

**Supplementary Data.** L1Hs Ta PCR Primers, Chromosomal Locations, and PCR Product Sizes

Name	Accession	Chr. Loc. <sup>1</sup>	5' Primer Sequence (5'-3')	3' Primer Sequence (5'-3')	A.T. <sup>2</sup>	Human Diversity <sup>3</sup>	Product Sizes <sup>4</sup>		
							Filled	Empty	Subfamily Specific
L1HS1	AC010739	2	AGGGAATGCTTATATTGTTGATGAG	ACTTCCTCAGGGTTAATAGCAAAG	60	FP	3877	159	224+
L1HS2	AC010305	16	ACCAAATATCTGGACACTTTCTGG	GAAGTCAGCAGTGGTTAATTTTACA	60	IF	6131	74	171
L1HS3	AC008572	5	GCTTCTAGAATTGGAAGTAATATGG	AGTAGCCTTGAATCATCTTTTG	56	FP	656	95	422+
L1HS5	AC020647	12	TCAACTACAAAGTTGAAGAATAGG	GTTTCCATCAACAAGATCATGTCAAG	58	LF	546	376	455+
L1HS6	AC016138	3	TTTATTTCCCTGCATCTGATTA	CCTGTTATTAGATAATGAGTCTAGTC	54	HF	402	122	219+
L1HS7	AC004773	7q11	CCTTAGACATATTCTTGAAATAG	CCAGAATATTTGGGTATTTTCATCTG	58	HF	326	169	256+
L1HS9	AC004694	7p	TCTTTCAATGGAACAAGAGGTATC	AGGGAGAGGGGACTGAGTTTAT	59	FP	6126	74	178
L1HS12	AC007538	Xq28	GTTAAAGCAATCAAGCAATCTACTG	TAACAAGGCCACTGTAGAAAAGATT	59	FP	6188	104	209
L1HS13	AC007938	7q31	ATGGGAAGGAACCCCATCTAT	AATTACTCCTCTCTTTGGCCTGTT	59	HF	745	128	220+
L1HS14	L05367	17q	AAGTGGATTAACAGTAACATACAGA	CCAAGCTGATAACTGATTATCTCA	55	IF	601	251	158
L1HS15	AC007556	2	AATGCATACCCATGAGGACAA	ATGGTGTGCACAACAAAAGAA	60	HF	6167	126	197
L1HS16	AP000220	21q	CCCTCACAGAGTGCTTGGTAA	GGGAAGGTAGGAAAACAGATT	56	IF	368	101	207+
L1HS18	AC005798	4	TTGAACAGCTTAGACTCGTCAGATA	GCAGTTAGACAGGAAAACAGAAAGA	60	HF	6174	87	212
L1HS20	AC009241	2	AATGGAAGAGCTCTCAAATTCCTTA	GCAACCATTCAAAAATTTACAACAG	61	IF	2302	62	181
L1HS21	AC008277	2	GTGTTGGCATATTTCTATTCCG	TAAAGGCTGAACCTTGCATTG	57	LF	2606	84	178+
L1HS24	AC004554	Xp22	GTGTATTTGCCTTTTGAACCAA	CAAAAACCTGTTTCACTTGATTTTTAG	59	IF	6148	101	181+
L1HS25	AC002385	7q31	GAGGACCTTATTCATTTATTGC	CCATCTGAGCTTTAGTTTTGTCATA	60	FP	6140	94	191+
L1HS26	AC003689	11q12	GCTTCAAGCTTAAAAGATGTAGACT	CCTACCCAAGTATCCACTGTCC	60	IF	2652	589	420+
L1HS27	AC007736	2	AGAACGTTGCCACATTATTTTGA	GTAGGAAGGTCTGGACTGGAGTATT	58	FP	3667	68	214+
L1HS28	AC002980	Xp22	CTTTTGTGACTGATTTCTAGC	CACTGTATATTGGAGCTGTTTTTCC	58	IF	6531	282	373
L1HS30	AL022166	Xp11	CCCTAAACAGAAAGGAAAATGAGAC	TCCTCATTGTGGTTCAAGTTATAC	60	IF	4795	97	175+
L1HS31	AC019212	X	GACAACACAAAGAAAACCAAGAT	CTTATGTCCCAAAGCTAGTGAGTGA	56	FP	2317	86	176
L1HS32	AC004911	7q	TCTCTAATCCAGCCTTTCAATTC	TGTTTCTTTTCTGTGTGTTTCC	57	IF	463	280	384
L1HS34	AC002122	5p15	ATGTCTGTCTTGACATTCCTAAGC	AATATGTAGAATGGCACAGGCTTC	58	IF	2177	284	328
L1HS35	AC010081	Y	CTACCACATAACTGAGTGACAGTTT	CAATGTGCATCCATATAGCTGTGTT	61	FP	6308	233	239
L1HS39	AC005690	4	AGAACCAATCTTGCCACAC	TGAGGAGTTTCTGAGTAACCTGGTA	60	HF	6337	155	189
L1HS43	AF172277	7q21	TTTATTGCACCTCCTGGTAAAGTAG	AGAGCACCATTAACAACACAAGAT	58	IF	6157	89	191
L1HS44	AC004883	7q	TAGCTGTGCTTGTATGTCCAGTT	GAATGAGTTTTGTGTGGTTCTGTG	57	VLF	2288	478	615+
L1HS45	AC004865	1	AATAGGCCAGCTATTAGATTTAGC	CCTTTAAACCTTTGAACACGATTT	53	FP	329	81	150+
L1HS46	AC006027	7p	CCTGTGTTCTTTTGTAAATCC	CAAATGTCTCTTCAAGGACTG	55	HF	6382	326	183+
L1HS48	AC005105	7p	CGAAAAGCTTAGGAACTGTTTGT	TAAGCAATCTTCAGTTTAGGAAA	58	FP	1242	810	420
L1HS51	AC008055	12q22	GCCCCTTACGTTAGAATAGAAAAC	TGGATTGGTCCATACTACTGT	55	FP	1094	272	239+
L1HS56	AC005908	12p13	CCATTCATCAGCCATTTGCTA	GTGGCTTTAAAACAACGAGATG	59	FP	6545	459	494+
L1HS57	AC006222	4	CAGCAAGACTCTGTCTCTAAAATGAT	GGACTTGAATTTGGTCTGTTTCTA	59	LF	589	195	284+

L1HS60	AC006465	7p	GAAGTATGGAAATTGAGTCACA	CCCTAAGCTGTATCACTTTAAACA	56	FP	445	104	246+
L1HS61	AC002288	16p12	ACGTTTGTGCTTCACTCTAAGTTCT	CAAAATACCGGGATTATAGTTGTGA	57	FP	353	68	175+
L1HS62	AC006840	4	ATTTAAAGGAATGGACATGCAACAC	CACTCCTTTGTCTCTCTCTCC	60	FP	6282	182	256+
L1HS69	AC004220	5	GGATGTTGATGATGGAGTCAGTC	TAACCATTGAAACCATTAGAGGTC	60	FP	1410	76	180
L1HS70	AL049588	Xq	GTTCAATTTGAGTGAGGGTACTGTCT	TAAGTCCCAAAAATTGCATCC	59	IF	3174	175	256+
L1HS72	AL133413	9q	CTGAGATGAGACAGCAGGTCTTC	TCTGCTGAGATTCTCCATTACC	60	FP	825	147	221
L1HS73	AC018822	3p	ATAAGGAGCCTAGGGAAGAACTTTT	CAAGCATGCCTGAAACATCTAT	55	HF	1126	462	162+
L1HS74	AC011990	17	CTGGACGTATTTCTTACAGAGTTGA	CCCTAAGTTATTTCTTGAGGCTA	60	LF	6163	125	186+
L1HS77	AB020867	8p	TTCCTAAATGGCCTTACTATCCTTT	TCAGAAGTGCTAACACTCTAGTAGGA	58	HF	990	78	233
L1HS78	AP000084	21q22	TAGTACCTCCCTTAAAGAGCTG	GAGGAAAAGAAAAGTGCCTGATA	59	IF	374	107	175+
L1HS81	AP000962	21q21	AAGTGTATATATTGGAGCAATTC	ACAAGACAATGCCAATTTAAGAGA	60	FP	848	148	401
L1HS85	AC008132	22q11	TTTGTATGCCTTGTGTTTGTATTG	AGGAGAGTCTCATCTCCAGAGTTAC	58	LF	593	79	183+
L1HS86	AL121825	22	TATTACACACAGAACAAGCAACT	GGAATATTCTCCCCTATCAGGAAT	60	HF	6527	483	227+
L1HS91	Z84572	13q12	ATACGTGCAAAACAGGAGATTTGA	TGTTTATGGTGAAGGATAAGTCTCA	59	FP	1619	78	167
L1HS92	AL022153	Xq	ACAATCCCTACTTCAGAAAGTT	CAACACTTTGATCATGAATAATAGCTC	57	FP	859	121	206
L1HS94	AL031586	Xq	TCGTATGAATAACCTTGTGTTCTTG	TTTAGATCCTCGTCACTCAAAGTGT	57	FP	6250	151	264
L1HS95	AL023284	6q	GGAAATCTCAAGCTCAAGTTAAAA	CTTTTAAAGTGTGTTCTCACAGTGG	60	FP	717	119	320+
L1HS97	AL030998	Xq	AACCAAACCCACAATCAGTAGAA	CTAGCTAAAGGTTTGCTATTTTT	58	FP	1640	182	407+
L1HS98	AL022099	6p	ATCTGCATTGGGCCAAGTTTT	TCTCCTGTAAGACAGCACCATA	60	FP	1561	129	242+
L1HS102	AL096677	20p	CCATTTGCCATAAATAAAGGCATC	ACTGTTACAAGTTTCCCAAATGT	59	FP	6741	611	542
L1HS104	AL096799	20	GAGATGTGGTTTTGTTTGAAGCTG	GCAGCTCACATAGTTTAGAGAAGAT	59	IF	6196	131	219+
L1HS106	AL117339	10	CTGACTGTTGAAACTTCTCCATTG	CAATAGACATGAAGGCATGGAAG	57	FP	3103	378	345
L1HS109	AL137191	14	GCCTTTCTATCTTTTGTCTTGGT	GACACATACCAATTACAGGCAAAG	59	FP	6549	501	381+
L1HS110	AL078623	20	GGATTCTGACCTTATTCTAACAGCA	AGTTGACTGTTGGTGTGATTGTGT	56	HF	6263	212	253
L1HS112	AC018755	19	AGGTTCCATCTCTAATACTGGATAA	TGATCACTTTGTTGTTAAGATGGAG	60	LF	1686	102	170
L1HS113	AL133386	6p	AGTTTTGGCCTGAGAGAGAAGTAGA	GGTAGGCTAGAGATCCCTCAATTA	55	FP	405	184	328+
L1HS116	AC024610	18	CTGTGCACTTTTCCATATGTTTGAC	TCTAATCTATGGTGGATGCTCTTTC	56	FP	252	76	189
L1HS117	AC005885	12q	TGCAGTGTCTATTTATGTCGTAGGT	CGAGAGAGGGAGGAAAAGTGAG	57	IF	6629	535	176+
L1HS118	AC020599	4	ATGCCAGAAATACCTCTTTTACCTT	CTAAGTGCAATTCTCTCAGATTTTG	60	IF	6321	286	277
L1HS119	AC005739	5	GGCTTATTTAGAGCACCTGGATTTA	GAGATCCAAAGCTTATGCTGTAAGT	60	FP	904	243	257+
L1HS124	AC004499	20q	TGACATAATTAATGGAGAAAACCAG	GAGATCCCTGTCTTGTGTGAT	60	FP	749	515	373+
L1HS125	AF001905	Xq25	CCTCACGTTTCTCCACATTGTA	TTCTGGCCTTCATAGTGTTTTA	60	HF	332	96	169
L1HS131	AL163152	14	TTGACTGTGTACTGCCAGTCTCT	GTAACCTACCAGTTTACAGTTACC	58	IF	381	179	212
L1HS132	AP001693	21	CCCTGATACACCAGTATATCTTA	GAAAAGAAAAGTGCCTGATA	56	IF	753	486	173+
L1HS133	AC008716	5	CATGGTGTCCAGTGTTAAAAA	TATCTCTTACCTCTTCTGCCATA	59	FP	3351	821	738+
L1HS134	AF265340	16	CACAGTCAACTCAACCACTGAATAA	AAGGAGATGGAAGTAAGTGCAAAC	60	FP	751	433	603+
L1HS135	AL137804	11p	TTTTTGAAGGGAGTACAGTAATAGGT	GCCTTCCATAGTTTCTATTTGC	58	FP	6475	429	500+
L1HS150	AP000966	21q21	CAAGAACAACGAAAATGCAGAT	CCCCTCAGTCTCTGGTTACCTA	58	FP	642	89	141+

L1HS151	AC019205	6	CTTTGATCAGTTCCTTGGAACTAGGA	CCTCTATGCCTTATTCATGCTTATC	60	FP	573	405	476+
L1HS153	Z84814	6p	CCAATTCACCTTTGTCTCCTAGAAAT	AGTTCACGAAGTTGAAAGCTTATGT	60	IF	931	169	219
L1HS155	AC019050	2	TGGCATGTCAATATATACCTGAAGA	GGAAAACAGAAATAAAAGACGGACA	60	FP	7004	596	720
L1HS157	ALO49842	6q	ATTCAGATTCCAGTAAGCTGTGTTT	GAACCTTTGGAAAATTCACAACCTACC	60	HF	892	143	245
L1HS158	AC008467	5	CAGCCCAGAGTAGTTCATGTTTT	GAAGGAAAAGGAGCTGCTTAGATA	59	IF	6194	147	207+
L1HS160	AL121938	6q	CTAAATAGGCAGAGGAAAGGAAAAAC	TAAACTTCCAAGAGATCAGCACTTC	60	HF	1071	99	225+
L1HS163	AL139114	9p	GGGACAGGGGTTAAGATTTTATTTT	AGTTCTCAACTGTAAAGGCAGTGTG	60	IF	2898	85	251
L1HS164	AB045357	1q	GGAAGGAAGTGGGGATAATAAGTAA	CCCAATTCAGTTTCTTCATTCTATG	60	FP	1507	193	267+
L1HS165	AC011666	1q21	CACAGTGATGGAGTTACAATCTTTG	GCTTTAAAGTCAGACAGGCTTGAGT	62	FP	1509	200	276+
L1HS166	AC021017	8	TGCCTGAAATGCTATTGGTAGTATC	GTGCCAGCCATAATATAAA	60	IF	6204	102	251
L1HS168	AC009492	2	CTTTTTCAAGGCCATCTGTGAG	AATCCTTACAATGAAAAGGGTGT	61	FP	666	97	180
L1HS169	AL118519	6q	TATTGAGGTGTAACCAGCATAACAAT	CCACACGAAAGATATATGAATTGC	60	IF	6289	214	288
L1HS171	AL137145	10	GAAAGTTCATGAAAGTTGTGATGC	ACAAGAGAATCTATCTCCTGAAGAA	60	IF	6157	91	198
L1HS172	AL133479	9p	CTAAGATCAGTCACAGGCTTAATGA	CAGGTGCAAGTGGTTAATTTTC	60	IF	1326	111	193+
L1HS173	AL359218	14	CACCATCTAGTGATTTTATGTTCTGC	AATAATCCCCATTGACTGTGTAAGT	55	HF	319	123	217+
L1HS177	AC017015	18	CAAGTTCCTCACCAAATGAAACTAC	TCCATTTTACTGATGTTGAATAGGC	58	HF	693	165	273+
L1HS178	AC023480	3p	GAATATTGAGCTTTCTTCACCTTT	CAAGCATGCCTGAAACATCTAT	60	HF	508	54	162+
L1HS180	AC009276	7	GGAGTGTAGAATACTGGGGAAAATC	CTTATTTCCCAATGAGCCCTGTA	56	IF	507	84	225+
L1HS185	AL157837	1q	CTGGCAGTTCCCTCAATGTAA	GAGTAGCTAGCAAAACAGGTAATGAA	60	FP	604	108	214+
L1HS186	AL359332	14	GGTCTAACAATATTCATGATGC	CCTCTTTTACCCTGTGAAGAAAAT	60	FP	6313	249	205+
L1HS191	AC007972	Y	TCCTCCAAGACCCCTCTAAAAATAAT	TTTTGTCTCCCTGAGTAAATTCTG	60	FP	2645	122	251
L1HS192	AC018680	4	TTTCACTTTTTCTATGGTGATGAGG	CTTAGAATGTTACACTTTTCCGACA	60	FP	6218	155	196
L1HS193	AC018503	3	CTACAGTGGCATTCTTTTAGGACAA	TATACAACAGAACTGAATCACTGAC	60	FP	6296	239	288
L1HS195	AC044791	15	GCTTACATCTCAAATCTGGTACCTT	CAGATGATTAAGGTGATGGTTCT	60	FP	1554	183	209
L1HS197	AC027332	5	TGGAGTAGAATCAAGCAAAGTAA	AGAGTTTATGATAGGTCCTTCT	60	HF	6226	97	260+
L1HS202	AL391097	20	TTGTACCTATGATTTGTGTGATAGGC	GCTCTACATAAAAAGATGTTCCACCA	60	FP	990	754	435
L1HS204	AL157815	13q	ACTAGTTGATGACAACTGGATGTG	GAGTGGCATAATCAATTGCTAGAGA	60	FP	647	126	182+
L1HS206	AL355382	6	GTTTGTCAAGTGACAGGAATCTCTT	GCTAAGTCATCAATAAGCCCCTAAT	60	FP	2704	154	186
L1HS207	AL354861	9	CTTTGCATATCTCTGTCATCCTACA	GATGAGATCATTACACACTTTCTG	60	FP	6208	164	170
L1HS208	AL354793	X	AACATTGGGAGAAGTTTGCAGTAT	CCAAGTTGTTAAGCACTCCATAGTT	60	FP	6639	570	689+
L1HS209	AL158159	9	GATGAGTTATCTTTGACGCTTTGAC	TGATAGATGAATGAGCTTTATGGTC	57	FP	508	118	213+
L1HS212	AL157700	Xq	TTCTAGCCCTCTACTAATGTCCTTG	TTCTAAGGTAGCTGCAGATAAGTGG	60	FP	1045	184	234+
L1HS213	AC087432	3p	AATGCCCTGATAAAAGTAGACACACC	GTGGGAATATATCTTCTGGGTTT	60	HF	1710	89	188+
L1HS214	AC007483	3	TAGCTGAGAAACCATAAGCCTAGAA	ACCTGAATGTCCACTCATTCACT	60	HF	4159	328	330+
L1HS216	AC023880	7	CTATACCAAATGCAGTCAGGATGTT	TCCCATAACTCTGTCACTAGAAA	59	FP	714	197	228
L1HS218	AC016910	2	TCTTACAGCACTATTCAGTGTGTTGC	TTCCTCTCAAGGAACTCAAACC	60	FP	6136	82	174
L1HS220	AC016635	5	ATTGGCCTTCAGAAGTGATTAAGAC	TAGATAGCCAGACAAACAAACCTTG	60	LF	6244	135	260+
L1HS222	AL445932	6	TCTTTCTCCTCTTGAATGTCTCAG	AAGATACTGTGCTTCACTCTTCTGG	60	LF	6195	118	238

L1HS224	AL358934	9	GATCTGAATCTTTGCTCTCCAGATA	ACGTGGTACAAAAGAAAACACTGTC	60	FP	1121	126	215
L1HS226	AL353153	6	CCCTAAGCCTGTCCAGAAAGTTAGTATC	GCCATGAAAGATAAAGGAGATAAGAG	60	LF	2114	120	359
L1HS228	AL353657	13q	AATATCCACTACCCAATTCCATAGG	GCTGCAATTTAGCAGGATTTCT	60	HF	1383	184	205
L1HS231	AL354896	13	GAGTATGAGAGCTCTGCTTTCTGTC	CTTGAAGGACTGGGATACTTGAAA	60	HF	2289	379	481
L1HS232	AL365367	1p32	TGCTACTCCAGTGATAGAAGCTAGA	ACAGTTAACTTCAAGGCAGGTTGAC	60	FP	1181	69	214+
L1HS233	AL357507	6	TAGTTGTCTACAACCAAGTGCTGAG	TCTGCATAGATCAGGAATTCTAAGG	59	IF	1232	81	174
L1HS235	AL158193	13	ACAGGATCTTAAGGTTGAAGGTTTG	GGTCTACCCAAAGTAGTCAAGAAA	59	IF	6441	420	179
L1HS238	AL357519	6	GCAGGTAGGATACATGTAAGCATT	ATCACAGCAATGGCATATCATC	60	FP	2155	374	360+
L1HS241	AP003112	8q23	GATAATCAGGTGATTGTGAAGTGTG	CTACCACCCTTTTACTCCCTTTAC	60	FP	366	148	206+
L1HS242	Z80899	6p21	AGTTCACGGTCTCTATCTCTCCTTT	AACCTGTCTTTGACTGTTGAGC	58	IF	576	125	276+
L1HS243	AC019041	2	CACTAACATTTCTGCATCTCACAATC	GTGGGAGGACATGAATAACACAT	58	FP	6148	96	202
L1HS245	AC017040	2	AAGGCTCTTATCACAGGAAGTACC	ACGTTAATCACCGATCATTGC	60	FP	2141	294	263+
L1HS247	AC009274	7	GTGTGAAGTATTACCTCGGTGTTG	CTGTGTGGAGCAATAGTAACCAGAT	60	FP	2238	286	275
L1HS248	AL360236	6	AGAACAAGTGAGTGGCTAAAACCTC	AGCCAACAATTTCCCATCTC	60	FP	6705	658	710
L1HS250	AL162373	13	AGTACCTGGTGAGTTCTCCTCAAC	GGTCTTTTGTGAGATGCATACCTG	57	FP	2055	110	194+
L1HS258	AC024905	3	GATTGGACTCCATTTCTCTTGTAT	ATAAATTCTGGACCTCTGCTTAAT	57	FP	1717	1011	643
L1HS260	AL354982	9	GGCAACGGAATAATAGCTTCA	GTCAGCACTCCCATCTTAAATGTCT	57	HF	6461	358	510+
L1HS262	AC013579	1	GATCCCTGTGTCTGGAGCACT	GGAATTCATGGAGAAGGTGAGTT	60	FP	1148	97	186
L1HS264	AL391643	9	GAGGAGGAAGAAGGCTGATAATATG	GACAGCCACTAAGTTAATGAGATCC	60	FP	284	133	174+
L1HS265	AC018938	9	GCATTATTTCTGGAGCACTCACT	GTCTTGTGCTATTAAGCCTGGTCT	60	FP	6087	105	207
L1HS268	AC025428	10	CTTTGCTCTCTTGCTCCATGTAT	TATCTGTTTACCAACCCATCTCACC	60	FP	6235	90	283+
L1HS272	AL157787	10	CTATGTCCTAGCCTTCCCAGATG	AGAAAAGACAAGACAGGATAGGG	58	FP	1125	201	223+
L1HS274	AC027118	10	GCACATGGCTTCTTAGCTAACTT	CTTTCTTGATAAATGACTCTGTCC	57	FP	2081	611	317
L1HS282	AP001002	11q	CTTACCTCCAGAGCATGCACATTAT	CCCCTCCTTCTCAATTTAAGGTTAC	61	FP	6448	156	249+
L1HS284	AC018619	11	AGATAGGAGAATCCTCTGGTCTTCT	CTATTGTTGGTACTTGGGTCCT	58	FP	1877	174	268+
L1HS287	AC021304	11	CCTTTTATCTGAAATAAGTGTTGG	CTTCTTTAGCTGGGCTGTTCTAAG	61	VLF	1693	95	216+
L1HS291	AC025410	6	CTCCCACTACTTTATGGGAAGGT	AGGACTTCCAATTCCTAGTATGCAG	58	HF	5658	216	271+
L1HS292	AC073915	12q	GACTCCCACTAGCTTCTTTGACTT	GAGACTCAGTTGACAAGGAGTTACC	60	FP	1117	117	213
L1HS293	AC026831	12	TTACAATGGATACGTTAGACAGCTC	CCATAATTGGTTAGGATGATGAGAC	60	LF	2517	417	317+
L1HS294	AC027442	12	CTTTACCTGTTCCACTAATCAC	GGCACAAGATGGATATAAAGGA	57	FP	6154	103	168
L1HS295	AC012144	13	GAGGAATGGTTGAACAGCTTG	ATGTGGCTGGAGAAATACCTCTAAG	61	FP	713	100	208+
L1HS297	AC064857	12	GTCCAGAGTGATGCATTTTATTTGG	GCATAGTCATTTAATGCATGTCAGC	58	FP	771	461	549+
L1HS298	AC025880	12	ATATACCATACTCCTTTCCCTTCC	TGAGCCCTGTATTTAATCACTTGT	60	LF	1037	80	235+
L1HS301	AC027382	1	CTATCCCATAGATGGTGGGTAGAAT	GAGGAAATAGCACAGGTATGGTAAA	61	IF	1770	685	431
L1HS303	AL451063	1	CTATGTTCTGGGAGAAGAGCTGAT	CTAGGGTCAGAAAGAACTTTGATGT	62	FP	780	87	170
L1HS305	AC016371	1	CAAAAAGCAGCCCTATATTAGC	GCCTGCCTCATTATCTTTTCATT	58	FP	3998	415	409+
L1HS308	AL390200	1	CCTACTAGGCCCTCTCTTTTGTAT	GTCTTGTTGTGCCAGACACTTTA	62	IF	3441	455	652+
L1HS314	AL357975	1	TGGCTAGCAAAAAGGTGGAC	AGGGCAGAGAAAATGGTCA	58	IF	6215	109	255+

L1HS315	AL139137	1	AAGTCCCAATTCCTAGTCTGTCT	GACACAGAATCATGTCACAATACCC	61	FP	6286	241	332
L1HS316	AC026905	1	CTTTAGCAGTTTTTCATGCCTCCT	AGGTTGATGGTAACCTGTAGGAAC	59	FP	6240	173	245
L1HS317	AL356323	1	CTCTGCCTCAAGTGTGTCTTGACTA	GAGAACACACCCTTGCTCAGTAAAT	59	FP	901	711	626+
L1HS320	AL357973	1	GGGATTCAAATGGGAAACAAG	CTCCTTTCCAGTATCTGCTCTTATG	60	IF	1748	140	305
L1HS326	AC025702	1	CTCACCGTTATCAAAGGGTAGAAAC	CTAGCCCCAAATTTGAGAAACAG	60	FP	6250	156	289+
L1HS327	AC018874	1	GGTACAATGTAATCATGGGTTGG	GAGTTAACCGTTAGTCCACAAGATG	58	FP	4695	172	413
L1HS329	AC058795	1	CTTCACCTCTGAATGACACACAT	GGCTTCATAATGCATCGCTAA	60	FP	1188	454	365+
L1HS332	AC008110	1	CATGTTAGAACTGGCTCAAGTATCC	CCTGCAGAAATTTGCCTTTAG	58	IF	2850	87	227+
L1HS334	AC026253	2	ACACTTCTGAGAAATTTCCCTGTG	TTACTCCCTCTTACTGTCTTGGTG	60	FP	1095	199	341
L1HS335	AC023434	1	CATGCATCTCTGAACTACTGACTTG	ATAAAAACCTGTTTAGGCCAAGG	60	IF	1276	395	284+
L1HS337	AC010890	2	GGTACAATATGAGGCATCACGTA	GTAGCATCCTTTATAGCTTTGCTGA	60	HF	3174	224	329+
L1HS342	AC018591	2	GAGACTCAGTTGACAAGGAGTTACC	AAACAGGACCTGCTGTCCATAA	60	FP	1087	78	183+
L1HS345	AC073509	2	CACAGCATTTACCAAAGCACTC	CTCAGTTCATTGCACAGTTTGG	60	LF	2587	192	229+
L1HS348	AC018378.3	2	GAAATGGGAAGAGGAGTTGACA	CCTATTTTTATCTCAGCTGATGTCG	60	HF	748	523	526+
L1HS349	AC009963	2	GGAGCTGGGAGAATTATTGAAAC	CCACTCTCAACTACTGTCCAACAAG	60	HF	229	114	182
L1HS350	AC022605	2	TGGTATATAGTTCTAAGGACCCACAG	GCTACTTTTGCTTCTGGGTGTT	58	FP	725	243	331+
L1HS353	AC019324	2	TCCATGATAGAACACACTCTTCC	AATCCCTGTCAAACCAATCC	59	HF	1822	426	167
L1HS356	AC009290	2	CATCCTGTTGAAGAACAGAGAGATG	ATAGAGTGACCAGAACTCCAGAGA	60	FP	6290	156	250+
L1HS358	AC019130	2	GAGACTCTTTGGACTCAGAGTATAACC	AGTCTGTGCATACCAGTTATTGGAC	59	FP	6621	128	673
L1HS360	AC023416	2	GAGGTCTTTGTGCAGAGGTATAAGA	CTCACCAACATCAGTTTCCTTTG	60	IF	3222	153	218+
L1HS361	AC073642	2	AGCCCATTAGATATATGTGGCTGT	CTTTTTATATTGGTCACCCCAAC	61	FP	6319	281	372+
L1HS363	AC010913	2	GTTAGACAGCGACATGCACAG	ACCTCTGTGCCTTACCAAAAAC	60	FP	577	223	198+
L1HS364	AC026860	3	CTTAGCCTCTGTCTTTAGGGAAAAC	CATGACCAACGGTGCATAATA	60	HF	6139	97	170+
L1HS366	AC083853	3	AGAAAACCTCCAGACACCTATCC	CTATGTCCTAGCCTTCCAGATG	60	FP	1088	163	183
L1HS367	AC078805	3	GACTCATATTACCCTGGACAACAAC	AGTCTCTCCTTGCTCAGTTTGGTAG	60	FP	6784	83	401+
L1HS370	AC068365	3	GCAATCAGTTTCACACTCAACTG	CATGTGATCTATTGTGTACCATCAGG	58	FP	3436	146	323+
L1HS372	AC022077.13	3	GAAGAGAAAGAGGAAATAGCACAGG	CTATCCCATAGATGGTGGGTAGAAT	60	IF	1779	599	431+
L1HS373	AC022838	3	GAAAGAGAGTTCTCTGTACCACACC	GTCATGTCCCAACAGGACATTT	60	VLF	6294	215	231
L1HS375	AC023139	3	TGTGGTACAGTCACTACAAAAG	GATAGCATACCCATCATGCACT	60	IF	3862	430	469+
L1HS377	AC078856	3q	GGGAGATGTAGAGTTTTATGTGACC	CTAATGTGCTGGGCAAACATAAGAT	57	FP	577	139	201
L1HS378	AC069225	3	CTCCCCTTTTTGCCTTACTTCT	CTTACTTGCAATAGCCCATTAC	60	IF	5569	646	369+
L1HS382	AC055732	3	GCAGACACTAGAAGCTTTTGCAT	GCCACAAAATCTGGCACTTATAG	58	FP	3357	426	185
L1HS383	AC017085	3	ATTAGTCAGTAATAGAGCCCCTGT	AAAGACTTCTTTCCAGCTCTACCC	60	FP	6493	267	515
L1HS389	AC024216	3	CATGTAGAGATGATCTTCAAAGCTG	GCCTGATAAAAGTAGACACACCTG	60	FP	1782	162	263
L1HS391	AC022040	4	GTGGACATCAGAGTATCCCTTTCT	AGAAGGGTACATGACAACCTGGTTAG	60	HF	889	113	203
L1HS393	AC013336	4	TACACAGAATCTGATGCTAGGAGAG	CGGGAACATAAAGTCATAGCGTAAC	61	LF	751	277	412+
L1HS395	AC067804	4	GTTGCATTTTGGAAAGGAAGG	TAGTGGAAAGACAGACAGTTTAGGG	61	IF	1218	119	214
L1HS396	AC007512	4	AGACTCAAACCTCAAACCTCTGTGT	TCACAAGCAGACATTTCTTACTGAA	60	FP	6643	562	373+

L1HS397	AL161439	6	ACTCATCCTAGAGCTTTACCCAGTT	CACAAAGTCAACAGGTTTGATCC	58	FP	1085	259	231+
L1HS404	AC021700	4	CCACCTTACGTTACAGCTGTTAAT	CGGTGATTAGGTGACAGCTTTT	60	LF	3262	163	231+
L1HS405	AC032017	4	ATCAAAAGTCCTGTGTGTTTGTCTT	GAAATTTTGTAGACATAGCTGTCC	60	FP	1206	396	202+
L1HS406	AC067842	4	GCAAGTTTTACCCATAGTACACAGG	GTATGTAGAAGGCAGGGGTACT	60	HF	3589	209	302
L1HS407	AC041010	4	CTCACCAGTACGAGAAGCAAGTT	TCTGACCTAGGGATGATTCTTCA	60	FP	413	227	217
L1HS408	AC019133	4	TTTTAGCCAAGCTCTTTGTTCC	CATTATGGCAGCGTAGACATTG	56	FP	2059	106	209
L1HS410	AC011633	4	GCTAAGCAATGGAGGAAAATATCG	TGTACATGGTGTGAGGTATGAA	57	IF	6211	100	244+
L1HS411	AC073338	4	ACACACACACGATGGAAAGTATCT	AGCACATCCTAAATCTTCTCTCT	60	FP	2670	136	246
L1HS413	AC023332	4	TCATGAGCATCACTCTTACCATGT	ACTCAGCTGACTTGCCATAAATGT	60	IF	6199	127	191
L1HS415	AC009816	4	TCAGACCCATATATGAGCATAACC	GCTTAGAAGAATTTTAGCCAGGTG	56	HF	1360	590	476+
L1HS416	AC068256	4	TTAGTCACTATGACTTGAGCCACTT	TAGTGATAGTGTAGAGAGGGGTTG	61	FP	822	238	284
L1HS418	AC011981	2	CGATTTCTGTCTTTGTGAACGTAGT	CCTTACAGAGTAGAAATCTCACGAT	60	IF	6380	328	358
L1HS423	AC022672	11	CTCCCTGTCTTCTGGGTTAAAATA	GGAAGTCCCCTTTTTCAGTAGAG	60	HF	5680	201	248+
L1HS426	AC023921	5	AGATTCCCTTTGGTATCCAAATCAC	GTTGCCATACTCCGCATAAAGTC	60	IF	3394	204	252
L1HS427	AC015990	4	TACGGGCAAAGACTGAGAGTACTAA	TTCAGCCTTCTGACATCAAAC	57	IF	2230	139	220+
L1HS430	AC024963	4	CAGAGAACCAACATGTAGGAACAA	GTTACAGGTCAAAGGAGGTCTGAG	60	LF	4034	127	223+
L1HS434	AC010437	5	ACCTGGGCCACATTTATTTTTC	TGTAGAAGAAGACCCGTCGTTAG	60	FP	2637	250	246+
L1HS435	AC026403	5	GACTCAGTTGACAAGGAGTTACCA	ACACTAGCTTCTTTGACTTCACCA	55	FP	1115	111	211+
L1HS437	AC023526	5	ATCTATCATTTATCTGCCCGTCT	ACAAGGATTAGCAGGAAGTCTGTT	60	IF	2954	256	201+
L1HS438	AC011433	5	TCCTCTACCAACCACATAAAGTA	ATCCCTTGGATACAAAGATGTGC	60	FP	1909	570	345
L1HS442	AC027325	5	GACGGTTACTCAGAAAAACACAAG	GTAGATGCCACTGTTACCCTGACT	60	IF	907	224	185+
L1HS443	AC021600	5	GCTAGACTCTCTACCTTTGGCTTT	TGATACCTGACTCTATGCACCACT	56	FP	891	261	382
L1HS444	AC027315	5	TTATTGGAATAGCTTCTCCTGTCC	GCTGTTCCCTAACTCTAGTCTCCA	60	FP	464	303	296+
L1HS446	AC010314	5	CTCGTGACATTTCCATCATATAGC	TTAAGTCACCTAAGGGTTGTAAGTG	56	LF	6142	109	182+
L1HS447	AC018759	5	GTACATCTCTTTGGACACTTCCACT	GTTAAGTCCAACATCTCTGTTCTG	59	IF	691	560	386
L1HS448	AC016545	5	GTCAATTAGAGCATGAAGAAACCAC	GTACATCTCTTTGGACACTTCCACT	60	IF	652	525	382+
L1HS449	AC011378	5	CTAGGGAGGTGAAAATTCAGATGT	GCATGTTGCACAACAGTATGTA	60	FP	1797	281	315+
L1HS450	AC011413	5	GTGAAGACTGTTGGTCAGTTACTTGT	GTCATTGAGATTGGCAGGTAAGAG	60	HF	6179	128	189+
L1HS455	AC027643	6	CATACACAAGGGCGAAGAGTAAA	GCCTCTTTTACATCAGTTACCACTC	60	FP	259	110	213+
L1HS456	AC026966	6	TAACACTTAGTGATTGCTGGGAGAG	GGACAAGGTGAAGTGGAAACTAGA	60	FP	1641	121	215
L1HS461	AL358992	6	ATCCAGCAAAGTATCCCTTAAGTA	TCCTGTCCCAATTCTTTGTATTAT	60	LF	4143	324	417
L1HS463	AL391336	6	ATTAATCTGTGTGGGAGTGG	AGGGTGACTTCAGTGATATCTTCA	60	FP	6304	247	346
L1HS469	AC020586	UL	GGTACTGGCTGTTTCAGTATTTTT	GTCTCAAAGCCCATTTTCATAGTTC	60	FP	6458	101	212+
L1HS479	AC079855	7	CACTCGAAGGGTAAGTGAGATTTT	CCACTAGCGCACCATTTTTCTAAT	58	FP	6223	146	276
L1HS480	AC021836	4	AGAGGTAACCACTACCTTGCAACT	GCCTCATGACAGGAGAAGAGATAAA	60	IF	2701	272	265
L1HS485	AC027189	8	CTCAGTTCCACATAAACCTTGACA	GAAGCAATTAACCTAGCAGTAGGAC	60	FP	548	74	183+
L1HS486	AL356516	9	CCCTCATCACAAATATCTGAGAA	AGCTGACAGTCTAGTGAATGAGGTC	60	IF	905	139	196
L1HS488	AL353649	9	CAAATTGTCAATGCTAACCCTCC	GGAAAAAGGCACCTTTGGCTTATC	62	FP	6787	724	472+

L1HS489	AC009284.2	9	TCTCCAGAAACCATCACAGTAAGA	AGGAGTTGAAAGTAGGATGGGTTT	60	FP	322	104	202+
L1HS490	AL358937	9	CAGCTGTCTTGCTAAGAATCCAT	AGACCACAGACTCTTTGAGGGTAAG	60	FP	2289	397	206
L1HS493	AL138764	10	GACTACCTTTCTGCGTATTCCTTTC	GTCTAACAGGTACACGAGACTCCAT	61	IF	1603	111	241+
L1HS496	AC024929	8	CCTTTGGAAGAGAAAAGAGGATATG	CTCCCAATGGAAGGAAGTGTAT	60	FP	617	70	177
L1HS497	AC060775	8	GCCTAGTGGGAAGACAAAAAGTATT	GCTGTAATGTTAACCTCGAAGTCGT	60	FP	950	346	439+
L1HS498	AC067844.3	8	AGGTTTCCCCAAAATTTACCC	CTGATGTGTGGATTCACTGTTCTT	58	FP	6281	184	295
L1HS500	AC009630.5	8	GTGTTGCCTTCACCACAATAGTA	TTTCTCCGAGTACAGGTTACGAG	60	FP	1145	206	227+
L1HS501	AC022207	12	GTTGGCAACTTACTCTCAAATGG	AAATACACTCGACTGGCCACTAA	60	FP	6254	199	306+
L1HS503	AC055118	13	GTGAGGAATGTTGAACAGCTT	TGTGGCTGGAGAAATACCTCTAA	60	FP	713	101	206+
L1HS508	AC048381	15	ACAGAACCTTTTAGAGGGGAATCG	CTCCGTGTGGTAAAATTAGCTGT	58	HF	6144	103	184
L1HS509	AL356017	14	CACTCATGACTGCCTGACTTCT	CAGGGTACTCTTCTGTTGTGG	61	FP	443	131	220+
L1HS512	AC021839	14	AAAGAGACAATCCACAGCATAGTTG	GATTTATTCTTCATGGAGATGTGC	61	HF	2071	722	266+
L1HS513	AL160156	13	CCAACTTGAGCCTCCTGTAATC	CCTTGAAATAAGCAGGAAGAAGC	61	IF	809	142	235+
L1HS514	AL138961	13	CCTCAGCTTTGGATCCTGTAGTT	AGAAGAATTGGGTCTGTTGAA	60	FP	6670	334	361
L1HS515	AL163537	13	GGATGGTAAAGGAGTGGCATAAT	TGTGGAGCCAGATCTTTTAAT	60	FP	637	106	193
L1HS516	AC044907	15	CCACAGTTTACACAGAAGCTGAA	GAAGGAGTGGATGTGTTTCAGTAA	60	IF	6151	101	212
L1HS521	AC067951	15	AAAGAGCAACCCTATACTTCATGC	CACCAAAAGGAGAAGCCAATAAAG	60	FP	1804	156	438+
L1HS523	AC009658.6	15	CGTGGAAGATGTTACGAGGATTA	AGAGAATGCGATGTCGATTAGAG	60	FP	570	105	204
L1HS526	AC025289	16	ACCCTCCAAGGTAAGTGAATCTTA	ATGCCATGCTTGTAGCTACTAC	60	IF	6076	223	324+
L1HS528	AC009021.4	16	CGGATGGGAGCACAAAATTAATA	TGCCTACTAAGATACCTTGAAAATG	61	FP	991	172	278
L1HS529	AC022164	16	TGAGTAATGTGGCGGTTTAGTTC	AACCAGTCAAGAAGCCAAAGAG	61	FP	6143	116	193+
L1HS532	AL356138	20	CCTCTAATCTATGGTGGATGCTCT	TGGTAGGGAGCTGGTAAAAGTCTA	61	FP	308	175	242+
L1HS543	AC009267	18	TACATTAGTCTGCCTCTGATTCCA	GGCCATTCTTTTCATCTGTTGTAG	61	FP	547	99	183
L1HS545	AC007768	18	TGGGAAGTCTGTTACAGTTTCAC	ATTTGTCATGATCACAGCCACCT	59	FP	2514	95	216
L1HS552	AP001564	18	CAGTGAAGTCTTTCTCACAAATC	CAAGAAGTTTCTGGAGTCTCTC	60	IF	4144	123	235
L1HS557	AP001019	18	ACAAAAGCACCTAGAAGCAGTCAT	CTTTTTCTCTATGCTCGTGGTAT	60	FP	2277	85	229+
L1HS558	AC015819	18	TGCTTTCTTTCTTTACATAGATCA	GCAGACACGAATCACAGTTTGTAT	61	HF	983	128	203+
L1HS561	AC013620	14	TACCCATTTAAAGGGCAAAGTG	CTACCCATTTAAACCACTAATGCTG	61	LF	430	114	239+
L1HS562	AC019175	X	TGTCTGTTTCAGTCTTTCTCACAT	AGCAAAATGTATGCCGAAGACT	59	FP	6170	115	181
L1HS564	AC034155.5	X	TGCAATTGACATAGATACTGCAGAG	CCCTTCCCTTTCTGTACATGTCTT	61	LF	2085	471	425+

1. Chromosomal location was determined from Accession information or by PCR analysis of NIGMS monochromosomal hybrid cell line DNA samples.
2. Amplification of each locus required 2:30 min @ 94°C initial denaturing, and 32 cycles for 1 min 94°C, 1 min Annealing Temperature (A.T.), and 1 min elongation at 72°C. A final extension time of 10 min at 72°C was also used.
3. Elements represented here are classified according to allele frequency as: high frequency (HF), intermediate (IF), low (LF), very low (VLF) or "private" insertion polymorphisms, or as fixed present (FP) insertions. Fixed present: every individual tested had the LINE element in both chromosomes. Low frequency insertion polymorphism: the element is present in no more than 1/3 (33%) alleles tested. Intermediate frequency insertion polymorphism: the element present in more than 1/3 (33%) of alleles tested and no more than 2/3 (67%) of the alleles. High frequency insertion polymorphism: the element is present in more than 2/3 or 67% but not all alleles tested. Indeterminable data is denoted (-).
4. PCR Product Sizes: Empty product size is calculated computationally by removing the L1Hs Ta elements and 1 direct repeat from identified filled site. Subfamily Specific product size is calculated from internal subfamily specific primer located in the 3' UTR to the proximal 3' primer. In cases where target site duplication sequence were not found flanking the element PCR product sizes may

vary from those reported. Elements with subfamily product size denoted “+” were found in 5′ → 3′ orientation in GenBank and are assayed using the internal subfamily specific primer and flanking reverse primer. All other elements were assayed using the internal subfamily specific primer and flanking forward primer.