# Supplementary Table Legends for "Transposable element detection from whole genome sequence data"

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## 1 Supplementary Tables

### 1.1 Supplementary Table 1

Text file containing the following columns: Chromosome, Start, End, TE Family (L1, ALU, or SVA), and a comma-delimited list of studies, abbreviated as follows: AE2010[1], AE2011[2], AK2014[3], CB2010[4], CS2011[5], DBRIP[6], DW2010[7], DW2013[8], EH2014[9], EL2012[10], FH2011 [11], JT2014[12], RI2010[13], RS2013[14], SS2012[15]. Where coordinates were originally relative to hg18, they were converted to hg19 using the liftOver tool. The final list was generated using BEDTools merge.

### 1.2 Supplementary Table 2

Overlaps between insertion sites identified by *(a)* TranspoSeq and Tea or *(b)* TranspoSeq and TraFiC, related to Figure 2. Each row shows the overlap for an individual sample, and the summation shown in Figure 2 is the bottom row for each panel. Jaccard distance between two insertion sets $A$ and $B$ is defined as $1 - \frac{|A \cap B|}{|A \cup B|}$.

## 2 Supplementary References

## References

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