

Supplemental Table 5: mRC-seq Read Counts for Mosaic Insertions

	% Prevalence: insertion #3	Reads: insertion #3	Reference L1 5' end sequencing depth (fold)
SRA Liver	7.5	0	34.79
SRA Brain	3.7	0	37.28
SRA Muscle	4.2	0	21.62
SRA Right Ovary	27.5	1	26.89
SRA Left Ovary	9.1	0	27.33

	% Prevalence: insertion #5	Reads: insertion #5	Reference L1 5' end sequencing depth (fold)
SRE Liver	0.2	0	53.59
SRE Brain	0.6	1	27.38
SRE Heart	0.2	0	27.60
SRE Right Ovary	1.5	0	30.16
SRE Left Ovary	0.4	0	31.14

	% Prevalence: insertion #7	Reads: insertion #7	Reference L1 5' end sequencing depth (fold)
SRCD14 Right Testicle	3.6	2	277.06
SRCD14 Left Testicle	11.5	13	238.56

Supplemental Table 5. mRC-seq read counts for mosaic insertions. For each insertion (#3, #5, #7) where the tissues of the appropriate mosaic animal were assayed individually by mRC-seq, the percent prevalence of the insertion and the mRC-seq read count are shown. As a reference for sequence capture efficiency and sequencing depth for each library, sequencing depth achieved for reference L1 5' ends is shown. For insertion #6 in mouse SRCD10, the tissues of mouse SRCD10 were not analyzed individually by mRC-seq, so read counts and reference L1 sequencing depth are denoted as n/a. Full statistics for each library can be found in Supplemental Table 1.