Supplementary Figure 7 - Branchpoint motif supporting read evidence and co-occurence with additional branchpoints in same intron. (A) Histogram depicting the number of supporting reads per mapped branchpoint, stratified by the matched premRNA-U2 alignment motif. Y-axis is the fraction of branchpoints that fall into each bin. X-axis is the number of supporting reads per unique branchpoint. (B) Co-occurrence of different branchpoint motif classes with an additional branchpoint in the same intron. Y-axis is the percent of introns in each motif class that has an additional branchpoint as described on the x-axis. The 'any' x-axis bin includes canonical branchpoints, non-canonical branchpoints, and no motif branchpoints (excludes circles and template switching events).Canonical BP introns fit the TRYTRAY motif. Non-canonical BP introns fit TRYTRANY, TRYTRCY, TRAYTRY, TRANYTRY, and TRANNYTRY motifs.