

Table S1 Number of syntenic breaks (SB), regions of elevated DNA flexibility and large genes within 13 human, eight cloned mouse (italic) CFSs and 21 stable control regions. CFS frequencies are shown for human (K. Stout-Weider, unpublished data) and mouse (this study) lymphocytes. Frequencies of FRA7K (Helmrich et al., in press) and FRA7G (Hellman et al. 2002), both within 7q31, are based on FISH results.

The frequencies of SBs and islands/clusters of increased helix flexibility are not elevated in CFSs compared to control regions. Large transcriptionally active genes are a specific feature of frequent CFSs.

Human and <i>mouse</i> chromosomal region (first – last marker/ BAC/gene) (reference)	Size (Mb)	No. of SB	No. of flexibility islands / Mb	No. of flexibility clusters / Mb	Genes > 650kb (Mb)	CFS levels per band in % of all lesions (gene expression values) ^a
G-band CFSs						
FRA1E (SHGC-836 40 – STSG32532 FS) (Hormozian et al. 2006)	0.6	0	48.3	3.3	<i>DPYD</i> (0.8)	1.7 (500)
FRA4F (RP11-466 G12 – 145G20) (Rozier et al. 2004)	8.0	≥ 1	39.7	1.9	<i>GRID2</i> (1.5)	0.8 ^b (330)
<i>Fra6C1</i> (<i>RP23-474E</i> 7 – <i>10A23</i>) (Rozier et al. 2004)	11.2	≥ 1	45.1	2.5	<i>Grid2</i> (0.8)	0.4
FRA6E (RH92608 – RH63999) (Denison et al. 2003)	3.2	0	31.2	1.2	<i>PARK2</i> (1.4)	0.5 (218)
FRA7E (D7S1934 – SHGC-1044 56) (Zlotorynski et al. 2003)	4.5	0	59.6	3.6	-	0.7
FRA7K (WI-5281– SHGC-7864 8) (Helmrich et al., in press)	0.5	0	33.2	0	<i>IMMP2L</i> (0.9)	2.0 (375)
<i>Fra12C1</i> (<i>RP23-75F2</i> 3 – <i>153D4</i>) (Helmrich et al., in press)	1.1	0	49.3	3.5	<i>Imp2l</i> (1.0)	5.4

FRA7I (SHGC-153 624 – SWSS2627) (Ciullo et al. 2002)	1.5	0	56.7	3.3	<i>CNTNAP2</i> (2.3)	0.0 (106)
FRA13A (SHGC-843 29 – RH80830) (Savelyeva et al. 2006)	0.6	0	29.8	3.1	<i>NBEA</i> (0.7)	1.1 (210)
FRA16D (RH54766 – SHGC-1400 02) (Krummel et al. 2000)	2.0	0	30.0	1.5	<i>WWOX</i> (1.1)	3.1 (551)
<i>Fra8E1</i> (<i>Wwox</i>) (Krummel et al. 2002)	1.0	0	48.8	4.3	<i>Wwox</i> (0.9)	1.8
R-band CFSs						
FRA2G (RH91148 – RH1293) (Limongi et al. 2003)	1.0	0	22.6	0	-	0.3
<i>Fra2D</i> (<i>RP23-10N1</i> 2 – <i>431M12</i>) (C)	1.1	0	39.4	0.9	-	0.2
FRA3B (SHGC-843 49 – RH16786) [FRA3B epicentre (RP11-70P2 0 – 154D3)] (Becker et al. 2002)	4.3 [2.7]	0	24.1 [24.3]	0.5 [0.7]	<i>FHIT</i> (1.5); <i>PTPRG</i> (0.7) [<i>FHIT</i> ; <i>PTPRG</i>]	3.3 (1000; 44)
<i>Fra14A2</i> (<i>Fhit</i> – <i>Ptprg</i>) (Glover et al. 1998)	2.7	0	38.5	1.1	<i>Fhit</i> (1.6); <i>Ptprg</i> (0.7)	1.1
FRA6F (SHGC-103 019 – 82095) (Morelli et al. 2002)	1.2	0	26.6	0	-	0.5

FRA7G (D7S767 – RH40796) (Hellman et al. 2002)	4.4	1	41.9	1.8	-	0.1
<i>Fra6A3.1</i> (RP23-117 H11 – 73G15) (°)	0.6	0	47.7	1.7	-	0.2
FRA7H (SWSS2777 – SHGC-3140 2) [FRA7H epicentre (AC008264 - 083872)] (Mishmar et al. 1998)	3.9 [2.7]	0	21.8 [21.1]	0.8 [1.1]	<i>SEC8</i> (0.8) [<i>SEC8</i> (0.8)]	2.4 (563)
<i>Fra6B1</i> (RP23-194E 21 – 255H4) (°)	2.6	0	32.6	0.4	<i>Sec8</i> (0.7)	1.6
FRA9E (SHGC-785 96 – RH62868) (Callahan et al. 2003)	9.7	0	29.7	0.8	-	0.7
<i>Fra4C2</i> (RP23-6A1 3 – 395A21) (°)	8.1	0	42.8	1.7	<i>Astn2</i> (1.0)	0.5
FRAXB (RH68074 – DXS1133) (Arlt et al. 2002)	0.5	n.a.	50.3	2.0	-	3.1
Human control regions		G-			R-	
		band	R-	G-		
7q31.1 (SHGC- 80779 – 112009)	3.0	n.a.	45.5	2.7	-	0.0
1q42 (STSG3 4203 – CHLC.G GAA6F0 6)	13.1	3	21.0	21.4	0.3	0.8
					-	0.0

4q13 (SHGC- 142150 – RH4862 5)	16.9	0	48.0	44.4	2.1	2.4	<i>LPHN3</i> (0.9)	0.1 (75)
4q32 (SHGC4 -1146 – SHGC4- 472)	14.7	≥ 1	45.0	64.6	2.0	3.9	<i>FSTL5</i> (0.8)	0.0 (93)
6q22 (RH6093 0 – AFM109 XA9)	15.6	≥ 1	39.2	30.8	1.4	0.0	<i>TCBA1</i> (1.0)	0.0 (230)
7q31.3 (BV0971 31 – CHLC.G ATA31D 01)	9.7	0	47.1	46.3	2.1	3.0	-	0.0
8q21 (SHGC- 14112 – SHGC-1 06250)	19.2	2	40.8	45.4	1.6	2.8	<i>LOC138 046</i> (0.7)	0.1 (50)
10q23 (SHGC- 13153 – RH5153 1)	14.1	1	33.1	25.1	0.8	1.1	-	0.0
13q12 (8K22_T 7 – WI-4416)	12.7	1		23.9		0.4	-	0.0
13q31 (SHGC- 146050 – MFD44)	15.9	0	54.6	93.5	2.9	7.8	<i>GPC5</i> (1.5); <i>GPC6</i> (1.2)	0.1 (158; 113)
15q24- q25 (RH3799 0 – SHGC-1 30309)	16.4	≥ 4	21.3	20.8	0.6	0.1	-	0.0
Mouse control regions								
<i>IC1.1</i> (<i>C78142</i> – <i>D1MIT5</i> 28)	6.1	0	51.0		2.0		-	0.0

2C3 (AU0155 84- D2MIT5 24)	9.1	0	53.6		2.5		-	0.0
2E1 (D2MIT2 48- PTPRJ)	10.0	2	52.6		2.7		-	0.0
3H2 (D3MIT3 51- D3MIT8 4)	4.3	1		57.4		3.5	-	0.0
4A3 (D4MIT3 17- D4MIT2 60)	10.0	1	44.4		2.0		-	0.0
5A3 (D5MIT1 78- D5MIT2 50)	9.0	0	51.7		2.7		-	0.0
8A3 (CHRNA 6-WRN)	5.9	0		59.0		3.2	-	0.0
14D3 (D14MIT 37- AI64653 1)	11.6	1		36.4		1.4	-	0.1
15D1 (D15MIT 152- HSH)	13.0	0	50.7		3.9		-	0.0
15D3 (D15MIT 50- D15MIT 105)	13.0	0	41.1		1.1		-	0.0

^aGene expression values were obtained from Su et al. 2002 ([HYPERLINK "http://symatlas.gnf.org/SymAtlas"](http://symatlas.gnf.org/SymAtlas)) in human T-lymphocytes.

^bSince chromosome bands 4q22-q24 are difficult to separate, CFS frequencies for 4q22 are based on mapping results for q22-q24.

^cThis study.

n.a.: not analyzed

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