Table S1   Standardized comments used by FlyBase for flagging exceptional transcripts

FlyBase transcript-associated standardized comments
Polycistronic transcript.
Dicistronic transcript.
Dicistronic transcript; alternative monocistronic transcript(s) exist.
Monocistronic transcript; alternative dicistronic transcript(s) exist.
Unconventional splice site postulated ([*splice donor-acceptor specified*]).
Unconventional splice site invoked ([*splice donor-acceptor specified*]): sequence altered due to transposon insertion; this splice may not occur in vivo.
Unconventional splice site(s) invoked due to gap in genomic sequence; this splice does not occur in vivo.
Unconventional splice site(s) invoked ([*splice donor-acceptor])*; within a dynamic region of nested TEs that may differ in different strains; this splice may not occur in vivo.
Unconventional splice site postulated: transcript subject to HAC1-type intron splice site recognition and cleavage.
Trans-spliced.
Unconventional translation start postulated ([*codon specified*] encoding Met).
Stop-codon suppression (UGA as Sec) postulated; reflected in aa sequence of predicted polypeptide.
Stop-codon suppression postulated *([codon specified])*; reflected in aa sequence of predicted polypeptide.
Double stop-codon suppression postulated *([codons specified])*; reflected in aa sequence of predicted polypeptide.
Translational frameshifting postulated: +1 frameshift reflected in aa sequence of predicted polypeptide.
TAA stop codon is completed by the addition of 3' A residues to the mRNA.
Start codon not determined.