|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Symbol | Chromosome | Start (10 kb upstream) | End (10 kb downstream) | Sequence length | *L1* length | *L1* % |
|  |  |  |  |  |  |  |
| *POTEA* | chr8 | 43282482 | 43373518 | 91036 | 43009 | **47.2** |
| *POTEB* | chr15 | 21836328 | 21887298 | 50970 | 9318 | **18.3** |
| *POTEB2* | chr15 | 20825371 | 20876314 | 50943 | 10252 | **20.1** |
| *POTEB3* | chr15 | 21398963 | 21450059 | 51096 | 9329 | **18.3** |
| *POTEC* | chr18 | 14501897 | 14553146 | 51249 | 10634 | **20.7** |
| *POTED* | chr21 | 13600176 | 13651585 | 51409 | 11060 | **21.5** |
| *POTEE* | chr2 | 131208066 | 131275278 | 67212 | 9016 | **13.4** |
| *POTEF* | chr2 | 130064029 | 130139222 | 75193 | 12994 | **17.3** |
| *POTEG* | chr14 | 19392485 | 19444341 | 51856 | 10518 | **20.3** |
| *POTEH* | chr22 | 15680025 | 15731522 | 51497 | 10457 | **20.3** |
| *POTEI* | chr2 | 130449454 | 130519666 | 70212 | 8739 | **12.4** |
| *POTEJ* | chr2 | 130601480 | 130668091 | 66611 | 8190 | **12.3** |
| *POTEKP* | chr2 | 131581751 | 131637266 | 55515 | 14662 | **26.4** |
| *POTEM* | chr14 | 18957433 | 19008903 | 51470 | 10602 | **20.6** |
|  |  |  |  |  |  |  |
| *All POTEs* (mean) | |  |  |  |  | **20.7%** |
| Nuclear Genes1 (mean) | |  |  |  |  | **14.1%** |
| Wilcoxon rank-sum p-value | |  |  |  |  | **0.0065** |

**Table S1. *LINE1* sequence composition in *POTE* genes + 10kb flanking regions.**

**1** Obtained from UCSC Genome Browser queried for human nuclear genes annotated in reference genome (hg38) and *L1* sequences. The annotated set of genes included protein-coding genes, non-coding RNA, and splice variants. Custom Python scripts were used to determine the length of *L1* sequences in each gene, and are available on request.