

Supplementary materials

a)

Primer A					
Score	Expect	Identities	Gaps	Strand	
1203 bits(651)	0.0	662/667(99%)	2/667(0%)	Plus/Plus	
Query	4	ATGGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAGAG	63		
Sbjct	94	ATGGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAGAG	153		
Query	64	GTTCCATTTTGC GTTCATCTGGAGGTGGACGCACAGCATCGGGAATACACAATGCCACTG	123		
Sbjct	154	GTTCCATTTTGC GTTCATCTGGAGGTGGACGCACAGCATCGGGAATACACAATGCCACTG	213		
Query	124	AATTGTGTACTTCAACATGGTCACAATGGCACAATCCTTTATTTTTGTAGAGACAGGGTG	183		
Sbjct	214	AATTGTGTACTTCAACATGGTCACAATGGCACAATCCTTTATTTTTGTAGAGACAGGGTG	273		
Query	184	TCACTGTGTTGCCAGGCTAGCCTCGAAGCTCGGGTTCAGGCTCTCCTTCCACCTCGGCCCT	243		
Sbjct	274	TCACTGTGTTGCCAGGCTAGCCTCGAAGCTCGGGTTCAGGCTCTCCTTCCACCTCGGCCCT	333		
Query	244	CCCAAAGTGCTGGGATTATAGGTGTGAGCCACCACACCTGGCCAAATTTGTGGGTTTTTT	303		
Sbjct	334	CCCAAAGTGCTGGGATTATAGGTGTGAGCCACCACACCTGGCCAAATTTGTGGGTTTTTT	393		
Query	304	ggTTTTTatgTTTTGAAACAGAGTTTCTCCCTTGTCACCTAGGCTGGAGTACAGTGGCG	363		
Sbjct	394	GGTTTTTATGTTTTGAAACAGAGTTTCTCCCTTGTCACCTAGGCTGGAGTACAGTGGCG	453		
Query	364	CGATCTTGGCTCACTGCAACCTTTACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCT	423		
Sbjct	454	CGATCTTGGCTCACTGCAACCTTTACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCT	513		
Query	424	CCCAAGTAGCTGGGATTACAGGCACCTGCCAACACACCCAGCTAATTTTTTCTATTTTTA	483		
Sbjct	514	CCCAAGTAGCTGGGATTACAGGCACCTGCCAACACACCCAGCTAATTTTTTCTATTTTTA	573		
Query	484	GTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGAT	543		
Sbjct	574	GTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGAT	633		
Query	544	CCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGGCGCTGCGCCAGCCA	603		
Sbjct	634	CCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGGCGCTGCGCCAGCCA	693		
Query	604	AAATTTGTGTTTTTAAATGTATGTTTAAACAATTTAAAAATCCTAGATCTCCCCACAGTT	663		
Sbjct	694	AAATTTGTGTTTTTAAATGTATGTTTAAACAATTTAAAAATCCTAGATCAT--CCACAGTT	751		
Query	664	TGCCAAA 670			
Sbjct	752	TGCCAAA 758			

Deletion Mutation ↓

Insertion Mutation ↓

Substitution Mutation ↓

b)

Primer B					
Score	Expect	Identities	Gaps	Strand	
894 bits(484)	0.0	494/498(99%)	3/498(0%)	Plus/Plus	
Query	22	CTGCTCT-G-AGAGCTCATGTTCCAGCAGGGACAGCTAACACCCAGGGGCTGCACGGGG	79		
Sbjct	46	CTGCTCTAGAAGAGCTCATGTTCCAGCAGGGACAGCTAACACCCAGGGGCTGCACGGGG	105		
Query	80	TGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCACC	139		
Sbjct	106	TGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCACC	165		
Query	140	CCAGGGCCAGGCCTGCTTGCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGGG	199		
Sbjct	166	CCAGGGCCAGGCCTGCTTGCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGGG	225		
Query	200	TCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACC GCATGTGATCAGTCTGGGT	259		
Sbjct	226	TCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACC GCATGTGATCAGTCTGGGT	285		
Query	260	GGGCAAGACTTCAAGAGAGCACGCCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCCG	319		
Sbjct	286	GGGCAAGACTTCAAGAGAGCACGCCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCCG	345		
Query	320	ACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAATG	379		
Sbjct	346	ACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAATG	405		
Query	380	AGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATCT	439		
Sbjct	406	AGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATCT	465		
Query	440	CACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCTGGCTCTGTTTATAAGCTG	499		
Sbjct	466	CACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCTGGCTCTGTTTATAAGCTG	525		
Query	500	TCTGGaaaaaggcaaaa	517		
Sbjct	526	TCTGGGAAAA-GGCAAAA	542		

Deletion Mutation ↓

Insertion Mutation ↓

Substitution Mutation ↓

Figure S1: DNA sequencing for autistic sample-2, a) Primer A and b) Primer B

a)

Primer A					
Score	Expect	Identities	Gaps	Strand	
1192 bits(645)	0.0	662/669(99%)	5/669(0%)	Plus/Plus	
Query	7	ATGGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAGAG			66
Sbjct	94	ATGGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAGAG			153
Query	67	GTTCCATTTTGCCTTCATCTGGAGGTGGACGCACAGCATCGGGAATACACTTAATGCCAC			126
Sbjct	154	GTTCCATTTTGCCTTCATCTGGAGGTGGACGCACAGCATCGGGAATACAC--AATGCCAC			211
Query	127	TGAATTGTGTACTTCAACATGGTCACAATGGCACATTCTTTATTTTTTTGTAGAGACAGGG			186
Sbjct	212	TGAATTGTGTACTTCAACATGGTCACAATGGCACATTCTTTATTTTTTTGTAGAGACAGGG			271
Query	187	TGTCACTGTGTTGCCAGGCTAGCCTCGAACTCGGGTTCAGGCTCTCCTTCCACCTCGGC			246
Sbjct	272	TGTCACTGTGTTGCCAGGCTAGCCTCGAACTCGGGTTCAGGCTCTCCTTCCACCTCGGC			331
Query	247	CTCCCAAAGTGCTGGGATTATAGGTGTGAGCCACCACACCTGGCCAAATTTGTGGGtttt			306
Sbjct	332	CTCCCAAAGTGCTGGGATTATAGGTGTGAGCCACCACACCTGGCCAAATTTGTGGGTTTT			391
Query	307	ttggTTTTTatgTTTTGAAACAGAGTTTCTCCCTTGTACCTAGGCTGGAGTACAGTGG			366
Sbjct	392	TTGGTTTTTATGTTTTGAAACAGAGTTTCTCCCTTGTACCTAGGCTGGAGTACAGTGG			451
Query	367	CGCGATCTTGGCTCACTGCAACCTTTACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGC			426
Sbjct	452	CGCGATCTTGGCTCACTGCAACCTTTACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGC			511
Query	427	CTCCCAAGTAGCTGGGATTACAGGCACCTGCCAACACACCCAGCTAATTTTTTCTATTTT			486
Sbjct	512	CTCCCAAGTAGCTGGGATTACAGGCACCTGCCAACACACCCAGCTAATTTTTTCTATTTT			571
Query	487	TAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTG			546
Sbjct	572	TAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTG			631
Query	547	ATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGGCGCTGCGCCAGC			606
Sbjct	632	ATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGGCGCTGCGCCAGC			691
Query	607	CAAAATTTGTGTTTTTAAATGTATGTTAACAATTTAAAAATCCTAGATCACGCCACCGG			666
Sbjct	692	CAAAATTTGTGTTTTTAAATGTATGTTAACAATTTAAAAATCCTAGATCAT-CCACAG-			749
Query	667	TATTGCAAA 675			
Sbjct	750	T-TTGCAAA 757			

Deletion Mutation ▼

Insertion Mutation ▲

Substitution Mutation ▼

b)

Primer B					
Score	Expect	Identities	Gaps	Strand	
902 bits(488)	0.0	495/498(99%)	1/498(0%)	Plus/Plus	
Query	3	CCTGCTCTAG-AGAGCTCATGTTCCAGCAGGGACAGCTGACACCCAGGGGCCTGCACGGG		61	
Sbjct	45	CCTGCTCTAGAAGAGCTCATGTTCCAGCAGGGACAGCTAACACCCAGGGGCCTGCACGGG		104	
Query	62	GTGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCAC		121	
Sbjct	105	GTGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCAC		164	
Query	122	CCCAGGGCCAGGCTGCTTGCCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGG		181	
Sbjct	165	CCCAGGGCCAGGCTGCTTGCCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGG		224	
Query	182	GTCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACC GCATGTGATCAGTCTGGG		241	
Sbjct	225	GTCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACC GCATGTGATCAGTCTGGG		284	
Query	242	TGGGCAAGACTTCAAGAGAGCACGCCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCC		301	
Sbjct	285	TGGGCAAGACTTCAAGAGAGCACGCCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCC		344	
Query	302	GACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAAT		361	
Sbjct	345	GACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAAT		404	
Query	362	GAGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATC		421	
Sbjct	405	GAGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATC		464	
Query	422	TCACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCTGGCTCTGTTTATAAGCT		481	
Sbjct	465	TCACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCTGGCTCTGTTTATAAGCT		524	
Query	482	GTCTGGAAAAAGGCAAAA		499	
Sbjct	525	GTCTGGGAAAAAGGCAAAA		542	

Deletion Mutation ↓

Insertion Mutation ↓

Substitution Mutation ↓

Figure S2: DNA sequencing for autistic sample-4, a) Primer A and b) Primer B

a)

Primer A					
Score	Expect	Identities	Gaps	Strand	
372 bits(201)	4e-107	418/517(81%)	37/517(7%)	Plus/Plus	
Query	2	AATGGGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAG			61
Sbjct	93	AAT-GGGGATTGTTAGGGACTGGGGGAGAGGAATGGGGAGTTGGCGTCTAGTGGGGACAG			151
Query	62	AGGTTCCATTTTGC GTTCATCTGGAGGTGGACGCACAGCATCGGGAATACACTTTGTGCC			121
Sbjct	152	AGGTTCCATTTTGC GTTCATCTGGAGGTGGACGCACAGCATCGGGAATACACAATGCCAC			211
Query	122	TGTGTTGTGTGTATCTCAATGTGGACACTGTGGCA ttttttttttttttGTGTAGACACGG			181
Sbjct	212	TGAATTGTGT--ACTTCAACATGGTCACAATGGCACATTCTTTATTTTTGTAGAGACAG			269
Query	182	GGTGTCTGTGTTTTGCCACGATACCCTCAAAC TC--GTTCTCGCGCTCCTTCT-CCTCT			238
Sbjct	270	GGTGTCACTGTGTTGCCAGGCTAGCCTCGA ACTCGGGTTCAGGCTCTCCTTCCACCTCG			329
Query	239	CCCTCTCCCAAAGTGGT--GATTTTATGTGTGAGAC-CCACCACCTGTGCAAAA ttt-tg			294
Sbjct	330	GCCTC-CC-AAAGTGCTGGGATTATAGGTGTGAGCCACCAC-ACCTG-GCCAAATTTGTG			385
Query	295	ggtttttttgg ttttatat tttttGAAACACAGATTCTCCCTTGTGTACCTACGGTAGTG			354
Sbjct	386	GGTTTTTGGTTTTTATGTTTTGAAACAGAGTTTCTCCCTTGT--CACCTAGGCTGGAG			443
Query	355	TACAG-GG-GCGATCTTGTGTACAGTGCCCTTTTACCTCG-GGGTCTCA--CGATACT			409
Sbjct	444	TACAGTGGCGGATCTTGGCTCAC--TGCAACCTTACCTCCTGGGT-TCAAGCGATTCT			500
Query	410	CTCGTGTCTCC-CCTCCCATGTA--TGGGATTACACGCGCACGTGCCAACACACCCA--T			464
Sbjct	501	C-C-TGCCTCAGCCTCCAAGTAGCTGGGATTACA-G-GCACCTGCCAACACACCCAGCT			556
Query	465	AATTTTT-CTATATTATAA TAGACA-GGG-TTTCACC			498
Sbjct	557	AATTTTTTCTATTTT-TAGTAGAGACGGGGTTTCACC			592

Deletion Mutation ↓

Insertion Mutation ↓

Substitution Mutation ↓

b)

Primer B					
Score	Expect	Identities	Gaps	Strand	
891 bits(482)	0.0	494/499(99%)	3/499(0%)	Plus/Plus	
Query	3	CTGCTCTAG-AGAGCTCATGTTCCAGCAGGGACAGCTGACACCCAGGGGCCTGCACGGGG	61		
Sbjct	46	CTGCTCTAGAAGAGCTCATGTTCCAGCAGGGACAGCTAACACCCAGGGGCCTGCACGGGG	105		
Query	62	TGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCACC	121		
Sbjct	106	TGGAGGGCTCTTCAGAGGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCACC	165		
Query	122	CCAGGGCCAGGCCTGCTTGCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGGG	181		
Sbjct	166	CCAGGGCCAGGCCTGCTTGCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGGG	225		
Query	182	TCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACCGCATGTGATCAGTCTGGGT	241		
Sbjct	226	TCATGTCTCAAGGGCAGCCACTGGGCCTGAAAAGCAGAACCGCATGTGATCAGTCTGGGT	285		
Query	242	GGGCAAGACTTCAAGAGAGCACGCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCCG	301		
Sbjct	286	GGGCAAGACTTCAAGAGAGCACGCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCCG	345		
Query	302	ACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAATG	361		
Sbjct	346	ACGTCCATGCCAGCCACCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAATG	405		
Query	362	AGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATCT	421		
Sbjct	406	AGTGGATGAAAAGCAGCGACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATCT	465		
Query	422	CACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCGTGGCTCTGTTTATAAGCTG	481		
Sbjct	466	CACGGAGGGAAGGAAGCAGGCTCGGGAGGTGCCGTGCCGCGTGGCTCTGTTTATAAGCTG	525		
Query	482	TCTGGAAAAAAGGGCAAAA	500		
Sbjct	526	TCTGGGAAAA-GG-CAAAA	542		

Deletion Mutation ↓

Insertion Mutation ↓

Substitution Mutation ↓

Figure S3: DNA sequencing for Autistic sample-6, a) Primer A and b) Primer B

The sequence for primer A

AATTGAGCCGGTCACAAAGGACACATTTTGTACTGTACAATTCCACTTGCATGAGGCACCTC
AAGTAGTCAGATTCAAGAAACAGACAGGAGAATGGGGATTGTTAGGGACTGGGGGAGAG
GAATGGGGAGTTGGCGTCTAGTGGGGACAGAGGTTCCATTTTGC GTTCATCTGGAGGTGG
ACGCACAGCATCGGGAATACACAATGCCACTGAATTGTGTACTTCAACATGGTCACAATGG
CACATTCTTTATTTTTTGTAGAGACAGGGTGTCACTGTGTTGCCAGGCTAGCCTCGAACTC
GGTTTCAGGCTCTCCTTCCACCTCGGCCTCCCAAAGTGCTGGGATTATAGGTGTGAGCCACC
ACACCTGGCCAAATTTGTGGGTTTTTTGGTTTTTATGTTTTTGAACAGAGTTTCTCCCTTGTC
ACCTAGGCTGGAGTACAGTGGCGGATCTTGGCTCACTGCAACCTTTACCTCCTGGGTTCAA
GCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACCTGCCAACACACCCAG
CTAATTTTTTCTATTTTTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACT
CCTGACCTCAGGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGG
CGCTGCGCCCAGCCAAAATTTGTGTTTTTAAATGTATGTTTAAACAATTTAAAAATCCTAGATC
ATCCACAGTTTGCAAAGCCACTGCTATCCATCTTGGAT

Forward Primer: AGGCACCTCAAGTAGTCAGA

Reverse Primer: TGCAAAGTGTGGATGATCTAGG

Product size: 702bp

The sequence for primer B

AAAAGTGCCAAAGTGTCCATCCCATGAATGCAAGACACACAGTGCCTGCTCTAGAAGAGCT
CATGTTCCAGCAGGGACAGCTAACACCCAGGGGCCTGCACGGGGTGGAGGGCTCTTCAGA
GGCAGGATCACCTCGGAGATGGGTGCAGGGGACCTCGGGCCACCCAGGGCCAGGCCTGC
TTGCCCTGCTTAGGAGCTGGGTCTCCCACTCAGGGAGGGAGGGTTCATGTCTCAAGGGCA
GCCACTGGGCCTGAAAAGCAGAACCGCATGTGATCAGTCTGGGTGGGCAAGACTTCAAGA
GAGCACGCCTACCCTCAAGGGATGGAAGCAGAGGCTGGTAGCCGACGTCCATGCCAGCCA
CCAACTCAGAGCCAGCACACTACCCGCATGTGCCTCTGCCAATGAGTGGATGAAAAGCAGC
GACCTACAGATGCAGGCAACCTGGATGAGTCTTGACTTTATCTCACGGAGGGAAGGAAGCA
GGCTCGGGAGGTGCCGTGCCGCTGGCTCTGTTTATAAGCTGTCTGGGAAAAGGCAAAC
CACAGTACAGAACACAG

Forward Primer: TGCCAAAGTGTCCATCCCAT

Reverse Primer: TTTGCCTTTTCCAGACAGC

Product size: 536bp

Figure S4: Sequences for Primers A and B