Table 1 | Classification of alternative splicing events

| Splicing event	Diagram	FlyBase r5.12	modENCODE	New events	Short poly(A)$^+$ RNA-Seq	Significantly changing
Cassette exons		793	2,717	2,014	2,369	1,539
Alternative 5′ splice sites		843	5,192	4,599	4,583	3,142
Alternative 3′ splice sites		879	6,253	5,505	5,579	3,242
Mutually exclusive exons		229	251	123	228	226
Coordinate cassette exons		301	1,227	979	992	467
Alternative first exons		1,767	4,936	3,442	4,473	3,996
Alternative last exons		227	604	432	553	471
Retained/unprocessed introns		1,434	2,679 (5,667)	1,275 (4,263)	2,439 (35,641)	868 (8,998)
Total		6,437	23,859 (26,847)	18,369 (21,478)	21,216 (54,418)	13,951 (22,081)

The number of retained/unprocessed introns in parentheses indicates the total number identified, whereas the number not in parentheses indicates the subset of identified events that have been validated by cDNA sequences or FlyBase 5.12 annotations.