| % Prevalence: | Reads: | Reference L1 5’ end sequencing depth (fold) |
|---------------|--------|--------------------------------------------|
| insertion #3  | insertion #3 |                                    |
| 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: | Reads: | Reference L1 5’ end sequencing depth (fold) |
|---------------|--------|--------------------------------------------|
| insertion #5  | insertion #5 |                                    |
| 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: | Reads: | Reference L1 5’ end sequencing depth (fold) |
|---------------|--------|--------------------------------------------|
| insertion #7  | insertion #7 |                                    |
| 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.