Supplementary Table 5

Quality control standards for evaluating manual annotations

QC remark	Criterion
A	1. Evidence for 100%+ of exons (RNAseq or proteomics is best, blast hits may be allowed)
	2. Final protein length +- 10% of similar gene in related species
	3. Similar exon count/order to gene in related species
B	1. Evidence for 90%+ of exons (RNAseq or proteomics is best, blast hits may be allowed)
	2. Final protein length +- 25% of similar gene in related species
C	1. Evidence for less than 90% of exons (RNAseq or proteomics is best, blast hits may be allowed)
	2. Final protein length +- 50% of similar gene in related species
D	Not accepted in current form