



Supp. Figure S1. Structures of the 3' ends of 11 potential *de novo* L1 insertions recovered by hybridisation enrichment, aligned to the human-specific L1 insertion, L1.3 (L19088). The names of the sequences include the target locus from which they originate. Bars are coloured to show the origin of the sequence: the L1 sequence is blue, the L1 poly A tail is red, regions of no alignable identity to the target locus are green (with chromosome origin shown above, where identified), regions of intermediate identity to the target sequence (>25% to <99%) are purple, and regions of high (>99%) identity to the target sequence are yellow. Regions containing Alu sequences likely involved in template switching are boxed and the size of the boxes reflects the length of the Alu tract.

Supp. Table S1. Biotinylated oligonucleotides used for hybridisation enrichment

Bio-oligo ID	Sequence (5'- 3')	Position (L1.3¹)
bio-L1U1	bio-GGCACATGTATACATATG	5956
bio-L1U2	bio-GAAATACCATTTGACCCA	5489
bio-L1U3	bio-TGACAAAGGGCTAATATC	5124
bio-L1U4	bio-ACTACCTGACTTCAAAC	4602

¹ The location of each bio-oligo with respect to L1.3 (accession L19088)

Supp. Table S2. Primary target site PCR primers used for multiplex PCR and their optimised concentrations

Target Locus	Primer ID	Sequence	Working concentration (μM)	Accession Number	Location ¹	Size, bp ²
HBB	PFHBBTF1	ATTTGCCTGGTATGCCTGGG	0.07	ac104389	175485	5005
	PFHBBTR1	CCTTGAAGCCAGGATGATGG	0.07	ac104389	180490	
DMD	PFDMDTF1	GTGCTTTAGACATTACCCAGG	0.12	al031643	111421	4908
	PFDMDTR1	CAACACATCTCTTCATACAGAGGTG	0.12	al031643	116329	
F9	PFFIXTF1	CACTGAGACCCCCTTCGG	0.08	al033433	17106	5551
	PFFIXTR1	CTGGTATAGTGCTGAGACAGG	0.08	al033433	22657	
MHC2	PFMH2TF1	TGCAGGGGCAGAAGAGGG	0.15	al662845	32532	5017
	PFMH2TR1	CCCCCTTGCTTGCTAAGGG	0.15	al662845	37549	
CHM	PFCHMTF1	TGAATGCTGGTTGTGGGAGG	0.05	al009175	57913	5677
	PFCHMTR1	ACCATCTATGGTGCTGCTGG	0.05	al009175	63590	
APC	PFAPCTF1	GGAAGCATTATGGGACATGG	0.025	ac008575	127059	5416
	PFAPCTR1	CCTGAACAGACGAATGTGTGG	0.025	ac008575	132475	
CYBB	PFCGDTF1	GTTGGCTAACCATCAGAGGG	0.07	al627245	38073	5159
	PFCGDTR1	CAGCAAACCTGAGGGATTGGG	0.07	al627245	43232	
RP2	PFRP2TF1	CACAGAAGAGGATTGGGAGG	0.03	al050307	86064	4773
	PFRP2TR1	TCTGTCATGCCCAACCTCTG	0.03	al050307	90837	
FKTN	PFFCMTF1	CCTTTCGGAAGAGTGCAAAGG	0.1	al158070	94766	5078
	PFFCMTR1	TGGAGCTAAGGTTTCCCAGG	0.1	al158070	99844	
HOXD	PFHODTF1	TTCGGTTCCTTCTCTGCTGG	0.1	ac009336	84862	4264
	PFHODTR1	CTCCTAAAATGGCTCCCTGG	0.1	ac009336	89126	
Control	PFLRCtrlA	TTAGGACGCCCACTACTGTG	0.1	ac008706	73112	12805
	PFLRCtrlB	GCCAATCCTGTAAGGCAAAGGG	0.1	ac008706	85917	
Al121819 L1 insertion	PF819LRA	CCTGCTTTCACCTCACAGGG	0.05	al121819	105131	6454
	PF819LRB	CAGGTAGAAACTTCCCAGGG	0.05	al121819	111585	

¹ Location of the primer within the sequence accession; ² Length of the primary PCR amplicon.

Supp. Table S3. PCR primers used for secondary TSP multiplex PCRs

Target Locus	Primer ID	Sequence	Concentration (μ M)	Accession Number	Location ¹	Size, bp ²
HBB	PFHBBTF2	CCTTGAAGCCAGGATGATGG	0.05	ac104389	175627	4724
	PFHBBTR2	AGCCAGAAGCACCATAAGGG	0.05	ac104389	180351	
DMD	PFDMDTF2	GTACCTCACAGCATAGAGGG	0.05	al031643	111738	4429
	PFDMDTR2	GTTCTGTGTTGTGACAGAGGG	0.05	al031643	116167	
F9	PFFIXTF2	TCTATGGAAGCTCTCCCCTGG	0.05	al033433	17217	5226
	PFFIXTR2	GCCATACGAACATGGAGTGG	0.05	al033433	22443	
MHC2	PFMH2TF2	TAGCAACTGACTCCATGAGG	0.05	al662845	32604	4814
	PFMH2TR2	GAAACCTGGATAGAGACGTGG	0.05	al662845	37418	
CHM	PFCHMTF2	ACCCTGAAGGAGACTTCTGG	0.05	al009175	57972	5404
	PFCHMTR2	CCTCACAAAGGACATAGGTGG	0.05	al009175	63376	
APC	PFAP2TR2	GACCTAGTGGGAGAAGCTGG	0.05	ac008575	127170	5234
	PFAPCTF2	TAGGCCTGCGAAGTACAAGG	0.05	ac008575	132404	
CYBB	PFCGDTF2	TCCTCACCTCATGTGTGGAG	0.05	al627245	38145	4985
	PFCGDTR2	CACGTACAATTCGTCTGGGTG	0.05	al627245	43130	
RP2	PFRP2TF2	GGTACAATTCTTGAGGGGGTG	0.05	al050307	86090	4697
	PFRP2TR2	TCTGTCATGCCAACCTCTG	0.05	al050307	90787	
FKTN	PFFCMTF2	TGGCTGAGCAGTGGAAGTTG	0.05	al158070	94837	4900
	PFFCMTR2	TTGGACTGACAAACCCAGGG	0.05	al158070	99737	
HOXD	PFHODTF2	CCTTAAGGCTTCCACGTTGG	0.05	ac009336	84995	4052
	PFHODTR2	CGGGTCTTTATGTGTCTGGG	0.05	ac009336	89047	
Al121819 flanking primers	PF819LRC	TGTTCTCACAGCCTGACAGG	0.05	al121819	105208	6328
	PF819LRD	CTGGCTTGTAGGTACCAAGG	0.05	al121819	111536	

¹ Location of primer within the sequence accession; ² Length of secondary PCR amplicon in base pairs.