APPENDIX A

 Table 18. The raw data for the relationship among CGG repeat numbers, haplotype and AGG interruption patterns. The position of an AGG is designated by A and the number refers to the triplet length of uninterrupted CGG repeats.

AC-W-AT-1-IV-2-3 (Hap)	AGG	19-28 (%)	29 (%)	<u>30</u> (%)	31-35 (%)	36 (%)	37-56 (%)
17-G-G-A-T-A-A (A)	9A9	1 (6.3)					
	9A13	1 (6.3)					
	11A12	1 (6.3)					
	21	2(12.5)					
	9A9A9		12 (70.6)				
	9A20			1(5.6)			
	9A9A12				2(15.4)		
	9A9A15				1 (7.7)		
	9A21				1 (7.7)		
	9A25				1 (7.7)		
	9A9A16					1(5.6)	
	19A6A9					2(11.1)	
	9A9A6A9					2(11.1)	
	9A29						1 (7.7)
	9A9A7A9						1 (7.7)
	9A9A9A9						1 (7.7)
	9A11A9A9						1 (7.7)
	43						1 (7.7)

Table	18.	(continued)
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AC-W-AT-1-IV-2-3 (Hap)	AGG	19-28 (%)	29 (%)	<u>30</u> (%)	31-35 (%)	36 (%)	37-56 (%)
17-C-G-T-T-A-A (C)	10A6A9	2(12.5)					
	12A6A9		2 (11.8)				
	9A23				1 (7.7)		
	9A9A6A9					13 (72.2)	
	9A9A6A6A9						4 (30.8)
	9A9A6A8A9						1(7.7)
<u> 18-C-A-T-C-G-C (B)</u>	10A9	2 (12.5)					
	12A9	3 (18.8)					
	10A7A9	1(6.3)					
	10A9A3	1(6.3)					
	10A9A5	1(6.3)					
	<u>10A9A9</u>			<u>16 (88.9)</u>			
	10A23				2 (15.4)		
	10A9A11				1 (7.7)		
	11A9A9				3(23.1)		
	10A27						1 (7.7)
	10A39						1(7.7)
	56						1 (7.7)

Table 18.	(continued)
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AC-W-AT-1-IV-2-3 (Hap)	AGG	19-28 (%)	29 (%)	<u>30</u> (%)	31-35 (%)	36 (%)	37-56 (%)
OTHER							
18-G-A-T-C-G-C	9A13	1 (6.3)					
18-C-G-T-C-G-C	9A9A9		2(11.8)				
19-C-G-T-C-G-C	9A9A9		1(5.9)				
19-C-A-T-C-G-C	20A9			1(5.6)			
17-C-G-T-C-G-C	10A12A9				1 (7.7)		
total	95	16(100.0)	17(100.0)	18(100.0)	13(100.0)	18(100.0)	13(100.0)

(AC = FRAXAC1, W = WEX5, AT = ATL1, 1 = rs25731, IV = IVS10, 2 = rs25702, 3 = rs25723)

Table 19. SNPs map in the FMR1 gene. All SNP loci are collected from both the study ofBrightwell (2002) and the dbSNP of NCBI (July, 2006). The nucleotide positionof each SNP is according to the FMR1 sequence of L29074 from GenBank.

SNP	Other Name	Allele	Location	Nucleotide Position
	WEX8	A/G	5' UTR	4018
	WEX3	DEL T	5' UTR	4197
rs10521868	WEX1	C/A	5' UTR	11768
rs12687886		C/G	5' UTR	11796
rs12687865	WEX4	T/C	5' UTR	11886
rs1805420	WEX5, FMR12570	C/G	5' UTR	12570
	WEX6	G/A	5' UTR	12872
rs28902	ATL4	C/G	5' UTR	13304
rs28900	ATL2,FMR14365	A/C	Intron1	14365
rs28901	ATL3	C/T	Intron1	14367
rs1805421	FMR15180	A/G	Intron1	15180
rs1805422	FMR15223	C/G	Intron1	15223
rs12013181		C/T	Intron1	15714
rs12388933		C/T	Intron1	16459
rs12007147		G/T	Intron1	18192
rs5951751		C/T	Intron1	18294
rs12836995		C/T	Intron1	18519
rs4949	ATL1	C/T	Intron1	19445
rs1805423	FMR19689	A/G	Intron1	19689
rs29294		A/T	Intron1	20028
rs1270096		A/G	Intron1	20256
rs1270095		A/G	Intron1	20278
rs1793968		C/T	Intron1	20286
rs1793969		A/C	Intron1	20291
rs1793970		-/C/CTTTT/T	Intron1	20338
rs3041857		-/TT	Intron1	20362
rs1270094		A/G	Intron1	21600
rs1270093		A/G	Intron1	21768
rs971000	FMR22057	C/T	Intron1	22057
rs25725	FMR23047	C/T	Intron1	23047

Table 19. (continued)

SNP	Other Name	Allele	Location	Nucleotide Position
rs4824257		G/T	Intron1	23256
rs25726	FMR23603	A/G	Intron1	23603
rs1270092		C/T	Intron2	23828
rs25727	FMR24058	C/T	Intron2	24058
rs29295		C/T	Intron2	24120
rs10567806		-/TT	Intron2	25284
rs1270091		C/T	Intron2	25537
rs6626955		A/G	Intron2	25674
rs29296		A/G	Intron2	25727
rs29297		A/T	Intron2	25904
rs25728	FMR26138	A/G	Intron2	26138
rs3999731		-/GT	Intron2	26282
rs5904814		A/T	Intron2	26296
rs25729	FMR27014	C/T	Intron2	27014
rs12837370		G/T	Intron2	27075
rs12862794		A/C	Intron2	27179
rs12862796		A/C	Intron2	27180
rs12837614		C/T	Intron2	27193
rs12837623		A/T	Intron2	27206
rs12837624		A/T	Intron2	27207
rs3737554		A/G	Intron3	27432
rs25731	FMR27484	A/T	Intron3	27484
rs29299		A/G	Intron3	27782
rs29300		A/T	Intron3	27838
rs29298		A/G	Intron3	27855
rs1805424	FMR28442	A/G	Intron3	28442
rs29277		C/T	Intron3	29218
rs29278		C/G	Intron3	29443
rs29279		A/G	Intron4	30422
rs25707	FMRb	G/A	Exon5	30584
rs25708	FMR30793	A/G	Intron5	30793
rs29280		A/T	Intron5	30978
rs29281		G/T	Exon6	31744
rs6626957		C/G	Splice-site	31910

Table 19. (continued)

SNP	Other Name	Allele	Location	Nucleotide Position
rs25699		C/T	Intron7	32550
rs29282		C/T	Intron7	32868
rs16994366		G/T	Intron7	33072
rs7885132		A/T	Intron7	33256
rs5951855		A/G	Intron7	33299
rs29283		A/G	Intron7	33968
rs4824232		C/T	Intron9	35224
rs4824233		C/T	Intron9	35285
rs11425567		-/T	Intron9	35989
rs25715		C/T	Intron9	37556
rs29284		C/T	Intron9	38193
rs25712	FMR38248	C/T	Intron9	38248
rs25714	FMR38410	C/T	Intron10	38410
rs5904650		G/T	Intron10	38804
rs25700	FMR39456	A/G	Intron11	39456
rs29285		G/T	Intron11	39750
rs29286		C/G	Intron12	40038
rs29287		C/G	Intron12	40638
rs11361700		-/T	Intron12	41531
rs7052022		A/T	Intron12	41560
rs12837819		A/G	Intron12	41753
rs12839483		A/C	Intron12	41754
rs12156753		C/T	Intron12	41771
rs5904815		A/T	Intron12	41786
rs7878418		A/C	Intron12	41963
rs2187601		C/G	Exon13	42401
rs25702	FMR42950	A/G	Intron13	42950
rs29288		A/G	Intron13	43472
rs11342854		-/C	Intron13	43487
rs10608929		-/CTC	Intron13	43505
rs25718		A/G	Intron13	43631
rs1805425	FMR43654	-/C	Intron13	43654
rs29289		A/G	Intron13	43897
rs29290		C/T	Intron13	44526

Table 19. (continued)

SNP	Other Name	Allele	Location	Nucleotide Position
rs29291		C/G	Intron14	46303
rs5904816		G/T	Intron14	46530
rs11293471		-/C	Intron14	46597
rs7054612		C/T	Intron15	46883
rs5904651		A/G	Intron16	47922
rs12012926		C/G	Intron16	48000
rs11390934		-/G	Intron16	48927
rs6626961		C/T	Intron16	49150
rs25723		A/C	Intron16	49567
rs25720	FMR49911	C/T	Intron16	49911
rs25721	FMR50303	A/G	Intron16	50303
rs11798323		A/T	3' UTR	51690
rs25704	FMR51802	C/T	3' UTR	51802
rs1051719		C/G	3' UTR	52575
rs1051722		C/G	3' UTR	52578
rs11541363		C/T	3' UTR	52698
rs29292		A/G	3' UTR	52851
rs25724		G/T	3' UTR	53212
rs25703		C/T	3' UTR	53270
	WEX20	T/G	3' UTR	59881
	WEX16	G/C	3' UTR	120380
	WEX17	C/T	3' UTR	121167
	WEX18	A/G	3' UTR	121305
rs215120	WEX51	T/C	3' UTR	157310
rs5904668	WEX52	G/A	3' UTR	158608

AC Repeat	Buyle et	Macpherson et al. (1994)	Oudet et al.	Chiurazzi	Limprasert et
	al.	Chiurazzi et al. (1996b)	(1993)	et al.	al.(2001)
	(1993)	Eichler et al. (1996)	Rousseau et al.	(1999)	Tzeng et al.
		Mingroni-Netto et al. (1999)	(1995)		(2005)
18	1	9	190	T36	18
19	2	8	192	T38	19
20	3	7	194	T40	20
21	4	6	196	T42	21
22	5	5	198	T44	22
23	6	4	200	T46	23
24	7	3	202	T48	24
25	8	2	204	T50	25
26	9	1	206	T52	26

Table 20. Allele nomenclature of DXS548

Table 21. Allele nomenclature of FRAXAC1.

AC Repeat	Richards et al.	Macpherson et al.	Jacobs et al.	Chiurazzi	Limprasert et
	(1992)	(1994)	(1993)	et al.	al.(2001)
	Jacobs et al.	Eichler et al. (1996)	Rousseau et al.	(1999)	Tzeng et al.
	(1993)	Mingroni-Netto et al.	(1995)		(2005)
	Chiurazzi et al.	(1999)			
	(1996b)				
	Mingroni-Netto et				
	al. (1999)				
16	F	6	102	T32	16
17	Е	5	104	T34	17
18	D	4	106	T36	18
19	С	3	108	T38	19
20	В	2	110	T40	20
21	А	1	112	T42	21
22	Z	0	114	T44	22

CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	06)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	l. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
10	10				1							
11	11											1
14	14									1		
15	15									1		
16	6A9								1			
17	17							1	1			
	7A9								2			1
18	8A9									2		
19	19							1				
	8A10								1			
	9A9	1				1			5			
20	9A10					2						
	10A9	2				1		3	3	26	2	3
	11A8								1			
21	21	2								1		
	9A11					1						
	11A9								1			

Table 22. The raw data of AGG interspersion patterns within nine ethnic groups.

CGG	AGG Pattorn	This	Hirst at al	Zhou	u ot al (90)	06)	Foredz at al	Larson at al	Hirst at al	Fighler et a	1 (1005)	Crawford at al
	AOO Fatterii	THIS		ZIIO	u et al. (20	(00)				Liciliei et a	1. (1995)	
Allele		study	(1997)				(2001)	(1999)	(1994)		1	(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
22	9A12										1	3
	10A11								1	1		4
	11A10								1	1		
	12A9	3			2				1	1		2
23	23				1				2	1		3
	9A13	2		3								
	11A11								1			
	12A10					1			1	3		1
	13A9					5			6	6		
24	24								1		1	
	10A13										1	1
	11A12	1										
	13A10								1	1	1	1
	14A9					1						4
	10A9A3	1			1							
25	25			1					1			
	10A14											2
	5A9A9										1	

Table 22. (continued)

Table 22	. (continued)
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CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	06)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et al. (1995)		Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
26	26									1		
	9A16				1					1		
	10A15									1		
	16A9			1								
	8A8A8										1	
	9A6A9							1				
	10A9A4A									1		
	10A9A5	1		1								
27	27								1			
	10A16				1							
	10A6A9	2	1									
	10A9A6					1						
28	9A18			1								1
	8A9A9								3			
	9A8A9										1	
	10A7A9	1			2							

Table	22.	(continued)

CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et al. (1995)		Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
29	29				1							
	9A19			3							1	
	10A18									1		
	19A9			1	5						1	3
	9A9A9	15		93	80	30		3	11	23	20	45
	10A8A9								1			
	10A9A8								1			
	12A6A9	2										
30	30											1
	9A20	1		1					1	1		2
	10A19				1	3				1	1	2
	20A9	1				1						3
	8A9A11										1	
	8A12A8								1			
	9A9A10			1					1	2	2	6
	9A10A9				1	2				4	2	6
	9A11A8							1				

Table 22.	(continued)
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CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	ıl. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
30	10A7A11								1			
	10A8A10											1
	10A9A9	16		31	49	33		45	27	54	10	45
	10A5A3A9					2						
31	31									1	1	
	9A21	1				1				2	1	1
	10A20			2	2					1	1	3
	21A9			2								
	8A9A12									1		
	8A11A10								1			
	9A9A11			3						1		
	9A10A10											2
	9A11A9								1	2	1	
	10A9A10			1					8	11	7	16
	10A10A9			1						7	2	13
	11A9A9	3										1

Table 22.	(continued)
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CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	l. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
32	9A22							1				1
	10A21				2	1						1
	22A9											2
	9A9A12	2		2	5				1			1
	9A10A11											1
	9A11A10										1	
	9A12A9							2	4			3
	10A9A11	1		2	1						4	1
	10A10A10									1		
	10A11A9										1	
	11A9A10								1			
33	33											1
	8A24								1			
	9A23	1										
	10A22				1							3
	12A20											1
	9A9A13							1	1	1	1	1

Table 22.	(continued)
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CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	l. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
33	9A13A9							1				
	10A9A12			1								
	10A12A9	1										
	9A6A6A9			1								
34	34									1		
	9A24			1								
	10A23	2										
	9A9A14							1				
	9A14A9				1							
35	9A25	1							1			1
	10A24					1						1
	9A9A15	1			1		1				1	
	9A15A9		1							1		
	9A5A9A9									1		
	9A9A6A8						1					

Table	22.	(continued)

CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	l. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
36	36											1
	9A26		1	1		1				1		
	10A25						1					
	13A22										1	
	26A9									1		
	9A9A16	1	1	2			3	2				
	9A16A9		3									
	19A6A9	2		1								
	9A9A6A9	15	15	15	11	7	16	16				
	12A6A6A9				1							
37	9A9A17					1		4				
	9A17A9			1	1							
	9A7A9A9									1		
	9A9A7A9	1							1			
38	9A28									1		1
	10A27	1			1							1
	10A7A19											1

Table 22.	(continued)
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CGG	AGG Pattern	This	Hirst et al.	Zho	u et al. (20	006)	Faradz et al.	Larsen et al.	Hirst et al.	Eichler et a	al. (1995)	Crawford et al.
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
38	9A9A6A11			1								
	10A9A6A10											1
39	9A29	1										1
	9A9A19											1
	9A9A9A9	1		1	5	2	2	1				6
	9A9A10A8						1					
40	10A29					1						
	9A9A20									1		
41	10A30											1
	8A9A22								1			
	21A9A9			1								
	9A11A9A9	1										
42	11A30											1
	12A29											1
	10A9A21							1		1		1
43	43	1										
	9A9A23									1		
	9A9A6A6A9	4		1								

CGG	AGG Pattern	This	Hirst et al.	Zhou et al. (2006)		Faradz et al.	Larsen et al.	Hirst et al.	Eichler et al. (1995)		Crawford et al.	
Allele		study	(1997)				(2001)	(1999)	(1994)			(2000)
		Thai	Japanese	Chinese	Malay	Indian	Javanese	Eskimo	Caucasian	Caucasian	African	African
											American	American
44	10A33						1					
45	10A34						1					
	8A9A26								1			
	9A9A6A8A9	1										
48	8A9A9A9A9								1			
49	9A9A29									1		
	9A9A9A9A9									1		
50	10A39	1										
56	56	1										
	total	95	22	177	178	99	27	86	102	175	69	213

Table 22. (continued)

Table 23. Relationship among CGG repeat numbers, haplotype (FRAXAC1-ATL1) andAGG interruption patterns in six different ethnic groups.

Thai –	This	study
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	1.00	10.00(22 (11)	22 (11)	01 05 (11)	22 (1)	07 50 ()
AC-AT	AGG	19-28 (%)	29 (%)	30 (%)	31-35 (%)	36 (%)	37-56 (%)
17-G	9+9+9		12(70.6)				
	9+9	1(6.3)					
	9+13	1(6.3)					
	11+12	1(6.3)					
	21	2(12.5)					
	9+20			1(5.6)			
	9+9+12				2(15.4)		
	9+9+15				1 (7.7)		
	9+21				1 (7.7)		
	9+25				1 (7.7)		
	9+9+6+9					15 (83.3)	
	9+9+16					1(5.6)	
	19+6+9					2 (11.1)	
	9+9+7+9						1 (7.7)
	9+9+9+9						1 (7.7)
	9+11+9+9						1 (7.7)
	9+29						1 (7.7)
	43						1 (7.7)
	10+6+9	2(12.5)					
	10+12+9				1 (7.7)		
	12+6+9		2 (11.8)				
	9+23				1 (7.7)		
	9+9+6+6+9						4 (30.8)
	9+9+6+8+9						1 (7.7)
18-A	10+9+9			16 (88.9)			
	10+9	2(12.5)					
	10+7+9	1 (6.3)					
	10+9+3	1 (6.3)					
	10+9+5	1 (6.3)					
	12+9	3 (18.8)					
	10+9+11				1 (7.7)		
	11+9+9				3 (23.1)		
	10+23				2 (15.4)		

Thai (continued)

AC-AT	AGG	19-28 (%)	29 (%)	30 (%)	31-35 (%)	36 (%)	37-56 (%)
18-A	10+27						1 (7.7)
	10+39						1(7.7)
	56						1(7.7)
	9+13	1 (6.3)					
OTHER							
18-G	9+9+9		2 (11.8)				
19-G	9+9+9		1 (5.9)				
19-A	20+9			1(5.6)			
total	95	16(100.0)	17(100.0)	18(100.0)	13(100.0)	18(100.0)	13(100.0)

Chinese - Zhou et al. (2006)

AC-AT	AGG	23-28(%)	29 (%)	30 (%)	31-34(%)	36 (%)	37-43(%)
16-G	9A9A9		2 (2.1)				
17-G	9A13	3 (42.9)					
	25	1(14.3)					
	16A9	1(14.3)					
	9A18	1 (14.3)					
	19A9		1 (1.0)				
	9A9A9		90 (92.8)				
	9A19		2(2.1)				
	9A9A10			1 (3.0)			
	9A20			1 (3.0)			
	10A9A9			1 (3.0)			
	9A9A11				3 (18.8)		
	21A9				1 (6.3)		
	9A9A12				2(12.5)		
	9A6A6A9				1 (6.3)		
	10A9A12				1 (6.3)		
	9A24				1 (6.3)		
	19A6A9					1(5.3)	
	9A9A6A9					14 (73.7)	
	9A9A16					2(10.5)	
	9A26					1(5.3)	
	9A17A9						1 (20.0)
	9A9A6A11						1 (20.0)
	9A9A9A9						1 (20.0)

AC-AT	AGG	23-28(%)	29 (%)	30 (%)	31-34(%)	36 (%)	37-43(%)
17-G	21A9A9						1 (20.0)
	9A9A6A6A9						1 (20.0)
18-A	10A9A5	1 (14.3)					
	10A9A9			29 (87.9)			
	21A9				1 (6.3)		
	10A10A9				1 (6.3)		
	10A9A10				1 (6.3)		
	10A20				2(12.5)		
	10A9A11				1 (6.3)		
18-G	9A9A9		1 (1.0)				
	9A19		1 (1.0)				
	9A9A6A9					1(5.3)	
	10A9A9			1 (3.0)			
	10A9A11				1 (6.3)		
total	177	7(100.0)	97(100.0)	33(100.0)	16(100.0)	19(100.0)	5(100.0)

Chinese (continued)

Malay - Zhou et al. (2006)

AC-AT	AGG	10-28(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-39(%)
17-G	10	1 (11.1)					
	9A16	1 (11.1)					
	19A9		5(5.8)				
	9A9A9		76 (88.4)				
	9A14A9				1 (7.7)		
	9A9A12				5(38.5)		
	9A9A6A9					9 (75.0)	
	9A9A15				1(7.7)		
	9A17A9						1(14.3)
	9A9A9A9						4 (57.1)
	12A6A6A9					1 (8.3)	
	29		1(1.2)				
18-A	9A9A6A9					2 (16.7)	
	10A9A3	1 (11.1)					
	10A9A9			49 (96.1)			
	10A7A9	2(22.2)					
	10A16	1 (11.1)					
	10A19			1 (2.0)			

3 6 1	(1)
Malav	(confinited)
Trutary	(commuca)

AC-AT	AGG	10-28(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-39(%)
18-A	10A20				2(15.4)		
	10A21				2(15.4)		
	10A22				1(7.7)		
	10A27						1(14.3)
	10A9A11				1(7.7)		
	12A9	2(22.2)					
	23	1 (11.1)					
18-G	9A9A9		4 (4.6)				
	9A9A9A9						1(14.3)
	9A10A9			1 (2.0)			
total	178	9(100.0)	86(100.0)	51(100.0)	13(100.0)	12(100.0)	7(100.0)

Indian - Zhou et al. (2006)

AC-AT	AGG	19-27(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-40(%)
17-A	9A26					1 (12.5)	
17-G	9A11	1 (7.7)					
	13A9	1 (7.7)					
	9A9A9		9 (30.0)				
	20A9			1(2.4)			
	9A9A6A9					5(62.5)	
	9A9A9A9						1 (25.0)
	9A10	1 (7.7)					
	9A10A9			1 (2.4)			
18-A	9A9A6A9					1 (12.5)	
	9A10	1 (7.7)					
	10A9	1 (7.7)					
	10A5A3A9			2 (4.9)			
	10A9A6	1 (7.7)					
	10A9A9			31 (75.6)			
	10A19			3(7.3)			
	10A21				1 (33.3)		
	10A24				1 (33.3)		
	10A29						1 (25.0)
	12A10	1 (7.7)					
	13A9	1 (7.7)					
1					•		1

Indian	(continued)
mutan	(commueu)

AC-AT	AGG	19-27(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-40(%)
18-A	14A9	1 (7.7)					
18-G	9A9A6A9					1 (12.5)	
	9A9A9		12 (40.0)				
	9A9A17						1(25.0)
	10A9A9			1 (2.4)			
	13A9	3 (23.1)					
19-A	10A9A9			1 (2.4)			
20-G	9A9	1 (7.7)					
	9A9A9		8 (26.7)				
	9A9A9A9						1(25.0)
	9A10A9			1(2.4)			
	9A21				1(33.3)		
20-A	9A9A9		1 (3.3)				
total	99	13(100.0)	30(100.0)	41(100.0)	3(100.0)	8(100.0)	4(100.0)

Caucasian - Gunter et al. (1998)

AC-AT	AGG	13-27(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-54(%)
18-G	9A16	1 (2.1)					
	9A20			2(2.8)			
	9A21				1(2.3)		
	9A26					1	
	9A7A13				1(2.3)		
	9A9A9		9(37.5)				
	9A9A10			3(4.2)			
	9A9A11				1(2.3)		
	9A10A9			2(2.8)			
	9A11A9				4 (9.3)		
	9A11A10				1(2.3)		
	9A12A9				3 (7.0)		
	9A15A9				1(2.3)		
	13A12A8				1(2.3)		
	9A5A9A9				1(2.3)		
19-A	8A9	1 (2.1)					
	9A9A9		2(8.3)				
	9A12A11				1(2.3)		
	10A9	23 (48.9)					

AC-AT	AGG	13-27(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-54(%)
19-A	10A9A9			55 (77.5)			
	10A10A9				4 (9.3)		
	10A6A9	2(4.3)					
	10A8A4A	1(2.1)					
	10A8A9		2(8.3)				
	10A9A10				14 (32.6)		
	10A10	1(2.1)					
	10A10A10				1(2.3)		
	10A11	1(2.1)					
	10A11A19						1(5.9)
	10A18		1(4.2)				
	10A19			1(1.4)			
	10A21				2(4.7)		
	10A9A12				1(2.3)		
	11A10	1(2.1)					
	12A10	2(4.3)					
	13A9	1(2.1)					
	13A10	1(2.1)					
	13	1(2.1)					
	21	1(2.1)					
	23	1 (2.1)					
19-G	9A9A9		6 (25.0)				
	9A9A10			3(4.2)			
	9A9A11				1(2.3)		
	9A9A19						1(5.9)
	9A9A9A10						1(5.9)
	9A10A9			1 (1.4)			
	10A9A9			2 (2.8)			
	10A9	1(2.1)					
	12A9	1 (2.1)					
	12A10	1 (2.1)					
	9A28						1 (5.9)
	10A20				1 (2.3)		
	13A9	4 (8.5)					
	24	1 (2.1)					
	26	1(2.1)					

AC-AT	AGG	13-27(%)	29 (%)	30 (%)	31-35(%)	36 (%)	37-54(%)
21-G	8A9A12				1(2.3)		
	9A9A9		4 (16.7)				
	9A9A9A9A9						1(5.9)
	9A9A10			1(1.4)			
	9A9A11				2(4.7)		
	9A9A13				1(2.3)		
	9A9A17						1 (5.9)
	9A9A18						1 (5.9)
	9A9A19						1 (5.9)
	9A9A20						2 (11.8)
	9A9A22						1 (5.9)
	9A9A23						1 (5.9)
	9A9A24						1 (5.9)
	9A9A25						1 (5.9)
	9A9A26						1(5.9)
	9A9A29						1 (5.9)
	9A20			1 (1.4)			
	54						1 (5.9)
total	203	47(100.0)	24(100.0)	71(100.0)	43(100.0)	1(100.0)	17(100.0)

Caucasian (continued)

African American - Crawford et al. (2000)

AC-AT	AGG	11-28 (%)	29 (%)	30 (%)	31-35 (%)	36 (%)	37-45 (%)
16-G	10A19			1(3.1)			
	10A22				1 (4.6)		
	10A24				2 (9.1)		
18-G	9A12	3 (17.7)					
	14A9	1(5.9)					
	9A18	1(5.9)					
	9A19		1 (4.8)				
	19A9		5(23.8)				
	20A9			3 (9.4)			
	9A22				1 (4.6)		
	22A9				1 (4.6)		
	9A23				1 (4.6)		
	9A25				1 (4.6)		
	9A28						1 (11.1)

AC-AT	AGG	11-28 (%)	29 (%)	30 (%)	31-35 (%)	36 (%)	37-45 (%)
18-G	10A11	1 (5.9)					
	5A9A9	1(5.9)					
	9A9A9		14(66.7)				
	9A10A9			1(3.1)			
	9A10A10				1 (4.6)		
	9A12A9				2 (9.1)		
	11	1(5.9)					
	23	1(5.9)					
	31				1 (4.6)		
	34				1 (4.6)		
19-A	9A12	1 (5.9)					
	10A9	1(5.9)					
	10A9A9			20~(62.5)			
	10A9A10				3 (13.6)		
	10A11	2 (11.8)					
	10A20				1 (4.6)		
	10A22				1 (4.6)		
	10A30						2(22.2)
	10A9A16						1 (11.1)
	11A9A9				1 (4.6)		
	12A10	1(5.9)					
	14A9	1(5.9)					
	38						1 (11.1)
19-G	9A9A10			5 (15.6)			
	10A10A9				4 (18.2)		
	10A14	1(5.9)					
	10A15	1(5.9)					
	10A30						1 (11.1)
21-G	9A9A9		1 (4.8)				
	9A9A23						1 (11.1)
	9A20			2 (6.3)			
	9A27						1 (11.1)
	9A33						1 (11.1)
total	101	17(100.0)	21(100.0)	32(100.0)	22(100.0)	-	9(100.0)

African American (continued)



APPENDIX B

Figure 10. The CGG alleles distribution in 337 normal Thai males.



Figure 11.1. The electropherograms of the CGG-21 allele with no AGG interruption sequenced in reverse strand. The boundary of the CGG repeat regions is squared (seen as CCG in the opposite strand).



Figure 11.2. The electropherograms of the CGG-29 allele with AGG configuration of 9A9A9 sequenced in reverse strand. The boundary of the CGG repeat regions is squared (seen as CCG in the opposite strand).



Figure 11.3. The electropherograms of the CGG-30 allele with AGG configuration of 10A9A9 sequenced in reverse strand. The boundary of the CGG repeat regions is squared (seen as CCG in the opposite strand).



Figure 11.4. The electropherograms of the CGG-33 allele with AGG configuration of 9A23 sequenced in reverse strand. The boundary of the CGG repeat regions is squared (seen as CCG in the opposite strand).



Figure 11.5. The electropherograms of the CGG-36 allele with AGG configuration of 9A9A6A9 sequenced in reverse strand. The boundary of the CGG repeat regions is squared (seen as CCG in the opposite strand).



Figure 11.6. The electropherograms of the CGG-43 allele with AGG configuration of 9A9A6A6A9 sequenced in forward strand. The boundary of the CGG repeat regions is squared.

APPENDIX C

8% Acrylamide solution (100 ml)		
Urea	42	g
10X TBE	10	ml
40% Acrylamide/Bis solution	20	ml
Deionized distilled water to 100 ml, store at 4°C		
25% Ammonium persulfate (1 ml)		
APS	0.25	g
Deionized distilled water	1	ml
Mix well, store at 4°C in the dark		
2.3M Citric acid (10 ml)		
Citric acid	4.83	g
Deionized distilled water	10	ml
Mix well, store at room temperature		
Developer solution (100 ml)		
2.3M Citric acid	10	μl
40% Formaldehyde	100	μl
Deionized distilled water to 100 ml		
2.5mM dNTPs Mix (400 µl)		
100mM dATP	10	μl
100mM dCTP	10	μl
100mM dGTP	10	μl
100mM dTTP	10	μl
Deionized distilled water	360	μl
Mix well, store at -20°C		
2.5mM dNTPs Mix with 50% 7-Deaza-dGTP (400 $\mu l)$		
100mM dATP	10	μl
100mM dCTP	10	μl
100mM dTTP	10	μl
100mM dGTP	5	μl
10mM 7-Deaza-dGTP	50	μl
Deionized distilled water	315	μl
Mix well, store at -20°C		

6X Gel loading buffer (4 ml)		
Glycerol	1.2	ml
Xylene cyanol FF	0.006	g
Deionized distilled water	2.8	ml
Mix well, store at 4°C		
10% Glutaraldehyde solution (50 ml)	
50% Glutaraldehyde solution	10	ml
Deionized distilled water	40	ml
Mix well, store at room tempe	erature in the dark	
Loading dye (10 ml)		
Formamide	9.5	ml
0.5M EDTA, pH 8.0	400	μl
Bromophenol blue	0.005	g
Xylene cyanol FF	0.005	g
Deionized distilled water	100	μl
Mix well, store at -20°C		
10% Methanol-Acetic acid solution ((200 ml)	
100% Methanol	20	ml
Glacial acetic acid	20	ml
Deionized distilled water	160	ml
Mix well, store at room tempe	erature	
8% Polyacrylamide gel (30 ml)		
8% Acrylamide solution	30	ml
TEMED	50	μl
25% APS	50	μl
Mix well		
20% Silver nitrate (20 ml)		
$AgNO_3$	4	g
Deionized distilled water	20	ml
Mix well, store at room tempe	erature in the dark	

Silver solution (50 ml)		
0.36% NaOH	10.5	ml
25% NH ₄ OH	700	μl
20% AgNO ₃	2	ml
Deionized distilled water to 50 ml		
0.36% Sodium hydroxide (200 ml)		
3.6% NaOH solution	20	ml
Deionized distilled water	180	ml
Mix well, store at room temperature		
50X TAE (1,000 ml)		
Tris base	242.28	g
Glacial acetic acid	57.1	ml
EDTA	18.61	g
Deionized distilled water to 1,000 ml, store at r	room temperature	
10X TBE (1,000 ml)		
Tris base	109.03	g
Boric acid	55.65	g
EDTA	7.45	g
Deionized distilled water to 1,000 ml, store at r	room temperature	

APPENDIX D

QIAquick PCR purification kit protocol using a microcentrifuge

- 1. Add 250 µl of Buffer PB to 50 µl of the PCR sample, mix
- 2. Place a QIAquick spin column in a provided 2 ml collection tube, apply the sample to the column
- 3. Centrifuge at 13,000 rpm for 1 min, discard flow through, place the column back into the same tube
- 4. Add 700 μ l Buffer PE to the column
- 5. Centrifuge at 13,000 rpm for 1 min, discard flow through, place the column back into the same tube
- 6. Centrifuge at 13,000 rpm for 1 min, place column in a clean 1.5 ml microcentrifuge tube
- 7. Add 30 μ l Buffer EB to the center of the membrane
- 8. Let the column stand for 5 min, centrifuge at 13,000 rpm for 1 min

DyeEx 2.0 spin protocol for dye-terminator removal

- 1. Gently vortex the spin column to resuspend the resin
- 2. Loosen the cap of the column a quarter turn
- 3. Snap off the bottom closure of the spin column
- 4. Place the spin column in a 2 ml collection tube
- 5. Centrifuge at 2,900 rpm for 3 min.
- 6. Carefully transfer the spin column to a clean 1.5 ml tube
- 7. Slowly apply the sequencing reaction to the gel bed
- 8. Centrifuge at 2,900 rpm for 3 min.
- 9. Remove the spin column from the microcentrifuge tube
- 10. Dry the sample in a vacuum centrifuge for 30 min