Spectrum of *CREBBP* mutations in Indian patients with Rubinstein–Taybi syndrome

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Supplementary tables and figures

Supplementary table 1. Details of the symptoms of Indian RSTS patients

	Patients	GM1LBL	GM3SF	RSTS3a	RSTS4a	RSTS5a	RSTS6a	RSTS7a	RSTS8a	RSTS9a	RSTS10a	RSTS11a	RSTS12a	RSTS13a
	Parents' sample available	No	No	Yes	Yes	Yes	Yes	No	only Mother	Yes	Yes	No	No	Unknown
1	Consanguinity	Unknown	Unknown	No	No	Yes	No	Unknown	Yes	No	Unknown	Unknown	Unknown	Unknown
2	Age	6 months	3 years	9 years	8 years	7 years	11 years	5 days	6 years	8 years	10 years	9 years	3 months	16 years
3	Sex	Male	Female	Male	Male	Male	Male	Female	Female	Male	male	Female	Female	Male
4	Growth retardation	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	Mental and psychometric retardation	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	Severity of mental and psychometric retardation	Severe	Severe	Severe	Mild	Severe	Mild	Severe	Severe	Severe	Severe	Severe	Severe	Severe
7	Heavy and arched eyebrows	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	Long eyelashes	Yes	Yes	Yes	Yes	Yes	Yes	Unknown	Yes	Yes	Yes	Yes	Unknown	Yes
9	Eye abnormality (myopia/ cataracts/ glaucoma/, coloboma)	Yes	Yes	Yes	Yes	Yes	Yes	Unknown	Yes	Yes	Yes	Unknown	Unknown	Yes
10	Prominent beaked nose	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	Low-set ears	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	Highly arched palate	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	Downward-slanting palpebral fissures	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	Radially deviated thumbs	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes
15	Broad thumb	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	Hypotonic	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	Microcepahaly	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	Deviation from classical	Classical	Classical	Classical	-	Classical	-	Classical	Classical	Classical	Classical	Classical	Classical	Classical

Supplementary table 2. Primers used for CREBBP gene amplification

Primer	Exons	Forward	Reverse
CBPE2	Exon2	5′-CTG TTT TCG CGA GCA GGT-3′	5′-ATC GGT ATC CGC GAC CAC-3′
CBPE3a	Exon3	5′-AACGTGGCAGTTGGAGAGC-3′	5′-GTGCTGGCTGCCTGTTTAG-3′
CBPE3b	Exon3	5′-TAAACAGGCAGCCAGCACC-3′	5′-TACCTTGGCCATGCCTCCTG-3′
CBPE4	Exon4	5′-TCACCACAGCTGATGTTACCTC-3′	5′-TCCTGTTGCTAGCTCATCACAG-3′
CBPE5	Exon5	5′-GTGGTCGGTATTATCCATCAGC-3′	5′-GGCAAATTCTTCCTGACCTC-3′
CBPE6	Exon6	5′-TGTTTGTAAGTTGAGGACTGCC-3′	5′-TGTACCTTGGGCTGCTGTC-3′
CBPE7	Exon7	5′-TTCCTTTCTCCCTAGGCTTG-3′	5′-GAGAGTTCCTTCACCTACCCAG-3′
CBPE8	Exon8	5′-GGTGGCATGTTGTTATCGTC	5′-AAGTCAGGAGAGCCAAGTGATG-3′
CBPE9	Exon9	5′-GTGGTGGCAGAAGAACCTTAC-3′	5′-AGAGTGTGGGAATCTCTGGC-3′
CBPE10	Exon10	5′-AGGTGATTCTCCCGCCTCAG-3′	5′-ATCTGGGAAGTCTCCTTGGTC-3′
CBPE11	Exon11	5′-GCCAGTGTACTCAATGAGGAAG-3′	5′-ACATCAACAGCTTCTGCAGG-3′
CBPE12	Exon12	5′-CTC TCT TGG GAA GGC CCT TTA C-3′	5′-GAG GCA GGA GAA TGG TGT GAA C-3′
CBPE13	Exon13	5′-TGTCCTCGTCCTTCCCTGGTAC -3′	5′-TGTGAGAGGGAGGGCTATCTGC -3′
CBPE14	Exon14	5′-TGTGCTTGCCATCCTCTGGG -3′	5′-TCATGGGTCCTTCTCACTCGC -3′
CBPE15	Exon15	5′-CTC TGT CCA TTT CTG GTA GGG -3′	5′-GGA TGG TCT TGA ACT CAT GGG -3′
CBPE16	Exon16	5′-TCTGGCTGCTGTTACCTCCCTC-3′	5′-TACCCATGGCAGGCTCCAAG -3′
CBPE17	Exon17	5′-CTG ACT CTG TGC TGA AGC GAC-3′	5′-CTC TCA CTC CTG CCA TGA GC-3′
CBPE18	Exon18	5′-CCACCATGCCCAGCCTGAAAT G-3′	5′-TCCAAGGACCAGGGCTTCATG-3′
CBPE19	Exon19	5′-CCCAGCCGATTCTATGTAGCAG -3′	5′-CTCCCAGTATACAGGCGTGGTC -3′
CBPE20	Exon20	5′-CTGAAGCGATGTGATGGGTG-3′	5′-TGTCGCCAAGGCTGATAAC-3′
CBPE21	Exon21	5′-GATGATGGCCTGTGATGTGTGC -3′	5′-TGGTCAAGGCTGCAGTGAGTC -3′
CBPE22	Exon22	5′-GGCGTGGTGGTTTGTACCTG -3′	5′-CCCACAACCCACTCCATAAGG-3′
CBPE23-24	Exon23&24	5′-CCCAGAGAACAAGGTGTGGAC G-3′	5′-TTGACAACCGAACCTCAGAACC -3′
CBPE25	Exon25	5′-ATCCATCTGCTCCGCCCTAGAG-3′	5′-GCTACTGCACGCATTCGCTG -3′
CBPE26	Exon26	5′-CATTCACAGAGGTGCAGTTCCC -3′	5′-TAGGTAAGAGCGGGTCCCACAC-3′
CBPE27	Exon27	5′-GAGCCCATGAGGTTGAGGTTGC -3′	5′-TTCAGGTGATCCACCGCAGCAG -3′
CBPE28	Exon28	5′-CCCAAGGGAGAAGTGTTGCAG -3′	5′-TGCCCACTGATGGAAACAGC-3′
CBPE29	Exon29	5′-CTGTTTCCATCAGTGGGCATTG -3′	5′-TTTACATCAGCGGGTTGTGTCC -3′
CBPE30	Exon30	5′-TGGAATCTTCCGCATCTGGTTG -3′	5′-CCTGATGCCTTGGGATGGAAC-3′
CBPE31	Exon31	5′-ATCAGGGCCATCAGGCTCAG-3′	5′-GCGGGTGTTTCCAGCCATTTAG-3′
CBPE32	Exon32(i)	5′-GCTGTTGCCAGGAGTGAAGGTC-3′	5′-GCTGGCGGAGCTTGTGTTTG-3′
CBPE32	Exon32(ii)	5′-TCATCGCCCTCTGCTGCTAC -3′	5′-TGGGCCTGCATGGATATCAC-3′
CBPE32	Exon32(iii)	5′-CCTGTACCGGGTGAACATCAAC -3′	5′-GCTGCCTCCGTAACATTTCTCG -3′
CBPE32	Exon32(iv)	5′-CATGAACCCAGGACACAACCC -3′	5′-GGGAGCATTGCACTCTGTTCG -3′

Supplementary table 3. List of eight groups classified on the basis of markers showing independent association or interdependency

First group					
S. No.	Markers	Alleles	Exact position	Samples	*dbSNP/Novel*
1	M2	C/A	3185	RSTS10a	Novel
2	M6	A/T	4503	RSTS10a	Novel
3	M10	C/T	5478	RSTS10a	Novel
Second group					
1	M7	C/T	4628	RSTS5a	Novel
2	M8	T/A	4794	RSTS5a	Novel
3	M53	T/C	65411	RSTS5a	Novel
4	M54	C/G	65427	RSTS5a	Novel
5	M56	A/C	65465	RSTS5a	Novel
6	M57	T/C	65467	RSTS5a,RSTS11a	Novel
7	M58	A/C	65527	RSTS5a	Novel
8	M59	T/G	65648	RSTS5a	Novel
9	M62	A/T	123800	RSTS11a	Novel
10	M65	T/G	124424	RSTS13a	Novel
11	M66	A/C	124262	RSTS13a	Novel
Third group					
1	M12	G/T	5540	C75,C76,C86	Novel
2	M29	T/G	18478	C75,C83	Novel
3	M52	C/T	65348	C86	Novel
Fourth group					
1	M13	C/T	9919	C2,C13,C17	Novel
2	M36	T/C	25081	C1,C2,C3,C6,C9,C13,C17,C19,C67,C69,RSTS6b	Novel
3	M38	G/A	25230	C20,C69	Novel
Fifth group					
1	M14	A/T	10029	C5	Novel
2	M15	A/C	10054	C5,C9,C16	Novel
3	M16	T/G	10107	C9	Novel
4	M17	T/C	10152	C5,C9	Novel
Sixth group					
1	M19	A/G	11755	GM1LBL	Novel
2	M26	T/G	13946	GM3SF,RSTS3a	Novel
3	M31	T/G	18607	GM1LBL	Novel
4	M32	C/G	18617	C21,C17,GM1LBL	Novel
5	M33	G/T	18724	C1,C23,GM1LBL,GM3SF,RSTS3a,RSTS3c,RSTS4a ,RSTS4b,RSTS6a,RSTS6b	*rs129974*
6	M61	C/T	98804	RSTS3a	Novel
7	M41	G/C	25445	C8,GM3SF,RSTS3a,RSTS3b,RSTS4b,RSTS4a,RSTS 4c,RSTS5a,RSTS5c,RSTS6c,RSTS7a	Novel
8	M60	C/T	98802	RSTS3a	Novel
9	M28	A/G	18455	GM1LBL	Novel
Seventh group					

1	M30	C/A	18547	RSTS12a	Novel
2	M69	A/T	23282	RSTS13a	Novel
3	M46	T/C	32284	RSTS12a	Novel
4	M48	T/C	51363	C2,C17,C63,RSTS4a,RSTS12a	*rs130002*
5	M49	C/A	52107	RSTS12a	Novel
6	M55	A/C	65439	RSTS11a,RSTS12a	Novel
7	M65	T/G	124424	RSTS13a	Novel
8	M66	A/C	124262	RSTS13a	Novel
9	M64	T/A	9600	RSTS13a	Novel
10	M67	G/C	3334	RSTS13a	Novel
11	M68	C/A	5533	RSTS13a	Novel
Eighth group					
1	M43	G/A	30603	C2,C19,C52,C69	Novel
2	M44	A/T	31015	C18	Novel
3	M45	A/C	31609	C62	Novel
4	M50	C/T	54071	C62	Novel

Supplementary table 4. Exon mutations in RSTS patients in the Indian population

S.No	Gene Position	Sense / Missense	Patient	Exon	Amino acid change	Novel/*de novo*/SNP	Domain
1	g.3276G>C	missense	RSTS13a	32	p.Thr1735Arg	Novel	CH3
2	g.4503A>T	missense	RSTS10a	31	p.Gln1765His	*De novo;* novel	CH3
3	g.4627C>T	missense	RSTS5a	31	p.Glu1724Lys	*De novo;* novel	CH3
4	g.4794T>A	missense	RSTS5a	31	p.Leu1668His	*De novo;* novel	HAT
5	g.9600T>A	missense	RSTS13a	29	p.Ser1533Cys	Novel	HAT
6	g.5262C>T	missense	RSTS13a	30	p.Val1613Met	Novel	HAT
7	g.12009C>T	missense	RSTS3a	27	p.Glu1459Asp	Novel	CH2
8	g.13140T>C	missense	RSTS6a	26	p.Glu1384Gly	*De novo;* novel	CH2
9	g.13946T>G	missense	GM3SF, RSTS3a	25	p.Asp1340Ala	Novel	CH2
10	g.25233A>T	missense	GM3SF, RSTS3a, RSTS4a, RSTS5a	21	p.His1235Gln	Novel	CH2
11	g.65427C>G	missense	RSTS5a	6	p.Lys439Asn	*De novo;* novel	CH1
12	g.65439A>C	missense	RSTS11a, RSTS12a	6	p.Asn435Lys	Novel	CH1
13	g.65465A>C	missense	RSTS5a	6	p.Cys427Gly	*De novo;* novel	CH1
14	g.65467T>C	missense	RSTS5a, RSTS11a	6	p.Asp426Gly	Novel	CH1
15	g.65527A>C	missense	RSTS5a	6	p.Val406Gly	*De novo;* novel	CH1
16	g.123800A>T	missense	RSTS11a	3	p.Leu243Gly	Novel	NTAD
17	g.124262A>C	missense	RSTS13a	3	p.Val89Gly	Novel	NHRD
18	g.124424T>G	missense	RSTS13a	3	p.Asp35Ala	Novel	NHRD
19	g.4808C>T	sense(silent)	RSTS5a	31	p.Gly1663Gly	*De novo;* novel	HAT
20	g.5284C>T	sense(silent)	RSTS10a	31	p.Lys1605Lys	*De novo;* novel	HAT
21	g.5341C>T	sense(silent)	RSTS12a	30	p.Lys1586Lys	Novel	HAT
22	g.13894A>G	sense(silent)	GM3SF, RSTS3a	25	p.Val1357Val	Novel	CH2
23	g.13929A>G	sense(silent)	GM3SF, RSTS3a	25	p.Leu1346Leu	Novel	CH2
24	g.54717T>G	sense(silent)	GM3SF	8	p.Pro532Pro	Novel	KIX
25	g.65472T>C	sense(silent)	RSTS5a	6	p.Arg424Arg	*De novo;* novel	CH1

Supplementary table 5. Intron mutations in RSTS patients in the Indian population

S.No	Gene position	Exact position	Patient	Splice site	Novel/*De novo*/SNP	Domain
1	g.3334G>C	c.3379-28G>C	RST13a	No	Novel	HAT
2	g.3185C>A	c.3379+76C>A	RSTS10a	No	Novel	HAT
3	g.5478C>T	c.4728-108C>T	RSTS10a	No	*De novo; novel*	HAT
4	g.5533C>A	c.4890-178C>A	RSTS13a	No	Novel	HAT
5	g.11755A>G	c.4394+238A>G	GM1LBL	No	Novel	HAT
6	g.12857A>G	c.4113-154A>G	RSTS6a	No	*De novo; novel*	HAT
7	g..12833G>A	c.4113-178G>A	RSTS6a	No	*De novo; novel*	HAT
8	g.14259G>A	c.3982-277G>A	RSTS4a	No	*De novo; novel*	HAT
9	g.18455A>G	c.3914-277A>A	GM1LBL	No	Novel	HAT
10	g.18547C>A	c.3914+164C>A	RSTS12a	No	Novel	HAT
11	g.18617C>G	c.3914+93C>G	GM1LBL	No	Novel	HAT
12	g.18607T>G	c.3914+103T>G	GM1LBL	No	Novel	HAT
13	g.23282A>T	c.3836-67A>T	RST13a	No	Novel	HAT
14	g.32284T>C	c.3369+3T>C	RSTS12a	No	Novel	BROMO
15	g.51363T>C	c.2113+81T>C	RSTS4a	No	*rs130002*	KIX
16	g.52107C>A	c.1941+26C>A	RSTS12a	No	Novel	KIX
17	g.54546C>T	c.1676-235C>T	RSTS3a	No	Novel	KIX
18	g.54548C>T	c.1676-237C>T	RSTS3a	No	Novel	KIX
19	g.65411T>C	c.1330+3T>C	RSTS5a	Part of donor splice site	*De novo; novel*	KIX
20	g.65648T>G	c.1216-121T>G	RSTS5a	No	*De novo; novel*	KIX

Supplementary table 6. List of fifteen nucleotide changes both in the patients as well as parents

S.No.	Position	Intron/Exon	Samples	Exact position/ change	dbSNP/Novel
1	g.25233A>G	Ex21	RSTS3c,RSTS5a	p.His1235HiS	Novel
2	g.23474C>T	IVS21	RSTS8a,GM1LBL,RSTS4b,RSTS6a,RSTS6b,RSTS8b	c.3779-358C>T	Novel
3	g.23289T>C	IVS21	GM3SF,RSTS3a,RSTS3c,RSTS3b,RSTS4a,RSTS5a,RSTS5b,RSTS6a,RSTS6c	c.3779-173T>C	Novel
4	g.25445G>C	IVS21	GM3SF,RSTS3a,RSTS3b,RSTS4a,RSTS4b,RSTS4c,RSTS5a,RSTS5c,RSTS6c,RSTS7a	c.3779-206G>C	Novel
5	g.10446C>A	IVS27	RSTS3a,RSTS3b,RSTS3c,RSTS4c,RSTS5a,RSTS5b,RSTS6a,RSTS6b	c.4394-198C>A	Novel
6	g.46880A>T	IVS14	RSTS3b,RSTS4c,RSTS5b,RSTS6b,RSTS6c,RSTS8a,RSTS9a,RSTS9b,	c.2463+304A>T	Novel
7	g.46900A>T	IVS14	RSTS3b,RSTS4c,RSTS5b,RSTS6b,RSTS6c,RSTS8a,RSTS9a,RSTS9b	c.2463-284A>T	Novel
8	g.46908A>C	IVS14	RSTS3b,RSTS4c,RSTS5b,RSTS6b,RSTS6c,RSTS8a,RSTS9a,RSTS9b	c.2463+176A>C	Novel
9	g.46966A>C	IVS14	RSTS3b,RSTS4c,RSTS5b,RSTS6b,RSTS6c,RSTS8a,RSTS9a,RSTS9b	c.2463+218A>C	Novel
10	g.47122_ 47133insA	IVS14	RSTS3c,RSTS5a,RSTS5c,RSTS6a,RSTS9c	c.24634+62insA	Novel
11	g.12969G>A	IVS25	RSTS6a,RSTS6b,GM1LBL,RSTS4b	c.4113-42G>A	Novel
12	g.13739T>C	IVS25	RSTS3c,RSTS4a,RSTS4b	c.4280+93T>C	Novel
13	g.18795G>A	IVS23	GM1LBL,GM3SF,RSTS3a,RSTS3c,RSTS4a,RSTS4b, RSTS6b	c.3982+9G>A	Novel
14	g.13190A>G	IVS26	RSTS6a,RSTS6b	c.4394+43A>G	Novel
15	g.52289T>C	IVS9	RSTS10b,RSTS10c,RSTS13a	c.1941-139T>C	Novel

Supplementary table 7. List of variants identified in the parents only

S.No.	Position	Intron/Exon	Samples	Exact position	dbSNP/Novel
1	g.23322A>T	IVS21	RSTS3c	c.3836-206A>T	Novel
2	g.23339A>C	IVS21	RSTS3c	c.3836-223A>C	Novel
3	g.12796C>T	IVS25	RSTS6b	c.4280-215C>T	Novel
4	g.25045A>C	IVS21	RSTS6c	c.3836+114A>C	Novel

Supplementary table 8. Single-nucleotide polymorphisms (SNPs) identified in the Indian population SNPs located in exons

S. No.	SNP	Synonymous/ Non-synonymous	Location	Amino acid change	Known SNP (dbSNP)	Samples
1	g.25230G>A	Synonmous	Exon21	p.Phe1236Phe	Novel	C20,C69
2	g.10107T>G	Synonmous	Exon28	p.Ala1512Ala	Novel	C9
3	g.10152T>C	Synonmous	Exon28	p.Lys1497Lys	Novel	C5, C9
4	g.18724G>T	Synonmous	Exon23	p.Ile1300Ile	*rs129974*	C1, C23, GM1LBL, GM3SF, RSTS3a, RSTS3c, RSTS4a,RSTS6a
5	g.3227G>T	Non-synonmous	Exon32	p.Asp1751Glu	Novel	C81
6	g.54203A>G	Synonmous	Exon9	p.His595His	Novel	C57
7	g.123970T>C	Synonmous	Exon3	p.Pro186Pro	Novel	C51

SNPs located in introns and I/E boundaries

S. No.	SNP	Intron	Exact position	Part of splice site	Known SNP (dbSNP)	Samples
1	g.65348C>T	Intron6	c.1330-3C>T	No	Novel	C86
2	g.54071C>T	Intron9	c.1823+94C>T	No	Novel	C62
3	g.51363T>C	Intron11	c.2113+81T>C	No	*rs130002*	C2, C17, C63, RSTS12a
4	g.31609A>C	Intron18	c.3369-128A>C	No	Novel	C62
5	g.31015A>T	Intron20	c.3698-295A>T	No	Novel	C18
6	g.30603G>A	Intron20	c.3698+58G>A	No	Novel	C2, C19, C52, C69
7	g.25469G>T	Intron20	c.3698-230G>T	No	Novel	C17
8	g.25445G>C	Intron20	c.3698-206G>C	No	Novel	C8, GM3SF, RSTS3a, RSTS3b, RSTS4b, RSTS4a, RSTS4c, RSTS5a, RSTS5c, RSTS6c,RSTS7a
9	g.25355T>G	Intron20	c.3698-116T>G	No	Novel	C19
10	g.25081T>C	Intron21	c.3779+77T>C	No	*rs129982*	C1, C2,C3, C6, C9, C13, C17, C19, C67, C69, CRSTS6b
11	g.24982G>T	Intron21	c.3779+177G>T	No	Novel	C4, C6, C10, C22, RSTS3c, RSTS5b, RSTS5c, RSTS6b, RSTS6c
12	g.23289T>C	Intron21	c.3779-173T>C	No	*rs129981*	C1, C8, C21, C24,GM3SF, RSTS3a, RSTS3c, RSTS4a, RSTS5a, RSTS5b, RSTS6a, RSTS6c
13	g.18617C>G	Intron23	c.3914+93C>G	No	Novel	C21, C17, GM1LBL
14	g.18478T>G	Intron23	c.3914+232T>G	No	Novel	C75, C83
15	g.13013C>A	Intron25	c.4113-3C>A	No	Novel	C53
16	g.12969G>A	Intron26	c.4280+42G>A	No	*rs129667*	C56,RSTS6a,RSTS6b, GM1LBL,RSTS4b
17	g.11973T>A	Intron27	c.4394+19T>A	No	Novel	C10
18	g.9919C>T	Intron28	c.4560+264C>T	No	Novel	C2, C13, C17

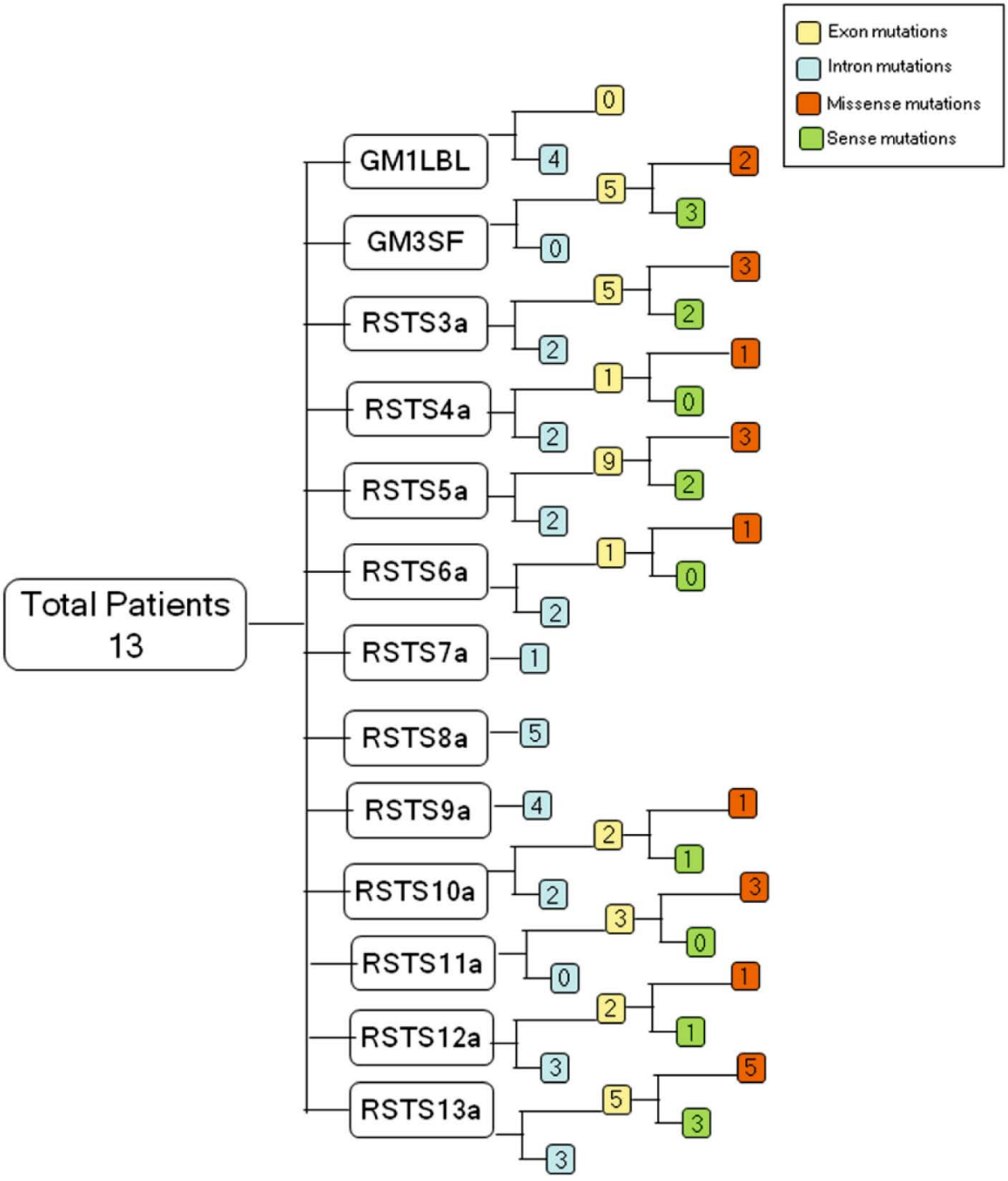
19	g.10029A>T	Intron28	c.4560+54A>T	No	Novel	C5
20	g.10054A>C	Intron28	c.4560+19A>C	No	Novel	C5, C9, C16
21	g.10268A>T	Intron28	c.4560-20A>T	Part of acceptor splice site*	Novel	C13,16
22	g.5540G>T	Intron30	c.4890-170G>T	No	Novel	C75, C76, C86
23	g.5522A>G	Intron30	c.4890-152A>G	No	Novel	C75, C76, C43, RSTS10b, C43
24	g.5148C>A	Intron31	c.5172+61C>A	No	Novel	C76
25	g.3425A>T	Intron31	c.5172-119A>T	No	Novel	C77, C78, C81, C82, C83, C85
26	g.3372C>T	Intron31	c.5172-65C>T	No	Novel	C75

Supplementary table 9. Calculated chi-square and P values (uncorrected) for the allele frequencies in RSTS cases vs controls

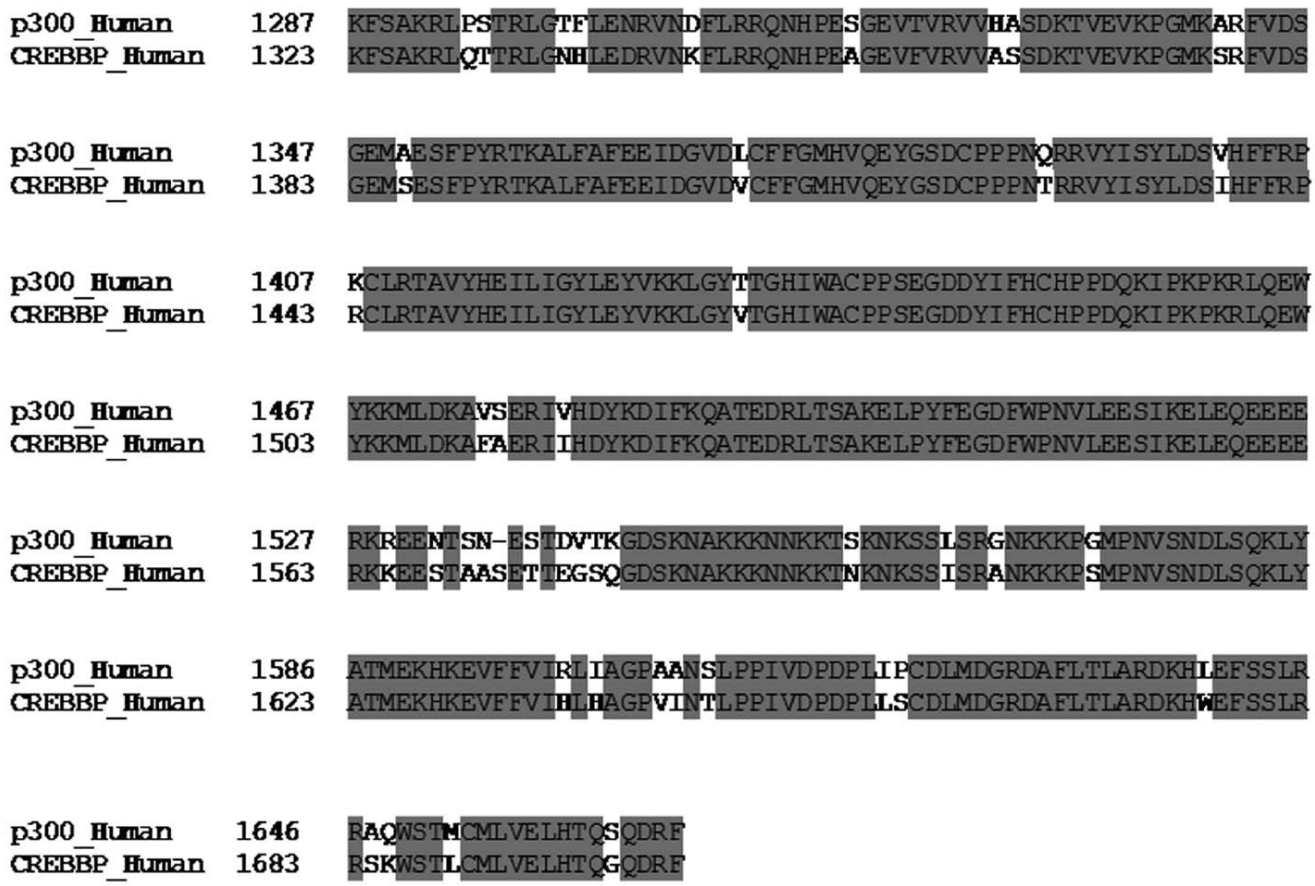
S.No.	Name	Chi-square values	Uncorrected *P* value
1	M1	0.116	0.734
2	M2	8.727	0.0031
3	M3	0.116	0.734
4	M4	0.116	0.734
5	M5	0.707	0.4004
6	M6	8.727	0.0031
7	M7	8.727	0.0031
8	M8	8.727	0.0031
9	M9	0.116	0.734
10	M10	8.727	0.0031
11	M11	0.468	0.4941
12	M12	0.349	0.5545
13	M13	0.349	0.5545
14	M14	0.116	0.734
15	M15	0.349	0.5545
16	M16	0.116	0.734
17	M17	0.232	0.6301
18	M18	0.232	0.6301
19	M19	8.727	0.0031
20	M20	0.116	0.734
21	M21	8.727	0.0031
22	M22	8.727	0.0031
23	M23	4.857	0.0275
24	M24	0.116	0.734
25	M25	8.727	0.0031
26	M26	17.524	2.84E-05
27	M27	8.727	0.0031
28	M28	8.727	0.0031
29	M29	0.116	0.734
30	M30	17.524	2.84E-05
31	M31	8.727	0.0031
32	M32	1.738	0.1874
33	M33	17.722	2.56E-05
34	M34	8.433	0.0037
35	M35	1.074	0.3001
36	M36	1.323	0.25
37	M37	0.116	0.734
38	M38	0.232	0.6301
39	M39	35.33	2.78E-09
40	M40	0.116	0.734
41	M41	8.433	0.0037
42	M42	0.468	0.4941
43	M43	0.116	0.734
44	M44	0.232	0.6301
45	M45	0.116	0.734
46	M46	17.524	2.84E-05
47	M47	0.116	0.734
48	M48	10.46	0.0012
49	M49	17.524	2.84E-05
50	M50	0.116	0.734
51	M51	0.116	0.734
52	M52	0.116	0.734
53	M53	8.727	0.0031
54	M54	8.727	0.0031
55	M55	26.391	2.79E-07
56	M56	8.727	0.0031
57	M57	17.524	2.84E-05
58	M58	8.727	0.0031
59	M59	8.727	0.0031
60	M60	8.727	0.0031
61	M61	8.727	0.0031
62	M62	8.727	0.0031
63	M63	0.116	0.734
64	M64	8.727	0.0031
65	M65	8.727	0.0031
66	M66	8.727	0.0031
67	M67	8.727	0.0031
68	M68	8.727	0.0031
69	M69	8.727	0.0031

Supplementary table 10. List of references with the number of patients reported in the study

Reference cited	Patient sample used in the study
Coupry *et al*. 2002	60
Bartsch *et al*. 2002	10
Kalkhoven *et al.* 2003	39
Bartsch *et al*. 2005	45
Udaka *et al*. 2005	21
Roelfsema *et al.* 2005	92
Bentivegna *et al*. 2006	31



Supplementary figure 1. Representation of the distribution of nucleotide changes in the *CREBBP* gene of RSTS patients. Numbers in the yellow block represent exon mutations and blue blocks represent intron mutations. Numbers in the red and green blocks represent the missense and the sense/silent mutations, respectively, in each of the patients.



Supplementary figure 2. Primary sequences corresponding to the minimal human p300 and CREBBP HAT domains are aligned with the same and conserved residues highlighted in black and white, respectively.