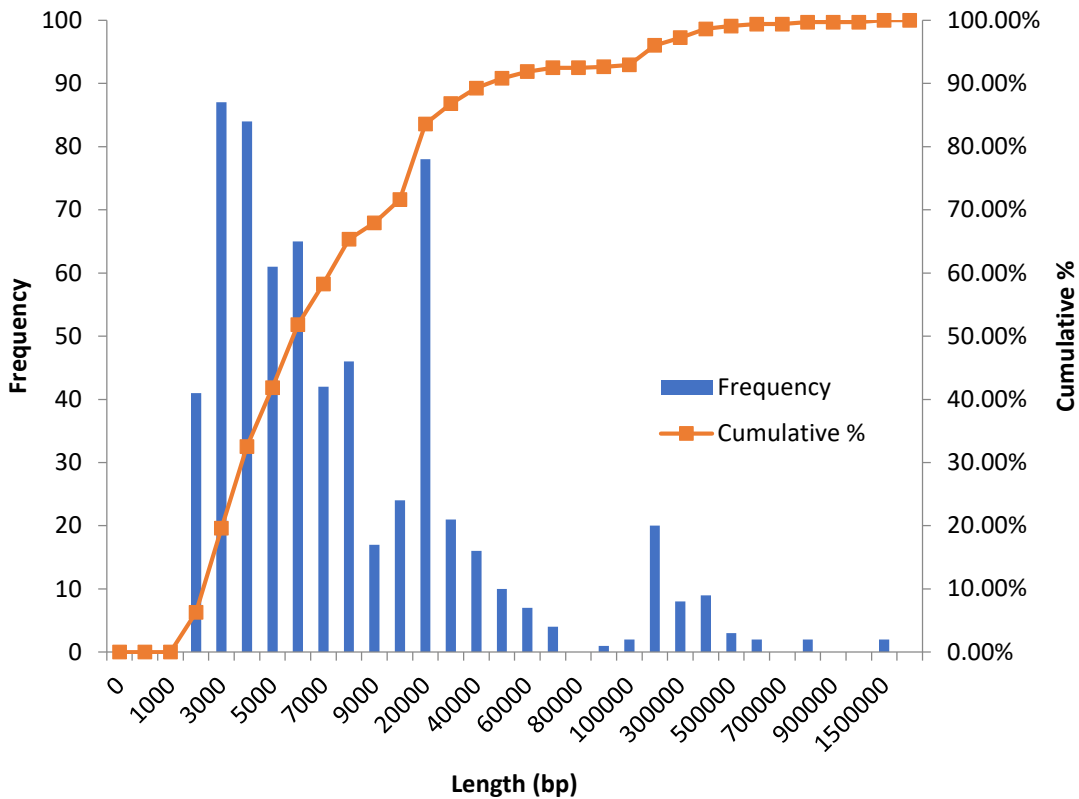
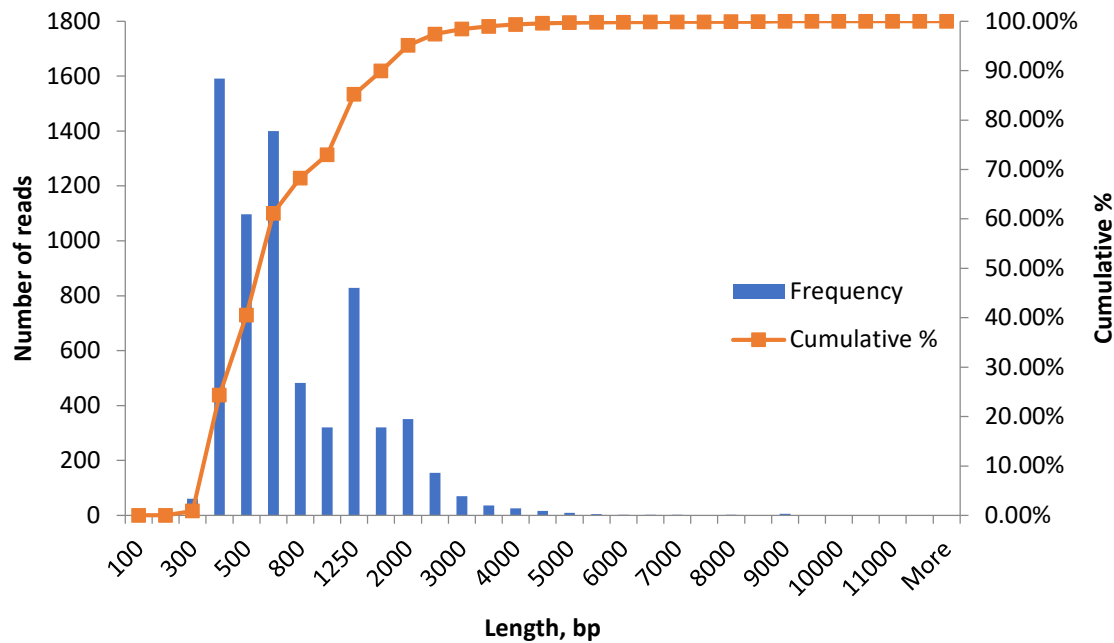


## Alpaca Y assembly contig lengths

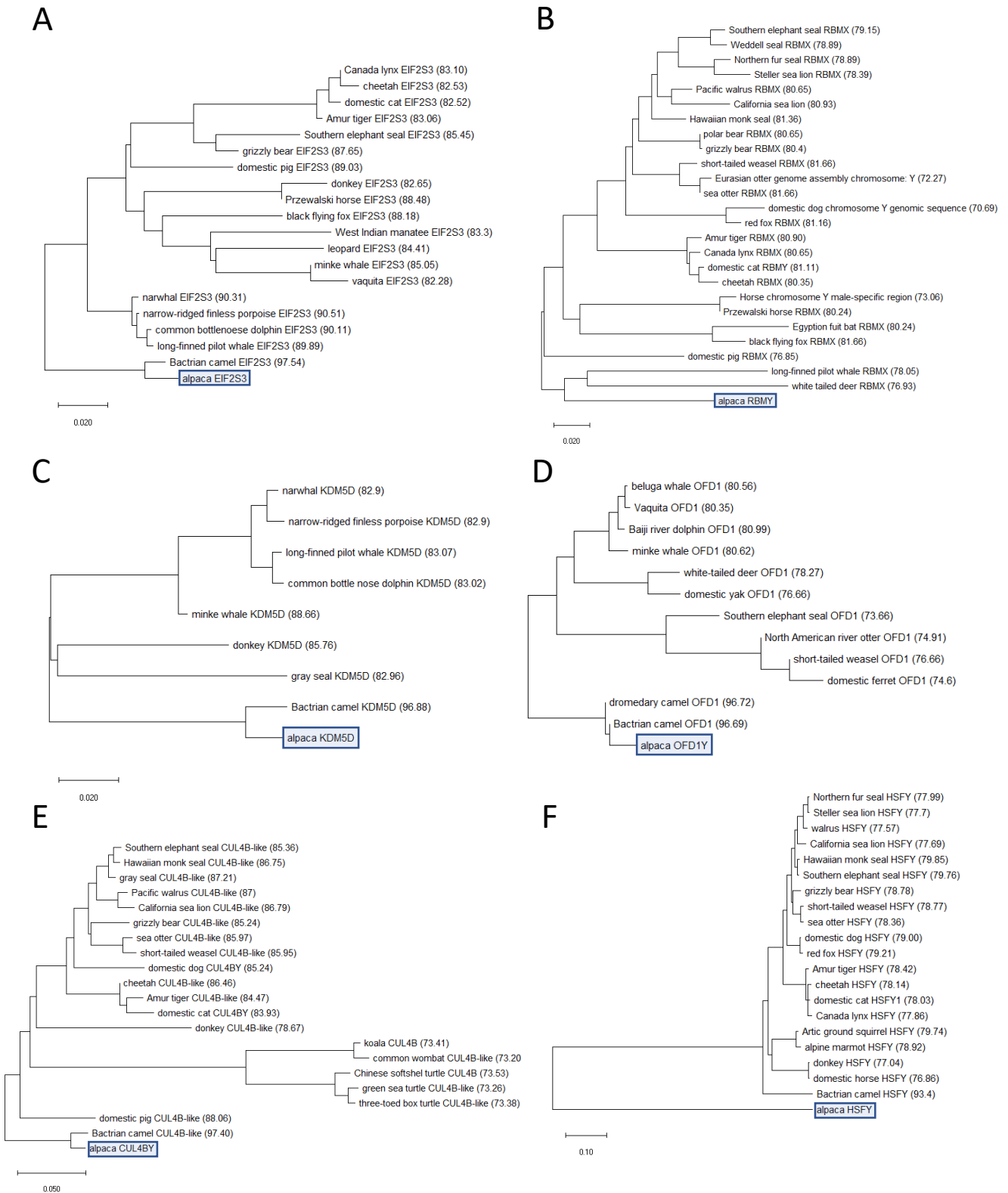




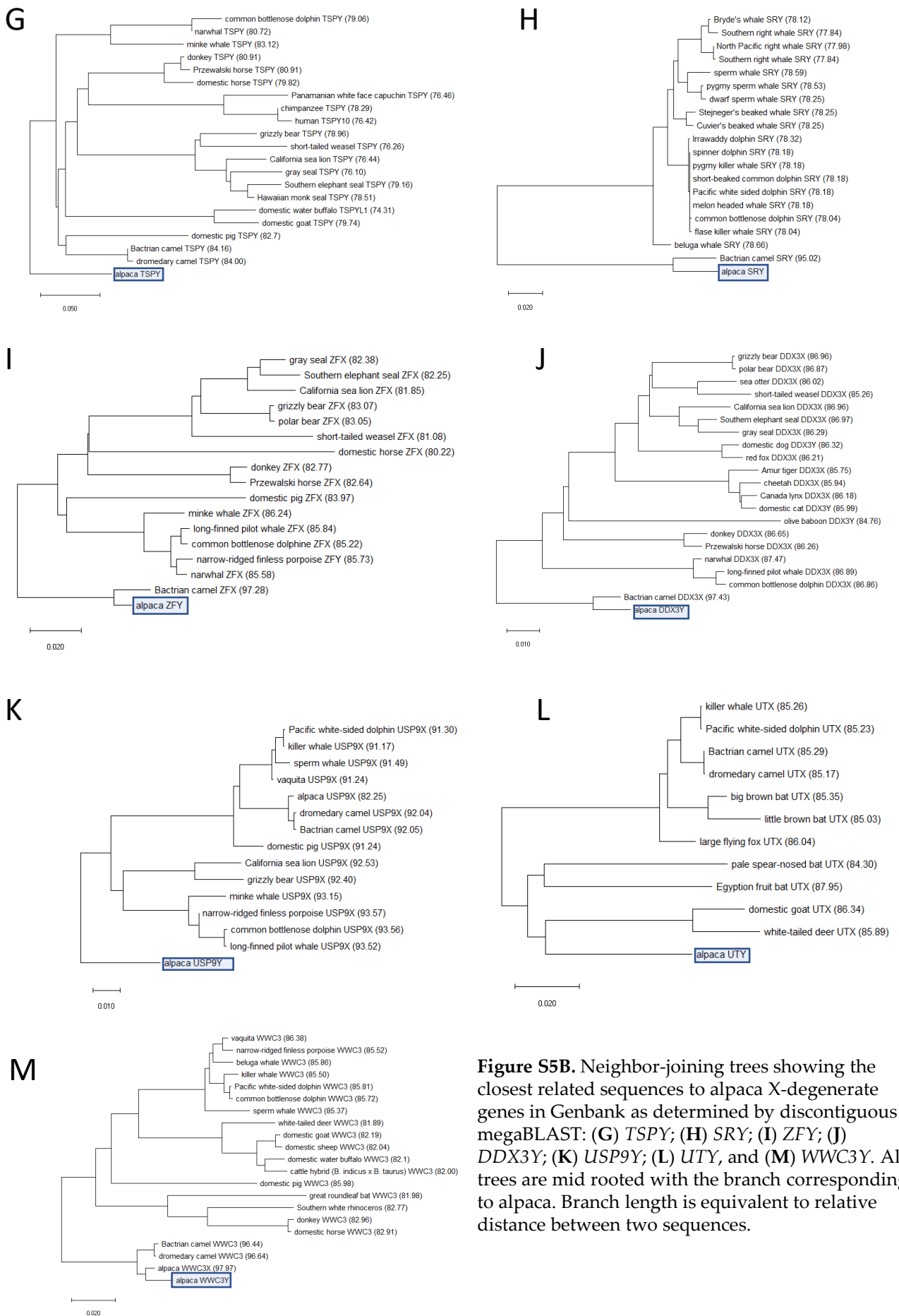
# Transcript length distribution



**Figure S4.** Length distribution of assembled transcripts with BLASTp results. The x-axis shows the length in base pairs, the y-axis shows the number of reads of a certain length, and the z-axis shows the cumulative percentage of reads of a particular size or shorter, denoted by the orange line.



**Figure S5A.** Neighbor-joining trees showing the closest related sequences to alpaca X-degenerate genes in Genbank as determined by discontinuous megaBLAST: **(A)** *EF2S3AY*; **(B)** *RBMY*; **(C)** *KDM5D*; **(D)** *OFD1Y*; **(E)** *CUL4BY*; **(F)** *HSFY*. All trees are mid rooted with the branch corresponding to alpaca. Branch length is equivalent to relative distance between two sequences.



**Figure S5B.** Neighbor-joining trees showing the closest related sequences to alpaca X-degenerate genes in Genbank as determined by discontinuous megaBLAST: (G) *TSPY*; (H) *SRY*; (I) *ZFX*; (J) *DDX3Y*; (K) *USP9Y*; (L) *UTY*, and (M) *WWC3Y*. All trees are mid rooted with the branch corresponding to alpaca. Branch length is equivalent to relative distance between two sequences.