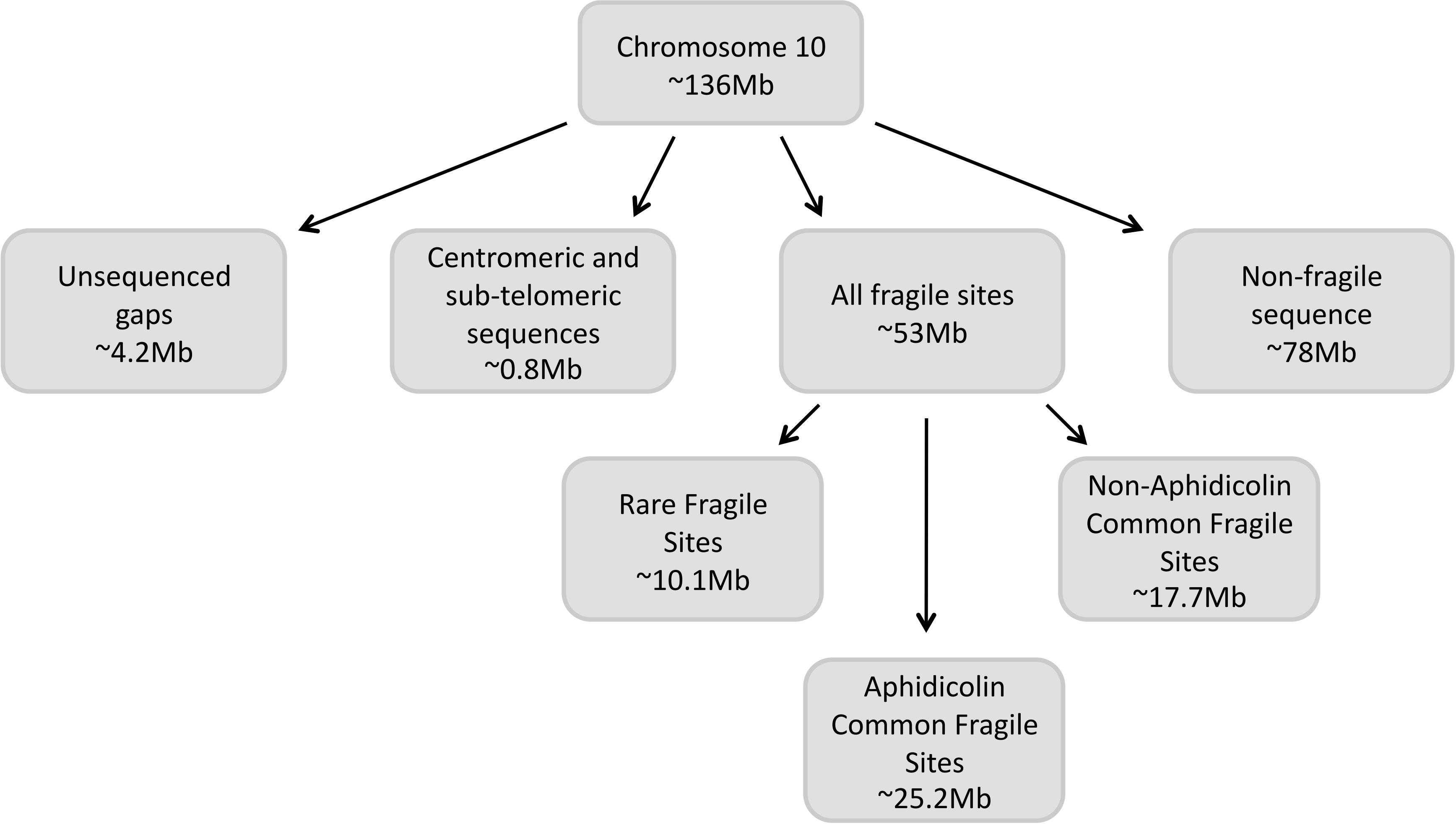


Figure S1. Division of the chromosome 10 sequence into non-fragile and fragile regions.

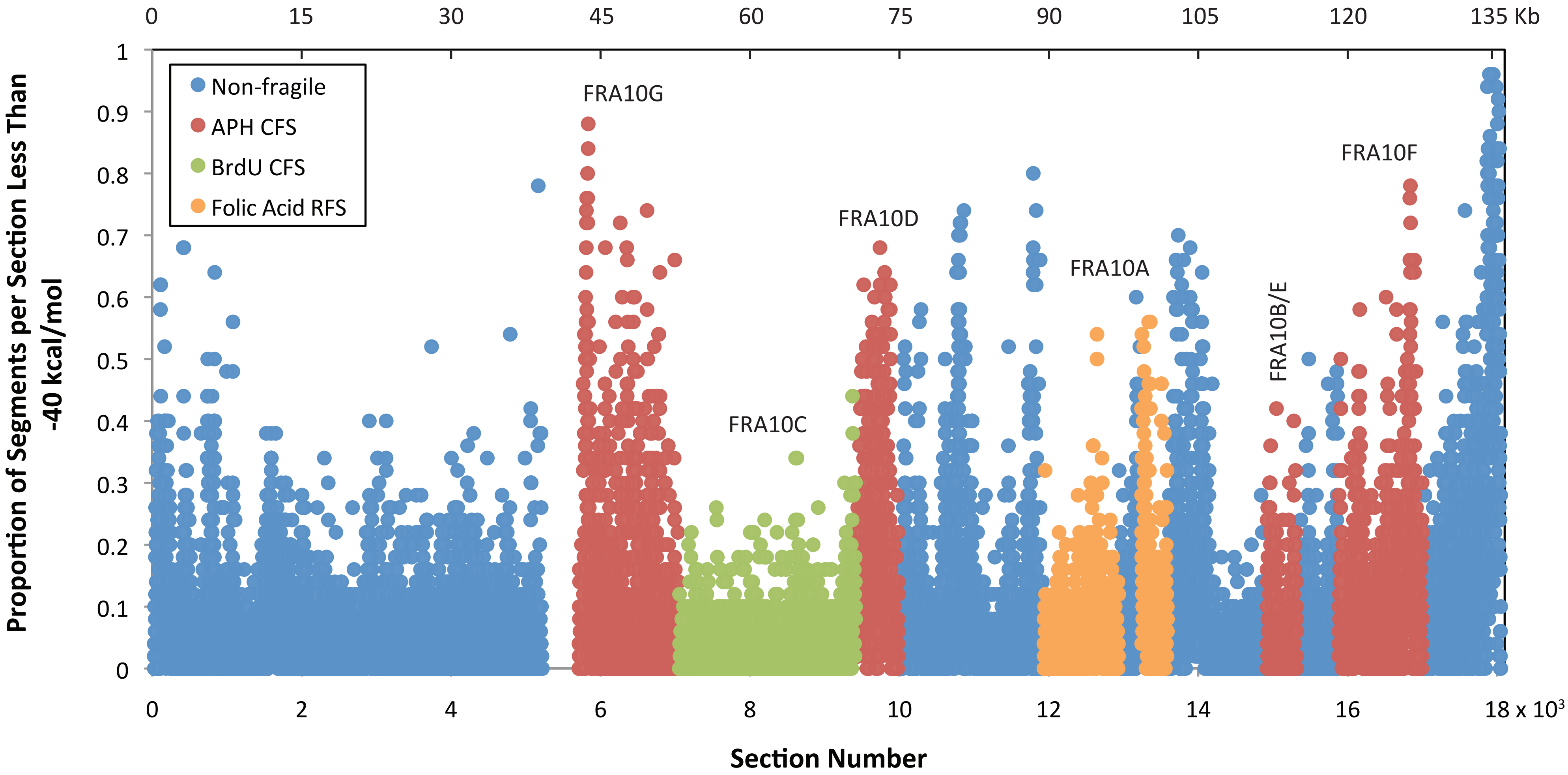


Figure S2. Density of Secondary Structure Forming Potential on Chromosome 10. The proportion of segments per section (consisting of 50 segments) with a predicted free energy value less than -40 kcal/mol is depicted for chromosome 10, where each data point represents 7650-nt. APH-induced common fragile sites (CFS) have high levels of DNA secondary structure clustering. BrdU-induced common fragile site FRA10C has low levels of clustering compared to the overall sequence. Folic acid rare fragile site (RFS) FRA10A has low levels of clustering in the 5’ half and higher levels in the 3’ section. Non-fragile DNA exhibits fluctuations in regions with low and high levels of clustering, with increasingly high levels of clustering approaching the 3’ telomere.

A. FRA3B

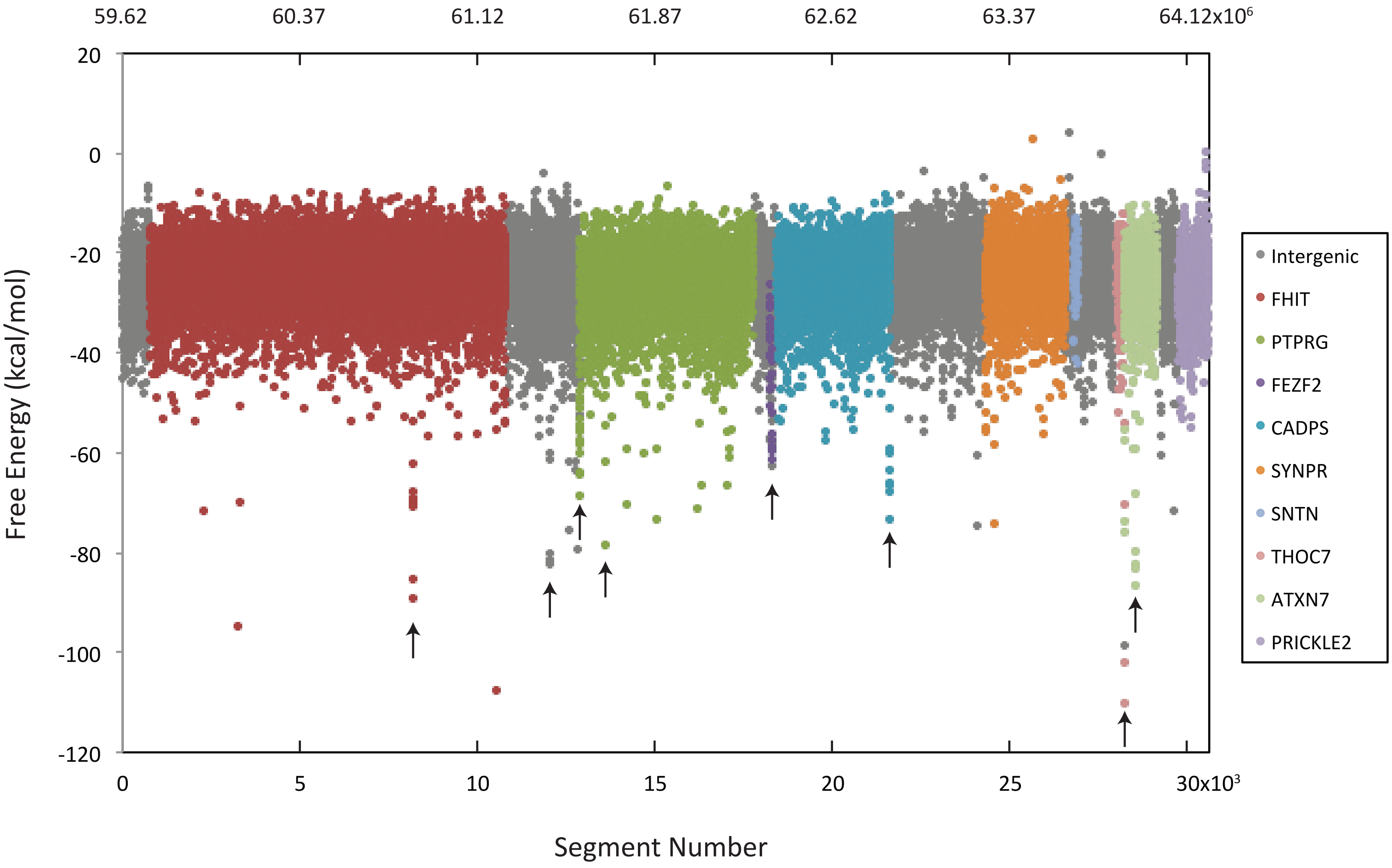


Figure S3. Free energy values for predicted DNA secondary structures at FRA3B (A) and FRA16D (B). The free energy value for the most favorable Mfold-predicted DNA secondary structure for each 300-nt segment, with 150-nt increments, of the FRA3B and FRA16D sequences is presented. The lower x axis depicts the segment number in the p to q arm direction on each chromosome, the upper x axis depicts the corresponding nucleotide number, and the y axis displays the free energy value of the predicted structure. The arrows indicate the regions identified by the fragility threshold.

B. FRA16D

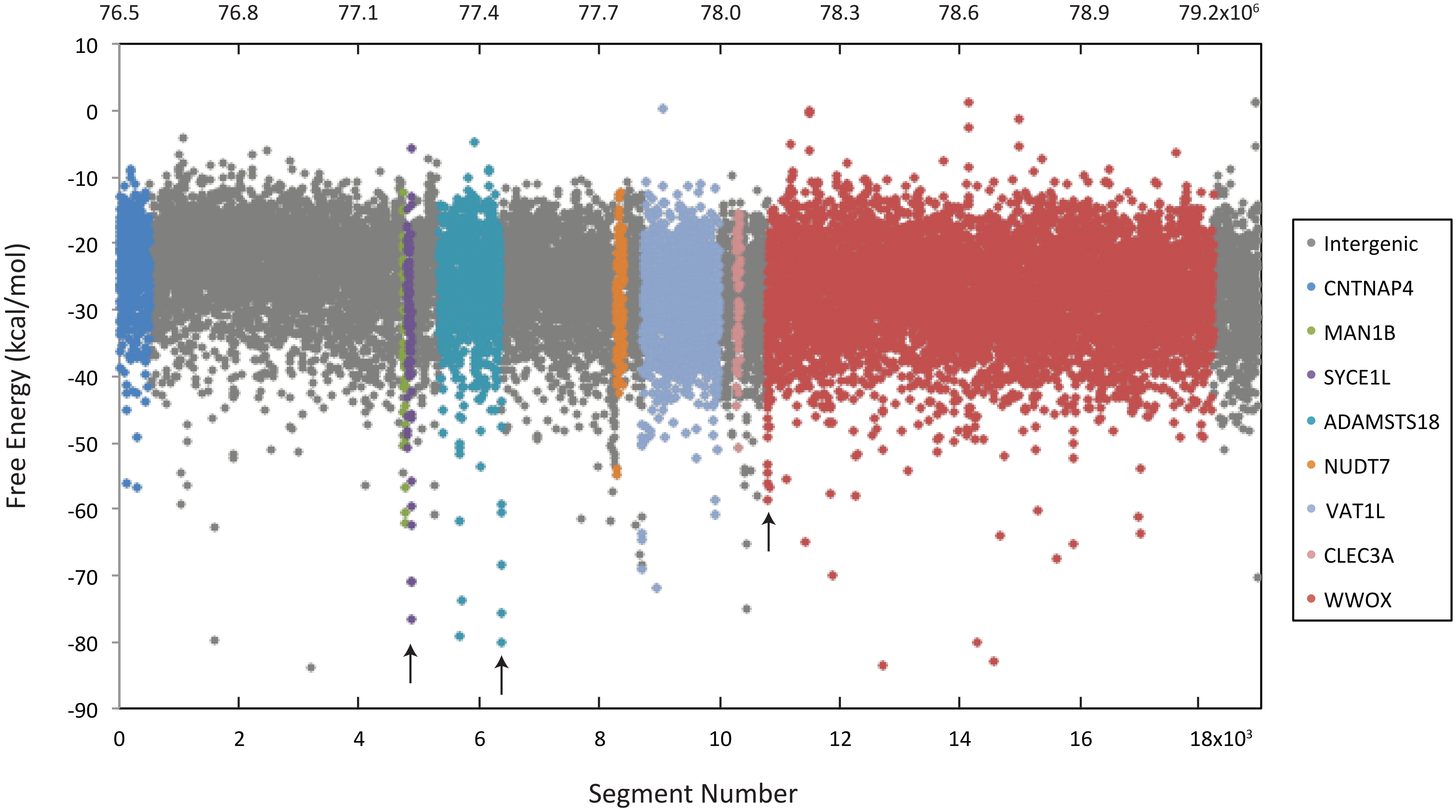


Figure S3. (Continued)

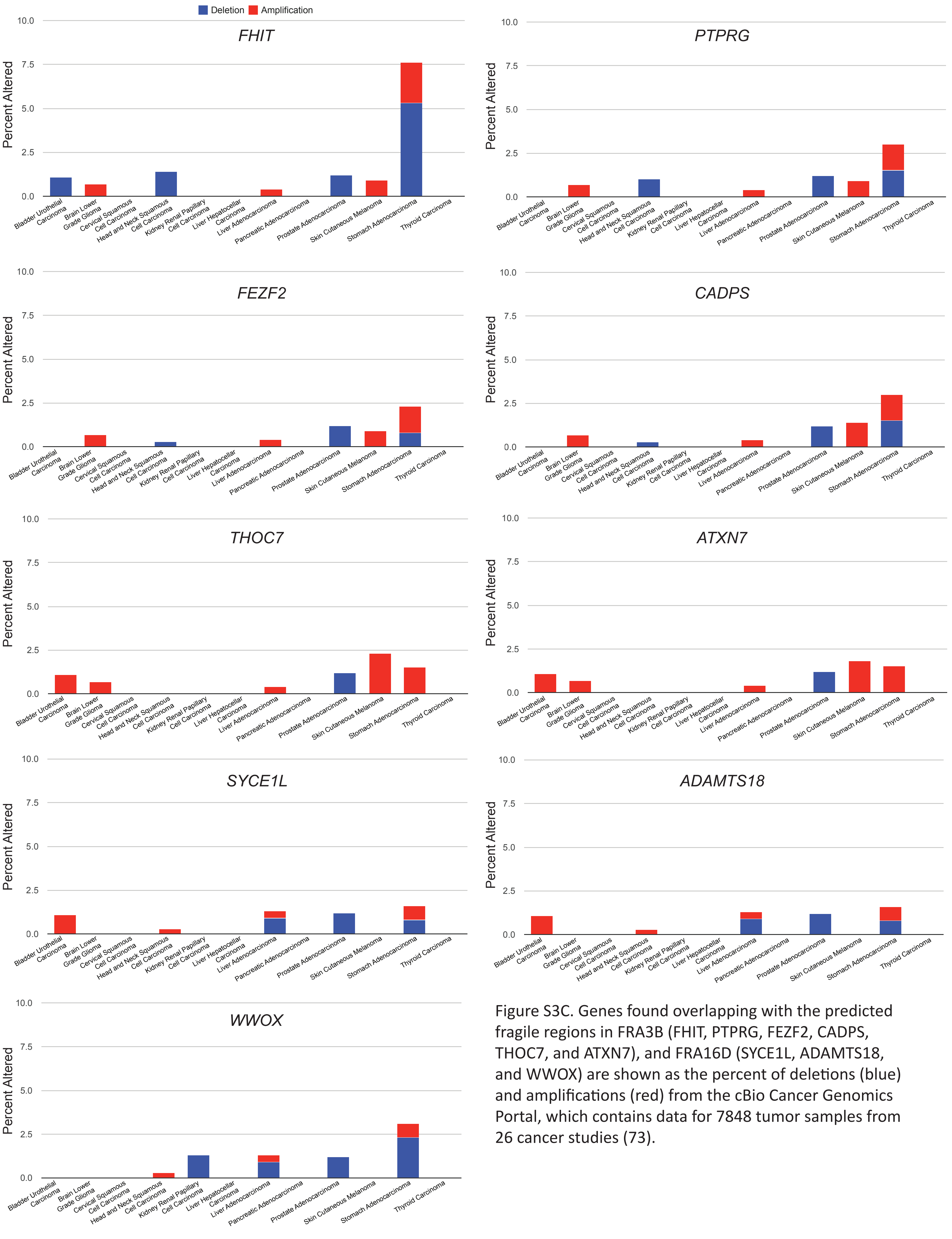


Figure S3C. Genes found overlapping with the predicted fragile regions in FRA3B (FHIT, PTPRG, FEZF2, CADPS, THOC7, and ATXN7), and FRA16D (SYCE1L, ADAMTS18, and WWOX) are shown as the percent of deletions (blue) and amplifications (red) from the cBio Cancer Genomics Portal, which contains data for 7848 tumor samples from 26 cancer studies (73).

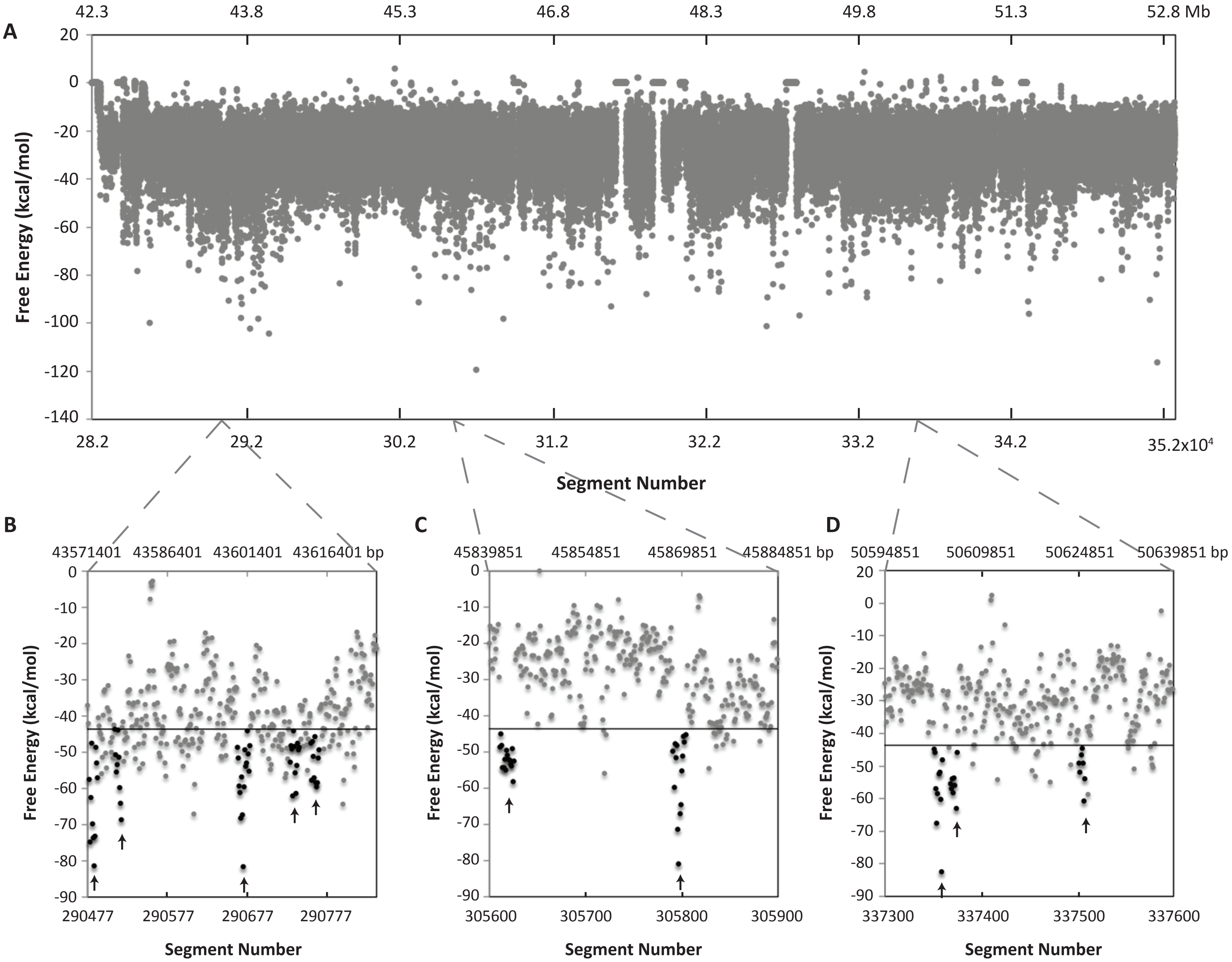


Figure S4. Free energy values for predicted DNA secondary structures at FRA10G. (A) The free energy value for the most favorable Mfold-predicted DNA secondary structure for each 300-nt segment, with 150-nt increments, of the FRA10G sequence is presented. The lower x axis depicts the segment number in the p to q arm direction on chromosome 10, the upper x axis depicts the corresponding nucleotide number, and the y axis displays the free energy value of the predicted structure. A zoomed in view of three sequence regions are presented in panels B-D, and their relative location in FRA10G is shown by the dashed lines. The 95% confidence interval for chromosome 10 (-43.61 kcal/mol) is depicted by the horizontal black line. Regions (black dots, arrows) predicted to be fragile using the prediction threshold- seven consecutive segments below -43.61 kcal/mol, exhibit sharp decreases in predicted free energy values compared to the surrounding sequence (grey dots). These fragile regions correspond to both genic and intergenic sequences: (B) five regions located within RET, (C) one intergenic region (nt 45,868501~45844050) and one region within ALOX5 (nt 45868501~45870750), and (D) three intergenic regions.

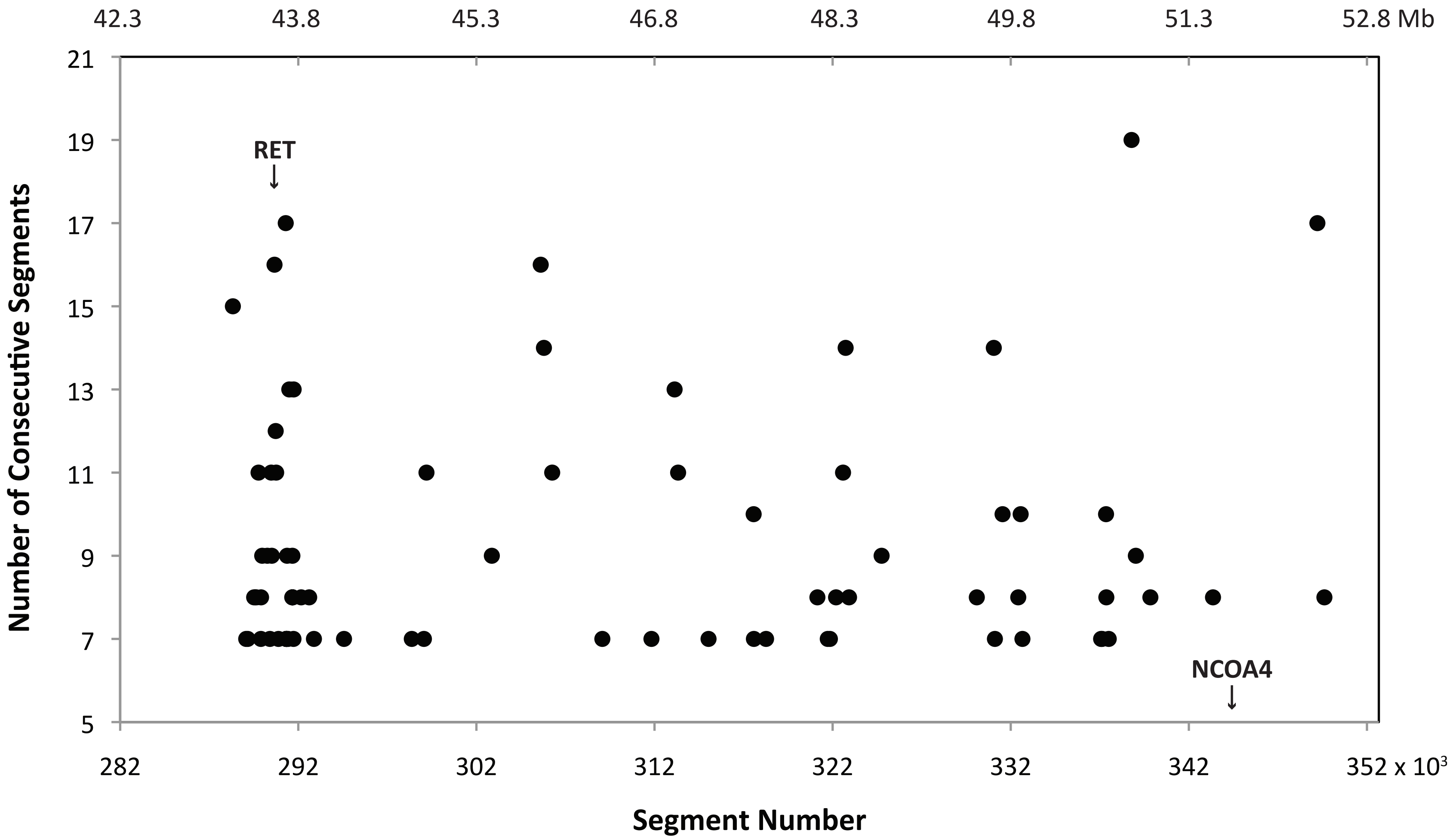
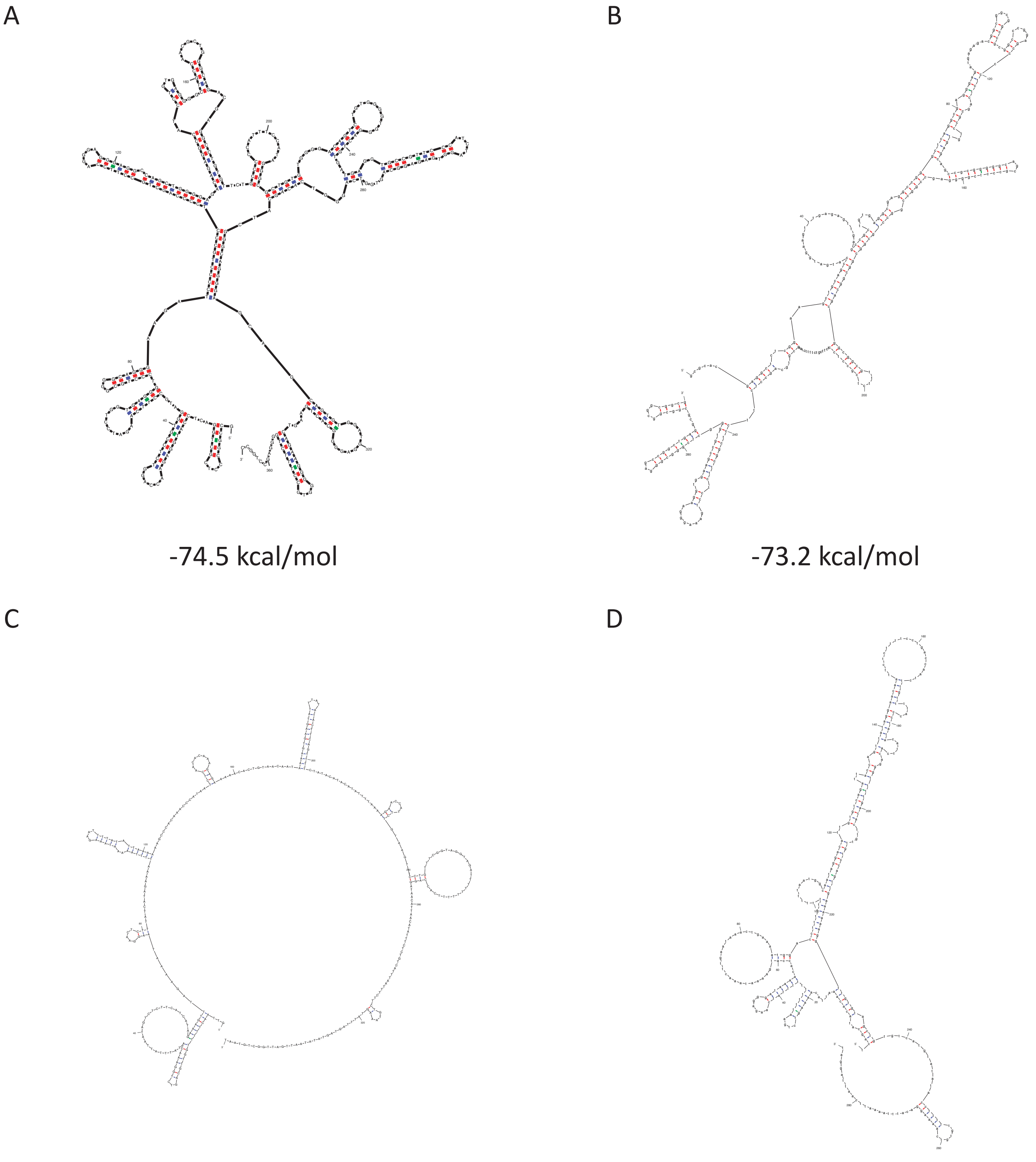


Figure S5. Regions predicted to exhibit fragile site breakage within APH-induced common fragile site FRA10G. Regions with at least seven consecutive segments with a predicted free energy values of less then -43.61 kcal/mol are presented. The lower x axis depicts the number of the first 300-nt segment isolated by the threshold, the upper x axis displays the corresponding chromosome 10 nucleotide number, and the y axis depicts the number of consecutive segments within the isolated region. The locations of two translocation participating genes, *RET* (segments 290482-290839)and *NCOA4* (343766-343939), are labeled. *RET* contains five significant regions, while *NCOA4* has none.



-74.5 kcal/mol

-73.2 kcal/mol

-20.1 kcal/mol

-23.2 kcal/mol

Figure S6. The most stable Mfold predicted DNA secondary structures and free energy values for DNA fragments analyzed by *in vitro* reduplexing assays: *RET* intron 11 (A), *PTEN* exon 1 (B), *NCOA4* intron 7 (C), and *PTEN* exon 9 (D).

Table S1. Classification of the Chromosome 10 Sequence Based on Fragile Site Location.

Region	**Cytogenetic location**	**Fragile Site Class**	**Mode of Induction**	**Number of segments**	**Number of Sections**
Non-fragile	-	-	-	517301	10334
FRA10G	10q11.2	common	APH	63867	1272
FRA10C	10q21	common	BrdU	118000	2360
FRA10D	10q22.1	common	APH	28668	574
FRA10A	10q23.3, 10q24.2	rare	folic acid	67335	1349
FRA10B	10q25.2	rare	BrdU	20001	401
FRA10E	10q25.2	common	APH	20001	401
FRA10F	10q26.1	common	APH	55665	1113

Table S2. Free Energy of Predicted DNA Secondary Structures for Fragile and Non-Fragile Regions of Chromosome 10.

Region	Chr 10	Non-fragile	FRA10G	FRA10C	FRA10D	FRA10A	FRA10B/E	FRA10F
Number of segments	870837	517301	63867	118000	28668	67335	20001	55665
Mean Free Energy (kcal/mol)	-27.2	-27.5	-28.1	-24.0	-32.0	-26.3	-27.2	-29.4
Standard Deviation	9.3	9.4	10.1	7.6	10.2	8.9	8.4	9.5

Table S3. Percentage of Segments with Free Energy Below -50 kcal/mol.

Region	**Non-fragile**	**FRA10G**	**FRA10C**	**FRA10D**	**FRA10A**	**FRA10B/E**	**FRA10F**
Segments ΔG>-50 kcal/mol*	506900 (98.0%)	61984 (97.1%)	117153 (99.3%)	27440 (95.7%)	66378 (98.6%)	19765 (98.8%)	54297 (97.5%)
Segments ΔG<-50 kcal/mol*	10401 (2.0%)	1883 (2.9%)	847 (0.7%)	1228 (4.3%)	4241 (1.4%)	236 (1.2%)	1368 (2.5%)
P-value**	-	1.77E-54	8.02E-203	2.07E-148	1.21E-113	1.28E-16	1.62E-12

*Total number of segments with a free energy value higher or lower than -50 kcal/mol, with the percentage of the total in parentheses

**P-value calculated by comparing each fragile site to non-fragile DNA using a Chi-square test.

***Fragile sites highlighted in grey have a significantly greater proportion of segments with a free energy value less than -50 kcal/mol compared to non-fragile DNA.

Table S4. Regions on Chromosome 10 with at Least Seven Consecutive Segments Below -43.61 kcal/mol

Segment start	Segment end	Number of Consecutive segments	Nucleotide start	Nucleotide end	Chromosomal Position	Fragile site	Gene	GC content (%)	LINEs (%)	SINEs (%)	LTR elements (%)	DNA transponsons (%)	simple repeats (%)
1,204	1,215	12	180,451	182,400	10p15.3		ZMYND11	74	0	0	0	0	9
2,450	2,459	10	367,351	369,000	10p15.3		DIP2C	68	0	0	0	0	0
3,216	3,222	7	482,251	483,450	10p15.3		DIP2C	60	0	0	0	0	0
4,166	4,172	7	624,751	625,950	10p15.3		DIP2C	39	0	0	0	0	65
4,467	4,473	7	669,901	671,100	10p15.3		DIP2C	62	0	0	0	0	0
4,898	4,910	13	734,551	736,650	10p15.3		DIP2C	71	0	3	0	0	13
5,210	5,219	10	781,351	783,000	10p15.3		none	64	0	0	0	0	0
5,531	5,544	14	829,501	831,750	10p15.3		none	68	0	0	0	0	0
8,340	8,346	7	1,250,851	1,252,050	10p15.3		ADARB2	63	0	0	13	0	0
9,365	9,377	13	1,404,601	1,406,700	10p15.3		ADARB2	69	0	0	16	0	0
10,042	10,048	7	1,506,151	1,507,350	10p15.3		ADARB2	65	46	0	0	0	0
11,384	11,390	7	1,707,451	1,708,650	10p15.3		ADARB2	61	19	0	0	0	0
11,859	11,867	9	1,778,701	1,780,200	10p15.3		ADARB2	64	0	0	0	0	0
20,735	20,742	8	3,110,101	3,111,450	10p15.2		PFKP	70	0	0	0	0	0
32,580	32,586	7	4,886,851	4,888,050	10p15.1		AKR1E2	64	0	0	68	0	0
39,540	39,551	12	5,930,851	5,932,800	10p15.1		ANKRD16, FBXO18	74	0	3	0	0	0
40,127	40,134	8	6,018,901	6,020,250	10p15.1		IL15RA	73	0	0	0	0	0
41,244	41,254	11	6,186,451	6,188,250	10p15.1		PFKFB3	70	0	0	0	0	0
41,629	41,637	9	6,244,201	6,245,700	10p15.1		PFKFB3	71	0	0	0	0	0
41,716	41,723	8	6,257,251	6,258,600	10p15.1		PFKFB3	61	0	0	0	13	12
45,845	45,861	17	6,876,601	6,879,300	10p14		none	22	0	0	0	0	84
49,696	49,702	7	7,454,251	7,455,450	10p14		none	65	0	0	0	0	4
53,943	53,960	18	8,091,301	8,094,150	10p14		none	67	0	0	0	0	0
55,406	55,413	8	8,310,751	8,312,100	10p14		none	9	0	0	0	0	93
73,730	73,738	9	11,059,351	11,060,850	10p14		CUGBP2	73	0	19	0	0	10
77,687	77,693	7	11,652,901	11,654,100	10p14		USP6NL	71	0	0	0	0	8
78,561	78,567	7	11,784,001	11,785,200	10p14		ECHDC3	71	0	18	0	0	10
79,411	79,417	7	11,911,501	11,912,700	10p14		C10orf47	71	0	0	0	0	0
79,573	79,580	8	11,935,801	11,937,150	10p14		none	65	0	0	0	0	0
82,604	82,617	14	12,390,451	12,392,700	10p13		CAMK1D	70	0	0	0	0	1
83,740	83,748	9	12,560,851	12,562,350	10p13		CAMK1D	74	0	0	0	0	0
88,943	88,949	7	13,341,301	13,342,500	10p13		PHYH	67	0	19	0	0	0
89,261	89,272	12	13,389,001	13,390,950	10p13		SEPHS1	70	0	0	0	0	1
90,468	90,475	8	13,570,051	13,571,400	10p13		none	79	0	0	0	0	19
91,324	91,331	8	13,698,451	13,699,800	10p13		FRMD4A	67	0	0	0	0	0
97,638	97,644	7	14,645,551	14,646,750	10p13		FAM107B	75	0	0	0	0	4
99,198	99,206	9	14,879,551	14,881,050	10p13		CDNF,HSPA14	66	0	0	0	0	0
99,469	99,475	7	14,920,201	14,921,400	10p13		SUV39H2	71	0	0	0	0	0
101,399	101,405	7	15,209,701	15,210,900	10p13		NMT2	73	0	0	0	0	12
102,750	102,756	7	15,412,351	15,413,550	10p13		FAM171A1	79	0	0	0	0	20
115,143	115,151	9	17,271,301	17,272,800	10p13		VIM	65	0	0	0	0	0
116,636	116,644	9	17,495,251	17,496,750	10p12.33		ST8SIA6	72	0	0	0	0	6
117,725	117,732	8	17,658,601	17,659,950	10p12.33		PTPLA	68	0	11	0	0	1
117,806	117,813	8	17,670,751	17,672,100	10p12.33		none	69	0	0	0	0	0
122,861	122,869	9	18,429,001	18,430,500	10p12.33		CACNB2	68	0	0	0	0	0
143,085	143,091	7	21,462,601	21,463,800	10p12.31		NEBL	72	0	0	0	0	0
145,231	145,238	8	21,784,501	21,785,850	10p12.31		C10orf114	69	0	0	0	0	0
145,323	145,330	8	21,798,301	21,799,650	10p12.31		none	65	0	0	0	0	0

148,613	148,619	7	22,291,801	22,293,000	10p12.31		DNAJC1	67	0	0	0	0	3
150,729	150,741	13	22,609,201	22,611,300	10p12.2		COMMD3, BMI1	73	0	0	0	0	22
150,827	150,839	13	22,623,901	22,626,000	10p12.2		none	66	0	0	0	0	0
151,504	151,510	7	22,725,451	22,726,650	10p12.2		none	67	0	0	0	0	0
151,766	151,772	7	22,764,751	22,765,950	10p12.2		none	65	0	0	0	0	0
153,349	153,359	11	23,002,201	23,004,000	10p12.2		PIP4K2A	73	0	0	0	0	10
156,415	156,427	13	23,462,101	23,464,200	10p12.2		none	66	0	0	0	0	0
156,537	156,549	13	23,480,401	23,482,500	10p12.2		PTF1A	71	0	0	0	0	2
156,586	156,592	7	23,487,751	23,488,950	10p12.2		none	66	0	0	0	0	0
158,185	158,196	12	23,727,601	23,729,550	10p12.2		OTUD1	75	0	0	0	0	8
166,297	166,310	14	24,944,401	24,946,650	10p12.1		ARHGAP21	74	76	0	0	0	0
166,744	166,754	11	25,011,451	25,013,250	10p12.1		ARHGAP21	72	0	0	0	0	3
169,763	169,771	9	25,464,301	25,465,800	10p12.1		GPR158	65	0	0	0	0	0
171,182	171,189	8	25,677,151	25,678,500	10p12.1		GPR158	59	0	0	0	0	0
183,900	183,908	9	27,584,851	27,586,350	10p12.1		none	69	0	0	0	0	0
186,875	186,886	12	28,031,101	28,033,050	10p12.1		MKX	66	0	0	0	0	0
192,141	192,153	13	28,821,001	28,823,100	10p12.1		WAC	70	0	14	0	0	2
193,106	193,115	10	28,965,751	28,967,400	10p12.1		BAMBI	71	0	0	0	0	2
199,901	199,908	8	29,985,001	29,986,350	10p11.23		SVIL	70	0	0	0	0	0
200,160	200,174	15	30,023,851	30,026,250	10p11.23		SVIL	71	0	0	0	0	0
202,318	202,324	7	30,347,551	30,348,750	10p11.23		KIAA1462	73	0	0	0	0	11
204,817	204,825	9	30,722,401	30,723,900	10p11.23		MAP3K8	67	0	0	0	0	0
210,722	210,729	8	31,608,151	31,609,500	10p11.22		ZEB1	73	0	0	0	0	9
211,004	211,011	8	31,650,451	31,651,800	10p11.22		ZEB1	67	0	6	0	0	0
213,655	213,661	7	32,048,101	32,049,300	10p11.22		none	67	0	0	0	7	0
214,780	214,789	10	32,216,851	32,218,500	10p11.22		ARHGAP12	69	0	0	0	0	10
215,059	215,067	9	32,258,701	32,260,200	10p11.22		none	76	0	7	0	0	2
217,568	217,578	11	32,635,051	32,636,850	10p11.22		EPC1	66	0	0	0	0	0
221,643	221,651	9	33,246,301	33,247,800	10p11.22		ITGB1	74	0	0	0	0	3
224,160	224,166	7	33,623,851	33,625,050	10p11.22		none	70	0	0	0	0	0
234,021	234,032	12	35,103,001	35,104,950	10p11.21		PARD3	74	0	0	0	0	9
237,500	237,510	11	35,624,851	35,626,650	10p11.21		CCNY	73	0	10	0	0	5
239,311	239,318	8	35,896,501	35,897,850	10p11.21		GJD4	66	0	0	0	0	0
239,522	239,546	25	35,928,151	35,932,050	10p11.21		FZD8	70	0	11	0	0	4
249,424	249,431	8	37,413,451	37,414,800	10p11.21		ANKRD30A	61	0	45	0	0	0
253,128	253,139	12	37,969,051	37,971,000	10p11.21		none	65	0	0	0	0	0
253,340	253,348	9	38,000,851	38,002,350	10p11.1		none	61	0	0	0	0	0
258,253	258,261	9	38,737,801	38,739,300	10p11.1		none	68	0	0	0	0	0
288,327	288,341	15	43,248,901	43,251,300	10q11.21	FRA10G	none	68	0	0	0	0	0
289,075	289,081	7	43,361,101	43,362,300	10q11.21	FRA10G	none	64	30	10	0	0	0
289,158	289,164	7	43,373,551	43,374,750	10q11.21	FRA10G	none	62	0	0	0	0	0
289,521	289,528	8	43,428,001	43,429,350	10q11.21	FRA10G	none	66	0	0	0	0	0
289,643	289,650	8	43,446,301	43,447,650	10q11.21	FRA10G	none	63	58	0	0	0	0
289,768	289,778	11	43,465,051	43,466,850	10q11.21	FRA10G	none	59	0	0	0	0	0
289,900	289,906	7	43,484,851	43,486,050	10q11.21	FRA10G	none	61	0	0	0	0	10
289,909	289,916	8	43,486,201	43,487,550	10q11.21	FRA10G	none	63	5	0	0	0	0
289,973	289,981	9	43,495,801	43,497,300	10q11.21	FRA10G	none	61	0	0	0	0	0
290,263	290,271	9	43,539,301	43,540,800	10q11.21	FRA10G	none	62	0	0	0	0	0
290,408	290,414	7	43,561,051	43,562,250	10q11.21	FRA10G	none	57	0	0	0	0	0
290,479	290,489	11	43,571,701	43,573,500	10q11.21	FRA10G	RET	71	0	4	0	0	13
290,511	290,519	9	43,576,501	43,578,000	10q11.21	FRA10G	RET	62	0	0	0	0	3
290,665	290,680	16	43,599,601	43,602,150	10q11.21	FRA10G	RET	63	0	19	0	0	0

290,731	290,742	12	43,609,501	43,611,450	10q11.21	FRA10G	RET	61	0	4	0	0	0
290,757	290,767	11	43,613,401	43,615,200	10q11.21	FRA10G	RET	62	0	0	0	0	0
290,887	290,893	7	43,632,901	43,634,100	10q11.21	FRA10G	CSGALNACT2	67	0	31	0	0	0
291,295	291,311	17	43,694,101	43,696,800	10q11.21	FRA10G	RASGEF1A	61	0	0	0	0	0
291,325	291,331	7	43,698,601	43,699,800	10q11.21	FRA10G	RASGEF1A	67	0	0	0	0	36
291,335	291,341	7	43,700,101	43,701,300	10q11.21	FRA10G	RASGEF1A	63	0	0	0	0	0
291,344	291,350	7	43,701,451	43,702,650	10q11.21	FRA10G	RASGEF1A	64	6	0	0	0	0
291,371	291,379	9	43,705,501	43,707,000	10q11.21	FRA10G	RASGEF1A	60	0	19	0	17	0
291,421	291,427	7	43,713,001	43,714,200	10q11.21	FRA10G	RASGEF1A	62	7	0	0	0	0
291,494	291,506	13	43,723,951	43,726,050	10q11.21	FRA10G	RASGEF1A	69	12	0	0	0	6
291,659	291,666	8	43,748,701	43,750,050	10q11.21	FRA10G	RASGEF1A	62	0	0	39	0	0
291,669	291,677	9	43,750,201	43,751,700	10q11.21	FRA10G	RASGEF1A	63	0	10	0	0	0
291,683	291,690	8	43,752,301	43,753,650	10q11.21	FRA10G	RASGEF1A	60	0	6	0	0	0
291,729	291,735	7	43,759,201	43,760,400	10q11.21	FRA10G	RASGEF1A	63	0	0	0	0	0
291,739	291,751	13	43,760,701	43,762,800	10q11.21	FRA10G	RASGEF1A	70	0	5	0	0	6
292,162	292,169	8	43,824,151	43,825,500	10q11.21	FRA10G	none	65	34	22	0	0	2
292,611	292,618	8	43,891,501	43,892,850	10q11.21	FRA10G	HNRNPF	69	0	0	0	7	3
292,878	292,884	7	43,931,551	43,932,750	10q11.21	FRA10G	none	64	0	19	0	0	0
294,567	294,573	7	44,184,901	44,186,100	10q11.21	FRA10G	none	65	11	0	0	0	0
298,372	298,378	7	44,755,651	44,756,850	10q11.21	FRA10G	none	57	0	0	0	0	0
299,053	299,059	7	44,857,801	44,859,000	10q11.21	FRA10G	none	55	0	0	0	0	2
299,197	299,207	11	44,879,401	44,881,200	10q11.21	FRA10G	CXCL12	68	0	0	0	0	4
302,866	302,874	9	45,429,751	45,431,250	10q11.21	FRA10G	TMEM72	59	0	0	0	0	0
305,611	305,626	16	45,841,501	45,844,050	10q11.21	FRA10G	none	66	0	0	0	0	3
305,791	305,804	14	45,868,501	45,870,750	10q11.21	FRA10G	ALOX5	65	43	5	0	0	2
306,255	306,265	11	45,938,101	45,939,900	10q11.21	FRA10G	ALOX5	69	0	0	0	0	0
309,071	309,077	7	46,360,501	46,361,700	10q11.22	FRA10G	none	65	0	0	0	0	0
311,828	311,834	7	46,774,051	46,775,250	10q11.22	FRA10G	none	70	0	0	0	0	0
313,128	313,140	13	46,969,051	46,971,150	10q11.22	FRA10G	SYT15	67	0	8	0	0	0
313,325	313,335	11	46,998,601	47,000,400	10q11.22	FRA10G	GPRIN2	64	0	7	0	4	0
315,033	315,039	7	47,254,801	47,256,000	10q11.22	FRA10G	none	70	0	0	0	0	0
317,566	317,575	10	47,634,751	47,636,400	10q11.22	FRA10G	none	57	0	0	0	9	0
317,580	317,586	7	47,636,851	47,638,050	10q11.22	FRA10G	none	62	8	0	0	0	0
318,263	318,269	7	47,739,301	47,740,500	10q11.22	FRA10G	none	60	0	10	0	0	0
321,145	321,152	8	48,171,601	48,172,950	10q11.22	FRA10G	none	61	0	0	0	0	0
321,727	321,733	7	48,258,901	48,260,100	10q11.22	FRA10G	ANXA8	58	0	7	0	0	0
321,847	321,853	7	48,276,901	48,278,100	10q11.22	FRA10G	none	61	0	0	0	0	0
322,193	322,200	8	48,328,801	48,330,150	10q11.22	FRA10G	none	58	31	0	0	0	0
322,585	322,595	11	48,387,601	48,389,400	10q11.22	FRA10G	RBP3	63	0	0	0	3	0
322,731	322,744	14	48,409,501	48,411,750	10q11.22	FRA10G	none	57	0	0	0	0	0
322,921	322,928	8	48,438,001	48,439,350	10q11.22	FRA10G	GDF10	70	0	0	0	27	3
324,750	324,758	9	48,712,351	48,713,850	10q11.22	FRA10G	none	61	0	10	0	8	0
330,095	330,102	8	49,514,101	49,515,450	10q11.22	FRA10G	none	70	0	0	0	0	0
331,049	331,062	14	49,657,201	49,659,450	10q11.22	FRA10G	ARHFAP22	65	0	0	0	0	0
331,111	331,117	7	49,666,501	49,667,700	10q11.22	FRA10G	ARHFAP22	61	0	0	0	3	0
331,541	331,550	10	49,731,001	49,732,650	10q11.22	FRA10G	ARHFAP22	68	17	0	0	7	0
332,422	332,429	8	49,863,151	49,864,500	10q11.22	FRA10G	none	69	0	0	0	0	5
332,557	332,566	10	49,883,401	49,885,050	10q11.22	FRA10G	none	20	0	0	0	0	98
332,657	332,663	7	49,898,401	49,899,600	10q11.22	FRA10G	WDFY4	59	0	0	71	0	0
337,074	337,080	7	50,560,951	50,562,150	10q11.23	FRA10G	none	55	0	0	4	0	0
337,122	337,128	7	50,568,151	50,569,350	10q11.23	FRA10G	none	59	0	14	0	0	0
337,351	337,360	10	50,602,501	50,604,150	10q11.23	FRA10G	none	67	0	0	0	0	0

337,368	337,375	8	50,605,051	50,606,400	10q11.23	FRA10G	none	64	0	0	0	0	0
337,502	337,508	7	50,625,151	50,626,350	10q11.23	FRA10G	none	64	0	0	0	0	0
338,783	338,801	19	50,817,301	50,820,300	10q11.23	FRA10G	CHAT, SLC18A3	69	0	0	0	0	0
339,024	339,032	9	50,853,451	50,854,950	10q11.23	FRA10G	CHAT	58	0	0	33	0	0
339,840	339,847	8	50,975,851	50,977,200	10q11.23	FRA10G	none	67	0	0	0	0	0
343,356	343,363	8	51,503,251	51,504,600	10q11.23	FRA10G	none	61	22	0	0	0	0
349,217	349,233	17	52,382,401	52,385,100	10q11.23	FRA10G	SGMS1	68	0	0	0	0	0
349,611	349,618	8	52,441,501	52,442,850	10q11.23	FRA10G	none	62	0	0	0	0	0
358,823	358,830	8	53,823,301	53,824,650	10q21.1	FRA10C	PRKG1	59	0	0	99	0	0
360,708	360,716	9	54,106,051	54,107,550	10q21.1	FRA10C	none	63	0	19	0	0	0
396,351	396,358	8	59,452,501	59,453,850	10q21.1	FRA10C	none	26	0	0	0	0	78
400,179	400,185	7	60,026,701	60,027,900	10q21.1	FRA10C	IPMK	67	0	0	0	0	23
400,630	400,636	7	60,094,351	60,095,550	10q21.1	FRA10C	UBE2D1	63	0	3	0	0	0
406,239	406,246	8	60,935,701	60,937,050	10q21.1	FRA10C	PHYHIPL	67	0	0	0	0	0
411,103	411,110	8	61,665,301	61,666,650	10q21.2	FRA10C	CCDC6	69	0	0	0	0	3
418,021	418,031	11	62,703,001	62,704,800	10q21.2	FRA10C	RHOBTB1	65	0	0	0	0	0
430,428	430,437	10	64,564,051	64,565,700	10q21.3	FRA10C	ADO	67	0	0	0	0	0
431,382	431,388	7	64,707,151	64,708,350	10q21.3	FRA10C	none	76	0	0	0	0	0
434,832	434,839	8	65,224,651	65,226,000	10q21.3	FRA10C	JMJD1C	67	0	0	0	0	2
435,205	435,211	7	65,280,601	65,281,800	10q21.3	FRA10C	REEP3	72	0	0	0	0	3
463,239	463,245	7	69,485,701	69,486,900	10q21.3	FRA10C	none	8	0	0	0	0	71
468,701	468,707	7	70,305,001	70,306,200	10q21.3	FRA10C	none	49	0	79	0	0	32
470,579	470,587	9	70,586,701	70,588,200	10q21.3	FRA10C	STOX1	74	0	16	0	0	0
472,556	472,562	7	70,883,251	70,884,450	10q22.1	FRA10D	VPS26A	68	0	0	0	0	0
473,851	473,861	11	71,077,501	71,079,300	10q22.1	FRA10D	HK1	68	0	8	0	0	2
475,545	475,555	11	71,331,601	71,333,400	10q22.1	FRA10D	NEUROG3	65	0	0	0	0	0
475,964	475,973	10	71,394,451	71,396,100	10q22.1	FRA10D	none	60	0	8	0	0	0
476,024	476,031	8	71,403,451	71,404,800	10q22.1	FRA10D	none	57	0	14	0	0	0
476,078	476,085	8	71,411,551	71,412,900	10q22.1	FRA10D	none	61	0	0	32	0	0
477,601	477,607	7	71,640,001	71,641,200	10q22.1	FRA10D	COL13A1	61	0	11	0	0	0
478,348	478,355	8	71,752,051	71,753,400	10q22.1	FRA10D	none	67	0	0	0	0	0
478,748	478,759	12	71,812,051	71,814,000	10q22.1	FRA10D	H2AFY2	65	0	0	0	0	3
479,365	479,375	11	71,904,601	71,906,400	10q22.1	FRA10D	TYSND1	67	0	0	0	0	4
479,989	480,002	14	71,998,201	72,000,450	10q22.1	FRA10D	none	67	0	0	0	0	0
480,097	480,103	7	72,014,401	72,015,600	10q22.1	FRA10D	NPFFR1	67	0	15	0	0	0
480,556	480,562	7	72,083,251	72,084,450	10q22.1	FRA10D	LRRC20	63	0	0	0	0	0
480,941	480,949	9	72,141,001	72,142,500	10q22.1	FRA10D	LRRC20	64	0	7	20	0	0
481,583	481,593	11	72,237,301	72,239,100	10q22.1	FRA10D	KIAA1274	68	0	4	0	0	0
481,979	481,986	8	72,296,701	72,298,050	10q22.1	FRA10D	KIAA1274	57	0	34	0	0	0
482,878	482,884	7	72,431,551	72,432,750	10q22.1	FRA10D	ADAMTS14	69	0	8	0	0	9
482,976	482,989	14	72,446,251	72,448,500	10q22.1	FRA10D	ADAMTS14	72	0	0	0	0	0
483,410	483,417	8	72,511,351	72,512,700	10q22.1	FRA10D	ADAMTS14	62	0	0	0	0	0
483,472	483,479	8	72,520,651	72,522,000	10q22.1	FRA10D	ADAMTS14	60	0	0	0	0	0
484,316	484,322	7	72,647,251	72,648,450	10q22.1	FRA10D	PCBD1	68	0	0	0	0	2
484,626	484,633	8	72,693,751	72,695,100	10q22.1	FRA10D	none	59	27	8	0	8	0
485,096	485,103	8	72,764,251	72,765,600	10q22.1	FRA10D	none	59	0	16	0	0	0
486,480	486,487	8	72,971,851	72,973,200	10q22.1	FRA10D	UNC5B	68	0	0	0	0	2
486,770	486,776	7	73,015,351	73,016,550	10q22.1	FRA10D	UNC5B	55	0	15	0	0	0
486,962	486,968	7	73,044,151	73,045,350	10q22.1	FRA10D	UNC5B	61	62	9	0	0	0
487,706	487,718	13	73,155,751	73,157,850	10q22.1	FRA10D	CDH23	70	12	0	0	0	8
488,051	488,057	7	73,207,501	73,208,700	10q22.1	FRA10D	CDH23	57	0	7	0	0	0
488,936	488,942	7	73,340,251	73,341,450	10q22.1	FRA10D	CDH23	54	0	0	0	14	0

489,815	489,821	7	73,472,101	73,473,300	10q22.1	FRA10D	CDH23, C10orf105	60	0	11	38	0	0
490,216	490,222	7	73,532,251	73,533,450	10q22.1	FRA10D	CDH23, C10orf54	65	0	6	0	0	0
490,324	490,336	13	73,548,451	73,550,550	10q22.1	FRA10D	CDH23	60	3	15	0	0	0
490,475	490,482	8	73,571,101	73,572,450	10q22.1	FRA10D	CDH23	64	0	0	0	0	0
490,859	490,866	8	73,628,701	73,630,050	10q22.1	FRA10D	none	68	0	0	0	0	0
491,488	491,497	10	73,723,051	73,724,700	10q22.1	FRA10D	CHST3	68	0	0	0	0	2
491,780	491,788	9	73,766,851	73,768,350	10q22.1	FRA10D	CHST3	67	0	0	0	0	0
492,267	492,274	8	73,839,901	73,841,250	10q22.1	FRA10D	SPOCK2	59	0	3	0	17	0
492,311	492,321	11	73,846,501	73,848,300	10q22.1	FRA10D	SPOCK2	68	0	0	0	0	0
493,551	493,557	7	74,032,501	74,033,700	10q22.1	FRA10D	DDIT4	63	0	0	0	0	0
493,897	493,906	10	74,084,401	74,086,050	10q22.1	FRA10D	none	64	0	20	0	0	0
493,919	493,927	9	74,087,701	74,089,200	10q22.1	FRA10D	none	61	0	0	94	0	0
493,963	493,969	7	74,094,301	74,095,500	10q22.1	FRA10D	DNAJB12	62	0	0	0	0	0
499,038	499,045	8	74,855,551	74,856,900	10q22.1	FRA10D	P4HA1	61	0	0	0	0	0
503,282	503,288	7	75,492,151	75,493,350	10q22.2		none	71	0	0	0	0	0
503,545	503,552	8	75,531,601	75,532,950	10q22.2		SEC24C, FUT11	65	0	0	0	0	0
503,804	503,811	8	75,570,451	75,571,800	10q22.2		NDST2	72	0	17	0	0	0
503,992	503,998	7	75,598,651	75,599,850	10q22.2		CAMK2G	65	0	10	0	14	0
504,222	504,231	10	75,633,151	75,634,800	10q22.2		CAMK2G	74	0	0	0	0	4
510,563	510,572	10	76,584,301	76,585,950	10q22.2		none	71	0	0	0	0	9
513,131	513,139	9	76,969,501	76,971,000	10q22.2		VDAC2	66	0	0	12	0	0
513,292	513,305	14	76,993,651	76,995,900	10q22.2		COMTD1	70	0	0	0	0	0
513,951	513,959	9	77,092,501	77,094,000	10q22.2		none	71	0	0	0	0	0
514,367	514,379	13	77,154,901	77,157,000	10q22.2		none	68	0	0	0	0	1
514,390	514,399	10	77,158,351	77,160,000	10q22.2		ZNF503	70	0	0	0	0	2
514,447	514,453	7	77,166,901	77,168,100	10q22.2		none	62	0	0	0	0	0
529,315	529,323	9	79,397,101	79,398,600	10q22.3		KCNMA1	74	0	0	0	0	9
531,237	531,246	10	79,685,401	79,687,050	10q22.3		DLG5	74	0	0	0	0	3
533,969	533,975	7	80,095,201	80,096,400	10q22.3		none	57	0	10	0	0	0
534,854	534,860	7	80,227,951	80,229,150	10q22.3		none	67	0	0	26	0	0
537,820	537,826	7	80,672,851	80,674,050	10q22.3		none	61	0	0	0	15	0
538,220	538,226	7	80,732,851	80,734,050	10q22.3		none	66	0	0	0	0	3
538,856	538,874	19	80,828,251	80,831,250	10q22.3		ZMIZ1	68	0	0	0	0	1
539,313	539,320	8	80,896,801	80,898,150	10q22.3		ZMIZ1	61	0	0	0	24	0
539,463	539,472	10	80,919,301	80,920,950	10q22.3		ZMIZ1	58	0	50	0	0	0
539,594	539,600	7	80,938,951	80,940,150	10q22.3		ZMIZ1	60	59	9	0	0	0
540,016	540,024	9	81,002,251	81,003,750	10q22.3		ZMIZ1	74	0	0	0	0	2
540,229	540,235	7	81,034,201	81,035,400	10q22.3		ZMIZ1	61	0	0	0	7	0
540,713	540,719	7	81,106,801	81,108,000	10q22.3		PPIF	66	0	13	0	7	0
541,001	541,007	7	81,150,001	81,151,200	10q22.3		ZCCHC24	59	0	25	0	0	0
541,140	541,148	9	81,170,851	81,172,350	10q22.3		ZCCHC24	59	0	7	0	0	0
541,363	541,370	8	81,204,301	81,205,650	10q22.3		ZCCHC24	72	0	0	0	0	7
541,775	541,782	8	81,266,101	81,267,450	10q22.3		none	59	0	0	0	0	0
542,955	542,961	7	81,443,101	81,444,300	10q22.3		none	60	0	0	0	0	0
543,123	543,130	8	81,468,301	81,469,650	10q22.3		none	63	0	0	0	0	0
543,903	543,912	10	81,585,301	81,586,950	10q22.3		none	71	0	0	0	0	2
544,043	544,051	9	81,606,301	81,607,800	10q22.3		FAM22E	62	0	0	24	0	0
544,942	544,948	7	81,741,151	81,742,350	10q22.3		none	70	6	0	0	0	0
548,090	548,097	8	82,213,351	82,214,700	10q23.1		TSPAN14	73	0	0	0	0	11
548,625	548,631	7	82,293,601	82,294,800	10q23.1		none	76	0	0	0	0	0
552,280	552,288	9	82,841,851	82,843,350	10q23.1		none	57	100	0	0	0	0
555,532	555,541	10	83,329,651	83,331,300	10q23.1		none	61	0	0	82	0	0

557,560	557,570	11	83,633,851	83,635,650	10q23.1		NRG3	74	0	0	27	0	6
573,027	573,036	10	85,953,901	85,955,550	10q23.1		CDHR1	66	0	0	0	0	0
574,046	574,052	7	86,106,751	86,107,950	10q23.1		FAM190B	65	0	0	0	0	0
575,335	575,341	7	86,300,101	86,301,300	10q23.1		none	64	0	0	0	0	0
586,540	586,548	9	87,980,851	87,982,350	10q23.2		GRID1	59	0	9	0	0	3
587,420	587,426	7	88,112,851	88,114,050	10q23.2		GRID1	61	11	0	0	0	0
587,504	587,516	13	88,125,451	88,127,550	10q23.2		GRID1	73	0	0	0	0	9
587,730	587,742	13	88,159,351	88,161,450	10q23.2		none	67	12	0	0	0	0
589,393	589,400	8	88,408,801	88,410,150	10q23.2		none	59	4	0	13	0	2
589,528	589,535	8	88,429,051	88,430,400	10q23.2		LDB3	60	0	0	11	0	0
589,595	589,610	16	88,439,101	88,441,650	10q23.2		LDB3	63	5	0	0	0	0
589,626	589,633	8	88,443,751	88,445,100	10q23.2		LDB3	60	0	17	0	0	0
589,734	589,740	7	88,459,951	88,461,150	10q23.2		LDB3	60	0	0	0	0	0
589,806	589,812	7	88,470,751	88,471,950	10q23.2		LDB3	70	0	0	0	0	0
590,103	590,113	11	88,515,301	88,517,100	10q23.2		BMPR1A	70	0	0	0	0	0
591,430	591,438	9	88,714,351	88,715,850	10q23.2		MMRN2	60	0	0	0	0	0
591,447	591,459	13	88,716,901	88,719,000	10q23.2		MMRN2, SNCG	62	0	4	0	0	1
591,537	591,547	11	88,730,401	88,732,200	10q23.2		AGAP11, C10orf116	65	0	0	0	0	0
592,358	592,368	11	88,853,551	88,855,350	10q23.2		GLUD1, FAM35A	70	0	8	0	0	2
593,155	593,162	8	88,973,101	88,974,450	10q23.2		none	59	0	0	0	0	0
593,271	593,278	8	88,990,501	88,991,850	10q23.2		FAM22A	63	0	0	0	0	0
594,010	594,019	10	89,101,351	89,103,000	10q23.2		none	71	0	0	0	0	7
594,153	594,160	8	89,122,801	89,124,150	10q23.2		FAM22D	63	0	0	0	0	0
597,486	597,493	8	89,622,751	89,624,100	10q23.31	FRA10A	KILLIN,PTEN	70	0	0	0	0	4
611,407	611,414	8	91,710,901	91,712,250	10q23.31	FRA10A	none	56	0	0	0	0	0
616,864	616,871	8	92,529,451	92,530,800	10q23.31	FRA10A	HTR7	60	0	0	85	0	0
619,481	619,492	12	92,922,001	92,923,950	10q23.32	FRA10A	none	71	0	0	0	0	5
620,551	620,558	8	93,082,501	93,083,850	10q23.32	FRA10A	none	67	0	0	0	0	0
621,129	621,136	8	93,169,201	93,170,550	10q23.32	FRA10A	HECTD2	70	0	0	0	0	0
627,564	627,577	14	94,134,451	94,136,700	10q23.33	FRA10A	none	78	0	0	0	0	0
628,888	628,895	8	94,333,051	94,334,400	10q23.33	FRA10A	IDE	69	0	12	0	0	0
629,559	629,570	12	94,433,701	94,435,650	10q23.33	FRA10A	none	74	0	0	0	0	0
629,658	629,669	12	94,448,551	94,450,500	10q23.33	FRA10A	HHEX	71	0	0	0	0	0
630,719	630,725	7	94,607,701	94,608,900	10q23.33	FRA10A	EXOC6	69	0	0	0	0	0
632,148	632,154	7	94,822,051	94,823,250	10q23.33	FRA10A	CYP25C1	68	6	0	0	0	0
632,186	632,192	7	94,827,751	94,828,950	10q23.33	FRA10A	CYP25C1	61	0	16	0	0	0
632,210	632,216	7	94,831,351	94,832,550	10q23.33	FRA10A	none	59	0	0	0	0	0
632,220	632,227	8	94,832,851	94,834,200	10q23.33	FRA10A	CYP26A1	65	0	5	0	0	0
635,735	635,741	7	95,360,101	95,361,300	10q23.33	FRA10A	RBP4	70	0	0	0	0	3
641,080	641,088	9	96,161,851	96,163,350	10q23.33	FRA10A	TBC1D12	68	0	0	0	0	3
650,460	650,467	8	97,568,851	97,570,200	10q24.1		ENTPD1	71	0	0	0	0	0
652,019	652,027	9	97,802,701	97,804,200	10q24.1		CCNJ	67	0	0	0	0	0
655,152	655,159	8	98,272,651	98,274,000	10q24.1		TLL2	67	0	0	0	0	5
655,640	655,646	7	98,345,851	98,347,050	10q24.1		TM9SF3	71	0	0	0	0	8
657,277	657,287	11	98,591,401	98,593,200	10q24.1		LCOR	72	0	0	0	0	0
658,389	658,395	7	98,758,201	98,759,400	10q24.1		SLIT1	59	0	0	0	0	0
658,404	658,413	10	98,760,451	98,762,100	10q24.1		SLIT1	62	13	0	0	0	0
659,489	659,498	10	98,923,201	98,924,850	10q24.1		SLIT1	60	0	0	22	0	0
659,632	659,639	8	98,944,651	98,946,000	10q24.1		SLIT1	69	0	0	0	0	3
660,235	660,245	11	99,035,101	99,036,900	10q24.1		ARHGAP19	79	0	0	0	0	0
660,525	660,533	9	99,078,601	99,080,100	10q24.1		FRAT1	71	0	0	0	0	3
660,623	660,632	10	99,093,301	99,094,950	10q24.1		FRAT2	72	0	0	0	0	0

661,719	661,729	11	99,257,701	99,259,500	10q24.1		MMS19, UBTD1	70	0	9	0	0	0
661,918	661,927	10	99,287,551	99,289,200	10q24.1		UBTD1	73	0	0	0	0	0
662,199	662,205	7	99,329,701	99,330,900	10q24.2	FRA10A	UBTD1	62	0	0	13	0	0
662,975	662,982	8	99,446,101	99,447,450	10q24.2	FRA10A	AVPI1	63	0	15	0	0	0
663,156	663,163	8	99,473,251	99,474,600	10q24.2	FRA10A	MARVELD1	72	0	0	0	0	6
663,539	663,545	7	99,530,701	99,531,900	10q24.2	FRA10A	SFRP5	72	0	0	0	0	2
663,874	663,880	7	99,580,951	99,582,150	10q24.2	FRA10A	none	56	12	0	0	0	0
665,058	665,064	7	99,758,551	99,759,750	10q24.2	FRA10A	CRTAC1	56	61	0	0	0	0
665,260	665,273	14	99,788,851	99,791,100	10q24.2	FRA10A	CRTAC1	69	0	0	75	0	8
667,845	667,852	8	100,176,601	100,177,950	10q24.2	FRA10A	HPS1	60	0	11	0	7	0
673,925	673,935	11	101,088,601	101,090,400	10q24.2	FRA10A	CNNM1	67	12	0	0	0	2
675,297	675,304	8	101,294,401	101,295,750	10q24.2	FRA10A	NKX2-3	66	0	0	0	0	4
677,318	677,334	17	101,597,551	101,600,250	10q24.2	FRA10A	ABCC2	76	0	0	0	0	0
677,673	677,679	7	101,650,801	101,652,000	10q24.2	FRA10A	DNMBP	67	16	0	0	0	0
679,013	679,024	12	101,851,801	101,853,750	10q24.2	FRA10A	none	73	0	7	0	0	6
680,246	680,253	8	102,036,751	102,038,100	10q24.31		BLOC1S2	78	0	0	0	0	0
680,707	680,714	8	102,105,901	102,107,250	10q24.31		SCD	64	0	19	0	0	0
682,772	682,778	7	102,415,651	102,416,850	10q24.31		none	66	0	0	0	0	3
683,396	683,404	9	102,509,251	102,510,750	10q24.31		PAX2	63	0	0	0	0	0
683,906	683,913	8	102,585,751	102,587,100	10q24.31		none	66	0	0	0	0	0
684,859	684,865	7	102,728,701	102,729,900	10q24.31		FAM178A	67	0	0	0	0	0
685,044	685,050	7	102,756,451	102,757,650	10q24.31		LZTS2	68	0	0	0	0	2
685,059	685,067	9	102,758,701	102,760,200	10q24.31		LZTS2	71	0	0	0	0	3
685,075	685,084	10	102,761,101	102,762,750	10q24.31		LZTS2	59	0	0	0	0	0
685,186	685,193	8	102,777,751	102,779,100	10q24.31		PDZD7	64	0	10	0	0	0
685,685	685,691	7	102,852,601	102,853,800	10q24.31		TLX1NB	62	22	0	0	0	8
686,036	686,043	8	102,905,251	102,906,600	10q24.31		none	63	0	0	0	0	0
688,868	688,874	7	103,330,051	103,331,250	10q24.32		none	66	0	0	0	0	0
690,227	690,242	16	103,533,901	103,536,450	10q24.32		FGF8	69	0	6	0	0	3
690,260	690,272	13	103,538,851	103,540,950	10q24.32		C10orf76	64	0	0	0	0	1
691,967	691,973	7	103,794,901	103,796,100	10q24.32		none	67	0	24	0	0	0
692,165	692,180	16	103,824,601	103,827,150	10q24.32		HPS6	66	5	5	0	0	0
692,492	692,498	7	103,873,651	103,874,850	10q24.32		LDB1	67	0	0	0	0	0
692,531	692,537	7	103,879,501	103,880,700	10q24.32		LDB1	70	0	0	0	0	4
692,985	692,991	7	103,947,601	103,948,800	10q24.32		none	56	0	0	87	0	0
693,265	693,272	8	103,989,601	103,990,950	10q24.32		PITX3	68	0	7	77	0	2
694,393	694,401	9	104,158,801	104,160,300	10q24.32		NFKB2	64	0	31	0	0	0
694,415	694,421	7	104,162,101	104,163,300	10q24.32		NFKB2,PSD	64	0	0	0	0	0
694,480	694,486	7	104,171,851	104,173,050	10q24.32		PSD	58	10	0	0	0	0
694,537	694,546	10	104,180,401	104,182,050	10q24.32		FBXL15	66	3	0	0	0	0
694,733	694,740	8	104,209,801	104,211,150	10q24.32		none	69	0	0	0	0	0
696,019	696,032	14	104,402,701	104,404,950	10q24.32		TRIM8	69	0	0	0	0	0
696,133	696,142	10	104,419,801	104,421,450	10q24.32		none	61	0	18	0	0	0
696,492	696,500	9	104,473,651	104,475,150	10q24.32		ARL3,SFXN2	66	0	21	0	0	2
697,848	697,862	15	104,677,051	104,679,450	10q24.32		CNNM2	65	0	0	0	0	2
699,257	699,264	8	104,888,401	104,889,750	10q24.32		NT5C2	78	0	0	0	0	0
699,681	699,687	7	104,952,001	104,953,200	10q24.33		NT5C2	68	0	0	0	0	5
700,242	700,253	12	105,036,151	105,038,100	10q24.33		INA	68	0	0	0	0	0
700,733	700,739	7	105,109,801	105,111,000	10q24.33		PCGF6	64	0	48	0	0	0
701,410	701,416	7	105,211,351	105,212,550	10q24.33		CALHM2	64	0	0	0	0	6
701,447	701,458	12	105,216,901	105,218,850	10q24.33		CALHM1	63	0	0	0	5	0
701,687	701,694	8	105,252,901	105,254,250	10q24.33		NEURL	70	0	0	0	0	2

702,343	702,349	7	105,351,301	105,352,500	10q24.33		NEURL	60	0	10	0	0	0
702,795	702,802	8	105,419,101	105,420,450	10q24.33		SH3PXD2A	61	0	0	0	0	0
702,806	702,812	7	105,420,751	105,421,950	10q24.33		SH3PXD2A	68	0	0	0	0	0
702,849	702,858	10	105,427,201	105,428,850	10q24.33		SH3PXD2A	61	0	7	0	0	0
704,098	704,104	7	105,614,551	105,615,750	10q24.33		SH3PXD2A	74	0	0	0	0	0
705,292	705,298	7	105,793,651	105,794,850	10q24.33		COL17A1	61	0	0	0	0	0
707,162	707,170	9	106,074,151	106,075,650	10q25.1		ITPRIP	62	0	0	0	0	0
709,330	709,336	7	106,399,351	106,400,550	10q25.1		SORCS3	65	0	0	0	0	0
709,340	709,348	9	106,400,851	106,402,350	10q25.1		SORC53	70	0	0	0	0	2
735,507	735,513	7	110,325,901	110,327,100	10q25.1		none	61	53	0	6	0	0
745,112	745,121	10	111,766,651	111,768,300	10q25.1		ADD3	67	0	0	35	0	0
748,381	748,390	10	112,257,001	112,258,650	10q25.2	RA10B/FRA10	DUSP5	71	9	0	0	0	0
752,250	752,261	12	112,837,351	112,839,300	10q25.2	RA10B/FRA10	ADRA2A	67	0	0	0	0	0
756,488	756,496	9	113,473,051	113,474,550	10q25.2	RA10B/FRA10	none	60	0	0	0	0	0
772,019	772,035	17	115,802,701	115,805,400	10q25.3		ADRB1	71	0	0	77	0	3
774,422	774,432	11	116,163,151	116,164,950	10q25.3		AFAP1L2	68	0	0	0	0	0
776,850	776,856	7	116,527,351	116,528,550	10q25.3		none	69	0	0	0	0	0
777,208	777,214	7	116,581,051	116,582,250	10q25.3		FAM160B1	70	0	0	0	0	0
779,015	779,026	12	116,852,101	116,854,050	10q25.3		ATRNL1	71	0	0	0	0	0
786,867	786,873	7	118,029,901	118,031,100	10q25.3		GFRA1	67	0	0	0	0	0
786,876	786,883	8	118,031,251	118,032,600	10q25.3		GFRA1	67	0	0	0	0	0
790,008	790,017	10	118,501,051	118,502,700	10q25.3		HSPA12A	75	0	0	0	0	2
791,761	791,767	7	118,764,001	118,765,200	10q25.3		KIAA1598	65	0	0	0	0	0
792,661	792,668	8	118,899,001	118,900,350	10q25.3		none	68	0	0	0	0	0
792,815	792,822	8	118,922,101	118,923,450	10q25.3		none	67	0	0	0	0	0
793,173	793,179	7	118,975,801	118,977,000	10q25.3		none	66	0	11	0	0	0
793,331	793,341	11	118,999,501	119,001,300	10q25.3		SLC18A2	68	0	0	0	0	0
794,225	794,236	12	119,133,601	119,135,550	10q26.11	FRA10F	PDZD8	69	0	0	0	0	0
795,293	795,301	9	119,293,801	119,295,300	10q26.11	FRA10F	none	67	0	0	0	0	0
798,704	798,710	7	119,805,451	119,806,650	10q26.11	FRA10F	RAB11FIP2	68	0	0	0	0	0
802,357	802,363	7	120,353,401	120,354,600	10q26.11	FRA10F	PRLHR	64	0	0	0	0	0
803,425	803,432	8	120,513,601	120,514,950	10q26.11	FRA10F	C10orf46	67	0	0	0	0	0
804,009	804,019	11	120,601,201	120,603,000	10q26.11	FRA10F	none	57	0	0	0	18	0
805,257	805,267	11	120,788,401	120,790,200	10q26.11	FRA10F	NANOS1	75	0	0	0	0	8
806,441	806,450	10	120,966,001	120,967,650	10q26.11	FRA10F	GRK5	71	0	0	0	0	4
808,019	808,029	11	121,202,701	121,204,500	10q26.11	FRA10F	GRK5	60	14	0	0	0	0
808,674	808,686	13	121,300,951	121,303,050	10q26.11	FRA10F	RGS10	68	0	9	0	0	3
809,035	809,042	8	121,355,101	121,356,450	10q26.11	FRA10F	TIAL1	62	0	0	0	0	2
809,403	809,411	9	121,410,301	121,411,800	10q26.11	FRA10F	BAG3	70	0	0	0	0	0
809,872	809,879	8	121,480,651	121,482,000	10q26.11	FRA10F	none	67	0	22	0	0	2
810,360	810,368	9	121,553,851	121,555,350	10q26.11	FRA10F	INPP5F	71	0	0	0	0	0
810,877	810,883	7	121,631,401	121,632,600	10q26.11	FRA10F	MCMBP	71	0	0	0	0	6
814,772	814,783	12	122,215,651	122,217,600	10q26.12	FRA10F	PPAPDC1A	67	0	0	0	0	0
818,056	818,062	7	122,708,251	122,709,450	10q26.12	FRA10F	none	59	84	10	0	0	0
822,377	822,387	11	123,356,401	123,358,200	10q26.13	FRA10F	FGFR2	69	0	0	0	0	2
824,580	824,587	8	123,686,851	123,688,200	10q26.13	FRA10F	ATE1	69	0	5	0	0	0
824,892	824,899	8	123,733,651	123,735,000	10q26.13	FRA10F	NSMCE4A	66	0	0	0	11	0
825,641	825,648	8	123,846,001	123,847,350	10q26.13	FRA10F	TACC2	61	0	0	0	0	0
825,813	825,821	9	123,871,801	123,873,300	10q26.13	FRA10F	TACC2	65	0	0	0	0	0
826,149	826,158	10	123,922,201	123,923,850	10q26.13	FRA10F	TACC2	66	0	0	0	0	0
826,397	826,406	10	123,959,401	123,961,050	10q26.13	FRA10F	TACC2	61	0	0	22	0	0
827,559	827,565	7	124,133,701	124,134,900	10q26.13	FRA10F	PLEKHA1	69	0	0	0	0	0

828,133	828,145	13	124,219,801	124,221,900	10q26.13	FRA10F	HTRA1	68	0	0	0	0	1
832,630	832,638	9	124,894,351	124,895,850	10q26.13	FRA10F	HXM3	69	0	0	0	0	2
832,641	832,648	8	124,896,001	124,897,350	10q26.13	FRA10F	HXM3	68	0	0	0	0	0
834,719	834,725	7	125,207,701	125,208,900	10q26.13	FRA10F	none	51	0	85	0	0	2
836,170	836,176	7	125,425,351	125,426,550	10q26.13	FRA10F	GPR26	71	0	0	0	0	0
838,340	838,346	7	125,750,851	125,752,050	10q26.13	FRA10F	none	64	0	26	0	0	15
838,626	838,632	7	125,793,751	125,794,950	10q26.13	FRA10F	CHST15	63	0	0	0	0	0
839,011	839,021	11	125,851,501	125,853,300	10q26.13	FRA10F	CHST15	72	0	0	0	0	2
840,514	840,520	7	126,076,951	126,078,150	10q26.13	FRA10F	none	65	0	0	12	0	0
840,712	840,718	7	126,106,651	126,107,850	10q26.13	FRA10F	OAT	69	0	0	0	0	0
840,904	840,910	7	126,135,451	126,136,650	10q26.13	FRA10F	NKX1-2	68	0	0	0	0	6
841,507	841,513	7	126,225,901	126,227,100	10q26.13	FRA10F	LHPP	62	0	5	0	0	0
841,533	841,541	9	126,229,801	126,231,300	10q26.13	FRA10F	LHPP	60	0	11	0	0	0
841,594	841,603	10	126,238,951	126,240,600	10q26.13	FRA10F	LHPP	66	0	8	0	0	0
841,749	841,755	7	126,262,201	126,263,400	10q26.13	FRA10F	LHPP	61	0	4	0	0	0
841,906	841,912	7	126,285,751	126,286,950	10q26.13	FRA10F	LHPP	61	22	7	45	0	0
841,943	841,959	17	126,291,301	126,294,000	10q26.13	FRA10F	LHPP	64	4	0	0	0	0
842,029	842,036	8	126,304,201	126,305,550	10q26.13	FRA10F	none	61	29	35	0	0	0
842,093	842,099	7	126,313,801	126,315,000	10q26.13	FRA10F	FAM53B	62	0	0	0	0	0
842,264	842,270	7	126,339,451	126,340,650	10q26.13	FRA10F	FAM53B	60	10	0	27	0	0
842,874	842,887	14	126,430,951	126,433,200	10q26.13	FRA10F	FAM53B	66	0	0	0	0	2
844,034	844,040	7	126,604,951	126,606,150	10q26.13	FRA10F	none	72	0	0	0	0	3
844,581	844,587	7	126,687,001	126,688,200	10q26.13	FRA10F	CTBP2	59	0	0	0	0	0
844,601	844,616	16	126,690,001	126,692,550	10q26.13	FRA10F	CTBP2	63	0	0	0	0	0
844,764	844,773	10	126,714,451	126,716,100	10q26.13	FRA10F	CTBP2	65	0	0	0	0	0
845,648	845,659	12	126,847,051	126,849,000	10q26.13	FRA10F	CTBP2	72	0	0	0	0	5
845,663	845,672	10	126,849,301	126,850,950	10q26.13	FRA10F	C10orf137	68	0	0	0	0	0
849,383	849,390	8	127,407,301	127,408,650	10q26.13	FRA10F	none	61	0	0	0	30	0
849,746	849,752	7	127,461,751	127,462,950	10q26.13	FRA10F	MMP21	69	0	0	0	0	0
849,756	849,762	7	127,463,251	127,464,450	10q26.13	FRA10F	MMP21	64	0	0	0	0	0
850,562	850,568	7	127,584,151	127,585,350	10q26.2		FANK1	70	0	0	0	0	4
853,840	853,848	9	128,075,851	128,077,350	10q26.2		ADAM12	66	0	0	0	0	0
857,289	857,299	11	128,593,201	128,595,000	10q26.2		none	71	4	0	0	0	0
859,959	859,968	10	128,993,701	128,995,350	10q26.2		DOCK1,FAM196A	72	0	0	0	0	5
863,562	863,574	13	129,534,151	129,536,250	10q26.2		FOXI2	68	0	0	0	0	0
863,579	863,585	7	129,536,701	129,537,900	10q26.2		FOXI2	66	0	0	0	0	0
864,699	864,707	9	129,704,701	129,706,200	10q26.2		PTPRE	71	0	0	0	0	0
866,720	866,730	11	130,007,851	130,009,650	10q26.2		none	67	1	25	0	0	3
867,108	867,114	7	130,066,051	130,067,250	10q26.2		none	60	0	0	0	0	0
871,851	871,857	7	130,777,501	130,778,700	10q26.3		none	59	0	0	0	0	0
875,098	875,105	8	131,264,551	131,265,900	10q26.3		MGMT	69	0	0	30	0	0
875,461	875,467	7	131,319,001	131,320,200	10q26.3		MGMT	62	0	3	0	0	0
877,050	877,056	7	131,557,351	131,558,550	10q26.3		MGMT	59	8	0	0	0	0
877,148	877,157	10	131,572,051	131,573,700	10q26.3		none	61	0	0	0	0	0
877,427	877,434	8	131,613,901	131,615,250	10q26.3		none	63	0	0	0	0	0
878,379	878,390	12	131,756,701	131,758,650	10q26.3		EBF3	66	0	0	0	0	0
878,409	878,424	16	131,761,201	131,763,750	10q26.3		EBF3	70	0	0	0	0	6
878,441	878,453	13	131,766,001	131,768,100	10q26.3		none	64	0	0	0	0	0
878,471	878,477	7	131,770,501	131,771,700	10q26.3		none	70	0	0	0	0	0
879,919	879,928	10	131,987,701	131,989,350	10q26.3		none	70	0	19	0	6	0
879,989	879,997	9	131,998,201	131,999,700	10q26.3		none	63	0	0	8	0	0
880,657	880,666	10	132,098,401	132,100,050	10q26.3		none	68	0	0	0	0	12

883,837	883,843	7	132,575,401	132,576,600	10q26.3		none	56	0	0	0	0	0
885,197	885,203	7	132,779,401	132,780,600	10q26.3		none	10	92	0	0	0	0
886,159	886,165	7	132,923,701	132,924,900	10q26.3		TCERG1L	57	0	0	0	0	13
886,779	886,786	8	133,016,701	133,018,050	10q26.3		TCERG1L	61	0	11	0	0	0
886,789	886,796	8	133,018,201	133,019,550	10q26.3		TCERG1L	64	0	0	0	0	0
886,864	886,870	7	133,029,451	133,030,650	10q26.3		TCERG1L	59	7	0	12	0	0
887,099	887,109	11	133,064,701	133,066,500	10q26.3		TCERG1L	61	0	0	69	6	0
887,394	887,406	13	133,108,951	133,111,050	10q26.3		TCERG1L	74	0	0	13	0	8
889,672	889,679	8	133,450,651	133,452,000	10q26.3		none	60	0	0	28	0	0
889,911	889,917	7	133,486,501	133,487,700	10q26.3		none	62	0	0	0	0	3
890,530	890,537	8	133,579,351	133,580,700	10q26.3		none	59	8	11	0	0	0
890,542	890,548	7	133,581,151	133,582,350	10q26.3		none	64	0	0	0	0	11
891,156	891,166	11	133,673,251	133,675,050	10q26.3		none	63	0	0	0	14	20
891,965	891,975	11	133,794,601	133,796,400	10q26.3		BNIP3	70	0	0	0	0	0
892,216	892,222	7	133,832,251	133,833,450	10q26.3		none	61	0	0	100	0	0
893,027	893,033	7	133,953,901	133,955,100	10q26.3		JAKMIP3	62	0	0	0	0	0
893,036	893,043	8	133,955,251	133,956,600	10q26.3		JAKMIP3	67	0	0	0	0	0
893,065	893,074	10	133,959,601	133,961,250	10q26.3		JAKMIP3	60	0	0	0	0	2
893,213	893,228	16	133,981,801	133,984,350	10q26.3		JAKMIP3	66	0	0	0	0	0
893,325	893,343	19	133,998,601	134,001,600	10q26.3		DPYSL4	72	0	0	0	0	4
893,394	893,403	10	134,008,951	134,010,600	10q26.3		DPYSL4	63	0	0	0	0	0
893,407	893,419	13	134,010,901	134,013,000	10q26.3		DPYSL4	65	0	0	0	0	0
893,422	893,430	9	134,013,151	134,014,650	10q26.3		DPYSL4	67	0	0	0	0	0
893,436	893,453	18	134,015,251	134,018,100	10q26.3		DPYSL4	64	0	0	0	0	0
893,473	893,481	9	134,020,801	134,022,300	10q26.3		STK32C	65	5	0	0	0	0
893,574	893,588	15	134,035,951	134,038,350	10q26.3		STK32C	66	0	0	0	0	0
893,621	893,631	11	134,043,001	134,044,800	10q26.3		STK32C	63	0	8	5	0	0
893,799	893,814	16	134,069,701	134,072,250	10q26.3		STK32C	64	0	0	0	0	0
893,873	893,879	7	134,080,801	134,082,000	10q26.3		STK32C	52	0	0	0	0	79
893,882	893,889	8	134,082,151	134,083,500	10q26.3		STK32C	58	0	0	0	0	53
893,975	893,981	7	134,096,101	134,097,300	10q26.3		STK32C	59	0	0	0	0	0
894,135	894,149	15	134,120,101	134,122,500	10q26.3		STK32C	70	0	0	0	0	6
894,300	894,306	7	134,144,851	134,146,050	10q26.3		LRRC27	69	0	0	11	0	0
894,682	894,690	9	134,202,151	134,203,650	10q26.3		none	69	0	0	0	0	0
894,726	894,743	18	134,208,751	134,211,600	10q26.3		PWWP2B	74	0	0	0	0	3
894,750	894,763	14	134,212,351	134,214,600	10q26.3		PWWP2B	64	2	0	0	0	0
894,767	894,773	7	134,214,901	134,216,100	10q26.3		PWWP2B	63	0	7	0	0	0
894,779	894,795	17	134,216,701	134,219,400	10q26.3		PWWP2B	67	0	0	0	0	0
894,799	894,810	12	134,219,701	134,221,650	10q26.3		PWWP2B	64	0	0	0	0	0
894,813	894,819	7	134,221,801	134,223,000	10q26.3		PWWP2B	67	0	0	0	0	0
894,825	894,833	9	134,223,601	134,225,100	10q26.3		PWWP2B	65	0	0	10	0	0
894,863	894,877	15	134,229,301	134,231,700	10q26.3		PWWP2B	64	0	0	4	0	0
894,880	894,890	11	134,231,851	134,233,650	10q26.3		none	65	0	0	0	3	0
894,897	894,906	10	134,234,401	134,236,050	10q26.3		none	66	9	0	0	0	2
894,950	894,956	7	134,242,351	134,243,550	10q26.3		none	65	0	0	0	0	0
894,995	895,007	13	134,249,101	134,251,200	10q26.3		none	60	0	0	2	6	9
895,062	895,073	12	134,259,151	134,261,100	10q26.3		C10orf91	66	0	0	0	0	0
895,093	895,114	22	134,263,801	134,267,250	10q26.3		none	65	0	5	0	0	10
895,126	895,138	13	134,268,751	134,270,850	10q26.3		none	63	0	0	0	0	0
895,172	895,186	15	134,275,651	134,278,050	10q26.3		none	65	0	0	0	0	0
895,202	895,210	9	134,280,151	134,281,650	10q26.3		none	65	0	0	0	0	0
895,273	895,282	10	134,290,801	134,292,450	10q26.3		none	66	0	0	0	0	0

895,341	895,347	7	134,301,001	134,302,200	10q26.3		none	63	0	0	54	0	0
895,533	895,540	8	134,329,801	134,331,150	10q26.3		none	62	0	0	0	0	13
895,668	895,677	10	134,350,051	134,351,700	10q26.3		INPP5A	73	0	0	0	15	11
895,836	895,844	9	134,375,251	134,376,750	10q26.3		INPP5A	61	0	0	8	0	3
896,426	896,432	7	134,463,751	134,464,950	10q26.3		INPP5A	63	0	0	0	0	0
896,466	896,473	8	134,469,751	134,471,100	10q26.3		INPP5A	64	0	0	0	0	0
896,480	896,489	10	134,471,851	134,473,500	10q26.3		INPP5A	59	2	0	0	0	0
896,750	896,760	11	134,512,351	134,514,150	10q26.3		INPP5A	64	0	0	0	0	0
896,847	896,853	7	134,526,901	134,528,100	10q26.3		INPP5A	66	0	0	0	0	0
896,948	896,954	7	134,542,051	134,543,250	10q26.3		INPP5A	62	0	0	0	0	0
896,962	896,969	8	134,544,151	134,545,500	10q26.3		INPP5A	60	0	0	0	0	0
896,995	897,004	10	134,549,101	134,550,750	10q26.3		INPP5A	61	0	0	0	0	0
897,055	897,063	9	134,558,101	134,559,600	10q26.3		INPP5A	64	0	0	0	0	0
897,140	897,148	9	134,570,851	134,572,350	10q26.3		INPP5A	65	0	0	0	79	1
897,153	897,159	7	134,572,801	134,574,000	10q26.3		INPP5A	65	0	0	0	0	0
897,179	897,187	9	134,576,701	134,578,200	10q26.3		INPP5A	57	0	0	0	0	35
897,258	897,270	13	134,588,551	134,590,650	10q26.3		INPP5A	64	0	0	0	0	0
897,281	897,290	10	134,592,001	134,593,650	10q26.3		INPP5A	62	0	0	0	0	0
897,316	897,354	39	134,597,251	134,603,250	10q26.3		NKX6-2	71	0	0	0	0	1
897,363	897,375	13	134,604,301	134,606,400	10q26.3		none	64	0	0	0	0	0
897,379	897,395	17	134,606,701	134,609,400	10q26.3		none	66	0	0	0	0	0
897,415	897,424	10	134,612,101	134,613,750	10q26.3		none	66	0	0	8	0	0
897,430	897,436	7	134,614,351	134,615,550	10q26.3		none	67	0	0	55	0	0
897,477	897,487	11	134,621,401	134,623,200	10q26.3		TTC40	65	0	0	0	0	8
897,490	897,509	20	134,623,351	134,626,500	10q26.3		TTC40	66	0	0	0	0	0
897,651	897,660	10	134,647,501	134,649,150	10q26.3		TTC40	63	0	0	0	0	0
897,728	897,740	13	134,659,051	134,661,150	10q26.3		TTC40	64	0	0	0	0	0
897,830	897,837	8	134,674,351	134,675,700	10q26.3		TTC40	63	0	0	0	0	0
897,952	897,962	11	134,692,651	134,694,450	10q26.3		TTC40	65	13	0	0	0	5
898,077	898,089	13	134,711,401	134,713,500	10q26.3		TTC40	65	4	0	0	0	0
898,152	898,159	8	134,722,651	134,724,000	10q26.3		TTC40	63	0	0	0	0	0
898,180	898,188	9	134,726,851	134,728,350	10q26.3		TTC40	68	0	13	0	25	0
898,213	898,228	16	134,731,801	134,734,350	10q26.3		TTC40	64	0	0	0	0	0
898,231	898,247	17	134,734,501	134,737,200	10q26.3		TTC40	66	0	0	11	0	0
898,475	898,483	9	134,771,101	134,772,600	10q26.3		none	62	0	0	0	0	0
898,486	898,496	11	134,772,751	134,774,550	10q26.3		none	66	0	0	0	0	0
898,574	898,584	11	134,785,951	134,787,750	10q26.3		none	65	0	0	0	0	0
898,702	898,712	11	134,805,151	134,806,950	10q26.3		none	64	0	0	0	0	0
898,802	898,808	7	134,820,151	134,821,350	10q26.3		none	64	0	0	18	0	0
898,871	898,880	10	134,830,501	134,832,150	10q26.3		none	63	0	0	0	0	10
898,891	898,898	8	134,833,501	134,834,850	10q26.3		none	65	0	12	0	0	0
898,967	898,975	9	134,844,901	134,846,400	10q26.3		none	64	22	0	0	0	0
899,016	899,025	10	134,852,251	134,853,900	10q26.3		none	62	0	0	0	0	0
899,087	899,095	9	134,862,901	134,864,400	10q26.3		none	64	0	0	0	0	0
899,125	899,131	7	134,868,601	134,869,800	10q26.3		none	58	0	30	0	0	0
899,157	899,163	7	134,873,401	134,874,600	10q26.3		none	65	0	0	0	0	0
899,234	899,240	7	134,884,951	134,886,150	10q26.3		none	66	0	0	0	0	0
899,254	899,260	7	134,887,951	134,889,150	10q26.3		none	63	0	0	0	0	0
899,300	899,309	10	134,894,851	134,896,500	10q26.3		none	63	0	0	0	0	0
899,325	899,336	12	134,898,601	134,900,550	10q26.3		none	63	0	0	0	0	0
899,341	899,353	13	134,901,001	134,903,100	10q26.3		GPR123	69	0	0	0	0	0
899,390	899,397	8	134,908,351	134,909,700	10q26.3		GPR123	64	0	0	9	0	0

899,404	899,411	8	134,910,451	134,911,800	10q26.3		GPR123	61	0	0	26	0	0
899,438	899,449	12	134,915,551	134,917,500	10q26.3		GPR123	65	0	0	0	0	0
899,512	899,518	7	134,926,651	134,927,850	10q26.3		GPR123	63	0	0	0	0	0
899,536	899,543	8	134,930,251	134,931,600	10q26.3		GPR123	64	0	0	0	0	0
899,599	899,606	8	134,939,701	134,941,050	10q26.3		GPR123	65	12	0	0	0	0
899,612	899,619	8	134,941,651	134,943,000	10q26.3		GPR123	70	0	0	0	0	0
899,696	899,704	9	134,954,251	134,955,750	10q26.3		none	66	0	0	0	0	0
899,814	899,836	23	134,971,951	134,975,550	10q26.3		KNDC1	69	1	0	0	0	1
899,848	899,864	17	134,977,051	134,979,750	10q26.3		KNDC1	63	3	0	0	0	5
899,870	899,876	7	134,980,351	134,981,550	10q26.3		KNDC1	66	0	0	0	0	2
899,951	899,958	8	134,992,501	134,993,850	10q26.3		KNDC1	60	22	0	0	0	0
899,974	899,980	7	134,995,951	134,997,150	10q26.3		KNDC1	66	0	13	0	0	0
900,057	900,074	18	135,008,401	135,011,250	10q26.3		KNDC1	63	0	5	13	27	0
900,078	900,085	8	135,011,551	135,012,900	10q26.3		KNDC1	71	0	0	0	0	0
900,088	900,102	15	135,013,051	135,015,450	10q26.3		KNDC1	68	0	0	0	0	0
900,115	900,121	7	135,017,101	135,018,300	10q26.3		KNDC1	61	0	0	0	12	0
900,131	900,144	14	135,019,501	135,021,750	10q26.3		KNDC1	62	0	14	0	0	0
900,161	900,170	10	135,024,001	135,025,650	10q26.3		KNDC1	65	0	0	0	0	0
900,175	900,182	8	135,026,101	135,027,450	10q26.3		KNDC1	66	0	0	0	0	21
900,216	900,228	13	135,032,251	135,034,350	10q26.3		KNDC1	68	0	0	0	0	0
900,287	900,299	13	135,042,901	135,045,000	10q26.3		UTF1	74	24	0	0	0	2
900,330	900,345	16	135,049,351	135,051,900	10q26.3		VENTX	71	0	0	0	0	0
900,364	900,371	8	135,054,451	135,055,800	10q26.3		VENTX	59	0	0	0	0	0
900,379	900,386	8	135,056,701	135,058,050	10q26.3		none	60	0	0	0	0	14
900,390	900,397	8	135,058,351	135,059,700	10q26.3		none	63	0	22	0	0	0
900,407	900,415	9	135,060,901	135,062,400	10q26.3		none	67	0	0	0	0	0
900,474	900,486	13	135,070,951	135,073,050	10q26.3		none	65	0	0	0	0	0
900,492	900,504	13	135,073,651	135,075,750	10q26.3		none	67	0	0	0	0	0
900,532	900,570	39	135,079,651	135,085,650	10q26.3		ADAM8	66	8	0	0	0	0
900,576	900,584	9	135,086,251	135,087,750	10q26.3		ADAM8	68	0	0	0	0	0
900,588	900,610	23	135,088,051	135,091,650	10q26.3		ADAM8	66	0	1	0	0	0
900,621	900,631	11	135,093,001	135,094,800	10q26.3		TUBGCP2	62	0	0	0	0	27
900,812	900,820	9	135,121,651	135,123,150	10q26.3		TUBGCP2, ZNF511	69	0	0	0	0	0
900,923	900,931	9	135,138,301	135,139,800	10q26.3		CALY	71	0	0	0	0	0
900,941	900,950	10	135,141,001	135,142,650	10q26.3		CALY	60	11	0	6	0	0
900,988	901,002	15	135,148,051	135,150,450	10q26.3		CALY	71	0	0	0	0	6
901,071	901,078	8	135,160,501	135,161,850	10q26.3		PRAP1	65	0	24	0	0	0
901,088	901,097	10	135,163,051	135,164,700	10q26.3		PRAP1	63	0	0	0	0	4
901,125	901,142	18	135,168,601	135,171,450	10q26.3		none	67	0	0	0	0	0
901,269	901,282	14	135,190,201	135,192,450	10q26.3		none	65	0	0	5	0	0
901,285	901,292	8	135,192,601	135,193,950	10q26.3		PAOX	72	0	0	0	0	13
901,547	901,554	8	135,231,901	135,233,250	10q26.3		MTG1	61	9	0	0	0	0
901,584	901,590	7	135,237,451	135,238,650	10q26.3		SPRN	73	0	0	0	0	0
901,639	901,646	8	135,245,701	135,247,050	10q26.3		CYP2E1	65	0	0	0	0	0
901,803	901,813	11	135,270,301	135,272,100	10q26.3		CYP2E1	65	0	0	0	9	0
901,817	901,823	7	135,272,401	135,273,600	10q26.3		CYP2E1	70	0	0	0	0	0
902,274	902,282	9	135,340,951	135,342,450	10q26.3		CYP2E1	63	0	0	0	0	0

Table S5. Genes Located in Regions Capable of Forming Highly Stable Secondary Structures and Disease Associations

Gene	Chromosomal Position	Fragile Site	Insertions, Deletions, and Translocations	Point Mutations	Reference*
PHYH	10p13			Refsum Disease	602026
NMT2	10p13		Hypogonadism and Testicular Atrophy		603801
VIM	10p13			Cataracts	193060
CACNB2	10p12.33			Brugada Syndrome 4	600003
NEBL	10p12.31		DiGeorge syndrome-2		605491
BMI1	10p12.2			Hematological Malignancies	[1]
PTF1A	10p12.2			Diabetes Mellitus, Cerebellar Agenesis	607194
MAP3K8	10p11.23			Lung Cancer	191195
ZEB1	10p11.22			Corneal Dystrophy	189909
RET	10q11.21	FRA10G	Papillary Thyroid Carcinoma, BCR-ABL(-) Myeloproliferative Disorders, Papillary Thyroid Carcinoma of the Ovary, Hirschprung's Disease	Hirschsprung Disease, Multiple Endocrine Neoplasia, Medullary Thyroid Carcinoma, Pheochromocytoma, Renal Abnormalities	164761, [1]
CXCL12	10q11.21	FRA10G		Resistance to AIDS	600835
ALOX5	10q11.21	FRA10G		Asthma, Atherosclerosis	152390
CHAT	10q11.23	FRA10G		Myasthenic Syndrome	118490
CCDC6	10q21.2	FRA10C	Papillary Thyroid Carcinoma, BCR-ABL(-) Myeloproliferative Disorders, Chronic Myeloid Leukemia		601985, [1]
RHOBTB1	10q21.2	FRA10C		Head and Neck Squamous Cell Carcinoma	[1]
STOX1	10q21.3	FRA10C		Preeclampsia	609397
HK1	10q22.1	FRA10D	Hemolytic Anemia		142600
NEUROG3	10q22.1	FRA10D		Diarrhea	604882
PCBD1	10q22.1	FRA10D		Hyperphenylalaninemia	126090
CDH23	10q22.1	FRA10D		Deafness, Usher syndrome	605516
CHST3	10q22.1	FRA10D		Spondyloepiphyseal Dysplasia	603799
KCNMA1	10q22.3			Epilepsy	600150
ZMIZ1	10q22.3		B-Cell Acute Lymphoblastic Leukemia		[2]
CDHR1	10q23.1			Cone-Rod Dystrophy 15	609502
LDB3	10q23.2			Cardiomyopathy, Myofibrillar Myopathy	605906
BMPR1A	10q23.2		Juvenile Polyposis Syndrome	Juvenile Polyposis Syndrome	601299
GLUD1	10q23.2			Hyperinsulinism-Hyperammonemia Syndrome	138130

PTEN	10q23.31	FRA10A	Bannayan-Riley-Ruvalcaba Syndrome; Endometrial, Prostate, Breast, Cervical, Squamous Cell, and Head and Neck Carcinoma	Malignant Melanom; Cowden Disease; Bannayan-Riley-Ruvalcaba, Lhermitte-Duclos, and Macrocephaly/Autism Syndromes	601728
RBP4	10q23.33	FRA10A		Retinol-Binding Protein Deficiency	180250
HPS1	10q24.2	FRA10A	Hermansky-Pudlak Syndrome 1		604982
ABCC2	10q24.2	FRA10A	Dubin-Johnson Syndrome	Dubin-Johnson Syndrome	601107
PAX2	10q24.31		Papillorenal Syndrome	Papillorenal Syndrome, Isolated Renal Hypoplasia	167409
PDZD7	10q24.31		Usher Syndrome		612971
FGF8	10q24.32			Kallmann Syndrome 6	600483
HPS6	10q24.32		Hermansky-Pudlak Syndrome 6	Hermansky-Pudlak Syndrome 6	607522
PITX3	10q24.32		Anterior Segment Mesenchymal Dysgenesis, Cataracts	Cataracts	602669
NFKB2	10q24.32		Hematological Malignancies		164012, [1]
CNNM2	10q24.32		Renal Hypomagnesemia 6	Renal Hypomagnesemia 6	607803
COL17A1	10q24.33		Epidermolysis Bullosa	Epidermolysis Bullosa	113811
ADD3	10q25.1		T-cell Acute Lymphblastic Leukemia		601568
ADRB1	10q25.3		Congestive Heart Failure	Congestive Heart Failure	109630
BAG3	10q26.11	FRA10F	Dilated Cardiomyopathy 1HH	Myofibrillar Myopathy, Dilated Cardiomyopathy 1HH	603883
FGFR2	10q26.13	FRA10F	Saethre-Chotzen, Apert, Pfeiffer, LADD,and Beare-Stevenson Cutis Gyrata Syndromes	Endometrial, Gastric, Lung, Breast, and Ovarian Cancers; Crouzon, Pfeiffer, Jackson-Weiss, Antley-Bixler, Beare-Stevenson Cutis Gyrata, Apert, and LADD Syndromes; Craniosynostosis; Axenfeld-Rieger Anomaly	176943, [1]
PLEKHA1	10q26.13	FRA10F		Age-Related Maculopathy	607772
HTRA1	10q26.13	FRA10F		Age-related Macular Degeneration, Cerebral Autosomal Recessive Arteriopathy with Subcortical Infarcts and Leukoencephalopathy	602194
OAT	10q26.13	FRA10F	Gyrate Atrophy of the Choroid and Retina	Gyrate Atrophy of the Choroid and Retina	613349
ADAM12	10q26.2			Breast Cancer	[1]

*Reference numbers refer to Online Mendelian Inheritance in Man entries. URL www.omim.org

[1] Atlas of Genetics and Cytogenetics in Oncology and Haematology. URL http://AtlasGeneticsOncology.org

[2] Soler, G. *et al*. (2008) *Leukemia*, **22**, 1278-1280.

Table S6. Copy Number Alterations That Overlap With Regions of Predicted High Levels of DNA Secondary Structure.

Cancer	Type	Nucleotide Start*	Nucleotide End*	Segment Start	Segment End
Glioma	Deletion	89,505,798	90,410,621	596,704	602,738
Glioma	Deletion	116,731,800	130,571,762	778,211	870,479
Breast	Amplification	79,120,871	81,735,347	527,471	544,903
Breast	Amplification	123,214,869	123,367,187	821,431	822,448
Breast	Amplification	101,955	12,088,176	678	80,588
Breast	Deletion	89,505,798	90,410,621	596,704	602,738
Breast	Deletion	100,166,329	135,071,762	667,774	900,479
Breast	Deletion	19,022,250	42,889,659	126,814	285,932
Colorectal	Deletion	86,049,212	120,513,596	573,660	803,424
Colorectal	Deletion	121,281,931	133,627,776	808,545	890,852
Colorectal	Deletion	101,955	12,248,313	678	81,656
Lung NSC	Deletion	52,319,777	53,165,029	348,797	354,434
Lung NSC	Deletion	101,955	1,001,958	678	6,680
Lung NSC	Deletion	104,446,715	135,071,762	696,310	900,479
Melanoma	Deletion	89,308,314	90,410,621	595,387	602,738
Melanoma	Deletion	129,149,375	135,071,762	860,994	900,479
Melanoma	Deletion	54,201,467	57,779,853	361,342	385,200
Ovarian	Amplification	75,589,696	80,443,337	503,930	536,289
Prostate	Amplification	74,192,290	82,019,313	494,614	546,796
Prostate	Amplification	61,909,390	66,364,553	412,728	442,431
Prostate	Deletion	101,955	44,811,377	678	298,743

*Location of deletions and amplifications obtained from Tumorscape (www.broadinstitute.org/tumorscape) and based on human genome build hg37.2