

Transduction-Specific ATLAS Reveals a Cohort of Highly Active L1 Retrotransposons in Human Populations

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ABSTRACT: Long INterspersed Element-1 (LINE-1 or L1) retrotransposons are the only autonomously active transposable elements in the human genome. The average human genome contains ~80–100 active L1s, but only a subset of these L1s are highly active or ‘hot’. Human L1s are closely related in sequence, making it difficult to decipher progenitor/offspring relationships using traditional phylogenetic methods. However, L1 mRNAs can sometimes bypass their own polyadenylation signal and instead utilize fortuitous polyadenylation signals in 3′ flanking genomic DNA. Retrotransposition of the resultant mRNAs then results in lineage specific sequence “tags” (i.e., 3′ transductions) that mark the descendants of active L1 progenitors. Here, we developed a method (Transduction-Specific Amplification Typing of L1 Active Subfamilies or TS-ATLAS) that exploits L1 3′ transductions to identify active L1 lineages in a genome-wide context. TS-ATLAS enabled the characterization of a putative active progenitor of one L1 lineage that includes the disease causing L1 insertion L1_{RP}, and the identification of new retrotransposition events within two other “hot” L1 lineages. Intriguingly, the analysis of the newly discovered transduction lineage members suggests that L1 polyadenylation, even within a lineage, is highly stochastic. Thus, TS-ATLAS provides a new tool to explore the dynamics of L1 lineage evolution and retrotransposon biology.

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KEY WORDS: human; retrotransposon; transduction; polyadenylation; genome

Introduction

Long INterspersed Element-1 (LINE-1 or L1) sequences are autonomously mobile non-LTR retrotransposons that are ubiquitous in mammalian genomes (reviewed in Beck et al. (2011)). In humans, L1s comprise ~17% of the genome and are responsible for the genesis of at least another 10% of DNA through the mobilization of nonautonomous retrotransposons (e.g., Alu and SVA elements), certain noncoding RNAs, and cellular mRNAs, which leads to the creation of processed pseudogenes [Buzdin et al., 2002; Bennett et al., 2004; Dewannieux et al., 2003; Esnault et al., 2000; Garcia-Perez et al., 2007; Gilbert et al., 2005; Hancks et al., 2011; Lander et al., 2001; Ostertag et al., 2003; Wei et al., 2001; Weber, 2006]. Despite their prevalence, there is a profound dearth of knowledge regarding the active L1s segregating in human populations.

In silico studies have been instrumental in identifying active (i.e., retrotransposition competent or RC-L1s) human L1 elements. RC-L1s contain an intact 5′ UTR harboring an internal RNA polymerase II promoter [Swergold, 1990] that drives transcription of an mRNA containing two open reading frames (ORF1 and ORF2) [Dombroski et al., 1991; Scott et al., 1987]. The L1-encoded proteins (ORF1p and ORF2p) are required for retrotransposition [Moran et al., 1996; Feng et al., 1996] and biochemical and genetic studies indicate that both proteins preferentially act in *cis* to mobilize their encoding transcript [Esnault et al., 2000; Kulpa and Moran, 2006; Wei et al., 2001].

The development of a cultured-cell retrotransposition assay [Moran et al., 1996] allowed quantification of the retrotransposition efficiency of individual L1s. In 2003, analysis of the Human Genome Working Draft (HGWD) sequence [Lander et al., 2001] indicated that 90 L1s had two intact ORFs [Brouha et al., 2003; Myers et al., 2002]. When 82 of the 90 potential RC-L1s were tested in the retrotransposition assay, 40 were active [Brouha et al., 2003]. The majority of these 40 L1s were weakly active; however, six elements, termed “hot” L1s, displayed robust retrotransposition activity in HeLa cells [Brouha et al., 2003]. Subsequent genome-wide studies have indicated that there are significantly more “hot” L1s in the human population than previously appreciated, and that ongoing L1 retrotransposition contributes significantly to human genetic diversity [Badge et al., 2003; Beck et al., 2010; Ewing and Kazazian, 2010; Huang et al., 2010; Iskow et al., 2010; Kidd et al., 2010; Mills et al., 2011], reviewed in Beck et al. [2011].

We previously developed a transposon display system (Amplification Typing of L1 Active Subfamilies or ATLAS) to selectively amplify human-specific L1 insertions [Badge et al., 2003]. Interestingly, three of seven (~43%) full-length elements in this study were “hot” L1s, which contrasts with the relatively low number of

Additional Supporting Information may be found in the online version of this article.

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“hot” L1s in the HGWD [Brouha et al., 2003]. Thus, a combination of *in silico* analyses, transposon display approaches, and a cultured cell retrotransposition assay can identify polymorphic, active L1s segregating in human populations.

Human-specific L1 subfamilies are evolutionarily young and are closely related in sequence—for example, the oldest human-specific L1 subfamily (pre-Ta) originated around 4.4 MYA and its members are on average 99.4% identical at the nucleotide level [Boissinot et al., 2000; Marchani et al., 2009]. Thus, it often is difficult to discern progenitor/offspring relationships among L1s by comparing their sequences. Previous work revealed that the transcription machinery frequently bypasses the native L1 polyadenylation (poly (A)) signal and instead terminates at a poly (A) signal in 3′ flanking genomic DNA [Goodier et al., 2000; Holmes et al., 1994; Moran et al., 1996, 1999; Pickeral et al., 2000]. The resultant retrotransposition events therefore acquire a sequence “tag” known as a 3′ transduction [Goodier et al., 2000; Holmes et al., 1994; Moran et al., 1996, 1999; Pickeral et al., 2000].

In principle, shared 3′ transductions can be used to identify related L1s and establish progenitor/offspring relationships. *In silico* studies suggest that ~15% of L1s contain 3′ transductions, and that 3′ transductions are responsible for generating between 19 and 30.5 Mb of human genomic sequence [Goodier et al., 2000; Pickeral et al., 2000]. Moreover, 3′ transductions have enabled the identification of putative progenitors of disease-producing L1 insertions and a number of “hot” L1 lineages [Beck et al., 2010; Brouha et al., 2002; Goodier et al., 2000; Holmes et al., 1994; Kidd et al., 2010; Selemé Mdel et al., 2006; Solyom et al., 2012; van den Hurk et al., 2003, 2007].

Here, we describe a system called Transduction-Specific ATLAS (TS-ATLAS) that allows the amplification of L1s containing shared 3′ transduced sequences. We report the discovery of new L1s related to three “hot” L1 lineages: L1_{RP} (AF148856), AC002980, and LRE3 (AC067958) [Brouha et al., 2002; Kimberland et al., 1999; Schwahn et al., 1998; Selemé Mdel et al., 2006]. Notably, we identified a likely progenitor of a lineage of elements that includes a disease-causing L1 insertion (L1_{RP}) [Kimberland et al., 1999; Schwahn et al., 1998] and demonstrated that this L1 is highly active in a cultured human cell retrotransposition assay. The AC002980 and LRE3 lineages are extensive (with 10 and eight members, respectively) and generally are polymorphic. They also have highly variable allele frequencies (from putatively “Private” insertions present in a single individual to 0.495), suggesting they have expanded in recent human history. Within the AC002980 lineage there is evidence for ongoing variation in poly (A) site selection, suggesting this may be a plastic feature of L1 evolution. Together, the above data reveal that ongoing L1 retrotransposition contributes to human genetic diversity and strongly suggest that these three lineages remain active in human populations.

Materials and Methods

Identification of L1s Related to AC002980, LRE3, and RP in Human Genomic Sequence Resources

BLAT searches of the UCSC genome (<http://genome.ucsc.edu>) Human March 2006 (NCBI 36/hg18) assembly (hereafter referred to as the Human Genome Reference, HGR) and BLAST searches of the NCBI nonredundant nucleotide databases (nr) (<http://www.ncbi.nlm.nih.gov>) were both performed using AC002980, LRE3 (Accession Number: AC067958), and L1_{RP} (Accession Number: AF148856) 3′ transduction sequences as probes [Altschul et al.,

1990; Kent, 2002]. Sequences with >95% identity that were preceded by an L1HS were aligned by hand to L1.3 (Accession Number: L19088 [Dombroski et al., 1993]) using the SIMMONIC sequence analysis package [Simmonds and Smith, 1999] to enable detailed examination of L1 length and structural hallmarks such as target-site duplications (TSDs) and poly (A) tails. L1 elements were named according to the accession number of the sequence into which they inserted.

TS-ATLAS DNA Samples and Extraction

TS-ATLAS was performed using peripheral blood lymphocyte and ejaculated sperm derived genomic DNA (gDNA) from nine healthy, anonymous volunteers, collected with informed consent under ethical approval from Leicestershire, Northamptonshire, and Rutland Research Ethics Committee (LNRREC Ref. No. 6659 UHL). After collection, assigning randomized identifiers anonymized the blood and sperm samples. Lymphoblastoid cell line genomic DNAs from 1 CEPH/FRENCH and 5 CEPH/UTAH pedigrees, obtained from the Centre d’Etude du Polymorphisme Humain (CEPH)/Fondation Jean Dausset were also utilized (Supp. Methods). Genomic DNA was isolated using the Genra Puregene Blood kit (Qiagen UK, Manchester, Lancs, UK) following the manufacturer’s instructions. DNA integrity was assessed by fractionation on 0.8% (w/v) agarose gels alongside intact bacteriophage λ DNA. DNA was visualized by ethidium bromide (0.5 μ g/ml) staining under UV illumination.

TS-ATLAS

TS-ATLAS is a modification of ATLAS [Badge et al., 2003] that uses transduction specific primers to selectively amplify loci containing transduced sequences from oligonucleotide-linked genomic libraries. All oligonucleotides (Supp. Table S1) were HPLC purified by the manufacturer (Sigma Aldrich UK, Gillingham, Dorset, UK) and resuspended at 50 μ M in 5 mM Tris–HCl, pH 7.5. All pre-PCR reaction set up was carried out in a Class II laminar flow hood (Walker Safety Cabinets, Glossop, Derbys., UK), decontaminated by UV exposure for at least 30 min before use.

Library Construction and Amplification

The method described below is the *VspI*-specific protocol for the L1_{RP} transduction lineage (Supp. Methods Protocol 1 and Supp. Fig. S1). Variations required for the *MspI*-specific L1_{RP} transduction lineage assay and AC002980 and LRE3 lineages are described in the Supp. Methods (Protocols 2–5 and Supp. Fig. S2–S4). Briefly, 600 ng of genomic DNA were digested to completion with 20 units of *VspI* (Promega, Madison, WI) in the manufacturer’s recommended buffer at 37°C for 3 hr. After incubation, reactions were heated to 65°C for 20 min to inactivate the restriction enzyme. Before setting up the ligation reaction, linker oligonucleotides were freshly annealed by mixing equal volumes of 20 μ M RBMSL2 and RBD3, heating to 65°C for 10 min, and then cooling to room temperature. An aliquot (100 ng) of the digested DNA was ligated to a 40-fold molar excess of the annealed suppression linker (2.7 μ l of 10 μ M annealed linker for *VspI* libraries) with 4 Weiss units T4 DNA ligase (Promega) in 1X Ligase Buffer (Invitrogen, Paisley, Renfrewshire, UK) overnight (~16 hr) at 15°C, in a final volume of 20 μ l. After ligation, the reaction was heated to 70°C for 10 min to inactivate the ligase. Excess linkers and short DNA fragments (i.e., <100 bp) were removed with the Qiaquick PCR purification system (Qiagen) following the manufacturer’s protocol, but eluting the DNA in 30 μ l

5 mM Tris-HCl pH 7.5. In our hands, the purification is ~80% efficient, resulting in a purified library containing approximately 2.7 ng/ μ l of genomic DNA. Libraries are sensitive to freeze/thaw, and so were aliquotted and stored frozen at -20°C. An aliquot (1 μ l) of ligated genomic DNA was amplified in 10 μ l PCR reactions containing 1 \times PCR buffer (45 mM Tris-HCl pH 8.8, 11 mM NH₄SO₄, 0.9 mM MgCl₂, 6.7 mM β -mercaptoethanol, 113 μ g/ml BSA, 1 mM dNTPs), 1.25 μ M RBX4 primer, 1.25 μ M RB3PA1 primer, and 0.4 units *Taq* DNA polymerase (ABgene, Epsom, Kent, UK). Reactions were cycled in a Tetrad 2 Thermal Cycler (MJ Research, Waltham, MA) using the following conditions: 96°C -1 min; 30 \times [96°C -30 sec; 58°C -30 sec; 72°C -1 min]; 72°C -10 min. Primary suppression PCR reactions were diluted 1:50 in Single Molecule Dilution Diluent (SMDD: 5 mM Tris-HCl pH 7.5, 5 ng/ μ l sonicated *Escherichia coli* genomic DNA), and 1 μ l diluted PCR reaction was added to 9 μ l secondary PCR reactions containing 1 \times PCR buffer, 0.625 mM RBY1 primer (Linker specific), 0.625 mM 011TD1 (L1_{RP} transduction specific), and 0.4 units *Taq* DNA polymerase (ABgene). Reactions were cycled in a Tetrad 2 Thermal Cycler (MJ Research) using the following conditions: 96°C -1 min; 30 \times [96°C -30 sec; 58°C -30 sec; 72°C -1 min]; 72°C -10 min.

Recovery and Analysis of TS-ATLAS Products

An aliquot (10 μ l) of secondary TS-ATLAS PCR products was fractionated on 2% Seakem LE (Cambrex, Rockland, ME) 0.5X TBE agarose gels alongside the 100 bp ladder (NEB, Ipswich, MA) size marker and visualized by ethidium bromide (0.5 μ g/ml) staining. Novel PCR products were excised from the gel and purified using

the Qiagen Minelute system (Qiagen) following the manufacturer's protocol, but eluting the DNA in 10 μ l of 5 mM Tris-HCl pH 7.5. Purified PCR products were directly sequenced with ABI BigDye Ver. 3.1 Ready Reaction, using 3.3 μ M RBY1 as the primer. Sequencing reactions were purified using Performa DTR spin columns (Edge BioSystems, Gaithersburg, MD) and the sequencing data collected using an ABI 3730 capillary sequencer by the PNAFL core DNA sequencing service (University of Leicester). The sequences of the TS-ATLAS amplicons were imported into the CHROMAS sequence viewer and the L1 3' transduction flanking sequences mapped to the HGR using BLAT (<http://genome.ucsc.edu>) [Kent, 2002]. Accession numbers of the DNA sequences encompassing the L1 insertion locations were verified using the National Center for Biotechnology Information (NCBI) BLASTN program (<http://www.ncbi.nih.gov>) [Altschul et al., 1990]. Recovered L1 elements that had previously been reported [Beck et al., 2010; Boissinot et al., 2000; Goodier et al., 2000; Myers et al., 2002] are listed in Supp. Table S2. Putative novel insertions were named using the convention followed in Badge et al. (2003) and Beck et al. (2010). The insertions were assigned to the accession of the completely sequenced large insert clone (BAC/PAC) containing the insertion empty site sequence, as represented in the human genome reference sequence (hg18), and are listed in Table 1.

Primer Design for Novel L1 Insertions Related to RP, AC002980, and LRE3

Upon identification of the insertion sites of novel L1s, flanking DNA sequences were obtained from the HGR, the repeats

Table 1. TS-ATLAS and Related Loci

Accession/L1	Family library	Presence in HGR	Detected in 1000G?	Location Chr (position)	Length	TSDs	Transduction length (nt)	Allele frequency ^a
AL050308 ^b	RP-VspI	-	Y	Xq27.2 (140342939, -)	FL	AAAAAGTTTAAATTT	0	0.149
AC005888 ^b	RP-MspI	-	Y	12q24.31 (125221192, +)	5' Truncated	AAAGAAATAAGG	11	Polymorphic
AC005939	RP	+	NA	17q24.3 (65966692, +)	FL	AAGATTTTGTG	10	0.327
AC093861	RP	+	NA	4p13 (44202069, -)	5' Truncated	None detected	11	NT
AL590011 ^c	RP	-	N	6q13 (72856236, +)	FL	TAAGAAAATGTGGCACA	11	0.210 ^c
AC019288 ^c	RP	-	Y	15q14 (33441423, -)	FL	AAAAAATGAAAATC	11	0.002 ^c
RP ^d	RP	-	NA	Xp11.3 (46582227, +)	FL	AAGACTGTAAGGTG	11	Private
AL118519	2980-VspI	+	NA	6q13 (70776960, +)	FL	CAAAACAAAACAAAGCAAAC	0	Polymorphic
AC002980	2980-NlaIII	+	NA	Xp22.2 (11869357, -)	FL	AAAAAAAATCACCA	174	0.495
AC010387	2980-VspI	+	NA	5p14.2 (24409194, -)	5' Truncated	AAATTTTGTTTTA	222	Polymorphic
AC004740 ^{b,c}	2980-NlaIII	-	Y	7p21.3 (8853240, +)	FL	AACAATATGTA	222	0.063 ^c
AP001604 ^b	2980-NlaIII	-	N	21q21.3 (27594286, -)	5' Truncated	AGAAAGTGCCCTGTAG	222	0.056
AC048382 ^b	2980-NlaIII	-	Y	15q25.2 (82941913, +)	FL	AAGATGTAAGTAGAAA	181	0.025
AP001029 ^{b,c}	2980-NlaIII	-	Y	18p11.21 (12481262, +)	FL	AAGAAAATCCT	173	0.016 ^c
AC069023 ^b	2980-NlaIII	-	NA	10p12.33	Undetermined	In Duplicon	174	NT
AC116311 ^b	2980-VspI	-	N	5q21.1 (100553773, +)	5' Truncated	AGAAATAATGTAA	406	0.037
AC010749 ^b	2980-NlaIII	-	Y	7p21.1 (17061239, +)	5' Truncated	TAAAAAATTTGTTTC	173	Polymorphic
LRE3/AC067958 ^{b,d}	LRE3-MseI	-	Y	2q24.1 (156236094, +)	FL	GAAAGAAAGAAAGAA	0	0.328
BX927359 ^e	LRE3-MseI	-	N	14q32.23 (104052295, +)	FL	AAAATGAAAATAAAAT	257	0.016
AC091138 ^e	LRE3-MseI	-	N	18q22.3 (68673030, -)	5' Truncated	GAAAGAAATAAGATATTTTG	273	0.016
AC068286 ^b	LRE3-MseI	-	N	2p24.3 (14899793, +)	FL	AGAAATAAGTGTCTA	263	0.0
AL592182 ^b	LRE3-MseI	-	N	1p33 (50455323, +)	FL	AGAAAACAACAGAGGGG	263	0.0
AL031584 ^b	LRE3-MseI	-	N	Xp11.3 (45671041, +)	5' Truncated	AAATCAACCACAGAAAACAAACC	263	0.04
AL353685 ^c	LRE3	-	N	9q31.1 (106675844, +)	FL	GAACAAGCCTGG	278	0.0 ^e
CYBB ^d	LRE3	-	NA	Xp11.4 (37538956, +)	5' Truncated	AA	280	Private

^aWhether an element was detected in our analysis of the 1000 Genomes dataset is recorded in column 4 as: Y = Yes, N = No, and NA = Not Analyzed (because the element is in the HGR, private to an individual with a disease causing insertion or not mapped uniquely). Allele frequencies are listed in this study as determined in a panel of 129 unrelated CEPH individuals, or when previously described [Beck et al., 2010] with their reported allele frequency. Loci discovered in one member of the blood donor panel, but absent from the CEPH genotyping panel, are listed with allele frequencies of 0.0, as the relatedness between the donor panel and CEPH panel is not known. Loci are described as "polymorphic" if they were not fully genotyped, but were present or absent in more than one individual in the blood donor or CEPH panels. Disease causing de novo insertions are described as "Private", FL = full length, NT = not tested.

^bIdentified in blood donor panel (this study).

^cDescribed in Beck et al. (2010).

^dDescribed as disease causing insertions [Brouha et al., 2002; Kimberland et al., 1999].

^eIdentified in CEPH panel (this study).

were masked using RepeatMasker (<http://www.repeatmasker.org/>), and PCR primers were designed using Primer 3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Primers were designed so that the 3' flanking primer (downstream of the L1 poly (A) tail) was 3' of the restriction site to which the library linker was ligated, which enabled independent verification of the ligation point. Where flanking sequence was highly repetitive, primers were positioned across the junction of repeats.

Verification of Novel L1s Containing 3' Transductions

The presence of L1s preceding 3' transductions related to RP, AC002980, or LRE3 was verified by PCR amplification using a unique 3' flanking primer and the primer RP3PA2, which is specific to the 3' end of human-specific L1s. Primer sequences are listed in Supp. Table S1. PCR products were separated on 2% agarose gels, purified using the Qiagen Minelute system (Qiagen), cloned using the pGEM-T easy kit (Promega), and transformed into ultra competent DH5 α *E. coli* cells. Plasmid DNA was recovered using a QIAprep Spin miniprep kit (Qiagen). An aliquot (20–30 ng/kb) of plasmid DNA was sequenced using the Big Dye Terminator v3.1 as above with 3.3 μ M sequencing primer (M13F or M13R) to determine the insert sequence.

Length and 5' TDSs of Novel L1 Loci

The length of novel L1 insertions was confirmed by amplifying with a unique 5' flanking primer and the primer RB5PA2 specific to the 5' end of a human specific L1s. Primer sequences are listed in Supp. Table S1. Where novel L1 insertions appeared to be 5' truncated such that no 5' specific amplicon was produced, the entire element was amplified using the unique 5' and 3' flanking DNA primers. In principle, this strategy would enable amplification of elements with 5' inversions, but none were detected in this study. TSDs and the L1 insertion site in the HGR were determined by excising amplicons from 2% agarose gels, purifying the DNA using the Qiagen Minelute system (Qiagen), and directly sequencing with ABI BigDye Ver. 3.1 ReadyReactions as described above, using the flanking region primers.

Presence/Absence Polymorphism

Dimorphism of L1 insertions related to L1_{RP}, AC002980, or LRE3 was determined using two PCR assays: the “filled” site reaction amplified the 3' end of the L1 and its 3' flanking DNA, whereas the “empty” site reaction amplified the DNA flanking the L1 insertion point in the absence of the L1, as described previously [Badge et al., 2003; Sheen et al., 2000]. A panel of unrelated Northern European CEPH genomic DNAs ($n = 129$) was used to estimate L1 insertion allele frequency. This subset was derived from unrelated individuals (grandparents and parents) from CEPH families 02, 12, 17, 21, 23, 28, 35, 37, 45, 66, 102, 104, 884, 1331, 1332, 1333, 1340, 1341, 1344, 1345, 1346, 1347, 1349, 1350, 1362, 1375, 1377, 1408, 1413, 1416, 1418, 1420, 1421, 1423, 1424, 13291, 13292 and 13293. The primers used are listed in Supp. Table S1.

Amplification and Sequencing of L1 AL050308

The full-length putative L1_{RP} progenitor AL050308 was amplified using a 5' primer positioned across the junction of the L1 and its 5' flanking genomic DNA and a 3' primer unique to the 3' flanking

genomic DNA of AL050308 (primer sequences listed in Supp. Table S1). An aliquot (40 ng) of sperm genomic DNA from a male donor who is hemizygous for the AL050308 insertion was subjected to long-range PCR amplification in 10 μ l PCR reactions containing 1 \times PCR buffer, 0.0625 μ M of each primer, and 0.05 units/ μ l *Taq/Pfu* mixed in the ratio 10:1 (ABgene/Stratagene, Agilent Technologies, Santa Clara, CA). Reactions were cycled in a Tetrad 2 Thermal Cycler (MJ Research) using the following conditions: 96°C –1 min; 28 \times [94°C –15 sec; 68°C –10 min]; 72°C –10 min. PCR products were separated on a 1% agarose gel and purified using a QIAquick gel extraction kit (Qiagen). The PCR products were directly sequenced using the flanking genomic primers and a set of L1 sequencing primers designed to the L1.3 (L19088) reference sequence.

AL050308 Cloning and Retrotransposition Assays

L1 AL050308 was amplified from volunteer donor sperm gDNA by long-range PCR using flanking genomic primers JM0308D and CM0308A. To enable amplification of error-free PCR products, long-range PCR using the Expand Long Range polymerase system (Roche Applied Science, Burgess Hill, Sussex, UK) was employed using 50 ng of template DNA and buffer 2. PCR products were then cloned by digesting PCR fragments with *AccI*, performing PCR clean up with the Zymoclean DNA gel recovery kit (Zymo Research, Irvine, CA), and ligation of fragments into appropriate restriction sites in the pBluescript-based vector pJCC9 containing the *mneol* retrotransposition indicator cassette [Beck et al., 2010]. Cloned L1_{RP} progenitor elements were sequenced in their entirety ($\sim 4 \times$ coverage) to identify clones with minimal sequence variation from the directly determined consensus.

Clones were tested for retrotransposition activity relative to L1.3 (accession L19088) alongside the retrotransposition defective negative control construct pJCC9 L1.3 D702A (RT-) as previously described [Beck et al., 2010; Moran et al., 1996; Wei et al., 2000, 2001]. HeLa cells were cultured as previously described [Beck et al., 2010; Moran et al., 1996]. Six-well tissue culture plates were seeded with approximately 5×10^3 , 2×10^4 , or 2×10^5 cells, and 24 hr later, three wells of each cell concentration were transfected with 1 μ g of plasmid using Fugene 6 transfection reagent (Roche) and Opti-mem media (Gibco, Grand Island, NY). Approximately 18–24 hr posttransfection culture media was aspirated and replaced. Media was replaced daily from 72 hr posttransfection with media plus 400 μ g/mL G418 (Gibco). Fourteen days after transfection, cells were washed, fixed, and stained with 0.1% crystal violet as previously described [Beck et al., 2010]. G418-resistant colonies were counted on the 5×10^3 or 2×10^4 plates. Transfection efficiencies were obtained using 2×10^4 and 2×10^5 cells transfected with pCEP/GFP as per the transient retrotransposition assay protocol [Beck et al., 2010; Moran et al., 1996; Wei et al., 2000].

Screening for Transduction Lineage Elements Within the 1000 Genomes Pilot Data

Briefly, Roche 454-acquired genomic sequence data (from 375 individuals) from the 1000 Genomes Project Pilots 1–3 [2010] were downloaded and filtered to exclude very short reads (<45 bp) resulting in database of ~ 1.6 billion reads. MegaBLAST [Zhang et al., 2000] searches using genomic sequences flanking the insertion points of novel TS-ATLAS-discovered elements were used to identify reads mapping to these loci. These reads were analyzed to find junctions between genomic DNA and L1 or transduction sequences. These junction reads were validated by realignment and manual inspection. The detailed computational procedure is described in the

Supporting Information and reads supporting the presence of novel TS-ATLAS insertions in the 1000 Genomes dataset listed in Supp. Table S3.

Results

Principle of TS-ATLAS

We modified 3' ATLAS [Badge et al., 2003] to selectively amplify L1s with shared 3' transduction sequences. These L1s were amplified from oligonucleotide-linkered genomic libraries in a method termed TS-ATLAS. Figure 1A illustrates this procedure as developed for the L1_{RP} transduction lineage, and is designed to equally amplify all members of the lineage. Other lineages (AC002980 and LRE3) required modifications that prevented the amplification of common lineage members. For example, the efficient amplification of AC002980 can outcompete novel lineage members with longer transductions (detailed in the Supp. Methods, Protocols 3 and 4).

Briefly, genomic DNA was digested to completion with restriction enzymes (Fig. 1A, diamond tipped lines) generating fragments containing L1 termini and their immediate 3' flanking genomic sequences. The digested DNA was then ligated to a GC-rich double stranded ATLAS linker (Fig. 1A, AL) and suppression PCR was performed using either an L1 3' UTR or 3' transduction specific primer in conjunction with a linker specific primer. Intramolecular annealing of DNA fragments that have linkers attached to both ends leads to the formation of stable "panhandle" structures that suppress PCR amplification [Badge et al., 2003; Broude et al., 2001; Lavrentieva et al., 1999]. This suppression is relieved if a 3' UTR or transduction specific primer anneals within the loop of the panhandle structure and is extended by *Taq* DNA polymerase, generating an amplicon with only one linkered end. The resultant amplicon then can serve as an exponential amplification template. For the L1_{RP} lineage, the primary PCR utilized the L1 3' UTR specific primer RB3PA1 and a secondary nested PCR was employed to enrich for DNA fragments containing the L1_{RP} specific 3' transduction (Fig. 1A, black arrow) and its associated flanking DNA sequences. In the case of L1_{RP} lineage elements that are not the progenitor, (Fig. 1A, right panel) this procedure generates fragments containing the L1_{RP} transduction sequence, upstream of a poly (A) tract and the 3' genomic DNA flanking the L1 insertion. In contrast a putative progenitor of the L1_{RP} insertion would terminate in its poly (A) tail, and the 3' flanking sequence subsequently identified as a transduction in offspring elements. This "transduction" sequence will be followed by 3' flanking genomic DNA which does not contain a second poly (A) tract, enabling its identification as a putative progenitor. Notably, TS-ATLAS amplification schemes also were developed for the 3' transduction sequences flanking AC002980 and LRE3 (Supp. Methods, Protocols 3–5). To validate the reproducibility of TS-ATLAS, three-generation CEPH pedigrees showing segregation of AC002980 (CEPH families 12, 1333, 1340, 1424, and 1347) and LRE3 (CEPH families 1333, 1340, 1424, and 13291) were analyzed using lineage-specific TS-ATLAS and insertion specific genotyping. In all cases, TS-ATLAS amplification patterns were entirely concordant with the genotypes of all family members (data not shown). The L1_{RP} specific amplification scheme was not applied to CEPH pedigrees as initial screening of unrelated donors revealed only one novel amplicon (see below).

Discovery of a Putative RP Lineage Progenitor

Application of the L1_{RP} lineage specific TS-ATLAS scheme to genomic DNA from a small panel of unrelated DNA donors ($n = 9$)

resulted in the recovery of a PCR product from one donor with a sequence consistent with it being a progenitor of the L1_{RP} lineage. Subsequent genotyping of a panel of 129 unrelated CEPH DNAs showed this progenitor was not rare (allele frequency = 0.149). Long-range PCR and direct sequencing confirmed that the allele from the original donor had intact open reading frames. Low-error rate long-range PCR was used to amplify representative PCR products and these were cloned into a retrotransposition assay vector, making use of conserved *Acd* sites at the element's termini [Beck et al., 2010; Sassaman et al., 1997]. Ten clones were sequenced at ~fourfold coverage and assayed for retrotransposition activity. One clone showed no nucleotide variation from the directly determined sequence and retrotransposed at ~170% the rate ($n = 6$) of a reference active L1 element (L1.3, L19088 [Dombroski et al., 1993]), as illustrated in Figure 1B.

Analyses of the above data, searches of sequence databases, and identification of L1_{RP} lineage members from the literature suggest that the L1_{RP} transduction family is composed of at least seven members (Table 1, and Fig. 2A). AC005939 and AC093861 are present in the human genome reference (HGR) sequence [Myers et al., 2002], whereas AL050308 and AC005888 were discovered in this study. Two L1_{RP}-related full-length polymorphic L1s (AL059011 and AC019288) were previously detected using a fosmid-based, paired-end DNA sequencing strategy [Beck et al., 2010]. In summary, the L1_{RP} transduction family contains the private mutagenic insertion L1_{RP}, its likely progenitor (AL050308), at least three additional polymorphic full-length elements (AC005939, AL059011, AC019288), and two 5' truncated L1s (AC005888, AC093861), whose allele frequencies range from 0.002 to 0.210.

TS-ATLAS with Common Allele Suppression

Next we developed TS-ATLAS schemes for two other disease causing lineages, AC002980 and LRE3 [Brouha et al., 2002; Myers et al., 2002]. Unlike the L1_{RP} lineage, members of these families are known to be common within human populations [Brouha et al., 2002; Seleme Mdel et al., 2006]. As suppression PCR is competitive, amplification of a common insertion potentially jeopardises amplification of novel elements with longer transductions or with restriction sites (for linker addition) distant from the L1. To overcome this technical hurdle, we suppressed amplification of known common lineage members by digesting the linkered libraries with a rare cutting restriction enzyme predicted to cut between the end of the transduced sequence and the flanking linker ligated restriction site. In the case of L1 AC002980 this was *MunI*, as illustrated in Figure 3A. Lack of *MunI* digestion allowed amplification only of AC002980 itself (Fig. 3B, lane 16), whereas libraries derived from our nine gDNA donors, pre-digested with *MunI*, yielded a constellation of potential AC002980 family members (Fig. 3B, lanes 1–9).

L1 Transduction Family: AC002980

TS-ATLAS identified 10 elements with transductions consistent with the AC002980 lineage. Three elements were present in the HGR (AC002980, AL118519, AC010387), including the putative lineage progenitor AL118519 and a related L1, AC010387 (Table 1). We identified seven other L1s that share the AC002980 3' transduction, two of which, AC004740 and AP001029, were previously detected by fosmid end sequencing [Beck et al., 2010]. Five of the L1s were full-length and four were 5' truncated, and all contained discernable TSDs (Table 1, and Fig. 4A). Also nine of the 10 L1s in the AC002980 lineage were dimorphic with respect to presence/absence, with

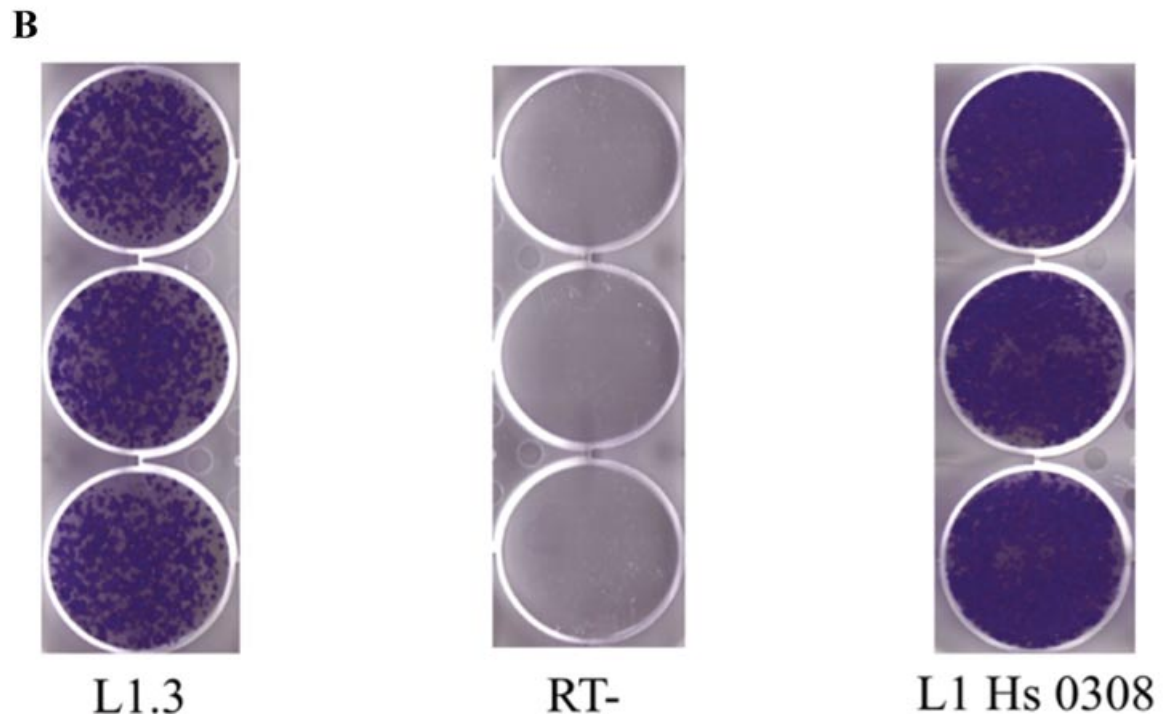
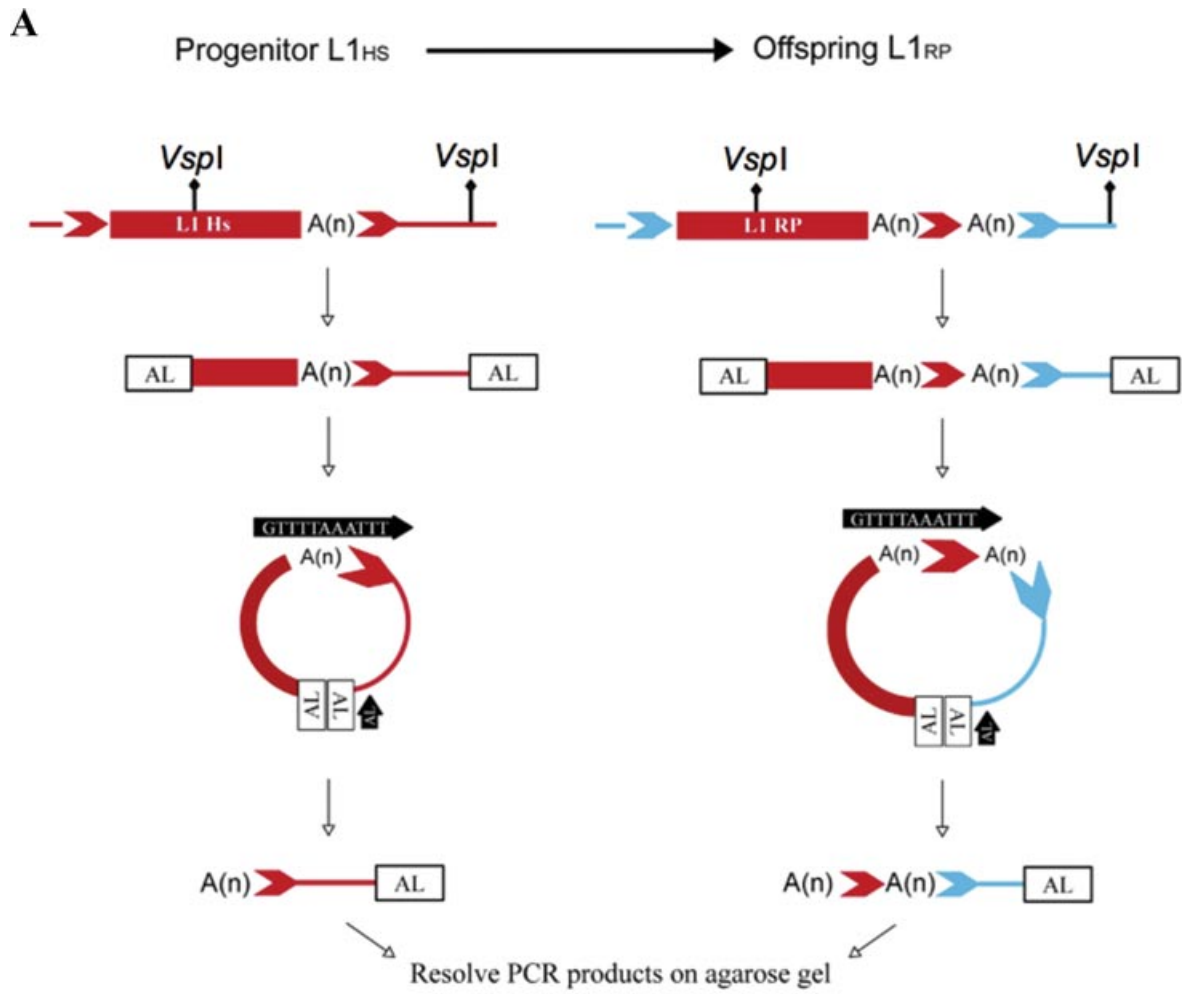


Figure 1. See figure legend on next page.

Figure 1. Schematic of RP-specific TS-ATLAS and activity of L1 AL050308. **A:** TS-ATLAS using a primer specific to the RP transduction shown on the right is an offspring L1 (red rectangle, labeled “L1 RP”) of a progenitor L1 (red rectangle to the left, labeled “L1 Hs”), which carries two poly (A) tails (A(n).) These poly (A) tails are separated by a short transduced sequence consisting of the progenitor’s TDS sequence (red chevron), and flanked by distinct TSDs (light blue chevrons). PCR reactions containing linker specific (black arrow, labeled “AL”) and transduction specific primers (black arrow, labeled with RP transduction sequence) and using linker genomic DNA libraries as a template enable specific amplification of both types of element. Offspring elements are identifiable by the presence of a poly (A) tail downstream of the transduction sequence (red chevron), whereas progenitor elements lack this. Sequencing of transduction PCR products enables their 3’ flanking genomic DNA to be used to determine if they originate from novel insertions. **B:** Retrotransposition of Putative Lineage Progenitor L1 AL050308 TS-ATLAS was used to identify a putative novel progenitor for the RP lineage, inserted into genomic accession AL050308. The three panels show the results of representative duplicate cell culture based retrotransposition assays using L1 elements cloned into standard assay vectors. L1.3 (Accession L10988) is a reference element: its ability to generate G418 resistant HeLa cell colonies (left panel) was compared with that of the putative L1RP progenitor, AL050308 (right panel). This clone of the AL050308 element has no nucleotide changes from the genomic consensus sequence of the L1, and retrotransposes at ~170% the rate of L1.3 ($n = 6$). As a negative control an L1 construct with an inactivating mutation in the RT domain of ORF2p in L1.3 [Wei et al., 2001, 2000] was assayed under the same conditions (middle panel, RT-).

allele frequencies ranging from 0.016 to 0.485 (Table 1). The tenth AC002980 member (AC069023) was embedded in a segmental duplication and thus, was intractable for genotyping and determination of L1 length (Table 1). Two additional members (ABC9_21 and ABC13_100) of the AC002980 family identified previously [Beck et al., 2010] were not detected in our panel using TS-ATLAS, likely due to the small number of individuals screened ($n = 9$).

L1 Transduction Family: LRE3

TS-ATLAS revealed five novel L1 insertions that share the 3’ transduction flanking the likely progenitor of a disease-producing insertion into the *CYBB* gene (MIM #300481), LRE3 ([Brouha et al., 2002], Table 1, and Fig. 2B). Three insertions, BX927359, AC068286, and AL592182 are full-length and represent potentially active L1s. Two of these, AC068286 and AL592182, appear to be rare as they were absent from the CEPH genotyping panel of 129 unrelated individuals. As these LRE3 lineage insertions occurred in a single donor also carrying the LRE3 progenitor element (AC067958) the sequence of the microsatellite region of the progenitor and offspring was compared with determine whether the progenitor had directly given rise to the novel element, as described previously [van den Hurk et al., 2007]. In both cases, at least two independent changes (microsatellite repeat number and substitutions) were observed between the progenitor allele and putative offspring elements (data not shown). Given the high error rate of the L1 RT [Gilbert et al., 2005] and the established instability of the LRE3 microsatellite [van den Hurk et al., 2007] we cannot absolutely exclude a direct descent relationship, but together these changes make this seem unlikely in these cases. L1s BX927359 and the 5’ truncated AC091138 are both present at a very low allele frequency of 0.016. The 5’ truncated element AL031584 is located on the X chromosome and has an allele frequency of 0.04. In summary, the LRE3 family appears to be the youngest transduction family examined by TS-ATLAS: 87.5% (7 of 8 tested) of its member L1s (including the *CYBB* disease causing insertion) are rare (present in only one individual) or at low allele frequencies (allele frequency < 0.04) within the human population analyzed [Beck et al., 2010; Brouha et al., 2002].

Variable Polyadenylation of AC002980 Lineage Members

Inspection of the 3’ transduction sequences of the AC002980 lineage revealed evidence for alternative polyadenylation. In some cases, polyadenylation occurred within the 3’ transduction sequence. The most parsimonious explanation of these data is that the putative progenitor of this transduction family, AL118519, gave rise to three sublineages with long, intermediate, or short transductions (Fig. 4A). Long transduction elements (insertions AC004740

and AC010387) likely utilize a predicted poly (A) site (highlighted in red in Fig. 4B) located 200 nts downstream of the native L1 poly (A) site. The single member of the intermediate transduction length sub-lineage, AC048382 (Fig. 4B, top alignment section and Supp. Fig. S5), likely utilized a predicted poly (A) site located 153 nucleotides downstream of the native L1 poly (A) site, but generated a transduction derived from AL118519, which is 41 nucleotides shorter than the long transductions. This transduction is 7–8 bp longer than the short transduction elements, which could equally be accounted for by variation in the reverse transcription initiation site, or variation in the position of the poly (A) addition site.

The four members of the short sub-lineage, AP001029, AC010749, AC069023, and AC002980 are polyadenylated within one nucleotide of each other, and likely use the same polyadenylation signal as the intermediate length L1 AC048382 (Fig. 4B, top alignment section and Supp. Fig. S5). Finally the ‘hot’ prototype element of this lineage, AC002980, has given rise to a lineage that includes two 5’ truncated elements that share sequences flanking the 3’ end of the 3’ TSD; these L1s also have different poly (A) tail lengths (Fig. 4A and B and Supp. Fig. S5). Insertion AC116311 apparently used a predicted poly (A) site 378 nucleotides downstream of the native AC002980 poly (A) site, whereas AP001604 apparently used a predicted poly (A) site 193 nucleotides downstream of the native L1 poly (A) site. Together, these data suggest that although the presence of a poly (A) tail is critical for retrotransposition, the usage of particular poly (A) sites is highly variable and apparently local sequence context dependent, explaining why many L1s are flanked by 3’ transduced sequences. However, the L1_{RP} and LRE3 lineage members analyzed here show stable poly (A) site utilization (Supp. Fig. S6 and S7), so this phenomenon could be peculiar to the AC002980 lineage.

Screening the 1000 Genomes Pilot Data for Novel TS-ATLAS Identified L1 Insertions

Notably, none of the novel elements reported here was recovered in the 1016 novel insertions reported by Ewing and Kazazian’s analyses of the pilot 1000 Genomes Project dataset [Ewing and Kazazian, 2011]. This may be a result of the difficulty of unambiguously mapping NGS-generated short reads derived from transduced sequences which are, by definition, not single copy. Additionally, the lack of identification of transduction-containing elements could be due to the low sequence coverage of the pilot data. To distinguish these possibilities, we screened the 1000 Genomes data for junction reads that corresponded to the sequences of TS-ATLAS identified novel (i.e., absent from the HGR) insertions. This revealed that eight of 18 nonreference insertions (excluding L1_{RP} and L1_{CYBB}) were supported by junction reads (Table 1), indicating

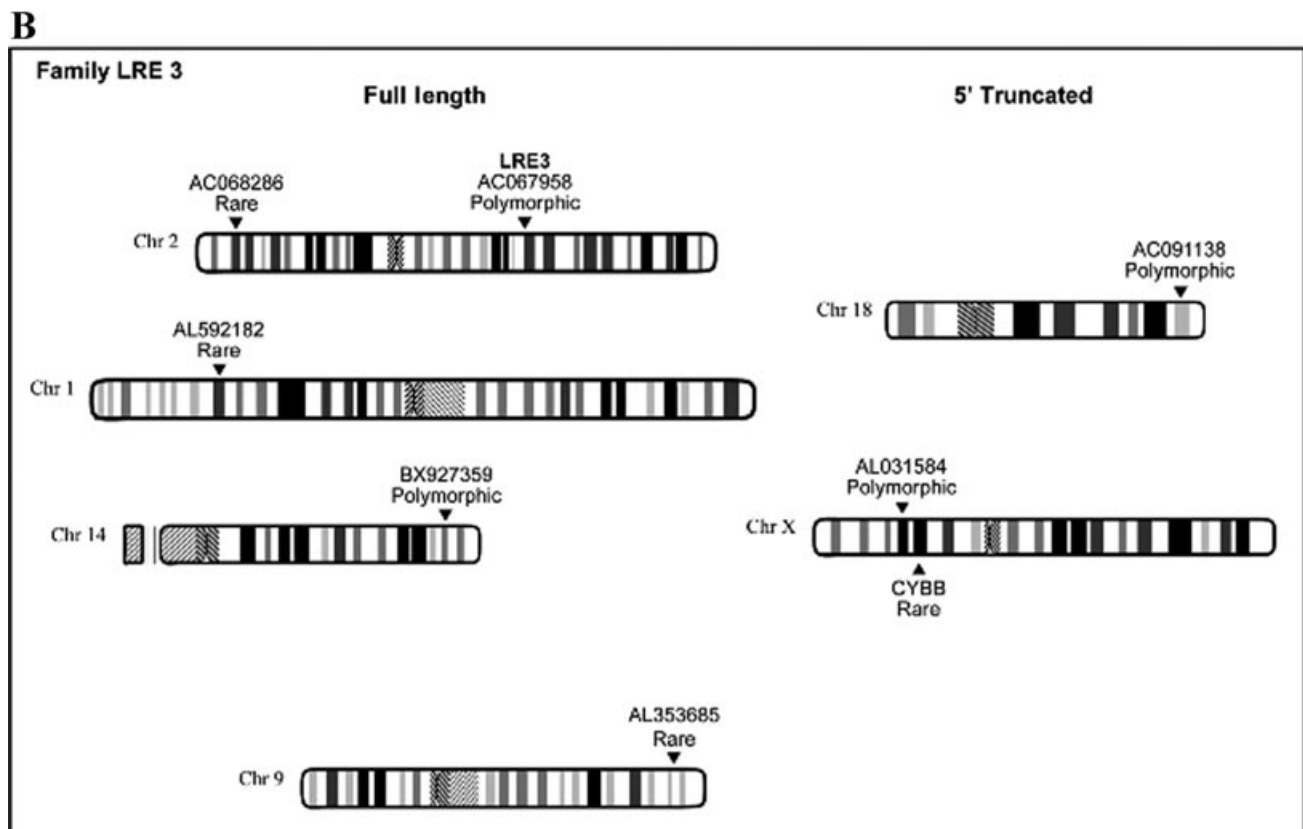
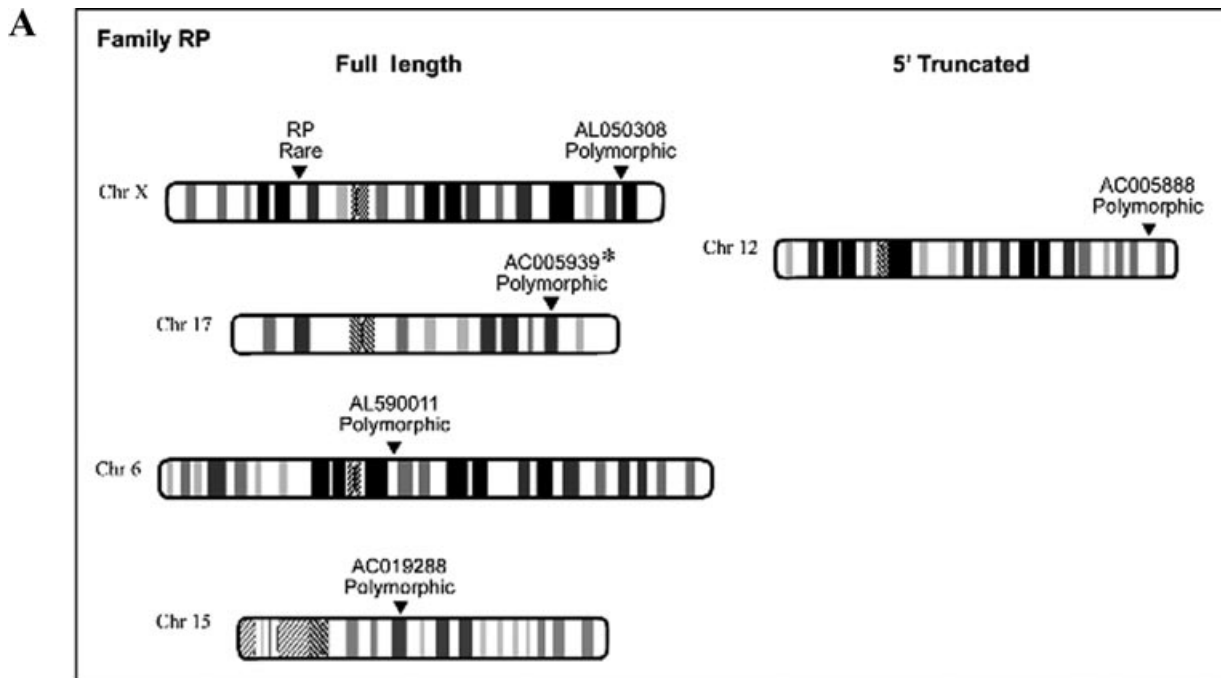


Figure 2. L1 transduction families data presented in Figure 3 are compiled from this and other studies [Beck et al., 2010; Brouha et al., 2002; Goodier et al., 2000; Kimberland et al., 1999; Myers et al., 2002]. Ideograms were adapted from the NCBI map viewer Website (<http://www.ncbi.nlm.nih.gov/projects/mapview/>). **A:** Transduction family RP. The RP family is characterized by a transduction putatively derived from the L1 locus AL050308. AL050308, AL590011, AC005939, AL019288, and L1_{RP} are full length and AC005888 is 5' truncated. L1_{RP} is a disease causing insertion [Kimberland et al., 1999]. Asterisks (*) denote L1s present in the human genome reference assembly (hg18). Insertion AC093861 is not included as the absence of TSDs (see Table 1) means we cannot exclude a non-TPRT mechanism for its mobilization. **B:** Transduction family LRE3. The LRE3 family is characterized by a transduction originally derived from the L1 locus LRE3. LRE3, BX927359, AC068286, AL592182, and AL353685 are full length. AC091138 and AL031584 are 5' truncated. L1_{CYBB} is a disease causing insertion [Meischl et al., 2000].

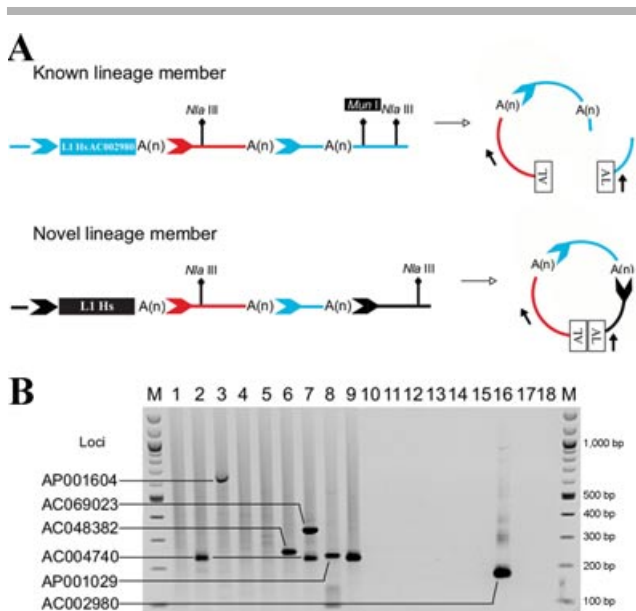


Figure 3. Schematic representation of TS-ATLAS with common allele suppression. **A:** Amplification of L1 AC002980 is prevented by digestion with *MnlI*. A commonly known transduction family member (upper panel, blue rectangle, labeled “L1Hs AC002980”) carries a lineage specific transduction (red line and chevron) and is flanked by distinct TSDs (light blue chevrons). L1 AC002980 competes with the amplification of novel lineage members. By selecting a rare restriction site (*MnlI*) in the 3' flanking DNA of this element, upstream of the *NlaIII* linker site, pre-digestion of linker genomic libraries suppresses its amplification. Novel lineage members directly derived from L1 AC002980 carry the lineage specific transduction (red line and chevron) and a second transduction (light blue line and chevron) and are flanked by distinct TSDs (black chevrons). Novel members most likely lack the combination of the rare cutting (*MnlI*) restriction enzyme upstream of a very common *NlaIII* site, and so their amplification is not suppressed. **B:** Representative TS-ATLAS display gel showing the results of applying the AC002980-specific (*NlaIII*) assay. Lanes 1–9 show display patterns of nine unrelated individuals each of whom carries the AC002980 L1. Control reactions in lanes 11, 13, 14, and 16 were setup using the same library sample as is shown in Lane 9. Lane 16 shows the amplification of the AC002980 locus, which is suppressed by digestion with *MnlI* in lanes 1–9. Lanes 2, 7, and 9 show amplification of the AC004740 locus. Lane 3 shows amplification of the AP001604 locus. Lane 6 shows amplification of the AC048382 locus. Lane 7 shows amplification of the AC069023 locus. Lane 8 shows amplification of the AP001029 locus. Lane 10—Reaction in the absence of genomic DNA. Lane 11—Reaction in the absence of restriction enzyme (*NlaIII*). Lane 12—Reaction in the absence of genomic DNA. Lane 13—Reaction in the absence of T4 Ligase. Lane 14—Reactions in the absence of linker. Lane 15—Reaction in the absence of digested genomic DNA. Lane 16—Reaction in the absence of suppression enzyme digestion (*MnlI*). Lane 17—Control for primary PCR with DNA omitted. Lane 18—Control for secondary PCR with DNA omitted. MW—molecular weight marker (100 bp ladder [NEB]). All labeled bands were sequenced to verify their origin.

that their novelty is not due to low genome sequencing coverage. The eight insertions identified (AL050308, AC005888, AC019288, AC004740, AC048382, AC010749, AP001029, and AC067958) have a range of allele frequencies, from 0.002 to 0.328, demonstrating the 1000 Genomes dataset's ability to capture both common and rare insertions.

Discussion

The 3' transduction of genomic sequences by L1 is a relatively common event. For example, there are at least five instances where

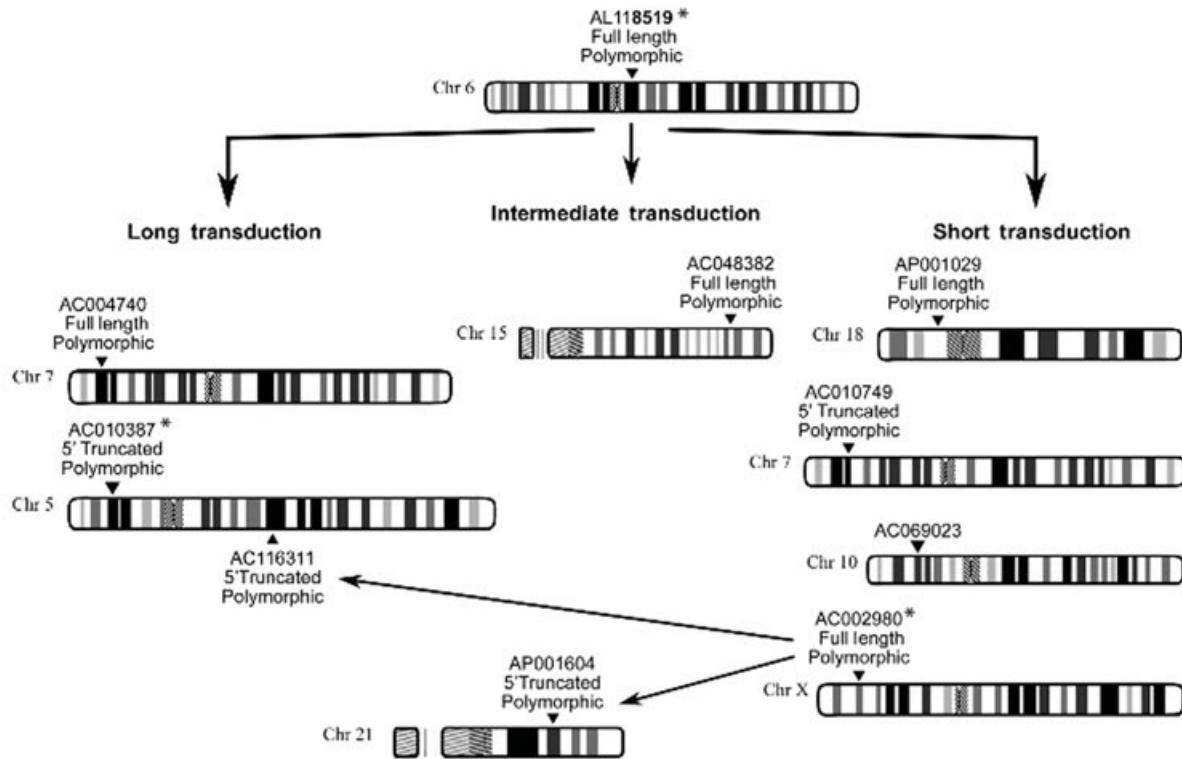
L1s carrying 3' transductions have disrupted human genes: *APC* (MIM #611731) [Miki et al., 1992]; *Dystrophin*, *DMD* (MIM #300377) [Holmes et al., 1994], *CYBB* (MIM #300481) [Meischl et al., 2000]; *RP2* (MIM #300757) [Schwahn et al., 1998]; and *CHM* (MIM #300390) [van den Hurk et al., 2003, 2007]. Here, TS-ATLAS was combined with previously published data [Beck et al., 2010; Brouha et al., 2002; Goodier et al., 2000; Kimberland et al., 1999; Myers et al., 2002] to enable the identification of 25 L1s from three active L1 transduction lineages (L1_{RP}, AC002980, and LRE3). On genotyping the novel elements revealed by TS-ATLAS, we noted that none of the elements reported here was recovered in the study by Ewing and Kazazian analyzing the pilot 1000 Genomes Project dataset [Ewing and Kazazian, 2011], despite some overlap between the study participants and our genotyping panel. Screening the 1000 Genomes data for junction reads that corresponded to the sequences of TS-ATLAS-identified insertions (Supp. Table S3), revealed eight of 18 insertions were supported by junction reads, indicating that their novelty is not due to low genome coverage in the pilot data. Thus, without lineage-specific molecular genomic approaches, capturing L1 transduction lineages in genome sequencing data will require refinement of existing bioinformatic approaches.

These results demonstrate that adapting transposon display methods is an effective means to selectively analyze active L1 lineages. Additionally, for some loci, the use of frequently cutting restriction enzymes can enable more comprehensive coverage of the human genome, allowing for the identification of more lineage members. For example, whole genome *in silico* restriction analyses showed that only ~12% of the genome is within suppression PCR range (<~1,000 bp) when libraries are constructed with *VspI*, but that ~80% of the genome is accessible using *NlaIII*. The relatively small number of coamplifying fragments generated in TS-ATLAS makes fractionation and isolation of novel loci by agarose gel electrophoresis straightforward. In principle, TS-ATLAS could be enhanced by the use of multiple restriction enzymes (dependent upon the particular transduction sequence), as used in a related display technique developed to analyze LTR retrotransposons in the mouse genome [Ray et al., 2011].

The application of TS-ATLAS to a small panel of nine unrelated individuals allowed the identification of 20 novel L1s. Strikingly the majority (11) of these elements were full-length raising the possibility that these lineages are not only adept at propagating 3' transductions but also generating full-length insertions. To estimate the rate of full-length offspring element production across the three lineages, we excluded putative progenitor elements that are necessarily full-length (AL050308, AL118519, AC067958, and AC002980), as well as disease causing elements that may be more likely to be full-length due to acquisition bias (L1_{RP} and L1_{CYBB}), and elements of unknown length (AC069023). This results in 59% (10 of 17) of novel elements observed here being full-length, a stark contrast with the ~30% of genomic Ta elements that are of similar size [Boissinot et al., 2000]. However, it is very likely that full-length insertions are selected against [Boissinot et al., 2001], leading to a reduction in average insert length over evolutionary time. To test whether the high fraction of full-length elements in transducing lineages is an intrinsic property of these elements or simply reflects their evolutionary young age could be tested using comparative quantitative retrotransposition assays of the progenitor elements, as carried out for L1_{RP} and LRE3 previously [Farley et al., 2004; Gilbert et al., 2005].

Of these 20 L1s, one (AL050308) is the putative progenitor of a mutagenic insertion (L1_{RP}) into the X-linked retinitis pigmentosa *RP2* gene [Schwahn et al., 1998] and retrotransposes at ~170% of the level of a 'hot' reference element, L1.3 (L19088 [Dombroski

A



B

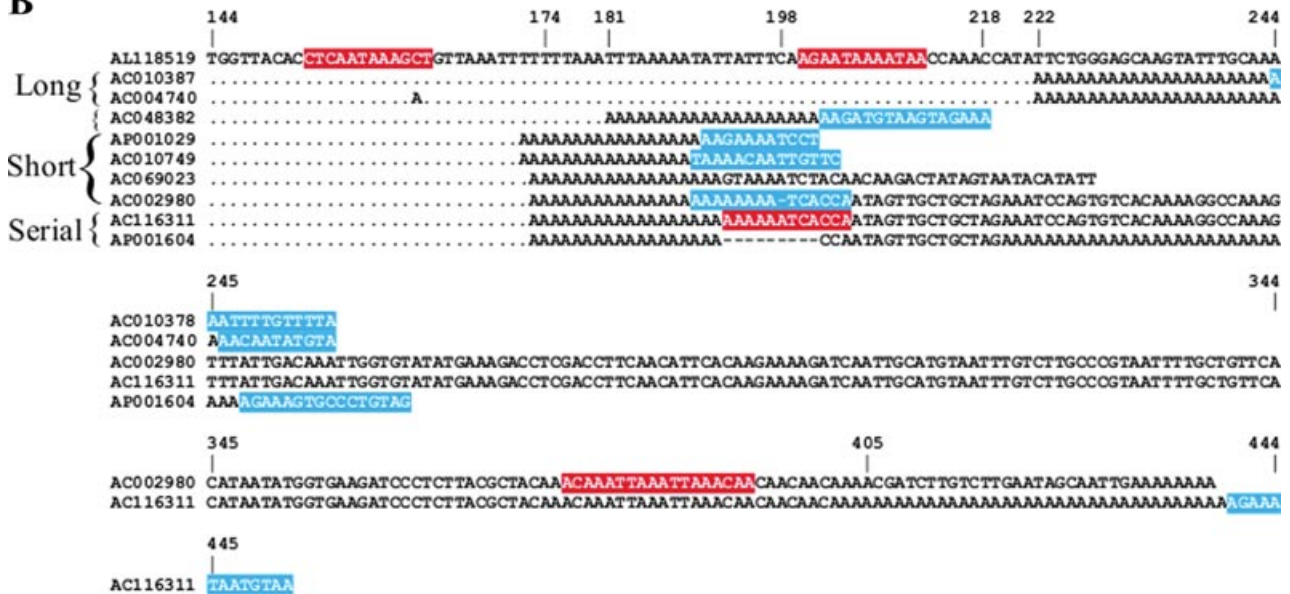


Figure 4. Variable transduction lengths in the AC002980 family. **A:** Characteristics and putative relationships of the AC002980 family. Data presented here are compiled from this study and other publications [Beck et al., 2010; Brouha et al., 2002; Goodier et al., 2000; Kimberland et al., 1999; Myers et al., 2002]. Putative relationships of L1 loci are indicated by arrows. Ideograms were adapted from the NCBI map viewer (<http://www.ncbi.nlm.nih.gov/projects/mapview/>). The AC002980 family contains elements characterized by alternative polyadenylation resulting in variable lengths of transduced sequence. The long, intermediate, and short transductions are derived from the progenitor locus AL118519. Loci AC004740 and AC010387 retain the long transduction, AC048382 contains an intermediate length transduction, whereas AP001029, AC010749, AC068023, and AC002980 have a shorter transduction. AP001604 and AC116311 contain sequences putatively derived from the AC002980 locus. Asterisks (*) denote L1s present in the human genome reference assembly (hg18). **B:** Multiple alignment showing variable transduction lengths and putative polyadenylation sites in the AC002980 lineage. The long, intermediate, and short transductions are derived from the progenitor locus AL118519. Short transduction lengths end at bases 173/174, The intermediate transduction of AC048382 ends at base 181, and long transduction lengths end at base 222. Following this (bases 198–405) the alignment shows the direct offspring of the AC002980 locus, with AP001604 ending at base 218 and AC116311 base 405. Sections highlighted in red are predicted poly (A) signal regions determined using the Hamming–Clustering (HC) network analysis ([http://zeus2.itb.cnr.it/~webgene/wwwHC_poly\(A\).html](http://zeus2.itb.cnr.it/~webgene/wwwHC_poly(A).html)). TSDs, confirmed by sequencing, are highlighted in blue.

et al., 1993]). The allele frequency (0.149) and activity of AL050308 suggest that the L1_{RP} lineage is actively amplifying in human populations. Previously reported members of the L1_{RP} lineage (AL590011 and AC019288, Table 1) show activities (~69% and ~120%, respectively, compared with L1.3) and allele frequencies (0.21 and 0.002, respectively) consistent with this hypothesis [Beck et al., 2010].

Comparison of L1s from the AC002980 transduction lineage revealed diversity in the site of L1 polyadenylation. Of the 9 L1s related to the progenitor element, AL118519, two pairs of events used precisely the same poly (A) addition site (AC010378/AC004740, AC010749/AP001029) but the five other sites were used only once. Thus, nine events utilized seven distinct poly (A) addition sites. These data are consistent with the notion that L1 polyadenylation is dependent upon local primary sequence context and can occur either at its native site or at suitable sites downstream of the L1 insertion. Indeed, these data are consistent with the observation of serial transductions, where sequences from multiple loci are sequentially mobilized by a particular L1 lineage [Brouha et al., 2002; Goodier et al., 2000; Holmes et al., 1994; Pickeral et al., 2000; van den Hurk et al., 2003]. Such events are well described in the case of the LRE3 lineage and are also apparent in AC002980 and L1_{RP} lineages [Beck et al., 2010]. A consequence of a highly variable, stochastic polyadenylation mechanism is that L1 3' ends might be expected to expand rapidly over evolution, eventually leading to the decay of the canonical Cleavage Polyadenylation Stimulating Factor 1 (CPSF1) binding site upstream of the encoded poly (A) tract. However, experimental observations suggest that the priming of Target-Primed Reverse Transcription (TPRT) in L1 retrotransposition is not strictly dependent upon a terminally located adenosine nucleotide, but can occur at internal sites in the L1 poly (A) tail [Kopera et al., 2011; Kulpa and Moran, 2006; Ovchinnikov et al., 2001]. As a result, in principle, TPRT could initiate within other poly (A) tracts, such as the "original" terminal poly (A) tract, upstream of transduced sequences, a process that has been observed for Alu constructs in cell culture assays [Wagstaff et al., 2012]. Such priming events would lead to loss of the transduced sequences that distinguish the lineage. A closely related group of three elements that may exemplify this process is transduction lineage IV (c.f. Fig. 5 Beck et al. 2010 [Beck et al., 2010]). Two elements (ABC11.27 and ABC11.35) share a short 3' transduction, which the third element lacks (ABC11.8). As the 3' transduction in this lineage does not include the TSD of ABC11.8, we can exclude the possibility that ABC11.8 is the progenitor of ABC11.27 and ABC11.35. Another possibility is that all three elements derive from the same progenitor, but ABC11.8 has been polyadenylated at the canonical L1 CPSF1 binding site, removing the transduced sequence. Thus, populations of L1 elements, some carrying 3' transductions and some with a canonical structure, might be maintained at equilibrium by these opposing processes. A theoretical consequence of such equilibrium would be a systematic underestimation of the number of elements belonging to particular active L1 lineages, even when applying technical innovations such as TS-ATLAS.

By selectively amplifying related active L1 elements only, we can simultaneously reduce the complexity of linkered PCR libraries and so increase their sensitivity. With effective destruction of known transduction primer targets by enzymatic suppression, the possibility of amplifying fragments present at less than constitutional levels arises. We are currently applying variants of these techniques to germline (sperm) and fetal DNA pools to detect germline and somatic mosaicism. Such mosaicism is likely to be common if endogenous elements retrotranspose in early embryogenesis [Garcia-Perez et al., 2007; Kano et al., 2009; van den Hurk et al., 2007]. Moreover, three highly active transduction-containing L1s are asso-

ciated with additional events, indicating they are donor 'hotspots' and have been active in modern human genomes [Beck et al., 2010; Kidd et al., 2010]. Phylogenetic analysis of novel, active L1 elements detected by fosmid end sequencing also captured additional transduction lineages [Beck et al., 2010]. Thus, application of TS-ATLAS to additional transduction families, and the use of this method within larger pedigrees will directly provide data on the activity of L1 lineages in the human population. Furthermore, as certain transduction lineages include some of the most active L1s in human populations, TS-ATLAS could be adapted to screen distinct cellular populations for elements that have retrotransposed in a tissue specific manner. Brain regions where endogenous L1 activity appears to be elevated [Baillie et al., 2011; Coufal et al., 2009; Muotri et al., 2005; Muotri et al., 2010] could be illuminating targets.

In conclusion, by utilizing 3' transduction sequences specific for active lineages it is possible to efficiently capture related active L1s. In addition, TS-ATLAS is flexible and can be readily adapted to analyze different lineages of interest. One unexpected discovery enabled by TS-ATLAS is the apparent plasticity of the polyadenylation location within a transduction family. Therefore, TS-ATLAS both readily identifies amplifying lineages of L1 across multiple individuals and provides novel insights into the mechanism of endogenous L1 retrotransposition.

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Disclosure statement: The authors declare no conflict of interest.

The authors assert that there are no Conflicts of Interest associated with the reported research. In the interests of full disclosure J.V.M. is an inventor on the following patent: Compositions and methods of use of human retrotransposons. Application No. 60/006,831; Patent number 6,150,160; Issued November 21, 2000. His involvement with this patent is disclosed voluntarily and does not influence the content or conclusions of this study.

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