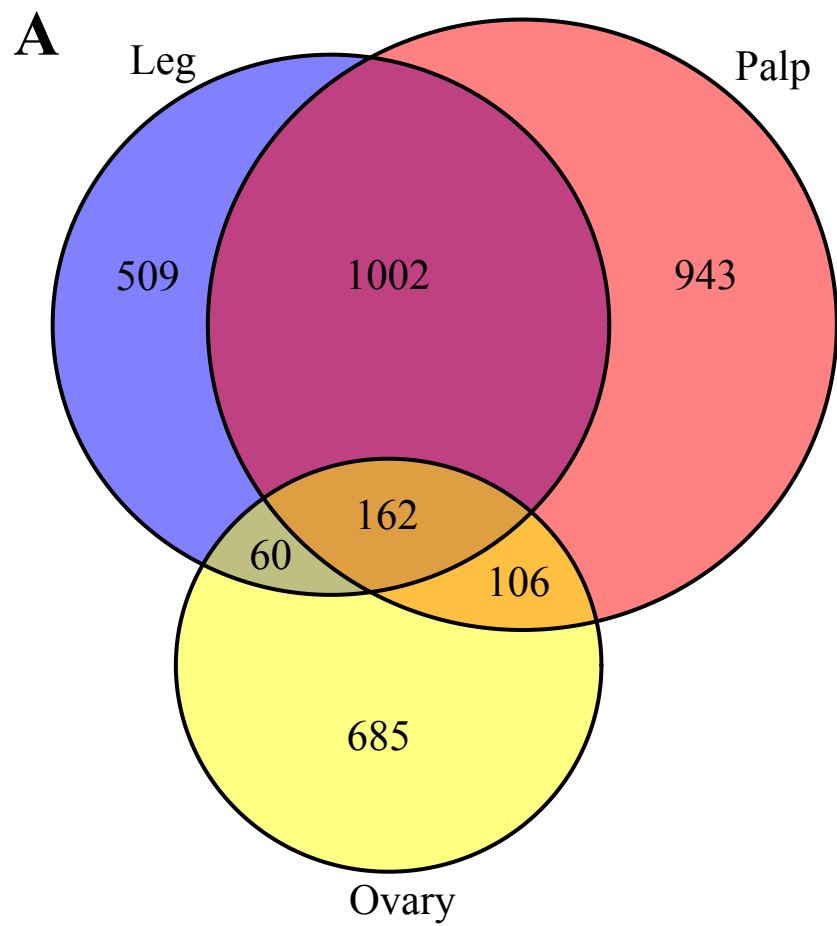


Figure S4

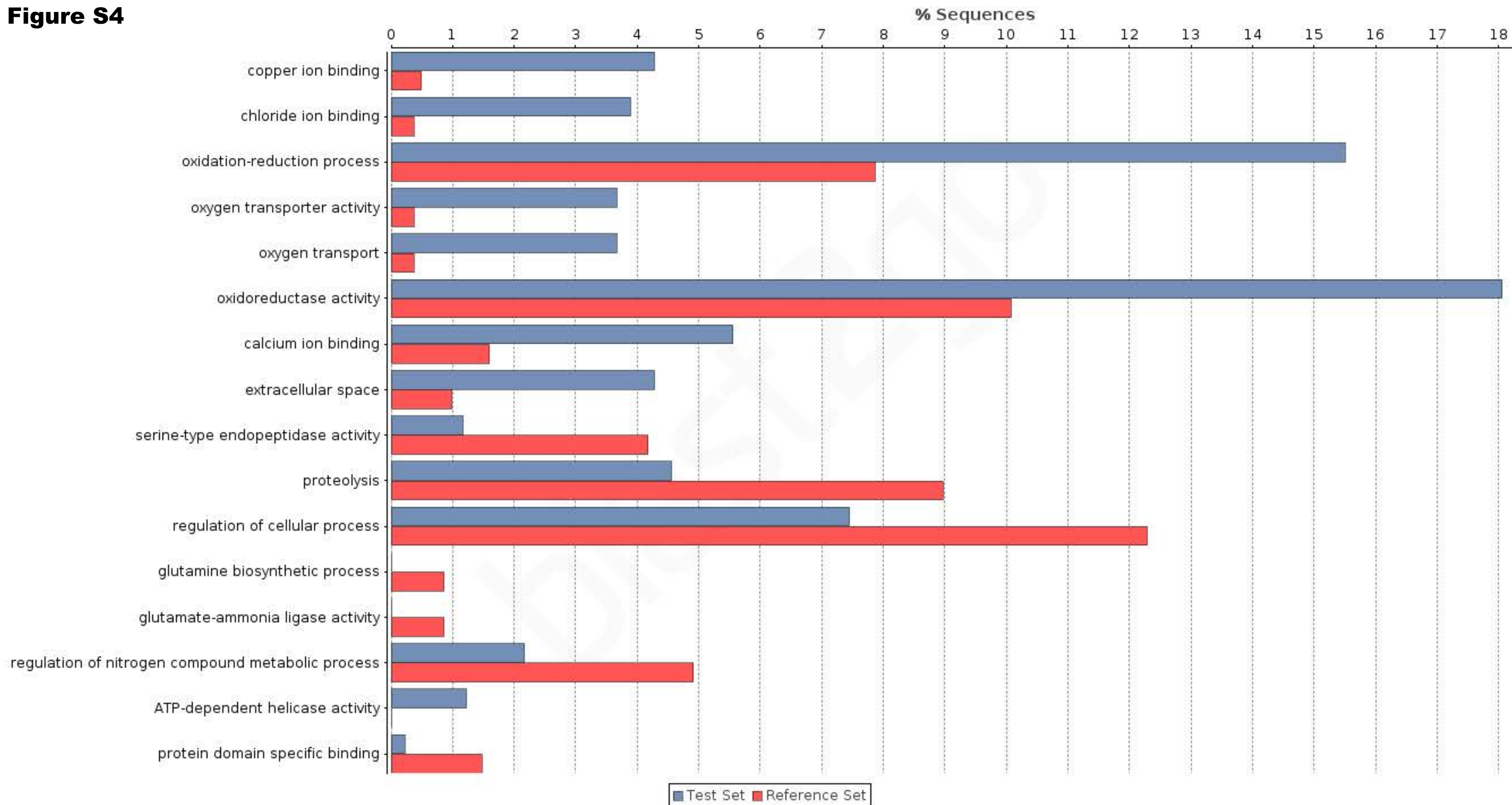


Figure S5A

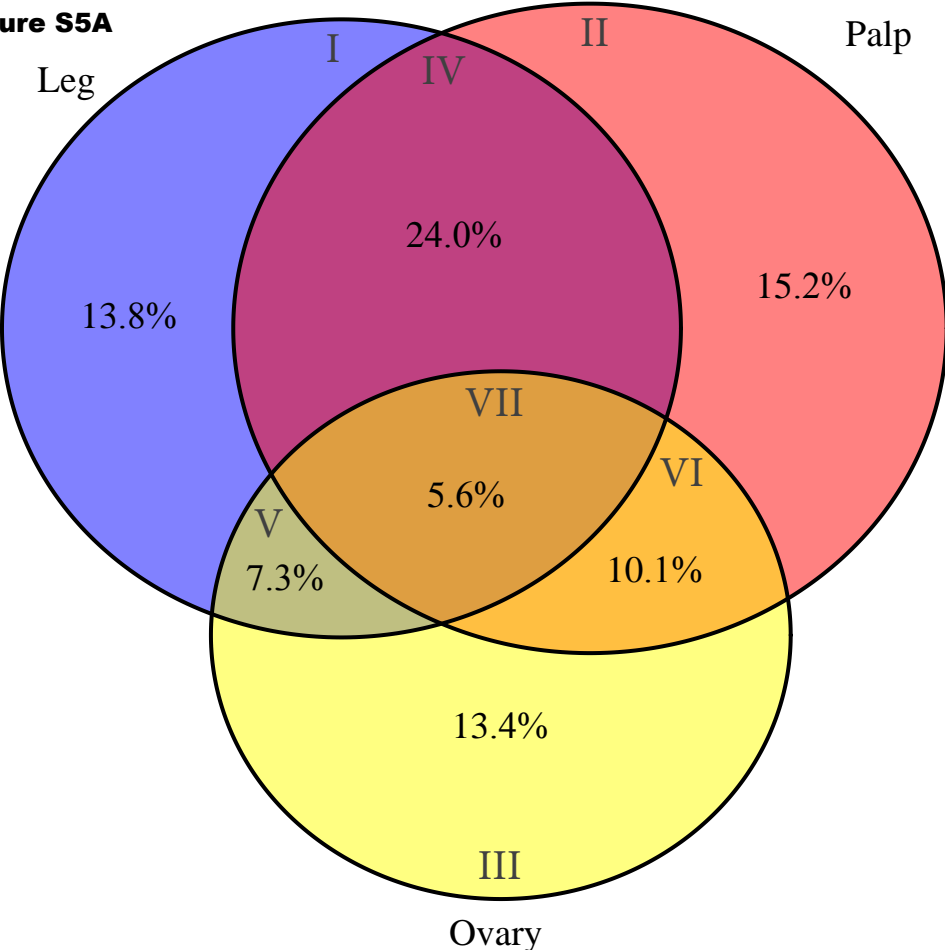


Figure S5B

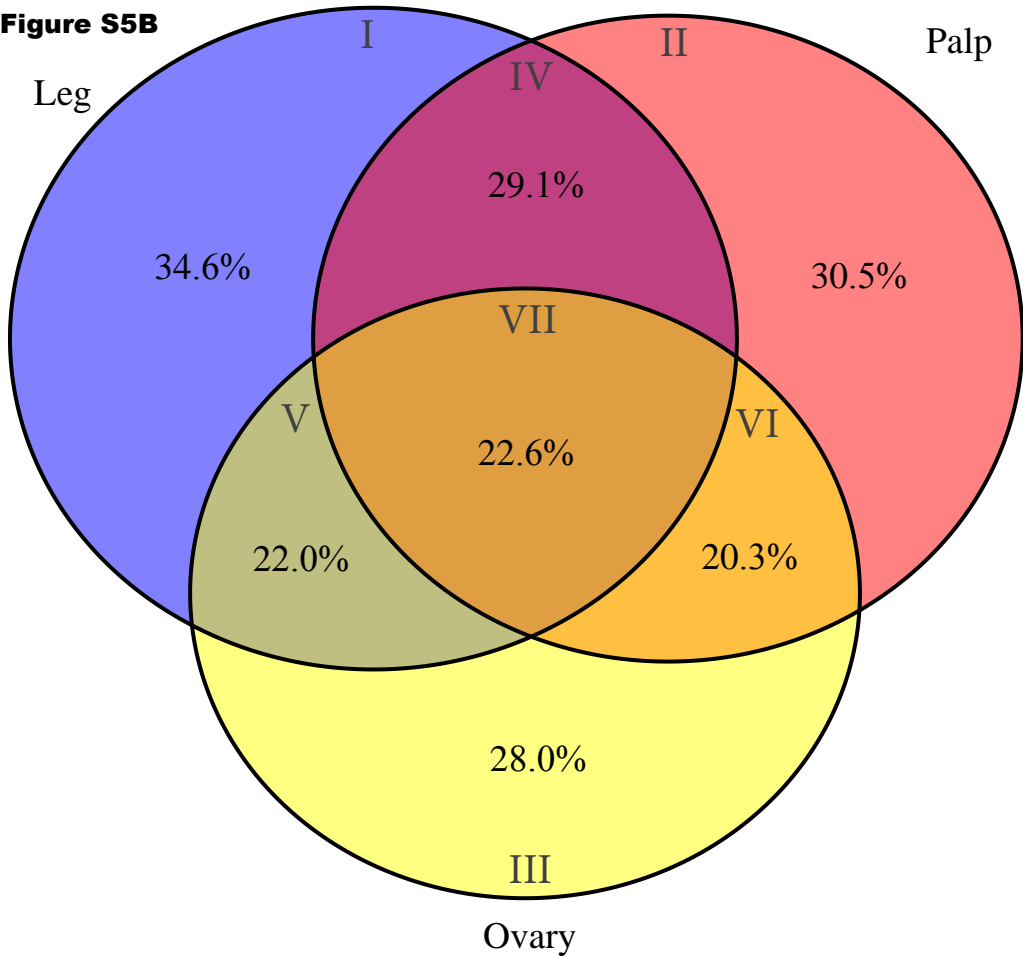


Figure 6A

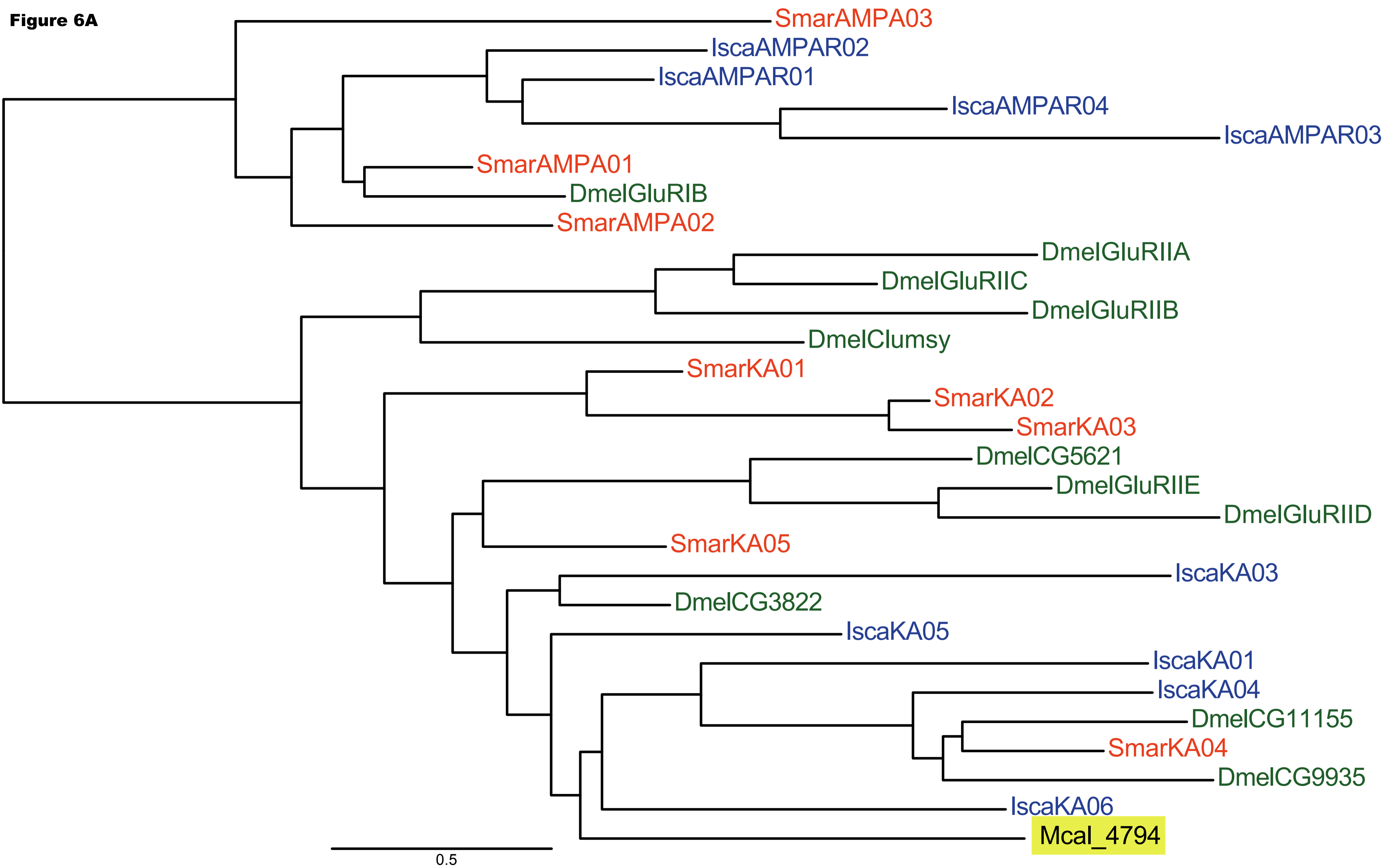


Figure 6B

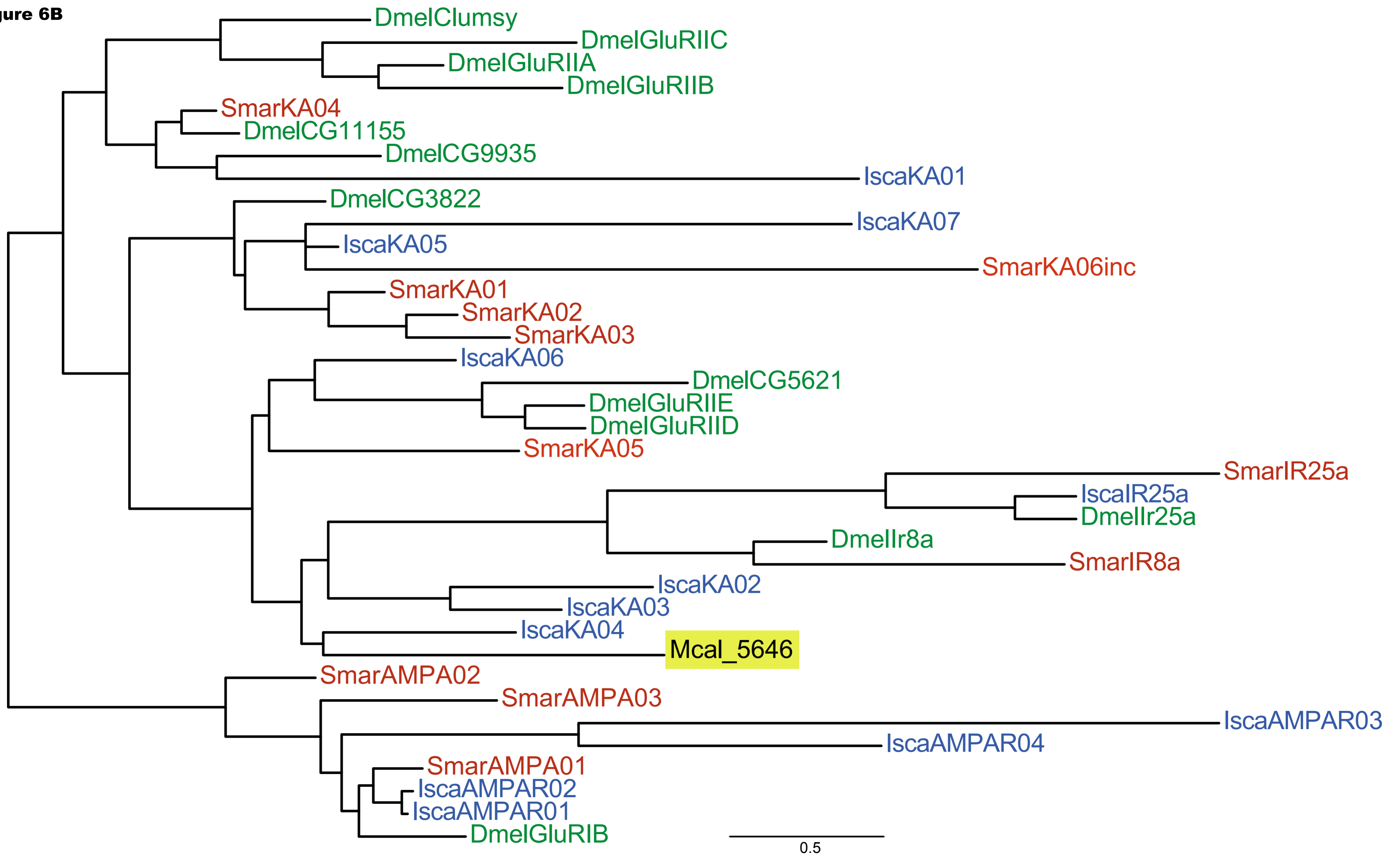


Figure 6C

