**Supplemental Material**

Supplemental Figure 1

Confirmation of amplicon size selection. Representative bioanalyzer trace showing the size distribution of the size selected final, Ta subfamily-enriched L1Hs-amplified sequencing library for an individual sample. Size selected amplicon products were distributed between 200-1000 base pairs (bp, x-axis). Y-axis is arbitrary florescent units (FU).



**Supplemental Oligomers**

L1HsACA primer

GGGAGATATACCTAATGCTAGATGACACA

Double stranded T-Linker

AGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAG/Phos/5’

TCTACACTCTTTCCCTACACGACGCTCTTCCGATC\*T

T-linker bottom strand primer

TCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Seq2-L1HsG primer

GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCACATGTACCCTAAAACTTAG

Adapt2-Seq1

AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Adapt1-Barcode-Seq2 - Index 1

CAAGCAGAAGACGGCATACGAGATACATCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

Adapt1-Barcode-Seq2 - Index 2

CAAGCAGAAGACGGCATACGAGATTGGTCAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

Adapt1-Barcode-Seq2 - Index 3

CAAGCAGAAGACGGCATACGAGATCACTGTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

Adapt1-Barcode-Seq2 - Index 4

CAAGCAGAAGACGGCATACGAGATATTGGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

Adapt1-Barcode-Seq2 - Index 5

CAAGCAGAAGACGGCATACGAGATGATCTGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

Adapt1-Barcode-Seq2 - Index 6

CAAGCAGAAGACGGCATACGAGATTACAAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC\*T

\* denotes a phosphorothioate bond and highlighting denotes barcode sequence