

Supplementary information

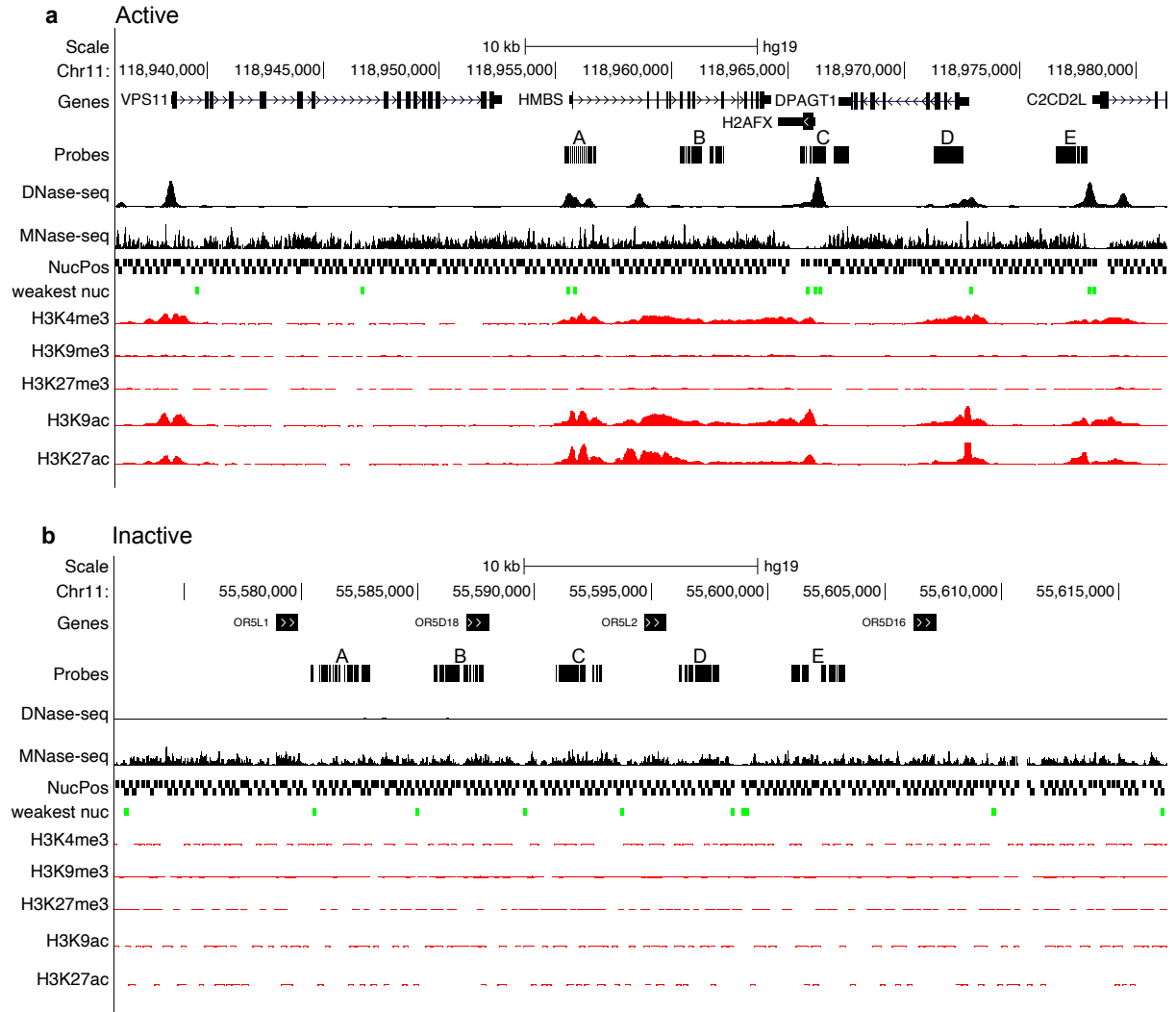
Differences in nanoscale organization of DNase I hypersensitive and insensitive chromatin in single human cells

Brandstetter et al.

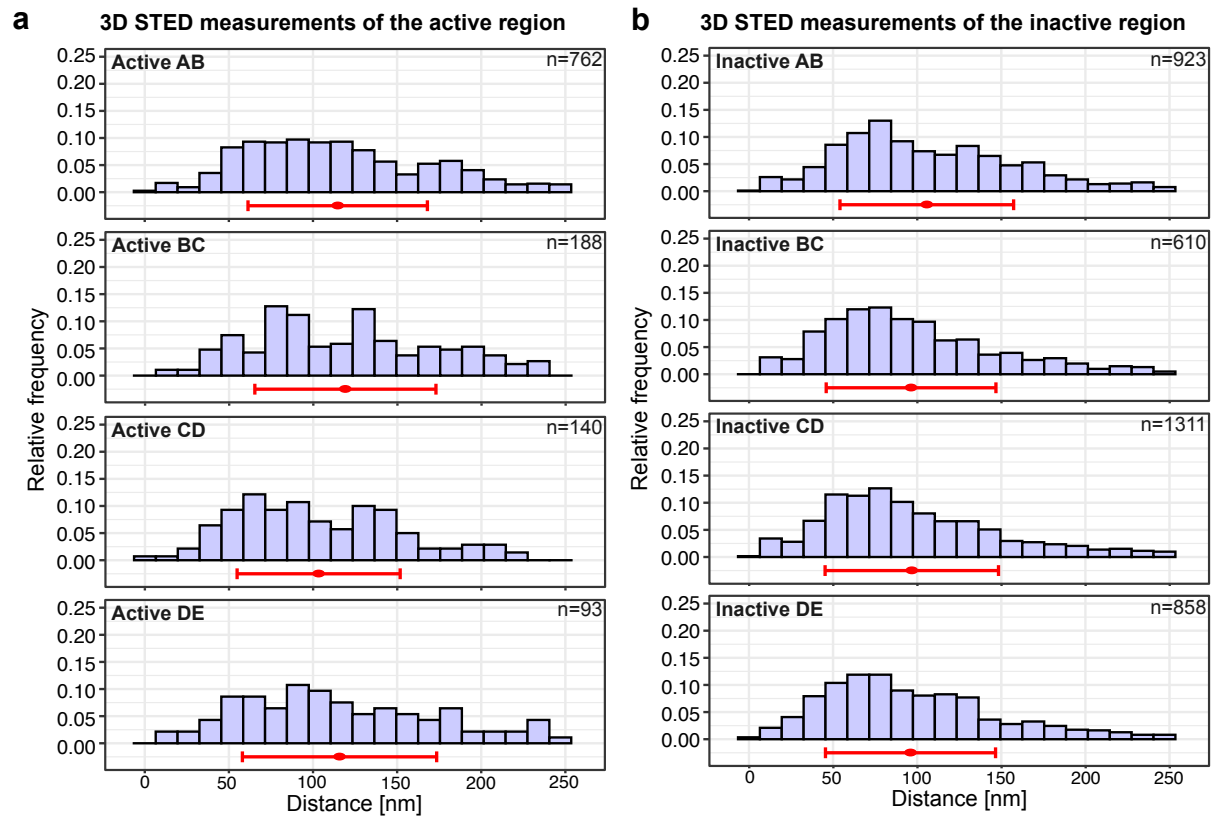
Supplementary Figures 1 – 5

Supplementary Table 1 – 4

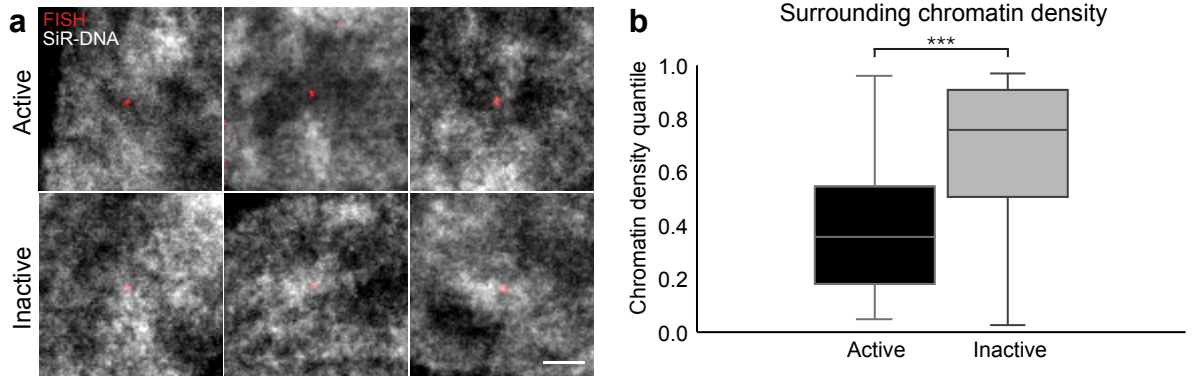
Supplementary figures with explanation



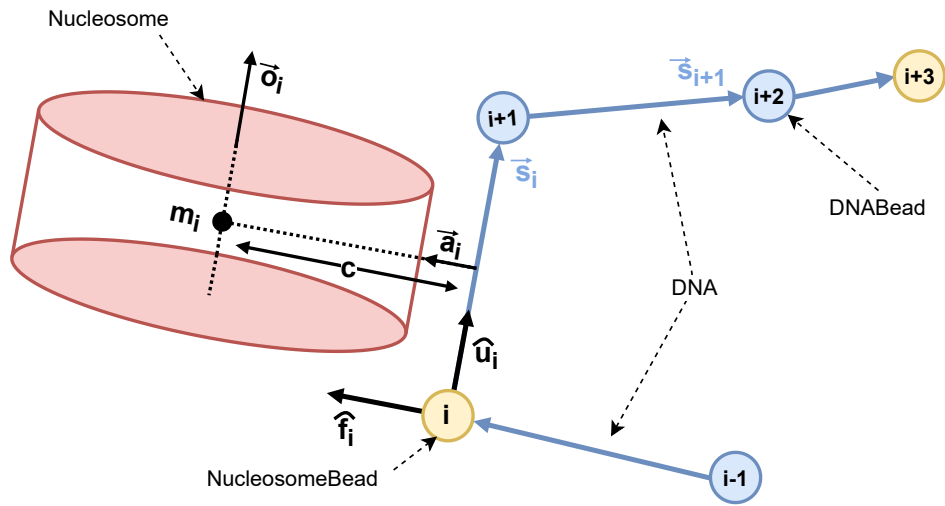
Supplementary Figure 1: Active (a) and inactive (b) genomic regions with genes, probe sets (A-E), DNase-seq, MNase-seq, nucleosome positions from NucPosSimulator, the weakest nucleosomes calculated by NucPosSimulator, H3K4me3, H3K9me3, H3K27me3, H3K9ac, H3K27ac. Tracks show that inactive region has almost no histone modifications while the active region contains active marks like H3K4me3, H3K9ac and H3K27ac. Notably, most of the weakest nucleosomes for the active region are located at DNase I hypersensitive sites.



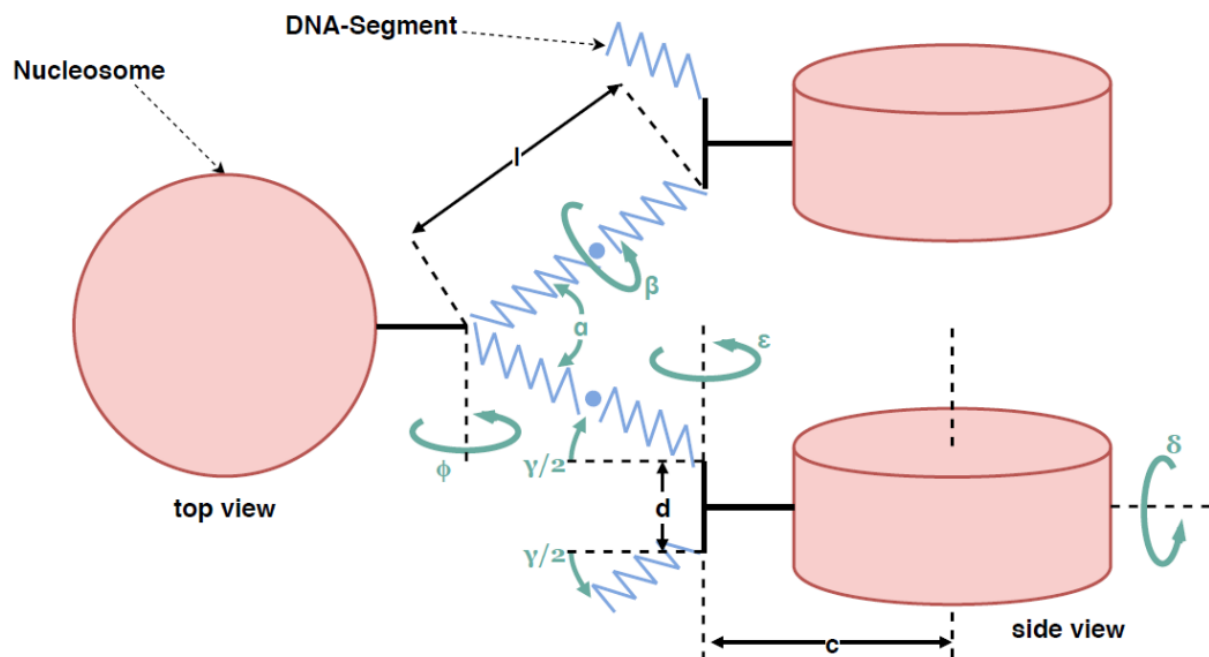
Supplementary Figure 2: Distance histograms from 3D STED measurements for all four intervals (AB, BC, CD, DE) in active (a) and inactive (b). The mean for each histogram is indicated by the red dot and the standard deviation by the red line. N-numbers can be found next to the respective histogram (for statistical data, see Supplementary Table 2).



Supplementary Figure 3: Chromatin environment of the active and inactive region. (a) Representative images for the active (upper row) and inactive (lower row) region labeled with one FISH probe set (red) and chromatin labeled with SiR-DNA (gray). Scale bar = 1 μm . (b) Chromatin density quantile for active (black, $n=43$) and inactive (gray, $n=38$) differ significantly (two-sided Wilcoxon rank sum test, $p = 9.890 \times 10^{-6}$). Inactive region is embedded in higher density chromatin, while active chromatin is surrounded by lower density chromatin.



Supplementary Figure 4: Model of a nucleosome chain. i represents the position of the bead in the chain, yellow circles indicate nucleosome bead positions, and blue circles indicate DNA bead positions. The nucleosome is represented by a red cylinder. The segment vector \vec{s}_i points from one bead to the next bead. A local coordination system $(\hat{u}_i, \hat{v}_i, \hat{f}_i)$ (not shown) describes the orientation of a bead. Vector \vec{a}_i describes the direction from the center of the segment to the nucleosome center m_i , c is its length, and vector \vec{o}_i describes the orientation of the nucleosome. Vector \vec{a}_i is defined by two rotations of vector \hat{v}_i (i) around \vec{u}_i by the angle ε (not shown), (ii) around vector \hat{f}_i by the angle ϕ (not shown).



Supplementary Figure 5: The relative orientation of the nucleosome is described by the angles $\alpha, \delta, \epsilon, \gamma, \phi$ (modified from (Rippe et al., 2012)). β is the torsional orientation of subsequent nucleosomes. l is the length of the DNA modeling the linker DNA, d the distance between the entry and the exit point of the linker DNA at the nucleosome, c the distance between the center of the nucleosome segment and the center of the oblate sphero-cylinder modeling of the nucleosome.

Supplementary tables with explanation

Supplementary Table 1: Statistical data for 2D STED datasets

Test: Wilcoxon rank sum test with continuity correction

Correction method: Bonferroni holm correction for multiple testing

Software: R studio

p-values for Active AB – BC – CD – DE

	Active AB	Active BC	Active CD
Active BC	0.03220	-	-
Active CD	0.02706	0.80123	-
Active DE	0.18970	0.00053	0.00053

p-values for Inactive AB – BC – CD – DE

	Inactive AB	Inactive BC	Inactive CD
Inactive BC	$3.3 * 10^{-7}$	-	-
Inactive CD	$5.8 * 10^{-9}$	0.451	-
Inactive DE	$1.2 * 10^{-12}$	0.071	0.451

p-value for all active vs. all inactive

	Active
Inactive	$<2 * 10^{-16}$

Supplementary Table 2: Statistical data for 3D STED datasets

Test: Wilcoxon rank sum test with continuity correction

Correction method: Bonferroni holm correction for multiple testing

Software: R studio

Significant: $p < 0.05$

p-values for Active AB – BC – CD – DE

	Active AB	Active BC	Active CD
Active BC	0.895	-	-
Active CD	0.138	0.076	-
Active DE	1.000	1.000	0.525

p-values for Inactive AB – BC – CD – DE

	Inactive AB	Inactive BC	Inactive CD
Inactive BC	$8 * 10^{-4}$	-	-
Inactive CD	$8.3 * 10^{-5}$	1.000	-
Inactive DE	$9.4 * 10^{-5}$	1.000	1.000

p-value for all active vs. all inactive

	Active
Inactive	$<2 * 10^{-16}$

Supplementary Table 3: Simulation Parameters and Constants

e_c	$1.602 \times 10^{-19} \text{ C}$	Electric charge unit
v	$-2/0.34 e_c \text{ nm}^{-1}$	Line charge density of DNA
ρ	$0.1 \times 10^{24} \text{ mol nm}^{-3}$	Molarity of the monovalent solution
N_A	$6.022 \times 10^{23} \text{ mol}^{-1}$	Avogadro constant
ε	80	Value for the dielectric value in the solution
ε_0	$(4\pi f)^{-1}$	Dielectric constant
f	$138.935 \text{ kJ nm mol}^{-1} e_c^{-2}$	Electric conversion factor
k_B	$8.314513 \times 10^{-3} \text{ kJ mol}^{-1} \text{ K}^{-1}$	Boltzmann constant
a	1.2 nm	Radius of the DNA model sphere
T	293 K	Temperature of the solution
	4×10^7	simulation steps for internucleosomal interaction strength $4 k_B T$
	8×10^7	simulation steps for internucleosomal interaction strength $8 k_B T$
	10 nm	maximum DNA segment length
	5.5 nm	nucleosome height
	11 nm	nucleosome diameter
	293 K	minimum temperature used for replica exchange procedure
	700 K	maximum temperature used for replica exchange procedure
	16	number of temperatures used for replica exchange procedure for internucleosomal interaction strength $4 k_B T$
	32	number of temperatures used for replica exchange procedure for internucleosomal interaction strength $8 k_B T$
	$4 k_B T$ and $8 k_B T$ (inactive)	ε for $E_{internuc}$
	5.5 nm	σ for $E_{internuc}$
	665	$a_{DNA}^{(s)}$
	665	$a_{NUC}^{(s)}$
	120.44	$a_{DNA}^{(b)}$
	120.44	$a_{NUC}^{(b)}$
	219.25	$a_{DNA}^{(t)}$
	782.85	$a_{NUC}^{(t)}$
	1.2 kJ mol^{-1}	Lennard jones ε for DNA
	2.0 kJ mol^{-1}	Lennard jones σ for DNA
	$S000 = 1.6957$	interaction potential nucleosome s-functions
	$Scc2 = -0.7641$	
	$S220 = -0.1480$	
	$S222 = -0.2582$	
	$S224 = 0.5112$	
	$E000 = 2.7206$	
	$Ecc2 = 6.0995$	
	$E220 = 3.3826$	
	$E222 = 7.1036$	
	$E224 = 3.2870$	

Supplementary Table 4: Oligo probe genomic coordinates and sequences

Chromosome	Start (hg38)	End (hg38)	Oligo name	Sequence	Dye
chr11	119084693	119084733	ActiveA_947	AAACTTAGCTTTGCTACAACCTTGAAATAGGCAGCATTTT	ATTO647N
chr11	119084735	119084775	ActiveA_948	AGCAAGTAGTGCAGCTTCTATGGCGCTTCCTTTGCTCTGT	ATTO647N
chr11	119084777	119084817	ActiveA_949	GGACCTCCCCATTCGACCACCCCATTCCCCAGCTGTGACA	ATTO647N
chr11	119084819	119084859	ActiveA_950	GAGGTCCCTCCCTCTGGGCGGGAATTGGAACATTGCGACA	ATTO647N
chr11	119084861	119084901	ActiveA_951	CCGCAGAGCCTCGCGTCACTTCCGGCGCCCTCCCTCGAAG	ATTO647N
chr11	119084903	119084943	ActiveA_952	CACGTGGGACCCGAGGTCGTCCTACAGTCTGACTCCTGGT	ATTO647N
chr11	119084945	119084985	ActiveA_953	GGCCCCGGGAAGCCGGGGGCTCCGGCCGGCGAGTACCGGG	ATTO647N
chr11	119084987	119085027	ActiveA_954	GCTTGAAAGTAGGCTGTGTGTGGGTGCCGCTAAGTCCC	ATTO647N
chr11	119085029	119085069	ActiveA_955	CACCGCCGTTGCAGCCGCATTGCCGTTACCAGACATGGCT	ATTO647N
chr11	119085071	119085111	ActiveA_956	TCGTCCAGAAGCCCAAAGTGTGCTGGTCACCGGCTCAGCA	ATTO647N
chr11	119085113	119085153	ActiveA_957	AGACGACTGAGGATGGCAACCTGGGGCCAATCGCTGCACG	ATTO647N
chr11	119085197	119085237	ActiveA_959	AACCGAGCTACTGGCCCTTTAAAAGCTACTCGGACCAAAA	ATTO647N
chr11	119085239	119085279	ActiveA_960	CAGTATCACCGCTCTCTGATTTCCCCATTCTTCCGGAGG	ATTO647N
chr11	119085281	119085321	ActiveA_961	GGGACCGGAGTTCGGTTCCAACAATCCTTCCACTCTTAA	ATTO647N
chr11	119085323	119085363	ActiveA_962	GTGCATCCCAGGCCTGATGGGAATCCCACCCAGATGCCCG	ATTO647N
chr11	119085365	119085405	ActiveA_963	TGTAGACGAACGTTCTTGGTCTGGGTCACTAAATCTAGAG	ATTO647N
chr11	119085407	119085447	ActiveA_964	GCATCCGCCTCAGCCCAGCCTCGAATGAAAGGACCCCGTC	ATTO647N
chr11	119085449	119085489	ActiveA_965	TGAATCAAAGTGGAAACGTGTCTTCCCAAAGGGGCGTAT	ATTO647N
chr11	119085491	119085531	ActiveA_966	CGTTTGTGTGCAGTTCGGAGGCTTGGCTGATACTCTCTCC	ATTO647N
chr11	119085533	119085573	ActiveA_967	TGGGAGACCACTATAACACAAAAAGAAGGCGCACTTCTAA	ATTO647N
chr11	119085575	119085615	ActiveA_968	GTAGGTGTGTCACAGCTGGGGACTTGGAGCGTTGGCTGTG	ATTO647N
chr11	119085617	119085657	ActiveA_969	TGGAAAGGCCACGGCGGCCTCCCACCCACGGTAGTAATT	ATTO647N
chr11	119085659	119085699	ActiveA_970	TTGTCTGTGCACAAGCCCAGGGCTCGGCAAGCAGGCTCGT	ATTO647N
chr11	119085701	119085741	ActiveA_971	TTCTTATCTCGGCCTGGCAGTGGCCTCCACCAGCTCTGCA	ATTO647N
chr11	119085743	119085783	ActiveA_972	CCAACAGGCTGGACAGGGGGAGATTAGCAGCTCCCCATCT	ATTO647N

chr11	119085785	119085825	ActiveA_973	AGGGCTCTGGAATGACTGCAAGAGCAAAGATCCCAGCCCT	ATTO647N
chr11	119085827	119085867	ActiveA_974	AGAGAGTTGGGGCCACAATTCAGATCTTCCTACTCCTAGT	ATTO647N
chr11	119085911	119085951	ActiveA_976	CACCTTTGGGACCATGTTACAGAAGCAACGGGTGGCATCA	ATTO647N
chr11	119085953	119085993	ActiveA_977	ATTGTTGTCGTCTCAAAAATCCTATCAGGTGGACAAGACA	ATTO647N
chr11	119085995	119086035	ActiveA_978	AAAACACTGAGCACTTCTATGTTGAAGCTATTGCTTTTGC	ATTO647N
chr11	119089649	119089689	ActiveB_1065	GTCCACTCTATAGAGATGGGAGAGGGGGGCAAAGAGAAAG	ATTO594
chr11	119089691	119089731	ActiveB_1066	AGGAAGCACAGTGGGCAGGTCCTTCAAGGAGTGAACAACC	ATTO594
chr11	119089733	119089773	ActiveB_1067	GCAAGACTCTTACTTGCAGATGGCTCCGATGGTGAAGCCA	ATTO594
chr11	119089775	119089815	ActiveB_1068	AAAGGTTACATGATGCCTACCCCTGCCAAGCCCTTAC	ATTO594
chr11	119089817	119089857	ActiveB_1069	AGATAACCCTGAAGCAGAGGGTCAGGCCCCAAAGGGAAAG	ATTO594
chr11	119089901	119089941	ActiveB_1071	GATCACCTCTATTCTCTCTCGATTGCCAACTCACTGGTAT	ATTO594
chr11	119089985	119090025	ActiveB_1073	GGGTGAAAGACAACAGCATCATGAGGGTTTTCCCGCCTGG	ATTO594
chr11	119090027	119090067	ActiveB_1074	CTCTTCTCTGGCAGGGTTTCTAGGGTCTTCCCAACAAATT	ATTO594
chr11	119090069	119090109	ActiveB_1075	CTGGGCACATCCCACCAAGCTGCCTATCCAGGCCCCACTT	ATTO594
chr11	119090153	119090193	ActiveB_1077	CACACTGCCCAGAGAGAAGTTACAATGAGATTTTAACACT	ATTO594
chr11	119090195	119090235	ActiveB_1078	TCTCTGCAGCTGGGCTGCTCTTCGCAGGGAGCTGGTTCCC	ATTO594
chr11	119090237	119090277	ActiveB_1079	CTAAAAGGATACAATACTCCTGAACTCCAGATGCGGGAAC	ATTO594
chr11	119090279	119090319	ActiveB_1080	GCTGCTGTCTCCGTCACTCTTCCAAAAGGATCCGTCACTC	ATTO594
chr11	119090321	119090361	ActiveB_1081	CTCCGGACTCCCAGAGCCCTCTAGACCTTGTCTTTTTCT	ATTO594
chr11	119090363	119090403	ActiveB_1082	GCCACTGACCCACGGGCTGCTTGCTGGAAGCCCCTTCCA	ATTO594
chr11	119090405	119090445	ActiveB_1083	CTGTAAATGAGTGGACGGATGAGTGCATGGAAAGACAGAC	ATTO594
chr11	119090447	119090487	ActiveB_1084	CTTGCACTCTGAACACTTGTCTGGGGCTAAGAAAACATTA	ATTO594
chr11	119090489	119090529	ActiveB_1085	ATGCAGGGAATGTTTATCTTGCTCACCATTATCCCAAT	ATTO594
chr11	119090531	119090571	ActiveB_1086	AGTATAACTGCATTATCCCTAAGTAAGACGTAAACTCTAC	ATTO594
chr11	119090573	119090613	ActiveB_1087	GAAGTACTCCCTATCCCTCCAGAAGTAGTCACTATTAGT	ATTO594
chr11	119090909	119090949	ActiveB_1095	CAAGACAATATAGTAGCATATAAAAATGGAAGTACTGACC	ATTO594
chr11	119090951	119090991	ActiveB_1096	AATTTAGTTTTATGAAATGTACTACATATTCATTGTAATA	ATTO594

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chr11	119091203	119091243	ActiveB_1102	CTGCTCTAAAAGTACTTTCCATATGTCAGCTCATTTCATC	ATTO594
chr11	119091287	119091327	ActiveB_1104	AGCTGGCTGACTTTTCAGTCATCTTCCAGCTCTCAGCTTAA	ATTO594
chr11	119091329	119091369	ActiveB_1105	CCTCGTGCGGTTCCCTCTGCCTGAGTCTGTCTTTCCCTCT	ATTO594
chr11	119091371	119091411	ActiveB_1106	TGTGGAGAGTTGCTAAGGACCACAGTGTCTGGGCAATCTGG	ATTO594
chr11	119091413	119091453	ActiveB_1107	TGCTCGTCCAGCTTCCGAAGCCGGGTGTTGAGTTTCCCC	ATTO594
chr11	119091455	119091495	ActiveB_1108	TGCAGGCCAGCTGTTGCCAGGATGATGGCACTGAACTCCT	ATTO594
chr11	119091497	119091537	ActiveB_1109	GCAGGCCCTACCTGCCCCACCCGGTTGTGCCAGCCCATGC	ATTO594

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chr11	119094899	119094939	ActiveC_1190	GCCAGGCCTCCCCATGCCACCACAAAGGCCCTTTTAAGGG	ATTO647N
chr11	119094941	119094981	ActiveC_1191	GGCCTCCAGGAGTACTAAGAGGGCCCGCGCCGCGGCCGG	ATTO647N
chr11	119094983	119095023	ActiveC_1192	CGTGGGGCCGAAGGCGCCCTCGGGCGGCAAGAAGGCCACC	ATTO647N
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chr11	119095361	119095401	ActiveC_1201	CGTAGCATGTGCGGGCCGCGGCAAGACTGGCGGCAAGGCC	ATTO647N
chr11	119095403	119095443	ActiveC_1202	TCTGTTCTAGTGTGTTGAGCCGTCGTGCTTCACCGGTCTAC	ATTO647N
chr11	119095445	119095485	ActiveC_1203	CCTCGCGGCGCGCGCGGACAGCAGTTACACTGCGGCGGG	ATTO647N
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chr11	119095529	119095569	ActiveC_1205	ACCGCAACCAACCGGAGGCGGGTATTGGAGAAAAGAGCCA	ATTO647N
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chr11	119095613	119095653	ActiveC_1207	CCTTTTCTCCCCGGGCAAAAGGTTTTCAAATTCGACCAAT	ATTO647N
chr11	119095655	119095695	ActiveC_1208	TCAGCGGATAGTTGGCAGTCTGCGTGCTACCCCTCCTCCT	ATTO647N
chr11	119095697	119095737	ActiveC_1209	TGTAGTGTAAATCTCGCGCGCTTACAAGGATTGGCTA	ATTO647N
chr11	119095739	119095779	ActiveC_1210	CTCAGACTCCACCCCTTTGGTCTTCCGCTTCTGGTTTCCG	ATTO647N
chr11	119095781	119095821	ActiveC_1211	ATCCTACGCCGGCACAGATTTCCAGACGCTCTCTAGGTG	ATTO647N
chr11	119095823	119095863	ActiveC_1212	GAGGGCTGCAGTAGCTATAATATTGACCCCTTTCCTTTAA	ATTO647N

chr11	119095865	119095905	ActiveC_1213	TCAGGTAGGAGAAGGGAGTAGGGAGTGACTGGACCTGGAA	ATTO647N
chr11	119096285	119096325	ActiveC_1223	GCATGGAGGGCCACAAAATTGAAGTTATCCTGTTTCCTGG	ATTO647N
chr11	119096369	119096409	ActiveC_1225	CAGACCCCGTCTAACAAGAAGTGAACAGAACTGAGACCAA	ATTO647N
chr11	119096411	119096451	ActiveC_1226	GGGGGTA CTCTCCAACAGGATGCCTATCTCTCTGCCCC	ATTO647N
chr11	119096453	119096493	ActiveC_1227	ATTCCTATATGGGCATTTTTGGGTAGATTGGGAGGGGTG	ATTO647N
chr11	119096537	119096577	ActiveC_1229	GATTAGTAAGAACTAAGCAGGGGGCCACATGCTCTCAATG	ATTO647N
chr11	119096579	119096619	ActiveC_1230	GCTCCACGGTGACATGTCATTTGATTGTAATTAAGTGTT	ATTO647N
chr11	119096621	119096661	ActiveC_1231	CTGGTTTTTGGGATAGA ACTTGGGCCAGGGCTAGGAACAC	ATTO647N
chr11	119096663	119096703	ActiveC_1232	TATCCACACTCACATTTTCAGAGTCCTGACTCTCAAGGAAC	ATTO647N
chr11	119096705	119096745	ActiveC_1233	TTGCAGCCTCATAGGGTGGGATACAGCAGCTTTTTTTGCA	ATTO647N
chr11	119096789	119096829	ActiveC_1235	CGTTTCTTGCCCTCTGCTGACTACTGATTGGATTTTACCT	ATTO647N
chr11	119096873	119096913	ActiveC_1237	TTGCCAGGCCTCTCTCACTCTTCATACTCCTCCAGATTT	ATTO647N

chr11	119100569	119100609	ActiveD_1325	TGCCCTATGGCACCTACTTCAGGGAACCCTTCCTGGTGC	ATTO594
chr11	119100611	119100651	ActiveD_1326	CTTGGCCTGCATCTGGACTTGGGTAGGTAGTCCTACCACT	ATTO594
chr11	119100653	119100693	ActiveD_1327	GGCAACACGACCATTGTGGTGCCCAAGCCCTCCGCCCGA	ATTO594
chr11	119100695	119100735	ActiveD_1328	GCTGCCTCACTACCTCTCCTCATGGTCTATTTACCAACT	ATTO594
chr11	119100737	119100777	ActiveD_1329	GTA CTGAATCTGCGCTGGCGCCATAAGCTGCTGCTACCTA	ATTO594
chr11	119100779	119100819	ActiveD_1330	CTTGCCATCTGCTGCATGATCTTCCTGGGCTTTGCGGATG	ATTO594
chr11	119100821	119100861	ActiveD_1331	TGCCCGAGCCTCCCCCAGTTTGTGGCCCTGATAGGTGCC	ATTO594
chr11	119100863	119100903	ActiveD_1332	ATTCTTAAAAGGTGGAATGGGAGCAGGCTTGAGTCATGGA	ATTO594
chr11	119100905	119100945	ActiveD_1333	GGCTTGTGGGAGGGGCTAAGAAATTATCAGAAAAGACAG	ATTO594
chr11	119100947	119100987	ActiveD_1334	GGCTGGGACCTGGGAGGTACCTGAGAGAACTGGGGTTATT	ATTO594
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chr11	119101031	119101071	ActiveD_1336	CCCTTCCTGAACTGCTTTGTGAAGGAGCAGTGTAAAGCAT	ATTO594
chr11	119101073	119101113	ActiveD_1337	GGTGCTGTTTTCTTATCATCCTCTTCTGCTTCATCCCTT	ATTO594
chr11	119101115	119101155	ActiveD_1338	TTGCTGCTGGGCCACAGCCCAGAATCCCAGGGAGTGATCA	ATTO594
chr11	119101157	119101197	ActiveD_1339	TAGTGAGTGACCACGCCCCCTTCTCTTCCCCCTCGCCC	ATTO594

chr11	119101199	119101239	ActiveD_1340	CGGGAATGAGAAGACCACTTTGGGTACTGTAACACCTGC	ATTO594
chr11	119101241	119101281	ActiveD_1341	TTCCTCCCTCCGCCCCCTCACCCTTACCAGAATAAAAA	ATTO594
chr11	119101283	119101323	ActiveD_1342	GTAGGGACCCTTGGGTATATCTGGGACTCTGGCAGTGGTG	ATTO594
chr11	119101325	119101365	ActiveD_1343	AGAGGTGATGAGCAGAACTTACTCGCATTGGGGAAAGGAT	ATTO594
chr11	119101367	119101407	ActiveD_1344	CACGTGAAGACTCAGAACTAACCCAGGCAGCCTGGAACTC	ATTO594
chr11	119101409	119101449	ActiveD_1345	AGGAGTGGCTAGGGCAGGGGCGGGAACCGGGTGCTTGAC	ATTO594
chr11	119101451	119101491	ActiveD_1346	AGCAGCGGCACACGGGTCCGGGCAGGGGGCAAGGGCTAAG	ATTO594
chr11	119101493	119101533	ActiveD_1347	CTGTGGTCAGGACCTCAACAAAACCAGCCGACAGCAGATG	ATTO594
chr11	119101535	119101575	ActiveD_1348	CCTCATCCCGGCCTTCCGGGGCCACTTCATTGCTGCGCGC	ATTO594
chr11	119101577	119101617	ActiveD_1349	CAATTTGATCGTCTCGCTGCTGGGATTTGTGGCCACAGTC	ATTO594
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chr11	119101703	119101743	ActiveD_1352	CCACTCCATACTGCTGAGGCCTCAGGACTGCTGCTCAGCT	ATTO594
chr11	119101745	119101785	ActiveD_1353	TTGCTCAGATTGGTGTGGGAAGAGCCTGCCTGTGGGGAGC	ATTO594
chr11	119101787	119101827	ActiveD_1354	CCCCGGTGTCCCGACGGCGGCTCAAGTCAGAGTTGCTGGG	ATTO594

chr11	119105819	119105859	ActiveE_1450	AAGACCCTCTTCCCCAAGAATCCTTCAGGAACCCTCAGA	ATTO647N
chr11	119105861	119105901	ActiveE_1451	CAGGTTATGCAGGAAGTTGTCCAGGTAGAAGCTTCCCTA	ATTO647N
chr11	119105903	119105943	ActiveE_1452	GAGGAAGCTGTCAGTGGGAAGAGCAGCTAGGGTTTAGGGG	ATTO647N
chr11	119105945	119105985	ActiveE_1453	ATCAAGGGAGGAGAGAACTCAGGGCCAGAACCAGGGATGC	ATTO647N
chr11	119105987	119106027	ActiveE_1454	AGAGTCTGGGTTTCTAATCTCAAAGGGAGGAGAAGACATG	ATTO647N
chr11	119106029	119106069	ActiveE_1455	CCCATGCATTGTCCTGACTGCCAAATCAGTGGAGATTC	ATTO647N
chr11	119106071	119106111	ActiveE_1456	GGGGAGAGGTGGGGGTGAATGAGGTAACCTCCTGTGGCCC	ATTO647N
chr11	119106113	119106153	ActiveE_1457	GGGGTAGCCTGGGCCTCCCTAGATTTCCCTGTAAGGAATG	ATTO647N
chr11	119106155	119106195	ActiveE_1458	TGACAGGTCAGCAACAGGTTTGTCTGAGCCAGAGGAGGTG	ATTO647N
chr11	119106197	119106237	ActiveE_1459	CAATGCCTTCTGAAGTGTGGGATGGCAGGGCTAGACAGAA	ATTO647N
chr11	119106239	119106279	ActiveE_1460	GTAGTTGTCTGAGGAATGAGCACATGAGAATAAGAGAATA	ATTO647N
chr11	119106281	119106321	ActiveE_1461	GGTAGGATGGAAAGGTGTTAAGTATCTTTCTCCCAAACCC	ATTO647N

chr11	119106323	119106363	ActiveE_1462	ACATGTGGGAAGGTCTTTGGCACACAGTCCCTTTCTTAAA	ATTO647N
chr11	119106365	119106405	ActiveE_1463	ATCCTGGGGGAATTCACATTCTCCCAAGAGCCCCTTCTTC	ATTO647N
chr11	119106407	119106447	ActiveE_1464	TGAGGACAGGGGAAGGAAATACCTGCAAAGGATTCAAAG	ATTO647N
chr11	119106449	119106489	ActiveE_1465	GTTGATTCAACCTCTACAGGACTGGGGCTCATCAATGCTT	ATTO647N
chr11	119106491	119106531	ActiveE_1466	CAACCTCTGGCCTCAGAAGCCATCTTTTCCTAGACTCAAG	ATTO647N
chr11	119106533	119106573	ActiveE_1467	TCCCAACAAGCTCCCAAGAAATGGTGCTGTAGGTACTG	ATTO647N
chr11	119106575	119106615	ActiveE_1468	ATAGATTCAGCCACAAGACCTTGCCACTCTAAGTATGTGA	ATTO647N
chr11	119106617	119106657	ActiveE_1469	TGGTAATGACAAGGGAGCTGGCAATGTAGCACTGGACTAT	ATTO647N
chr11	119106659	119106699	ActiveE_1470	CCATAGTAACAGCTCCTGCCTATGGAGCACGTGTAGAGGG	ATTO647N
chr11	119106743	119106783	ActiveE_1472	CCCATTAACCTCCTTGCTCGTGTAGGTTTGTCTGGAGAT	ATTO647N
chr11	119106785	119106825	ActiveE_1473	TCATCACCTCCTTCTCTTGGAGCTTGGACCCAGAAACA	ATTO647N
chr11	119106827	119106867	ActiveE_1474	AGAGGTTGAGAGTAGAACACCGAATTTGAATCCCCCAC	ATTO647N
chr11	119106911	119106951	ActiveE_1476	GACGCAGAGCGTCCCTCCAGATAGAAGTGTCTGGCAGAG	ATTO647N
chr11	119106953	119106993	ActiveE_1477	TAGCTTCCCATTTCTGGGGGAAGCTAGGCCAGGGTAAG	ATTO647N
chr11	119106995	119107035	ActiveE_1478	TCACCGCCCCCTTCTCCCAACACCCCCAGACTCAGCGACT	ATTO647N
chr11	119107037	119107077	ActiveE_1479	CGGACGCCTGTGAGGTTAAGAAGGAGGTGACCCCTGTGGA	ATTO647N
chr11	119107079	119107119	ActiveE_1480	GCTGCCTTTGCTTTCCCTATGCTTGTAGATTTCCACAG	ATTO647N
chr11	119107121	119107161	ActiveE_1481	CACACTCAGCTCAAGGCAAGAGTAACTTCACTTACCTAAG	ATTO647N
chr11	55812948	55812988	InactiveA_64	AAAGTTCCAATGACACTGGAAACTAAAACAACAGCAAGAA	ATTO647N
chr11	55812990	55813030	InactiveA_65	TGAAATTATTATGTTTTTCATCTATCATATAACATATTAT	ATTO647N
chr11	55813284	55813324	InactiveA_72	ACAGAGATTAAAAGTCCTCTTATAAGTGTGAGTAAGCATG	ATTO647N
chr11	55813368	55813408	InactiveA_74	AATTCAGAAATGTGGTTGGGGTACATATGGAAAGTAAAT	ATTO647N
chr11	55813410	55813450	InactiveA_75	AGTCACAAAGAAAGCATCAATGGTGCATATAATTCAATAT	ATTO647N
chr11	55813494	55813534	InactiveA_77	TTCACACGGTATCATAGTATAAAATTTTTCTGAATCTTGT	ATTO647N
chr11	55813578	55813618	InactiveA_79	CACTTAAATAAGTACTTGTCTTTATTAAGTTTGCTTCCAC	ATTO647N
chr11	55813620	55813660	InactiveA_80	TGTGATTCTTTTCTCATTTGCTGGCAAACCTTTGTTTTAAT	ATTO647N
chr11	55813746	55813786	InactiveA_83	AAGAATGTTACAGTGACTCTGTTATGGCTTTTAGTGGTA	ATTO647N

chr11	55813872	55813912	InactiveA_86	GTTTAGAGATAAAAGGTTTCCTTTTAGAGAAAATTTGGAA	ATTO647N
chr11	55813998	55814038	InactiveA_89	AGAGACAATCTGATTAAGTGTGACAGTATTCTAGCTTCC	ATTO647N
chr11	55814040	55814080	InactiveA_90	TAAACCAGTGGCAGCAATTTCAAATCTCTTCCTATGTGTC	ATTO647N
chr11	55814124	55814164	InactiveA_92	TTTTTAGTATCTAGATAGAAACATACATGAGGCCTTTAAA	ATTO647N
chr11	55814166	55814206	InactiveA_93	GACAACCATTAGTAGTAATCAATGATTTCTTATATTTTTT	ATTO647N
chr11	55814376	55814416	InactiveA_98	CCTAATGATTGTTATGTTTCATTGAAGTCACCTTGATCCAC	ATTO647N
chr11	55814502	55814542	InactiveA_101	GAGAAGCATATGATAACTGGTTGATGACAAGTATTGTCC	ATTO647N
chr11	55814544	55814584	InactiveA_102	TTCTTCATTGATTTTTCTGACTACTGTTGGTTGCAGTCCA	ATTO647N
chr11	55814586	55814626	InactiveA_103	TATTAGCTCAGGTTTCATTCTTTTAGTGTCTTTTAGGCAA	ATTO647N
chr11	55814670	55814710	InactiveA_105	TGTATTTGGCTTAGTGCTTCATTTTGTGTCATTGTATATA	ATTO647N
chr11	55814796	55814836	InactiveA_108	ATTCAGATAAATATGGTTGTTATAAAAAGTTTACTTTGTTA	ATTO647N
chr11	55814838	55814878	InactiveA_109	ATTGTCTCAAAGGCATATTTTTTCCAGTTAGTTTGAATCA	ATTO647N
chr11	55814922	55814962	InactiveA_111	CACTCATGCCAAAAGTGCACCTAACAAAATCATCATTATA	ATTO647N
chr11	55814964	55815004	InactiveA_112	TTATCACTTTTTGATTGGAGAGTCTTTAATGTTTGAACCA	ATTO647N
chr11	55815132	55815172	InactiveA_116	GCAGGCCAAAAGTATCGACTTCTGATTAGAGTATTTTCATT	ATTO647N
chr11	55815174	55815214	InactiveA_117	TCCCTTCAGTTCCTCCAGGGCATGGCGATGCTGAAGTACA	ATTO647N
chr11	55815216	55815256	InactiveA_118	GTCTTCCCGCTCCACCCAGTTAGATCCCACTTGATTCCCT	ATTO647N
chr11	55815258	55815298	InactiveA_119	AAGCAGACCTAGAGAAAAAGTTGAAATTTGAGCGCATTGT	ATTO647N
chr11	55815342	55815382	InactiveA_121	TATGGGAAGATCAGATAAAATTAAGAACTCATGTAAGTAT	ATTO647N
chr11	55815384	55815424	InactiveA_122	AATTAGAAAGCACTCTTTCTAAACAATTGGCCTATTGGCA	ATTO647N
chr11	55815426	55815466	InactiveA_123	TGAGCCACCATGCTCCGCCCAAGCCTTCCCTATTAAAAAA	ATTO647N
chr11	55818240	55818280	InactiveB_190	CAAGAAAGATGTTAATTTACATGCAAGACCAACATATTCA	ATTO594
chr11	55818282	55818322	InactiveB_191	ATATCTATTCACATAACCCACCCAAATTTTTAGACGGCCT	ATTO594
chr11	55818324	55818364	InactiveB_192	GCTATCATATCTGTAATCTCTTTCTCTATCATAATAGACA	ATTO594
chr11	55818450	55818490	InactiveB_195	TATGAAGGAGAAGAACTAAAAGTGGAGATAGTACAGCAA	ATTO594
chr11	55818492	55818532	InactiveB_196	CCTTCAAGACACATTATATATTCATTGTGTCCATCTATTA	ATTO594
chr11	55818576	55818616	InactiveB_198	GTGTAAGAGTCTGACTTGCAAAGTCCCTTTTCTTCTAGG	ATTO594

chr11	55818702	55818742	InactiveB_201	TAAGCAGACTAGAGAATCTACATAGTCCAGTGACAGTTAC	ATTO594
chr11	55818744	55818784	InactiveB_202	TACTAACACATTCCCTTCATTAATAACCATACTTTCAATT	ATTO594
chr11	55818786	55818826	InactiveB_203	CCTTTACCCGCACCAAACCTCTGCTCCATTATCTAGGTCTGA	ATTO594
chr11	55818828	55818868	InactiveB_204	CTGTGACTAGGGTTTTGATCCTTGAACCTCCTAGACATGTA	ATTO594
chr11	55818870	55818910	InactiveB_205	TGAATTTCCCTATCGATATGCCCAGGAAGGCCAATCTACAC	ATTO594
chr11	55818912	55818952	InactiveB_206	TTCTTTATTCTATAGGTGACAAAGTAGAAGCCAGAGAAGC	ATTO594
chr11	55818954	55818994	InactiveB_207	AAATAATAAATATCGAATAGTCAATACAGATACCCTTGTT	ATTO594
chr11	55818996	55819036	InactiveB_208	AATCAGGCTGTACTAATTATCAATCCTTCCTCATTGCTTG	ATTO594
chr11	55819038	55819078	InactiveB_209	CAAATAACAGCTGAACTAATTGTTTCAGAGCGTATGCTCC	ATTO594
chr11	55819080	55819120	InactiveB_210	ATATAGCAGTTTAATGTTTGTCTGACCCAGAAAATTTGAC	ATTO594
chr11	55819164	55819204	InactiveB_212	TAGTTTTCACATAATTTGTTTATACGATGACATTAECTAT	ATTO594
chr11	55819248	55819288	InactiveB_214	CTACATAAATGATCTTCCTCGTATAATATGATGACTGATT	ATTO594
chr11	55819500	55819540	InactiveB_220	ACGGCTCCTGAAGGATGAAGCAAATATCTCTTCCGGAATC	ATTO594
chr11	55819584	55819624	InactiveB_222	CTGTTTCTTCGAATCTGAAAGTTAGTTCTGAAAACAAAAA	ATTO594
chr11	55819626	55819666	InactiveB_223	ACGTGGTCCCACCTTGTATTTCTATCAGTCAGCAGCATCGC	ATTO594
chr11	55819710	55819750	InactiveB_225	GCACAGTGACATTGTAGATGGCCAGAAAACCAGGAAGAG	ATTO594
chr11	55819752	55819792	InactiveB_226	TGGGGTTGATTTTGTATGATCACAATCAACCCAATATTCCC	ATTO594
chr11	55819878	55819918	InactiveB_229	CTAAAAATGAAATGGTTCTGTCTTTGACAACAAGGTTAC	ATTO594
chr11	55820004	55820044	InactiveB_232	GGGACATGTAACTGTGTAGAGCAGAGGGTTGCAAATGGC	ATTO594
chr11	55820046	55820086	InactiveB_233	CCCAGGCATAGGATCCCACAACCAGCAGCACGCAGAGTTT	ATTO594
chr11	55820172	55820212	InactiveB_236	TGTAAGTATCAGAGCAAGAAAGGGAGAGTAGTGAGGAGAA	ATTO594
chr11	55820214	55820254	InactiveB_237	TTTCATTAAGGTGGCAAGAAAGAATAGCAGCCACTGGTT	ATTO594
chr11	55820256	55820296	InactiveB_238	CAATGAACGCATAAGATGTGAGAACGATGAGTAGTGTGCT	ATTO594
chr11	55820298	55820338	InactiveB_239	TGCGGCGCCCACTGACTGAACGCATCTTGAGGATGGTTAC	ATTO594
chr11	55823448	55823488	InactiveC_314	CGGGGGTTACAGACCACCTTGGGCATAATGGAAGAACCTT	ATTO647N
chr11	55823532	55823572	InactiveC_316	ATAGAACCTTGCCCAGGTGTGGTGATTAATGCCCTGATC	ATTO647N
chr11	55823574	55823614	InactiveC_317	CTTTTCATTGAAAAGAATCGCAGTTGACATGTACTATAGC	ATTO647N

chr11	55823616	55823656	InactiveC_318	CAAATCCATGATATGACTTGTTTTCTATGGTGTTTGTA	ATTO647N
chr11	55823658	55823698	InactiveC_319	TGTTATTCATGAGGGTTGAAGTTGTCTTTAATCGAAACAC	ATTO647N
chr11	55823742	55823782	InactiveC_321	GATTTCTCTAATCCATTACATACTTACCATGTGAATCACTC	ATTO647N
chr11	55823784	55823824	InactiveC_322	ATTCTCACACAGCTTTTTCTCTCGCTCTTTAAAAAAGCAT	ATTO647N
chr11	55823826	55823866	InactiveC_323	CTGCATTGTAGGAGGCTTTCTGGGTTTCCTTTTGTAECTA	ATTO647N
chr11	55823910	55823950	InactiveC_325	AAGAGAAACCAACATTTCAATAATTCCATTGATATAAGC	ATTO647N
chr11	55823952	55823992	InactiveC_326	CAACCTGAATGAGCAGTGTTCAAAGCACAGTCTGTGTGCC	ATTO647N
chr11	55823994	55824034	InactiveC_327	TCTCCCCAAGTTCTGCTTCCTTCTTGACTAATACAGCAAT	ATTO647N
chr11	55824036	55824076	InactiveC_328	CTATTCAATGCTAGTGGCCATTAATGGGAATATCTCAAG	ATTO647N
chr11	55824078	55824118	InactiveC_329	GGAAGAGCAGAGCTCCAGAGTGGTACCGGGGGTGCAGACT	ATTO647N
chr11	55824120	55824160	InactiveC_330	TCAAGTGTGGCTTTTTGGCTTGTGCCATCTGTGCAACCAT	ATTO647N
chr11	55824162	55824202	InactiveC_331	AACTCACCCACAGTCACACATAGAATCCCTGATAGAGACA	ATTO647N
chr11	55824204	55824244	InactiveC_332	ATTTCCCCTTTCAAATAAGGTTATAGAGGCACAGCAGGT	ATTO647N
chr11	55824246	55824286	InactiveC_333	ACACATTTTATCTTCATAAACTGGTTGACATTAGTACTG	ATTO647N
chr11	55824288	55824328	InactiveC_334	GTA CTGCTCATGTACCAGATACTATTCTAAATACAATTAT	ATTO647N
chr11	55824330	55824370	InactiveC_335	GAATACTAATAATTGCTGATACTAATACTAATAATTTACT	ATTO647N
chr11	55824372	55824412	InactiveC_336	AAATACCAGAAAGGGGTGGGGATAAAGGAGTCCCTTTTACT	ATTO647N
chr11	55824456	55824496	InactiveC_338	TAAATAGGCATTATAAAATTTGTTTCACACTCAAAGCTC	ATTO647N
chr11	55824498	55824538	InactiveC_339	TGAGCCAGTACTCACATTGCCATTTTCATGTTATGAAATTA	ATTO647N
chr11	55824540	55824580	InactiveC_340	AAATTGCATAACATTGTATGCCACATCCAAGCATTGCCTC	ATTO647N
chr11	55824582	55824622	InactiveC_341	CATATTATTATAATGTAACACAATTACATTCAGACTTCAT	ATTO647N
chr11	55824666	55824706	InactiveC_343	CAAGGAAACCATCCTATCCTGGGACTCCAACAATTATTGA	ATTO647N
chr11	55825002	55825042	InactiveC_351	AAATTATCTAATACCATTACCATCCTTTTGAATTCCCCTT	ATTO647N
chr11	55825170	55825210	InactiveC_355	CTAATAGCTGTTATAAGATGTTTGGTTTTACAGATTAAT	ATTO647N
chr11	55825212	55825252	InactiveC_356	AAGTGCTTATGCCAATGTCTTCACACTGCTTTACATCTCA	ATTO647N
chr11	55825296	55825336	InactiveC_358	TAGGAAAATCTCCATGCAGTCTTAACCAAGTCGCATGGAC	ATTO647N
chr11	55825338	55825378	InactiveC_359	CCGTGGGCCTCCTACTGCCACCCTCAGCACTAGGATGACT	ATTO647N

chr11	55828698	55828738	InactiveD_439	TAGAGTCCGCTGCAATTATTATTTTCGTCATCTATCAAAT	ATTO594
chr11	55828740	55828780	InactiveD_440	AGCTCTTTTTATGTGATTCCAGCTTCCTTAATGCAATTC	ATTO594
chr11	55828782	55828822	InactiveD_441	GAGAGAGAGACAATAAATTATGTTCCAGGGATTATTC	ATTO594
chr11	55828950	55828990	InactiveD_445	TTTAGGGTTAGTATGAAGATAAGCAGTAAAGATAAAGTGA	ATTO594
chr11	55828992	55829032	InactiveD_446	TAAAAGTCATAAGTGTGAGTAAGCATCTCTTCATCAATAG	ATTO594
chr11	55829118	55829158	InactiveD_449	GCATTAATGGTGCATATAATTCAACAGGGAATTAAGAAAT	ATTO594
chr11	55829160	55829200	InactiveD_450	AATGAGGAAATTGACATAAGTCGTAATGGAATCACAAATA	ATTO594
chr11	55829244	55829284	InactiveD_452	TCGGTTTTGAAAACTCAAACCTATTGCTTTTCTAATATT	ATTO594
chr11	55829286	55829326	InactiveD_453	AATTACTTGACAAATTAAAAAACCAGGGTCAAACACCCAA	ATTO594
chr11	55829412	55829452	InactiveD_456	CACTGAGTCTCTTCCTGATGTCAGTAAGTACACATATGCT	ATTO594
chr11	55829454	55829494	InactiveD_457	AGTTAAATAAACCCCAAGCTTCAATGACTTCATTTAGATA	ATTO594
chr11	55829496	55829536	InactiveD_458	TAAAAACTTCTCATATGCCACTGATGATGAAGTAGATAA	ATTO594
chr11	55829580	55829620	InactiveD_460	TAATCTGCATAGTAATCCCAATATGCTTACCATAAATTCA	ATTO594
chr11	55829622	55829662	InactiveD_461	ACAATGTGGACCAACTCACAGTTCTTGAAGTCTCTCGAAA	ATTO594
chr11	55829664	55829704	InactiveD_462	ATTTGTTTTCTAAGTAGACCATGACTGCTAGAACATTCCG	ATTO594
chr11	55829706	55829746	InactiveD_463	GCCTCTAATCGCTAACATTTTCATGAATTAGATCCTGCAGA	ATTO594
chr11	55829748	55829788	InactiveD_464	ACAATCTTTAATAATACAGCATCTCCTGTGTGCTCTTTT	ATTO594
chr11	55829790	55829830	InactiveD_465	TTGCCCTCTAATATCAAGAGCAATAGTTACTTCCTAAAGT	ATTO594
chr11	55829832	55829872	InactiveD_466	TCCACGAAGCTCTGAGGTTCTGGGGACAATGTTTCTTCCC	ATTO594
chr11	55829874	55829914	InactiveD_467	TGTCTCTTCCTCAAGGGATTAACACCCGGCGGACTGAGCTG	ATTO594
chr11	55829916	55829956	InactiveD_468	AGTCCTAACCCAGCCTCAGAGGCCCTGACACACTAAGCGT	ATTO594
chr11	55829958	55829998	InactiveD_469	GGACCATGTCTGAGCGTGCCACAGGACACTGGAAATCTGC	ATTO594
chr11	55830000	55830040	InactiveD_470	CCTCTTCAGAGGCAGGAGCAGCCATCTAGCACAGCCTTCT	ATTO594
chr11	55830042	55830082	InactiveD_471	AGCCACAGTGGATACTTGGTGTGTTCCAGCTTTCCATGAT	ATTO594
chr11	55830168	55830208	InactiveD_474	TTAGATCCGCCAGAGGAAGTAAGGGGGTAAGGGGAGGAG	ATTO594
chr11	55830210	55830250	InactiveD_475	TGCAAACCTGTATTCCCAGATGTCCTATCTAGCTGCCTTC	ATTO594
chr11	55830252	55830292	InactiveD_476	CCACTCTCCTAGTCCTTATGCTGTGATCTTGCTGCTGGGG	ATTO594
chr11	55830294	55830334	InactiveD_477	CCTCAGAAGCTGTGTTTGTGAACCTAGTCTCATTTTCAT	ATTO594

chr11	55830336	55830376	InactiveD_478	AGAGGGTTTTCTTGTACCCTGTGCATTGTACACCGCAAG	ATTO594
chr11	55830378	55830418	InactiveD_479	GTTTCAGATACAGAAAGATGTACACACTCTAGGTAATAGGA	ATTO594
chr11	55833528	55833568	InactiveE_554	TTGCATTTGAATCCATACCATATTTAATCTATTCTAAGTC	ATTO647N
chr11	55833570	55833610	InactiveE_555	CATTGTTGTTCTTTTTCCCAACAGAATTCTAGCAAAGATC	ATTO647N
chr11	55833654	55833694	InactiveE_557	GGTATGAATATCTAATAGTTGTGAATTGAAAAGTCTTGAC	ATTO647N
chr11	55833696	55833736	InactiveE_558	CCTACCTTAAGCCTTACCTTATGGTATGATCCTCACATCT	ATTO647N
chr11	55833738	55833778	InactiveE_559	ATTACGTTATAGCCTCCTGATTTTCACTCTGTACTIONTAG	ATTO647N
chr11	55833780	55833820	InactiveE_560	AGACCATATGTTAGTTGCCACAGCCAGAAATAAATCACAG	ATTO647N
chr11	55833822	55833862	InactiveE_561	GCTCTCTGATACTCTTCATGTTAGGAGTAAGGCTATGGTT	ATTO647N
chr11	55833948	55833988	InactiveE_564	AAATTATTCATCTTTACCTCTGTATCCACCTCAGATATT	ATTO647N
chr11	55833990	55834030	InactiveE_565	ATGGCTTTCTCTCTAACTAGAGTGTGGATTCTGGAGATA	ATTO647N
chr11	55834032	55834072	InactiveE_566	CTCAGGTCACAGTGTGACGTAGCTATCTGCTTATACATTT	ATTO647N
chr11	55834074	55834114	InactiveE_567	GGGTACTIONACAATTTCTGTGAACAGCCTGTATTTTATTGT	ATTO647N
chr11	55834116	55834156	InactiveE_568	TGAGACATTTTCTGACTCCTCCCAACCAAGTTCAGTATTT	ATTO647N
chr11	55834158	55834198	InactiveE_569	TTATCCATACAGCAAACATTGCTGAGTTGTGAAACTIONTC	ATTO647N
chr11	55834200	55834240	InactiveE_570	TGGCTCCCAACAACTIONTAGTCCACTGCTAAATTGTCATTTA	ATTO647N
chr11	55834830	55834870	InactiveE_585	ACAATAGGATTATTTCCCCAGCATGTAAATCTTAGTGATTT	ATTO647N
chr11	55834914	55834954	InactiveE_587	TGTAAAACATGCAAATCTCACCAACTIONTCATGAGTTGTGC	ATTO647N
chr11	55834956	55834996	InactiveE_588	AACTGCAACAATTTGGATAATTAACGTGTAATCAAATTGT	ATTO647N
chr11	55835124	55835164	InactiveE_592	GAGAAAGTGGACCATGTGAATATACTIONATTCCAAAAT	ATTO647N
chr11	55835166	55835206	InactiveE_593	ATGCCTATACTIONGGGAGTTTTTGCAGGGCTGATATAATAA	ATTO647N
chr11	55835250	55835290	InactiveE_595	TCACTIONCCACTAAAATAACTIONCTTTACAAATAAATIONCTAC	ATTO647N
chr11	55835292	55835332	InactiveE_596	TTGGTCTTATGCCTATAAATTTACTIONCTTATATATGCC	ATTO647N
chr11	55835334	55835374	InactiveE_597	CATTTTATAATTTAACACTIONTGCACTIONTTCATAGCCTCCA	ATTO647N
chr11	55835460	55835500	InactiveE_600	TCCTCTTTGGTTCTGATTTACCATATAAATTTCACTIONCAAGC	ATTO647N
chr11	55835544	55835584	InactiveE_602	CTGATGTTGTTGCAAACACTIONCCACACTIONCTGTAAACAAA	ATTO647N
chr11	55835586	55835626	InactiveE_603	CATAAGAAACTIONTACGTCTIONCTACAACCAACTIONATATTAAGGT	ATTO647N

chr11	55835628	55835668	InactiveE_604	GGACAGGACTGCAAACGTTTGGAAATTTGTTTCTCAGTGTC	ATTO647N
chr11	55835670	55835710	InactiveE_605	GCCAAGGATATTAGATGCAGATCCGATCTTCATGTATAGA	ATTO647N
chr11	55835712	55835752	InactiveE_606	GAGATTCTTCCTTCAGGTCTCTCATCTGCTTAGTTAATTA	ATTO647N
chr11	55835754	55835794	InactiveE_607	TAACTGTTCTCTCTGTTACACTAACCACACAAGAGATGCA	ATTO647N
chr11	55835796	55835836	InactiveE_608	TATTTCTTATATATCTACCATGCCCTTGGTCTTTGCAAAT	ATTO647N