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Adenovirus small E1A directs activation of *Alu* transcription at YAP/TEAD- and AP-1-bound enhancers through interactions with the EP400 chromatin remodeler

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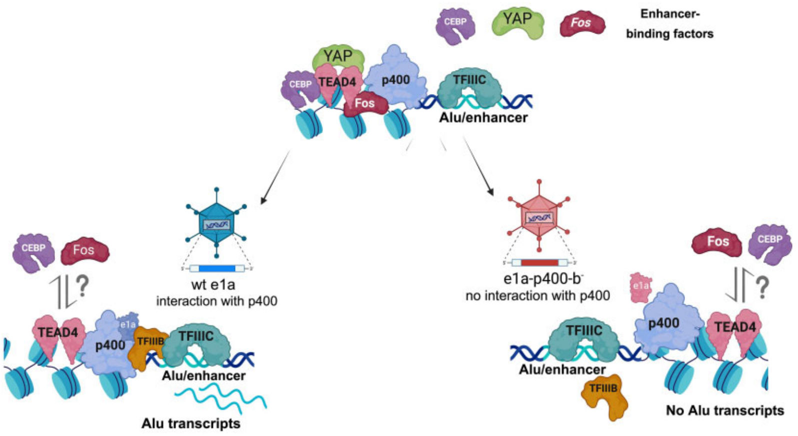
Abstract

Alu retrotransposons, which form the largest family of mobile DNA elements in the human genome, have recently come to attention as a potential source of regulatory novelties, most notably by participating in enhancer function. Even though *Alu* transcription by RNA polymerase III is subjected to tight epigenetic silencing, their expression has long been known to increase in response to various types of stress, including viral infection. Here we show that, in primary human fibroblasts, adenovirus small e1a triggered derepression of hundreds of individual *Alu*s by promoting TFIIIB recruitment by *Alu*-bound TFIIIC. Epigenome profiling revealed an e1a-induced decrease of H3K27 acetylation and increase of H3K4 monomethylation at derepressed *Alu*s, making them resemble poised enhancers. The enhancer nature of e1a-targeted *Alu*s was confirmed by the enrichment, in their upstream regions, of the EP300/CBP acetyltransferase, EP400 chromatin remodeler and YAP1 and FOS transcription factors. The physical interaction of e1a with EP400 was critical for *Alu* derepression, which was abrogated upon EP400 ablation. Our data suggest that e1a targets a subset of enhancer *Alu*s whose transcriptional activation, which requires EP400 and is mediated by the e1a-EP400 interaction, may participate in the manipulation of enhancer activity by adenoviruses.

Graphical abstract



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Introduction

Alu elements are primate-specific members of the short-interspersed element (SINE) family of retrotransposons and constitute a large fraction (∼11%) of the human genome. Like other types of retrotransposons, *Alu*s are subjected to tight epigenetic silencing, required to limit their inherently mutagenic mobilization (1,2). *Alu* transcription is thought to mostly depend on the RNA polymerase (Pol) III machinery, through the recognition of A- and B-box promoter DNA sequences within the transcribed region by the multi-subunit transcription factor TFIIIC. The TFIIIC-promoter DNA complex is bound, ∼30 bp upstream of the *Alu* transcription start site (TSS), by the Pol III initiation factor TFIIIB, which includes the TATA-binding protein (TBP) subunit required for initiation by all three of the eukaryotic nuclear RNA polymerases (3). Even though many *Alu* transcription units occur throughout the genome, the level of *Alu* transcription is normally kept very low by chromatin structure-based repression mechanisms (4). Recently, it has become possible to profile expression of specific *Alu*s by determining the precise sequences of their transcripts, which allows mapping them to individual *Alu* genes, most of which have unique sequences due to sequence variation in a small percentage of positions (5–7). Similar advances have been reported for the expression profiling of other SINEs in mouse (8,9). Through these studies, some common features of *Alu* transcriptomes have emerged. First, in every human cell type analyzed the expressed *Alu* loci represent a very small fraction (∼0.3% at most) of the total *Alu* copies in the genome. Second, the majority of *Alus* with detectable transcripts are expressed in a cell type-specific manner, while only a limited number of *Alu* elements are expressed ubiquitously. Consequently, the total number of *Alu* elements expressed in at least one cell type/tissue amounts to ∼1.5% of the ∼1.2 million *Alus* annotated in the human genome. Third, histone post-translational modifications associated with expressed *Alus* tend to display epigenetic marks that are typically enriched at enhancers and promoters for RNA polymerase II. These include the histone H2A variant Z (H2A.Z), indicative of repeated disassembly and re-assembly of the TSS-region nucleosomes, and histone H3 lysine 4 monomethylation (H3K4me1). This observation agrees with the hypothesis that a subset of *Alu* elements have evolved the properties of cell type-specific enhancers (7,10). Lastly, expressed *Alu* elements tend to be bound not only by the Pol III transcription machinery, but also by transcription factors typically involved in Pol II regulation, which potentially modulate *Alu* expression in a cell type-specific manner (5,7). This cell type-specific expression, as well as possible functions related to controlling Pol II enhancers, have also been reported for a small subset of mammalian-wide interspersed repeats (MIRs), the second most numerous family of SINEs in the human genome (11–13), and are increasingly recognized as a general property of transposable elements (14). A recent study further indicated that *Alu* elements contribute to human gene regulation by rewiring of the 3D chromatin architecture through an interaction network involving TFIIIC, ADNP, CTCF looping and TFIIIC-dependent histone H3 lysine 18 acetylation (H3K18ac) (15). Such properties may have contributed to the evolutionary impact of *Alu*s and other SINEs (16).

Further pointing to the existence of highly organized chromatin at *Alu* elements, *Alu*s and other SINEs typically are associated with translationally stable nucleosomes. In the case of full-length *Alu* elements, two nucleosomes are approximately centered on the left and right arms, where they might in principle mask access to the transcriptional machinery (17,18). Such a nucleosome arrangement is likely to be instrumental to *Alu* repression, together with DNA CpG methylation and H3K9 methylation (19–21), and represents a scaffold which every activation mechanism must confront.

Alu expression is known to increase in response to different types of cell stress, such as viral infection (22,23), heat shock and cycloheximide treatment (24), as well as under altered cellular conditions that occur with some pathologies including cancer (25). Induction of SINE expression by viral infection also occurs in mouse (8). The mechanisms leading to increased *Alu* RNA levels are still largely unexplored. According to previous studies, they may be both transcriptional, involving increased chromatin accessibility (26), and post-transcriptional, due to reduced DICER-dependent turnover of *Alu* RNA (27). *Alu* upregulation upon viral infection is of particular interest, because it occurs in response to different viruses, including the dsDNA adenovirus and herpes simplex virus (23,28,29), and it reflects a general property of SINEs in different mammals (8,30–33). In the case of human adenovirus type 5 (HAdV-C5), infection of cultured human cells was found to cause *Alu* activation in different cell lines (22), possibly as the result of overcoming chromatin-mediated repression (4). This observation came in the context of a more general phenomenon of Pol III transcription activation by the Ad5 immediate early protein E1A (34,35). Studies of the mechanisms of Pol III activation by E1A identified TFIIIC as a possible regulatory target of this viral oncoprotein (36,37), and identified an E1A-dependent increase in the number of active Pol III transcription complexes assembled *in vitro* with nuclear extracts from infected versus uninfected cells (38). To what extent these phenomena impact *in vivo* transcription of Pol III target genes coding for either canonical untranslated RNAs (e.g. tRNAs, 5S rRNA, U6 snRNA) or RNAs expressed from retrotransposons (*Alu* and other SINEs) has not been extensively investigated.

More recently, genome-wide studies of the effects of an E1A protein variant lacking the conserved region CR3 (referred to as small E1A, or ‘e1a’) revealed its surprising ability to alter global patterns of histone modifications as part of an epigenetic reprogramming process leading to cellular transformation (39,40). A pivotal role in this process is played by interactions of small e1a with key chromatin regulatory proteins such as the lysine acetylases EP300 and its paralog CREB Binding Protein (CREBBP, or CBP) and the tumor suppressor RB and related RB family members (41). Another chromatin regulator whose interaction with e1a is required for cell transformation is EP400, a SWI2/SNF2 DNA helicase-related chromatin remodeler (42). Other proteins found to be part of the same EP400 complex co-purified with E1A are the large multidomain protein TRRAP/PAF400, the TAP54 DNA helicase (RVB2), the oncogenic transcription factor MYC, actin-like proteins, the human homolog of the Polycomb protein (EPC1) (42), and the ∼20 subunit TIP60 lysine acetylase complexes (43). Importantly, cellular proteins bound by the N-terminus of e1a include EP400 and TRRAP associated with a variety of related cellular multiprotein complexes with histone acetyl-transferase activity supplied by the TIP60 subunits. The TIP60/EP400 complexes are often recruited by binding of their chromodomains to H3K4me1. This can increase chromatin accessibility at enhancers by promoting incorporation of the H2A.Z histone variant (44).

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To explore the breadth of the epigenetic mechanisms through which *Alu*s are likely to reconcile their predominant silencing and their frequent exaptation as regulatory elements, we investigated the mechanisms of their derepression in response to adenovirus e1a expression. We surmised that e1a, by virtue of its reported abilities to reprogram the epigenome of human IMR90 primary fibroblasts and to affect Pol III-dependent transcription, would prove to be sufficient for *Alu* upregulation, thus unveiling key regulatory interactions. *Alu* expression profiling at single locus resolution, ChIP-seq characterization of histone modification and regulatory protein enrichment at expressed and silenced *Alu*s, and e1a mutants specifically affected in interactions with key chromatin regulators were used together to study the complex epigenetic context operating at *Alu* transcription units.

Materials and methods

Cell culture and viruses

IMR90 primary human fetal lung fibroblasts were purchased from the American Type Culture Collection (ATCC). Cells were grown in Dulbecco's modified medium supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin and 100 μg/ml streptomycin at 37°C in 5% CO_2.

Ad5 *dl*1500 containing a 9-bp deletion removing the 13S E1A mRNA 5′-splice site was described (45). The ΔE1A deletion mutant *dl*312 was isolated as previously described (46). Small e1a binding mutants (e1a_RB-b^-, e1a_p300-b^-, e1a_p400-b^-) were constructed as in (41) and afterwards incorporated into the *dl*1500 background. *dl*1500 and e1a binding mutant constructs were cloned into shuttle plasmid pAdlox. LoxP recombination between the HAdV-C5 backbone Ψ5 and the shuttle plasmid pAdlox, as well as propagation of viruses, were performed as described (47).

RNA extraction and total RNA-seq library preparation

IMR90 cells were grown to confluence in 60-mm Petri dishes and incubated two more days without changing the medium to arrest cells in G1/0. On the day of infection, the medium was collected (conditioned medium) and confluent cells were incubated with mock or with the indicated Ad5-based vectors for 1 h in PBS. At the end of the infection, cells were washed and transferred back to conditioned medium. The infections were performed at multiplicity of infection (MOI) 40 for *dl*1500 and *dl*312, 160 MOI for e1a_RB-b^-, 60 MOI for e1a_p300-b^- and 6 MOI for e1a_p400-b^-, in order to achieve comparable amounts of wt and mutant e1a protein expression as assayed by Western blotting (48). 24 hours post-infection, cells were lysed with Trizol and total RNA was extracted using Direct-zol RNA MiniPrep Plus (Zymo research). After elution, RNA was subjected to DNaseI treatment (Invitrogen), followed by inactivation for 10 minutes at 65°C in the presence of 2 mM EDTA.

For the experiment in Figure 1, total RNA (1 μg) from *dl*1500, *dl*312 and mock infections (performed in duplicate) was processed using a Ribo-Zero rRNA Removal Kit (Epicentre) to remove rRNA. Total RNA-seq libraries were prepared using the Illumina TruSeq stranded RNA library Preparation kit. Libraries were sequenced using a HiSeq4000 Illumina Sequencer to obtain 100-base-long paired-end reads, using a sequencing depth of about 60 million reads per sample.

For the experiments in Figure 5, total RNA (1 μg) from wt e1a (*dl*1500), e1a_RB-b^-, e1a_p300-b^-, e1a_p400-b^- and mock infections (performed in duplicate) was processed using the RiboCop rRNA Depletion Kit (Lexogen), and total RNA-seq libraries were prepared as described above. Libraries were sequenced using a NovaSeq Illumina sequencer to obtain 150 base-long stranded paired-end reads, using a sequencing depth of about 100 million reads per sample.

RNA-seq reads were aligned to the GRCh38 human reference genome using STAR (49). Only uniquely mapped reads were considered for downstream analyses and subjected to counting with the featureCounts tool of the SubRead Python package (50). The pipeline for *Alu* RNA profiling was essentially as previously described (6), with some improvements to reduce the rate of false positives. Specifically, we added parameters allowing for setting the cut-off value for the ratio of the expression coverage between the *Alu* body and its upstream and downstream regions. We also added a parameter controlling the fraction of the *Alu* body sequence that should be covered by reads to enable the identification of shorter, processed *Alu* transcripts. In the present study, *Alu*s identified by the pipeline were subsequently filtered for an expression coverage of at least 1000 nt, corresponding to 5 paired-end reads of length 100 nt. The union of these *Alu*s from all the samples in the experiment of Figure 1 constitutes the single, comprehensive list of expression-positive *Alu*s (ep*Alu*s). Differentially expressed *Alu* sequences were identified using the DESeq2 package (51). *Alu* sequences with a $\log_2$ fold-change ≥ 0.5 or ≤ -0.5 and an adjusted *P*-value <0.05 were deemed differentially expressed.

Alu proximity to protein-coding genes

GENCODE annotation v24 (human genome assembly GRCh38/hg38) was used to analyse *Alu* distance to protein-coding genes. RepeatMasker tracks were downloaded from the UCSC Genome Browser for human genome assembly hg38. *Alu* sequences that are positioned outside of protein-coding genes (intergenic *Alu*) and *Alu*s that map to introns or exons of annotated genes in an antisense orientation (antisense *Alu*) were selected to obtain the intergenic/antisense *Alu* subset (802 571 *Alu* elements). The expression of intergenic/antisense *Alu*s was considered only for the elements belonging to the single, comprehensive list of ep*Alu*s, whereas the remaining intergenic/antisense annotated *Alu* sequences were used as a control for unexpressed *Alu*s. The presence of an *Alu* within protein-coding genes was analysed using the intersect tool of the BEDtools program package v2.29.1 (52) and custom R scripts. Enrichment analyses were performed using a two-tailed Fisher's exact test.

The transcription start site (TSS) position of protein-coding genes was extracted as the first or last nucleotide (forward or reverse strand, respectively) of the 'gene' feature in the *gtf* annotation file. The distance of *Alu* elements to the TSS was analysed using the closest tool from BEDtools (52) and custom R scripts. Gene expression was calculated as the average expression (TPM) across all samples. The difference in distribution of gene expression was determined to be statistically significant using a two-sided Wilcoxon rank-sum test. A two-tailed Fisher's exact test was used to analyse the difference between the fraction of the set of all of expression-positive *Alus* and the fraction of the set of all unexpressed *Alu*s within each genomic range.

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ChIP-seq analyses

ChIPs of TFIIIC (GTF3C2) and BDP1 were performed using procedures and antibodies described in (15) and references therein (53,54). All data was aligned to the hg38 human genome reference (GRCh38) and processed as in (15). The average ChIP signal and heatmap profiles were visualized using the tools plotHeatmap from the deepTools package v3.5.1 (55). Sources for publicly available ChIP-seq data are detailed in the Data Availability section.

Western blot

Cells infected with the adenovirus-based vectors were detached by scraping from a 60 mm plate and lysed in EBC buffer (50 mM Tris–Cl pH 8.0, 120 mM NaCl, 0.5% NP-40) with Roche cOmplete™ protease inhibitor cocktail. Samples were prepared in Laemmli buffer and heated for 5 minutes at 65°C. Protein extracts were resolved in a 9% SDS-polyacrylamide gel and electrotransferred to a polyvinylidene difluoride (PVDF) membrane. Blocking was performed in 5% skim milk in TBS-Tween 0.1% for 10 minutes. Extracts were probed with antibodies against E1A (anti-e1a MAb M73) (56), Ku86 H-300 (sc-9034; Santa Cruz) and p400 (Thermo Fisher A300-541A) at manufacturer recommended dilutions for 1 h at room temperature or O/N at 4°C. Membranes were washed 3 times with TBS–Tween 0.1% for 10 min at room temperature. Incubation with secondary antibodies was performed using anti-mouse or anti-rabbit IgG antibodies (Bio-Rad) in TBS–Tween 0.1% buffer with 5% skim milk for 1 h at room temperature. Membranes were washed three times with TBS–Tween 0.1% for 10 min at room temperature before visualization with the Pierce ECL Western Blotting substrate (Thermo Fisher).

siRNA EP400 knockdown

Dharmacon SMART ON-TARGETplus pool siRNA against human EP400 (L-021272-05-0005) and D-001810-10-05 ON-TARGETplus Non-Targeting Pool were used to carry out EP400 knockdown in IMR90 cells. Cells were seeded in the absence of antibiotics and culture for 16h prior to transfection with lipofectamine (Lipofectamine 3000, Invitrogen). siRNAs were used at 30 nM and cells were left in culture for 24 h in the presence of the siRNA, followed by adenoviral *dl*1500- and e1a_p400-b- and mock-infection for other 24 h. The knockdown efficiency was evaluated by RT-qPCR after total RNA extraction (Trizol) and reverse transcription to obtain cDNA. Knockdown efficiencies of EP400 were around 50–60% depletion in different experiments. Interferon response was monitored by RT-qPCR of STAT1 and IFIT2 expression.

Reverse transcription and real-time PCR

RNA extracted from infected cells (500 ng) was reverse-transcribed using SuperScript III Reverse Transcriptase (Thermo Fisher) with random hexamer primers. The Real Time PCR reaction was performed using 20 ng of cDNA and the PowerUp SYBR Green Master Mix (Applied Biosystems), in a 20 μl final volume with 300 nM primer concentration. Runs were performed using a 7500 Real-Time PCR System (Applied Biosystems). Expression levels were normalized using U1 snRNA as internal control and the ΔΔCt method was used to evaluate expression relative to mock-infections. Data are presented as an average of two replicates ± standard deviation. Expression levels of *Alus* for siRNA knockdown experiments were calculated using ΔΔCt (siEP400-siCTRL) method for each infection and compared to respective non-siRNA infections relative to mock. Primers used are listed in Supplementary Table S1.

TF binding motif analysis

DNA sequences upstream of expression-positive *Alu*s (200 bp) were analysed using Analysis of Motif Enrichment (AME) from the MEME suite (57). The Jaspar 2020 collection was used as motif database (58) and the DNA sequences of 200 bp upstream of 20 000 random unexpressed *Alu*s were used as a control.

Results

Small E1A upregulates *Alu* transcription in human fibroblasts

To investigate alterations in *Alu* expression caused by adenovirus e1a, we performed *Alu* expression profiling in contact-inhibited, G1-arrested IMR90 primary human fibroblasts infected with HAdV-C5 mutant *dl*1500, which expresses e1a with little or no expression of other viral genes, versus infection with HAdV-C5 mutant *dl*312, with deletion of the complete e1a coding region (46). Mock-infected cells subjected to the same changes in medium, but without the addition of virus, served as a further control. *Alu* expression before and after infection was evaluated by RNA-seq through an analysis enabling quantitation of the expression of individual *Alu* elements to profile *Alu* expression at single-locus resolution (5,6). To minimize detection of bystander *Alu* RNA embedded within longer, Pol II-dependent transcripts, the analysis was restricted to *Alu*s that are not within any annotated protein-coding or ncRNA gene (intergenic) and *Alu*s that map to introns or exons of annotated genes in an antisense orientation (antisense). Most of the members of this intergenic/antisense *Alu* subset, amounting to 802 431 *Alu* elements, are likely to represent independent Pol III transcription units, and are thus more suitable than the complete genomic *Alu* inventory for evaluating a possible *Alu* transcriptional response to e1a.

As shown in Figure 1A, the *Alu* transcriptome expanded considerably in response to e1a expression. 1783 different *Alu*s were detected as expressed 24 h after infection with *dl*1500, versus 973 in mock-infected and 974 in *dl*312-infected cells. More precisely, 666 more *Alu*s could be detected as expressed in *dl*1500-infected cells compared to *dl*312/mock-infected cells. From now on, we will refer to the entire set of *Alu*s whose expression is detected in at least one of the three conditions as ‘expression-positive’ *Alu*s (ep*Alu*s). We prefer this term, instead of simply ‘expressed’ *Alu*s, because it indicates that an *Alu* element which is not expressed in just one or two conditions is nevertheless well distinguishable from the much larger number of *Alu*s that are not expressed in any of the conditions. In general, we observed a >75% overlap between the two replicates of each infection (Supplementary Figure S1). The global effect of e1a on *Alu* expression can be observed in the profiles in Figure 1B, showing a ∼4-fold increase in average *Alu* expression in response to e1a expression. The viral e1a protein is thus able to derepress *Alu* elements genome-wide, likely as a part of its global epigenome reprogramming properties. As it is further evident from Figure 1A, *dl*312- and mock-infected cells are

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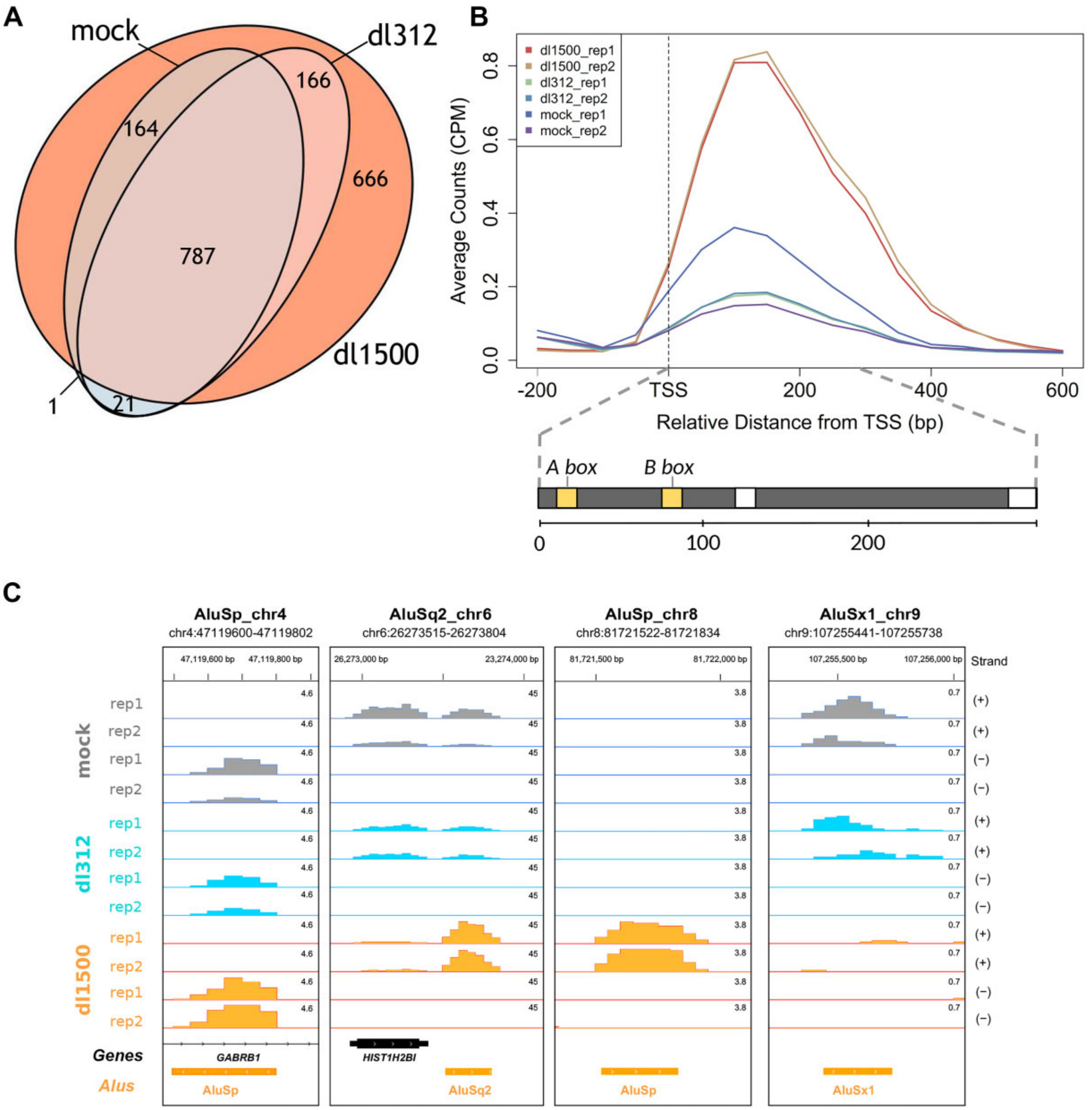

Figure 1. Upregulation of *Alu* expression by e1a in IMR90 cells. (**A**) Venn-diagram showing the number of expressed *Alu* elements in *dl*1500-, *dl*312- and mock-infected cells. The whole experiment was performed in duplicate. Expressed *Alu*s included elements whose expression was detected by the pipeline in at least one replicate. (**B**) Average *Alu* expression profiles in the presence/absence of e1a, generated from normalized read counts (Counts Per Million, CPM) of the 1805 expression-positive *Alu*s. Shown in the lower part of the panel is the structure of a typical full-length *Alu* element. The approximate positions of the A and B box internal control regions (yellow bars) are indicated above, those of internal and terminal poly(dA) motifs are indicated by white bars. The approximate position and extension of *Alu* internal sequence elements are indicated below (bp, base pairs). The upper graph reports the average read count for both replicates of each sample (*dl*1500, *dl*312 and mock), labelled by different colours as indicated. The vertical dashed line marks the position of the *Alu* transcription start site (TSS). (**C**) Base resolution expression profiles, shown as Integrated Genome Browser views (119), of 4 *Alu*s representative of different types of response to e1a. For the *Alu* in the first view on the left (AluSp_chr4), no substantial expression changes were observed under the different conditions. The *Alu* in the second view from the left (AluSq2_chr6) is detected as expressed in *dl*312- and mock-infected cells and its expression is strongly increased by e1a. The expression of the *Alu* in the third view from the left (AluSp_chr8) is only detected in *dl*1500-infected cells. The rightmost view (AluSx1_chr9) illustrates one of the very few examples of e1a-dependent downregulation. Orange boxes represent the orientation of repetitive elements as evidenced by the RepeatMasker track. The chromosomal coordinates of each annotated *Alu* are shown above each view. Bigwig RNA-seq data are normalized as Counts Per Million. The profiles of both replicates on (+) and (–) strands are shown for each sample (mock-, *dl*312- and *dl*1500-infected cells).

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Table 1. Subfamily distribution of expression-positive *Alus*[a]

	***Alu*J**	***Alu*S**	***Alu*Y**	**No family**	**Tot**
Annotated	213 441 (26.6%)	484 941 (60.43%)	100 903 (12.57%)	3146 (0.39%)	802 431
Expressed (*dl*1500)	187 (10.49%)	1499 (84.07%)	96 (5.38%)	1 (0.05%)	1783
Subfamily enrichment[b]	0.39	1.39	0.43		
P-value[c]	$<2.2 \times 10^{-16}$	$<2.2 \times 10^{-16}$	$<2.2 \times 10^{-16}$		
Expressed (*dl*312)	155 (15.91%)	748 (76.8%)	70 (7.19%)	1 (0.1%)	974
Subfamily enrichment	0.60	1.27	0.57		
P-value	2.3×10^{-15}	$<2.2 \times 10^{-16}$	6.9×10^{-08}		
Expressed (mock)	153 (15.72%)	750 (77.08%)	69 (7.09%)	1 (0.1%)	973
Subfamily enrichment	0.59	1.28	0.56		
P-value	6.8×10^{-16}	$<2.2 \times 10^{-16}$	3.9×10^{-08}		

[a] Reported for each *Alu* subfamily (columns) is the absolute number of intergenic/antisense *Alus* and (in parentheses) their percentage. In the first row, the subfamily distribution of annotated *Alus* is reported. The other rows report the subfamily distribution of *Alus* expressed in *dl*1500, *dl*312 and mock-infected IMR90 cells.

[b] For each sample, the subfamily enrichment was calculated as the ratio between the percentage of each subfamily out of all expressed *Alus* and the percentage of each subfamily out of all annotated *Alus*.

[c] The *P*-value for subfamily enrichment (in italics) was calculated using a two-tailed Fisher's exact test.

characterized by an incomplete overlap of expressed *Alu* sets, which may result from the interaction of cellular and viral receptors and the exposure of viral nucleic acids during the injection of viral DNA-protein complexes from the cell surface into the nucleus (59). However, most of these elements were also expressed in *dl*1500-infected cells, where many of them were upregulated. Of 1805 observed ep*Alus*, almost 37% were exclusive to *dl*1500-infected cells, ∼62% were also expressed in *dl*312/mock cells, whereas only ∼1% were detected in *dl*312/mock-infected cells but not in *dl*1500-infected cells. Among the 953 *Alu*s expressed in both *dl*312- and *dl*1500-infected cells, 385 were differentially expressed with FDR < 0.05. With just one exception, all differentially expressed *Alu*s were upregulated in *dl*1500-infected cells. The coordinates of ep*Alu*s, including information on differentially expressed *Alu*s and the corresponding expression values are reported in Supplementary Table S2.

In agreement with previous studies showing that only a small fraction of *Alu* elements is expression-positive in each cell type (5,7), e1a-dependent *Alu* upregulation was very limited on a genome-wide scale. Only 0.22% of the total intergenic/antisense *Alu* sequences could be detected as expressed after *dl*1500 infection, which nonetheless represented a remarkable increase with respect to the percentage of constitutively expressed *Alu* loci (0.12%) (see Table 1). Such low percentages might also reflect the detection limits of the technique. A few examples of individual *Alu* expression profiles, representative of different e1a effects on *Alu* expression, are shown in Figure 1C.

Alu elements are classified into three main subfamilies, called *Alu*J, *Alu*S and *Alu*Y, with *Alu*Y being the evolutionarily youngest, and thus the less degenerate in sequence. Accordingly, *Alu*Y is the only known subfamily which is at present actively retrotransposing in the human genome (60). Despite their retrotransposition activity, *Alu*Y elements were not found to be more expressed than the other two subfamilies in previous studies (5,7). We thus investigated the contribution (in terms of ep*Alu* fraction) of *Alu*J, S and Y subfamilies to the total expression of *Alu* sequences in IMR90 cells subjected or not to e1a-dependent reprogramming. As detailed in Table 1, a highly significant enrichment in *Alu*S subfamily elements was observed among expressed *Alus* in both control and *dl*1500-infected cells, while *Alu*Y- and *Alu*J-derived transcripts were significantly underrepresented in *Alu* transcriptomes. As recently suggested, the relatively low contribution of *Alu*Y to *Alu* transcriptomes is consistent with the possibility that specific repression systems tend to be more efficient on *Alu*s with higher retrotransposition-dependent mutagenic potential (7). The underrepresentation of *Alu*J transcripts might be related to the higher number of mutations accumulated in these old elements (61), making them less able to support transcription, in particular in response to e1a. An evaluation of A- and B-box promoter elements of ep*Alu*s confirmed the results of previous analyses (5), showing a substantial match with canonical tRNA gene-derived consensus sequences for the two internal control regions (A-box: TRGYnnAnnnG; B-box: GWTCRAnnC), with the exception of the last position of the A-box, which in *Alu*s is C instead of G (data not shown).

To check whether e1a-dependent derepression also occurs in other SINEs in addition to *Alu*s, we analyzed the expression of mammalian-wide interspersed repeats (MIRs). With ∼500 000 copies in the human genome, MIRs are the second most numerous subgroup of human SINEs. As is the case for *Alu*s, it has recently been shown that only a tiny percentage of MIRs are expressed in different cell lineages (11). Out of a total of 404 371 intergenic/antisense MIRs (defined as detailed above for *Alus*), only 137 were expression-positive, i.e. detected as expressed in at least one sample, with no evidence of *dl*1500-dependent upregulation (data not shown). The effect of e1a thus appears to be restricted to the *Alu* subgroup of human SINEs.

It was recently reported that expressed *Alu* elements tend to reside closer to the transcription start sites of Pol II-transcribed genes than unexpressed *Alu*s, a property that may be associated with their ability to function as cell type-specific enhancers for nearby genes (7). To investigate the possible relevance of *Alu* expression for protein-coding gene expression in our experimental system, we first asked whether there is any bias in the distribution of ep*Alus* between protein-coding genes and the remaining genomic regions. As shown in Supplementary Figure S2, the fraction of intragenic *Alu*s (limited to those with antisense orientation) was significantly lower (and, correspondingly, the fraction of extra-genic elements was higher) for ep*Alu*s than for unexpressed *Alu*s (panel A). Furthermore, there was a significant overrepresentation of ep*Alu*s within 32 kb from the TSSs of protein-coding genes (more marked upstream than downstream of the TSS), while at distances of more than 64 kb ep*Alu*s were sig-

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nificantly underrepresented (panel B). The expression levels (normalized for gene length) of protein-coding genes flanked by ep*Alu*s were generally higher than those of genes flanked by unexpressed *Alu*s (panel C). Altogether, these data provide general support to the idea that ep*Alu*s are overrepresented in regions relatively close to the TSSs of protein-coding genes, where their expression tends to parallel the expression of nearby genes. However, we did not find evidence for differential expression of protein-coding genes paralleling the e1a-dependent induction of nearby *Alu*s (data not shown).

e1a-dependent *Alu* derepression occurs through increased TFIIIB recruitment without changes in TFIIIC occupancy

Previous reports suggested that e1a affects TFIIIC activity (36,37) and that human TFIIIC can influence the epigenetic state of *Alu* elements genome-wide (15). We thus asked whether e1a induces changes in the genome-wide distribution of TFIIIC and TFIIIB in IMR90 cells, and whether such changes could explain at least in part the observed e1a-dependent *Alu* upregulation.

The genome-wide location of TFIIIC and TFIIIB in IMR90 cells in the presence or absence of e1a was assessed by ChIP-seq using antibodies targeting the 110 kDa subunit of TFIIIC and the Bdp1 component of TFIIIB. TFIIIC/TFIIIB-associated loci in IMR90 cells were classified into four combinatorial clusters according to their enrichment for TFIIIC and Bdp1 (Figure 2A). Loci of the first two clusters were characterized by the association of both TFIIIC and Bdp1, and their overlap with all repetitive elements was strongly enriched in tRNA genes (Figure 2B). Cluster 1 loci were characterized by an e1a-dependent increase in Bdp1 association, without any appreciable change in TFIIIC enrichment. An increase in both TFIIIC and TFIIIB association was instead observed at cluster 2 targets. Loci belonging to clusters 3 and 4 were generally found to be enriched in TFIIIC but not Bdp1. These two clusters turned out to be strongly enriched in SINEs, primarily *Alu* but also MIR elements (Figure 2B). The presence of human TFIIIC in the absence of other components of the Pol III machinery has previously been reported to occur at SINE loci (62,63). A distinctive feature of cluster 4 is an e1a-dependent decrease of TFIIIC association. Genomic Regions Enrichment of Annotations Tool (GREAT) analysis (64) found that the *Alu*s of this cluster are significantly associated with genes involved in embryonic lethality (Supplementary Figure S3A), suggesting that e1a-dependent TFIIIC removal from these sites might participate in viral manipulation of cell identity and differentiation pathways (40,41,65).

The analyses reported in Figure 2A and B related to TFIIIC and Bdp1 enrichment across the whole genome. To assess in a more accurate and sensitive way whether there was a correlation between the presence of TFIIIC/Bdp1 at individual *Alu* loci and their expression, we focused the ChIP-seq data analysis on the 1805 ep*Alu*s. We found that ep*Alu*s were globally characterized by a significant TFIIIC association independently from the presence of e1a (Figure 2C). Therefore, *Alu* upregulation in response to e1a does not appear to involve increased TFIIIC recruitment at ep*Alu*s. However, no comparable TFIIIC occupancy was observed in random *Alu* sets, considered to be representative of unexpressed *Alu*s. As ep*Alu*s were ranked based on their levels of expression (from high to low) in Figure 2C, our results show marked TFIIIC occupancy for highly expressed ep*Alu*s for both *dl*1500- and mock-infected cells. This suggests that TFIIIC occupancy is higher at *Alu*s with higher transcriptional potential and that the presence of e1a could eventually turn this potential into active transcription.

No specific signal was observed at ep*Alu*s in mock-infected cells through Bdp1 ChIP-seq analysis, while a specific Bdp1 association profile at ep*Alu*s was detected in *dl*1500-infected cells (Figure 2C), although it was weaker than the TFIIIC signal, possibly due to low efficiency of immunoprecipitation elicited by anti-Bdp1 antibodies and to the generally low level of *Alu* transcription activation. When the Bdp1 enrichment analysis was limited to differentially expressed *Alu*s, and more specifically to those among them whose expression levels in the presence of e1a falls in the first quartile, a clear increase in Bdp1 enrichment was observed at an upstream position where TFIIIB is expected to be recruited by DNA-bound TFIIIC (Figure 2D). The Genome browser profiles of TFIIIC/Bdp1 occupancy along with expression profiles for three *Alu*s included in the heatmap of Figure 2D are also reported (Supplementary Figure S3B). Altogether, the data suggest that *Alu* upregulation by e1a does not entail increased TFIIIC occupancy but does involve increased Bdp1 (and thus very likely TFIIIB) recruitment on an appreciable subset of ep*Alu*s.

Epigenetic signatures of expression-positive and e1a-upregulated *Alu* elements

Since *Alu* expression control is supposed to be mainly epigenetic, with the vast majority of *Alus* undergoing chromatin-mediated silencing (2), we asked whether some key histone modifications, as well as the association of chromatin regulatory proteins, could be associated with ep*Alu*s, and whether they are affected by e1a. We first made use of publicly available nucleosome mapping of IMR90 cells (66), which showed clear evidence for two strong nucleosomes positioned not only on ep*Alu*s, but also on random *Alu* sets (Supplementary Figure S4, panel A). As revealed by ATAC-seq analysis of the same cells (67), however, ep*Alus* displayed more accessible chromatin upstream of TSS than random unexpressed *Alus* (Supplementary Figure S4, panel B). These preliminary observations prompted us to search for patterns of histone modifications at ep*Alu*s.

To gain insight into the epigenetic state of *Alus* and its possible e1a-induced changes, we employed ChIP-seq analysis of IMR90 cells, either mock- or *dl*1500-infected, for the following histone modifications: H3K9ac, H3K18ac, H3K27ac and H3K4me1 (the last three modifications being landmarks of enhancers). As shown in Figure 3A, the most noticeable e1a-dependent changes in the average profiles at ep*Alu*s were observed for H3K27ac, which was generally depleted in the presence of e1a, and for H3K4me1, whose presence upstream of ep*Alu*s was generally increased in response to e1a. More subtle and less specific changes in enrichment profiles were observed for H3K9ac and H3K18ac. The comparison of histone modification profiles of ep*Alu* with random *Alu* sets revealed clear differences between expressed and unexpressed *Alus* in H3K4me1 and H3K27ac profiles. This supports the idea that ep*Alu*s bear enhancer-like chromatin marks and are epigenetically remodeled by e1a towards a state marked by H3K4me1 but lacking H3K27ac, reminiscent of poised enhancers (10).

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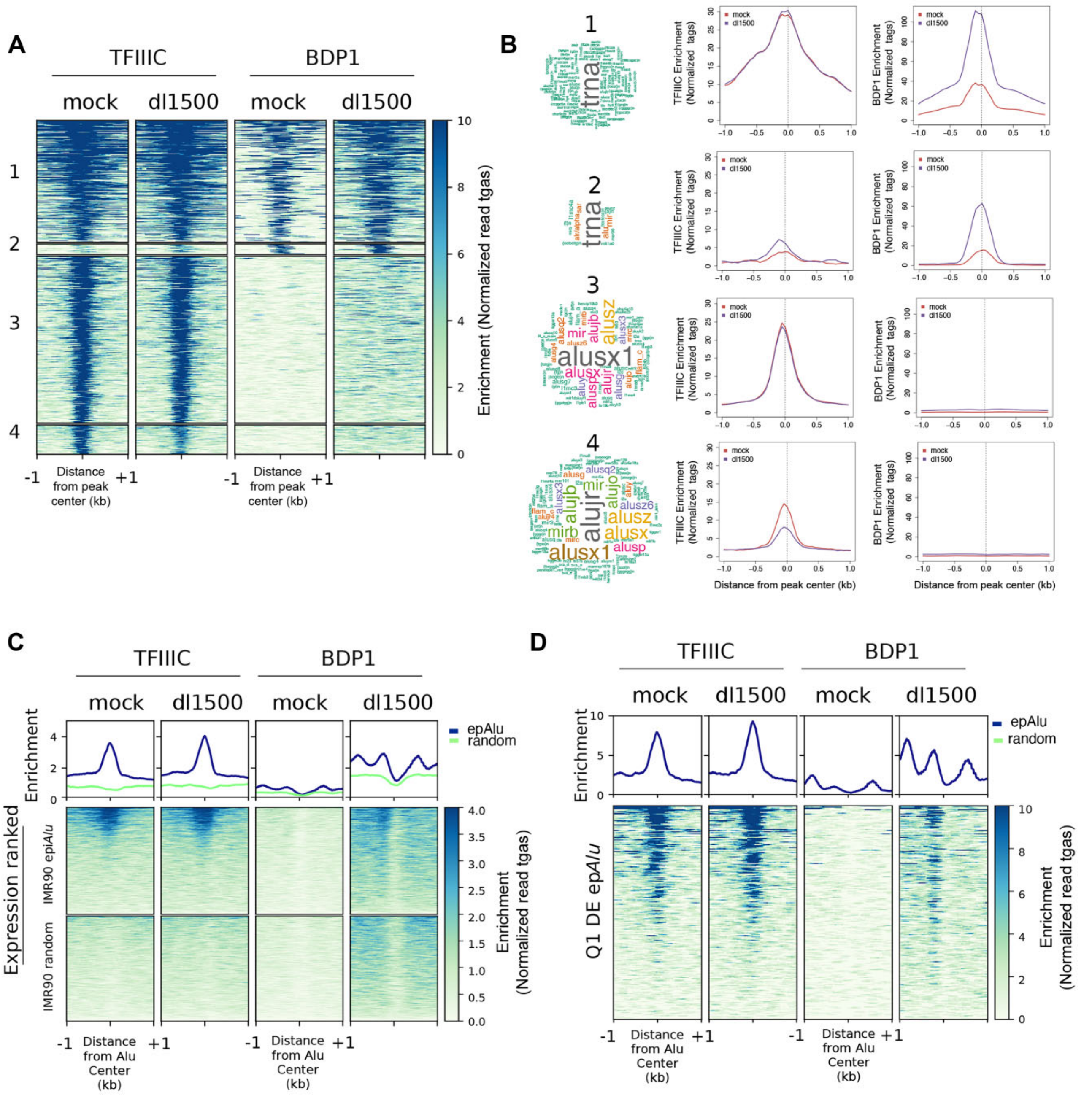

Figure 2. Genome-wide location analysis of TFIIIC and TFIIIB in the presence/absence of e1a. (**A**) Heatmap of TFIIIC (GTF3C2) and Bdp1 spanning ±1 kb across all TFIIIC-bound sites in mock- and *dl*1500-infected cells. Clusters 1 to 4 were created by combinatorial clustering of the two factors across all regions bound. Color bar scale with increasing shades of color stands for increasing enrichment (normalized read tags). (**B**) Shown on the left is the word cloud analysis of repetitive elements associated with regions occupied by TFIIIC and Bdp1 in the four clusters. Font size reflects enrichment for the indicated term. Reported on the right are the results of *sitepro* analysis (120) of TFIIIC and Bdp1 enrichment (normalized read tags) for each cluster reported in panel A. Enrichment is shown spanning 2 kb from the center of the peaks. (**C**) Shown in the upper part of the panel are the average ChIP-seq enrichment profiles (normalized read tags) of the TFIIIC 110 kDa subunit (left) or the Bdp1 component of TFIIIB (right) in either mock-infected or *dl*1500-infected IMR90 cells across the 1805 ep*Alu*s and across random *Alu*s. Reported below the plots are heatmaps of TFIIIC and Bdp1 enrichment at the same *Alu*s, sorted according to their expression level in *dl*1500-infected cells (top, high expression; bottom, low expression). (**D**) Enrichment profiles (normalized read tags) of TFIIIC and Bdp1, in either mock-infected or *dl*1500-infected IMR90 cells, at differentially expressed *Alu*s whose expression levels in the presence of e1a falls in the first quartile (Q1 DE ep*Alu*), sorted according to their expression level in *dl*1500-infected cells (top, high expression; bottom, low expression).

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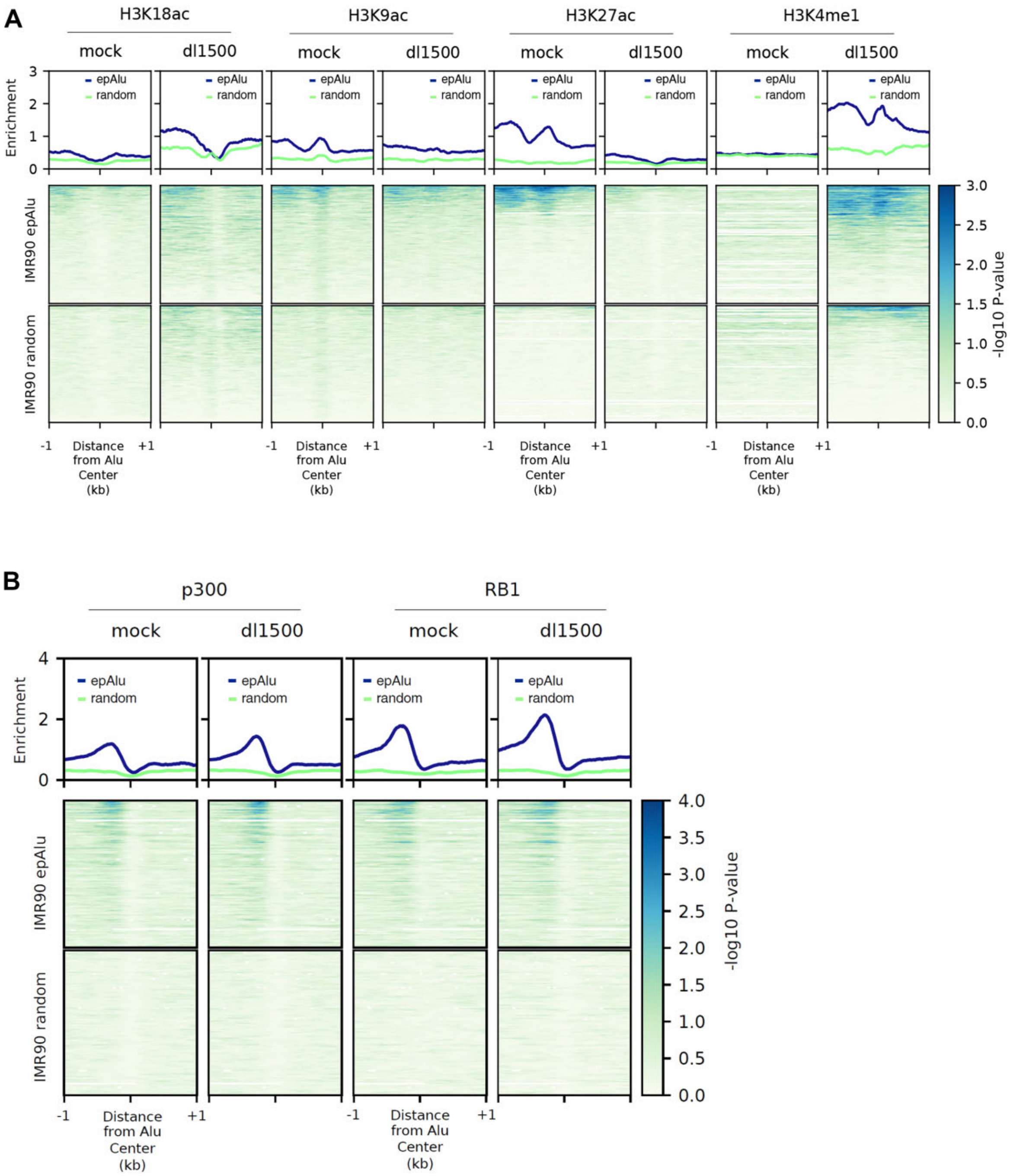

Figure 3. Histone modification and chromatin regulator enrichment profiles of ep*Alu*s in the presence/absence of e1a. (**A**) Shown in the upper graphs are the average ChIP-seq enrichment (–log$_{10}$ of the Poisson *P*-value) profiles of (from left to right) H3K18ac, H3K9ac, H3K27ac and H3K4me1 across the 1805 ep*Alu*s in either mock-infected or *dl*1500-infected IMR90 cells. Reported below the plots are the heatmaps of the same histone modification enrichments, with ep*Alus* and random *Alus* ranked according to enrichment expressed as –log$_{10}$ of the Poisson *P*-value. (**B**) Shown in the upper part of the panel are the average ChIP-seq enrichment profiles (–log$_{10}$ of the Poisson *P*-value) of EP300 (left) and RB1 (right) in either mock-infected or *dl*1500-infected IMR90 cells across the 1805 ep*Alu*s and across random *Alu*s. Reported below the plots are heatmaps of EP300 and RB1 association to the same *Alu*s, sorted according to their expression level in *dl*1500-infected cells (top, high expression; bottom, low expression).

Given the importance of e1a-EP300 and e1a-Rb interactions for e1a-dependent epigenome reprogramming (41), we also investigated by ChIP-seq the enrichment and possible redistribution of these two proteins at *Alu* loci. Ep*Alu*s were generally characterized by the presence of a p300 peak just upstream of the *Alu* body (Figure 3B). As in the case of TFIIIC, however, the average p300 association profile was not dramatically affected by e1a (Figure 3B). A similar behavior was observed for RB1, with a peak at the same position as the p300 peak (Figure 3B). Remarkably, the p300 and the RB1 association profiles were not present when random sets of *Alu*s were compared with ep*Alu*s, thus pointing to a relevant role of these proteins in establishing the chromatin state of ep*Alu*s. Importantly, ep*Alu*s characterized by higher expression levels in *dl*1500-infected cells (top positions in the heatmaps) also generally displayed higher p300 and RB1 occupancy both in

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*dl*1500- and in mock-infected cells (Figure 3B). Therefore, as in the case of TFIIIC, the presence of p300 and Rb proteins appears to correlate with the *Alu* transcriptional potential.

Transcription factor signature of ep*Alu*s

A number of transcription factors (TFs) have previously been shown to be enriched at expressed *Alu* elements (5,7), and the evolution of *Alu* elements towards enhancers has been suggested to be accompanied by the acquisition of TF binding sites over evolutionary timescales (10). To gain insight into the possible contribution of specific TFs to the epigenetic state of ep*Alu*s and their e1a-dependent upregulation, we searched for TF binding motifs enriched in the 200-bp region upstream of ep*Alu*s through the Analysis of Motif Enrichment (AME) tool (68). As shown in Figure 4A, the most significant enrichment was for motifs recognized by the Fos- and Jun-related factor heterodimers collectively referred to as AP-1 (69). In order of significance, the first AP-1-unrelated TF binding motif found to be enriched upstream of ep*Alu*s was the one recognized by TEAD1. Remarkably, TEAD2, TEAD3 and TEAD4 motifs were also significantly enriched. Other enriched motifs included those recognized by Nuclear Factor I (NFIX), CCCTC-binding factor (CTCF), Zinc finger and BTB domain-containing protein 7A (ZBTB7A), ETS Variant Transcription Factor 6 (ETV6), Basic Helix-Loop-Helix family member A15 (BHLHA15) and CCAAT Enhancer Binding Protein Epsilon (CEBPE). Some of these TFs or TFs of the same family (namely AP-1, CTCF, CEBPB), as well as the corresponding binding motifs, were previously found to occupy loci of expressed *Alu*s in several cell lines (5,7). To further characterize the role of closely bound TFs in *Alu* expression, we took advantage of the Cistrome ToolKit (70) to perform an unbiased search for DNA binding proteins enriched, in any cell type or tissue, at the set of ep*Alu*s identified in this study (Figure 4B). We found that, in addition to components of the basal Pol III transcription machinery (POLR3D, POLR3A, GFT3C2, GTF3C5, TBP), the top 20 factors displaying the highest-ranking scores for ep*Alu*s included chromatin proteins and TFs whose presence suggests a complex regulatory scenario. Indeed, all three components of the ChAHP complex (CHD4, ADNP, CBX3), recently proposed to counteract CTCF binding by competing for the same sites in correspondence of mouse B2 SINEs (71), were found (Figure 4B). Importantly, we also identified TFs and chromatin regulators expected to be recruited to the enriched regulatory motifs of Figure 4A, such as: YAP1 (or YAP), a coactivator acting together with the paralogous TAZ protein to regulate target genes mainly through binding to DNA-bound TEAD TFs (72), and recently shown to be affected by e1a (73); bromodomain-containing protein 4 (BRD4), known to be physically engaged genome-wide by YAP/TAZ (74); the AP-1 subunits JUN and FOSL1; CEBPB, whose binding site specificity is the same as CEBPE (Figure 4B). As this analysis used ChIP-seq data from a wide range of cell types and tissues, we wanted to gain more insight into the relevance of these observations for the regulatory properties of our IMR90 ep*Alu*s. We thus further focused on publicly available CEBPB, FOS, YAP1 and BRD4 ChIP-seq data in IMR90 cells (75–79). We calculated the enrichment for all these ChIP-seq over the IMR90 ep*Alu*s. Our analysis unveiled a clear enrichment for YAP1, CEBPB and FOS peaking at the ep*Alu* upstream region (Figure 4C), precisely where the corresponding binding sites were revealed by the DNA motif analysis. BRD4 was also found to be specifically enriched upstream of ep*Alu*s, while no corresponding signals were detected for random *Alu*s (Figure 4C). Some representative profiles, showing the TF enrichment upstream of individual ep*Alu*s, are reported in Supplementary Figure S5.

Interaction of e1a with chromatin remodeler EP400 is required for *Alu* upregulation

The above analyses revealed a complex epigenetic infrastructure at ep*Alu*s but did not provide direct information on the molecular mechanism of e1a-dependent *Alu* upregulation. To address this issue, we analysed the functions of e1a interactions with host proteins by taking advantage of e1a mutants that are specifically impaired in their ability to interact with either RB-family proteins, EP300 and its paralog CREBBP, or EP400 (41,80,81). These mutants will henceforth be referred to as e1a_RB-b$^-$, e1a_p300-b$^-$ and e1a_p400-b$^-$ (b$^-$ standing for 'binding minus').

Alu expression profiling was carried out through RNA sequencing of IMR90 cells infected with the three e1a mutant strains, compared to cells infected in parallel with mock- or *dl*1500. We first identified the proper MOI for the different mutants to obtain similar amounts of e1a protein with the different strains. RNA-seq and Western blot confirmed the proper expression of e1a binding mutants, with e1a_RB-b$^-$ expressed at significantly lower levels (Supplementary Figure S6). Samples from two rounds of infections performed as biological replicates were subjected to RNA-seq analysis. We then calculated *Alu* differential expression upon infection observed for each of the four e1a variants compared to mock-infected cells and reported the results as a heatmap (Figure 5A). Despite the lower expression levels of e1a_RB-b$^-$, a slightly higher number of differentially expressed *Alu*s were observed in its presence compared to wt e1a. A reduction in the number of differentially expressed *Alu*s was instead observed with e1a_p300-b$^-$ and, much more markedly, with e1a_p400-b$^-$. Therefore, RB-family proteins (RB, RBL1 and RBL2) appear to exert at best a negative modulatory effect on e1a-dependent *Alu* upregulation. By contrast, EP300/CREBBP appear to act positively in the same process, in accordance with their reported stimulatory activity on Pol III chromatin templates (82). But the major e1a function required for *Alu* derepression turned out to be the interaction with EP400, whose involvement in the regulation of *Alu* or any Pol III-transcribed gene has not been previously reported. Of the *Alu*s activated by wt e1a, ∼90% were no longer activated by its mutant defective in EP400 binding.

The effect of the e1a mutations on *Alu* expression regulation was further confirmed by RT-qPCR on two individual ep*Alu*s whose unique 3′-trailer sequence was long enough to allow for unambiguous detection of *Alu* transcripts from the individual loci (Figure 5B, upper panel). Expression profiles of the same RT-qPCR tested loci reconstructed from RNA-seq data supported the same conclusion (Figure 5B, lower panel). For these two *Alus*, upregulation was strongly impaired with e1a_p400-b$^-$, and it was also negatively affected, to a lower extent, by the loss of e1a interaction with RB and EP300/CREBBP (the behaviour of RB at these *Alu*s thus deviates from the generally observed one). In contrast to these effects of e1a and its interaction mutants on *Alu* expression, no e1a-dependent expression modulation was observed for other non-*Alu* Pol III transcripts (7SL RNA, 7SK RNA, U6 snRNA,

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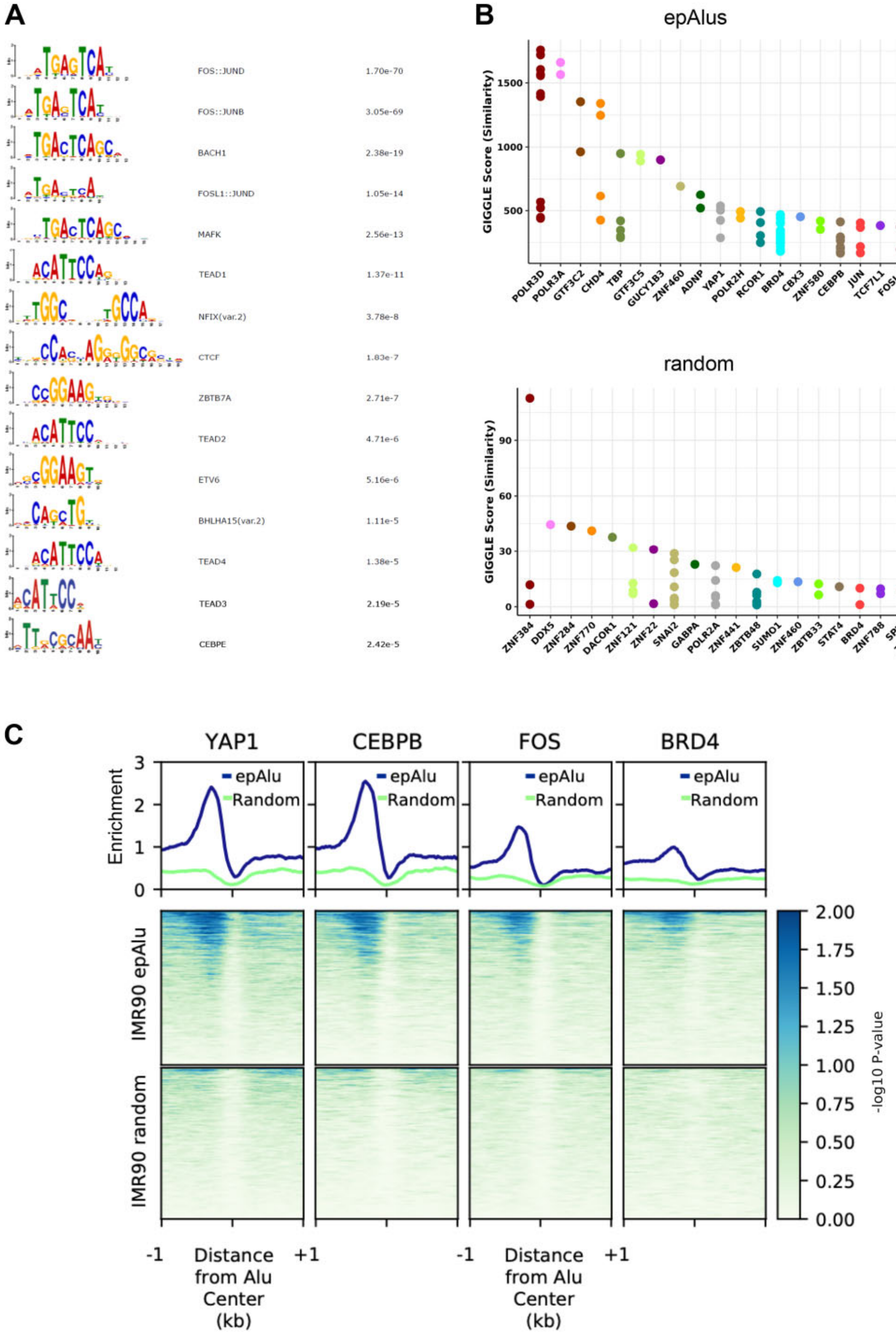

Figure 4. TF binding motifs and ChIP-seq enrichment at ep*Alu*s. (**A**) TF binding motifs enriched in the 200 bp upstream of the TSS of ep*Alu*s with (right column) their corresponding *P*-values adjusted for multiple testing with Bonferroni correction. (**B**) Cistrome Toolkit (http://dbtoolkit.cistrome.org/) analysis of ep*Alu* and random *Alu* sets. Giggle score is calculated by using the genome coordinates of the two sets of *Alu*s to retrieve which factors bind those intervals among all curated experiment in the Cistrome database (70). (**C**) Plotheatmap of ChIP-seq of YAP1, CEBPB, FOS and BRD4 at the 1805 ep*Alu*s and at random *Alu*s based on data from (75–79). Ranking is according to enrichment of YAP1 reported as $-\log_{10}$ of the Poisson *P*-value.

RNase P RNA, tRNA$^{\text{His}}$) whose genes are characterized by different types of promoter organization (83) (Figure 5C-D). As e1a-dependent *Alu* upregulation was found to entail increased Bdp1 recruitment (Figure 2), we wondered whether the weakening of *Alu* activation caused by the loss of e1a-EP400 interaction could be due to reduced Bdp1 recruitment. We thus employed Bdp1 ChIP-seq to systematically address whether Bdp1 enrichment at *dl*1500-differentially expressed *Alus* and ep*Alus* was affected genome-wide by expression of e1a_p400-b^{-}. By comparing Bdp1 enrichment profiles upon infection of IMR90 with *dl*312 (no e1a), *dl*1500 (wt e1a) and the e1a_p400-b^{-} mutant, we found that infection with the latter led to a significant decrease in Bdp1 recruitment at both set of *Alu*s (Figure 5E and F).

To find support for a general role of EP400 in *Alu* epigenetic control, we took advantage of the availability of ChIP-seq data for EP400 in K562 cells (84). Even though IMR90 and K562 represent different cell lineages and thus display

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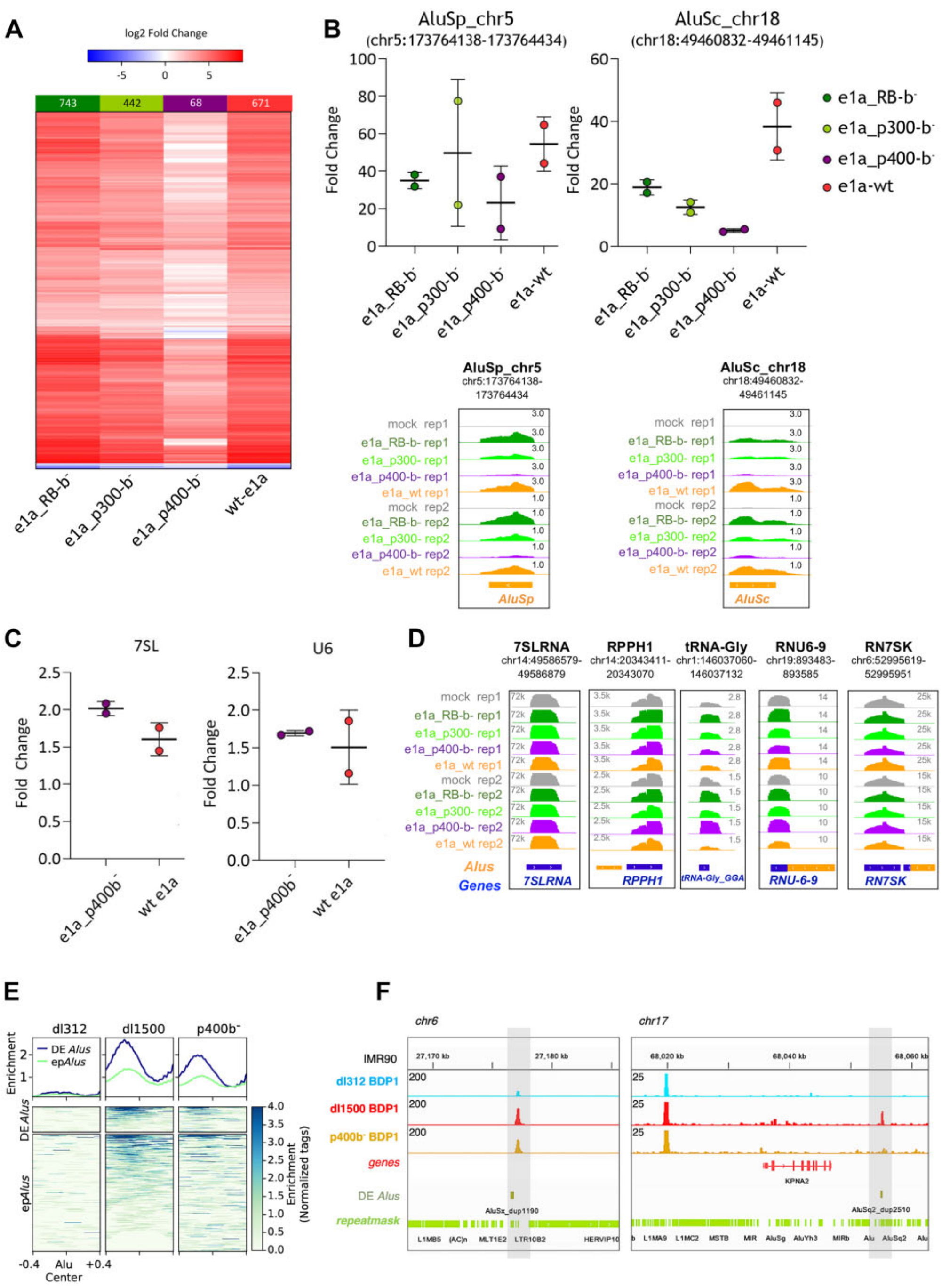

Figure 5. Dependence of *Alu* upregulation on e1a interaction with chromatin regulators. (**A**) Heatmap showing increased (red) or decreased (blue) expression of *Alu* elements triggered by wt e1a or e1a mutants defective in interaction with RB (e1a_RB-b⁻), p300 (e1a_p300-b⁻) or p400 (e1a_p400-b⁻), as compared to mock-infected cells. Boxed above each heatmap are the numbers of differentially expressed *Alu*s ($\log_2$ fold-change ≥ 0.5 or ≤ -0.5 and an adjusted P-value < 0.05). The experiment was performed in two biological replicates. (**B**) Expression levels of two individual *Alu*s as measured by RT-qPCR (upper graphs) and RNA-seq (lower views). Fold changes estimated by RT-qPCR are relative to the expression in mock-infected cells, after normalization to U1 snRNA gene expression. Primers were chosen to target the unique sequence of *Alu* elements within the 3′ trailer region. RT-qPCR data relative to each independent experiment are represented as dots. Indicated by horizontal bars are the means ± standard deviation between the replicates. RNA-seq data (lower subpanels) are presented as genome browser views of the same *Alu* elements analysed in the upper plots. Orange boxes represent the orientation of repetitive elements as evidenced by the RepeatMasker track. The chromosomal coordinates of each annotated *Alu* are shown in the upper part of each subpanel. Bigwig tracks are normalized per CPM. (**C**) Expression changes of 7SL RNA (left graph) and U6 snRNA (right graph) genes induced by either wt e1a or e1a_p400-b⁻ mutant, as measured by RT-qPCR. Fold change is relative to mock-infected cells, after normalization to U1 snRNA gene expression. RT-qPCR data from each of two independent experiments are represented as dots. Indicated by horizontal bars are the means ± standard deviation between the replicates. (**D**) Genome browser views of the expression of RN7SL1, RPPH1, tRNA-His-GTG-1–1 (GtRNAdb), RNU6-9 and RN7SK genes, coding for 7SL RNA, Ribonuclease P RNA component H1, tRNA^{Gly}(GGA), U6 snRNA and 7SK RNA, respectively. Expression profiles are based on RNA-seq analysis of IMR90 cells infected as indicated on the left. (**E**) Heatmap and enrichment profiles (normalized read tags) of Bdp1 ChIP-seq occupancy at differentially expressed *Alu*s (DE ep*Alus*) and ep*Alus* in IMR90 infected with *dl*312, *dl*1500 and p400-b⁻ viruses. (**F**) Genome browser views Bdp1 ChIP-seq data of two highly *dl*1500-induced *Alu* elements as evidenced by the RepeatMasker track. The chromosomal coordinates of each annotated *Alu* are shown above each view. Bigwig tracks are normalized for the library size.

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largely different sets of expression-positive *Alu*s, we observed nevertheless that 285 *Alu*s are expression-positive in both cell lineages (Supplementary Figure S7A). Both the Pol III machinery and EP400 turned out to be strongly enriched at these *Alu*s in K562 cells (Figure 6A). When the whole set of IMR90 ep*Alu*s was considered, EP400 enrichment was still significant (Mann–Whitney *U* test), while no enrichment signal was observed with random *Alu* subsets of similar size (Figure 6B, left subpanel). When the same analysis was carried out on the subset of *Alu*s that are expression-positive in K562 cells, as expected EP400 was found to be even more enriched (Figure 6C, left subpanel). As EP400 has been implicated in the deposition of H2A.Z histone variant at nucleosomes (85), with the potential to influence both transcription and DNA repair, we compared the H2A.Z ChIP-seq profiles at expression-positive *Alu*s of K562 cells and found an appreciable enrichment of H2A.Z compared to a random set (Figure 6B-C, right subpanels). To gain more mechanistic insight into the function of EP400 at *Alus* upregulated by e1a, we implemented siRNA knockdown of EP400 prior to infection with *dl*1500 and e1a_p400-b$^-$ adenovirus (Figure 6D-E, Supplementary Figure S7B and C). Our data show that siRNA depletion of EP400 did not cause any increase in ep*Alu* expression in mock-infected cells, thus excluding that EP400 is a mere *Alu* repressor counteracted by e1a. In contrast, EP400 depletion from IMR90 cells abrogated e1a-mediated upregulation of AluSp and AluSc, thereby attesting that EP400 is actively involved in the induction of *Alus* caused by wt e1a expression (Figure 6E). *Alu* upregulation by e1a thus critically depends on previously unrecognized epigenetic features of ep*Alu*s involving the active role of p400 chromatin remodeler and possibly its histone exchange activity.

Discussion

Alu expression has long been known to be upregulated in response to viral infection (86). Our study shows that the Adenovirus 5 e1a oncoprotein is responsible by itself for derepression of several hundred *Alu* elements across the human genome in IMR90 fibroblasts by virtue of its interaction with the host ATPase chromatin remodeler EP400. Our data show that many of the e1a-responsive *Alu*s display features of YAP/TAZ- and AP-1-associated enhancers where e1a appears to reconfigure key histone modifications, most notably H3K27 acetylation. These effects can best be framed into the context of e1a epigenome reprogramming properties required for maximal viral DNA replication in permissive human cells and cell transformation of baby rat kidney cells (40). An impressive range of interactions with host proteins is exploited by e1a to induce cell cycling and dedifferentiation (87). Two of the best well-characterized e1a-host protein interactions take place with the tumour suppressor RB1 and the lysine acetyltransferases EP300/CREBBP. These interactions are key to the e1a-induced gene dysregulation underlying cell transformation. Their mechanistic contribution to this process has been widely studied and shown to involve, in addition to the displacement of RB1 from E2F transcription factors, a complex interplay with chromatin regulatory proteins (41,88–91). The less extensively investigated e1a-EP400 interaction has been known for twenty years to function in the e1a transforming process (42), and later was shown to stabilize MYC and to promote formation of MYC-EP400 complexes on chromatin leading to activation of MYC target genes (92). Our finding that derepression of a subset of ep*Alu*s strongly depends on the e1a-p400 interaction adds an important element to our knowledge of e1a-dependent epigenome reprogramming, by showing that it might also rely on the exploitation of a chromatin remodeler at a subset of retrotransposons. Whether such an epigenetic switch, operating at hundreds of loci throughout the genome, also involves the MYC family of transcription factors, or some other EP400-interacting proteins like TRRAP, remains to be established. In support of a possible involvement of Myc proteins, N-Myc was recently shown to interact with TFIIIC by proteomic analysis and to colocalize with TFIIIC at thousands of sites (93). c-Myc was also previously found to activate Pol III-dependent transcription of tRNA and 5S rRNA genes through a mechanism involving TRRAP and Gcn5 recruitment (94) and more generally to be present at Pol III-transcribed genes at the genome-wide scale (95). TRRAP recruitment was also previously reported to be required for cell transformation by E1A (96). Myc proteins could therefore participate in the complex interaction network expolited by e1a to epigenetically deregulate *Alu*s.

Through its histone exchange activity, EP400 is likely to promote H2A.Z deposition at ep*Alu*s, whose enrichment was correlated with *Alu* expression in this and previous studies (7). Notably, we find that EP400 is actively involved in wt e1a induction of *Alu*s in agreement with findings reporting EP400 to be necessary for H2A.Z and H3.3 deposition into enhancers and promoters *in vivo* (97). Another possible mechanistic facet of *Alu* activation through e1a-EP400 interaction is suggested by the ability of the TIP60/p400 complex to recognize H3K4me1 through its TIP60 component (44). As part of the *Alu* epigenetic switch, the e1a-EP400 interaction might favour H3K4me1-mediated TIP60/p400 recruitment, which would in turn promote *Alu* transcription. The presence at specific *Alu* loci of regulators of chromatin architecture might not be limited to p400, as another chromatin remodeler, CHD4, recently shown to associate to evolutionarily younger mouse SINEs as part of the ChAHP complex (71), was found to be enriched at a subset of *Alu* elements in human breast cancer cells (15).

The use of e1a mutants specifically defective in interaction with chromatin regulatory proteins also allowed us to exclude the possibility that e1a acts by relieving Rb-mediated repression at *Alu* elements. With an e1a mutant unable to interact with Rb, the number of upregulated *Alu*s and the extent of upregulation was even higher than with wt e1a, thus suggesting that the e1a-Rb interaction impacts negatively on *Alu* expression. As to the e1a-p300 interaction, its loss only slightly weakened *Alu* expression upregulation. Collectively, these effects are in line with the complex interplay between e1a, Rb and p300 previously shown to lie behind activating and repressing chromatin conformations in Ad5-infected cells (41).

A possible key to understanding the epigenetic features of *Alu* elements, including their expression leading to *Alu* RNA, is their recently recognized nature of *cis*-regulatory elements serving as a repertoire for the *de novo* birth of enhancers (7,10). Such enhancer-like properties extend to different types of SINEs in different species, suggesting a relevant role of SINEs in the evolution of complex regulatory networks (98,99). Results in our study both confirm and expand the notion of *Alus* as enhancer-like elements. In mock-infected and e1a-expressing IMR90 cells, ep*Alus* differed for two key histone modifications, H3K4me1 and H3K27ac, whose

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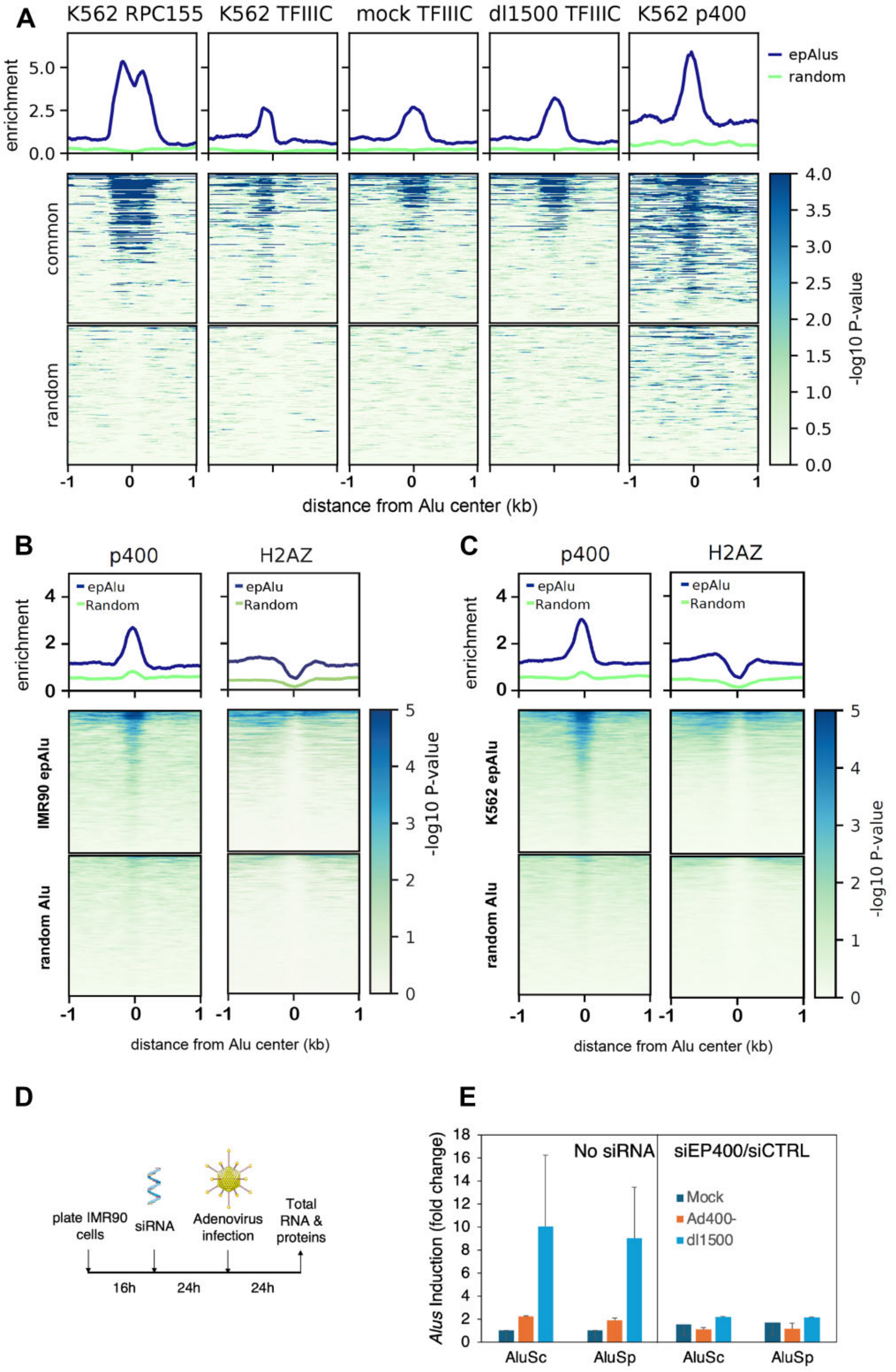

Figure 6. Enrichment of EP400 and H2A.Z at ep*Alu*s and effects of EP400 depletion. (**A**) ChIP-seq enrichment profiles of Pol III (RPC155 subunit), TFIIIC and EP400 (p400) at the 285 *Alu* elements that are expression-positive in both IMR90 (this study) and K562 cells (76,78). Plotheatmap of ChIP-seq data. From left to right: Pol III enrichment in K562 cells, TFIIIC enrichment in K562 cells, TFIIIC enrichment in mock-infected and *dl*1500-infected IMR90 cells and EP400 enrichment in K562 cells. Ranking is according to enrichment of Pol III in K562 cells reported as -log$_{10}$ of the Poisson *P*-value. (**B**) Plotheatmap of ChIP-seq enrichment of EP400 (left) and the H2A.Z histone variant (right) in K562 cells (76,78) across either the 1805 IMR90 ep*Alu*s or random *Alu*s. Ranking is according to enrichment of EP400 in K562 cells reported as -log$_{10}$ of the Poisson *P*-value. (**C**) Plotheatmap of ChIP-seq enrichment of EP400 (left) and the H2A.Z histone variant (right) in K562 cells across either the 3764 *Alu*s detected as expressed in K562 cells or random *Alu*s. Ranking is according to enrichment of p400 in K562 cells reported as -log$_{10}$ of the Poisson *P*-value. (**D**) Schematic representation of the protocol of siRNA-mediated EP400 knock down (KD) followed adenoviral infection (time of each incubation is reported). (**E**) RT-qPCR for measuring expression of two ep*Alu* loci (the same as in Figure 5B) comparing mock-, e1a_p400-b— and *dl*1500-infection in conditions of absence of silencing RNA (non-siRNA) or presence of siRNA against p400 (siEP400) compared to a scramble set of siRNA control (siCTRL). Standard error bars are indicated, as a result of two biological replicates.

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concomitant presence is an epigenetic hallmark of active enhancers. Specifically, we observed a general e1a-dependent increase of H3K4me1 and a general depletion of the H3K27ac marker. This epigenetic signature at ep*Alu*s in the presence of e1a roughly resembles the previously reported enhancer-like *Alu* epigenetic profile reminiscent of poised enhancers, marked by H3K4me1, but lacking H3K27ac (10). The association of p300 upstream of ep*Alu*s is also consistent with an enhancer-like state of these elements. At these sites, however, the acetyltransferase activity of p300 towards H3K27 appears to be inhibited by e1a, as it occurs at many enhancers and other genomic locations as part of the epigenome reprogramming effects of e1a (41). The ability of e1a to alter some *Alu*s towards the epigenetic state of poised enhancers, corresponding to a cellular state preceding differentiation (100), might contribute to e1a's ability to promote cell dedifferentiation (73). On this regard, our finding that the YAP/TAZ coactivators associate to ep*Alu*s in unperturbed IMR90 cells (most likely through TEAD TFs recognizing their cognate DNA motif upstream of ep*Alu*s) appears as particularly relevant. As recently shown, e1a causes YAP/TAZ cytoplasmic sequestration, with consequent genome-wide loss of YAP/TAZ and H3K27ac at enhancers involved in cell differentiation (73). Even though we have not addressed the e1a-dependent YAP/TAZ dynamics at ep*Alu*s, it appears reasonable to hypothesize that e1a-dependent *Alu* derepression contributes, through unexplored mechanisms, to enhancer manipulation by e1a. Possibly related to these mechanisms are the previously reported interaction of YAP/TAZ with EP400 and the so far unreported enrichment at ep*Alus* of BRD4, which is known to mediate YAP/TAZ-dependent transcriptional regulation in cancer cells (74).

Another related issue that deserves proper investigation is the role of two other families of enhancer-associated transcription factors, AP-1 and C/EBP. We found an overrepresentation of their cognate sites upstream of expression-positive *Alu*s, as well as an enrichment of members of the two TF families at ep*Alu*s based on ChIP-seq data analysis, an observation also reported by previous studies (5,7). AP-1 and C/EBP TFs might play a role in *Alu* transcription and/or *Alu* enhancer-like function through recruitment of coactivators like p300/CBP (101,102). However, the interplay between the presence of these factors at ep*Alu*s and their e1a-dependent upregulation needs to be clarified, as e1a was previously shown to counteract Fos-dependent transcriptional activation by competing for p300/CBP binding (103). Of note, the concomitant presence of AP-1 and YAP/TAZ/TEAD at growth-controlling enhancers was previously associated to oncogenesis (104), thus reinforcing the idea that e1a-triggered *Alu* derepression participates in key cell-controlling enhancer functions. The identity of *Alu*-associated TF family members is another issue awaiting further clarification. The different isoforms of C/EBP (α, β, γ, δ, ε, ζ) have binding site specificities that are almost identical (with the exception of C/EBP$_\zeta$) (105). Therefore, ChIP studies can tell more reliably than DNA sequence motif analysis which isoforms are more likely to be involved than others. Remarkably, C/EBP$_\beta$ was previously reported to be significantly enriched at ep*Alu*s in HeLa, HepG2 and K562 cells based on analysis of ENCODE ChIP-seq data (5). The same association, again based on ENCODE ChIP-seq data, was observed in this study in the case of IMR90 cells. Moreover, C/EBP$_\beta$ (*alias* CEBPB) has recently been shown to mediate the Pol III-dependent transcription of a microRNA transcription unit (miR-138) in human glioblastoma cell lines, and the same study provided evidence for a more general involvement of C/EBP$_\beta$ in the recruitment of Pol III transcription complexes to their target genes (106). Notably, all the above mentioned ep*Alu*-associated TFs were found to associate with target sites located upstream of the *Alu* body, suggesting a co-evolution of ep*Alu*s with these TF binding sites which may be relevant for *Alu* exaptation as regulatory elements, as well as for *Alu* transcription. In fact, the internal pol III elements (A and B boxes) are likely to synergize with the upstream flanking region for Alu transcription (5). The mostly random insertion of *Alu* elements into the genome creates a likelihood that the majority will land in regions that do not support transcription even under epigenetically open chromatin, due to the lack of appropriate upstream sequences. This could also explain why the relative number of ep*Alu* loci is so small.

Viewing ep*Alu*s as enhancers or proto-enhancers suggests possible implications for their expression and their virus-dependent upregulation. A key to understanding these processes may in fact be provided by the tendency of enhancers to act as templates for noncoding enhancer RNA (eRNA) synthesis in a manner linked to their activity (107). Ep*Alu*-encoded RNA may possibly be considered as a special case of eRNA, with the potential to influence transcription of genes placed under the control of the *Alu* enhancer, as shown for the regulation of *FOS* gene transcription by a SINE-encoded eRNA in mouse cortical neurons (98). Moreover, a recent work has revealed that ∼38% of the enhancer–promoter RNA interaction sites are overlapped with *Alu* sequences (108). It should be added, however, that *Alu*-associated TFIIIC has the potential to participate in organizing the landscape of chromatin loops, and thus in controlling gene expression at distance, just by virtue of its protein-protein interactions with transcription factors and/or architectural proteins such as ADNP and CTCF (15), even in the absence of RNA production. How frequently and to what extent *Alu* transcripts, or even the mere act of their transcription, participate in the enhancer-like activity of *Alu*s still awaits further investigation (see below).

Another, more general issue that has still to be satisfactorily understood is the impact of ep*Alu* derepression on the processes leading to cell transformation. In principle, *Alu* RNA accumulation might contribute to sustained cell proliferation via remodulation of the mRNA transcriptome which may occur both transcriptionally and post-transcriptionally (109,110). However, the actual amount of Alu transcripts elicited by e1a is probably low compared to the one obtained by artificial Alu RNA overexpression, and the duration and stability of e1a-dependent Alu RNA increase has not been evaluated. It is therefore somewhat difficult to attribute to increased Alu RNA a causative role in e1a-dependent cell transformation. Alternatively, the transcripts resulting from ep*Alu* derepression might be considered to some extent as by-products of an epigenetic transition whose contribution to cell transformation is not due to the RNA products themselves but possibly to ep*Alu*-triggered genome architectural rewiring (15).

Another property of e1a with the potential to contribute to cellular transformation is its previously reported ability to increase the activity of both TFIIIC and TFIIIB, at least in part by overcoming the repressive effect of Rb (35,37,111). Derepressed Pol III-dependent transcription of genes coding for RNAs required for protein synthesis and trafficking, such as tRNAs, 5S rRNA and 7SL RNA, would in turn contribute to

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cell transformation (112). Although our study did not address systematically the expression of canonical Pol III-transcribed genes, whose study at single-locus resolution is especially challenging for tRNA genes (113), expression analysis of a few of them showed the lack of an e1a-dependent upregulation comparable to the one of ep*Alu*s. At the same time, an e1a-dependent increase of Bdp1 (but not TFIIIC) association was generally observed for tRNA gene loci. According to a commonly accepted model, mainly based on *in vitro* studies, Rb sequesters a TFIIIB component without associating itself to DNA. In doing so, it impairs the TFIIIC-dependent recruitment of TFIIIB at promoters and subsequent transcription by Pol III. By interacting with Rb, e1a would release TFIIIB from repression (112). According to more recent analyses of ChIP-seq data, however, Rb stably associates to a relevant percentage of tRNA gene loci in IMR90 cells (114). This leaves open the possibility that Rb might participate in tRNA gene transcriptional regulation by influencing steps subsequent to TFIIIB recruitment, as it occurs in the case of Pol III-transcribed genes with a Type 3 promoter (e.g. the U6 snRNA gene) (115).

The most evident e1a-dependent change in TFIIIC enrichment occurred at a subset of TFIIIC genomic targets, strongly enriched in *Alu* elements, where marked depletion of TFIIIC occurred upon *dl*1500 infection. This *Alu* subset overlaps only marginally to the one of ep*Alu*s, thus implying that the modulation of TFIIIC association to these elements does not entail changes in *Alu* expression. Rather, TFIIIC depletion at these *Alu* loci might result in epigenetic changes possibly contributing to e1a interference with the cellular differentiation state, as suggested by the involvement of neighbouring genes in embryonic development.

In conclusion, molecular characterization of *Alu* upregulation in response to adenovirus infection led us to identify e1a as a key player in this phenomenon through its epigenome reprogramming properties. We uncovered an unexpectedly complex epigenetic landscape at ep*Alu* elements. In some respects, our findings confirm the idea that ep*Alu*s represent a tiny subset of the whole *Alu* complement that have been -or are being- exapted to enhancer function (7,10). The observation that ep*Alu*s are enriched in older *Alu*S element is also suggestive of evolutionary selection. We speculate that, among the >1 200 000 *Alu* elements in the human genome, such evolutionarily exapted *Alu*s are likely to constitute a small set of non-silenced elements, sharing some basic epigenetic features that endow them with a certain transcriptional potential. Different subsets of such *Alu*s would then be activated in different cell types due to further epigenetic changes accompanying cell differentiation. Whether and how *Alu* transcription and its modulation by different cues mechanistically contribute to enhancer function remains to be established. The fact that some derepressed *Alu*s display features of YAP/TAZ enhancers, that are known to undergo e1a-dependent inactivation, supports an inverse relationship between Pol III transcription activation and enhancer activity. This would be in contrast with a previously proposed role of enhancer SINE Pol III transcription in activating Pol II-dependent transcription of the target gene (98). Other studies, however, provided evidence for a complex interplay between Pol III and Pol II transcription at regulatory SINEs (116,117), leaving room for the possibility that at enhancer *Alu*s Pol III transcription counteracts Pol II-dependent eRNA synthesis and thus enhancer activity. In other respects, our study of the ability of e1a to turn on the *Alu* epigenetic switch revealed a possible unexpected role of chromatin remodelling in this process, with EP400 and possibly other chromatin remodelers performing a key activating function during induction of expression-prone *Alu*s. As exemplified by the subtle control of promoter-bound nucleosome positioning by ATP-dependent remodeling complexes at rRNA genes (118), chromatin remodelers offer the possibility to rapidly switch between chromatin states of different transcriptional accessibility without radically changing the overall nucleosomal architecture. They are thus likely to be key players at exapted *Alu* loci where facilitation of accessibility changes may favour the evolutionary exploration of novel regulatory possibilities.

Data availability

Data of RNA-seq and ChIP-seq generated in this study are available at GEO under accession number GSE208717. Publicly available data were retrieved from the following sources: GSE32340 for H3K4me1 ChIP-seq (*dl*1500-infected IMR90 cells) and H3K9ac ChIP-seq (40); GSE43070 for H3K4me1 ChIP-seq (uninfected IMR90 cells) (40); GSE59693 for ChIP-seq of H3K27ac, EP300, Pol II and RB (mock- and *dl*1500-infected IMR90 cells) (41); GSM2828526 for EP400 ChIP-seq (K562 cells); GSM935372 for Pol III (RPC155 subunit) ChIP-seq (K562 cells); GSM935343 for TFIIIC (GTF3C2 subunit) ChIP-seq (K562 cells); GSM733786 for H2A.Z ChIP-seq (K562 cells); GSM3289968 for ATAC-seq (IMR90 cells); GSM935519 for CEBPB ChIP-seq (IMR90 cells); GSM818008 for H2A.Z ChIP-seq (IMR90 cells); GSM2825448 for FOS ChIP-seq (IMR90 cells); GSM1696207 for YAP1 ChIP-seq (IMR90 cells); GSM1915116 for BRD4 ChIP-seq (IMR90 cells).

Supplementary data

Supplementary Data are available at NAR Online.

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Conflict of interest statement

None declared.

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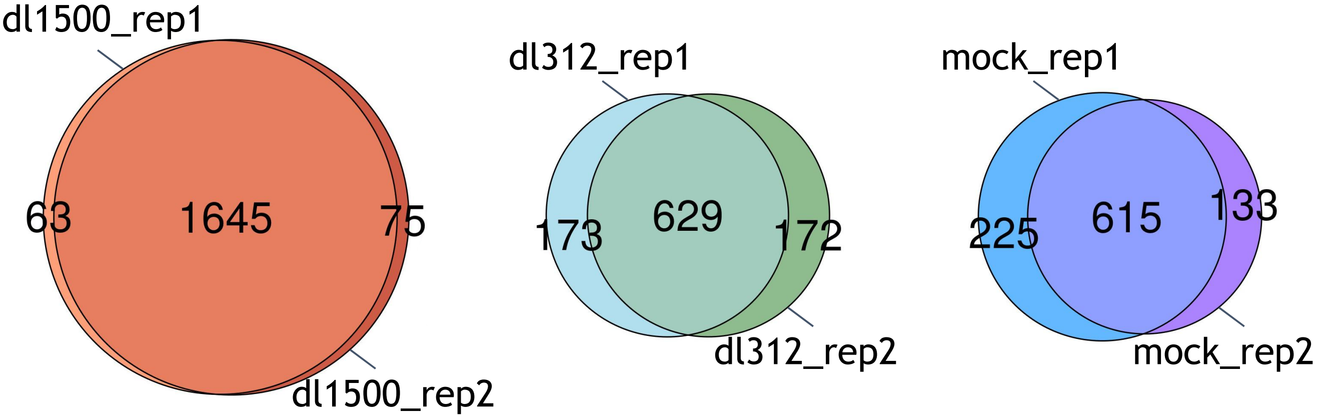
Supplementary Table S1. List of primers used for *Alu* and Pol III gene expression analysis in RT-qPCR

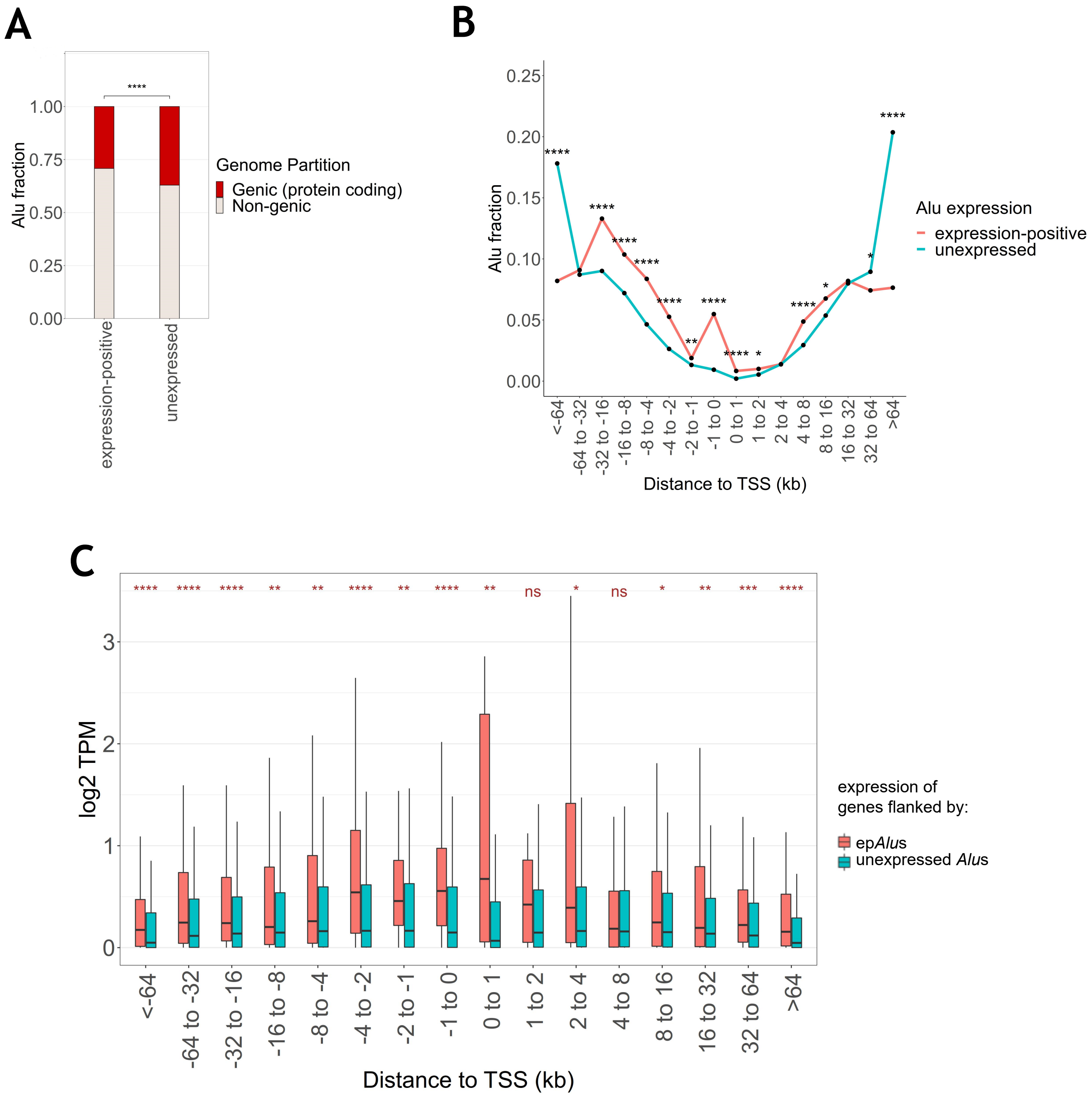
Primer	Sequence (5’-3’)
*Alu*Sp_qRT_fw	TCACTCTGTCGCTTCCCAGTTG
*Alu*Sp_qRT_rev	TTAAAACTCTGCTCTGTTCACGCAG
*Alu*Sc_qRT_fw	GCTAGAGTCAACCTCACCTGC
*Alu*Sc_qRT_rev	TTAAGCCGCCAGAACGAGC
U1_fw	AGGGCGAGGCTTATCCATTG
U1_rev	GCAGTCGAGTTTCCCACATTTG
7SL_fw	CACCAGGTTGCCTAAGGAGG
7SL_rev	GCTGGAGTGCAGTGGCTATTC
U6_fw	CGCTTCGGCAGCACATATAC
U6_rev	AAAATATGGAACGCTTCACGA
EP_400_fw	*GTGTTCGAGCGGTCACTTCT*
Ep_400_rev	*CTGAACTCCTGTGGCTTGGG*

Suppl. Figure S1



Supplementary Figure S1. Venn diagrams showing the number of expressed *Alu* elements in the two replicates of (from left to right) dl1500-, dl312- and mock-infected IMR90 cells.

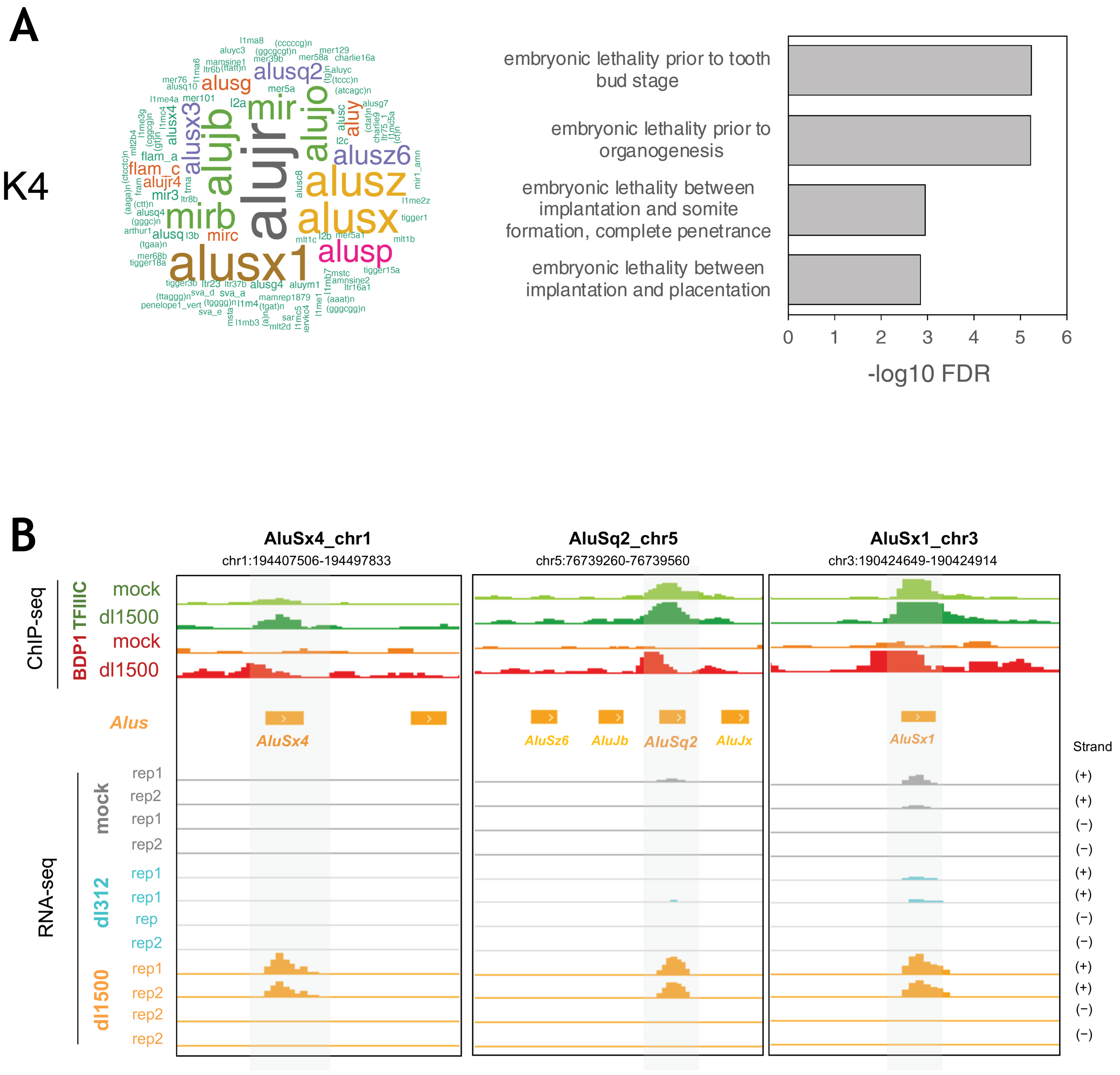
Suppl. Figure S2



Supplementary Figure S2.

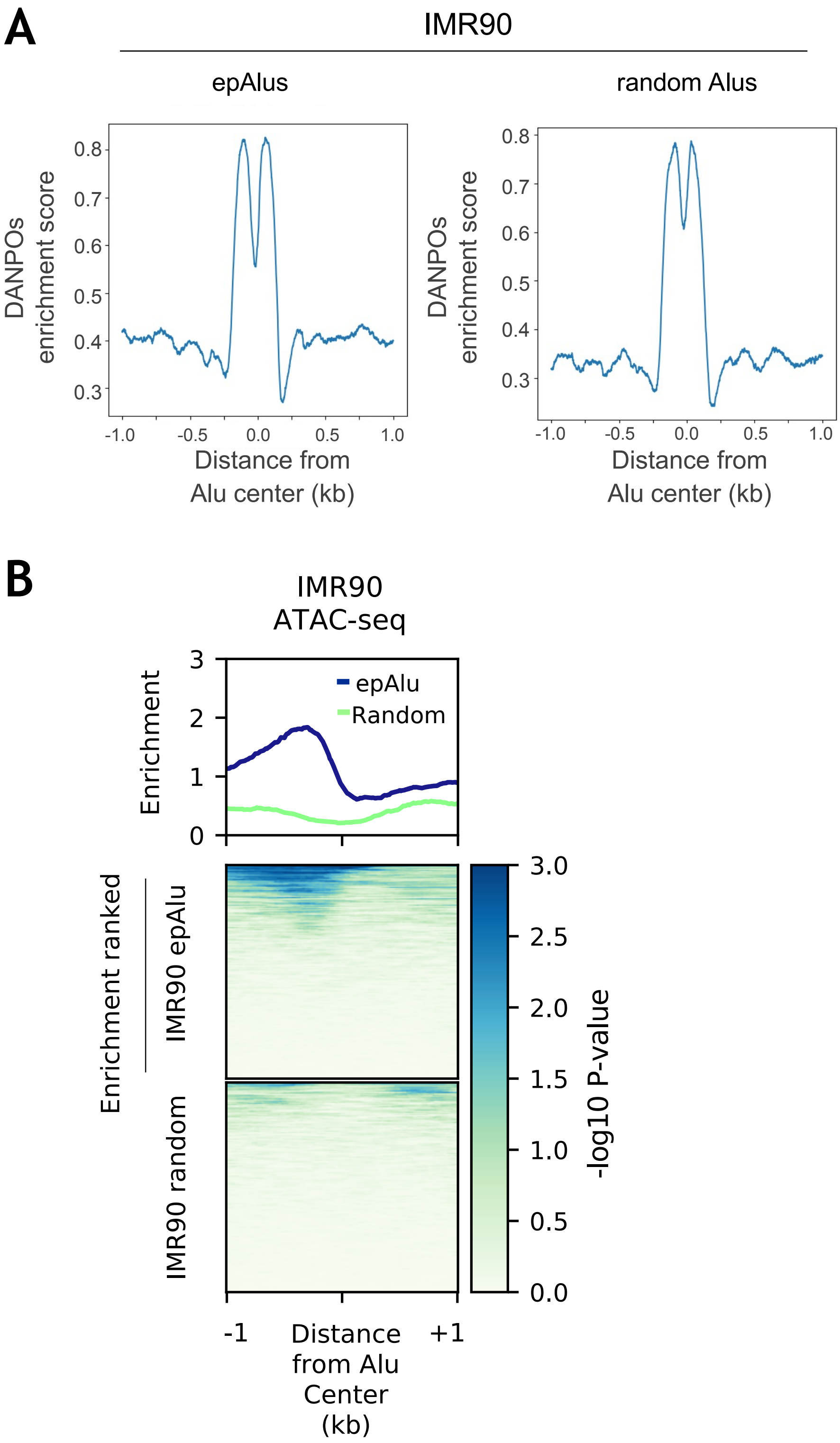
Proximity relationships of expressed *Alu*s with protein-coding genes. (**A**) Stacked plots representing the fraction of *Alu*s whose genomic location is internal (red, Genic) or external (grey, Non-genic) to protein-coding genes. Reported are the values for the 1805 ep*Alu*s (left vertical bar) and for the complementary set of 800626 unexpressed *Alu*s (right vertical bar). P value: **** ≤0.0001 as inferred by a two-tailed Fisher's exact test. (**B**) The graph reports, for each range of distance from protein coding genes (reported on the *x* axis), the fraction of the set of all expression-positive *Alu*s (orange line) and the fraction of the set of all unexpressed *Alu*s (blue line) located within the distance range. P-values were inferred by a two-tailed Fisher´s exact test. * < 0.05, ** < 0.01, *** < 0.001, **** < 0.0001. (**C**) Box plot of expression levels of protein-coding genes located at the distance intervals reported below from either ep*Alu*s (orange) or unexpressed *Alu*s (blue). Gene expression was quantified as the average TPM among all the infections (dl1500, dl312 and mock). Wilcoxon rank-sum test p-values were calculated for the comparison between the genes flanking expressed and unexpressed *Alu*s at each distance interval: * < 0.05, ** < 0.01, *** < 0.001, **** < 0.0001, ns = not significant.

Suppl. Figure S3



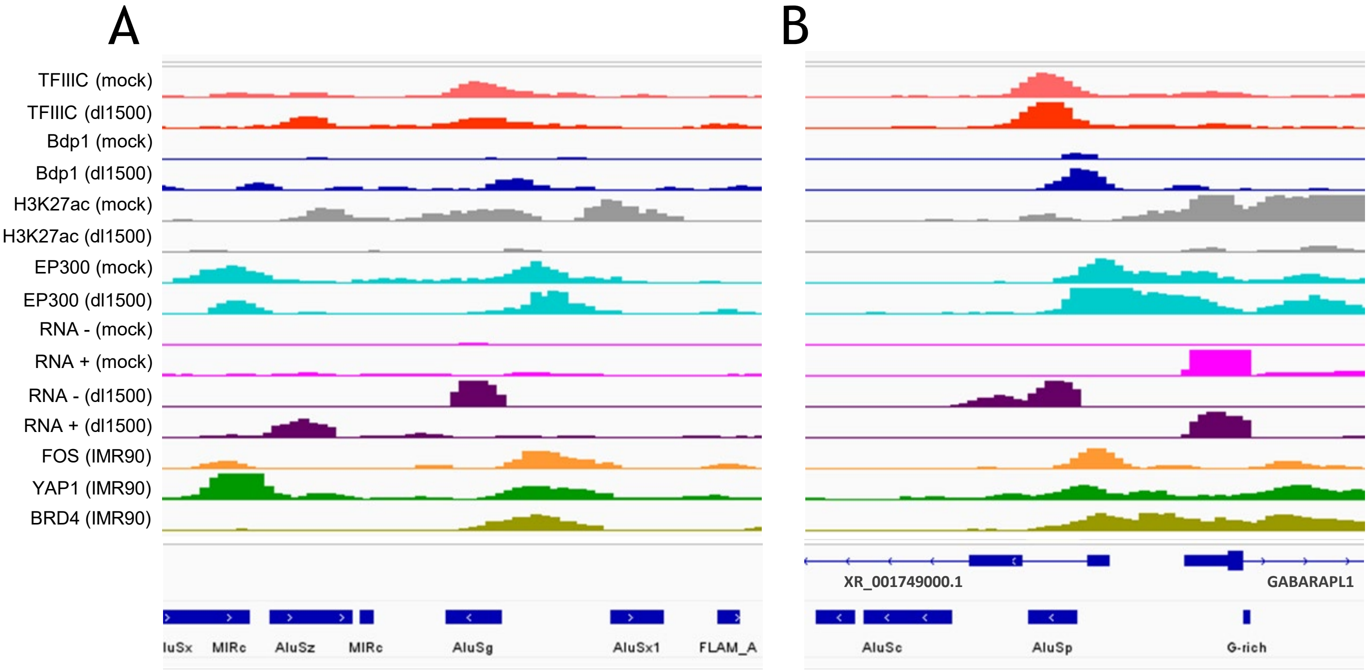
Supplementay Figure S3. **(A)** *Left*, word cloud analysis of repetitive elements associated with regions occupied by TFIIIC and Bdp1 of cluster 4 (K4) as reported in Figure 2A; font size reflects enrichment for the indicated elements. *Right*, bar plots of GREAT gene ontology (GO) enrichment for TFIIIC-bound regions of cluster 4 as reported in Figure 2A; GO terms (Human Phenotypes) were ranked from the lowest to the highest p-value. **(B)** Genome browser views of TFIIIC and Bdp1 ChIP-seq and RNA-seq data of three highly expressed Alu elements. Yellow arrows represent the position and orientation of repetitive elements as evidenced by the RepeatMasker track. The chromosomal coordinates of each annotated Alu are shown above each view. Bigwig tracks are normalized for the library size.

Suppl. Figure S4



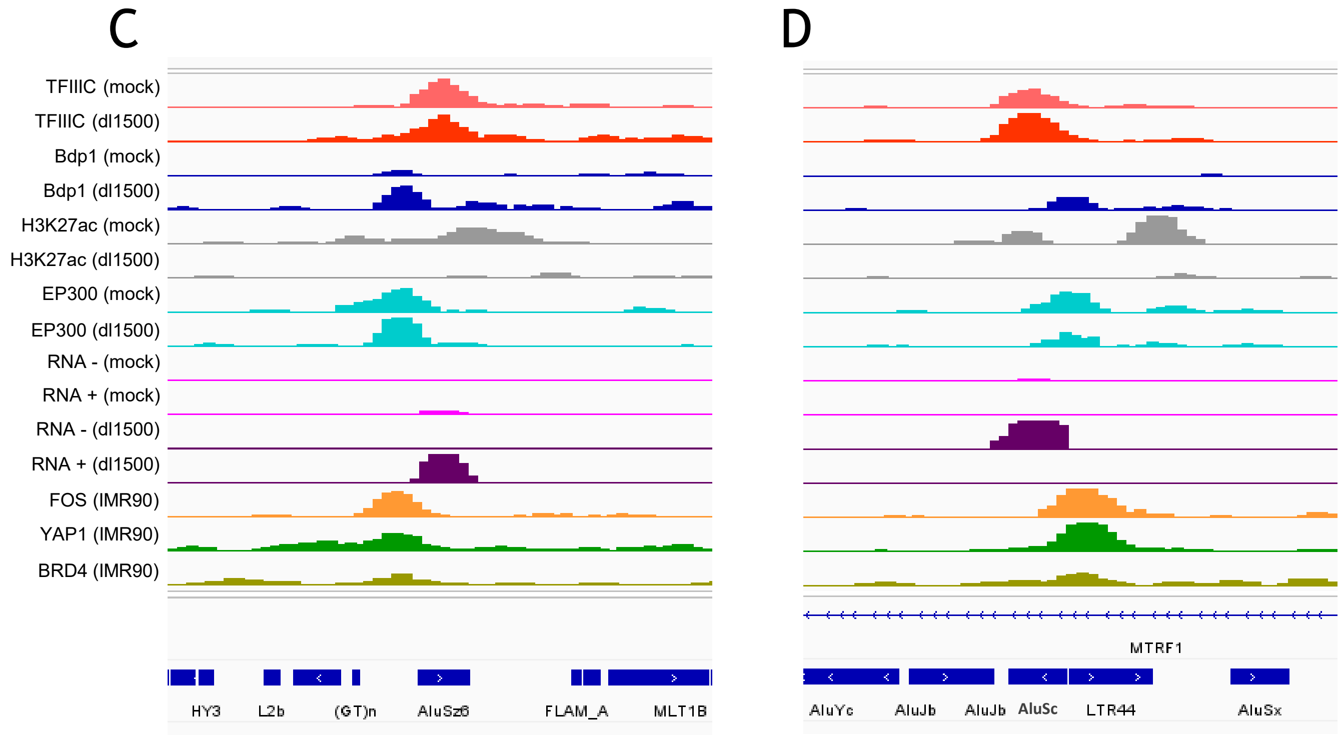
Supplementary Figure S4. (**A**) Nucleosome density as mapped by MNase digestion across epAlusand random *Alu*s in IMR90 cells using the DANPOS score. The plot has been produced using NucMap (Zhao et al., 2019, *Nucleic Acids Res* 47:D163-D169). Note the presence of two nucleosomes. (**B**) Plotheatmap of ATAC-seq signal around ep*Alu*s (top) and random *Alu*s (bottom) in IMR90 cells. Ranking is according to enrichment of ATAC-seq reported as -log10 of the Poisson p-value.

Suppl. Figure S5



AluSg
(chr16:71816314-71816632)

AluSp
(chr12:10211956-10212242)

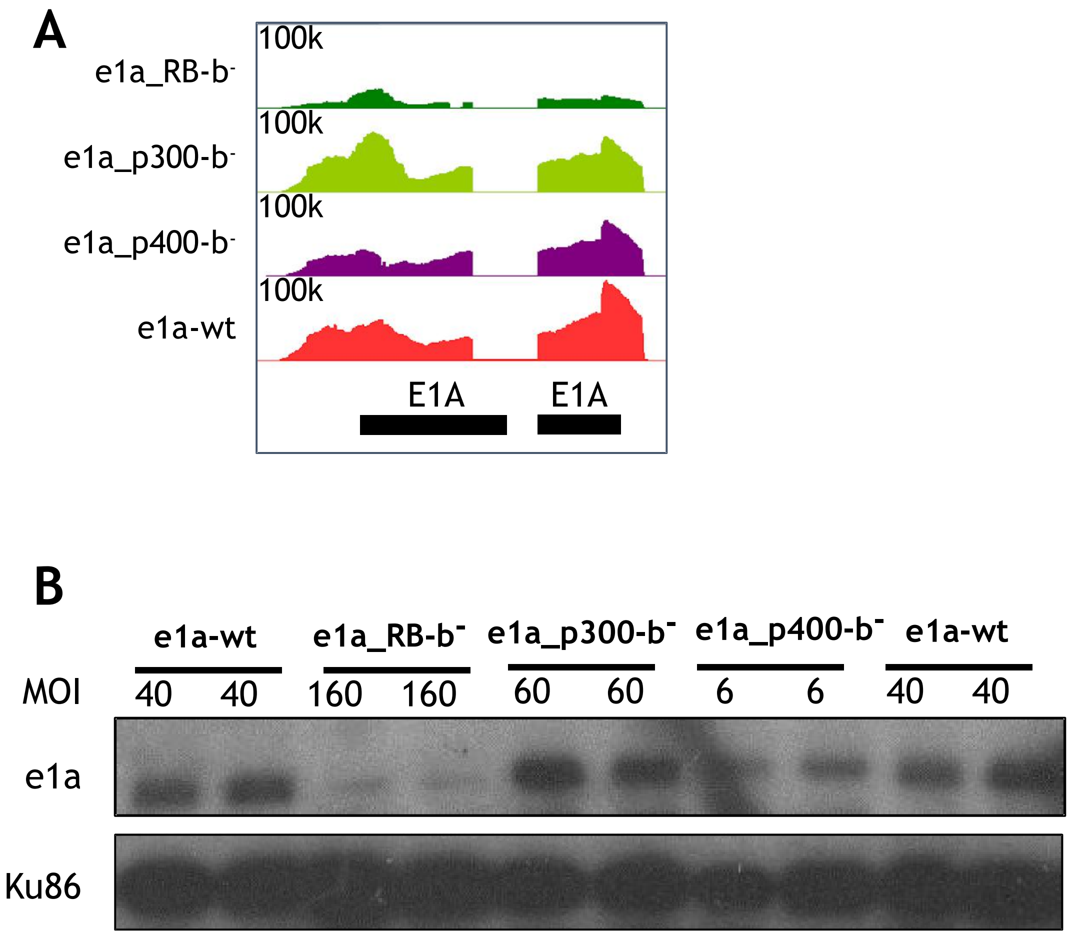


AluSz6
(chr4:185112386-185112669)

AluSc
(chr13:41284641-41284698)

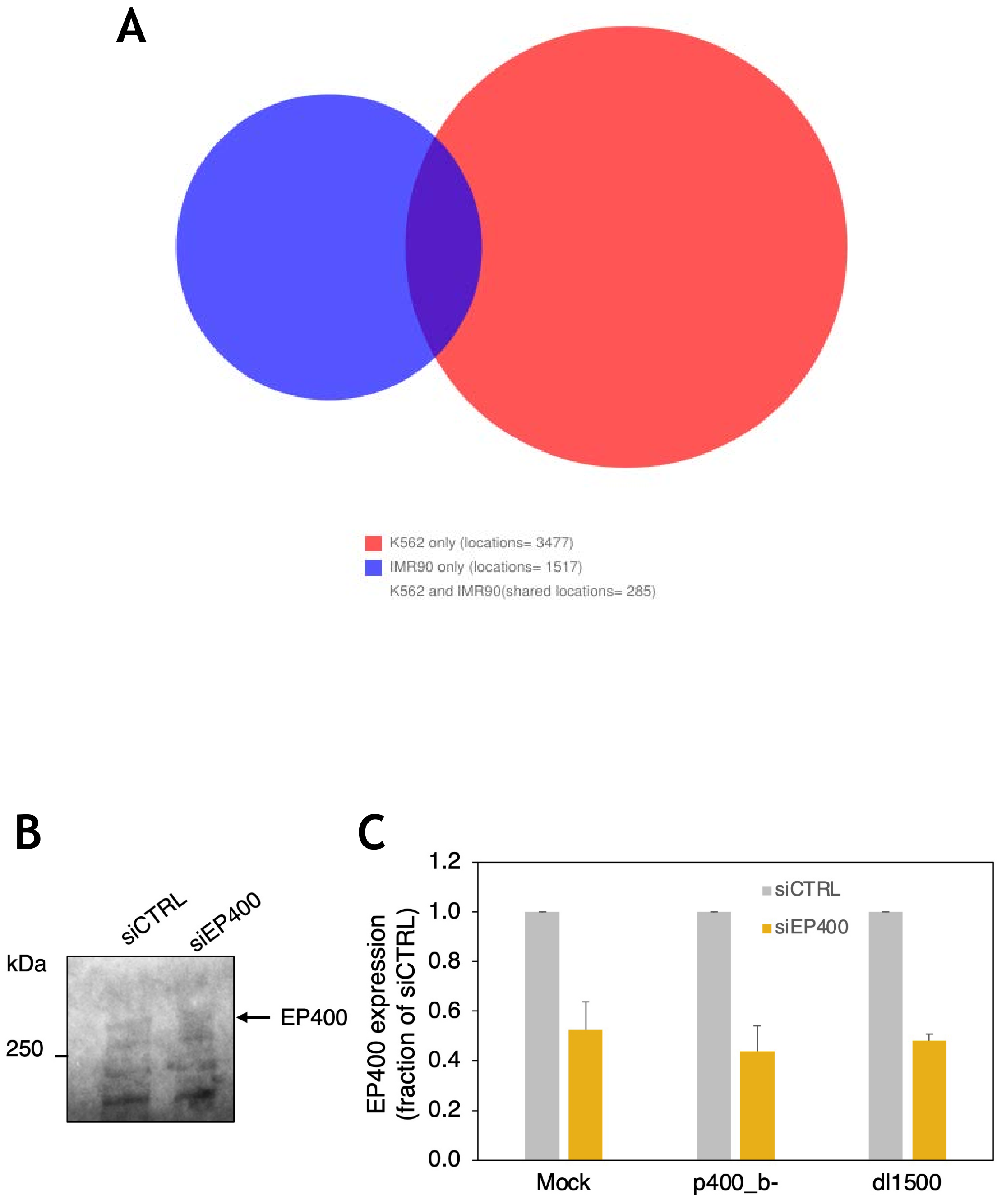
Supplementary Figure S5. **(A-D)** Genome browser views of TFIIIC, Bdp1, H3K27ac and EP300 ChIP-seq data and representative RNA-seq data of four differentially expressed *Alu* elements obtained in this study either in the absence (mock) or in the presence (*dl*1500) of e1a, along with the views of publicly available ChIP-seq data for FOS, YAP1 and BRD4 in IMR90 cells. The chromosomal coordinates of each annotated *Alu* are shown under each view, in correspondence of the position of the e1a-induced *Alu*.

Suppl. Figure S6



Supplementary Figure S6. (**A**) Expression profiles, shown as Integrated Genome Browser views, of the E1A gene in IMR90 infected with dl1500 (e1a-wt) or its interaction mutants. (**B**) Western blot showing protein levels of wt e1a and e1a interaction mutants obtained from virus infections of IMR90 cells at the MOIs used for the experiment in Figure 6. Ku86 was used as a loading control.

Suppl. Figure S7



Supplementary Figure S7. (A) Venn diagram of overlapping peaks for epAlus from K562 and IMR90 cells. B) Westerblot of EP400 KD in IMR90 fibroblasts treated with scramble siCTRL or siRNA smart pool against EP400. Arrow indicates the band corresponding to EP400. C) qRT-PCR measuring the expression of EP400 transcript upon treatment with siRNA smart pool against EP400. Levels of EP400 in IMR90 fibroblasts treated with scramble siCTRL are set to one.

chrom	start	end	name	strand	dl1500_rep1	dl1500_rep2
chr1	1608440	1608756	AluJo_dup72	+	6.388521053	4.721944081
chr1	6408239	6408537	AluSp_dup126	+	6.388521053	15.34631826
chr1	8830207	8830514	AluSq2_dup242	+	5.323767544	0
chr1	8885403	8885691	AluSx1_dup479	+	9.582781579	21.24874836
chr1	9164313	9164617	AluSz6_dup164	+	6.388521053	10.62437418
chr1	9208575	9208876	AluSp_dup198	+	7.453274561	12.98534622
chr1	9615960	9616251	AluJb_dup655	-	7.453274561	16.52680428
chr1	10010113	10010415	AluSx_dup704	-	25.55408421	14.16583224
chr1	10402528	10402822	AluY_dup630	-	6.388521053	4.721944081
chr1	10421813	10422108	AluJo_dup469	+	6.388521053	0
chr1	11050852	11051066	AluSx1_dup743	-	5.323767544	2.36097204
chr1	12539619	12539921	AluJr_dup505	-	15.97130263	16.52680428
chr1	15433148	15433444	AluSz_dup877	+	53.23767544	54.30235693
chr1	17014404	17014737	AluJb_dup1362	-	7.453274561	4.721944081
chr1	20677571	20677870	AluSx_dup1586	+	10.64753509	4.721944081
chr1	21275312	21275610	AluSq2_dup720	+	8.51802807	2.36097204
chr1	23377761	23378070	AluSx3_dup420	+	38.33112632	48.39992683
chr1	24629239	24629547	AluSz6_dup680	+	7.453274561	5.902430101
chr1	24718676	24718975	AluSz_dup1586	-	162.9072868	131.0339482
chr1	25709742	25710044	AluSq2_dup912	-	6.388521053	7.082916121
chr1	26671278	26671552	AluSx1_dup1938	-	9.582781579	8.263402142
chr1	27013704	27014016	AluSx3_dup507	-	8.51802807	8.263402142
chr1	27863875	27864176	AluSq2_dup1059	-	5.323767544	2.36097204
chr1	27874966	27875278	AluSx1_dup2083	-	24.4893307	31.87312255
chr1	28235333	28235639	AluSx_dup2330	-	43.65489386	41.31701071
chr1	28346052	28346291	AluSx1_dup2137	-	247.022814	213.6679697
chr1	28829356	28829668	AluSx1_dup2209	-	7.453274561	2.36097204
chr1	29140904	29141208	AluSx_dup2472	-	12.77704211	15.34631826
chr1	31091222	31091501	AluSg_dup741	+	5.323767544	1.18048602
chr1	31955658	31955939	AluSp_dup1119	+	8.51802807	4.721944081
chr1	32218140	32218444	AluSq_dup433	+	6.388521053	1.18048602
chr1	32288543	32288726	AluSx3_dup666	+	6.388521053	5.902430101
chr1	35220806	35221099	AluSz_dup2297	-	7.453274561	4.721944081
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chr1	36297444	36297742	AluSx3_dup763	-	7.453274561	5.902430101
chr1	36377254	36377557	AluSg_dup882	+	14.90654912	14.16583224
chr1	37989010	37989321	AluSg_dup907	+	31.94260526	35.41458061
chr1	41753378	41753670	AluSq2_dup1615	+	7.453274561	3.541458061
chr1	44058281	44058588	AluSg_dup1026	-	10.64753509	15.34631826
chr1	44745464	44745769	AluSp_dup1524	-	5.323767544	1.18048602
chr1	45830181	45830472	AluSg_dup1083	-	8.51802807	5.902430101
chr1	52058604	52058899	AluSp_dup1716	-	8.51802807	12.98534622
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chr1	53147793	53148097	AluSz_dup3301	-	9.582781579	4.721944081
chr1	53789533	53789817	AluSq2_dup1972	+	5.323767544	4.721944081
chr1	54771886	54772196	AluY_dup3116	-	216.1449623	238.4581761
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chr1	66467875	66468173	AluSx1_dup4141	+	9.582781579	15.34631826
chr1	78061706	78061916	AluSx_dup4678	-	7.453274561	5.902430101
chr1	92805000	92805127	AluJb_dup6063	+	29.81309825	30.69263653

chr1	92974343	92974627	AluSg_dup1573	-	9.582781579	12.98534622
chr1	93254941	93255250	AluSg4_dup301	-	31.94260526	44.85846877
chr1	94673311	94673602	AluSx_dup5128	+	23.42457719	27.15117847
chr1	94949274	94949558	AluSp_dup2336	-	6.388521053	9.443888162
chr1	109049653	109049906	AluJb_dup6605	+	15.97130263	10.62437418
chr1	109667774	109667870	AluJo_dup3778	-	8.51802807	7.082916121
chr1	109871861	109872169	AluSz_dup4766	-	6.388521053	2.36097204
chr1	113117487	113117779	AluSg_dup1778	-	5.323767544	0
chr1	120180629	120180930	AluSx1_dup5395	+	22.35982368	28.33166449
chr1	144071262	144071573	AluSx1_dup5475	+	15.97130263	8.263402142
chr1	145968570	145968870	AluSx3_dup1679	-	14.90654912	11.8048602
chr1	146035979	146036276	AluSq_dup969	-	137.3532026	165.2680428
chr1	146038383	146038685	AluSg_dup1912	-	38.33112632	38.95603867
chr1	149893497	149893798	AluSx1_dup5689	-	8.51802807	1.18048602
chr1	150876980	150877276	AluSq_dup1017	+	144.8064772	169.9899869
chr1	153502830	153503135	AluSg_dup2051	+	8.51802807	8.263402142
chr1	153671904	153672193	AluSx1_dup5958	+	34.07211228	29.51215051
chr1	153684380	153684689	AluSc_dup1768	-	11.7122886	14.16583224
chr1	154901291	154901597	AluSx3_dup1852	-	22.35982368	44.85846877
chr1	155158226	155158529	AluY_dup5687	+	6.388521053	10.62437418
chr1	155274096	155274402	AluSg_dup2126	+	8.51802807	9.443888162
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chr1	155509515	155509801	AluSx_dup6646	+	7.453274561	1.18048602
chr1	155742024	155742309	AluSx_dup6682	-	6.388521053	7.082916121
chr1	155857447	155857739	AluSx_dup6699	+	5.323767544	7.082916121
chr1	156255258	156255569	AluSq2_dup3456	+	8.51802807	9.443888162
chr1	156263987	156264295	AluSg_dup2172	+	9.582781579	22.42923438
chr1	156457865	156458168	AluSg_dup2175	+	29.81309825	20.06826234
chr1	156686838	156687151	AluSz_dup5843	-	6.388521053	3.541458061
chr1	161033375	161033655	AluSg4_dup437	+	5.323767544	0
chr1	161729838	161730139	AluSx1_dup6480	-	13.84179561	16.52680428
chr1	171393227	171393538	AluSz_dup6266	-	21.29507018	25.97069244
chr1	173858582	173858882	AluSz_dup6330	+	9.582781579	10.62437418
chr1	174035339	174035625	AluSx1_dup6817	-	11.7122886	11.8048602
chr1	181086660	181086967	AluSx1_dup7082	-	75.59749912	80.27304938
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chr1	185016241	185016536	AluSx_dup7761	+	6.388521053	3.541458061
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chr1	200404471	200404769	AluSx3_dup2278	-	7.453274561	3.541458061
chr1	201972534	201972702	AluSz6_dup3414	-	36.2016193	55.48284295
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chr1	202077112	202077420	AluSc_dup2279	+	9.582781579	7.082916121
chr1	203460574	203460870	AluSx4_dup802	+	5.323767544	3.541458061
chr1	203780162	203780461	AluSq2_dup4253	+	15.97130263	25.97069244
chr1	203926743	203927058	AluSx_dup8292	+	9.582781579	10.62437418
chr1	204508217	204508526	AluSx3_dup2356	+	14.90654912	16.52680428
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chr1	225979121	225979424	AluSx_dup9092	+	10.64753509	7.082916121
chr1	226036298	226036587	AluSq_dup1454	-	6.388521053	11.8048602
chr1	226053060	226053371	AluSx_dup9103	+	7.453274561	2.36097204
chr1	226953020	226953327	AluSg_dup2980	-	5.323767544	1.18048602
chr1	231059052	231059336	AluSz_dup8213	-	21.29507018	14.16583224
chr1	234822811	234823103	AluSg_dup3064	+	6.388521053	9.443888162
chr1	241641978	241642176	AluJo_dup6709	+	8.51802807	5.902430101
chr1	244764250	244764556	AluSx_dup9980	-	10.64753509	3.541458061
chr1	244822738	244823046	AluSx1_dup9403	+	7.453274561	5.902430101
chr1	246769580	246769888	AluSx1_dup9512	+	44.71964737	55.48284295
chr10	5853575	5853688	AluYh3a3	-	6.388521053	10.62437418
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chr10	72697426	72697732	AluSx3_dup785	-	5.323767544	0
chr10	73587191	73587488	AluY_dup2580	+	6.388521053	12.98534622
chr10	73918214	73918528	AluSx1_dup3209	+	11.7122886	5.902430101
chr10	73966642	73966925	AluSx1_dup3219	+	14.90654912	14.16583224
chr10	74029117	74029412	AluY_dup2618	-	27.68359123	36.59506663
chr10	75190975	75191255	AluSz_dup3058	-	10.64753509	15.34631826
chr10	76251226	76251551	AluYb8_dup65	-	12.77704211	14.16583224
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chr10	91142295	91142606	AluSx_dup3795	+	44.71964737	54.30235693
chr10	91390383	91390684	AluSz_dup3461	-	9.582781579	7.082916121
chr10	97024987	97025311	AluSq_dup647	+	22.35982368	9.443888162
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chr10	98692486	98692792	AluY_dup3417	+	8.51802807	10.62437418
chr10	101106084	101106370	AluSq_dup675	+	37.26637281	35.41458061
chr10	102169695	102169992	AluYk3_dup47	+	155.4540123	173.531445
chr10	102855153	102855454	AluSg_dup1326	-	29.81309825	27.15117847
chr10	103151181	103151479	AluSp_dup1812	+	5.323767544	4.721944081
chr10	110307641	110307944	AluJb_dup5125	-	5.323767544	5.902430101
chr10	116212237	116212523	AluSq2_dup2562	+	7.453274561	12.98534622
chr10	119160226	119160538	AluSx3_dup1322	+	10.64753509	37.77555265
chr10	119190666	119190973	AluSz_dup4634	+	17.03605614	16.52680428
chr10	130033352	130033632	AluSg_dup1612	+	53.23767544	42.49749673
chr10	132474185	132474490	AluSx1_dup5442	+	23.42457719	28.33166449
chr11	785424	785723	AluSg_dup18	-	11.7122886	7.082916121
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chr11	3813401	3813683	AluJb_dup201	-	10.64753509	7.082916121
chr11	7190268	7190582	AluSx_dup275	+	9.582781579	3.541458061
chr11	8900143	8900449	AluY_dup378	+	6.388521053	1.18048602
chr11	9321855	9322154	AluSg_dup103	-	192.7203851	182.9753331
chr11	9360940	9361242	AluSg_dup108	-	6.388521053	5.902430101
chr11	9599189	9599478	AluSg_dup120	+	21.29507018	17.7072903
chr11	12647256	12647578	AluSz_dup401	-	9.582781579	7.082916121
chr11	14850825	14851122	AluY_dup605	-	8.51802807	12.98534622
chr11	46406898	46407233	AluSg_dup438	+	12.77704211	27.15117847
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chr11	47539370	47539550	AluSx_dup1492	+	6.388521053	7.082916121
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chr11	47932075	47932385	AluSg_dup505	+	69.20897807	69.64867519
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chr11	62427164	62427465	AluSx_dup1950	-	11.7122886	20.06826234
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chr11	64326109	64326385	AluSx_dup2130	+	13.84179561	22.42923438
chr11	64825783	64826088	AluSz_dup1895	+	7.453274561	15.34631826
chr11	65152560	65152842	AluSg_dup705	-	7.453274561	2.36097204
chr11	65221939	65222254	AluSx_dup2218	-	7.453274561	2.36097204
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chr11	66032649	66032941	AluSx1_dup2281	-	14.90654912	20.06826234
chr11	66399898	66400207	AluSg4_dup147	+	30.87785175	40.13652469
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chr11	66580597	66580856	AluSc8_dup464	-	12.77704211	17.7072903
chr11	66892565	66892867	AluSg4_dup148	+	11.7122886	11.8048602
chr11	66995104	66995397	AluSg_dup762	-	10.64753509	17.7072903
chr11	67011239	67011541	AluSq2_dup1271	-	7.453274561	7.082916121
chr11	67065373	67065660	AluSz6_dup986	-	9.582781579	15.34631826
chr11	68111129	68111429	AluSq2_dup1326	+	8.51802807	2.36097204
chr11	71783011	71783301	AluSx1_dup2745	-	6.388521053	11.8048602
chr11	77970548	77970759	AluJb_dup3506	+	9.582781579	1.18048602
chr11	83155781	83156073	AluSc_dup927	-	7.453274561	8.263402142
chr11	93893102	93893401	AluSz_dup3062	-	6.388521053	2.36097204
chr11	102242456	102242756	AluJb_dup4143	+	11.7122886	9.443888162
chr11	102278215	102278496	AluSz_dup3207	-	5.323767544	3.541458061

chr11	108434224	108434519	AluSz_dup3366	+	10.64753509	5.902430101
chr11	110326935	110327199	AluSx3_dup1039	-	9.582781579	4.721944081
chr11	111311201	111311481	AluSx_dup3802	-	7.453274561	2.36097204
chr11	119166172	119166467	AluSx1_dup4234	-	13.84179561	14.16583224
chr12	6286642	6286936	AluSx3_dup71	-	37.26637281	20.06826234
chr12	6557860	6558165	AluSz_dup218	+	5.323767544	5.902430101
chr12	6568651	6568942	AluSq_dup41	+	41.52538684	44.85846877
chr12	6969617	6969917	AluSx1_dup280	+	18.10080965	15.34631826
chr12	8655013	8655315	AluSx1_dup397	+	15.97130263	11.8048602
chr12	9782236	9782556	AluYh3_dup13	-	17.03605614	15.34631826
chr12	10211956	10212242	AluSp_dup293	-	68.14422456	66.10721713
chr12	12858353	12858645	AluSx4_dup61	-	8.51802807	7.082916121
chr12	19151864	19152165	AluY_dup894	-	8.51802807	14.16583224
chr12	49501608	49501917	AluSx_dup1740	-	12.77704211	8.263402142
chr12	49728805	49729110	AluSc5_dup112	-	6.388521053	10.62437418
chr12	50036735	50036985	AluSp_dup871	+	12.77704211	12.98534622
chr12	50364755	50365057	AluSq2_dup1005	+	10.64753509	15.34631826
chr12	51035014	51035333	AluSg_dup619	-	7.453274561	10.62437418
chr12	51336361	51336643	AluSx_dup1954	+	21.29507018	27.15117847
chr12	51875611	51875916	AluSg_dup654	+	12.77704211	30.69263653
chr12	52980658	52980928	AluSz_dup1791	-	19.16556316	18.88777632
chr12	53135822	53136125	AluSc5_dup123	+	6.388521053	5.902430101
chr12	53365726	53366032	AluSq2_dup1143	-	6.388521053	1.18048602
chr12	53386940	53387250	AluSx3_dup611	-	35.13686579	21.24874836
chr12	53691423	53691719	AluY_dup2157	+	8.51802807	5.902430101
chr12	54287614	54287879	AluSx1_dup2009	-	6.388521053	1.18048602
chr12	55904311	55904625	AluSx3_dup645	+	26.61883772	37.77555265
chr12	56045940	56046233	AluSx1_dup2090	-	6.388521053	5.902430101
chr12	56195600	56195889	AluSc_dup675	-	6.388521053	0
chr12	56196600	56196905	AluSp_dup1144	-	34.07211228	30.69263653
chr12	56696887	56697182	AluSq_dup345	-	9.582781579	16.52680428
chr12	57847422	57847721	AluSg7_dup195	+	7.453274561	10.62437418
chr12	64565294	64565430	AluSx_dup2603	+	5.323767544	3.541458061
chr12	68803187	68803480	AluSz_dup2426	-	13.84179561	9.443888162
chr12	68807301	68807602	AluSx1_dup2582	-	18.10080965	31.87312255
chr12	68864162	68864462	AluSx1_dup2595	+	5.323767544	0
chr12	76753408	76753681	AluSx4_dup282	-	91.56880175	103.8827698
chr12	79747855	79748175	AluSg7_dup236	-	36.2016193	17.7072903
chr12	87158054	87158360	AluSp_dup1558	+	159.7130263	149.9217246
chr12	92956674	92956976	AluSx1_dup3121	-	10.64753509	8.263402142
chr12	95608081	95608393	AluSg_dup1111	-	8.51802807	1.18048602
chr12	101129854	101130155	AluSx1_dup3518	+	96.8925693	101.5217977
chr12	101460128	101460428	AluSx1_dup3543	+	12.77704211	4.721944081
chr12	104181831	104182131	AluSx1_dup3642	-	11.7122886	11.8048602
chr12	104314730	104315042	AluSz_dup3454	-	6.388521053	4.721944081
chr12	106545491	106545800	AluSc_dup1181	+	15.97130263	28.33166449
chr12	109794735	109795034	AluSq_dup602	+	7.453274561	1.18048602
chr12	110087090	110087205	AluJo_dup2872	-	6.388521053	0
chr12	112147672	112147968	AluSg7_dup323	-	14.90654912	8.263402142
chr12	118063155	118063461	AluSx1_dup4568	+	8.51802807	4.721944081
chr12	119882733	119883041	AluY_dup4276	+	122.4466535	157.0046407

chr12	119941216	119941512	AluSq_dup709	+	234.2457719	254.9849804
chr12	120292320	120292608	AluSg4_dup278	+	24.4893307	11.8048602
chr12	120319649	120319930	AluSx_dup4937	-	12.77704211	9.443888162
chr12	120328662	120328953	AluSp_dup2206	+	64.94996403	64.92673111
chr12	122464666	122464978	AluSx3_dup1389	+	61.75570351	46.03895479
chr12	122525091	122525393	AluSq2_dup2593	+	6.388521053	8.263402142
chr12	124172026	124172323	AluJb_dup6426	-	10.64753509	11.8048602
chr12	124899280	124899551	AluSx1_dup5331	+	15.97130263	8.263402142
chr12	124908077	124908379	AluYm1_dup202	+	9.582781579	9.443888162
chr13	19680935	19681234	AluJr_dup71	+	13.84179561	22.42923438
chr13	27272127	27272432	AluSq_dup95	-	41.52538684	48.39992683
chr13	27285201	27285475	AluSx1_dup414	-	6.388521053	15.34631826
chr13	30428989	30429302	AluSq2_dup342	+	11.7122886	5.902430101
chr13	31958027	31958335	AluSx1_dup615	+	21.29507018	25.97069244
chr13	32656595	32656894	AluSz6_dup273	-	31.94260526	24.79020642
chr13	37226826	37227122	AluSx_dup779	-	18.10080965	5.902430101
chr13	41108239	41108545	AluSg_dup273	+	5.323767544	3.541458061
chr13	41284641	41284698	AluSc_dup276	-	111.7991184	155.8241547
chr13	41284698	41284952	AluSx1_dup902	-	258.7351026	266.7898406
chr13	47898506	47898807	AluY_dup1208	-	35.13686579	43.67798275
chr13	49587712	49587991	AluSz6_dup514	+	6.388521053	7.082916121
chr13	62302656	62302828	AluJb_dup1623	+	26.61883772	22.42923438
chr13	66574890	66575183	AluSq2_dup894	+	23.42457719	24.79020642
chr13	67383197	67383504	AluSg_dup530	-	12.77704211	10.62437418
chr13	93882147	93882442	AluJb_dup2277	-	6.388521053	4.721944081
chr13	95366014	95366280	AluSp_dup969	-	21.29507018	27.15117847
chr13	95369812	95370112	AluSz_dup2010	+	6.388521053	2.36097204
chr13	95382299	95382538	AluSx_dup2102	-	7.453274561	16.52680428
chr13	97134881	97135193	AluSz_dup2065	+	46.84915439	36.59506663
chr13	97478842	97479150	AluSx1_dup2214	-	19.16556316	40.13652469
chr13	98155505	98155818	AluJb_dup2462	-	7.453274561	5.902430101
chr13	98667269	98667566	AluSg_dup772	+	6.388521053	3.541458061
chr13	110707364	110707659	AluSx_dup2570	+	8.51802807	10.62437418
chr14	20625994	20626290	AluSc_dup28	+	75.59749912	62.56575907
chr14	20633950	20634242	AluSq2_dup49	+	45.78440088	49.58041285
chr14	20650471	20650785	AluSp_dup52	+	18.10080965	25.97069244
chr14	22244612	22244920	AluY_dup179	-	58.56144298	76.73159131
chr14	50026157	50026456	AluSg4_dup67	+	51.10816842	48.39992683
chr14	52110159	52110433	AluSx_dup1163	-	14.90654912	11.8048602
chr14	93151442	93151751	AluSz6_dup1274	-	22.35982368	21.24874836
chr14	100179954	100180263	AluSx_dup3201	+	28.74834474	22.42923438
chr14	102310626	102310856	AluSg7_dup258	-	123.511407	113.3266579
chr14	103075954	103076272	AluSx1_dup3228	+	61.75570351	63.74624509
chr15	22785785	22786095	AluY_dup157	-	89.43929474	86.17547948
chr15	22837743	22838048	AluSg_dup44	-	6.388521053	5.902430101
chr15	28960757	28961058	AluSp_dup244	-	10.64753509	16.52680428
chr15	32701083	32701381	AluY_dup876	-	58.56144298	57.84381499
chr15	37180600	37180908	AluSg_dup213	-	6.388521053	3.541458061
chr15	40244384	40244697	AluSq_dup132	-	8.51802807	10.62437418
chr15	40596266	40596575	AluSg_dup246	-	8.51802807	10.62437418
chr15	40757520	40757789	AluSg_dup251	+	10.64753509	8.263402142

chr15	40804720	40805010	AluSz_dup606	+	9.582781579	5.902430101
chr15	41120426	41120739	AluSx_dup849	+	6.388521053	2.36097204
chr15	41545546	41545841	AluSx_dup956	+	12.77704211	5.902430101
chr15	43723551	43723772	AluSg4_dup78	-	6.388521053	1.18048602
chr15	43826579	43826872	AluSq2_dup566	-	7.453274561	7.082916121
chr15	44155152	44155452	AluSc_dup332	+	8.51802807	12.98534622
chr15	50411237	50411531	AluSp_dup722	+	10.64753509	24.79020642
chr15	50690595	50690906	AluSq_dup239	+	6.388521053	3.541458061
chr15	50763617	50763925	AluSg_dup474	+	7.453274561	0
chr15	50777350	50777651	AluSx_dup1425	+	13.84179561	16.52680428
chr15	50885578	50885876	AluSc5_dup80	+	17.03605614	28.33166449
chr15	58756833	58757147	AluSx_dup1742	-	35.13686579	34.23409459
chr15	63096859	63097155	AluSp_dup958	-	71.33848509	62.56575907
chr15	63162134	63162439	AluSz_dup1640	+	7.453274561	2.36097204
chr15	64473188	64473496	AluSg_dup682	-	6.388521053	2.36097204
chr15	64790978	64791272	AluSx1_dup1913	-	6.388521053	2.36097204
chr15	65044453	65044758	AluSc8_dup379	+	61.75570351	46.03895479
chr15	65872434	65872733	AluSp_dup1098	-	55.36718246	55.48284295
chr15	72227462	72227774	AluSq2_dup1269	+	6.388521053	5.902430101
chr15	73879202	73879517	AluSx1_dup2428	-	18.10080965	21.24874836
chr15	74914766	74915051	AluSx3_dup693	-	6.388521053	2.36097204
chr15	75547316	75547465	AluSg7_dup206	+	38.33112632	44.85846877
chr15	75574659	75574972	AluSq2_dup1402	+	8.51802807	10.62437418
chr15	75636824	75637109	AluSz_dup2386	-	5.323767544	3.541458061
chr15	78434963	78435263	AluSg_dup930	+	12.77704211	24.79020642
chr15	78506876	78507013	AluSx_dup2771	-	15.97130263	18.88777632
chr15	79793300	79793601	AluSx1_dup2765	+	37.26637281	23.6097204
chr15	80011242	80011546	AluSq2_dup1495	+	84.11552719	70.82916121
chr15	81362975	81363266	AluSx4_dup298	+	6.388521053	3.541458061
chr15	84569720	84570009	AluSx1_dup2964	+	22.35982368	31.87312255
chr15	88974726	88974996	AluJb_dup3820	+	13.84179561	5.902430101
chr15	90356116	90356496	AluSz_dup3025	-	19.16556316	16.52680428
chr15	90681809	90682107	AluSx_dup3322	+	20.23031667	12.98534622
chr15	90823929	90824225	AluSg7_dup262	+	11.7122886	21.24874836
chr15	90847882	90848189	AluSx4_dup349	+	22.35982368	44.85846877
chr15	92837837	92838146	AluY_dup3472	+	9.582781579	9.443888162
chr15	101104842	101105124	AluJr_dup2540	-	23.42457719	21.24874836
chr16	71565157	71565453	AluSg_dup2	-	113.9286254	108.6047139
chr16	188421	188594	AluJb_dup29	-	6.388521053	2.36097204
chr16	1328552	1328659	AluSg7_dup9	+	5.323767544	4.721944081
chr16	1578599	1578742	AluSg7_dup12	+	10.64753509	12.98534622
chr16	2275248	2275540	AluSz_dup101	+	6.388521053	7.082916121
chr16	2722913	2723197	AluSx_dup219	-	21.29507018	15.34631826
chr16	2983920	2984215	AluSq2_dup119	+	11.7122886	15.34631826
chr16	3263366	3263666	AluSx4_dup29	-	269.3826377	277.4142148
chr16	3907330	3907625	AluSg_dup132	+	12.77704211	10.62437418
chr16	4308878	4309186	AluSz_dup282	-	12.77704211	16.52680428
chr16	4767448	4767677	AluSp_dup211	+	10.64753509	11.8048602
chr16	9127396	9127534	AluSx_dup756	-	7.453274561	15.34631826
chr16	9217893	9218203	AluSx1_dup849	-	5.323767544	1.18048602
chr16	11532399	11532700	AluSz_dup826	+	8.51802807	2.36097204

chr16	11639854	11640073	AluJb_dup956	-	22.35982368	18.88777632
chr16	12028749	12029045	AluSq2_dup445	-	39.39587982	30.69263653
chr16	15892826	15893122	AluSp_dup471	-	7.453274561	0
chr16	20929846	20930145	AluSq2_dup758	-	12.77704211	5.902430101
chr16	21360822	21361121	AluSg_dup477	-	22.35982368	42.49749673
chr16	25050152	25050443	AluSx3_dup460	-	13.84179561	16.52680428
chr16	25053926	25054213	AluSc_dup471	-	7.453274561	1.18048602
chr16	25342897	25343194	AluSz6_dup909	-	5.323767544	9.443888162
chr16	28967252	28967430	AluJr_dup2181	+	5.323767544	0
chr16	29054952	29055255	AluSg_dup632	+	7.453274561	0
chr16	29340001	29340300	AluSg_dup637	-	185.2671105	191.2387353
chr16	29828378	29828679	AluSx1_dup2866	-	6.388521053	2.36097204
chr16	29965760	29966034	AluSg_dup672	-	6.388521053	14.16583224
chr16	30558832	30559140	AluSx_dup2694	+	7.453274561	2.36097204
chr16	30630939	30631221	AluSx_dup2705	-	6.388521053	4.721944081
chr16	30946194	30946503	AluSx1_dup3026	-	9.582781579	12.98534622
chr16	31175758	31176041	AluSz_dup2462	+	9.582781579	2.36097204
chr16	46921159	46921471	AluSz_dup2615	-	6.388521053	3.541458061
chr16	48458114	48458415	AluSx1_dup3333	-	13.84179561	11.8048602
chr16	56419510	56419806	AluSx_dup3309	+	38.33112632	49.58041285
chr16	56628215	56628515	AluSx3_dup718	+	10.64753509	4.721944081
chr16	56966591	56966912	AluSq2_dup1576	-	7.453274561	3.541458061
chr16	57835669	57835971	AluSz_dup3114	+	8.51802807	5.902430101
chr16	58643561	58643853	AluSq2_dup1643	-	7.453274561	9.443888162
chr16	66029349	66029657	AluJo_dup2900	+	6.388521053	0
chr16	66980518	66980814	AluSx1_dup4057	-	8.51802807	11.8048602
chr16	66982847	66983160	AluSz_dup3405	+	6.388521053	4.721944081
chr16	67389068	67389337	AluSg_dup999	-	8.51802807	7.082916121
chr16	67427475	67427788	AluSx_dup3753	-	10.64753509	7.082916121
chr16	67751633	67751921	AluSx_dup3800	+	6.388521053	3.541458061
chr16	67970280	67970585	AluSx1_dup4155	+	6.388521053	4.721944081
chr16	69412675	69412992	AluJb_dup4159	-	5.323767544	0
chr16	69509231	69509501	AluSx1_dup4344	+	5.323767544	1.18048602
chr16	70136748	70137041	AluSz_dup3712	-	9.582781579	16.52680428
chr16	70155553	70155689	AluSp_dup1446	-	17.03605614	33.05360857
chr16	70536798	70537108	AluSx4_dup358	-	12.77704211	12.98534622
chr16	70574487	70574792	AluSz6_dup1721	-	7.453274561	5.902430101
chr16	71815327	71815622	AluSz_dup3817	+	38.33112632	46.03895479
chr16	71816314	71816632	AluSg_dup1154	-	44.71964737	64.92673111
chr16	73082901	73083223	AluSq2_dup2086	+	21.29507018	38.95603867
chr16	74701346	74701554	AluSx_dup4450	+	9.582781579	2.36097204
chr16	81181500	81181804	AluSx1_dup5096	+	24.4893307	33.05360857
chr16	84470372	84470670	AluSx1_dup5265	+	7.453274561	1.18048602
chr16	84802086	84802384	AluSx_dup4993	-	10.64753509	27.15117847
chr16	84881640	84881775	AluJo_dup3725	-	13.84179561	16.52680428
chr16	84962072	84962379	AluSp_dup1782	+	13.84179561	15.34631826
chr16	85024994	85025280	AluSz_dup4535	+	9.582781579	4.721944081
chr16	89850824	89851120	AluSx1_dup5671	-	5.323767544	7.082916121
chr17	870460	870773	AluJb_dup101	+	13.84179561	3.541458061
chr17	1633401	1633701	AluSx1_dup253	+	5.323767544	8.263402142
chr17	3749735	3750039	AluSg7_dup29	+	8.51802807	3.541458061

chr17	4391826	4392142	AluSp_dup160	+	13.84179561	15.34631826
chr17	4421727	4422038	AluSq2_dup229	+	6.388521053	8.263402142
chr17	5260206	5260512	AluY_dup481	+	34.07211228	22.42923438
chr17	7773722	7774029	AluSx1_dup997	-	6.388521053	7.082916121
chr17	8212892	8213037	AluSx1_dup1040	+	4.259014035	3.541458061
chr17	8224376	8224681	AluSg7_dup69	+	17.03605614	10.62437418
chr17	8281402	8281715	AluSg_dup285	-	9.582781579	3.541458061
chr17	12003173	12003457	AluSx3_dup358	+	9.582781579	8.263402142
chr17	15290023	15290315	AluSc8_dup273	+	10.64753509	15.34631826
chr17	15830996	15831269	AluSp_dup601	-	11.7122886	9.443888162
chr17	17300470	17300760	AluSp_dup684	-	41.52538684	40.13652469
chr17	19860942	19861085	AluSq2_dup862	+	9.582781579	9.443888162
chr17	30255617	30255904	AluSx3_dup635	+	15.97130263	31.87312255
chr17	30294410	30294704	AluSg_dup693	-	11.7122886	20.06826234
chr17	30367968	30368274	AluSx_dup2110	+	45.78440088	47.21944081
chr17	30683533	30683839	AluSx1_dup2086	-	6.388521053	8.263402142
chr17	31936290	31936586	AluSx3_dup686	+	14.90654912	18.88777632
chr17	32097156	32097468	AluYm1_dup94	-	18.10080965	22.42923438
chr17	35141265	35141584	AluSc_dup691	+	13.84179561	7.082916121
chr17	37458694	37458976	AluJb_dup2369	-	21.29507018	18.88777632
chr17	37808687	37809003	AluSp_dup1234	-	8.51802807	10.62437418
chr17	38670686	38670983	AluSc5_dup132	-	5.323767544	8.263402142
chr17	38867172	38867494	AluSx3_dup785	-	34.07211228	36.59506663
chr17	39057270	39057577	AluSx1_dup2685	-	7.453274561	15.34631826
chr17	39180372	39180689	AluSx1_dup2698	+	9.582781579	5.902430101
chr17	40002659	40002975	AluSx_dup2878	-	50.04341491	48.39992683
chr17	41841315	41841612	AluSg_dup976	-	8.51802807	15.34631826
chr17	42034846	42035148	AluSx_dup3033	+	6.388521053	9.443888162
chr17	42292644	42292927	AluSg7_dup236	-	5.323767544	3.541458061
chr17	42360362	42360660	AluSp_dup1469	+	6.388521053	12.98534622
chr17	42398262	42398507	AluSg7_dup238	-	13.84179561	22.42923438
chr17	42428026	42428348	AluJb_dup2867	-	17.03605614	3.541458061
chr17	42638047	42638358	AluJb_dup2901	-	8.51802807	4.721944081
chr17	42914599	42914896	AluJo_dup1843	+	8.51802807	2.36097204
chr17	43103184	43103488	AluSx_dup3183	+	12.77704211	7.082916121
chr17	43421622	43421929	AluSg4_dup232	+	10.64753509	5.902430101
chr17	43711702	43712012	AluSx3_dup909	+	9.582781579	5.902430101
chr17	44186037	44186335	AluSp_dup1614	+	12.77704211	7.082916121
chr17	44434622	44434677	AluSx3_dup936	+	6.388521053	8.263402142
chr17	44560730	44561013	AluSx4_dup314	-	23.42457719	22.42923438
chr17	44754642	44754860	AluYi6_4d_dup3	-	7.453274561	8.263402142
chr17	45027705	45028012	AluSg_dup1090	+	6.388521053	5.902430101
chr17	48009159	48009458	AluSx_dup3698	-	19.16556316	7.082916121
chr17	49071100	49071233	AluJb_dup3646	-	3.194260526	1.18048602
chr17	49241310	49241602	AluSg4_dup276	-	5.323767544	0
chr17	50090622	50090921	AluSx_dup3898	+	6.388521053	3.541458061
chr17	50222759	50223054	AluSx1_dup3765	+	6.388521053	3.541458061
chr17	50757805	50758102	AluSx3_dup1087	+	8.51802807	3.541458061
chr17	59853747	59854031	AluSp_dup2133	+	6.388521053	7.082916121
chr17	60427425	60427712	AluSx_dup4449	-	8.51802807	12.98534622
chr17	62774773	62775087	AluSg4_dup330	+	17.03605614	20.06826234

chr17	64667820	64668129	AluSg7_dup362	-	6.388521053	11.8048602
chr17	64737369	64737672	AluSp_dup2313	-	8.51802807	1.18048602
chr17	64826921	64827243	AluSx_dup4854	+	17.03605614	36.59506663
chr17	66280417	66280702	AluSg4_dup347	-	7.453274561	4.721944081
chr17	68054921	68055229	AluSq2_dup2510	-	18.10080965	16.52680428
chr17	69394544	69394831	AluSx1_dup5027	-	9.582781579	3.541458061
chr17	75028169	75028476	AluY_dup4389	+	15.97130263	16.52680428
chr17	75127600	75127894	AluJb_dup5425	-	8.51802807	2.36097204
chr17	76127514	76127814	AluSc8_dup1027	+	6.388521053	1.18048602
chr17	78284513	78284811	AluSg_dup1797	+	23.42457719	22.42923438
chr17	78363372	78363672	AluSx_dup5903	-	11.7122886	22.42923438
chr17	78377686	78377995	AluSq_dup970	-	9.582781579	10.62437418
chr17	78889837	78890117	AluSx3_dup1599	+	6.388521053	1.18048602
chr17	78960464	78960760	AluSx1_dup5786	+	10.64753509	8.263402142
chr17	81892524	81892822	AluSx_dup6189	-	7.453274561	4.721944081
chr17	82498372	82498672	AluSc_dup1578	+	6.388521053	4.721944081
chr18	2827350	2827648	AluSx_dup115	+	7.453274561	5.902430101
chr18	9419703	9419997	AluSg_dup98	-	17.03605614	27.15117847
chr18	9654223	9654540	AluSg_dup99	-	5.323767544	4.721944081
chr18	11929037	11929334	AluSx_dup467	-	10.64753509	8.263402142
chr18	12630380	12630662	AluSx_dup513	+	10.64753509	9.443888162
chr18	21607913	21608210	AluSg7_dup59	+	6.388521053	3.541458061
chr18	23117051	23117342	AluSg_dup231	+	10.64753509	4.721944081
chr18	23488460	23488751	AluSx3_dup221	+	9.582781579	12.98534622
chr18	24076009	24076279	AluSx1_dup836	-	19.16556316	30.69263653
chr18	25687481	25687771	AluJr4_dup197	+	10.64753509	4.721944081
chr18	26012854	26013153	AluSp_dup336	-	5.323767544	0
chr18	46094391	46094691	AluSc_dup430	+	6.388521053	2.36097204
chr18	49313183	49313492	AluSg_dup440	+	6.388521053	3.541458061
chr18	49460832	49461145	AluSc_dup462	+	236.3752789	241.9996341
chr18	58793758	58794048	AluSz6_dup787	+	27.68359123	36.59506663
chr18	59744530	59744830	AluSz_dup1732	-	12.77704211	16.52680428
chr18	59953403	59953715	AluSq2_dup1031	+	5.323767544	1.18048602
chr18	63428132	63428441	AluSx4_dup197	-	7.453274561	12.98534622
chr18	69307430	69307713	AluSg7_dup163	+	6.388521053	2.36097204
chr18	70361573	70361878	AluSx1_dup2054	-	14.90654912	7.082916121
chr19	770559	770855	AluSz_dup50	+	46.84915439	48.39992683
chr19	1332383	1332688	AluSx1_dup190	-	12.77704211	20.06826234
chr19	1367925	1368221	AluSx4_dup8	-	5.323767544	2.36097204
chr19	1888821	1889127	AluSg7_dup11	-	8.51802807	2.36097204
chr19	3501316	3501452	AluJb_dup322	+	19.16556316	27.15117847
chr19	3999723	4000000	AluSx3_dup135	-	30.87785175	33.05360857
chr19	4796189	4796488	AluSx3_dup168	-	24.4893307	23.6097204
chr19	4809354	4809657	AluSq_dup119	+	9.582781579	20.06826234
chr19	4964648	4964951	AluSx_dup733	-	6.388521053	3.541458061
chr19	6328208	6328529	AluSx1_dup1090	+	28.74834474	34.23409459
chr19	6335887	6336200	AluSq2_dup315	-	6.388521053	3.541458061
chr19	6779043	6779352	AluJr_dup690	-	18.10080965	12.98534622
chr19	7238337	7238644	AluSz_dup689	+	9.582781579	16.52680428
chr19	10239993	10240304	AluY_dup1219	-	17.03605614	11.8048602
chr19	10351207	10351503	AluSq2_dup578	+	24.4893307	28.33166449

chr19	13659944	13660254	AluSx1_dup2274	-	8.51802807	12.98534622
chr19	13832341	13832636	AluSx_dup1960	-	7.453274561	11.8048602
chr19	14027044	14027345	AluSx3_dup530	-	12.77704211	4.721944081
chr19	14538525	14538829	AluSg_dup581	-	8.51802807	11.8048602
chr19	14540405	14540691	AluSx1_dup2447	-	22.35982368	8.263402142
chr19	15128656	15128947	AluSx1_dup2521	+	13.84179561	5.902430101
chr19	16063740	16063970	AluJo_dup1831	-	5.323767544	3.541458061
chr19	16077755	16078072	AluSx3_dup584	-	14.90654912	22.42923438
chr19	16105376	16105666	AluSp_dup868	+	7.453274561	5.902430101
chr19	16149201	16149502	AluSz_dup1825	-	14.90654912	16.52680428
chr19	16489202	16489336	AluSx_dup2305	+	7.453274561	7.082916121
chr19	16823410	16823721	AluSp_dup908	+	8.51802807	7.082916121
chr19	18089345	18089641	AluSz_dup2121	+	15.97130263	7.082916121
chr19	18416013	18416314	AluSx1_dup3095	-	8.51802807	4.721944081
chr19	18714312	18714605	AluSg_dup700	-	6.388521053	1.18048602
chr19	19267086	19267398	AluSp_dup1048	+	9.582781579	8.263402142
chr19	29875384	29875693	AluSx1_dup3715	+	6.388521053	7.082916121
chr19	33167787	33168017	AluSz_dup2818	-	8.51802807	1.18048602
chr19	33171770	33172063	AluSx3_dup867	-	175.6843289	178.2533891
chr19	35263657	35263795	AluJr4_dup375	-	6.388521053	1.18048602
chr19	35564150	35564455	AluSx_dup3648	-	8.51802807	4.721944081
chr19	35684219	35684335	AluSx3_dup911	-	5.323767544	7.082916121
chr19	35814606	35814909	AluSg4_dup227	-	28.74834474	35.41458061
chr19	39328599	39328904	AluSz_dup3432	+	12.77704211	18.88777632
chr19	40268844	40269125	AluSp_dup1812	+	8.51802807	15.34631826
chr19	40310254	40310341	AluJb_dup3442	+	12.77704211	18.88777632
chr19	42259735	42260043	AluSx_dup4444	-	33.00735877	35.41458061
chr19	42340215	42340528	AluSz6_dup1448	-	5.323767544	9.443888162
chr19	43720533	43720802	AluSg_dup1264	-	11.7122886	16.52680428
chr19	44608735	44609032	AluSx1_dup5030	+	10.64753509	4.721944081
chr19	45009071	45009380	AluSx1_dup5082	-	12.77704211	15.34631826
chr19	45042615	45042915	AluSz_dup3926	-	6.388521053	7.082916121
chr19	45371046	45371359	AluSp_dup2016	+	20.23031667	23.6097204
chr19	45376640	45376944	AluSx3_dup1183	+	11.7122886	2.36097204
chr19	47079616	47079909	AluSx3_dup1244	+	40.46063333	66.10721713
chr19	47277495	47277662	AluSx1_dup5435	-	4.259014035	10.62437418
chr19	47312978	47313274	AluSg_dup1386	-	7.453274561	12.98534622
chr19	48071865	48072174	AluSx4_dup444	+	6.388521053	2.36097204
chr19	49524011	49524306	AluSx1_dup5879	-	6.388521053	0
chr19	49817641	49817951	AluSx1_dup5928	+	54.30242895	48.39992683
chr19	50098955	50099087	AluYa5_dup88	-	12.77704211	4.721944081
chr19	50137195	50137327	AluYa5_dup96	-	138.4179561	153.4631826
chr19	50929633	50929944	AluSx1_dup6084	-	17.03605614	9.443888162
chr19	52109395	52109673	AluSx1_dup6184	-	9.582781579	5.902430101
chr19	57305517	57305800	AluJo_dup4433	-	6.388521053	5.902430101
chr19	57309668	57309968	AluSx_dup6239	-	9.582781579	7.082916121
chr19	58420704	58421003	AluSg_dup1829	-	10.64753509	9.443888162
chr2	8406519	8406826	AluSx_dup168	+	7.453274561	3.541458061
chr2	9708501	9708786	AluSz_dup195	-	8.51802807	2.36097204
chr2	23280725	23281036	AluSg_dup182	+	7.453274561	5.902430101
chr2	23942967	23943254	AluSx3_dup162	-	6.388521053	3.541458061

chr2	25192697	25192983	AluSz_dup630	+	52.17292193	56.66332897
chr2	26622078	26622388	AluSx1_dup873	+	6.388521053	4.721944081
chr2	26737561	26737849	AluSg_dup256	+	8.51802807	11.8048602
chr2	26962160	26962471	AluY_dup801	+	13.84179561	21.24874836
chr2	27259212	27259509	AluSc5_dup52	+	15.97130263	20.06826234
chr2	27418486	27418797	AluSx_dup945	-	6.388521053	3.541458061
chr2	27603939	27604226	AluSx_dup967	-	5.323767544	0
chr2	28296682	28296987	AluSx1_dup983	-	7.453274561	1.18048602
chr2	28893962	28894280	AluSg7_dup60	-	10.64753509	8.263402142
chr2	30091086	30091421	AluSz6_dup439	+	7.453274561	3.541458061
chr2	33462367	33462676	AluSx1_dup1229	-	8.51802807	8.263402142
chr2	38685734	38686012	AluSz_dup1263	-	6.388521053	10.62437418
chr2	39230097	39230356	AluSp_dup597	+	42.59014035	44.85846877
chr2	43151299	43151599	AluSg_dup474	-	5.323767544	2.36097204
chr2	44106355	44106653	AluSq_dup251	-	10.64753509	12.98534622
chr2	61830398	61830704	AluSz_dup2107	+	9.582781579	11.8048602
chr2	65028670	65028940	AluSx_dup2544	+	29.81309825	20.06826234
chr2	69894663	69894977	AluSg_dup787	-	8.51802807	9.443888162
chr2	70249485	70249795	AluSx1_dup2621	+	7.453274561	10.62437418
chr2	70828671	70828964	AluSx1_dup2647	-	11.7122886	8.263402142
chr2	75248487	75248787	AluSx_dup2932	-	11.7122886	24.79020642
chr2	84958986	84959290	AluSx1_dup2986	-	17.03605614	4.721944081
chr2	85406019	85406271	AluSz_dup2836	+	9.582781579	3.541458061
chr2	85499398	85499678	AluSx_dup3113	+	45.78440088	44.85846877
chr2	85615637	85615929	AluSp_dup1362	-	13.84179561	22.42923438
chr2	85971344	85971484	AluSz6_dup1371	-	10.64753509	10.62437418
chr2	100751993	100752286	AluSg7_dup263	-	34.07211228	36.59506663
chr2	106322014	106322332	AluYb8_dup101	-	47.91390789	72.00964723
chr2	107891176	107891312	AluJb_dup4260	+	29.81309825	17.7072903
chr2	112005878	112006181	AluSz_dup3615	-	66.01471754	66.10721713
chr2	112655694	112656000	AluSq2_dup2211	-	5.323767544	1.18048602
chr2	121693926	121694247	AluSp_dup1857	-	7.453274561	8.263402142
chr2	121925701	121925997	AluSz_dup3883	+	8.51802807	9.443888162
chr2	128534424	128534727	AluSx_dup4598	+	9.582781579	8.263402142
chr2	131093944	131094242	AluSq2_dup2522	-	11.7122886	16.52680428
chr2	158895371	158895682	AluSq2_dup2883	-	6.388521053	7.082916121
chr2	159920407	159920701	AluSg_dup1672	-	35.13686579	29.51215051
chr2	165031507	165031820	AluY_dup5428	-	23.42457719	44.85846877
chr2	169547613	169547914	AluSx3_dup1674	+	11.7122886	11.8048602
chr2	177168612	177168901	AluSg_dup1856	+	6.388521053	7.082916121
chr2	189484557	189484853	AluSg_dup1944	-	7.453274561	3.541458061
chr2	196598658	196598947	AluSx1_dup6185	+	7.453274561	9.443888162
chr2	197624679	197624962	AluSz_dup5567	+	7.453274561	14.16583224
chr2	201111470	201111774	AluSx3_dup1946	+	7.453274561	1.18048602
chr2	207654440	207654737	AluSp_dup2959	+	11.7122886	20.06826234
chr2	208046482	208046795	AluSx1_dup6705	-	6.388521053	4.721944081
chr2	218374560	218374789	AluSg_dup2274	+	21.29507018	24.79020642
chr2	219953980	219954290	AluY_dup7207	+	6.388521053	0
chr2	223727939	223728233	AluSg4_dup489	+	14.90654912	12.98534622
chr2	223734758	223735054	AluSx1_dup7183	-	8.51802807	7.082916121
chr2	227881743	227882051	AluSx1_dup7359	-	8.51802807	20.06826234

chr2	230617453	230617760	AluSx_dup7633	+	9.582781579	14.16583224
chr2	235327988	235328274	AluSc_dup2526	+	13.84179561	16.52680428
chr2	237947704	237948011	AluSx_dup8077	-	28.74834474	25.97069244
chr2	238157095	238157385	AluSx1_dup7926	-	12.77704211	5.902430101
chr2	241756527	241756820	AluSq2_dup4417	-	7.453274561	4.721944081
chr20	1242234	1242531	AluJb_dup72	-	26.61883772	28.33166449
chr20	1900091	1900383	AluSp_dup48	-	5.323767544	4.721944081
chr20	2638905	2639194	AluSx3_dup26	-	12.77704211	2.36097204
chr20	3160065	3160391	AluSx_dup164	+	10.64753509	3.541458061
chr20	3208378	3208669	AluSp_dup90	-	9.582781579	11.8048602
chr20	4015792	4016099	AluY_dup180	+	84.11552719	87.3559655
chr20	5611300	5611594	AluSx_dup357	+	38.33112632	33.05360857
chr20	5613296	5613617	AluSq2_dup200	-	22.35982368	31.87312255
chr20	5743414	5743729	AluSq2_dup207	-	13.84179561	10.62437418
chr20	19885383	19885701	AluSz_dup696	+	34.07211228	36.59506663
chr20	31503371	31503653	AluSx_dup941	+	10.64753509	2.36097204
chr20	31764182	31764467	AluJb_dup1172	-	5.323767544	8.263402142
chr20	32325655	32325966	AluSq_dup148	-	12.77704211	28.33166449
chr20	33435315	33435602	AluSz6_dup558	+	8.51802807	16.52680428
chr20	35596377	35596499	AluSz_dup1306	+	5.323767544	4.721944081
chr20	36864404	36864713	AluSg_dup496	+	29.81309825	16.52680428
chr20	37284411	37284717	AluSg_dup509	-	8.51802807	9.443888162
chr20	41330195	41330482	AluSz_dup1647	-	5.323767544	7.082916121
chr20	47307837	47308133	AluSg4_dup129	+	12.77704211	10.62437418
chr20	47316050	47316346	AluSg_dup631	+	8.51802807	25.97069244
chr20	47378433	47378742	AluSg_dup636	+	13.84179561	12.98534622
chr20	47380173	47380482	AluSx1_dup2092	+	8.51802807	9.443888162
chr20	47444188	47444485	AluSg4_dup132	+	13.84179561	12.98534622
chr20	49625404	49625666	AluJr_dup1736	-	5.323767544	5.902430101
chr20	50492756	50493068	AluSq_dup347	-	29.81309825	21.24874836
chr20	50969964	50970109	AluSx_dup2442	-	44.71964737	35.41458061
chr20	51369271	51369584	AluSx1_dup2428	+	6.388521053	7.082916121
chr20	53552414	53552711	AluSz_dup2432	+	6.388521053	0
chr20	53787438	53787731	AluSp_dup1106	-	8.51802807	12.98534622
chr20	62795774	62796066	AluSq2_dup1554	-	7.453274561	4.721944081
chr21	17454672	17454759	AluSp_dup144	-	194.8498921	230.1947739
chr21	24814211	24814513	AluSg7_dup48	+	7.453274561	3.541458061
chr21	26762346	26762645	AluSc_dup200	+	22.35982368	27.15117847
chr21	29054600	29054911	AluYm1_dup32	-	7.453274561	1.18048602
chr21	31424773	31425079	AluSz_dup485	+	17.03605614	12.98534622
chr21	31890234	31890529	AluSx1_dup613	-	17.03605614	17.7072903
chr21	34176395	34176589	AluJr4_dup167	-	20.23031667	14.16583224
chr21	42968236	42968420	AluSx3_dup361	-	83.05077368	120.4095741
chr21	43788796	43789099	AluSg_dup387	-	27.68359123	49.58041285
chr21	45013930	45014230	AluSx_dup1331	-	7.453274561	4.721944081
chr22	17171203	17171328	AluJo_dup104	-	38.33112632	49.58041285
chr22	17442541	17442846	AluSg7_dup25	-	25.55408421	40.13652469
chr22	17979264	17979549	AluSq_dup33	+	6.388521053	1.18048602
chr22	19157313	19157492	AluSx_dup271	+	6.388521053	14.16583224
chr22	20931826	20932109	AluY_dup508	-	13.84179561	10.62437418
chr22	21744460	21744767	AluSg_dup159	+	6.388521053	7.082916121

chr22	22258000	22258312	AluSx1_dup495	+	60.69095	57.84381499
chr22	22587183	22587474	AluSc5_dup30	+	50.04341491	60.20478703
chr22	22804954	22805266	AluSz6_dup200	-	228.9220044	211.3069976
chr22	24790578	24790793	AluSx1_dup654	-	10.64753509	12.98534622
chr22	28674538	28674836	AluSz_dup655	+	7.453274561	11.8048602
chr22	29210250	29210535	AluSp_dup399	-	5.323767544	1.18048602
chr22	29843143	29843436	AluSc8_dup211	+	11.7122886	8.263402142
chr22	30087008	30087160	AluSp_dup435	-	15.97130263	8.263402142
chr22	30905134	30905440	AluSg_dup314	-	5.323767544	2.36097204
chr22	31405167	31405465	AluSx4_dup106	-	18.10080965	17.7072903
chr22	33506618	33506915	AluSx_dup1255	+	24.4893307	11.8048602
chr22	36001781	36002086	AluSq2_dup724	+	15.97130263	12.98534622
chr22	36531475	36531778	AluSg7_dup141	-	9.582781579	8.263402142
chr22	37272016	37272233	AluSx_dup1477	+	33.00735877	27.15117847
chr22	37590725	37591035	AluY_dup1596	+	19.16556316	8.263402142
chr22	37613389	37613698	AluY_dup1601	-	23.42457719	28.33166449
chr22	37687463	37687757	AluSx_dup1521	-	5.323767544	9.443888162
chr22	37731468	37731754	AluSz_dup1255	-	9.582781579	4.721944081
chr22	37820009	37820304	AluSz_dup1265	-	8.51802807	23.6097204
chr22	37923229	37923526	AluSx_dup1564	-	5.323767544	9.443888162
chr22	38043987	38044293	AluSx1_dup1556	+	8.51802807	0
chr22	38507941	38508186	AluSg4_dup105	-	6.388521053	2.36097204
chr22	40756867	40757166	AluSz6_dup676	-	15.97130263	7.082916121
chr22	41329258	41329558	AluSx1_dup1948	-	17.03605614	12.98534622
chr22	41376224	41376527	AluSx1_dup1954	-	6.388521053	2.36097204
chr22	41511162	41511471	AluSz6_dup713	-	4.259014035	4.721944081
chr22	41980129	41980435	AluSq4_dup23	-	10.64753509	9.443888162
chr22	42729666	42729975	AluSx3_dup654	-	10.64753509	8.263402142
chr22	44551516	44551804	AluSq2_dup1174	+	7.453274561	9.443888162
chr22	45280347	45280640	AluSz_dup1851	+	10.64753509	7.082916121
chr3	12667203	12667479	AluSp_dup118	+	9.582781579	5.902430101
chr3	13452232	13452542	AluSg_dup146	+	10.64753509	12.98534622
chr3	23139447	23139751	AluSx3_dup193	+	17.03605614	18.88777632
chr3	27503286	27503559	AluSx1_dup812	-	60.69095	64.92673111
chr3	27606428	27606610	AluJb_dup1068	-	11.7122886	10.62437418
chr3	29255928	29256202	AluSz_dup834	-	11.7122886	1.18048602
chr3	29268900	29269022	AluJr_dup718	+	26.61883772	25.97069244
chr3	30511340	30511626	AluSp_dup344	-	22.35982368	29.51215051
chr3	32040124	32040412	AluSx_dup900	+	11.7122886	15.34631826
chr3	32611829	32612140	AluSz_dup918	-	19.16556316	9.443888162
chr3	38067752	38068053	AluSx_dup1152	-	19.16556316	36.59506663
chr3	38984515	38984809	AluSq2_dup560	-	11.7122886	14.16583224
chr3	48109311	48109637	AluSg4_dup100	+	8.51802807	14.16583224
chr3	48135017	48135313	AluSg7_dup117	+	14.90654912	15.34631826
chr3	48139630	48139849	AluSg_dup505	+	5.323767544	9.443888162
chr3	48153598	48153910	AluSq2_dup765	-	8.51802807	10.62437418
chr3	48920948	48921253	AluSg_dup535	-	10.64753509	15.34631826
chr3	49107124	49107422	AluSg4_dup108	-	21.29507018	29.51215051
chr3	49262864	49263166	AluSq2_dup846	-	8.51802807	15.34631826
chr3	58038048	58038328	AluSq2_dup1092	-	6.388521053	10.62437418
chr3	58056073	58056400	AluSg_dup724	-	18.10080965	9.443888162

chr3	61451781	61452065	AluSz_dup2249	-	11.7122886	22.42923438
chr3	72518356	72518649	AluSg_dup855	+	24.4893307	33.05360857
chr3	100204912	100205207	AluSq_dup536	+	5.323767544	0
chr3	102447070	102447363	AluSc_dup1046	-	11.7122886	16.52680428
chr3	129226041	129226333	AluSg_dup1278	-	8.51802807	7.082916121
chr3	129246057	129246361	AluSz_dup3750	+	8.51802807	4.721944081
chr3	133969149	133969415	AluSx3_dup1154	+	22.35982368	18.88777632
chr3	140884788	140885098	AluSx_dup4287	-	10.64753509	4.721944081
chr3	141637758	141638062	AluSp_dup1942	+	7.453274561	0
chr3	155859379	155859682	AluSx_dup4707	-	6.388521053	1.18048602
chr3	156796519	156796807	AluSx1_dup4716	+	14.90654912	4.721944081
chr3	161138137	161138446	AluSp_dup2193	-	11.7122886	9.443888162
chr3	169763177	169763457	AluSx_dup4963	+	13.84179561	25.97069244
chr3	170409264	170409566	AluSx4_dup499	-	5.323767544	1.18048602
chr3	172029251	172029556	AluSx1_dup5043	-	48.9786614	60.20478703
chr3	172498530	172498812	AluSp_dup2328	+	9.582781579	3.541458061
chr3	172626512	172626812	AluSg_dup1711	+	15.97130263	36.59506663
chr3	176722769	176723062	AluJo_dup3598	+	6.388521053	2.36097204
chr3	177243869	177244038	AluSz_dup4973	+	27.68359123	22.42923438
chr3	177245021	177245313	AluSx3_dup1559	-	10.64753509	1.18048602
chr3	184793494	184793785	AluSx1_dup5541	-	72.4032386	74.37061927
chr3	185873737	185874031	AluSz6_dup2657	-	9.582781579	1.18048602
chr3	190424649	190424914	AluSx1_dup5849	+	348.1743974	351.784834
chr3	196144756	196144872	AluJr_dup4486	-	46.84915439	38.95603867
chr3	196435986	196436295	AluSz_dup5669	-	26.61883772	51.94138489
chr3	196504044	196504355	AluSx1_dup6139	+	76.66225263	96.79985366
chr4	7078598	7078885	AluSx_dup329	-	10.64753509	3.541458061
chr4	8260454	8260732	AluJo_dup240	-	166.1015474	185.3363052
chr4	10761713	10762001	AluSx4_dup37	-	7.453274561	5.902430101
chr4	17330316	17330628	AluSx1_dup645	+	7.453274561	5.902430101
chr4	39392248	39392558	AluSz_dup1042	+	7.453274561	1.18048602
chr4	40022899	40023212	AluSq2_dup681	+	169.2958079	185.3363052
chr4	40505206	40505506	AluSz_dup1183	+	57.49668947	34.23409459
chr4	40745146	40745443	AluSz_dup1225	-	7.453274561	16.52680428
chr4	43505136	43505442	AluSx1_dup1509	+	78.79175965	67.28770315
chr4	44709760	44709957	AluJr_dup892	+	8.51802807	5.902430101
chr4	47119495	47119802	AluSp_dup665	-	46.84915439	72.00964723
chr4	54253679	54253984	AluSz_dup1538	-	9.582781579	8.263402142
chr4	56945110	56945406	AluSx1_dup1850	+	29.81309825	40.13652469
chr4	77831189	77831485	AluSz6_dup962	+	8.51802807	7.082916121
chr4	83034354	83034644	AluY_dup2432	-	7.453274561	3.541458061
chr4	83256564	83256861	AluY_dup2459	-	30.87785175	15.34631826
chr4	83319778	83320050	AluSz_dup2286	+	7.453274561	8.263402142
chr4	86843896	86844205	AluY_dup2559	+	9.582781579	8.263402142
chr4	87309877	87310197	AluSz_dup2438	+	5.323767544	3.541458061
chr4	88138867	88139156	AluSg_dup788	+	9.582781579	10.62437418
chr4	118461248	118461555	AluSz6_dup1417	-	10.64753509	14.16583224
chr4	121727870	121728164	AluSx_dup3179	-	24.4893307	51.94138489
chr4	139202706	139203011	AluSp_dup1710	+	86.24503421	99.1608257
chr4	139225942	139226235	AluSx3_dup1151	+	6.388521053	8.263402142
chr4	145640094	145640411	AluSz_dup3619	-	6.388521053	7.082916121

chr4	147142892	147143204	AluSx_dup3736	-	69.20897807	29.51215051
chr4	169069065	169069361	AluSc_dup1603	+	5.323767544	2.36097204
chr4	169385160	169385470	AluSq2_dup2489	-	47.91390789	49.58041285
chr4	173443988	173444273	AluSq2_dup2546	-	22.35982368	17.7072903
chr4	183368438	183368751	AluSx_dup4664	+	11.7122886	1.18048602
chr4	185112386	185112669	AluSz6_dup2138	+	251.2818281	177.072903
chr4	186746393	186746693	AluSx1_dup4963	-	31.94260526	29.51215051
chr4	187218589	187218880	AluSz_dup4603	-	21.29507018	18.88777632
chr4	188111677	188111929	AluSz_dup4618	+	33.00735877	36.59506663
chr5	10551031	10551324	AluSq2_dup124	-	35.13686579	28.33166449
chr5	10922265	10922542	AluSq2_dup131	+	7.453274561	7.082916121
chr5	14087638	14087928	AluSq2_dup157	+	11.7122886	16.52680428
chr5	14097618	14097928	AluSz_dup267	+	15.97130263	12.98534622
chr5	17033744	17034044	AluSx4_dup37	+	6.388521053	3.541458061
chr5	18194198	18194488	AluSg_dup157	-	14.90654912	8.263402142
chr5	35047157	35047461	AluJb_dup865	+	9.582781579	16.52680428
chr5	36265691	36266000	AluSx1_dup920	+	13.84179561	17.7072903
chr5	37279360	37279661	AluSc8_dup196	+	6.388521053	14.16583224
chr5	37285057	37285316	AluSq10_dup16	+	58.56144298	77.91207733
chr5	55169831	55170133	AluY_dup1462	+	8.51802807	0
chr5	55583400	55583717	AluSx3_dup456	-	18.10080965	12.98534622
chr5	55815759	55816085	AluSz6_dup507	-	15.97130263	7.082916121
chr5	56054527	56054813	AluSz6_dup512	-	8.51802807	3.541458061
chr5	56133158	56133453	AluSg_dup459	+	7.453274561	5.902430101
chr5	65879979	65880293	AluSx1_dup1583	+	6.388521053	1.18048602
chr5	69071974	69072277	AluSp_dup799	+	7.453274561	8.263402142
chr5	69485129	69485446	AluJo_dup953	+	6.388521053	10.62437418
chr5	73082876	73083183	AluSc5_dup138	-	61.75570351	103.8827698
chr5	73542959	73543279	AluSq2_dup1138	+	7.453274561	10.62437418
chr5	76739259	76739560	AluSq2_dup1221	+	680.3774921	714.1940422
chr5	76861343	76861638	AluSx1_dup2038	-	37.26637281	31.87312255
chr5	77679614	77679911	AluSx1_dup2073	-	7.453274561	12.98534622
chr5	79611682	79611982	AluSg_dup728	-	13.84179561	22.42923438
chr5	82632713	82633008	AluY_dup2349	-	53.23767544	62.56575907
chr5	83023123	83023415	AluY_dup2365	-	14.90654912	11.8048602
chr5	91279719	91280029	AluY_dup2564	-	94.76306228	101.5217977
chr5	96293771	96294059	AluSx1_dup2590	-	12.77704211	10.62437418
chr5	110876121	110876287	AluSz6_dup1268	-	4.259014035	1.18048602
chr5	112963509	112963804	AluSz_dup2614	-	8.51802807	15.34631826
chr5	112977967	112978274	AluSg7_dup251	-	6.388521053	11.8048602
chr5	115375646	115375942	AluSx_dup2910	-	50.04341491	67.28770315
chr5	119725558	119725863	AluSz_dup2721	+	7.453274561	4.721944081
chr5	132447821	132448133	AluSx1_dup3329	-	26.61883772	38.95603867
chr5	132967224	132967519	AluSx_dup3346	+	21.29507018	16.52680428
chr5	134683029	134683318	AluSg_dup1176	-	6.388521053	5.902430101
chr5	134907246	134907540	AluSg_dup1196	-	9.582781579	10.62437418
chr5	138360568	138360891	AluSx1_dup3645	-	13.84179561	3.541458061
chr5	139405043	139405345	AluSx1_dup3736	-	9.582781579	7.082916121
chr5	140313918	140314178	AluSz6_dup1697	-	7.453274561	11.8048602
chr5	142251325	142251466	AluSq2_dup2255	-	14.90654912	8.263402142
chr5	147350361	147350667	AluSx1_dup4046	-	6.388521053	2.36097204

chr5	149484534	149484836	AluSc8_dup809	+	10.64753509	4.721944081
chr5	149562439	149562745	AluY_dup4268	-	22.35982368	18.88777632
chr5	172298744	172299036	AluSq2_dup2807	+	5.323767544	3.541458061
chr5	173764138	173764434	AluSp_dup2321	-	408.8653474	426.1554533
chr5	176539407	176539700	AluSg_dup1740	+	6.388521053	9.443888162
chr5	181164964	181165264	AluYf1_dup111	+	15.97130263	16.52680428
chr5	181183488	181183817	AluSc_dup1881	+	28.74834474	22.42923438
chr5	181210636	181210939	AluSp_dup2538	-	5.323767544	4.721944081
chr5	181215994	181216282	AluSq2_dup3073	-	15.97130263	24.79020642
chr5	181218547	181218855	AluY_dup5553	+	29.81309825	47.21944081
chr6	3803384	3803687	AluSz6_dup33	-	6.388521053	10.62437418
chr6	3871046	3871155	AluSx3_dup38	+	5.323767544	7.082916121
chr6	4174420	4174713	AluSg_dup65	+	7.453274561	8.263402142
chr6	10886421	10886713	AluSz_dup329	-	42.59014035	25.97069244
chr6	11767090	11767335	AluJb_dup420	+	10.64753509	8.263402142
chr6	13780407	13780710	AluSg_dup194	+	6.388521053	3.541458061
chr6	17086686	17086984	AluSz_dup539	+	7.453274561	18.88777632
chr6	21637782	21638090	AluSx4_dup86	-	15.97130263	15.34631826
chr6	25174377	25174684	AluSx4_dup107	+	11.7122886	9.443888162
chr6	26125749	26126038	AluSq_dup215	-	22.35982368	28.33166449
chr6	26180258	26180564	AluSx_dup1136	-	9.582781579	9.443888162
chr6	26273515	26273804	AluSq2_dup685	+	784.7233359	787.3841755
chr6	26327015	26327333	AluSx3_dup338	-	8.51802807	4.721944081
chr6	26328470	26328766	AluSz_dup893	-	19.16556316	25.97069244
chr6	26341509	26341646	AluSg_dup376	-	62.82045702	56.66332897
chr6	26342425	26342736	AluSz6_dup436	-	8.51802807	7.082916121
chr6	26511290	26511584	AluSx_dup1163	+	12.77704211	15.34631826
chr6	26573437	26573733	AluSx1_dup1117	+	9.582781579	3.541458061
chr6	27087728	27088033	AluSq_dup222	+	6.388521053	4.721944081
chr6	27163598	27163908	AluSg_dup389	+	9.582781579	4.721944081
chr6	27167593	27167752	AluSz_dup944	-	13.84179561	18.88777632
chr6	27176569	27176881	AluSx_dup1190	+	37.26637281	43.67798275
chr6	27244665	27244967	AluSz_dup950	+	24.4893307	18.88777632
chr6	27544082	27544387	AluSc8_dup253	-	13.84179561	7.082916121
chr6	27594430	27594745	AluSx3_dup365	+	18.10080965	23.6097204
chr6	28475605	28475920	AluSz_dup999	-	11.7122886	7.082916121
chr6	28600354	28600647	AluSz6_dup502	+	9.582781579	15.34631826
chr6	28722231	28722528	AluSp_dup616	+	6.388521053	2.36097204
chr6	28760732	28761036	AluSg_dup419	+	9.582781579	14.16583224
chr6	28809512	28809794	AluSq_dup237	+	19.16556316	20.06826234
chr6	28836838	28837139	AluSx3_dup395	+	7.453274561	8.263402142
chr6	28837819	28838120	AluY_dup1122	+	9.582781579	8.263402142
chr6	28898108	28898411	AluSg_dup421	-	162.9072868	151.1022106
chr6	28935962	28936229	AluJb_dup1227	-	25.55408421	20.06826234
chr6	28973972	28974268	AluSx_dup1309	-	6.388521053	5.902430101
chr6	28984677	28984982	AluY_dup1141	-	34.07211228	30.69263653
chr6	30489007	30489272	AluSp_dup672	-	11.7122886	10.62437418
chr6	30503212	30503511	AluSc_dup430	-	6.388521053	14.16583224
chr6	30512353	30512647	AluSg_dup448	+	6.388521053	4.721944081
chr6	30673435	30673731	AluSx_dup1368	+	23.42457719	23.6097204
chr6	30674127	30674434	AluSg_dup458	-	8.51802807	10.62437418

chr6	30784281	30784587	AluJb_dup1327	-	6.388521053	4.721944081
chr6	32839124	32839420	AluSq2_dup890	+	7.453274561	5.902430101
chr6	33241581	33241891	AluSx1_dup1454	+	12.77704211	30.69263653
chr6	34609876	34610190	AluY_dup1440	+	10.64753509	8.263402142
chr6	34666277	34666575	AluSp_dup841	+	7.453274561	5.902430101
chr6	36565115	36565426	AluY_dup1587	+	5.323767544	7.082916121
chr6	36581438	36581735	AluSz_dup1396	+	9.582781579	10.62437418
chr6	37135517	37135806	AluSc5_dup101	+	6.388521053	7.082916121
chr6	41353801	41354103	AluSg_dup677	+	37.26637281	35.41458061
chr6	41988033	41988331	AluSp_dup1030	+	6.388521053	4.721944081
chr6	73598348	73598645	AluSz_dup2324	+	10.64753509	10.62437418
chr6	85644895	85645197	AluY_dup2858	+	5.323767544	2.36097204
chr6	106824537	106824836	AluSx_dup3641	-	6.388521053	3.541458061
chr6	107060012	107060310	AluSq10_dup70	-	20.23031667	21.24874836
chr6	111468877	111469189	AluSz_dup3269	+	6.388521053	4.721944081
chr6	112260414	112260720	AluSx_dup3940	-	10.64753509	10.62437418
chr6	128538558	128538859	AluSp_dup1985	-	46.84915439	41.31701071
chr6	129702717	129703026	AluSx_dup4254	+	7.453274561	3.541458061
chr6	131751232	131751513	AluSg_dup1464	-	7.453274561	2.36097204
chr6	131926502	131926813	AluSq2_dup2485	+	7.453274561	2.36097204
chr6	137451702	137451992	AluSz_dup3850	-	7.453274561	2.36097204
chr6	149496484	149496780	AluSq2_dup2803	-	7.453274561	2.36097204
chr6	151188650	151188820	AluSz6_dup2226	+	7.453274561	1.18048602
chr6	155062594	155062874	AluSq2_dup2977	-	8.51802807	2.36097204
chr6	157235315	157235614	AluSc5_dup338	-	55.36718246	43.67798275
chr6	158236790	158237108	AluSg_dup1798	-	6.388521053	4.721944081
chr6	163621222	163621465	AluSx_dup5557	+	8.51802807	4.721944081
chr7	2265829	2266132	AluJr_dup148	+	13.84179561	24.79020642
chr7	2445455	2445728	AluSx3_dup38	-	40.46063333	33.05360857
chr7	5504148	5504407	AluSx1_dup499	+	5.323767544	2.36097204
chr7	6316541	6316850	AluSc_dup112	-	6.388521053	5.902430101
chr7	7046268	7046575	AluSx_dup659	+	7.453274561	4.721944081
chr7	13111047	13111328	AluY_dup673	-	6.388521053	0
chr7	22702341	22702643	AluSx_dup970	-	17.03605614	15.34631826
chr7	23330004	23330302	AluSx3_dup272	+	5.323767544	11.8048602
chr7	25015180	25015477	AluSx3_dup288	+	7.453274561	1.18048602
chr7	26017393	26017692	AluSc_dup320	+	6.388521053	7.082916121
chr7	39520167	39520447	AluSg_dup519	+	7.453274561	8.263402142
chr7	44848862	44849030	AluSp_dup680	-	12.77704211	12.98534622
chr7	44856674	44856986	AluY_dup1632	-	21.29507018	25.97069244
chr7	45846410	45846715	AluSz6_dup744	-	20.23031667	15.34631826
chr7	46240109	46240401	AluSx3_dup488	+	31.94260526	22.42923438
chr7	47654271	47654572	AluSz_dup1542	+	14.90654912	12.98534622
chr7	66204302	66204515	AluSx1_dup2682	-	9.582781579	18.88777632
chr7	66432736	66433029	AluSx_dup2638	+	6.388521053	1.18048602
chr7	67390768	67390897	AluSq10_dup55	-	8.51802807	12.98534622
chr7	72843695	72843991	AluSx1_dup3354	+	13.84179561	11.8048602
chr7	73403192	73403503	AluSp_dup1270	+	10.64753509	14.16583224
chr7	73629453	73629737	AluJo_dup2498	+	15.97130263	9.443888162
chr7	74230057	74230362	AluY_dup2855	+	17.03605614	4.721944081
chr7	74867804	74868107	AluSx3_dup907	-	30.87785175	30.69263653

chr7	75075985	75076288	AluSx3_dup911	+	20.23031667	14.16583224
chr7	75838057	75838364	AluSq2_dup1854	+	6.388521053	1.18048602
chr7	75913699	75913993	AluSx1_dup3980	-	6.388521053	5.902430101
chr7	76391151	76391454	AluSz_dup3251	+	43.65489386	41.31701071
chr7	76417051	76417358	AluSp_dup1443	-	6.388521053	4.721944081
chr7	80221664	80221939	AluSc5_dup205	-	5.323767544	5.902430101
chr7	92604442	92604741	AluSx_dup4266	-	11.7122886	5.902430101
chr7	99330305	99330614	AluSx1_dup4768	-	8.51802807	14.16583224
chr7	99472126	99472435	AluSx_dup4563	-	44.71964737	38.95603867
chr7	100086654	100086943	AluSz6_dup1735	-	6.388521053	4.721944081
chr7	100318935	100319209	AluSz6_dup1749	-	6.388521053	4.721944081
chr7	100664948	100665255	AluSz_dup3980	+	6.388521053	2.36097204
chr7	100669219	100669533	AluJr_dup4516	+	13.84179561	22.42923438
chr7	101116784	101117053	AluSz_dup4046	+	10.64753509	10.62437418
chr7	101192791	101193107	AluY_dup3955	+	10.64753509	12.98534622
chr7	101255076	101255384	AluSx_dup4774	+	6.388521053	7.082916121
chr7	101809167	101809475	AluSq_dup771	-	75.59749912	72.00964723
chr7	101810395	101810707	AluSz_dup4140	+	7.453274561	2.36097204
chr7	104965118	104965408	AluSx3_dup1254	+	5.323767544	3.541458061
chr7	128641958	128642065	AluJb_dup5272	+	4.259014035	0
chr7	129991297	129991599	AluSx1_dup6048	-	5.323767544	0
chr7	132763801	132764107	AluSz_dup5107	-	83.05077368	70.82916121
chr7	149668988	149669294	AluSz_dup5822	-	10.64753509	5.902430101
chr7	157308802	157309105	AluSp_dup2604	-	22.35982368	12.98534622
chr8	1996273	1996566	AluSq2_dup26	-	18.10080965	24.79020642
chr8	6801522	6801818	AluSz_dup163	+	41.52538684	27.15117847
chr8	8793905	8794206	AluSz_dup274	+	7.453274561	3.541458061
chr8	17838865	17839178	AluSx_dup561	-	20.23031667	25.97069244
chr8	26189358	26189660	AluSx1_dup1018	+	176.7490825	204.2240815
chr8	27409726	27410021	AluSq2_dup462	-	6.388521053	11.8048602
chr8	30059945	30060255	AluSx1_dup1220	+	28.74834474	27.15117847
chr8	30265082	30265378	AluSq2_dup543	+	18.10080965	24.79020642
chr8	33419846	33420151	AluJb_dup1464	+	5.323767544	7.082916121
chr8	38388751	38389065	AluSx_dup1468	-	7.453274561	5.902430101
chr8	39764731	39765026	AluSx_dup1547	+	7.453274561	5.902430101
chr8	41151342	41151640	AluSq2_dup807	-	21.29507018	18.88777632
chr8	42248599	42248890	AluSx4_dup128	+	11.7122886	8.263402142
chr8	42421522	42421818	AluSp_dup584	+	5.323767544	3.541458061
chr8	42592625	42592919	AluSx_dup1706	-	5.323767544	0
chr8	42658043	42658326	AluSx_dup1711	-	6.388521053	5.902430101
chr8	43094108	43094335	AluSx1_dup1962	-	6.388521053	11.8048602
chr8	48102486	48102768	AluSz_dup1817	-	10.64753509	12.98534622
chr8	48626948	48627255	AluYk2_dup8	-	6.388521053	11.8048602
chr8	49083061	49083351	AluSz_dup1840	+	9.582781579	5.902430101
chr8	52109722	52110028	AluSq_dup305	+	11.7122886	14.16583224
chr8	66546122	66546427	AluJb_dup2551	-	13.84179561	12.98534622
chr8	68244488	68244808	AluSx_dup2473	+	17.03605614	23.6097204
chr8	69548448	69548758	AluSz_dup2382	-	9.582781579	9.443888162
chr8	79709961	79710254	AluSz_dup2612	+	6.388521053	2.36097204
chr8	81721522	81721834	AluSp_dup1096	+	92.63355526	113.3266579
chr8	89813974	89814256	AluSz6_dup1254	+	14.90654912	18.88777632

chr8	98001455	98001777	AluSz6_dup1376	-	10.64753509	5.902430101
chr8	99019204	99019499	AluSq_dup501	-	10.64753509	11.8048602
chr8	121323085	121323388	AluSp_dup1576	+	87.30978772	96.79985366
chr8	123103421	123103721	AluSx_dup4048	-	10.64753509	9.443888162
chr8	124830457	124830757	AluSx_dup4179	-	6.388521053	10.62437418
chr8	124846062	124846299	AluSz_dup3922	+	30.87785175	35.41458061
chr8	125402265	125402567	AluSp_dup1671	+	5.323767544	8.263402142
chr8	127765323	127765635	AluSx_dup4283	+	12.77704211	24.79020642
chr8	130518527	130518836	AluY_dup3899	-	13.84179561	17.7072903
chr8	133340479	133340785	AluSg7_dup291	+	7.453274561	9.443888162
chr8	133590126	133590390	AluJo_dup3143	-	17.03605614	4.721944081
chr8	140491857	140492156	AluSz_dup4305	+	181.0080965	178.2533891
chr8	140646157	140646459	AluY_dup4160	+	108.6048579	115.68763
chr8	141145853	141146145	AluSc8_dup819	-	9.582781579	8.263402142
chr8	143906443	143906721	AluSq2_dup2464	-	11.7122886	12.98534622
chr9	752482	752783	AluSq2_dup23	+	8.51802807	15.34631826
chr9	6775012	6775314	AluSz_dup233	-	13.84179561	9.443888162
chr9	19148440	19148740	AluSg_dup168	+	8.51802807	7.082916121
chr9	27088416	27088709	AluY_dup797	-	7.453274561	3.541458061
chr9	34056020	34056228	AluSx_dup905	-	8.51802807	8.263402142
chr9	35951552	35951843	AluSx_dup1008	-	13.84179561	20.06826234
chr9	36297321	36297619	AluY_dup1150	-	10.64753509	15.34631826
chr9	72376389	72376682	AluSx3_dup482	+	17.03605614	4.721944081
chr9	72379533	72379793	AluSx_dup1745	-	6.388521053	11.8048602
chr9	76926074	76926362	AluSx1_dup1861	-	11.7122886	8.263402142
chr9	86738095	86738384	AluSx4_dup233	-	36.2016193	34.23409459
chr9	92009436	92009747	AluSx3_dup688	-	5.323767544	0
chr9	92115680	92115979	AluSp_dup1153	-	26.61883772	16.52680428
chr9	97964601	97964822	AluYh3_dup75	+	7.453274561	1.18048602
chr9	105078046	105078340	AluY_dup3502	+	8.51802807	0
chr9	107618432	107618740	AluSg_dup1000	-	7.453274561	9.443888162
chr9	110343923	110344211	AluSg_dup1027	+	125.640914	115.68763
chr9	113485094	113485388	AluYh3_dup82	-	79.85651316	62.56575907
chr9	114320918	114321228	AluSz_dup2968	+	68.14422456	67.28770315
chr9	122828827	122829135	AluSx1_dup3542	+	9.582781579	9.443888162
chr9	124794610	124794921	AluSx_dup3842	-	9.582781579	8.263402142
chr9	124812162	124812460	AluSq2_dup2134	-	31.94260526	22.42923438
chr9	125199787	125200098	AluYb8_dup120	+	12.77704211	17.7072903
chr9	125305371	125305668	AluSg7_dup312	-	5.323767544	10.62437418
chr9	127919796	127919911	AluJb_dup4388	+	2.129507018	0
chr9	127919955	127920120	AluJb_dup4389	+	7.453274561	1.18048602
chr9	127924086	127924235	AluSx1_dup3909	+	15.97130263	8.263402142
chr9	128024620	128024909	AluSx1_dup3930	+	6.388521053	4.721944081
chr9	128060610	128060920	AluSg_dup1277	-	24.4893307	20.06826234
chr9	128158541	128158841	AluSg_dup1281	-	11.7122886	17.7072903
chr9	128171445	128171766	AluSx3_dup1136	+	5.323767544	3.541458061
chr9	129762845	129763155	AluSq2_dup2393	+	10.64753509	12.98534622
chr9	129824317	129824595	AluSx1_dup4156	+	10.64753509	10.62437418
chr9	130145449	130145729	AluSx1_dup4202	-	5.323767544	18.88777632
chr9	131373777	131374077	AluY_dup4486	+	33.00735877	18.88777632
chr9	133482731	133483032	AluSg_dup1446	-	10.64753509	15.34631826

chr9	134249863	134250159	AluSq2_dup2574	+	7.453274561	2.36097204
chr9	136706647	136706958	AluSx1_dup4676	+	6.388521053	11.8048602
chr9	136834488	136834777	AluSc_dup1607	-	18.10080965	11.8048602
chr9	137117985	137118287	AluSx1_dup4712	-	18.10080965	10.62437418
chr9	137424431	137424737	AluSx1_dup4740	-	7.453274561	5.902430101
chrX	2664275	2664576	AluSx3_dup102	-	11.7122886	20.06826234
chrX	2929512	2929825	AluSx_dup376	+	18.10080965	14.16583224
chrX	9357205	9357509	AluJb_dup531	+	8.51802807	9.443888162
chrX	10003365	10003666	AluSc_dup126	-	10.64753509	8.263402142
chrX	13488450	13488755	AluSg_dup204	+	19.16556316	14.16583224
chrX	24053562	24053857	AluY_dup813	-	8.51802807	3.541458061
chrX	34526017	34526318	AluSx4_dup117	+	8.51802807	4.721944081
chrX	41027705	41028002	AluSp_dup604	+	136.2884491	148.7412385
chrX	41300457	41300766	AluSz_dup1456	+	19.16556316	28.33166449
chrX	44652039	44652337	AluSg_dup536	+	15.97130263	11.8048602
chrX	49127325	49127606	AluSx1_dup2252	+	8.51802807	9.443888162
chrX	49127633	49127659	AluSx1_dup2253	+	2.129507018	4.721944081
chrX	68462510	68462808	AluSz_dup2255	+	29.81309825	31.87312255
chrX	68475440	68475646	AluSx_dup2605	-	15.97130263	9.443888162
chrX	77896069	77896377	AluSq_dup464	-	9.582781579	14.16583224
chrX	85003067	85003378	AluY_dup2241	-	5.323767544	2.36097204
chrX	119609910	119610213	AluSg7_dup271	-	8.51802807	9.443888162
chrX	129612961	129613255	AluSx1_dup4020	+	7.453274561	9.443888162
chrX	134521429	134521732	AluSg_dup1339	-	7.453274561	7.082916121
chrX	134903758	134904065	AluSg_dup1345	+	7.453274561	4.721944081
chrX	154330588	154330881	AluSx_dup4713	+	9.582781579	3.541458061
chr1	1375700	1376008	AluSx1_dup82	+	10.64753509	8.263402142
chr1	6538390	6538690	AluSx1_dup299	+	4.259014035	7.082916121
chr1	8129280	8129583	AluSx_dup431	-	0	5.902430101
chr1	8823613	8823914	AluSx1_dup468	+	2.129507018	8.263402142
chr1	8942113	8942423	AluSx_dup522	-	4.259014035	8.263402142
chr1	9139790	9140044	AluSx1_dup513	+	4.259014035	12.98534622
chr1	10139709	10140020	AluSp_dup263	-	3.194260526	7.082916121
chr1	16454044	16454358	AluSp_dup511	-	0	7.082916121
chr1	16616417	16616718	AluSz_dup1016	+	2.129507018	7.082916121
chr1	17063328	17063626	AluSx1_dup1194	-	4.259014035	11.8048602
chr1	19494312	19494609	AluSx_dup1515	+	4.259014035	11.8048602
chr1	19514991	19515283	AluSq10_dup20	+	4.259014035	12.98534622
chr1	20613206	20613503	AluSq2_dup692	-	0	9.443888162
chr1	22991971	22992277	AluYk4_dup8	+	1.064753509	7.082916121
chr1	23302949	23303234	AluJo_dup1114	-	6.388521053	11.8048602
chr1	23680395	23680707	AluY_dup1341	-	5.323767544	8.263402142
chr1	24741615	24741914	AluSp_dup761	-	2.129507018	8.263402142
chr1	27625658	27625966	AluSx4_dup184	+	3.194260526	12.98534622
chr1	28425125	28425416	AluSg_dup673	-	3.194260526	9.443888162
chr1	31976125	31976429	AluSx1_dup2396	+	4.259014035	7.082916121
chr1	35193859	35193996	AluSq2_dup1352	+	1.064753509	10.62437418
chr1	37570249	37570546	AluSg_dup897	+	7.453274561	10.62437418
chr1	40375942	40376250	AluSq2_dup1583	-	0	5.902430101
chr1	44671646	44671938	AluSx1_dup3189	+	1.064753509	8.263402142
chr1	46202410	46202724	AluSz_dup2966	+	1.064753509	7.082916121

chr1	47256712	47256978	AluSp_dup1624	+	1.064753509	7.082916121
chr1	52105297	52105595	AluSx3_dup1034	+	1.064753509	7.082916121
chr1	77824983	77825304	AluSz_dup4006	-	4.259014035	8.263402142
chr1	78191348	78191644	AluSq2_dup2357	-	4.259014035	5.902430101
chr1	86436698	86437011	AluSp_dup2183	-	2.129507018	5.902430101
chr1	94633422	94633729	AluSg7_dup364	+	5.323767544	11.8048602
chr1	100189058	100189370	AluSz_dup4557	+	0	5.902430101
chr1	109234178	109234323	AluSz_dup4743	-	2.129507018	3.541458061
chr1	109638058	109638380	AluSq2_dup2761	-	0	5.902430101
chr1	145928380	145928728	AluSz_dup5221	-	1.064753509	7.082916121
chr1	146378413	146378688	AluSx_dup6009	+	1.064753509	5.902430101
chr1	148061234	148061353	AluY_dup5247	-	4.259014035	4.721944081
chr1	151247120	151247426	AluSx3_dup1766	-	1.064753509	5.902430101
chr1	151254129	151254428	AluSx3_dup1767	-	10.64753509	10.62437418
chr1	151258013	151258327	AluSq_dup1026	-	1.064753509	9.443888162
chr1	154133867	154134160	AluSq_dup1056	+	0	5.902430101
chr1	154462814	154463103	AluSz6_dup2737	-	5.323767544	8.263402142
chr1	155743632	155743762	AluSx_dup6683	-	3.194260526	8.263402142
chr1	156193471	156193761	AluSx_dup6733	-	43.65489386	27.15117847
chr1	157069155	157069464	AluSg_dup2191	-	2.129507018	7.082916121
chr1	171441571	171441870	AluSg_dup2332	+	0	7.082916121
chr1	203563855	203564167	AluSx1_dup7686	-	4.259014035	10.62437418
chr1	203599417	203599717	AluSz6_dup3467	+	5.323767544	8.263402142
chr1	225934533	225934837	AluSx1_dup8484	-	3.194260526	11.8048602
chr1	226024068	226024352	AluSx1_dup8498	+	2.129507018	7.082916121
chr1	226088974	226089294	AluSg_dup2963	-	1.064753509	15.34631826
chr10	6160924	6161235	AluSq2_dup111	-	1.064753509	7.082916121
chr10	11820666	11820959	AluSx_dup445	-	4.259014035	8.263402142
chr10	14914662	14914954	AluSx_dup718	+	1.064753509	7.082916121
chr10	21554810	21555120	AluSq_dup181	-	1.064753509	9.443888162
chr10	22816620	22816923	AluSx_dup1170	-	8.51802807	11.8048602
chr10	27130577	27130870	AluSq2_dup619	+	0	7.082916121
chr10	27187469	27187765	AluSz6_dup576	+	9.582781579	12.98534622
chr10	28756379	28756659	AluSq4_dup22	-	1.064753509	7.082916121
chr10	45943593	45943855	AluJb_dup2127	+	1.064753509	5.902430101
chr10	49387376	49387690	AluSz_dup2113	+	36.2016193	25.97069244
chr10	49912682	49912945	AluJb_dup2277	+	5.323767544	7.082916121
chr10	68807635	68807922	AluSg4_dup164	+	1.064753509	5.902430101
chr10	68932271	68932559	AluSz_dup2625	-	0	7.082916121
chr10	72648605	72648749	AluJb_dup3194	-	7.453274561	9.443888162
chr10	73942410	73942701	AluSg_dup938	+	0	5.902430101
chr10	73992376	73992669	AluSx1_dup3223	+	2.129507018	7.082916121
chr10	74737038	74737331	AluSx_dup3275	-	1.064753509	7.082916121
chr10	97637432	97637708	AluSx3_dup1057	-	0	7.082916121
chr10	102455335	102455452	AluJb_dup4822	-	0	5.902430101
chr10	102455452	102455576	AluJo_dup3347	-	0	3.541458061
chr10	103200758	103201060	AluSz_dup4145	-	4.259014035	5.902430101
chr10	110624278	110624598	AluSx_dup4783	-	1.064753509	7.082916121
chr10	114736906	114737042	AluSz6_dup2075	+	1.064753509	5.902430101
chr10	114874499	114874803	AluSq_dup777	-	4.259014035	7.082916121
chr11	9366509	9366817	AluSz6_dup137	-	2.129507018	7.082916121

chr11	9638405	9638716	AluSx1_dup432	-	4.259014035	5.902430101
chr11	10750396	10750697	AluSx1_dup464	-	29.81309825	16.52680428
chr11	33147314	33147592	AluSg_dup320	+	3.194260526	7.082916121
chr11	46310248	46310567	AluSx1_dup1354	-	0	7.082916121
chr11	46736457	46736597	AluJo_dup929	-	2.129507018	10.62437418
chr11	47336206	47336519	AluSx1_dup1460	+	6.388521053	7.082916121
chr11	47838723	47839029	AluSg_dup500	+	3.194260526	8.263402142
chr11	61284675	61284972	AluSz_dup1666	+	2.129507018	7.082916121
chr11	62170935	62171277	AluSx_dup1931	-	4.259014035	9.443888162
chr11	62423977	62424274	AluSq_dup304	+	2.129507018	5.902430101
chr11	62847424	62847709	AluSx_dup2023	+	0	7.082916121
chr11	62862931	62863220	AluSz_dup1769	-	4.259014035	5.902430101
chr11	63672486	63672767	AluSx1_dup2035	+	1.064753509	8.263402142
chr11	63858366	63858652	AluSg_dup664	-	4.259014035	8.263402142
chr11	65506778	65507076	AluSx3_dup626	-	0	10.62437418
chr11	65512040	65512333	AluSz6_dup930	+	5.323767544	9.443888162
chr11	65986795	65987087	AluSx1_dup2269	+	4.259014035	8.263402142
chr11	67809565	67809863	AluSx1_dup2476	+	6.388521053	9.443888162
chr11	72079259	72079554	AluSg7_dup195	+	5.323767544	8.263402142
chr11	73635979	73636277	AluSq_dup463	-	4.259014035	5.902430101
chr11	73843221	73843523	AluSx3_dup761	-	3.194260526	14.16583224
chr11	74026687	74026983	AluSc_dup814	+	4.259014035	10.62437418
chr11	78125877	78126175	AluY_dup2837	+	1.064753509	12.98534622
chr11	110515667	110515969	AluSz_dup3456	+	9.582781579	12.98534622
chr11	111441776	111442081	AluSz_dup3473	+	5.323767544	8.263402142
chr11	111827586	111827883	AluSx_dup3829	+	1.064753509	5.902430101
chr11	122153419	122153734	AluSz_dup3932	+	4.259014035	7.082916121
chr12	1723984	1724280	AluSx3_dup38	-	1.064753509	5.902430101
chr12	12036278	12036579	AluSc_dup173	+	2.129507018	7.082916121
chr12	13018990	13019295	AluSz_dup561	-	4.259014035	7.082916121
chr12	32036107	32036418	AluSx1_dup1147	-	2.129507018	11.8048602
chr12	43831546	43831842	AluSx4_dup151	-	6.388521053	16.52680428
chr12	45991280	45991576	AluSz_dup1382	+	17.03605614	30.69263653
chr12	48682600	48682908	AluSp_dup776	+	18.10080965	18.88777632
chr12	49934253	49934537	AluSx_dup1769	-	2.129507018	5.902430101
chr12	50027545	50027826	AluSx1_dup1675	+	1.064753509	5.902430101
chr12	50305076	50305378	AluSq_dup273	+	1.064753509	5.902430101
chr12	51294287	51294589	AluSg_dup642	+	1.064753509	5.902430101
chr12	51990312	51990614	AluJb_dup2385	-	3.194260526	9.443888162
chr12	55843688	55843985	AluSx1_dup2063	+	0	5.902430101
chr12	56501725	56502010	AluSz_dup1993	-	0	9.443888162
chr12	56661731	56661794	AluY_dup2318	-	1.064753509	7.082916121
chr12	56662467	56662603	AluJb_dup2723	-	5.323767544	5.902430101
chr12	57682345	57682642	AluSx_dup2413	+	3.194260526	9.443888162
chr12	76017845	76018139	AluSq2_dup1621	-	3.194260526	9.443888162
chr12	77109647	77109957	AluSz_dup2662	-	3.194260526	5.902430101
chr12	77845651	77845951	AluSp_dup1472	-	6.388521053	18.88777632
chr12	92727595	92727890	AluSq2_dup1790	-	0	7.082916121
chr12	96486974	96487257	AluSx1_dup3370	-	4.259014035	9.443888162
chr12	101890749	101891048	AluSc_dup1130	-	5.323767544	11.8048602
chr12	104191065	104191376	AluSz_dup3450	-	3.194260526	5.902430101

chr12	111799008	111799161	AluSx3_dup1202	-	2.129507018	7.082916121
chr12	121234993	121235291	AluSx1_dup4897	-	5.323767544	5.902430101
chr12	121672784	121673060	AluSz_dup4779	-	1.064753509	7.082916121
chr12	121687361	121687662	AluSq2_dup2543	+	2.129507018	8.263402142
chr12	121924426	121924729	AluSq2_dup2557	-	173.5548219	197.1411654
chr12	122258698	122259007	AluSx_dup5231	+	5.323767544	8.263402142
chr12	122415957	122416221	AluSg7_dup367	+	1.064753509	7.082916121
chr12	122509166	122509479	AluSx3_dup1390	+	4.259014035	7.082916121
chr12	122746822	122747116	AluSq2_dup2616	+	4.259014035	10.62437418
chr12	122758070	122758369	AluSg4_dup296	-	4.259014035	8.263402142
chr12	123537852	123538156	AluSx1_dup5234	-	3.194260526	11.8048602
chr12	123586347	123586649	AluSz_dup5045	-	4.259014035	10.62437418
chr13	19811801	19811938	AluSz6_dup47	+	4.259014035	5.902430101
chr13	27301450	27301743	AluSz6_dup186	+	0	8.263402142
chr13	30972624	30972936	AluSz6_dup246	-	0	8.263402142
chr13	41433763	41434067	AluSx3_dup257	-	4.259014035	10.62437418
chr13	49538428	49538730	AluJb_dup1304	+	1.064753509	8.263402142
chr13	73031454	73031759	AluSq2_dup966	-	5.323767544	5.902430101
chr13	79443142	79443451	AluSc_dup641	+	3.194260526	9.443888162
chr13	95334376	95334674	AluSz_dup2003	+	1.064753509	7.082916121
chr13	113380842	113381162	AluY_dup3006	+	1.064753509	8.263402142
chr14	22803137	22803437	AluSx_dup206	+	8.51802807	12.98534622
chr14	34538097	34538379	AluSx_dup586	+	6.388521053	12.98534622
chr14	54947057	54947329	AluSp_dup575	+	4.259014035	16.52680428
chr14	76989845	76990135	AluSg_dup775	+	4.259014035	12.98534622
chr14	102078543	102078841	AluSx1_dup3114	+	5.323767544	16.52680428
chr14	104815004	104815299	AluSx1_dup3344	-	25.55408421	23.6097204
chr15	22838058	22838357	AluY_dup172	-	4.259014035	11.8048602
chr15	42934563	42934871	AluSz_dup775	+	1.064753509	5.902430101
chr15	50879870	50880179	AluSx1_dup1301	+	3.194260526	10.62437418
chr15	50930072	50930366	AluSp_dup753	-	3.194260526	7.082916121
chr15	63520554	63520862	AluSq2_dup1001	-	0	5.902430101
chr15	64628636	64628924	AluSp_dup1016	-	6.388521053	8.263402142
chr15	65222145	65222457	AluSz_dup1816	-	6.388521053	10.62437418
chr15	74012182	74012473	AluSg7_dup195	-	7.453274561	11.8048602
chr15	79934373	79934652	AluSx1_dup2770	+	3.194260526	5.902430101
chr15	80765352	80765649	AluSg_dup962	-	10.64753509	14.16583224
chr15	81116305	81116596	AluSx_dup2884	-	4.259014035	8.263402142
chr15	84420868	84421160	AluSx1_dup2954	+	7.453274561	12.98534622
chr15	85367238	85367521	AluSz_dup2809	+	6.388521053	12.98534622
chr15	89843657	89843809	AluSq_dup563	+	2.129507018	11.8048602
chr15	92761961	92762247	AluSz_dup3153	+	1.064753509	5.902430101
chr15	101746248	101746383	AluY_dup3783	+	4.259014035	3.541458061
chr16	581760	582054	AluSg_dup38	-	4.259014035	8.263402142
chr16	595593	595900	AluSg_dup39	-	2.129507018	7.082916121
chr16	3151542	3151826	AluSg_dup101	+	2.129507018	8.263402142
chr16	4136736	4137037	AluSq_dup63	-	2.129507018	8.263402142
chr16	11639712	11639854	AluSz_dup846	+	2.129507018	9.443888162
chr16	11747636	11747929	AluSx_dup935	+	2.129507018	14.16583224
chr16	11955427	11955749	AluSc8_dup187	+	4.259014035	9.443888162
chr16	14914800	14915115	AluSc5_dup54	-	7.453274561	12.98534622

chr16	15829852	15830145	AluSx_dup1311	+	3.194260526	8.263402142
chr16	15942110	15942410	AluSp_dup474	-	5.323767544	10.62437418
chr16	22196567	22196873	AluSq2_dup834	-	5.323767544	10.62437418
chr16	24580973	24581266	AluSz_dup1941	+	11.7122886	16.52680428
chr16	25039066	25039341	AluJo_dup1629	-	5.323767544	10.62437418
chr16	28378180	28378257	AluJr_dup2108	-	0	1.18048602
chr16	30052084	30052381	AluSq2_dup1165	+	2.129507018	9.443888162
chr16	30320269	30320584	AluSx3_dup563	+	3.194260526	10.62437418
chr16	46787323	46787634	AluSz6_dup1177	+	5.323767544	10.62437418
chr16	50127018	50127312	AluSx1_dup3395	+	3.194260526	7.082916121
chr16	67703121	67703403	AluSp_dup1298	+	2.129507018	7.082916121
chr16	69544314	69544598	AluSx1_dup4351	-	1.064753509	9.443888162
chr16	69635023	69635310	AluSq2_dup1963	-	4.259014035	7.082916121
chr16	70145224	70145435	AluSg_dup1105	-	4.259014035	7.082916121
chr16	70440659	70440942	AluSg4_dup260	+	3.194260526	7.082916121
chr16	71790258	71790557	AluSp_dup1513	+	3.194260526	7.082916121
chr16	88541594	88541897	AluSx1_dup5535	-	3.194260526	14.16583224
chr16	89814660	89814970	AluSg_dup1429	+	2.129507018	8.263402142
chr17	2754053	2754185	AluSc5_dup11	-	1.064753509	7.082916121
chr17	4361657	4361981	AluSz6_dup133	+	3.194260526	8.263402142
chr17	5494305	5494623	AluSz_dup388	+	7.453274561	14.16583224
chr17	7149077	7149352	AluSg_dup240	-	5.323767544	9.443888162
chr17	7185831	7186137	AluSx3_dup228	-	4.259014035	11.8048602
chr17	7198865	7199049	AluJb_dup620	+	2.129507018	4.721944081
chr17	8296737	8297046	AluSx1_dup1051	+	3.194260526	8.263402142
chr17	8329243	8329552	AluSq_dup196	+	4.259014035	12.98534622
chr17	16431292	16431598	AluSx_dup1409	-	2.129507018	7.082916121
chr17	17237823	17238123	AluSq_dup297	-	2.129507018	5.902430101
chr17	19309142	19309428	AluSc_dup472	-	3.194260526	10.62437418
chr17	28945853	28946150	AluSx3_dup604	+	11.7122886	25.97069244
chr17	31818574	31818877	AluSx1_dup2197	+	0	7.082916121
chr17	38525719	38526012	AluSq4_dup49	-	0	5.902430101
chr17	38678162	38678449	AluSx_dup2708	-	2.129507018	8.263402142
chr17	38803347	38803644	AluSx_dup2717	+	6.388521053	16.52680428
chr17	40047379	40047691	AluSx3_dup832	+	4.259014035	8.263402142
chr17	40137949	40138250	AluSg_dup939	+	2.129507018	8.263402142
chr17	40239686	40239996	AluSx1_dup2823	-	8.51802807	17.7072903
chr17	42269927	42270214	AluSx_dup3065	+	0	5.902430101
chr17	42390775	42391074	AluSq2_dup1532	+	4.259014035	5.902430101
chr17	42399433	42399730	AluSx1_dup2995	+	1.064753509	5.902430101
chr17	44491209	44491508	AluSg7_dup252	+	3.194260526	5.902430101
chr17	44946838	44947142	AluSq2_dup1689	+	6.388521053	15.34631826
chr17	48010663	48010966	AluSz_dup2767	-	5.323767544	9.443888162
chr17	49861893	49862204	AluSp_dup1920	+	4.259014035	8.263402142
chr17	60582493	60582803	AluSq2_dup2208	-	5.323767544	9.443888162
chr17	61190594	61190900	AluSq2_dup2226	-	4.259014035	7.082916121
chr17	63843360	63843659	AluSq2_dup2335	+	8.51802807	18.88777632
chr17	67237707	67238005	AluSz_dup3978	+	2.129507018	7.082916121
chr17	67812199	67812498	AluSq2_dup2490	-	2.129507018	7.082916121
chr17	76109789	76110008	AluJo_dup3383	+	1.064753509	7.082916121
chr17	76616274	76616576	AluSg_dup1757	-	0	7.082916121

chr17	77315288	77315585	AluSg_dup1781	-	3.194260526	7.082916121
chr17	77485837	77486115	AluSz_dup4685	-	3.194260526	5.902430101
chr17	78922535	78922794	AluSq2_dup2909	+	5.323767544	7.082916121
chr17	78970647	78970942	AluSx1_dup5788	+	4.259014035	11.8048602
chr17	80341807	80342097	AluSz_dup4876	-	0	5.902430101
chr17	80484137	80484444	AluSx1_dup5884	+	3.194260526	8.263402142
chr17	80496006	80496315	AluSx1_dup5886	-	7.453274561	8.263402142
chr17	82522803	82523092	AluSc5_dup311	-	6.388521053	7.082916121
chr18	9644785	9645072	AluSx1_dup380	-	2.129507018	5.902430101
chr18	9647176	9647481	AluSx1_dup381	-	1.064753509	9.443888162
chr18	9879836	9880125	AluSx1_dup398	-	1.064753509	5.902430101
chr18	21462438	21462749	AluSx_dup652	-	0	5.902430101
chr18	48985821	48986133	AluSp_dup599	-	3.194260526	8.263402142
chr18	57767505	57767801	AluSq2_dup965	+	6.388521053	9.443888162
chr18	57821287	57821576	AluSq2_dup968	+	4.259014035	11.8048602
chr18	59716505	59716802	AluSz_dup1730	+	1.064753509	7.082916121
chr18	69131842	69132139	AluSg_dup634	+	1.064753509	7.082916121
chr18	69190811	69191147	AluYm1_dup92	+	5.323767544	8.263402142
chr19	774497	774770	AluSg_dup24	-	1.064753509	7.082916121
chr19	1134765	1135069	AluSg7_dup9	+	9.582781579	12.98534622
chr19	1537814	1538094	AluSq2_dup47	+	4.259014035	5.902430101
chr19	1989112	1989375	AluJo_dup142	+	15.97130263	10.62437418
chr19	2084211	2084505	AluSz_dup123	+	2.129507018	16.52680428
chr19	3103984	3104118	AluSx1_dup508	-	3.194260526	5.902430101
chr19	3182691	3182990	AluSx_dup419	-	1.064753509	7.082916121
chr19	3788206	3788342	AluSq10_dup5	+	0	4.721944081
chr19	4069959	4070109	AluSp_dup178	-	2.129507018	7.082916121
chr19	4596873	4597179	AluSx1_dup817	-	4.259014035	10.62437418
chr19	4621707	4622001	AluSg_dup190	-	1.064753509	8.263402142
chr19	4790740	4791047	AluSq2_dup231	+	4.259014035	15.34631826
chr19	4900737	4901031	AluSp_dup227	+	7.453274561	9.443888162
chr19	9197101	9197399	AluSx4_dup61	-	2.129507018	5.902430101
chr19	10585418	10585700	AluSc_dup296	+	4.259014035	10.62437418
chr19	11149467	11149592	AluJr4_dup148	+	0	9.443888162
chr19	12779867	12780172	AluSz_dup1414	+	5.323767544	15.34631826
chr19	13721577	13721875	AluSc_dup402	+	0	5.902430101
chr19	13846056	13846360	AluSz_dup1546	-	5.323767544	7.082916121
chr19	13929007	13929304	AluSx4_dup135	-	9.582781579	10.62437418
chr19	14605102	14605395	AluSq_dup356	-	2.129507018	5.902430101
chr19	16317024	16317166	AluJr_dup1914	+	2.129507018	4.721944081
chr19	17233942	17234240	AluSg_dup648	+	4.259014035	10.62437418
chr19	17586571	17586870	AluJb_dup2005	+	2.129507018	5.902430101
chr19	18152070	18152372	AluSp_dup978	+	2.129507018	8.263402142
chr19	18297073	18297369	AluSg_dup685	+	6.388521053	15.34631826
chr19	20201000	20201276	AluSx_dup2830	+	2.129507018	7.082916121
chr19	23219389	23219675	AluSx1_dup3544	-	57.49668947	61.38527305
chr19	38325120	38325414	AluSx4_dup355	-	4.259014035	7.082916121
chr19	39387855	39388151	AluSx_dup4148	+	4.259014035	8.263402142
chr19	39493895	39494105	AluSg_dup1156	-	2.129507018	5.902430101
chr19	40187925	40188223	AluSg_dup1169	-	2.129507018	10.62437418
chr19	40522348	40522651	AluSx_dup4269	-	6.388521053	10.62437418

chr19	40637009	40637297	AluSx_dup4283	-	4.259014035	7.082916121
chr19	44762521	44762819	AluSz_dup3853	-	2.129507018	7.082916121
chr19	45426100	45426401	AluSx4_dup414	+	5.323767544	11.8048602
chr19	46282651	46282939	AluSx1_dup5273	+	4.259014035	9.443888162
chr19	47129298	47129592	AluSx3_dup1255	-	1.064753509	7.082916121
chr19	47324880	47325192	AluSx_dup4965	+	5.323767544	8.263402142
chr19	49627522	49627826	AluSz_dup4500	+	1.064753509	7.082916121
chr19	49728065	49728346	AluSq2_dup2380	+	1.064753509	8.263402142
chr19	49733481	49733783	AluSx3_dup1355	+	12.77704211	18.88777632
chr19	49756777	49757078	AluSx_dup5347	+	5.323767544	12.98534622
chr2	8598527	8598832	AluSz6_dup71	+	7.453274561	16.52680428
chr2	11106538	11106854	AluJr_dup194	+	0	7.082916121
chr2	20226932	20227162	AluSp_dup203	-	2.129507018	7.082916121
chr2	25683709	25684014	AluSz6_dup317	-	1.064753509	7.082916121
chr2	25831037	25831319	AluSz_dup669	+	2.129507018	8.263402142
chr2	27642564	27642864	AluSp_dup376	-	5.323767544	7.082916121
chr2	30106825	30107142	AluSp_dup411	+	14.90654912	15.34631826
chr2	33415378	33415677	AluSq2_dup666	+	3.194260526	14.16583224
chr2	42953553	42953862	AluSz_dup1432	+	1.064753509	7.082916121
chr2	47392262	47392481	AluSx_dup1865	-	1.064753509	10.62437418
chr2	54006155	54006446	AluSq10_dup41	-	1.064753509	8.263402142
chr2	58045843	58046144	AluSq_dup350	-	4.259014035	7.082916121
chr2	69677240	69677529	AluSx_dup2681	-	4.259014035	8.263402142
chr2	74544021	74544335	AluSx_dup2915	+	1.064753509	9.443888162
chr2	84869697	84869991	AluSz6_dup1344	+	5.323767544	7.082916121
chr2	85007769	85008062	AluSz_dup2797	-	2.129507018	8.263402142
chr2	85040752	85041059	AluSg_dup932	-	4.259014035	14.16583224
chr2	85382521	85382815	AluSx_dup3099	-	6.388521053	8.263402142
chr2	85413297	85413612	AluSq_dup506	+	5.323767544	9.443888162
chr2	85439735	85440027	AluSz_dup2843	+	2.129507018	9.443888162
chr2	85440331	85440627	AluSx1_dup3025	-	2.129507018	11.8048602
chr2	85478664	85478829	AluSx1_dup3030	+	4.259014035	9.443888162
chr2	96227832	96228136	AluSp_dup1470	-	0	8.263402142
chr2	96242936	96243210	AluSx1_dup3325	+	4.259014035	7.082916121
chr2	100759119	100759386	AluSx1_dup3558	+	3.194260526	9.443888162
chr2	111700099	111700405	AluSx1_dup3960	+	1.064753509	8.263402142
chr2	113013132	113013439	AluSx_dup4128	+	4.259014035	9.443888162
chr2	121726356	121726518	AluJr4_dup781	-	42.59014035	64.92673111
chr2	127824446	127824755	AluSg7_dup329	+	4.259014035	10.62437418
chr2	135739673	135739971	AluSg_dup1476	-	2.129507018	5.902430101
chr2	171242408	171242710	AluSx1_dup5556	-	5.323767544	10.62437418
chr2	177396928	177397236	AluSg4_dup388	-	2.129507018	11.8048602
chr2	191083981	191084274	AluSg_dup1961	+	2.129507018	7.082916121
chr2	223695302	223695572	AluSz6_dup3082	-	2.129507018	10.62437418
chr2	226730735	226731032	AluSg7_dup543	-	2.129507018	9.443888162
chr2	227562093	227562383	AluSq_dup1202	+	2.129507018	7.082916121
chr2	231421728	231421819	AluSz_dup6804	+	4.259014035	7.082916121
chr2	237963386	237963678	AluSg_dup2527	-	4.259014035	8.263402142
chr2	241568420	241568717	AluSx1_dup8027	-	0	7.082916121
chr20	3073616	3073921	AluSq_dup16	+	2.129507018	8.263402142
chr20	5652955	5653263	AluSz_dup318	+	4.259014035	10.62437418

chr20	25429915	25430210	AluSx4_dup71	-	2.129507018	8.263402142
chr20	31642018	31642152	AluJo_dup718	-	2.129507018	7.082916121
chr20	32264075	32264384	AluSq2_dup620	+	3.194260526	5.902430101
chr20	32287872	32288180	AluSg_dup318	-	4.259014035	11.8048602
chr20	32753079	32753391	AluSx1_dup1162	+	6.388521053	9.443888162
chr20	34390443	34390749	AluSx_dup1245	-	0	5.902430101
chr20	35417040	35417309	AluSx4_dup113	-	0	5.902430101
chr20	44647152	44647458	AluSp_dup847	+	4.259014035	7.082916121
chr20	44869736	44870042	AluJb_dup2193	+	5.323767544	7.082916121
chr20	45846925	45847231	AluSz6_dup912	+	7.453274561	9.443888162
chr20	50104001	50104298	AluSc_dup571	+	1.064753509	7.082916121
chr20	61185509	61185837	AluSq2_dup1543	-	15.97130263	14.16583224
chr21	31737396	31737707	AluSx1_dup602	-	5.323767544	10.62437418
chr21	31738167	31738467	AluSg_dup222	-	4.259014035	7.082916121
chr22	20426653	20426941	AluSx1_dup347	+	3.194260526	10.62437418
chr22	22480006	22480307	AluSx1_dup501	-	5.323767544	10.62437418
chr22	24452054	24452361	AluSg_dup203	+	4.259014035	7.082916121
chr22	29321099	29321409	AluSx1_dup881	-	4.259014035	10.62437418
chr22	31144483	31144813	AluJr_dup965	+	2.129507018	14.16583224
chr22	33935482	33935767	AluSg_dup401	+	2.129507018	8.263402142
chr22	36391241	36391536	AluSx3_dup453	-	5.323767544	10.62437418
chr22	36441219	36441520	AluSx1_dup1403	-	1.064753509	7.082916121
chr22	38044805	38045100	AluSx_dup1582	-	9.582781579	20.06826234
chr22	38103580	38103881	AluSx_dup1590	+	5.323767544	9.443888162
chr22	41096612	41096917	AluSq_dup286	-	1.064753509	16.52680428
chr22	41186866	41187160	AluY_dup1898	+	5.323767544	15.34631826
chr22	43074144	43074457	AluSp_dup976	+	5.323767544	5.902430101
chr22	45478666	45478954	AluSg_dup716	+	2.129507018	11.8048602
chr22	45544088	45544386	AluSx_dup2324	-	5.323767544	9.443888162
chr22	50235659	50235958	AluSg_dup779	+	2.129507018	9.443888162
chr22	50543884	50544138	AluSx1_dup2681	-	6.388521053	7.082916121
chr3	31784056	31784348	AluSz_dup867	+	1.064753509	8.263402142
chr3	32508955	32509233	AluSx1_dup954	+	0	7.082916121
chr3	39397987	39398273	AluSz6_dup541	+	1.064753509	7.082916121
chr3	47352439	47352747	AluSx1_dup1509	+	2.129507018	5.902430101
chr3	47490709	47490884	AluSz6_dup715	-	1.064753509	7.082916121
chr3	48077161	48077472	AluSp_dup678	+	1.064753509	5.902430101
chr3	58014726	58015026	AluSg_dup721	-	4.259014035	10.62437418
chr3	66024525	66024830	AluSq2_dup1190	+	3.194260526	7.082916121
chr3	93841449	93841766	AluSg_dup983	-	1.064753509	8.263402142
chr3	120434937	120435243	AluSx1_dup3585	+	0	5.902430101
chr3	125181904	125182035	AluJb_dup4708	+	3.194260526	7.082916121
chr3	129181371	129181668	AluSg_dup1277	+	0	5.902430101
chr3	149317722	149318044	AluSx3_dup1314	-	2.129507018	5.902430101
chr3	167927841	167928139	AluSx4_dup488	-	1.064753509	5.902430101
chr3	183152894	183153201	AluSx1_dup5373	+	0	5.902430101
chr3	184154566	184154861	AluSp_dup2596	-	3.194260526	8.263402142
chr3	190186887	190187170	AluSx1_dup5844	+	4.259014035	9.443888162
chr3	196328019	196328313	AluSg_dup2062	+	5.323767544	10.62437418
chr4	838299	838591	AluSx1_dup62	+	1.064753509	5.902430101
chr4	17549523	17549815	AluY_dup620	+	5.323767544	7.082916121

chr4	25281586	25281868	AluJr_dup522	+	4.259014035	10.62437418
chr4	39647047	39647347	AluSp_dup533	-	5.323767544	9.443888162
chr4	40039321	40039619	AluSq2_dup686	+	5.323767544	10.62437418
chr4	70851763	70851861	AluSz_dup1930	+	3.194260526	5.902430101
chr4	81276875	81277180	AluSx1_dup2317	+	0	5.902430101
chr4	121140053	121140361	AluSx4_dup366	+	10.64753509	9.443888162
chr4	127878484	127878789	AluJb_dup3920	-	3.194260526	7.082916121
chr4	153174996	153175319	AluSq4_dup68	-	3.194260526	8.263402142
chr4	168673928	168674214	AluSz_dup4137	-	2.129507018	9.443888162
chr4	183026312	183026590	AluSx_dup4642	+	3.194260526	16.52680428
chr5	14105454	14105781	AluSp_dup117	+	2.129507018	14.16583224
chr5	34572154	34572470	AluSz_dup761	+	1.064753509	7.082916121
chr5	50643584	50643883	AluSz_dup1037	-	3.194260526	12.98534622
chr5	55586332	55586619	AluSg_dup443	-	4.259014035	5.902430101
chr5	69186007	69186102	AluJo_dup921	-	3.194260526	8.263402142
chr5	76795841	76796157	AluSx1_dup2028	-	4.259014035	11.8048602
chr5	76797613	76797921	AluSq2_dup1228	+	5.323767544	10.62437418
chr5	134039322	134039627	AluY_dup3693	-	3.194260526	10.62437418
chr5	139482943	139483222	AluSq_dup619	+	6.388521053	15.34631826
chr5	139737435	139737716	AluSg_dup1290	-	3.194260526	7.082916121
chr5	154607498	154607698	AluSx_dup4279	+	4.259014035	7.082916121
chr5	154886149	154886318	AluSx_dup4310	-	2.129507018	4.721944081
chr5	163447982	163448167	AluJb_dup5213	+	4.259014035	10.62437418
chr5	172832176	172832477	AluSx_dup4958	-	2.129507018	10.62437418
chr5	172983143	172983442	AluSz_dup4431	-	5.323767544	7.082916121
chr5	173087813	173088114	AluSx3_dup1529	-	2.129507018	5.902430101
chr5	176518464	176518765	AluSx1_dup5158	-	3.194260526	8.263402142
chr5	177375704	177376051	AluSx3_dup1585	-	4.259014035	8.263402142
chr6	12021671	12021964	AluSq_dup107	-	25.55408421	21.24874836
chr6	13732654	13732945	AluSx_dup528	+	0	9.443888162
chr6	18082643	18082950	AluSz_dup600	-	5.323767544	10.62437418
chr6	20503649	20503953	AluSz_dup677	+	2.129507018	5.902430101
chr6	20508782	20509097	AluJr4_dup148	+	2.129507018	7.082916121
chr6	26218398	26218707	AluSx1_dup1098	+	7.453274561	9.443888162
chr6	26568130	26568437	AluSz6_dup446	+	5.323767544	12.98534622
chr6	27147858	27148123	AluSx_dup1185	-	8.51802807	14.16583224
chr6	27213183	27213478	AluSp_dup565	+	1.064753509	8.263402142
chr6	27276437	27276740	AluSq2_dup717	-	8.51802807	16.52680428
chr6	27547299	27547533	AluJb_dup1160	+	1.064753509	5.902430101
chr6	27903426	27903739	AluSz6_dup482	-	3.194260526	8.263402142
chr6	28752400	28752703	AluSx_dup1292	+	5.323767544	10.62437418
chr6	28790369	28790670	AluSp_dup618	+	6.388521053	10.62437418
chr6	30756725	30757034	AluSg_dup462	-	1.064753509	9.443888162
chr6	31192357	31192651	AluSq2_dup841	-	0	5.902430101
chr6	31612044	31612345	AluSx3_dup437	+	4.259014035	9.443888162
chr6	31679765	31680067	AluSx_dup1433	+	1.064753509	7.082916121
chr6	31732840	31733140	AluSx_dup1439	+	1.064753509	8.263402142
chr6	33275324	33275618	AluSx1_dup1459	-	0	7.082916121
chr6	34708167	34708464	AluSx_dup1659	-	0	5.902430101
chr6	35175546	35175847	AluSg7_dup130	+	5.323767544	8.263402142
chr6	37420037	37420335	AluSg_dup642	-	3.194260526	12.98534622

chr6	37769081	37769383	AluSz_dup1469	-	3.194260526	11.8048602
chr6	41610367	41610651	AluSx1_dup1963	+	4.259014035	7.082916121
chr6	42079571	42079853	AluSz6_dup796	-	0	5.902430101
chr6	42872786	42873093	AluSp_dup1085	+	2.129507018	7.082916121
chr6	42880502	42880812	AluSx_dup2184	-	3.194260526	7.082916121
chr6	48084721	48085033	AluSx3_dup717	-	3.194260526	7.082916121
chr6	73573253	73573555	AluSz_dup2318	+	3.194260526	5.902430101
chr6	100203631	100203928	AluJb_dup3720	+	4.259014035	10.62437418
chr6	141823036	141823191	AluJo_dup2976	-	5.323767544	9.443888162
chr6	148600320	148600631	AluSc_dup1746	+	4.259014035	7.082916121
chr6	151517421	151517741	AluSx3_dup1526	-	5.323767544	7.082916121
chr6	154968813	154969105	AluSq2_dup2968	-	0	7.082916121
chr6	158007967	158008272	AluSx_dup5323	-	5.323767544	8.263402142
chr6	158106552	158106829	AluSx_dup5332	+	0	5.902430101
chr6	170575008	170575248	AluJo_dup3517	-	4.259014035	9.443888162
chr7	950574	950886	AluSx1_dup60	+	1.064753509	7.082916121
chr7	1151451	1151540	AluSx_dup48	-	9.582781579	5.902430101
chr7	2393241	2393548	AluSc5_dup5	+	3.194260526	8.263402142
chr7	2556794	2557099	AluSq2_dup70	-	2.129507018	7.082916121
chr7	2624826	2625157	AluJb_dup149	-	2.129507018	7.082916121
chr7	5590525	5590824	AluSx3_dup95	+	4.259014035	7.082916121
chr7	6047393	6047687	AluSx1_dup604	+	0	5.902430101
chr7	6076877	6077175	AluSg_dup147	-	10.64753509	12.98534622
chr7	6077578	6077712	AluSq2_dup209	+	5.323767544	10.62437418
chr7	6314971	6315265	AluSg_dup155	-	1.064753509	10.62437418
chr7	6336398	6336698	AluSz6_dup167	+	0	9.443888162
chr7	20288363	20288652	AluSq2_dup418	+	3.194260526	7.082916121
chr7	28267370	28267673	AluSx1_dup1232	-	4.259014035	7.082916121
chr7	44672631	44672940	AluSg_dup597	-	7.453274561	16.52680428
chr7	73613316	73613623	AluSz6_dup1245	+	2.129507018	9.443888162
chr7	74181743	74182014	AluSg4_dup195	-	3.194260526	9.443888162
chr7	74208832	74208978	AluSx_dup3449	-	4.259014035	7.082916121
chr7	74417068	74417351	AluSx1_dup3653	+	2.129507018	7.082916121
chr7	75004867	75005166	AluSx1_dup3802	-	8.51802807	8.263402142
chr7	75778796	75778911	AluSx3_dup927	+	1.064753509	3.541458061
chr7	101098002	101098299	AluSq2_dup2343	-	2.129507018	7.082916121
chr7	129099819	129099949	AluSx_dup5731	-	3.194260526	4.721944081
chr7	157326686	157326986	AluY_dup5809	-	1.064753509	7.082916121
chr8	8288092	8288341	AluSz_dup220	-	3.194260526	7.082916121
chr8	20120056	20120352	AluSq2_dup323	+	9.582781579	17.7072903
chr8	22318308	22318617	AluSx_dup739	-	5.323767544	8.263402142
chr8	30298890	30299189	AluSg_dup317	+	4.259014035	11.8048602
chr8	37739475	37739765	AluSg7_dup83	-	0	7.082916121
chr8	42330505	42330806	AluSx3_dup449	-	3.194260526	10.62437418
chr8	42355028	42355337	AluSx3_dup451	-	4.259014035	5.902430101
chr8	42381716	42382026	AluSz_dup1663	+	1.064753509	7.082916121
chr8	42507877	42508182	AluSx_dup1699	+	4.259014035	7.082916121
chr8	74081653	74081935	AluSg_dup821	-	5.323767544	7.082916121
chr8	93724986	93725281	AluJb_dup3512	-	0	8.263402142
chr8	123241662	123241949	AluSp_dup1612	+	2.129507018	5.902430101
chr8	141130691	141130984	AluSg_dup1418	-	2.129507018	8.263402142

chr9	8012778	8013087	AluSx_dup317	-	6.388521053	22.42923438
chr9	33076867	33077171	AluSp_dup380	+	22.35982368	24.79020642
chr9	33432612	33432919	AluSx_dup842	-	1.064753509	5.902430101
chr9	34097650	34097954	AluSq2_dup506	+	4.259014035	7.082916121
chr9	35695278	35695579	AluSg_dup336	+	2.129507018	5.902430101
chr9	36299535	36299838	AluSg_dup344	-	0	5.902430101
chr9	37466642	37466940	AluSx1_dup1084	+	5.323767544	15.34631826
chr9	72433654	72433961	AluSp_dup800	-	4.259014035	12.98534622
chr9	95375864	95376163	AluSx3_dup745	-	4.259014035	8.263402142
chr9	99340018	99340296	AluSc5_dup194	-	4.259014035	8.263402142
chr9	100422133	100422426	AluSx_dup2903	+	5.323767544	7.082916121
chr9	111952873	111953165	AluSx3_dup929	+	0	8.263402142
chr9	120785747	120786043	AluSx_dup3617	+	2.129507018	9.443888162
chr9	127634909	127635216	AluSq2_dup2244	-	6.388521053	11.8048602
chr9	128698631	128698923	AluSg_dup1312	+	19.16556316	14.16583224
chr9	128772486	128772772	AluSx_dup4255	+	14.90654912	7.082916121
chr9	130712062	130712365	AluSp_dup1925	-	7.453274561	9.443888162
chr9	133347237	133347531	AluSx1_dup4514	+	1.064753509	9.443888162
chrX	3815241	3815539	AluY_dup302	+	63.88521053	60.20478703
chrX	41287734	41288022	AluSz_dup1452	+	1.064753509	8.263402142
chrX	41490783	41491096	AluSq2_dup857	+	1.064753509	7.082916121
chrX	53455843	53456152	AluSp_dup910	-	2.129507018	8.263402142
chrX	74291174	74291470	AluSz6_dup1076	+	2.129507018	7.082916121
chrX	103655865	103656158	AluSg_dup1054	+	6.388521053	7.082916121
chrX	110226323	110226636	AluSx3_dup904	+	5.323767544	8.263402142
chrX	122080114	122080403	AluSx4_dup345	+	4.259014035	5.902430101
chrX	136261553	136261791	AluJo_dup2905	+	5.323767544	8.263402142
chr1	32689660	32689957	AluSc_dup596	+	0	1.18048602
chr1	92805181	92805334	AluJb_dup6064	+	17.03605614	21.24874836
chr1	182837203	182837513	AluSx_dup7648	-	1.064753509	0
chr1	211597638	211597941	AluY_dup7449	+	4.259014035	5.902430101
chr1	247345761	247346056	AluSz_dup8921	-	3.194260526	3.541458061
chr10	17717080	17717353	AluSx1_dup946	+	1.064753509	4.721944081
chr10	47500001	47500205	AluJb_dup2191	-	2.129507018	4.721944081
chr10	74713992	74714287	AluJb_dup3428	+	6.388521053	2.36097204
chr10	87044942	87045234	AluSx_dup3692	-	5.323767544	1.18048602
chr12	19380985	19381268	AluSx_dup828	+	6.388521053	0
chr12	31997756	31997960	AluJb_dup1470	+	2.129507018	4.721944081
chr12	64621487	64621771	AluSp_dup1314	-	4.259014035	5.902430101
chr13	19672148	19672442	AluSp_dup27	-	3.194260526	8.263402142
chr15	70648328	70648615	AluSx_dup2370	-	2.129507018	4.721944081
chr16	69344490	69344797	AluSx_dup4017	+	8.51802807	12.98534622
chr16	69715485	69715776	AluSz_dup3674	+	3.194260526	1.18048602
chr17	32392409	32392704	AluSx1_dup2267	+	1.064753509	0
chr17	61418259	61418551	AluSq2_dup2233	+	0	2.36097204
chr17	62451480	62451609	AluSx1_dup4442	+	22.35982368	31.87312255
chr17	81340216	81340514	AluY_dup4802	-	5.323767544	2.36097204
chr18	45959194	45959346	AluSx1_dup1309	+	0	0
chr19	9647570	9647866	AluSq2_dup515	+	1.064753509	4.721944081
chr19	18283140	18283443	AluSz_dup2154	+	5.323767544	5.902430101
chr19	52513448	52513746	AluY_dup3909	+	7.453274561	5.902430101

chr2	84960188	84960356	AluJb_dup3495	-	3.194260526	2.36097204
chr2	231500113	231500421	AluSq2_dup4162	-	1.064753509	1.18048602
chr20	3179775	3180005	AluJr4_dup44	-	5.323767544	2.36097204
chr20	30401878	30402002	AluJo_dup680	+	1.064753509	1.18048602
chr22	22275239	22275542	AluSq2_dup273	-	1.064753509	1.18048602
chr3	44738253	44738393	AluJo_dup1004	+	1.064753509	1.18048602
chr3	130747745	130748035	AluYc_dup200	-	53.23767544	44.85846877
chr3	136858924	136859230	AluSx3_dup1198	+	4.259014035	2.36097204
chr4	13629252	13629549	AluJr_dup350	+	1.064753509	0
chr4	71577557	71577872	AluSz_dup1968	+	4.259014035	0
chr5	42997599	42997903	AluJo_dup556	-	1.064753509	2.36097204
chr5	76737787	76738090	AluSz6_dup897	+	2.129507018	1.18048602
chr5	83938395	83938687	AluSz_dup2130	-	1.064753509	0
chr5	172208783	172209044	AluJo_dup3074	-	6.388521053	2.36097204
chr6	26249688	26250003	AluSz_dup890	-	12.77704211	10.62437418
chr6	42879092	42879211	AluSx_dup2183	-	2.129507018	1.18048602
chr6	110700924	110701211	AluSg4_dup222	+	72.4032386	68.46818917
chr6	150827067	150827192	AluJb_dup5630	-	0	1.18048602
chr7	56098480	56098650	AluJr_dup1766	-	2.129507018	1.18048602
chr7	65081636	65081738	AluJo_dup1784	+	1.064753509	2.36097204
chr7	72838315	72838602	AluSz_dup2653	+	3.194260526	2.36097204
chr8	1779239	1779544	AluSz_dup40	-	3.194260526	4.721944081
chr8	6760184	6760416	AluJr_dup98	+	22.35982368	21.24874836
chr8	23187326	23187635	AluSx1_dup917	-	73.4679921	62.56575907
chr8	38221182	38221456	AluSc5_dup88	+	0	5.902430101
chr9	88516208	88516523	AluSp_dup1088	-	4.259014035	4.721944081
chr9	133336825	133337105	AluSx_dup4713	-	3.194260526	1.18048602
chrX	34625054	34625365	AluSx3_dup360	-	1.064753509	1.18048602
chr1	23297451	23297752	AluSz_dup1455	-	2.129507018	4.721944081
chr1	25221931	25222223	AluSx1_dup1785	-	4.259014035	3.541458061
chr1	192992628	192992922	AluJo_dup5373	-	4.259014035	0
chr1	236915940	236916214	AluSp_dup4500	+	0	0
chr10	31131931	31132203	AluSx_dup1654	-	0	0
chr10	73105571	73105880	AluSx4_dup271	-	0	2.36097204
chr10	110145802	110146112	AluSp_dup1914	+	1.064753509	1.18048602
chr11	27493241	27493286	Alu_dup39	-	3.194260526	0
chr11	85956631	85956914	AluJb_dup3772	-	2.129507018	3.541458061
chr12	50822057	50822344	AluJb_dup2265	+	4.259014035	0
chr12	71605967	71606257	AluYj4_dup69	-	1.064753509	10.62437418
chr12	95302943	95303235	AluSx1_dup3284	+	7.453274561	5.902430101
chr13	44637916	44638213	AluSg_dup312	-	0	1.18048602
chr13	95396386	95396511	AluJo_dup1479	-	2.129507018	1.18048602
chr15	59691801	59692105	AluSx1_dup1666	+	1.064753509	0
chr15	65040967	65041033	AluJo_dup1349	-	7.453274561	9.443888162
chr16	28531338	28531636	AluSx1_dup2643	-	2.129507018	4.721944081
chr16	29857797	29858089	AluJb_dup2535	-	8.51802807	11.8048602
chr16	89257881	89258011	AluJo_dup3896	-	1.064753509	0
chr17	38846648	38846808	AluJr_dup1556	-	3.194260526	7.082916121
chr17	39452914	39453172	AluSz_dup2030	+	3.194260526	2.36097204
chr19	2947229	2947342	AluSz_dup207	-	0	0
chr19	38217921	38218227	AluSc_dup844	+	0	0

chr19	44237398	44237696	AluSc8_dup694	+	3.194260526	4.721944081
chr19	58543718	58543855	AluJb_dup5301	-	3.194260526	3.541458061
chr20	50593290	50593583	AluSq_dup350	+	3.194260526	0
chr21	46573379	46573673	AluJb_dup1337	+	2.129507018	0
chr22	17577975	17578270	AluJb_dup180	-	13.84179561	9.443888162
chr22	41297686	41297857	AluSx4_dup185	-	0	0
chr3	37180979	37181162	AluJo_dup806	+	2.129507018	1.18048602
chr3	42649563	42649696	AluSz_dup1289	+	3.194260526	4.721944081
chr3	195923484	195923782	AluSz_dup5629	-	3.194260526	4.721944081
chr4	99068756	99069032	AluSz_dup2693	-	4.259014035	3.541458061
chr4	183462403	183462694	AluSz_dup4462	-	6.388521053	3.541458061
chr5	61157310	61157597	AluSg_dup508	-	24.4893307	18.88777632
chr5	69598721	69599018	AluSg_dup585	+	5.323767544	5.902430101
chr5	70148106	70148417	AluSc_dup653	-	2.129507018	1.18048602
chr5	70577559	70577874	AluSq_dup307	-	0	0
chr5	71137497	71137808	AluSz_dup1645	-	2.129507018	3.541458061
chr5	118836233	118836535	AluSg7_dup265	-	10.64753509	14.16583224
chr6	42928291	42928571	AluJo_dup1345	-	5.323767544	2.36097204
chr6	99564142	99564444	AluSx_dup3509	+	1.064753509	0
chr7	42906296	42906599	AluJb_dup1629	-	0	3.541458061
chr7	42906976	42907281	AluSq2_dup798	-	4.259014035	2.36097204
chr7	66547478	66547771	AluSx1_dup2717	-	1.064753509	0
chr7	97968392	97968694	AluJr_dup4132	-	3.194260526	8.263402142
chr7	110279038	110279341	AluJb_dup4784	-	1.064753509	0
chr7	118182594	118182767	AluSq2_dup2697	-	4.259014035	0
chr7	139192874	139193107	AluJr_dup5830	+	4.259014035	12.98534622
chr7	155006225	155006498	AluSz_dup6062	+	1.064753509	2.36097204
chr8	100154305	100154423	AluJr_dup2875	+	1.064753509	1.18048602
chr9	19051314	19051618	AluJr_dup397	+	3.194260526	2.36097204
chr9	26902116	26902430	AluJr_dup536	-	1.064753509	2.36097204
chr9	107255441	107255738	AluSx1_dup2935	+	1.064753509	0
chr9	111702828	111703131	AluJr_dup2176	+	5.323767544	5.902430101
chrX	75740203	75740496	AluSp_dup1176	-	2.129507018	1.18048602
chrX	101001236	101001535	AluJr_dup2304	-	1.064753509	3.541458061
chrX	131652459	131652749	AluJo_dup2749	-	3.194260526	1.18048602
chr1	113688711	113689023	AluSc8_dup992	+	5.323767544	5.902430101
chr1	146035369	146035649	AluJb_dup7321	-	0	0
chr1	150521964	150522273	AluSx_dup6214	+	0	2.36097204
chr1	168256596	168256909	AluSz6_dup2963	+	0	4.721944081
chr1	235106044	235106351	AluSq2_dup4923	-	3.194260526	7.082916121
chr10	18390219	18390511	AluSx4_dup65	-	3.194260526	5.902430101
chr10	28521123	28521420	AluSp_dup434	-	15.97130263	10.62437418
chr10	52436491	52436777	AluSz6_dup960	-	3.194260526	3.541458061
chr11	114456951	114457072	AluJb_dup4584	+	1.064753509	1.18048602
chr12	24112521	24112839	AluJb_dup1036	-	10.64753509	4.721944081
chr12	120502646	120502950	AluSx3_dup1333	-	1.064753509	0
chr13	20617787	20618083	AluSz_dup133	-	12.77704211	5.902430101
chr13	23823547	23823827	AluJr4_dup39	+	0	1.18048602
chr13	77003660	77003952	AluSz_dup1710	+	2.129507018	2.36097204
chr15	35890832	35891126	AluSq2_dup326	+	0	4.721944081
chr15	82481602	82481913	AluY_dup3076	+	2.129507018	1.18048602

chr15	83015383	83015673	AluJr_dup2101	-	0	1.18048602
chr16	1843416	1843717	AluSz_dup78	+	8.51802807	4.721944081
chr16	30916635	30916945	AluSz_dup2435	-	5.323767544	4.721944081
chr16	69346481	69346770	AluSq2_dup1940	+	6.388521053	7.082916121
chr16	85511244	85511547	AluSp_dup1794	+	0	0
chr17	29254856	29255144	AluJo_dup1037	-	1.064753509	0
chr17	40116664	40116984	AluJr4_dup378	-	5.323767544	3.541458061
chr17	42559048	42559252	AluSx_dup3107	-	0	0
chr17	64540947	64541240	AluJb_dup4755	-	2.129507018	1.18048602
chr17	67744614	67744910	AluSz_dup4050	+	4.259014035	5.902430101
chr19	36177307	36177600	AluSq2_dup1654	-	7.453274561	1.18048602
chr19	36683069	36683359	AluJb_dup3060	-	10.64753509	10.62437418
chr19	37000304	37000599	AluSc8_dup573	+	13.84179561	4.721944081
chr19	37731727	37732016	AluSz_dup3206	-	2.129507018	4.721944081
chr19	40311678	40311956	AluSz_dup3505	-	2.129507018	2.36097204
chr19	44178897	44179188	AluSx_dup4537	+	6.388521053	7.082916121
chr19	57335365	57335665	AluSc_dup1281	+	4.259014035	2.36097204
chr19	57764480	57764784	AluSp_dup2743	+	3.194260526	0
chr2	27651864	27652179	AluSz_dup827	+	6.388521053	4.721944081
chr2	46769250	46769560	AluSx1_dup1775	+	4.259014035	2.36097204
chr2	55519116	55519403	AluSx_dup2150	-	8.51802807	5.902430101
chr2	65225849	65226143	AluSx_dup2566	-	1.064753509	1.18048602
chr2	69317308	69317603	AluJo_dup1736	-	7.453274561	4.721944081
chr2	112577567	112577852	AluJb_dup4460	+	27.68359123	22.42923438
chr2	121724392	121724525	AluSx_dup4380	-	0	0
chr2	130348235	130348365	AluJr_dup3196	+	8.51802807	7.082916121
chr2	186357186	186357498	AluSx1_dup5956	-	0	2.36097204
chr2	191698963	191699272	AluJb_dup7017	+	5.323767544	5.902430101
chr2	218599592	218599890	AluSz6_dup2990	+	1.064753509	0
chr2	232347202	232347454	AluJr4_dup1500	+	4.259014035	3.541458061
chr2	241697802	241698100	AluSx_dup8207	+	1.064753509	0
chr20	28577969	28578094	AluJo_dup649	-	2.129507018	4.721944081
chr21	33364160	33364440	AluSz_dup600	+	1.064753509	3.541458061
chr22	24576243	24576550	AluSq2_dup332	-	3.194260526	9.443888162
chr22	30980659	30980959	AluSx1_dup1026	+	7.453274561	1.18048602
chr3	37178513	37178797	AluJb_dup1423	+	9.582781579	5.902430101
chr3	37184778	37185075	AluSq2_dup529	+	0	0
chr3	179395768	179396061	AluJb_dup6482	+	6.388521053	7.082916121
chr4	92050	92290	AluSg	+	5.323767544	3.541458061
chr4	1714259	1714554	AluJo_dup40	+	2.129507018	4.721944081
chr4	26760280	26760588	AluJb_dup908	+	5.323767544	3.541458061
chr4	76939519	76939610	AluJr4_dup376	-	1.064753509	1.18048602
chr4	76945890	76946191	AluSx_dup2193	-	29.81309825	35.41458061
chr4	89115813	89116106	AluSz_dup2516	+	15.97130263	9.443888162
chr4	163167010	163167299	AluSg_dup1423	+	5.323767544	5.902430101
chr5	17381395	17381678	AluSz_dup394	+	0	2.36097204
chr5	32351983	32352284	AluSq2_dup462	-	2.129507018	1.18048602
chr5	34903964	34904268	AluJr_dup509	-	6.388521053	4.721944081
chr5	54660350	54660451	AluJb_dup1283	-	4.259014035	4.721944081
chr5	66084132	66084434	AluJb_dup1737	+	7.453274561	8.263402142
chr5	79363809	79364104	AluSz_dup1966	-	0	0

chr5	134396434	134396705	AluJo_dup2111	-	0	2.36097204
chr5	179529114	179529270	AluSg_dup1792	-	7.453274561	2.36097204
chr6	48091639	48091942	AluSx_dup2405	-	3.194260526	5.902430101
chr6	76953788	76954066	AluY_dup2681	-	1.064753509	2.36097204
chr6	77111119	77111416	AluSx1_dup2875	-	2.129507018	3.541458061
chr6	91492951	91493224	AluJb_dup3560	+	1.064753509	1.18048602
chr6	95567782	95568084	AluSg4_dup193	-	0	0
chr6	99395144	99395439	AluSx_dup3492	-	1.064753509	0
chr7	271086	271350	AluJr_dup13	+	0	0
chr7	23492872	23493174	AluSx_dup1032	-	1.064753509	1.18048602
chr7	56009169	56009476	AluSz_dup1730	-	2.129507018	7.082916121
chr7	72956851	72957142	AluSz_dup2665	+	3.194260526	1.18048602
chr7	74876285	74876590	AluSz_dup3007	-	1.064753509	4.721944081
chr7	74877986	74878335	AluJb_dup3131	-	2.129507018	1.18048602
chr7	76675419	76675713	AluJb_dup3355	+	2.129507018	3.541458061
chr7	77668767	77669068	AluJb_dup3410	+	1.064753509	2.36097204
chr7	99545880	99546168	AluJb_dup4096	-	0	0
chr7	150777478	150777805	AluJb_dup6335	-	0	3.541458061
chr8	19397919	19398249	AluSc5_dup42	+	6.388521053	9.443888162
chr8	42834391	42834690	AluSx_dup1725	-	1.064753509	2.36097204
chr8	53512977	53513274	AluSz_dup1939	-	7.453274561	1.18048602
chr8	66920238	66920519	AluSx_dup2409	-	12.77704211	0
chr8	93638477	93638705	AluSx1_dup3243	+	3.194260526	2.36097204
chr8	117742894	117743203	AluSx1_dup3968	-	1.064753509	5.902430101
chr9	15473625	15473955	AluSx_dup450	+	3.194260526	7.082916121
chr9	40995625	40995846	AluY_dup1511	-	4.259014035	5.902430101
chr9	41406167	41406465	AluJr4_dup280	+	6.388521053	3.541458061
chr9	63411479	63411661	AluJr_dup1033	+	1.064753509	4.721944081
chr9	65648419	65648719	AluSz_dup1275	+	1.064753509	3.541458061
chr9	82611669	82611969	AluY_dup2604	+	2.129507018	5.902430101
chr9	111801687	111801980	AluSx3_dup925	+	3.194260526	2.36097204
chrX	233658	233962	AluYk2_dup1	+	2.129507018	0
chrX	20123255	20123560	AluSx1_dup1108	-	1.064753509	2.36097204
chrX	24219009	24219286	AluSq2_dup532	+	3.194260526	2.36097204
chrX	54567364	54567664	AluSp_dup964	+	2.129507018	9.443888162
chr1	77225861	77226153	AluSx3_dup1248	+	1.064753509	0
chr1	84527732	84528030	AluSx_dup4794	-	0	4.721944081
chr1	113686536	113686839	AluSx1_dup5231	+	10.64753509	10.62437418
chr1	155744701	155745018	AluJr_dup4497	-	4.259014035	2.36097204
chr1	168254975	168255147	AluJr_dup4794	+	1.064753509	1.18048602
chr1	247350592	247350883	AluJr_dup7153	+	2.129507018	3.541458061
chr12	49528756	49529039	AluSp_dup851	+	1.064753509	0
chr12	108575796	108576101	AluSg7_dup290	-	14.90654912	16.52680428
chr16	29931016	29931311	AluSq2_dup1160	+	2.129507018	4.721944081
chr16	75625320	75625611	AluSz_dup4091	-	1.064753509	5.902430101
chr17	786095	786267	AluSg_dup20	-	0	1.18048602
chr18	69225448	69225645	AluSx_dup2026	+	3.194260526	1.18048602
chr19	41260298	41260611	AluSz_dup3640	-	0	0
chr19	46906806	46907101	AluJb_dup4168	+	1.064753509	0
chr2	26138157	26138456	AluSx_dup839	+	14.90654912	7.082916121
chr2	31851730	31851995	AluSz_dup971	-	4.259014035	5.902430101

chr2	112367326	112367620	AluSc_dup1268	-	6.388521053	3.541458061
chr2	113881876	113882191	AluJb_dup4507	-	5.323767544	5.902430101
chr2	169642778	169642930	AluJo_dup3713	+	2.129507018	3.541458061
chr4	82421833	82422086	AluSz6_dup1014	-	2.129507018	4.721944081
chr5	13953693	13954007	AluSx1_dup293	-	0	0
chr5	37072668	37072948	AluJb_dup924	+	1.064753509	3.541458061
chr5	66097007	66097315	AluSx_dup1665	+	1.064753509	3.541458061
chr5	70855760	70856072	AluSz_dup1609	+	10.64753509	5.902430101
chr5	75040183	75040276	AluSx3_dup653	-	1.064753509	1.18048602
chr5	115574661	115574961	AluSg7_dup258	-	11.7122886	8.263402142
chr6	35432836	35432956	AluJr_dup1176	+	2.129507018	0
chr6	77258906	77259204	AluJo_dup1832	-	0	0
chr7	23503474	23503764	AluSc8_dup174	-	3.194260526	4.721944081
chr7	43651714	43652008	AluJb_dup1661	+	0	0
chr7	100045606	100045712	AluJo_dup3586	+	0	0
chr7	110427606	110427899	AluSx_dup5345	-	0	1.18048602
chr8	48069652	48069927	AluJb_dup2034	+	2.129507018	0
chr9	6507721	6507991	AluJo_dup141	+	3.194260526	1.18048602
chr9	27087511	27087798	AluJb_dup884	+	0	0
chr9	35761871	35762097	AluSz_dup883	+	2.129507018	2.36097204
chr9	93434467	93434764	AluSz6_dup984	-	3.194260526	4.721944081

dl312_rep1	dl312_rep2	mock_rep1	mock_rep2	log2FC_vs_dl312
0	0.904528319	0	0.916840356	NA
0	0	0	0.916840356	5.983379879
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0	0	0	NA
0	0	0	0	6.125830078
0	0.904528319	0.970095843	0	5.419422597
0	0.904528319	0	0	NA
0.960861216	2.713584956	0.970095843	0	NA
0	0	0	0	NA
0	1.809056637	0	1.833680712	4.141566051
1.921722432	0.904528319	2.91028753	0.916840356	5.261806258
1.921722432	0	2.91028753	0	NA
0.960861216	0	0.970095843	0	NA
0	0	0.970095843	0	NA
2.882583649	2.713584956	3.880383374	0	3.954016844
2.882583649	0.904528319	0.970095843	3.667361424	NA
8.647750946	8.140754868	19.40191687	6.417882493	4.13119497
4.804306081	1.809056637	5.820575061	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0	0	0	NA
0.960861216	2.713584956	2.91028753	2.750521068	3.925198252
0	0	2.91028753	2.750521068	7.952960993
45.16047716	34.37207611	54.32536723	30.25573175	2.536273578
0	0	0	0	NA
0.960861216	0	1.940191687	0.916840356	4.908324386
0	0	0	0	NA
0.960861216	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	6.405541746
0.960861216	0	0	0	6.171072411
0	0	0.970095843	0.916840356	NA
0	0	0	0	6.243044363
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0	NA
16.33464068	8.140754868	18.43182103	11.00208427	4.222809588
0.960861216	2.713584956	5.820575061	2.750521068	6.872478522
0	0	0	0	6.182469956
0	1.809056637	0	0.916840356	NA
18.25636311	7.23622655	32.01316283	14.6694457	NA

0	0	0	0	6.039312054
5.765167297	7.23622655	2.91028753	1.833680712	2.558996803
0	0.904528319	1.940191687	0.916840356	5.764536681
0	4.522641594	0.970095843	0	NA
0	0	0	0	6.27793704
3.843444865	5.427169912	4.850479217	5.501042137	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
0.960861216	0	0.970095843	0	5.759842045
11.53033459	9.949811506	13.58134181	12.83576499	NA
0	0	0	0	6.283793822
27.86497527	16.28150974	39.77392958	22.00416855	2.780429154
0.960861216	1.809056637	2.91028753	1.833680712	4.792519819
0	0	0	0	NA
63.41684027	48.84452921	94.09929681	49.50937923	1.488096213
0	0	0	0	NA
8.647750946	5.427169912	28.13277946	3.667361424	NA
0	0	0	0	6.237024598
17.29550189	17.18603806	17.46172518	2.750521068	NA
0	0	0	0	NA
0	0.904528319	1.940191687	0	NA
24.98239162	27.13584956	34.92345036	22.00416855	5.237769178
0	0	0	0	NA
5.765167297	3.618113275	3.880383374	1.833680712	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	2.713584956	0	0	4.178101654
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	6.467899174
1.921722432	0.904528319	0.970095843	0	4.072680311
24.0215304	13.56792478	19.40191687	12.83576499	NA
0	1.809056637	0.970095843	0	NA
0.960861216	0	2.91028753	0.916840356	7.383809516
0.960861216	2.713584956	0.970095843	1.833680712	4.942463409
0	0.904528319	0	0	NA
0	0	0.970095843	0	5.849542193
15.37377946	14.4724531	11.64115012	0.916840356	5.4178176
5.765167297	17.18603806	10.67105428	8.251563205	NA
2.882583649	0	1.940191687	1.833680712	5.021072216
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
3.843444865	3.618113275	13.58134181	2.750521068	NA
0.960861216	1.809056637	0	0.916840356	NA
1.921722432	0	0	0	NA
1.921722432	0.904528319	0	0	4.917360858
2.882583649	0	2.91028753	0.916840356	NA
5.765167297	7.23622655	13.58134181	7.334722849	2.883682263
0	0	0	0	NA

0	0	0	0	NA
3.843444865	8.140754868	5.820575061	0.916840356	NA
0.960861216	0	2.91028753	0	6.645835778
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0.904528319	0	0	NA
0.960861216	1.809056637	0.970095843	1.833680712	3.672272313
0	0	0	0	NA
0	0.904528319	0	0	NA
0.960861216	0	0	2.750521068	NA
0	0	0	0	NA
70.14286878	48.84452921	81.48805085	49.50937923	NA
5.765167297	0	3.880383374	1.833680712	NA
8.647750946	5.427169912	11.64115012	6.417882493	NA
0.960861216	0	0	0	NA
5.765167297	7.23622655	8.730862591	4.584201781	NA
0	0	0	0	6.653424695
1.921722432	0.904528319	4.850479217	0.916840356	NA
0.960861216	0	3.880383374	0	NA
3.843444865	4.522641594	5.820575061	4.584201781	4.459781225
4.804306081	7.23622655	4.850479217	3.667361424	5.879007109
0	0	0	0	6.195036862
0	0	0	0.916840356	6.797863468
2.882583649	1.809056637	0	0	NA
0	0.904528319	0.970095843	1.833680712	NA
0.960861216	0	0	0	5.139593068
7.68688973	2.713584956	5.820575061	3.667361424	NA
0	0	0	0	NA
0	0	0.970095843	0	NA
61.49511784	68.74415222	155.215335	44.92517745	2.331887352
0	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0.916840356	NA
1.921722432	3.618113275	3.880383374	0	3.295874992
0	0	0	0	NA
0.960861216	0.904528319	0	0	NA
1.921722432	2.713584956	2.91028753	2.750521068	NA
4.804306081	6.331698231	6.790670904	2.750521068	NA
7.68688973	6.331698231	5.820575061	4.584201781	2.197160981
1.921722432	6.331698231	0.970095843	0	NA
0	0	0	0	6.295409098
0	0	0	0	NA
0	0	0	0	NA
10.56947338	10.85433982	11.64115012	7.334722849	NA
0	4.522641594	1.940191687	0.916840356	4.426731625
0	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0	NA

4.804306081	4.522641594	4.850479217	9.168403561	NA
0	2.713584956	2.91028753	0	NA
0	0	0	0	7.727493694
36.51272622	37.08566107	76.63757163	20.17048783	2.160017422
2.882583649	2.713584956	3.880383374	0.916840356	3.348599708
0	0	0	0	NA
0	0	0	0	NA
4.804306081	0	1.940191687	0	NA
0	0	0	0	NA
0	0	0	0	6.612710308
15.37377946	10.85433982	13.58134181	5.501042137	1.871143801
0	0	0.970095843	0	7.236938721
0	0	0.970095843	0	5.777628176
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0.970095843	0	NA
0	0	0	0	NA
0	0.904528319	0.970095843	0	8.655806504
0	0	0	0	NA
0	0	0	0	6.829807115
0	0	0	0	NA
0.960861216	0	0	1.833680712	NA
0	0	0	0	NA
31.70842013	40.70377434	51.4150797	18.33680712	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	0	0.970095843	1.833680712	NA
27.86497527	16.28150974	19.40191687	11.00208427	1.656225521
1.921722432	5.427169912	2.91028753	0	4.645396192
0	0	0	0	NA
0	0	0.970095843	0	NA
0.960861216	0	0.970095843	0	5.274609399
0	0	0	0	6.053140561
0	0.904528319	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	0.904528319	0	0	3.636475902
0.960861216	0	0	0.916840356	6.247234848
2.882583649	0	5.820575061	2.750521068	4.50695
0	2.713584956	0	0	NA
0	0	0.970095843	0	6.099456731
0	0	0	0	6.368140942
0	0	0	0	NA
0	0	0	0	6.182469956
0	0	0	0	NA
3.843444865	0.904528319	0	1.833680712	NA
1.921722432	2.713584956	0	0	NA
2.882583649	2.713584956	5.820575061	1.833680712	NA
0	0	0.970095843	0	NA
0	0.904528319	5.820575061	0	NA
0	0	0	0.916840356	NA

0	0	0	0	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	6.351525172
1.921722432	0.904528319	0	1.833680712	4.354130285
0	0	1.940191687	0	NA
0.960861216	2.713584956	3.880383374	2.750521068	4.540492749
0.960861216	0	0	0	5.158703245
0	0.904528319	0	0	NA
6.726028513	2.713584956	10.67105428	8.251563205	NA
6.726028513	8.140754868	6.790670904	3.667361424	3.172894782
0	0	0	0	NA
2.882583649	4.522641594	8.730862591	3.667361424	NA
0	0.904528319	0	0	NA
0	0	0	0	NA
0.960861216	0	0	0	NA
0	0	0	2.750521068	6.242929662
0	0.904528319	0	0	NA
0	0.904528319	0	0	5.703034992
0.960861216	0	0	0	5.534847312
0	0.904528319	0	0	5.356108898
0	0	0	0	NA
0	0	0	0	NA
6.726028513	4.522641594	15.5215335	1.833680712	NA
0	0	0	0	NA
0	0	0	0.916840356	NA
0	0	0	0	7.551792528
0	0	0	0	NA
0	0	0	0	NA
2.882583649	11.75886814	13.58134181	7.334722849	NA
0	0.904528319	0	1.833680712	NA
3.843444865	0.904528319	5.820575061	5.501042137	NA
0	0	0	0	NA
9.608612162	7.23622655	13.58134181	6.417882493	NA
2.882583649	1.809056637	0	3.667361424	3.415800697
0	0.904528319	0	0	NA
0	0	2.91028753	1.833680712	9.154137953
0	0	0	0	NA
34.59100378	30.75396284	55.29546308	27.50521068	2.245346527
1.921722432	0.904528319	0	0	NA
0	0	0	0	NA
9.608612162	10.85433982	13.58134181	10.08524392	3.275884902
0.960861216	0.904528319	0	0.916840356	NA
0.960861216	0	0	0	NA
0	0	0.970095843	0	NA
2.882583649	1.809056637	5.820575061	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	0	0	0	NA
3.843444865	4.522641594	3.880383374	0.916840356	NA
16.33464068	10.85433982	12.61124596	3.667361424	3.364288621

4.804306081	4.522641594	0.970095843	0.916840356	5.713752732
0	1.809056637	1.940191687	0.916840356	4.301545384
0	0	0	0	6.018403682
25.94325284	14.4724531	17.46172518	11.91892463	1.687631598
15.37377946	9.045283187	9.700958434	9.168403561	2.147519934
0.960861216	0	1.940191687	0	NA
1.921722432	0	0.970095843	0	NA
3.843444865	7.23622655	3.880383374	0.916840356	NA
1.921722432	0.904528319	0	1.833680712	NA
6.726028513	10.85433982	4.850479217	4.584201781	NA
11.53033459	6.331698231	12.61124596	3.667361424	2.335336051
0	0	0	0	5.983871625
0	0	0	0	NA
1.921722432	2.713584956	0.970095843	0	3.345498634
15.37377946	15.37698142	20.37201271	10.08524392	NA
0	0	0	0	6.131230744
0	0	0	0	NA
9.608612162	5.427169912	8.730862591	5.501042137	4.159609309
21.13894676	16.28150974	28.13277946	10.08524392	3.814076559
7.68688973	6.331698231	7.760766748	2.750521068	2.491791638
0	0	0	0	NA
4.804306081	10.85433982	20.37201271	3.667361424	NA
3.843444865	4.522641594	4.850479217	2.750521068	2.525006145
0.960861216	0	0.970095843	0	NA
1.921722432	0.904528319	2.91028753	0.916840356	NA
0	0	0	0	7.141519935
0	0	0	0	NA
0	3.618113275	3.880383374	0.916840356	NA
3.843444865	0	0.970095843	2.750521068	4.467511468
0	0.904528319	0	0	5.993327385
1.921722432	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0.970095843	0	NA
1.921722432	0	1.940191687	1.833680712	6.205999438
0	1.809056637	0	0	5.68618776
0	0	0	0.916840356	7.004558188
19.21722432	14.4724531	16.49162934	11.00208427	2.006447772
2.882583649	3.618113275	1.940191687	3.667361424	3.933386841
0	0	1.940191687	1.833680712	6.284153661
0	0	0.970095843	0	6.990540717
0	0	0	0	7.221937025
38.43444865	27.13584956	48.50479217	33.00625282	1.855384072
7.68688973	8.140754868	14.55143765	7.334722849	2.986472624
25.94325284	23.51773629	30.07297115	15.58628605	1.828832859
0	0	0	0	NA
0	0	0	0	6.306946828
1.921722432	3.618113275	7.760766748	0.916840356	4.385463038
0	0	0	0	NA
0	0	0	0	NA
0	2.713584956	0.970095843	0.916840356	NA
0	1.809056637	0	0.916840356	NA

0	0	0	0	NA
0.960861216	0	0.970095843	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0.904528319	0.970095843	0.916840356	NA
0	2.713584956	2.91028753	0.916840356	NA
0	1.809056637	0	0	NA
0	0	0	0	NA
0	3.618113275	0	0	NA
0	0	0	0	6.467899174
1.921722432	1.809056637	2.91028753	2.750521068	3.602600739
0	1.809056637	0	0	5.229810654
0.960861216	0.904528319	4.850479217	1.833680712	6.167129267
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0.970095843	1.833680712	6.856543468
18.25636311	5.427169912	17.46172518	5.501042137	2.232568987
0.960861216	0	1.940191687	0.916840356	NA
0	0	0	0	6.841701121
3.843444865	0.904528319	1.940191687	0	NA
0	0.904528319	0	0	6.481985379
0	0	0	0	NA
1.921722432	0.904528319	1.940191687	0	NA
0	0	1.940191687	0.916840356	6.773125937
0.960861216	0	0	0.916840356	5.218343576
4.804306081	2.713584956	3.880383374	4.584201781	3.02539361
0.960861216	2.713584956	7.760766748	8.251563205	5.382288951
0	0.904528319	0.970095843	0	NA
0	2.713584956	0.970095843	0	4.294551397
18.25636311	16.28150974	19.40191687	3.667361424	NA
0	0	0	0	6.701763503
0	0.904528319	0.970095843	0.916840356	5.161214679
0	0	0	0	NA
0.960861216	0	3.880383374	0	6.165893873
0	0	0	0	NA
0	0	0	0	7.025441892
13.45205703	13.56792478	25.22249193	8.251563205	3.041990159
1.921722432	0.904528319	0.970095843	0	NA
0	0	0.970095843	0	NA
0	0	0	0	6.106069692
4.804306081	1.809056637	8.730862591	0.916840356	NA
0.960861216	1.809056637	1.940191687	0.916840356	3.719085445
0.960861216	1.809056637	0.970095843	0	NA
11.53033459	11.75886814	13.58134181	12.83576499	4.552901557
0	0	0	0	6.09280559
0	0	0	0	6.416213452
0	0.904528319	1.940191687	0	NA
0	0	0.970095843	0	6.052736662
0	0	0	0	NA
0	0	1.940191687	0	NA

0.960861216	1.809056637	7.760766748	2.750521068	3.888726699
5.765167297	9.045283187	12.61124596	4.584201781	2.240293891
0	0	0	0	NA
0	0.904528319	0	0	NA
8.647750946	10.85433982	7.760766748	0.916840356	NA
0	0.904528319	0	0	5.030800546
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0.904528319	0.970095843	3.667361424	NA
0	0	0	0	NA
44.19961595	31.65849116	45.59450464	32.08941246	2.313451329
0	0	0	0	NA
0	0	0	0	NA
1.921722432	0.904528319	1.940191687	1.833680712	NA
0.960861216	0	0	0	NA
0	0	0	0	6.039312054
0	0	0	0	NA
0	0	0	0	NA
0	1.809056637	0	0.916840356	NA
7.68688973	17.18603806	10.67105428	11.91892463	1.81514643
0	0	0	0.916840356	NA
0.960861216	0	0	0	NA
0	0	0.970095843	0	NA
0	0	0	1.833680712	NA
0	0	0	0	NA
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0	0	0	0	6.23098777
0	0	0.970095843	0	NA
10.56947338	13.56792478	9.700958434	1.833680712	NA
2.882583649	4.522641594	3.880383374	2.750521068	3.88119231
3.843444865	0	1.940191687	2.750521068	3.992442049
0	0	0	0.916840356	NA
1.921722432	11.75886814	10.67105428	1.833680712	NA
0	0	0	0	NA
0	0	0	0	NA
5.765167297	2.713584956	6.790670904	0.916840356	NA
0	0	0	0	6.41088563
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA

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0	0	0	0	NA
2.882583649	4.522641594	9.700958434	2.750521068	2.929111934
0.960861216	0	0	0	NA
1.921722432	0	0	0	NA
0.960861216	1.809056637	0.970095843	0.916840356	NA
0	1.809056637	0	0.916840356	NA
0.960861216	0	0	0	NA
2.882583649	3.618113275	0.970095843	0	NA
0.960861216	0.904528319	0.970095843	0.916840356	NA
0	0	0	0	7.895534536
0	1.809056637	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	8.082982119
0	0	0	0	NA
0.960861216	0	0.970095843	0	5.173174741
3.843444865	5.427169912	6.790670904	3.667361424	NA
0.960861216	0	0	0	NA
0.960861216	0	1.940191687	1.833680712	5.425968147
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0	0	0	0	NA
2.882583649	0.904528319	0	0.916840356	4.235704276
0	0	0	0	6.053140561
0	0	0.970095843	0	NA
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0	0	0	2.750521068	6.119040062
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
2.882583649	2.713584956	1.940191687	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	1.809056637	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0.904528319	0	0	NA
0	0	0	0	NA
1.921722432	1.809056637	0.970095843	0	3.620382894
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0	0	1.940191687	0	NA
0	0	0	0	NA
2.882583649	10.85433982	4.850479217	4.584201781	NA
0	0.904528319	0	0.916840356	NA
0.960861216	0.904528319	3.880383374	1.833680712	NA
1.921722432	5.427169912	11.64115012	3.667361424	NA
0	0	0	0.916840356	5.969060455
0	0	0	0	6.756933666

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0	0	0	0	NA
0	4.522641594	2.91028753	2.750521068	NA
1.921722432	2.713584956	2.91028753	0	NA
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0	0	0	0	7.06292832
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2.882583649	4.522641594	0.970095843	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	1.809056637	0.970095843	0.916840356	NA
0	1.809056637	0	0	NA
0.960861216	1.809056637	1.940191687	0	3.986340514
0	0	0	0	NA
1.921722432	0	0.970095843	0	NA
5.765167297	5.427169912	2.91028753	3.667361424	NA
1.921722432	0	0	0	NA
0	0	0.970095843	0	NA
0.960861216	0.904528319	0	0	NA
4.804306081	8.140754868	9.700958434	7.334722849	NA
0	0	0	0	NA
2.882583649	4.522641594	1.940191687	1.833680712	NA
0	0	0	0	NA
0	0	0	0	NA
5.765167297	3.618113275	7.760766748	4.584201781	5.679602294
0.960861216	5.427169912	0.970095843	4.584201781	3.31677819
0	0	0.970095843	2.750521068	6.415931858
0	0	0	0	NA
0	0	0	0	NA
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0	0.904528319	0	0	NA
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0	0	0	0	6.580347618
0	0.904528319	0	0	NA
0	0	0	0	NA
1.921722432	2.713584956	0	0.916840356	3.315720286
6.726028513	7.23622655	3.880383374	3.667361424	2.194018194
0	0	0	0	7.131878045
0	0	0	0	NA
0	0	0	0	NA
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0	0	0	0.916840356	NA
0.960861216	0	0	0	5.053070544
0	0	0	0	6.249055027
1.921722432	0.904528319	0	0	NA
4.804306081	3.618113275	7.760766748	4.584201781	2.650881303

0.960861216	0.904528319	1.940191687	0.916840356	NA
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0	0	0	0	NA
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0	0	0	0	NA
1.921722432	0.904528319	0.970095843	0	NA
0	0	0	0.916840356	NA
1.921722432	0	1.940191687	0	4.305038377
2.882583649	0	1.940191687	1.833680712	NA
0	0.904528319	1.940191687	0.916840356	5.079523289
0	0	0	0	NA
0	0	0	0	NA
0	2.713584956	0.970095843	0.916840356	NA
1.921722432	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	8.140754868	3.880383374	5.501042137	NA
11.53033459	9.949811506	20.37201271	6.417882493	4.043931871
8.647750946	9.949811506	7.760766748	7.334722849	NA
0	0	0	0	NA
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0	0	0	0	6.527682232
0	0	0	0.916840356	6.118914574
2.882583649	7.23622655	13.58134181	3.667361424	NA
0.960861216	0	1.940191687	0	6.19399396
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0	0	0	0	6.362611555
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0	0.904528319	0	0	NA
3.843444865	4.522641594	6.790670904	0.916840356	NA
0.960861216	0.904528319	0	1.833680712	NA
0.960861216	2.713584956	2.91028753	2.750521068	4.841892664
21.13894676	17.18603806	25.22249193	13.75260534	NA
0	0	0	0	NA
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0	0	0	0	NA
13.45205703	11.75886814	12.61124596	8.251563205	2.027993509
0.960861216	0.904528319	0	0	NA
30.74755892	32.56301947	28.13277946	26.58837033	2.203928979
0	0	0	0	NA
5.765167297	4.522641594	6.790670904	6.417882493	NA
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2.882583649	2.713584956	0.970095843	0.916840356	NA
0	1.809056637	1.940191687	0	NA
0.960861216	0	0	0	NA
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1.921722432	0.904528319	0	0	NA
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0	0.904528319	0	0	NA
0	0	3.880383374	0.916840356	5.630405248
7.68688973	6.331698231	4.850479217	6.417882493	2.642692653
0	0	0	0	NA
0	0	0	0	6.106069692
0	0	0	0	5.962029998
6.726028513	4.522641594	0	0	NA
0	1.809056637	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	NA
5.765167297	4.522641594	3.880383374	1.833680712	NA
0.960861216	3.618113275	0.970095843	1.833680712	NA
0	0	0	0	NA
11.53033459	4.522641594	12.61124596	4.584201781	2.503970832
1.921722432	0.904528319	1.940191687	0.916840356	3.688970456
5.765167297	6.331698231	2.91028753	1.833680712	NA
1.921722432	0.904528319	0.970095843	0.916840356	4.654854427
29.7866977	20.80415133	26.19258777	16.50312641	NA
19.21722432	17.18603806	28.13277946	31.17257211	NA
8.647750946	14.4724531	14.55143765	3.667361424	2.511276493
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0	0	0.970095843	2.750521068	7.558976575
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0	0	0	0.916840356	6.532362884
1.921722432	1.809056637	0	1.833680712	NA
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9.608612162	6.331698231	8.730862591	4.584201781	NA
1.921722432	0.904528319	0.970095843	0	NA
1.921722432	0	0	0.916840356	NA

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2.882583649	6.331698231	5.820575061	0.916840356	NA
17.29550189	18.99509469	31.04306699	16.50312641	NA
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0	0	0	0	NA
9.608612162	7.23622655	3.880383374	2.750521068	NA
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3.843444865	2.713584956	1.940191687	0	NA
3.843444865	9.045283187	1.940191687	2.750521068	NA
16.33464068	10.85433982	5.820575061	7.334722849	2.660220742
0.960861216	4.522641594	5.820575061	0	3.690840064
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0	0	0	0	6.157193062
3.843444865	3.618113275	4.850479217	5.501042137	3.243853442
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2.882583649	0	0.970095843	0.916840356	3.854721941
0.960861216	0	0	0.916840356	NA
0	0	0	0	NA
4.804306081	0	0.970095843	1.833680712	3.289299207
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1.921722432	2.713584956	0.970095843	1.833680712	NA
2.882583649	0.904528319	0.970095843	0.916840356	3.767322512
3.843444865	3.618113275	1.940191687	1.833680712	3.426536948
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136.4422927	123.9203797	206.6304147	141.1934148	NA
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3.843444865	4.522641594	4.850479217	1.833680712	NA
9.608612162	0	14.55143765	2.750521068	NA
2.882583649	2.713584956	1.940191687	0	NA
2.882583649	0	0	2.750521068	NA
0	0	0	0	9.211535356
5.765167297	5.427169912	13.58134181	11.00208427	2.785085952
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35.551865	24.42226461	38.80383374	38.50729496	NA
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2.882583649	9.949811506	10.67105428	4.584201781	NA
1.921722432	0	0	0.916840356	NA

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0	0	0	0.916840356	5.809846409
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4.804306081	0.904528319	2.91028753	2.750521068	NA
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0	0	0	0	6.706110711
1.921722432	0	0	0	4.265396553
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2.882583649	2.713584956	0.970095843	0	NA
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0.960861216	0	0.970095843	0.916840356	NA
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0	0	0	0.916840356	NA
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2.882583649	0.904528319	0	0	NA
0.960861216	0	1.940191687	0	NA
0	0	0	0	NA
0	0.904528319	0	0	NA
3.843444865	1.809056637	0	1.833680712	NA
0	0.904528319	0	0	5.272849557
1.921722432	2.713584956	0.970095843	0.916840356	4.754764939
1.921722432	0	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	7.260615073
0	0.904528319	0.970095843	0.916840356	5.800606912
0	0.904528319	0	0	NA
0.960861216	0	3.880383374	0	NA
0	0.904528319	0	0	5.904735438
0	0	0	0	6.237024598
0	0	0	0	6.046230549
0	0	0	0	6.462763254
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	6.243044363
2.882583649	0.904528319	0.970095843	0	3.757140368
0	0	0	0	6.119248624
0	0	0	0	NA
0	0	0	0	NA

0	0	0	0.916840356	6.635484708
0	0	0	0	7.389623346
0	0	0	0	NA
0	0	0	2.750521068	6.362516823
0	0	0	0	NA
0	0	0	0	NA
0.960861216	1.809056637	0.970095843	0.916840356	3.888951275
0	0	0	0	NA
0	0	0	0	NA
0	1.809056637	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	5.947354724
0	0	1.940191687	0	6.857341576
0	1.809056637	2.91028753	1.833680712	NA
0	0.904528319	0	0	6.873636528
0.960861216	6.331698231	1.940191687	0.916840356	NA
0	0	0	0	NA
0.960861216	0	0.970095843	0	NA
5.765167297	4.522641594	11.64115012	8.251563205	2.287850593
0	0.904528319	0	0	NA
2.882583649	0.904528319	4.850479217	0	5.29230312
0	0	0	0	NA
66.29942392	66.93509558	97.97968019	53.17674065	2.393230163
14.41291824	24.42226461	43.65431296	13.75260534	NA
0	0	0	0	NA
0.960861216	2.713584956	3.880383374	4.584201781	5.543762269
0	0	0	0	NA
18.25636311	9.949811506	14.55143765	12.83576499	3.645213366
0	1.809056637	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
9.608612162	0.904528319	8.730862591	3.667361424	5.097410187
23.06066919	14.4724531	30.07297115	12.83576499	NA
2.882583649	0.904528319	0	0	NA
0	0.904528319	0	0	7.294233636
0.960861216	4.522641594	0.970095843	0.916840356	NA
25.94325284	15.37698142	27.16268362	12.83576499	NA
0	0	0	0	NA
1.921722432	4.522641594	5.820575061	3.667361424	3.429532625
0	0	0.970095843	0.916840356	NA
0.960861216	0	0	0	NA
11.53033459	2.713584956	10.67105428	7.334722849	NA
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0	0	NA
2.882583649	2.713584956	2.91028753	0.916840356	NA
0.960861216	0	0	1.833680712	NA
0	0.904528319	1.940191687	0	6.358741296
2.882583649	0.904528319	1.940191687	0.916840356	5.631084547
0	0	0	0	NA
0	0.904528319	1.940191687	3.667361424	NA

2.882583649	5.427169912	2.91028753	0.916840356	3.566741465
0	0	0	0	NA
2.882583649	3.618113275	1.940191687	1.833680712	3.903555747
0	2.713584956	0.970095843	2.750521068	3.860783806
0	0	0	0	NA
26.90411405	17.18603806	34.92345036	15.58628605	3.284162235
1.921722432	2.713584956	0	0.916840356	3.724930199
6.726028513	5.427169912	9.700958434	0.916840356	NA
0.960861216	0	2.91028753	0	6.218391531
1.921722432	0.904528319	0	0	4.499942635
0.960861216	0	0	0	NA
0	0	0	0	6.362611555
0	0	0	0	6.400174938
0	0	0	0	NA
2.882583649	0	1.940191687	1.833680712	NA
3.843444865	4.522641594	7.760766748	0.916840356	NA
0	0.904528319	0	2.750521068	5.085240583
0	0	0	0	NA
4.804306081	6.331698231	1.940191687	5.501042137	3.611232056
0	0	0.970095843	0	NA
0	0	0	0	6.50286034
1.921722432	1.809056637	0.970095843	0.916840356	NA
3.843444865	4.522641594	1.940191687	2.750521068	NA
0	0	0.970095843	1.833680712	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	1.809056637	0	0	NA
8.647750946	1.809056637	3.880383374	0.916840356	3.997538728
0	0	0.970095843	0	NA
57.65167297	65.12603895	94.09929681	43.09149674	3.505020646
1.921722432	0	0.970095843	0	5.201924776
3.843444865	2.713584956	3.880383374	0.916840356	NA
4.804306081	0.904528319	5.820575061	0.916840356	NA
0.960861216	0.904528319	0.970095843	0	5.956616818
22.09980797	9.045283187	30.07297115	16.50312641	NA
4.804306081	3.618113275	6.790670904	5.501042137	4.546510444
0.960861216	0	0.970095843	1.833680712	NA
11.53033459	5.427169912	8.730862591	7.334722849	NA
0	0	1.940191687	0	6.118995328
1.921722432	0	0	0	NA
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0	0	0.970095843	0	7.577826844
0	0.904528319	0.970095843	0	5.347759382
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
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0	0	0	0	6.079374707
0.960861216	0	0	0	NA

0.960861216	0	0	0	NA
0.960861216	0	2.91028753	0.916840356	5.463579167
0	0	0	0	NA
0	1.809056637	3.880383374	0.916840356	8.809161119
0	0	0	0.916840356	NA
0	0.904528319	1.940191687	0	5.128438079
0.960861216	0.904528319	7.760766748	0	4.779390687
0	0	0	0	NA
3.843444865	0	2.91028753	0.916840356	3.425253919
3.843444865	1.809056637	0	0.916840356	3.775358223
0	0	0	0	NA
0	0	0	0	NA
1.921722432	1.809056637	1.940191687	1.833680712	NA
0	0	1.940191687	0.916840356	7.644663109
1.921722432	2.713584956	5.820575061	3.667361424	NA
0	0.904528319	0	0.916840356	NA
2.882583649	0	1.940191687	0	NA
0	0	0	0	6.512841769
1.921722432	0	0	0	NA
1.921722432	1.809056637	5.820575061	1.833680712	3.763966958
5.765167297	0.904528319	0.970095843	1.833680712	NA
192.1722432	163.7196257	252.2249193	103.6029602	2.143459391
0	0.904528319	0.970095843	1.833680712	NA
0.960861216	3.618113275	4.850479217	0	NA
1.921722432	1.809056637	0.970095843	1.833680712	5.002526567
0	0	0	0.916840356	NA
0	0	0	0	6.357075348
0	0	0	0.916840356	NA
0	0	0	0	NA
1.921722432	0	0	0	NA
0.960861216	2.713584956	1.940191687	1.833680712	NA
2.882583649	4.522641594	3.880383374	1.833680712	3.444564286
1.921722432	2.713584956	1.940191687	0	3.223651334
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0.960861216	0	0	0	5.477094669
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0	0	0	0.916840356	6.182204697
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0	0	0	0	6.112664923
0	0	1.940191687	0.916840356	6.837712693
0	0	1.940191687	0	NA
0	1.809056637	2.91028753	0	NA
12.49119581	18.09056637	17.46172518	11.00208427	3.356622131
0.960861216	0	0	0	5.608380771
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1.921722432	2.713584956	0.970095843	0.916840356	3.800534772
1.921722432	0.904528319	2.91028753	1.833680712	NA
5.765167297	0.904528319	6.790670904	5.501042137	NA
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0	1.809056637	0	0	4.672611406
0	1.809056637	0	3.667361424	NA

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0.960861216	2.713584956	1.940191687	0	3.551767336
0	0	0.970095843	5.501042137	5.785989582
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	1.833680712	NA
6.726028513	5.427169912	9.700958434	4.584201781	2.582471675
0	0	0	0	NA
0.960861216	2.713584956	2.91028753	1.833680712	NA
0	4.522641594	0.970095843	3.667361424	NA
0	0	0.970095843	0	NA
2.882583649	9.949811506	4.850479217	4.584201781	NA
0	0	0.970095843	0	NA
0	0	0	0	5.954711773
4.804306081	2.713584956	9.700958434	0.916840356	3.557499418
0	0	0	0	NA
0	0.904528319	0.970095843	0	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
1.921722432	1.809056637	0.970095843	0	NA
0	0	0.970095843	0.916840356	NA
0	0	0	0.916840356	NA
12.49119581	9.045283187	7.760766748	2.750521068	2.204566582
0	0	0	0	NA
0.960861216	0	0	0	NA
0	0.904528319	1.940191687	1.833680712	5.374753673
0	0	0	0	7.744347793
0	0	0	0	NA
0	0.904528319	0	0	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
1.921722432	2.713584956	2.91028753	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	1.833680712	NA
1.921722432	0.904528319	0	0.916840356	NA
0	2.713584956	1.940191687	0	NA
0	0	0	0.916840356	7.105973663
0.960861216	0	0	0	5.248381412
3.843444865	3.618113275	7.760766748	2.750521068	2.867491088
0	0	0	0.916840356	6.346037755
0.960861216	1.809056637	0.970095843	0.916840356	NA
0	2.713584956	2.91028753	1.833680712	NA
1.921722432	8.140754868	8.730862591	7.334722849	NA
4.804306081	4.522641594	7.760766748	2.750521068	NA
0	0	0	0	6.176181554
2.882583649	1.809056637	2.91028753	0.916840356	NA
0	0	0	0	NA
10.56947338	5.427169912	8.730862591	2.750521068	NA

0.960861216	4.522641594	1.940191687	2.750521068	NA
0	0	0	0	NA
0	1.809056637	3.880383374	0.916840356	NA
0	0.904528319	0	0	6.513140927
0	0	0	0	NA
0	0	1.940191687	4.584201781	NA
8.647750946	3.618113275	4.850479217	2.750521068	NA
1.921722432	0	0.970095843	0	NA
3.843444865	7.23622655	7.760766748	0.916840356	2.912445261
3.843444865	0.904528319	1.940191687	0.916840356	NA
5.765167297	0.904528319	1.940191687	0.916840356	NA
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0	0	0	0	6.723401097
0	0.904528319	0.970095843	0	NA
0	2.713584956	0	0	NA
0.960861216	0.904528319	0	0	NA
8.647750946	10.85433982	18.43182103	4.584201781	2.918452091
0	0	0	0	NA
0	0	0	0	NA
3.843444865	3.618113275	1.940191687	5.501042137	NA
0	0	0	0	NA
6.726028513	4.522641594	13.58134181	6.417882493	3.779288839
1.921722432	3.618113275	0.970095843	0.916840356	NA
0.960861216	1.809056637	0.970095843	0	3.66832467
2.882583649	5.427169912	1.940191687	1.833680712	NA
5.765167297	1.809056637	1.940191687	0.916840356	3.192354771
3.843444865	0.904528319	4.850479217	0	NA
0.960861216	0.904528319	2.91028753	2.750521068	4.63022207
35.551865	26.23132124	40.74402542	23.83784926	2.626080222
0	0	0	0	NA
0	0	0	0	7.348764043
0.960861216	0	1.940191687	0.916840356	5.518274846
5.765167297	9.045283187	3.880383374	4.584201781	NA
0	0	0	0	NA
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0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0.916840356	NA
6.726028513	2.713584956	2.91028753	1.833680712	NA
0.960861216	2.713584956	0.970095843	0.916840356	NA
1.921722432	1.809056637	3.880383374	0.916840356	NA
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0	0	0	0	6.621948645

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1.921722432	7.23622655	9.700958434	0.916840356	NA
7.68688973	5.427169912	7.760766748	2.750521068	3.815062936
1.921722432	0.904528319	3.880383374	0.916840356	NA
0	0.904528319	0	0	NA
6.726028513	6.331698231	17.46172518	9.168403561	2.343736131
0	0	0	0	NA
0	0	0	0	NA
0	0	0	1.833680712	6.522654874
0	0	0	0	NA
2.882583649	3.618113275	1.940191687	0.916840356	NA
6.726028513	4.522641594	8.730862591	8.251563205	5.003423109
12.49119581	10.85433982	4.850479217	8.251563205	3.265377451
2.882583649	4.522641594	0.970095843	1.833680712	NA
5.765167297	2.713584956	3.880383374	0	NA
0	5.427169912	2.91028753	2.750521068	NA
6.726028513	2.713584956	3.880383374	0	NA
0	0	0	0	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
1.921722432	0.904528319	0.970095843	0.916840356	3.592114138
2.882583649	0	0	0	NA
0.960861216	0.904528319	2.91028753	1.833680712	NA
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0	0.904528319	0	0	NA
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0	0	0	0	NA
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31.70842013	16.28150974	20.37201271	10.08524392	2.33427687
13.45205703	17.18603806	19.40191687	6.417882493	2.216101861
27.86497527	18.99509469	31.04306699	10.08524392	NA
4.804306081	0	3.880383374	0	NA
0	0	0	0	NA
2.882583649	0	1.940191687	0.916840356	4.265092525
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2.882583649	0	0	0.916840356	3.974371837
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1.921722432	2.713584956	1.940191687	1.833680712	NA
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4.804306081	2.713584956	4.850479217	3.667361424	2.795239797
0	0.904528319	0	0.916840356	NA

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0	0	0.970095843	0	NA
9.608612162	20.80415133	10.67105428	13.75260534	NA
1.921722432	0.904528319	4.850479217	0.916840356	NA
0	0	0	0	NA
2.882583649	7.23622655	13.58134181	12.83576499	NA
0	2.713584956	0	0	NA
0.960861216	0	0.970095843	0	NA
1.921722432	0	0	0	NA
2.882583649	3.618113275	4.850479217	1.833680712	NA
7.68688973	2.713584956	6.790670904	2.750521068	NA
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6.726028513	5.427169912	13.58134181	6.417882493	4.554416435
7.68688973	9.949811506	4.850479217	3.667361424	NA
0.960861216	0.904528319	0	3.667361424	NA
0	1.809056637	0	0	NA
0	1.809056637	0	0	NA
0	0	0	0.916840356	7.490523335
2.882583649	0.904528319	2.91028753	0	NA
2.882583649	0.904528319	0.970095843	0	NA
0	0	1.940191687	0.916840356	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
6.726028513	8.140754868	0.970095843	0.916840356	NA
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0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0.916840356	NA
0.960861216	0	0.970095843	0.916840356	NA
0	0	0	0	NA
1.921722432	2.713584956	3.880383374	0	NA
0	0	0	0	NA
0.960861216	0	0.970095843	2.750521068	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
11.53033459	18.09056637	21.34210856	17.41996677	NA
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	0	0	NA
0.960861216	0	0.970095843	0	NA
0	0	0	0	NA
0	0	1.940191687	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA

0	0	0	0	NA
0	0	0	0	NA
9.608612162	2.713584956	6.790670904	4.584201781	NA
0	0	0.970095843	0	NA
0.960861216	0	0.970095843	0.916840356	NA
1.921722432	0	1.940191687	0	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	0.904528319	0	0.916840356	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
3.843444865	0	3.880383374	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	2.713584956	0.970095843	0	NA
1.921722432	3.618113275	5.820575061	3.667361424	NA
14.41291824	12.66339646	20.37201271	18.33680712	NA
0	0	0	0	NA
0	0	0	0	NA
0	1.809056637	0.970095843	1.833680712	NA
0	0	0	0	NA
0	0	1.940191687	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	0.904528319	0	0.916840356	NA
0	0	0	0	NA
0	0.904528319	0	0	NA
0	0	0	0	NA
6.726028513	4.522641594	0.970095843	3.667361424	NA
0	0	0	0	NA
1.921722432	4.522641594	0.970095843	1.833680712	NA
0.960861216	4.522641594	11.64115012	5.501042137	3.489397292
1.921722432	2.713584956	0	1.833680712	NA
0	0	1.940191687	0	NA
0	0	0	0	NA
2.882583649	5.427169912	5.820575061	0	NA
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0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0.916840356	NA
0	0	0	0	NA
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2.882583649	0	0	0	NA
0	0	0	0	NA

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5.765167297	5.427169912	13.58134181	6.417882493	NA
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0	0	0	0	NA
0	0	0	0	NA
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0	0	0	0	NA
0	0	0	0	NA
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0	0	0	0	NA
0	0	0	0.916840356	NA
0	0.904528319	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
2.882583649	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
2.882583649	5.427169912	2.91028753	0	NA
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0	0	2.91028753	0	NA
0	0.904528319	0	0	NA
1.921722432	2.713584956	0	3.667361424	NA
7.68688973	3.618113275	3.880383374	5.501042137	NA
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0	0	0	0	NA
0	0	0	3.667361424	NA
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3.843444865	3.618113275	0	0	NA
1.921722432	4.522641594	5.820575061	3.667361424	NA
0	3.618113275	0.970095843	0	NA
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1.921722432	0.904528319	0.970095843	0.916840356	NA
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0.960861216	0	3.880383374	3.667361424	NA
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0.960861216	0	0	0.916840356	NA
0	0	0.970095843	0	NA
0.960861216	0.904528319	1.940191687	0	NA
7.68688973	1.809056637	1.940191687	0	5.305057901
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0	0	0	0	NA
0	0	0	0	NA
1.921722432	0	1.940191687	0	NA
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0	0	0.970095843	0	5.990577655
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2.882583649	0.904528319	3.880383374	0	NA
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0.960861216	0	1.940191687	1.833680712	NA
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7.68688973	9.045283187	6.790670904	7.334722849	NA

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0	0	0	0	NA
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0	0	0	0	NA
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0	0	0	0	NA
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1.921722432	0	0.970095843	0	NA
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3.843444865	0.904528319	2.91028753	1.833680712	NA
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1.921722432	0	4.850479217	3.667361424	NA
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0	0	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	4.522641594	1.940191687	3.667361424	NA
0	0	0	0.916840356	NA
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0	0	0	0	NA
0	0	0	0	NA

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0	0	0.970095843	0	NA
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13.45205703	12.66339646	20.37201271	16.50312641	NA
12.49119581	20.80415133	12.61124596	14.6694457	NA
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0	0	0	0	NA
4.804306081	3.618113275	6.790670904	2.750521068	NA
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0	0	0	0	NA
1.921722432	0	0	0	NA
0.960861216	1.809056637	0.970095843	0	NA
0	0	0	0.916840356	NA
0	0	0	0	5.983871625
4.804306081	13.56792478	4.850479217	1.833680712	NA
1.921722432	6.331698231	12.61124596	9.168403561	3.834552156
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0	0	0	0	NA

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0	0.904528319	0.970095843	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	1.809056637	2.91028753	5.501042137	NA
0	0	0	0	NA
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3.843444865	0	0	0.916840356	NA
3.843444865	0	0	0	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
0	0	0.970095843	1.833680712	NA
0.960861216	1.809056637	0	0	NA
3.843444865	4.522641594	1.940191687	0	NA
0	0	0	0.916840356	6.46275373
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0	0	0.970095843	0	NA
1.921722432	0.904528319	0	0	NA
0	0	0	0	NA
2.882583649	0.904528319	0	1.833680712	NA
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0	0	0	0	NA
5.765167297	5.427169912	10.67105428	8.251563205	NA
0	0	0.970095843	0	NA
0	0	0	0	NA
0	0.904528319	0	0	NA
24.98239162	23.51773629	29.1028753	28.42205104	NA
0	0	0	0	NA
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0	0	0.970095843	1.833680712	5.536508792
3.843444865	3.618113275	3.880383374	1.833680712	NA
0	0	0	0	NA
0	0	0.970095843	0.916840356	NA
12.49119581	7.23622655	7.760766748	6.417882493	NA
2.882583649	5.427169912	0.970095843	3.667361424	NA
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0	0	0	0	NA
0	0	0.970095843	0	NA

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0	0	0	0	NA
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0	0	0.970095843	0.916840356	NA
11.53033459	10.85433982	10.67105428	7.334722849	NA
0	0	0	0	NA
1.921722432	0.904528319	5.820575061	2.750521068	3.424548366
3.843444865	0.904528319	2.91028753	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0.904528319	2.91028753	0	NA
0	0	0	0.916840356	NA
0.960861216	0	0.970095843	0.916840356	NA
1.921722432	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0.916840356	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0.960861216	2.713584956	0	0	NA
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0	0	0	0	NA
0.960861216	0	2.91028753	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0.970095843	0	NA
3.843444865	2.713584956	1.940191687	0.916840356	NA
0.960861216	0	0	0	NA
1.921722432	1.809056637	3.880383374	2.750521068	NA
0	0.904528319	0	0	NA
1.921722432	1.809056637	2.91028753	0	NA
0	0.904528319	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
1.921722432	1.809056637	0	0.916840356	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0	NA
0	0	0	0.916840356	NA
0	0	0	0	NA
6.726028513	0.904528319	2.91028753	0.916840356	NA
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0	0	0	0	NA

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4.804306081	2.713584956	2.91028753	6.417882493	NA
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1.921722432	4.522641594	9.700958434	1.833680712	NA
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0	0.904528319	0	0	NA
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3.843444865	0.904528319	5.820575061	0.916840356	NA
0	0	0	0	NA
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0.960861216	0	0	1.833680712	NA
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0	0	0	0	NA
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20.17808554	22.61320797	25.22249193	29.3388914	NA
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0	0.904528319	0	0	NA
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2.882583649	3.618113275	0.970095843	0.916840356	2.846521346
0	0	0	0	NA
1.921722432	2.713584956	0.970095843	3.667361424	NA
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1.921722432	1.809056637	5.820575061	1.833680712	NA
1.921722432	0.904528319	0.970095843	1.833680712	NA
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0.960861216	1.809056637	0.970095843	0.916840356	NA
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0.960861216	0	0	0	NA
5.765167297	14.4724531	7.760766748	28.42205104	NA
0	0	0	0	NA
0.960861216	0.904528319	5.820575061	0.916840356	NA
6.726028513	7.23622655	13.58134181	4.584201781	NA
1.921722432	1.809056637	2.91028753	0.916840356	NA
0.960861216	0	0	0	NA
0	0	0	0	NA
1.921722432	0	3.880383374	2.750521068	NA
0.960861216	2.713584956	0.970095843	1.833680712	NA
5.765167297	4.522641594	4.850479217	10.08524392	NA
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1.921722432	0	0	0.916840356	NA
13.45205703	11.75886814	14.55143765	8.251563205	NA
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0	0	0.970095843	0	NA
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6.726028513	5.427169912	3.880383374	7.334722849	NA
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0	0	0.970095843	0	NA
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1.921722432	0	0.970095843	0	4.14324595
0.960861216	0	3.880383374	3.667361424	NA
0	0	0.970095843	0	NA
0	1.809056637	2.91028753	0.916840356	NA
5.765167297	3.618113275	9.700958434	7.334722849	3.731301895
0	0	0	0	NA
2.882583649	0.904528319	0.970095843	1.833680712	NA
0	0	0.970095843	0	NA
0	2.713584956	0	0	NA
0	0	1.940191687	0	NA
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5.765167297	0	0	0.916840356	NA
17.29550189	6.331698231	21.34210856	9.168403561	NA
4.804306081	0	0.970095843	3.667361424	NA
5.765167297	0.904528319	0.970095843	0.916840356	NA
10.56947338	10.85433982	10.67105428	5.501042137	NA
9.608612162	12.66339646	5.820575061	12.83576499	NA
9.608612162	12.66339646	1.940191687	3.667361424	NA
6.726028513	0	3.880383374	6.417882493	NA
12.49119581	14.4724531	12.61124596	3.667361424	NA
5.765167297	5.427169912	0.970095843	1.833680712	NA
4.804306081	5.427169912	8.730862591	7.334722849	NA
5.765167297	9.949811506	11.64115012	4.584201781	NA
6.726028513	10.85433982	4.850479217	9.168403561	NA
7.68688973	12.66339646	16.49162934	22.00416855	NA
15.37377946	6.331698231	3.880383374	4.584201781	NA
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