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(54) Title: METHOD FOR ASSESSING THE QUALITY OF VARIOUS CELLS INCLUDING INDUCED PLURIPOTENT STEM CELLS

(57) Abstract: The present invention relates to a method for assessing the quality, utility and applicability of a cell according to the said method comprising the following steps: a) analyzing the expression of the TEs of said cell in order to set up an expression profile of the TEs of said cell; b) comparing the expression profile obtained in step a) to a reference.



Method for assessing the quality of various cells including induced pluripotent stem cells

5 **FIELD OF THE INVENTION**

The present invention is directed to methods for assessing the quality of various cells including induced pluripotent stem cells and differentiated cells.

BACKGROUND OF THE INVENTION

10 The recent discovery of factors that reprogram somatic cells from patients into induced pluripotent stem cells (iPSCs) has led to a further increase in the number of pluripotent cell lines available to the research community. Because of this progress and because iPS cells are similar to embryonic stem (ES) cells without being hampered by the same ethical and immunological concerns, it is now believed
15 that iPSCs cells, by allowing a patient's own cells to become a source of therapeutic tissue, have the potential to become a platform for personalized medicine. Thus, iPSC has become a strong and highly promising therapeutic strategy for treating incurable human diseases.

 However, a major limitation encountered with the use of such cells is that
20 their genomic integrity may be compromised during their generation or during *ex vivo* culture. Indeed, at the end of the reprogramming of human somatic cells into iPS cells, several colonies that at first sight look like acceptable iPSCs are obtained, but they are not all equivalent as they have not reached the same level of reprogramming and not all of them have acquired the same differentiation potential.
25 Moreover, some could display phenotypes incompatible with clinical applications, such as block in some differentiation pathways, predisposition to oncogenic changes, release of bioactive molecules, and altered immunogenicity.

 Thus, it has become clear that not all human pluripotent cell lines are equally suited for every purpose. This suggests that any new research project should perform
30 a deliberate and informed selection of the cell lines that are most qualified for an application of interest. However, there is little information or guidance concerning how to select cell lines that are most appropriate for each application.

There is thus an unfulfilled need for a novel, effective and efficient method that can assess the quality and developmental stage or state of a given cell, in particular induced pluripotent human cell lines, and predict their behavior.

5 SUMMARY OF THE INVENTION

The inventors met the burden to show, for the first time, that the expression of transposable elements (TEs) may constitute a signature for a given cell, such as induced pluripotent stem cells as well as differentiated cells.

10 Thus, **in a first aspect**, the invention relates to a method for assessing the quality and/or utility of a cell, said method comprising the following steps:

- a) analyzing the expression of the transposable elements of the said cell in order to set up an expression profile of the TEs of said cell;
- b) comparing the expression profile obtained in step a) to a reference;

15 wherein said cell is selected from the group consisting of :

- induced pluripotent stem cells (iPSC);
- pluripotent stem cells and precursor cells selected from the group consisting of embryonic stem (ES) cells, somatic stem cells, hematopoietic stem cells, leukemic stem cells, skin stem cells, intestinal stem cells, gonadal stem cells, brain stem cells, muscle stem cells, mammary stem cells, neural stem cells;
- differentiated cells; and
- cells of the embryonic developmental stages from zygote to fetus, including zygote, cells of morula, cells of blastula, cells of gastrula, cells of blastocytes.

In a first embodiment, said cell is an induced pluripotent stem cell (iPSC).

In a second embodiment, said cell is a CD34⁺ hematopoietic stem cell.

In a third embodiment, said cell is a differentiated cell.

30 **In a second aspect**, the invention pertains to the signatures of TEs as independently defined in table 1, table 2, table 3, table 4, table 5 and table 6. The invention also relates to the uses of said signatures for assessing the quality of a given cell.

In a first embodiment, the signatures as defined in table 1 or table 2 are used for discriminating iPSC based on their TE expression signature, that is, a TE expression pattern closest to that seen in bona fide ES cells, rather than that associated with differentiated tissue or disease phenotypes.

In a second embodiment, the signature as defined in table 3 is used for selecting hematopoietic stem cells that can be used for all relevant clinical or research applications such as hematopoietic stem cells transplantation.

In a third embodiment, the signature as defined in table 4 is used for selecting hepatocytes that are most appropriate for research or clinical applications such as disease modeling, toxicology studies or cell therapy.

In a fourth embodiment, the signature as defined in tables 5 and 6 are used for selecting respectively resting and activated CD4+ T lymphocytes.

In a third aspect, the invention relates to a kit comprising means for detecting the expression of TEs as independently defined in table 1, table 2, table 3 table 4, table 5 and table 6.

DETAILED DESCRIPTION OF THE INVENTION

Definition

"Transposable elements" or "TEs" refer to mobile genetic elements of a genome that have or had (many have lost this ability and are now domesticated by the host cell for regulatory purposes) the ability to move from one location to another in the genome. Transposable elements constitute a normal and ubiquitous component of genomes. Transposable elements may cause genetic changes and make important contributions to the evolution of genomes by inserting into genes; inserting into regulatory sequences; or modification of gene expression through a variety of mechanisms, both transcriptional and post-transcriptional. TEs account for over half of the mouse or human genome, and their potential as insertional mutagens and transcriptional perturbators is suppressed by early embryonic epigenetic silencing.

Recent findings demonstrate that certain classes of TEs or specific TE loci are essential to reach and maintain the pluripotent state.

TEs replicate in two main ways, involving either a DNA or an RNA intermediate, and they have been accordingly divided into two classes, namely: DNA transposons and retrotransposons. TEs have the ability to move from place to place in the genome, hence their designation as mobile DNAs. DNA transposons spread by a non-amplifying “cut-and-paste” mechanism, whereas retrotransposons use a copy-and-paste process that increases their genomic representation. Thus, transposable elements facilitate genome evolution, support genome structure and provide numerous cis-acting elements such as promoters, enhancers, alternative exons, transcription terminators and splice junctions to protein-coding loci or to non coding RNAs.

'Retrotransposons', *"endogenous retroelements"* and *"retroposons"* refer to a subset of transposable elements that go through an RNA intermediate that is reverse transcribed before re-integration at a novel genome site, in a “copy and paste” mechanism. Hence, these elements do not excise when they transpose. Instead, they make a copy that inserts elsewhere. Although transcription of retrotransposons is an integral part of their life cycle, elements may be transcriptionally active without this resulting in proliferation of the elements within the host genome.

They can be further classified based on their structure.

LTR elements or endogenous retroviruses (ERVs) are characterised by long terminal repeats and include (or included as older elements often lose part of this structure through mutation or recombination) the *gag*, *pol*, and *env* genes. These evolved as a consequence of retroviral infection of germ cells, so that they are inherited through generations.

Non-LTR retrotransposons include long and short interspersed repeat elements (LINEs and SINEs) and SVA elements that are a composite of sequences derived from other repeats (SINE, VNTR [variable number tandem repeat], and *Alu*).

There are only three highly active elements in the human genome:

- (1) a subset of LINEs;
- (2) *Alu* elements that are a family of primate-specific SINEs; and
- (3) SVA elements.

Impacts of the retrotransposons on the transcriptome may be considered transcriptional (or co-transcriptional) and posttranscriptional. The former mechanisms refer to any TE related transcriptional effect and include provision of an alternative promoter that may be tissue- or stage-specific in its activity; promotion of
5 alternative splicing either through prevention of the splicing machinery from recognising a splice acceptor site in an endogenous exon (exon skipping) or through incorporation of the TE into the mature transcript (exonization); promotion of alternative polyadenylation (poly(A)) either by providing an alternative polyadenylation signal or by promoter activity interfering with host gene
10 transcription and causing upstream polyadenylation; and by introducing transcription factor binding sites that may confer tissue- or stage-specific expression, or link a gene into a transcriptional network.

"Embryonic stem cells" are pluripotent stem cells derived from the inner cell mass of a blastocyst, an early-stage embryo. They are unique in the ability to
15 maintain pluripotency over significant periods in culture, making them leading candidates for use in cell therapy. Embryonic stem cell differentiation involves epigenetic mechanisms to control lineage-specific gene expression patterns. ES cell-based therapies hold great promise for the treatment of many currently intractable heritable, traumatic, and degenerative disorders. The distinguishing characteristics of
20 an embryonic stem cell define an embryonic stem cell phenotype. Accordingly, a cell has the phenotype of an embryonic stem cell if it possesses one or more of the unique characteristics of an embryonic stem cell such that that cell can be distinguished from other cells. Exemplary distinguishing embryonic stem cell characteristics include, without limitation, gene expression profile, proliferative capacity, differentiation
25 capacity, karyotype, responsiveness to particular culture conditions.

It has become clear that pluripotency encompasses more than one stage of development. The earlier **"naïve"** stage is closest to the preimplantation inner cell mass or even slightly earlier stages, whereas, the **"primed"** stage is akin to the post-implantation epiblast. The primed ES stage is generally referred to as human ES cells
30 (hESCs). Therefore, naïve and primed ES cells basically differ by their stage of development. Naïve ES are the developmentally earliest state described for human established cultured cells to date. Existing human ES cell lines in the later primed

state can be reverse toggled to the naïve state by exposure to appropriate culture conditions

The term "*reprogramming*" as used herein refers to a process that alters or reverses the differentiation state of a differentiated cell.

5 The term "*induced pluripotent stem cell*" or "*iPS cell*" or "*iPSC*" refers to a type of pluripotent stem cell artificially derived from a non-pluripotent, adult somatic cell, by compulsory dedifferentiation (reprogramming). Typically, said iPS cells are reprogrammed by the expression of the transcription factors Oct4 (also known as POU5F1), Sox2, Klf4, and c-Myc (OKSM, or other variations of reprogramming
10 cocktails).

The term "*pluripotent*" as used herein refers to a cell with the capacity, under different conditions, to differentiate to cell types characteristic of all three germ cell layers (endoderm, mesoderm and ectoderm). Pluripotent cells are characterized primarily by their ability to differentiate to all three germ layers, using, for example,
15 an immuno-deficient mouse teratoma formation assay. A pluripotent cell is an undifferentiated cell.

The term "*differentiated cell*" refers to any primary cell that is not, in its native form, pluripotent as that term is defined herein. It is noteworthy that placing many primary cells in culture can lead to some loss of fully differentiated
20 characteristics. Thus, simply culturing such cells is included in the term "differentiated cells" and does not render these cells non-differentiated cells (e.g. undifferentiated cells) or pluripotent cells. The transition of a differentiated cell to pluripotency requires a reprogramming stimulus beyond the stimuli that lead to partial loss of differentiated character in culture. Reprogrammed cells also have the
25 characteristic of the capacity of self-renewal (extended passaging) without loss of growth potential, relative to primary parental cells, which generally have capacity for only a limited number of divisions in culture. In some embodiments, the term "differentiated cell" also refers to a cell of a more specialized cell type derived from a cell of a less specialized cell type (e.g. from an undifferentiated cell or a
30 reprogrammed cell) where the cell has undergone a cellular differentiation process.

As used herein, the term "*somatic cell*" refers to any cell other than an ES, iPS or germ cell. In mammals, germline cells (also known as "gametes") are the

spermatozoa and oocytes, which fuse during fertilization to produce a cell called a zygote, from which the entire mammalian embryo develops.

As used herein, the term "*adult cell*" refers to a cell found throughout the body after embryonic development.

5 The term "*cell line*" refers to a population of largely or substantially identical cells that has typically been derived from a single ancestor cell or from a defined and/or substantially identical population of ancestor cells.

Method for assessing the quality of a cell

10

The inventors have showed that endogenous retroelements (EREs) are markedly upregulated during the reprogramming into iPS cells of either mouse embryonic fibroblasts, human CD34+ cells or human primary hepatocytes, with hundreds of ERE loci not associated with pluripotency aberrantly unleashed. The
15 inventors have thus thoroughly analyzed all TE integrants (loci) during iPS reprogramming and they identified clusters of TEs that are specific of reprogramming time-points, which likely reflect cellular sub-states on the path to pluripotency.

Surprisingly, they also observe that thousands of TEs, which were broadly
20 thought to be inactivated at this stage, are in fact highly expressed in somatic cells ranging from primary hepatocytes to neural committed cells and CD34+ hematopoietic stem cells. Therefore the inventors met the burden to show, for the first time, that the expression of retroelements may constitute a signature for a given cell such as induced pluripotent stem cells, as well as differentiated cells.

25 Moreover, a large fraction of expressed TEs in each cell are highly specific of that cell type, thereby providing the opportunity to accurately and predictively describe the unique expression profile of all the TEs, also referred as "*transcriptome*", of distinct cellular states. Therefore, the inventors met the burden to identify signatures that may be used as a precise marker of cellular states
30 with broad applications in quality control.

Such a precise cell stage gauge and quality control method should prove crucial in the assessment of induced pluripotent stem cell attributes. Indeed, iPS clones are very heterogeneous in terms of phenotypes that include differentiation

capacity and potentially predisposition to oncogenic changes. The inventors observed that certain iPS clones failed to differentiate in certain lineages and that this phenotype correlated with a distinct pattern of TE expression. Similarly, Yamanaka and al observed (Koyanagi-Aoi et al., PNAS 2013) that seven iPS clones that were
5 defective for neural differentiation showed increased expression of several genes, many of which were driven by the promoter (LTR7) of a human specific endogenous retroelements (HERVH). Moreover, Ohnuki et al. (Ohnuki, PNAS 2014) proposed that general HERVH levels need to be reduced to an ES-like level in iPS clones following a peak of expression during reprogramming in order to be differentiation
10 competent. These data are in agreement with the inventors' own demonstration of TE dysregulation during reprogramming (Friedli et al., Genome Res 2014) and recent observation that differentiation-defective iPS clones show a distinct TE expression signature.

The inventors met the burden to identify and disclose the expression profiles
15 of the TEs of several cell stages for each of about 4 million TE integrants. The result is a highly accurate and specific signature akin to a unique barcode descriptive and predictive of each cell stage or state. These TE signatures are approximately two orders of magnitude above that of tissue-specific genes, with thousands of TEs uniquely expressed in a specific cell type.

20

Therefore, **in a first aspect**, the present invention relates to a method for assessing the quality and/or utility of a cell, said method comprising the following steps:

a) analyzing the expression of the TEs of said cell in order to set up an
25 expression profile of all TEs, more precisely of all TE integrants (loci) of said cell;

b) comparing the expression profile obtained in step a) to a reference;

wherein said cell is selected from the group consisting of :

- induced pluripotent stem cells (iPSC);
- 30 – pluripotent stem cells and precursor cells selected from the group consisting of embryonic stem (ES) cells, somatic stem cells, hematopoietic stem cells, leukemic stem cells, skin stem cells, intestinal

stem cells, gonadal stem cells, brain stem cells, muscle stem cells, mammary stem cells, and neural stem cells;

- differentiated cells; and
- cells of the embryonic developmental stages from zygote to fetus, including zygote, cells of morula, cells of blastula, cells of gastrula, cells of blastocytes.

The method of the invention allows for a high throughput screening which provides for the rapid identification and selection of cells, which are suitable for further uses such as research, modeling, therapeutic or bioprocessing applications.

The invention thus harnesses the power of genetic by providing specific signatures of TE expression that give essential information regarding a cell line.

Step a) of the method of the invention consists of an analysis of the expression of all TE integrants (loci) of a cell. Step a) allows establishing the expression profile of the TE of said cell. Preferably, said TEs are retrotransposons.

As used herein, the expression "***expression profile of the TEs***" refers to qualitative and/or quantitative expression of the TEs in a cell. The expression profile is a repository of the expression level data that can be used to compare the expression levels of different TEs, in whatever units are chosen. Put in other words, step a) consists in setting up a collection of all the TEs of the cells, i.e. setting up the "transcriptome" of said cell. In the context of the invention, the terms "***expression profile of the TEs***", "***transposable element (TE) transcriptome***" and "***transcriptome***" can be used interchangeably, and refer to the collection of all transcripts containing TE and TE-derived sequences in a specific cell. Basically, the transcriptome encompasses all the transposable elements transcribed in any cell type or developmental stage/state.

In a preferred embodiment, the transcriptome according to the invention refers to the collection of all transcripts containing retrotransposons and retrotransposons-derived sequences in a specific cell.

The inventors met the burden to specifically identify the loci of the TEs (TE integrants). Thus, the expression "***transcriptome***" preferably refers to the collection of all transcripts containing TE and TE-derived sequences in a specific cell, and the precise identifications of the locus from which they originate.

Typically, step a) of analyzing the expression profile of TEs consists in identifying and quantifying the transcripts originating from all TEs, more precisely all TE integrants (loci).

Said step is carried out by RNA Sequencing, also referred to as "**RNAseq**".

5 RNAseq has been widely adopted as a gene-expression measurement tool due to the detail, resolution, and sensitivity of transcript characterization that the technique provides. It falls within the general knowledge of person skilled in the art to carry out a RNA sequencing for identifying accurately mapping, and quantifying TEs.

In another embodiment, the step of analyzing the expression of TEs of a cell
10 consists in identifying the transposable element integrants within the DNA of the cell. Said step is carried by the unambiguous mapping of individual TE reads (sequences) to specific unique genomic loci. This step requires:

- Sufficient depth of sequencing (typically > 40 million reads per RNA sample);
- 15 – Sufficient length of reads (100bp or more);
- Paired-end and stranded protocols desirable.

Typically, step a) can be performed on an Illumina platform according to the manufacturer's standard protocols.

As used herein, "**cell quality**" relates to technical features of a cell that render
20 such cell appropriate for given intended uses. Typically, quality control relates to features such as cell identity/morphology, cell phenotype, cell genotype, levels of cell contamination, degree of pluripotency, differentiation or reprogramming potential, cell viability, contamination levels, and/or cell safety especially with regards to potential predisposition to oncogenic changes or uncontrolled and anarchic
25 cell growth.

For stem cells, quality is usually defined as self-renewal capacity, expression of specific markers, differentiation ability, ability to be converted to the naïve state, and absence of detrimental phenotypes such as predisposition to oncogenic changes, release of bioactive molecules, and altered immunogenicity.

30 Preferably, as used herein, a cell which proves to be of acceptable quality is a cell that does not show any potential predisposition to oncogenic changes or uncontrolled and anarchic growth. Thus, in the context of the present invention, the expression "**assessing the quality of a cell**" preferably refers to the determination of

an absence of a potential predisposition to oncogenic changes or uncontrolled and anarchic cell growth.

As used herein, the expression "*cell utility*" or "*cell use*" refers to the intended purposes of the target cell. Said purposes include but are not limited to
5 research, therapeutic or diagnostic purposes.

In prior art, the assessment of the quality of a cell is implemented with tests that may involve the use of DNA profiling techniques, immunohistochemistry, alkaline phosphatase staining, flow cytometry, gene expression analysis (perhaps
10 using expression arrays and the like), blood group typing, karyotypes, microorganism screening (using PCR and immunological based techniques), teratoma and embryoid body formation (particularly relevant where the pluripotency of a stem cell is being tested) and simple live/dead (trypan blue) stains to determine viability. By establishing a reference indicative of a certain cell "*quality standard*", the inventors
15 developed a method that allows controlling the quality of cells by comparison of TE transcriptome (transposcriptome) to a reference.

It should be understood that the term "standard" or "quality standard" may relate to defined criteria or features which any given cell must exhibit prior to being used. Such standards may be set by regulatory bodies but may also relate to locally
20 determined cell features and/or characteristics which render cells suitable for particular uses - for example uses in assays, or in therapeutic purposes.

Typically, the reference of step b) can be determined experimentally, empirically, or theoretically. Preferably, said reference is the expression profile of the TEs of a cell having known or defined qualities. More preferably, said reference
25 is a signature of TE expression of a cell having known or defined qualities.

In a first embodiment, said cell is an induced pluripotent stem cell.

The method of the invention thus relates to a method of characterization of various cells, especially pluripotent stem cells such as induced pluripotent stem cells
30 (iPSCs). iPSC are very heterogeneous in terms of phenotypes. Presently, existing methods cannot predict how a pluripotent stem cell line will behave in a given directed differentiation paradigm.

The method of the invention addresses the limitations of prior art by enabling to forecast the differentiation efficiency of iPSC and their quality, especially with regards to the absence of any potential predisposition to oncogenic changes or uncontrolled and anarchic cell growth. The method of the invention thus allows a
5 quality control that proves crucial in the assessment of iPSC.

Preferably, step **b)** consists in a step **b1)** of comparing the expression profile of step a) to the expression profile of the TEs of a naïve embryonic stem cell or a primed embryonic stem cell, preferably of a primed embryonic stem cell. In this embodiment, said iPSC is considered as showing an acceptable quality and/or to
10 show genomic integrity if the expression profile obtained in step a) comprises at least 80%, 85%, 90%, 95% or more preferably 100% of the TEs of the expression profile of said naïve embryonic stem cell or said primed embryonic stem cell.

Alternatively, said step **b)** consists in a step **b2)** of comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 1 or table
15 2. In this embodiment, the iPSC is considered as showing an acceptable quality and/or to show genomic integrity if at least 80%, preferably 85%, preferably 90%, preferably 95% or more preferably 100% of the TEs as disclosed in table 1 or 2 are present in the expression profile as obtained in step a).

As used herein, the expression "**genomic integrity**" refers to an apparent
20 absence of mutation or any risk of malignant transformation of the iPSC's genome.

Preferably, said step **b)** consists in a step **b2)** of comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 2.

Table 1 represents the TEs expressed in a naïve embryonic stem cell. The list of TEs of table 1 thus constitutes a unique signature of naïve embryonic stem cells.

25 Table 2 represents the TEs expressed in a primed embryonic stem cell. The list of TEs of table 1 thus constitutes a unique signature of primed embryonic stem cells.

As used herein, the expressions "**signature**", "**signature of TE expression**" or "**TE signature**" refer to the expression of TEs in a given cell that proved to be
30 specific to a given cell type, a stage of development and/or a state of said cell. It is noteworthy that a "signature" in the sense of the present invention does not comprise all the TEs of the cells (i.e. the transcriptome). Quite the reverse, a signature

comprises only the TEs that are found to be specific to a given cell type, state or stage of development.

By comparing the TE transcriptome of an iPS cell to the TE signatures of naïve ES or primed ES cells, as respectively defined in tables 1 and 2, the person skilled in the art can identify an iPS cell that shows high quality, especially with regards to its differentiation ability.

Thus, in a specific embodiment, the invention relates to a method for assessing the quality of an iPS cell comprising the steps of :

- a) analyzing the expression of the TEs of said iPS cell in order to set up an expression profile of the TEs of said iPS cell; and
- b) comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 1 or 2, preferably in table 2.

In a second embodiment, said cell is a hematopoietic stem cell.

In this embodiment, step **b)** consists in a **step b3)** of comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 3. In this embodiment, the hematopoietic stem cell is considered as showing an acceptable quality if at least 80%, preferably 85%, preferably 90%, preferably 95% or more preferably 100% of the TEs disclosed in table 3 are present in the expression profile as obtained in step a).

Table 3 represents the transposable elements expressed in a CD34+ hematopoietic stem cell. The list of the transposable elements of table 3 thus constitutes a unique signature of CD34+ hematopoietic stem cells.

Thus, in a specific embodiment, the invention relates to a method for assessing the quality of a hematopoietic stem cell comprising the steps of :

- a) analyzing the expression of the TEs of said hematopoietic stem cell in order to set up an expression profile of the TEs of said cell; and
- b) comparing the expression profile obtained in step a) to the expression of all the TE disclosed in table 3.

In this particular embodiment, the method of the invention allows the identification of hematopoietic stem cells that are of higher quality for broad applications. Indeed abnormal CD34+ cell levels are known to be associated with a poor prognosis of several cancers, especially acute myeloid leukemia. Acute myeloid

leukemia (AML) is a malignancy of immature cells. Intensive chemotherapy is the mainstay of treatment, but primary resistance and relapse after an apparent initial remission are frequently observed. Various factors are considered to be responsible for the difference in response to chemotherapy and to serve as prognostic parameters predicting outcome of therapy.

One of the promising therapeutic strategies for said disease may require transplantation of relevant CD34+ hematopoietic cells. The method of the invention allows the identification hematopoietic cells that are highly appropriate for such transplantation. The method of the invention thus allows the identification of hematopoietic stem cells that constitute good candidates for hematopoietic stem cell transplantation.

In a third embodiment, said cell is a differentiated cell.

Preferably, said cell is selected among neuronal cells and hepatocytes. More preferably, said cell is a hepatocyte.

The inventors have met the burden to show, for the very first time, that differentiated cell line can be identified and characterised thanks to the expression of TEs. They thus have shown that the method of the invention may give sensitive and important information regarding differentiated cells. Said information include: the cell type, the cell quality, and the degree of differentiation of said cell, the activation state of said cell. This information is critical for the assessment of cells envisioned for each application whether for basic research, diseases, modelling, drug screening or clinical applications.

In this embodiment, step **b)** consists in a **step b4)** of comparing the expression profile obtained in step a) to the expression of all the TEs as disclosed in table 4. In this embodiment, the hepatocyte is considered as showing an acceptable quality if at least 80%, preferably 85%, preferably 90%, preferably 95%, or more preferably 100% of the transposable elements disclosed in table 4 are present in the expression profile as obtained in step a).

Thus, in a specific embodiment, the invention relates to a method for assessing the quality of a hepatocyte comprising the steps of :

a) analyzing the expression of the TEs of said hepatocyte in order to set up an expression profile of the TEs of said cell; and

b) comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 4.

In a fourth embodiment, said cell is a CD4+ T lymphocyte.

5 The inventors have shown that CD4+ T lymphocytes can be identified and characterised thanks to the expression of TEs. The method of the invention allows the identification of resting and activated CD4+ T lymphocytes.

10 In this embodiment, step **b)** consists in a **step b5)** of comparing the expression profile obtained in step a) to the expression of all the TEs as disclosed in tables 5 and 6.

The CD4+ T lymphocyte is considered as resting if at least 80%, preferably 85%, preferably 90%, preferably 95%, or more preferably 100% of the transposable elements disclosed in table 5 are present in the expression profile as obtained in step a).

15 The CD4+ T lymphocyte is considered as activated if at least 80%, preferably 85%, preferably 90%, preferably 95%, or more preferably 100% of the transposable elements disclosed in table 6 are present in the expression profile as obtained in step a).

20 **Signature and uses thereof**

25 **In a second aspect**, the invention relates to specific signatures of TE expression. As indicated above, said signatures give various indication regarding a given cell line. The invention thus relates to uses for assessing the quality of a cell line.

Said signature gives comprehensive information regarding the quality of a cell and allow the discriminating cells depending on their quality, especially when compared to the expression profile of TEs of a cell having known or defined qualities.

30 The use of signature may allow discriminating induced pluripotent cells depending on their quality, especially their differentiation ability, developmental stage/state, and safety. The "**differentiation ability**" of an iPSC refers to its ability of differentiating in any kind of cells.

The use of said signature may also discriminate differentiated cells depending on their predisposition to oncogenic changes or uncontrolled and anarchic growth.

The invention thus pertains to the signatures of TEs as independently defined in table 1, table 2, table 3 and table 4.

5 The inventors have shown that said signatures are highly useful for assessing the quality of a given cell.

More precisely, the signatures as defined in tables 1 and 2 are used for assessing the quality of an iPSC. More specifically, the signature disclosed in tables
10 1 and 2 are compared to the expression profile of the TEs of a given iPSC for determining the general quality and differentiation potential of said iPSC. Thus, **in a first embodiment**, said signature is useful for discriminating cells depending on their differentiation ability. Said signature is also useful for discriminating cells depending on their ability to convert to the naïve state, their safety, and their general
15 research or clinical applications.

In a second embodiment, the signature as defined in table 3 is useful for assessing the quality of hematopoietic stem cells. More specifically, said signature is useful for selecting hematopoietic stem cells that are appropriate for research or
20 clinical applications including hematopoietic stem cells transplantation.

In a third embodiment, the signature as defined in table 4 is useful for assessing the quality of a hepatocyte. More specifically, said signature is useful for selecting hepatocytes that do not show a predisposition to oncogenic changes or
25 uncontrolled and anarchic growth and that are generally appropriate for research, disease modeling, drug screening, and cell therapy.

In a fourth embodiment, the signatures as defined in tables 5 and 6 are used for selecting respectively resting and activated CD4⁺ T lymphocytes.

Kits

The inventors have carried out a comprehensive analysis of the transposable elements of different kinds of cells.

- 5 Thus, **in a third aspect**, the invention relates to a kit comprising means for detecting the expression of the transposable elements as independently defined in tables 1, 2, 3, 4, 5 and 6.

TABLES

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Table 1: Retrotransposon signature specific to naive embryonic stem cell

Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chr17	15770110	15771695	SVA_D	Retroposon/SVA
chr19	23880259	23882993	L1PB1	LINE/L1
chr4	48187835	48189464	SVA_B	Retroposon/SVA
chr7	63539735	63542971	L1PREC2	LINE/L1
chr21	40528523	40530124	SVA_D	Retroposon/SVA
chr9	134782584	134784280	SVA_D	Retroposon/SVA
chr3	9890329	9890417	SVA_F	Retroposon/SVA
chr16	8164386	8165934	SVA_D	Retroposon/SVA
chr7	54733678	54734688	MLT1J2-int MLT1J2-int MLT1J2	LTR/ERV1-MaLR
chr11	83026662	83028894	SVA_D	Retroposon/SVA
chr1	24261449	24262991	SVA_D	Retroposon/SVA
chr4	3539599	3541490	SVA_D	Retroposon/SVA
chr12	101880933	101881146	L1PB4	LINE/L1
chr19	23876389	23877924	L1PB1	LINE/L1
chr7	63543278	63544295	L1PREC2	LINE/L1
chr1	24014645	24016257	SVA_D	Retroposon/SVA
chr19	23887175	23889043	THE1A THE1A-int	LTR/ERV1-MaLR
chr7	64725150	64726046	LTR5_Hs	LTR/ERV1
chr14	63988691	63990445	SVA_D	Retroposon/SVA
chr7	129115405	129117062	SVA_C	Retroposon/SVA
chr20	52472472	52473184	LTR8	LTR/ERV1
chr20	52470321	52471772	SVA_D	Retroposon/SVA
chr12	101882374	101882678	L1M2	LINE/L1
chr3	186591073	186592864	SVA_D	Retroposon/SVA
chr7	139204682	139205837	SVA_E	Retroposon/SVA
chr20	4014724	4015629	LTR5_Hs	LTR/ERV1

chr19	39287788	39289464	SVA_D	Retroposon/SVA
chr4	161583304	161589197	LTR12_ HERV9N-int HERV9N-int LTR12_	LTR/ERV1
chr13	46736400	46737787	SVA_C	Retroposon/SVA
chr5	79596365	79598167	SVA_D	Retroposon/SVA
chr13	50166317	50168382	SVA_F	Retroposon/SVA
chr2	11042073	11044034	SVA_F	Retroposon/SVA
chr4	123732308	123734357	SVA_D	Retroposon/SVA
chr19	20406577	20408040	SVA_D	Retroposon/SVA
chr19	23879028	23879960	L1PB1	LINE/L1
chr6	4342143	4343300	L1ME2z	LINE/L1
chr11	71890974	71891292	L1MC4	LINE/L1
chr1	50846651	50848247	SVA_D	Retroposon/SVA
chr19	23883363	23884258	MER41C PRIMA41-int	LTR/ERV1
chr12	56468876	56470558	SVA_F	Retroposon/SVA
chr11	107787145	107787939	LTR1A1	LTR/ERV1
chr7	123402309	123403788	LTR12C	LTR/ERV1
chr19	23878220	23878997	L1PB1	LINE/L1
chr19	22500220	22500587	L1PA6	LINE/L1
chr20	32721509	32724384	HERVK-int LTR5B	LTR/ERVK
chr1	226302000	226303681	SVA_F	Retroposon/SVA
chr19	22507210	22508143	MER50 MER50 MER50-int MER50-int	LTR/ERV1
chr19	22502165	22503664	L1MA8	LINE/L1
chr10	95729763	95731384	SVA_D	Retroposon/SVA
chr20	35753579	35755544	SVA_D	Retroposon/SVA
chr20	5007569	5009319	SVA_F	Retroposon/SVA
chr17	42314809	42316928	SVA_D	Retroposon/SVA
chr15	56404611	56405876	L1PA10	LINE/L1
chr6	123168926	123171462	SVA_F	Retroposon/SVA
chr7	48033440	48033737	HAL1	LINE/L1
chr3	48770906	48772886	SVA_D	Retroposon/SVA
chr12	101881320	101881630	AluY	SINE/Alu
chr20	52471952	52472263	AluSx	SINE/Alu
chr3	186583377	186584275	LTR5_Hs	LTR/ERVK
chr8	59588380	59589853	SVA_C	Retroposon/SVA
chr6	43392359	43393744	SVA_C	Retroposon/SVA
chr2	26132612	26134450	SVA_D	Retroposon/SVA
chr7	64726049	64726204	AluSx	SINE/Alu
chr3	39268580	39270084	SVA_D	Retroposon/SVA
chr3	39301261	39302248	L1MA7	LINE/L1
chr12	4814512	4814994	L1MCA	LINE/L1
chr18	70916201	70916749	L1MDa	LINE/L1

chr7	139204545	139204681	AluYc	SINE/Alu
chr4	165940373	165942121	SVA_D	Retroposon/SVA
chr4	165920887	165924068	HERVK-int HERVK-int LTR5_Hs	LTR/ERVK
chr20	52473548	52473761	MIRb	SINE/MIR
chr4	165983987	165984263	L1MC5a	LINE/L1
chr9	29188016	29190063	SVA_D	Retroposon/SVA
chr1	150753326	150755021	SVA_F	Retroposon/SVA
chr4	165966823	165967128	AluSp	SINE/Alu
chr19	52945422	52945881	MER9a3	LTR/ERVK
chr5	1114663	1115304	L1MC5	LINE/L1
chr4	6978804	6980483	SVA_D	Retroposon/SVA
chr9	134782054	134782580	MER41B	LTR/ERV1
chr8	42560048	42560472	MLT1J	LTR/ERVL-MaLR
chr17	3756901	3758383	SVA_D	Retroposon/SVA
chr12	101882732	101883218	L1MA7	LINE/L1
chr20	18305332	18305985	PABL_A	LTR/ERV1
chr15	40974273	40976457	SVA_D	Retroposon/SVA
chr20	4012514	4013564	SVA_E	Retroposon/SVA
chr6	34753553	34755313	SVA_D	Retroposon/SVA
chr1	76577139	76579019	SVA_D	Retroposon/SVA
chr19	20414708	20415010	AluSq2	SINE/Alu
chr17	20587728	20589414	SVA_D	Retroposon/SVA
chr6	4344781	4344979	MIRb	SINE/MIR
chr19	41153273	41155109	SVA_D	Retroposon/SVA
chr6	76142398	76144922	L1PA5	LINE/L1
chr11	107782497	107784211	SVA_D	Retroposon/SVA
chr1	46189675	46191131	SVA_E	Retroposon/SVA
chr5	37012586	37014358	SVA_D	Retroposon/SVA
chr3	136441507	136443460	SVA_D	Retroposon/SVA
chr17	36786462	36787421	SVA_D	Retroposon/SVA
chr9	125818761	125820365	SVA_D	Retroposon/SVA
chr11	71890445	71890732	AluJb	SINE/Alu
chr19	54265764	54265863	AluJb	SINE/Alu
chr1	151572086	151574215	SVA_E	Retroposon/SVA
chr19	54266823	54267130	AluSp	SINE/Alu
chr20	52473227	52473406	MIRb	SINE/MIR
chr1	109595266	109596821	SVA_B	Retroposon/SVA
chr6	4344308	4344552	L2c	LINE/L2
chr22	22237233	22239139	SVA_D	Retroposon/SVA
chr13	108434371	108436230	SVA_D	Retroposon/SVA
chr16	47033359	47035214	SVA_D	Retroposon/SVA

chr20	4013593	4014746	SVA_E	Retroposon/SVA
chr7	64081547	64083188	HUERS-P3-int HUERS-P3-int HUERS-P3-int	LTR/ERV1
chr12	101883521	101883945	L1MA7	LINE/L1
chr4	165983816	165983983	AluJr	SINE/Alu
chr19	54265864	54266162	AluSz6	SINE/Alu
chr20	35604150	35606104	SVA_D	Retroposon/SVA
chr4	165916840	165920578	LTR5_Hs HERVK-int HERVK-int	LTR/ERVK
chrX	72172451	72174198	L1PB1	LINE/L1
chr7	48032839	48033439	L1MB8	LINE/L1
chr17	26785169	26786798	SVA_D	Retroposon/SVA
chr19	52944488	52944781	AluJo	SINE/Alu
chr2	71387605	71389222	SVA_A	Retroposon/SVA
chr4	165964310	165965146	MER54A	LTR/ERV1
chr15	40976459	40978237	L1M1	LINE/L1
chr3	186581371	186583393	SVA_E	Retroposon/SVA
chr7	139204141	139204544	SVA_E	Retroposon/SVA
chr3	39376270	39376407	AluSx	SINE/Alu
chr19	54266163	54266233	AluJb	SINE/Alu
chr1	192825472	192827531	SVA_D	Retroposon/SVA
chr1	44600852	44600983	L1ME3D	LINE/L1
chr4	151884302	151885990	SVA_B	Retroposon/SVA
chr13	50168726	50169527	LTR16A ERV3-16A3_I-int	LTR/ERV1
chr2	27037157	27038455	LTR12C	LTR/ERV1
chr8	42560477	42560836	MSTD	LTR/ERV1-MaLR
chr19	23886394	23887162	PRIMA41-int	LTR/ERV1
chr10	29984905	29986738	SVA_D	Retroposon/SVA
chr17	57576809	57578521	SVA_B	Retroposon/SVA
chr19	23151100	23153323	L1MA8	LINE/L1
chr6	15189507	15190821	SVA_F	Retroposon/SVA
chr19	23896285	23896582	AluSg	SINE/Alu
chr3	50121078	50123316	SVA_D	Retroposon/SVA
chr3	121030359	121031216	L1PA4	LINE/L1
chr19	22680976	22682355	LTR12C	LTR/ERV1
chr14	31715142	31715449	AluSx1	SINE/Alu
chr7	26300894	26302656	SVA_D	Retroposon/SVA
chr9	110033456	110034082	SVA_D	Retroposon/SVA
chr19	23885339	23886121	PRIMA41-int PRIMA41-int	LTR/ERV1
chr15	72688143	72689984	SVA_D	Retroposon/SVA
chr4	58038670	58040267	SVA_D	Retroposon/SVA
chr13	52653457	52655042	SVA_C	Retroposon/SVA
chr11	47913824	47915299	SVA_B	Retroposon/SVA

chr3	132188839	132191094	SVA_F	Retroposon/SVA
chr12	4813994	4814080	MER58B	DNA/hAT-Charlie
chr4	165983511	165983815	AluSq2	SINE/Alu
chr20	18304673	18305099	MER41-int	LTR/ERV1
chr13	41529696	41530730	SVA_D	Retroposon/SVA
chr14	31714370	31714678	AluSx	SINE/Alu
chr11	71890733	71890859	L1MC5a	LINE/L1
chrX	71983920	71984619	L1MA4A	LINE/L1
chr12	101883219	101883520	AluSz	SINE/Alu
chr19	23877925	23878219	AluSx	SINE/Alu
chr13	52669997	52672329	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr7	105050469	105052241	SVA_D	Retroposon/SVA
chr20	4015982	4016061	L2b	LINE/L2
chr19	54244999	54245305	AluSq2	SINE/Alu
chr14	89971592	89973486	SVA_D	Retroposon/SVA
chr19	23879961	23880258	AluSq	SINE/Alu
chr19	41692479	41692875	LTR7	LTR/ERV1
chr10	43959822	43961656	SVA_C	Retroposon/SVA
chr11	61413206	61413543	MLT1K MLT1K	LTR/ERV1-MaLR
chr17	15769852	15769992	L1ME3	LINE/L1
chr13	32577542	32578177	L1PA14	LINE/L1
chr20	18304063	18304534	MER4C MER4-int MER4-int LTR49	LTR/ERV1
chrX	41473225	41473534	L1MD1	LINE/L1
chr2	27775051	27775922	L1MEg	LINE/L1
chr16	8233583	8234101	L1MB5	LINE/L1
chr10	112526084	112528030	SVA_D	Retroposon/SVA
chr11	61414316	61414631	MamRep4096	DNA/hAT-Tip100
chr6	32351967	32353899	SVA_D	Retroposon/SVA
chr11	107786228	107786667	LTR45B	LTR/ERV1
chr1	43966927	43968647	SVA_D	Retroposon/SVA
chr11	107793577	107794003	MLT1C	LTR/ERV1-MaLR
chr13	21759854	21761595	SVA_F	Retroposon/SVA
chr13	50170171	50170939	ERV3-16A3_I-int	LTR/ERV1
chr5	76107394	76109518	SVA_D	Retroposon/SVA
chr19	22389493	22391465	L1PREC2	LINE/L1
chr1	225802716	225804045	SVA_B	Retroposon/SVA
chr1	50848248	50849275	L1MA9	LINE/L1
chr11	61413986	61414288	AluSx1	SINE/Alu
chr18	70920435	70921773	L1MDa	LINE/L1
chr1	109217717	109219338	SVA_F	Retroposon/SVA
chr19	22676746	22679398	HUERS-P2-int LTR1A1	LTR/ERV1

chr19	54260417	54260703	AluJb	SINE/Alu
chr6	29645990	29646576	Tigger7	DNA/TcMar-Tigger
chr12	4813926	4813987	L1ME4c	LINE/L1
chr11	71890312	71890444	L1MC5a	LINE/L1
chr4	165981885	165981937	MIRb	SINE/MIR
chr5	23237704	23238008	AluSp	SINE/Alu
chr11	60933230	60934781	SVA_D	Retroposon/SVA
chrX	70560547	70562436	SVA_C	Retroposon/SVA
chr4	165983173	165983342	FRAM	SINE/Alu
chr20	31702735	31704284	SVA_D	Retroposon/SVA
chr10	103489613	103489920	AluY	SINE/Alu
chr6	74369588	74371468	SVA_C	Retroposon/SVA
chr3	121007924	121011883	L1PB1	LINE/L1
chr7	57533454	57535302	THE1D THE1D-int THE1D-int THE1D	LTR/ERV1-MaLR
chr1	212952813	212953862	SVA_D	Retroposon/SVA
chr19	58559848	58560124	AluSz	SINE/Alu
chr20	10374960	10376436	SVA_C	Retroposon/SVA
chr1	27129383	27131339	SVA_D	Retroposon/SVA
chr16	8162561	8162857	AluY	SINE/Alu
chr16	2449054	2449311	L1M2	LINE/L1
chr7	112191105	112192655	SVA_D	Retroposon/SVA
chr13	69795758	69799468	LTR17 HERV17-int	LTR/ERV1
chr10	101597224	101599876	SVA_F	Retroposon/SVA
chr3	46535391	46537171	SVA_F	Retroposon/SVA
chr2	81095685	81096145	LTR33A	LTR/ERV1
chr11	61415767	61416077	MLT2B2	LTR/ERV1
chrX	71986292	71988039	L1PB1	LINE/L1
chr7	1076934	1078817	SVA_F	Retroposon/SVA
chr11	107789575	107789821	L2a	LINE/L2
chr2	81096196	81096657	MLT1D	LTR/ERV1-MaLR
chr4	790157	790370	AluSx4	SINE/Alu
chr7	63542972	63543277	AluSx	SINE/Alu
chr11	61415321	61415458	MLT2B2	LTR/ERV1
chr4	49512875	49512931	MER47C	DNA/TcMar-Tigger
chrX	18851136	18851856	LTR1C	LTR/ERV1
chr19	39345611	39347332	SVA_D	Retroposon/SVA
chr19	40430692	40430984	AluSz	SINE/Alu
chr17	36787422	36788520	SVA_D	Retroposon/SVA
chr14	31714226	31714369	AluJb	SINE/Alu
chr9	110034403	110035367	SVA_D	Retroposon/SVA
chr11	71889460	71889592	FLAM_C	SINE/Alu

chr17	20587494	20587634	L1ME3	LINE/L1
chr6	88460109	88461852	SVA_D	Retroposon/SVA
chr2	128110253	128111835	SVA_D	Retroposon/SVA
chr13	50169528	50170170	L1PA8	LINE/L1
chr4	165983346	165983510	AluJr	SINE/Alu
chr20	4015642	4015788	AluSq2	SINE/Alu
chr19	22387958	22388858	L1PREC2	LINE/L1
chr20	30709007	30711015	SVA_D	Retroposon/SVA
chr19	54260726	54260803	L1M4	LINE/L1
chr19	23884559	23885030	PRIMA41-int	LTR/ERV1
chr7	48033745	48033811	MIR3	SINE/MIR
chr19	23041288	23041588	AluSx1	SINE/Alu
chr20	2803682	2804830	SVA_D	Retroposon/SVA
chr4	78904328	78905941	SVA_D	Retroposon/SVA
chr4	48364787	48366925	SVA_D	Retroposon/SVA
chr20	5681972	5683380	SVA_D	Retroposon/SVA
chr7	105049872	105050208	MLT1H2	LTR/ERV1-MaLR
chr2	25856057	25857939	SVA_D	Retroposon/SVA
chr16	46901480	46903318	THE1C THE1C-int THE1C	LTR/ERV1-MaLR
chr19	58566175	58566437	MER102b	DNA/hAT-Charlie
chr16	2449312	2450819	SVA_D	Retroposon/SVA
chr12	101882006	101882227	AluJb	SINE/Alu
chr22	30253578	30255009	SVA_D	Retroposon/SVA
chr18	70914485	70914592	MLT1I	LTR/ERV1-MaLR
chr4	57559027	57560508	SVA_D	Retroposon/SVA
chr16	5248498	5248790	MLT1O	LTR/ERV1-MaLR
chr1	227319849	227321658	SVA_D	Retroposon/SVA
chr19	58560126	58560413	AluJr	SINE/Alu
chr16	2851338	2852861	SVA_F	Retroposon/SVA
chr6	56688784	56690317	SVA_D	Retroposon/SVA
chr19	52943752	52944048	AluSx1	SINE/Alu
chr5	61809573	61810412	SVA_D	Retroposon/SVA
chr7	20707377	20709366	SVA_E	Retroposon/SVA
chr7	100119840	100122236	SVA_D	Retroposon/SVA
chr1	176026481	176027908	SVA_D	Retroposon/SVA
chr19	52943041	52943340	AluSp	SINE/Alu
chr5	76279689	76281775	SVA_D	Retroposon/SVA
chr16	7928055	7928499	L1PA16	LINE/L1
chr5	138111733	138113595	SVA_D	Retroposon/SVA
chr7	54734725	54736467	SVA_D	Retroposon/SVA
chr1	199870432	199870931	MER87B	LTR/ERV1

chr3	39375913	39376224	Tigger4	DNA/TcMar-Tigger
chr19	52942715	52943029	AluY	SINE/Alu
chrX	71954831	71956606	L1PA17	LINE/L1
chr7	64078444	64080981	LTR9C HUERS-P3b-int HUERS-P3b-int	LTR/ERV1
chr8	48047751	48048397	L1MA4A	LINE/L1
chr10	99288544	99289549	SVA_D	Retroposon/SVA
chr2	25859898	25861236	L1PA5	LINE/L1
chrX	71951365	71951693	L1MD3	LINE/L1
chr2	27776808	27777430	MLT1A0-int MLT1A0	LTR/ERV1-MaLR
chr11	79210252	79211876	SVA_B	Retroposon/SVA
chr11	107792597	107792978	L2d	LINE/L2
chr17	37489563	37490741	SVA_B	Retroposon/SVA
chr6	74035136	74035437	AluSq2	SINE/Alu
chr3	186584278	186584433	AluSq2	SINE/Alu
chr11	61415459	61415766	AluSz	SINE/Alu
chrX	72175874	72176573	L1MA4A	LINE/L1
chr14	31714067	31714197	MER34A	LTR/ERV1
chr6	76150704	76152495	SVA_D	Retroposon/SVA
chr2	71384218	71384347	MIR3	SINE/MIR
chr11	107791477	107791787	AluSx1	SINE/Alu
chr10	120940814	120942736	SVA_D	Retroposon/SVA
chr7	73210949	73212455	SVA_D	Retroposon/SVA
chr10	99287254	99288526	SVA_D	Retroposon/SVA
chr3	142803458	142804255	MER54A	LTR/ERV1
chr19	21957962	21959468	SVA_D	Retroposon/SVA
chr19	22674607	22676427	LTR1A1 HUERS-P2-int HUERS-P2-int	LTR/ERV1
chr9	125816713	125817493	L1MC3	LINE/L1
chr6	32350553	32351040	MLT1F	LTR/ERV1-MaLR
chr19	23883060	23883362	AluYm1	SINE/Alu
chr9	90859008	90860914	SVA_D	Retroposon/SVA
chr1	217696518	217698243	SVA_D	Retroposon/SVA
chr11	107788651	107788928	AluSz6	SINE/Alu
chr11	107792289	107792585	AluJr	SINE/Alu
chr16	31264295	31264723	L2a	LINE/L2
chr4	165963561	165963881	Tigger4b	DNA/TcMar-Tigger
chr13	41530816	41531127	AluSz	SINE/Alu
chr5	43086628	43089269	SVA_E	Retroposon/SVA
chr8	48004539	48006516	L1PB3	LINE/L1
chr14	64503852	64505606	SVA_D	Retroposon/SVA
chr1	92482372	92482909	L2	LINE/L2
chr8	9059237	9059648	L1MC4a	LINE/L1

chr15	84489998	84491992	SVA_D	Retroposon/SVA
chr16	8232213	8232518	AluSx3	SINE/Alu
chr19	54260256	54260414	AluSx	SINE/Alu
chr1	45341423	45342884	SVA_D	Retroposon/SVA
chr7	2200739	2202237	SVA_B	Retroposon/SVA
chr17	3367299	3369093	SVA_D	Retroposon/SVA
chrX	96492564	96492879	AluYk4	SINE/Alu
chr12	31804693	31805308	LTR9	LTR/ERV1
chr5	116934695	116936530	SVA_D	Retroposon/SVA
chr16	28427206	28429157	SVA_D	Retroposon/SVA
chr6	4345757	4346191	MLT1F	LTR/ERV1-MaLR
chr19	54266241	54266550	AluY	SINE/Alu
chr8	42560864	42561006	MamTip3	DNA/hAT-Tip100
chr6	73934216	73934517	AluY	SINE/Alu
chr19	22360320	22360618	AluSx1	SINE/Alu
chr19	21890180	21891511	SVA_C	Retroposon/SVA
chr4	186160924	186162680	SVA_D	Retroposon/SVA
chr12	12564290	12565828	L1PA6	LINE/L1
chr11	107791307	107791476	AluJo	SINE/Alu
chr19	358740	359184	MLT1D MLT1D	LTR/ERV1-MaLR
chr3	142804467	142806480	SVA_F	Retroposon/SVA
chr15	63390455	63391986	SVA_D	Retroposon/SVA
chr2	38639211	38639870	LTR8	LTR/ERV1
chr1	92425562	92426266	L1MB2	LINE/L1
chr19	23043050	23043361	AluSx1	SINE/Alu
chr10	15105592	15106098	Charlie1b	DNA/hAT-Charlie
chr19	18028421	18030317	SVA_C	Retroposon/SVA
chr7	26315462	26315779	AluJb	SINE/Alu
chr16	2447975	2449000	MER21A MER21A	LTR/ERV1
chr1	24316771	24317253	L1PB1	LINE/L1
chr3	51641123	51642906	SVA_B	Retroposon/SVA
chr19	41691646	41691891	L1MA4A	LINE/L1
chr1	166965744	166966030	L1ME3E	LINE/L1
chrX	71984931	71985738	L1M2	LINE/L1
chr20	52475038	52475408	L1PB1	LINE/L1
chr2	170711860	170713335	SVA_B	Retroposon/SVA
chr12	4815014	4817742	L1Mca	LINE/L1
chr1	12144182	12144399	L2	LINE/L2
chr20	32723312	32723398	SVA_F	Retroposon/SVA
chr1	147420874	147423219	SVA_D	Retroposon/SVA
chr19	22355321	22357565	L1MA8	LINE/L1

chr1	229089264	229090044	LTR17	LTR/ERV1
chr19	23042742	23043045	AluY	SINE/Alu
chr16	7926506	7927056	L1ME1	LINE/L1
chr7	64037208	64038509	SVA_D	Retroposon/SVA
chr11	107789277	107789574	AluSp	SINE/Alu
chr5	23237607	23237703	MER51B	LTR/ERV1
chr13	41528557	41529679	SVA_D	Retroposon/SVA
chr19	6354799	6356476	SVA_D	Retroposon/SVA
chr14	31714840	31714991	AluJb	SINE/Alu
chr6	155007801	155009399	SVA_D	Retroposon/SVA
chr2	172755757	172757482	SVA_D	Retroposon/SVA
chr2	201547372	201549498	SVA_E	Retroposon/SVA
chr6	150106543	150108468	SVA_D	Retroposon/SVA
chr19	1498618	1500000	SVA_D	Retroposon/SVA
chr9	114379147	114380572	SVA_C	Retroposon/SVA
chr9	34136813	34138764	SVA_D	Retroposon/SVA
chr7	72697295	72699311	SVA_F	Retroposon/SVA
chr2	27041125	27041519	MLT1N2	LTR/ERV1-MaLR
chr19	20258715	20259162	MER57E3	LTR/ERV1
chr10	34641257	34642637	SVA_B	Retroposon/SVA
chr15	63402392	63402834	MLT1D	LTR/ERV1-MaLR
chr21	30382964	30385103	SVA_D	Retroposon/SVA
chr3	130586183	130587085	SVA_D	Retroposon/SVA
chr8	42571120	42571418	AluSx1	SINE/Alu
chr10	98698003	98699439	L1M4b	LINE/L1
chr10	103489392	103489612	THE1C	LTR/ERV1-MaLR
chr1	166966068	166966362	AluSx3	SINE/Alu
chr19	54266551	54266626	AluJb	SINE/Alu
chr8	47918372	47919087	HUERS-P3-int	LTR/ERV1
chr4	49512111	49512432	L1MB8	LINE/L1
chr17	44329740	44331154	SVA_D	Retroposon/SVA
chr20	18306784	18309640	MER4-int	LTR/ERV1
chr16	8162501	8162560	LTR8	LTR/ERV1
chr14	31714679	31714838	AluSx1	SINE/Alu
chr6	15188722	15189488	SVA_F	Retroposon/SVA
chr10	15105136	15105429	AluJb	SINE/Alu
chr19	23882995	23883059	MER41C	LTR/ERV1
chr4	3539154	3539468	AluSz	SINE/Alu
chr17	3466973	3468327	SVA_D	Retroposon/SVA
chr4	165923010	165923104	SVA_F	Retroposon/SVA
chr4	165963917	165964159	L2a	LINE/L2

chr14	100646601	100648282	SVA_D	Retroposon/SVA
chr19	58563476	58563597	MER45A	DNA/hAT-Tip100
chr10	98504436	98504737	AluJb	SINE/Alu
chr21	47204396	47206040	SVA_D	Retroposon/SVA
chr15	84489546	84489847	AluSz	SINE/Alu
chr11	107787940	107788205	AluJb	SINE/Alu
chr19	54260165	54260255	AluJb	SINE/Alu
chr2	27043798	27044168	MER57B2	LTR/ERV1
chr8	17765202	17765411	LTR5B	LTR/ERVK
chr19	22509377	22509685	AluSx	SINE/Alu
chr11	68628325	68629825	SVA_D	Retroposon/SVA
chr1	43970477	43970773	AluSz	SINE/Alu
chrX	41470918	41472901	SVA_D	Retroposon/SVA
chr2	38982396	38983898	SVA_D	Retroposon/SVA
chr19	22561244	22564234	L1PA5	LINE/L1
chr16	21000022	21001529	LTR12C	LTR/ERV1
chr19	54240371	54240532	AluSx	SINE/Alu
chr6	29646577	29646822	AluSz	SINE/Alu
chr20	37089308	37091248	SVA_D	Retroposon/SVA
chr17	1143497	1144030	LTR8	LTR/ERV1
chr19	58559751	58559840	FLAM_C	SINE/Alu
chr18	71016648	71016760	L2	LINE/L2
chr7	48029276	48030236	LTR5_Hs	LTR/ERVK
chr6	148500002	148500890	SVA_D	Retroposon/SVA
chr19	22384404	22385698	LTR70	LTR/ERV1
chr6	32348776	32349578	L1ME2z	LINE/L1
chr17	65326883	65328694	THE1B THE1B-int THE1B	LTR/ERVL-MaLR
chr4	165983023	165983159	FLAM_C	SINE/Alu
chrX	72174757	72175562	L1M2	LINE/L1
chr1	150700421	150702439	SVA_F	Retroposon/SVA
chr2	81097412	81097495	LFSINE_Vert	SINE/tRNA
chr17	19378636	19380007	SVA_D	Retroposon/SVA
chr4	61787	62490	L1MA9	LINE/L1
chr1	50859391	50859890	LTR54	LTR/ERV1
chr8	142211648	142213293	SVA_D	Retroposon/SVA
chr19	22517559	22517837	AluSx1	SINE/Alu
chr8	47995826	47999262	L1PA13	LINE/L1
chr7	123512062	123512369	L1PB4	LINE/L1
chr1	1518174	1518616	MLT1H	LTR/ERVL-MaLR
chr20	18304637	18304792	MER4-int	LTR/ERV1
chr9	77467371	77468789	SVA_B	Retroposon/SVA

chr19	54249058	54250092	LTR13	LTR/ERVK
chr19	23156186	23156493	AluSx1	SINE/Alu
chr10	99600778	99602222	SVA_D	Retroposon/SVA
chr19	41692260	41692478	LTR26C	LTR/ERV1
chr20	30018520	30019328	HAL1	LINE/L1
chr10	15106664	15106955	AluSx	SINE/Alu
chr15	56401269	56402283	SVA_D	Retroposon/SVA
chr3	121032303	121033431	SVA_E	Retroposon/SVA
chr16	8230773	8230976	MER63A	DNA/hAT-Blackjack
chr19	21891564	21891859	AluSp	SINE/Alu
chr10	116546458	116548105	SVA_D	Retroposon/SVA
chr20	35697236	35698894	SVA_F	Retroposon/SVA
chr7	64080656	64081255	HUERS-P3-int	LTR/ERV1
chr19	23889354	23889813	THE1A-int THE1A	LTR/ERVL-MaLR
chr11	61403958	61404032	MIRb	SINE/MIR
chr8	80288622	80290025	LTR12C	LTR/ERV1
chr1	146856097	146856262	X7C_LINE	LINE/CR1
chr6	148499305	148500000	SVA_D	Retroposon/SVA
chr1	150698385	150698690	AluSx1	SINE/Alu
chr11	73485427	73486985	SVA_C	Retroposon/SVA
chr19	22516552	22516833	AluSp	SINE/Alu
chr19	23053678	23055249	SVA_D	Retroposon/SVA
chr2	217089983	217092321	SVA_E	Retroposon/SVA
chr16	57233841	57235903	SVA_C	Retroposon/SVA
chr3	121019784	121021506	L1PA4	LINE/L1
chr10	98509585	98509877	AluSx1	SINE/Alu
chr20	32719617	32721485	SVA_D	Retroposon/SVA
chr19	22366857	22373132	L1PA8	LINE/L1
chr12	4813776	4813925	L1PA15	LINE/L1
chr7	112192738	112193021	AluSx3	SINE/Alu
chr9	29186918	29187148	MIRc	SINE/MIR
chr2	27044752	27045082	LTR37-int LTR37-int	LTR/ERV1
chr10	103461772	103461958	L1MC3	LINE/L1
chr1	23829729	23831478	SVA_D	Retroposon/SVA
chr1	229101977	229104134	L1ME3A	LINE/L1
chr10	98700092	98702237	SVA_E	Retroposon/SVA
chr11	107789913	107790044	MER112	DNA/hAT-Charlie
chr1	166967924	166970032	Tigger1	DNA/TcMar-Tigger
chr1	112144894	112145087	MIRb	SINE/MIR
chr19	58563170	58563269	MIRc	SINE/MIR
chr22	41138470	41138865	MLT2B1	LTR/ERVL

chr1	166966978	166967335	L1ME3E	LINE/L1
chr8	42561024	42561771	L2a	LINE/L2
chr3	5154919	5156388	SVA_D	Retroposon/SVA
chr19	22184724	22186690	L1PREC2	LINE/L1
chr16	8165967	8166573	LTR8	LTR/ERV1
chr19	22720129	22721945	L1ME1	LINE/L1
chr1	166967049	166967421	L1P4	LINE/L1
chr11	89716059	89717682	SVA_D	Retroposon/SVA
chr11	107790959	107791269	AluSc8	SINE/Alu
chr3	121031326	121032289	SVA_E	Retroposon/SVA
chr19	54240275	54240370	AluJb	SINE/Alu
chr2	207129410	207129731	AluJr	SINE/Alu
chr10	98510719	98510876	L1ME1	LINE/L1
chr9	134784393	134784666	L2b	LINE/L2
chr22	41140158	41142441	SVA_E	Retroposon/SVA
chr6	108590444	108592150	SVA_A	Retroposon/SVA
chr3	121025103	121026923	L1M4b	LINE/L1
chr20	30014070	30016242	SVA_D	Retroposon/SVA
chr10	98501443	98501740	AluJr	SINE/Alu
chr12	49829449	49831664	SVA_D	Retroposon/SVA
chr10	98504738	98505005	MLT1C2	LTR/ERV1-MaLR
chr17	37491172	37491656	LTR15	LTR/ERV1
chr8	30103461	30105395	SVA_E	Retroposon/SVA
chr6	29645695	29645989	AluSx	SINE/Alu
chr1	43969625	43969996	MER20B	DNA/hAT-Charlie
chr2	161294770	161296575	SVA_D	Retroposon/SVA
chr8	38724786	38725153	L2b	LINE/L2
chr10	98498040	98498489	L1MC2	LINE/L1
chr10	134817679	134818117	LTR7Y	LTR/ERV1
chr3	39300767	39301049	L1ME4a	LINE/L1
chr9	125818130	125818487	L1MC3	LINE/L1
chr2	27043070	27043467	MLT1C2	LTR/ERV1-MaLR
chr4	170599566	170601099	SVA_B	Retroposon/SVA
chr11	61413840	61413984	MER5B	DNA/hAT-Charlie
chr19	54240535	54240818	AluSx	SINE/Alu
chr12	7869019	7869190	L1MC1	LINE/L1
chr2	198482776	198484482	SVA_D	Retroposon/SVA
chr17	3366515	3367100	Tigger3c	DNA/TcMar-Tigger
chr10	98509202	98509505	AluSz6	SINE/Alu
chr12	10284931	10285124	MER67B	LTR/ERV1
chr1	24357920	24359387	SVA_A	Retroposon/SVA

chr9	131541764	131543445	SVA_D	Retroposon/SVA
chr4	165940032	165940372	L1MA5A	LINE/L1
chr11	61422097	61422200	LTR79	LTR/ERV1
chr6	32350126	32350415	AluJr	SINE/Alu
chr1	150699529	150699823	AluSq2	SINE/Alu
chr1	43969257	43969516	MER20B	DNA/hAT-Charlie
chr7	48032187	48032466	HAL1	LINE/L1
chr4	165965483	165965667	Tigger2a	DNA/TcMar-Tigger
chr1	46194168	46194466	AluJb	SINE/Alu
chr4	165965192	165965482	AluJo	SINE/Alu
chr1	150695711	150696641	Tigger1	DNA/TcMar-Tigger
chr18	70921781	70922199	MSTB1	LTR/ERV1-MaLR
chr16	7927175	7927466	AluSc8	SINE/Alu
chr1	24317548	24317887	L1PB1	LINE/L1
chr4	165920579	165920886	AluSp	SINE/Alu
chr18	11959025	11960661	SVA_D	Retroposon/SVA
chr1	199871099	199871400	AluJr	SINE/Alu
chr16	7929199	7929478	AluJo	SINE/Alu
chr14	93377080	93379075	SVA_D	Retroposon/SVA
chr19	58564330	58564623	AluSg	SINE/Alu
chr12	10285318	10285575	MER39	LTR/ERV1
chr11	107793260	107793576	AluSz	SINE/Alu
chr11	61413097	61413177	MIRb	SINE/MIR
chr11	107785601	107785918	AluSq2	SINE/Alu
chr7	26063174	26063819	L1PB1	LINE/L1
chr19	22360884	22361179	AluSx	SINE/Alu
chr12	4814135	4814203	L1MCa	LINE/L1
chr1	92483218	92483704	L2	LINE/L2
chr14	21656418	21657641	SVA_D	Retroposon/SVA
chr1	215089203	215089705	L2a	LINE/L2
chr1	166966363	166966563	MER30	DNA/hAT-Charlie
chr19	54240851	54241078	L1MB7	LINE/L1
chr11	61422349	61422453	LTR79	LTR/ERV1
chr8	9058229	9058962	L1MC4a	LINE/L1
chr6	74034736	74035037	AluSx1	SINE/Alu
chr18	70918624	70919160	L1MC3	LINE/L1
chr19	22566085	22567876	L1PA5	LINE/L1
chr7	64722828	64723915	SVA_E	Retroposon/SVA
chr7	64084039	64084328	HUERS-P3-int	LTR/ERV1
chr1	229087994	229089063	L1MA4	LINE/L1
chr5	12563973	12566251	THE1B THE1B-int THE1B	LTR/ERV1-MaLR

chr19	22150245	22150487	AluSx	SINE/Alu
chr12	10285577	10285825	MER39	LTR/ERV1
chr11	107790722	107790855	MIR3	SINE/MIR
chr1	229090045	229090552	MER50	LTR/ERV1
chrX	53748041	53749425	SVA_B	Retroposon/SVA
chr20	18305103	18305331	MER4-int	LTR/ERV1
chr13	49951566	49952844	SVA_F	Retroposon/SVA
chr16	28459273	28460903	SVA_D	Retroposon/SVA
chr17	42314420	42314734	AluSq2	SINE/Alu
chr12	21921259	21923405	Tigger1	DNA/TcMar-Tigger
chr10	73628416	73630264	SVA_D	Retroposon/SVA
chr9	102829439	102831589	SVA_D	Retroposon/SVA
chrX	53530399	53532064	SVA_C	Retroposon/SVA
chr11	61411954	61412278	AluSc8	SINE/Alu
chr20	18355741	18356961	SVA_F	Retroposon/SVA
chr20	33749902	33752848	L1PA7	LINE/L1
chr5	4853939	4854878	L1MD2	LINE/L1
chr18	70919166	70919505	L1MC3	LINE/L1
chr7	105048819	105049228	L1MA3	LINE/L1
chr12	26937305	26938286	SVA_D	Retroposon/SVA
chr3	121022862	121024871	L1MEc	LINE/L1
chr5	61808435	61809561	SVA_D	Retroposon/SVA
chr7	26309877	26310363	Tigger1	DNA/TcMar-Tigger
chr10	98508967	98509201	L1ME1	LINE/L1
chr9	29186778	29186901	MIR	SINE/MIR
chr2	207035705	207037316	SVA_D	Retroposon/SVA
chr1	65587849	65591390	L1PA6	LINE/L1
chr1	150674449	150675395	L1PA10	LINE/L1
chr16	28676801	28678371	SVA_D	Retroposon/SVA
chr19	54244836	54244998	AluSq	SINE/Alu
chr1	24318177	24318554	L1PB1	LINE/L1
chr13	25449194	25450430	HSMAR2	DNA/TcMar-Mariner
chr8	9053919	9054221	AluSz	SINE/Alu
chr7	123514456	123514758	AluSx3	SINE/Alu
chr8	9053211	9053504	AluJr	SINE/Alu
chr1	24226501	24226925	LTR8	LTR/ERV1
chr1	150756343	150756649	AluSz	SINE/Alu
chr17	5030947	5031282	MER2	DNA/TcMar-Tigger
chr14	31715007	31715141	Charlie1	DNA/hAT-Charlie
chr3	196708253	196708878	L1MC1	LINE/L1
chr18	70919534	70920423	L1MC3	LINE/L1

chr7	132861688	132863088	SVA_D	Retroposon/SVA
chr7	22839829	22841483	SVA_D	Retroposon/SVA
chr16	8207441	8207751	AluSx	SINE/Alu
chr19	22682836	22683161	AluSx4	SINE/Alu
chr9	114385293	114385680	THE1C	LTR/ERV1-MaLR
chr17	1145235	1145408	L1MC4	LINE/L1
chr5	65253069	65254500	SVA_C	Retroposon/SVA
chr11	107785942	107786227	AluSx1	SINE/Alu
chr19	5562661	5562957	AluSz	SINE/Alu
chr6	29645217	29645334	MIR	SINE/MIR
chr22	41139479	41139746	AluSz	SINE/Alu
chr1	147420033	147420419	L2a	LINE/L2
chr19	22564539	22565783	L1PA5	LINE/L1
chr19	41688212	41688554	AluSx	SINE/Alu
chr16	64379132	64380456	MER52A	LTR/ERV1
chr4	124458891	124460599	LTR12C	LTR/ERV1
chr17	3761668	3762348	MER21B	LTR/ERV1
chr6	4428861	4428948	MER5A	DNA/hAT-Charlie
chr3	82036872	82040824	MER61-int MER61-int MER61A	LTR/ERV1
chr18	55299329	55301135	SVA_D	Retroposon/SVA
chr20	5693084	5693825	L1MEg	LINE/L1
chr7	48031696	48032177	HAL1	LINE/L1
chr4	153787034	153788705	SVA_D	Retroposon/SVA
chr1	199872986	199874527	SVA_D	Retroposon/SVA
chr8	142207259	142207698	MLT1C2	LTR/ERV1-MaLR
chr4	37669824	37671675	SVA_D	Retroposon/SVA
chr1	92485312	92485632	AluJr	SINE/Alu
chr11	61412651	61412740	L2a	LINE/L2
chr16	31182943	31183946	LTR13	LTR/ERV1
chr19	34622799	34624603	SVA_C	Retroposon/SVA
chr11	107790045	107790338	AluJr	SINE/Alu
chr5	37562549	37564679	SVA_D	Retroposon/SVA
chr17	41124316	41126029	SVA_F	Retroposon/SVA
chr20	52474578	52474654	MIRb	SINE/MIR
chr19	23156761	23157053	AluSx3	SINE/Alu
chr11	64251313	64251773	LTR7B	LTR/ERV1
chr17	37086259	37087544	SVA_D	Retroposon/SVA
chr16	8031629	8032112	MLT1F	LTR/ERV1-MaLR
chr11	107790468	107790642	AluSp	SINE/Alu
chr2	207129098	207129266	MER21B	LTR/ERV1
chr8	38725223	38725999	LTR17	LTR/ERV1

chr3	121012732	121014124	L2a	LINE/L2
chr1	46222068	46226738	HERVIP10B3-int	LTR/ERV1
chr4	3756528	3757250	MER72	LTR/ERV1
chr3	196707310	196707742	L1MD	LINE/L1
chr11	107791788	107791920	AluJo	SINE/Alu
chr12	28028460	28029603	L1MB3	LINE/L1
chr3	39285399	39285804	L2b	LINE/L2
chr5	115301657	115302215	L1MD3	LINE/L1
chr18	71011207	71012378	L1MC5a	LINE/L1
chr2	215699040	215701068	SVA_E	Retroposon/SVA
chrX	71950940	71951091	MSTB	LTR/ERV1-MaLR
chr11	47060247	47061054	SVA_D	Retroposon/SVA
chr19	23896091	23896283	MIR	SINE/MIR
chr19	20285192	20285485	AluSx	SINE/Alu
chr16	8233436	8233579	MIR	SINE/MIR
chr8	47921795	47924048	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr22	38182207	38183623	SVA_D	Retroposon/SVA
chr21	30393121	30393646	L1ME2z	LINE/L1
chr11	20570171	20571176	SVA_E	Retroposon/SVA
chr7	34691968	34692273	AluSc	SINE/Alu
chr20	43298870	43305415	LTR7B HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr8	142208317	142208629	L1MEc	LINE/L1
chr20	18303168	18303924	MER4E1	LTR/ERV1
chr19	22151705	22151925	AluYk3	SINE/Alu
chr19	30389241	30392602	SVA_F	Retroposon/SVA
chr10	15104180	15104369	MIR	SINE/MIR
chr19	58560913	58560973	Tigger3d	DNA/TcMar-Tigger
chr4	189139686	189140245	LTR1A2	LTR/ERV1
chr13	52659576	52659999	MamRep137	DNA/TcMar-Tigger
chr19	20324672	20326120	SVA_D	Retroposon/SVA
chr20	3421099	3422526	SVA_D	Retroposon/SVA
chr2	207128099	207128420	MER31-int	LTR/ERV1
chr10	15104404	15104737	L1ME4a	LINE/L1
chr20	55251167	55251418	MLT1C2	LTR/ERV1-MaLR
chr1	199871472	199871736	AluSx1	SINE/Alu
chr19	6499054	6499326	AluSx3	SINE/Alu
chr2	27045383	27045674	LTR37-int	LTR/ERV1
chr13	25543831	25545367	SVA_D	Retroposon/SVA
chr19	37508359	37509463	L1MB3	LINE/L1
chr12	122430471	122430775	AluJb	SINE/Alu
chr11	61414633	61414937	AluSc	SINE/Alu

chr12	12718331	12719858	SVA_D	Retroposon/SVA
chrX	99978130	99979868	SVA_C	Retroposon/SVA
chr19	20251576	20252209	L1PREC2	LINE/L1
chr20	19658353	19660203	SVA_D	Retroposon/SVA
chr17	26786814	26787119	AluSz	SINE/Alu
chr7	805337	805629	AluJo	SINE/Alu
chr6	29644033	29644340	AluSg	SINE/Alu
chr11	107784791	107785011	L2	LINE/L2
chr19	22582724	22583474	L1M3a	LINE/L1
chr11	107785306	107785518	MamGypLTR2b	LTR/Gypsy
chr19	370649	370778	L1ME2	LINE/L1
chr1	229090554	229091155	L1MA4	LINE/L1
chr1	150755078	150755371	AluSx	SINE/Alu
chr17	56150628	56152572	SVA_D	Retroposon/SVA
chr1	166966771	166966954	AluJr	SINE/Alu
chr14	100648311	100648422	L2d2	LINE/L2
chr13	32576321	32576621	AluSx1	SINE/Alu
chr12	10284627	10284930	AluY	SINE/Alu
chr6	123167118	123167552	L1MEc	LINE/L1
chr12	55872248	55873908	SVA_D	Retroposon/SVA
chr7	123487550	123487834	AluSc8	SINE/Alu
chr3	46537969	46538238	MER49	LTR/ERV1
chr2	207128460	207128767	AluSp	SINE/Alu
chr22	50109583	50109760	AluJb	SINE/Alu
chr4	34124481	34125225	L2a	LINE/L2
chr4	22618208	22618756	MLT2A2	LTR/ERV1
chr5	21032660	21033077	LOR1b	LTR/ERV1
chr1	109078098	109079480	SVA_D	Retroposon/SVA
chr10	15104738	15105037	AluSz	SINE/Alu
chr1	92485007	92485311	L1ME4a	LINE/L1
chr19	53314114	53316035	SVA_E	Retroposon/SVA
chr7	26303761	26304374	MER4B	LTR/ERV1
chr14	63990621	63991071	Tigger10	DNA/TcMar-Tigger
chr19	55439621	55439785	AluSz	SINE/Alu
chr10	121318452	121320006	SVA_C	Retroposon/SVA
chr11	19880686	19882618	SVA_D	Retroposon/SVA
chr16	24475893	24476252	THE1B	LTR/ERV1-MaLR
chr12	31779160	31779504	THE1B	LTR/ERV1-MaLR
chr6	29647385	29647663	AluSp	SINE/Alu
chr16	5249820	5250155	MSTD	LTR/ERV1-MaLR
chr17	57597661	57598339	L1MB3	LINE/L1

chr12	8056992	8057287	AluSp	SINE/Alu
chr11	107793179	107793259	MLT1C	LTR/ERV1-MaLR
chr1	24225593	24225755	MIRb	SINE/MIR
chr19	20257370	20257651	AluSp	SINE/Alu
chr8	47926951	47927577	L1M1	LINE/L1
chr8	47930332	47936375	L1PA3	LINE/L1
chr20	35603505	35603975	L1ME1	LINE/L1
chr13	111256098	111257166	HSMAR1	DNA/TcMar-Mariner
chr12	4814204	4814511	AluSg	SINE/Alu
chr2	27042554	27042770	LTR37A	LTR/ERV1
chr16	7999554	8000000	L1MB8	LINE/L1
chr3	194121172	194121919	SVA_E	Retroposon/SVA
chr11	71891714	71891849	L2a	LINE/L2
chrX	71984628	71984885	L1MD	LINE/L1
chr8	48081580	48083178	L1P4	LINE/L1
chr1	227463285	227464792	SVA_A	Retroposon/SVA
chr12	8054266	8054575	AluSg	SINE/Alu
chr7	123520767	123521656	L1MC5	LINE/L1
chr17	57602718	57603442	HAL1	LINE/L1
chr6	151450937	151451799	THE1D-int THE1D	LTR/ERV1-MaLR
chr10	75448772	75450383	SVA_D	Retroposon/SVA
chr14	65360983	65363441	SVA_E	Retroposon/SVA
chr2	81098440	81099196	LTR17	LTR/ERV1
chr10	101593811	101593937	AluSp	SINE/Alu
chr16	8231335	8231437	MamTip2	DNA/hAT-Tip100
chr6	155286733	155288566	SVA_D	Retroposon/SVA
chr18	70998584	70998978	MLT2D	LTR/ERV1
chr16	8230977	8231035	MIR1_Amn	SINE/MIR
chr19	6585039	6585256	AluSq2	SINE/Alu
chr17	40600472	40602063	SVA_D	Retroposon/SVA
chr2	128544428	128547239	SVA_F	Retroposon/SVA
chr1	92423396	92423699	AluSz	SINE/Alu
chr19	22482896	22484174	LTR70	LTR/ERV1
chr7	57229003	57229886	THE1D THE1D-int	LTR/ERV1-MaLR
chr1	112141210	112141818	MER21B	LTR/ERV1
chr11	107784337	107784616	MLT1J	LTR/ERV1-MaLR
chr3	5127011	5127318	AluSz6	SINE/Alu
chr9	125817494	125817810	AluJb	SINE/Alu
chr3	39283193	39283592	MLT1K	LTR/ERV1-MaLR
chr2	55877310	55878924	SVA_C	Retroposon/SVA
chr1	214996418	214997735	L1PA17	LINE/L1

chr8	47917882	47918102	AluSx	SINE/Alu
chr6	29685650	29688054	SVA_E	Retroposon/SVA
chr12	12562155	12564288	L1PA4	LINE/L1
chr7	26314110	26314549	L1ME3A	LINE/L1
chr1	229092382	229093086	LTR8	LTR/ERV1
chr4	6837193	6838107	L1PA6	LINE/L1
chr17	37493247	37494802	SVA_D	Retroposon/SVA
chr7	64723933	64725166	SVA_E	Retroposon/SVA
chr4	165938727	165939211	L1PA10	LINE/L1
chr15	52577645	52579153	SVA_D	Retroposon/SVA
chr19	41155111	41155197	L1M1	LINE/L1
chr1	147409176	147410223	MER11A	LTR/ERVK
chr12	8053959	8054263	AluSz	SINE/Alu
chr1	199901151	199901541	MLT1A1	LTR/ERVL-MaLR
chr6	93341292	93341735	MLT1C2	LTR/ERVL-MaLR
chr19	58555007	58555333	AluJb	SINE/Alu
chr2	27046082	27046366	AluYk2	SINE/Alu
chr1	146986939	146987351	LTR37A	LTR/ERV1
chr7	26308283	26308829	L1MB8	LINE/L1
chr2	204071105	204072520	SVA_D	Retroposon/SVA
chr19	58568570	58568772	MamRep4096	DNA/hAT-Tip100
chr9	95592348	95593330	SVA_D	Retroposon/SVA
chr20	33740705	33741902	SVA_F	Retroposon/SVA
chrX	134528454	134529499	HERVL-int MLT2A1 MLT2A1	LTR/ERVL
chr5	23231776	23233590	LTR54B MER57-int MER57-int	LTR/ERV1
chr19	22376043	22379350	HERVK3-int HERVK3-int LTR3	LTR/ERVK
chr19	22683600	22683838	MIR	SINE/MIR
chr4	781172	781473	MLT1C2	LTR/ERVL-MaLR
chrX	53751739	53752824	MSTB1-int	LTR/ERVL-MaLR
chrX	71969990	71972887	L1PA6	LINE/L1
chr7	104554181	104554489	AluY	SINE/Alu
chr11	61416900	61417211	AluJr	SINE/Alu
chr19	37759202	37759494	AluSp	SINE/Alu
chr8	144124138	144124231	MIR3	SINE/MIR
chr2	85714148	85716186	SVA_D	Retroposon/SVA
chr12	49829113	49829407	AluSz	SINE/Alu
chr8	47927674	47928057	L1M3c	LINE/L1
chrX	48517223	48519002	SVA_C	Retroposon/SVA
chr19	41155198	41155494	AluSz6	SINE/Alu
chr2	127065301	127066140	LTR1A2	LTR/ERV1
chr7	55469355	55471173	SVA_D	Retroposon/SVA

chr19	22687226	22687424	MIRc	SINE/MIR
chr16	28708507	28710833	SVA_F	Retroposon/SVA
chr1	24317254	24317547	AluSx	SINE/Alu
chr19	20252540	20252894	L1PREC2	LINE/L1
chr19	52944153	52944455	AluSc8	SINE/Alu
chr16	31188357	31188732	L2c	LINE/L2
chrX	71985930	71986235	L1PB1	LINE/L1
chr10	98497704	98497965	AluJr4	SINE/Alu
chr19	41689830	41690139	AluSc8	SINE/Alu
chr8	48046920	48047436	L1MA4A	LINE/L1
chr1	43969997	43970306	AluSx1	SINE/Alu
chr11	68629984	68630220	L2a	LINE/L2
chr19	40623100	40625294	SVA_F	Retroposon/SVA
chr1	207860707	207861054	L1ME3	LINE/L1
chr19	41692876	41693092	LTR26C	LTR/ERV1
chr22	17129395	17129695	AluSz	SINE/Alu
chr19	23154851	23155145	AluSq2	SINE/Alu
chr6	33026723	33028586	SVA_D	Retroposon/SVA
chr2	202148007	202149437	SVA_E	Retroposon/SVA
chr19	5548587	5553223	LTR7Y HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr4	62497	63405	L1MA9	LINE/L1
chr1	149196674	149198801	SVA_D	Retroposon/SVA
chr17	1129356	1129504	L2a	LINE/L2
chr2	198560178	198562182	SVA_D	Retroposon/SVA
chr2	204236653	204238195	SVA_D	Retroposon/SVA
chr19	6497664	6497936	AluYe5	SINE/Alu
chr22	43376472	43378895	SVA_E	Retroposon/SVA
chr8	142207704	142207830	MIRb	SINE/MIR
chr8	9057230	9057543	AluSx1	SINE/Alu
chr1	154259376	154260904	SVA_D	Retroposon/SVA
chr11	82843633	82845216	SVA_C	Retroposon/SVA
chr17	41528222	41528459	SVA_E	Retroposon/SVA
chr4	135560476	135561707	BLACKJACK	DNA/hAT-Blackjack
chr6	108123914	108125270	SVA_D	Retroposon/SVA
chr13	52660775	52661229	MLT1C2	LTR/ERV1-MaLR
chr17	1134735	1135001	L2c	LINE/L2
chr8	48087656	48088615	LTR5_Hs	LTR/ERV1
chr12	62543	64507	SVA_E	Retroposon/SVA
chrX	114581077	114582891	SVA_F	Retroposon/SVA
chr18	71019037	71020440	L1M3f	LINE/L1
chr1	40378152	40379739	SVA_D	Retroposon/SVA

chr10	103461950	103462148	L1MC3	LINE/L1
chr1	151623072	151624718	SVA_F	Retroposon/SVA
chr4	34336558	34337827	LTR12C	LTR/ERV1
chr19	41685628	41687748	SVA_D	Retroposon/SVA
chr16	2849977	2850279	Tigger3	DNA/TcMar-Tigger
chr1	92482910	92483217	AluSz	SINE/Alu
chr17	1131341	1131408	MIR3	SINE/MIR
chr8	99063335	99064743	SVA_B	Retroposon/SVA
chr2	171005573	171007431	SVA_D	Retroposon/SVA
chrX	41472909	41473105	L1ME4a	LINE/L1
chr8	42571554	42571955	MER66B	LTR/ERV1
chr18	71027512	71028740	L1MB5	LINE/L1
chr6	71975116	71977144	SVA_D	Retroposon/SVA
chr17	15997860	15999635	SVA_D	Retroposon/SVA
chr8	47918103	47918246	AluSp	SINE/Alu
chr19	41690889	41691185	AluSz	SINE/Alu
chr19	58563624	58563748	AluJr	SINE/Alu
chr2	54312189	54312833	MER6A	DNA/TcMar-Tigger
chr17	1131166	1131306	L2d2	LINE/L2
chr18	7097867	7099486	SVA_D	Retroposon/SVA
chr14	73650003	73652346	SVA_F	Retroposon/SVA
chr19	22359733	22359926	L1MA2	LINE/L1
chr4	184739242	184740749	SVA_C	Retroposon/SVA
chr8	101903704	101905572	SVA_D	Retroposon/SVA
chr1	150672940	150673385	L1MB8	LINE/L1
chr13	49953981	49954274	AluY	SINE/Alu
chr8	48087570	48087655	AluY	SINE/Alu
chrX	73045399	73045570	MER58C	DNA/hAT-Charlie
chr10	98505325	98505461	MLT1C2	LTR/ERV1-MaLR
chr19	58568977	58569166	MER102b	DNA/hAT-Charlie
chr2	27044232	27044478	LTR37-int	LTR/ERV1
chr3	183325148	183327575	SVA_E	Retroposon/SVA
chr22	41137994	41138214	ERV1-int MLT2B1	LTR/ERV1
chr1	153554815	153556385	SVA_D	Retroposon/SVA
chr11	90796049	90797650	SVA_A	Retroposon/SVA
chr5	132318084	132319679	SVA_D	Retroposon/SVA
chr1	55079966	55080295	L2b	LINE/L2
chr3	41346683	41348664	SVA_D	Retroposon/SVA
chr4	65859	66940	L1MB1	LINE/L1
chr20	25227679	25228208	LTR65	LTR/ERV1
chr1	212951732	212953069	SVA_D	Retroposon/SVA

chr7	805630	805764	AluJo	SINE/Alu
chr3	46541564	46541637	MIR3	SINE/MIR
chr10	98505806	98505998	MIRb	SINE/MIR
chr18	3358114	3358593	L3	LINE/CR1
chr16	58879422	58880991	SVA_D	Retroposon/SVA
chr16	24476910	24477128	MER58A	DNA/hAT-Charlie
chr3	109033628	109033939	AluSz	SINE/Alu
chr8	9046174	9046659	MER50B	LTR/ERV1
chr4	170966873	170968713	SVA_D	Retroposon/SVA
chr5	107894091	107895876	SVA_D	Retroposon/SVA
chr19	41690606	41690875	AluSx3	SINE/Alu
chr1	146886161	146886753	MLT1E2	LTR/ERVL-MaLR
chr12	6241598	6243149	LTR12C	LTR/ERV1
chr4	63882	64105	L1M3a	LINE/L1
chr4	113878190	113879804	SVA_C	Retroposon/SVA
chr22	24712269	24714505	SVA_D	Retroposon/SVA
chr3	142765182	142766165	SVA_D	Retroposon/SVA
chr1	27614842	27616533	SVA_D	Retroposon/SVA
chr9	136979899	136984158	SVA_F	Retroposon/SVA
chr13	31412722	31414778	SVA_D	Retroposon/SVA
chr16	24477884	24478406	MLT1F	LTR/ERVL-MaLR
chr1	199868287	199868439	L2c	LINE/L2
chr19	23875490	23876388	LTR5_Hs	LTR/ERVK
chr9	134784292	134784392	MER41B	LTR/ERV1
chr9	125629748	125631014	SVA_D	Retroposon/SVA
chr6	29643409	29643472	L2b	LINE/L2
chr22	41137375	41137597	AluJr	SINE/Alu
chr19	41690468	41690605	L2a	LINE/L2
chr1	113611439	113612657	SVA_F	Retroposon/SVA
chr4	123936339	123938331	SVA_D	Retroposon/SVA
chr12	8052802	8052889	AluJb	SINE/Alu
chr8	42559177	42559459	MLT1B	LTR/ERVL-MaLR
chr4	129003969	129005815	SVA_C	Retroposon/SVA
chr1	166966602	166966767	L1ME3E	LINE/L1
chr1	207859118	207859318	LTR33C	LTR/ERVL
chr12	4812771	4813186	LTR44	LTR/ERV1
chr1	146949968	146950508	LTR3B_ LTR3B_	LTR/ERVK
chr4	64106	64245	FLAM_C	SINE/Alu
chr10	101596895	101597193	AluSp	SINE/Alu
chr9	86418138	86420398	SVA_D	Retroposon/SVA
chr11	77200456	77202190	SVA_D	Retroposon/SVA

chr1	155804317	155804617	MER41B	LTR/ERV1
chr11	89593163	89594788	SVA_D	Retroposon/SVA
chr19	22063054	22071157	LTR13 HERVK13-int	LTR/ERVK
chr17	781379	781617	L2b	LINE/L2
chr1	192827532	192827643	MER5B	DNA/hAT-Charlie
chrX	48512913	48513664	LTR17	LTR/ERV1
chr1	150681666	150682689	LTR5A	LTR/ERVK
chr5	23236767	23237606	MER57-int MER57-int	LTR/ERV1
chr1	173651967	173652910	MER4-int MER4-int MER4-int MER4-int MER4A1	LTR/ERV1
chr8	48006713	48012603	L1PA2	LINE/L1
chr6	84953493	84955309	SVA_D	Retroposon/SVA
chr6	159301418	159303542	LTR7B HERVH-int	LTR/ERV1
chr7	100842585	100842893	AluSp	SINE/Alu
chr10	98502568	98502900	MER46C	DNA/TcMar-Tigger
chr2	204072523	204072723	HAL1b	LINE/L1
chr12	4813531	4813775	L1ME4c	LINE/L1
chr10	71747641	71749083	L1ME3G	LINE/L1
chr3	47297211	47298640	SVA_D	Retroposon/SVA
chr2	203399005	203400834	SVA_F	Retroposon/SVA
chr21	45702743	45703660	LTR5_Hs	LTR/ERVK
chr5	112289881	112291497	SVA_D	Retroposon/SVA
chr6	5037244	5039107	SVA_E	Retroposon/SVA
chr12	96234887	96236196	SVA_E	Retroposon/SVA
chr2	207121886	207122451	MER54A	LTR/ERVL
chrX	47875724	47877252	SVA_A	Retroposon/SVA
chr1	31648617	31650508	SVA_D	Retroposon/SVA
chr7	123511699	123511825	MIRc	SINE/MIR
chr2	201906659	201908168	SVA_B	Retroposon/SVA
chr21	27067288	27068746	SVA_C	Retroposon/SVA
chr7	34694875	34695293	MLT2B4	LTR/ERVL
chr12	70861742	70862767	MER61A MER61-int	LTR/ERV1
chr8	47918246	47918346	AluSx	SINE/Alu
chr19	22573098	22573412	AluSx	SINE/Alu
chr17	1133814	1134116	AluSp	SINE/Alu
chr8	17762793	17763244	LTR85b	LTR/Gypsy?
chr19	46150773	46152484	SVA_D	Retroposon/SVA
chr2	205012266	205013211	L1MA9	LINE/L1
chr12	31780179	31780479	AluSx1	SINE/Alu
chr2	25945508	25947023	SVA_D	Retroposon/SVA
chr13	111258023	111259669	SVA_D	Retroposon/SVA
chr12	122430912	122432883	SVA_F	Retroposon/SVA

chr10	70243419	70243720	AluSx	SINE/Alu
chr10	98505006	98505324	AluSx	SINE/Alu
chrX	73061652	73061776	MIRc	SINE/MIR
chr5	23234215	23234908	LTR9B	LTR/ERV1
chr6	29641589	29641901	AluSp	SINE/Alu
chr12	70932052	70932235	MIRc	SINE/MIR
chr19	20289351	20290288	LTR70	LTR/ERV1
chr1	92482201	92482371	MER5A	DNA/hAT-Charlie
chr1	15445073	15445208	MER5A1	DNA/hAT-Charlie
chr1	92480405	92480710	AluJb	SINE/Alu
chr9	114387167	114387814	L1M5	LINE/L1
chr10	98488781	98489332	L1MEb	LINE/L1
chr8	9050957	9051353	MLT1A	LTR/ERVL-MaLR
chr8	144122156	144123228	MER11C	LTR/ERVK
chr8	47919333	47920706	HUERS-P3-int HUERS-P3-int	LTR/ERV1
chr4	67235	67575	L1MB2	LINE/L1
chr1	25158769	25161354	SVA_E	Retroposon/SVA
chr10	98508378	98508673	AluSz	SINE/Alu
chr4	66961	67068	L1MB1	LINE/L1
chr10	98503688	98503858	L1ME4a	LINE/L1
chr19	6499327	6499505	MIRb	SINE/MIR
chr1	92484579	92484836	AluSc	SINE/Alu
chr4	73764339	73764644	AluY	SINE/Alu
chr17	29310373	29310671	AluSx1	SINE/Alu
chr13	32573590	32575276	SVA_D	Retroposon/SVA
chr5	81278385	81280235	SVA_D	Retroposon/SVA
chr18	71010530	71011184	L2	LINE/L2
chr15	23821419	23821733	MSTD	LTR/ERVL-MaLR
chr20	35603985	35604110	AluJb	SINE/Alu
chr7	804808	804933	MIR	SINE/MIR
chr6	123167939	123168526	L1MEc	LINE/L1
chr14	35511753	35512045	AluJb	SINE/Alu
chr1	53374324	53374631	AluSx1	SINE/Alu
chr1	146855427	146856063	CR1_Mam	LINE/CR1
chr12	31803766	31804179	LTR47A	LTR/ERVL
chr7	13141600	13143290	SVA_D	Retroposon/SVA
chr9	128541535	128543849	SVA_D	Retroposon/SVA
chr19	20281606	20281964	MER21C	LTR/ERVL
chr8	48000187	48000863	L1PA12	LINE/L1
chr12	8056050	8056190	AluSx3	SINE/Alu
chr13	41473906	41476048	SVA_D	Retroposon/SVA

chr15	59157687	59157840	MER77	LTR/ERV1
chr10	32257987	32258872	SVA_E	Retroposon/SVA
chr4	125246433	125247178	FordPrefect	DNA/hAT-Tip100
chr11	107790339	107790428	MER112	DNA/hAT-Charlie
chr8	9054580	9054843	AluSp	SINE/Alu
chr8	47928098	47928533	L1M3c	LINE/L1
chr2	54314916	54315487	LTR78	LTR/ERV1
chr17	1130256	1130413	MER91A	DNA/hAT-Tip100
chr19	6597897	6599996	Harlequin-int Harlequin-int	LTR/ERV1
chr1	207861336	207861620	AluJr	SINE/Alu
chr8	47917738	47917881	PABL_A-int	LTR/ERV1
chr20	30059229	30060256	SVA_D	Retroposon/SVA
chr7	139237880	139240188	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr5	43085842	43086400	LTR49-int	LTR/ERV1
chr1	212493291	212495586	SVA_D	Retroposon/SVA
chr4	153684717	153685089	MLT1A	LTR/ERV1-MaLR
chr6	4347033	4347170	MIRb	SINE/MIR
chr17	6128948	6130411	SVA_D	Retroposon/SVA
chr7	64066184	64066715	HERV1_LTRd	LTR/ERV1
chr5	23233987	23234214	MER41-int	LTR/ERV1
chr3	142824769	142827758	LTR25-int LTR25-int	LTR/ERV1
chrX	96529641	96531307	SVA_C	Retroposon/SVA
chr19	41695458	41695719	L2	LINE/L2
chr19	6584874	6584939	AluSz	SINE/Alu
chr22	17133966	17134250	AluJr	SINE/Alu
chr20	18313557	18319732	L1PA4	LINE/L1
chr8	28737804	28738763	SVA_E	Retroposon/SVA
chr1	207860455	207860665	L1M5	LINE/L1
chr8	9052883	9053184	AluSz	SINE/Alu
chr15	59156934	59156998	MIR	SINE/MIR
chr11	20569323	20570156	SVA_E	Retroposon/SVA
chr1	33516945	33517945	SVA_F	Retroposon/SVA
chr4	67081	67199	L1PA13	LINE/L1
chr19	21903126	21905526	SVA_E	Retroposon/SVA
chr16	24477155	24477554	Tigger2a	DNA/TcMar-Tigger
chr11	50240124	50241155	MER11A	LTR/ERV1
chr8	9057711	9058003	AluSq	SINE/Alu
chr1	207860078	207860394	MLT1A0	LTR/ERV1-MaLR
chr7	806342	806459	AluJb	SINE/Alu
chr19	6497287	6497576	AluJb	SINE/Alu
chr1	147420474	147420873	L2a	LINE/L2

chr19	53725485	53726902	SVA_D	Retroposon/SVA
chr5	23231113	23231904	MER51B HERV4_I-int LTR54B	LTR/ERV1
chr1	146989266	146989967	LTR12_	LTR/ERV1
chr16	8826076	8827671	SVA_D	Retroposon/SVA
chr12	8056198	8056485	AluSz	SINE/Alu
chr3	121407005	121408513	SVA_D	Retroposon/SVA
chr8	47924049	47925888	HUERS-P3-int	LTR/ERV1
chr7	4620517	4622001	Ricksha_c	DNA/MULE-MuDR
chr4	119712665	119714060	SVA_B	Retroposon/SVA
chr19	6584597	6584873	AluJr	SINE/Alu
chr4	61035	61327	AluSx1	SINE/Alu
chr19	22928179	22934876	LTR17 HERV17-int HERV17-int HERV17-int LTR17	LTR/ERV1
chr6	44266151	44266257	MIRb	SINE/MIR
chr2	63948844	63950437	SVA_F	Retroposon/SVA
chr12	8052953	8053087	AluSx	SINE/Alu
chr3	61419455	61421381	SVA_F	Retroposon/SVA
chr19	359565	359928	MLT1A0	LTR/ERV1-MaLR
chr9	131543725	131544226	LOR1a	LTR/ERV1
chr1	227042772	227044342	MER4-int MER4A1	LTR/ERV1
chrX	48511116	48511662	MER74B	LTR/ERV1
chr19	38281798	38282244	MER31A	LTR/ERV1
chrX	69898785	69900446	SVA_D	Retroposon/SVA
chr8	47917370	47917656	AluSx1	SINE/Alu
chr12	32715349	32716995	SVA_D	Retroposon/SVA
chr1	53373900	53374199	AluSx1	SINE/Alu
chr12	4742313	4742436	AluJb	SINE/Alu
chr19	36559254	36560956	SVA_C	Retroposon/SVA
chr16	9075315	9076587	SVA_C	Retroposon/SVA
chr6	125710006	125711315	SVA_E	Retroposon/SVA
chr19	22143901	22145028	MER11A	LTR/ERV1
chrX	48512471	48512864	MLT1A0-int	LTR/ERV1-MaLR
chr1	53369114	53369278	AluJo	SINE/Alu
chr1	207858551	207859113	ERV1-E-int	LTR/ERV1
chr3	8480704	8482932	SVA_D	Retroposon/SVA
chr5	23236499	23236748	MER4A1	LTR/ERV1
chr19	6498754	6498839	MIR	SINE/MIR
chr5	150688566	150690104	LTR12C	LTR/ERV1
chr19	6500139	6500442	AluJb	SINE/Alu
chr1	13433219	13434635	SVA_E	Retroposon/SVA
chr3	10111178	10112829	SVA_D	Retroposon/SVA
chr1	45203717	45204806	SVA_B	Retroposon/SVA

chr20	35651522	35651824	AluSz	SINE/Alu
chr16	87855431	87855964	MER92B	LTR/ERV1
chr5	23235183	23236498	MER57-int	LTR/ERV1
chr22	43086014	43086470	MLT1L MLT1L	LTR/ERV1-MaLR
chr19	20336898	20336996	L1PREC2	LINE/L1
chr17	2409546	2411437	SVA_D	Retroposon/SVA
chr22	43085737	43086013	MLT1J	LTR/ERV1-MaLR
chr1	33517915	33519087	SVA_F	Retroposon/SVA
chr1	227897703	227899534	SVA_D	Retroposon/SVA
chr19	20279928	20280217	AluSp	SINE/Alu
chr19	20233701	20233997	MLT1E1A	LTR/ERV1-MaLR
chr22	17132888	17133052	MER5A1	DNA/hAT-Charlie
chr10	32259130	32260541	SVA_E	Retroposon/SVA
chr1	23831501	23831834	L2c	LINE/L2
chr21	30392902	30393074	MER20	DNA/hAT-Charlie
chr12	12567383	12568513	SVA_D	Retroposon/SVA
chr8	47916963	47917212	HUERS-P3-int	LTR/ERV1
chr2	65565401	65566852	SVA_D	Retroposon/SVA
chrX	73056273	73057558	L1MC3	LINE/L1
chr2	192605967	192608132	SVA_D	Retroposon/SVA
chr5	55309746	55311848	SVA_D	Retroposon/SVA
chr7	63937218	63940296	L1MA8	LINE/L1
chr4	64714	65170	L1M3a	LINE/L1
chr5	104534199	104539643	L1PA5	LINE/L1
chr9	6806927	6808710	SVA_F	Retroposon/SVA
chr2	38629801	38631536	SVA_D	Retroposon/SVA
chr19	22047545	22049645	SVA_F	Retroposon/SVA
chr8	47943650	47945382	L1PBa	LINE/L1
chr20	55250835	55251120	AluJo	SINE/Alu
chr10	98512995	98513275	AluSz	SINE/Alu
chr11	73646671	73648711	SVA_D	Retroposon/SVA
chr13	25159501	25159657	L2d2	LINE/L2
chr19	55512965	55513277	AluJo	SINE/Alu
chr10	85977177	85977355	MIRb	SINE/MIR
chr1	150667600	150667912	AluSz	SINE/Alu
chr19	55431753	55431847	MLT1B	LTR/ERV1-MaLR
chr1	13654013	13655327	SVA_E	Retroposon/SVA
chr17	1305937	1307355	SVA_D	Retroposon/SVA
chr1	53345046	53345107	L2d2	LINE/L2
chr9	125628646	125629747	SVA_D	Retroposon/SVA
chr12	4813189	4813481	AluSx4	SINE/Alu

chr18	70998208	70998578	THE1B	LTR/ERV1-MaLR
chr14	42142257	42144843	SVA_D	Retroposon/SVA
chr7	150716673	150716751	L2d2	LINE/L2
chr19	30388911	30389210	AluSp	SINE/Alu
chr10	98511758	98512061	AluSz6	SINE/Alu
chr1	207859530	207859954	L1M5	LINE/L1
chr22	17134259	17134574	AluSq2	SINE/Alu
chr22	24197057	24198491	SVA_E	Retroposon/SVA
chr1	26921947	26924007	SVA_D	Retroposon/SVA
chr10	98506341	98506567	MIRb	SINE/MIR
chr4	153685788	153687290	SVA_B	Retroposon/SVA
chr19	47512359	47513891	SVA_D	Retroposon/SVA
chrX	47997984	47999513	SVA_A	Retroposon/SVA
chr1	207861038	207861333	L1ME3	LINE/L1
chr5	43085540	43085841	AluY	SINE/Alu
chr1	53353269	53353514	AluJr	SINE/Alu
chr5	23234909	23235167	MER41-int	LTR/ERV1
chr1	207861813	207863949	L1ME3	LINE/L1
chr7	157231100	157231456	MLT1C2	LTR/ERV1-MaLR
chr9	110018355	110020828	SVA_F	Retroposon/SVA
chr10	98497445	98497703	L1MC2	LINE/L1
chr1	53368138	53368261	AluJr	SINE/Alu
chr1	154316120	154316342	L1MA9	LINE/L1
chr6	28469292	28470908	SVA_B	Retroposon/SVA
chr2	161304818	161306349	SVA_B	Retroposon/SVA
chr19	20234022	20234225	FordPrefect	DNA/hAT-Tip100
chr8	47987138	47992107	L1PA4	LINE/L1
chr19	20281105	20281399	AluSx1	SINE/Alu
chr14	23105172	23106844	SVA_D	Retroposon/SVA
chrX	67545680	67547637	SVA_E	Retroposon/SVA
chr1	21379037	21380979	SVA_D	Retroposon/SVA
chr6	93433043	93434724	LTR12C	LTR/ERV1
chr12	8051844	8052123	AluY	SINE/Alu
chr4	83401804	83402516	L2a	LINE/L2
chr4	40142202	40143764	SVA_D	Retroposon/SVA
chr19	55431597	55431751	MER20	DNA/hAT-Charlie
chr19	6584940	6585038	L1PA10	LINE/L1
chr19	6585359	6585652	AluJb	SINE/Alu
chr8	47921000	47921794	HUERS-P3-int	LTR/ERV1
chr6	56758416	56760857	SVA_E	Retroposon/SVA
chr19	20283121	20283407	AluSq2	SINE/Alu

chr10	98498490	98498777	Tigger1	DNA/TcMar-Tigger
chr12	8052214	8052398	AluSx1	SINE/Alu
chr12	4812639	4812770	AluJo	SINE/Alu
chr11	61416129	61416257	MLT1H	LTR/ERV1-MaLR
chr7	2306935	2309168	SVA_F	Retroposon/SVA
chr19	20283459	20283749	AluSg	SINE/Alu
chr10	12560509	12562924	SVA_E	Retroposon/SVA
chr3	72836852	72838245	SVA_B	Retroposon/SVA
chr3	21622601	21623035	L2c	LINE/L2
chr12	8053096	8053157	AluSx	SINE/Alu
chr16	2850574	2850930	Tigger3	DNA/TcMar-Tigger
chr19	20281400	20281596	MER92B	LTR/ERV1
chr16	24477555	24477883	L1ME3B	LINE/L1
chr19	20282799	20283110	AluSp	SINE/Alu
chr14	101300986	101301075	L2b	LINE/L2
chr7	53832729	53833759	L1MC1	LINE/L1
chr12	8054579	8054884	AluSc	SINE/Alu
chr19	6582821	6583014	THE1-int	LTR/ERV1-MaLR
chr1	207857611	207857872	L1ME4a	LINE/L1
chr20	35627864	35630179	SVA_D	Retroposon/SVA
chr7	805893	805990	L1ME4a	LINE/L1
chr10	98507018	98507329	AluSq	SINE/Alu
chr1	146934493	146941668	L1PA14	LINE/L1
chr22	24587221	24587550	LTR33A_	LTR/ERV1
chr19	20279658	20279923	AluSx4	SINE/Alu
chr10	98499208	98499355	AluJb	SINE/Alu
chr19	20280479	20280697	MER92B	LTR/ERV1
chr19	37798037	37798531	LTR53 LTR53-int	LTR/ERV1
chr1	45353788	45354925	MER41-int MER41-int	LTR/ERV1
chr1	207863950	207864412	MLT1C2	LTR/ERV1-MaLR
chr16	87854104	87854645	LTR8A	LTR/ERV1
chr1	53346772	53346958	MIRb	SINE/MIR
chr19	55440455	55440746	AluSz	SINE/Alu
chr1	53374632	53374960	L1MB4	LINE/L1
chr22	17122219	17125789	L1PA16	LINE/L1
chr8	48014478	48015704	L1MEc	LINE/L1
chr19	6582367	6582820	L1PA5	LINE/L1
chr19	6499610	6499712	L2b	LINE/L2
chr10	98507330	98507490	AluJb	SINE/Alu
chr19	53016702	53016999	AluY	SINE/Alu
chr19	22757824	22764561	LTR5_Hs HERVK-int HERVK-int HERVK-int LTR5_Hs	LTR/ERV1

chr1	228121574	228121997	L1MB7	LINE/L1
chr19	6600109	6602013	HERVE_a-int LTR2 LTR2	LTR/ERV1
chr14	101295803	101295973	MIRb	SINE/MIR
chr12	39190359	39193447	L1P1	LINE/L1
chr22	22201317	22202740	SVA_B	Retroposon/SVA
chr19	20334374	20334667	AluSp	SINE/Alu
chr16	5251748	5253790	SVA_E	Retroposon/SVA
chr19	55502961	55503233	AluSx	SINE/Alu
chr19	6498289	6498742	L2a	LINE/L2
chrX	73044838	73044890	MIRc	SINE/MIR
chr1	53368934	53369062	L1PB1	LINE/L1
chr7	139158439	139158523	AluSp	SINE/Alu
chr3	23912168	23913892	SVA_D	Retroposon/SVA
chr6	24672890	24673596	MER4-int MER4-int MER4-int	LTR/ERV1
chr2	175972255	175973916	SVA_C	Retroposon/SVA
chr12	8052401	8052466	Alu	SINE/Alu
chr4	6838275	6839679	SVA_B	Retroposon/SVA
chrX	128987627	128993336	L1PA5	LINE/L1
chr21	45671236	45671402	L1MA10	LINE/L1
chr1	53374962	53375098	MER2	DNA/TcMar-Tigger
chr19	20278889	20279180	AluSg	SINE/Alu
chr22	24586598	24586713	L2c	LINE/L2
chr19	20282525	20282796	L1PREC2	LINE/L1
chr6	103230443	103232771	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr12	131456808	131457094	MER121	DNA/hAT?
chrX	73042269	73042349	L2a	LINE/L2
chr19	20283750	20284228	L1PREC2	LINE/L1
chr7	152274186	152274275	LTR8A	LTR/ERV1
chr7	804426	804778	AluJr	SINE/Alu
chr19	20278723	20278882	LTR10B2	LTR/ERV1
chr2	54322027	54324009	SVA_D	Retroposon/SVA
chr2	54312006	54312188	L1MC4	LINE/L1
chr22	43080067	43080294	MIRc	SINE/MIR
chr12	132412193	132412429	L2	LINE/L2
chr1	207857422	207857609	L3	LINE/CR1
chr8	115323399	115324824	LTR12C	LTR/ERV1
chr19	53017028	53017297	AluSx	SINE/Alu
chr19	20237315	20237520	L1MA8	LINE/L1
chr12	95628448	95630244	SVA_D	Retroposon/SVA
chr11	6726113	6726293	AluSg4	SINE/Alu
chr18	71028739	71031552	L1MB5	LINE/L1

chrX	75438330	75439598	SVA_F	Retroposon/SVA
chr7	64426237	64427310	L1P4	LINE/L1
chr12	8776917	8778111	SVA_D	Retroposon/SVA
chr5	150690105	150692905	L1M1	LINE/L1
chr1	53375099	53375322	MER30	DNA/hAT-Charlie
chr17	2349925	2351365	SVA_D	Retroposon/SVA
chrX	73043930	73043999	MIRc	SINE/MIR
chr19	14251142	14251446	AluSc8	SINE/Alu
chr19	53018216	53018516	AluSq2	SINE/Alu
chr10	88839663	88841720	SVA_D	Retroposon/SVA
chr1	53367837	53368127	AluSz6	SINE/Alu
chr1	53373816	53373899	L1MB4	LINE/L1
chr2	170431030	170432685	SVA_D	Retroposon/SVA
chr19	55431914	55432177	AluJr	SINE/Alu
chr5	23233578	23233977	MER61-int	LTR/ERV1
chr1	45352605	45353328	MER41-int	LTR/ERV1
chr4	113877187	113877910	MER44C	DNA/TcMar-Tigger
chr12	123211538	123211835	AluJr	SINE/Alu
chr19	20237027	20237314	AluSz	SINE/Alu
chr12	8055138	8055418	AluSp	SINE/Alu
chr7	140061313	140063510	SVA_E	Retroposon/SVA
chr19	20339289	20341821	L1PA5	LINE/L1
chr1	207859991	207860077	L1MB7	LINE/L1
chr1	217663251	217664200	L1ME1	LINE/L1
chr1	112149661	112151521	SVA_D	Retroposon/SVA
chr2	122567097	122567570	MLT1F	LTR/ERV1-MaLR
chr2	195244164	195248290	MER57A1 MER57-int	LTR/ERV1
chr16	24476391	24476769	MSTA	LTR/ERV1-MaLR
chr19	54605304	54605601	AluY	SINE/Alu
chr22	32914380	32914695	L1ME4a	LINE/L1
chr7	139153492	139153895	MLT1B	LTR/ERV1-MaLR
chr10	11925708	11926425	MER63C	DNA/hAT-Blackjack
chr22	41690028	41691719	SVA_D	Retroposon/SVA
chr18	70998985	70999569	L1MC5a	LINE/L1
chr14	101296554	101296681	MIRc	SINE/MIR
chr1	113440247	113441932	SVA_F	Retroposon/SVA
chr14	35510673	35511005	LTR84b	LTR/ERV1
chr10	98514319	98514434	AluJr	SINE/Alu
chr20	35640259	35642008	SVA_D	Retroposon/SVA
chr1	53357042	53357335	L1MEd	LINE/L1
chr14	101528923	101529447	Eutr11	DNA

chrX	73044222	73044279	MIRc	SINE/MIR
chr1	53355922	53356205	AluSx3	SINE/Alu
chr2	54319597	54320296	ERV3-16A3_I-int LTR16	LTR/ERV1
chr9	119612732	119612922	MIRb	SINE/MIR
chr13	48321251	48321807	MLT1F1	LTR/ERV1-MaLR
chr11	78902140	78903817	SVA_D	Retroposon/SVA
chr17	8276459	8277959	SVA_B	Retroposon/SVA
chr19	52899901	52900191	AluJr	SINE/Alu
chr14	101529782	101530215	MER4A1	LTR/ERV1
chr17	17447584	17447877	AluSq2	SINE/Alu
chrX	73044011	73044061	L2b	LINE/L2
chr8	9029398	9029543	MIR3	SINE/MIR
chr4	3538610	3539016	MER57A-int MER57A-int	LTR/ERV1
chr14	101296722	101296821	MIRc	SINE/MIR
chr14	101298108	101298232	MIRb	SINE/MIR
chr1	53344329	53344651	AluSq2	SINE/Alu
chr7	139158221	139158437	HAL1	LINE/L1
chr19	49386505	49386781	MER41B	LTR/ERV1
chr20	32204287	32204546	AluSz6	SINE/Alu
chr7	100842282	100842582	AluSg	SINE/Alu
chr1	53354030	53354329	AluSq2	SINE/Alu
chr4	188962875	188963629	LTR1A2	LTR/ERV1
chr18	77656266	77658800	L1M4b	LINE/L1
chr2	15751006	15753178	SVA_D	Retroposon/SVA
chr14	101296945	101297034	L2c	LINE/L2
chr10	94734302	94736433	SVA_D	Retroposon/SVA
chr20	32206900	32207253	AluSz	SINE/Alu
chr1	53373694	53373805	L2b	LINE/L2
chr20	32113459	32113759	AluJr	SINE/Alu
chr19	20288738	20289035	AluSq10	SINE/Alu
chr9	119610934	119611783	MER21B	LTR/ERV1
chr1	15439708	15439968	MER106B	DNA/hAT-Charlie
chr20	32201103	32201521	MER68B	LTR/ERV1
chr13	55627766	55635877	LTR17 HERV17-int HERV17-int HERV17-int HERV17-int LTR17	LTR/ERV1
chr9	119600706	119601009	AluSq2	SINE/Alu
chr19	6496683	6496836	AluSx3	SINE/Alu
chr14	101396853	101397066	MER20	DNA/hAT-Charlie
chr3	21621111	21621528	MLT1C2	LTR/ERV1-MaLR
chr1	53374200	53374323	L1MB4	LINE/L1
chr19	37798564	37798997	MER51E	LTR/ERV1

chr22	38805406	38806730	SVA_B	Retroposon/SVA
chr14	101297698	101297917	L2	LINE/L2
chr13	25160431	25160707	AluSx1	SINE/Alu
chr6	24674960	24676907	L1PA5	LINE/L1
chr7	139158524	139158627	HAL1	LINE/L1
chr16	31114923	31117030	SVA_D	Retroposon/SVA
chrX	73043321	73043383	L2a	LINE/L2
chr1	202159949	202161640	SVA_F	Retroposon/SVA
chr14	36293178	36294838	SVA_D	Retroposon/SVA
chr14	101536322	101536417	MIR3	SINE/MIR
chr19	20278570	20278648	AluSz	SINE/Alu
chr7	34692274	34692740	MER92B	LTR/ERV1
chr14	31715568	31720344	LTR7Y HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr19	55503293	55503580	AluSg	SINE/Alu
chr19	22040886	22046695	LTR7C HERVH-int HERVH-int HERVH-int LTR7C	LTR/ERV1
chr19	20288105	20288393	LTR70	LTR/ERV1
chr19	5559344	5559645	AluY	SINE/Alu
chr1	207864413	207865166	L1ME3	LINE/L1
chr1	150668594	150669034	L2c	LINE/L2
chrX	73067240	73067354	FLAM_C	SINE/Alu
chr1	222660309	222662729	SVA_D	Retroposon/SVA
chr20	18292592	18292955	Tigger4b	DNA/TcMar-Tigger
chr19	52897504	52897786	AluSx3	SINE/Alu
chr11	6726475	6726767	AluSx	SINE/Alu
chr1	207857982	207858138	L1ME4a	LINE/L1
chr14	35512359	35512584	MIR	SINE/MIR
chr19	9576387	9576690	AluSx	SINE/Alu
chr19	55432192	55432308	AluSx	SINE/Alu
chr19	20600332	20600617	AluSx	SINE/Alu
chr1	53357397	53357574	L1MEd	LINE/L1
chr1	143421323	143425437	L1PA13	LINE/L1
chrX	71903331	71903779	L1ME1	LINE/L1
chr2	204072724	204073017	AluJr	SINE/Alu
chr2	3637710	3639834	SVA_D	Retroposon/SVA
chr12	76334786	76336717	SVA_D	Retroposon/SVA
chr7	64709270	64709560	AluSz	SINE/Alu
chr14	101299604	101299894	AluSg	SINE/Alu
chr12	70594939	70596066	SVA_E	Retroposon/SVA
chr17	80334508	80334602	L1MB5	LINE/L1
chr6	24676916	24683328	HERV17-int LTR17	LTR/ERV1
chr14	101327149	101327343	MIRb	SINE/MIR

chr12	122841149	122843002	SVA_D	Retroposon/SVA
chr19	53019460	53019547	AluSz	SINE/Alu
chr1	53346099	53346674	MLT1E1A	LTR/ERV1-MaLR
chr21	30566036	30566367	AluSz	SINE/Alu
chr10	85963178	85963471	AluSx3	SINE/Alu
chr3	21584131	21584522	MER61A MER61-int	LTR/ERV1
chr19	53019143	53019396	L2	LINE/L2
chr19	55433864	55434175	AluSq2	SINE/Alu
chr4	167120727	167124603	MER61-int MER61A	LTR/ERV1
chr5	133808756	133809938	L1MB8	LINE/L1
chr8	9032012	9032067	MLT1G3	LTR/ERV1-MaLR
chr17	19345738	19347628	MSTA-int MSTA	LTR/ERV1-MaLR
chr4	77837254	77838467	SVA_D	Retroposon/SVA
chr4	55238	56751	LTR70	LTR/ERV1
chr3	186528655	186530271	SVA_D	Retroposon/SVA
chr13	25169002	25169594	MER54A	LTR/ERV1
chr14	101534235	101534360	L2a	LINE/L2
chr1	53356275	53356541	AluJr	SINE/Alu
chr4	165886944	165887684	HAL1	LINE/L1
chr20	25268339	25268637	AluJb	SINE/Alu
chr19	55493162	55493445	AluSp	SINE/Alu
chr14	105544938	105546382	SVA_D	Retroposon/SVA
chr19	55499129	55499427	AluSx3	SINE/Alu
chr19	12153665	12153946	AluJr	SINE/Alu
chr14	101536763	101536827	L2c	LINE/L2
chr19	53772639	53773979	SVA_D	Retroposon/SVA
chr19	36800915	36801209	AluSz	SINE/Alu
chr4	53687	53873	MER57E3	LTR/ERV1
chr4	54783	55080	AluY	SINE/Alu
chr6	29642322	29642421	MER94	DNA/hAT-Blackjack
chr1	76294517	76300619	L1PA5	LINE/L1
chr1	53345460	53345735	AluSc	SINE/Alu
chr1	179008867	179010821	SVA_D	Retroposon/SVA
chr19	37799810	37800365	MLT1G	LTR/ERV1-MaLR
chr17	27859374	27860875	SVA_A	Retroposon/SVA
chr14	101535660	101535791	MIR	SINE/MIR
chr10	70284655	70284823	AluSz	SINE/Alu
chr2	78638491	78638868	L2a	LINE/L2
chr19	55503925	55504225	AluSx	SINE/Alu
chr3	109366436	109372250	L1PA7	LINE/L1
chr19	20288394	20288684	AluSp	SINE/Alu

chr20	32203392	32203533	AluY	SINE/Alu
chr19	49385668	49386195	LTR10C	LTR/ERV1
chr20	32199314	32199604	AluJr	SINE/Alu
chr17	29310672	29311564	L1MB2	LINE/L1
chr19	36801471	36801682	L2d	LINE/L2
chrX	29350787	29353389	SVA_E	Retroposon/SVA
chr8	9034271	9034360	AluJo	SINE/Alu
chr9	133381302	133382739	SVA_D	Retroposon/SVA
chr19	12152640	12152792	AluJb	SINE/Alu
chr3	23911375	23911922	MLT1F1	LTR/ERV1-MaLR
chr1	78334618	78336825	SVA_E	Retroposon/SVA
chr10	70282291	70282595	AluSc8	SINE/Alu
chr19	5560909	5561088	L2b	LINE/L2
chr3	10112843	10113445	L1MA3	LINE/L1
chr1	228131700	228132235	L1MB7	LINE/L1
chr3	124468263	124470217	SVA_D	Retroposon/SVA
chr12	4812468	4812583	L1ME4c	LINE/L1
chr10	70281654	70281946	AluSz	SINE/Alu
chr19	47758814	47759119	AluY	SINE/Alu
chr20	32200619	32200897	AluJr	SINE/Alu
chr19	52898486	52898653	L1MD	LINE/L1
chr1	53356568	53356871	AluSq	SINE/Alu
chr5	12490324	12494592	LTR7Y HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr19	52912962	52913267	AluSx	SINE/Alu
chr8	9037020	9037258	MIRb	SINE/MIR
chr14	76387332	76390632	L1P2	LINE/L1
chr12	8980048	8981840	L1MA3	LINE/L1
chr9	45613532	45616610	LTR25-int LTR25-int MER61D	LTR/ERV1
chr19	55431532	55431588	L1PB2	LINE/L1
chr1	53343798	53344257	MLT1H2	LTR/ERV1-MaLR
chr20	25265385	25265699	MamRep1151	LTR?
chr13	20193925	20194106	L1M3c	LINE/L1
chr1	53361202	53361506	AluJb	SINE/Alu
chr19	55434556	55434642	MER58B	DNA/hAT-Charlie
chr19	54312039	54312221	MER20	DNA/hAT-Charlie
chr11	65006066	65007793	SVA_F	Retroposon/SVA
chr1	161250134	161250576	L2-3_Crp	LINE/L2
chr13	20194148	20194450	AluSx	SINE/Alu
chr3	150537209	150539615	SVA_E	Retroposon/SVA
chr1	53354354	53354520	AluJr	SINE/Alu
chr1	235471756	235473508	SVA_D	Retroposon/SVA

chr2	234062069	234062794	HAL1	LINE/L1
chr19	9575806	9576113	AluSc	SINE/Alu
chr13	25158356	25158934	L1MC5	LINE/L1
chr8	66574290	66575782	SVA_D	Retroposon/SVA
chr9	86423643	86423985	MLT1I	LTR/ERV1-MaLR
chr21	45669175	45669889	MER49	LTR/ERV1
chr11	62126034	62126618	Zaphod	DNA/hAT-Tip100
chr9	119605337	119605654	L1PA16	LINE/L1
chr2	78768383	78770304	L1PBa1	LINE/L1
chr19	5558780	5558830	MIR	SINE/MIR
chr8	9036940	9037011	L2d2	LINE/L2
chr1	203810286	203811750	SVA_B	Retroposon/SVA
chr19	37492194	37492504	AluSg	SINE/Alu
chr7	23675523	23676345	SVA_E	Retroposon/SVA
chr21	30565341	30565995	MER50B	LTR/ERV1
chr14	76386616	76389331	L1PA6	LINE/L1
chr10	70244182	70244476	AluJr	SINE/Alu
chr2	32518143	32520141	SVA_D	Retroposon/SVA
chr14	101534514	101534618	L2a	LINE/L2
chr5	116347033	116348299	HSMAR1	DNA/TcMar-Mariner
chr4	167119312	167120483	MER61A MER61-int MER61-int	LTR/ERV1
chr19	53016275	53016573	AluSp	SINE/Alu
chr4	188926399	188926745	MLT1B	LTR/ERV1-MaLR
chr19	41697257	41697486	L1ME2z	LINE/L1
chr14	101537175	101537404	L2b	LINE/L2
chr2	78637173	78637788	L1M5	LINE/L1
chr17	17814966	17816551	SVA_D	Retroposon/SVA
chr10	70283574	70283710	AluSz	SINE/Alu
chr1	27387867	27387962	L2	LINE/L2
chr19	39014967	39015163	MIRb	SINE/MIR
chr20	3731730	3731895	MIRb	SINE/MIR
chr17	29308417	29309716	L1MB4	LINE/L1
chr6	44263693	44263922	MIRb	SINE/MIR
chr19	20826632	20827415	L1M3a	LINE/L1
chr7	77145863	77146144	L2c	LINE/L2
chrX	122867344	122868845	SVA_D	Retroposon/SVA
chr4	175215198	175216908	SVA_D	Retroposon/SVA
chr1	160902415	160903956	SVA_B	Retroposon/SVA
chr13	20195985	20196297	AluJb	SINE/Alu
chr8	9035423	9035727	AluSx1	SINE/Alu
chr19	55497923	55498215	AluSx1	SINE/Alu

chr14	101373180	101373358	MIRb	SINE/MIR
chr7	152274409	152274768	LTR8A	LTR/ERV1
chr10	98687553	98689972	Tigger1	DNA/TcMar-Tigger
chr19	53017919	53018208	AluSg	SINE/Alu
chr2	27761995	27764309	SVA_E	Retroposon/SVA
chr20	25270374	25270473	L1MC5	LINE/L1
chr5	134216900	134218561	SVA_D	Retroposon/SVA
chr1	15440372	15440556	MIRb	SINE/MIR
chr9	46628936	46631996	LTR25-int LTR25-int MER61D	LTR/ERV1
chr7	64680102	64680592	MLT1H	LTR/ERV1-MaLR
chr19	54226961	54227261	AluSx	SINE/Alu
chr8	115259913	115260357	MER4A1	LTR/ERV1
chr13	87034915	87035767	MER52A	LTR/ERV1
chr8	9032074	9032371	AluJr	SINE/Alu
chr19	12154438	12154537	AluJo	SINE/Alu
chr17	80334690	80335356	SVA_D	Retroposon/SVA
chr14	103143562	103144580	SVA_D	Retroposon/SVA
chr19	54605602	54605749	L2c	LINE/L2
chr8	115260723	115261139	L1MC4a	LINE/L1
chr7	139161864	139162509	L1MB3	LINE/L1
chr19	36981365	36983060	SVA_E	Retroposon/SVA
chr4	53893	54246	MER21C	LTR/ERV1
chr18	3355763	3357421	L1MA9	LINE/L1
chr7	139136713	139137021	AluSx3	SINE/Alu
chr19	55499661	55499914	AluSx1	SINE/Alu
chr4	575347	576617	L1ME1	LINE/L1
chr5	76273102	76274496	Tigger1	DNA/TcMar-Tigger
chr10	70281014	70281301	AluSz	SINE/Alu
chr1	15440786	15440883	MIR	SINE/MIR
chr10	85959054	85959646	L1ME4a	LINE/L1
chr1	27387219	27387387	AluY	SINE/Alu
chr19	12154134	12154417	AluSp	SINE/Alu
chr10	70284886	70285191	AluSz	SINE/Alu
chr1	21141297	21142266	SVA_D	Retroposon/SVA
chr21	44342876	44345058	HERVH48-int	LTR/ERV1
chr15	52751372	52752877	SVA_B	Retroposon/SVA
chr4	65439	65858	MSTA	LTR/ERV1-MaLR
chr1	142665075	142666063	MER4-int LTR49 MER4-int MER4-int	LTR/ERV1
chr8	9031614	9031748	L2d	LINE/L2
chrX	71823242	71823385	X12_DNA	DNA/TcMar-Tigger
chr5	1440640	1441037	MLT1B	LTR/ERV1-MaLR

chr11	18664801	18671021	LTR7B HERVH-int HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chrX	40722954	40723849	MSTC-int MSTC	LTR/ERV1-MaLR
chr19	20286142	20287623	SVA_A	Retroposon/SVA
chr6	74098369	74098469	MIRb	SINE/MIR
chr4	152311328	152312938	SVA_E	Retroposon/SVA
chr17	47248007	47254052	MER9a3 HERVK9-int HERVK9-int MER9a3	LTR/ERVK
chr19	53248276	53253707	HERVK-int HERVK-int HERVK-int LTR5B	LTR/ERVK
chr1	21142235	21143752	SVA_E	Retroposon/SVA
chr1	53343686	53343794	MIR	SINE/MIR
chr17	52278935	52279902	LTR5_Hs	LTR/ERVK
chr7	48133886	48134088	AluSx1	SINE/Alu
chr19	54226660	54226953	AluSx	SINE/Alu
chr19	55500624	55500849	AluSx	SINE/Alu
chr19	9576741	9577045	AluSx	SINE/Alu
chr1	15447075	15447268	MIRb	SINE/MIR
chr20	25270000	25270309	AluJb	SINE/Alu
chr22	35580773	35584460	L1PREC2	LINE/L1
chr19	12152801	12153218	LTR39	LTR/ERV1
chr8	9035292	9035422	Arthur1A	DNA/hAT-Tip100
chr6	111452221	111459276	LTR17 HERV17-int HERV17-int HERV17-int LTR17	LTR/ERV1
chr10	70282156	70282290	AluSz	SINE/Alu
chr8	9027086	9027292	MER2	DNA/TcMar-Tigger
chr19	20300179	20301009	L1MB2	LINE/L1
chr10	70281948	70282155	L1ME1	LINE/L1
chr1	27387963	27388258	AluJr	SINE/Alu
chr19	41698348	41698539	MIR	SINE/MIR
chr1	27389631	27389924	AluSx1	SINE/Alu
chr20	25265109	25265361	AluJb	SINE/Alu
chr4	574733	575335	L1ME3B	LINE/L1
chr1	228119722	228121386	Tigger1	DNA/TcMar-Tigger
chr8	9034533	9034634	AluSx3	SINE/Alu
chr13	20180374	20180725	MLT1J2	LTR/ERV1-MaLR
chr11	62127800	62128661	Zaphod	DNA/hAT-Tip100
chr8	9034019	9034103	L2c	LINE/L2
chr10	102036227	102038579	SVA_D	Retroposon/SVA
chr9	42075047	42078106	MER61D LTR25-int LTR25-int	LTR/ERV1
chrX	40721215	40722923	SVA_A	Retroposon/SVA
chr19	55500018	55500185	AluSg	SINE/Alu
chr10	70278964	70279262	AluSg7	SINE/Alu
chr12	132410280	132411662	SVA_D	Retroposon/SVA

chr19	55490713	55491018	AluSq2	SINE/Alu
chr7	139136397	139136509	MIRb	SINE/MIR
chr4	188920448	188920585	AluJb	SINE/Alu
chr11	85820949	85823186	SVA_D	Retroposon/SVA
chr4	167372963	167373293	L1M5	LINE/L1
chr14	93089213	93091887	HERVIP10B3-int HERVIP10B3-int	LTR/ERV1
chr4	167374024	167374434	MLT1H	LTR/ERV1-MaLR
chr5	133783176	133783467	AluJr4	SINE/Alu
chr1	78333916	78334211	AluSz	SINE/Alu
chr19	55491864	55492195	MER83	LTR/ERV1
chr19	5558344	5558493	L2c	LINE/L2
chr20	25268005	25268317	AluJr	SINE/Alu
chr19	53019741	53020173	LTR7B	LTR/ERV1
chr14	101376538	101376657	MIRc	SINE/MIR
chr11	62135963	62138471	LTR5_Hs HERVK-int	LTR/ERVK
chr4	146761409	146761570	MER91B	DNA/hAT-Tip100
chrX	73787742	73789694	SVA_D	Retroposon/SVA
chr9	19250526	19252409	THE1B-int THE1B	LTR/ERV1-MaLR
chr19	20823959	20824405	L1MB2	LINE/L1
chr4	3950467	3950766	AluSq2	SINE/Alu
chr16	67221866	67222178	AluSz	SINE/Alu
chr3	129702648	129703065	LTR16C	LTR/ERV1
chr8	9038174	9038357	AluJb	SINE/Alu
chr7	139135567	139135826	MLT1G1	LTR/ERV1-MaLR
chr14	35863132	35863567	MER110A	LTR/ERV1
chr19	20505971	20506249	AluSx	SINE/Alu
chr7	139137050	139137199	L1PA7	LINE/L1
chr8	9033089	9033390	AluSx1	SINE/Alu
chr17	29309881	29310328	L1MB2	LINE/L1
chr11	536488	536774	AluSz	SINE/Alu
chr2	35742246	35746163	MER61C MER61-int	LTR/ERV1
chr12	8976974	8979044	L1MA3	LINE/L1
chr12	14886306	14886584	AluSz	SINE/Alu
chr11	61422485	61423448	LTR5_Hs	LTR/ERVK
chr5	116281324	116281873	LTR7	LTR/ERV1
chr19	20575130	20575408	AluSx	SINE/Alu
chr10	85959944	85960108	L1ME4a	LINE/L1
chr4	37673504	37674066	MER21C	LTR/ERV1
chr19	20226984	20227275	AluSx	SINE/Alu
chr18	12873245	12875325	SVA_D	Retroposon/SVA
chr19	49384939	49385074	AluSx	SINE/Alu

chr14	65416157	65416470	AluSx	SINE/Alu
chr7	139135964	139136253	AluSx1	SINE/Alu
chr15	51585732	51587195	SVA_D	Retroposon/SVA
chr5	133780444	133780914	MLT1F	LTR/ERV1-MaLR
chr7	22844716	22848217	MER61-int MER61-int MER61B	LTR/ERV1
chr13	20195025	20195330	AluJr	SINE/Alu
chr13	25285970	25286110	LTR85a	LTR/Gypsy?
chr17	20306559	20308676	L1PA11	LINE/L1
chr19	12151914	12152038	AluJo	SINE/Alu
chr5	133780915	133781200	MLT1J	LTR/ERV1-MaLR
chr18	26876670	26880072	MLT2A2 HERVL-int HERVL-int HERVL-int	LTR/ERV1
chr6	111499100	111499225	FLAM_A	SINE/Alu
chr4	167373029	167373310	L1MD	LINE/L1
chr10	128446651	128447194	MER67A	LTR/ERV1
chr14	101400692	101402095	L1M2	LINE/L1
chr8	9031184	9031493	AluJr	SINE/Alu
chr5	178956283	178956593	AluY	SINE/Alu
chr8	144372197	144372485	AluJr	SINE/Alu
chr1	228125106	228125544	MLT1C2	LTR/ERV1-MaLR
chr7	152275352	152275656	AluSq2	SINE/Alu
chr20	32113791	32114019	Tigger17a	DNA/TcMar-Tigger
chr19	20227870	20228139	AluSx1	SINE/Alu
chr4	188923364	188923632	L2a	LINE/L2
chr1	27387650	27387861	MIR	SINE/MIR
chr19	53016151	53016247	AluSz	SINE/Alu
chr22	29883338	29883651	AluJr	SINE/Alu
chr8	9027792	9028128	LTR16C	LTR/ERV1
chr22	43114257	43114569	AluSz	SINE/Alu
chr2	65855035	65855595	MLT1G1	LTR/ERV1-MaLR
chr5	101577533	101579212	L1M1	LINE/L1
chr6	74310675	74312172	SVA_D	Retroposon/SVA
chr7	77144423	77144946	MLT1F	LTR/ERV1-MaLR
chr4	170490644	170492323	SVA_F	Retroposon/SVA
chr14	101380942	101381683	MER54A	LTR/ERV1
chr10	70283235	70283531	AluSx	SINE/Alu
chr19	12153224	12153355	AluY	SINE/Alu
chr8	121063640	121063812	MIRb	SINE/MIR
chr19	20220661	20221082	L1MB2	LINE/L1
chr4	119223618	119223880	AluSz	SINE/Alu
chr7	152274769	152275052	AluJr	SINE/Alu
chr1	15439259	15439445	MER5A	DNA/hAT-Charlie

chr10	70285201	70285399	AluJb	SINE/Alu
chr20	25230487	25230784	AluSx3	SINE/Alu
chr13	20200029	20200195	AluJr	SINE/Alu
chr20	25233024	25233765	MER21C	LTR/ERV1
chr5	116282259	116282615	L2a	LINE/L2
chr12	132411830	132411960	L1MC1	LINE/L1
chr17	18444328	18444760	L1MC4	LINE/L1
chr2	25378720	25378831	FLAM_C	SINE/Alu
chr14	101398942	101399945	L1MC1	LINE/L1
chr5	178955405	178955706	AluSz	SINE/Alu
chr4	3887545	3888544	L1MB3	LINE/L1
chr14	38023876	38025731	SVA_D	Retroposon/SVA
chr8	9039260	9039567	AluSp	SINE/Alu
chr2	25379148	25379462	AluSz	SINE/Alu
chr4	3761718	3761959	MLT1L	LTR/ERV1-MaLR
chr15	65090618	65092291	SVA_D	Retroposon/SVA
chr7	64709597	64710001	MLT1K	LTR/ERV1-MaLR
chr4	170862159	170862495	LTR26C	LTR/ERV1
chrX	71824351	71824478	X12_DNA	DNA/TcMar-Tigger
chr12	14888800	14889188	MLT1A	LTR/ERV1-MaLR
chr7	64710540	64710687	MIRb	SINE/MIR
chr4	188919514	188920011	Tigger3	DNA/TcMar-Tigger
chr19	20223127	20223430	AluSx	SINE/Alu
chr9	124139778	124140969	L1MC1	LINE/L1
chr8	9028717	9029020	AluSx	SINE/Alu
chr9	141067771	141069361	PRIMA41-int	LTR/ERV1
chr14	51423000	51423996	SVA_B	Retroposon/SVA
chr12	14887492	14888798	L2a	LINE/L2
chr1	27386763	27387218	LTR2	LTR/ERV1
chr17	60753999	60754219	MIR	SINE/MIR
chr11	8998936	9000000	SVA_D	Retroposon/SVA
chr19	41698579	41698671	MIR3	SINE/MIR
chr19	55490348	55490652	AluSx1	SINE/Alu
chr1	27388488	27388802	AluSz	SINE/Alu
chr19	20221083	20221371	AluSx1	SINE/Alu
chr7	23680133	23681172	L1MB4	LINE/L1
chr4	73976074	73976182	FLAM_A	SINE/Alu
chr19	22858134	22860408	L1PA5	LINE/L1
chr4	158558123	158558996	SVA_F	Retroposon/SVA
chr1	143161537	143162527	MER4-int LTR49 MER4-int MER4-int	LTR/ERV1
chr16	23605597	23605688	MER5B	DNA/hAT-Charlie

chr19	20226677	20226980	AluSz	SINE/Alu
chr7	152275053	152275316	LTR8A	LTR/ERV1
chr1	27389358	27389409	MIRb	SINE/MIR
chr4	170862496	170862873	LTR7	LTR/ERV1
chr19	55430507	55431531	LTR13	LTR/ERVK
chr10	70284320	70284654	AluSz	SINE/Alu
chr17	45497282	45499010	SVA_D	Retroposon/SVA
chr12	4826910	4827799	L1MDa	LINE/L1
chr1	244978836	244979303	MER41A MER41-int	LTR/ERV1
chr4	240701	241790	MER11B	LTR/ERVK
chr7	139146211	139150158	LTR7 HERVH-int HERVH-int	LTR/ERV1
chr12	4809609	4810376	L2c	LINE/L2
chr19	20826511	20826631	FLAM_A	SINE/Alu
chr4	119223174	119223585	L1MD	LINE/L1
chr13	20183160	20183464	AluSx	SINE/Alu
chr13	25165731	25166668	LTR5_Hs	LTR/ERVK
chr2	65785912	65786291	MLT1A1	LTR/ERV1-MaLR
chr8	121067198	121067472	AluJb	SINE/Alu
chr11	4157999	4159344	SVA_D	Retroposon/SVA
chr3	101424918	101425212	AluSq	SINE/Alu
chr13	20197681	20198114	LTR75	LTR/ERV1
chr4	167373318	167373597	AluJr4	SINE/Alu
chr4	3761046	3761156	MIR3	SINE/MIR
chr3	101420970	101421212	MER45C	DNA/hAT-Tip100
chr14	101396223	101396326	L1ME5	LINE/L1
chr13	20194451	20194716	L2	LINE/L2
chr20	32202210	32202640	L1MB3	LINE/L1
chr1	15440164	15440366	AluSx1	SINE/Alu
chr20	32204772	32205052	AluJr	SINE/Alu
chr1	149397994	149398183	MER20	DNA/hAT-Charlie
chr1	142633286	142636080	MER57-int MER52A MER52A MER57-int MER57A1	LTR/ERV1
chr5	116282617	116282759	L1MB5	LINE/L1
chr19	36744013	36744304	AluSc	SINE/Alu
chr3	32837219	32838362	HERVH-int HERVH-int LTR7	LTR/ERV1
chr19	12152323	12152633	AluY	SINE/Alu
chr19	38316454	38318636	Tigger1	DNA/TcMar-Tigger
chr1	52779403	52780071	L1ME1	LINE/L1
chr4	188922716	188922866	MER58B	DNA/hAT-Charlie
chr4	188921178	188921411	Tigger4a	DNA/TcMar-Tigger
chr1	15438393	15438518	MamTip2b	DNA/hAT-Tip100

chr13	20192557	20193156	L1M3c	LINE/L1
chr7	77147000	77147613	L2c	LINE/L2
chr8	121064638	121064948	AluSz	SINE/Alu
chr8	121065981	121066273	AluSx4	SINE/Alu
chr7	139152151	139153119	LTR5_Hs	LTR/ERVK
chr4	3950767	3950899	AluSg	SINE/Alu
chr1	244980605	244980906	AluSg	SINE/Alu
chr7	139165866	139166106	MLT1D	LTR/ERV1-MaLR
chr19	20127710	20128748	L1MA9	LINE/L1
chr19	19965986	19967242	LTR70	LTR/ERV1
chrX	71903006	71903272	AluJr	SINE/Alu
chr1	244979313	244979489	AluSx	SINE/Alu
chr1	45983854	45984171	AluSp	SINE/Alu
chr4	3950057	3950254	L1MD2	LINE/L1
chr8	9028129	9028547	LTR16	LTR/ERV1
chr1	45983172	45983476	AluY	SINE/Alu
chr19	20223988	20224299	AluSp	SINE/Alu
chr14	101363669	101364055	L1ME3G	LINE/L1
chr7	22841524	22843708	MER61B MER61-int	LTR/ERV1
chr4	3763562	3763717	L2c	LINE/L2
chr1	27388881	27389170	AluSq2	SINE/Alu
chr19	53154794	53154964	AluSp	SINE/Alu
chrX	71823533	71823770	L2d2	LINE/L2
chr13	20199542	20199822	AluJr	SINE/Alu
chr19	12152058	12152289	AluSg	SINE/Alu
chr2	230878129	230878432	AluSq2	SINE/Alu
chr4	251781	252199	L1MA8	LINE/L1
chr17	20306110	20306539	L1MC4	LINE/L1
chr1	228119073	228119214	L1MEd	LINE/L1
chr4	167374748	167377026	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr22	23852043	23852398	MLT1G	LTR/ERV1-MaLR
chr10	81807450	81807739	AluY	SINE/Alu
chr4	109329997	109331742	SVA_E	Retroposon/SVA
chr1	244983250	244985040	MER41-int MER41A	LTR/ERV1
chr19	55974300	55974540	L2a	LINE/L2
chr1	244979534	244979736	MER41-int	LTR/ERV1
chr4	261642	261933	AluSg	SINE/Alu
chr1	45982015	45982140	FLAM_A	SINE/Alu
chr13	20195331	20195543	L2	LINE/L2
chr16	58434989	58435605	LTR12_	LTR/ERV1
chr11	457540	457984	L1ME1	LINE/L1

chr7	48140508	48140801	AluSx1	SINE/Alu
chr10	70282754	70282831	L1ME1	LINE/L1
chr6	44276334	44276638	AluSz	SINE/Alu
chr19	23999440	23999775	THE1B	LTR/ERV1-MaLR
chr22	31422297	31424136	SVA_D	Retroposon/SVA
chr1	228122004	228122405	L1MEd	LINE/L1
chr6	42093811	42094114	AluSg	SINE/Alu
chr7	139150465	139152150	HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr10	70280287	70280596	AluSp	SINE/Alu
chr3	1282421	1286776	LTR7Y HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr2	233282529	233282645	MIRc	SINE/MIR
chr11	86589268	86591501	SVA_D	Retroposon/SVA
chr19	53155023	53155121	AluSz	SINE/Alu
chr10	122557456	122558843	SVA_B	Retroposon/SVA
chr1	27389306	27389357	MIR	SINE/MIR
chr4	65169	65438	L1MB1	LINE/L1
chr1	15438573	15438794	MIR	SINE/MIR
chr19	37807574	37807868	AluSx1	SINE/Alu
chr6	42093683	42093808	MamRep38	DNA/hAT
chrX	23471836	23475985	L1PA4	LINE/L1
chr8	9037823	9038017	MER91A	DNA/hAT-Tip100
chr1	27386621	27386762	AluY	SINE/Alu
chr19	37807262	37807571	AluSq2	SINE/Alu

Table 2: Retrotransposon signature specific to primed embryonic stem cell

Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chrX	16194447	16195172	L1ME3F	LINE/L1
chr10	6831435	6832025	L1MEg1	LINE/L1
chrX	16196297	16197284	L1MEi	LINE/L1
chrX	16191449	16191752	AluSz	SINE/Alu
chrX	16190084	16190490	MSTB	LTR/ERV1-MaLR
chrX	16191753	16193115	L1M4	LINE/L1
chr6	131652433	131653964	MER41-int MER41B	LTR/ERV1
chr13	54698674	54698799	MER94	DNA/hAT-Blackjack
chr13	56149763	56150041	L1MA8	LINE/L1
chrX	124520881	124521559	MER4D1	LTR/ERV1
chrX	16195278	16195517	Arthur1B	DNA/hAT-Tip100
chr14	48730987	48731598	L1MA4	LINE/L1

chr13	54698955	54700151	Tigger3b	DNA/TcMar-Tigger
chrX	16194317	16194446	MIRb	SINE/MIR
chr3	90132134	90135878	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	16180432	16181665	THE1C-int THE1C	LTR/ERV1-MaLR
chrX	16190491	16190575	L2b	LINE/L2
chr10	6832027	6832691	L1MEg1	LINE/L1
chrX	124521657	124522291	MER51C	LTR/ERV1
chrX	16195547	16195640	MIR3	SINE/MIR
chrX	16177769	16178096	L1ME4b	LINE/L1
chr8	72615582	72615985	L4_A_Mam	LINE/RTE-X
chr13	56148848	56149660	Charlie21a	DNA/hAT-Charlie
chr1	63218928	63228332	LTR12C HERV9NC-int HERV9NC-int LTR12C	LTR/ERV1
chr15	24930507	24936174	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	7262918	7263692	L1M4b	LINE/L1
chr1	114576653	114577219	MER41C	LTR/ERV1
chr10	6829730	6829902	MIRb	SINE/MIR
chr10	6833697	6833767	MLT1J	LTR/ERV1-MaLR
chr13	54695002	54695381	MSTA	LTR/ERV1-MaLR
chrX	121380847	121381707	MER4D	LTR/ERV1
chr8	72615343	72615465	MIRb	SINE/MIR
chrX	16186184	16186491	AluJo	SINE/Alu
chr16	9763424	9763698	MLT1K	LTR/ERV1-MaLR
chr9	14717824	14717975	MIR	SINE/MIR
chr10	6830265	6830393	L3b	LINE/CR1
chr2	8031403	8031734	L1M4	LINE/L1
chr10	6830007	6830161	MIR3	SINE/MIR
chr5	25413672	25413943	AluSx	SINE/Alu
chr13	56145304	56145583	MER67D	LTR/ERV1
chr13	56150062	56150145	Charlie21a	DNA/hAT-Charlie
chr13	56145584	56145920	THE1B	LTR/ERV1-MaLR
chrX	16193116	16193286	L1MB7	LINE/L1
chrX	16179665	16180431	LTR1A1	LTR/ERV1
chrX	16196175	16196300	L1MEi	LINE/L1
chr1	223192615	223193196	MER4B	LTR/ERV1
chrX	124520292	124520880	MER41C	LTR/ERV1
chr9	14717445	14717578	MIRb	SINE/MIR
chrX	16166970	16167281	ERV3-16A3_LTR	LTR/ERV1
chr2	67564736	67564857	AluJb	SINE/Alu
chr11	94380613	94381303	L2b	LINE/L2
chr11	27643290	27643643	L1ME4b	LINE/L1

chr2	8031727	8031823	L1M4	LINE/L1
chr1	223197433	223197736	MER4A1	LTR/ERV1
chr8	72614867	72615159	AluSx1	SINE/Alu
chr11	27644708	27644915	MIR	SINE/MIR
chr20	12740289	12740631	THE1A	LTR/ERV1-MaLR
chr20	12742342	12742534	MIRb	SINE/MIR
chr4	87395924	87401673	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	33487954	33496479	LTR12C HERV9NC-int LTR12C	LTR/ERV1
chr13	54700534	54700879	L2	LINE/L2
chr2	67566400	67566633	MIR	SINE/MIR
chr1	223227106	223228589	L2	LINE/L2
chr1	223195228	223195599	MLT1O	LTR/ERV1-MaLR
chr13	56145921	56146174	MER67D	LTR/ERV1
chr20	12744705	12745587	L2a	LINE/L2
chrX	16168205	16168375	MER96	DNA/hAT-Tip100
chr14	48723170	48724391	L1MC1	LINE/L1
chr13	54692781	54693238	LTR40b	LTR/ERV1
chr5	135066688	135070234	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr9	14718014	14718075	MADE2	DNA/TcMar-Mariner
chr1	223186587	223187134	L1ME3G	LINE/L1
chr20	44394328	44394540	MER20	DNA/hAT-Charlie
chr13	54689371	54689663	L2	LINE/L2
chr8	72614486	72614866	L1ME3A	LINE/L1
chrX	124518779	124519166	MER57B2	LTR/ERV1
chr1	114572294	114575106	HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	27644198	27644549	LTR16C	LTR/ERV1
chr10	6828834	6829281	L1ME2	LINE/L1
chr8	72615160	72615297	L1ME3A	LINE/L1
chr2	8032165	8032852	L1ME3G	LINE/L1
chrX	124522394	124522684	LTR29	LTR/ERV1
chr6	131658923	131659539	MLT1G	LTR/ERV1-MaLR
chrX	16169254	16169391	MIRb	SINE/MIR
chr5	7262450	7262855	LTR7	LTR/ERV1
chrX	16166490	16166655	LTR79	LTR/ERV1
chr20	12742571	12742717	Charlie15a	DNA/hAT-Charlie
chrX	16179256	16179664	THE1C-int	LTR/ERV1-MaLR
chr1	223187987	223188163	MLT1N2	LTR/ERV1-MaLR
chr20	44395440	44395655	AluJb	SINE/Alu
chr2	67565107	67565567	MLT1D	LTR/ERV1-MaLR
chr6	131654397	131654707	MER2	DNA/TcMar-Tigger

chr1	223187464	223187652	MIRb	SINE/MIR
chr1	223190961	223191308	THE1A	LTR/ERV1-MaLR
chr12	97958192	97958443	MIRb	SINE/MIR
chr8	72613177	72613841	Charlie29a	DNA/hAT-Charlie
chrX	16166791	16166920	L2c	LINE/L2
chr8	7759377	7760938	MSTB MSTB-int	LTR/ERV1-MaLR
chr8	72601110	72602518	L1MC5a	LINE/L1
chr8	72610844	72611256	L1ME3A	LINE/L1
chrX	16172450	16172563	MIR3	SINE/MIR
chrX	121374005	121374740	L1PA16	LINE/L1
chrX	121373632	121373935	AluSz	SINE/Alu
chr10	91044477	91050644	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	72603054	72603551	MLT1D	LTR/ERV1-MaLR
chr12	59715844	59716239	LTR88c	LTR/Gypsy?
chr5	25431898	25432192	AluSx1	SINE/Alu
chr1	223188556	223188734	LTR67B	LTR/ERV1
chrX	121379209	121379930	LTR8	LTR/ERV1
chrX	16165285	16165777	L1MC5a	LINE/L1
chr1	223193197	223193501	Tigger3a	DNA/TcMar-Tigger
chr6	131616299	131616496	MER61A	LTR/ERV1
chr14	48702982	48703438	L1MB1	LINE/L1
chr11	27644927	27645136	L2b	LINE/L2
chrX	16166249	16166414	LTR79	LTR/ERV1
chrX	16178437	16178694	L1ME4b	LINE/L1
chr16	9763305	9763398	MLT1K	LTR/ERV1-MaLR
chr2	8023336	8023766	MLT1B	LTR/ERV1-MaLR
chr11	27635870	27636504	L1MC5a	LINE/L1
chr14	48730211	48730976	L1MC1	LINE/L1
chr1	232259844	232262247	L1MB5	LINE/L1
chr11	81736450	81742056	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	223194914	223195206	AluSx	SINE/Alu
chr9	14717118	14717425	L1ME3Cz	LINE/L1
chr5	25434742	25436929	L1MC1	LINE/L1
chr10	6838005	6838530	MER74A	LTR/ERV1
chr2	67565757	67566187	MSTB1	LTR/ERV1-MaLR
chr11	27636985	27637128	MIRb	SINE/MIR
chrX	16167901	16168128	L1MA8	LINE/L1
chr13	56144658	56144818	MER5A	DNA/hAT-Charlie
chr1	232262718	232264966	L1MB5	LINE/L1
chrX	16167393	16167531	ERV3-16A3_LTR	LTR/ERV1

chr16	9764166	9764384	MIR	SINE/MIR
chr6	131656386	131656618	MIRb	SINE/MIR
chr6	131655256	131655528	AluJr	SINE/Alu
chrX	16178097	16178436	MER44A	DNA/TcMar-Tigger
chr5	123639451	123645169	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	16167282	16167392	MER81	DNA/hAT-Blackjack
chr8	7265699	7267260	MSTB-int MSTB	LTR/ERV1-MaLR
chr16	9761841	9761958	FLAM_A	SINE/Alu
chr11	27641002	27641308	MLT2C2	LTR/ERV1
chr1	223189501	223189661	MLT10	LTR/ERV1-MaLR
chr1	223188736	223188881	LTR90B	LTR
chr8	72612413	72612682	AluJr	SINE/Alu
chrX	121361641	121365128	MER41-int	LTR/ERV1
chrX	121371956	121372684	MER41-int MER41-int	LTR/ERV1
chrX	124520093	124520291	MER4D1	LTR/ERV1
chr14	48721978	48722525	THE1C-int THE1C	LTR/ERV1-MaLR
chr1	223191490	223191632	MIRb	SINE/MIR
chr6	131667077	131667599	MER34A1	LTR/ERV1
chr8	72607355	72607571	L2c	LINE/L2
chr7	145912984	145913401	LTR16C	LTR/ERV1
chr2	67564927	67565075	L1ME1	LINE/L1
chr11	27643910	27644027	MIR3	SINE/MIR
chr4	171049309	171055034	HERVK14C-int LTR14C	LTR/ERV1
chr11	87776578	87782950	LTR7B LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7 HERVH-int LTR7B	LTR/ERV1
chr16	9762425	9762679	AluSx1	SINE/Alu
chr3	189883315	189884326	L1M3	LINE/L1
chrX	121378960	121379208	LTR16A	LTR/ERV1
chr11	27643036	27643288	MamGypLTR1a	LTR/Gypsy
chr11	27642612	27642980	MamGypLTR1a	LTR/Gypsy
chr5	147041248	147041405	MER5A1	DNA/hAT-Charlie
chr2	67558649	67564733	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	56146348	56146489	MIR3	SINE/MIR
chr1	232267840	232268634	MER21B	LTR/ERV1
chrX	16182655	16182878	MER58A	DNA/hAT-Charlie
chr16	9761376	9761601	MIR	SINE/MIR
chr21	38961987	38964810	HERVH-int LTR7	LTR/ERV1
chr8	72607028	72607329	Kanga1c	DNA/TcMar-Tc2
chr5	25426847	25427019	AluSp	SINE/Alu
chr8	72608826	72609899	MER11C	LTR/ERV1
chr5	25432674	25432893	L1MEd	LINE/L1

chr11	27642155	27642461	AluJb	SINE/Alu
chrX	121375429	121375676	MIR	SINE/MIR
chr13	54676148	54678061	Tigger1	DNA/TcMar-Tigger
chr5	25422585	25422949	L1PA8	LINE/L1
chr15	89081365	89083782	LTR6B HERVS71-int	LTR/ERV1
chrX	121367882	121371953	L1PB1	LINE/L1
chr20	44394861	44395002	MamTip1b	DNA/hAT-Tip100
chr13	54692316	54692564	MamTip1	DNA/hAT-Tip100
chr1	232270118	232270547	MER51B	LTR/ERV1
chr6	160655992	160659250	MER41-int MER41-int MER41-int MER41A	LTR/ERV1
chr3	176009016	176009880	L1ME3A	LINE/L1
chr10	6832800	6832877	L2a	LINE/L2
chr14	48721446	48721878	MER110A	LTR/ERV1
chr1	223230226	223232833	MER57A1 MER57-int	LTR/ERV1
chr5	166721061	166721484	L2c	LINE/L2
chr1	232274993	232275603	LTR9B	LTR/ERV1
chr7	20006227	20008019	L2a	LINE/L2
chr20	12744123	12744315	MIRc	SINE/MIR
chr11	27636813	27636946	L1MC5a	LINE/L1
chr13	54689795	54689908	MIRb	SINE/MIR
chr11	94380478	94380616	MIRc	SINE/MIR
chr8	72603874	72604365	L1MC5a	LINE/L1
chr8	39762016	39763369	LTR49-int	LTR/ERV1
chr11	27636505	27636812	AluSz	SINE/Alu
chr7	125568841	125569165	L1PA7	LINE/L1
chr11	27638176	27638592	MSTB	LTR/ERV1-MaLR
chrX	16173197	16173500	AluSp	SINE/Alu
chr6	131666035	131666643	MER39	LTR/ERV1
chr3	97909932	97915635	LTR7 HERVH-int HERVH-int LTR7	LTR/ERV1
chr7	75409321	75412836	HERVH-int LTR7 HERVH-int HERVH-int	LTR/ERV1
chrX	121365572	121367558	L1PB1	LINE/L1
chr12	59714173	59714462	X26_DNA	DNA/TcMar-Tigger
chr1	223226516	223226895	THE1D	LTR/ERV1-MaLR
chr11	27639204	27639315	MamTip2	DNA/hAT-Tip100
chr8	72610643	72610819	ERV3-16A3_I-int	LTR/ERV1
chr5	25425709	25425881	MER58A	DNA/hAT-Charlie
chr6	131615825	131616049	LTR78	LTR/ERV1
chr5	25431402	25431756	MER2	DNA/TcMar-Tigger
chrX	16175379	16175453	MADE2	DNA/TcMar-Mariner
chr1	232266639	232267091	MER61D	LTR/ERV1
chr7	145932476	145932881	LTR16C	LTR/ERV1

chr6	131650283	131650505	L1ME4b	LINE/L1
chr13	56123941	56126285	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr8	72603674	72603872	MER107	DNA/hAT-Charlie
chr3	63110406	63110781	LTR16A	LTR/ERV1
chr11	27637538	27637606	L2b	LINE/L2
chr11	27638804	27638952	L2b	LINE/L2
chr5	135070535	135073175	HERVH-int LTR7	LTR/ERV1
chrX	121377888	121378113	MER20	DNA/hAT-Charlie
chr16	9902016	9902214	MIR	SINE/MIR
chr11	131137680	131143370	L1PA7	LINE/L1
chr2	8019166	8019587	LTR16	LTR/ERV1
chr15	89084751	89089461	HERVS71-int HERVS71-int HERVS71-int LTR6B	LTR/ERV1
chrX	16197325	16202557	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr16	9902368	9902579	MIRb	SINE/MIR
chr16	9761969	9762238	AluSc	SINE/Alu
chr1	223228592	223228823	L1ME3	LINE/L1
chr1	223192263	223192359	MER5A1	DNA/hAT-Charlie
chr6	167647449	167647881	LTR37A LTR37A	LTR/ERV1
chr6	167648666	167648784	MIRc	SINE/MIR
chrX	121378516	121378761	L2d	LINE/L2
chr1	232325380	232326189	LTR39	LTR/ERV1
chr5	25433912	25434220	AluY	SINE/Alu
chrX	121376652	121376894	MIRc	SINE/MIR
chr5	146939463	146939616	MER5A1	DNA/hAT-Charlie
chr4	126476578	126477913	MSTD MSTD-int	LTR/ERV1-MaLR
chr11	83053028	83056621	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	35238972	35241209	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr3	96991307	96996394	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	223192118	223192253	MER3	DNA/hAT-Charlie
chr11	27637157	27637228	MIRb	SINE/MIR
chrX	16172913	16173092	CR1_Mam	LINE/CR1
chr10	6834432	6834597	MamGypLTR2b	LTR/Gypsy
chr14	87701035	87707135	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr16	9899833	9900376	Eutr11	DNA
chr1	223193628	223193728	MIRb	SINE/MIR
chr3	163791286	163793148	MER57-int MER57-int	LTR/ERV1
chrX	121367559	121367840	AluY	SINE/Alu
chr16	9901613	9901815	MIRc	SINE/MIR
chrX	16378200	16384341	L1PA3	LINE/L1

chrX	121365152	121365500	L1PB1	LINE/L1
chr20	37253132	37253621	L2a	LINE/L2
chr11	131170588	131170778	L2a	LINE/L2
chr1	114561713	114563990	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr7	125719135	125719530	LTR52	LTR/ERV1
chrX	121372685	121373151	MER61D	LTR/ERV1
chr1	223197214	223197373	MER5A1	DNA/hAT-Charlie
chr6	167641163	167645287	HUERS-P1-int	LTR/ERV1
chr5	7272501	7272890	MLT1C2	LTR/ERV1-MaLR
chr5	166719675	166720034	L2b	LINE/L2
chr5	7273213	7273650	MLT1J1	LTR/ERV1-MaLR
chr6	98222474	98224265	L1PA10	LINE/L1
chr11	27637914	27638171	L2d	LINE/L2
chr16	9902639	9902994	L1ME3G	LINE/L1
chrX	16175225	16175286	MIRc	SINE/MIR
chr5	25426202	25426350	MER5B	DNA/hAT-Charlie
chr7	145930557	145931825	L1PA3	LINE/L1
chr4	187163110	187168738	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	54694375	54694685	AluSq2	SINE/Alu
chr12	59714487	59714786	AluY	SINE/Alu
chr9	14716822	14717110	L2a	LINE/L2
chr7	75413130	75416681	HERVH-int	LTR/ERV1
chr5	147032265	147036560	L1PA8	LINE/L1
chr3	189893959	189895402	LTR12C	LTR/ERV1
chr8	72593174	72593523	MER1B	DNA/hAT-Charlie
chr13	54691260	54691435	AluJb	SINE/Alu
chr9	102902464	102908804	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	8028829	8029120	MLT1J2	LTR/ERV1-MaLR
chr6	63605060	63606734	L1ME3Cz	LINE/L1
chr3	63108880	63109138	L3	LINE/CR1
chr1	223188187	223188488	AluSc	SINE/Alu
chr5	95501187	95502134	MER63C	DNA/hAT-Blackjack
chr20	37256516	37256915	MER66A	LTR/ERV1
chr20	44393915	44394027	MER5A1	DNA/hAT-Charlie
chr6	167645603	167647400	HUERS-P1-int LTR8	LTR/ERV1
chr5	138882528	138890961	LTR12 HERV9-int HERV9-int LTR12	LTR/ERV1
chr12	30954518	30954903	MLT1H2	LTR/ERV1-MaLR
chr12	59713999	59714152	MIR3	SINE/MIR
chr1	223192547	223192614	Tigger3a	DNA/TcMar-Tigger
chr1	232272062	232272502	MER74A	LTR/ERV1
chr4	17005697	17006230	MER34B	LTR/ERV1

chr13	54700308	54700528	MER3	DNA/hAT-Charlie
chr7	145937897	145938312	MSTA	LTR/ERV1-MaLR
chr12	75761350	75761879	L1M5	LINE/L1
chr4	62620337	62626523	L1PA4	LINE/L1
chr3	176009873	176010520	L1MC	LINE/L1
chrX	121381708	121381835	MIR	SINE/MIR
chr1	209627779	209628167	Tigger3a	DNA/TcMar-Tigger
chr8	72611251	72611463	L1ME3E	LINE/L1
chr3	189867994	189868827	LTR78	LTR/ERV1
chr4	171135075	171137514	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr5	25427214	25427352	MER104	DNA/TcMar-Tc2
chr12	59713666	59713790	MIRb	SINE/MIR
chr5	25438396	25438718	AluSp	SINE/Alu
chr5	25434221	25434476	L1MEd	LINE/L1
chr8	72613034	72613133	MIRb	SINE/MIR
chr5	166725633	166730683	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	232279095	232279585	MER67A	LTR/ERV1
chr6	167650263	167651024	MER4D1	LTR/ERV1
chr8	72602774	72603053	L1MC5a	LINE/L1
chr5	118285936	118288341	HERVH-int LTR7	LTR/ERV1
chrX	121377401	121377724	MER33	DNA/hAT-Charlie
chr3	189882410	189883205	L1M1	LINE/L1
chr6	132237379	132237738	THE1B	LTR/ERV1-MaLR
chr6	167664840	167665142	MLT1F1	LTR/ERV1-MaLR
chr6	131615421	131615659	MER4C	LTR/ERV1
chr8	72603552	72603665	L1MC5a	LINE/L1
chr16	9903643	9903935	AluSx	SINE/Alu
chr8	72593598	72594190	L1ME3Cz	LINE/L1
chr1	223189179	223189479	AluSz	SINE/Alu
chr11	67386324	67394513	LTR12C HERV9NC-int HERV9NC-int LTR12C LTR12C	LTR/ERV1
chr16	9902995	9903299	AluSz	SINE/Alu
chr14	21290876	21297018	LTR10F HERVIP10FH-int LTR10F	LTR/ERV1
chr14	24053109	24054656	LTR12C	LTR/ERV1
chrX	121375757	121376133	MER61D	LTR/ERV1
chr6	131665773	131666034	L1ME3G	LINE/L1
chr2	188519338	188524240	MER61A MER61-int MER61-int MER61A	LTR/ERV1
chr6	167660278	167660499	MLT1H	LTR/ERV1-MaLR
chrX	16593395	16594839	LTR12C	LTR/ERV1
chr1	209629834	209630119	L2d2	LINE/L2
chr6	167658459	167659140	MER4D	LTR/ERV1

chr6	167659495	167659785	AluSq2	SINE/Alu
chr8	72596961	72597307	L1ME2z	LINE/L1
chr6	167660659	167660739	MLT1H	LTR/ERV1-MaLR
chrX	121376134	121376212	LTR27	LTR/ERV1
chr3	189879358	189880425	MER11C	LTR/ERV1
chr10	26020741	26022028	L1MB4	LINE/L1
chr11	27637607	27637913	AluSq2	SINE/Alu
chr5	25433834	25433911	L1MEd	LINE/L1
chr2	67565578	67565654	L1ME3D	LINE/L1
chr10	6835214	6835350	Charlie4a	DNA/hAT-Charlie
chr3	176010890	176011324	MSTB1	LTR/ERV1-MaLR
chr9	76706568	76707015	MER4D	LTR/ERV1
chr2	8024898	8025140	L1MC4	LINE/L1
chr1	232265623	232265845	MIRc	SINE/MIR
chr13	56111186	56112397	L1M4b	LINE/L1
chr6	160649683	160655354	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	121380746	121380846	MIR	SINE/MIR
chr10	6884489	6884905	LTR19A	LTR/ERV1
chr5	166167063	166171655	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	35014886	35021123	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr16	9900688	9901045	THE1B	LTR/ERV1-MaLR
chr3	62935909	62938204	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr2	210188321	210188794	MER51E	LTR/ERV1
chr5	166720535	166720981	LTR86A2	LTR/ERV1
chr4	126479008	126479652	MSTD-int MSTD	LTR/ERV1-MaLR
chrX	121378174	121378270	MamRTE1	LINE/RTE-BovB
chr8	72602546	72602758	MER30	DNA/hAT-Charlie
chr13	54684125	54684263	L2c	LINE/L2
chrX	93948066	93950107	L1P4a	LINE/L1
chr1	95032034	95036345	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr2	8026012	8026202	MIR	SINE/MIR
chr5	25444290	25444904	L1MEf	LINE/L1
chr10	6881457	6881648	L1M5	LINE/L1
chr17	42638099	42638381	AluSx4	SINE/Alu
chr6	77271171	77271373	LTR40A1	LTR/ERV1
chrX	16183849	16184146	AluSx1	SINE/Alu
chr12	75762291	75762667	L1M5	LINE/L1
chrX	130823747	130824551	MER4D1	LTR/ERV1
chr8	72596420	72596692	L2b	LINE/L2

chr1	232262248	232262717	MER4A1	LTR/ERV1
chr1	114671177	114672133	L2a	LINE/L2
chrX	16182048	16182333	AluJb	SINE/Alu
chr8	39767815	39768198	MER34-int LTR48B	LTR/ERV1
chr10	6835736	6835980	L1ME4a	LINE/L1
chr5	25443891	25444256	L1MEf	LINE/L1
chr8	72604691	72604834	MIR	SINE/MIR
chrX	121379931	121380065	LTR16A	LTR/ERV1
chr6	167645288	167645602	AluSx	SINE/Alu
chr10	6883475	6883646	Tigger19a	DNA/TcMar-Tigger
chr1	232322981	232323217	MIR	SINE/MIR
chr7	75431673	75432137	MER41B	LTR/ERV1
chr6	167648790	167649453	MER52C	LTR/ERV1
chrX	121381832	121381930	MIRb	SINE/MIR
chr3	189882037	189882409	MLT2A1	LTR/ERV1
chr5	146985070	146991203	L1PA7	LINE/L1
chr16	9904255	9904660	MLT1C2	LTR/ERV1-MaLR
chr6	131666773	131667057	AluSz	SINE/Alu
chr20	37257348	37257522	MIRb	SINE/MIR
chr16	9761299	9761382	L2c	LINE/L2
chrX	65477887	65478614	L2d	LINE/L2
chr13	56109186	56109611	LTR80B	LTR/ERV1
chr5	123649551	123650074	MER44B	DNA/TcMar-Tigger
chr6	132235312	132235641	MSTD	LTR/ERV1-MaLR
chr5	25411665	25411790	L2c	LINE/L2
chr5	146998018	146998334	AluSq2	SINE/Alu
chr7	75416993	75417880	HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	131644436	131650277	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	8022541	8022674	L2b	LINE/L2
chr1	223186433	223186568	L2c	LINE/L2
chr4	171128259	171134414	L1PA5	LINE/L1
chr2	188526357	188527439	L1PA12	LINE/L1
chr8	72594822	72595072	L1MEi	LINE/L1
chr15	89446704	89447020	AluSx1	SINE/Alu
chr9	14709127	14710907	L1MA8	LINE/L1
chr15	89445649	89445716	L2c	LINE/L2
chr20	44395999	44396200	L1PA15	LINE/L1
chr9	118285277	118285991	MamGypLTR3	LTR/Gypsy
chr20	37277940	37278361	LTR16A1	LTR/ERV1
chr1	232269680	232269885	L1ME3G	LINE/L1
chr4	62609440	62615587	L1PA3	LINE/L1

chr7	19988344	19994458	L1PA6	LINE/L1
chrX	124519302	124519424	MIRc	SINE/MIR
chr7	120416677	120422939	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	176006636	176006906	L1ME3Cz	LINE/L1
chr1	64612496	64612721	MIRb	SINE/MIR
chr16	9903451	9903642	MIR	SINE/MIR
chrX	16181984	16182047	MER5B	DNA/hAT-Charlie
chr7	125565201	125565436	L2c	LINE/L2
chrX	107916381	107916608	MIRc	SINE/MIR
chr1	223197374	223197432	LTR8A	LTR/ERV1
chr4	134178387	134181851	MER4A1 MER4-int	LTR/ERV1
chrX	124517027	124517530	L1MA6	LINE/L1
chr10	6883229	6883321	MIR3	SINE/MIR
chr7	20085128	20085461	ERV3-16A3_I-int	LTR/ERV1
chr6	126011038	126015491	L1PB2	LINE/L1
chr5	25441981	25442264	MLT1A	LTR/ERV1-MaLR
chr6	167664435	167664649	LTR90B	LTR
chr12	30955238	30955536	AluSx1	SINE/Alu
chr1	232322232	232322534	AluJb	SINE/Alu
chr7	19953825	19955115	Tigger1	DNA/TcMar-Tigger
chr8	72596700	72596959	L1P4	LINE/L1
chr15	89445248	89445362	L2d	LINE/L2
chr10	6881661	6881874	L2a	LINE/L2
chr5	147016992	147017269	AluSx1	SINE/Alu
chr9	76707311	76707741	MER4D	LTR/ERV1
chr3	189878038	189878550	L2	LINE/L2
chr1	209627349	209627529	L1MA4A	LINE/L1
chr1	28283132	28284237	L2a	LINE/L2
chr3	176038199	176039188	L1PA16	LINE/L1
chr3	3893019	3893236	MIRb	SINE/MIR
chr5	147022296	147022738	MLT2A2	LTR/ERV1
chrX	107854747	107856413	L1ME1	LINE/L1
chr20	37254968	37255120	MER5A	DNA/hAT-Charlie
chrX	121380580	121380669	MIRb	SINE/MIR
chr1	232266480	232266607	FLAM_A	SINE/Alu
chrX	71367649	71367827	MamTip2	DNA/hAT-Tip100
chr5	146974786	146975181	MLT1A1	LTR/ERV1-MaLR
chr7	100519902	100525640	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	72606904	72607029	Kanga1d	DNA/TcMar-Tc2
chr1	232327236	232328011	LTR1	LTR/ERV1
chr7	145935753	145936124	THE1D	LTR/ERV1-MaLR

chr12	59716819	59716925	X26_DNA	DNA/TcMar-Tigger
chr1	232271742	232271884	MLT1J-int	LTR/ERV1-MaLR
chr8	7758091	7758597	MLT1D	LTR/ERV1-MaLR
chr16	77916364	77916567	MIR	SINE/MIR
chr7	121666928	121667490	L2a	LINE/L2
chr8	8029783	8038106	HERVE-int LTR2C	LTR/ERV1
chr6	132237739	132237871	MSTA	LTR/ERV1-MaLR
chr7	131194523	131194754	MIRb	SINE/MIR
chr3	154965196	154966960	Tigger2	DNA/TcMar-Tigger
chr7	142654046	142654673	L2c	LINE/L2
chr3	176010579	176010854	L1MEg2	LINE/L1
chr2	8023950	8024299	THE1B	LTR/ERV1-MaLR
chr10	6836893	6837100	L1PA14	LINE/L1
chr20	37252626	37253113	MLT1G3	LTR/ERV1-MaLR
chr8	132320886	132321077	L1MCa	LINE/L1
chr19	43867036	43867373	Tigger3a	DNA/TcMar-Tigger
chrX	2852073	2852398	AluSz	SINE/Alu
chr4	176379617	176379931	MER2	DNA/TcMar-Tigger
chr4	171057613	171058888	HERVL32-int LTR32	LTR/ERV1
chr7	43899298	43904584	MER9a3 HERVK9-int HERVK9-int HERVK9-int MER9a3	LTR/ERV1
chrX	15856669	15856749	MER112	DNA/hAT-Charlie
chr2	210189210	210189504	L1PA13	LINE/L1
chr5	7270252	7270582	L1M4b	LINE/L1
chr2	8029813	8030037	LTR90B	LTR
chrX	102683983	102690366	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	188532605	188534309	Tigger1	DNA/TcMar-Tigger
chr1	223210645	223211386	LTR1B1	LTR/ERV1
chr11	94381923	94382144	MIRb	SINE/MIR
chrX	107843819	107844388	MLT2B3 MLT2B3	LTR/ERV1
chrX	71370025	71370247	X6b_DNA	DNA/TcMar-Tigger
chr8	23046249	23046670	MSTA	LTR/ERV1-MaLR
chr21	37480225	37481546	HERVIP10F-int	LTR/ERV1
chr14	95230453	95230758	AluSz6	SINE/Alu
chr1	114701023	114701261	MIRb	SINE/MIR
chr1	232279612	232280000	Charlie7	DNA/hAT-Charlie
chr7	125719019	125719112	MER2B	DNA/TcMar-Tigger
chr4	186564169	186564779	L2b	LINE/L2
chrX	107914744	107915160	MER31B	LTR/ERV1
chr4	6101870	6103331	L1MB7	LINE/L1
chr3	33496539	33496802	MER57A-int	LTR/ERV1
chr3	63104538	63104676	MER5B	DNA/hAT-Charlie

chr6	167656024	167656583	HERVL-int HERVL-int	LTR/ERV1
chr5	141695160	141695358	MIR	SINE/MIR
chr20	44395840	44395960	L1ME4a	LINE/L1
chr1	232325133	232325379	L1MC1	LINE/L1
chr7	125680244	125681964	MER52A	LTR/ERV1
chrX	15853804	15853908	L3	LINE/CR1
chrX	16182334	16182454	MER5B	DNA/hAT-Charlie
chr7	75430259	75430554	AluSx1	SINE/Alu
chr4	171043312	171043942	LTR8	LTR/ERV1
chr6	167651550	167652103	LTR1C3	LTR/ERV1
chr4	126477914	126478289	THE1C	LTR/ERV1-MaLR
chrX	16314834	16317043	Tigger1	DNA/TcMar-Tigger
chr14	87696026	87697440	THE1C THE1C-int	LTR/ERV1-MaLR
chr15	89446622	89446703	MER5A1	DNA/hAT-Charlie
chr9	76707016	76707310	AluSg4	SINE/Alu
chr6	167665743	167666006	AluJr	SINE/Alu
chr18	32819233	32819617	MLT1H	LTR/ERV1-MaLR
chr5	141697768	141698088	AluSx1	SINE/Alu
chrX	121382338	121382459	L2d	LINE/L2
chr2	8025173	8025305	MER58A	DNA/hAT-Charlie
chr13	56246123	56246763	MER50	LTR/ERV1
chr4	171055657	171057280	L1PBa	LINE/L1
chr8	42231066	42231348	AluSx3	SINE/Alu
chr6	167660174	167660274	MIRc	SINE/MIR
chr15	89443874	89443959	MIR3	SINE/MIR
chr7	125573791	125574320	MLT1H1	LTR/ERV1-MaLR
chrX	93944336	93946477	THE1B THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr6	167660777	167660831	MIRc	SINE/MIR
chr1	232265281	232265408	MIR3	SINE/MIR
chrX	15856867	15857170	AluSz6	SINE/Alu
chr2	188501015	188502931	SVA_A	Retroposon/SVA
chr6	132234433	132234540	AluJb	SINE/Alu
chr6	132238237	132238458	L2a	LINE/L2
chr3	106554530	106557172	LOR1-int LOR1-int LOR1-int LOR1a	LTR/ERV1
chr6	94525121	94525790	L1ME1	LINE/L1
chr7	75431180	75431369	MER41B	LTR/ERV1
chr8	72599651	72599756	MER5A1	DNA/hAT-Charlie
chr13	56113272	56114528	L1M4b	LINE/L1
chr6	132237142	132237378	MSTA	LTR/ERV1-MaLR
chr2	8030553	8030743	L1ME3G	LINE/L1
chr1	232259694	232259843	AluJb	SINE/Alu

chr6	143657591	143658573	MLT1B MLT1B-int	LTR/ERV1-MaLR
chrX	132433444	132433673	L1ME4b	LINE/L1
chr1	232269907	232270043	L1ME3G	LINE/L1
chr20	37256953	37257245	AluYk3	SINE/Alu
chrX	124516270	124516511	LTR16A	LTR/ERV1
chr9	85357774	85358267	MLT2B2	LTR/ERV1
chr5	142091000	142091713	LTR66	LTR/ERV1
chr5	18593283	18595882	MSTA MSTA-int MSTA MSTA	LTR/ERV1-MaLR
chr4	62603656	62604249	L1PB1	LINE/L1
chr2	8019795	8019940	L2a	LINE/L2
chr6	132238076	132238192	L2c	LINE/L2
chr5	25442306	25442597	L1M4c	LINE/L1
chr8	72599145	72599450	AluSz	SINE/Alu
chr7	31069697	31070217	L2a	LINE/L2
chrX	122552142	122552976	L1MB7	LINE/L1
chr5	25439225	25439408	MER20	DNA/hAT-Charlie
chr11	58898342	58899976	THE1D-int	LTR/ERV1-MaLR
chr8	138412266	138417578	L1PA13	LINE/L1
chr6	77273170	77274527	L1PB4	LINE/L1
chr6	132230215	132230514	AluSp	SINE/Alu
chr9	76716866	76720438	L1PA11	LINE/L1
chr3	189896235	189896961	Arthur1	DNA/hAT-Tip100
chrX	107851614	107853248	L1ME2z	LINE/L1
chr1	232313666	232314420	LTR8B	LTR/ERV1
chrX	107856611	107857645	L1ME1	LINE/L1
chrX	107923155	107923639	MER101B	LTR/ERV1
chr3	176036237	176036525	MLT1B	LTR/ERV1-MaLR
chr1	114557525	114557718	MIRc	SINE/MIR
chr7	89843788	89844514	L2d	LINE/L2
chrX	107967618	107967896	Tigger19a	DNA/TcMar-Tigger
chr3	146122793	146129944	LTR6B HERVS71-int HERVS71-int HERVS71-int LTR6B	LTR/ERV1
chr20	37254048	37254361	AluSx	SINE/Alu
chr3	189887751	189887934	L1M3	LINE/L1
chr1	223205929	223206476	MER41A	LTR/ERV1
chr4	93182095	93182228	L2a	LINE/L2
chr7	75430556	75430666	LTR16C	LTR/ERV1
chr2	8030884	8031093	L1ME3G	LINE/L1
chr1	223206946	223207645	LTR8A	LTR/ERV1
chr3	189878859	189879227	L2	LINE/L2
chr4	62615936	62616142	MIRb	SINE/MIR

chrX	71370732	71370876	MER58C	DNA/hAT-Charlie
chr2	188524422	188525689	L1PA3	LINE/L1
chr15	89446546	89446601	MIR3	SINE/MIR
chr3	176012009	176012459	L2c	LINE/L2
chr4	41267314	41267613	AluSz	SINE/Alu
chr3	63108653	63108896	L2b	LINE/L2
chr6	77271308	77271424	LTR68	LTR/ERV1
chr6	77272017	77272409	LTR7	LTR/ERV1
chr5	141701762	141702049	AluSg	SINE/Alu
chrX	71370877	71371173	AluSc	SINE/Alu
chr18	33477444	33483600	L1PA4	LINE/L1
chrX	132433102	132433405	AluSz	SINE/Alu
chrX	51200838	51203688	HUERS-P3-int HUERS-P3-int HUERS-P3-int HUERS-P3-int HUERS-P3-int	LTR/ERV1
chrX	16594840	16597709	MER4A1 MER4-int MER4-int MER4-int MER4-int MER4-int MER4-int	LTR/ERV1
chr7	121696679	121698254	L1ME3F	LINE/L1
chr2	8020721	8020807	MER5A	DNA/hAT-Charlie
chr9	102901473	102901857	L2a	LINE/L2
chr17	72635495	72635859	MLT1A0	LTR/ERV1-MaLR
chr20	37276336	37276672	L2b	LINE/L2
chr1	223236688	223237074	L2a	LINE/L2
chr3	189881165	189881657	L1M1	LINE/L1
chr8	39764617	39765330	LTR49-int	LTR/ERV1
chr9	101082168	101083277	L1PA3	LINE/L1
chr6	63604052	63604523	MER66C	LTR/ERV1
chr20	38412763	38413231	MLT1D	LTR/ERV1-MaLR
chr5	123840499	123840828	LTR81B	LTR/Gypsy
chr4	93179909	93180216	L1ME3A	LINE/L1
chr13	78489581	78489804	MIRb	SINE/MIR
chr4	101872723	101872940	AluY	SINE/Alu
chr11	92676735	92683297	MER11D HERVK11D-int HERVK11D-int HERVK11D-int HERVK11D-int MER11D	LTR/ERV1
chr12	75761944	75762086	L1M5	LINE/L1
chr4	101866346	101866936	L1ME3	LINE/L1
chr9	38622683	38623064	L1MC	LINE/L1
chr2	26520789	26529263	LTR15 HERV15-int HERV15-int HERV15-int HERV15-int LTR15	LTR/ERV1
chr2	8030297	8030420	MER94	DNA/hAT-Blackjack
chr1	64610201	64610441	MIR	SINE/MIR
chr3	189872500	189872945	MER110 MER110	LTR/ERV1
chr8	133085914	133086368	L2	LINE/L2
chr4	171199459	171200179	L2	LINE/L2

chr1	216185314	216185479	AluYb9	SINE/Alu
chr1	223226252	223226337	MIR3	SINE/MIR
chr13	56112556	56113242	L1M4b	LINE/L1
chr8	72594631	72594767	L1MEi	LINE/L1
chr1	232271681	232271736	MER74A	LTR/ERV1
chr12	93399952	93400009	L2b	LINE/L2
chr10	6779260	6779650	MLT1H	LTR/ERV1-MaLR
chr2	8022387	8022477	L2d2	LINE/L2
chr14	101760957	101763231	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr11	94374767	94380477	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr10	26005350	26011855	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	64613507	64613721	MER20	DNA/hAT-Charlie
chr12	30956284	30958504	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr1	114579270	114579696	MER50	LTR/ERV1
chr6	167666287	167666690	MSTA	LTR/ERV1-MaLR
chr6	132230574	132231016	L1MB2	LINE/L1
chr5	141694918	141695135	MIR	SINE/MIR
chr7	75408230	75409095	LTR7 HERVH-int	LTR/ERV1
chr5	166720201	166720524	AluSp	SINE/Alu
chr8	39775037	39775259	L2d	LINE/L2
chrX	93821695	93823748	L1M1	LINE/L1
chr5	147036873	147039060	L1PA8	LINE/L1
chr2	238493038	238493130	MER58B	DNA/hAT-Charlie
chr2	188903874	188904896	THE1C-int THE1C	LTR/ERV1-MaLR
chrX	93831932	93833733	L1M1	LINE/L1
chr8	39763673	39764309	LTR49-int	LTR/ERV1
chr5	166718863	166719226	THE1B	LTR/ERV1-MaLR
chr3	176006173	176006317	FRAM	SINE/Alu
chr11	125357998	125358290	MER44A	DNA/TcMar-Tigger
chr15	89443187	89443491	AluSx1	SINE/Alu
chr1	223220740	223221320	MLT2B3	LTR/ERV1
chr3	189709406	189709758	L2	LINE/L2
chr16	9901469	9901534	MIR3	SINE/MIR
chr1	232276858	232277135	AluSp	SINE/Alu
chr19	6656146	6657137	LTR6A HERVS71-int	LTR/ERV1
chr1	64609352	64610097	L2a	LINE/L2
chr6	131631410	131633624	L1MEc	LINE/L1
chr6	63606861	63607162	AluSc	SINE/Alu
chr3	189874799	189875158	L1ME3Cz	LINE/L1
chr13	54678057	54678199	Tigger1	DNA/TcMar-Tigger

chr2	8028701	8028804	LTR84b	LTR/ERV1
chr3	163910410	163916338	L1PA16	LINE/L1
chr4	87404831	87405250	L2c	LINE/L2
chr1	209627626	209627746	L2d2	LINE/L2
chr8	12342588	12350911	LTR2C HERVE-int	LTR/ERV1
chrX	124518082	124518344	L1MB5	LINE/L1
chr7	75428821	75428880	MER5B	DNA/hAT-Charlie
chr10	6880428	6880545	L2c	LINE/L2
chr9	101027595	101028757	LTR7 HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr6	132228776	132228848	FLAM_A	SINE/Alu
chrX	65477248	65477603	LTR79	LTR/ERV1
chr1	232332298	232337384	MLT2A1 MLT2A1 MLT2A1 HERVL-int	LTR/ERV1
chr3	189886051	189886129	MER5A	DNA/hAT-Charlie
chr2	188531436	188532028	Tigger1	DNA/TcMar-Tigger
chr6	132239222	132239368	L1M1	LINE/L1
chr4	93186912	93187033	MLT1L	LTR/ERV1-MaLR
chr7	20046835	20047173	MLT1J1	LTR/ERV1-MaLR
chr6	167660068	167660168	MIRc	SINE/MIR
chr3	63107825	63107973	MIRc	SINE/MIR
chr17	6832141	6833931	L1MA4	LINE/L1
chr3	189709873	189710182	AluSq2	SINE/Alu
chr2	188525812	188526256	L1P1	LINE/L1
chrX	121388665	121391118	L1PA3	LINE/L1
chr12	75761072	75761317	Tigger3b	DNA/TcMar-Tigger
chr15	24920043	24920348	AluSx	SINE/Alu
chrX	101148543	101149114	L2c	LINE/L2
chr15	89448425	89448546	MIR3	SINE/MIR
chr3	176031601	176031975	MLT1B	LTR/ERV1-MaLR
chrX	107921944	107922849	L1MC4	LINE/L1
chr7	75431370	75431672	AluSx	SINE/Alu
chr5	166714808	166714953	MER135	DNA
chr10	21776309	21776560	AluSz	SINE/Alu
chr7	125719598	125719790	L1M4a2	LINE/L1
chr5	147050367	147050918	L2a	LINE/L2
chr1	238644460	238649445	MER61A MER61-int MER61-int MER61A	LTR/ERV1
chr2	210171695	210172678	MER52D	LTR/ERV1
chrX	15852605	15852906	AluSg4	SINE/Alu
chrX	124515846	124516256	MSTB	LTR/ERV1-MaLR
chr6	132234541	132235126	L1MD2	LINE/L1
chr15	48447396	48447971	L1ME4a	LINE/L1

chr7	131192565	131192617	Eutr18	LTR?
chr15	48446725	48447015	L1ME4a	LINE/L1
chr1	223224876	223225134	MER115	DNA/hAT-Tip100
chr5	7263693	7269444	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	125358295	125358604	AluSg	SINE/Alu
chr5	123648649	123648933	AluY	SINE/Alu
chr6	167664051	167664200	AluJo	SINE/Alu
chrX	128587332	128588623	L1PA7	LINE/L1
chr2	8023233	8023335	MIR	SINE/MIR
chr4	93181403	93181472	L4_A_Mam	LINE/RTE-X
chr5	7815923	7816310	MLT1B	LTR/ERV1-MaLR
chr10	6837306	6837465	L1PA14	LINE/L1
chr5	25406854	25407172	MLT1G1	LTR/ERV1-MaLR
chr6	63607163	63607314	L1ME3Cz	LINE/L1
chr6	132229987	132230209	AluJr	SINE/Alu
chr14	21276504	21278265	MER89-int MER89-int MER89	LTR/ERV1
chr5	25402842	25403829	HERVL-int	LTR/ERV1
chr4	93191519	93191718	LTR16A	LTR/ERV1
chr14	96391413	96391623	MIRb	SINE/MIR
chr11	85413592	85415684	L1MEg	LINE/L1
chr16	77915147	77915412	L2b	LINE/L2
chr7	20068357	20068791	L1ME3G	LINE/L1
chr4	182896974	182897284	MLT1B	LTR/ERV1-MaLR
chr1	211539332	211539434	MIRb	SINE/MIR
chr18	40571462	40576774	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	101145882	101146713	L2b	LINE/L2
chr7	19969358	19969665	AluY	SINE/Alu
chr8	7758598	7758907	MER2	DNA/TcMar-Tigger
chr7	125564677	125564824	L2-2_Mam	LINE/L2
chr20	37252296	37252434	L2a	LINE/L2
chr7	145939017	145939213	MIR	SINE/MIR
chr15	89445826	89446018	LTR86B1	LTR/ERV1
chr5	5137717	5138772	LTR12C	LTR/ERV1
chr20	12746150	12746568	L1ME3G	LINE/L1
chr8	72599451	72599568	MIRb	SINE/MIR
chr9	76619288	76621127	L1PA5	LINE/L1
chrX	107919055	107919292	MIR	SINE/MIR
chr7	19937265	19938195	L1PA2	LINE/L1
chr15	89456103	89456190	MIR3	SINE/MIR
chr11	94382760	94383068	AluSx1	SINE/Alu

chr5	38313212	38313710	L1ME4a	LINE/L1
chr7	145939350	145939659	AluSx3	SINE/Alu
chrX	15854484	15854568	L1ME4b	LINE/L1
chr11	58649062	58650733	L1PA6	LINE/L1
chr11	14616307	14622422	L1PA6	LINE/L1
chr9	14706342	14708161	L1MA8	LINE/L1
chr1	232297711	232298092	MSTB	LTR/ERV1-MaLR
chr5	38314197	38314478	L1ME4a	LINE/L1
chr10	10826080	10826826	LTR1B	LTR/ERV1
chr2	8028545	8028613	MADE1	DNA/TcMar-Mariner
chr15	89445487	89445573	MIRb	SINE/MIR
chr6	131659940	131665704	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	131182891	131188573	L1PA6	LINE/L1
chr5	147061632	147062056	L2c	LINE/L2
chr5	146973898	146974190	AluJb	SINE/Alu
chr1	114638279	114638580	AluY	SINE/Alu
chr4	182897699	182898106	L2a	LINE/L2
chr3	189886342	189886464	FLAM_A	SINE/Alu
chr2	121721942	121722317	L2c	LINE/L2
chr7	93269247	93274864	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr15	89454672	89454983	AluY	SINE/Alu
chr4	129562049	129567764	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	225027638	225033784	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	114639668	114639776	MIRc	SINE/MIR
chr18	25529286	25529655	L1ME3G	LINE/L1
chr6	131630333	131631410	L1MEc	LINE/L1
chr2	8023767	8023894	MIR	SINE/MIR
chr13	54678252	54678706	Tigger1	DNA/TcMar-Tigger
chr13	23473666	23475108	LTR12C	LTR/ERV1
chr1	82820252	82826239	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	188904897	188905370	LTR2	LTR/ERV1
chr1	223203655	223204248	LTR8A	LTR/ERV1
chr15	64653576	64653863	AluJb	SINE/Alu
chr2	57456676	57462340	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	12373168	12373476	LTR16C	LTR/ERV1
chr8	7267730	7268041	MER2	DNA/TcMar-Tigger
chr8	39772595	39772741	MIR	SINE/MIR

chr17	20806630	20807193	L2	LINE/L2
chr6	132232172	132233902	L1MD2	LINE/L1
chr7	75429037	75429312	AluJo	SINE/Alu
chrX	2851120	2851429	AluSz	SINE/Alu
chrX	107843094	107843633	L1ME3B	LINE/L1
chr7	75430817	75431143	AluSp	SINE/Alu
chr8	23045173	23045568	LOR1-int	LTR/ERV1
chr4	93191830	93192234	LTR16B2	LTR/ERV1
chrX	107237749	107238331	L2	LINE/L2
chr6	126006395	126007160	L1ME3Cz	LINE/L1
chr7	75428519	75428816	AluSq2	SINE/Alu
chr3	33496480	33496538	AluSq2	SINE/Alu
chr12	93412913	93413509	Tigger12c	DNA/TcMar-Tigger
chr2	238493766	238493853	L2a	LINE/L2
chr6	98238704	98239793	LTR2752	LTR/ERV1
chr5	142138903	142139151	MIRb	SINE/MIR
chr6	126007986	126009758	L1PB2	LINE/L1
chr5	25415943	25416337	LTR52	LTR/ERV1
chr2	210170462	210170934	MER52D	LTR/ERV1
chr7	131193192	131193315	AluJr	SINE/Alu
chrX	71369668	71369848	MIR3	SINE/MIR
chr5	142088413	142089013	Tigger1	DNA/TcMar-Tigger
chrX	125997030	126002975	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	5133955	5134437	MLT1H	LTR/ERV1-MaLR
chr5	25420566	25421604	Tigger3b	DNA/TcMar-Tigger
chr6	132234114	132234386	AluSx3	SINE/Alu
chr7	128375880	128376361	LTR72	LTR/ERV1
chr19	6657436	6657902	HERVS71-int	LTR/ERV1
chr1	232266418	232266479	MER81	DNA/hAT-Blackjack
chr4	93192237	93192517	ERV3-16A3_L-int	LTR/ERV1
chr10	53793517	53799321	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr14	95232263	95232563	AluSz	SINE/Alu
chr7	128375123	128375477	L2a	LINE/L2
chr4	48888360	48891355	L1PA5	LINE/L1
chr16	9903300	9903361	L1ME3G	LINE/L1
chr4	93190752	93191022	L2a	LINE/L2
chr14	38675130	38675875	L1MB5	LINE/L1
chr10	94833129	94833198	MIR3	SINE/MIR
chr2	210187912	210188260	L3	LINE/CR1

chr1	223208602	223209149	LTR9A1	LTR/ERV1
chr10	94832591	94832765	MIRc	SINE/MIR
chr1	64613334	64613506	MIRc	SINE/MIR
chr3	110916719	110917022	LTR82B	LTR/ERV1
chr6	126009759	126011037	HSMAR1	DNA/TcMar-Mariner
chrX	107842322	107842870	L1ME3B	LINE/L1
chr18	47926821	47930564	LTR6A HERVS71-int	LTR/ERV1
chrX	15859995	15860228	MIRb	SINE/MIR
chrX	110796846	110797563	L1PA7	LINE/L1
chr14	21282677	21284889	LTR7B HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chrX	130825172	130826229	MER4B-int MER4D1 MER4B-int MER4B-int	LTR/ERV1
chr12	4400888	4401299	L1MB4	LINE/L1
chr12	30953216	30953607	MSTD	LTR/ERV1-MaLR
chr2	84019934	84021604	HERVH-int LTR7	LTR/ERV1
chr19	41485662	41487823	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr2	169990293	169993316	HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	140258824	140261374	L1MB7	LINE/L1
chr7	128374358	128374718	L2a	LINE/L2
chr5	25407988	25408329	L1PREC2	LINE/L1
chr16	9810439	9810876	MLT1C2	LTR/ERV1-MaLR
chr3	162430248	162436046	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	133079177	133079669	LTR33A_	LTR/ERV1
chrX	132432347	132432635	AluJr	SINE/Alu
chr21	37482018	37483288	HERVIP10FH-int LTR10F HERVIP10FH-int LTR10F	LTR/ERV1
chr14	96390814	96391150	THE1B	LTR/ERV1-MaLR
chr2	188525684	188525765	L1P1	LINE/L1
chr12	8973326	8973790	LTR8	LTR/ERV1
chr1	114683305	114685552	Tigger1	DNA/TcMar-Tigger
chr8	7268042	7268545	MLT1D	LTR/ERV1-MaLR
chr1	48701643	48701847	MIRc	SINE/MIR
chrX	110370843	110371153	L4_A_Mam	LINE/RTE-X
chr19	42503799	42504769	L2a	LINE/L2
chr16	77914502	77915052	L1PA16	LINE/L1
chrX	15854022	15854078	AluJb	SINE/Alu
chr10	3084750	3085175	L1ME1	LINE/L1
chr13	98185177	98185546	THE1D	LTR/ERV1-MaLR
chr2	210170935	210171694	LTR17	LTR/ERV1
chr1	64611449	64611669	MIRb	SINE/MIR
chrX	2811147	2811495	MSTA	LTR/ERV1-MaLR
chr14	96391151	96391342	MamTip2	DNA/hAT-Tip100

chr8	8009011	8009175	MLT1I	LTR/ERV1-MaLR
chrX	107915161	107915279	MIR3	SINE/MIR
chr7	19963858	19965022	L2a	LINE/L2
chr21	38960033	38960196	MLT1C	LTR/ERV1-MaLR
chr1	114636089	114636271	MIR3	SINE/MIR
chrX	71371719	71371803	OldhAT1	DNA/hAT-Ac
chr7	31032908	31034171	LTR12D	LTR/ERV1
chr8	12384731	12385075	MSTA	LTR/ERV1-MaLR
chr1	64613767	64613964	MIRb	SINE/MIR
chr6	131668171	131668470	AluSz6	SINE/Alu
chr8	132322422	132328094	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	232276574	232276857	L1MB3	LINE/L1
chr6	132231625	132231748	L2c	LINE/L2
chr5	142139597	142139827	MIRb	SINE/MIR
chr8	12377417	12384732	LTR6B HERVS71-int HERVS71-int HERVS71-int HERVS71-int LTR6B	LTR/ERV1
chrX	93946479	93947142	MER4B-int MER4B-int	LTR/ERV1
chr4	93178786	93179157	L1ME3A	LINE/L1
chr8	6664501	6665005	MER90	LTR/ERV1
chr10	21776601	21777016	MLT1H	LTR/ERV1-MaLR
chrX	16597888	16598172	MER4-int MER4-int	LTR/ERV1
chr4	134933367	134939535	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	107229308	107234827	L1PA4	LINE/L1
chr1	160374196	160374582	L1MB5	LINE/L1
chr10	47006927	47007318	THE1D	LTR/ERV1-MaLR
chr14	101771591	101777584	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	114689367	114689595	MIR	SINE/MIR
chr6	132236879	132237081	MER63D	DNA/hAT-Blackjack
chr2	188898225	188903863	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	48701622	48701745	MIR3	SINE/MIR
chr11	96464727	96465094	L1MA4	LINE/L1
chr2	188530154	188530869	L1M5	LINE/L1
chr12	96138287	96139769	L1MEc	LINE/L1
chr1	211541593	211541710	L2c	LINE/L2
chrX	107916990	107917273	AluSx1	SINE/Alu
chrX	71365926	71366051	AluJo	SINE/Alu
chr8	133077560	133077828	AluY	SINE/Alu
chr2	36039116	36043843	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	201341198	201341973	LTR1D1	LTR/ERV1

			LTR6B HERVS71-int HERVS71-int HERVS71-int LTR6B	
chr3	164051797	164059685		LTR/ERV1
chr8	7995625	7995969	MSTA	LTR/ERVL-MaLR
chrX	16598539	16602071	MER4-int MER4A1 MER4A1 MER4A1	LTR/ERV1
chr11	13017239	13018652	L1PA13	LINE/L1
chrX	15854106	15854279	L1ME4b	LINE/L1
chr5	18548177	18550102	MSTA MSTA-int MSTA	LTR/ERVL-MaLR
chr5	12652212	12652504	L1MEc	LINE/L1
chr9	38547739	38549333	THE1D-int	LTR/ERVL-MaLR
chr4	93179450	93179854	MSTA	LTR/ERVL-MaLR
chr1	64124446	64124812	THE1B	LTR/ERVL-MaLR
chr3	170389966	170396051	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	166724636	166725326	LTR7 HERVH-int	LTR/ERV1
chr5	25416981	25417529	MLT2B4	LTR/ERVL
chr5	142137043	142138081	L2a	LINE/L2
chr1	211542114	211542247	MIR	SINE/MIR
chr1	211541850	211542045	L2c	LINE/L2
chrX	103223808	103224813	L1PA8	LINE/L1
chr9	85540048	85540657	MLT1E1A	LTR/ERVL-MaLR
chr8	132320509	132320885	LTR7	LTR/ERV1
chrX	15857621	15857910	AluJb	SINE/Alu
chr13	23477101	23477720	MER9a1 HERVK9-int	LTR/ERVK
chr4	41269249	41269562	AluY	SINE/Alu
chr5	142089264	142089897	Tigger1	DNA/TcMar-Tigger
chrX	107236104	107236518	MSTA	LTR/ERVL-MaLR
chr14	62174027	62175497	L1PA4	LINE/L1
chr6	132228915	132229420	MLT1H	LTR/ERVL-MaLR
chr1	38765828	38766338	L1ME4a	LINE/L1
chr7	131193319	131193423	MIR3	SINE/MIR
chr21	15484389	15484961	L1MA8	LINE/L1
chr17	20807581	20807871	AluSp	SINE/Alu
chrX	107969164	107969327	Tigger19a	DNA/TcMar-Tigger
chr3	162440606	162445017	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr15	64656874	64657182	AluSx	SINE/Alu
chr6	16259243	16265124	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	131616497	131622336	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	12350912	12354452	HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	133080667	133081044	Eutr5	LTR?

chr2	238491793	238491976	AluSz6	SINE/Alu
chr21	15476882	15477436	LTR6A	LTR/ERV1
chrX	110798070	110798841	L1MD2	LINE/L1
chr2	238488726	238488839	MIRb	SINE/MIR
chr4	62616646	62616901	MER1B	DNA/hAT-Charlie
chr4	41268102	41268237	AluJo	SINE/Alu
chr1	64609300	64609376	L2a	LINE/L2
chr8	8013473	8014487	L1PA4	LINE/L1
chrX	15861398	15861696	AluSp	SINE/Alu
chr6	132233903	132234113	AluJb	SINE/Alu
chr1	64124865	64125204	L2	LINE/L2
chr3	176006384	176006480	MER5A	DNA/hAT-Charlie
chrX	128589592	128591364	Tigger1	DNA/TcMar-Tigger
chrX	124522687	124528409	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	211541720	211541843	L2a	LINE/L2
chr8	133078758	133078946	MIR3	SINE/MIR
chr8	7995508	7995624	MER58A	DNA/hAT-Charlie
chr7	128372634	128374190	L2a	LINE/L2
chr21	37481547	37482017	LTR2C	LTR/ERV1
chr5	12653511	12653989	L1PB1	LINE/L1
chr12	95924659	95924968	AluY	SINE/Alu
chr1	211540342	211540585	AluSz	SINE/Alu
chrX	110371621	110371856	MIRb	SINE/MIR
chr8	7993985	7994189	L2b	LINE/L2
chr8	133078393	133078624	MIRb	SINE/MIR
chr9	118235460	118241197	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	144919207	144920060	MER4D1	LTR/ERV1
chr17	6816967	6819294	L1PBb	LINE/L1
chr4	104862425	104868186	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	110915397	110915563	MIRb	SINE/MIR
chrX	107971680	107971877	MIRc	SINE/MIR
chr1	211541156	211541454	L2c	LINE/L2
chr5	18595955	18597209	ERV3-16A3_LTR ERV3-16A3_I-int	LTR/ERV1
chr21	37476566	37481175	LTR10F HERVIP10FH-int	LTR/ERV1
chr7	79088912	79089103	L2	LINE/L2
chr2	238489102	238489398	AluSz	SINE/Alu
chrX	15856206	15856432	MER20	DNA/hAT-Charlie
chr3	3853774	3854189	L2b	LINE/L2
chr3	176036618	176036877	L2d	LINE/L2

chr8	7995968	8003278	LTR6B HERVS71-int HERVS71-int HERVS71-int HERVS71-int LTR6B	LTR/ERV1
chr1	48701925	48702065	L2c	LINE/L2
chr8	38279925	38280219	AluJr	SINE/Alu
chr19	42504788	42505047	MLT1F	LTR/ERV1-MaLR
chr8	12366197	12367211	L1PA4	LINE/L1
chr17	7965610	7967219	HERVK-int	LTR/ERVK
chr5	142090315	142090621	AluJr	SINE/Alu
chr6	121941170	121941518	MamTip3	DNA/hAT-Tip100
chr2	238489750	238490032	AluJb	SINE/Alu
chrX	110370176	110370522	L1ME4a	LINE/L1
chr11	122695136	122697277	LTR7 HERVH-int	LTR/ERV1
chr11	10318146	10318714	L1MB5	LINE/L1
chr3	163633990	163636375	MLT2A2 HERVL-int MLT2A2	LTR/ERV1
chr5	173136539	173136662	L2a	LINE/L2
chr6	136690721	136692048	L1MB2	LINE/L1
chrX	93947472	93948065	MER4B	LTR/ERV1
chrX	2870373	2870507	FLAM_C	SINE/Alu
chr5	146773977	146774149	MIRb	SINE/MIR
chr12	95925930	95926243	AluSx1	SINE/Alu
chr5	141698444	141698666	MIR	SINE/MIR
chrX	128586418	128586693	MER103C	DNA/hAT-Charlie
chr12	95916577	95917334	MER21B	LTR/ERV1
chr1	48674674	48680493	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr19	6658211	6659352	HERVS71-int	LTR/ERV1
chrX	107239716	107240785	MER11C	LTR/ERVK
chr6	132231490	132231576	L1MA7	LINE/L1
chr7	128374719	128375116	MLT1J2	LTR/ERV1-MaLR
chr13	23465395	23467342	MER4-int MER4A1	LTR/ERV1
chr6	126007172	126007585	L1MC4a	LINE/L1
chr7	128375502	128375879	MSTA	LTR/ERV1-MaLR
chrX	15854722	15855032	AluJr	SINE/Alu
chrX	16597934	16598118	MER66-int	LTR/ERV1
chr1	211538955	211539149	MIR3	SINE/MIR
chr9	38623062	38623298	L1MA7	LINE/L1
chr14	95233056	95233246	MIR	SINE/MIR
chr21	15476215	15476881	L1M1	LINE/L1
chr3	154992226	154998587	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	134182091	134182761	MER4-int	LTR/ERV1
chr4	93173977	93175337	THE1B THE1B-int	LTR/ERV1-MaLR

chr1	114675396	114675625	MIRb	SINE/MIR
chr1	114675174	114675247	MIRc	SINE/MIR
chrX	107913990	107914252	AluSx	SINE/Alu
chrX	15855729	15856027	AluSc5	SINE/Alu
chr5	145430749	145431443	L2a	LINE/L2
chr2	121713171	121713967	L2a	LINE/L2
chr1	114689636	114690098	Charlie22a	DNA/hAT-Charlie
chr11	7920872	7921779	LTR3A HERVK3-int HERVK3-int	LTR/ERVK
chr19	42505035	42505348	MER74B	LTR/ERV1
chr6	14284658	14284767	MER91A	DNA/hAT-Tip100
chrX	107842871	107843093	MER58A	DNA/hAT-Charlie
chr10	1391211	1396765	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	114690313	114690496	MIRb	SINE/MIR
chr2	33883863	33886990	HERV17-int HERV17-int	LTR/ERV1
chr6	118897874	118899612	HERVIP10B3-int HERVIP10B3-int LTR10B1	LTR/ERV1
chr6	144920931	144923135	Tigger1	DNA/TcMar-Tigger
chr6	48043312	48044390	Tigger1	DNA/TcMar-Tigger
chr7	151081311	151081823	MLT1J	LTR/ERV1-MaLR
chrX	2807047	2807564	MER50B	LTR/ERV1
chr5	25402103	25402583	MLT2B5	LTR/ERV1
chr6	126007767	126007983	L1PB2	LINE/L1
chr3	110919216	110919321	MIRc	SINE/MIR
chrX	128306350	128314034	L1MA2	LINE/L1
chr10	3085551	3085829	AluSq2	SINE/Alu
chr2	8012837	8019022	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	173136306	173136518	L2c	LINE/L2
chr4	93180326	93181013	L1PA6	LINE/L1
chr8	12362313	12366199	L1PA4	LINE/L1
chrX	107969328	107969579	Tigger16b	DNA/TcMar-Tigger
chrX	12957984	12963656	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	64121794	64122238	L1MA9	LINE/L1
chrX	15863104	15863169	Tigger19a	DNA/TcMar-Tigger
chr12	111396421	111396751	MLT1L MLT1L	LTR/ERV1-MaLR
chr19	42505380	42505678	AluSx1	SINE/Alu
chr1	175070212	175078158	LTR12C HERV9NC-int HERV9NC-int HERV9NC-int LTR12C	LTR/ERV1
chr14	95229915	95230051	MIRb	SINE/MIR
chr9	130990848	130990981	L1ME4c	LINE/L1
chr10	17053187	17060974	LTR12 HERV9-int LTR12	LTR/ERV1
chrX	130826450	130830339	MER4B-int MER4B-int MER4B-	LTR/ERV1

			int MER4B-int MER4D1	
chr8	7993672	7993984	AluJr	SINE/Alu
chr5	18546361	18547037	LTR8A	LTR/ERV1
chr1	81710968	81716892	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr7	120525754	120531445	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	93175338	93176617	L1PA10	LINE/L1
chr7	128372181	128372476	AluJb	SINE/Alu
chr5	142085195	142085506	Tigger1	DNA/TcMar-Tigger
chr4	41268649	41268919	AluJr	SINE/Alu
chr8	12373916	12374266	MLT10	LTR/ERV1-MaLR
chr3	110917072	110917335	LTR82B	LTR/ERV1
chr15	48452166	48452242	LFSINE_Vert	SINE/tRNA
chrX	15855075	15855184	FLAM_A	SINE/Alu
chr2	238491502	238491765	AluSz	SINE/Alu
chrX	15854288	15854387	L1M5	LINE/L1
chr2	171479084	171485181	L1PA5	LINE/L1
chr5	142089014	142089263	MLT2A2 MLT2A2	LTR/ERV1
chr17	20806173	20806461	L1MA8	LINE/L1
chr20	38723295	38727650	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr2	150969231	150975078	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	14289186	14289408	MLT1J2	LTR/ERV1-MaLR
chr4	62616228	62616530	AluYa5	SINE/Alu
chr5	142090766	142090999	THE1C	LTR/ERV1-MaLR
chr13	91489878	91490397	L2a	LINE/L2
chr19	53447835	53448814	LTR5B	LTR/ERV1
chr4	41264685	41264924	AluSz	SINE/Alu
chr21	43131830	43132332	MLT1C	LTR/ERV1-MaLR
chr3	110919685	110919826	MIRc	SINE/MIR
chr12	8939679	8948723	LTR12C HERV9NC-int HERV9NC-int LTR12C	LTR/ERV1
chr13	23457699	23463986	LTR2B Harlequin-int Harlequin-int Harlequin-int LTR2B	LTR/ERV1
chrX	16602075	16602284	MER34	LTR/ERV1
chr6	132235716	132235984	Zaphod4a	DNA/hAT-Tip100
chr8	8004816	8005262	MER4A1	LTR/ERV1
chrX	103016087	103017827	LTR7 HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr4	56148581	56151984	L1MA9	LINE/L1
chr8	12386719	12387047	AluJr	SINE/Alu
chrX	130830890	130831580	L1PA7	LINE/L1
chrX	128586736	128587331	Tigger1	DNA/TcMar-Tigger

chrX	15860870	15861174	AluSx	SINE/Alu
chrX	30467049	30472978	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	2870511	2870662	MLT1A0	LTR/ERV1-MaLR
chr5	123832728	123838432	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr7	20160332	20166178	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	64149073	64153551	L1PBa	LINE/L1
chr4	41264197	41264467	AluSz	SINE/Alu
chr5	18663701	18664778	L1PA16	LINE/L1
chr15	89443525	89443588	X24_LINE	LINE/L2
chrX	110369422	110369669	Tigger20a	DNA/TcMar-Tigger
chr3	176039407	176045151	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	110918649	110918701	X7B_LINE	LINE/CR1
chr11	7923057	7927779	HERVK3-int LTR3A	LTR/ERVK
chrX	91355104	91355237	L1MC5a	LINE/L1
chr4	16999370	17005548	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	18665797	18666462	HSMAR2	DNA/TcMar-Mariner
chr21	15484167	15484388	L1PB4	LINE/L1
chr9	100978315	100978523	MIR	SINE/MIR
chr8	12375433	12375879	MER4A1	LTR/ERV1
chr13	109917438	109923464	LTR7Y HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr5	25408330	25409074	L1PA7	LINE/L1
chrX	110369708	110369901	MIRc	SINE/MIR
chrX	103014672	103014971	AluY	SINE/Alu
chrX	2801001	2801304	AluSz6	SINE/Alu
chrX	2851430	2851629	MLT1B	LTR/ERV1-MaLR
chr4	93176683	93178677	L1M2	LINE/L1
chr9	130990622	130990743	AluJr	SINE/Alu
chr1	195817044	195817727	LTR7Y HERVH-int LTR7	LTR/ERV1
chr5	18662412	18662656	L1MEc	LINE/L1
chr5	34060600	34062284	THE1B THE1B-int	LTR/ERV1-MaLR
chr5	18615580	18617889	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr12	8948738	8949027	AluYk2	SINE/Alu
chr8	12385546	12385673	AluSz	SINE/Alu
chr5	12654317	12654827	L1ME3Cz	LINE/L1
chr21	15483275	15484166	L1MA8	LINE/L1
chr8	8003536	8003836	AluSp	SINE/Alu
chr9	22658526	22664061	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1

chr7	124871462	124872007	BLACKJACK	DNA/hAT-Blackjack
chr20	44100760	44107254	L1PA13	LINE/L1
chr5	12653033	12653165	AluJo	SINE/Alu
chr4	75033558	75034398	L2a	LINE/L2
chrX	2807565	2808102	MER41A	LTR/ERV1
chr5	18646108	18648622	L1MA3	LINE/L1
chrX	128584018	128584440	MLT1B	LTR/ERV1-MaLR
chr5	89802287	89802345	OldhAT1	DNA/hAT-Ac
chrX	121355857	121361638	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	132240460	132242191	L1PA13	LINE/L1
chr3	110918825	110919209	CR1_Mam	LINE/CR1
chr21	29533753	29539243	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	171472170	171475960	MER11D HERVK11D-int MER11D	LTR/ERVK
chr19	35988856	35989022	FRAM	SINE/Alu
chrX	103017828	103017988	AluSx1	SINE/Alu
chr6	132239393	132240456	L1PA13	LINE/L1
chrX	128598650	128599236	L1MC4	LINE/L1
chrX	70491433	70492681	HERVH-int HERVH-int LTR7B	LTR/ERV1
chr15	48454539	48454667	MIR	SINE/MIR
chr9	38550153	38552392	MSTA MSTA-int MSTA MSTA MSTA-int	LTR/ERV1-MaLR
chrX	103017989	103022234	HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	101912850	101918632	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	76963685	76972373	LTR12C HERV9NC-int HERV9NC-int LTR12C	LTR/ERV1
chr8	38292379	38292687	AluSp	SINE/Alu
chr9	38407283	38407429	MIR3	SINE/MIR
chr6	14287108	14287472	MER21C	LTR/ERV1
chr19	56040481	56040776	AluJr	SINE/Alu
chrX	107846558	107848938	Tigger1	DNA/TcMar-Tigger
chr9	130991666	130991902	AluJb	SINE/Alu
chr8	8014485	8018371	L1PA4	LINE/L1
chr8	12386514	12386718	L2b	LINE/L2
chr5	142090636	142090765	LTR103b_Mam	LTR/ERV1?
chr15	93054537	93060655	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	227021204	227026105	LTR7C HERVH-int HERVH-int HERVH-int LTR7C	LTR/ERV1
chr6	14284944	14285113	AluJo	SINE/Alu
chr8	38291301	38291691	L1MB8	LINE/L1
chr9	85352677	85353146	MLT1C2	LTR/ERV1-MaLR
chr8	8026245	8029782	LTR7 HERVH-int HERVH-int	LTR/ERV1

chr21	15482676	15483161	L1MA8	LINE/L1
chr9	130990982	130991291	AluSx4	SINE/Alu
chr5	12655803	12657634	L1MEc	LINE/L1
chr5	146777548	146777769	L3	LINE/CR1
chrY	23199944	23207131	HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	18653983	18654059	L1MA3	LINE/L1
chr12	95924586	95924657	L1ME4c	LINE/L1
chr17	47124738	47124832	MIR	SINE/MIR
chr2	224854537	224854914	LTR33	LTR/ERV1
chr3	189861107	189861400	AluSg	SINE/Alu
chr4	134183107	134184559	MER4-int MER4-int MER4-int MER4-int MER4A1	LTR/ERV1
chrX	113283263	113288757	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr5	146787127	146787241	MIRb	SINE/MIR
chr1	211540625	211540836	MIR	SINE/MIR
chr4	41264955	41265140	MIR	SINE/MIR
chr10	6839045	6844915	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr15	48454441	48454505	MIRb	SINE/MIR
chr21	40976833	40976938	MIRc	SINE/MIR
chr8	7929213	7929521	AluSx	SINE/Alu
chr9	130988707	130988916	MIRb	SINE/MIR
chr9	38408687	38408832	MIR3	SINE/MIR
chr12	111397300	111397597	L2c	LINE/L2
chrX	130831615	130833635	MLT1A0 MLT1A0-int	LTR/ERV1-MaLR
chr4	41267152	41267313	MIR	SINE/MIR
chr7	22742977	22748932	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	126115474	126119695	L1MA2	LINE/L1
chr6	132231900	132232064	AluSx	SINE/Alu
chr8	8006427	8006777	MLT1O	LTR/ERV1-MaLR
chr5	25401224	25401708	LTR22B	LTR/ERV1
chr6	14289520	14289910	L1PA6	LINE/L1
chr3	163625318	163631776	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	103014981	103015134	FRAM	SINE/Alu
chr2	215954662	215960754	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	111398605	111399029	MLT1L LTR67B	LTR/ERV1-MaLR
chr22	35230599	35236015	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	7922164	7922604	L2b	LINE/L2
chr3	3893523	3893646	MIRb	SINE/MIR
chr4	176382318	176388337	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1

			int HERVH-int HERVH-int HERVH-int LTR7	
chr1	114677155	114677362	L2d	LINE/L2
chr3	3855589	3855976	L2	LINE/L2
chr5	142084999	142085179	MER8	DNA/TcMar-Tigger
chr4	93187643	93188089	LTR37B	LTR/ERV1
chr12	59716969	59722767	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	85356167	85356542	MLT1B	LTR/ERV1-MaLR
chrX	128588774	128589591	L1PA7	LINE/L1
chr4	93190417	93190571	MER5A1	DNA/hAT-Charlie
chr17	20806470	20806592	AluSx3	SINE/Alu
chr1	155153429	155153720	AluSg	SINE/Alu
chr8	7995030	7995157	AluSz	SINE/Alu
chrX	154582722	154589205	L1PA13	LINE/L1
chr21	15464390	15465856	LTR12C	LTR/ERV1
chrX	70148945	70149240	AluSx	SINE/Alu
chrX	130872165	130872463	AluSc	SINE/Alu
chr5	18668505	18668946	L2a	LINE/L2
chr21	40976241	40976524	AluYk4	SINE/Alu
chrX	31395839	31401487	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	90028312	90034154	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	16604195	16604814	MER41B	LTR/ERV1
chr12	30209014	30215449	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	39619323	39625109	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	38288734	38288979	L2b	LINE/L2
chr1	114679402	114679795	MLT1I	LTR/ERV1-MaLR
chr8	22996193	22996575	L1MC	LINE/L1
chr2	141183963	141189971	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	165361210	165361695	MLT1D	LTR/ERV1-MaLR
chr18	40229438	40229802	MLT1A0	LTR/ERV1-MaLR
chr13	23475109	23476495	MER4-int	LTR/ERV1
chrX	154711019	154717502	L1PA13	LINE/L1
chr5	18550982	18552348	LTR12C	LTR/ERV1
chr4	93184004	93184161	MIRc	SINE/MIR
chr8	38300550	38300890	L1MA7	LINE/L1
chr1	64122279	64122783	L1MA9	LINE/L1
chr5	142088119	142088412	AluJb	SINE/Alu
chrX	107238897	107239715	L1PB1	LINE/L1

chrX	115946058	115946140	L1M2	LINE/L1
chr1	48829476	48835601	L1PA3	LINE/L1
chr19	28194362	28204218	MER11C HERVK11-int HERVK11-int MER11C	LTR/ERVK
chrX	86936680	86942644	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	83685780	83686595	L1ME4b	LINE/L1
chr5	18649127	18653939	L1MA3	LINE/L1
chr5	137427317	137427587	AluJr	SINE/Alu
chr9	38407647	38407874	MIRc	SINE/MIR
chr15	53719041	53724660	LTR7Y HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr15	101599617	101600116	L1MC5	LINE/L1
chr4	113625740	113626077	L2	LINE/L2
chr5	142086943	142088118	Tigger1	DNA/TcMar-Tigger
chr5	173134814	173135406	L1ME3E	LINE/L1
chrX	15847859	15848104	L1MB2	LINE/L1
chr1	211539708	211540132	L2c	LINE/L2
chr1	114696684	114696867	MIRc	SINE/MIR
chr5	18665183	18665492	HSMAR2	DNA/TcMar-Mariner
chr5	142086033	142086220	AluJo	SINE/Alu
chr13	91490398	91491026	L1MA2	LINE/L1
chr2	165362902	165363622	L1MB5	LINE/L1
chr9	130986046	130986354	AluY	SINE/Alu
chr5	142083179	142084996	L1MEg	LINE/L1
chr4	120923016	120923389	L2d	LINE/L2
chr11	87840714	87842297	L1P2	LINE/L1
chr12	8949049	8949207	MLT-int	LTR/ERV1-MaLR
chr3	42629614	42629919	AluSx3	SINE/Alu
chr9	100978977	100979276	AluJr	SINE/Alu
chr8	22999032	22999503	L1PA16	LINE/L1
chr9	100977641	100977799	MIRb	SINE/MIR
chrX	70484230	70486737	LTR7B HERVH-int	LTR/ERV1
chr4	155839481	155845715	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	38553086	38555494	MSTA-int MSTA MSTA-int MSTA MSTA MSTA-int	LTR/ERV1-MaLR
chr2	163201841	163202356	Charlie2a	DNA/hAT-Charlie
chr6	14289929	14290038	Tigger22N1	DNA/TcMar-Tigger
chr14	38671087	38671426	L2a	LINE/L2
chr9	25668927	25675215	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	77340072	77346502	MLT2A1 HERV1-int MLT2A1	LTR/ERV1
chr2	163209007	163209697	HAL1	LINE/L1
chr8	38293611	38293904	AluJr	SINE/Alu

chr13	54904479	54906417	L1MC1	LINE/L1
chr2	69670143	69676473	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	130990308	130990621	AluSq	SINE/Alu
chr1	114674614	114674809	MIRb	SINE/MIR
chr12	95915273	95915562	AluSz	SINE/Alu
chr4	88857074	88858699	LTR7 HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr13	61779816	61785413	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	118758680	118758975	AluSc8	SINE/Alu
chr11	27650619	27656473	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	53104975	53105173	MER112	DNA/hAT-Charlie
chr5	146778181	146778550	MLT1I	LTR/ERV1-MaLR
chr4	88842955	88847147	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr6	14297028	14297170	L1MC1	LINE/L1
chr8	38290837	38291140	AluSz	SINE/Alu
chr17	51533034	51533484	LTR7	LTR/ERV1
chr12	8121626	8121826	AluJr	SINE/Alu
chr7	125550019	125555793	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	38295559	38295693	MIR	SINE/MIR
chr22	36631869	36632508	HAL1	LINE/L1
chr5	25416599	25416879	AluSc	SINE/Alu
chr11	7956140	7957177	L1PA5	LINE/L1
chr2	189399917	189403050	L1PA16	LINE/L1
chr14	38670457	38670940	MER115	DNA/hAT-Tip100
chr5	146787374	146787554	L1ME3A	LINE/L1
chrX	115946113	115946411	L1M1	LINE/L1
chrX	128581575	128581746	MER104	DNA/TcMar-Tc2
chrX	130890617	130890738	AluJr	SINE/Alu
chr21	38960228	38961714	HERVH-int HERVH-int HERVH-int	LTR/ERV1
chrX	118757164	118757504	L1MC5	LINE/L1
chr4	134182809	134183106	AluSg	SINE/Alu
chr5	34063694	34064918	HERV17-int LTR17	LTR/ERV1
chr6	81137396	81143344	L1PA7	LINE/L1
chr7	121203703	121209722	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr16	86773401	86773759	MLT1B	LTR/ERV1-MaLR
chr1	65155342	65155750	L2c	LINE/L2
chr9	130987669	130987779	MER91C	DNA/hAT-Tip100
chr1	31652212	31652484	AluSx	SINE/Alu
chr1	113366164	113368676	HERVH-int LTR7	LTR/ERV1
chr6	14281841	14281944	MIR3	SINE/MIR

chr17	6757049	6757728	L1PBa1	LINE/L1
chrX	16597710	16597886	LTR8	LTR/ERV1
chr5	103367411	103373014	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	38890786	38896451	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	23485953	23488919	L1ME1	LINE/L1
chr9	38408129	38408448	AluJb	SINE/Alu
chr5	142086694	142086928	L1MEg	LINE/L1
chr6	55875537	55881584	HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	54896357	54896723	L1PA15	LINE/L1
chr6	14280312	14280686	MLT1A	LTR/ERV1-MaLR
chr6	14287675	14288188	MER21C MER21C	LTR/ERV1
chr4	116896856	116902379	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	130991402	130991665	AluJr4	SINE/Alu
chr1	53803960	53804799	L1ME3E	LINE/L1
chr6	64035503	64043151	LTR12C HERV9NC-int HERV9NC-int LTR12C	LTR/ERV1
chr17	20795566	20796001	Tigger2a	DNA/TcMar-Tigger
chr6	167687014	167687774	MER4D1	LTR/ERV1
chr14	38671459	38671512	LTR91A	LTR
chr14	38668643	38668885	LTR78	LTR/ERV1
chr9	130994027	130994196	MIR	SINE/MIR
chr1	155153105	155153416	AluSp	SINE/Alu
chr8	38276366	38276704	THE1B	LTR/ERV1-MaLR
chr5	83684755	83685016	MIR	SINE/MIR
chr9	100977800	100978087	AluJr	SINE/Alu
chr9	130995222	130995347	L2c	LINE/L2
chrX	130873906	130874293	LTR4	LTR/ERV1
chr21	18493759	18500075	LTR7 HERVH-int HERVH-int HERVH-int LTR7 LTR7	LTR/ERV1
chr18	33424026	33430382	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	130989655	130989960	AluSx	SINE/Alu
chr7	124879111	124880726	Tigger1	DNA/TcMar-Tigger
chr22	38127476	38127761	AluSz	SINE/Alu
chr2	214262432	214263638	L2a	LINE/L2
chr9	100979622	100979815	MIR3	SINE/MIR
chr7	125557611	125564164	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	18658616	18659340	L1MD2	LINE/L1
chrX	16603553	16604158	LTR35	LTR/ERV1
chr9	130993474	130993779	AluSp	SINE/Alu

chr8	12387048	12387687	L2b	LINE/L2
chr8	7472741	7473309	ERVL-B4-int	LTR/ERVL
chr7	124895144	124895771	L1M5	LINE/L1
chr9	130987238	130987487	MIRc	SINE/MIR
chr12	111397799	111398085	AluSx1	SINE/Alu
chr14	84966594	84972317	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	14294214	14294297	L2b	LINE/L2
chr18	47931542	47935100	HERVS71-int HERVS71-int HERVS71-int LTR6A	LTR/ERV1
chrX	113300333	113300777	MER4E1	LTR/ERV1
chr8	12459401	12459841	L2b	LINE/L2
chr12	8116052	8116387	MER58B	DNA/hAT-Charlie
chrX	115945786	115946009	L1PB3	LINE/L1
chr4	41266956	41267151	MER58A	DNA/hAT-Charlie
chr9	38556338	38558571	MSTA MSTA-int MSTA MSTA MSTA-int	LTR/ERVL-MaLR
chrX	119279501	119280305	Harlequin-int	LTR/ERV1
chr2	157576596	157582356	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	203015958	203016183	X7B_LINE	LINE/CR1
chrX	53095854	53096651	Charlie17	DNA/hAT-Charlie
chr11	89893519	89894535	LTR37-int LTR37A	LTR/ERV1
chr1	209622150	209627347	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	90613147	90614147	L1MA2	LINE/L1
chr6	129067251	129067732	LTR7	LTR/ERV1
chrX	115854285	115860680	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	73932955	73933180	AluJr	SINE/Alu
chr2	188535210	188540996	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	62266015	62266522	L1MA9	LINE/L1
chr12	8949031	8949796	MSTA-int MSTA-int MSTA	LTR/ERVL-MaLR
chr5	12660494	12661271	LTR17	LTR/ERV1
chr5	12661451	12661846	LTR9C	LTR/ERV1
chr1	80104447	80110172	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	170399547	170407095	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	14296733	14297025	AluSg	SINE/Alu
chr2	163209994	163211371	HAL1	LINE/L1
chr8	12387464	12387732	L2a	LINE/L2
chr5	146785957	146786162	MIRb	SINE/MIR
chr12	8118791	8119085	AluSx	SINE/Alu
chr1	24485731	24485907	MIR	SINE/MIR

chr6	114734701	114734999	MLT2C1	LTR/ERV1
chrX	70487034	70489460	HERVH-int HERVH-int	LTR/ERV1
chr7	124869461	124871442	THE1D THE1D-int	LTR/ERV1-MaLR
chrX	15846733	15847312	L1MC5a	LINE/L1
chr3	182993390	182993713	AluJr	SINE/Alu
chr5	145136147	145136509	Tigger15a	DNA/TcMar-Tigger
chr6	114738272	114738392	L2b	LINE/L2
chr22	31745545	31745845	AluSx	SINE/Alu
chr14	38669465	38669631	MIR	SINE/MIR
chr12	8470084	8477521	LTR6B HERVS71-int HERVS71-int HERVS71-int LTR6B	LTR/ERV1
chr6	14288245	14288680	MLT1H2	LTR/ERV1-MaLR
chr1	113362767	113365854	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr5	12658489	12658810	L1PREC2	LINE/L1
chrX	51644036	51644617	L1MA7	LINE/L1
chr5	12663172	12663439	LTR9C	LTR/ERV1
chr18	32795992	32802476	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	173477402	173477687	AluSq2	SINE/Alu
chr5	18655086	18658127	L1MD2	LINE/L1
chr15	25267957	25268128	L1ME3G	LINE/L1
chr6	18754375	18760101	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	222157977	222159320	HSMAR2	DNA/TcMar-Mariner
chr14	38667782	38667992	MIR	SINE/MIR
chr17	47125077	47125377	AluJb	SINE/Alu
chr5	36032844	36033724	MER70-int MER70A	LTR/ERV1
chr14	45964165	45968935	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chrX	53104055	53104747	L2a	LINE/L2
chr8	84416938	84423155	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	8119133	8119419	AluSg	SINE/Alu
chr3	21009033	21014723	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr17	47124534	47124641	MIRb	SINE/MIR
chr12	8119881	8120040	THE1D	LTR/ERV1-MaLR
chr2	173477727	173478119	ERV3-16A3_LTR	LTR/ERV1
chr19	49313424	49313831	LTR65	LTR/ERV1
chr2	97745702	97746722	L1PA12	LINE/L1
chr7	145940911	145946317	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	108895249	108895650	LTR7	LTR/ERV1
chr12	8949813	8950057	ERV3-16A3_I-int LTR16B1	LTR/ERV1

chr2	69663958	69664122	MIR3	SINE/MIR
chr2	173478191	173478341	FRAM	SINE/Alu
chr5	18658128	18658615	MER66B	LTR/ERV1
chr5	8998484	9002586	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr8	12460703	12461263	ERVL-B4-int	LTR/ERVL
chr12	79941114	79941210	MamTip2b	DNA/hAT-Tip100
chr3	42626847	42627494	L2	LINE/L2
chr4	126482775	126488611	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	38125230	38125488	AluJr	SINE/Alu
chr12	8957475	8963172	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	153576559	153578015	HUERS-P3b-int LTR9B	LTR/ERV1
chr6	81219513	81225520	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	238515427	238521297	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr14	38670068	38670227	L1ME4a	LINE/L1
chr8	7992201	7992298	L2b	LINE/L2
chr8	38305431	38305761	L1ME4a	LINE/L1
chr4	90606850	90607253	MLT1H MLT1H	LTR/ERVL-MaLR
chr2	69666187	69666383	L2	LINE/L2
chr22	38127154	38127448	AluJb	SINE/Alu
chr9	137726328	137726601	L2b	LINE/L2
chr9	130993082	130993381	AluSz	SINE/Alu
chr1	64061650	64061862	L2-3_Crp	LINE/L2
chr10	104971436	104973414	HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr13	54893684	54894047	THE1B	LTR/ERVL-MaLR
chr2	173475339	173475639	AluSx1	SINE/Alu
chr12	72608789	72609235	LTR7	LTR/ERV1
chr13	56229066	56234937	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	131198994	131199352	L3b	LINE/CR1
chr8	12398293	12398862	MLT1E1	LTR/ERVL-MaLR
chr7	148006508	148012707	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	83683989	83684178	MIRb	SINE/MIR
chr1	64815626	64821444	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr21	46911917	46911990	MIR	SINE/MIR
chr1	233199218	233200569	L1MEd	LINE/L1
chr9	99998835	99999592	L1M5	LINE/L1
chr13	54872353	54873208	L1PA15	LINE/L1

chr5	140494104	140496069	L1M4	LINE/L1
chr1	114679187	114679280	L2d	LINE/L2
chr9	100976291	100976470	Chap1_Mam	DNA/hAT-Charlie
chr7	124897951	124898422	MER4A1	LTR/ERV1
chr8	72587172	72592895	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	37608161	37612747	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr8	38294360	38294454	OldhAT1	DNA/hAT-Ac
chr20	35175663	35175852	MIR	SINE/MIR
chr22	38124163	38124461	AluSc8	SINE/Alu
chr8	91661483	91662136	L2a	LINE/L2
chr15	25283100	25283920	L1MC4	LINE/L1
chr15	77578042	77578611	L1P1	LINE/L1
chr20	30774876	30775163	AluJr	SINE/Alu
chr6	158121674	158127614	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	38124583	38124675	L1MC1	LINE/L1
chr2	173474547	173474849	AluSx1	SINE/Alu
chr9	100981738	100981989	Tigger3c	DNA/TcMar-Tigger
chr1	200996384	200996563	MIR3	SINE/MIR
chr5	12658028	12658488	L1PREC2	LINE/L1
chr8	7992982	7993671	L2b	LINE/L2
chrX	102748217	102750364	L1MA2	LINE/L1
chr9	4531072	4537200	L1PA4	LINE/L1
chr13	43426291	43426970	L1ME3A	LINE/L1
chrX	103015414	103015711	AluJb	SINE/Alu
chr4	99934579	99943059	LTR10C HERVIP10B3-int LTR10C	LTR/ERV1
chr22	38127762	38127896	AluJo	SINE/Alu
chrX	53104789	53104961	L2	LINE/L2
chr18	44809639	44810268	L1ME5	LINE/L1
chr1	35597626	35603626	HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	12410024	12410320	AluSg	SINE/Alu
chrX	130928383	130928508	FLAM_A	SINE/Alu
chr12	111375874	111376181	AluJr	SINE/Alu
chr6	14281961	14282133	UCON105	DNA/hAT?
chr9	130990128	130990307	AluJr	SINE/Alu
chrX	86236887	86242490	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	33889527	33891520	MER61-int	LTR/ERV1
chr1	99266611	99272414	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	42631454	42631587	MIR	SINE/MIR

chr11	61590744	61590923	MIR3	SINE/MIR
chr17	47125605	47125916	AluSx	SINE/Alu
chr1	203016777	203016996	MIR	SINE/MIR
chrY	21153222	21153521	AluSx1	SINE/Alu
chrX	103009924	103010081	AluSx	SINE/Alu
chr10	92567046	92573015	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7 LTR7	LTR/ERV1
chr2	96682548	96682913	THE1B	LTR/ERV1-MaLR
chr9	38562354	38564717	MSTA-int MSTA MSTA-int MSTA MSTA MSTA-int	LTR/ERV1-MaLR
chr19	51917121	51917619	LTR3B_	LTR/ERV1
chr17	39974832	39974919	MER91A	DNA/hAT-Tip100
chr18	44809331	44809626	AluSx	SINE/Alu
chr9	130986373	130986506	MIR1_Amn	SINE/MIR
chr8	7995158	7995464	AluSx1	SINE/Alu
chr5	36028639	36031345	MER70A MER70-int MER70-int MER70-int	LTR/ERV1
chr20	35136083	35136648	MLT1G3	LTR/ERV1-MaLR
chr3	143516287	143524767	LTR7 HERVH-int LTR7	LTR/ERV1
chr4	16778691	16779267	L2a	LINE/L2
chr12	46583394	46583728	THE1B	LTR/ERV1-MaLR
chr5	100652585	100656301	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	57245361	57251297	MER48 HERVH48-int HERVH48-int HERVH48-int HERVH48-int HERVH48-int MER48	LTR/ERV1
chr7	124874009	124874497	LTR16D2	LTR/ERV1
chr9	38559419	38561660	MSTA MSTA-int MSTA MSTA MSTA-int	LTR/ERV1-MaLR
chr8	138421660	138426131	HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	54902832	54904488	L1MC1	LINE/L1
chrX	2792327	2792730	L2a	LINE/L2
chr13	54896029	54896349	MLT2A2	LTR/ERV1
chr5	142089980	142090154	MER102a	DNA/hAT-Charlie
chr20	12320915	12326587	LTR7Y HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7Y	LTR/ERV1
chr12	100111978	100115515	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	65024216	65025344	L1PA14	LINE/L1
chr8	38294464	38294659	AluSz6	SINE/Alu
chr12	8122836	8123144	AluSx	SINE/Alu
chr5	82872035	82872948	L1ME3E	LINE/L1
chr18	44808459	44809010	MLT1L	LTR/ERV1-MaLR
chr14	71590924	71596723	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	38307944	38313654	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1

			int LTR7	
chr7	124877875	124879102	L1MEf	LINE/L1
chrX	2788558	2789447	L1MEg	LINE/L1
chr3	161439703	161445565	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	81517262	81523721	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr20	153413	159494	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	12661847	12663171	LTR12C	LTR/ERV1
chr12	13412573	13418453	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	38126667	38126974	AluSx1	SINE/Alu
chr3	137314443	137320032	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	28090000	28090424	LTR7C	LTR/ERV1
chr17	43346385	43346678	AluJr	SINE/Alu
chr13	43425195	43425474	L1ME1	LINE/L1
chr5	161702434	161708166	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	38125939	38126003	L2a	LINE/L2
chr6	14294878	14295181	L1M1	LINE/L1
chr12	8950058	8950203	AluSz	SINE/Alu
chr11	121183650	121184458	L1ME2	LINE/L1
chr3	42624022	42624346	L2c	LINE/L2
chr2	149869638	149870089	MLT1J	LTR/ERV1-MaLR
chrX	53090943	53091738	MSTD MSTD-int	LTR/ERV1-MaLR
chr9	130989961	130990127	L1ME3Cz	LINE/L1
chrX	115944181	115944331	L2a	LINE/L2
chr12	111383250	111384730	MLT1G1 MLT1G1-int	LTR/ERV1-MaLR
chr12	8116627	8116929	AluSx	SINE/Alu
chr10	20659775	20660223	LTR7	LTR/ERV1
chrX	130921460	130922695	L1MA4	LINE/L1
chr1	169457390	169457978	MLT1E2	LTR/ERV1-MaLR
chr16	86771858	86772479	MER83 MER83 MER83	LTR/ERV1
chr9	100978674	100978852	MIRb	SINE/MIR
chr5	70435038	70435446	L1PA10	LINE/L1
chr6	14292324	14292497	LTR33	LTR/ERV1
chr15	101612692	101618498	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	192713434	192719177	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	55508441	55508869	MSTB1	LTR/ERV1-MaLR
chr6	14295968	14296020	MIRb	SINE/MIR

chrX	137346517	137352494	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7 LTR7	LTR/ERV1
chr21	18264530	18270560	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	97744490	97745391	L1PA12	LINE/L1
chr5	18629458	18631830	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr11	89900185	89901538	LTR12C	LTR/ERV1
chr6	114733566	114734700	L1MC3	LINE/L1
chr9	137723970	137724279	AluSx	SINE/Alu
chr12	29288864	29293734	HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	83685214	83685459	L2d	LINE/L2
chr13	43438262	43438565	AluYk2	SINE/Alu
chr8	12399323	12400289	L1P1	LINE/L1
chr3	120119158	120119312	MER5B	DNA/hAT-Charlie
chr12	79939593	79939769	LTR78B	LTR/ERV1
chr1	93590329	93590474	L3	LINE/CR1
chr4	118521277	118524884	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr6	30806371	30806671	AluSc	SINE/Alu
chr19	35999839	36000000	AluSx1	SINE/Alu
chr6	30805089	30805764	L1MC4a	LINE/L1
chr3	15691374	15691568	MIRb	SINE/MIR
chr2	210164037	210169656	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	114736544	114736806	MER110A	LTR/ERV1
chrX	24336221	24336832	MLT2F	LTR/ERV1
chr13	48575677	48575738	MIRc	SINE/MIR
chr5	12655069	12655767	L1MEf	LINE/L1
chr12	79940093	79940619	MER41A	LTR/ERV1
chr13	78507358	78513514	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	130513456	130519367	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	8950549	8950695	AluSz	SINE/Alu
chr7	31506474	31511993	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	64127876	64133645	L1PA7	LINE/L1
chr2	69665229	69665374	MER5A	DNA/hAT-Charlie
chr1	200447516	200447767	L2b	LINE/L2
chr13	43430636	43430802	MLT1A	LTR/ERV1-MaLR
chr1	93727418	93729363	THE1D THE1D-int	LTR/ERV1-MaLR
chr11	6091052	6097114	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	9079523	9080341	L2c	LINE/L2
chr13	43430264	43430560	AluJr4	SINE/Alu

chr18	51838319	51842291	L1PA16	LINE/L1
chr11	67527156	67532835	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	96125930	96126289	L1M5	LINE/L1
chr16	13446440	13451918	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	16598173	16598538	LTR7	LTR/ERV1
chr2	109004760	109005401	L2d2	LINE/L2
chr5	126174536	126175019	L1MEd	LINE/L1
chr6	114727790	114728172	L1PB1	LINE/L1
chr5	5515636	5521277	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr10	118588561	118588912	THE1B	LTR/ERV1-MaLR
chr10	104968394	104971155	HERVH-int	LTR/ERV1
chr6	14292487	14292642	LTR33	LTR/ERV1
chrX	129344808	129344989	MER5A	DNA/hAT-Charlie
chr1	55496626	55498904	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr22	38124757	38124917	L1MC1	LINE/L1
chrX	103014474	103014656	AluSp	SINE/Alu
chr13	43440026	43440233	LTR16A	LTR/ERV1
chr6	14297173	14303054	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr5	12623996	12626435	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr18	29383746	29390019	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	51757970	51758309	L2	LINE/L2
chr3	101350889	101360900	LTR6A HERVS71-int LTR6A	LTR/ERV1
chr12	9081354	9081747	L1ME3F	LINE/L1
chr19	39904903	39905513	L2b	LINE/L2
chr11	3468656	3478209	LTR5A HERVK-int LTR5A	LTR/ERV1
chr2	64477208	64477893	L2a	LINE/L2
chr2	219038743	219044609	LTR7B HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr12	73209892	73210370	LTR7	LTR/ERV1
chr8	12388514	12395551	MER11C HERVK11-int HERVK11-int HERVK11-int HERVK11-int MER11C	LTR/ERV1
chr11	131124430	131130174	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	8117325	8117633	AluSz	SINE/Alu
chrX	106295361	106298101	LTR17 HERV17-int HERV17-int	LTR/ERV1
chr2	155723741	155731072	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr7	131000001	131006360	L1PA8	LINE/L1
chrX	57243074	57245360	L1PB1	LINE/L1
chr6	33411857	33411974	L2a	LINE/L2
chr13	98294572	98300463	LTR7 HERVH-int HERVH-int HERVH-int	LTR/ERV1

			int HERVH-int HERVH-int LTR7	
chr4	139848990	139854697	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	189254350	189261963	L1PB3	LINE/L1
chr13	54890512	54892874	HERV9NC-int LTR12D	LTR/ERV1
chr15	25280971	25281449	L1ME3G	LINE/L1
chr12	79942812	79943126	AluSx1	SINE/Alu
chr1	232253861	232259691	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	62525209	62525813	MER21B	LTR/ERVL
chr22	38124677	38124753	AluJr	SINE/Alu
chrX	130923990	130925378	L1M4	LINE/L1
chr9	103154467	103156164	SVA_A	Retroposon/SVA
chr11	121180996	121181164	MLT1A1	LTR/ERVL-MaLR
chr14	69585390	69585626	MIR	SINE/MIR
chrX	37339302	37344090	HERVIP10FH-int LTR10F	LTR/ERV1
chr13	54893134	54893354	MamTip2b	DNA/hAT-Tip100
chr1	113365855	113366163	AluY	SINE/Alu
chr15	101589540	101589593	MIRc	SINE/MIR
chr1	185917411	185923348	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	77687309	77689358	THE1B THE1B-int THE1B	LTR/ERVL-MaLR
chr1	43197143	43197301	L1MC5a	LINE/L1
chr9	96122228	96122402	MER4B-int	LTR/ERV1
chr9	35855397	35855690	AluSp	SINE/Alu
chr13	43438728	43438859	FLAM_C	SINE/Alu
chr12	8078713	8078986	AluSx1	SINE/Alu
chr3	78633483	78638069	HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr4	93192643	93198799	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	137725722	137725972	L2c	LINE/L2
chr10	64932262	64932687	L2a	LINE/L2
chr12	8122385	8122691	AluSx	SINE/Alu
chr8	12395724	12395938	X30_DNA	DNA
chr13	43425621	43425833	L1ME4c	LINE/L1
chr13	43439877	43440018	BLACKJACK	DNA/hAT-Blackjack
chr3	191788898	191794647	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr15	25276999	25277270	L1MEf	LINE/L1
chr19	9857983	9859333	L1PA6	LINE/L1
chrX	53100457	53100917	MER20B	DNA/hAT-Charlie
chr4	167637276	167643205	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1

chr13	48575742	48575820	L2a	LINE/L2
chr3	8218718	8224403	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	114741956	114742326	L2c	LINE/L2
chr14	96439368	96445197	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	130867454	130867746	L1MB5	LINE/L1
chr17	47126004	47126334	MER1B	DNA/hAT-Charlie
chr11	124819047	124819980	HSMAR1	DNA/TcMar-Mariner
chr15	25280040	25280236	MER58A	DNA/hAT-Charlie
chr1	43424936	43425055	MIR	SINE/MIR
chr4	186348632	186348935	AluSx1	SINE/Alu
chr15	25273115	25273411	AluSq2	SINE/Alu
chr7	124898423	124898819	MLT2B4 MLT2B4	LTR/ERV1
chr1	43446834	43447008	L2b	LINE/L2
chr3	42631016	42631320	MER1B	DNA/hAT-Charlie
chr15	25268129	25268422	AluSx	SINE/Alu
chrX	115013148	115013644	MER4A	LTR/ERV1
chr7	143304833	143305010	HAL1ME	LINE/L1
chr9	99976776	99982296	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	125211553	125212937	LTR7Y HERVH-int	LTR/ERV1
chr11	27703965	27710419	L1PA7	LINE/L1
chr6	46129980	46130548	Tigger22N1	DNA/TcMar-Tigger
chr7	124898882	124899380	LTR7	LTR/ERV1
chr9	76700499	76706352	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	69666384	69667279	LTR12C	LTR/ERV1
chrX	130846053	130851792	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr12	8950204	8950492	AluSx	SINE/Alu
chr6	114737968	114738211	L2	LINE/L2
chr5	34165093	34165551	MLT2B3	LTR/ERV1
chr14	86198781	86204945	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chrX	70150004	70150165	MIRb	SINE/MIR
chr12	111376182	111376337	L2a	LINE/L2
chr3	42625046	42625691	MLT2B3	LTR/ERV1
chr12	79942411	79942724	AluJr	SINE/Alu
chr3	108410267	108410605	MER39	LTR/ERV1
chr2	84016071	84019824	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	69665381	69665678	AluJr	SINE/Alu

chr13	43426064	43426273	MamRTE1	LINE/RTE-BovB
chr1	43446229	43446754	LTR48	LTR/ERV1
chr3	97514277	97516583	HAL1	LINE/L1
chr9	35003290	35009330	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr20	292462	293017	L1MC3	LINE/L1
chr6	14292975	14293095	MIR	SINE/MIR
chr11	70060778	70066262	HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	43440991	43441292	AluJr	SINE/Alu
chrX	97542856	97544245	HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr4	62629936	62635743	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr18	40317011	40322310	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr18	14074465	14075238	THE1B-int THE1B	LTR/ERV1-MaLR
chr8	73937706	73938015	AluY	SINE/Alu
chr1	193209062	193211771	L1MA4A	LINE/L1
chr6	28395893	28396513	L2c	LINE/L2
chr12	73102783	73107205	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int	LTR/ERV1
chr3	42624616	42625045	L2c	LINE/L2
chr15	93589271	93589745	MLT1D	LTR/ERV1-MaLR
chr11	118592691	118592779	SVA_F	Retroposon/SVA
chr4	42287455	42294913	LTR17 HERV17-int HERV17-int HERV17-int HERV17-int LTR17	LTR/ERV1
chr13	43441738	43442136	BLACKJACK	DNA/hAT-Blackjack
chr1	68851687	68857675	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr11	3514187	3520281	L1PA4	LINE/L1
chr1	231965418	231971394	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr7	86952700	86956041	MER61-int	LTR/ERV1
chr5	120033241	120039106	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	239264536	239270362	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr22	38123971	38124066	L1MB7	LINE/L1
chr22	31745846	31746227	L1MB5	LINE/L1
chr9	12958985	12959098	LTR77	LTR/ERV1
chr16	28299281	28300247	LTR16B2 ERV3-16A3_l-int	LTR/ERV1
chr2	58502511	58503292	LTR17	LTR/ERV1
chr2	69665687	69665751	MER5A	DNA/hAT-Charlie
chr11	121182360	121182466	MIR	SINE/MIR
chr3	42628011	42628774	L2	LINE/L2

chr11	96458635	96464674	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	200996981	200997198	MIRb	SINE/MIR
chr8	12400290	12400732	MLT1F2	LTR/ERV1-MaLR
chr1	55488381	55494042	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	96124989	96125290	AluSz	SINE/Alu
chr18	75289712	75295837	L1PA6	LINE/L1
chr11	121181165	121181468	AluY	SINE/Alu
chr8	89754446	89759757	LTR7B HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr3	98115593	98116040	LTR7	LTR/ERV1
chr3	120120433	120120717	AluJb	SINE/Alu
chr6	126022994	126028909	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	178183290	178184565	L1MB8	LINE/L1
chr5	70435447	70435741	MLT1F2-int	LTR/ERV1-MaLR
chr1	55514933	55515181	L3	LINE/CR1
chr9	96121871	96122146	MER4-int	LTR/ERV1
chr10	64933201	64933508	AluJr4	SINE/Alu
chr9	83623999	83630196	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr1	93593833	93594131	AluSx	SINE/Alu
chr6	33418747	33419100	MamRep434	DNA/TcMar-Tigger
chr2	188397007	188403469	L1PA7	LINE/L1
chr20	296972	297370	L1MB8	LINE/L1
chr13	43441593	43441732	ERV3-16A3_LTR	LTR/ERV1
chrX	93953819	93960088	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7 LTR7	LTR/ERV1
chr1	53890009	53895701	LTR7B HERVH-int HERVH-int HERVH-int HERVH-int LTR7B	LTR/ERV1
chr1	150621550	150622083	L1MB4	LINE/L1
chr5	34169817	34170725	L1MA10	LINE/L1
chr15	25277280	25277477	MER20	DNA/hAT-Charlie
chrX	102746080	102746579	LTR45B	LTR/ERV1
chr3	167149074	167154918	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr9	2287794	2288567	LTR1B	LTR/ERV1
chr11	67612629	67620956	LTR2C HERVE-int	LTR/ERV1
chr18	54722473	54722674	MIR	SINE/MIR
chr8	73935621	73935865	L1MEg1	LINE/L1
chrX	103007917	103008020	MIRc	SINE/MIR
chr6	6036332	6036781	LTR7	LTR/ERV1
chr17	43345919	43346225	L1ME5	LINE/L1
chr13	54887037	54887807	LTR12D	LTR/ERV1

chr13	54895296	54896028	L1PBb	LINE/L1
chr2	173478463	173479560	MER52C	LTR/ERV1
chr5	179739598	179739770	AluJb	SINE/Alu
chr3	164059969	164065637	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr16	77773030	77773616	MER41B	LTR/ERV1
chr12	54730526	54730831	AluSx4	SINE/Alu
chr10	27754239	27759866	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr2	173476041	173476580	L1MD	LINE/L1
chrX	131202782	131203310	L2a	LINE/L2
chr1	222122106	222125444	HERVH-int	LTR/ERV1
chr11	121179830	121180169	MLT1J2	LTR/ERV1-MaLR
chr11	118600884	118602564	HERVH-int LTR7	LTR/ERV1
chr1	241597189	241603182	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr3	170535404	170541550	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr8	8025304	8025455	MER5A1	DNA/hAT-Charlie
chr5	18668952	18674707	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr13	43430803	43433427	L1PA3	LINE/L1
chr10	118582673	118584095	L1MB7	LINE/L1
chr13	54894539	54894915	MSTB	LTR/ERV1-MaLR
chr13	54813916	54814677	L2a	LINE/L2
chrX	53092014	53093066	MST-int	LTR/ERV1-MaLR
chr3	65356901	65359300	Tigger1	DNA/TcMar-Tigger
chr9	100000081	100000353	AluSg4	SINE/Alu
chr11	3494759	3502941	LTR2C HERVE-int HERVE-int HERVE-int	LTR/ERV1

Table 3: Retrotransposon signature specific to CD34+ hematopoietic stem cells

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Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chr17	56351369	56351513	L2d2	LINE/L2
chr17	56351224	56351334	MIRc	SINE/MIR
chr17	56351899	56352209	AluJb	SINE/Alu
chr17	56352747	56352884	MIRb	SINE/MIR
chr17	56356025	56356103	MamTip2	DNA/hAT-Tip100
chr17	56353148	56353492	L2d2	LINE/L2
chr17	56352218	56352523	AluY	SINE/Alu
chrX	65239797	65240011	MER103C	DNA/hAT-Charlie
chr17	56354616	56354813	MER3	DNA/hAT-Charlie

chrX	65238052	65238281	MIRb	SINE/MIR
chr12	10135249	10135855	L1PB4	LINE/L1
chr17	56353523	56353670	MER117	DNA/hAT-Charlie
chr17	56354188	56354482	AluSx3	SINE/Alu
chr4	75111199	75115930	L1PA3	LINE/L1
chr1	161567632	161568601	MER34B-int MER34B-int MER34B-int	LTR/ERV1
chr1	36942054	36942230	L2c	LINE/L2
chr15	95026464	95027085	L1PA13	LINE/L1
chr6	137109263	137110081	L1P4	LINE/L1
chr11	47402680	47403242	L1PB4	LINE/L1
chr7	150454261	150454937	L1MC2	LINE/L1
chr14	106396650	106396956	L1MA7	LINE/L1
chr10	20011009	20011138	L2b	LINE/L2
chr4	154609520	154615579	MER9a3 HERVK9-int HERVK9-int MER9a3	LTR/ERVK
chr11	47403552	47403850	AluJb	SINE/Alu
chr3	148610758	148612583	L1MDa	LINE/L1
chr1	36942096	36942256	L2b	LINE/L2
chr10	20011238	20011548	AluJr	SINE/Alu
chr17	56349655	56349829	MIRb	SINE/MIR
chr11	59832893	59834361	L2a	LINE/L2
chr15	50159765	50160367	L1MEj	LINE/L1
chr17	3815137	3815425	MLT1K	LTR/ERV1-MaLR
chr1	161565452	161565916	MER57F	LTR/ERV1
chr1	161566844	161567497	MER34B-int	LTR/ERV1
chrX	65235631	65235772	MIR3	SINE/MIR
chr1	161568746	161569213	LTR54	LTR/ERV1
chrX	65237812	65237940	MIR3	SINE/MIR
chr12	54938196	54938500	L1MD2	LINE/L1
chr12	54938977	54939205	MIRc	SINE/MIR
chr4	75195915	75196170	AluJr	SINE/Alu
chrX	65235999	65236162	MIR3	SINE/MIR
chr1	67237811	67238230	MSTB	LTR/ERV1-MaLR
chr6	32554151	32554877	L2a	LINE/L2
chr15	57597637	57597687	L2a	LINE/L2
chr6	36687219	36687733	L2a	LINE/L2
chr11	60159407	60159931	L1MEd	LINE/L1
chr1	192133805	192134803	MER11B	LTR/ERVK
chr12	69745517	69745712	L1ME4a	LINE/L1
chr19	52021583	52021885	AluSz	SINE/Alu
chr15	50160397	50160915	L1MEj	LINE/L1
chr6	6711038	6711268	MER92-int	LTR/ERV1

chr6	6711666	6712036	MLT1B	LTR/ERV1-MaLR
chr8	24195357	24195591	L1M5	LINE/L1
chr9	137794068	137795410	L1MDa	LINE/L1
chr3	46405041	46407074	Tigger1	DNA/TcMar-Tigger
chr11	47403912	47404041	L2c	LINE/L2
chr4	154618028	154619904	MER57A-int	LTR/ERV1
chr22	37326095	37326347	MIRb	SINE/MIR
chrX	37654306	37654785	LTR16A2	LTR/ERV1
chr4	154629683	154630287	MER61F	LTR/ERV1
chr12	54939862	54940166	AluSz	SINE/Alu
chr12	10093786	10094537	L2a	LINE/L2
chr12	54938501	54938807	AluSx	SINE/Alu
chr1	161485978	161486946	MER34B-int MER34B-int	LTR/ERV1
chr2	43216616	43222642	L1PA3	LINE/L1
chr17	33695255	33696609	L1MA1	LINE/L1
chr1	67240186	67240596	LTR33	LTR/ERV1
chr19	52021886	52021965	L1MEd	LINE/L1
chr19	15974066	15974209	MIR3	SINE/MIR
chr11	59864075	59864389	AluSx3	SINE/Alu
chr15	50164526	50165244	L1MD3	LINE/L1
chr15	57592352	57592476	MIRb	SINE/MIR
chr19	8557483	8557598	L1MA6	LINE/L1
chr2	209720102	209722995	L1PA15	LINE/L1
chr17	33696601	33699647	L1MA1	LINE/L1
chr4	38794210	38794565	L1ME4c	LINE/L1
chr1	67239466	67239619	MamGypLTR4	LTR/Gypsy
chr19	855158	855289	AluJb	SINE/Alu
chr10	20011137	20011224	MIR3	SINE/MIR
chr6	36700122	36700285	L1ME4a	LINE/L1
chr4	38793616	38793757	MIRb	SINE/MIR
chr6	32555189	32555728	L2a	LINE/L2
chr1	161569266	161569484	MER34B-int	LTR/ERV1
chr17	56348578	56348634	MER91A	DNA/hAT-Tip100
chr15	57597159	57597267	MIRb	SINE/MIR
chr4	154621458	154622279	L1MEg	LINE/L1
chr4	154615689	154617732	L1MA3	LINE/L1
chr12	69742775	69743082	AluSx3	SINE/Alu
chr1	67238537	67238713	MIRb	SINE/MIR
chr12	10090282	10090664	MLT1B	LTR/ERV1-MaLR
chr17	56346313	56346482	MIRc	SINE/MIR
chr12	54938808	54938955	L1MD2	LINE/L1

chr11	47403851	47403911	L1PB4	LINE/L1
chr8	24197188	24197300	L2b	LINE/L2
chrX	65240235	65240380	MIR3	SINE/MIR
chr7	150455361	150455657	AluSc	SINE/Alu
chr2	68540935	68541413	L2c	LINE/L2
chr3	121840999	121842886	THE1C-int THE1C	LTR/ERV1-MaLR
chr4	38797248	38797632	LTR16C	LTR/ERV1
chr7	150456135	150456732	L1MC	LINE/L1
chr10	17361513	17361591	X9_LINE	LINE/L1
chrX	65237012	65237187	MIRc	SINE/MIR
chr7	150455881	150456341	L1MEc	LINE/L1
chr11	59943765	59943950	MIR3	SINE/MIR
chr9	137801234	137801340	MIRc	SINE/MIR
chrX	30576208	30576511	AluSq2	SINE/Alu
chr4	95222664	95223285	L1MC5	LINE/L1
chr12	69744558	69744849	AluJr	SINE/Alu
chr17	3816425	3816720	AluSx	SINE/Alu
chrX	30575678	30576016	MER58B	DNA/hAT-Charlie
chr12	10127419	10129678	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr21	39601832	39606061	L1MB8	LINE/L1
chr7	150456780	150457049	L1MC	LINE/L1
chr17	56344333	56344481	MIR	SINE/MIR
chr6	6711277	6711665	MER92C	LTR/ERV1
chr13	21885590	21888415	ERV1-E-int	LTR/ERV1
chr3	148612984	148613438	L2a	LINE/L2
chr2	113105784	113111580	Harlequin-int Harlequin-int Harlequin-int LTR2	LTR/ERV1
chr2	102031613	102031964	MLT1A0	LTR/ERV1-MaLR
chr12	116958111	116958623	L2a	LINE/L2
chr12	69745166	69745288	L1ME4a	LINE/L1
chr4	95227842	95228549	HAL1	LINE/L1
chr2	102032085	102032537	L2b	LINE/L2
chr8	24194375	24194527	L1M6B	LINE/L1
chr1	25420713	25421179	MLT1J	LTR/ERV1-MaLR
chr1	67239247	67239409	MIR	SINE/MIR
chr8	134048211	134048645	L2b	LINE/L2
chr8	27306473	27306681	MER20	DNA/hAT-Charlie
chr19	15975266	15975570	AluSx3	SINE/Alu
chr1	161565920	161566116	MER34B-int	LTR/ERV1
chr8	24194944	24195091	L2b	LINE/L2
chr17	62468640	62468913	Tigger3a	DNA/TcMar-Tigger

chr11	59830835	59831210	L1PB	LINE/L1
chr1	158581974	158582092	L2c	LINE/L2
chr11	60151596	60151986	L2a	LINE/L2
chr4	75144235	75144495	MLT1H	LTR/ERV1-MaLR
chr1	67238916	67239023	MLT1K	LTR/ERV1-MaLR
chr6	110800274	110800685	MSTB	LTR/ERV1-MaLR
chr6	6732128	6733619	L1MC1	LINE/L1
chr17	3802498	3802660	FRAM	SINE/Alu
chr19	8557599	8557900	AluSx1	SINE/Alu
chr9	93647278	93648704	L1M2	LINE/L1
chr11	33897482	33897974	L2a	LINE/L2
chr1	158582174	158582345	L2c	LINE/L2
chr1	192156108	192156321	MIRb	SINE/MIR
chr2	102969720	102970703	L1M5	LINE/L1
chr1	158585896	158586732	L1MA4	LINE/L1
chr6	32549892	32550091	MIR	SINE/MIR
chr6	32624593	32624691	Tigger13a	DNA/TcMar-Tigger
chr15	50166253	50166672	L2a	LINE/L2
chr19	845866	845973	AluYc3	SINE/Alu
chr1	89587852	89590038	L1MC4a	LINE/L1
chr4	154607494	154608571	L1MEg	LINE/L1
chr9	124217907	124218003	L2b	LINE/L2
chr11	47379123	47379415	AluSq2	SINE/Alu
chr4	38815931	38818311	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr19	854867	855151	AluSc8	SINE/Alu
chr11	59986091	59991426	HERV1-int MLT2A2	LTR/ERV1
chr1	158592241	158592434	MIRc	SINE/MIR
chr15	50125417	50131564	L1PA4	LINE/L1
chr1	25422666	25423012	MamRep4096	DNA/hAT-Tip100
chr8	24209804	24210164	MLT1A	LTR/ERV1-MaLR
chr17	56346871	56346951	L2b	LINE/L2
chr1	203745499	203745842	L1MC4	LINE/L1
chr3	148618521	148618880	MLT1J	LTR/ERV1-MaLR
chr17	62469955	62470204	L1ME1	LINE/L1
chr1	206240600	206240732	MIR3	SINE/MIR
chr6	137107033	137107162	Tigger16a	DNA/TcMar-Tigger
chr8	24196541	24196655	MIRc	SINE/MIR
chr11	1929183	1929422	MIRb	SINE/MIR
chr4	38793351	38793557	MIR	SINE/MIR
chr17	7044911	7045529	LTR8	LTR/ERV1
chr11	5247320	5247415	L1MA6	LINE/L1

chr6	32484975	32485094	L1MA8	LINE/L1
chr12	54939734	54939857	AluJo	SINE/Alu
chr19	55149007	55149576	L1M5	LINE/L1
chr6	32553154	32553301	MIRb	SINE/MIR
chr15	50185572	50186008	L1MB2	LINE/L1
chr9	124217697	124217816	MIR	SINE/MIR
chr1	158804271	158808967	L1MB2	LINE/L1
chr17	3816357	3816407	L3	LINE/CR1
chr8	24196359	24196472	MIR	SINE/MIR
chr9	137796645	137797094	L1MEg	LINE/L1
chr6	6731045	6731575	MLT1F1	LTR/ERV1-MaLR
chr4	175421319	175422020	L1MC1	LINE/L1
chr1	161568630	161568722	MER34-int	LTR/ERV1
chr6	6698919	6699358	L1MC1	LINE/L1
chr10	17488186	17488646	L1M6	LINE/L1
chr6	110796808	110796894	MIR	SINE/MIR
chr17	3810024	3810524	MLT1K	LTR/ERV1-MaLR
chr1	67241293	67241555	L2b	LINE/L2
chr12	10094623	10094898	L2c	LINE/L2
chr20	48894680	48895121	L2a	LINE/L2
chr14	52777785	52778277	MLT2B1	LTR/ERV1
chr5	131621495	131623496	LTR57-int LTR57	LTR/ERV1
chr16	21651242	21651558	AluSx3	SINE/Alu
chr6	6712037	6712193	MER92C	LTR/ERV1
chr1	161487093	161487558	LTR54	LTR/ERV1
chr2	102030728	102031036	AluSz	SINE/Alu
chr1	161485187	161485858	MER34B-int	LTR/ERV1
chr8	27305409	27305582	L2d2	LINE/L2
chr6	6730515	6730891	HAL1	LINE/L1
chr17	3817484	3817573	MIRb	SINE/MIR
chr7	37853328	37854487	L1PA15	LINE/L1
chr6	46666320	46666378	L1MEf	LINE/L1
chr19	847024	847316	AluJr	SINE/Alu
chr1	247688440	247689267	MER21B	LTR/ERV1
chr10	134668152	134671008	L1MB5	LINE/L1
chr1	248061633	248069197	LTR2 Harlequin-int Harlequin-int LTR2	LTR/ERV1
chr4	75140663	75141763	L1PA10	LINE/L1
chr2	158270632	158270823	MIRb	SINE/MIR
chr3	45117847	45120139	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr11	59945168	59945271	L1MC3	LINE/L1
chr4	38824818	38825053	Tigger3b	DNA/TcMar-Tigger

chr2	43222710	43223587	L1ME1	LINE/L1
chr17	3818010	3818123	MIR3	SINE/MIR
chr19	15963704	15964158	MLT1C2	LTR/ERV1-MaLR
chr10	20013654	20014088	L1MB4	LINE/L1
chr11	123948812	123949732	MER21A	LTR/ERV1
chr1	206241713	206242008	AluSz	SINE/Alu
chr19	856297	856407	AluJb	SINE/Alu
chr6	137109007	137109259	MER58B	DNA/hAT-Charlie
chr19	844820	844946	AluJr	SINE/Alu
chr1	192132135	192132357	MIRc	SINE/MIR
chr19	40224137	40224471	L1ME4c	LINE/L1
chr2	102963882	102964126	L2d2	LINE/L2
chr9	137798087	137798634	MamRep1151	LTR?
chr19	40225975	40226254	AluJb	SINE/Alu
chr8	24195651	24195782	L1M5	LINE/L1
chr5	130559872	130560439	L2	LINE/L2
chr6	29466214	29467595	L1M1	LINE/L1
chr19	844696	844819	L2a	LINE/L2
chr7	38296252	38296527	AluSx	SINE/Alu
chr11	59940906	59941113	MIRc	SINE/MIR
chr11	123954498	123955318	L1MA7	LINE/L1
chr2	68540316	68540934	L1ME1	LINE/L1
chr15	32754093	32754396	AluSx1	SINE/Alu
chr2	124490609	124496628	L1MB4	LINE/L1
chr2	102033656	102033962	AluJr4	SINE/Alu
chr2	102030044	102030191	MIRb	SINE/MIR
chr1	153331105	153331381	L2a	LINE/L2
chr19	854163	854446	AluSx3	SINE/Alu
chr12	63961124	63962411	L1ME1	LINE/L1
chr11	33898292	33898522	MIRb	SINE/MIR
chr6	6712801	6712939	X7B_LINE	LINE/CR1
chr4	38790652	38790966	MER63D	DNA/hAT-Blackjack
chr11	59942096	59942245	LTR101_Mam	LTR/ERV1
chr19	51676352	51676550	L2c	LINE/L2
chr1	192155414	192155483	L2c	LINE/L2
chr10	20014464	20016031	L1MB4	LINE/L1
chr20	30670704	30671169	MLT1D	LTR/ERV1-MaLR
chr1	192133632	192133804	L1MC3	LINE/L1
chr2	102970989	102971794	L1M5	LINE/L1
chr15	50161120	50161408	AluSq2	SINE/Alu
chr15	50163276	50163460	MIRb	SINE/MIR

chr11	59832178	59832535	L2a	LINE/L2
chr1	36942257	36942569	AluJb	SINE/Alu
chr15	50162196	50162477	L1MC4a	LINE/L1
chr6	68590889	68598779	LTR7C HERVH-int HERVH-int	LTR/ERV1
chr1	25423039	25423252	MER20	DNA/hAT-Charlie
chr2	43230933	43231148	MLT1B	LTR/ERV1-MaLR
chr11	59831211	59831498	L1PB1	LINE/L1
chr4	38796309	38796416	L2d2	LINE/L2
chr1	25423992	25424261	L1MEf	LINE/L1
chr11	59943514	59943579	MADE1	DNA/TcMar-Mariner
chr1	203745844	203745967	MER21C	LTR/ERV1
chr3	52549801	52549924	MIR3	SINE/MIR
chr1	25421546	25421728	L2b	LINE/L2
chr12	117098348	117099725	LTR12C	LTR/ERV1
chr14	22887039	22887229	MIRc	SINE/MIR
chr3	148613915	148614202	Tigger19a	DNA/TcMar-Tigger
chr6	32552547	32552703	L2b	LINE/L2
chr17	62469043	62469184	L1MEh	LINE/L1
chr19	845248	845417	AluJr	SINE/Alu
chr1	206242602	206242831	L3b	LINE/CR1
chr11	60160412	60160605	AluSx3	SINE/Alu
chr11	59976533	59977081	MLT1D	LTR/ERV1-MaLR
chr15	95025417	95026353	L2	LINE/L2
chr6	2836944	2837120	AluJb	SINE/Alu
chr4	75074930	75081376	L1PA7	LINE/L1
chr16	11024580	11024742	LTR16C	LTR/ERV1
chr4	95221734	95222129	L2b	LINE/L2
chr15	57592490	57592770	AluSg	SINE/Alu
chr19	8561327	8561638	AluSz	SINE/Alu
chr19	54863512	54863693	MER31A	LTR/ERV1
chr6	36688626	36688855	L2d	LINE/L2
chr20	61065857	61066303	MLT2A2	LTR/ERV1
chr20	30682797	30683064	L1MB8	LINE/L1
chr2	182377713	182378067	L2b	LINE/L2
chr6	6730360	6730506	MLT1L	LTR/ERV1-MaLR
chr5	130545533	130545936	MSTB	LTR/ERV1-MaLR
chr11	60154257	60154468	MIRb	SINE/MIR
chrX	55048738	55049472	L1ME3G	LINE/L1
chr8	2520655	2521463	L1PA8	LINE/L1
chr14	21254696	21255003	FordPrefect_a	DNA/hAT-Tip100
chr6	36686689	36686932	AluYc	SINE/Alu

chr6	6785876	6787521	HAL1	LINE/L1
chr4	95229128	95229463	Tigger4b	DNA/TcMar-Tigger
chr2	185459380	185459927	Charlie29a	DNA/hAT-Charlie
chr2	190440499	190440581	MIR3	SINE/MIR
chr10	17493141	17493576	L1PB4	LINE/L1
chr8	24193815	24194122	AluY	SINE/Alu
chr4	154626986	154627203	MamSINE1	SINE/tRNA-RTE
chr6	32622514	32622832	AluSx	SINE/Alu
chr3	121681119	121686223	L1PA12	LINE/L1
chr19	52020158	52020611	L1PA13	LINE/L1
chr5	149786931	149787135	MamRep1879	DNA/hAT-Tip100?
chr15	57596761	57597108	L1MD3	LINE/L1
chr14	52778741	52779015	MER115	DNA/hAT-Tip100
chr1	36943751	36943847	MER58C	DNA/hAT-Charlie
chr10	17356507	17357854	L1ME1	LINE/L1
chr14	106393549	106393973	MLT1D	LTR/ERV1-MaLR
chr6	32616051	32618621	L1PA6	LINE/L1
chr6	32487702	32487901	MIR	SINE/MIR
chr1	25421205	25421327	L3	LINE/CR1
chr11	59975547	59976036	MLT1E MLT1E	LTR/ERV1-MaLR
chr19	15963392	15963498	MIRb	SINE/MIR
chr8	134048081	134048352	L2b	LINE/L2
chr6	137107230	137107540	AluSz	SINE/Alu
chr4	106060155	106060377	MIRc	SINE/MIR
chr11	60158999	60159109	L1MEd	LINE/L1
chr6	32555953	32556245	AluJb	SINE/Alu
chr19	8559991	8560283	AluSx	SINE/Alu
chr1	36944167	36944451	AluJb	SINE/Alu
chr4	95227458	95227836	HAL1	LINE/L1
chr20	1521291	1526977	L1PA7	LINE/L1
chr11	73120163	73120503	L2c	LINE/L2
chr4	38794944	38795077	MIRb	SINE/MIR
chr9	136134193	136134543	L1MB3	LINE/L1
chr19	51674109	51675151	L1MB7	LINE/L1
chr19	51635196	51635574	MSTB1	LTR/ERV1-MaLR
chr8	65713176	65713735	MER49	LTR/ERV1
chr19	52031771	52031954	MLT1C	LTR/ERV1-MaLR
chr1	158590785	158590902	L2d	LINE/L2
chr5	71736781	71736942	Charlie15a	DNA/hAT-Charlie
chr6	32552779	32552847	MER53	DNA/hAT
chr19	40222345	40222520	L2b	LINE/L2

chr4	154629022	154629181	MLT2A1	LTR/ERV1
chr8	24194139	24194310	L1MA8	LINE/L1
chr1	36931376	36931461	AmnSINE1	SINE/5S-Deu-L2
chr17	62466065	62466208	L1MB3	LINE/L1
chr11	60155732	60155845	MIR3	SINE/MIR
chr3	148618940	148619105	MIR1_Amn	SINE/MIR
chr12	10126276	10127182	L2a	LINE/L2
chr1	92944970	92945112	L2a	LINE/L2
chr1	158590940	158591145	Tigger19a	DNA/TcMar-Tigger
chr17	62467791	62467908	AluJo	SINE/Alu
chr19	8560284	8560423	AluSz	SINE/Alu
chr1	158625587	158626000	L2c	LINE/L2
chr2	43228427	43228495	L2c	LINE/L2
chr4	38824466	38824817	THE1B	LTR/ERV1-MaLR
chr9	137803189	137803496	AluSc8	SINE/Alu
chr1	153332858	153332988	MIRb	SINE/MIR
chr4	75196174	75196662	LTR15	LTR/ERV1
chr1	92943182	92943360	MIRc	SINE/MIR
chr4	80622560	80624218	L1MDa	LINE/L1
chr4	154630654	154630832	L2a	LINE/L2
chr4	75135895	75137648	L1PA5	LINE/L1
chr10	73516569	73516810	MamRep434	DNA/TcMar-Tigger
chr4	95228628	95229127	HAL1	LINE/L1
chrY	21246661	21249383	HERV17-int HERV17-int LTR17	LTR/ERV1
chr1	25421885	25422277	L3	LINE/CR1
chr21	15886259	15886655	LTR16B	LTR/ERV1
chr12	47603057	47603277	AluSx	SINE/Alu
chr11	60154707	60154818	MER81	DNA/hAT-Blackjack
chr11	1920224	1922126	MER57A-int	LTR/ERV1
chr6	110800159	110800273	L1M4	LINE/L1
chr1	111435932	111436243	AluSp	SINE/Alu
chr6	32553740	32553838	L2a	LINE/L2
chr19	854512	854646	AluJb	SINE/Alu
chr9	93644937	93646416	L1M2	LINE/L1
chr15	50177230	50177729	L2a	LINE/L2
chr6	25988712	25988967	AluSz6	SINE/Alu
chr20	5476260	5476509	L2c	LINE/L2
chrX	37648069	37648664	MLT1E1A	LTR/ERV1-MaLR
chr13	49109920	49110045	L2	LINE/L2
chr19	8561018	8561321	AluSg	SINE/Alu
chr1	36943665	36943740	L3	LINE/CR1

chr12	54683221	54683454	AluSz	SINE/Alu
chr11	72958093	72958914	L1MC5a	LINE/L1
chr4	154621042	154621457	MSTB	LTR/ERV1-MaLR
chr16	2869629	2869836	MIR	SINE/MIR
chr11	59972741	59972894	L2b	LINE/L2
chr1	161567447	161567507	LTR57-int	LTR/ERV1
chr10	70857928	70858248	L1MB7	LINE/L1
chr4	95226991	95227226	MIR	SINE/MIR
chr9	136129790	136129861	AluJr	SINE/Alu
chr17	56369441	56371189	L1MEf	LINE/L1
chr3	130582436	130584698	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr5	130544985	130545227	LTR43	LTR/ERV1
chr12	10091817	10092192	L2c	LINE/L2
chr4	95229464	95229700	HAL1	LINE/L1
chr11	60152257	60152446	L3	LINE/CR1
chr15	57597778	57598078	AluSx	SINE/Alu
chr22	37257616	37257904	L2a	LINE/L2
chr4	38794103	38794201	FRAM	SINE/Alu
chr1	202117976	202118278	AluSx1	SINE/Alu
chr18	43596580	43596765	MLT1E1	LTR/ERV1-MaLR
chr4	154627897	154628049	MIRb	SINE/MIR
chr18	43597599	43597891	L1MA8	LINE/L1
chr7	37855152	37856104	L1MCa	LINE/L1
chr13	32872578	32873145	L2a	LINE/L2
chr1	198680448	198681631	L1ME2	LINE/L1
chr5	360118	361084	MLT1A MLT1A-int	LTR/ERV1-MaLR
chr4	95213555	95213834	AluSx1	SINE/Alu
chr2	68614567	68614713	MER113A	DNA/hAT-Charlie
chr15	50539147	50539588	L1MA3	LINE/L1
chr12	66587093	66587688	L1MC3	LINE/L1
chr1	244471810	244472263	MLT1C	LTR/ERV1-MaLR
chr10	54265878	54268955	LOR1-int	LTR/ERV1
chr2	102037129	102037440	L2c	LINE/L2
chr6	6731752	6732007	AluSx1	SINE/Alu
chr15	50536060	50536218	L1MB4	LINE/L1
chr11	1923877	1924440	MER41A	LTR/ERV1
chr9	125141553	125141837	MamGypLTR3a	LTR/Gypsy
chr5	149785967	149786153	MIRc	SINE/MIR
chr11	59972946	59973202	MIR	SINE/MIR
chr2	182378105	182378283	L2b	LINE/L2
chr1	92945131	92945435	AluSz6	SINE/Alu

chr19	8557128	8557438	AluSq2	SINE/Alu
chr17	3803936	3804156	L2c	LINE/L2
chr19	52020670	52021582	L1MEd	LINE/L1
chr19	40226548	40226827	L1M5	LINE/L1
chr12	11983662	11984118	L3	LINE/CR1
chr17	4344400	4344536	Charlie2b	DNA/hAT-Charlie
chr10	17489823	17490099	AluSx1	SINE/Alu
chr15	50162064	50162137	L1MC4a	LINE/L1
chr2	127291493	127292139	MER39	LTR/ERV1
chr10	17358225	17358625	L1ME5	LINE/L1
chr3	107857117	107857320	Tigger1	DNA/TcMar-Tigger
chr5	71738142	71738313	MER5B	DNA/hAT-Charlie
chr15	50181377	50181543	MIR3	SINE/MIR
chr22	37257389	37257558	MIR3	SINE/MIR
chr19	51637122	51637386	L1ME2	LINE/L1
chr1	192131430	192131712	AluSz	SINE/Alu
chr6	137108657	137108762	MIRc	SINE/MIR
chr1	192146990	192147922	L2c	LINE/L2
chr11	33881950	33882027	MER5A	DNA/hAT-Charlie
chr5	71736484	71736612	MER94	DNA/hAT-Blackjack
chr12	66632104	66632285	MIRb	SINE/MIR
chrX	37653343	37653836	MER90	LTR/ERV1
chr12	66634669	66634893	Eutr10	LTR/ERV1?
chr6	36670775	36671134	MSTD	LTR/ERV1-MaLR
chr11	33897448	33897646	L2d	LINE/L2
chrY	21241824	21246375	LTR17 HERV17-int HERV17-int	LTR/ERV1
chr12	10093601	10093710	L2a	LINE/L2
chr5	363283	363981	LTR78	LTR/ERV1
chr10	73524168	73524504	MER102b	DNA/hAT-Charlie
chr11	33893310	33893414	MIR	SINE/MIR
chr4	95222421	95222618	L1MC5	LINE/L1
chr4	55600920	55601441	Charlie4a	DNA/hAT-Charlie
chr1	25423455	25423675	L1MEf	LINE/L1
chr6	36700967	36701253	AluJr	SINE/Alu
chr1	150721222	150722018	Tigger1	DNA/TcMar-Tigger
chr11	59941788	59942095	AluSg4	SINE/Alu
chr2	182379708	182379884	MER5A	DNA/hAT-Charlie
chr2	190446148	190446240	MIR3	SINE/MIR
chrX	37656895	37657126	MIRb	SINE/MIR
chr17	62465234	62465354	Charlie5	DNA/hAT-Charlie
chr1	158816831	158817100	L1PB3	LINE/L1

chr11	60151427	60151587	L2a	LINE/L2
chr19	15964258	15964920	L1PA10	LINE/L1
chr2	182365979	182367821	L2a	LINE/L2
chr2	102091228	102091338	MER5B	DNA/hAT-Charlie
chr17	62468316	62468612	AluSx	SINE/Alu
chr1	92943456	92943654	MIRb	SINE/MIR
chr11	33881567	33881634	MamTip2b	DNA/hAT-Tip100
chr2	102029904	102029996	MIRb	SINE/MIR
chr8	144276894	144278327	HERVL- int MLT2A2 MLT2A2 MLT2A2	LTR/ERV
chr20	30683065	30683359	AluSz	SINE/Alu
chr2	68610197	68610412	MIR	SINE/MIR
chr6	110799690	110799865	MamTip2	DNA/hAT-Tip100
chr15	50176036	50176370	Charlie1b	DNA/hAT-Charlie
chr20	30677528	30677770	L2c	LINE/L2
chr19	52032280	52032566	MLT1C	LTR/ERV-MaLR
chr12	10092067	10092481	L2a	LINE/L2
chr9	137802505	137802681	MER103C	DNA/hAT-Charlie
chr20	48894970	48895339	L2a	LINE/L2
chr15	50165388	50165741	L1ME4a	LINE/L1
chr17	3812081	3812308	MIRb	SINE/MIR
chr12	66622419	66622768	MER47A	DNA/TcMar-Tigger
chr18	43602814	43603240	L1PA13	LINE/L1
chr11	118078686	118078974	AluJb	SINE/Alu
chr10	17492440	17492740	AluSz	SINE/Alu
chr1	114398412	114398609	Charlie17a	DNA/hAT-Charlie
chr4	154628441	154628727	AluJb	SINE/Alu
chr18	43596224	43596345	AluSx3	SINE/Alu
chr3	132089392	132089686	AluSx	SINE/Alu
chr9	136135559	136136005	MLT1G1	LTR/ERV-MaLR
chr12	66634097	66634567	Eutr10	LTR/ERV?
chr17	72695487	72695878	MLT1C2	LTR/ERV-MaLR
chr10	70862071	70862263	L2a	LINE/L2
chr4	55601956	55602357	MLT1J	LTR/ERV-MaLR
chr2	182353278	182353584	AluYk2	SINE/Alu
chr1	161569659	161569991	MER57F	LTR/ERV1
chr11	60166487	60167264	L2b	LINE/L2
chrX	154015423	154015921	L1M5	LINE/L1
chr19	55095130	55097367	L1P2	LINE/L1
chr7	37801599	37802216	L1PA16	LINE/L1
chr19	44483507	44484564	MLT2C1 ERVL-B4-int ERVL-B4-int	LTR/ERV
chr11	57156969	57157121	MIRc	SINE/MIR

chr17	62399448	62399764	AluSq	SINE/Alu
chr1	244470745	244471281	L1MC4	LINE/L1
chr12	58351230	58357709	L1PB1	LINE/L1
chr2	68611923	68612046	MIRc	SINE/MIR
chr2	182379887	182380125	MIR	SINE/MIR
chr6	114188956	114189242	L1MC5	LINE/L1
chr20	30671338	30671587	MIR	SINE/MIR
chr17	7045530	7046020	LTR7B	LTR/ERV1
chr12	69744396	69744517	L1ME3Cz	LINE/L1
chrX	37652611	37652782	MIR3	SINE/MIR
chr1	25187804	25187972	MIRb	SINE/MIR
chr1	36943364	36943658	AluY	SINE/Alu
chr19	55402458	55402862	LTR101_Mam	LTR/ERV1
chr4	75142809	75143252	MER70B	LTR/ERV1
chr2	231255090	231255306	MIRb	SINE/MIR
chr19	36397609	36397918	AluSp	SINE/Alu
chr14	91718091	91718268	MIRc	SINE/MIR
chr11	60163514	60163734	MIRb	SINE/MIR
chr12	10093015	10093176	L2	LINE/L2
chr2	68611370	68611622	AluSp	SINE/Alu
chr2	68612252	68612398	L1MA6	LINE/L1
chr1	248085585	248086323	L1ME2z	LINE/L1
chr5	131624358	131625221	ERV1-E-int ERV1-E-int ERV1-E-int	LTR/ERV1
chr4	100785695	100785791	Zaphod2	DNA/hAT-Tip100
chr11	2335166	2335267	MER45A	DNA/hAT-Tip100
chrY	21742395	21748497	L1PA5	LINE/L1
chr9	137796343	137796644	AluSz	SINE/Alu
chrX	55048020	55048219	MIRb	SINE/MIR
chr20	30683562	30683645	L1ME3	LINE/L1
chr3	128201277	128201457	MER3	DNA/hAT-Charlie
chr1	117030657	117030998	L2d2	LINE/L2
chr12	54684715	54685023	AluSp	SINE/Alu
chr10	134666197	134667802	L1M5	LINE/L1
chr20	30680320	30680740	L2a	LINE/L2
chr19	52031955	52032279	AluSc	SINE/Alu
chr11	47401972	47402100	L2d2	LINE/L2
chr12	9865527	9865858	LTR2B	LTR/ERV1
chrY	14803386	14803767	MLT1F2	LTR/ERV1-MaLR
chr9	127149244	127149550	AluY	SINE/Alu
chr14	105401825	105402399	MLT1F2	LTR/ERV1-MaLR
chr11	33895057	33895130	L2d2	LINE/L2

chr22	37330414	37330597	L3b	LINE/CR1
chr12	66630813	66631018	MIRb	SINE/MIR
chr19	845762	845857	AluSp	SINE/Alu
chr11	60159110	60159406	AluSx	SINE/Alu
chr9	136126761	136127062	AluSx1	SINE/Alu
chr4	154608627	154609067	MER57D	LTR/ERV1
chr3	148606199	148606556	MamRTE1	LINE/RTE-BovB
chr5	66477732	66477908	Tigger16a	DNA/TcMar-Tigger
chr9	139601411	139602087	HERVL40-int	LTR/ERV1
chr8	66891241	66893521	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr20	61063679	61063897	L2c	LINE/L2
chr17	3814611	3814761	Charlie8	DNA/hAT-Charlie
chr1	153332157	153332464	AluSp	SINE/Alu
chr15	50131568	50136976	HERVK22-int LTR22A	LTR/ERV1
chr19	42120615	42120731	L2b	LINE/L2
chr17	62468971	62469045	L1ME4b	LINE/L1
chr12	66631815	66632011	L2d	LINE/L2
chr11	118077935	118078178	MIRb	SINE/MIR
chr11	34484597	34484857	Tigger19a	DNA/TcMar-Tigger
chr20	1541906	1542830	L1MC3	LINE/L1
chrY	2870478	2874472	LTR4 HERV3-int HERV3-int HERV3-int LTR4	LTR/ERV1
chr4	175454985	175455283	L2a	LINE/L2
chr19	40226263	40226405	MIR	SINE/MIR
chr6	36702864	36703064	MIR	SINE/MIR
chr15	50164386	50164480	MIRb	SINE/MIR
chr3	121840794	121840995	MIR	SINE/MIR
chr1	145134943	145136105	L1MB7	LINE/L1
chr18	61672278	61672537	L1ME3	LINE/L1
chr15	50550284	50550464	MIRb	SINE/MIR
chr6	137108828	137108969	MIR3	SINE/MIR
chr4	38793992	38794101	L1ME4c	LINE/L1
chr7	38297500	38297904	L1M5	LINE/L1
chr22	37260288	37260487	MER20	DNA/hAT-Charlie
chr20	48893322	48894135	L2a	LINE/L2
chrX	37657131	37657286	MIRb	SINE/MIR
chr5	130545436	130545528	L1ME1	LINE/L1
chrY	3006420	3007224	L1PA14	LINE/L1
chr1	247730463	247736938	L1PA8	LINE/L1
chr11	33882481	33882581	MIRc	SINE/MIR
chr21	15885898	15886256	L2a	LINE/L2
chr1	198723830	198724378	MLT1H	LTR/ERV1-MaLR

chr11	33882350	33882471	MER5A	DNA/hAT-Charlie
chr20	30677194	30677329	L2c	LINE/L2
chr3	128217151	128217589	L2a	LINE/L2
chr6	6699359	6699641	AluJb	SINE/Alu
chr11	33888190	33888390	AluSq2	SINE/Alu
chr6	6731624	6731751	HAL1	LINE/L1
chr1	36943848	36944157	AluSx1	SINE/Alu
chr6	137110066	137110153	L1PA16	LINE/L1
chr4	75143671	75143857	Charlie10b	DNA/hAT-Charlie
chr5	149788359	149788500	MLT1A1	LTR/ERV1-MaLR
chr17	3814265	3814581	AluJb	SINE/Alu
chr11	33893438	33893496	MIR	SINE/MIR
chr15	50276513	50277022	LTR33	LTR/ERV1
chr2	143809114	143811385	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr6	137108593	137108686	MIR3	SINE/MIR
chr10	73522756	73522911	MIRb	SINE/MIR
chr3	107856968	107857124	Tigger1	DNA/TcMar-Tigger
chr15	50185012	50185188	L1MEd	LINE/L1
chr19	3175886	3176367	LTR3B_	LTR/ERV1
chr6	29465083	29465447	THE1D	LTR/ERV1-MaLR
chr4	38790348	38790651	AluJr4	SINE/Alu
chr15	51753600	51753727	Eutr2B	DNA
chr11	34485025	34485223	MIR3	SINE/MIR
chr1	109146744	109147018	L2a	LINE/L2
chr6	147688794	147691374	L1ME1	LINE/L1
chr2	47184324	47184471	MIR3	SINE/MIR
chr1	161552870	161552924	L2a	LINE/L2
chr2	68619637	68620028	L2d2	LINE/L2
chr9	125141279	125141429	MIR1_Amn	SINE/MIR
chr2	6974618	6975770	L1MEf	LINE/L1
chr6	110799356	110799431	L2c	LINE/L2
chrY	15999559	16001226	LTR12C LTR12C	LTR/ERV1
chr16	2870091	2870321	MIR	SINE/MIR
chrX	12943099	12943867	L1MA1	LINE/L1
chr4	95224390	95224619	Tigger4a	DNA/TcMar-Tigger
chr2	43232000	43232157	MIRb	SINE/MIR
chr14	21255239	21255436	Eutr18	LTR?
chr6	36703891	36704052	MER5B	DNA/hAT-Charlie
chr10	17357933	17358130	MIRb	SINE/MIR
chr9	125229479	125231469	ERV24B_Prim-int	LTR/ERV1
chr6	6732008	6732131	HAL1	LINE/L1

chr2	68614143	68614399	AluSz	SINE/Alu
chr10	17487467	17487689	L1M6	LINE/L1
chr17	25975490	25975578	L2c	LINE/L2
chrY	3007776	3008122	L1PA14	LINE/L1
chr1	192148543	192149170	L1MD1	LINE/L1
chr6	32409593	32409756	MIRb	SINE/MIR
chr19	687853	688132	L2b	LINE/L2
chr19	51636315	51636547	L1ME2	LINE/L1
chr20	30677164	30677286	MIR1_Amn	SINE/MIR
chr11	34491219	34491512	AluSx	SINE/Alu
chr15	50163564	50163710	MIRb	SINE/MIR
chr3	148616474	148616764	AluJb	SINE/Alu
chr4	156654253	156654392	L2a	LINE/L2
chr20	5475895	5476256	AluJb	SINE/Alu
chr19	36395687	36396028	L2b	LINE/L2
chr4	57897837	57897912	MIRc	SINE/MIR
chr4	156657333	156657435	Charlie7	DNA/hAT-Charlie
chr12	66587699	66587984	AluJb	SINE/Alu
chr4	56743572	56743628	L3	LINE/CR1
chr17	56375388	56376162	L1MEf	LINE/L1
chr1	244470117	244470444	L1MA3	LINE/L1
chr15	50535767	50535912	MER91A	DNA/hAT-Tip100
chr11	34487306	34488042	L1MEg	LINE/L1
chr20	61061488	61061614	MIRb	SINE/MIR
chr5	138859863	138860147	AluSx1	SINE/Alu
chr6	110768689	110769652	L1MB7	LINE/L1
chr5	130559412	130559864	L2-3_Crp	LINE/L2
chr4	175456147	175456694	L3	LINE/CR1
chr20	30682201	30682519	AluJr	SINE/Alu
chr4	175413637	175413834	MIRb	SINE/MIR
chr19	52022269	52022571	AluY	SINE/Alu
chr1	117058737	117058814	FLAM_A	SINE/Alu
chr2	127293582	127293949	L2a	LINE/L2
chr2	182380991	182381173	MLT1L	LTR/ERV1-MaLR
chr8	24174110	24175266	L1M4c	LINE/L1
chr5	169687413	169687523	MIRb	SINE/MIR
chr9	123609195	123609289	MIR3	SINE/MIR
chr11	59925759	59926540	L1MB1	LINE/L1
chr11	33896636	33896809	MIR	SINE/MIR
chr13	50037471	50038153	LTR76	LTR/ERV1
chr6	32556520	32556590	MADE2	DNA/TcMar-Mariner

chr19	15974630	15974938	AluY	SINE/Alu
chr11	34490834	34490933	MIRc	SINE/MIR
chr15	50186022	50186133	MIR	SINE/MIR
chrY	3007233	3007773	LTR27D	LTR/ERV1
chr3	148610159	148610469	AluSx	SINE/Alu
chr2	175491181	175491773	L2a	LINE/L2
chr1	161483795	161484259	MER57F	LTR/ERV1
chr2	58967397	58968035	MLT1E3	LTR/ERV1-MaLR
chr17	4344885	4345203	AluSq2	SINE/Alu
chr3	148608797	148609030	MIR	SINE/MIR
chr1	156556999	156557189	MIR	SINE/MIR
chr15	50179009	50179306	AluSq	SINE/Alu
chr11	34490314	34490432	FLAM_A	SINE/Alu
chr11	94347775	94348723	L1MA9	LINE/L1
chr9	137802767	137802924	MIRb	SINE/MIR
chr1	161572016	161572790	L2a	LINE/L2
chr15	50178432	50178589	MIRb	SINE/MIR
chr20	61192281	61192557	AluJr	SINE/Alu
chr21	15859960	15860089	L3b	LINE/CR1
chr6	32554878	32555188	AluSc8	SINE/Alu
chr19	51672073	51673065	LTR13	LTR/ERVk
chr19	55091668	55095305	L1HS	LINE/L1
chr1	146363185	146365100	L2a	LINE/L2
chr19	51724543	51726098	L1ME1	LINE/L1
chr4	154607002	154607480	MSTD MSTD	LTR/ERV1-MaLR
chr14	21253026	21253225	MER5B	DNA/hAT-Charlie
chr18	43596430	43596569	L2b	LINE/L2
chr5	32794813	32799690	L1PA8A	LINE/L1
chr1	203153071	203153277	MIRb	SINE/MIR
chr8	27306393	27306472	L2b	LINE/L2
chr19	830459	830579	AluSz	SINE/Alu
chr11	33895881	33896117	MIRb	SINE/MIR
chr10	73523977	73524143	MIR	SINE/MIR
chr17	4385174	4385480	AluSc	SINE/Alu
chr5	49910089	49911825	L1PA5	LINE/L1
chr9	137802339	137802462	MIRc	SINE/MIR
chr12	47604267	47604553	AluSx	SINE/Alu
chr17	4348671	4348971	AluSp	SINE/Alu
chr15	90339164	90339464	AluJr	SINE/Alu
chr11	59830272	59830571	AluSz	SINE/Alu
chr19	845440	845744	AluSq	SINE/Alu

chr2	231312011	231312824	MER21C MER21C	LTR/ERV1
chr22	37330980	37331212	L2c	LINE/L2
chr5	76214360	76215344	L1MC1	LINE/L1
chr6	147668450	147668807	HAL1b	LINE/L1
chr11	33893984	33894055	MIRb	SINE/MIR
chr7	37799789	37800153	L1PA16	LINE/L1
chr1	158607671	158607799	Tigger19a	DNA/TcMar-Tigger
chr11	33901158	33901687	L1MB3	LINE/L1
chr3	158385293	158385601	AluJb	SINE/Alu
chr8	27302774	27302945	AluJb	SINE/Alu
chr12	10130058	10130468	L2a	LINE/L2
chr20	61191933	61192280	L1MC4a	LINE/L1
chr6	32622833	32622966	L1MA7	LINE/L1
chr11	33883462	33883520	Plat_L3	LINE/CR1
chr8	134047702	134048048	L1M5	LINE/L1
chr16	11016414	11016617	MIR	SINE/MIR
chr5	131642439	131642825	L1MB7	LINE/L1
chr1	235113106	235113409	MLT1B	LTR/ERV1-MaLR
chr17	72516020	72516384	L1MB1	LINE/L1
chr12	116962468	116962700	MIRb	SINE/MIR
chr4	74851674	74851913	MIR	SINE/MIR
chr3	148619283	148619372	Charlie4z	DNA/hAT-Charlie
chr4	95213976	95214407	L1MC	LINE/L1
chr19	55402182	55402266	AluJr	SINE/Alu
chr9	125134696	125134868	MIRc	SINE/MIR
chr9	10000332	10001203	HUERS-P3-int LTR9B	LTR/ERV1
chr4	38789163	38789418	MER33	DNA/hAT-Charlie
chr19	37124366	37124993	L1ME1	LINE/L1
chr9	139602398	139602983	HERV140-int	LTR/ERV1
chr11	118065186	118065418	MIRb	SINE/MIR
chr7	30588926	30589143	MIRb	SINE/MIR
chr14	101586934	101587193	MLT1J2	LTR/ERV1-MaLR
chr6	6720853	6721449	L1MB3	LINE/L1
chr12	10272337	10272914	L1MEg	LINE/L1
chr1	168011608	168011933	CR1_Mam	LINE/CR1
chr19	16262634	16262945	AluSx1	SINE/Alu
chr6	6698131	6698282	MER5B	DNA/hAT-Charlie
chr1	158608331	158608528	AluSg	SINE/Alu
chr4	106061983	106062149	MER5B	DNA/hAT-Charlie
chr20	1543141	1543857	Tigger6a	DNA/TcMar-Tigger
chr12	29618196	29618494	THE1D	LTR/ERV1-MaLR

chr9	123615178	123615265	L2d	LINE/L2
chr6	110771933	110773217	L1ME3B	LINE/L1
chr21	21629639	21630000	MLT1A1	LTR/ERV1-MaLR
chr2	102962690	102962856	MIR	SINE/MIR
chr2	102036412	102036633	L2c	LINE/L2
chr1	117039216	117039761	L2a	LINE/L2
chr10	70859888	70860164	AluJb	SINE/Alu
chr11	33900167	33900478	L2d	LINE/L2
chr11	33874847	33875906	L1MC4	LINE/L1
chr10	17359953	17360214	MamRTE1	LINE/RTE-BovB
chr1	109147031	109147134	MLT1J	LTR/ERV1-MaLR
chr4	175419114	175419397	AluJb	SINE/Alu
chr7	38383621	38383912	L1MC5a	LINE/L1
chr20	30685415	30685518	L1MEd	LINE/L1
chr19	829808	829936	AluJr	SINE/Alu
chr11	2335268	2335407	FLAM_C	SINE/Alu
chr4	175427613	175427863	MIR	SINE/MIR
chr8	142147070	142147378	AluSx1	SINE/Alu
chr1	198825509	198826615	L2	LINE/L2
chr11	118096518	118096609	MER63D	DNA/hAT-Blackjack
chr12	10090968	10091026	MIRb	SINE/MIR
chr6	110820377	110827271	MER9a1 HERVK9-int MER9a1	LTR/ERV1
chr21	15861450	15861552	MamSINE1	SINE/tRNA-RTE
chr5	39384287	39384616	MER44A	DNA/TcMar-Tigger
chr15	50172364	50172839	L2a	LINE/L2
chrY	14801815	14802111	AluSc	SINE/Alu
chr21	15861357	15861426	MamSINE1	SINE/tRNA-RTE
chr6	6699792	6699950	MIR3	SINE/MIR
chr22	44599052	44599154	L2a	LINE/L2
chr2	192907161	192910824	ERV1-B4-int	LTR/ERV1
chr13	108944327	108946034	L1MB5	LINE/L1
chr6	114188768	114188955	MLT1B	LTR/ERV1-MaLR
chr17	72692451	72692610	MIR3	SINE/MIR
chr6	6714140	6714346	AluJr	SINE/Alu
chr1	161486975	161487067	MER34-int	LTR/ERV1
chr11	118096610	118096846	Tigger4a	DNA/TcMar-Tigger
chr13	32983208	32983603	L3	LINE/CR1
chr17	40455804	40456090	L2a	LINE/L2
chr1	117029717	117030144	MLT1J MLT1J	LTR/ERV1-MaLR
chr2	201646982	201647666	L4_C_Mam	LINE/RTE-X
chr1	244471583	244471795	L1MC4	LINE/L1

chr20	30678609	30678709	MIRb	SINE/MIR
chr12	10140841	10141971	L1PA4	LINE/L1
chr21	15890356	15890742	L2a	LINE/L2
chr2	182378457	182378758	L2b	LINE/L2
chr7	23288845	23289993	L1MD1	LINE/L1
chr19	17947088	17947380	AluSx	SINE/Alu
chr12	54682426	54682683	AluSx3	SINE/Alu
chr6	137107933	137108079	AluJb	SINE/Alu
chr6	6729813	6729938	HAL1	LINE/L1
chr8	41658434	41658627	L1ME3E	LINE/L1
chr6	110797089	110797239	MIRb	SINE/MIR
chr19	846746	846986	AluSx1	SINE/Alu
chr20	34062058	34062471	L2d	LINE/L2
chr19	40222722	40223434	L1PA2	LINE/L1
chr1	158591652	158591953	AluY	SINE/Alu
chr2	6971208	6972350	L1ME1	LINE/L1
chr19	844947	845247	AluSz	SINE/Alu
chr3	171326028	171326939	L1ME4a	LINE/L1
chr17	33699648	33699832	L1MA2	LINE/L1
chr2	201658313	201658587	Charlie15b	DNA/hAT-Charlie
chr15	50184825	50184914	MER103C	DNA/hAT-Charlie
chr11	47403243	47403549	AluSq	SINE/Alu
chr17	62467928	62468120	L1ME4b	LINE/L1
chr22	44597531	44597836	MLT1H2	LTR/ERV1-MaLR
chr17	72735053	72735217	MIR	SINE/MIR
chr7	38298640	38298880	MIRb	SINE/MIR
chr15	90336651	90336954	AluSx	SINE/Alu
chr4	154617733	154617919	MER57A-int	LTR/ERV1
chr4	174381148	174384290	L1MB4	LINE/L1
chr1	92942670	92942913	MamTip2b	DNA/hAT-Tip100
chr5	71737176	71737260	MamRTE1	LINE/RTE-BovB
chr17	72696926	72697310	MLT1B	LTR/ERV1-MaLR
chr19	16260959	16261067	AluJo	SINE/Alu
chr19	51636867	51636985	L1ME2	LINE/L1
chr4	38790208	38790347	MER63D	DNA/hAT-Blackjack
chr19	42123516	42123571	Chap1a_Mam	DNA/hAT-Charlie
chr11	47404810	47404903	MIR3	SINE/MIR
chr8	41658773	41659495	L1ME3E	LINE/L1
chr1	198679032	198679941	L1M4	LINE/L1
chr5	131638707	131638908	L1M4	LINE/L1
chr3	195793840	195794155	L3	LINE/CR1

chr3	88047192	88047409	L2d	LINE/L2
chr1	161570065	161570363	AluSz6	SINE/Alu
chr11	33899912	33900150	MIRb	SINE/MIR
chr11	118079150	118079233	L2a	LINE/L2
chr15	50189825	50190013	MIRc	SINE/MIR
chr6	144285011	144285179	MamGypLTR1d	LTR/Gypsy
chr8	2584506	2585024	L1PBa1	LINE/L1
chr8	41658015	41658240	L1ME3E	LINE/L1
chr14	106381615	106381989	L1ME3B	LINE/L1
chr8	2521463	2521819	L1PA8	LINE/L1
chr7	150600	151006	MER31B	LTR/ERV1
chr19	16261861	16262164	AluSq2	SINE/Alu
chr11	33887899	33888176	AluJb	SINE/Alu
chr11	121459366	121459758	MLT1B	LTR/ERV1-MaLR
chr4	175419632	175419813	L1ME1	LINE/L1
chr19	51635934	51636042	MSTB1	LTR/ERV1-MaLR
chr1	183537304	183537600	AluSz	SINE/Alu
chr15	50174569	50175141	L1ME3B	LINE/L1
chr12	10139419	10140394	MER4B-int	LTR/ERV1
chr4	95250892	95251305	L3	LINE/CR1
chr6	36702591	36702677	L3b	LINE/CR1
chr3	146224794	146224924	LTR101_Mam	LTR/ERV1
chr19	44472739	44473486	L1PA11	LINE/L1
chr12	66626143	66626378	LFSINE_Vert	SINE/tRNA
chr5	149787915	149787991	MIR1_Amn	SINE/MIR
chr2	234053977	234054225	L2a	LINE/L2
chr6	49578959	49579277	L1MA9	LINE/L1
chr1	25423676	25423991	AluSz	SINE/Alu
chr20	61065248	61065433	MIR	SINE/MIR
chr16	81800420	81800591	L2c	LINE/L2
chrX	70417768	70417883	L2d2	LINE/L2
chr15	50175698	50175880	MIR	SINE/MIR
chrY	2733911	2734222	AluY	SINE/Alu
chr5	149437241	149437536	L3	LINE/CR1
chr12	66637367	66637533	MIRb	SINE/MIR
chr20	58860731	58862395	HERV4_I-int MER51A	LTR/ERV1
chr19	51636053	51636203	L1ME2	LINE/L1
chr1	235836004	235838432	HERVIP10B3-int	LTR/ERV1
chr11	59836701	59836811	HAL1b	LINE/L1
chrX	153911284	153912186	HAL1	LINE/L1
chr4	175455509	175456094	LTR31	LTR/ERV1

chr4	95230277	95236442	L1PA4	LINE/L1
chr2	225632181	225632566	MER87B	LTR/ERV1
chr16	11016621	11016694	MADE2	DNA/TcMar-Mariner
chr1	158588522	158588729	MIRc	SINE/MIR
chr3	28394000	28394392	Charlie2b	DNA/hAT-Charlie
chr8	65723804	65726090	ERV-L-E-int ERV-L-E-int	LTR/ERV-L
chr4	175410503	175410789	MLT1K	LTR/ERV-L-MaLR
chr19	21625543	21625643	MIRb	SINE/MIR
chr6	137110154	137110476	AluJr	SINE/Alu
chr4	56800333	56801694	L1MA3	LINE/L1
chr10	54269992	54272059	LOR1-int LOR1-int LOR1-int LOR1a	LTR/ERV1
chr2	207545579	207547082	L1P3	LINE/L1
chr20	30668302	30668591	AluSz6	SINE/Alu
chr11	59977403	59977508	L2a	LINE/L2
chr12	9865867	9865965	L2	LINE/L2
chr11	33873962	33874846	LTR28B	LTR/ERV1
chr11	1924441	1924675	AluJo	SINE/Alu
chr21	46342807	46343536	L1MC5	LINE/L1
chr15	75436223	75438388	MER52-int MER52D	LTR/ERV1
chr6	116763473	116763886	L2a	LINE/L2
chr19	8605877	8606036	AluJb	SINE/Alu
chr19	847320	847436	AluSx3	SINE/Alu
chr5	14627710	14628163	L1MA9	LINE/L1
chr17	4388543	4388679	MIR	SINE/MIR
chrY	7202641	7202860	L1MC5a	LINE/L1
chr2	175495807	175496353	L1MB2	LINE/L1
chr15	32879086	32879389	AluSx1	SINE/Alu
chr4	175419474	175419631	L1MA10	LINE/L1
chr4	106062684	106062906	MIRb	SINE/MIR
chr4	95226788	95226945	MIR	SINE/MIR
chr6	119675528	119676003	L1MA7	LINE/L1
chr6	36668896	36669184	AluSz	SINE/Alu
chr6	36694878	36695216	L1ME4b	LINE/L1
chrX	154017735	154017948	L1ME3G	LINE/L1
chr17	7013826	7014006	MIR	SINE/MIR
chr14	21251082	21251391	AluSx	SINE/Alu
chr8	24211072	24211187	L2d2	LINE/L2
chr4	38748174	38750493	MSTA MSTA-int MSTA	LTR/ERV-L-MaLR
chr7	36551154	36551271	L2b	LINE/L2
chr6	32545312	32545672	MLT1L	LTR/ERV-L-MaLR
chr7	35121948	35122795	L1ME1	LINE/L1

chr1	247688116	247688412	L1ME3G	LINE/L1
chr2	102970704	102970988	AluSp	SINE/Alu
chr4	174204809	174209152	LTR25-int LTR25-int LTR25-int LTR25-int	LTR/ERV1
chr22	37265281	37265492	MIR	SINE/MIR
chr2	89464095	89465958	L1PA7	LINE/L1
chrY	23415344	23415540	AluSc	SINE/Alu
chr2	68613021	68613110	L2b	LINE/L2
chr1	160809216	160809560	MER2	DNA/TcMar-Tigger
chr2	99385293	99385663	MLT1B	LTR/ERV1-MaLR
chr2	43215894	43216199	AluJb	SINE/Alu
chr20	48895886	48895999	MIRc	SINE/MIR
chr1	117043523	117044076	L2a	LINE/L2
chr4	74851948	74852012	MIRb	SINE/MIR
chr15	50121332	50121802	L2c	LINE/L2
chr11	118080578	118080743	FRAM	SINE/Alu
chr2	97542633	97542868	MIRb	SINE/MIR
chr1	109147147	109147368	L2a	LINE/L2
chr17	25975199	25975295	L2c	LINE/L2
chr4	174200223	174200631	MSTA	LTR/ERV1-MaLR
chr22	44593142	44593381	MIR	SINE/MIR
chr10	134673361	134673535	AluSc5	SINE/Alu
chr2	24486979	24487285	AluSp	SINE/Alu
chr15	56380423	56380620	MIRb	SINE/MIR
chr11	123948223	123948482	AluJr	SINE/Alu
chr16	50749016	50749226	MIR	SINE/MIR
chr7	37800477	37800968	L1MA9	LINE/L1
chr6	135530372	135530671	AluSx1	SINE/Alu
chr1	183538734	183539024	AluSz	SINE/Alu
chr11	33896842	33897143	AluSq2	SINE/Alu
chr11	33892856	33893135	AluJr	SINE/Alu
chr17	40453905	40454191	AluJr	SINE/Alu
chr19	42129694	42130283	L1MCA	LINE/L1
chr1	198823031	198823891	L1MA7	LINE/L1
chr4	55602441	55602543	MIRc	SINE/MIR
chr11	44637244	44637448	L1ME3	LINE/L1
chr2	97905939	97906544	L1MEc	LINE/L1
chr17	56376173	56376462	MER70B	LTR/ERV1
chr6	132057883	132058330	MLT1C2	LTR/ERV1-MaLR
chr21	17069524	17071469	L1PA7	LINE/L1
chr19	44484676	44485131	ERV1-B4-int	LTR/ERV1
chr6	36671698	36671961	L2a	LINE/L2

chr2	43199823	43200211	MLT1F	LTR/ERV1-MaLR
chr7	37794139	37795221	L1MA9	LINE/L1
chr16	55461207	55461751	MLT1F2 MLT1F2	LTR/ERV1-MaLR
chr7	142159769	142160379	MLT2E	LTR/ERV1
chr11	118079974	118080106	Charlie15a	DNA/hAT-Charlie
chrY	21041899	21043334	LTR12C	LTR/ERV1
chr21	39762290	39762708	MLT1B	LTR/ERV1-MaLR
chr9	137795387	137795462	L1ME1	LINE/L1
chr11	73118762	73118918	L2c	LINE/L2
chr15	50120094	50120497	MLT1F2	LTR/ERV1-MaLR
chr17	72694785	72695011	L1PA15	LINE/L1
chr11	60147308	60147630	L1MB3	LINE/L1
chr19	687395	687704	AluSx	SINE/Alu
chrX	55048294	55048512	MIR	SINE/MIR
chr17	3814102	3814217	L2a	LINE/L2
chr9	139600313	139600791	HERV140-int	LTR/ERV1
chr14	88478679	88479078	L1MB7	LINE/L1
chr1	109144502	109144846	L2a	LINE/L2
chr12	10011712	10014260	L1ME3	LINE/L1
chr1	158585761	158585892	MER106B	DNA/hAT-Charlie
chr12	11988757	11988995	MIR	SINE/MIR
chrX	55049941	55050120	MIRb	SINE/MIR
chr22	37332792	37332868	L3b	LINE/CR1
chr8	41515950	41516080	MIRc	SINE/MIR
chr1	116614411	116614786	L1ME3Cz	LINE/L1
chr9	21009548	21009808	L1MA7	LINE/L1
chrX	37652136	37652386	MIR	SINE/MIR
chr7	150491552	150491941	ERV3-16A3_LTR	LTR/ERV1
chr2	238675532	238675846	AluJb	SINE/Alu
chr5	149438409	149438559	MIR3	SINE/MIR
chr17	3804302	3804360	LTR85a	LTR/Gypsy?
chr2	182341861	182343174	L1MA9	LINE/L1
chr11	14533639	14533939	AluSp	SINE/Alu
chr6	135511917	135512230	AluJr	SINE/Alu
chr10	54264810	54265877	MER11A	LTR/ERV1
chr2	102940832	102946961	L1PA4	LINE/L1
chr9	125145112	125145459	L2b	LINE/L2
chr2	182345315	182345400	MIR	SINE/MIR
chr1	159018523	159018884	LTR82A	LTR/ERV1
chr19	686402	686556	MIR	SINE/MIR
chr22	44597950	44598057	MIR	SINE/MIR

chr6	114192353	114192654	AluSz	SINE/Alu
chr7	40577995	40578279	LTR90A	LTR
chr18	77573498	77574608	L1MD2	LINE/L1
chr16	85945706	85945911	Tigger15a	DNA/TcMar-Tigger
chr2	201632659	201632839	L2c	LINE/L2
chr15	57593312	57593626	AluSx1	SINE/Alu
chr1	40883165	40884940	L1MC4	LINE/L1
chr15	57598104	57598167	MIR3	SINE/MIR
chr19	8562334	8562404	FLAM_C	SINE/Alu
chr11	59941452	59941787	LTR101_Mam	LTR/ERV1
chr17	3815613	3815924	AluSz	SINE/Alu
chr3	87141401	87147541	L1PA4	LINE/L1
chr4	5020402	5020586	MIR	SINE/MIR
chr6	36688429	36688552	MIR	SINE/MIR
chr12	47599577	47600264	LTR8	LTR/ERV1
chr9	123616243	123616986	MER99	DNA/hAT?
chr15	57596459	57596760	AluSx	SINE/Alu
chr8	24210858	24210999	L2a	LINE/L2
chr11	33883589	33883783	LTR16A2	LTR/ERV1
chrX	154012738	154012816	L2	LINE/L2
chr6	2835790	2835926	FLAM_A	SINE/Alu
chr18	9912292	9912669	LTR12_	LTR/ERV1
chr19	8562058	8562333	AluJo	SINE/Alu
chr12	54683561	54683805	AluJr	SINE/Alu
chr22	37262254	37262659	L2	LINE/L2
chr1	67245826	67252009	L1PA4	LINE/L1
chr4	95221110	95221519	L1MC5a	LINE/L1
chr12	54687770	54688041	AluYm1	SINE/Alu
chr8	27305094	27305404	AluSz	SINE/Alu
chr9	123583765	123584435	L1MB3	LINE/L1
chr7	150494429	150494845	MER65A	LTR/ERV1
chr19	8562426	8562542	L2	LINE/L2
chr6	2838372	2838473	L1MB2	LINE/L1
chr16	11025316	11025429	MER113	DNA/hAT-Charlie
chr14	91706077	91707166	MER11B	LTR/ERV1
chr10	17494477	17495045	L1ME4a	LINE/L1
chr15	51753260	51753378	L1ME4b	LINE/L1
chr4	174209462	174211067	LTR25-int LTR25-int MER61F	LTR/ERV1
chr9	136125760	136126382	MER4B	LTR/ERV1
chr2	241572247	241574527	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr20	30676656	30677101	MLT1H2	LTR/ERV1-MaLR

chr19	8558678	8558981	AluSz	SINE/Alu
chr9	66468616	66469020	MLT1H1	LTR/ERV1-MaLR
chr3	146225239	146226503	MLT1A-int MLT1A-int MLT1A MLT1A-int	LTR/ERV1-MaLR
chr11	33882028	33882349	AluJb	SINE/Alu
chr1	203745975	203746116	LTR78B	LTR/ERV1
chr15	57594521	57594827	MER2	DNA/TcMar-Tigger
chr9	136141832	136142518	L1ME2	LINE/L1
chr2	97904374	97905590	L1MEc	LINE/L1
chr16	21651790	21652117	AluSx	SINE/Alu
chr5	149783489	149783643	L3	LINE/CR1
chr6	147573918	147576513	L1PA7	LINE/L1
chr7	37782333	37782463	L1PA13	LINE/L1
chr3	121603756	121604749	L2a	LINE/L2
chr11	46386086	46386166	MamRTE1	LINE/RTE-BovB
chr17	62469490	62469731	L1MEh	LINE/L1
chr7	150463391	150465424	MER31-int	LTR/ERV1
chr2	43207372	43207511	MIR	SINE/MIR
chr4	175414989	175415582	Tigger17a	DNA/TcMar-Tigger
chr7	37850833	37853023	L1PA15	LINE/L1
chr5	361369	362479	MLT1A-int MLT1A	LTR/ERV1-MaLR
chr19	44479187	44479863	L1PA11	LINE/L1
chr15	57596255	57596458	L1MD3	LINE/L1
chr14	93164143	93165118	L1MC3	LINE/L1
chr1	109145641	109146742	L1MEg	LINE/L1
chr11	47401228	47401582	L1PB4	LINE/L1
chr3	152168554	152168697	MER102a	DNA/hAT-Charlie
chr2	166666433	166666743	AluSz	SINE/Alu
chr20	30678258	30678337	Charlie15a	DNA/hAT-Charlie
chr3	132088077	132088279	MamGypLTR1b	LTR/Gypsy
chr5	149790551	149790773	MIR	SINE/MIR
chr8	144634015	144634295	AluSx	SINE/Alu
chr2	188205886	188207163	L1MB8	LINE/L1
chr19	20046561	20046861	AluSx1	SINE/Alu
chr14	21251409	21251712	AluSx1	SINE/Alu
chr11	94345100	94346941	L1MA9	LINE/L1
chr6	29843427	29849606	MER9a1 HERVK9-int HERVK9-int MER9a1	LTR/ERV1
chr21	16741276	16741974	L1MB8	LINE/L1
chr16	11024366	11024481	MIRc	SINE/MIR
chr4	175420564	175421061	L2	LINE/L2
chr16	11024911	11025178	AluJr	SINE/Alu
chr11	59971619	59971728	L2	LINE/L2

chr5	41938628	41939211	MLT1E3	LTR/ERV1-MaLR
chr12	9870239	9871122	L1MCc	LINE/L1
chr5	149789902	149790078	MIRb	SINE/MIR
chr9	66478268	66484289	L1PA6	LINE/L1
chr2	231255426	231256203	L1MB7	LINE/L1
chr6	46667611	46667735	L1ME4a	LINE/L1
chr6	32547142	32547598	LTR12	LTR/ERV1
chr12	54684363	54684663	AluSp	SINE/Alu
chr10	43010370	43010491	L1MA3	LINE/L1
chr4	103559652	103559848	LTR86A1	LTR/ERV1
chr2	68544609	68544737	MER5B	DNA/hAT-Charlie
chr15	57594244	57594328	MLT1H1	LTR/ERV1-MaLR
chr22	37320171	37321987	L2a	LINE/L2
chr11	73119962	73120128	L2c	LINE/L2
chr9	66465885	66465962	L2a	LINE/L2
chr2	96492243	96492727	L1PA10	LINE/L1
chr10	38654802	38655046	MIRb	SINE/MIR
chr18	43601105	43601547	L1MC5a	LINE/L1
chr1	206242068	206242573	L2a	LINE/L2
chr6	36686399	36686537	MIRb	SINE/MIR
chr6	25987856	25988153	L1MC1	LINE/L1
chr9	90301038	90301263	LTR33	LTR/ERV1
chr22	44595347	44595768	L2c	LINE/L2
chr1	208056014	208056391	L2c	LINE/L2
chr8	79850993	79852347	THE1C THE1C-int THE1C	LTR/ERV1-MaLR
chr6	32408854	32409160	AluSc	SINE/Alu
chr15	34398270	34398351	MER90	LTR/ERV1
chr4	154620850	154621041	L1MEg	LINE/L1
chr17	62466209	62466509	AluSx1	SINE/Alu
chr6	143797021	143798130	L2a	LINE/L2
chr4	5019880	5020123	L1ME4a	LINE/L1
chr18	8913645	8921363	LTR2 Harlequin-int LTR2	LTR/ERV1
chr17	5111101	5111709	L2b	LINE/L2
chr12	54687353	54687650	AluSx	SINE/Alu
chrX	155240885	155241002	MLT1C2	LTR/ERV1-MaLR
chr21	45840030	45840137	L2a	LINE/L2
chr2	231030612	231030906	AluSg	SINE/Alu
chr15	50185303	50185389	Kanga1b	DNA/TcMar-Tc2
chr17	41842143	41842265	L2d2	LINE/L2
chr20	30685868	30686133	AluSx1	SINE/Alu
chr20	48896000	48896315	AluJr	SINE/Alu

chr6	6185363	6191484	L1PA3	LINE/L1
chr2	163209698	163209993	AluSc	SINE/Alu
chr1	236702561	236702629	MER102b	DNA/hAT-Charlie
chr1	203150139	203150228	MIRb	SINE/MIR
chr12	117141871	117142437	L1MB7	LINE/L1
chr12	57874893	57875021	L2b	LINE/L2
chr12	116985013	116985096	MIR	SINE/MIR
chr20	30683360	30683589	L1MB8	LINE/L1
chr7	73641004	73641355	L2a	LINE/L2
chr4	103558008	103558372	THE1B	LTR/ERV1-MaLR
chr9	125142791	125143007	MER58A	DNA/hAT-Charlie
chr1	156144027	156144451	L2a	LINE/L2
chr4	5017690	5018079	MSTD	LTR/ERV1-MaLR
chr3	10330513	10330676	MIRc	SINE/MIR
chr4	144400718	144402823	L1ME3B	LINE/L1
chr21	45841372	45841657	AluJo	SINE/Alu
chr15	65240767	65241063	AluSx1	SINE/Alu
chr16	11026403	11026512	MER30	DNA/hAT-Charlie
chr9	71566647	71567703	HAL1	LINE/L1
chr3	158545210	158545504	AluJb	SINE/Alu
chr12	66625171	66625588	L2c	LINE/L2
chr6	32919424	32919734	AluSx	SINE/Alu
chr5	149791522	149791827	AluSx	SINE/Alu
chr11	58914046	58914142	MIRc	SINE/MIR
chr4	103554269	103554428	MLT1N2	LTR/ERV1-MaLR
chr13	21877776	21877902	MIR	SINE/MIR
chr2	182354389	182354567	L1PB4	LINE/L1
chr10	97625532	97625821	AluJr	SINE/Alu
chr15	51753049	51753243	MER3	DNA/hAT-Charlie
chr8	144633115	144633267	AluSg4	SINE/Alu
chr9	136139572	136140173	L1ME2	LINE/L1
chr17	40455446	40455746	AluSp	SINE/Alu
chr5	126389934	126390836	L1PA6	LINE/L1
chr19	51720975	51723531	L1PB4	LINE/L1
chr12	57878351	57878426	MIR	SINE/MIR
chr1	31983446	31984513	HERV1-int MLT2A1	LTR/ERV1
chr3	121637721	121638584	LTR27D	LTR/ERV1
chr15	90351162	90351737	L2b	LINE/L2
chr9	136129529	136129789	L1M2	LINE/L1
chr6	39279261	39279406	MIR	SINE/MIR
chr20	61141790	61142177	MSTB	LTR/ERV1-MaLR

chr4	79788085	79788354	AluSz	SINE/Alu
chr6	135530067	135530234	MER3	DNA/hAT-Charlie
chr2	239439015	239441080	MSTA MSTA-int MSTA	LTR/ERV1-MaLR
chr17	62466510	62466613	L1MB3	LINE/L1
chr17	4382242	4382535	AluSq2	SINE/Alu
chr11	33883364	33883458	MIR3	SINE/MIR
chr5	131640789	131641497	L1MB7	LINE/L1
chr4	95247064	95249513	L1M2	LINE/L1
chr5	69774822	69775130	AluJo	SINE/Alu
chr10	17483871	17484165	AluSg	SINE/Alu
chr5	76212005	76212660	L1MD	LINE/L1
chr12	66633920	66634041	MIRb	SINE/MIR
chr17	72740282	72740385	L2d2	LINE/L2
chr15	30712712	30713014	AluSx1	SINE/Alu
chr4	39144099	39144863	L1MD2	LINE/L1
chr7	37781864	37782148	L1PA7	LINE/L1
chr5	131638912	131640032	L1MB7	LINE/L1
chr12	3721514	3721737	MIRb	SINE/MIR
chr9	66473930	66475921	L1PA4	LINE/L1
chr9	21010555	21011071	MER1A	DNA/hAT-Charlie
chr19	8559817	8559990	AluSz	SINE/Alu
chr9	136145425	136146495	L1MB7	LINE/L1
chr6	96988841	96989190	L2b	LINE/L2
chr3	50376058	50376742	L2	LINE/L2
chr4	154620334	154620764	MER57A-int	LTR/ERV1
chr20	30680741	30681047	AluSz6	SINE/Alu
chr10	70861167	70861532	L2a	LINE/L2
chr2	160631463	160631771	L2a	LINE/L2
chr5	70292332	70292640	AluY	SINE/Alu
chr2	68544859	68545035	MER5A	DNA/hAT-Charlie
chr20	49212176	49212446	MLT1K	LTR/ERV1-MaLR
chr17	7047437	7047911	MER41B	LTR/ERV1
chr2	190436887	190437062	MIR3	SINE/MIR
chr20	30682046	30682192	L1ME3	LINE/L1
chr3	58403946	58404132	MIRb	SINE/MIR
chr6	119677466	119678090	L1MB8	LINE/L1
chr4	175415857	175416179	L2	LINE/L2
chr17	56424332	56424546	MIR	SINE/MIR
chr11	72949655	72949852	MIRb	SINE/MIR
chr5	131625522	131626581	ERV1-E-int	LTR/ERV1
chr6	2840355	2840494	L2a	LINE/L2

chr11	73119543	73119843	AluJb	SINE/Alu
chr17	72515224	72515653	L1MA5	LINE/L1
chr19	20008624	20010614	HERVIP10F-int HERVIP10F-int	LTR/ERV1
chr12	57875334	57875902	L2b	LINE/L2
chr11	72952878	72952974	LTR33	LTR/ERV1
chr19	28367856	28376825	LTR9B HUERS-P3-int HUERS-P3-int LTR9B	LTR/ERV1
chr2	7009904	7014058	MER101 MER101-int	LTR/ERV1
chr19	16015405	16018481	L1M2	LINE/L1
chr10	17491379	17491660	LTR81B	LTR/Gypsy
chrX	153929872	153931132	L1MA2	LINE/L1
chr7	155099635	155099738	MIR1_Amn	SINE/MIR
chrY	59344568	59344666	MLT1C2	LTR/ERV1-MaLR
chr10	45926310	45926964	L1ME3G	LINE/L1
chr15	57593103	57593309	L1MC5a	LINE/L1
chr3	101576663	101576758	MIR	SINE/MIR
chr7	102046188	102047380	HSMAR1	DNA/TcMar-Mariner
chr3	15786125	15790602	L1PBa	LINE/L1
chr15	90343780	90344083	AluSp	SINE/Alu
chr3	132087583	132087889	AluJr	SINE/Alu
chr8	74942769	74943525	LTR9 HUERS-P3-int LTR9	LTR/ERV1
chr7	142644640	142644909	AluSz6	SINE/Alu
chr15	51752843	51752995	Eutr2B	DNA
chr5	149783692	149783779	MIR3	SINE/MIR
chr10	17361808	17361873	Tigger7	DNA/TcMar-Tigger
chr3	132327091	132329059	L1P3	LINE/L1
chr12	48452109	48453841	L1MEc	LINE/L1
chr8	27305605	27305812	L2d2	LINE/L2
chr6	32919772	32919949	MER91A	DNA/hAT-Tip100
chr7	150461027	150462193	L1MD3	LINE/L1
chr1	116613606	116614109	L1ME3Cz	LINE/L1
chr3	132089100	132089370	MER41C	LTR/ERV1
chr9	139932029	139932415	MLT2A1	LTR/ERV1
chr11	72951591	72951733	MIR3	SINE/MIR
chr11	57176143	57176243	MIRb	SINE/MIR
chr6	25988968	25989575	L1MC1	LINE/L1
chr20	30682083	30682200	L1ME3	LINE/L1
chr13	39627001	39627548	MLT2A2	LTR/ERV1
chr7	37781667	37781734	L3b	LINE/CR1
chr15	91429773	91429939	MER45A	DNA/hAT-Tip100
chr6	147624297	147626059	THE1C THE1C-int	LTR/ERV1-MaLR
chr9	125149675	125150044	MLT1B	LTR/ERV1-MaLR

chr3	58402355	58402649	AluSz	SINE/Alu
chr5	150172704	150174246	L1PB1	LINE/L1
chr10	43011430	43011731	AluJb	SINE/Alu
chr6	32546327	32546453	L1MA8	LINE/L1
chr19	563123	563561	HERVIP10B3-int	LTR/ERV1
chr10	43010506	43010765	MSTA	LTR/ERV1-MaLR
chr1	168009130	168009785	L2a	LINE/L2
chr6	79678351	79678845	HAL1	LINE/L1
chr10	17492941	17493140	MIR	SINE/MIR
chr19	16014804	16015404	MLT2A2 MLT2A2 MLT2A2	LTR/ERV1
chr12	54682891	54683204	AluSx1	SINE/Alu
chr4	5019585	5019721	MIR3	SINE/MIR
chr9	66467421	66467490	L2c	LINE/L2
chr5	69416888	69417205	AluY	SINE/Alu
chr15	90344084	90344243	MIR	SINE/MIR
chr22	44599162	44599367	MER103C	DNA/hAT-Charlie
chr15	57599566	57599799	ORSL	DNA/hAT-Tip100
chr10	70861533	70861816	AluJb	SINE/Alu
chr20	30642697	30642926	L1ME3Cz	LINE/L1
chr6	6729572	6729794	Charlie9	DNA/hAT-Charlie
chr8	32902790	32903498	L1MD1	LINE/L1
chr4	95209324	95209532	L1MC5a	LINE/L1
chr4	103559299	103559610	AluJb	SINE/Alu
chr7	142646482	142646750	L2a	LINE/L2
chr8	41515690	41515833	MIRc	SINE/MIR
chr21	16131546	16132779	L1MB1	LINE/L1
chr3	48372016	48375292	LTR17 HERV17-int HERV17-int HERV17-int HERV17-int	LTR/ERV1
chr2	68542827	68543023	AluJr	SINE/Alu
chr12	57877318	57877535	L2b	LINE/L2
chr16	11028061	11028314	MER113	DNA/hAT-Charlie
chr12	123899681	123899819	MER104	DNA/TcMar-Tc2
chr10	91340465	91340855	L2a	LINE/L2
chr20	30668649	30668909	AluJo	SINE/Alu
chr10	119251320	119251802	LTR33	LTR/ERV1
chr3	132381567	132381782	MIRb	SINE/MIR
chrX	154016129	154017407	L1ME3A	LINE/L1
chr3	133337365	133337424	L2c	LINE/L2
chr13	50568350	50568810	MER4A1	LTR/ERV1
chr4	141210256	141211206	ERV3-16A3_L-int	LTR/ERV1
chr1	117060603	117060852	MIR	SINE/MIR
chr5	102511313	102511486	L2a	LINE/L2

chr10	104523421	104523554	MIRc	SINE/MIR
chr10	17496968	17497181	MER58A	DNA/hAT-Charlie
chr10	135079014	135079322	AluY	SINE/Alu
chr10	104523227	104523312	MIRc	SINE/MIR
chr2	98134078	98135023	L1M4	LINE/L1
chr10	17396797	17396907	Charlie4z	DNA/hAT-Charlie
chr2	160632664	160633084	L1MB3	LINE/L1
chr5	176933039	176933254	AluSx	SINE/Alu
chr21	16742134	16742352	MIRc	SINE/MIR
chr15	90337745	90339066	HAL1	LINE/L1
chr17	26557545	26566365	LTR2C HERVE-int LTR2C	LTR/ERV1
chr3	139284207	139290327	L1PA4	LINE/L1
chr19	52027959	52030548	L1PREC2	LINE/L1
chr19	48759591	48759885	AluSc8	SINE/Alu
chr3	121651608	121657633	L1PA3	LINE/L1
chr7	38365791	38366120	L1MA9	LINE/L1
chr4	95252991	95253860	LTR28B	LTR/ERV1
chr15	56930379	56930977	Charlie1a	DNA/hAT-Charlie
chr8	27306682	27306806	L2b	LINE/L2
chr1	169830298	169830802	MLT1H1	LTR/ERV1-MaLR
chr6	32920422	32920555	MIRb	SINE/MIR
chr22	29575936	29576341	L1M5	LINE/L1
chr11	72952485	72952856	LTR78B	LTR/ERV1
chr6	119503038	119503692	L1M3	LINE/L1
chr4	56739600	56739698	MamRTE1	LINE/RTE-BovB
chr16	11028906	11029059	MIRb	SINE/MIR
chr2	190431146	190432071	L2a	LINE/L2
chr1	207814327	207814464	L1ME4b	LINE/L1
chr1	43818659	43818927	L2a	LINE/L2
chr6	32897510	32898526	L1MB2	LINE/L1
chr12	66584772	66585283	MER89	LTR/ERV1
chr9	66467575	66467715	L2c	LINE/L2
chr9	66466178	66466706	LTR6A	LTR/ERV1
chr2	192564829	192565593	L1MC5a	LINE/L1
chr3	58408386	58408492	MamSINE1	SINE/tRNA-RTE
chr5	94240522	94241489	L2a	LINE/L2
chr3	132088492	132088709	MamGypLTR1b	LTR/Gypsy
chr10	45930711	45932518	L1PA17	LINE/L1
chr15	91432027	91432316	AluSx	SINE/Alu
chr3	121605566	121606062	L1MC1	LINE/L1
chr20	30685557	30685697	L1MEd	LINE/L1

chr15	91429660	91429744	MIR3	SINE/MIR
chr7	102916287	102916591	AluSz	SINE/Alu
chr3	122443497	122444278	SVA_A	Retroposon/SVA
chr3	111703760	111704093	L2c	LINE/L2
chr10	17497191	17497524	MER57D	LTR/ERV1
chr18	12887057	12887615	L1ME3A	LINE/L1
chr2	9580864	9580997	FLAM_C	SINE/Alu
chr11	14532956	14533638	L1M5	LINE/L1
chr6	160195483	160195772	AluJo	SINE/Alu
chr9	136128859	136129382	L1M2	LINE/L1
chr22	42446688	42447673	L1MC2	LINE/L1
chr2	43207540	43208098	LTR85c	LTR/Gypsy?
chr6	39279422	39279655	L2d2	LINE/L2
chr18	43599485	43599789	AluSz	SINE/Alu
chr1	47668309	47670054	L1MA4A	LINE/L1
chr16	27463264	27463342	L2a	LINE/L2
chr7	87474592	87474954	MER1B	DNA/hAT-Charlie
chr1	183597590	183597989	L2c	LINE/L2
chr19	8606091	8606172	FLAM_C	SINE/Alu
chr16	30962574	30962795	MIR	SINE/MIR
chr4	95252421	95252990	L1M2	LINE/L1
chr7	73642011	73642223	AluJb	SINE/Alu
chr16	11026549	11026759	AluSx	SINE/Alu
chr10	94444111	94445934	Tigger1	DNA/TcMar-Tigger
chr2	181921055	181921431	MSTA1	LTR/ERV1-MaLR
chr5	151108942	151110019	MER11B	LTR/ERV1
chr12	63957192	63958985	L1ME1	LINE/L1
chr11	58728779	58729301	L1MEj	LINE/L1
chr10	89074291	89074714	MSTB1	LTR/ERV1-MaLR
chr10	15824366	15824506	HAL1	LINE/L1
chr12	123894896	123895049	MIRc	SINE/MIR
chr12	112605838	112606023	MIRb	SINE/MIR
chr20	33856421	33856547	MIRc	SINE/MIR
chr4	103556713	103556935	MIRc	SINE/MIR
chrX	47784256	47784357	L1ME2z	LINE/L1
chr17	43587714	43587823	L2d2	LINE/L2
chr1	182796484	182797374	L1MEd	LINE/L1
chr2	162085554	162086187	L2c	LINE/L2
chr10	15825927	15826073	MIRb	SINE/MIR
chr17	62852174	62852312	MER2B	DNA/TcMar-Tigger
chr12	65855605	65855910	L2a	LINE/L2

chr13	50054796	50054991	MIR	SINE/MIR
chr1	40886222	40886905	L1MC4	LINE/L1
chr6	4992717	4993495	L1MD2	LINE/L1
chr8	90729648	90729956	MLT1I	LTR/ERV1-MaLR
chr4	103618513	103623791	L1PA3	LINE/L1
chr10	98461704	98461975	L1MA9	LINE/L1
chr5	131652901	131653509	L1MB7	LINE/L1
chr7	142647904	142648144	MIR	SINE/MIR
chr20	30678740	30678950	MIR	SINE/MIR
chr6	135529819	135530064	L1MC5a	LINE/L1
chrX	49000779	49001150	HERVE-int HERVE-int	LTR/ERV1
chr17	56420575	56420867	AluJb	SINE/Alu
chr11	33885426	33885642	MIRb	SINE/MIR
chr4	95240919	95247072	L1PA5	LINE/L1
chr10	28804536	28805966	L1MB5	LINE/L1
chr3	158385907	158386242	MER2	DNA/TcMar-Tigger
chr1	85048795	85049381	LTR9	LTR/ERV1
chr10	135077554	135077864	AluJb	SINE/Alu
chr7	102858440	102859496	L1MC4	LINE/L1
chr10	45928839	45929627	LTR39	LTR/ERV1
chr16	11026145	11026359	MIR	SINE/MIR
chr1	235990268	235990345	L1ME2	LINE/L1
chr15	75376124	75379282	L1P2	LINE/L1
chr6	46676217	46676448	DNA1_Mam	DNA/TcMar
chr7	128584532	128585049	L1ME4b	LINE/L1
chr12	123895440	123895572	AluJr	SINE/Alu
chr17	73597900	73598055	MIRb	SINE/MIR
chr17	70814304	70814900	L3	LINE/CR1
chr1	117067179	117068397	L1MC1	LINE/L1
chr5	43046230	43046543	AluSx1	SINE/Alu
chr3	158386502	158386630	Tigger19a	DNA/TcMar-Tigger
chr6	147566719	147567159	MLT1C2	LTR/ERV1-MaLR
chr16	84761100	84761664	L1MC4	LINE/L1
chr11	33885673	33885949	L1ME3F	LINE/L1
chr3	129627122	129627675	LTR35A	LTR/ERV1
chr1	6141535	6141947	MLT1C2	LTR/ERV1-MaLR
chr11	58726283	58726535	LTR9D	LTR/ERV1
chr9	70906691	70909918	L1PB1	LINE/L1
chr9	69209548	69212773	L1PB1	LINE/L1
chr21	39758119	39758585	ORSL-2b	DNA/hAT-Tip100
chr16	11029068	11029307	MER113	DNA/hAT-Charlie

chr22	29576395	29576675	AluJb	SINE/Alu
chr17	72740029	72740167	MER117	DNA/hAT-Charlie
chr10	101400325	101406444	L1PA5	LINE/L1
chr2	196590220	196590810	L1ME1	LINE/L1
chr8	41657724	41657938	MIR	SINE/MIR
chr6	27726629	27727256	LTR38C	LTR/ERV1
chrX	129197988	129198095	L1PA8	LINE/L1
chr15	51754538	51754833	AluSp	SINE/Alu
chr5	149783140	149783446	AluSz	SINE/Alu
chr2	202578841	202579363	MER68B	LTR/ERV1
chrX	49000340	49000641	AluY	SINE/Alu
chr1	84760302	84762649	Tigger1	DNA/TcMar-Tigger
chr9	90297988	90298295	AluSx4	SINE/Alu
chr8	41514986	41515131	L2d2	LINE/L2
chr3	195790520	195790822	AluSx1	SINE/Alu
chr3	158548943	158549285	L1ME4a	LINE/L1
chr6	146877129	146879121	L1PA3	LINE/L1
chr15	90350650	90350944	AluSg7	SINE/Alu
chr17	80908194	80908301	Tigger1	DNA/TcMar-Tigger
chr8	142153515	142153800	AluJr	SINE/Alu
chr5	70292716	70292913	L1MB5	LINE/L1
chr1	231116434	231117938	L2a	LINE/L2
chr11	58914178	58914417	L1MC5a	LINE/L1
chr17	41840959	41841626	L1MC1	LINE/L1
chr6	36050822	36056217	L1PA10	LINE/L1
chr9	136128666	136128884	L1MDa	LINE/L1
chr3	129153046	129153297	MIR	SINE/MIR
chr19	44473801	44478910	L1PA11	LINE/L1
chr16	11026760	11026867	MER30	DNA/hAT-Charlie
chr11	71797581	71797682	L2c	LINE/L2
chr6	147670328	147670654	L1ME2z	LINE/L1
chr11	46384074	46384248	MIRb	SINE/MIR
chr4	56741949	56742080	FLAM_C	SINE/Alu
chr6	30237914	30239853	L1MA9	LINE/L1
chr19	8606173	8606241	MER5A	DNA/hAT-Charlie
chr15	91431322	91431636	AluSz	SINE/Alu
chr1	235991772	235991994	L1M5	LINE/L1
chr15	51753762	51754035	AluSx	SINE/Alu
chr7	102913341	102913534	MIRb	SINE/MIR
chr1	41504796	41504900	MIRb	SINE/MIR
chr16	21637226	21637523	AluSx	SINE/Alu

chr5	69415856	69416355	HAL1	LINE/L1
chr16	27462748	27463051	AluJr	SINE/Alu
chr12	94689363	94689947	L2c	LINE/L2
chr1	169830921	169831313	MLT1C2	LTR/ERV1-MaLR
chr8	144632659	144633101	LTR27	LTR/ERV1
chr15	100240731	100241917	L1MD3	LINE/L1
chr6	27728333	27728660	L1ME5	LINE/L1
chr20	252239	252337	MIRc	SINE/MIR
chr10	89702038	89703160	Tigger3b	DNA/TcMar-Tigger
chr12	62653054	62653181	L2a	LINE/L2
chr1	22051963	22052258	AluSp	SINE/Alu
chr13	51525662	51525888	CR1_Mam	LINE/CR1
chr6	144284599	144284817	MIRb	SINE/MIR
chr9	66463730	66463813	MER103C	DNA/hAT-Charlie
chr5	68919397	68919657	HAL1	LINE/L1
chr5	70293284	70293828	L1MB5	LINE/L1
chr1	235990383	235990685	AluSz6	SINE/Alu
chr1	41504516	41504702	MIRc	SINE/MIR
chr8	21848853	21849163	Charlie13b	DNA/hAT-Charlie
chr18	34361335	34361617	AluSc5	SINE/Alu
chr14	53508678	53508759	MIR3	SINE/MIR
chr10	91337824	91338456	L1MB8	LINE/L1
chr5	176933334	176933639	AluSx	SINE/Alu
chr11	72951944	72952313	MLT1A0	LTR/ERV1-MaLR
chr5	68925415	68926815	THE1B-int THE1B	LTR/ERV1-MaLR
chr19	562284	562821	HERVIP10B3-int	LTR/ERV1
chr6	147567204	147567290	L2c	LINE/L2
chr13	21876960	21877263	AluSc8	SINE/Alu
chr3	98508351	98508526	L1ME3G	LINE/L1
chr8	41514747	41514986	MIR	SINE/MIR
chr1	33591387	33591480	L2a	LINE/L2
chr3	15715761	15716494	L2a	LINE/L2
chr9	70642083	70642762	L1ME3B	LINE/L1
chr9	88914786	88914967	MIRb	SINE/MIR
chr4	77861602	77862041	MSTA1	LTR/ERV1-MaLR
chr1	47054727	47055132	L2c	LINE/L2
chr19	13946022	13946156	AluJr	SINE/Alu
chr18	12888794	12889031	L1ME3	LINE/L1
chr12	66595629	66596269	L1MC4a	LINE/L1
chr3	195788684	195788781	MER5A	DNA/hAT-Charlie
chr4	16218052	16218928	L2c	LINE/L2

chrX	153652679	153653056	MLT1C	LTR/ERV1-MaLR
chr7	108113416	108114202	L1ME1	LINE/L1
chr1	6135169	6135738	L3	LINE/CR1
chr4	95251988	95252413	MER57A1	LTR/ERV1
chr4	77860997	77861601	L1ME1	LINE/L1
chr1	33594790	33595361	LTR51	LTR/ERV1
chr8	30022390	30022591	MLT1J	LTR/ERV1-MaLR
chr9	114136787	114136947	L1ME4a	LINE/L1
chr1	161186706	161186941	MIRc	SINE/MIR
chr12	64053689	64054078	L1ME3Cz	LINE/L1
chr15	51744306	51745437	L1PB2	LINE/L1
chr12	117477304	117477467	MIRc	SINE/MIR
chr9	75780552	75780700	L4_C_Mam	LINE/RTE-X
chr2	163213786	163213852	L2c	LINE/L2
chr12	11984644	11984935	L1ME4c	LINE/L1
chr3	122445282	122445411	L1MEg	LINE/L1
chr5	70292987	70293283	AluSz	SINE/Alu
chr8	24216865	24218287	L1PA7	LINE/L1
chr15	51752607	51752712	Eutr2B	DNA
chr22	29574941	29575607	L1M5	LINE/L1
chr11	14532833	14532930	L1M5	LINE/L1
chr9	66458644	66460514	L1M1	LINE/L1
chr5	121367335	121367827	L1MB7	LINE/L1
chr9	70631546	70631719	MER58A	DNA/hAT-Charlie
chr13	51526160	51526317	FAM	SINE/Alu
chr15	91441312	91442121	L1MEg2	LINE/L1
chr2	197641771	197642029	MER102a	DNA/hAT-Charlie
chr15	101612358	101612690	L1ME4b	LINE/L1
chr5	69393682	69393892	L2b	LINE/L2
chr15	59945581	59946854	L2a	LINE/L2
chr2	162085059	162085553	Tigger3c	DNA/TcMar-Tigger
chr15	90350488	90350633	MIRb	SINE/MIR
chr2	91814038	91814402	MLT1A0	LTR/ERV1-MaLR
chr3	146226952	146227668	Tigger13a	DNA/TcMar-Tigger
chr12	123895576	123895875	AluSg	SINE/Alu
chr6	143804337	143804877	L2b	LINE/L2
chr1	167511846	167511904	Charlie30a	DNA/hAT-Charlie
chr16	25088763	25089113	AluJr	SINE/Alu
chr9	125143251	125143441	L1MC5a	LINE/L1
chrX	155241562	155241660	MLT1C2	LTR/ERV1-MaLR
chr13	21877264	21877432	L1MA2	LINE/L1

chr19	13946159	13946467	AluSx	SINE/Alu
chr20	30679098	30679293	MIR	SINE/MIR
chr1	33595805	33596354	MLT1F2	LTR/ERV1-MaLR
chr9	90300632	90301003	MER113	DNA/hAT-Charlie
chr6	136592269	136592435	MIRb	SINE/MIR
chr2	61159447	61161869	L1MA8	LINE/L1
chr22	29575608	29575935	AluSc	SINE/Alu
chr2	64144243	64144471	MIRb	SINE/MIR
chr7	139055203	139055498	AluSx	SINE/Alu
chr6	4059542	4059698	L2d2	LINE/L2
chr5	69774532	69774792	HAL1	LINE/L1
chr22	29579269	29579559	AluJr	SINE/Alu
chr9	88912461	88912582	AluJr	SINE/Alu
chr5	68923565	68924176	L1ME3D	LINE/L1
chr6	27725939	27726138	L1M3	LINE/L1
chr17	56425441	56425524	MIRb	SINE/MIR
chr22	29576343	29576394	L1ME1	LINE/L1
chr22	29579081	29579268	L2a	LINE/L2
chr17	42453970	42454280	AluSz	SINE/Alu
chr4	103557406	103557662	Tigger3a	DNA/TcMar-Tigger
chr12	102138433	102138791	MLT1A1	LTR/ERV1-MaLR
chr5	69417558	69417855	AluSz	SINE/Alu
chr3	111701834	111702137	L2d	LINE/L2
chr6	144288189	144288371	MIRb	SINE/MIR
chr6	39280272	39280494	MIR	SINE/MIR
chr3	58407028	58407315	AluSg	SINE/Alu
chr4	56740034	56740326	L2d	LINE/L2
chrX	102165970	102167251	L1PB1	LINE/L1
chr10	51588241	51589088	Tigger1	DNA/TcMar-Tigger
chrX	62617482	62620203	MER57-int LTR54B MER57-int MER57-int MER57B1	LTR/ERV1
chr3	158546273	158546462	L1ME4a	LINE/L1
chr9	66460488	66462772	L1PREC2	LINE/L1
chr10	120894810	120895306	L1MB4	LINE/L1
chr5	176934834	176935121	L2a	LINE/L2
chr1	45094594	45095032	MLT1H	LTR/ERV1-MaLR
chr12	62789148	62789812	L1MA1	LINE/L1
chr6	143764594	143764683	FRAM	SINE/Alu
chr12	47046190	47046442	LTR79	LTR/ERV1
chr5	176934741	176934942	L2b	LINE/L2
chr15	91431637	91431977	L2a	LINE/L2
chr5	150651170	150651353	L1MC4a	LINE/L1

chr8	28917021	28917086	L2d2	LINE/L2
chr6	3022662	3022966	AluSz	SINE/Alu
chr1	156557190	156557345	Tigger13a	DNA/TcMar-Tigger
chr5	14613331	14613430	L1MB3	LINE/L1
chr1	43819571	43819794	MIR	SINE/MIR
chr13	49083185	49083480	AluJb	SINE/Alu
chr3	139092877	139093070	MIRb	SINE/MIR
chr9	123166504	123166877	L2b	LINE/L2
chr11	73126298	73126375	MIR3	SINE/MIR
chr3	50375729	50376010	AluSq2	SINE/Alu
chr10	17396728	17396780	L3	LINE/CR1
chr19	44410622	44411824	L1M4	LINE/L1
chr8	135797479	135798870	L1ME3Cz	LINE/L1
chr3	58404596	58404980	MER39B	LTR/ERV1
chr1	156160994	156161851	L1MB5	LINE/L1
chr3	158543222	158543301	Charlie21a	DNA/hAT-Charlie
chr11	10525408	10525465	Charlie1b	DNA/hAT-Charlie
chr15	55631913	55632222	L1PB2	LINE/L1
chr22	42451479	42452712	L1MB7	LINE/L1
chr4	106320929	106321282	Tigger7	DNA/TcMar-Tigger
chr11	57184609	57185115	MLT1H	LTR/ERV1-MaLR
chr17	45090752	45090967	L1MC4	LINE/L1
chr15	67498205	67499237	L1MC4a	LINE/L1
chr1	207964521	207965047	MER44B	DNA/TcMar-Tigger
chr5	69776320	69776638	AluY	SINE/Alu
chr19	36232732	36233025	AluSq2	SINE/Alu
chr7	50504696	50505384	MER21A MER21A	LTR/ERV1
chr11	72401472	72401724	AluJr	SINE/Alu
chr16	81994382	81994612	Charlie2b	DNA/hAT-Charlie
chr13	50093659	50093757	L2d2	LINE/L2
chr4	107241042	107241177	MIRb	SINE/MIR
chr1	167511651	167511768	MER5A1	DNA/hAT-Charlie
chr2	127440118	127440287	L3	LINE/CR1

Table 4: Retrotransposon signature specific to hepatocytes

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Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chr6	53424848	53428222	MER4-int MER4-int MER4A1	LTR/ERV1
chr5	78385337	78385467	L2d	LINE/L2
chr9	104116414	104118547	MLT1A0 MLT1A0-int MLT1A0	LTR/ERV1-MaLR

chr3	177614398	177615201	L1M3c	LINE/L1
chr10	96701025	96701336	AluSg	SINE/Alu
chr3	177615134	177615866	L1M3c	LINE/L1
chr1	236127691	236130878	L1PB1	LINE/L1
chr6	3907470	3908226	MER4E	LTR/ERV1
chr6	53420618	53423327	MER4A1 MER4-int MER4-int	LTR/ERV1
chr10	96701337	96701431	MIRb	SINE/MIR
chr10	5015441	5015931	MLT1H	LTR/ERV1-MaLR
chr10	5007027	5007449	MER68	LTR/ERV1
chr3	177616640	177617913	LTR2752	LTR/ERV1
chr7	99265371	99265996	L1MD	LINE/L1
chr9	42892619	42893205	LTR26	LTR/ERV1
chr3	177626396	177631859	L1P2	LINE/L1
chr6	3905395	3905911	L1ME3Cz	LINE/L1
chr4	70344014	70345066	L1PB2	LINE/L1
chr1	207266860	207267532	L1ME3G	LINE/L1
chr1	159573553	159579692	L1PA3	LINE/L1
chr8	128220205	128220738	MER1A	DNA/hAT-Charlie
chr1	20480603	20486721	LTR2C HERVE-int HERVE-int HERVE-int HERVE-int HERVE-int	LTR/ERV1
chr7	155760000	155761077	L1MA4	LINE/L1
chr5	56975067	56975658	MLT1E2	LTR/ERV1-MaLR
chr9	67254200	67254786	LTR26	LTR/ERV1
chr12	14992694	14993009	L2c	LINE/L2
chr1	236125828	236127394	L1PB1	LINE/L1
chr3	190019307	190020194	L2a	LINE/L2
chr11	18260062	18260534	L1MA2	LINE/L1
chr19	15762665	15763158	LTR40A1	LTR/ERV1
chr9	42608708	42609294	LTR26	LTR/ERV1
chr8	128220739	128220916	MIR	SINE/MIR
chr10	47134430	47134766	MLT1D	LTR/ERV1-MaLR
chr6	3900004	3900620	LTR18B	LTR/ERV1
chr10	96614750	96614990	MLT1D	LTR/ERV1-MaLR
chr12	103247349	103247522	LTR79	LTR/ERV1
chr10	96681089	96682173	L1PA15-16	LINE/L1
chr10	95357988	95358235	MIR	SINE/MIR
chr6	3898914	3899566	LTR1C1	LTR/ERV1
chr12	14992299	14992693	MSTD	LTR/ERV1-MaLR
chr8	128195044	128196635	L1PA8	LINE/L1
chr19	18498070	18498330	AluJr	SINE/Alu
chr2	149011214	149017451	LTR18A HERVL18-int HERVL18-int LTR18A	LTR/ERV1
chr12	103248300	103248439	MIRb	SINE/MIR

chr10	96442356	96442871	MER61D	LTR/ERV1
chr4	114336129	114338583	L1PB1	LINE/L1
chr14	57951235	57952109	L2a	LINE/L2
chr6	8652328	8652687	MLT1A	LTR/ERV1-MaLR
chr3	177618911	177619539	L1M3c	LINE/L1
chr10	5036523	5037013	MLT1H	LTR/ERV1-MaLR
chr2	169778659	169779266	HAL1	LINE/L1
chr10	47138814	47138922	Charlie13a	DNA/hAT-Charlie
chr10	47134806	47134971	FRAM	SINE/Alu
chr7	155029905	155035897	MER9a1 HERVK9-int HERVK9-int MER9a1	LTR/ERV1
chr8	128220950	128221113	L2b	LINE/L2
chr8	128221342	128221527	AluSq	SINE/Alu
chr8	128197795	128198180	MLT1J1	LTR/ERV1-MaLR
chr6	3908630	3908895	L1ME3A	LINE/L1
chr6	3905917	3906001	L1M5	LINE/L1
chr6	86098671	86099184	MLT1H	LTR/ERV1-MaLR
chr3	177618029	177618625	L1M3c	LINE/L1
chr3	120361149	120361332	LTR33	LTR/ERV1
chr2	31749680	31749916	UCON44	DNA/TcMar
chr4	155492374	155492639	AluSx4	SINE/Alu
chr4	70345252	70345601	L1PB2	LINE/L1
chr1	94628135	94632777	HERVL-int HERVL-int HERVL-int MLT2A1	LTR/ERV1
chr14	57955306	57956261	L1PA11	LINE/L1
chr3	120362881	120363122	MIRb	SINE/MIR
chr19	45121124	45121291	LTR33	LTR/ERV1
chr2	31749984	31750199	MER102a	DNA/hAT-Charlie
chr4	185540479	185540614	LTR26B	LTR/ERV1
chr10	101554872	101555148	Charlie4a	DNA/hAT-Charlie
chr9	104139832	104141489	L1P3	LINE/L1
chr7	99262079	99262760	L1MB7	LINE/L1
chr16	55845408	55845866	MER67B	LTR/ERV1
chr10	33370790	33370887	MLT1J	LTR/ERV1-MaLR
chr1	159559006	159559199	Tigger15a	DNA/TcMar-Tigger
chr8	38605558	38607094	L1MEa	LINE/L1
chr9	69616189	69616775	LTR26	LTR/ERV1
chr12	104674303	104674730	MLT2D	LTR/ERV1
chr19	48370790	48371099	AluSp	SINE/Alu
chr8	128218936	128219062	MIRb	SINE/MIR
chr10	47137041	47137139	L2c	LINE/L2
chr3	177613375	177613529	FRAM	SINE/Alu
chr19	6709179	6709485	AluSc	SINE/Alu

chr4	129489495	129489669	MIRb	SINE/MIR
chr5	68325390	68325617	X4a_DNA	DNA/TcMar
chr9	75475541	75476642	L1PB2	LINE/L1
chr10	96442999	96443062	MER5B	DNA/hAT-Charlie
chr3	170712990	170713137	MIRb	SINE/MIR
chr5	173213844	173214276	L2b	LINE/L2
chr10	5041188	5041363	L2	LINE/L2
chr10	101554650	101554734	MIR3	SINE/MIR
chr16	4956214	4956525	AluY	SINE/Alu
chr6	107219507	107220056	MLT1K	LTR/ERV1-MaLR
chr10	91197909	91198208	MER58B	DNA/hAT-Charlie
chr17	48735083	48735239	MIRb	SINE/MIR
chr3	177616070	177616636	MER52A	LTR/ERV1
chr2	138877275	138877952	L1ME3	LINE/L1
chr19	18498431	18498481	L2b	LINE/L2
chr3	177615871	177616068	MER44A	DNA/TcMar-Tigger
chr10	96490418	96490855	L1PA16	LINE/L1
chr12	52629483	52629638	MIR3	SINE/MIR
chr1	9485160	9485406	MIR	SINE/MIR
chr2	235776100	235777004	Tigger17d	DNA/TcMar-Tigger
chr10	101556289	101556471	AluSx	SINE/Alu
chr9	75518910	75519155	MIRb	SINE/MIR
chr3	177635079	177636386	MER52A	LTR/ERV1
chr10	96682191	96683340	Tigger1	DNA/TcMar-Tigger
chr9	69621250	69625205	L1PA10	LINE/L1
chr6	3897709	3898086	L2a	LINE/L2
chr10	71019319	71019702	MSTA	LTR/ERV1-MaLR
chr10	33280783	33281178	L1MC3	LINE/L1
chrX	146966443	146966895	LTR06	LTR/ERV1
chr2	44105901	44106257	THE1C	LTR/ERV1-MaLR
chr19	6704937	6705049	AluJo	SINE/Alu
chr10	33287833	33290177	L1PA16	LINE/L1
chr2	235775063	235775430	THE1C	LTR/ERV1-MaLR
chr10	95357822	95357959	MIR3	SINE/MIR
chr16	20425482	20427242	MLT1D MLT1D-int	LTR/ERV1-MaLR
chr19	48371175	48371462	AluYj4	SINE/Alu
chr6	3904596	3904719	LTR85b	LTR/Gypsy?
chr10	5012588	5012730	L1MC5a	LINE/L1
chr10	91197095	91197326	MIRc	SINE/MIR
chr10	5012758	5013165	L1PA2	LINE/L1
chr10	96710576	96711328	L1PA7	LINE/L1

chr20	38641322	38641668	L2a	LINE/L2
chr10	47137285	47137376	MIR1_Amn	SINE/MIR
chr2	151008840	151009356	L1MC1	LINE/L1
chr10	47137624	47137767	MIR3	SINE/MIR
chr5	148587719	148588358	MLT1K MLT1K	LTR/ERV1-MaLR
chr6	25781707	25782112	MSTB1	LTR/ERV1-MaLR
chr9	38476803	38477617	L1M1	LINE/L1
chr11	46761152	46761281	FRAM	SINE/Alu
chr6	133010647	133011847	L2c	LINE/L2
chr10	95350713	95350923	MIRb	SINE/MIR
chr14	88552891	88553225	L1PA13	LINE/L1
chr3	170706071	170708379	L1PB4	LINE/L1
chr6	53428433	53428628	MIRb	SINE/MIR
chr7	155761236	155761679	L1M1	LINE/L1
chr8	128155295	128159498	LOR1a LOR1-int LOR1-int	LTR/ERV1
chr10	33370592	33370677	MER81	DNA/hAT-Blackjack
chr7	155038328	155038790	L2a	LINE/L2
chr19	48371798	48372106	AluSx1	SINE/Alu
chr8	123682377	123682742	Tigger2a	DNA/TcMar-Tigger
chr10	115350753	115350963	MIRb	SINE/MIR
chr1	207265588	207265962	L1ME4a	LINE/L1
chr6	29520305	29520710	MER57F	LTR/ERV1
chr3	170705291	170706060	Charlie2a	DNA/hAT-Charlie
chr6	53485982	53486270	L1M6	LINE/L1
chr10	33271447	33271696	AluSz6	SINE/Alu
chr3	170713173	170713265	L2c	LINE/L2
chr10	96615008	96615159	MIR	SINE/MIR
chr3	190035437	190035673	MER8	DNA/TcMar-Tigger
chr10	74691015	74691263	AluJr4	SINE/Alu
chr5	148635400	148635579	MIRb	SINE/MIR
chr6	86098261	86098420	MIR3	SINE/MIR
chr3	81583444	81583559	L2b	LINE/L2
chr10	5145602	5146059	MLT1H	LTR/ERV1-MaLR
chr4	114320813	114323098	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr10	33282342	33282636	L1MC2	LINE/L1
chr7	87102358	87103041	L2a	LINE/L2
chr14	57950831	57951214	MLT1C	LTR/ERV1-MaLR
chr6	133006578	133007163	HAL1	LINE/L1
chr10	47136067	47136165	MIRb	SINE/MIR
chr6	3753150	3753263	L1ME3G	LINE/L1
chr10	5010607	5010782	L2	LINE/L2

chr4	155493436	155493859	LTR32	LTR/ERV1
chr6	86097462	86097574	L1MC5a	LINE/L1
chr10	33282015	33282316	AluSz	SINE/Alu
chr12	120079485	120079915	MER113	DNA/hAT-Charlie
chr6	3905274	3905381	AluJo	SINE/Alu
chr8	38604546	38605562	L1MC1	LINE/L1
chr5	67100303	67100606	MLT2B1 MLT2B1	LTR/ERV1
chr6	3898774	3898913	L1MC5	LINE/L1
chr8	38603815	38604240	L1MEf	LINE/L1
chr10	110307837	110308124	AluSx	SINE/Alu
chr1	219155867	219157428	MER52A	LTR/ERV1
chr6	86097082	86097452	L1ME2z	LINE/L1
chr3	190033045	190033157	MER81	DNA/hAT-Blackjack
chr19	15761680	15761979	AluSg	SINE/Alu
chr14	57939957	57940936	L2b	LINE/L2
chr10	96487641	96488343	L1MC4	LINE/L1
chr8	38604234	38604573	L1MEa	LINE/L1
chr11	18249848	18250723	L2	LINE/L2
chr10	96484996	96485702	L1MEg1	LINE/L1
chr10	33278390	33278648	L1MB3	LINE/L1
chr1	219261793	219268105	L1MA4	LINE/L1
chr7	45930673	45930850	L1MB3	LINE/L1
chr10	95356795	95356988	MER5A	DNA/hAT-Charlie
chr19	15761176	15761257	LTR40A1	LTR/ERV1
chr5	148633399	148633751	THE1B	LTR/ERV1-MaLR
chr3	170704141	170704726	HAL1	LINE/L1
chr15	67276394	67276842	MSTA1	LTR/ERV1-MaLR
chr21	23409541	23411362	L1PA13	LINE/L1
chr3	120361333	120361541	MER63A	DNA/hAT-Blackjack
chr17	48739011	48739260	L2c	LINE/L2
chr8	128217687	128217813	MIR3	SINE/MIR
chr3	177784614	177784868	MIRb	SINE/MIR
chr9	35455414	35458921	LTR10F HERVIP10FH-int	LTR/ERV1
chr11	120092985	120093286	AluSx	SINE/Alu
chr1	145757314	145757455	MIR	SINE/MIR
chr1	220085895	220086205	AluYk3	SINE/Alu
chr10	33276651	33276966	AluJb	SINE/Alu
chr10	5037773	5037851	MER5A	DNA/hAT-Charlie
chr11	62926747	62929252	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr14	57957191	57957401	MIRb	SINE/MIR
chr3	177618626	177618910	AluSx3	SINE/Alu

chr10	47135527	47135903	ORSL-2a	DNA/hAT-Tip100
chr20	37006449	37006582	MIR	SINE/MIR
chr5	56974628	56975017	MLT1J2	LTR/ERV1-MaLR
chr5	148637058	148637164	L1MC4	LINE/L1
chr12	76707509	76707721	MIRb	SINE/MIR
chr3	177783980	177784264	AluSz6	SINE/Alu
chr8	131452767	131453026	L2c	LINE/L2
chr20	38636810	38637167	MLT1H2	LTR/ERV1-MaLR
chr7	155037928	155038290	L2a	LINE/L2
chr20	38672624	38673114	LTR45B	LTR/ERV1
chr10	33278649	33278959	AluSz	SINE/Alu
chr6	132165338	132166183	Tigger6a	DNA/TcMar-Tigger
chr3	190033414	190033526	L3b	LINE/CR1
chr8	128216540	128217294	L1ME3	LINE/L1
chr1	236132184	236132634	MLT1G3	LTR/ERV1-MaLR
chr10	96666546	96667865	L1MA6	LINE/L1
chr9	38491655	38494297	L1P3	LINE/L1
chr6	53423567	53424097	MER4-int	LTR/ERV1
chr8	123682764	123683528	HAL1	LINE/L1
chr6	64531147	64532005	LTR78	LTR/ERV1
chr20	38641669	38641875	MER20	DNA/hAT-Charlie
chr2	138849214	138851218	L2a	LINE/L2
chr12	76698318	76698793	MLT1J	LTR/ERV1-MaLR
chr2	216278259	216278690	HAL1	LINE/L1
chr5	148583344	148583576	MIR	SINE/MIR
chr9	116822870	116823004	MIRb	SINE/MIR
chr5	95549205	95549511	AluJr	SINE/Alu
chr3	120361542	120361796	LTR33	LTR/ERV1
chr4	114338581	114339495	L1PB1	LINE/L1
chr5	131696584	131696760	MLT2B2	LTR/ERV1
chr14	57954046	57954179	L2a	LINE/L2
chr4	185541095	185541393	AluSx1	SINE/Alu
chr4	77234620	77234742	AluJr	SINE/Alu
chr10	96490856	96491163	AluYf1	SINE/Alu
chr10	33280492	33280782	AluSz	SINE/Alu
chr10	5014014	5014176	L1MC4	LINE/L1
chr6	133002184	133002693	MLT1F2	LTR/ERV1-MaLR
chr3	190036747	190036927	L3b	LINE/CR1
chr1	236131189	236131476	L1PB1	LINE/L1
chr18	56201853	56201913	MER5A1	DNA/hAT-Charlie
chr1	63072597	63072887	AluSx	SINE/Alu

chr1	236107722	236107961	MIRb	SINE/MIR
chr7	14318496	14324646	L1PA3	LINE/L1
chr7	99248570	99248826	L1MC5	LINE/L1
chr1	200336008	200336068	MIRb	SINE/MIR
chr12	103250109	103255760	L1PA5	LINE/L1
chr19	6705320	6705657	AluJr	SINE/Alu
chr9	67065660	67066246	LTR26	LTR/ERV1
chr10	96523531	96532539	LTR12 HERV9-int	LTR/ERV1
chr9	99076057	99076265	L1M4b	LINE/L1
chr6	107193026	107193650	LTR82A	LTR/ERV1
chr15	50504302	50508802	L1PB1	LINE/L1
chr6	86097689	86097980	AluJr	SINE/Alu
chr10	49199008	49199451	L2c	LINE/L2
chr10	74691882	74692072	MIRb	SINE/MIR
chr5	173215487	173215964	MLT1K	LTR/ERV1-MaLR
chr7	155761080	155761216	FLAM_C	SINE/Alu
chr4	155493382	155493435	L1MA10	LINE/L1
chr3	149211425	149211668	L2c	LINE/L2
chr10	47138923	47139994	L1P4	LINE/L1
chr9	75517733	75517880	MER5A1	DNA/hAT-Charlie
chr15	67279825	67279968	MLT1K	LTR/ERV1-MaLR
chr8	128178557	128181118	L1MC1	LINE/L1
chr10	101564599	101565004	L2a	LINE/L2
chr2	44106710	44107091	L1MC4	LINE/L1
chr10	33277589	33277814	L1MB3	LINE/L1
chr7	99568884	99569019	MIRb	SINE/MIR
chr1	78608872	78609371	L2a	LINE/L2
chr1	196690449	196692894	L1PA15-16	LINE/L1
chr6	3898094	3898391	AluSx1	SINE/Alu
chr1	236119484	236119606	MIRb	SINE/MIR
chr2	169777960	169778356	HAL1	LINE/L1
chr3	188655969	188656765	LTR17	LTR/ERV1
chr1	78607278	78607726	L2a	LINE/L2
chr10	101555616	101555762	FRAM	SINE/Alu
chr22	24913720	24913850	L1ME4c	LINE/L1
chr2	169775473	169776370	HAL1	LINE/L1
chr10	5142203	5142503	AluSp	SINE/Alu
chr22	30883330	30883449	AluJo	SINE/Alu
chr5	148636020	148636415	L1MC5a	LINE/L1
chr18	68003108	68003178	MIRc	SINE/MIR
chr7	155035899	155036446	L1MB2	LINE/L1

chr3	149209539	149209736	L2c	LINE/L2
chr15	67280492	67283492	L1M1	LINE/L1
chr9	67063624	67065622	L1PA10	LINE/L1
chr4	185545896	185546438	L2	LINE/L2
chr10	96455314	96461393	L1PA4	LINE/L1
chr1	236107477	236107669	MER5A	DNA/hAT-Charlie
chrX	146966934	146967244	AluJb	SINE/Alu
chr7	134218873	134219172	AluSz	SINE/Alu
chr1	207266459	207266606	L1ME3G	LINE/L1
chr4	187211140	187211283	L2a	LINE/L2
chr14	76040883	76041325	HAL1	LINE/L1
chr5	149016861	149017141	AluSx	SINE/Alu
chr12	104674085	104674291	L2-3_Crp	LINE/L2
chr2	234673865	234674326	L1PA8A	LINE/L1
chr14	103674437	103674738	AluSg	SINE/Alu
chr3	151548103	151549170	L1PB1	LINE/L1
chr6	3900641	3901085	L1MC5	LINE/L1
chr5	148632844	148633116	MIR	SINE/MIR
chr4	77159896	77161305	L1MB3	LINE/L1
chr1	196806760	196807574	L1MA9	LINE/L1
chr5	131696780	131696931	MIRb	SINE/MIR
chr18	56207999	56208054	L2b	LINE/L2
chr17	48738666	48738899	MIRb	SINE/MIR
chr14	94853201	94853378	MIRb	SINE/MIR
chr3	177784265	177784536	L1MD1	LINE/L1
chr2	128183347	128183425	MIRc	SINE/MIR
chr7	155043098	155043400	AluSz	SINE/Alu
chr10	71020689	71020852	MIRb	SINE/MIR
chr11	61518273	61518956	L2a	LINE/L2
chr6	64276004	64276464	LTR42	LTR/ERV
chr12	12557637	12557934	AluSx1	SINE/Alu
chr14	94763652	94765918	THE1A THE1A-int THE1A	LTR/ERV-MaLR
chr10	5049827	5050548	MST-int	LTR/ERV-MaLR
chr2	20792723	20792932	L2c	LINE/L2
chr6	31970739	31970979	L3b	LINE/CR1
chr18	56209729	56210089	LTR41B	LTR/ERV
chr15	80490363	80490828	LTR85c	LTR/Gypsy?
chr7	106210455	106211057	L4_A_Mam	LINE/RTE-X
chr2	233738826	233739357	L1MC4	LINE/L1
chr10	5034862	5035151	AluSx3	SINE/Alu
chr20	37011101	37011223	L1ME4b	LINE/L1

chr3	120361853	120361980	MER5A	DNA/hAT-Charlie
chrX	99912925	99913885	L1MA4A	LINE/L1
chr11	126200278	126200545	MIR	SINE/MIR
chr10	47141668	47144039	L1M4	LINE/L1
chr5	67103911	67104170	MIRb	SINE/MIR
chr10	5016504	5017241	L1MEd	LINE/L1
chr5	78375437	78375727	AluSx1	SINE/Alu
chr6	29520719	29520819	L3	LINE/CR1
chr9	42876335	42876563	L2b	LINE/L2
chr9	112150045	112151134	L3	LINE/CR1
chr16	80189502	80189614	MIRb	SINE/MIR
chr10	33423433	33423859	LTR45B	LTR/ERV1
chr10	33278090	33278389	AluSx1	SINE/Alu
chr16	55845895	55846097	MER67A	LTR/ERV1
chr6	53423328	53423566	LTR8	LTR/ERV1
chr5	148584195	148584428	MIRb	SINE/MIR
chr17	48765879	48765965	MIRb	SINE/MIR
chr1	236133153	236133302	L1ME4a	LINE/L1
chr8	128123068	128124053	L1MA7	LINE/L1
chr16	83996145	83996556	MER4A1	LTR/ERV1
chr7	134218105	134218261	MIRc	SINE/MIR
chr20	38640482	38640688	MLT1O	LTR/ERV1-MaLR
chr12	7652735	7653037	AluSq10	SINE/Alu
chr10	96492880	96493019	MIR3	SINE/MIR
chr3	33836712	33837055	MLT1J2	LTR/ERV1-MaLR
chr7	130600663	130600797	MIRc	SINE/MIR
chr1	27238781	27239030	MIR	SINE/MIR
chr8	38603736	38603808	L1MEa	LINE/L1
chr3	142660453	142660763	L4_C_Mam	LINE/RTE-X
chr11	75441487	75441657	MIRb	SINE/MIR
chr8	17746777	17747061	AluSx	SINE/Alu
chr10	5014599	5014677	MER5A	DNA/hAT-Charlie
chr5	148634363	148634511	MER5B	DNA/hAT-Charlie
chr9	75476928	75477195	L1PB2	LINE/L1
chr1	150153507	150153809	AluSx1	SINE/Alu
chr17	48762693	48762793	MIR	SINE/MIR
chr14	105213853	105214135	AluSg	SINE/Alu
chr12	88072634	88072806	L1ME3F	LINE/L1
chr8	122156931	122157375	MLT2A2	LTR/ERV1
chr5	148634872	148635365	L2a	LINE/L2
chr1	196722077	196722891	L1MA9	LINE/L1

chr10	80216105	80216414	AluSg	SINE/Alu
chr17	17348005	17348276	AluSp	SINE/Alu
chr8	131454504	131454626	MIR3	SINE/MIR
chr12	104665848	104666292	LTR10F	LTR/ERV1
chr10	110321509	110321914	ERV3-16A3_LTR ERV3-16A3_LTR	LTR/ERV1
chr4	1197052	1197656	L1MB7	LINE/L1
chr12	52646415	52646660	MER102c	DNA/hAT-Charlie
chr6	53499685	53499997	MLT1C	LTR/ERV1-MaLR
chr10	29712892	29713015	MIR1_Amn	SINE/MIR
chr19	6705658	6705984	AluSx1	SINE/Alu
chr20	38641876	38642002	L2a	LINE/L2
chr17	77709703	77710001	AluSq2	SINE/Alu
chr3	177783871	177783979	L1MD1	LINE/L1
chr22	24900194	24900683	HAL1	LINE/L1
chr11	76476340	76476669	L2c	LINE/L2
chr5	148583583	148584105	L3	LINE/CR1
chr11	114176069	114177511	L1PA5	LINE/L1
chr9	38475825	38476499	L1M1	LINE/L1
chr10	29747748	29748038	AluJr	SINE/Alu
chr5	148633122	148633308	L2d2	LINE/L2
chr5	148584441	148584609	L3	LINE/CR1
chr3	178668031	178668452	MLT1C2	LTR/ERV1-MaLR
chr3	177632368	177632824	L1PA7	LINE/L1
chr17	77013366	77014223	MER41-int MER41B	LTR/ERV1
chr14	54260004	54260142	MIR	SINE/MIR
chr4	1195724	1195893	L1MB7	LINE/L1
chr15	58574316	58574812	MLT1H	LTR/ERV1-MaLR
chr8	128214509	128215565	L1ME3	LINE/L1
chr3	127464130	127464537	L1PB4	LINE/L1
chr6	133006457	133006526	L2	LINE/L2
chr7	95026657	95026887	MIRb	SINE/MIR
chr22	30883904	30884204	AluSz	SINE/Alu
chr12	122287241	122287442	MIR	SINE/MIR
chr18	56201822	56201925	MER5A	DNA/hAT-Charlie
chr8	123670412	123670648	MER4D	LTR/ERV1
chr5	62671526	62677794	L1PA7	LINE/L1
chrX	99932539	99933159	L2a	LINE/L2
chr10	5148661	5148956	AluSx	SINE/Alu
chr3	177619772	177619910	L1M3c	LINE/L1
chr10	91196438	91196549	MER30	DNA/hAT-Charlie
chr8	123698056	123698351	MLT1J	LTR/ERV1-MaLR

chr20	25815062	25815351	AluSx	SINE/Alu
chr12	88072930	88073407	MLT1H	LTR/ERV1-MaLR
chr3	120391520	120391648	MIRb	SINE/MIR
chr10	33370889	33371095	hAT-N1_Mam	DNA/hAT-Tip100?
chr5	172234044	172234193	MIRc	SINE/MIR
chr15	80491546	80491704	MER5A1	DNA/hAT-Charlie
chr5	67102283	67102404	MIRc	SINE/MIR
chr16	83998200	83998429	MIR	SINE/MIR
chr7	149928742	149929630	L1MC3	LINE/L1
chr20	26003586	26003907	L1MB8	LINE/L1
chr12	21071527	21073147	L1MA6	LINE/L1
chr10	114567034	114567316	MLT1C2	LTR/ERV1-MaLR
chr2	96189284	96189576	AluJr	SINE/Alu
chr6	86099852	86100178	L2c	LINE/L2
chr5	179254307	179254583	AluY	SINE/Alu
chr14	94749229	94749284	MIR3	SINE/MIR
chr3	177625619	177626041	L1P2	LINE/L1
chr6	133007304	133007596	AluSz	SINE/Alu
chr10	74692826	74693136	AluSx	SINE/Alu
chr8	26618875	26619216	MLT1B	LTR/ERV1-MaLR
chr8	128200212	128200344	MIR	SINE/MIR
chr1	16941817	16942127	AluJb	SINE/Alu
chr11	72464239	72464493	MIRb	SINE/MIR
chr12	120079978	120080282	AluSz	SINE/Alu
chr2	44106498	44106647	MER5A1	DNA/hAT-Charlie
chr1	236107365	236107476	MIR3	SINE/MIR
chr4	69929858	69930516	LTR76	LTR/ERV1
chr3	177783573	177783870	AluJb	SINE/Alu
chr8	105394173	105394326	MIRb	SINE/MIR
chr18	56210837	56210994	LTR41B	LTR/ERV1
chr3	142660249	142660351	L4_C_Mam	LINE/RTE-X
chr8	131452865	131453337	L2b	LINE/L2
chr14	88566877	88568694	L1MEc	LINE/L1
chrX	99927405	99927637	MIR	SINE/MIR
chr15	67279980	67280166	MER53	DNA/hAT
chr1	150508433	150508717	L2d	LINE/L2
chr16	57812689	57812845	FRAM	SINE/Alu
chr21	34598178	34598384	L1MCa	LINE/L1
chr20	38659390	38659811	L2	LINE/L2
chr10	74690716	74690994	L1M5	LINE/L1
chr3	33483027	33483220	AluSz	SINE/Alu

chr11	120090050	120090218	MLT1J	LTR/ERV1-MaLR
chr22	24911662	24911971	AluSz	SINE/Alu
chr1	209911945	209912399	MLT1C2	LTR/ERV1-MaLR
chr17	66990317	66991742	L2	LINE/L2
chr6	133000009	133001130	L1PA16	LINE/L1
chr21	36216237	36216525	MamTip2b	DNA/hAT-Tip100
chr16	1348843	1348961	MLT1D	LTR/ERV1-MaLR
chr10	71000650	71001236	L2a	LINE/L2
chr10	96739065	96740730	L1MA1	LINE/L1
chrX	99911183	99911875	L1MA4A	LINE/L1
chr15	84697467	84699867	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr11	20081937	20082013	MamTip2b	DNA/hAT-Tip100
chr21	36218772	36218968	MIR3	SINE/MIR
chr4	77161294	77162921	L1MB3	LINE/L1
chr5	60545290	60545977	L1PA10	LINE/L1
chr10	5019195	5019296	MER68	LTR/ERV1
chr3	187013697	187014559	Ricksha_0	DNA/MULE-MuDR
chr6	53416511	53418800	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr1	95337189	95337620	Charlie20a	DNA/hAT-Charlie
chr8	128167492	128169545	L1PB1	LINE/L1
chrX	37724826	37727119	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr22	24832715	24832936	L2b	LINE/L2
chr1	145757536	145757868	L3	LINE/CR1
chr1	63076146	63076735	L1PA7	LINE/L1
chr3	9990014	9990191	AluJb	SINE/Alu
chr10	101608993	101609166	L2c	LINE/L2
chr19	17925110	17925419	AluSz6	SINE/Alu
chr1	159569093	159569190	LTR91	LTR
chr22	30883818	30883888	MIR1_Amn	SINE/MIR
chr3	177617914	177618022	Tigger7	DNA/TcMar-Tigger
chr10	114567338	114567640	AluSq2	SINE/Alu
chr1	236136777	236137813	L1MB4	LINE/L1
chr20	36768808	36769266	Charlie4a	DNA/hAT-Charlie
chr8	128197457	128197738	AluSz	SINE/Alu
chr5	133844665	133844895	L2c	LINE/L2
chr2	91812103	91812226	MER5A	DNA/hAT-Charlie
chr14	57930447	57930862	LTR16C	LTR/ERV1
chr4	1168321	1168658	Charlie1a	DNA/hAT-Charlie
chr7	134219620	134219740	MER5B	DNA/hAT-Charlie
chr18	32484985	32487285	THE1C THE1C-int THE1C	LTR/ERV1-MaLR
chr10	29772315	29772477	MER5B	DNA/hAT-Charlie

chr13	80635938	80639553	MLT2A1 MLT2A1 HERVL-int MLT2A1	LTR/ERV
chr17	67066439	67069915	L1P3	LINE/L1
chr14	28730290	28732796	L1PREC2	LINE/L1
chr3	148891706	148892317	L1MC4	LINE/L1
chr7	134219742	134219987	AluJr	SINE/Alu
chr20	26002121	26002404	AluSq2	SINE/Alu
chr14	57953199	57953326	MER5B	DNA/hAT-Charlie
chr2	88986274	88986487	MER20	DNA/hAT-Charlie
chr6	86098566	86098630	L2b	LINE/L2
chr18	24333828	24334122	AluSz	SINE/Alu
chr5	78374311	78374469	MIRb	SINE/MIR
chr10	46967107	46967163	L2b	LINE/L2
chr6	107218337	107218539	MER3	DNA/hAT-Charlie
chr20	36998164	36998535	LTR33A_	LTR/ERV
chr9	19126759	19127047	AluSx1	SINE/Alu
chr12	122287866	122287967	L2b	LINE/L2
chr4	185539742	185540209	MER4A1	LTR/ERV1
chr1	145759030	145759324	AluSz	SINE/Alu
chr20	36775733	36776163	L2b	LINE/L2
chr8	128231034	128231109	MIR	SINE/MIR
chr3	125835877	125836096	AluJb	SINE/Alu
chr5	95545932	95548535	L1MD	LINE/L1
chr6	53499364	53499670	AluSq2	SINE/Alu
chr9	6723408	6723534	HERVL40-int	LTR/ERV
chr9	114350291	114350476	AluJb	SINE/Alu
chr3	145784175	145784575	L1M1	LINE/L1
chr11	63335313	63335646	L1ME3F	LINE/L1
chr10	47124444	47124837	MLT1K	LTR/ERV-MaLR
chr2	120244211	120244374	MIR	SINE/MIR
chr7	134220711	134220846	MER91A	DNA/hAT-Tip100
chr1	16491206	16491415	MIRb	SINE/MIR
chr12	21392811	21393782	Tigger1	DNA/TcMar-Tigger
chr12	122290894	122291252	L1PA11	LINE/L1
chr22	30883451	30883750	AluY	SINE/Alu
chr10	5000323	5001050	MST-int	LTR/ERV-MaLR
chr2	110775132	110777591	L1PA3	LINE/L1
chr21	40284281	40284701	L1MB7	LINE/L1
chr9	104130999	104131169	Charlie4z	DNA/hAT-Charlie
chr12	126782643	126783259	MLT1F1 MLT1F1-int	LTR/ERV-MaLR
chr10	109969578	109975705	L1PBa	LINE/L1
chr16	82041532	82043792	THE1B THE1B-int THE1B	LTR/ERV-MaLR

chr3	186967438	186967580	MIR3	SINE/MIR
chr2	169776676	169777082	HAL1	LINE/L1
chr11	112050731	112051058	MER2B	DNA/TcMar-Tigger
chr2	111139363	111139672	AluSc	SINE/Alu
chr12	103238242	103238836	MLT2B3	LTR/ERV1
chr5	173217736	173217902	MER115	DNA/hAT-Tip100
chr2	234674465	234675333	LTR1A2	LTR/ERV1
chr7	99248401	99248495	MamRep137	DNA/TcMar-Tigger
chr1	63075509	63075819	AluSg	SINE/Alu
chr8	128194662	128195016	THE1B	LTR/ERV1-MaLR
chr2	169778357	169778658	AluY	SINE/Alu
chr16	1343860	1344280	MER41A	LTR/ERV1
chr2	29380457	29380845	L3	LINE/CR1
chr4	1167461	1167586	L1MC4a	LINE/L1
chr10	110212738	110212973	MIRb	SINE/MIR
chr3	125835694	125835764	MIR	SINE/MIR
chr18	56210995	56211092	MIRb	SINE/MIR
chr6	136415455	136415964	L2a	LINE/L2
chr1	9485863	9486067	MIRb	SINE/MIR
chr18	55473546	55473680	L2a	LINE/L2
chr1	8077006	8077133	L2c	LINE/L2
chr3	177619679	177619745	L1M2	LINE/L1
chr7	75704584	75704738	LTR41	LTR/ERV1
chr5	147267655	147268358	L2b	LINE/L2
chr3	127463849	127464093	MIRb	SINE/MIR
chr20	36770833	36771123	AluSx	SINE/Alu
chr17	48724668	48725072	L2	LINE/L2
chr3	119537354	119537560	hAT-1_Mam	DNA/hAT-Tag1
chr22	24871069	24871150	FRAM	SINE/Alu
chr16	57818022	57818128	L2a	LINE/L2
chr3	115325654	115327245	L1PB1	LINE/L1
chr10	29713853	29713943	MIRb	SINE/MIR
chr8	101210866	101211670	L1MB7	LINE/L1
chr16	71615992	71616275	AluY	SINE/Alu
chr18	24485871	24485999	L2c	LINE/L2
chr9	116824195	116824544	L2b	LINE/L2
chr2	138871466	138871946	LTR19A	LTR/ERV1
chr20	25814776	25815059	AluSq2	SINE/Alu
chr10	80210399	80210500	L1ME3A	LINE/L1
chr10	47123768	47124082	THE1D	LTR/ERV1-MaLR
chr8	79724055	79728214	L1MA8	LINE/L1

chr10	11889406	11889717	AluSx1	SINE/Alu
chr6	3728378	3728629	L1PB2	LINE/L1
chrX	154355993	154356076	MER76-int	LTR/ERV1
chr1	75165127	75165344	MER8	DNA/TcMar-Tigger
chr9	75487100	75487392	L2c	LINE/L2
chr12	52632663	52633249	LTR71B	LTR/ERV1
chr8	123671145	123671215	L2b	LINE/L2
chr11	102047747	102047915	L2b	LINE/L2
chr3	42937525	42941143	MER50-int MER50-int MER50C	LTR/ERV1
chr18	55473768	55474077	AluJb	SINE/Alu
chr10	11903173	11903437	L2c	LINE/L2
chr6	160007971	160008680	L1MEj	LINE/L1
chr20	36764275	36764470	MIRc	SINE/MIR
chr7	44572048	44572429	Tigger2a	DNA/TcMar-Tigger
chr16	1346823	1347313	LTR10A	LTR/ERV1
chr14	57933031	57933492	L2a	LINE/L2
chr3	151544040	151544249	MIRc	SINE/MIR
chr6	150985174	150985305	MLT1L	LTR/ERV1-MaLR
chr18	24304222	24304977	L1ME1	LINE/L1
chr10	6015189	6015465	L1M5	LINE/L1
chr2	211052192	211052493	AluSg	SINE/Alu
chr1	236099097	236099806	L1MC4	LINE/L1
chr10	33277933	33278089	L1MB3	LINE/L1
chr4	1196802	1197027	MLT1A1 MLT1A1	LTR/ERV1-MaLR
chr14	54173412	54173740	L3	LINE/CR1
chr11	120093341	120093649	AluSc	SINE/Alu
chr3	81145008	81145431	LFSINE_Vert	SINE/tRNA
chr3	93676693	93676961	AluSx	SINE/Alu
chr1	100147196	100147418	MER20	DNA/hAT-Charlie
chr15	29976110	29976380	L1M4	LINE/L1
chr12	104667090	104667400	AluSg	SINE/Alu
chr1	223721773	223722134	MLT1A0	LTR/ERV1-MaLR
chr6	3897489	3897707	L1ME3F	LINE/L1
chr7	55225482	55225869	L1MC4a	LINE/L1
chr1	236133435	236133669	L1ME4a	LINE/L1
chr10	47130364	47130828	LTR33	LTR/ERV1
chr12	103244584	103244896	AluJr	SINE/Alu
chr8	62571431	62571492	L2a	LINE/L2
chr9	101918415	101919932	L1MB7	LINE/L1
chr9	124115955	124116408	L2c	LINE/L2
chr5	95549142	95549204	L1ME4b	LINE/L1

chr1	16490623	16490866	L2a	LINE/L2
chr10	4276751	4277557	Tigger2	DNA/TcMar-Tigger
chr1	236131949	236132183	Tigger4a	DNA/TcMar-Tigger
chr3	52855492	52855635	MIR1_Amn	SINE/MIR
chrX	99934604	99934751	MIR	SINE/MIR
chr12	104500939	104501220	L2a	LINE/L2
chr20	42215586	42215887	AluSp	SINE/Alu
chr3	81551334	81551470	Charlie23a	DNA/hAT-Charlie
chr10	5044110	5044621	MER68	LTR/ERV
chr8	123676717	123676880	MIRb	SINE/MIR
chr2	170568760	170574103	HERVL18-int HERVL18-int HERVL18-int LTR18B	LTR/ERV
chr3	127472150	127472291	Tigger15a	DNA/TcMar-Tigger
chr12	120069927	120070181	MIR	SINE/MIR
chr10	82022000	82022865	HSMAR2	DNA/TcMar-Mariner
chr16	13339970	13340331	THE1B	LTR/ERV-MaLR
chr17	58163357	58163535	MER117	DNA/hAT-Charlie
chr10	47119808	47120075	L1ME2z	LINE/L1
chr8	19259197	19259432	MIR	SINE/MIR
chr14	62023054	62023253	CR1-3_Croc	LINE/CR1
chr6	160457553	160457666	L3	LINE/CR1
chr6	3735037	3735323	AluJo	SINE/Alu
chr8	128213283	128213349	L2b	LINE/L2
chr12	27451818	27452144	L2	LINE/L2
chr1	201371338	201371644	AluSz6	SINE/Alu
chr17	79282475	79282780	AluSx1	SINE/Alu
chr20	26001647	26001825	AluSq2	SINE/Alu
chr1	78949258	78954747	L1PA8A	LINE/L1
chr5	176012598	176012662	MIRb	SINE/MIR
chr11	86146665	86147094	LTR16	LTR/ERV
chr14	94778315	94778605	Tigger20a	DNA/TcMar-Tigger
chr19	6671650	6671971	AluSx1	SINE/Alu
chr2	45876309	45876462	MER96B	DNA/hAT-Tip100
chr10	71022810	71023154	AluJb	SINE/Alu
chr11	76478495	76478638	MIR3	SINE/MIR
chr9	72049711	72055847	L1PA4	LINE/L1
chr16	29849867	29850167	AluJr	SINE/Alu
chr12	76697517	76698145	MER41B	LTR/ERV1
chr6	26112890	26113187	MLT1J	LTR/ERV-MaLR
chr7	149927833	149928314	L1MC3	LINE/L1
chr3	119530755	119530895	MER5A	DNA/hAT-Charlie
chr12	52649537	52649617	L2b	LINE/L2

chr12	96053070	96053370	AluJb	SINE/Alu
chr4	1195374	1195670	AluY	SINE/Alu
chr8	19259707	19259856	MER63A	DNA/hAT-Blackjack
chr9	4654276	4655017	LTR1A2	LTR/ERV1
chr3	120348391	120349645	L1PREC2	LINE/L1
chr9	38476500	38476802	AluSz6	SINE/Alu
chr10	47118501	47119802	L1MA3	LINE/L1
chr3	151550866	151551780	L2	LINE/L2
chr7	95027282	95027395	L2b	LINE/L2
chr9	67057162	67062587	L1PA10	LINE/L1
chr3	81583404	81583496	L2c	LINE/L2
chr11	61519050	61519335	AluSx	SINE/Alu
chr5	90608956	90609141	MamRTE1	LINE/RTE-BovB
chr15	67346976	67347543	L2c	LINE/L2
chr10	101612957	101613075	MER94	DNA/hAT-Blackjack
chr10	5034178	5034381	L1MEd	LINE/L1
chr1	16940831	16941382	L2b	LINE/L2
chr10	5017767	5017970	L1MEd	LINE/L1
chr6	3753856	3754211	MER51B	LTR/ERV1
chr6	32004956	32005262	MLT10	LTR/ERV1-MaLR
chr18	56158340	56159050	LTR8	LTR/ERV1
chr10	101555838	101555979	AluSx	SINE/Alu
chr17	79281686	79282029	L2	LINE/L2
chr20	43053919	43054283	L2c	LINE/L2
chr9	67257861	67263285	L1PA10	LINE/L1
chr4	69911256	69912793	L1PB2	LINE/L1
chr9	114349107	114349394	AluSq2	SINE/Alu
chr9	38462802	38464937	L1ME1	LINE/L1
chr9	42884616	42888073	L1PA10	LINE/L1
chr10	80191591	80192520	L1MC4a	LINE/L1
chr3	38457285	38457631	THE1D	LTR/ERV1-MaLR
chr6	32003476	32003716	L3b	LINE/CR1
chr19	6705051	6705295	Zaphod4a	DNA/hAT-Tip100
chr20	42214676	42214970	AluSz	SINE/Alu
chr6	64532006	64532304	AluSx	SINE/Alu
chr4	77843862	77844129	AluSz	SINE/Alu
chr10	115349938	115350184	MIR	SINE/MIR
chr5	132162780	132163026	L2a	LINE/L2
chr7	100770846	100771154	AluJb	SINE/Alu
chr13	94876547	94877847	HSMAR2	DNA/TcMar-Mariner
chr10	74693505	74693784	AluJr	SINE/Alu

chr18	24487770	24488100	L1MB3	LINE/L1
chrX	54996773	55000000	L1PA3	LINE/L1
chr17	48729145	48729780	MER92-int	LTR/ERV1
chr10	47097505	47097615	MLT1K	LTR/ERV1-MaLR
chr2	128182133	128182270	FLAM_C	SINE/Alu
chr9	42884120	42884766	L1PA10	LINE/L1
chr1	94636223	94636531	L1M5	LINE/L1
chr7	100778185	100778495	AluSz	SINE/Alu
chr3	120350107	120350369	L1MA2	LINE/L1
chr11	120085018	120085185	MIRb	SINE/MIR
chr10	92673469	92673706	MER102a	DNA/hAT-Charlie
chr12	49750290	49750613	L3	LINE/CR1
chr18	56154350	56154762	MLT1C	LTR/ERV1-MaLR
chr19	18498624	18498941	AluSx1	SINE/Alu
chr2	114153621	114155189	L1M1	LINE/L1
chr10	5028324	5028835	MER9a2	LTR/ERV1
chr19	17925450	17925737	AluJb	SINE/Alu
chr3	52856787	52857113	L2b	LINE/L2
chr9	99077038	99077392	L1M4b	LINE/L1
chr6	52613077	52614103	LTR5A	LTR/ERV1
chr10	47090023	47090477	LTR47B2	LTR/ERV1
chr18	24489290	24489437	MER5A	DNA/hAT-Charlie
chr8	128159810	128160881	LOR1-int LOR1-int	LTR/ERV1
chr1	177906870	177907772	MER49	LTR/ERV1
chr10	47097657	47098075	MLT1A MLT1A	LTR/ERV1-MaLR
chr12	52638832	52639058	MIRb	SINE/MIR
chr5	176012388	176012630	MIR	SINE/MIR
chr1	16116710	16117013	AluSz	SINE/Alu
chr11	45831916	45832111	L2c	LINE/L2
chr15	84695038	84696194	L1MB8	LINE/L1
chr10	118656703	118656793	MARNA	DNA/TcMar-Mariner
chr19	4526571	4526893	AluJo	SINE/Alu
chr15	58573716	58573881	HAL1ME	LINE/L1
chr10	47091761	47092446	L1ME4a	LINE/L1
chr10	47122669	47123179	MLT1C2	LTR/ERV1-MaLR
chr4	980084	980384	MER2	DNA/TcMar-Tigger
chr5	55517194	55523327	L1PA5	LINE/L1
chr10	106031788	106032002	L1MC1	LINE/L1
chr21	36224182	36224466	AluSc8	SINE/Alu
chr9	99076266	99076542	AluSz	SINE/Alu
chr10	47132198	47132571	HAL1ME	LINE/L1

chr5	179256816	179257108	AluJb	SINE/Alu
chr3	52857128	52857323	MIRc	SINE/MIR
chr10	47096263	47096381	L2	LINE/L2
chr2	128181770	128182074	AluSp	SINE/Alu
chr10	5028836	5029471	Tigger1	DNA/TcMar-Tigger
chr11	120091119	120091568	L2c	LINE/L2
chr3	81581468	81581924	L2c	LINE/L2
chr2	203929076	203929687	L1MC4	LINE/L1
chrX	57680116	57682979	MER61-int MER61C	LTR/ERV1
chr5	172196281	172196493	MIRb	SINE/MIR
chr1	201352959	201353398	L2c	LINE/L2
chr9	97782918	97783218	AluSz	SINE/Alu
chr15	63443441	63443732	AluSz	SINE/Alu
chr1	94635002	94636216	L1MC4	LINE/L1
chr9	67254824	67256823	L1PA10	LINE/L1
chr20	42215063	42215299	MIR	SINE/MIR
chr4	979702	980009	AluJr	SINE/Alu
chr20	19866028	19866345	AluSz	SINE/Alu
chr17	6940389	6940685	AluSg	SINE/Alu
chr6	64532585	64533194	L1ME3G	LINE/L1
chr10	106031639	106031787	MER58B	DNA/hAT-Charlie
chr4	77215838	77216265	LTR16B	LTR/ERV1
chr8	65504463	65504755	AluSx1	SINE/Alu
chr10	118657474	118657556	MamRep434	DNA/TcMar-Tigger
chr3	52856536	52856718	MIR	SINE/MIR
chr19	10350670	10350980	AluY	SINE/Alu
chr10	5026076	5026365	L1PBb	LINE/L1
chr10	46972107	46972383	MLT1D	LTR/ERV1-MaLR
chr7	100779922	100780213	AluJr	SINE/Alu
chr16	57808436	57808738	AluJr	SINE/Alu
chr16	18609083	18609428	L1ME4b	LINE/L1
chr10	33186110	33186564	L1MB4	LINE/L1
chr14	76106078	76106315	MIRc	SINE/MIR
chr11	33725744	33725899	MIRb	SINE/MIR
chrX	57682980	57688759	PRIMA4-int PRIMA4-int PRIMA4-int	LTR/ERV1
chr5	145436963	145437125	MIRb	SINE/MIR
chr22	36626470	36626554	MER96	DNA/hAT-Tip100
chr1	16116515	16116709	L1MB3	LINE/L1
chr15	63434735	63435619	MLT1F MLT1F-int	LTR/ERV1-MaLR
chr1	16488368	16488487	MIRb	SINE/MIR
chr19	45421248	45421538	AluSg	SINE/Alu

chr12	104665255	104665569	LTR7B	LTR/ERV1
chr14	71005677	71006749	MER11D MER11D	LTR/ERVK
chr18	55472384	55472504	AluJo	SINE/Alu
chr11	114184886	114185106	MER58A	DNA/hAT-Charlie
chr10	47096414	47096916	LTR16E2	LTR/ERV1
chr16	55818122	55818321	L1PA15	LINE/L1
chr17	53370861	53371103	MIR	SINE/MIR
chr11	66841064	66841357	AluSq	SINE/Alu
chr3	120153785	120154090	AluSx1	SINE/Alu
chr2	165505285	165506780	L1M2	LINE/L1
chr1	145930139	145930304	L3	LINE/CR1
chr11	19733288	19733472	MIRb	SINE/MIR
chr10	5035193	5035947	L1MEd	LINE/L1
chr6	34236620	34237912	LTR12C	LTR/ERV1
chr7	100773000	100773311	AluJr	SINE/Alu
chr6	53489271	53489731	LTR16C	LTR/ERV1
chr11	45828128	45828365	MIR	SINE/MIR
chr3	38456993	38457284	AluSx	SINE/Alu
chr10	47096930	47097428	MLT1C	LTR/ERV1-MaLR
chr5	131700912	131701198	LTR32	LTR/ERV1
chrX	82325443	82326307	MER11D	LTR/ERVK
chr12	49748329	49748727	L1ME3	LINE/L1
chr5	172382773	172382898	MIRb	SINE/MIR
chr7	100774016	100774315	AluJr	SINE/Alu
chr1	178005342	178005663	MER1B	DNA/hAT-Charlie
chr11	120088349	120088433	MIRc	SINE/MIR
chr5	179256382	179256815	HAL1	LINE/L1
chr9	114351923	114352213	AluSx1	SINE/Alu
chr12	56081272	56081573	AluSz	SINE/Alu
chr12	49750628	49750788	MIR3	SINE/MIR
chr20	43055646	43055850	MER20	DNA/hAT-Charlie
chr15	101842631	101842933	AluSq	SINE/Alu
chr9	131124866	131125084	MIR	SINE/MIR
chr11	12553776	12553980	MER103C	DNA/hAT-Charlie
chr12	76685500	76691563	LTR7 HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1
chr6	143516377	143516508	L2	LINE/L2
chr14	24090655	24097283	MER50 MER50-int MER50-int MER50-int MER50	LTR/ERV1
chrX	57614985	57617072	L1ME3B	LINE/L1
chr5	179255361	179255672	AluSp	SINE/Alu
chr6	3727054	3727186	MIRc	SINE/MIR
chr5	172348749	172348927	L2c	LINE/L2

chr3	188658971	188659166	MIR3	SINE/MIR
chr5	133844380	133844625	MLT1C2	LTR/ERVL-MaLR
chr1	231657020	231657257	L2a	LINE/L2
chr20	39822640	39823767	L1MB4	LINE/L1
chr5	133844097	133844379	AluJo	SINE/Alu
chrX	117902462	117902902	MLT1C2	LTR/ERVL-MaLR
chr4	77842810	77843090	AluSx1	SINE/Alu
chr4	978776	978974	L1MEg	LINE/L1
chr1	153578489	153578799	AluSp	SINE/Alu
chr20	43055940	43056125	MIR	SINE/MIR
chr22	37959267	37959400	MIRc	SINE/MIR
chr9	114353290	114353603	AluSp	SINE/Alu
chr9	114327415	114327694	MLT1B	LTR/ERVL-MaLR
chr11	12555434	12555742	AluSc8	SINE/Alu
chr16	57811932	57812209	AluJb	SINE/Alu
chr17	1616277	1616393	OldhAT1	DNA/hAT-Ac
chr4	77842508	77842809	Tigger1	DNA/TcMar-Tigger
chr7	100772590	100772895	AluSz6	SINE/Alu
chr16	30933273	30933421	MIRb	SINE/MIR
chr2	111138948	111139362	L1MB8	LINE/L1
chr3	196733808	196733942	MIRb	SINE/MIR
chr9	114352377	114352645	L1M5	LINE/L1
chr20	43055162	43055462	AluSz6	SINE/Alu
chr9	114352646	114352938	AluSz6	SINE/Alu
chr1	37944207	37944451	MIR	SINE/MIR
chr7	100772226	100772529	AluYm1	SINE/Alu
chr12	49746014	49746350	AluSx	SINE/Alu
chr9	114352939	114353165	L1M5	LINE/L1
chr9	114330083	114331109	MER11A	LTR/ERVK
chr11	1620311	1621161	L1PA16	LINE/L1
chr11	12555743	12555797	Tigger2a	DNA/TcMar-Tigger
chr1	19592432	19592799	L1MB7	LINE/L1

Table 5 : Retrotransposon signature specific to resting CD4+ T lymphocytes

Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chr2	242970841	242971830	L1ME1	LINE/L1
chr11	11173851	11174255	MSTD	LTR/ERVL-MaLR
chr2	242965365	242965653	MLT2B4 MLT2B4	LTR/ERVL
chr2	242962670	242965035	MLT2B4 MLT2B4 MLT2B4 MLT2B4 MLT2B4 MLT2B4 MLT2B4 MLT2B 4 MLT2B4	LTR/ERVL

chr17	74153976	74154328	L2a	LINE/L2
chr11	11168644	11168841	MER20	DNA/hAT-Charlie
chr2	242969922	242970091	L2	LINE/L2
chr11	11167839	11168050	MIRc	SINE/MIR
chr16	68028804	68029100	AluSz6	SINE/Alu
chr2	242966998	242967558	MLT2B4 MLT2B4	LTR/ERV1
chr8	126930164	126930379	MIRb	SINE/MIR
chr22	39643039	39643275	MIR	SINE/MIR
chr13	74839617	74841262	ERV1-E-int ERV1-E-int	LTR/ERV1
chr5	133471904	133471963	MIRb	SINE/MIR
chr14	92223751	92224049	L3	LINE/CR1
chr13	74832930	74833363	LTR16C	LTR/ERV1
chr8	126953786	126954190	L2d2	LINE/L2
chr7	5896137	5896395	L1MEc	LINE/L1
chr17	74156201	74156688	L1ME4a	LINE/L1
chr11	11167046	11167345	L1MB3	LINE/L1
chr22	20918185	20918472	L1MB7	LINE/L1
chr11	11167360	11167510	MIR	SINE/MIR
chr16	68029940	68030157	AluJb	SINE/Alu
chr11	11174902	11175098	MIR	SINE/MIR
chr13	74844238	74844997	MER21B	LTR/ERV1
chr2	242968453	242968754	L1ME3E	LINE/L1
chr4	38609514	38609640	MIRc	SINE/MIR
chr7	5901817	5902990	MER4CL34	LTR/ERV1
chr11	11170817	11171042	L2c	LINE/L2
chr13	114636138	114636691	L1ME1	LINE/L1
chr2	242968955	242969493	L1ME3E	LINE/L1
chr11	11166754	11167042	AluSc8	SINE/Alu
chr2	242972557	242973030	LOR1a	LTR/ERV1
chr11	11171043	11171268	AluSz	SINE/Alu
chr2	242969806	242969880	L1ME3E	LINE/L1
chr11	11175379	11175583	MIRb	SINE/MIR
chr4	38600074	38601659	L1MEg	LINE/L1
chr17	19064306	19064730	LTR16C	LTR/ERV1
chr6	166838772	166842934	L1PA3	LINE/L1
chr13	74831577	74831876	MamGypLTR1d	LTR/Gypsy
chr2	242969494	242969805	AluSx1	SINE/Alu
chr11	11168977	11169348	LTR33	LTR/ERV1
chr16	68031250	68031557	AluY	SINE/Alu
chr22	23107637	23108124	ERV1-E-int ERV1-E-int	LTR/ERV1
chr4	38616209	38616563	L1ME3G	LINE/L1

chr8	126930569	126930780	MIRb	SINE/MIR
chrX	70995670	70996436	L1PA13	LINE/L1
chr14	92225456	92225878	L1PB4	LINE/L1
chr8	126954435	126954814	MER92C	LTR/ERV1
chr11	64505192	64505243	L1ME3B	LINE/L1
chr7	5898417	5898753	AluSz	SINE/Alu
chr17	74155865	74156082	L1ME4a	LINE/L1
chr2	242967700	242967917	MLT1K	LTR/ERV1-MaLR
chr14	92228223	92228625	MSTB	LTR/ERV1-MaLR
chr13	46353113	46353518	MER63B	DNA/hAT-Blackjack
chr11	11171395	11171589	L2	LINE/L2
chr8	126932652	126932944	AluY	SINE/Alu
chr20	31101385	31101674	AluJr	SINE/Alu
chr22	39641341	39641480	MIR	SINE/MIR
chr16	68022068	68022136	L1ME2	LINE/L1
chr6	166848211	166848562	L1ME4b	LINE/L1
chr16	68030949	68031232	AluSp	SINE/Alu
chr14	92228626	92228911	L1PA15-16	LINE/L1
chr17	74156083	74156200	AluJr	SINE/Alu
chr17	74154874	74154999	MIR3	SINE/MIR
chr3	112645552	112646453	HAL1	LINE/L1
chr7	5906347	5906465	LTR33C	LTR/ERV1
chr7	5905671	5905947	AluJr	SINE/Alu
chr16	68029120	68029249	AluJr	SINE/Alu
chr7	5898885	5899188	AluJr	SINE/Alu
chr13	74982091	74982466	MSTA	LTR/ERV1-MaLR
chr11	11166466	11166615	L2a	LINE/L2
chr11	11176935	11177216	AluJr	SINE/Alu
chr7	5897804	5897951	L1MEc	LINE/L1
chr1	149233802	149235735	LTR49 LTR49-int LTR49-int	LTR/ERV1
chr11	11169403	11169540	L2c	LINE/L2
chr7	5895863	5896136	AluJr	SINE/Alu
chr4	38520554	38520736	CR1_Mam	LINE/CR1
chr7	5894704	5894980	AluSq2	SINE/Alu
chr16	68024366	68024666	AluSz	SINE/Alu
chr2	37831549	37832183	L1MA9	LINE/L1
chr4	38602221	38602582	MLT1A0	LTR/ERV1-MaLR
chr4	109231195	109232023	LTR1E	LTR/ERV1
chr17	74154666	74154758	FLAM_C	SINE/Alu
chr2	234331414	234332195	L1MD1	LINE/L1
chr11	11171816	11171980	LTR88b	LTR/Gypsy?

chr22	31682264	31682348	MIRc	SINE/MIR
chr22	40054382	40054774	Charlie4a	DNA/hAT-Charlie
chr17	75427144	75427415	AluJr	SINE/Alu
chr9	136521273	136521393	MIRb	SINE/MIR
chr8	126956180	126956672	MER31B	LTR/ERV1
chr8	19234903	19235840	L1ME3Cz	LINE/L1
chrX	70924839	70925605	L1PA13	LINE/L1
chr8	23123149	23123421	L1M5	LINE/L1
chr4	38519483	38519774	AluSx	SINE/Alu
chr4	38518593	38518801	MIRb	SINE/MIR
chrX	70928911	70929193	L1MC4	LINE/L1
chr1	160797025	160797221	L2d	LINE/L2
chr7	5897374	5897506	L1MEc	LINE/L1
chrX	70928761	70928910	AluJb	SINE/Alu
chr13	46353675	46353899	MIR	SINE/MIR
chr14	92224079	92224384	AluJo	SINE/Alu
chr7	5903463	5903683	L2	LINE/L2
chr2	242965879	242966070	MLT2B4 MLT2B4	LTR/ERV1
chr20	31099876	31100104	MER102c	DNA/hAT-Charlie
chr13	114629304	114629736	L1MB5	LINE/L1
chr7	5903689	5903999	AluJb	SINE/Alu
chrX	103366382	103366556	L1MC5a	LINE/L1
chr4	38520777	38520956	MIR	SINE/MIR
chr1	5621720	5623334	MSTA MSTA MSTA-int	LTR/ERV1-MaLR
chr16	68029589	68029866	AluSx	SINE/Alu
chr22	39644033	39644312	AluSx1	SINE/Alu
chr17	74153034	74153346	AluSc8	SINE/Alu
chr2	241996298	241996513	L1M4a1	LINE/L1
chr7	5905204	5905288	MADE1	DNA/TcMar-Mariner
chr11	11166616	11166681	L1PA4	LINE/L1
chr4	156842685	156843890	MLT2A2 HERV1-int	LTR/ERV1
chr4	38626448	38626527	L4_C_Mam	LINE/RTE-X
chr22	23109195	23109458	Charlie6	DNA/hAT-Charlie
chr13	46354119	46354349	MamTip2b	DNA/hAT-Tip100
chr10	47579468	47580078	L1M4	LINE/L1
chr13	74838151	74838553	ERV1-E-int	LTR/ERV1
chrX	70929971	70930326	L1M5	LINE/L1
chr16	15856132	15856713	LTR8	LTR/ERV1
chr22	23106904	23107325	ERV1-E-int	LTR/ERV1
chr2	242966147	242966631	MLT2B4 MLT2B4	LTR/ERV1
chr1	17021403	17021634	L2c	LINE/L2

chr7	5901250	5901361	L1M5	LINE/L1
chr6	166835379	166835687	AluSx	SINE/Alu
chr4	38626627	38626926	AluSz	SINE/Alu
chr1	160794489	160794791	AluY	SINE/Alu
chrX	70992080	70992364	L1MC4	LINE/L1
chr13	74842444	74842733	ERV1-E-int	LTR/ERV1
chr18	68314726	68315027	L1MC5	LINE/L1
chr1	160796206	160796343	MER85	DNA/PiggyBac
chr2	37829794	37830401	L1MEg	LINE/L1
chr9	100655963	100656405	L1MEf	LINE/L1
chr7	5900777	5901068	AluSq2	SINE/Alu
chr8	23123422	23123638	MER20	DNA/hAT-Charlie
chr18	68316710	68317039	L1PA4	LINE/L1
chr8	23129449	23130684	LTR12C	LTR/ERV1
chr17	18995021	18995181	MIR1_Amn	SINE/MIR
chr17	18929984	18930104	MIRb	SINE/MIR
chrX	70928146	70928396	L1MC4	LINE/L1
chr2	241993774	241994000	AluJb	SINE/Alu
chr17	18927199	18927302	L2a	LINE/L2
chr22	39643320	39643398	MIRc	SINE/MIR
chr8	23124209	23124519	AluJr	SINE/Alu
chr2	234335075	234335672	L1ME3A	LINE/L1
chr7	5904304	5904583	AluSp	SINE/Alu
chr2	242000079	242000368	AluJo	SINE/Alu
chr7	5920108	5920405	AluSx	SINE/Alu
chr17	75424092	75424264	MIRb	SINE/MIR
chr7	5903163	5903462	AluSx3	SINE/Alu
chr4	38514373	38514634	L2d2	LINE/L2
chr17	182219	182346	L2b	LINE/L2
chrX	17760375	17760454	L1MC3	LINE/L1
chr1	23964178	23964327	MIRc	SINE/MIR
chr8	126930810	126931118	AluY	SINE/Alu
chr2	241993605	241993771	L1MEh	LINE/L1
chrX	70992879	70993129	L1MC4	LINE/L1
chr22	20918029	20918183	L1MB8	LINE/L1
chr12	32151946	32152211	AluSg	SINE/Alu
chr7	5899342	5899618	AluSq2	SINE/Alu
chr8	126932171	126932233	MIR	SINE/MIR
chr14	106629182	106630091	L1MC3	LINE/L1
chr1	6512774	6512905	MIRb	SINE/MIR
chr1	160794795	160795012	AluJb	SINE/Alu

chr22	23109453	23109799	Charlie6	DNA/hAT-Charlie
chr5	79408488	79408791	AluJr	SINE/Alu
chr22	39642489	39642629	L1MA10	LINE/L1
chr19	16354893	16355270	L1MEg	LINE/L1
chr14	92223341	92223417	L3	LINE/CR1
chr11	121314219	121314781	LTR82B	LTR/ERV1
chr1	6513436	6513667	L2c	LINE/L2
chr11	121310196	121310417	MIRb	SINE/MIR
chr7	5896700	5897071	L1MEc	LINE/L1
chr20	31101115	31101384	L1MB4	LINE/L1
chr4	38625895	38626124	MIRc	SINE/MIR
chr7	5895172	5895457	AluJb	SINE/Alu
chr9	136521374	136521506	L2a	LINE/L2
chr12	32148994	32149277	AluSx	SINE/Alu
chr8	126956673	126956728	MER92-int	LTR/ERV1
chr20	31099506	31099834	AluJb	SINE/Alu
chrX	50933770	50936217	MSTB MSTB-int MSTB	LTR/ERV1-MaLR
chr7	5897507	5897803	AluJr	SINE/Alu
chr7	5901530	5901691	FAM	SINE/Alu
chr4	38613521	38613602	MIRc	SINE/MIR
chr4	38517808	38518166	Tigger6a	DNA/TcMar-Tigger
chr6	166838380	166838742	MER34A1	LTR/ERV1
chr13	74842889	74843486	ERV1-E-int	LTR/ERV1
chr12	53013886	53014187	AluSp	SINE/Alu
chr12	52994578	52994756	MIR	SINE/MIR
chr14	92228921	92229518	MER4E	LTR/ERV1
chrX	70992365	70992514	AluJb	SINE/Alu
chr6	166838042	166838158	MIR	SINE/MIR
chrX	70927657	70928060	MSTA	LTR/ERV1-MaLR
chr11	11175607	11175971	MLT1F2	LTR/ERV1-MaLR
chr15	29000859	29001034	AluJo	SINE/Alu
chr8	126948520	126949081	MER34A1	LTR/ERV1
chr16	68022166	68022296	AluSz	SINE/Alu
chr12	92310221	92310948	LTR50	LTR/ERV1
chr14	92226031	92226441	MSTA	LTR/ERV1-MaLR
chr14	92223581	92223743	MIR3	SINE/MIR
chr10	33362778	33362979	MIR3	SINE/MIR
chrX	70930673	70930739	L1ME3B	LINE/L1
chr17	19051319	19051609	AluY	SINE/Alu
chr9	130700862	130700944	L2b	LINE/L2
chr19	35348322	35348625	AluSz	SINE/Alu

chr7	105550115	105550475	L2d2	LINE/L2
chr2	241994553	241994896	L1MEh	LINE/L1
chr1	24824048	24824384	L1ME2	LINE/L1
chr7	5896396	5896699	AluSz	SINE/Alu
chr21	48003451	48003833	MSTD	LTR/ERV1-MaLR
chr11	113249856	113250723	L1PA16	LINE/L1
chrX	70929391	70929652	L1M5	LINE/L1
chr7	99766646	99766945	AluSq2	SINE/Alu
chr7	5894148	5894444	AluJo	SINE/Alu
chr2	241997131	241997230	L1MEg	LINE/L1
chr12	53014188	53014382	Tigger12A	DNA/TcMar-Tigger
chr13	74841456	74842000	L1MA4	LINE/L1
chr8	126956729	126957019	AluSg	SINE/Alu
chr17	42300694	42300900	MIRc	SINE/MIR
chr22	25459012	25459297	MER41D	LTR/ERV1
chr17	75424943	75425073	MIRb	SINE/MIR
chr6	36512785	36513095	AluSx1	SINE/Alu
chr8	23116879	23117170	AluSg	SINE/Alu
chr19	4912510	4912768	L1ME2z	LINE/L1
chr22	31683001	31683304	AluJb	SINE/Alu
chr2	75497166	75498485	L1MA4	LINE/L1
chr2	242000369	242001023	L1ME3F	LINE/L1
chr7	5895469	5895765	AluSx1	SINE/Alu
chr7	105589148	105591496	L1PA5	LINE/L1
chr10	33405586	33405694	MIR1_Amn	SINE/MIR
chr2	199017893	199019155	L1MEc	LINE/L1
chr1	25924702	25925242	LTR67B	LTR/ERV1
chr7	5903008	5903162	L2	LINE/L2
chr4	38609969	38610269	AluSz	SINE/Alu
chr22	24556903	24557077	MIRb	SINE/MIR
chr11	121312684	121313061	LTR82A	LTR/ERV1
chr8	141105759	141105963	L2a	LINE/L2
chr8	126931735	126932092	LTR16 LTR16	LTR/ERV1
chr2	241995832	241995933	L1MEg	LINE/L1
chr4	38613942	38614055	MIRb	SINE/MIR
chr2	232652847	232653145	AluSz6	SINE/Alu
chr3	111365294	111366091	L1PA15	LINE/L1
chrX	50903596	50904163	MER77B	LTR/ERV1
chr8	126934460	126934818	L2c	LINE/L2
chr6	166833720	166834295	L1MB3	LINE/L1
chr7	5906128	5906284	MamGypLTR1a	LTR/Gypsy

chr17	37227398	37227541	MIR	SINE/MIR
chr13	74842001	74842297	MLT1C2	LTR/ERV1-MaLR
chr7	5901378	5901509	FLAM_C	SINE/Alu
chr8	19237544	19238557	L1MB3	LINE/L1
chr9	136523172	136523376	L2	LINE/L2
chr3	16431209	16431728	MLT1G1	LTR/ERV1-MaLR
chr8	126931217	126931271	Alu	SINE/Alu
chr10	47588117	47588212	L2	LINE/L2
chr4	38608237	38609047	LTR1A1	LTR/ERV1
chr19	35345393	35345671	AluSp	SINE/Alu
chr4	38514947	38515114	MIRb	SINE/MIR
chr5	79418389	79418902	MLT1E3	LTR/ERV1-MaLR
chr7	5160403	5160703	AluSx1	SINE/Alu
chrX	70926815	70927339	L1ME3B	LINE/L1
chr3	111366091	111366235	L1MC4a	LINE/L1
chr2	242001024	242001301	AluSq4	SINE/Alu
chr9	132000587	132000896	AluSx	SINE/Alu
chr2	241994002	241994251	L1MEh	LINE/L1
chr1	25926538	25926764	MIR	SINE/MIR
chr4	38627871	38628008	L2b	LINE/L2
chr11	11176789	11176910	MIRb	SINE/MIR
chr12	32147165	32147449	AluSg	SINE/Alu
chr13	74841275	74841455	MLT1C2	LTR/ERV1-MaLR
chr4	38516586	38516743	Tigger6a	DNA/TcMar-Tigger
chr12	51608060	51608200	MIRb	SINE/MIR
chr13	46352808	46353112	MER2	DNA/TcMar-Tigger
chr11	113240385	113240560	MIRb	SINE/MIR
chr8	23122361	23122496	FLAM_C	SINE/Alu
chr7	5898754	5898864	MIRb	SINE/MIR
chr20	31100500	31100821	L1ME4a	LINE/L1
chr11	11173198	11173290	MIR3	SINE/MIR
chr12	32146863	32147162	AluSx1	SINE/Alu
chr22	31683779	31683956	MIR	SINE/MIR
chrX	70929251	70929368	L1MC4	LINE/L1
chr3	42574096	42574203	L2a	LINE/L2
chr7	5897972	5898270	AluSp	SINE/Alu
chr2	234334283	234334792	L1ME4b	LINE/L1
chr15	29000694	29000815	L1MA5	LINE/L1
chr1	144545925	144546284	Tigger20a	DNA/TcMar-Tigger
chr12	51605842	51606175	AluSg	SINE/Alu
chr22	24554786	24554896	L2b	LINE/L2

chr16	21805595	21805742	MLT1H	LTR/ERV1-MaLR
chr6	166834802	166835315	MER34B	LTR/ERV1
chr15	29401294	29401381	L2c	LINE/L2
chrX	70993936	70994460	L1ME3B	LINE/L1
chr11	113249071	113249293	MIRb	SINE/MIR
chr1	23964791	23965029	MIR	SINE/MIR
chr1	144531214	144531716	LTR23-int LTR56	LTR/ERV1
chr13	114634093	114634292	L1ME3	LINE/L1
chr17	18925926	18926037	MIR3	SINE/MIR
chrX	70993215	70993618	MSTA	LTR/ERV1-MaLR
chr8	29974195	29974588	MER21C	LTR/ERV1
chr1	6512948	6513253	AluSx1	SINE/Alu
chr19	35340620	35340928	AluSx	SINE/Alu
chr1	207087774	207088069	AluJb	SINE/Alu
chr17	74153458	74153888	L2d2	LINE/L2
chr12	32151808	32151945	AluSx	SINE/Alu
chr16	68022541	68022839	AluJr	SINE/Alu
chr22	17669907	17670200	AluSx	SINE/Alu
chr2	241998086	241998379	AluYf1	SINE/Alu
chr7	105652561	105653190	L2a	LINE/L2
chr20	31107807	31108105	AluY	SINE/Alu
chr3	127402256	127402540	AluSx1	SINE/Alu
chr8	26299568	26299868	AluSz	SINE/Alu
chr1	160792684	160792987	L2c	LINE/L2
chr17	19057294	19057605	AluSg	SINE/Alu
chr10	47565386	47565754	MLT1A0	LTR/ERV1-MaLR
chr1	23965269	23965460	L2b	LINE/L2
chr11	121289330	121289965	MER66D	LTR/ERV1
chr2	241995709	241995831	AluJo	SINE/Alu
chr4	109188969	109189981	L1PA3	LINE/L1
chr17	18937285	18937567	AluSz	SINE/Alu
chr14	92331516	92331698	X30_DNA	DNA
chr10	51456447	51457808	MER4-int MER4-int	LTR/ERV1
chr1	160791622	160791857	MIR	SINE/MIR
chr10	73501078	73501302	MIR	SINE/MIR
chr7	5898347	5898416	MER84	LTR/ERV1
chr12	51607172	51607297	FLAM_C	SINE/Alu
chrX	103366627	103366756	AluJr	SINE/Alu
chr16	1045888	1046225	L1M5	LINE/L1
chr3	111365006	111365206	L1MC4a	LINE/L1
chr2	241996836	241997124	AluJr	SINE/Alu

chr5	79417043	79417389	MSTA	LTR/ERV1-MaLR
chr16	50681612	50681703	LTR16C	LTR/ERV1
chr19	56150480	56150672	MER20	DNA/hAT-Charlie
chr20	31101675	31101725	L1MB4	LINE/L1
chr4	38613663	38613941	AluSg4	SINE/Alu
chrX	100190382	100190834	LTR16B2	LTR/ERV1
chr22	23115615	23115850	LTR16	LTR/ERV1
chr9	100638001	100638596	L1ME3A	LINE/L1
chr6	166842946	166843237	AluSz6	SINE/Alu
chr9	136519859	136519917	MIR	SINE/MIR
chr12	52994214	52994572	THE1A	LTR/ERV1-MaLR
chr22	31674093	31674256	MIR	SINE/MIR
chr7	6645328	6645629	AluSx1	SINE/Alu
chr1	53148896	53149200	AluJo	SINE/Alu
chr19	4915924	4916039	Charlie1b	DNA/hAT-Charlie
chrX	70925918	70926076	L1ME1	LINE/L1
chr17	33561210	33562187	L1PA7	LINE/L1
chrX	70993628	70993982	L1M5	LINE/L1
chr17	66190355	66190937	L1MEf	LINE/L1
chr1	65518747	65519050	AluSx	SINE/Alu
chr4	38596092	38596581	MLT1F	LTR/ERV1-MaLR
chr6	166834578	166834768	MIRc	SINE/MIR
chr17	18928914	18929226	AluYk3	SINE/Alu
chr17	18927049	18927137	MIRc	SINE/MIR
chrX	70995395	70995639	L1ME3B	LINE/L1
chr5	110765506	110768313	L1MA1	LINE/L1
chr12	32152348	32152436	Charlie1b	DNA/hAT-Charlie
chr5	180632822	180633385	L2b	LINE/L2
chr12	32152212	32152347	AluSx	SINE/Alu
chr1	3424599	3424675	MER117	DNA/hAT-Charlie
chrX	70927293	70927647	L1M5	LINE/L1
chr8	19238861	19239848	L1MB3	LINE/L1
chr1	144527491	144527819	PRIMA4-int	LTR/ERV1
chr2	242001302	242001525	L1ME3F	LINE/L1
chr2	199017094	199017514	L1MEc	LINE/L1
chr12	32147760	32147815	Tigger3b	DNA/TcMar-Tigger
chr19	56150673	56150819	AluJb	SINE/Alu
chr1	23963679	23963976	AluSg	SINE/Alu
chr13	52388206	52388574	L4_B_Mam	LINE/RTE-X
chr12	113739461	113739677	MIRb	SINE/MIR
chr18	47003870	47004170	AluSp	SINE/Alu

chr12	103689644	103691152	L1PA5	LINE/L1
chr6	37508622	37508760	MIR	SINE/MIR
chr8	23122641	23122936	AluSx1	SINE/Alu
chr4	38603686	38603979	AluJb	SINE/Alu
chr7	5909495	5909642	Zaphod	DNA/hAT-Tip100
chr12	32149278	32149452	Tigger3b	DNA/TcMar-Tigger
chr20	3787083	3787377	AluSx4	SINE/Alu
chr16	50674152	50674203	MamTip1b	DNA/hAT-Tip100
chr14	92227466	92227736	L1PA15-16	LINE/L1
chr10	17254633	17255333	LTR78	LTR/ERV1
chr17	18938663	18938852	MIR	SINE/MIR
chr12	106735277	106735860	MLT1K	LTR/ERV1-MaLR
chr11	113246163	113246670	MLT1K	LTR/ERV1-MaLR
chr1	53119961	53120572	L1MD	LINE/L1
chr19	4916353	4916532	Charlie1	DNA/hAT-Charlie
chr5	139481983	139482319	L2a	LINE/L2
chr22	39643740	39643894	AluJr	SINE/Alu
chr18	77147822	77151279	L1M4b	LINE/L1
chr1	25925268	25925708	MLT1G3	LTR/ERV1-MaLR
chr17	18994409	18994755	L2b	LINE/L2
chr2	86729633	86729897	AluJb	SINE/Alu
chr7	5897072	5897373	AluSx	SINE/Alu
chr13	74832421	74832587	MIR3	SINE/MIR
chr1	160790974	160791309	L1ME4b	LINE/L1
chr17	18928493	18928804	AluYk3	SINE/Alu
chr13	74834411	74834690	AluJr	SINE/Alu
chr3	42576975	42577171	MER5A1	DNA/hAT-Charlie
chrX	70990955	70991289	L1M5	LINE/L1
chr1	65519260	65519501	AluJb	SINE/Alu
chr1	25929721	25931423	SVA_F	Retroposon/SVA
chr17	4959162	4959501	AluSc8	SINE/Alu
chr3	16393184	16393690	Tigger13a	DNA/TcMar-Tigger
chr1	25932489	25933128	L1MA8	LINE/L1
chr13	114633541	114633643	MER5A	DNA/hAT-Charlie
chr22	39642324	39642481	FRAM	SINE/Alu
chr10	6701307	6702239	L1MB7	LINE/L1
chr19	56151277	56151415	MER3	DNA/hAT-Charlie
chr8	126963099	126963206	MER92-int	LTR/ERV1
chr1	53135743	53135857	Charlie4z	DNA/hAT-Charlie
chrX	70991623	70991884	L1M5	LINE/L1
chr1	220036913	220042937	L1PA3	LINE/L1

chr17	66186661	66186894	THE1B	LTR/ERV1-MaLR
chr14	92227737	92228035	AluY	SINE/Alu
chr1	26124024	26124432	L2b	LINE/L2
chr11	11155740	11156677	L1MEg	LINE/L1
chr16	1042758	1043056	AluSx4	SINE/Alu
chr9	130710770	130710974	MIRb	SINE/MIR
chr12	53013195	53013288	L2c	LINE/L2
chr10	1256307	1256372	L3	LINE/CR1
chr2	37832184	37832569	MLT1A1	LTR/ERV1-MaLR
chr13	52385053	52385482	LTR16A1	LTR/ERV1
chr17	19053699	19053965	AluSz	SINE/Alu
chr16	68022347	68022535	AluSz	SINE/Alu
chr9	100656692	100657277	L1MEf	LINE/L1
chr22	39642165	39642309	MIR	SINE/MIR
chr8	143723403	143724539	MER4A1 MER4-int	LTR/ERV1
chr7	5878712	5879018	L2c	LINE/L2
chr2	241997733	241997932	L1MEg	LINE/L1
chr11	95346622	95348760	MER57-int MER57-int MER57-int MER57A1	LTR/ERV1
chr12	53015231	53018472	L1MD1	LINE/L1
chr18	68452823	68453245	MLT1E MLT1E	LTR/ERV1-MaLR
chr1	143750612	143751615	MER31-int MER31-int MER31A	LTR/ERV1
chr22	25459298	25459684	L1PB2	LINE/L1
chr2	234329794	234330511	L2a	LINE/L2
chr1	144527820	144528116	AluSx	SINE/Alu
chr16	3618443	3618743	AluJb	SINE/Alu
chr19	4907717	4908023	AluSp	SINE/Alu
chr9	136571203	136571714	L1MB5	LINE/L1
chr12	32146585	32146744	AluJb	SINE/Alu
chr7	5901692	5901768	L1M5	LINE/L1
chr6	166843238	166843434	MER34A1	LTR/ERV1
chr5	42998227	42998521	AluSx	SINE/Alu
chr8	23106453	23106623	MIRb	SINE/MIR
chrX	70998091	70998215	L2	LINE/L2
chr4	89650367	89650507	MIRb	SINE/MIR
chr1	23962659	23962754	L2b	LINE/L2
chr17	37226850	37226948	L2c	LINE/L2
chr1	144478312	144478753	LTR49	LTR/ERV1
chr17	19058309	19058648	AluJb	SINE/Alu
chr17	19051060	19051162	MIR3	SINE/MIR
chr17	74602070	74607593	LTR7 HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int HERVH-int LTR7	LTR/ERV1

chr5	79411186	79411300	X7B_LINE	LINE/CR1
chr7	5889337	5889578	L1MEd	LINE/L1
chr13	52386004	52386521	LTR53B	LTR/ERV1
chr19	18123114	18123421	AluSz	SINE/Alu
chr1	202845865	202846165	AluJb	SINE/Alu
chr9	130713815	130714123	AluYf1	SINE/Alu
chr5	79411302	79411457	L2c	LINE/L2
chr20	3151159	3151467	AluSx	SINE/Alu
chr1	23962931	23963027	L1MB8	LINE/L1
chr10	48893502	48894860	MER4-int MER4-int	LTR/ERV1
chr4	38611105	38611333	MIR	SINE/MIR
chr16	68030819	68030899	AluJb	SINE/Alu
chr6	37528328	37528699	MLT1I	LTR/ERV1-MaLR
chr8	87345701	87346972	HSMAR2	DNA/TcMar-Mariner
chr7	5898274	5898346	AluSz	SINE/Alu
chr16	50674588	50674703	Charlie18a	DNA/hAT-Charlie
chr1	147993603	147993726	Charlie4	DNA/hAT-Charlie
chr2	242019716	242020639	L1MC5a	LINE/L1
chr12	32151629	32151734	Tigger3b	DNA/TcMar-Tigger
chr1	149661507	149661847	L1ME2	LINE/L1
chr1	53144355	53144438	MER5A1	DNA/hAT-Charlie
chrX	70925636	70925880	L1ME3B	LINE/L1
chrX	51071261	51071405	MIRb	SINE/MIR
chr2	199015605	199016505	L1MB7	LINE/L1
chr17	19052793	19053087	AluSx3	SINE/Alu
chr14	92330351	92330717	LTR39	LTR/ERV1
chr14	92331122	92331414	AluSz	SINE/Alu
chr16	67583845	67584306	L2b	LINE/L2
chr1	53147342	53147633	AluSp	SINE/Alu
chr11	113250714	113251500	L1PB1	LINE/L1
chr9	130714124	130714250	MIRb	SINE/MIR
chr4	6689667	6689862	L2b	LINE/L2
chr12	32147638	32147759	Charlie1a	DNA/hAT-Charlie
chr13	74805581	74805694	MIRc	SINE/MIR
chr1	3539982	3540348	LTR40c LTR40c	LTR/ERV1
chr1	23963276	23963369	MIRb	SINE/MIR
chr13	74839192	74839462	ERV1-E-int	LTR/ERV1
chr5	133470952	133471913	L2b	LINE/L2
chr4	38514737	38514948	MIRb	SINE/MIR
chr11	113247692	113247924	L2b	LINE/L2
chr22	31683316	31683615	AluSx3	SINE/Alu

chr2	241412566	241413085	L1M3c	LINE/L1
chr12	113741686	113741984	AluSz	SINE/Alu
chr10	6670938	6671059	MIRb	SINE/MIR
chr4	38517002	38517516	Tigger6a	DNA/TcMar-Tigger
chr1	53136790	53137083	AluSp	SINE/Alu
chr9	130700965	130701087	FLAM_C	SINE/Alu
chr1	148243665	148243892	LOR1a	LTR/ERV1
chr12	52993629	52993716	MIR	SINE/MIR
chr10	47564402	47564939	L2a	LINE/L2
chr16	22622031	22622178	MLT1H	LTR/ERV1-MaLR
chr5	180020251	180020884	L1MB3	LINE/L1
chrX	70991907	70992024	L1MC4	LINE/L1
chr11	121309759	121310193	L1ME2	LINE/L1
chr3	50147364	50147660	AluSc8	SINE/Alu
chr3	112646499	112647132	HAL1	LINE/L1
chr3	111353466	111353755	AluSp	SINE/Alu
chr10	33362365	33362727	THE1B	LTR/ERV1-MaLR
chr8	126959953	126960247	AluSc8	SINE/Alu
chr3	16376208	16376685	MLT1D	LTR/ERV1-MaLR
chr12	69722465	69722675	Charlie20a	DNA/hAT-Charlie
chr17	18931567	18931721	L2b	LINE/L2
chr1	160796351	160796495	L2d2	LINE/L2
chr7	142559297	142559694	L1ME4b	LINE/L1
chr2	241413847	241414650	L1PREC2	LINE/L1
chr12	32151119	32151295	AluSx3	SINE/Alu
chr10	1257347	1257455	L2c	LINE/L2
chr3	194113754	194114561	L1M5	LINE/L1
chr12	68075420	68076384	HAL1	LINE/L1
chr2	242016512	242017517	L1MB7	LINE/L1
chr9	136519225	136519503	AluSx1	SINE/Alu
chr8	2154845	2155388	MLT2A2	LTR/ERV1
chr5	42975530	42975851	LTR57-int	LTR/ERV1
chr19	36825775	36826075	AluSq2	SINE/Alu
chr12	32150922	32151118	Tigger3b	DNA/TcMar-Tigger
chr6	36512381	36512670	AluSx3	SINE/Alu
chr22	39535427	39535737	AluY	SINE/Alu
chr12	53013054	53013222	MIRc	SINE/MIR
chr9	130701130	130701207	L2b	LINE/L2
chr7	150445561	150445661	MIR3	SINE/MIR
chr1	154925303	154925419	L2d2	LINE/L2
chr12	32150574	32150687	Tigger3b	DNA/TcMar-Tigger

chr16	3617862	3618120	AluSg	SINE/Alu
chr17	66188996	66189629	L1MA5	LINE/L1
chr2	175410859	175410946	MIR3	SINE/MIR
chr4	89643381	89643519	MIRb	SINE/MIR
chr21	38530018	38530159	MIR3	SINE/MIR
chr17	18931569	18931765	L2c	LINE/L2
chr13	114634772	114635844	L1ME1	LINE/L1
chr4	54865324	54865616	AluJr	SINE/Alu
chr12	53018595	53019898	L1MD1	LINE/L1
chr6	36510847	36511141	AluY	SINE/Alu
chr1	144528117	144529125	PRIMA4-int	LTR/ERV1
chr15	81612692	81613398	Charlie2b	DNA/hAT-Charlie
chr20	60289485	60290395	L1PB3	LINE/L1
chr1	149612124	149612495	MLT1H	LTR/ERVL-MaLR
chr6	36480438	36480736	AluSx	SINE/Alu
chr14	92245749	92246042	AluY	SINE/Alu
chr5	133466560	133466813	L2b	LINE/L2
chr17	5143168	5144876	LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C LTR7C	LTR/ERV1
chr6	36511423	36511710	AluSx	SINE/Alu
chrX	17768650	17768771	MIR	SINE/MIR
chr17	75424620	75424748	MIRc	SINE/MIR
chr2	241999605	241999898	AluSx1	SINE/Alu
chr1	25931589	25932266	L1MA8	LINE/L1
chrX	17761327	17761456	X12_DNA	DNA/TcMar-Tigger
chr22	39643455	39643615	L2b	LINE/L2
chr7	5890269	5890570	AluSg	SINE/Alu
chr1	100980931	100981236	AluSx	SINE/Alu
chr1	6512610	6512772	MER5A1	DNA/hAT-Charlie
chr1	167475612	167475824	AluSx3	SINE/Alu
chr1	53141995	53142135	MIRb	SINE/MIR
chr1	160796150	160796205	Tigger2b_Pri	DNA/TcMar-Tigger
chr11	113246727	113247265	MER65D	LTR/ERV1
chr19	35345928	35346706	L1MA5	LINE/L1
chr5	133470652	133470951	AluJr	SINE/Alu
chr12	32147478	32147599	AluJb	SINE/Alu
chr17	19052361	19052671	AluSg4	SINE/Alu
chr19	35343098	35343213	AluYc	SINE/Alu
chr6	36508404	36508650	AluSp	SINE/Alu
chr1	53144193	53144300	L2b	LINE/L2
chr3	16386489	16386820	MLT1E2 MLT1E2	LTR/ERVL-MaLR

chr9	136525367	136525526	MIR	SINE/MIR
chr13	52383706	52383953	AluY	SINE/Alu
chr14	92333184	92333560	MER121	DNA/hAT?
chr10	47567386	47567933	L1MB4	LINE/L1
chr15	29404889	29405356	L1MB3	LINE/L1
chr20	31100295	31100400	L1ME4a	LINE/L1
chr5	79407569	79408476	LTR5B	LTR/ERVK
chr8	23120165	23120275	LTR104_Mam	LTR/Gypsy
chr10	121253480	121253688	L2b	LINE/L2
chr1	23962356	23962658	AluSz	SINE/Alu
chr11	113247266	113247539	L2a	LINE/L2
chr22	22119318	22119434	Tigger10	DNA/TcMar-Tigger
chr1	53148774	53148895	L1MB2	LINE/L1
chr6	108037925	108038074	MLT1J	LTR/ERV1-MaLR
chr5	42999501	42999865	L1PA17	LINE/L1
chr4	140325932	140326297	L1ME1	LINE/L1
chr17	19049620	19049969	AluSx	SINE/Alu
chr7	99759760	99759885	AluJr	SINE/Alu
chr1	23962851	23962930	L3	LINE/CR1
chr12	69720762	69721054	AluYk3	SINE/Alu
chr9	136570851	136571195	MLT1B	LTR/ERV1-MaLR
chr2	69679437	69679724	LTR88c	LTR/Gypsy?
chr2	241995296	241995691	L1MEg	LINE/L1
chr15	75935415	75935671	L2a	LINE/L2
chr11	121309455	121309758	AluSx4	SINE/Alu
chr14	92226642	92226998	L1PB4	LINE/L1
chr11	14920389	14920917	LTR31	LTR/ERV1
chr6	37538633	37538961	LTR16A1	LTR/ERV1
chr1	228454914	228455799	L1M5	LINE/L1
chr8	126960820	126961132	AluSx1	SINE/Alu
chr15	29405458	29405509	FRAM	SINE/Alu
chr19	4913265	4913566	AluSq	SINE/Alu
chr12	32146126	32146425	AluYf1	SINE/Alu
chr5	79413441	79413744	MLT1C2	LTR/ERV1-MaLR
chr17	19048119	19048308	L2a	LINE/L2
chr12	106709063	106709346	L2b	LINE/L2
chr12	32149725	32150024	AluSx	SINE/Alu
chr17	66127264	66127432	AluJb	SINE/Alu
chr7	99758991	99759302	AluSz	SINE/Alu
chr1	40221505	40221588	MIR3	SINE/MIR
chr7	5891614	5891891	AluJb	SINE/Alu

chr9	136525970	136526042	MER3	DNA/hAT-Charlie
chr7	5893701	5893802	L2a	LINE/L2
chr11	64553733	64553828	MIRb	SINE/MIR
chr6	108035503	108035863	L2c	LINE/L2
chr2	241997405	241997720	L1MEg	LINE/L1
chr19	24261862	24263353	PRIMA41-int	LTR/ERV1
chr5	133458649	133458826	MIRb	SINE/MIR
chr7	99762006	99762306	AluSx1	SINE/Alu
chr9	130707288	130707416	MIR	SINE/MIR
chr9	95594757	95595522	L1MA4A	LINE/L1
chr14	92241048	92241568	MER34A	LTR/ERV1
chr8	19236605	19237237	L1MB3	LINE/L1
chr17	33878307	33879612	HERV17-int LTR17	LTR/ERV1
chr14	92227163	92227465	AluSz	SINE/Alu
chr12	32152478	32152768	AluJb	SINE/Alu
chr17	18933873	18934011	MIR3	SINE/MIR
chr10	48891558	48892168	L1M4	LINE/L1
chr22	39642764	39642914	L2a	LINE/L2
chrX	50937461	50939497	THE1B THE1B-int THE1B THE1B	LTR/ERV1-MaLR
chr2	241994252	241994552	AluSx	SINE/Alu
chr14	92237608	92238428	L1PA15	LINE/L1
chr7	150331735	150336494	L1PA7	LINE/L1
chr15	86287386	86287499	MIRb	SINE/MIR
chr12	106732637	106732944	AluSz	SINE/Alu
chr10	1257542	1257939	MER63B	DNA/hAT-Blackjack
chr8	26302302	26302553	MLT1K	LTR/ERV1-MaLR
chr12	53014531	53014752	L2d	LINE/L2
chr12	53013397	53013531	L2a	LINE/L2
chr5	79358356	79359431	L1PA5	LINE/L1
chr7	5889050	5889336	AluJr	SINE/Alu
chr2	75498809	75500000	L1MA4	LINE/L1
chr7	5918531	5918844	AluJb	SINE/Alu
chr6	24811457	24811764	AluSz	SINE/Alu
chr1	160791874	160792455	LTR9	LTR/ERV1
chr10	46706967	46708328	MER4-int MER4-int	LTR/ERV1
chr4	6689947	6690177	MIRb	SINE/MIR
chr16	53425683	53425963	L1ME4a	LINE/L1
chr5	133464724	133464850	MIR	SINE/MIR
chr21	34178331	34178913	LTR88a	LTR/Gypsy?
chr6	108030476	108030618	MIRb	SINE/MIR
chr8	26303802	26304067	L1MB3	LINE/L1

chr1	53142821	53142940	L2b	LINE/L2
chr9	100651842	100652172	MLT1A0	LTR/ERV1-MaLR
chr17	19049426	19049601	L2b	LINE/L2
chr1	53143701	53143810	FLAM_C	SINE/Alu
chr9	130715297	130715424	AluSx3	SINE/Alu
chr8	126933431	126933494	MIR	SINE/MIR
chr7	99763215	99763442	AluJr	SINE/Alu
chr14	102522359	102522822	LTR2B	LTR/ERV1
chr12	9412080	9413516	MLT1D-int MLT1D	LTR/ERV1-MaLR
chr12	44922348	44924240	L2a	LINE/L2
chr8	143727577	143727793	LTR8	LTR/ERV1
chr5	1054904	1054999	OldhAT1	DNA/hAT-Ac
chr17	33556624	33557014	MLT1B	LTR/ERV1-MaLR
chr5	79414823	79415060	MIR	SINE/MIR
chr3	112630448	112634658	L1PA4	LINE/L1
chr2	69680663	69681059	MER57B2	LTR/ERV1
chr1	53139267	53139506	MIR	SINE/MIR
chr6	29928543	29930052	MER21C MER21-int	LTR/ERV1
chr16	50676361	50676586	MIRb	SINE/MIR
chr1	207066370	207066618	MIRc	SINE/MIR
chr16	3621011	3621339	L1M5	LINE/L1
chr19	4914935	4915105	MER20	DNA/hAT-Charlie
chr2	241561846	241562048	MER30	DNA/hAT-Charlie
chr12	32143849	32144144	AluJo	SINE/Alu
chr3	16385823	16385981	Charlie15a	DNA/hAT-Charlie
chr5	79417430	79417834	MSTB	LTR/ERV1-MaLR
chr6	30777730	30778027	AluSz	SINE/Alu
chr11	64495890	64496204	AluY	SINE/Alu
chr17	42300481	42300607	AluJo	SINE/Alu
chr17	18931199	18931548	AluSx	SINE/Alu
chr1	3424753	3424974	L2a	LINE/L2
chr2	37821341	37827470	L1PA6	LINE/L1
chr3	16373264	16373984	HAL1	LINE/L1
chr1	100617350	100617506	FAM	SINE/Alu
chr17	18933990	18934287	L2a	LINE/L2
chr1	53142615	53142758	MIRb	SINE/MIR
chr16	50681097	50681215	MLT1L	LTR/ERV1-MaLR
chr5	133466138	133466287	MER91A	DNA/hAT-Tip100
chr1	53145542	53145839	AluY	SINE/Alu
chr5	133472832	133473146	AluSx1	SINE/Alu
chr12	53006545	53006668	MIRb	SINE/MIR

chr17	33557645	33558463	L1PA13	LINE/L1
chr19	35345714	35345925	MER58C	DNA/hAT-Charlie
chr17	66186248	66186401	AluSx	SINE/Alu
chr11	121311111	121311717	MER39	LTR/ERV1
chr16	21805885	21806415	MamRep1527	LTR
chr6	166843440	166843754	AluSx3	SINE/Alu
chr9	100649876	100650063	LTR37-int	LTR/ERV1
chr22	31679897	31680189	AluSp	SINE/Alu
chr5	133435266	133435573	AluJr	SINE/Alu
chr8	87350270	87350757	MLT1F1	LTR/ERV1-MaLR
chr20	62363099	62363383	MER2	DNA/TcMar-Tigger
chr7	5890079	5890268	L1MB3	LINE/L1
chr8	29967960	29968263	AluSz	SINE/Alu
chr1	207088447	207088730	L2c	LINE/L2
chr7	5889632	5889784	L1MEd	LINE/L1
chr7	5892983	5893279	AluJo	SINE/Alu
chr1	160795052	160795244	MIRc	SINE/MIR
chr19	58298625	58298891	AluJb	SINE/Alu
chr16	3624304	3624420	MER5B	DNA/hAT-Charlie
chr1	65518214	65518479	AluY	SINE/Alu
chr13	114635845	114636137	AluSz	SINE/Alu
chrX	50912103	50913743	LTR49 LTR49-int LTR49-int LTR49-int	LTR/ERV1
chr13	114636698	114637375	L1MD2	LINE/L1
chr17	66190024	66190354	AluSc	SINE/Alu
chr12	51605029	51605099	Charlie15a	DNA/hAT-Charlie
chr1	148246265	148246483	L1MEf	LINE/L1
chr1	36801168	36802005	HERVHF21-int	LTR/ERV1
chr19	50480305	50480508	L2b	LINE/L2
chr2	241411035	241411476	L1M3c	LINE/L1
chr19	56149598	56149900	AluSc	SINE/Alu
chr17	19046061	19046268	MIR	SINE/MIR
chr2	175411892	175412132	LTR78	LTR/ERV1
chr3	111374971	111375712	L1MC4a	LINE/L1
chr19	4913820	4914137	AluSp	SINE/Alu
chr17	30734890	30735179	AluJb	SINE/Alu
chr5	133431403	133431594	MER3	DNA/hAT-Charlie
chr8	23121504	23122319	LTR48 LTR48	LTR/ERV1
chr1	148243187	148243489	AluSx1	SINE/Alu
chr1	147996348	147996567	LOR1b	LTR/ERV1
chr2	241996514	241996797	AluSq2	SINE/Alu
chr12	32152769	32152895	MLT1F2	LTR/ERV1-MaLR

chr17	19043605	19043914	AluSz	SINE/Alu
chr17	19050732	19050863	MIRb	SINE/MIR
chr1	151840932	151841381	L1MB5	LINE/L1
chr10	121275482	121275780	AluSx	SINE/Alu
chr3	16383061	16383142	L1MC1	LINE/L1
chr17	18932860	18933049	L2d	LINE/L2
chr7	5892219	5892498	AluJr	SINE/Alu
chr9	136526043	136526179	AluJo	SINE/Alu
chr17	5411773	5412257	L1ME4c	LINE/L1
chr17	18930301	18930435	MIRb	SINE/MIR
chr1	53140010	53140310	AluSx	SINE/Alu
chr1	146471282	146471693	L1MEc	LINE/L1
chr1	160795720	160796162	Tigger2	DNA/TcMar-Tigger
chr3	108578990	108579266	MLT1J	LTR/ERV1-MaLR
chr1	53147699	53147987	AluJr	SINE/Alu
chr9	136526600	136526902	AluSp	SINE/Alu
chr8	66626568	66626691	L2b	LINE/L2
chr2	242022342	242022910	L2a	LINE/L2
chr15	29400993	29401070	L2b	LINE/L2
chr8	126961133	126961751	MER92-int MER92-int	LTR/ERV1
chr1	207093518	207093816	AluSx	SINE/Alu
chr5	55448561	55448644	L1ME3G	LINE/L1
chr8	26304366	26304710	L1MB3	LINE/L1
chr2	232647579	232648440	L1ME3	LINE/L1
chr6	130374967	130376089	L2a	LINE/L2
chr4	109228867	109229591	LTR8	LTR/ERV1
chr3	72792847	72793200	L2d2	LINE/L2
chr11	67214035	67214344	AluYf1	SINE/Alu
chr1	160775573	160778610	L1PB4	LINE/L1
chr10	6377195	6377493	AluSq4	SINE/Alu
chr8	23105990	23106216	MIRb	SINE/MIR
chr1	207093817	207094131	L2c	LINE/L2
chr1	53143013	53143265	L3	LINE/CR1
chr21	43856948	43857521	MLT1E3	LTR/ERV1-MaLR
chr5	79423040	79423362	MLT1I	LTR/ERV1-MaLR
chr2	242085388	242086319	L1ME3F	LINE/L1
chr8	29976041	29976903	LTR5B LTR5B	LTR/ERV1
chr8	26300418	26300774	MLT1J	LTR/ERV1-MaLR
chr1	53106301	53107185	MER21C	LTR/ERV1
chr8	66629129	66629426	MER33	DNA/hAT-Charlie
chr8	126961752	126962060	AluSc	SINE/Alu

chr1	144545211	144545357	Tigger20a	DNA/TcMar-Tigger
chr6	36509597	36509911	AluSx1	SINE/Alu
chr1	193448293	193448721	LTR06	LTR/ERV1
chr6	36508665	36508976	AluY	SINE/Alu
chr5	133417803	133418575	L1ME1	LINE/L1
chr17	19051938	19052249	AluYk3	SINE/Alu
chr7	150389036	150389344	AluYc	SINE/Alu
chr17	18936512	18936890	MSTB	LTR/ERV1-MaLR
chr1	25920195	25920589	MER47B	DNA/TcMar-Tigger
chr1	53145366	53145541	MamTip1	DNA/hAT-Tip100
chr14	92226685	92227161	L1PA15-16	LINE/L1
chr17	4959504	4959795	AluSp	SINE/Alu
chr16	28483452	28483733	AluJo	SINE/Alu
chr8	126963714	126963972	MER92-int	LTR/ERV1
chr1	53141262	53141546	AluSq2	SINE/Alu
chr1	144532308	144532950	LTR8	LTR/ERV1
chr3	112644066	112644624	L1MC1	LINE/L1
chr12	56540699	56540984	MLT1J	LTR/ERV1-MaLR
chr7	99758871	99758990	AluJr	SINE/Alu
chr5	42997702	42998005	AluJr	SINE/Alu
chr3	15305693	15306054	LTR37A	LTR/ERV1
chr6	37509027	37509129	MIR	SINE/MIR
chr7	99759315	99759759	L1PA8	LINE/L1
chr8	19240522	19241349	L1MB3	LINE/L1
chr11	134107970	134108103	MER5B	DNA/hAT-Charlie
chr19	1079218	1079521	AluSx1	SINE/Alu
chr3	127401598	127401705	MIR1_Amn	SINE/MIR
chr1	144544113	144544448	L2b	LINE/L2
chr1	53143289	53143422	MIRb	SINE/MIR
chr6	108019998	108020082	MIR3	SINE/MIR
chr14	102301837	102301964	L4_C_Mam	LINE/RTE-X
chr5	79420343	79420828	MLT1O	LTR/ERV1-MaLR
chr17	19044282	19044660	MSTB	LTR/ERV1-MaLR
chr10	1279383	1279497	X2a_DNA	DNA
chr16	50674407	50674495	L2c	LINE/L2
chr2	106702983	106706609	L1MDa	LINE/L1
chr4	38512704	38512991	MLT1B	LTR/ERV1-MaLR
chr12	51610211	51610278	L2a	LINE/L2
chr21	48002698	48003450	L1M4b	LINE/L1
chr19	4916040	4916340	AluJr	SINE/Alu
chr5	133466863	133467032	MIR	SINE/MIR

chr1	53143539	53143656	L2b	LINE/L2
chr14	61768281	61768566	AluJo	SINE/Alu
chr8	26304068	26304365	AluSx1	SINE/Alu
chr1	104107249	104107351	MamRep1894	DNA/hAT
chr14	92224540	92224814	MLT2D	LTR/ERV1
chr4	103709290	103709570	L1MEd	LINE/L1
chr12	32148822	32148993	Tigger3b	DNA/TcMar-Tigger
chr5	133470482	133470561	Charlie17a	DNA/hAT-Charlie
chr2	242016225	242016511	AluYc	SINE/Alu
chr1	149283165	149283347	L1MEc	LINE/L1
chr1	100618319	100618582	AluSz6	SINE/Alu
chr7	43705798	43709360	HUERS-P3b-int HUERS-P3b-int LTR9B	LTR/ERV1
chr1	23963400	23963678	AluY	SINE/Alu
chr1	143746648	143747524	MER31A MER31-int	LTR/ERV1
chr1	53141553	53141905	AluJo	SINE/Alu
chr4	6690224	6690638	MLT1C	LTR/ERV1-MaLR
chr1	53137821	53137897	MIR	SINE/MIR
chr3	16383175	16383530	L1ME4a	LINE/L1
chr11	11177779	11178182	LTR16A LTR16A	LTR/ERV1
chr10	47581400	47582764	MER4-int MER4-int	LTR/ERV1
chr19	41345934	41346336	MSTA	LTR/ERV1-MaLR
chr3	59732954	59733272	THE1B	LTR/ERV1-MaLR
chr17	62128274	62129444	L1MC4	LINE/L1
chr15	75935999	75936336	L2-3_Crp	LINE/L2
chr17	33559627	33561166	ERV3-16A3_I-int	LTR/ERV1
chr3	122463637	122464257	L1MC5a	LINE/L1
chr1	53138262	53138553	AluSp	SINE/Alu
chr19	1072047	1072358	AluSz	SINE/Alu
chr16	22622321	22622852	MamRep1527	LTR
chr10	47565840	47566220	THE1C	LTR/ERV1-MaLR
chr11	113239525	113239604	MADE1	DNA/TcMar-Mariner
chr6	108024790	108024940	MER91A	DNA/hAT-Tip100
chr3	112313746	112314424	Kanga1a	DNA/TcMar-Tc2
chr17	75426791	75427101	AluSz	SINE/Alu
chr10	121255728	121256239	MER74A	LTR/ERV1
chr12	32148629	32148821	Tigger4a	DNA/TcMar-Tigger
chr11	77945121	77945428	AluJb	SINE/Alu
chr1	204597515	204597586	MIRb	SINE/MIR
chr1	207083841	207084017	MIRb	SINE/MIR
chr12	32150285	32150573	AluSx1	SINE/Alu
chr19	56150997	56151276	AluSx	SINE/Alu

chr1	53143817	53144124	AluSz6	SINE/Alu
chr17	44640556	44640846	AluJb	SINE/Alu
chr14	61765967	61766369	MER50	LTR/ERV1
chr17	33558866	33559281	LTR16B2	LTR/ERV1
chr1	204598542	204598884	THE1A	LTR/ERV1-MaLR
chr5	133470348	133470479	MIRc	SINE/MIR
chr17	46186295	46186588	AluSz6	SINE/Alu
chr7	99761157	99761456	AluJr	SINE/Alu
chr6	24811034	24811332	AluSx	SINE/Alu
chr7	150438475	150438734	L2	LINE/L2
chr11	68755642	68756937	L1MEd	LINE/L1
chr7	5893352	5893645	AluSx1	SINE/Alu
chr7	5888690	5888985	AluSx	SINE/Alu
chr5	133463640	133463813	MIR	SINE/MIR
chr2	242021895	242022057	MIR3	SINE/MIR
chr2	98102482	98103182	L1PA12	LINE/L1
chr1	53148023	53148317	AluSx	SINE/Alu
chr12	106731384	106731607	MIRb	SINE/MIR
chr1	53140742	53140889	MER45A	DNA/hAT-Tip100
chr19	4915444	4915748	AluSx	SINE/Alu
chr14	22544634	22545900	L1M4b	LINE/L1
chr11	77947050	77947359	L1M5	LINE/L1
chr12	32150220	32150284	Tigger3b	DNA/TcMar-Tigger
chr9	100431557	100431713	L1M5	LINE/L1
chr1	65517659	65517917	AluJo	SINE/Alu
chr18	47004406	47004625	AluJr	SINE/Alu
chr1	25577856	25578158	AluSp	SINE/Alu
chr7	45092122	45093720	ERV3-16A3_I-int	LTR/ERV1
chr18	21580134	21580519	MLT1B	LTR/ERV1-MaLR
chr19	35345090	35345318	LTR87	LTR/ERV1?
chrX	50907050	50908023	PRIMA4-int	LTR/ERV1
chr17	8128149	8128475	AluSx3	SINE/Alu
chr1	149570911	149573082	MER31-int MER31-int	LTR/ERV1
chr1	148600247	148600478	L1MEc	LINE/L1
chr12	47697790	47698194	Zaphod3	DNA/hAT-Tip100
chr8	29966866	29967068	Tigger15a	DNA/TcMar-Tigger
chr10	46705712	46706508	MER4A1 MER4-int	LTR/ERV1
chr10	28623787	28624403	MLT1F MLT1F	LTR/ERV1-MaLR
chr2	98081924	98082031	FLAM_C	SINE/Alu
chr14	100583168	100583280	MIR3	SINE/MIR
chr11	273659	274250	L1MC	LINE/L1

chr16	53521793	53522322	L1ME1	LINE/L1
chr14	75323021	75323205	L4_C_Mam	LINE/RTE-X
chr4	110463635	110464508	L2a	LINE/L2
chr12	106709905	106710622	L2a	LINE/L2
chr1	782121	782273	L2d	LINE/L2
chr6	138182434	138182611	Kanga11a	DNA/TcMar-Tc2
chr22	50652577	50652754	AluSx	SINE/Alu
chr3	16382359	16383060	L1MC1	LINE/L1
chr22	19874556	19874727	L1M5	LINE/L1
chr17	66185765	66186246	BLACKJACK	DNA/hAT-Blackjack
chr7	150913900	150914542	MER6	DNA/TcMar-Tigger
chr1	26645970	26646107	AluSq	SINE/Alu
chr11	14920082	14920250	MIR3	SINE/MIR
chr14	92229638	92230295	L1PA15-16	LINE/L1
chr7	5892042	5892169	MIR	SINE/MIR
chr1	160795418	160795714	AluSq2	SINE/Alu
chr20	55978247	55978388	MIR	SINE/MIR
chr19	56149373	56149597	MSTB	LTR/ERV1-MaLR
chr5	133462113	133462219	L2b	LINE/L2
chr3	111343353	111343653	L2a	LINE/L2
chr5	133441774	133441975	MIR	SINE/MIR
chr6	108023986	108024535	MER41A	LTR/ERV1
chr3	16385607	16385746	L3	LINE/CR1
chr3	16384344	16384408	MER5A	DNA/hAT-Charlie
chr19	42704047	42704552	L2a	LINE/L2
chr2	175411813	175411870	LTR78	LTR/ERV1
chr17	6900875	6901178	AluYm1	SINE/Alu
chr7	99763493	99763812	AluJr	SINE/Alu
chr2	219121921	219122136	MIRb	SINE/MIR
chr17	47443787	47444098	AluSp	SINE/Alu
chr2	20077499	20077778	AluJr	SINE/Alu
chr3	127400940	127401243	AluSx	SINE/Alu
chr22	20852864	20853374	MER39 MER34B-int MER34B-int	LTR/ERV1
chr18	72785576	72785720	MIRb	SINE/MIR
chr1	8494536	8495136	MLT1G3	LTR/ERV1-MaLR
chr14	102294098	102294389	Charlie18a	DNA/hAT-Charlie
chr12	106730326	106730588	AluSc	SINE/Alu
chr20	3150855	3151152	AluSz	SINE/Alu
chr4	68303958	68305710	L1MC3	LINE/L1
chr8	29976904	29977224	MLT1B MLT1B	LTR/ERV1-MaLR
chr9	136528546	136528674	MER117	DNA/hAT-Charlie

chr19	18115527	18115825	AluSz	SINE/Alu
chr19	56149034	56149284	MIR	SINE/MIR
chr19	18123422	18123548	MER2	DNA/TcMar-Tigger
chr22	27191336	27191697	MLT1I	LTR/ERV1-MaLR
chr8	125467943	125468497	MER4CL34	LTR/ERV1
chr12	106731940	106732636	L1PA15	LINE/L1
chr7	150107023	150107139	MIRb	SINE/MIR
chr9	130718682	130718989	AluSq2	SINE/Alu
chr9	5314974	5316306	L1M2a	LINE/L1
chr16	50674228	50674304	MamTip1b	DNA/hAT-Tip100
chr5	79408802	79409257	L1ME4a	LINE/L1
chr16	907000	907438	L1MD1	LINE/L1
chr11	559771	559924	FRAM	SINE/Alu
chr14	100576167	100576399	MIRc	SINE/MIR
chr12	2963197	2963490	AluSp	SINE/Alu
chr19	56148620	56148927	AluSz	SINE/Alu
chr3	107745876	107745998	Charlie9	DNA/hAT-Charlie
chr3	111376775	111377656	L1MC4	LINE/L1
chr3	16384640	16384710	MER5A	DNA/hAT-Charlie
chr21	43484312	43484653	MLT2B4	LTR/ERV1
chr16	21807284	21807516	LTR89	LTR/ERV1?
chr8	126960248	126960819	MER92-int	LTR/ERV1
chr16	911656	912177	L1MD1	LINE/L1
chr10	47576866	47577084	MER58A	DNA/hAT-Charlie
chr12	32150072	32150213	AluJo	SINE/Alu
chr3	111344289	111344868	L1ME3F	LINE/L1
chr8	26301727	26302169	MLT1C2	LTR/ERV1-MaLR
chr14	92240090	92240534	L2b	LINE/L2
chr12	68066235	68068459	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr10	103561962	103562148	L2c	LINE/L2
chr17	8124627	8124677	MIRc	SINE/MIR
chr17	66181926	66182797	MER89 MIR89-int	LTR/ERV1
chr5	133462605	133462754	MIRb	SINE/MIR
chr10	112628633	112628798	MER103C	DNA/hAT-Charlie
chr7	99759888	99760190	AluSg4	SINE/Alu
chr20	62260862	62261267	MLT1D	LTR/ERV1-MaLR
chr6	36463821	36464118	AluSc	SINE/Alu
chr11	22838072	22838510	L1M4	LINE/L1
chr1	207089527	207090075	L3	LINE/CR1
chr10	6653478	6653678	L2c	LINE/L2
chr13	22071567	22071869	AluJo	SINE/Alu

chr13	114633688	114633780	MIR	SINE/MIR
chr12	32147816	32148106	AluSz	SINE/Alu
chr22	39142585	39142749	MIRc	SINE/MIR
chr7	5889795	5890075	AluSq	SINE/Alu
chr10	47580146	47580941	MER4A1 MER4-int	LTR/ERV1
chr1	149285260	149285554	AluSz	SINE/Alu
chr7	99766947	99767016	MIRc	SINE/MIR
chr19	56147890	56148319	L2b	LINE/L2
chr1	207084911	207085013	MamTip2b	DNA/hAT-Tip100
chr2	46863611	46864331	HAL1	LINE/L1
chr5	79409977	79410194	THE1D	LTR/ERV1-MaLR
chr1	154925071	154925216	MIRb	SINE/MIR
chr9	130714251	130714350	MIRb	SINE/MIR
chr1	111224477	111224785	AluSz	SINE/Alu
chr5	55450412	55450715	AluSz6	SINE/Alu
chr16	89585034	89585382	L1MD1	LINE/L1
chrX	148598596	148599660	L1PA16	LINE/L1
chr1	207082282	207082533	L3	LINE/CR1
chr19	4913624	4913702	MIR	SINE/MIR
chr21	43484654	43484964	AluSq2	SINE/Alu
chr8	66627489	66627614	AluJr	SINE/Alu
chr5	79413001	79413246	MIRb	SINE/MIR
chr12	106732945	106733480	L1PA15	LINE/L1
chr7	5887554	5887854	AluSx1	SINE/Alu
chr16	50673175	50673348	MER5A	DNA/hAT-Charlie
chr22	31682159	31682224	MIR	SINE/MIR
chr19	35343270	35343490	AluSx	SINE/Alu
chr7	99761473	99761640	MIRb	SINE/MIR
chr1	144544588	144544866	AluSz6	SINE/Alu
chr17	3837207	3837510	AluSz	SINE/Alu
chr19	56149901	56150072	MSTB	LTR/ERV1-MaLR
chr18	47004633	47004931	AluSz6	SINE/Alu
chr2	241560662	241560969	AluSg	SINE/Alu
chr17	62764608	62765647	L1ME4b	LINE/L1
chr4	54869931	54870226	AluSx	SINE/Alu
chr16	89587881	89588208	AluJr	SINE/Alu
chr3	16392323	16393029	L3	LINE/CR1
chr9	130702465	130702542	MIRc	SINE/MIR
chr5	79419842	79420316	MER89	LTR/ERV1
chr2	175411276	175411389	LTR79	LTR/ERV1
chr6	138182626	138182977	L2a	LINE/L2

chr13	114639529	114639948	LTR8A	LTR/ERV1
chr1	53121431	53121730	L2	LINE/L2
chr6	108020150	108020229	L3	LINE/CR1
chr7	45106501	45106794	AluY	SINE/Alu
chr1	144539566	144539697	L2c	LINE/L2
chr4	108994264	108994557	AluSz6	SINE/Alu
chr20	3150243	3150550	AluSz6	SINE/Alu
chr10	6659103	6659310	AluSx1	SINE/Alu
chr6	111983551	111983662	MER58C	DNA/hAT-Charlie
chr1	167475185	167475394	MIR3	SINE/MIR
chr20	55976707	55977002	L2a	LINE/L2
chr1	52814006	52814269	L1MC4	LINE/L1
chr3	16386920	16387411	MLT2B1 MLT2B1	LTR/ERV1
chr17	33554675	33555042	MLT1C2	LTR/ERV1-MaLR
chr22	31677133	31677425	AluSp	SINE/Alu
chr3	45056011	45058222	ERV1-E-int ERV1-E-int	LTR/ERV1
chr19	3182989	3183155	MLT1C	LTR/ERV1-MaLR
chr7	96293444	96294013	MLT1E2	LTR/ERV1-MaLR
chr14	92244446	92244849	L2b	LINE/L2
chr5	133462312	133462604	AluSg	SINE/Alu
chr9	130713704	130713780	MIRb	SINE/MIR
chr12	32142049	32142349	AluY	SINE/Alu
chr1	29442663	29442965	AluSz	SINE/Alu
chr2	175413963	175414255	AluSc8	SINE/Alu
chr10	47566221	47566545	L2a	LINE/L2
chr1	53144504	53144634	L1MA9	LINE/L1
chr11	1496850	1497458	Tigger7	DNA/TcMar-Tigger
chr22	31681338	31681470	MIR	SINE/MIR
chr1	149614398	149614748	MER72	LTR/ERV1
chr18	47005605	47005764	HAL1	LINE/L1
chr3	16384409	16384639	AluJr	SINE/Alu
chr3	72788596	72788759	MIRb	SINE/MIR
chr2	20085472	20085746	LTR79	LTR/ERV1
chr4	109178306	109179205	MER63C	DNA/hAT-Blackjack
chr16	28485851	28486140	L1M4	LINE/L1
chr1	207064166	207064670	MER44B	DNA/TcMar-Tigger
chr16	66445307	66446519	L1ME1	LINE/L1
chr17	76787209	76787500	AluSp	SINE/Alu
chr1	161340406	161340592	MIR	SINE/MIR
chr3	195443049	195443250	LTR10A	LTR/ERV1
chr16	89587271	89587403	L1ME4c	LINE/L1

chr10	103562614	103562912	AluSx	SINE/Alu
chr1	202846605	202846889	AluSg	SINE/Alu
chr15	52949668	52949778	L2a	LINE/L2
chr2	112978415	112978730	L1PA14	LINE/L1
chr19	17842477	17842771	AluSx1	SINE/Alu
chr5	139481349	139481637	AluSz6	SINE/Alu
chr22	20852330	20852544	MLT1A0	LTR/ERV1-MaLR
chr10	1300280	1300481	L1PA4	LINE/L1
chr10	1300332	1304338	L1PA2	LINE/L1
chr11	129582444	129588556	L1PA4	LINE/L1
chr7	99758703	99758860	MIRb	SINE/MIR
chr6	26409386	26409490	L1ME4b	LINE/L1
chr22	31679580	31679710	FLAM_C	SINE/Alu
chr4	89639910	89640144	L1MD3	LINE/L1
chr1	207090969	207091261	AluJb	SINE/Alu
chr6	30777291	30777546	Charlie8	DNA/hAT-Charlie
chr2	242017518	242017826	AluSx1	SINE/Alu
chr19	3184281	3184591	L2b	LINE/L2
chr10	33339617	33340446	L1PB3	LINE/L1
chr16	15087003	15089858	L1PA4	LINE/L1
chr2	242088050	242088212	L2	LINE/L2
chrX	78536207	78538531	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr22	27139236	27139416	MLT1K	LTR/ERV1-MaLR
chr2	74934654	74935460	L1MEc	LINE/L1
chr11	118185716	118185870	MamRep38	DNA/hAT
chr16	27244483	27244696	L1ME4c	LINE/L1
chr12	6844838	6845458	L1MD2	LINE/L1
chr9	130711313	130711615	AluY	SINE/Alu
chr22	24573081	24573181	MIR	SINE/MIR
chr2	241413113	241413513	L1M3c	LINE/L1
chr1	160798256	160798572	AluSz	SINE/Alu
chr16	31060695	31061021	MLT11-int	LTR/ERV1-MaLR
chr10	47556520	47557536	L1MD1	LINE/L1
chr21	34118150	34119544	L1PA10	LINE/L1
chr12	106733759	106733849	MIRb	SINE/MIR
chr1	53146554	53146852	AluSx	SINE/Alu
chr14	102294499	102294737	L1MB5	LINE/L1
chr1	53145235	53145365	MIRb	SINE/MIR
chr7	150387661	150387771	MIR	SINE/MIR
chr7	99760277	99760450	L1PA8	LINE/L1
chr19	56150073	56150401	AluSx	SINE/Alu

chr5	35872919	35873120	L1M5	LINE/L1
chr19	18430092	18430396	AluSx4	SINE/Alu
chr11	77944381	77944651	L1M5	LINE/L1
chr11	274251	274550	AluJr	SINE/Alu
chr20	5801046	5801181	L2b	LINE/L2
chr16	1045040	1045149	MER81	DNA/hAT-Blackjack
chr10	121332000	121332204	AluSx3	SINE/Alu
chrX	152208921	152209262	L2c	LINE/L2
chr6	37531666	37532066	LTR33	LTR/ERV
chr6	29930717	29932043	L1PA7	LINE/L1
chr2	242030027	242030309	AluSx1	SINE/Alu
chr1	144478794	144478900	L2	LINE/L2
chr7	5887924	5888205	AluSx3	SINE/Alu
chr7	150439073	150439199	Charlie4z	DNA/hAT-Charlie
chr8	23123639	23123802	L1M5	LINE/L1
chr3	111383550	111383859	L1MC4	LINE/L1
chr5	133462237	133462311	MIRb	SINE/MIR
chr16	237737	237998	AluSx1	SINE/Alu
chr3	128882657	128882770	MLT1D	LTR/ERV-MaLR
chr5	133454461	133454687	AluJr	SINE/Alu
chr19	42704711	42704955	MLT1K	LTR/ERV-MaLR
chr9	136561647	136564187	L1MB8	LINE/L1
chr3	16375392	16375694	AluY	SINE/Alu
chr12	19724008	19727323	L1PREC2	LINE/L1
chr4	4270751	4271416	L1MD1	LINE/L1
chr9	5313716	5314979	L1M2a	LINE/L1
chr4	108967828	108968075	Plat_L3	LINE/CR1
chr7	142520614	142522660	L1M3	LINE/L1
chr16	3619921	3620149	MIRb	SINE/MIR
chr5	35872744	35872800	L3	LINE/CR1
chr4	68305770	68307764	L1PA6	LINE/L1
chr2	113002949	113003235	AluSz	SINE/Alu
chr15	29002900	29003265	THE1B	LTR/ERV-MaLR
chr20	31107611	31107775	FRAM	SINE/Alu
chr5	79415970	79416316	MLT1J2	LTR/ERV-MaLR
chr2	113001663	113001949	HAL1ME	LINE/L1
chr2	113005621	113005921	AluSz	SINE/Alu
chr12	68417769	68418630	L2a	LINE/L2
chr5	133470586	133470651	L2b	LINE/L2
chr11	67211999	67212294	AluSx1	SINE/Alu
chr2	242019418	242019715	AluSz	SINE/Alu

chr11	118185880	118186134	MIRb	SINE/MIR
chr4	110607773	110608045	AluJr	SINE/Alu
chr1	16780317	16780458	L2a	LINE/L2
chr22	22119727	22119908	MIR	SINE/MIR
chr22	39535308	39535426	AluSz	SINE/Alu
chr15	29402837	29402890	MIR	SINE/MIR
chr19	44561957	44564243	MER70A MER70-int	LTR/ERV1
chr6	30773414	30773702	AluSx1	SINE/Alu
chr13	20243654	20243949	AluSx1	SINE/Alu
chr14	50797671	50797958	AluSx	SINE/Alu
chr6	167349160	167349460	AluSg	SINE/Alu
chr2	97501977	97502277	AluSp	SINE/Alu
chr3	16375695	16376057	L1MC5a	LINE/L1
chr17	19046885	19047094	L2a	LINE/L2
chr2	127809379	127809580	MIRb	SINE/MIR
chr10	6668253	6668523	L2a	LINE/L2
chr7	128305144	128305880	L1MC5a	LINE/L1
chr1	144852968	144853120	MIR3	SINE/MIR
chr6	111983696	111983810	L1ME1	LINE/L1
chr6	108029845	108029998	L2b	LINE/L2
chr16	3624978	3625128	MER53	DNA/hAT
chr11	67213432	67213619	L2a	LINE/L2
chr12	68076515	68076872	HAL1ME	LINE/L1
chr19	49987746	49988047	AluSg	SINE/Alu
chr7	150446617	150446679	MamTip2	DNA/hAT-Tip100
chr3	52742494	52742640	MER3	DNA/hAT-Charlie
chr16	3594666	3594993	AluJb	SINE/Alu
chr15	74347184	74347480	AluSx	SINE/Alu
chr12	122234666	122234954	AluSp	SINE/Alu
chr7	142517119	142518750	L1MEc	LINE/L1
chr1	248624982	248625214	L1MA7	LINE/L1
chr9	100649116	100649355	L1MA1	LINE/L1
chr1	207084340	207084413	L2a	LINE/L2
chrX	103350637	103350858	MER20	DNA/hAT-Charlie
chr5	180270066	180270997	L1MEg	LINE/L1
chr6	166832151	166832252	MIRc	SINE/MIR
chr16	1028935	1029146	L2a	LINE/L2
chr17	33558470	33558838	L1MC4	LINE/L1
chr1	165690001	165690642	Tigger13a	DNA/TcMar-Tigger
chr9	130717523	130717722	MIRb	SINE/MIR
chr15	42187518	42187773	L2d2	LINE/L2

chr11	121309017	121309454	L1ME2	LINE/L1
chr11	64554382	64554432	L1MC5	LINE/L1
chr20	43712092	43712145	L1ME3A	LINE/L1
chr8	87347980	87348642	L1ME1	LINE/L1
chr19	38220597	38220908	AluSp	SINE/Alu
chr8	133720867	133721271	MLT1D	LTR/ERV1-MaLR
chr11	67214345	67214530	LTR8	LTR/ERV1
chr17	6565678	6566090	LTR50	LTR/ERV1
chr6	36510279	36510437	AluSx3	SINE/Alu
chr4	108974003	108974194	MIRb	SINE/MIR
chr12	32155866	32156553	ERV1-E-int ERV1-E-int	LTR/ERV1
chr16	3626659	3626970	AluSz	SINE/Alu
chr2	242016009	242016107	AluSz	SINE/Alu
chr7	150106574	150106701	MIRb	SINE/MIR
chr20	3789104	3789451	L1ME3	LINE/L1
chr2	241411956	241412260	L1M3c	LINE/L1
chr5	55450716	55450776	LTR54	LTR/ERV1
chr7	150169147	150169666	MER90a	LTR/ERV1
chr2	242049226	242049409	MER58A	DNA/hAT-Charlie
chr17	76786673	76786768	AluSx1	SINE/Alu
chr5	133467776	133467992	MIR	SINE/MIR
chr11	61176367	61176664	AluJr4	SINE/Alu
chr5	179719807	179720118	AluSx1	SINE/Alu
chr6	36477140	36477618	LTR22C0	LTR/ERV1
chr1	75165654	75166181	L1ME3G	LINE/L1
chr8	23120409	23120691	AluJr	SINE/Alu
chr11	118221940	118222337	L1ME3A	LINE/L1
chr16	3621662	3621964	AluSg	SINE/Alu
chr20	42851732	42852123	MSTB	LTR/ERV1-MaLR
chr21	46715624	46715852	MLT1A MLT1A	LTR/ERV1-MaLR
chr8	29966160	29966444	AluSz6	SINE/Alu
chr11	118222658	118222958	AluSx	SINE/Alu
chr3	108579382	108579432	MADE1	DNA/TcMar-Mariner
chr2	242086482	242086687	HAL1ME	LINE/L1
chr10	47569107	47569473	MLT1A	LTR/ERV1-MaLR
chr11	77946497	77947046	THE1A-int THE1A	LTR/ERV1-MaLR
chr1	58988253	58989289	Tigger2	DNA/TcMar-Tigger
chr19	35513907	35514088	MIRb	SINE/MIR
chr15	23200540	23200919	L1ME4a	LINE/L1
chr13	52382797	52383541	L1MB3	LINE/L1
chr3	125609302	125618439	LTR5_Hs LTR5_Hs HERVK-int LTR5_Hs LTR5_Hs	LTR/ERV1

chr7	6643714	6643883	AluSc	SINE/Alu
chr2	232648912	232649207	AluJr	SINE/Alu
chr13	75884773	75885148	L1PA15	LINE/L1
chr19	18115055	18115355	AluSp	SINE/Alu
chr9	100664250	100664573	L3	LINE/CR1
chr10	105623749	105624034	L1ME3	LINE/L1
chr9	100664574	100664883	AluSz	SINE/Alu
chr13	28012343	28012618	AluJr	SINE/Alu
chr8	23105130	23105319	MIRc	SINE/MIR
chr9	130709917	130710203	L2b	LINE/L2
chr2	98363155	98364219	L1MB7	LINE/L1
chr1	121203273	121203455	MIR	SINE/MIR
chr14	102300817	102301806	L4_C_Mam	LINE/RTE-X
chr16	22623721	22623953	LTR89	LTR/ERV1?
chr7	6643482	6643653	AluJr	SINE/Alu
chr3	107761211	107761731	MLT1K	LTR/ERV1-MaLR
chr12	32141039	32141184	MIRb	SINE/MIR
chr12	44905074	44905441	L1MEb	LINE/L1
chr6	37508761	37509026	AluSx	SINE/Alu
chr5	79417982	79418377	MLT2A1	LTR/ERV1
chr1	53137512	53137820	AluSx1	SINE/Alu
chr2	88065419	88065873	L1ME1	LINE/L1
chr6	167295445	167297328	L1MEc	LINE/L1
chr14	92250144	92250234	MIR3	SINE/MIR
chr1	202846331	202846396	L1MEg	LINE/L1
chr5	133454947	133455202	L1MB7	LINE/L1
chr13	25056019	25056956	Tigger1	DNA/TcMar-Tigger
chr20	3788142	3788228	MIR3	SINE/MIR
chr2	232648446	232648615	FAM	SINE/Alu
chr2	113006785	113007013	MLT1C	LTR/ERV1-MaLR
chr10	121252347	121252654	AluSz	SINE/Alu
chr1	144840755	144842859	L1P2	LINE/L1
chr1	149658230	149658738	MER66C	LTR/ERV1
chr2	198068007	198068838	L1MB5	LINE/L1
chr16	29923763	29924060	AluSp	SINE/Alu
chr2	242018844	242019417	L1MC5a	LINE/L1
chr9	130581948	130582034	MIR3	SINE/MIR
chr3	108579433	108579730	AluSg	SINE/Alu
chr11	121412649	121413604	L1MC4	LINE/L1
chr18	72785822	72786202	THE1D	LTR/ERV1-MaLR
chr2	219121009	219121143	AluJo	SINE/Alu

chr11	67212793	67212919	MIRb	SINE/MIR
chr11	67212966	67213143	L2a	LINE/L2
chr5	35884291	35884596	L2c	LINE/L2
chr16	956677	957120	L1M5	LINE/L1
chr10	112629147	112629200	L2b	LINE/L2
chr16	50680847	50680929	L2a	LINE/L2
chr2	238011630	238012009	L1MC4	LINE/L1
chr2	190342546	190343043	L1M4b	LINE/L1
chr1	53139464	53139555	MIR	SINE/MIR
chr19	49988862	49989072	AluSp	SINE/Alu
chr12	32144642	32144781	AluSx	SINE/Alu
chr9	130720305	130720665	L1MB7	LINE/L1
chr8	23109997	23110363	L1ME4a	LINE/L1
chr3	72788840	72789208	LTR16B1	LTR/ERV1
chr3	72789294	72789738	MLT1K	LTR/ERV1-MaLR
chr2	242051391	242051475	L1MC5	LINE/L1
chr18	47006851	47007161	AluJb	SINE/Alu
chr3	194115265	194115481	L1M5	LINE/L1
chr22	39142755	39143049	AluY	SINE/Alu
chr14	61769281	61769730	L1MEf	LINE/L1
chr1	65311448	65311565	MIRb	SINE/MIR
chr2	242023869	242025271	L1MEc	LINE/L1
chr22	36516750	36517311	MLT2A2	LTR/ERV1
chr2	242038208	242038312	L2a	LINE/L2
chr13	114764133	114764279	L1MC4	LINE/L1
chr6	105763490	105764510	Tigger1	DNA/TcMar-Tigger
chr16	3620359	3620754	L2a	LINE/L2
chr7	90700551	90706986	L1PA8	LINE/L1
chr1	53146097	53146464	L2	LINE/L2
chr15	52407882	52408367	L1MB7	LINE/L1
chr13	114768947	114769517	LTR10E	LTR/ERV1
chr3	16383531	16384106	L1MB8	LINE/L1
chr2	113003236	113003431	Tigger1	DNA/TcMar-Tigger
chr1	202846399	202846595	AluJr	SINE/Alu
chr19	35513270	35513498	L2b	LINE/L2
chr16	1599422	1599732	AluSq2	SINE/Alu
chr8	22444426	22444573	MIR3	SINE/MIR
chr10	17260297	17260511	MIR	SINE/MIR
chr9	130714822	130714989	L1ME4a	LINE/L1
chr6	108022159	108022281	UCON34	DNA/hAT-Charlie
chr6	167375904	167376233	L1PA16	LINE/L1

chr11	65140726	65140778	MIR1_Amn	SINE/MIR
chr17	44424781	44425086	AluSx1	SINE/Alu
chr13	114769679	114770684	L1PB4	LINE/L1
chr4	48896228	48896518	AluSx1	SINE/Alu
chr5	39127510	39127575	Alu	SINE/Alu
chr19	38872509	38872740	MIRb	SINE/MIR
chr9	95781134	95781431	AluSq	SINE/Alu
chr2	242087061	242087269	HAL1ME	LINE/L1
chr1	101694421	101695572	HAL1	LINE/L1
chr14	92230278	92231470	L1PB4	LINE/L1
chr14	61768934	61769279	LTR47A	LTR/ERV1
chr1	151865139	151865225	MIR	SINE/MIR
chr16	3619033	3619329	AluSz	SINE/Alu
chr4	10070521	10070604	MIRb	SINE/MIR
chr16	3624009	3624291	AluSx1	SINE/Alu
chr7	142519054	142520453	L1MEc	LINE/L1
chr17	42300228	42300423	Arthur1A	DNA/hAT-Tip100
chrX	152221040	152221509	MLT1C	LTR/ERV1-MaLR
chr1	154921139	154921615	L2d2	LINE/L2
chr7	26210434	26210637	AluJr	SINE/Alu
chr1	149670807	149671100	AluSz	SINE/Alu
chr14	102298592	102298874	MER113A	DNA/hAT-Charlie
chr21	45587613	45587679	L1M3	LINE/L1
chr2	113006315	113006490	MLT1C	LTR/ERV1-MaLR
chr7	150170368	150170706	L1ME3	LINE/L1
chr11	65334825	65335123	AluY	SINE/Alu
chr20	55978015	55978243	MER20	DNA/hAT-Charlie
chr12	122086664	122086842	L1ME4b	LINE/L1
chr17	66181383	66181516	MIR	SINE/MIR
chr1	53137084	53137463	MamRep137	DNA/TcMar-Tigger
chr3	16378969	16379273	AluSc	SINE/Alu
chr9	130714990	130715295	AluSz6	SINE/Alu
chr8	143732157	143734134	MER4-int MER4A1	LTR/ERV1
chr16	15693660	15693936	MER31B	LTR/ERV1
chr19	49987546	49987745	AluSq2	SINE/Alu
chr22	31684089	31684392	AluJr	SINE/Alu
chr12	32142504	32142794	AluSx	SINE/Alu
chr13	75886442	75886560	FRAM	SINE/Alu
chr15	50641532	50641734	MIR	SINE/MIR
chr10	121331696	121331988	AluSx1	SINE/Alu
chr8	143727794	143728748	MER4-int MER4-int	LTR/ERV1

chr1	207063066	207063833	MER21C	LTR/ERV1
chr2	242049411	242049726	L1MB2	LINE/L1
chrX	103370708	103370975	AluJr	SINE/Alu
chr2	242086785	242087056	AluJr	SINE/Alu
chr10	103561622	103561916	AluSg	SINE/Alu
chr19	17840316	17840481	AluJr	SINE/Alu
chr1	149277177	149277322	L1MEb	LINE/L1
chr17	76106165	76106244	MER5B	DNA/hAT-Charlie
chr2	88331665	88332101	Tigger3b	DNA/TcMar-Tigger
chr8	143734435	143734771	LTR8A	LTR/ERV1
chr2	98369517	98370044	LTR24C	LTR/ERV1
chr21	46710698	46710940	L1M5	LINE/L1
chr8	133721640	133722109	MLT1D	LTR/ERV1-MaLR
chr11	67213144	67213431	AluJr	SINE/Alu
chr19	56151854	56151923	MIRc	SINE/MIR
chr11	59575430	59575556	AluJr	SINE/Alu
chr12	2961536	2961829	AluJr	SINE/Alu
chr1	3441314	3441662	MLT1C2	LTR/ERV1-MaLR
chr16	57289189	57289497	AluSc8	SINE/Alu
chr7	65994520	65994792	L2	LINE/L2
chr1	193434568	193434682	L1ME3A	LINE/L1
chr10	73842335	73842638	AluJb	SINE/Alu
chr6	108027724	108028256	MLT1D	LTR/ERV1-MaLR
chr2	112978731	112979132	MSTA	LTR/ERV1-MaLR
chr16	3619396	3619698	AluSz	SINE/Alu
chr11	129730197	129730490	AluSc	SINE/Alu
chr1	53140443	53140542	L3	LINE/CR1
chr10	6669025	6669311	AluSz	SINE/Alu
chr17	43291125	43291423	AluSx1	SINE/Alu
chr3	111377657	111378475	L1PA16	LINE/L1
chr9	95781042	95781133	L1ME4b	LINE/L1
chr1	144300371	144300514	L1M5	LINE/L1
chr14	61772182	61773403	L1MEf	LINE/L1
chr19	49988679	49988861	AluSp	SINE/Alu
chr9	111632544	111633879	Tigger2	DNA/TcMar-Tigger
chr1	52813841	52814005	FRAM	SINE/Alu
chr4	147120396	147121069	L1M2	LINE/L1
chr10	6377494	6377597	MIR	SINE/MIR
chr14	64994047	64994340	AluSx3	SINE/Alu
chr5	43052162	43052456	AluSp	SINE/Alu
chr14	102298207	102298398	L4_C_Mam	LINE/RTE-X

chr2	113006491	113006784	AluSz6	SINE/Alu
chr17	16254252	16254544	AluSp	SINE/Alu
chr6	167346675	167346733	Cheshire	DNA/hAT-Charlie
chr3	111345180	111345856	L1ME3F	LINE/L1
chrY	21617487	21617806	AluJb	SINE/Alu
chr4	108975266	108975474	MIRb	SINE/MIR
chr10	6680859	6682013	L1MEf	LINE/L1
chr16	3620899	3620966	L1MD	LINE/L1
chr22	41262224	41262632	L2c	LINE/L2
chr17	66126936	66127263	L1MC4	LINE/L1
chr14	64997055	64997332	AluSx3	SINE/Alu
chr16	89609347	89609653	AluY	SINE/Alu
chr16	3595164	3595523	AluSx1	SINE/Alu
chr20	62897629	62897909	AluSg	SINE/Alu
chr22	36538810	36539238	MER31B	LTR/ERV1
chr3	98221491	98221575	MamTip2b	DNA/hAT-Tip100
chr9	130701770	130702062	AluSx1	SINE/Alu
chr17	44642447	44642556	MER2B	DNA/TcMar-Tigger
chr2	204635890	204636989	L1M5	LINE/L1
chr1	159836893	159837148	L2b	LINE/L2
chr19	50989461	50989742	AluSz	SINE/Alu
chr14	98054304	98056558	MSTB MSTB-int MSTB	LTR/ERV1-MaLR
chr1	207091262	207091959	L2	LINE/L2
chr6	24838738	24839030	AluSx1	SINE/Alu
chr3	16374365	16374976	Tigger17a	DNA/TcMar-Tigger
chr20	62262369	62262662	AluJr	SINE/Alu
chr1	151843519	151843830	AluSz6	SINE/Alu
chr22	39532290	39532770	MLT1F	LTR/ERV1-MaLR
chr12	9854406	9855213	LTR1E	LTR/ERV1
chr22	51212624	51213072	MLT1G3 MLT1G3	LTR/ERV1-MaLR
chr14	92229519	92229883	L1PB4	LINE/L1
chr2	55851048	55851226	HAL1	LINE/L1
chr7	150059689	150060196	MER34B	LTR/ERV1
chr16	66446700	66447105	MSTB	LTR/ERV1-MaLR
chr14	98402533	98404170	HAL1	LINE/L1
chrX	50908472	50909268	ERV24B_Prim-int	LTR/ERV1
chr20	61280329	61280818	MLT2B4	LTR/ERV1
chr8	133718132	133718484	MLT1A0	LTR/ERV1-MaLR
chr21	17261700	17262071	L1ME3G	LINE/L1
chr22	39142127	39142299	MER5B	DNA/hAT-Charlie
chr9	37774042	37774298	AluJb	SINE/Alu

chr7	141493132	141493367	MIRc	SINE/MIR
chr10	73845667	73845739	MER91C	DNA/hAT-Tip100
chr5	35872312	35872594	AluSx1	SINE/Alu
chr1	23961696	23961908	MIR	SINE/MIR
chr19	49988493	49988677	AluSp	SINE/Alu
chr9	140453433	140454438	LTR13	LTR/ERVK
chr20	51586199	51587511	L1PB3	LINE/L1
chr19	12356869	12357038	LTR33C	LTR/ERV1
chr22	27114857	27115039	MamTip2b	DNA/hAT-Tip100
chr4	6689133	6689629	LTR2C	LTR/ERV1
chr20	33582599	33582746	L2b	LINE/L2
chr6	30779729	30779918	L2a	LINE/L2
chr16	3620711	3620818	AmnSINE1	SINE/5S-Deu-L2
chr6	108032600	108032807	Tigger3c	DNA/TcMar-Tigger
chr1	149274177	149274517	MER57B2	LTR/ERV1
chr7	102126511	102126820	AluJr	SINE/Alu
chr15	52436676	52437320	MER77B	LTR/ERV1
chr1	26645663	26645969	AluY	SINE/Alu
chr21	17252681	17255626	L1PA11	LINE/L1
chr9	5316307	5316898	L1PA7	LINE/L1
chr7	102184474	102184604	AluJb	SINE/Alu
chr2	99212714	99214452	L1MB2	LINE/L1
chr9	130720666	130720973	AluJr4	SINE/Alu
chr17	4959890	4960174	AluSz6	SINE/Alu
chr16	50677496	50678140	Tigger17a	DNA/TcMar-Tigger
chr22	36517312	36517415	L2b	LINE/L2
chr20	21607758	21608462	HAL1	LINE/L1
chr22	27116758	27116968	LTR33	LTR/ERV1
chr8	133718879	133719415	L1MC5	LINE/L1
chr19	18424328	18424625	AluJb	SINE/Alu
chr1	149283941	149284196	AluSz	SINE/Alu
chr7	2885081	2885605	L1PB1	LINE/L1
chr15	50639971	50640256	AluSx1	SINE/Alu
chr16	29924566	29924751	L1M5	LINE/L1
chr15	50642367	50642583	MIR	SINE/MIR
chr11	64554118	64554381	L1MC	LINE/L1
chr12	54790464	54790769	AluJo	SINE/Alu
chr3	16381707	16382097	MLT1H2	LTR/ERV1-MaLR
chr1	202845471	202845750	L1MEg	LINE/L1
chr1	58991042	58991852	L1MEg	LINE/L1
chr6	149819674	149819975	AluJr	SINE/Alu

chr1	100499097	100499750	L1MC4	LINE/L1
chr11	77947496	77947900	L1M5	LINE/L1
chr16	3624682	3624977	AluSx1	SINE/Alu
chr1	149662894	149663792	MER49	LTR/ERV1
chr3	111378476	111379802	L1PA16	LINE/L1
chr3	195254803	195255156	L1PB1	LINE/L1
chr12	47698880	47699663	LTR1A2	LTR/ERV1
chr3	107746158	107746710	L1MA5	LINE/L1
chr16	89610357	89610589	L1MC5a	LINE/L1
chr12	113739139	113739443	AluSq2	SINE/Alu
chr1	207085326	207085631	L2c	LINE/L2
chr16	1409569	1409823	L1M3	LINE/L1
chr9	100649593	100649874	AluSz	SINE/Alu
chr19	19742818	19743113	AluSp	SINE/Alu
chr3	52845224	52845617	L2c	LINE/L2
chr3	52933313	52933460	Plat_L3	LINE/CR1
chr19	18114748	18114881	AluSx1	SINE/Alu
chr1	202846899	202847666	L1MEg	LINE/L1
chr10	6670201	6670512	AluSz	SINE/Alu
chr5	35881167	35881410	MLT1E1A	LTR/ERV1-MaLR
chr14	61764856	61765162	L2	LINE/L2
chr4	108970115	108970208	Charlie9	DNA/hAT-Charlie
chr11	62371847	62372148	AluSz	SINE/Alu
chr5	69288624	69288887	HAL1	LINE/L1
chr20	43287684	43288049	MSTD	LTR/ERV1-MaLR
chr1	167405249	167405312	FordPrefect_a	DNA/hAT-Tip100
chr1	207088803	207089060	L2d	LINE/L2
chr3	111382897	111383525	L1PA16	LINE/L1
chr17	44423101	44423399	AluSz	SINE/Alu
chr12	106731033	106731203	MIR3	SINE/MIR
chr4	108973800	108973911	MIR3	SINE/MIR
chr10	6658819	6659102	L1PA5	LINE/L1
chr1	9703185	9703510	AluSx3	SINE/Alu
chr12	44903015	44903185	L2c	LINE/L2
chr17	78985661	78986124	LTR10D	LTR/ERV1
chr22	31684584	31684650	OldhAT1	DNA/hAT-Ac
chr17	44643762	44643944	MIR	SINE/MIR
chr16	17321493	17321868	L2c	LINE/L2
chr7	142437063	142438322	HAL1	LINE/L1
chr8	29966445	29966597	AluSz6	SINE/Alu
chr17	47789098	47789174	L3b	LINE/CR1

chr2	88060435	88061142	L1MCa	LINE/L1
chr22	31679390	31679570	MIR	SINE/MIR
chr13	30931281	30931497	AluJr	SINE/Alu
chr14	61761590	61761882	AluSz6	SINE/Alu
chr6	37532324	37533035	L2c	LINE/L2
chr12	32141203	32141537	MER2	DNA/TcMar-Tigger
chr11	60783855	60783913	MER5A	DNA/hAT-Charlie
chr3	195382264	195383255	L1ME1	LINE/L1
chr8	23109164	23109708	L1ME4a	LINE/L1
chr6	30774495	30775782	LTR12C	LTR/ERV1
chr9	130712238	130712465	MIR	SINE/MIR
chr1	151149581	151149892	AluSg	SINE/Alu
chr17	44643022	44643309	AluSc	SINE/Alu
chr2	84973818	84976312	MSTB MSTB-int MSTB	LTR/ERV1-MaLR
chr19	1984715	1984998	AluSx1	SINE/Alu
chr22	39533905	39534209	AluY	SINE/Alu
chr21	46716713	46716937	MER58A	DNA/hAT-Charlie
chr4	120425110	120425667	L1PA17	LINE/L1
chr11	58261554	58261614	MIR	SINE/MIR
chr2	158251143	158251475	Tigger13a	DNA/TcMar-Tigger
chr22	28382086	28382429	THE1D	LTR/ERV1-MaLR
chr3	183915067	183915327	AluJr	SINE/Alu
chr5	133455865	133456436	L2c	LINE/L2
chr15	28961497	28962017	MLT1H2	LTR/ERV1-MaLR
chr2	73973205	73973559	LTR16D1	LTR/ERV1
chr11	6418173	6418238	MIRc	SINE/MIR
chr2	98386746	98388594	L4_C_Mam	LINE/RTE-X
chr5	44826936	44827044	MIRb	SINE/MIR
chr1	204598312	204598444	L2c	LINE/L2
chr20	3149745	3149887	MER96	DNA/hAT-Tip100
chr7	150442749	150443049	MER58B	DNA/hAT-Charlie
chr11	104776777	104777098	L1MA10	LINE/L1
chr19	42428418	42428623	MIR	SINE/MIR
chr21	35309123	35309273	MIRb	SINE/MIR
chr18	23617606	23617659	X6a_DNA	DNA/TcMar-Tigger
chr1	53139838	53140002	MIR	SINE/MIR
chr9	130708254	130708517	L2b	LINE/L2
chr5	1066243	1067056	MLT1C2-int MLT1C2	LTR/ERV1-MaLR
chr16	3620188	3620269	AluSz	SINE/Alu
chr6	108028259	108028535	AluSx1	SINE/Alu
chr15	42697219	42697434	Charlie8	DNA/hAT-Charlie

chr16	89610055	89610352	AluSx3	SINE/Alu
chr20	3787658	3787716	MIRc	SINE/MIR
chr6	108028621	108028704	MIRb	SINE/MIR
chr14	92250292	92250390	Charlie15a	DNA/hAT-Charlie
chr3	107746711	107747001	AluSp	SINE/Alu
chr19	44347492	44348423	Charlie1a	DNA/hAT-Charlie
chrX	100252238	100252498	L1MC4a	LINE/L1
chr14	50216914	50217191	L2c	LINE/L2
chr17	62560541	62561016	MLT1C2	LTR/ERV1-MaLR
chr16	89585788	89586088	AluSp	SINE/Alu
chr19	17841127	17841424	AluJr	SINE/Alu
chr12	29551946	29552208	L1ME3F	LINE/L1
chr5	139504654	139504792	Charlie4z	DNA/hAT-Charlie
chr9	130872542	130872856	AluSx	SINE/Alu
chr4	108999042	108999225	AluJb	SINE/Alu
chr2	46855245	46855547	AluSg4	SINE/Alu
chr11	60783925	60784272	MLT1J MLT1J	LTR/ERV1-MaLR
chr13	28012651	28012930	AluJr	SINE/Alu
chr2	219120860	219120999	Tigger11a	DNA/TcMar-Tigger
chr4	2225307	2226396	Tigger3b	DNA/TcMar-Tigger
chr11	65316887	65317188	AluSc	SINE/Alu
chr4	48894174	48894399	MIR	SINE/MIR
chr1	151865565	151865875	AluSz	SINE/Alu
chr1	151844811	151844888	MADE2	DNA/TcMar-Mariner
chr3	112629347	112630448	L1M3	LINE/L1
chr20	31973058	31973274	MIRb	SINE/MIR
chr7	6644612	6644919	AluSx1	SINE/Alu
chr17	33876993	33877266	L2c	LINE/L2
chrX	152216227	152216522	AluJb	SINE/Alu
chr14	77497373	77497518	MIR	SINE/MIR
chr11	67214845	67215252	LTR8	LTR/ERV1
chr7	35676123	35676233	MIRb	SINE/MIR
chr15	74348854	74349188	L1ME3	LINE/L1
chr14	31563815	31563943	AluJr	SINE/Alu
chr3	113432583	113432854	AluSp	SINE/Alu
chr19	39078509	39078960	L2b	LINE/L2
chr12	122041863	122042172	AluSp	SINE/Alu
chr9	136222154	136222447	AluSp	SINE/Alu
chr4	10070297	10070378	L2b	LINE/L2
chr16	3622589	3622727	L1M5	LINE/L1
chr16	27357400	27357562	AluJb	SINE/Alu

chr10	103562149	103562444	AluSp	SINE/Alu
chr10	47558069	47558938	L1ME3	LINE/L1
chr19	54950227	54950530	MER46C	DNA/TcMar-Tigger
chr1	27851257	27851546	AluSz6	SINE/Alu
chr11	107187581	107187883	AluSq2	SINE/Alu
chr10	6679119	6680321	MLT1E1A MLT1E1A-int	LTR/ERV-L-MaLR
chr22	39535738	39535949	AluSz	SINE/Alu
chr7	150155664	150158208	ERV-L-B4-int	LTR/ERV-L
chr8	143350863	143350987	AluJr	SINE/Alu
chr2	113006075	113006271	AluSp	SINE/Alu
chr12	122236011	122236127	MIRb	SINE/MIR
chr3	183914756	183915055	AluSx1	SINE/Alu
chr3	44963088	44963336	MIRb	SINE/MIR
chr16	29924779	29925151	MLT1F	LTR/ERV-L-MaLR
chr10	6669884	6670194	L3	LINE/CR1
chr6	108020529	108020646	MARNA	DNA/TcMar-Mariner
chr2	98361802	98362812	L1MB4	LINE/L1
chr6	167297457	167298147	MER21B	LTR/ERV-L
chr17	17118852	17119033	MIRb	SINE/MIR
chr17	76125045	76125126	MIRc	SINE/MIR
chr5	176875939	176876235	MER102a	DNA/hAT-Charlie
chr6	37508199	37508557	MSTA	LTR/ERV-L-MaLR
chr1	781350	782005	L1MC1	LINE/L1
chr2	87235436	87236147	L1MCa	LINE/L1
chr14	77495980	77496283	AluSx1	SINE/Alu
chr2	242017827	242018235	L1MB7	LINE/L1
chr16	3597683	3597970	AluSx	SINE/Alu
chr7	150159411	150161154	L1M2	LINE/L1
chr17	73563571	73563740	AluSg4	SINE/Alu
chr16	89585383	89585691	AluSg	SINE/Alu
chr2	112999561	112999672	HAL1ME	LINE/L1
chr9	130514996	130515344	L2b	LINE/L2
chr6	37507869	37507985	MIR3	SINE/MIR
chr9	98634815	98635311	Tigger18a	DNA/TcMar-Tigger
chr21	47993587	47995877	L1M4c	LINE/L1
chr7	99165885	99166171	AluSc8	SINE/Alu
chr6	24837651	24837937	AluJb	SINE/Alu
chr15	52880286	52880449	MER5A1	DNA/hAT-Charlie
chr9	95596014	95596483	LTR22B	LTR/ERV-K
chrX	281828	282014	AluJr	SINE/Alu
chr5	176949368	176949508	MER2	DNA/TcMar-Tigger

chr20	55980131	55980355	L2b	LINE/L2
chr19	50480072	50480136	L2b	LINE/L2
chr5	133461322	133461396	MIR3	SINE/MIR
chr1	151864435	151864550	FLAM_C	SINE/Alu
chr19	42389833	42390111	AluSz	SINE/Alu
chr22	47128431	47128790	L1ME3G	LINE/L1
chr2	241415232	241415747	L1M3c	LINE/L1
chr17	66179699	66179855	L1M5	LINE/L1
chr1	53135954	53136271	AluSz	SINE/Alu
chr12	124008802	124009397	L1MB7	LINE/L1
chr1	144302553	144302903	MER72	LTR/ERV1
chr2	107008677	107008902	MIRb	SINE/MIR
chr11	67661306	67661465	L2b	LINE/L2
chr16	66442346	66442604	LTR91	LTR
chr9	130723744	130724207	L2a	LINE/L2
chr15	40982356	40982410	Helitron1Nb_Mam	RC/Helitron
chr7	150442533	150442662	LTR85b	LTR/Gypsy?
chr19	19899197	19899498	AluSq2	SINE/Alu
chr7	142433502	142435754	THE1A THE1A-int THE1A	LTR/ERV1-MaLR
chr1	151867079	151867293	L2	LINE/L2
chr22	39536509	39536675	MIRc	SINE/MIR
chr5	171472529	171472637	MER5A	DNA/hAT-Charlie
chr2	37066363	37066528	L2a	LINE/L2
chr21	33936552	33939507	L1P4a	LINE/L1
chr12	112278743	112278877	AluSz	SINE/Alu
chr10	73842168	73842334	MLT1A	LTR/ERV1-MaLR
chr6	112019329	112019635	AluSp	SINE/Alu
chr17	10621139	10621438	AluSq2	SINE/Alu
chr1	144480109	144480612	L1M4c	LINE/L1
chr9	95781597	95781860	L1ME4b	LINE/L1
chr4	187144024	187146341	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr2	74914134	74914692	L2a	LINE/L2
chr6	31351519	31355060	LTR16B2 ERV3-16A3_I-int ERV3-16A3_I-int ERV3-16A3_I-int	LTR/ERV1
chr13	33085178	33085266	MIRb	SINE/MIR
chr16	930390	930671	AluJo	SINE/Alu
chr9	95781432	95781560	L1ME4b	LINE/L1
chr2	232649520	232649819	AluSx	SINE/Alu
chr14	92270324	92271312	L1ME3B	LINE/L1
chr7	102283579	102283709	AluJb	SINE/Alu
chr1	53139556	53139837	AluJr	SINE/Alu
chr3	195251921	195252250	MER2	DNA/TcMar-Tigger

chr3	127393560	127394100	L2a	LINE/L2
chr5	110830947	110831262	MLT1A0	LTR/ERV1-MaLR
chr22	27195423	27195528	L2b	LINE/L2
chr17	16337501	16337806	AluY	SINE/Alu
chr8	10964077	10964382	AluSx1	SINE/Alu
chr7	141493764	141494270	L1MA9	LINE/L1
chr16	16197155	16197458	AluSx1	SINE/Alu
chr22	24569522	24569808	AluSc	SINE/Alu
chr1	40220632	40220691	MER58A	DNA/hAT-Charlie
chr1	149271981	149272564	PRIMA41-int PRIMA41-int	LTR/ERV1

Table 6: Retrotransposon signature specific to activated CD4+ lymphocytes

Position (chromosome)	start	end	Name of the transposable elements	Type of TE
chr12	47764384	47764926	Tigger13a	DNA/TcMar-Tigger
chr8	101393712	101394064	MLT1J1	LTR/ERV1-MaLR
chr4	123531749	123531827	MIR3	SINE/MIR
chr4	154291971	154293486	Tigger1	DNA/TcMar-Tigger
chr7	129101035	129101350	L2-1_AMi	LINE/L2
chr12	47763833	47764149	AluJr	SINE/Alu
chr7	129097458	129097613	L1ME4a	LINE/L1
chr2	10341305	10342447	PABL_A-int	LTR/ERV1
chr10	6086139	6086630	MER66B	LTR/ERV1
chr4	123632755	123634495	Ricksha_c	DNA/MULE-MuDR
chr6	135958423	135960479	Charlie6	DNA/hAT-Charlie
chr10	74060187	74061778	LTR12C	LTR/ERV1
chr12	47764153	47764244	MLT1K	LTR/ERV1-MaLR
chr1	93042898	93043038	MLT2C2	LTR/ERV1
chr2	234759127	234759378	LTR82A	LTR/ERV1
chr10	6080696	6081521	L1MEd	LINE/L1
chr1	67672890	67673104	L1PA16	LINE/L1
chr12	47763420	47763806	MLT1L MLT1L	LTR/ERV1-MaLR
chr1	36484332	36485361	MER57A-int	LTR/ERV1
chr10	6078195	6078273	MIR3	SINE/MIR
chr6	149348472	149348554	MIRc	SINE/MIR
chr10	6080355	6080554	MIRb	SINE/MIR
chr7	129084042	129090075	MLT2A1 HERVL-int	LTR/ERV1
chr6	481504	483081	L1P1	LINE/L1
chr7	129096978	129097299	Tigger3a	DNA/TcMar-Tigger
chr4	123546442	123546552	MamRep1879	DNA/hAT-Tip100?
chr1	17766806	17767234	L2c	LINE/L2

chr12	12254325	12255598	L1MEc	LINE/L1
chr12	68551150	68551330	MIR3	SINE/MIR
chr1	42021310	42022800	L1MB3	LINE/L1
chr2	196415386	196416932	Tigger1	DNA/TcMar-Tigger
chr17	57280191	57280407	AluJr	SINE/Alu
chr21	44480263	44480390	Tigger19b	DNA/TcMar-Tigger
chr2	234759980	234760150	MER58A	DNA/hAT-Charlie
chr1	42014559	42017887	L1PA6	LINE/L1
chr10	6075307	6075874	L1ME2z	LINE/L1
chr10	6083378	6083818	L1ME3Cz	LINE/L1
chr10	6078851	6078973	MER5A1	DNA/hAT-Charlie
chr1	7977291	7977810	L1M5	LINE/L1
chr3	111294424	111294808	MLT1A1	LTR/ERV1-MaLR
chr1	995756	996006	L2	LINE/L2
chr13	43060052	43060355	AluSx	SINE/Alu
chr14	106470478	106471036	L1MC	LINE/L1
chr10	74061779	74061961	L1ME3A	LINE/L1
chr4	123548423	123549027	L1ME3G	LINE/L1
chr4	123529035	123530179	L2	LINE/L2
chr8	101324186	101324396	L2c	LINE/L2
chr1	42018453	42021302	L1PA6	LINE/L1
chr3	17815754	17816433	LTR12	LTR/ERV1
chr6	33375207	33375720	L1MC5a	LINE/L1
chr8	129290904	129294581	L1ME3A	LINE/L1
chr4	123544323	123544822	MLT1D	LTR/ERV1-MaLR
chr1	36480490	36481293	MER21B	LTR/ERV1
chr1	995467	995755	AluSg	SINE/Alu
chr4	123627457	123627539	L3	LINE/CR1
chr12	4667243	4667451	L1ME4c	LINE/L1
chr7	129096898	129096962	MamSINE1	SINE/tRNA-RTE
chr1	79104091	79105430	L1MD2	LINE/L1
chr21	26821492	26823803	THE1D THE1D-int THE1D	LTR/ERV1-MaLR
chr12	47761008	47761457	LTR54B	LTR/ERV1
chr2	196417232	196417732	Tigger1	DNA/TcMar-Tigger
chr4	123627647	123627740	FLAM_A	SINE/Alu
chr6	479268	480214	L1MEa	LINE/L1
chr6	477469	477866	L1MC4a	LINE/L1
chr21	26886064	26886464	MSTA	LTR/ERV1-MaLR
chr10	6079993	6080160	MIR3	SINE/MIR
chr2	10342507	10342947	LTR19A	LTR/ERV1
chr1	36482083	36483219	MER57B2 MER57A-int	LTR/ERV1

chr1	7976853	7976991	L1M5	LINE/L1
chrX	53740832	53741218	EUTREP15	LTR/ERV1?
chr14	106490059	106491156	L1M4b	LINE/L1
chr1	67727804	67728160	L2a	LINE/L2
chr12	47751235	47752182	HAL1	LINE/L1
chr10	6098980	6099202	L2c	LINE/L2
chr10	6077823	6078026	MamTip2	DNA/hAT-Tip100
chr4	89403491	89403873	MER115	DNA/hAT-Tip100
chr6	401121	401338	MER103C	DNA/hAT-Charlie
chr10	6101280	6101439	MIRb	SINE/MIR
chr17	38676713	38677014	L1M8	LINE/L1
chr6	33376156	33376467	L1MC5a	LINE/L1
chr7	138758227	138758536	AluSx1	SINE/Alu
chr15	52827917	52828234	AluSx3	SINE/Alu
chr1	234866997	234867543	hAT-4b_Ther	DNA/hAT-Tip100
chr9	92334259	92334724	MLT1G3	LTR/ERV1-MaLR
chr7	129099945	129100048	L2c	LINE/L2
chr7	129123887	129124182	L1MC5a	LINE/L1
chr3	72029533	72032336	MLT2A1 HERVL-int	LTR/ERV1
chr17	57282108	57282408	AluJr	SINE/Alu
chr13	80117009	80117311	AluSx1	SINE/Alu
chr1	7978350	7978443	L1M5	LINE/L1
chrX	53743337	53743795	MLT1L	LTR/ERV1-MaLR
chr1	79087476	79088055	L1MA4A	LINE/L1
chr6	483078	483268	L1MEa	LINE/L1
chr2	10340258	10340990	PABL_A-int	LTR/ERV1
chr21	44474236	44474533	AluSz6	SINE/Alu
chr13	80116508	80116737	L1MD	LINE/L1
chr1	36481458	36481783	MER57B2	LTR/ERV1
chrX	53741416	53741908	MLT1N2	LTR/ERV1-MaLR
chr10	6092212	6092314	MIR	SINE/MIR
chrX	13022338	13022644	AluSg	SINE/Alu
chr3	33015867	33016473	MLT2B4 MLT2B4	LTR/ERV1
chr4	123629158	123629420	AluJb	SINE/Alu
chr1	7977828	7977934	AluJo	SINE/Alu
chr2	231821652	231822217	MER44C	DNA/TcMar-Tigger
chr16	81063172	81063462	AluSz	SINE/Alu
chr1	7976992	7977290	AluSx	SINE/Alu
chr18	9088434	9088838	MLT1A1	LTR/ERV1-MaLR
chr10	6082734	6082928	L1MEd	LINE/L1
chr19	47741223	47741513	AluJb	SINE/Alu

chr1	1149947	1150242	AluSx1	SINE/Alu
chr6	25113385	25113637	L1PB4	LINE/L1
chr8	101323665	101323975	AluY	SINE/Alu
chr4	123545351	123545959	Tigger9b	DNA/TcMar-Tigger
chrX	53727871	53728442	MLT1E2	LTR/ERV1-MaLR
chr1	79098650	79100670	L1M1	LINE/L1
chr6	475793	476119	L1MC	LINE/L1
chr10	6085390	6085699	AluSx1	SINE/Alu
chr10	6084117	6084586	L1ME3Cz	LINE/L1
chr1	36486884	36487663	MER57A-int MER57A-int	LTR/ERV1
chr8	27663165	27663448	AluJb	SINE/Alu
chr19	50839363	50839664	AluSx	SINE/Alu
chr13	43060495	43060766	L1ME4a	LINE/L1
chr1	67726450	67726581	FRAM	SINE/Alu
chr12	47765092	47765395	AluY	SINE/Alu
chr6	480088	480546	L1MEf	LINE/L1
chr6	25111106	25111290	MIRc	SINE/MIR
chr8	27663816	27664111	L1MC	LINE/L1
chr4	123544026	123544321	MamRep38	DNA/hAT
chr4	15783403	15783948	MLT1H1-int MLT1H1	LTR/ERV1-MaLR
chr12	46903936	46911144	L1PA14	LINE/L1
chr19	47742410	47742557	MIR	SINE/MIR
chr4	89404082	89404292	L1MEd	LINE/L1
chr10	6090463	6090591	MIRb	SINE/MIR
chr12	113348225	113348705	L2a	LINE/L2
chr5	162907021	162908149	L1ME3F	LINE/L1
chr7	105904667	105904744	Tigger19a	DNA/TcMar-Tigger
chr1	67864278	67864383	L2b	LINE/L2
chr14	106469427	106470301	L1MC3	LINE/L1
chr7	100953508	100954205	L1M2	LINE/L1
chr4	123625369	123625868	MER87B	LTR/ERV1
chr9	36679316	36680245	L1MB7	LINE/L1
chr8	101391914	101392055	MER20	DNA/hAT-Charlie
chr10	6101570	6101909	L2c	LINE/L2
chr21	44474729	44475030	AluJo	SINE/Alu
chr1	36484034	36484331	AluSc8	SINE/Alu
chr22	19490799	19491215	MER41-int MER41-int	LTR/ERV1
chr18	9074223	9074502	AluSc	SINE/Alu
chr1	79089681	79089980	AluSz	SINE/Alu
chr18	2579726	2579926	L1M5	LINE/L1
chr8	101299563	101299630	L2a	LINE/L2

chr7	105904847	105905064	Tigger4a	DNA/TcMar-Tigger
chr1	79088173	79088741	MLT1E1A	LTR/ERV1-MaLR
chr10	6084583	6085389	L1ME3Cz	LINE/L1
chr10	6102285	6102431	L1PB1	LINE/L1
chr6	398461	398598	MIR3	SINE/MIR
chr9	102598510	102598788	L3	LINE/CR1
chr1	996698	996764	L2	LINE/L2
chr10	6085700	6085845	L1ME3Cz	LINE/L1
chr2	158335814	158338372	L1M1	LINE/L1
chr17	38682254	38682718	MLT1J	LTR/ERV1-MaLR
chr16	79747528	79748100	MLT1F2	LTR/ERV1-MaLR
chr3	121210936	121211248	LTR78B	LTR/ERV1
chr10	6090150	6090420	L2	LINE/L2
chr7	138754404	138754723	L4_A_Mam	LINE/RTE-X
chr12	47759625	47760222	MER41B	LTR/ERV1
chr2	10340991	10341304	AluSx	SINE/Alu
chrX	53718361	53719289	L1ME3G	LINE/L1
chr5	68470311	68470557	AluY	SINE/Alu
chr12	47761458	47763298	L2a	LINE/L2
chr2	102980114	102980608	LTR82B	LTR/ERV1
chr1	7978062	7978345	AluSq2	SINE/Alu
chr1	27997500	27997583	MIRb	SINE/MIR
chr4	123626024	123626216	MLT1H	LTR/ERV1-MaLR
chr8	101299530	101299614	MIRb	SINE/MIR
chr8	27664134	27664431	AluSq2	SINE/Alu
chrX	53737755	53738098	MLT1B	LTR/ERV1-MaLR
chr20	865289	865384	MIR3	SINE/MIR
chr4	15789306	15789746	LTR22A	LTR/ERV1
chr12	12253503	12253933	L2c	LINE/L2
chr6	406262	406562	AluSg	SINE/Alu
chr7	154989103	154989551	L1M5	LINE/L1
chr1	996353	996653	AluSq	SINE/Alu
chr1	212860506	212860658	L1ME1	LINE/L1
chr4	123630804	123631109	AluSz	SINE/Alu
chr1	235091772	235092005	UCON58	DNA?
chr8	101391817	101391911	L2c	LINE/L2
chr4	123527619	123527977	MSTA	LTR/ERV1-MaLR
chr1	67817953	67818305	MLT1J	LTR/ERV1-MaLR
chr18	2579418	2579725	AluSx	SINE/Alu
chr11	11383479	11386547	L1MC5	LINE/L1
chr1	996929	997045	FLAM_A	SINE/Alu

chr9	80933327	80933764	MLT1C2	LTR/ERVl-MaLR
chrX	53736431	53736670	L1MC5a	LINE/L1
chr1	998098	998175	MLT1B	LTR/ERVL-MaLR
chr4	104091441	104094706	L1MA8	LINE/L1
chr10	6088776	6088887	Charlie8	DNA/hAT-Charlie
chr10	6090943	6091478	MLT2B2	LTR/ERVL
chr1	212872150	212872308	MIRb	SINE/MIR
chr7	129123579	129123886	AluJb	SINE/Alu
chr19	47739974	47740184	AluSz6	SINE/Alu
chr22	37477279	37477470	MIRb	SINE/MIR
chr4	15782450	15782747	AluSz	SINE/Alu
chr1	159041297	159041599	AluSq	SINE/Alu
chr6	476243	476620	L1MC	LINE/L1
chr10	85898200	85898506	AluSz	SINE/Alu
chr12	92950831	92951460	L2	LINE/L2
chr8	19036838	19038584	Arthur1	DNA/hAT-Tip100
chr8	6431228	6431660	L1MEd	LINE/L1
chr11	64847885	64848111	AluJb	SINE/Alu
chr7	138760178	138760485	AluJb	SINE/Alu
chr1	67865442	67865906	MER41B	LTR/ERV1
chr15	91368568	91370060	LTR12C	LTR/ERV1
chr1	67728787	67729067	AluJb	SINE/Alu
chr3	72147862	72148184	LTR16A	LTR/ERVL
chr8	27664593	27665069	L1M5	LINE/L1
chr10	91154704	91155595	MER54A	LTR/ERVL
chr17	38680424	38680636	L1MEh	LINE/L1
chrX	53729275	53729728	MLT1J	LTR/ERVL-MaLR
chr2	113855744	113857281	L1PBa	LINE/L1
chr14	100822459	100822531	MIRb	SINE/MIR
chr13	42967825	42968262	MLT1K MLT1K MLT1K	LTR/ERVL-MaLR
chr7	130632808	130633364	L1MB3	LINE/L1
chr6	400584	400791	L1ME4a	LINE/L1
chr2	40162746	40163855	L1P4	LINE/L1
chr8	6432053	6432477	L1MEd	LINE/L1
chr4	123621353	123621824	MER70A	LTR/ERVL
chr10	6082059	6082117	MIRc	SINE/MIR
chr20	862439	862555	L2b	LINE/L2
chr1	79097381	79098615	Charlie1a	DNA/hAT-Charlie
chr1	212862273	212862488	L2d	LINE/L2
chr11	15084505	15092088	MER11B HERVK11-int HERVK11-int HERVK11-int HERVK11-int HERVK11-int MER11B	LTR/ERVK

chrX	53732788	53733176	MLT1E2	LTR/ERV1-MaLR
chr22	19503229	19503377	MIRb	SINE/MIR
chr1	27996801	27997096	AluJb	SINE/Alu
chr8	103108463	103108608	MLT1B	LTR/ERV1-MaLR
chr7	138759138	138759708	Charlie1b	DNA/hAT-Charlie
chrX	53740567	53740737	EUTREP15	LTR/ERV1?
chr1	67826494	67827671	L1MCa	LINE/L1
chr10	6098184	6098250	L2b	LINE/L2
chr2	112237619	112238033	MLT1C	LTR/ERV1-MaLR
chr12	113347183	113347476	AluJo	SINE/Alu
chr16	22207889	22208194	AluSp	SINE/Alu
chr21	26841224	26841671	MLT1E2	LTR/ERV1-MaLR
chr1	67864397	67864752	MER4A	LTR/ERV1
chr10	6065284	6065598	AluSz	SINE/Alu
chr4	89403903	89404081	AluSz	SINE/Alu
chr1	212860685	212860773	L2a	LINE/L2
chr21	26938950	26939163	MIR	SINE/MIR
chr4	123526973	123527618	L2a	LINE/L2
chr14	100825866	100825997	MER85	DNA/PiggyBac
chr10	6103070	6103354	AluJb	SINE/Alu
chr7	130638704	130639214	L1ME2	LINE/L1
chr2	28632601	28632907	AluSq2	SINE/Alu
chr12	94597562	94597939	MSTD	LTR/ERV1-MaLR
chr12	47752961	47753765	L1PA15	LINE/L1
chr2	163132831	163133141	AluJb	SINE/Alu
chr6	394492	394764	AluJr	SINE/Alu
chr8	129289731	129290906	L1ME3A	LINE/L1
chrX	119631658	119631933	AluSx	SINE/Alu
chr6	475206	475790	MER4CL34	LTR/ERV1
chr9	36653143	36653442	AluJo	SINE/Alu
chr1	67729312	67729560	AluSz	SINE/Alu
chr11	64850234	64850412	L2c	LINE/L2
chr2	103000344	103000598	L1M4a1	LINE/L1
chr7	154987180	154988238	L1MEf	LINE/L1
chrX	53740437	53740566	L1ME1	LINE/L1
chr20	866810	867138	L1ME4b	LINE/L1
chr2	217378680	217379402	L1MEg	LINE/L1
chr6	33376480	33376608	FRAM	SINE/Alu
chr1	211837760	211837980	L2a	LINE/L2
chr10	62546870	62547147	MER47A	DNA/TcMar-Tigger
chr12	12836346	12836591	MIR	SINE/MIR

chr12	68549514	68549702	MIRc	SINE/MIR
chr1	234864231	234864312	MIR3	SINE/MIR
chr12	113406759	113406868	MER117	DNA/hAT-Charlie
chr8	6431661	6432052	MLT1C	LTR/ERV1-MaLR
chr1	79089981	79090712	L1M3	LINE/L1
chr22	18654756	18654881	AluJo	SINE/Alu
chr1	27996136	27996333	MIR	SINE/MIR
chr1	163302194	163302698	MLT1D	LTR/ERV1-MaLR
chr1	67818977	67819275	AluJb	SINE/Alu
chr5	110861470	110862726	HSMAR1	DNA/TcMar-Mariner
chr7	138759731	138759919	MER20	DNA/hAT-Charlie
chr14	91289454	91290561	MER11A	LTR/ERV1
chr1	234864777	234864830	MIR1_Amn	SINE/MIR
chr1	79089174	79089639	MLT2B3	LTR/ERV1
chr1	67726827	67726953	MER94	DNA/hAT-Blackjack
chrX	53838578	53838970	L1P3	LINE/L1
chr10	6102189	6102311	L1PB1	LINE/L1
chr1	67809569	67809799	L2b	LINE/L2
chr21	43819505	43819837	L1MA9	LINE/L1
chr18	2581378	2581666	AluSz6	SINE/Alu
chr3	111297273	111297382	MER96	DNA/hAT-Tip100
chr19	21684007	21686213	MER57A-int MER57B1	LTR/ERV1
chr17	6665763	6666025	L2d	LINE/L2
chr4	123544941	123545225	LTR103b_Mam	LTR/ERV1?
chr1	67830090	67831237	L1Mca	LINE/L1
chr14	100825998	100826135	L1MB7	LINE/L1
chr8	101324461	101324549	MER5B	DNA/hAT-Charlie
chr7	138756620	138756818	L4_A_Mam	LINE/RTE-X
chr18	9062414	9062824	L2a	LINE/L2
chr20	32268431	32268847	MLT1F1 MLT1F1	LTR/ERV1-MaLR
chr2	231522907	231523218	AluSx3	SINE/Alu
chr1	67726106	67726286	MER117	DNA/hAT-Charlie
chr12	47747558	47748132	L2	LINE/L2
chr2	238341683	238341870	OldhAT1	DNA/hAT-Ac
chrX	53733920	53734144	MER101	LTR/ERV1
chr3	18962717	18962995	LTR88b	LTR/Gypsy?
chr19	21185188	21187904	LTR2 Harlequin-int	LTR/ERV1
chr10	6102438	6102746	AluSg	SINE/Alu
chr16	31370135	31370440	AluJr	SINE/Alu
chr4	169162046	169164369	THE1B THE1B-int THE1B	LTR/ERV1-MaLR
chr17	43014420	43015345	L1M5	LINE/L1

chrX	53730132	53730388	AluJb	SINE/Alu
chr6	52104637	52104952	Tigger19b	DNA/TcMar-Tigger
chr19	2457229	2457521	AluSz	SINE/Alu
chr4	123376647	123376889	MIR	SINE/MIR
chr1	27997891	27998196	AluY	SINE/Alu
chr6	159108855	159109453	L1ME4a	LINE/L1
chr17	38682885	38683338	LTR79	LTR/ERV1
chr1	79101871	79102016	L2b	LINE/L2
chr4	123631381	123631547	Tigger19b	DNA/TcMar-Tigger
chr1	159039634	159040136	L2b	LINE/L2
chr6	33373628	33373750	L2a	LINE/L2
chr22	37477034	37477254	MIR	SINE/MIR
chr1	117353538	117353859	AluSg	SINE/Alu
chr1	79086966	79087256	AluSz	SINE/Alu
chr1	234865157	234865208	L2c	LINE/L2
chr14	62192130	62192438	AluSz6	SINE/Alu
chr14	100824098	100824472	L1M4	LINE/L1
chr6	480585	481507	L1MEf	LINE/L1
chr7	138753514	138753970	LTR69	LTR/ERV1
chr1	67864724	67864955	MER4A	LTR/ERV1
chr10	6094347	6094440	L2c	LINE/L2
chr9	36656904	36657176	Tigger3a	DNA/TcMar-Tigger
chr1	7972926	7973535	LTR36	LTR/ERV1
chr6	16436526	16437469	L2a	LINE/L2
chr9	36601556	36602203	L1MB2	LINE/L1
chr1	67811747	67811949	MIR	SINE/MIR
chr10	6095131	6095369	MIRb	SINE/MIR
chr3	186760051	186760195	L2b	LINE/L2
chr1	169531555	169533851	L1MEc	LINE/L1
chr10	6098434	6098725	AluSz6	SINE/Alu
chr1	79088751	79089074	L1M3	LINE/L1
chr15	91370134	91370258	MIRc	SINE/MIR
chr5	76035085	76035385	AluSq2	SINE/Alu
chr10	6058007	6058411	MSTD	LTR/ERV1-MaLR
chr7	129125098	129125297	L1ME4b	LINE/L1
chrX	100419316	100419620	AluSx1	SINE/Alu
chr14	100823802	100824097	AluSq2	SINE/Alu
chr11	64848197	64848613	L2a	LINE/L2
chr12	7063607	7063696	AluJb	SINE/Alu
chr17	38679575	38679890	L2c	LINE/L2
chr21	43821653	43821758	L1M4	LINE/L1

chr11	64849605	64849926	L2c	LINE/L2
chr8	19038872	19039666	Arthur1	DNA/hAT-Tip100
chr1	1150291	1150385	MLT1B	LTR/ERV1-MaLR
chr2	113870708	113871346	L1MA10	LINE/L1
chr10	95270091	95270345	L1MC4	LINE/L1
chr7	130644751	130644832	MER20B	DNA/hAT-Charlie
chr7	30645152	30645306	AluJb	SINE/Alu
chr1	79103204	79104023	L1MD2	LINE/L1
chr10	6059536	6059839	AluSx1	SINE/Alu
chr18	9109624	9109813	MIRb	SINE/MIR
chr6	52105257	52105525	Tigger19b	DNA/TcMar-Tigger
chr6	479149	479259	MIR3	SINE/MIR
chrX	53725234	53726731	L1PA2	LINE/L1
chr6	402750	403027	AluSz6	SINE/Alu
chr14	100821487	100821546	MER5B	DNA/hAT-Charlie
chr16	81053982	81054124	FRAM	SINE/Alu
chr4	123543736	123543917	MIR	SINE/MIR
chr20	32273329	32273546	MIR	SINE/MIR
chr7	154989667	154989825	Tigger1	DNA/TcMar-Tigger
chr14	76002345	76002729	L2a	LINE/L2
chr12	113351754	113352544	L1PB1	LINE/L1
chr2	10351874	10352040	L1ME3A	LINE/L1
chr21	42803253	42803391	Charlie2b	DNA/hAT-Charlie
chr11	93441203	93444654	L1MA3	LINE/L1
chr21	42802947	42803252	AluSx	SINE/Alu
chr7	105896993	105897288	MER47A	DNA/TcMar-Tigger
chr10	6099807	6100110	AluSx1	SINE/Alu
chr1	160646338	160646760	MER45B	DNA/hAT-Tip100
chr2	231850497	231850973	MLT2C2	LTR/ERV1
chr22	37478189	37478315	MIRb	SINE/MIR
chr17	38678492	38678771	LTR103_Mam	LTR/ERV1?
chr15	91370809	91371103	AluSz	SINE/Alu
chr15	91413525	91413705	MIR	SINE/MIR
chr20	865467	865593	MIR1_Amn	SINE/MIR
chr17	38679939	38680134	MIRb	SINE/MIR
chr22	41604750	41605043	AluSg7	SINE/Alu
chr1	27997097	27997492	MER21B	LTR/ERV1
chr6	28865886	28866188	AluY	SINE/Alu
chr4	15782996	15783402	MLT2D	LTR/ERV1
chr6	33374904	33375206	AluJb	SINE/Alu
chr6	33375868	33376125	L1MC5a	LINE/L1

chr12	102549166	102549917	LTR17	LTR/ERV1
chr10	63831670	63832271	LTR50	LTR/ERV1
chr9	36656615	36656903	AluJb	SINE/Alu
chr2	163126848	163126927	MER117	DNA/hAT-Charlie
chr12	113345494	113345960	MER61F MER61F	LTR/ERV1
chr10	6083077	6083377	AluY	SINE/Alu
chr1	67866624	67866929	AluSz6	SINE/Alu
chr13	40656149	40656314	MIRb	SINE/MIR
chr11	60771458	60771559	L2c	LINE/L2
chrX	151927735	151928014	MLT2C2	LTR/ERV1
chr14	25114335	25115267	L1PA12	LINE/L1
chr1	70910326	70910526	AluJr	SINE/Alu
chr8	101147839	101148133	AluSz	SINE/Alu
chr12	6956805	6957010	L2	LINE/L2
chr16	81062998	81063171	AluJb	SINE/Alu
chrX	135721869	135721993	MIR3	SINE/MIR
chr10	6097029	6097192	MER5A1	DNA/hAT-Charlie
chr9	80934568	80934784	L2d	LINE/L2
chr11	118753552	118753753	MIR3	SINE/MIR
chr7	138756415	138756615	Charlie15a	DNA/hAT-Charlie
chr9	33306213	33306548	L2c	LINE/L2
chr2	231135460	231136281	MLT1D MLT1D-int	LTR/ERV1-MaLR
chr7	130639523	130639851	L1ME2	LINE/L1
chr2	163125118	163125393	AluSx1	SINE/Alu
chr21	40553068	40553361	AluJr	SINE/Alu
chr10	96362610	96362905	L2	LINE/L2
chr1	27998302	27998388	MIR3	SINE/MIR
chr13	43059476	43059680	MLT1H	LTR/ERV1-MaLR
chrX	30738428	30738679	L2d2	LINE/L2
chr1	67818392	67818817	L1M5	LINE/L1
chr20	48219632	48220022	MLT1B	LTR/ERV1-MaLR
chr14	100835021	100835311	AluSp	SINE/Alu
chr3	33033954	33034168	MIRb	SINE/MIR
chr1	25286372	25286741	L2c	LINE/L2
chr3	33031560	33031982	L2c	LINE/L2
chr12	27576253	27576561	AluY	SINE/Alu
chr11	64849156	64849427	AluJb	SINE/Alu
chr17	41276799	41277006	AluSg	SINE/Alu
chr21	43813154	43813373	AluSx	SINE/Alu
chr1	166878212	166878758	MLT1K	LTR/ERV1-MaLR
chr1	117348619	117349084	LTR16D1	LTR/ERV1

chr7	130642502	130642809	AluSz	SINE/Alu
chr2	204582337	204582522	MER8	DNA/TcMar-Tigger
chr6	33376668	33376962	AluY	SINE/Alu
chr1	117337212	117337505	AluSc	SINE/Alu
chr10	6096833	6096959	FLAM_C	SINE/Alu
chr10	74087037	74087321	AluSp	SINE/Alu
chr7	138753250	138753396	MER3	DNA/hAT-Charlie
chr7	105897340	105897610	AluSq	SINE/Alu
chr18	9105612	9105680	Tigger5b	DNA/TcMar-Tigger
chr3	121209619	121209907	AluSx1	SINE/Alu
chr2	231136679	231137050	L1PA13	LINE/L1
chr8	27663674	27663815	MER44C	DNA/TcMar-Tigger
chr4	123631942	123632211	UCON78	DNA
chr1	159044357	159045219	L1M5	LINE/L1
chr3	146259493	146259762	MSTD	LTR/ERV1-MaLR
chr2	102999253	102999997	L1M5	LINE/L1
chr7	130631463	130631794	L1ME4a	LINE/L1
chr3	18962127	18962622	MamGypLTR1d	LTR/Gypsy
chr21	43821838	43822630	L1ME3	LINE/L1
chr12	12257063	12257452	MSTB	LTR/ERV1-MaLR
chr4	89383706	89383884	MIR3	SINE/MIR
chr21	26954406	26955175	L1ME3Cz	LINE/L1
chr1	93451541	93451835	AluJr	SINE/Alu
chr17	16374309	16374723	MLT1C2	LTR/ERV1-MaLR
chr1	27997695	27997887	MIRb	SINE/MIR
chr16	81064682	81065123	LTR06	LTR/ERV1
chr7	97490624	97491359	L1M4	LINE/L1
chr8	42607461	42607756	AluJb	SINE/Alu
chr4	15782748	15782995	MLT1H1-int	LTR/ERV1-MaLR
chr3	189031732	189032149	L2b	LINE/L2
chr12	47767430	47770652	L1PA16	LINE/L1
chr15	91421724	91421806	AluJr	SINE/Alu
chr21	43825841	43825903	L2c	LINE/L2
chr21	43810556	43810863	AluSq	SINE/Alu
chr22	38937815	38939188	L1M1	LINE/L1
chr12	113349619	113349857	MIRc	SINE/MIR
chr7	105899877	105900167	AluSc	SINE/Alu
chr21	43811478	43811956	LTR40a	LTR/ERV1
chr7	130639215	130639522	AluSz	SINE/Alu
chr10	6092318	6092614	AluSz6	SINE/Alu
chr21	43822631	43822942	AluSx	SINE/Alu

chr4	89423249	89423388	L1ME3A	LINE/L1
chr18	9104239	9104530	L2b	LINE/L2
chr10	70195771	70196356	L1MB5	LINE/L1
chr2	7056433	7056600	AluJb	SINE/Alu
chr2	231848401	231848707	MLT1C2	LTR/ERV1-MaLR
chr1	117336726	117337211	LTR38B	LTR/ERV1
chr17	6671741	6672600	L1MEd	LINE/L1
chr1	160646027	160646319	MER45B	DNA/hAT-Tip100
chr21	43820647	43821376	L1M4	LINE/L1
chr10	27454883	27455135	AluSx1	SINE/Alu
chr1	36488553	36489365	MER57A-int MER57B2	LTR/ERV1
chr7	130642059	130642420	HAL1	LINE/L1
chr7	97491585	97492114	L1MC2	LINE/L1
chr7	105910942	105911376	MLT1H	LTR/ERV1-MaLR
chr5	138733237	138733539	AluSx1	SINE/Alu
chr15	91413930	91414188	MIRb	SINE/MIR
chr2	163131531	163131617	MamTip2b	DNA/hAT-Tip100
chr1	67865907	67866205	AluSx	SINE/Alu
chr12	113392401	113397286	L1PA5	LINE/L1
chr10	35497837	35498051	MIR	SINE/MIR
chr20	32270975	32271278	AluSz	SINE/Alu
chr7	130643054	130643362	AluSx	SINE/Alu
chr3	33032922	33033452	MLT1G3	LTR/ERV1-MaLR
chr12	113352711	113353636	L1PB1	LINE/L1
chr1	117346652	117346882	L1MEd	LINE/L1
chr12	113406869	113407095	Tigger4a	DNA/TcMar-Tigger
chr22	30660663	30660750	L2a	LINE/L2
chr17	54971603	54971909	AluSz6	SINE/Alu
chr10	27454611	27454843	AluJb	SINE/Alu
chr17	38682012	38682159	L1M5	LINE/L1
chr22	37471661	37471964	AluSp	SINE/Alu
chr2	231135939	231136507	MLT-int	LTR/ERV1-MaLR
chr6	495824	496803	L1MEf	LINE/L1
chr2	103050612	103051461	L3	LINE/CR1
chr12	48234358	48235113	CR1_Mam	LINE/CR1
chr4	89402219	89402503	AluJb	SINE/Alu
chr12	47748542	47748939	MLT2A1	LTR/ERV1
chr10	6065029	6065208	MIRc	SINE/MIR
chr20	32268848	32269143	AluJr	SINE/Alu
chr8	42606476	42606785	AluSp	SINE/Alu
chr12	47779863	47780512	Eutr2B	DNA

chr3	56725725	56727051	LTR12C	LTR/ERV1
chr11	110210640	110211069	MER57A1	LTR/ERV1
chr1	160598197	160598303	LTR85a	LTR/Gypsy?
chr1	160643493	160643900	LTR78B	LTR/ERV1
chr22	30660505	30660623	MIR3	SINE/MIR
chr1	160600410	160600597	L2c	LINE/L2
chr6	33376963	33377085	L1MC5a	LINE/L1
chr21	42818648	42818777	MLT1A0	LTR/ERV1-MaLR
chr12	113347891	113348195	AluSz	SINE/Alu
chr2	203161764	203161853	L3	LINE/CR1
chr15	91415881	91415962	MIR3	SINE/MIR
chr1	117348016	117348477	L1MEd	LINE/L1
chr10	6058412	6058467	L1MB5	LINE/L1
chr10	76814605	76814899	AluJr	SINE/Alu
chr7	130643366	130643655	AluSx1	SINE/Alu
chr3	18405665	18406131	Charlie4a	DNA/hAT-Charlie
chr12	92977638	92977997	MLT1H	LTR/ERV1-MaLR
chr17	54981875	54982490	L1ME3C	LINE/L1
chrX	135723009	135723130	L2c	LINE/L2
chr3	111305346	111307640	THE1B THE1B-int THE1B THE1B	LTR/ERV1-MaLR
chr4	7973225	7973308	MIRc	SINE/MIR
chr2	28587832	28588293	MLT1C2	LTR/ERV1-MaLR
chr10	6057804	6058006	L1MB5	LINE/L1
chr7	138757760	138758074	AluSq2	SINE/Alu
chr4	104047045	104050614	L1MC1	LINE/L1
chr2	231139933	231142265	Tigger1	DNA/TcMar-Tigger
chr15	91423614	91423717	MER20	DNA/hAT-Charlie
chr22	37467495	37467578	L2d2	LINE/L2
chr17	47282393	47282672	AluJr	SINE/Alu
chr20	32269431	32269510	L2c	LINE/L2
chr4	123626480	123626609	AluJo	SINE/Alu
chr1	160598343	160598458	L2d2	LINE/L2
chr3	111296804	111296956	MER5B	DNA/hAT-Charlie
chr1	67866930	67867409	MER21A	LTR/ERV1
chr1	120273326	120273875	L3	LINE/CR1
chr22	37470113	37470250	MIRb	SINE/MIR
chr14	62191645	62192068	L2d2	LINE/L2
chr14	50526748	50526937	L2a	LINE/L2
chrX	135724081	135724322	L2c	LINE/L2
chr19	50392138	50392444	AluSx	SINE/Alu
chr8	42606859	42607168	AluSz	SINE/Alu

chr1	79117778	79118064	AluSx3	SINE/Alu
chr7	26136992	26137297	AluSg	SINE/Alu
chr8	27671546	27672388	L1M5	LINE/L1
chr1	117336193	117336725	L1MC1	LINE/L1
chr1	159033564	159033987	Tigger2a	DNA/TcMar-Tigger
chr3	33002636	33003081	L1M7	LINE/L1
chr4	113509351	113509496	MIRc	SINE/MIR
chr12	27576606	27576767	MIR3	SINE/MIR
chr10	30728457	30728755	AluSx1	SINE/Alu
chr9	80941564	80941871	MLT1H	LTR/ERV1-MaLR
chr1	117355306	117356453	HAL1	LINE/L1
chr21	43822943	43823216	L1ME3	LINE/L1
chr17	38681034	38681971	L1MEh	LINE/L1
chr1	40849563	40849871	AluSz6	SINE/Alu
chr10	76805140	76805585	L2a	LINE/L2
chr10	6055487	6055795	MER63B	DNA/hAT-Blackjack
chr8	27663564	27663675	Tigger7	DNA/TcMar-Tigger
chr8	101324872	101325179	AluSz6	SINE/Alu
chr2	191879280	191880314	L2b	LINE/L2
chr17	40453569	40453673	AluJo	SINE/Alu
chr7	105907464	105907536	L2a	LINE/L2
chr17	47283221	47283390	L2c	LINE/L2
chr2	103043131	103048776	L1MA8	LINE/L1
chr1	67808789	67809064	AluJb	SINE/Alu
chr17	16374123	16374235	MLT1C2	LTR/ERV1-MaLR
chr1	169490044	169490756	L1MDa	LINE/L1
chr3	182845963	182846403	L1ME4b	LINE/L1
chr2	191876289	191876615	THE1D	LTR/ERV1-MaLR
chr1	27996470	27996800	MER21B	LTR/ERV1
chr22	37470373	37470517	MIR1_Amn	SINE/MIR
chr6	33377085	33377180	L1MC5a	LINE/L1
chr6	28863598	28863898	AluY	SINE/Alu
chr10	6055796	6056081	AluJr	SINE/Alu
chr2	7568886	7569067	LTR78	LTR/ERV1
chr2	231137424	231138839	L1PA13	LINE/L1
chr2	7569849	7570369	LTR78	LTR/ERV1
chr6	25095279	25095385	L2d2	LINE/L2
chr7	130630964	130631266	AluJr	SINE/Alu
chr17	6672751	6673342	L1MEd	LINE/L1
chr2	87769274	87769688	MLT1C	LTR/ERV1-MaLR
chr17	16367003	16367100	MIRc	SINE/MIR

chr1	159029143	159029265	MIR3	SINE/MIR
chr21	43810864	43811173	MLT1C2	LTR/ERV1-MaLR
chr15	91415765	91415870	Charlie15a	DNA/hAT-Charlie
chr20	32265483	32265594	MIRb	SINE/MIR
chr1	79089112	79089170	L1M3	LINE/L1
chr12	47780915	47781225	AluSp	SINE/Alu
chr12	12833629	12833922	AluSx1	SINE/Alu
chr12	113353633	113353850	L1MEd	LINE/L1
chr12	12833441	12833628	AluJb	SINE/Alu
chr2	191618902	191619274	L1MDa	LINE/L1
chr17	16375410	16375541	L3	LINE/CR1
chr1	89592278	89592580	AluJo	SINE/Alu
chr6	25094261	25094317	L2d2	LINE/L2
chr7	138756249	138756313	LTR106_Mam	LTR
chr4	89422953	89423248	AluSc8	SINE/Alu
chr18	9105338	9105446	MIRc	SINE/MIR
chr1	67805279	67805508	MIRb	SINE/MIR
chr2	163125431	163125583	Plat_L3	LINE/CR1
chr14	31031376	31032353	LTR13	LTR/ERVK
chr2	203161441	203161755	AluY	SINE/Alu
chr2	7056602	7056756	MIR	SINE/MIR
chr17	47282823	47283191	L2c	LINE/L2
chr10	91156012	91156474	MSTB2	LTR/ERV1-MaLR
chr7	138756819	138756898	MADE1	DNA/TcMar-Mariner
chr2	17935917	17936100	L2c	LINE/L2
chr6	487409	487704	AluSc	SINE/Alu
chr16	87799748	87800052	AluJr	SINE/Alu
chr8	120848564	120850075	L2	LINE/L2
chr21	43812145	43812246	MIR3	SINE/MIR
chr17	54988345	54988648	AluJr4	SINE/Alu
chr15	91422443	91422565	MIR3	SINE/MIR
chr1	93451836	93452141	L1ME1	LINE/L1
chr4	89402996	89403178	MER115	DNA/hAT-Tip100
chr17	47283413	47283588	L2c	LINE/L2
chr21	26939687	26939925	L2c	LINE/L2
chr6	484779	484999	MIR	SINE/MIR
chr4	15790348	15790783	LTR37B	LTR/ERV1
chr6	135304778	135305264	L2a	LINE/L2
chr1	44448126	44449414	L2c	LINE/L2
chr21	42818074	42818312	MLT1A0	LTR/ERV1-MaLR
chr10	6058535	6058824	AluSq	SINE/Alu

chr4	103984726	103985102	L1MA8	LINE/L1
chr2	231315837	231316895	L1MA8	LINE/L1
chr21	47742223	47742316	Charlie15b	DNA/hAT-Charlie
chr11	60770923	60771216	AluSz6	SINE/Alu
chrX	53724103	53724544	LTR79	LTR/ERV1
chr1	160647695	160647837	MLT1J2	LTR/ERV1-MaLR
chr1	79114304	79114548	L2a	LINE/L2
chr4	15791155	15791594	MSTC	LTR/ERV1-MaLR
chr11	9779989	9780181	MIR	SINE/MIR
chr20	32271298	32271607	AluSz6	SINE/Alu
chr10	76813745	76813975	L2d2	LINE/L2
chr1	117338423	117338564	LTR38B	LTR/ERV1
chr1	79111980	79112038	MamGyp-int	LTR/Gypsy
chr12	68599033	68601363	Tigger2	DNA/TcMar-Tigger
chr15	55511813	55512434	Charlie25	DNA/hAT-Charlie
chr17	6667988	6668450	L2b	LINE/L2
chr2	7053744	7053886	MamGypLTR1a	LTR/Gypsy
chr1	117092446	117094348	Tigger1	DNA/TcMar-Tigger
chr1	27994300	27994604	AluSx	SINE/Alu
chr3	18476074	18476224	MIRc	SINE/MIR
chr11	57314874	57314976	MIRc	SINE/MIR
chr15	77527245	77529377	THE1C THE1C-int THE1C	LTR/ERV1-MaLR
chr1	117347303	117347670	LTR79	LTR/ERV1
chr1	159027862	159028156	AluSz	SINE/Alu
chr7	138756943	138757232	AluSx	SINE/Alu
chr10	27457748	27458209	Charlie20a	DNA/hAT-Charlie
chr10	6054936	6055090	AluSg	SINE/Alu
chr12	9909870	9910509	L1ME2	LINE/L1
chr2	202000359	202000649	AluJo	SINE/Alu
chr2	7058626	7058921	AluYd8	SINE/Alu
chrX	30743764	30744069	AluSg4	SINE/Alu
chr18	9105722	9105801	Tigger5b	DNA/TcMar-Tigger
chr13	30116310	30116600	AluSq2	SINE/Alu
chr3	18403934	18404095	Tigger15a	DNA/TcMar-Tigger
chr21	18979029	18979271	L1ME4a	LINE/L1
chr15	91354884	91355187	AluSz	SINE/Alu
chr16	12625700	12626474	MER99	DNA/hAT?
chr4	103984962	103985943	L1MA6	LINE/L1
chr1	79114996	79115230	L2	LINE/L2
chr17	16375939	16376444	MamRep1151	LTR?
chr4	7974848	7974955	L2c	LINE/L2

chr21	42824927	42825293	THE1B	LTR/ERV1-MaLR
chr10	27458511	27458579	Charlie20a	DNA/hAT-Charlie
chr2	26602576	26603883	L1MC5	LINE/L1
chr10	27455430	27455687	AluJr	SINE/Alu
chr4	89402506	89402755	L1MEd	LINE/L1
chr21	42815860	42816006	MER5A1	DNA/hAT-Charlie
chr1	67866416	67866623	MER21A MER21A	LTR/ERV1
chr7	104602276	104602775	LTR67B LTR67B	LTR/ERV1
chr1	159031495	159032005	L1MD	LINE/L1
chr1	160599465	160599603	MLT1J	LTR/ERV1-MaLR
chr2	204582072	204582330	LTR33	LTR/ERV1
chr2	191876867	191877154	AluSx	SINE/Alu
chr12	113406352	113406619	AluSz	SINE/Alu
chr20	32819696	32820949	LTR40c HERVL40-int HERVL40-int	LTR/ERV1
chr2	163180513	163183016	LTR1A2 HUERS-P2-int	LTR/ERV1
chr12	113421329	113423631	L1MA4	LINE/L1
chr10	6055191	6055390	MER3	DNA/hAT-Charlie
chr15	30940629	30940834	MIRb	SINE/MIR
chr22	37473476	37473957	Charlie1b	DNA/hAT-Charlie
chr5	138731062	138731141	MIR3	SINE/MIR
chr1	160602835	160602960	MIRc	SINE/MIR
chr8	8779767	8780070	AluSx	SINE/Alu
chr10	6057382	6057540	MER5A	DNA/hAT-Charlie
chr12	113446433	113446732	AluSz	SINE/Alu
chr10	96363882	96364176	AluSz	SINE/Alu
chr5	35615360	35617279	L1MA4A	LINE/L1
chr3	105912464	105913029	MLT1F2	LTR/ERV1-MaLR
chr12	113354941	113355190	MIRb	SINE/MIR
chr10	6057740	6057796	MER5B	DNA/hAT-Charlie
chr8	129355888	129361920	L1PA3	LINE/L1
chr10	6057044	6057342	AluSz	SINE/Alu
chr10	27457464	27457747	AluSq2	SINE/Alu
chr7	105139465	105139810	L2	LINE/L2
chr11	57314230	57314320	L2a	LINE/L2
chr4	17837115	17838282	L1MB5	LINE/L1
chr3	197391053	197391459	L1MA4	LINE/L1
chrX	100419721	100419860	L1M2	LINE/L1
chr7	97490082	97490335	L1M4	LINE/L1
chr21	43817599	43817980	L2b	LINE/L2
chr10	27458210	27458510	AluSx	SINE/Alu
chr4	89417386	89417990	L1M5	LINE/L1

chr12	113350599	113351633	L1MEd	LINE/L1
chr12	121456390	121456698	AluSg4	SINE/Alu
chr1	79116768	79117277	MER1A	DNA/hAT-Charlie
chr7	148520745	148520906	FRAM	SINE/Alu
chr21	26941999	26942243	MamTip2b	DNA/hAT-Tip100
chr18	9114504	9114683	MIRc	SINE/MIR
chr1	93452142	93452520	MLT1A	LTR/ERV1-MaLR
chr1	79112099	79114290	THE1C THE1C-int THE1C	LTR/ERV1-MaLR
chr1	160645410	160645495	MER5A1	DNA/hAT-Charlie
chr15	65588879	65589217	AluY	SINE/Alu
chr1	173768458	173768551	L2c	LINE/L2
chr2	55891147	55891465	L1ME1	LINE/L1
chr1	159040876	159041082	X6A_LINE	LINE/CR1
chr12	113417923	113421020	L1MA4	LINE/L1
chr2	55890318	55890831	L1ME1	LINE/L1
chr1	117337506	117337692	LTR38B	LTR/ERV1
chr2	103055607	103055925	L2b	LINE/L2

The invention will be further illustrated by the following examples. However, these examples should not be interpreted in any way as limiting the scope of the present invention.

EXAMPLE

Through an ongoing study of the RNAseq data using state of the art transposcriptome analysis pipeline, the inventors have identified thousands of TE loci specific and likely predictive of cellular states.

When analyzing the transposcriptome of intermediate reprogramming time-points of CD34⁺ hematopoietic on the path to induced pluripotency (iPSCs), the inventors rapidly observed clusters of TEs scattered throughout the genome with acute expression patterns peaking at specific days of reprogramming. For example, the LTRs associated with HERVH-int (a human restricted ERV) were transcribed at precise time-points likely representing intermediate cellular or developmental stages, as iPSC reprogramming represents a paradigm of reversed developmental course. Of 50 full-length HERVH integrants expressed at day 4 of reprogramming, 39 (78%)

were associated with LTR7B while LTR7C vastly predominates at other time-points (e.g. 31/32, 97% at d14).

The inventors hypothesized that many more integrants specific of intermediate cell stages could be observed and eventually used as markers of cell state and quality. To this end, they generated and analyzed RNAseq of several somatic cell types including primary human hepatocytes, CD34+ hematopoietic stem cells, neural committed cells, along with iPSC, differentiation intermediates and human ES cells as comparisons. As predicted, the inventors found thousands of specific TE loci uniquely expressed in each somatic cell type thus providing an accurate and high-resolution description cell states. For example, at least 2'500 TE loci where only expressed in CD34+ cells as compared to hepatocytes, neural committed cells, ES, iPSC, and differentiation intermediates on the path to hepatocyte (endoderm) or neural commitment (ectoderm). Likewise, thousands of TEs uniquely tagged primary human hepatocytes and neural committed cells.

The inventors next compared human naïve ES cells and their primed counterparts. Again, they found thousands of TEs specifically tagging each of these pluripotent states.

When looking at overrepresented TEs, they found that SVA elements, particularly SVA-D, where highly enriched in the catalogue of naïve ES specific TEs. Indeed, of 892 over-expressed SVA-D in one state compared to the other (2 fold cut-off, p val <0.05), 891 (99.9%) were more expressed in naïve ES cells. Moreover of the top 10 over-expressed TEs in naïve versus primed ES cells, 6 were SVA-D integrants and 1 was a SVA-F, with expression fold changes higher than 1000 fold. Interestingly, all SVA subfamilies (SVA-F 419/422, SVA-E 155/165, SVA-C 167/168, SVA-B 169/177) bar SVA-A were over-represented in naïve ES cells. Most SVA-As were unchanged (143/226) when comparing the two states. As previously reported, HERVH and LTR7 were the two families most overrepresented in the catalogue of primed ES cells. Interestingly, the potential controllers such as KRAB-ZFPs, are also highly specific of cellular sub-states. This indicates that they indeed rewire species-specific transcriptional networks through the specific binding of species-restricted TEs.

The postranscriptome of hepatocytes and CD34+ hematopoietic stem cells does not show such clear cut enrichment for specific TE families. However, the

inventors provide a list of hundreds of TEs providing specific signatures for both cell types. CD34+ hematopoietic stem cells seem to display a modest enrichment for expression of LTR retrotransposons, while hepatocytes show a mild bias toward LINEs.

5

RNA-seq method for the quantification of integrant specific TE expression.

In order to identify TEs specific and predictive of cellular stages and quality, the inventors have generated the following RNAseq datasets (100bp, single end, non stranded unless otherwise stated):

- 10 - Reprogramming CD34+ to iPSC: 9 intermediate time-points of RNAseq samples (same donor), over 21 days, 6 resulting iPS clones;
- Somatic cells, differentiation, and reprogramming: 3 CD34+ (same donor) samples, 1 iPSC (unrelated to above) d1, d3, d4 of its neural differentiation, 1 resulting neural committed cell line, 3 primary hepatocytes,
- 15 3 reprogramming time-points of hepatocytes (hep) on the path to pluripotency, 2 resulting iPS clones, 14 differentiation time points of hep iPSC on the path to hepatocytic differentiation (3 different starting clones, 2 Hep-like cells (final differentiation stage);
- Human ES cells: 11 RNA Seqs: 3 RNA-seqs from H1 Trono lab, 6
- 20 UCLA (1-6), H1 from UCLA, H9 UCLA; and
- Human primed and Naïve ES cells: 12 RNA-seqs, 100bp, paired-end, stranded. 8 naïve (3 of which embryo-derived), 4 primed.

Conclusion

25 The inventors have showed that the specificity of each cell type can be accurately described and predicted using the transposcriptome with tens of thousands expressed in each cell type providing a unique signature to each cell state, far more accurate than the expression of tissue specific genes.

 The results confirm that the method presented here can be used for a broad
30 range of cell stage and quality assessment such as quality control of various types of cell, such as iPSC. Good iPS clones should display a TE signature closely resembling that of human ES cells and should be convertible to the naïve state of pluripotency, with the matching TE expression pattern.

CLAIMS

1. A method for assessing the quality and/or utility of a cell, said method comprising the following steps:

- 5 a) analyzing the expression of the transposable elements (TEs) of said cell in order to set up an expression profile of the TEs of said cell;
 b) comparing the expression profile obtained in step a) to a reference,

wherein said cell is selected from the group consisting of :

- induced pluripotent stem cells (iPSC);
- 10 - pluripotent stem cells and precursor cells selected from the group consisting of embryonic stem (ES) cells, somatic stem cells, hematopoietic stem cells, leukemic stem cells, skin stem cells, intestinal stem cells, gonadal stem cells, brain stem cells, muscle stem cells, mammary stem cells, neural stem cells;
- 15 - differentiated cells; and
- cells of the embryonic developmental stages from zygote to fetus, including zygote, cells of morula, cells of blastula, cells of gastrula, cells of blastocytes.

20 **2.** The method according to claim **1**, wherein the expression profile of step a) consists of a collection of all the TEs of said cell.

3. The method according to claims **1 or 2**, wherein step a) is performed by RNA sequencing.

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4. The method according to claims **1 to 3**, wherein said cell is an induced pluripotent stem cell (iPSC).

5. The method according to claim **4**, wherein :

- 30 - step b) consists in a step b1) of comparing the expression profile obtained in step a) to the expression profile of the TEs of a naïve embryonic stem cell or a primed embryonic stem cell; and

- said iPSC is considered as showing an acceptable quality and/or to show genomic integrity if the expression profile obtained in step a) comprises at least 80%, preferably 85%, preferably 90%, preferably 95% or more preferably 100% of the TEs of the expression profile of said naïve embryonic stem cell or said primed embryonic stem cell.

6. The method according to claim **4**, wherein :

- said step b) consists in a step b2) of comparing the expression of TEs of step a) to the expression of all the TEs disclosed in table 1 or table 2; and
- said iPSC is considered as showing an acceptable quality and/or to show genomic integrity if at least 80%, preferably 85%, preferably 90%, preferably 95% or more preferably 100% of the TEs disclosed in table 1 or 2 are present in the expression profile as obtained in step a).

7. The method according to claims **1 to 3**, wherein said cell is a hematopoietic stem cell.

8. The method according to claim **7**, wherein:

- said step b) consists in a step b3) of comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 3; and
- said hematopoietic stem cell is considered as showing an acceptable quality if at least 80%, preferably 85%, preferably 90%, preferably 95% or more preferably 100% of the TEs disclosed in table 3 are present in the expression profile obtained in step a).

9. The method according to claims **1 to 3**, wherein said differentiated cell is a hepatocyte.

10. The method according to claim **9**, wherein:

- said step b) consists in a step b4) of comparing the expression profile obtained in step a) to the expression of all the TEs disclosed in table 4; and

- said hepatocyte is considered as showing an acceptable quality if at least 80%, 85%, 90%, 95% or more preferably 100% of the TEs disclosed in table 4 are present in the expression profile as obtained in step a).

5 **11.** Signatures of TE expression as independently defined in table 1, table 2, table 3, table 4, table 5 and table 6.

12. Use of the signatures as defined in claim **11** for assessing the quality of a cell.

10 **13.** Use of the signatures as defined in table 1 or table 2 for discriminating iPSC depending on their differentiation ability.

14. Use of the signature as defined in table 3 for selecting hematopoietic stem cells that can be used for hematopoietic stem cells transplantation.

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15. Use of the signature as defined in table 4 for selecting hepatocytes that do not show a predisposition to oncogenic changes or uncontrolled and anarchic growth.

20 **16.** Use of the signature as defined in table 5 for selecting resting CD4⁺ T lymphocytes.

17. Use of the signature as defined in table 6 for selecting activated CD4⁺ T lymphocytes.

25 **18.** A kit comprising means for detecting the expression of the TEs as independently defined in tables 1, 2, 3, 4, 5 and 6.

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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/061986A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FEDERICO A SANTONI ET AL: "HERV-H RNA is abundant in human embryonic stem cells and a precise marker for pluripotency", RETROVIROLOGY, vol. 9:111, no. 1, 20 December 2012 (2012-12-20), pages 1-15, XP055290812, GB	1,3-5
Y	ISSN: 1742-4690, DOI: 10.1186/gb-2009-10-3-r25 page 6, column 2; figure 8 page 12, column 1, paragraph 3 - column 2, paragraph 2 page 2, column 2 - page 3, column 1 ----- -/--	2,6-17



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

26 July 2016

Date of mailing of the international search report

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Schmitt, Anja

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/061986

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	page 1256, column 2 page 1252 - page 1254	1-17
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Y	the whole document page 568, column 1, paragraph 3	1-17
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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/061986

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	XINYI LU ET AL: "The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity", NATURE STRUCTURAL AND MOLECULAR BIOLOGY, vol. 21, no. 4, 30 March 2014 (2014-03-30) , pages 423-425, XP055290889, US ISSN: 1545-9993, DOI: 10.1038/nsmb.2799 the whole document -----	1-17
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2016/061986

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