1 Subjects & Methods

1.1 Samples

For assay assessment, we sequenced AML cell lines (n = 3), samples from healthy volunteers (n = 2, from peripheral blood (PB)) and AML patient samples (n = 57 samples, from bone marrow aspirates (BM)). In total, and including all technical replicates, we sequenced and analyzed 90 samples.

The human AML cell lines HL-60 (FLT3-ITD negative control¹), MOLM-14 (FLT3-ITD positive control, 21 bp ITD¹) and PL-21 (FLT3-ITD positive control, 126 bp ITD¹) were obtained from the German cell line repository DSMZ (Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany). The 57 AML samples were derived from 28 AML patients who were all included in the AMLSG BiO Registry study (ClinicalTrials.gov identifier: NCT01252485) and gave their informed consent for both biobanking and genomic analysis of leukemia samples according to the Declaration of Helsinki.

For initial assay assessment, we sequenced 3 FLT3-ITD negative controls (healthy volunteers, n=2; AML cell line HL-60), 2 FLT3-ITD positive controls (AML cell lines MOLM-14 and PL-21) and diagnosis samples of 28 AML patients who previously tested FLT3-ITD positive by PCR- and capillary electrophoresis-based fragment analysis (FA). To further evaluate our assay in the context of MRD monitoring of FLT3-ITD positive AML, we sequenced 29 follow-up samples of 10 of these AML patients, five of whom achieved continuous complete remission and five of whom relapsed from the disease. For all patients, at least one sample from complete remission, following induction therapy, and at least one additional follow-up sample, either from continued complete remission or the time of relapse,

were sequenced. All of these 10 patients were also enrolled in the AMLSG 16-10 trial (ClinicalTrials.gov identifier: NCT01477606). Within this trial, patients were treated with intensive induction chemotherapy in combination with midostaurin followed by allogeneic stem cell transplantation (HSCT) as first priority for consolidation or an age-adapted high-dose cytarabine (HDAC) based chemotherapy regimen in combination with midostaurin. A one-year maintenance therapy with midostaurin was intended for all patients, starting after chemotherapy-based consolidation or 30 days after HSCT.

A detailed sample overview is provided in Table S2, including the attained sequencing coverage and FLT3-ITD statistics.

1.2 FLT3-ITD detection by NGS and getITD

Next-generation sequencing: Patient samples had been enriched for mononuclear cells by Ficoll gradient centrifugation and purified cells were biobanked at -80 °C. Of these samples, genomic DNA was isolated using the AllPrep Mini Kit (Qiagen, Hilden, Germany) according to the manufacturers instructions. *FLT3* exons 14–15 were amplified by PCR, using 1 μL (50 ng) of genomic sample DNA, 20 μL of 2x KAPA HiFi HotStart ReadyMix (KAPA Biosystems, Wilmington, Massachusetts, USA) and 1.2 μL of 10 μM forward and reverse primer (forward primer: TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGA + GCAATTT-AGGTATGAAAGCCAGCTAC, reverse primer: CCAACGGCAGTTTTACGA-CTTTC + AGACAGAGAATATGTGTAGAGGCTCGGGTGCTCTG, each consisting of *FLT3* locus-specific sequence and the required sequencing adapter). The PCR comprised an initial denaturation step (95 °C 3 min), 30 amplification cycles

(denaturation 98 °C 20 s, annealing 65 °C 30 s, elongation 72 °C 1 min) and a final elongation step (72 °C 5 min). PCR products were prepared for sequencing as detailed in the Illumina 16S Metagenomics Sequencing Protocol (16S Metagenomic Sequencing Library Preparation, Illumina, San Diego, California, USA) using either single or double unique indices for sample multiplexing. The resulting libraries were sequenced to high-coverage on the Illumina MiSeq using 250 bp paired-end reads (500-cycles MiSeq Reagent Kit V2, Illumina) and 7% phiX control spike-in (Kit V3, Illumina; coverage: 0.04–4.2 million, mean 1.6 million paired-end reads). In total, library preparation takes 6 h, with roughly 3 h of hands-on time. Se-

In total, library preparation takes 6 h, with roughly 3 h of hands-on time. Sequencing takes an additional 39 h, so that samples are fully processed within 48 h. For our validation experiments, we have aimed for a rather high coverage and pooled 8 samples per MiSeq run, generating on average around 2 million paired-end reads per sample. With this setup, assay costs amount to about 150 Euro per sample. However, more than 90 % of these costs are spent on sequencing and only a minor fraction covers the sequencing library preparation. Costs could thus be reduced to about 100 Euro per sample if 16 instead of 8 samples were pooled, which would still generate a sufficient coverage of around 1 million reads per sample.

Sample indexing: We tested our assay with both single and double unique indices for sample barcoding and multiplexing. Comparing 14 technical replicates, derived from 14/28 FLT3-ITD positive AML patients analyzed for assay assessment, we found significant index mis-assignment, so-called index hopping, when using single indices only². Index hopping causes reads to be mis-assigned to the wrong sample in a pooled library—when FLT3-ITD mutated reads are mis-assigned, they are then detected as false positive contaminated variants in these samples. For exam-

ple, in our 14 replicates sequenced with single unique indices, 22/61 FLT3-ITDs could be traced to index hopping. We therefore sequenced all of our AML patient samples thereafter using double unique indices, found zero ITDs attributable to index hopping, and thus recommend others also use double indexing whenever low-allelic variants are of interest. Details of the ITDs detected with either index design are provided in Table S3.

getITD: We developed the bioinformatics program *getITD* for the analysis of our assays sequencing data and the identification of respective ITDs. In brief, *getITD* aligns high-quality sequencing reads to the wild type (WT) amplicon, identifies insertions relative to this reference and then determines whether these qualify as ITDs. Insertions and ITDs are both extensively annotated and reported to the user.

By default, high-quality sequencing reads are those with an average base quality score (BQS) of at least 30, equivalent to a sequencing error probability below 0.1%, whose sequence is not unique in a given sample. Each of these reads is aligned to the WT sequence of the target amplicon using the Needleman-Wunsch alignment algorithm³, with alignment scores optimized for the detection of long insertions (match: 5, mismatch: -15, gap opening: -36, gap extension: -0.5). Only alignments with gap-free primer sequences and an alignment score of at least 50% of the maximum possible score are processed further.

This alignment score, which quantifies the similarity between the reference sequence and each of the samples reads, is calculated for each read as a running sum that increases whenever bases match between the read and the reference and decreases when they do not. Very low scores are indicative of PCR artefacts and

respective reads are thus filtered out.

From passing reads, insertions relative to the reference are extracted which are (i) in-frame, (ii) at least 6 bp / 2 amino acids long and (iii) free of ambiguous bases (N). Inserts at the very 5' or 3' end of a read, which we call trailing inserts, are not required to be in-frame - since they are not fully covered by the read, their exact length is unknown. Detected insertions, both trailing and non-trailing, are considered ITDs if they are adjacent to a second repeat of their own sequence (Figure 1B). These repeats, the respective ITDs WT tandems, are identified by realigning the insert to the WT reference and again require an alignment score of at least 50% of the maximum possible score. From all ITDs identified in this way, a set of high-confidence calls is obtained by filtering for those with a VAF of at least 0.006% and two or more distinct supporting reads.

While this is the primary output of interest, all of the insertions and ITDs identified as part of the analysis are annotated and reported. Specifically, each insertion and ITD is annotated with insertion length, site, sequence and frequency. ITD frequencies are provided as VAFs and, calculated from these as shown below in equation 1, allelic ratios (ARs). Insertion sites are given as coordinates relative to the amplicon, genome, transcript and protein.

Detailed results of getITD are presented in Table S3 for all 210 FLT3-ITDs described in the manuscript.

$$AR = \frac{VAF}{100 - VAF} \tag{1}$$

All analysis parameters are user-adjustable and can be tuned to accommodate for example single-end, merged or trimmed reads as well as reads generated from other sequencing technologies or target regions⁴. Limits on the maximum detectable ITD length are imposed only by the sequencing data used for the analysis, not by *getITD* itself.

Code availability & details: getITD is implemented in python3, runs on Linux, Mac and Windows and is freely available for download at https://github.com/tjblaette/getitd. It may be run directly from the command-line or via a wrapper program that offers a simple graphical interface to supply input files and parameters. Analysis of a single sample with one million paired-end reads takes, depending on the computational resources available, 20 min with and up to 60 min without parallelization across multiple cores. Analysis of the data described in this manuscript was performed with default parameters and without any manual curation of results.

Fragment analysis: All patient samples were independently screened for FLT3-ITDs at diagnosis and relapse using the established diagnostic FA, a PCR-based amplification of FLT3 exons 14 and 15 followed by capillary electrophoresis as described previously⁵. ITD insertion sites were determined by conventional Sanger sequencing⁵. To compare ITDs detected by FA and by NGS, which report mutation frequencies as ARs and VAFs respectively, the AR determined using the GeneScan platform was converted to the corresponding VAF as follows:

$$VAF = \frac{AR}{AR+1} * 100 \tag{2}$$

Supplementary references

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- Kircher M, Sawyer S, and Meyer M. Double indexing overcomes inaccuracies in multiplex sequencing on the Illumina platform. *Nucleic Acids Res* 2011; 40: e3–e3.
- Needleman SB and Wunsch CD. A general method applicable to the search for similarities in the amino acid sequence of two proteins. J Mol Biol 1970; 48: 443–453.
- 4. Rücker FG, Du L, Blätte TJ, Benner A, Krzykalla J, Gathmann I, et al. Prognostic Impact of Insertion Site in Acute Myeloid Leukemia (AML) with FLT3 Internal Tandem Duplication: Results from the Ratify Study (Alliance 10603). *Blood* 2018: 435 (abstract).
- Kayser S, Schlenk RF, Londono MC, Breitenbuecher F, Wittke K, Du J, et al. Insertion of FLT3 internal tandem duplication in the tyrosine kinase domain-1 is associated with resistance to chemotherapy and inferior outcome. *Blood* 2009; 114: 2386–2392.

MOLM-14: HL-60	1:100	1:1000	1:10000
Expected VAF (%)	0.67	0.067	0.0067
VAF by NGS (%)	0.88043	0.08545	0.00483
VAF by NGS (%)	0.72653	0.07486	0.01509
VAF by NGS (%)	0.72068	0.05967	0.00073
VAF by NGS (%)			0.00075
Mean	0.77588	0.07333	0.00535
Standard deviation	0.09059	0.01296	0.00677
Coefficient of variation (CV)	0.11676	0.17677	1.26592

Table S1: Replicates of the serial dilution: For the three dilutions with expected FLT3-ITD frequencies 0.67%, 0.067% and 0.0067%, 3–4 independent technical replicates were analyzed using our NGS-based assay. Reported here are the exact variant allele frequencies (VAFs) estimated in each replicate, also plotted in Figure 1A of the manuscript, and the standard deviation, mean and coefficient of variation (CV, standard deviation / mean) for each of the three dilutions. Note that independent serial dilutions were pipetted for all replicates.

Dilution Patient ID	Cohort_sensitivity Co	hort_specificity Co	ohort_accuracy Coho	ort_reproducibility	Cohort_mrd-rl	Cohort_mrd+	rl Material Tir	ne point N	umber of ITDs (FA)	AR of ITDs (FA)	VAF of ITDs (FA / calculated) I	TD1 length & site (FA / Sanger)	ITD2 length & site (FA / Sanger) Numb	er of ITDs (getITD) T	otal ITD VAF (getITD) Number of FA-fe	ound ITDs (getITD) Total VAF of	FA-found ITDs (getITD)	Sample indexing (Coverage (read pairs)
- 1			yes	yes			BM	dx	1	0.192	16.10738255	54 (AS 598/599)		2	13.2897	1	12.958	double	121444
- 1			yes	yes			BM BM	dx dx	1	0.192 0.617	16.10738255 38.15708101	54 (AS 598/599) 72 (AS 606/607)		6	13.1415 33.7071	1	12.68 33.695	single double	502823 1139145
. 3			yes	yes			BM	dx	1	0.789	44.10285075	21 (AS 600/601)		1	43.489	1	43.489	double	1143537
- 3			jus	yes			BM	dx	ī	0.789	44.10285075	21 (AS 600/601)		3	44.4894	1	44.45	single	283201
- 4			yes	yes			BM	dx	1	17.169	94.49611976	39 (AS 593)		1	94.653	1	94.653	double	143104
- 4				yes			BM	dx	1	17.169	94.49611976	39 (AS 593)		6	89.1975	1	89.111	single	642035
- 5			yes	yes			BM BM	dx dx	1	0.861 0.861	46.26544868 46.26544868	42 (AS 602) 42 (AS 602)		1 3	44.728 47.0621	1	44.728 47.007	double single	2092251 321840
- 6			yes	yes yes	yes		BM	dx	1	0.552	35.56701031	27 (AS 599)		5	37.2114	1	34.127	double	2110204
- 6			,	yes	,		BM	dx	ī	0.552	35.56701031	27 (AS 599)		5	38.6549	1	33.755	single	271565
- 6					yes		BM cr	cy2_c1						0	0	0	0	double	2668487
- 6					yes			fu_m11						0	0	0	0	double	1987005
- 7			yes yes	yes	yes		BM BM	dx dx	1	0.752 0.686	42.92237443 40.68801898	33 (AS 596/597) 36 (AS 608/609)		5	43.7485 44.7312	1	43.702 44.718	double	1602251 1358468
- 8			yes	yes	yes		BM	dx	1	0.686	40.68801898	36 (AS 608/609)		1	46.784	1	46.784	single	285460
- 8				,	yes		BM cr	cy2_c1				(ō	0	0	0	double	2415099
- 8					yes		BM ci	fu_m3						0	0	0	0	double	2950217
- 8					yes		BM cr	fu_m12						0	0	0	0	double	1895959
- 9			yes yes				BM BM	dx dx	1 2	0.103 0.347	9.338168631 25.76095026	48 (AS 610) 24 (AS 598)	33 (AS 594)	1 12	3.4012 25.5057	1	3.4012 24.677	double double	779831 2324362
- 10			yes	yes			BM	dx	1	0.452	31.12947658	45 (AS 590/591)	33 (AS 594)	1	24.702	1	24.702	double	182304
- 11			jus	yes			BM	dx	ī	0.452	31.12947658	45 (AS 590/591)		3	27.636	i	27.6	single	1344506
- 12			yes	yes	yes		BM	dx	1	0.768	43.43891403	45 (AS 598)		2	42.2052	1	41.874	double	2076011
- 12				yes			BM	dx	1	0.768	43.43891403	45 (AS 598)		2	42.3822	1	42.105	single	543655
- 12					yes		BM cr	cy2_c1						0	0	0	0	double	1856671
- 12 - 13			yes	yes	yes	yes	BM cr.	fu_m12 dx	2	0.276	21.63009404	60 (AS 613)	39 (AS 595/596)	0	22.2246	3	22.2246	double double	1887112 1423217
- 13			yes	yes		yes	BM	dx	2	0.276	21.63009404	60 (AS 613)	39 (AS 595/596)	3	22.2663		22.2529	single	383536
- 13				,		yes	BM cr	cy2_c1	-			(,		ō	0	0	0	double	1708522
- 13						yes	BM cr	eot_c4						0	0	0	0	double	2962904
- 13						yes	BM ci	_fu_m3						0	0	0	0	double	2013235
- 13 - 13						yes	BM ci BM ci	fu_m6 fu_m9						0	0	0	0	double double	2220894 1426831
- 13						yes		_ru_m9 fu_m11	0	0	0			2	0.21863	0	0	double	1888212
- 14			yes			yes	BM II	dx dx	2	0.765	43.3427762	18 (AS 603)	30 (AS 593)	2	42.581	2	42.581	double	2474806
- 15			yes	yes			BM	dx	1	0.525	34.42622951	24 (AS 601/602)		1	31.827	1	31.827	double	38989
- 15				yes			BM	dx	1	0.525	34.42622951	24 (AS 601/602)		9	31.0303	1	30.846	single	549621
- 16			yes				BM	dx	1	0.863	46.32313473	18 (AS 598)		5	42.8743	1	41.651	double	2601573
- 17 - 18			yes		yes		BM BM	dx dx	2	0.412 5.419	29.17847025 84.42124942	54 (AS 613) 27 (AS 608)	90 (AS 606)	11	29.2862 78.7967	2	28.646 78.789	double double	1203484 1160877
- 18			yes	yes yes	yes		BM	dx	1	5.419	84.42124942	27 (AS 608)		1	77.659	1	77.659	single	237902
- 18				yes	yes			cy2_c1	-	0.410	04.42124342	27 (10 000)		Ô	0	Ō	0	double	2331331
- 18					yes		BM cr	eot_c4						0	0	0	0	double	2178063
- 19			yes			yes	BM	dx	2	0.195	16.31799163	36 (AS 596)	93 (AS 611/612)	16	13.6331	2	8.0268	double	1268768
- 19 - 19						yes	BM cr BM cr	_cy2_i2 _eot_tx						4	0.654645 0.03156	0	0	double double	1480411 1241329
- 19						yes		_eot_ix _fu_m4	1	0.299	23.01770593	93 (AS 611/612)			17.9518	1	17.484	double	1071694
- 20			yes			yes	BM	dx	ī	0.51	33.77483444	39 (AS 593)		3	28.6368	î	28.364	double	1454110
- 21			yes	yes		yes	BM	dx	1	0.632	38.7254902	87 (AS 609/610)		4	38.2656	1	38.089	double	2486855
- 21				yes			BM	dx	1	0.632	38.7254902	87 (AS 609/610)		3	34.866	1	34.724	single	238719
- 21						yes	BM cr	_cy2_i2						1	0.93816	0	0	double	2709486
- 21 - 21						yes yes		_eot_tx fu_m3						1	0 0.060832	0	0	double double	2857166 1131351
- 21						ves		fu_m5	1	0.646	39.24665857	87 (AS 609/610)		1	35.688	1	35.688	double	745374
- 22			yes			,	BM	dx	1	0.892	47.14587738	39 (AS 611/612)		3	46.1544	1	46.136	double	1095411
- 23			yes		yes		BM	dx	1	0.76	43.18181818	54 (AS 600)		2	41.2423	1	41.156	double	1633097
- 23					yes		BM cr	cy2_c1						0	0	0	0	double	1942717
- 23 - 24					yes		BM cr BM	_eot_c4 dx	1	0.788	44.07158837	66 (AS 610)		0	0 39.744	0	39 744	double	1394662 2526191
- 24			yes yes	yes		yes	BM BM	dx	2	0.788	44.07158837 28.46924177	42 (AS 590)	60 (AS 598)	7	39.744 29.083	2	39.744 27.903	double	736243
- 25			jus	yes		yes	BM	dx	2	0.398	28.46924177	42 (AS 590)	60 (AS 598)	8	29.5654	2	28.573	single	789474
- 25				-		yes	BM cr	cy2_c1					* *	6	2.22909	0	0	double	2705254
- 25						yes		_eot_c4						1	0.63748	0	0	double	1862886
- 25						yes	BM rl BM	_fu_m1	1	0.744	42.66055046	60 (AS 598) 36 (AS 608/609)		2	37.1815	1	37.103	double	1478562
- 26 - 27			yes yes				BM BM	dx dx	1	0.178 0.861	15.11035654 46.26544868	36 (AS 608/609) 96 (AS 613)		3	15.5536 48.3012	1	15.505 48.29	double double	2254869 1160877
- 28			yes	yes		yes	BM	dx	î	0.386	27.84992785	198 (AS 614/615)		6	10.326	1	9.9464	double	1022779
- 28			•	yes			BM	dx	1	0.386	27.84992785	198 (AS 614/615)		8	20.9549	1	20.593	single	340073
- 28						yes		cy2_c1						0	0	0	0	double	1483295
- 28						yes	BM rl	fu_m4	0 KNOWN 0	0 KNOWN 0	0			1	0.055593	0	0	double	2069770
 HL-60 healthy_volunteer1 		yes yes					cell_line PB		KNUWNU	KNOWN U	U			0	0	0	0	double double	4164257 1137581
- healthy_volunteer2		yes yes					PB PB	-						0	0	0	0	double	2441834
10-0 MOLM-14	yes	,					cell_line	-	1	KNOWN 2, FA 2.451	KNOWN 66.7, FA 71.02289192	21 (AS 599)		1	64.979	1	64.979	double	1797368
10-1 MOLM-14	yes						cell_line	-	1	KNOWN 0.0718	KNOWN 6.7	21 (AS 599)		1	8.6377	1	8.6377	double	2698207
10-2 MOLM-14	yes						cell_line	-	1	KNOWN 0.00675	KNOWN 0.67	21 (AS 599)		1	0.72068	1	0.72068	double	1686834
10-2 MOLM-14	yes						cell_line	-	1	KNOWN 0.00675	KNOWN 0.67	21 (AS 599)		1	0.72653		0.72653	double	1629789
10-2 MOLM-14 10-3 MOLM-14	yes yes						cell_line cell_line	-	1	KNOWN 0.00675 KNOWN 0.000670	KNOWN 0.67 KNOWN 0.067	21 (AS 599) 21 (AS 599)		1	0.88043 0.059666	1	0.88043 0.059666	double double	2681959 1139435
10-3 MOLM-14 10-3 MOLM-14	yes						cell_line	2	1	KNOWN 0.000670	KNOWN 0.067	21 (AS 599) 21 (AS 599)		1	0.059666		0.059000	double	1261903
10-3 MOLM-14	yes						cell_line	-	1	KNOWN 0.000670	KNOWN 0.067	21 (AS 599)		î	0.085454	1	0.085454	double	2850841
10-4 MOLM-14	yes						cell_line	-	1	KNOWN 0.0000670	KNOWN 0.0067	21 (AS 599)		1	0.0048347		0.0048347	double	2408074
10-4 MOLM-14	yes						cell_line	-	1	KNOWN 0.0000670	KNOWN 0.0067	21 (AS 599)		1	0.015087	1	0.015087	double	1609750
10-4 MOLM-14 10-4 MOLM-14	yes						cell_line cell_line	-	1	KNOWN 0.0000670 KNOWN 0.0000670	KNOWN 0.0067 KNOWN 0.0067	21 (AS 599) 21 (AS 599)		1	0.00073096		0.00073096	double	1742353 1562426
10-4 MOLM-14 10-0 PL-21	yes yes						cell_line cell line	-	1	KNOWN 0.0000670 KNOWN 0.5	KNOWN 0.0067 KNOWN 33.3	21 (AS 599) KNOWN 126 (AS 613)		1	0.00074673 18.641	1	18.641	double	1562426 2249360
10-0 PL-21	yes						cell_line		î	KNOWN 0.0341	KNOWN 3.3	KNOWN 126 (AS 613)		î	2.6228	ī	2.6228	double	2353158
10-2 PL-21	yes						cell_line	-	1	KNOWN 0.00331	KNOWN 0.33	KNOWN 126 (AS 613)		1	0.26	1	0.26	double	2198641
10-3 PL-21	yes yes						cell_line	-	1	KNOWN 0.000330	KNOWN 0.033	KNOWN 126 (AS 613)		1	0.014983	1	0.014983	double	1432778

Table S2: Sample overview: Listed are all of the samples processed and described in the manuscript with results obtained by fragment analysis (FA) and our NGS-based assay and *getITD*-based analysis.

Nution Patient ID Time point Sample indexing Index - 1 dx double - 1 dx double	k hopping artefact ITD length (bp) Star no 21 no 54		The property of the property	Instalt sequence GREACHEATHEATHCATECT GREACHEGETCETCAGARAATGAGTACTTCTACGTTGATTTCAGAGAARATGAA	Insert domains: [[com.ldM.D. pipenfoot*] [com.ldM.D. pipenfoot*] [com.ldM.D. pipenfoot*]	Series A.	(bp, in transcript) Start (AA, in 1792 594 1741 591	Earl Sp., to ch 13] Cris Earl Sp., to ch 13] Cris 200000000000000000000000000000000000	(bp., in transcript) End (AA, is 1902 60 1794 56		Insertion site (bp. in transcript) I 2803 1795 1803 1798	section site (AA, in protein) Insection site domain 601 excel4_3MD_zippenfoot 599 excel4_3MD_zippenfoot
- 1 dx single - 1 dx single - 1 dx single	no 21 yes 29 yes 45	79 0.386 0.00397 65135 56 0.039 0.0003 436196 90 0.007 0.00007 436196	247 Falter 9549 Falter 1778 Falter 124 Falter 22 Falter 55309 Falter 97 Falter	GANGANATGANTANTAN ANGAGNATUTCHGGATGANTGANAT ANATGATCTGANTGGAGTTTCCAAGAGAAATTAGAGTTTG	[Passmald_JMLD_plankled]] [Passmald_JMLD_dathCollection(#_(mostAd	28608274 28608297 28608263	1792 594 1759 597 1793 598	20000254 20000259 20000219	1802 66 1704 56 1802 66 1797 56 1827 61 1704 55 1826 66	31 28608253 89 28608258 13 28608218	1903 1798	601 excel4_MD_ripperMotf 600 excel4_MD_ripperMotf - inten14_spliceDonor
- 1 dx single - 1 dx single	yes 54 yes 65	70 0.022 0.0002 436196 72 0.018 0.00038 436196	97 False 78 False	GIGACIGAE CE FORMANICAM INC. I CIRCUI TRAN I FORMANICAM COTTGATTICAGA ANXIGAMENTA CETCAMA TOGGA GATTICCAGA GAMA TGATTICAGA GANTATGA TATAGA TICCAA ANTIGGA GAAAANTTAGA GATTICGA TA	[waste_Jubunactived; waste_Juboppinions] [waste_Jubunactived; waste_Jubprepartie; prant_Jubinquisequer] [waste_Jubunatthier; waste_Jubprepartie; yaste_Jubinquisequer; waste_Jubunatthier; waste_JupicoCosso*; waste_Jubunatthier; waste_Jubunat	2800213 2800212 2800220	1713 591 1775 592	28608230 28608215	1826 60	99 29608229 - 29608214	1795 1927	609 exch14_MO_hingeRegion - intron14
- 2 dx double - 2 dx double	no 22 no 21	44 23.695 0.50019 1036513 77 43.499 0.70857 1054593	222 Fallon 2385027 Fallon 458027 Fallon 50912 Fallon 26 Fallon	GGCTCCTCAGATAATGAGTACTTCAGAGTAATTGAGAGTATGAATGA	[mont.], M.D., geografied / mont.], M.D. Sappilegen() [mont.], M.D., geografied / mont.], M.D., geografied [mont.], M.D.,	2800257 2800209 28000276	1747 582 1780 594	20000220 20000230 20000256	1919 60 1900 60	96 29608227 20 29608255	1919 1901	607 exch1_MD_tingsRegion 601 exch1_MD_tippsRegion
- 2 dx single - 2 dx single - 2 dx single	yes 42 yes 54	61 0.022 0.00023 114212 25 0.017 0.00017 114212	26 False 29 False 29 False	CCTITICAGGITGATTOGAGGITGATCTCAA ACAGATGGTAGAGCGGGCCCCTCAGARAAGGAGTACTCCACGATTATTC	[manta_last_Officerary] [manta	2800276 2800292 2800228	1764 588 1764 576 1728 576	28608251 28608275	1900 60 1900 60 1905 60 1791 55 1779 56	20 28608250 24 28608274	1825 1810 1801 1801 1804 1806 1702 1779 1888 1779	602 exceld_JMD_ripperModi 504 exceld_JMD_ripperModi 504 exceld_JMD_ripperModi
	yes 179 no 29	1966 1966	22 True 429505 False	CICCICAGAIANTAGAIACTICIAC GGTGACCGGTCCTCAGAIANTAGTCTTCTAC GGTGACCGGTCCTCAGAIANTAGTCTTCTACTTGA	[mont4_MO_switchfootf,mont4_MO_logical_MO_logical_mont4_MO_logical_mont4_MO_logical_mont4_mont4_spiceDonor_intent4_spiceAcceptor] [mont4_MO_switchfootf,mont4_MO_logical_mont4_MO_logical_mont4_MO_logical_mont4_mont4_spiceAcceptor] [mont4_MO_switchfootf,mont4_	28508207 28508216	1749 582 1740 580	2000029 20000270 20000270	1779 56	29608277 29608277		612 exon15_TKD1_beta1Sheet 592 exon14_MD_ripperMotF
- 4 dx single - 4 dx single	yes Si	41 0.026 0.00006 482100 70 0.020 0.00000 482100	127 False 95 False	AGGACTICTCAGATANGAGTICTTCAGTTGATTCAGAGAANGAATAY CGTTGATTCAGAGAANGAGTAGTCAAATGGGAGTTCCAAGAGAANGAATAY	The control of the co	28608282 28608282	1744 592 1773 591	20000259 2000259	1797 55 1826 60	99 29508258 99 29508259	1798 1827	600 excrt4_MD_tipperMotf 609 excrt4_MD_hingsRegion
- 5 dx double - 5 dx single	no 62 yes 21	61 64.729 0.80923 1899947 77 0.064 0.0004 129798	027665 Falso 61 Falso	CCITTICOAGTIGATIOAGAANIGAATIGATCOA	[mania_mo_manumam_mania_mo_mo_mo_mo_mo_mo_mo_mo_mo_mo_mo_mo_mo_	28608292 28608276	1764 588 1780 594	29608251 29608256	1905 60 1900 60	2 28508250 20 28508255	1806 1801	602 excel4_MD_ripperMotif 601 excel4_MD_ripperMotif
- 5 dx single - 6 dx double	yes 56 no 21	25 0.011 0.0001 129798 65 0.008 0.0008 1827296 66 24.177 0.51807 1827296	25 Falter 247 Falter 673049 Falter	ACAGNEGIAACOGCICCICOGANAIGAS WCTICIACOTTGATT ACACNEGIGATIVAGAGA CONGICTION ACAGNETICAGAGA CONGICTION ACAGNETICAGAGA	[construct_non_c	28608228 28608288 28608287	1728 576 1768 590 1769 590	28608275 28608268 28608261	1701 56 1700 56	M 29608276 86 29608267 96 29608267	1800 1 18	SS4 excit_XMD_ripperMotif SS7 excit_XMD_ripperMotif SS0 excit_XMD_ripperMotif
- G dx double - G dx double - G dx double	no 20 no 22 no 66	61 0.050 0.0058 1837396 29 0.265 0.0036 1837396 42 2.733 0.0283 1837396	1071 False 5241 False 50215 False	TGGGGCCTACGTTGATTTCAGAGAANTGA GTGGTACAGGTGACCGGCTCCTCAGTAAGGG GCCCAACCTCAGATAAGGATCACCGGCTCCTCAGATAAGGG GCCCAACCTCAGATAAGAATCTCTCAGAGTGATTCAGAAATGGATTGAATTGA	[count_d, Standarder count_d, Mar. questions' count_d, Mar. questions'] [count_d, Mar. questions' count_d, Mar. questions' count_d, Mar. questions'] [count_d, Mar. questions' count_d, Mar. questions']	2808292 2808224 2808211	1764 588 1732 578 1745 582	28608262 28608292 28608246	1788 55 1792 55 1792 55 1792 55 1704 55 1810 65 1793 55 1794 55 1794 55 1810 66 1795 55 1794 55 1795 55 1795 55 1795 55 1795 55	98 29508262 98 29508291 94 29508245	1794 1765 1911	SSS exceld_3MD_ripperMost SSS exceld_3MD_switchMost SSS exceld_3MD_binosRosion
- G dx single - G dx single - G dx single	no 21 no 27 no 30	71 0.012 0.00012 120472 66 22.755 0.50955 120472 61 0.061 0.00061 120472	14 False 40005 False 74 False	GGTGATTTCAGAGAAXATGAA CCTAGGTTGATTCAGAGAAXAGAAT TIGGGGCCTAGGTTGATTCAGAGAAXAGAA	Trends, 200, market result, 200, market result, 200, generally [Second Second	28608282 28608287 28608292	1774 592 1769 590 1764 588	28608262 28608261 28608262	1794 56 1795 50 1793 56	98 29508261 99 29508260 98 29508262	1795 1796 1794	500 exact AVD piperholf 500 exact AVD piperholf 500 exact AVD piperholf 500 exact AVD piperholf
- G dx single - G dx single - 7 dx double	no 22 no 66 no 18	29 0.328 0.0029 120472 42 4.499 0.04711 120472 67 0.024 0.0008 1428432	295 Falce 5420 Falce 345 Falce	GTGGTACAGGTGACCGGCTCCTCAGATAATGAG GCCCAACCTCAGATAATGAGTACTTCAGCATTAATTCAGAGAATATGAGTCTCAAATGAG CINCCTTGAGTTCAGAGAATATGAGATATGAGAT	[contal_A,DAIO_intelligents", total A_JAIO_intelligents (_Coll_A,Baino) [rospil_A,DAIO_intelligents (_Coll_A,Baino), Tell_A,DAIO_intelligents (_Coll_A,DAIO_intelligents (_Coll_A,DAIO_	28608224 28608211 28608285	1722 578 1745 582 1770 590	28608292 28608246 28608269	1764 56 1810 60 1797 56	88 29508291 36 29508265 96 29508268	1765 1811 1788	589 exon14_3MD_switchMost 604 exon14_3MD_bingeRegion 586 exon14_3MD_pipperMost
- 7 dx double - 7 dx double - 7 dx double	no 27 no 23 no 48	67 0.007 0.0007 1428422 52 43.702 0.77626 1428432 89 0.006 0.0006 1428432	98 False 624249 False 89 False	CINCUTTANTITCAGAGARIATGARA GATAGAGTACTICTUCGITGATTCAGAGAA GATAGAGTCTCAAATGAGATTTCCAGAGAAAATTTGAGTTGGT	[worsta_JMD_suschMost*] worsta_JMD_paperMost*] [worsta_JMD_paperMost*] [worsta	28508285 28508200 28508254	1770 590 1756 585 1792 598	28608260 28608268 28608217	1796 56 1788 56	99 29508259 96 29508267 - 29508216		599 excel4_3MD_xipperMotif 597 excel4_3MD_xipperMotif - intron14
- 7 dx double - 8 dx double - 8 dx double	no 66 no 36 no 72	20 0.009 0.0009 1428432 86 64.718 0.0089 1198294 50 0.012 0.00012 1198294	132 False 535998 False 158 False	GATATIGAG TACTICTACGTTGATTCAAGAAGAATANTIGAG TACTICTACSTTGATTCAAGAA TAGAANTGATCTCAAATGGGGGTTTCCAAGAGA TAGAANTGATCCAAATGGGAGTTCCAAGAAATATGAATGGATTCCAAGAGAA	[wood_A_MD_bindpulser] "wood_A_MD_inpulser[wood_A_MD_inpulser[wood_A] [wood_A_MD_inpulser] [wood_A_MD_inpulser[wood_A_MD_inpulser] [wood_A_MD_inpulser[wood_A] [wood_A_MD_inpulser[wood_A] [wood_A_MD_inpulser[wood_A] [wood_A_MD_inpulser[wood_A] [wood_A] [wood_A_MD_inpulser[wood_A] [wood_A] [woo	28608222 28608267 28608202	1722 575 1789 597 1752 585	28608268 28608232 28608232	1788 55 1824 60 1824 60	96 29608267 58 29608231 58 29608231	1788 1805 1805 1805 1806 1794 1796 1796 1798 1798 1798	597 excn24_3MD_pipperMotif 609 excn24_3MD_hingeRegion 609 excn24_3MD_hingeRegion
- 9 dx single - 9 dx double - 30 dx double	no 36 no 49 no 15	86 46.784 0.87913 123939 79 2.601 0.03521 746478 76 0.013 0.00013 2023998	52662 False 25269 False 264 False	TATGAMMIGATICTOMATIGGAGATTTCOMGAGAA CAGAGAMATGAMATGAGAGTTTCOMGAGAAAATTT TTTOMAGAMATGA TATGAAGAMATGA	[excatd_AMD_ippenfelor("xcatd_AMD_inepenfegors) [excatd_AMD_ippenfelor("xcatd_AMD_inepenfegors("xcatd_AMD_inepenfegors("xcatd_AMD_inepenfegors("xcatd_AMD_inepenfegors("xcatd_AMD_inepenfegors(") [excatd_AMD_inepenfelors(")	2866827 28668274 28668277	1799 597 1792 594 1779 593	28608232 28608227 28608263	1826 60 1829 61 1793 56	58 29608221 10 29608226 98 29608262	1925 1920 1794	609 excn14_MD_hingeRegion 610 excn14_MD_tipperMotif 698 excn14_MD_tipperMotif
- 20 dx double - 20 dx double - 20 dx double	no 21 no 26 no 27	72 0.026 0.0006 2023998 67 8.717 0.0950 2023998 28 0.009 0.0009 2023998	175428 False 175 False	TTGATTICAGAGANIGAN CIPACITIGATICAGAGANIGA GTGACCGGCTCCTCAGANATGAGTAC	[wants_MD_watchMed", wants_MD_openMedi"] [wants_MD_watchMed", wants_MD_MD_openMedi"] [wants_MD_watchMedi"]	2806281 2806286 2806215	1775 592 1770 590 1741 581	28606261 28606263 28606289	1795 55 1793 55 1767 56	99 29608260 98 29608262 99 29608288	1796 1794 1768	S99 excel4_3MD_sipperMost S90 excel4_3MD_sipperMost S90 excel4_3MD_switchMost
- 90 dx double - 90 dx double	no 27 no 30 no 23	61 0.006 0.0006 2023998 45 15.960 0.18991 2023998	129 False 222022 False	GRAD RECTEMENT INTO TRANSPORT GRECTEMENT INTO ANALYSISA GETECTO ANALYSISATION ANALYSISATION GETECTO ANALYSISATION ANALYSISATION GETECTO ANALYSISATION ANALYSIS	[washed_Jule_machinery.wash_Jule_populators] [washed_Jule_machinery] [washed_Jule_machinery.wash_Jule_putebors] [washed_Jule_machinery.washed_Jule_putebors]	2800294 2800292 2800308	1764 588 1768 583	28608282 28608276	1792 55 1790 55	96 29608262 96 29608275		SSG exceld_SMD_pipperMost SSG exceld_SMD_pipperMost SSG exceld_SMD_pipperMost
- 90 dx double - 90 dx double	no 69	62 0.016 0.00015 2022898 42 0.155 0.00156 2022898	222 False 222 False 2145 False	ACTICIAGATICAGAGAARIGAARIGACTOAARIGAATICAGAAAAAATTIGAGT CCGGCTCCTOAATAATGAGTACTICIAGATGATTICOAARIGAARIGAARIGAARITICOAARIGAAATTICOAARIGAAATTICOAARIGAARIA	Intensity Alloy American Control (Alloy American Contr	2800290 2800290 2800211	1766 589 1765 589 1745 582	28608222 28608231	1824 61 1825 60	12 29608221 29 29608220	1825 1826 1822	612 exon14_TKD1_bets1Sheet 609 exon14_TMD_bingsRegion
- 20 dx double - 20 dx double - 11 dx double	no 96	29 0.086 0.0006 2022998 29 0.086 0.0006 2022998 22 24.702 0.3286 82612	1722 False 1739 False 20607 False	TRACCISCICCIO DARMINIA INCIDEI TICATI TO DARAMINI ANTIDE TO CANDIDATI	[microid_Abo_selectation*, microid_Abo_Speciments*, microid_Abo_selectation_Ab	28608214 28608214 28608230	1742 S81 1742 S81 1736 S76	20000235 20000219 20000206	1827 61 1770 56	12 28608218 10 28608218 80 28608285		- introd 4, pilos Donor 591 econt 4, MD , switch Molf
- 11 dx single - 11 dx single - 12 dx single	no 45	22 27,600 0.38122 1355054 72 0.017 0.00017 1355058 67 0.231 0.0022 1055550	221550 Falter 202 Falter 5047 Falter	CGACCGGAAAATGGTCGGTCGCTCAGATAATGAGTACTTC GGGAAATTCAGAGAATGAATGAATGAGTCCTCCAAGAG CTGCCTTGGTTGGGAAATGTCAGAGAGTCCTCCAAGAG	[world_MD pintphoff (world_MD putchfort]] [world_MD putchfort] [world_MD putchfort] [world_MD putchfort] [world_MD putchfort] [world_MD pintphoff [world_MD putchfort]] [world_MD putchfort] [world_MD putchfort] [world_MD putchfort] [world_MD putchfort]	28608230 28608281 28608285	1726 576 1775 592 1730 590	20000236 20000234 20000234	1770 55 1822 66	00 29808295 08 29808222 00 29808222	1771 1805 1771 1822 1794 1794 1794 1794	SS1 exon14_MD_switchholf SS0 exon14_MD_hingeRegion SS0 exon14_MD_ringeRegion
- 12 dx double - 12 dx single	no 45 no 24	46 41.874 0.72040 1825658 67 0.277 0.00278 244605 46 42.105 0.72726 244605	764492 False 679 False 103992 Ealse	CCTCCTCGATANTOAGTACTTCTACGTTGATTCAGAGAATANGA CTACGTTGATTCAGAGAATANGA CTCCTCGATATAAGTACTCTTGATGATTCAGAGAATANGA	[examis_JMC]_muschMedf_examis_JMC_appententf] [examis_JMC]_muschMedf_examis_JMC_appententf] [examis_JMC]_muschMedf_examis_JMC_appententf] [examis_JMC]_muschMedf_examis_JMC_appententf]	28608207 28608286 28608207	1749 582 1770 590	20000262 20000262 20000262	1792 56 1793 56	98 29608262 98 29608262 99 29608262	1794 1794 1794	SSB excel4_3MD_ripperMotif SSB excel4_3MD_ripperMotif SSB excel4_3MD_ripperMotif
- 13 dx double - 13 dx double - 13 d m11 double	no 29 no 60 no 21	45 1.910 0.01947 120222 77 20.315 0.25494 120222 72 0.016 0.00016 1797023	25211 False 250254 False 292 False	GCTCCTCAGATAATGAGTACTTCTACGTTGATTCAGAG TTCAGAGAATATGACTCCAATGGGAGTTTCCAGAGAAAATTAGAGTTTGGT TTGATTCAGAGAATATGAT TTGATTCAGAGAATATGAT	[recontd_JMD_contentMostF_contd_JMD_pipenhostF] [recontd_JMD_pipenhostF_contd_JMD_pipenhostF] [recontd_JMD_pipenhostF_contd_JMD_pipenho	28508208 28508276 28508281	1748 582 1780 594 1775 592	28608270 28608217 28608261	1786 56 1795 56	96 29508259 - 29508216 99 29508250	1797 1796	SSG exceld_MC_ripperMost introduct SSG exceld_MC_ripperMost
- 13 ri_m11 double - 13 dx single - 13 dx single	no 60 yes 197 no 39	77 0.202 0.0003 1797022 22 0.012 0.00012 156759 45 1.920 0.01864 201651	3625 False 21 True 3690 False	TTCKGAGAADITGATCTCAARIGGGAGTTTCCAAGAGAAARTTKGGT CONOGGTGACGGCTCCTCA GCTCCTCAGARAARAGADITCTCKGGTTGAFTCAGAG	[mont4_MD_appendedf_wont4_MD_impendedf_wont4_MD_impendededf_mont4_MD_impendedf_mont4	28608276 28608221 28608208	1790 594 1725 579 1748 582	28608217 28608125 28608270	1941 61 1786 56	- 29508216 14 29508124 96 29508269	1942 1797	intox14 614 excn15_TXD1_betx1Sheet 656 excn14_3MD_spperMotE
- 13 dx single - 14 dx double - 14 dx double	no 60 no 18 no 30	77 20.423 0.25664 201651 87 15.753 0.18699 2117395 46 25.828 0.36664 2117395	41194 Falce 223546 Falce 558054 Falce	TTCKGAGAADITGATCTCAAATGGGAGTTTCCAAGAGAAATTTKGGT TGAADITGATCTCAAF CACCTCAGADATGATGATCTTGA		28608276 28608265 28608207	1790 594 1790 597 1749 582	28608217 28608249 28608278	1907 60 1779 56	- 29508216 33 29508248 83 29508277		602 excel4_3MD_ripperMotif 502 excel4_3MD_ripperMotif
- 15 dx double - 15 dx single - 15 dx single	no 26 no 19 yes 21	77 21.827 0.6666 25997 70 0.054 0.0004 657648 81 0.022 0.0002 657648	8274 False 298 False 102 False	TICAGAGANINGANINGATICAC CGTIGATTICAGAGANIA GAGANINGANIGACICA GAGANINGANIGACICA	[round_A_De_invelocity round_A_De_inpended/] [round_A_De_inpended/] [round_A_De_inpended/] [round_A_De_inpended/] [round_A_De_invelocity round_A_De_inpended/] [round_A_De_inpended/]	28608276 28608282 28608272	1790 594 1773 591 1784 595	26606253 26606266 26606252	1903 60 1790 56 1904 60	01 28608252 97 28608265 02 28608251	1904 1791 1905	602 excel4_3MD_zipperMotif 597 excel4_3MD_zipperMotif 602 excel4_3MD_zipperMotif
- 25 dx single - 25 dx single - 25 dx single	no 26 yes 29 yes 45	77 20.845 0.44505 457648 27 0.007 0.00007 457648 22 0.018 0.00028 457648	144252 False 23 False 84 False	TITICAGAGAMATIGAGITAGATTIC GGTGACCOGGCTCCTCAGARIAATGAGITACTICTACGTTGA CGACCIGGAAAANIGGTCGGTCGGCTCCTCAGARIAATGAGITAGTTCT CGACCIGGAAAANIGGTCGGTCGGCTCCTCAGARIAATGAGITACTTC	[WALL-JAMO_Open-Model] [wash_JAMO_witholderi(_Open-JAMO_Open-Model] [wash_JAMO_Open-JA	28608276 28608216 28608230	1780 594 1780 580 1726 576	30000000000000000000000000000000000000	1903 66 1778 56 1770 56	01 28608252 83 28608277 80 28608285	1908 1779 1804 1791 1805 1806 1779 1771 1822	592 excrt4_3MD_ripperMotif 592 excrt4_3MD_ripperMotif 591 excrt4_3MD_switchMotif
- 25 dx single - 25 dx single - 25 dx single	yes 40 yes 57 no 62	72 0.028 0.00028 467648 78 0.010 0.00020 467648 27 0.022 0.00022 467648	154 False 48 False 103 False	GGGANTONGAGANIGANINGA/TECHNATIGGGGATTTECHNAG TONGGANTGANIGATCHAGAGGGGATTECGAGAGAMATTIGAGATTIG GGTGACCGGCTCCTC/GATANTGAGTACTTCT/CGTTGATTTONGAGATANTGANIGATCT	South, July,	28608211 28608275 28608216	1775 592 1781 594 1780 580	20000234 20000219 20000254	1827 61 1827 61	58 29608223 13 29608218 31 29608253	1923	608 excn14_MD_tingsRegion - intron14_spliceConor 601 excn14_MD_tipperMotif
- 15 dx single - 15 dx double - 15 dx double	yes 99 no 19 no 33	36 0.009 0.0009 467648 72 41.651 0.71393 2223663 52 0.015 0.00015 2223663	40 False 925144 False 343 False	ACGTGACCGGCTCCTCAGABATGAGTACTTCTACGGTTGATTTCAGAGATAGAGAGAGAG	[weerd.4_MC_matchMost*, weard_Most_properlays*, weard_MO_insperlays*, weard_MOSt_benistSwert] [weerd.4_MC_matchMost*, weard_MOSt_properlays*, properlays*, properlay	2800217 280020 280020	1739 590 1776 592 1756 596	26606219 26606262 26606268	1927 61 1793 56 1788 56	13 29608218 98 29608262 96 29608267	1794 1799	- intron14_spiceConor SSB exceL4_3MD_sipperMost SS7 exceL4_3MD_sipperMost
- 35 dx double - 35 dx double - 35 dx double	no 40 no 70 no 96	43 0.012 0.00012 2223603 23 1.187 0.0120 2223603 13 0.009 0.0009 2223603	260 False 26207 False 210 False	CGGCTCCTCMATARTIAG THETTICKGTTGATTGATAGAGAKRIGA TINCHGRIGGTGACGGCTCCTCAGATAGAGAGACGTGATTCAGAGAKRIGA TINCHGRIGGTGACGGCTCCTCAGATAGAGAGACTGCGAGAGATATGAGATATGAGATCTC TGAMGCCHGCTACHGRIGGTRCAGGTGACCGGCTCCTCHGATAATGAGTACTTCTACGTTGATTTCAGAGAATRIGARTRIGATCTCAARTGGGA	[wanta_JMC_purples[] [Amount_Moder_woods_JMC_purples[]] [[wanta_JMC_purples[] [Amount_Moder_woods_JMC_purple	2800210 2800230 2800240	1765 582 1726 576 1716 572	26606252 26606252 26606246	1793 55 1803 56 1811 66	98 29608262 31 29608262 36 29608264	1794 1799 1794 1804 1812 1788 1782 1784 1821	SSB exceld_SMD_sipperMost 602 exceld_SMD_sipperMost 604 exceld_SMD_singeRegion
- 17 dx double - 17 dx double - 17 dx double	no 26 no 42	52 0.080 0.0000 130867 44 0.021 0.00031 130867 29 0.028 0.00038 130867	366 False 410 False	GGCTCCTCAGATATGAGTACTTCAGTTGATTCC CACCCAATTCCTCAGATAATGAGTACTTCACGTTGATTCA	[exacts_Jun_jun_contenter_vicoso_Jun_zoppontentr] [exacts_Jun_jun_jun_jun_jun_jun_jun_jun_jun_jun_j	28508309 28508309 28508314	1767 SE2 1762 SE2	28608274 28608273	1782 56 1783 56	66 29608272 96 29608272	1782 1784	SSG exceld_SVD_ripperVote SSG exceld_SVD_ripperVote SSG exceld_SVD_ripperVote SSG
- 17 dx double - 17 dx double - 17 dx double	no 51	25 0.012 0.00012 1200567 82 16.565 0.19655 1200567	1/0 False 160 False 182316 False	GEAGNIGANCIA GRANISTA I I COMMISSIONALI I I COMMISSIONALI I I COMMISSIONALI I COMMISSIONALI I COMMISSIONALI I COMMISSIONALI I COMMISSIONALI CO	[record_and_peperson_conta_box_repressor_conta_box_repressor_conta_box_repressor_conta_conta_repressor_ [record_and_persor_conta_box_repressor_con	28508228 28508271 28508271	1789 576 1798 576 1785 595	28608278 28608218 28608218	1778 55	29608277 - 29608277		502 exceld_MD_pipperMoti - introd4_splceDonor
- 17 dx double - 17 dx double - 17 dx double	no 69	11 0.229 0.0029 1100567 70 0.011 0.00011 1100567 27 0.256 0.00057 1100567	2515 False 121 False 2610 Dales	CCGGAAAGCOACTACAGATAGTACAGTGACCGCCCCCAAAAAGAGTACTCACATTGATTC AATTGATTCAGAAAATGAAATG	Personal, July, Securitary and July, July (1994). A presentation of the personal process of the person	28508342 28508282 28508283	1714 572 1772 591	20000274 20000215 20000215	1792 56	M 29508272 - 29508214 N 29508210	1903 1793	SSS exceld_MD_ripperMotil - intentil 666 exceld_MD_ripperMotil
- 17 dx double - 18 dx double	no 90 no 18	25 12.080 0.13740 1100567 71 0.008 0.0008 1005759 94 79.789 3.71450 1072004	132944 Falton 80 Falton 844505 Calton	GGGGACGGTRAGGCGGCTCCTCAGRANTAGATACTTCTACGTTGATTCAGGAATATGAARTGATCCCAAATGGGAGTTTCC CAGATTCAGAGATAT TOATCTCAATGGGGGTTCCAGGGA	[exan14_JMD_switchMotif\exan14_JMD_sigperMotif]	28608228 28608282 28608282	1728 576 1774 592 1797 599	20000239 20000205 20000233	1917 66 1791 56	205 20508228 27 20508226 20 20508272	1918 1792 1924	606 excn14_3MD_hingsRegion 598 excn14_3MD_hingsRegion 609 excn14_3MD_hingsRegion
- 12 dx single - 12 cr <y2-12 double<="" td=""><td>no 27 no 36</td><td>94 77.659 3.47630 101431 49 0.475 0.00177 1464299 34 0.011 0.00013 1464299</td><td>78770 False 6861 False 164 False</td><td>TGATCTOANTGGAGTTTCOAGGA GGGCGARATGGAGTTTCTAGTTCAGAGA AGGGCGARATGAGTTCTTCAGTTGATTCAGAGA</td><td>[month_JMC_paperson_month_JMC_paperson] [month_JMC_paperson] [month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_paperson] [month_JMC_</td><td>2800259 2800204 2800204</td><td>1797 599 1752 584 1777 579</td><td>20000232 20000239 20000275</td><td>1823 66 1797 56</td><td>08 29508232 36 29508236 34 29508274</td><td>1924 1798 1792</td><td>600 excel4_MD_hingsRegion 566 excel4_MD_ringsRefion 564 excel4_MD_ringsRefion</td></y2-12>	no 27 no 36	94 77.659 3.47630 101431 49 0.475 0.00177 1464299 34 0.011 0.00013 1464299	78770 False 6861 False 164 False	TGATCTOANTGGAGTTTCOAGGA GGGCGARATGGAGTTTCTAGTTCAGAGA AGGGCGARATGAGTTCTTCAGTTGATTCAGAGA	[month_JMC_paperson_month_JMC_paperson] [month_JMC_paperson] [month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_matchled" (month_JMC_paperson] [month_JMC_paperson] [month_JMC_	2800259 2800204 2800204	1797 599 1752 584 1777 579	20000232 20000239 20000275	1823 66 1797 56	08 29508232 36 29508236 34 29508274	1924 1798 1792	600 excel4_MD_hingsRegion 566 excel4_MD_ringsRefion 564 excel4_MD_ringsRefion
- 29 cr-cy2-2 double - 29 cr-cy2-2 double	no 63 no 93	1	100 100	COGGACOGGCCCCAGARAGGAGACCTCCCAGARAGGAGACTCCAGGTGACTTCAGGAGATAGGATAG	Percit_AEC_proposite reset_AEC_proposite res	28008317 28008315 28008315	1739 500 1741 501	28608255 28608223 28608273	1901 60 1923 61	28608254 11 28608222 11 28608222	1818 1818 1818 1792 1805 1805 1805 1805 1805 1805 1805 1805	601 exceld_MD_ripperMotif 612 exceld_TKD1_bets1Sheet 612 exceld_TKD1_bets1Sheet
- 19 dx double - 19 dx double - 19 dx double	no 194 no 21 no 30	35 0.103 0.00103 981039 77 0.015 0.00015 113606 61 0.012 0.00012 113606	1007 True 173 False 125 False	COGGTGACCGGCTCCTCAGAF TTCAGAGAARTGAARTGA CTRCTCCAGGTTCAGAGAARTGA	[world_MO_watchbotf;world_MO_zepenbotf;world_MO_begoingon;world_TXO_bealSheet;world_upinConor;world_twronld_plonAcoptor;world_TXO_bealSheet] [world_MO_zepenbotf] [world_MO_zepenbotf]	2800218 2800276 2800282	1728 580 1780 594 1764 588	20060223 AMDRIGHT STATE	1941 61 1900 60 1793 56	14 29009124 30 29008255 80 29008262	1962 1901 1796	G14 excels_TKDs_beta1Sheet G01 excels_MC_ripperMost S90 excels_MC_ripperMost
- 19 dx double - 19 dx double - 19 dx double	no 25 no 45 no 51	49 4.520 0.04734 1135405 34 1.941 0.01875 1135405 25 0.007 0.00007 1135405	51261 False 20921 False 85 False	GGGCGARAIGAGTACTTCIRCGTGARTTCAGAGA AAGGGGGCCGCGCCCCAGARATGAGTACTTCATTGATT CCAGAGGGACAGGCCCCCCAGARATGAGTACTTCATCAGTGA CCAGAGGGACAGGACGCCCCCCAGAGAATGAGTACTTCACGTTGA	[exant4_NO_switchMost*; exant4_NO_sipenMost*] [exant4_NO_switchMost*; exant4_NO_sipenMost*] [exant4_NO_sidenMost*; exant4_NO_sipenMost*] [exant4_NO_sidenMost*; exant4_NO_sidenMost*]	28508304 28508219 28508228	1752 584 1737 579 1728 576	28608269 28608275 28608278	1797 56 1791 56 1779 56	96 29608268 96 29608276 92 29608277	1788 1782 1779	SSG exceld_SVD_piperMost SS4 exceld_SVD_piperMost SS2 exceld_SVD_piperMost
- 29 dx double - 29 dx double - 29 dx double	no 54 no 54 no 57	27 0.255 0.00256 1125605 81 0.017 0.00017 1125605 28 0.279 0.00280 1125605	2998 False 197 False 2258 False	GGTGACCGGCTCCTCAGAAAGGAGTKCTTCAGATTCAGAAAAATATGA CCTCKIATGAAXIATGATCCAAATGGGAGTTTCCAAGAGAAAATTKGAGTTTG GATGGTACAGCGGCTCCTCAGAAAATGAGATCTTCAAGTTGATTCAGAGA	"(Substitution), (Substitution), (Substitution	28608216 28608272 28608225	1780 590 1784 595 1731 577	29608262 29608219 29608269	1793 56 1827 61 1797 56	98 29508262 12 29508218 96 29508268	1794 - 1798	SSS exceld_MD_ripperMost - introx14_splceDonor SSG exceld_MD_ripperMost
- 29 dx double - 29 dx double - 29 dx double	no 57 no 60 no 63	78 0.016 0.00015 1126406 75 0.218 0.00218 1126406 26 2.728 0.02804 1126406	179 False 2473 False 21000 False	AGGGGANTGANTGATCTONATGGGAGTTTCONGAGANATTRAGGTTTG ATTCAGAGANTGANTGATCTONATGGGAGTTTCCNGAGANATTRAGGTTG CCGTGACCGCCCCCCGNATGAGAGTCTCTCAGTTCAGAGANATAGAGTTG CCGTGACCGCCCCCCGNATGAGAGATCTCTAGGTTGATTCAGAGANTGATTGATCC	[woxsld_JMO_jripenfold(_woxsld_JMO_hripenfoldor(_woxsld_JMO_bringnfo	28608275 28608278 28608217	1781 594 1778 592 1729 590	28608219 28608219 28608255	1927 61 1927 61 1901 60	13 28608218 13 28608218 01 28608254	1802 1820	- introx14_pplceDonor introx14_pplceDonor - excel4_MD_zipperMotif
- 29 dx double - 29 dx double - 29 dx double	no 72 no 87 no 93	45 0.050 0.0050 1125405 48 0.057 0.0057 1125405 28 2.507 0.0825 1125405	570 False 649 False 29656 False	ACTICETOARMATIAGRATECTICEAGATTGATTCAGAGARKIIGAATKICAGCTCAARTGGGAGTTTCCAA CCTCAGARANGAGTACTTCIAGATGATTGATGAGARKIIGAATKICAGCTCAARTGGGGATTTCCAAGAGAAAAATTIAGAGTTTG GTGACCGGCTCCTCAGARANGAGAGTCCTCACTTCACAGAGAKARAARTAINGACTCAARTGGAGTTTCCAGAGAAAAATTIAGAG GTGACCGGCTCCTCAGARANGAGACTCTCACCTTGATTCAGAGAAKARGAARTIGGATCCAARTGGAGTTTCCAGAGAAAAATTIAGAG	[Pamella, J.M., Janebart (mark J.M.), papelage (J.M.), Lincon] [Pamella, J.M., Lincoln (J.M.), Lincoln (J.M.), Lincoln (J.M.), papelage	28508208 28508205 28508215	1749 592 1751 594 1741 591	28608237 28608219 28608223	1819 60 1827 61 1823 61	77 29808236 13 29808218 11 29808222		607 excn14_3MD_hingeRegion - introx14_spliceDonor 612 excn14_TKD1_bets1Sheet
- 29 dx double - 29 rt_m4 double - 29 rt_m4 double	no 96 no 194 no 21	35 0.021 0.00001 125606 35 0.021 0.00021 772271 77 0.011 0.00011 96206	96 False 163 True 104 False	GGBLAGGTGACOSCTCCTOAANAYGAGBACTTCHCGTTGATTCOAAGAANAYGACCTCAAANGGGAGTTTCOAAGAAAANTT CCGGTGACCOGGCTCCTCAGAT TTCAGAGANAYGAGATGAT	[excold_MO_webchilderf_excold_MO_zipperhiosf_excold_MO_hingeRegion(excold_TXO0_beta1Sheer()mixedd_spliceConor(/mixedd_spliceAcceptor(excold_TXO0_beta1Sheer)] [excold_MO_zipperhiosf]	2800022 2800218 2800276	1734 578 1738 580 1780 594	28608227 28608225 28608256	1829 61 1941 61 1800 60	10 29008226 14 29008124 30 29008255	Made	610 exon14_TKD1_bets1Sheet 614 exon15_TKD1_bets1Sheet 601 exon14_MD_xipperMosf
- 29 fl.m4 double - 29 fl.m4 double - 29 fl.m4 double	no 51 no 54	25 0.086 0.0006 942046 27 0.021 0.00021 942046	100 100	COMBINISTANCIA CONTROL TECNICAL THAN TO CAMBAN COMBINISTANCIA CONTROL TO CONT	[Tabalwago, Jan. Lacana, Walkana, Mul. Lakana, Walkana) [Tabalwago, Mi. Lakana, "Mathana, Mul. Lakana, "Indulana, G.M., Lakana)] [Tabalwago, G.M., Lakana, "Mathana, G.M., Lakana) [Tabalwago, G.M., Lakana, "Mathana, G.M., Lakana," Mathana, G.M., Lakana)]	28508228 28508228 28508216	1728 576 1720 580	28606276 28606263	1797 56 1779 56 1792 56	60 29608277 80 29608262	1779 1794	SS2 excit, MD_ripperMost SS2 excit, MD_ripperMost SS6 excit, MD_ripperMost
- 29 ft.m4 double - 29 ft.m4 double - 29 ft.m4 double	no 62 no 92	26 0.179 0.00179 96206 26 17.484 0.21199 96206	1505 False 1507 False 154712 False	COSTAGA DE ADECEMBRAÇÃO DE CENTRA DE CENTRA DE CENTRA DE CENTRA DE COSTAGA DE	[exceld_4_MAD_swatchModf_1condl_4_MAD_rispenModf_1condl_4_MAD_rispenModf] [exceld_4_MAD_swatchModf_1condl_4_MAD_rispenModf_1co	28608215 28608215	1731 577 1739 580 1741 581	28608256 28608253	1901 60 1923 61	01 28008254 11 28008254 11 28008222	1768 1802 1834	601 exceld_MD_ripperMost 602 exceld_MD_ripperMost 602 exceld_MDI_beta1Sheet
- 20 dx double - 20 dx double	no 29	27 28.264 0.39595 1228941 20 0.198 0.00199 1228941	251279 False 2458 False	GGGGCGGCTCCTOAGAWTGAGTCTCTCACGTTGA CACCUCAATGGTCACGGCGCCCCCAGAWTGAGGCTCTC	[mank_AMO_methoder] [excusl_AMO_methoder] [excusl_AMO_methoder] [mank_AMO_methoder] [m	28508215 28508222	1740 580 1723 575	28508278 28508285	1778 56 1770 56	22 28508277 80 28508285	1779 1771	SS2 excit_MD_reperior SS1 excit_MD_retributer SS1 excit_MD_retributer
- 21 cr-tu-m3 double - 21 dx double	no 87 no 21	28 0.061 0.0061 1076742 68 0.101 0.00101 226556 26 0.009 0.0009 234556	655 Falter 2251 Falter 100 Falter	CCCACCGGGTCCTCAGATAATGAGTACTTCTACGTTGATTCAGAGAGATATGAATATGATCTCAAATGGGAGTTTCCAAGAGAAAAT CCCTTTGATTCAGAGAAATAT GAGGTGGTBCAGGTGATCCGCTCTCCGGATATGAGTTCTTCATCGTTGATTCC	[monile_JMD_matchMatlf'(monile_JMD_properMort(monile_JMD_propeRegion)] [monile_JMD_matchMatlf'(monile_JMD_properMort[)] [monile_JMD_inderMort(monile_JMD_properMort[)] [monile_JMD_inderMort(monile_JMD_properMort[)] [monile_JMD_inderMort(monile_JMD_properMort[)] [monile_JMD_inderMort(monile_JMD_properMort[)] [monile_JMD_inderMort(monile_JMD_properMort[)] [monile_JMD_inderMort[]] [monile_JMD_inde	28608215 28608285 28608277	1741 591 1771 591 1779 577	20000229 20000205 20000274	1827 66 1791 56 1792 56	295 29508228 87 29508264 54 29508272	1828 1792 1792	610 excel4_TXD1_beta1Sheet 580 excel4_MD_xipperMotf 566 excel4_MD_xipperMotf
- 22 dx double - 21 dx double - 21 rl m5 double	no 57 no 87	22 0.058 0.0058 2245256 28 28.069 0.51522 2245256 28 25.588 0.55492 674926	1527 False 655512 False 240959 False	AGGGAGGTGACCGGCTCCTCAGARWIGAGTACTCTCAGGTGATTCAGAGAART CCCACCGGGTCCTCAGARWIGAGTACTCACCTGGATTCAGAGAARTGAARGACTCAATGGGAGTTTCAAGAGAAAT CCCACCGGGTCCTCAGARWIGAGTACTCACCTGGATTCAGAGAAATGAARTGAATGACTCAAATGGGAGTTTCAAGAGAAAAT CCCACCGGGTCCTCAGARWIGAGGACTCTCACGTGGTTTCAAGAGAAARTGAARTGAATGATCAAATGGGAGTTTCAAGAGAAAAT	[wastel_NO_matchlern(_wastel_NooninputMatf] [wastel_NO_matchlern(_wastel_Noon_inputMatf_wastel_Noon_inputMat	28608221 28608215 28608215	1725 579 1741 581 1741 581	20000205 20000229 20000229	1791 55 1827 66 1827 66	27 2808264 39 2808229 39 2808229	1792 1828 1828	550 exceld_MD_xipperModf 650 exceld_TNDi_betaiSheet 650 exceld_TNDi_betaiSheet
- 21 dx single - 21 dx single - 21 dx single	no 21 no 57 no 87	68 0.029 0.0009 107012 22 0.112 0.0012 107012 28 24.724 0.52196 107012	21 False 121 False 27159 False	CCCACGGGTCCTCAGATAVGAGTACTAGATTCAGAGAATAT CCCACGGGGTCCTCAGATAVGAGTACGGTCCTCAGATATGAGATATTCAGAGAATAT CCCACGGGTCCTCAGATAVGAGTACTTCTAGGTTGATTCAGAGAATATTCAAGAATAT	[exant4_NO_nuichMost] (wom14_NO_poperMost] [exant4_NO_pouchMost] (wom24_NO_poperMost] [exant4_NO_pouchMost] (wom24_NO_poperMost] [exant4_NO_pouchMost] (wom14_NO_poperMost]	28508285 28508221 28508215	1771 591 1735 579 1741 591	28608265 28608265 28608229	1791 56 1791 56 1827 66	97 29608264 97 29608264 99 29608228	1792 1792 1828	SSB exceld_SMD_ripperMost SSB exceld_SMD_ripperMost 610 exceld_TMD1_beta1Sheet
- 22 dx double - 22 dx double - 22 dx double	no 39 no 79 no 9	92 46.136 0.85653 979941 54 0.008 0.0008 979941 79 0.010 0.0000 115571	452104 Falce 79 Falce 12 Falce	ATGATCTCMATGGGAGTTTCCMGAGAMATTTAGAGT ATGATCTCMATGGGAGTTTCCAAGAGAMATTTAGAGT ATGATCTCMATGGGAGTTTCCAAGAGAMATTTAGAGTTGAGAGAGATTTCCAAGAGAMATTTAGAGT GAGAGGGA	["excel_CMC_DMC_DMC_DMC_DMC_DMC_DMC_DMC_DMC_DMC	28508250 28508299 28508274	1795 599 1757 595 1782 594	28608222 28608222 28608266	1834 61 1834 61 1790 56	12 29608221 12 29608221 87 29608265	1925 1925 1791	612 exon14_TKD1_bets1Sheet 612 exon14_TKD1_bets1Sheet 987 exon14_DKD_sipperModf
- 23 dx double - 23 dx double - 24 dx double	no 54 no 57 no 66	42 41.155 0.59941 1411441 28 0.085 0.00085 1411441 61 29.744 0.55859 2125903	580999 False 1219 False 949995 False	GGGCTCCTCAGTANTIAGTACTICTICGTTCAGTTCAGAGARIIGARIGA CCCAGTACAGGGGCCCTCGGGTAATGAGTCCTCTCAGGTGGTTCAGGGA CCTGCGGGGCGGG	[excent.6_MAD_count.6_MAD_count.flow.com.6_MAD_coun	28608210 28608225 28608292	1745 582 1724 577 1764 588	28608257 28608269 28608227	1799 60 1797 56 1829 61	2868256 286258 10 2868258	1900 1798 1920	600 excel4_3MD_ripperMotif 596 excel4_3MD_ripperMotif 610 excel4_7KD1_beta1Sheet
- 25 σ_gg_c1 double - 25 σ_gg_c1 double - 25 σ_gg_c1 double	no 21 no 35 no 39	82 0.053 0.0053 2565761 41 0.061 0.0061 2565761 40 0.050 0.0060 2565761	1254 False 1551 False 1295 False	TOTAGGATOMATICATORA GTOGGCTOCTOGAGATOGATCTOA GACOGGCTOCTOGAGATATGAGTTCTACGTTGAT GACOGGCTOCTOGAGATATGAGTACTTCTACGTTGATT	[rount], MO_spendorf] [rount], MO_suntiled Front, Mo, Spendorf]	2800271 2800212 2800213	1785 595 1744 592 1743 591	20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 200000200 20000200 20000200 20000200 20000200 20000200 20000200 2000000	1905 60 1779 55 1781 56	22 29808250 83 29808276 84 29808274	1906 1780 1792	SS4 excel4_3MD_pipperMost SS4 excel4_3MD_pipperMost SS4 excel4_3MD_pipperMost
- 25 σ_cy2_c1 double - 25 σ_cy2_c1 double - 25 σ_cy2_c1 double	no 42 no 42 no 60	25 0.040 0.00048 2565761 44 0.012 0.00012 2565761 31 2.004 0.02045 2565761	1235 False 219 False 51428 False	GGTCCETTCCTHAGTGAAGGGCTCCTCAGATAATGACTACET AGCTCCTCAGATAATGACTACTTCTCAGATGAAGACTTCAAGAA GCCACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTACGTTGATTTCAGAGAATATGA	[munch_Alphone_Count_Alphone_C	280023 2800309 2800322	1728 576 1747 582 1734 578	26606267 26606268 26606262	1769 55 1788 55 1793 56	0 2900206 6 2900267 8 2900262	1770 1789 1794	SSO exon14_3MD_swechMost SS7 exon14_3MD_sipperMost SS0 exon14_3MD_sipperMost
- 25 dx double - 25 dx double	no 21 no 24	82 0.718 0.00723 705386 54 0.008 0.00008 672529	5065 False 53 False	GEDERAGI GACEGGETECTONANAMINASIAETTE TENGETTAAT TENGERANIAGA TAAGAGAGAGTACTICTACGTTGATT	promote and the control of the contr	28508227 28508271 28508299	1785 595 1787 586	28608251 28608276	1905 60 1700 56	96 29608250 96 29608275	1906 1906 1791	602 exceld_MD_ripperMotil 504 exceld_MD_ripperMotil
- 25 dx double - 25 dx double	no 29	40 0.367 0.00009 672529 40 0.367 0.00089 672529 25 15.830 0.18807 672529	505 Falton 2471 Falton 106450 Falton 81102 Falton 78 Falton 602209 Falton 4026 Falton 41 Falton	GACCOGCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOC		28508212 28508228 28508228	1743 581 1743 581 1728 575	28608275 28608275 28608287	1791 56 1781 56 1769 56	28508276 36 28508274 30 28508285	1782 1792	SS4 exceld_SMD_paperMost SS4 exceld_SMD_paperMost SS0 exceld_SMD_parketMost
- 25 dx double - 25 rt_m1 double	no 92 no 42	29 0.012 0.00012 672529 44 0.079 0.00079 1225595	78 False 1042 False	CCCGCCGCTCCTCAGATANTGAGTACTTCAGGTGATTCAGAGGAATTGAGAGAATTGAGAGAATTCAGAGGAATTCAGAGGAATTCAGAGGAATTGAGAGAAATTAGAGT AGCTCCTCAGATAGGAGATACTCAGAGGAATTCAGAGAAAATTAGAGAAATTAGAGAAAAATTAGAGAAAAATTAGAGAAAAATTAGAGAAAAATTAGAGAAAAAA	[world_MD_matchest_MD_pends(f) world_MD_pends(f)	28508214 28508209	1742 SR1 1747 SR2	20000222 20000200	1824 61 1788 56	12 29608221 86 29608267	1925 1789	612 exon14_TKD1_bets1Sheet 597 exon14_TMD_pipperMotif
- 25 dx single - 25 dx single	no 21 no 24	82 0.610 0.00614 428572 54 0.010 0.0000 428573 41 0.020 0.00020 428573	2515 False 41 False 220 False	TORGANDAMINATION ANATAGENETICACTICAT ANATAGENETICACTICAT GEOGETETETETETAGET	[reard, A.D. Josepherf von L.D. A.D. Josepherf von L.D. A.D. Josepherf von L.D. A.D. Josepherf [reard, A.D. Josepherf von L.D. Jose	28608271 28608299 28608112	1785 595 1757 586 1744 502	28608251 28608276 28608277	1905 66 1790 56	20000250 36 2000275 20 2000276	1906 1791 1790	602 excit4_MD_zipperMotif 564 excit4_MD_zipperMotif 564 excit4_MD_zipperMotif
- 25 dx single - 25 dx single	no 36 no 39	56 0.006 0.0006 428572 40 0.280 0.0028 428573 25 16.260 0.19573 429573	26 False 1200 False 70149 False	CGAGGGGGGTTCRCGTTGATTCAGGAGARATGAA GACCGGCTCCTCAGATAATGAGTACTTCAGGTGATT GGTCCTTCCTTAGGTAAGGGGTCCTCCAGGTGATTT		28608212 28608297 28608213 28608228 28608228 28608224	1759 587 1743 581 1779 576	28606277 28606262 28606275 28606287 28606262	1794 56 1791 56 1799 50	98 29608261 94 29608274 90 29608296	1795 1792 1770	599 excel4_MD_ripperMotif 594 excel4_MD_ripperMotif 590 excel4_MD_ripperMotif
- 25 dx single - 25 dx single	no 60 no 93	40 0.280 0.0028 428572 25 16.388 0.18671 428572 31 12.285 0.13802 428573 29 0.007 0.00007 428573	52200 False 21 False 755 False	GCCACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTCGGTTGATTCAGAGAGAG	[mont4, Julio dischipated" (worst4, Julio puinchhard") [mont4, Julio puinchhard"] [mont4, Julio puinchhard", Julio	2800822 28008214 2800826	1734 578 1742 581 1730 590	28608262 28608222 28608209	1792 56 1824 61 1797 56	98 29608262 12 29608221 96 29608268	1794 1825 1700	598 excit_3MD_rippeMotif 612 excit4_TKD1_bets1Sheet 656 excit4_TKD1_rippeMotif
- 26 dx double - 26 dx double - 27 dx double	no 23 no 36 no 72	52 0.010 0.00010 1991236 86 15.505 0.18250 1991236 40 0.011 0.00011 1649051	207 False 207192 False 185 False		[counts]_MD_countsMortF_counts_(_MDrepentator) [counts_MD_copentator]_counts_MD_copentator] [counts_MD_copentator]_counts_MD_copentator_counts_MD_counts_MD_copentator_counts_M	2800200 2800207 2800212	1756 586 1789 597 1743 581	28608249 28608232 28608242	1700 56 1824 66 1814 66	96 2969267 26 2969221 26 2969241	1709 1825 1815	597 exceld_MD_ripperMotif 609 exceld_MD_hingsRegion 605 exceld_MD_hingsRegion
- 27 dx double - 28 dx double - 28 dx double	no 96 no 197 no 36	29 68.290 0.93285 1548051 22 9.965 0.11045 942988 54 0.047 0.00047 945585	795840 Falce 92794 True 441 Falce	COMPAGGTGACCGGCTCCTCA GGGTCCCGTTGATTTCAGAGAATATGATCT	[record_AMC_watchMost /coord_AMC_properfoot	28508214 28508221 28508289	1742 581 1735 579 1767 589 1775 592	28608219 28608125 28608254	1926 60 1916 60 1927 61 1981 63 1992 66 1921 61 1922 61 1927 66	13 29608218 14 29608124 01 29608253	1905 1915 	- introst4_spliceDonor 614 exon15_TKD1_bets1Sheet 601 exon14_MD_sipperMotF
- 28 dx double - 28 dx double - 28 dx double	no 57 no 60 no 75	72 0.007 0.0007 94585 70 0.028 0.0008 94585 50 0.029 0.0009 94585	68 Falce 255 Falce 277 Falce	TIGATTICAGAGAARRIGARKIGAICTCAARRIGGGGTTTICCAAGAGAAARTTRG CGITGATTICAGAGAARRIGARRIGARRIGECCAARGIGGGTTICCAAGAGAAARTTRGA CCAGARRIGAGACHCTCCACGTGRATTICAGAGARRICAARTIGAARGAARTICAARGAARTICAARGAARTICAARGAARTICAARGAARTICAARGAARTI	[words_AMO_peabMedf_words_AMO_peabMedf_words_AMO_peabfor(words_AMO_peabfor(words_TMO_pead_Deer] [words_AMO_peabMedf_words_AMO_peabMedf_words_AMO_peabfor(words_AMO_peabfor(words_TMO_peabfor(words_AMO_peabfor(wor	28608281 28608282 28608302	1775 592 1772 591 1753 585	28608225 28608224 28608229	1821 61 1822 61 1827 60	11 29608224 11 29608223 39 29608228	1932 1923 1929	- INDIGE SPECIAL SPECI
- 20 dx	no 94 no 197 no 19	51 0.259 0.0050 946585 22 0.056 0.0055 1953684 73 0.014 0.00014 154729	2452 False 1095 True 21 False	TRANSAIGAG PACTERACETIGATTO AGAMANG ANA TRANSAIGAG TITCAAGAGAAAATTAGAGTTIG COOKAGTIGACGGCCCCCCCA TRANSAIGAG PACTERACETIGATTO AGAMANG AGAMATTAGAGTTIG COOKAGTIGACGGCCCCCCCA	[word_AMD_matching*,word_AMD_paperholf*,word_AMD_paperholf*,word_aMD_paperholf*,word_amd_paperholf*,word_a	28608202 28608221 28608280	1754 585 1725 579 1775 592	28608219 28608125 28608262	1937 61 1941 61 1792 56	12 29608218 14 29608124 98 29608262	1942 1794	- inton14 spiceDonor 614 excn15_TXD1_beta1Sheet 658 exce14_3M0_sipperMotf
- 28 dx single - 28 dx single - 28 dx single	no 197 no 23 no 36	22 20.582 0.25823 154196 41 0.010 0.0000 154729 64 0.062 0.0002 154729	31752 True 35 Falter 95 Falter	CORAGGIFACOGGITACTOR ACCIGITATION AGRAPATION TO THE TOTAL CONTROL OF THE T	[mon4_MD_makthhatf_won14_MD_spenhatf_won14_MD_breedingst_won14_MOS_breakfact] [mon14_MO_makthhatf_won14_mon1	28608221 28608212 28608289	1725 579 1744 582 1767 589	28608125 28608280 28608254	1941 61 1776 56 1902 60	14 29509124 92 29509279 51 29609252	1962 1777 1903	- intend L, uples Coron C Gold Record Type, Described Gold Record L, MC, Dysperking Gold Record L, MCD, Described Gold R
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28 dx single 10^0 MOLM-14 - double 10^1 MOLM-14 - double	no 21 no 21	72 64.979 1.85540 1608216 72 8.628 0.09454 2534728	200 False 2005001 FALSE 218942 False	TOWNSHIP HE HELD I HERE I HERE I HERE HERE AND AND ANTICOME SA ANTICAMENT TO ANTICAMENT AND ANTI	[worse_mos_reconser_worse_mos_mos_mos_mos_mos_mos_mos_mos_mos_mos	280022 2800281 2800281	175 592 1775 592 1775 592	28508251 28508251 28508251	1765 56 1765 56	29608218 39 29608260 39 29608260	1796 1796	intro 1.5 julice Donor 509 excel.4_3MD_ripperMost 509 excel.4_3MD_ripperMost
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10"-4 MOLM-14 - double 10"-4 MOLM-14 - double 10"-6 MOLM-14 - double	no 21 no 21 no 21	72 0.015 0.00015 151789 72 0.001 0.00001 164666 72 0.001 0.00001 14730***	229 FALSE 22 FALSE 11 D-77	COMMITTACION CONTROLLA CON	[woods MO. paschider].	28608281 28608281 28608281	1775 592 1775 592 1775 592	20000251 20000251 20000261	1827 d 1 1841 d 6 1904 d 6 1904 d 6 1904 d 6 1905 d 6 1906 d 6 190	29508250 39 29508250 39 29508250	1842 1794 1842 1842 1842 1843 1843 1843 1843 1845 1796 1796 1796 1796 1796 1796 1796 1796	500 markl_AVD_repentual
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10~3 PL-21 - double	no 125	24 0.015 0.00015 1361676	204 True	TCAMICGGTACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTACGTTGATTTCAGAGAATATGATGATCTCCAATGGGGAGTTTCCAAGAGAAAAT	[months_MO_binderplotef; months_MO_switchhoof; months_MO_zappenhoof; months_MO_bingeRegion; months_MOS_bentSweet; mirrorld_spiceConor; mirrorld]	28000229	1727 576	28608205		29608204		- inton14

Table S3: getITD results: Shown are the detailed results obtained by getITD for each FLT3-ITD that was detected by our assay in the samples listed in Table S1. Genomic coordinates are based on hg19, transcriptomic and proteomic coordinates refer to NCBI NM_004119.

Patient ID	Age at dx (years)	Sex	Type of AML	Time from dx to rl (days)	CR after induction	BM blasts at dx (%)	PB blasts at dx (%)	BM blasts at rl (%)	PB blasts at rl (%)	NPM1-mutated at dx	NPM1 transcripts at dx (in BM)	NPM1 transcripts at rl (in BM)	Induction cycles (Dauna-ARAC 7+3)	Consolidation cycles (High dose ARAC)	Transplanted in 1st CR	WBC at dx (G/I)	WBC at rl (G/I)
13	65.15	male	de novo	561.00	CRi	95	98	5	0	yes	104882	22022	1	4	no	166.6	5.2
19	25.03	male	de novo	182.00	CR	69	11	32	na	no	na	na	2	0	yes	10.7	na
21	52.14	male	de novo	325.00	CRi	90	59	43	4	no	na	na	2	0	yes	na	2.3
25	53.49	male	de novo	245.00	CR	80	37	90	25	yes	537470	3682990	1	4	no	na	6.6
28	51.52	male	de novo	289.00	CRi	80	29	na	8	no	na	na	1	3	no	52.8	3.5

 $\textbf{Table S4:} \ \textbf{Clinical data:} \ \textbf{Provided are clinical details of five } \textit{FLT3-ITD positive AML patients that relapsed during follow-up (Figure 2A).}$