

Supplementary Table 5a

Quality control remark key

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

Supplementary Table 5b

Gene naming conventions

1	Use only gene name. Do not add Dcitr to the gene name! It will be done automatically
	Criterion
a	Evidence for 100%+ of exons (RNAseq or proteomics is best, blast hits may be allowed)
b	Final protein length +- 10% of similar gene in related species
c	Similar exon count/order to gene in related species
2	Add "partial" after the gene name in all other cases, especially for misassembly
	Criterion
a	Evidence for 90%+ of exons (RNAseq or proteomics is best, blast hits may be allowed)
b	Final protein length +- 25% of similar gene in related species