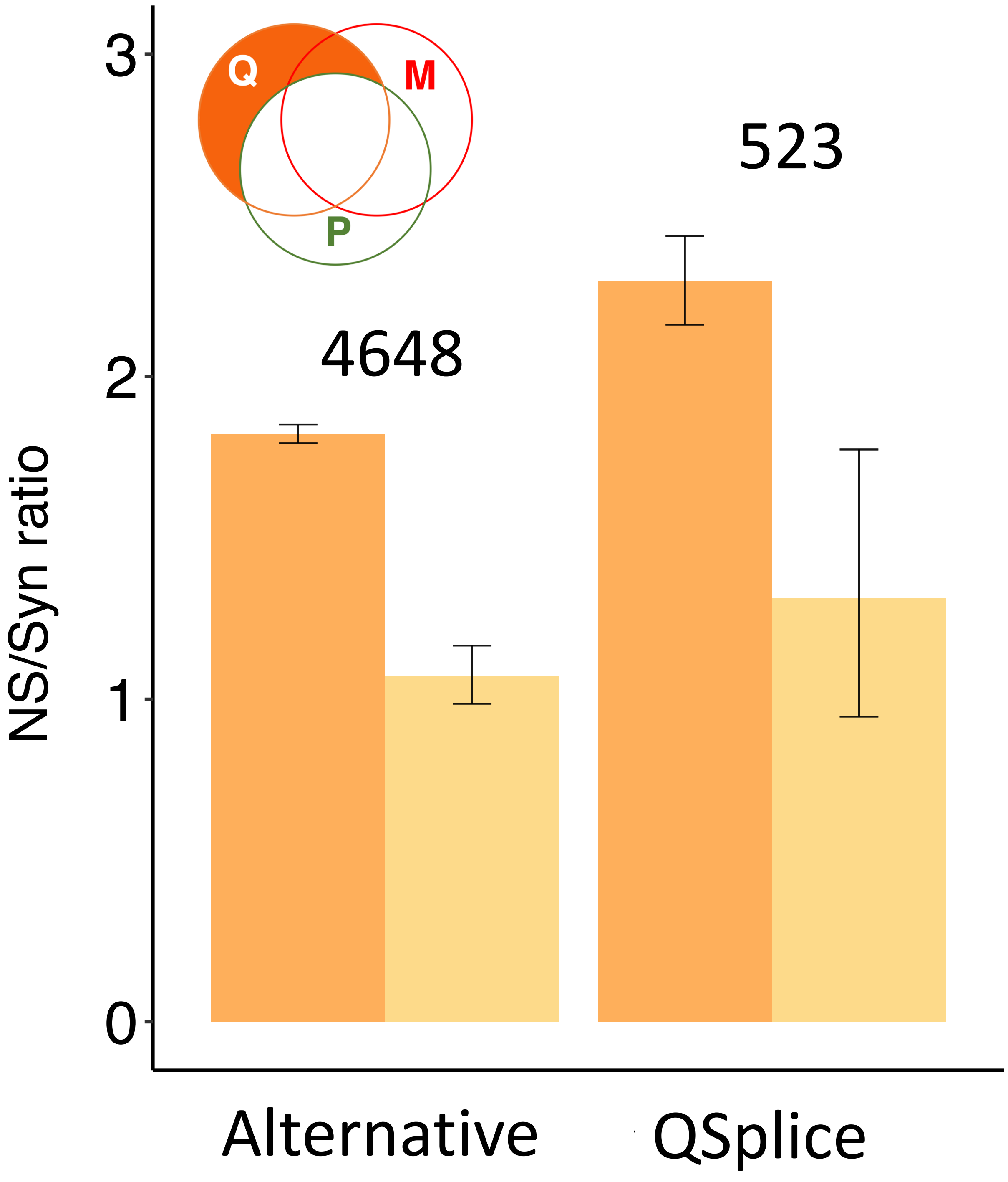
APPRIS principal versus MANE Select	Frequency	NS/Syn	Min error	Max error
Principal, not MANE Select	Rare	2.127	1.971	2.291
Principal, not MANE Select	Common	1.174	0.774	1.708
Alternative (but MANE Select)	Rare	2.059	1.982	2.138
Alternative (but MANE Select)	Common	1.487	1.229	1.784
Principal 263 exons, alternative 801				
MANE Select versus principal	Frequency	NS/Syn	Min error	Max error
MANE Select, not principal	Rare	2.066	1.942	2.196
MANE Select, not principal	Common	1.710	1.281	2.236
Alternative (but principal)	Rare	2.268	2.142	2.399
Alternative (but principal)	Common	1.966	1.489	2.547
MANE Select exons 293, alternative 529				
Longest versus MANE Select	Frequency	NS/Syn	Min error	Max error
Longest, not MANE Select	Rare	2.492	2.407	2.578
Longest, not MANE Select	Common	2.419	2.114	2.757
Shorter (but MANE Select)	Rare	1.884	1.796	1.976
Shorter (but MANE Select)	Common	0.949	0.717	1.233
Longest isoform exons 1578, alternative 1149				

Supplementary Table 1. Non-synonymous to synonymous ratios for reference and alternative exons.
Non-synonymous to synonymous ratios for rare and common variants, along with 95% confidence intervals. Non-synonymous to synonymous ratios are shown for exons from reference and alternative transcripts for subsets of MANE Select transcripts, longest isoforms and principal isoforms. Reference transcripts from which exons are selected are (from top to bottom) those that produce APPRIS principal isoforms, but not MANE Select variants, those that generate MANE Select variants, but not APPRIS principal isoforms, and those that produce the longest isoforms, but not MANE Select variants. The number of exons in each reference and alternative set is indicated below each table.



Supplementary Figure 1. Non-synonymous to synonymous ratios for reference and alternative exons using RNAseq information.
Non-synonymous to synonymous ratios for rare (dark orange bars) and common (light orange bars) variants, along with error bars showing 95% confidence intervals. The Venn diagram indicates the subset of exons; exons "Q" are those that produce the transcript with the highest QSplice score, "M" are present in MANE Select transcripts, and "P" produce principal isoforms. Here we compare the non-synonymous to synonymous ratios for exons that produce the transcript with the highest QSplice score and do not overlap with exons from principal transcripts (QSplice), against exons from transcripts alternative to QSplice reference transcripts (Alternative). The number of exons in the reference and alternative sets is indicated.