

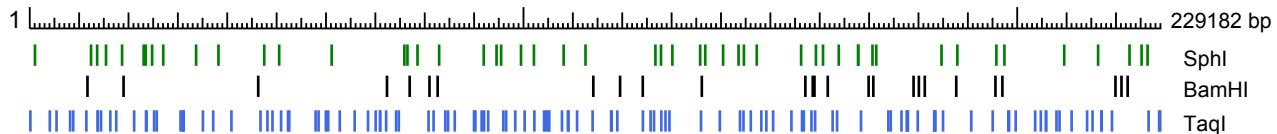
Supplement

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Figure S1 and Table S1: Restriction map of *PBX1* intron 2 and list of restriction sites



#	Site	Enzyme	#	Site	Enzyme	#	Site	Enzyme	#	Site	Enzyme
1	128/130	TaqI	50	61156/61152	SphI	99	114144/114148	BamHI	148	170689/170685	SphI
2	1058/1054	SphI	51	62794/62796	TaqI	100	117749/117751	TaqI	149	170853/170857	BamHI
3	4066/4068	TaqI	52	65808/65810	TaqI	101	117865/117867	TaqI	150	171452/171448	SphI
4	5427/5429	TaqI	53	68518/68520	TaqI	102	119004/119006	TaqI	151	173901/173903	TaqI
5	8174/8176	TaqI	54	70057/70059	TaqI	103	119564/119568	BamHI	152	174386/174388	TaqI
6	8814/8816	TaqI	55	70958/70960	TaqI	104	124161/124165	BamHI	153	176559/176561	TaqI
7	11467/11469	TaqI	56	70965/70967	TaqI	105	124184/124186	TaqI	154	177615/177617	TaqI
8	11693/11697	BamHI	57	72184/72186	TaqI	106	125742/125744	TaqI	155	177796/177798	TaqI
9	12415/12411	SphI	58	72355/72359	BamHI	107	126441/126443	TaqI	156	177864/177866	TaqI
10	13655/13651	SphI	59	74204/74206	TaqI	108	126726/126722	SphI	157	179006/179010	BamHI
11	13772/13774	TaqI	60	74745/74747	TaqI	109	127851/127847	SphI	158	179855/179857	TaqI
12	13783/13785	TaqI	61	75874/75870	SphI	110	127921/127923	TaqI	159	180083/180087	BamHI
13	14440/14442	TaqI	62	76499/76495	SphI	111	128767/128769	TaqI	160	181280/181284	BamHI
14	15449/15445	SphI	63	76954/76958	BamHI	112	129567/129569	TaqI	161	183189/183191	TaqI
15	16321/16323	TaqI	64	78535/78531	SphI	113	130158/130154	SphI	162	183284/183286	TaqI
16	17518/17520	TaqI	65	80769/80771	TaqI	114	135784/135780	SphI	163	183317/183319	TaqI
17	18703/18699	SphI	66	80967/80971	BamHI	115	135955/135957	TaqI	164	183418/183420	TaqI
18	19002/19006	BamHI	67	81792/81794	TaqI	116	136120/136124	BamHI	165	184666/184662	SphI
19	21143/21145	TaqI	68	82617/82621	BamHI	117	136819/136815	SphI	166	184976/184978	TaqI
20	23068/23064	SphI	69	82914/82910	SphI	118	139769/139771	TaqI	167	187877/187873	SphI
21	23478/23474	SphI	70	84173/84175	TaqI	119	140431/140427	SphI	168	190690/190692	TaqI
22	23551/23553	TaqI	71	84724/84726	TaqI	120	143561/143557	SphI	169	195039/195041	TaqI
23	23659/23661	TaqI	72	86080/86082	TaqI	121	143855/143857	TaqI	170	195776/195772	SphI
24	24783/24779	SphI	73	89982/89984	TaqI	122	144562/144564	TaqI	171	197404/197400	SphI
25	25194/25196	TaqI	74	90258/90260	TaqI	123	144646/144642	SphI	172	198201/198203	TaqI
26	25724/25726	TaqI	75	91526/91528	TaqI	124	146037/146039	TaqI	173	198352/198354	TaqI
27	27041/27037	SphI	76	91950/91946	SphI	125	147248/147244	SphI	174	199688/199690	TaqI
28	30547/30549	TaqI	77	92028/92030	TaqI	126	148172/148174	TaqI	175	203637/203639	TaqI
29	31021/31023	TaqI	78	92852/92854	TaqI	127	149190/149192	TaqI	176	204782/204784	TaqI
30	31031/31033	TaqI	79	94546/94542	SphI	128	150566/150568	TaqI	177	205808/205810	TaqI
31	31190/31192	TaqI	80	95471/95467	SphI	129	154272/154274	TaqI	178	205868/205870	TaqI
32	33698/33694	SphI	81	95928/95930	TaqI	130	156237/156233	SphI	179	207954/207956	TaqI
33	35075/35077	TaqI	82	96493/96495	TaqI	131	156416/156418	TaqI	180	208571/208573	TaqI
34	37156/37158	TaqI	83	98334/98336	TaqI	132	156779/156781	TaqI	181	209518/209514	SphI
35	38227/38223	SphI	84	99501/99497	SphI	133	157093/157097	BamHI	182	211018/211020	TaqI
36	40848/40850	TaqI	85	100237/100239	TaqI	134	158327/158329	TaqI	183	214148/214150	TaqI
37	46277/46281	BamHI	86	102121/102117	SphI	135	158586/158590	BamHI	184	215257/215259	TaqI
38	46738/46740	TaqI	87	102208/102210	TaqI	136	158935/158939	BamHI	185	216385/216381	SphI
39	47495/47491	SphI	88	104169/104171	TaqI	137	159068/159070	TaqI	186	217037/217039	TaqI
40	48147/48149	TaqI	89	104535/104537	TaqI	138	159241/159237	SphI	187	217110/217112	TaqI
41	49165/49167	TaqI	90	105034/105036	TaqI	139	160666/160662	SphI	188	219194/219196	TaqI
42	50518/50514	SphI	91	105231/105233	TaqI	140	161628/161632	BamHI	189	222748/222744	SphI
43	50909/50911	TaqI	92	107799/107801	TaqI	141	162615/162617	TaqI	190	225191/225187	SphI
44	52320/52322	TaqI	93	108139/108135	SphI	142	163516/163518	TaqI	191	226403/226399	SphI
45	52561/52563	TaqI	94	108987/108989	TaqI	143	163859/163855	SphI	192	226609/226611	TaqI
46	57896/57898	TaqI	95	109126/109128	TaqI	144	167786/167782	SphI	193	228732/228734	TaqI
47	58503/58505	TaqI	96	110850/110852	TaqI	145	167790/167786	SphI	194	228957/228959	TaqI
48	59976/59978	TaqI	97	112562/112558	SphI	146	168362/168364	TaqI			
49	60458/60460	TaqI	98	114001/114003	TaqI	147	169903/169907	BamHI			

Table S2: Alignment of the *TCF3* hotspot region

ID	<i>TCF3</i>	filler sequence	<i>PBX1</i>
5974	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	TTTCAACCATTCAGAGATTCATGACTCTTGACCGTGTCTCGCTGTA	
7236	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	GTCGCTAGATTTTCGGGTCACATGACTCTTGACCGTGTCTCGCTGAA	
ML11220	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	GAGAACAGTGCCTGGGGAGGTGCTAA	
ML4853	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	TTCAGAAGTTCATGGATGATTTAAACATTCATAATGTTGAAAGTGTT	
7613	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	GAGGATTATTTGGAAAGAAAGTCCCAAATAACCTCAATGACCTC	
3786	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	ACAGAAAGCTGAAGATTCATGTCATGTTGGATTG	CCT
3120	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	CTCCCTTGTCACCCAGGTGGAGTGCGATGCACTCGGCTCACTG	CC
ML11543	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	GCCAGGGTCACIGTGCGGCCACGGCTCAGTCATGCGCTCCAAA	AACATTAAAGCGGGGG
ML4316	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	GATGGTCGATCTCGACCTGTGATCCACATGCGCTTGCC	ATATC
4946	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	CTGCCAATAAAGCTCCAGTGTACATTTGACACTTGAGACATGAGACAT	TCTTTTTA
4297	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	AACCTTAACTCATAATCTATCCGCTTTTATCTTCACAAAGGGATC	GAAGCGAGAAGTTCGGCGCGAC
7979	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	ACACAGCTTCGTCATCTGAGAGGCCTGGCGCTACTGCGCATCCA	GATAGCCCTTAACACAAGGGCCGGGGCG
5489	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	ACCTGTCACAGGGCTCTTCATTAATGGGGATTTGTGGGAGGAA	GGGGG
5741	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGCCATCT	ACCCCCCTTGGTCCCTGGAGAAGCTTGTGATTAAGTTTGTTGTTAT	GCCTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		GCAGGTGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		GATTGACTCTTGGRACACAGGAACTCTTCCTTGTCCTCCATT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		TTCAGCAACCTCTCTCTCTCTGACCCCTTCAGCTTAAAGGGCTCT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		TTCAGCTCTGAGCTTGGGAGCTGTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		GACCCATTTCCTTCGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		TTTCAGCTCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		CAAGAAGCCACCAATAAAGTCAGACATTGGCCAGAGGAGGAGGAGGAA	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		AGAAACCT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		GAAAGATGGGAGAAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		CAACAGTCAGGTCAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		GTGGGAAATCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		TAICGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		TAATATGGAGGGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		CT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		ACCT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		CTCCAGGGCCAGAATCTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		ACACCTACCCGGGGAAAGGGACCTAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		ACACT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		AACTCTCACTGGCAAGGGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGTTCAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA
		CCCCCA	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
3999	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	GGTTCAGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
5752	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	ATACGTTCTACGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
3596	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	TGAGCCC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
7601	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	ACAGGCTCTCTTTCAGTCCCCTGGGA	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML9516	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	CG	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML2764	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	AGTGGAGACGGT	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
5850	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	CCC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
6776	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	TCTTTTTTTCGGAGACACCTCTGGTACTTATTTGTC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
4167	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	TCCACTTCTGGTTTTCGGGATAAA	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
7533	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	ATTTACCCATC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML11358	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	CGGGGGCA	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
6255	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	ACTCTAGGCCCCAAAAAA	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML5947	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	AGGGGCC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
7431	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	CCCCCCAGGGAGGACGCC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML13772	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	ACGGTGG	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML5319	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	AGATAT	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
7911	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	GTCGGG	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT
ML10287	TTCAGGAGAAGCTTCCAACTACCTTGATCTACCTCCTAGGGCATCT	GATTC	GGGCTTGGGAGCTTGGGAGCTTGGCAAGTGTAGTTTGTAT

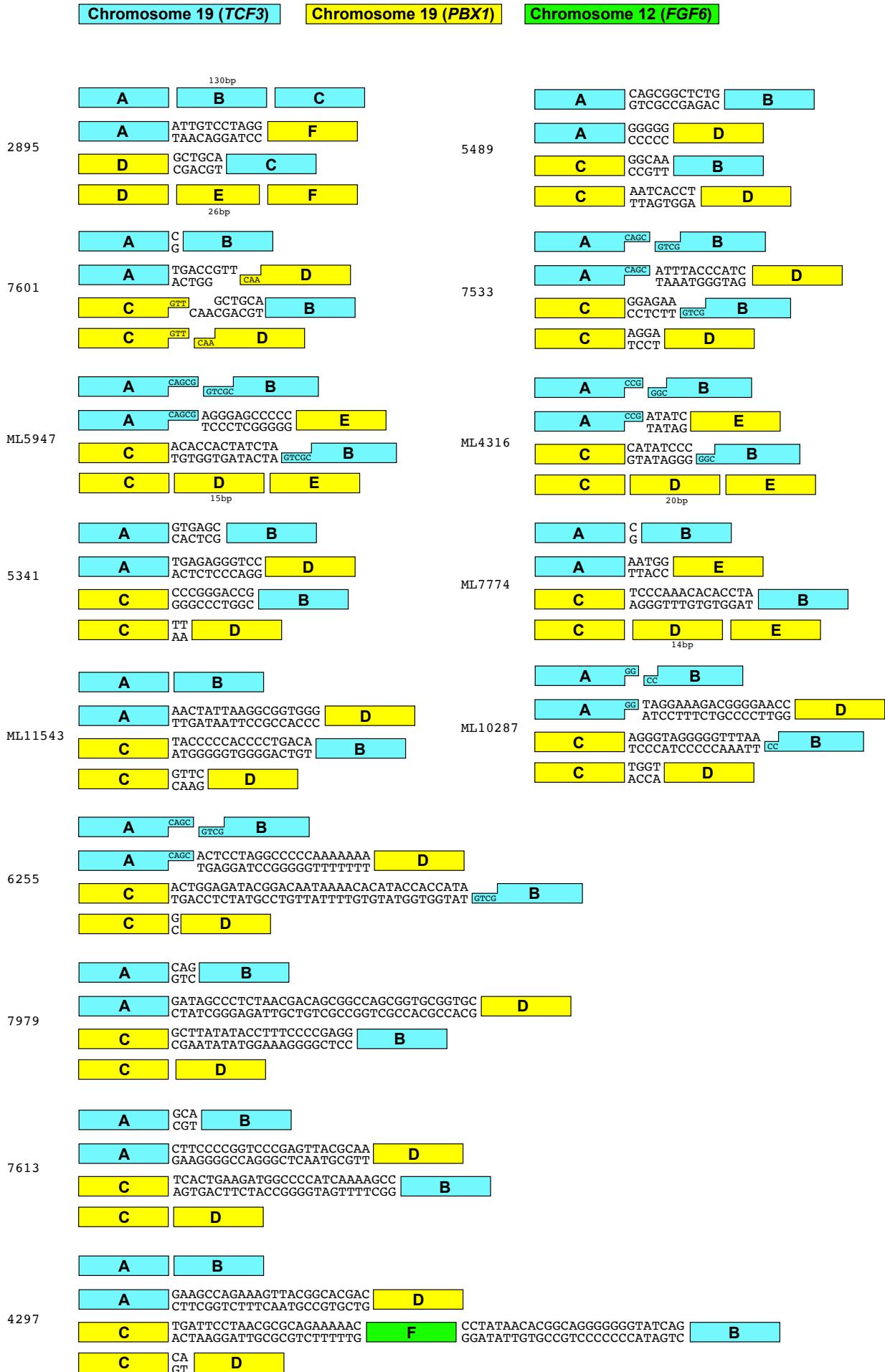
Figure S3: Chromosomal breakpoint and repair patterns

Table S4: Repeats in *PBX1* intron 2

#	query	%div.	%del.	%ins.	begin	end	orientation	repeat	class/family
1	PBX1 intron 2	0.0	4.8	0.0	947	967	+	(TATT)n	Simple repeat
2	PBX1 intron 2	15.5	0.0	0.0	1505	1533	+	(TA)n	Simple repeat
3	PBX1 intron 2	0.0	0.0	0.0	2112	2142	+	(AC)n	Simple repeat
4	PBX1 intron 2	20.5	0.0	0.0	3852	3893	+	(TG)n	Simple repeat
5	PBX1 intron 2	23.6	3.2	0.4	5858	6108	+	MIR	SINE/MIR
6	PBX1 intron 2	13.4	4.9	1.0	6236	6546	-	AluSx	SINE/Alu
7	PBX1 intron 2	6.4	0.3	0.3	6899	7763	-	L1PA7	LINE/L1
8	PBX1 intron 2	17.9	2.3	7.3	7853	8498	-	L1MB7	LINE/L1
9	PBX1 intron 2	9.8	0.0	3.9	8508	8560	-	L1MA10	LINE/L1
10	PBX1 intron 2	0.0	0.0	0.0	8563	8605	+	(TA)n	Simple repeat
11	PBX1 intron 2	12.5	3.5	0.0	8608	8895	-	AluSx	SINE/Alu
12	PBX1 intron 2	17.7	22.8	0.0	9132	9210	-	MamTip2	DNA/hAT-Tip100
13	PBX1 intron 2	34.5	4.4	0.7	9315	9451	+	MIRb	SINE/MIR
14	PBX1 intron 2	8.7	6.8	2.2	9771	9946	-	Charlie5	DNA/hAT-Charlie
15	PBX1 intron 2	14.8	3.0	9.0	9958	10173	-	MER33	DNA/hAT-Charlie
16	PBX1 intron 2	8.7	2.7	0.7	10174	10473	-	AluSx	SINE/Alu
17	PBX1 intron 2	15.7	2.6	7.9	10474	10574	-	MER33	DNA/hAT-Charlie
18	PBX1 intron 2	27.6	5.7	10.6	10946	11098	+	MIRc	SINE/MIR
19	PBX1 intron 2	9.4	2.4	0.0	11390	11677	+	AluSx	SINE/Alu
20	PBX1 intron 2	38.5	1.9	0.0	15183	15286	-	L2d2	LINE/L2
21	PBX1 intron 2	23.9	0.0	1.1	16556	16648	-	MIR	SINE/MIR
22	PBX1 intron 2	8.4	0.0	0.7	16972	17269	-	AluSx	SINE/Alu
23	PBX1 intron 2	11.3	0.0	1.0	17273	17566	-	AluSx	SINE/Alu
24	PBX1 intron 2	7.7	0.7	0.0	17918	18214	-	AluSx	SINE/Alu
25	PBX1 intron 2	12.5	2.6	5.3	18653	18691	+	(TTAT)n	Simple repeat
26	PBX1 intron 2	25.7	2.0	6.0	18924	19109	-	L4 A Mam	LINE/RTE-X
27	PBX1 intron 2	9.3	0.0	0.7	19110	19412	-	AluSx	SINE/Alu
28	PBX1 intron 2	25.7	2.0	6.0	19413	19469	-	L4 A Mam	LINE/RTE-X
29	PBX1 intron 2	35.0	10.3	1.6	19489	19662	+	L2c	LINE/L2
30	PBX1 intron 2	34.2	5.6	3.7	19708	19868	-	L2c	LINE/L2
31	PBX1 intron 2	22.9	2.2	19.8	20665	20800	+	L2c	LINE/L2
32	PBX1 intron 2	19.5	0.0	3.7	20907	20991	+	7SLRNA	srpRNA
33	PBX1 intron 2	26.1	0.0	0.0	20935	21026	-	SVA A	Retroposon/SVA
34	PBX1 intron 2	3.0	0.0	0.0	21040	21073	+	(GA)n	Simple repeat
35	PBX1 intron 2	7.7	3.3	3.3	21701	21730	+	(TAA)n	Simple repeat
36	PBX1 intron 2	0.0	0.0	0.0	22641	22666	+	(CATT)n	Simple repeat
37	PBX1 intron 2	24.2	5.7	10.1	23205	23328	+	MIRc	SINE/MIR
38	PBX1 intron 2	26.7	3.9	2.9	24017	24120	+	MIR3	SINE/MIR
39	PBX1 intron 2	0.0	0.0	0.0	25163	25189	+	(T)n	Simple repeat
40	PBX1 intron 2	17.4	2.9	2.9	25830	25864	+	GA-rich	Low complexity
41	PBX1 intron 2	24.0	2.5	4.5	26151	26307	+	MER135	DNA
42	PBX1 intron 2	32.8	0.0	0.0	26463	26523	-	MIR3	SINE/MIR
43	PBX1 intron 2	16.0	0.7	1.7	26616	26913	+	AluJb	SINE/Alu
44	PBX1 intron 2	15.7	0.0	0.0	27535	27700	-	AluSx	SINE/Alu
45	PBX1 intron 2	10.0	0.3	0.0	27701	28000	-	AluSx	SINE/Alu
46	PBX1 intron 2	27.0	8.3	3.0	28058	28405	+	MamRep434	DNA/TcMar-Tigger
47	PBX1 intron 2	13.0	0.0	0.7	29644	29946	-	AluSx	SINE/Alu
48	PBX1 intron 2	32.0	4.4	2.9	30173	30307	+	MIRb	SINE/MIR
49	PBX1 intron 2	19.3	19.1	0.9	30759	30847	-	MIRb	SINE/MIR
50	PBX1 intron 2	25.0	0.0	3.9	30913	30966	-	MIR3	SINE/MIR
51	PBX1 intron 2	8.9	5.0	0.3	30987	31269	-	AluSx	SINE/Alu
52	PBX1 intron 2	14.1	14.1	0.0	31300	31548	-	MER33	DNA/hAT-Charlie
53	PBX1 intron 2	18.7	0.0	5.1	31549	31611	-	MIR3	SINE/MIR
54	PBX1 intron 2	27.3	2.4	4.0	32803	32928	+	MamRep1151	LTR
55	PBX1 intron 2	12.0	4.0	1.3	33131	33206	+	MER20	DNA/hAT-Charlie
56	PBX1 intron 2	27.4	8.2	0.0	33372	33444	+	MIRc	SINE/MIR

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57	PBX1 intron 2	24.7	1.1	1.1	33586	33679	-	MIR1 Amn	SINE/MIR
58	PBX1 intron 2	21.3	1.8	5.7	34494	34548	+	(AATT)n	Simple repeat
59	PBX1 intron 2	21.0	5.5	3.5	34602	34932	-	MSTD	LTR/ERVL-MaLR
60	PBX1 intron 2	20.7	2.1	2.1	34970	35017	+	(TTCTCTT)n	Simple repeat
61	PBX1 intron 2	23.4	5.4	3.5	35018	35025	+	(TTCC)n	Simple repeat
62	PBX1 intron 2	29.5	10.4	0.0	35507	35699	-	MIRc	SINE/MIR
63	PBX1 intron 2	29.6	0.0	0.0	35732	35777	+	(TT)n	Simple repeat
64	PBX1 intron 2	34.4	0.8	0.8	36753	36875	-	MER94B	DNA/hAT-Blackjack
65	PBX1 intron 2	8.9	1.0	0.0	36936	37237	-	AluSx	SINE/Alu
66	PBX1 intron 2	30.4	0.7	2.0	37352	37502	+	MamSINE1	SINE/tRNA-RTE
67	PBX1 intron 2	8.2	1.0	0.7	37644	37951	+	AluSx	SINE/Alu
68	PBX1 intron 2	15.8	4.5	2.2	40469	40512	+	(TTTTAAG)n	Simple repeat
69	PBX1 intron 2	34.1	5.8	2.2	40542	40618	-	MIR	SINE/MIR
70	PBX1 intron 2	0.0	0.0	0.0	40619	40651	+	(T)n	Simple repeat
71	PBX1 intron 2	13.5	0.4	0.4	40662	40929	-	AluSx	SINE/Alu
72	PBX1 intron 2	34.1	5.8	2.2	40930	41014	-	MIR	SINE/MIR
73	PBX1 intron 2	10.8	0.0	12.8	41121	41173	-	L2c	LINE/L2
74	PBX1 intron 2	35.6	6.2	4.1	41707	41946	-	L2c	LINE/L2
75	PBX1 intron 2	27.1	12.4	4.6	42411	42693	+	MamRep434	DNA/TcMar-Tigger
76	PBX1 intron 2	13.9	0.0	0.0	42897	43126	+	AluSx	SINE/Alu
77	PBX1 intron 2	15.3	0.0	9.2	43143	43272	+	AluSx	SINE/Alu
78	PBX1 intron 2	22.1	7.1	0.0	43314	43453	+	L2a	LINE/L2
79	PBX1 intron 2	33.6	7.8	1.6	44050	44524	-	L2c	LINE/L2
80	PBX1 intron 2	19.5	0.0	0.0	44698	44738	+	MER117	DNA/hAT-Charlie
81	PBX1 intron 2	29.6	3.4	3.4	44738	44856	+	MER117	DNA/hAT-Charlie
82	PBX1 intron 2	17.7	1.6	0.0	44873	44934	-	L2b	LINE/L2
83	PBX1 intron 2	25.4	1.7	1.7	44899	44958	+	L2a	LINE/L2
84	PBX1 intron 2	31.7	0.0	0.0	45210	45291	-	MIRc	SINE/MIR
85	PBX1 intron 2	27.5	0.0	2.0	46434	46537	+	L2b	LINE/L2
86	PBX1 intron 2	3.0	0.0	0.3	47927	48226	-	AluY	SINE/Alu
87	PBX1 intron 2	28.6	7.1	0.0	49498	49707	+	MIR	SINE/MIR
88	PBX1 intron 2	18.4	16.7	4.1	49754	49861	-	L1ME4b	LINE/L1
89	PBX1 intron 2	35.8	7.3	1.3	50008	50225	+	L2b	LINE/L2
90	PBX1 intron 2	32.0	2.6	2.6	50880	51033	-	MIR3	SINE/MIR
91	PBX1 intron 2	13.7	0.0	0.7	51462	51763	-	AluSx	SINE/Alu
92	PBX1 intron 2	28.2	1.2	1.7	53456	53697	-	MIR	SINE/MIR
93	PBX1 intron 2	27.2	11.4	1.1	53854	54098	+	MamSINE1	SINE/tRNA-RTE
94	PBX1 intron 2	27.1	9.4	4.5	54231	54400	+	MER103C	DNA/hAT-Charlie
95	PBX1 intron 2	31.5	2.1	5.7	56294	56438	-	Charlie4z	DNA/hAT-Charlie
96	PBX1 intron 2	13.7	5.8	6.9	56581	56871	+	AluJb	SINE/Alu
97	PBX1 intron 2	11.2	0.0	0.0	57366	57670	-	AluSx	SINE/Alu
98	PBX1 intron 2	9.6	1.1	0.0	57691	57971	-	AluSx	SINE/Alu
99	PBX1 intron 2	25.4	0.0	6.1	57995	58046	+	(TCTT)n	Simple repeat
100	PBX1 intron 2	25.7	0.0	2.1	59454	59502	+	(CA)n	Simple repeat
101	PBX1 intron 2	9.3	4.1	0.0	59512	59801	-	AluSx	SINE/Alu
102	PBX1 intron 2	27.7	2.3	6.8	61193	61544	+	Charlie23a	DNA/hAT-Charlie
103	PBX1 intron 2	9.3	0.0	0.0	62390	62412	+	(TG)n	Simple repeat
104	PBX1 intron 2	4.3	0.0	0.0	62499	62522	+	(A)n	Simple repeat
105	PBX1 intron 2	20.8	2.1	0.0	63256	63303	-	L3b	LINE/CR1
106	PBX1 intron 2	15.9	0.0	0.0	65400	65427	+	(TC)n	Simple repeat
107	PBX1 intron 2	20.9	9.0	1.4	65428	65694	-	UCON64	Unknown
108	PBX1 intron 2	34.3	3.9	1.1	66148	66327	-	MIR3	SINE/MIR
109	PBX1 intron 2	28.1	15.0	0.0	67301	67453	-	MIRb	SINE/MIR
110	PBX1 intron 2	4.5	0.0	0.0	67965	67987	+	(T)n	Simple repeat
111	PBX1 intron 2	29.9	12.4	0.0	69611	69747	-	MIR3	SINE/MIR
112	PBX1 intron 2	11.2	0.0	0.0	69835	70138	-	AluSx	SINE/Alu
113	PBX1 intron 2	24.4	5.5	2.7	70336	70588	+	MIR	SINE/MIR
114	PBX1 intron 2	12.0	3.7	0.0	73547	73573	+	(TG)n	Simple repeat
115	PBX1 intron 2	29.4	0.0	1.5	74124	74192	+	MIR3	SINE/MIR
116	PBX1 intron 2	10.7	0.0	0.0	75259	75288	+	(AC)n	Simple repeat

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117	PBX1 intron 2	31.7	5.9	1.1	75685	75853	+	MIRb	SINE/MIR
118	PBX1 intron 2	17.3	0.0	0.0	76254	76355	+	U6	snRNA
119	PBX1 intron 2	18.7	0.3	0.3	76356	76650	-	AluJb	SINE/Alu
120	PBX1 intron 2	12.2	0.0	0.3	77235	77538	-	AluSx	SINE/Alu
121	PBX1 intron 2	20.5	5.0	0.0	78701	78740	+	(TTTG)n	Simple repeat
122	PBX1 intron 2	27.4	0.0	0.0	79401	79473	-	L2d2	LINE/L2
123	PBX1 intron 2	33.5	5.4	2.2	80329	80551	-	MIRb	SINE/MIR
124	PBX1 intron 2	26.6	5.8	1.2	82565	82720	+	MIR1 Amn	SINE/MIR
125	PBX1 intron 2	27.2	12.3	0.7	84104	84225	+	MIR3	SINE/MIR
126	PBX1 intron 2	22.0	0.0	3.5	84358	84503	+	MER5B	DNA/hAT-Charlie
127	PBX1 intron 2	6.0	0.0	0.3	84505	84803	-	AluY	SINE/Alu
128	PBX1 intron 2	29.6	2.4	1.2	85199	85362	-	MIRb	SINE/MIR
129	PBX1 intron 2	14.5	1.0	0.0	86906	87209	-	AluSx	SINE/Alu
130	PBX1 intron 2	20.9	4.5	0.0	88246	88289	+	GA-rich	Low complexity
131	PBX1 intron 2	0.0	0.0	0.0	88620	88659	+	(GT)n	Simple repeat
132	PBX1 intron 2	11.6	2.2	0.0	88757	88980	-	AluSx	SINE/Alu
133	PBX1 intron 2	34.3	3.8	2.1	89077	89311	-	MIRc	SINE/MIR
134	PBX1 intron 2	23.7	12.7	3.0	89387	89562	-	L1ME2	LINE/L1
135	PBX1 intron 2	13.7	1.0	0.0	89563	89855	-	AluSx	SINE/Alu
136	PBX1 intron 2	23.7	12.7	3.0	89856	90039	-	L1ME2	LINE/L1
137	PBX1 intron 2	13.4	1.1	0.0	90180	90448	+	AluSx	SINE/Alu
138	PBX1 intron 2	11.6	0.3	0.3	91790	92101	-	AluSx	SINE/Alu
139	PBX1 intron 2	14.0	5.9	1.9	92679	92729	+	Mam R4	LINE/Dong-R4
140	PBX1 intron 2	13.1	8.0	0.0	93494	93553	+	(TTATA)n	Simple repeat
141	PBX1 intron 2	30.4	3.2	1.6	93744	94120	+	Mam R4	LINE/Dong-R4
142	PBX1 intron 2	5.6	0.0	0.0	94856	94874	+	(A)n	Simple repeat
143	PBX1 intron 2	28.2	0.0	0.0	95352	95436	+	MIRb	SINE/MIR
144	PBX1 intron 2	23.5	3.3	1.7	95436	95690	-	MIR	SINE/MIR
145	PBX1 intron 2	29.5	0.0	0.0	96612	96740	+	MLT1N2	LTR/ERVL-MaLR
146	PBX1 intron 2	9.3	0.0	0.0	98114	98415	-	AluSx	SINE/Alu
147	PBX1 intron 2	13.8	0.0	0.0	98736	99031	+	AluSx	SINE/Alu
148	PBX1 intron 2	18.6	0.0	1.8	99822	99998	+	(CCTT)n	Simple repeat
149	PBX1 intron 2	6.7	9.4	0.0	99999	100030	+	(CT)n	Simple repeat
150	PBX1 intron 2	18.6	0.0	1.8	100031	100053	+	(CCTT)n	Simple repeat
151	PBX1 intron 2	10.7	5.4	1.9	101303	101654	-	THE1B	LTR/ERVL-MaLR
152	PBX1 intron 2	15.4	0.0	0.6	101963	102275	-	AluSx	SINE/Alu
153	PBX1 intron 2	29.2	3.5	3.5	102534	102675	-	MLT1N2	LTR/ERVL-MaLR
154	PBX1 intron 2	4.9	0.0	0.0	103036	103056	+	(ATT)n	Simple repeat
155	PBX1 intron 2	24.2	0.0	14.5	103101	103187	+	Mam R4	LINE/Dong-R4
156	PBX1 intron 2	28.9	1.6	2.7	103210	103394	+	Mam R4	LINE/Dong-R4
157	PBX1 intron 2	33.8	4.3	0.5	103485	103695	-	MIRb	SINE/MIR
158	PBX1 intron 2	25.0	6.1	0.0	104021	104151	+	(AT)n	Simple repeat
159	PBX1 intron 2	26.4	10.6	0.5	104301	104479	+	Tigger12	DNA/TcMar-Tigger
160	PBX1 intron 2	20.1	2.9	0.0	106496	106650	-	L1M3	LINE/L1
161	PBX1 intron 2	32.6	0.0	0.0	108668	108739	+	(TTT)n	Simple repeat
162	PBX1 intron 2	20.2	1.7	1.7	109597	109605	+	(TCTTTT)n	Simple repeat
163	PBX1 intron 2	17.7	0.0	0.0	109609	109640	+	(T)n	Simple repeat
164	PBX1 intron 2	20.2	1.7	1.7	109643	109655	+	(TCTTTT)n	Simple repeat
165	PBX1 intron 2	8.3	0.0	0.0	110155	110323	-	AluSx	SINE/Alu
166	PBX1 intron 2	15.4	5.1	0.0	110660	110698	-	MIR3	SINE/MIR
167	PBX1 intron 2	13.2	0.0	0.0	111537	111561	+	(C)n	Simple repeat
168	PBX1 intron 2	28.7	2.3	0.0	111616	111839	-	MIRc	SINE/MIR
169	PBX1 intron 2	6.4	1.3	0.0	112032	112109	+	MADE1	DNA/TcMar-Mariner
170	PBX1 intron 2	30.0	2.9	1.9	113308	113409	+	MIR	SINE/MIR
171	PBX1 intron 2	3.0	0.0	2.3	113773	114080	-	AluY	SINE/Alu
172	PBX1 intron 2	28.1	5.4	3.2	114134	114225	-	L2d2	LINE/L2
173	PBX1 intron 2	22.8	0.0	6.2	116476	116578	-	MIRc	SINE/MIR
174	PBX1 intron 2	15.6	0.0	1.0	117070	117166	-	L1PA16	LINE/L1
175	PBX1 intron 2	24.8	8.7	5.8	117379	117562	-	L3	LINE/CR1
176	PBX1 intron 2	16.4	9.6	0.4	117671	117878	+	AluJb	SINE/Alu

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177	PBX1 intron 2	25.1	0.0	2.6	118020	118059	+	(TATACA)n	Simple repeat
178	PBX1 intron 2	13.8	0.0	0.0	118346	118533	+	L1PA15	LINE/L1
179	PBX1 intron 2	22.4	0.8	9.2	119088	119205	-	L2a	LINE/L2
180	PBX1 intron 2	34.1	9.4	0.0	119949	120086	-	MIRc	SINE/MIR
181	PBX1 intron 2	31.1	10.4	0.0	120087	120274	-	MIRc	SINE/MIR
182	PBX1 intron 2	18.1	4.6	4.6	120491	120806	-	AluJb	SINE/Alu
183	PBX1 intron 2	32.3	5.2	2.0	121654	121846	-	MIRc	SINE/MIR
184	PBX1 intron 2	29.5	9.2	5.4	122292	122542	-	MIRb	SINE/MIR
185	PBX1 intron 2	29.6	10.6	2.6	122647	122892	+	MIRb	SINE/MIR
186	PBX1 intron 2	7.0	0.4	0.7	123402	123676	+	AluY	SINE/Alu
187	PBX1 intron 2	33.8	4.6	8.1	123747	123969	+	MamRep38	DNA/hAT-Tip100
188	PBX1 intron 2	14.4	0.7	0.7	123970	124277	+	AluJb	SINE/Alu
189	PBX1 intron 2	33.8	4.6	8.1	124278	124333	+	MamRep38	DNA/hAT-Tip100
190	PBX1 intron 2	28.4	3.5	8.1	124920	125061	+	X6a DNA	DNA/TcMar-Tigger
191	PBX1 intron 2	18.4	0.0	0.0	125983	126033	+	(T)n	Simple repeat
192	PBX1 intron 2	20.7	0.0	2.9	126458	126492	+	(CTTT)n	Simple repeat
193	PBX1 intron 2	23.3	4.1	0.0	127180	127252	+	7SLRNA	srpRNA
194	PBX1 intron 2	22.4	5.6	0.0	127197	127303	-	SVA A	Retroposon/SVA
195	PBX1 intron 2	36.6	2.9	1.9	127472	127574	-	MIRc	SINE/MIR
196	PBX1 intron 2	10.3	0.3	0.0	127701	128001	-	AluSx	SINE/Alu
197	PBX1 intron 2	16.0	2.3	1.1	128468	128814	+	Tigger4b	DNA/TcMar-Tigger
198	PBX1 intron 2	32.8	0.0	0.0	129029	129086	+	L2a	LINE/L2
199	PBX1 intron 2	14.7	2.6	0.0	129402	129439	+	(ATATTGT)n	Simple repeat
200	PBX1 intron 2	33.5	8.8	1.3	129488	129635	-	MIRc	SINE/MIR
201	PBX1 intron 2	32.8	11.8	1.3	130814	131017	+	L2c	LINE/L2
202	PBX1 intron 2	32.2	0.0	0.0	131061	131175	+	L2b	LINE/L2
203	PBX1 intron 2	36.2	5.6	6.5	131502	131717	+	L2c	LINE/L2
204	PBX1 intron 2	20.4	8.7	0.9	131747	131954	+	Chap1a Mam	DNA/hAT-Charlie
205	PBX1 intron 2	33.7	13.5	2.7	132009	132416	+	L2c	LINE/L2
206	PBX1 intron 2	22.7	12.5	0.0	133174	133261	+	L3	LINE/CR1
207	PBX1 intron 2	21.7	0.0	0.0	133433	133464	+	(TTGACT)n	Simple repeat
208	PBX1 intron 2	31.7	5.3	2.3	133598	133768	+	MIRb	SINE/MIR
209	PBX1 intron 2	27.7	10.1	0.4	133771	133998	-	MIR	SINE/MIR
210	PBX1 intron 2	30.9	10.8	0.0	135248	135441	+	Tigger15a	DNA/TcMar-Tigger
211	PBX1 intron 2	26.0	10.7	0.4	135450	135673	-	MIR	SINE/MIR
212	PBX1 intron 2	25.0	10.7	9.9	135707	135986	+	Tigger15a	DNA/TcMar-Tigger
213	PBX1 intron 2	26.4	3.8	1.8	137491	137737	+	MIRc	SINE/MIR
214	PBX1 intron 2	26.7	3.3	0.0	138236	138295	+	AmnL2-1	LINE/L2
215	PBX1 intron 2	19.7	3.5	0.0	139715	140003	-	7SLRNA	srpRNA
216	PBX1 intron 2	3.6	13.8	0.0	140651	140679	+	GA-rich	Low complexity
217	PBX1 intron 2	15.8	0.9	0.5	141729	141944	-	MER20	DNA/hAT-Charlie
218	PBX1 intron 2	27.4	1.0	1.0	142995	143097	-	X6b DNA	DNA/TcMar-Tigger
219	PBX1 intron 2	31.7	1.2	0.0	143323	143404	-	AmnL2-1	LINE/L2
220	PBX1 intron 2	0.0	0.0	0.0	144084	144107	+	(GT)n	Simple repeat
221	PBX1 intron 2	0.0	0.0	0.0	144108	144145	+	(GA)n	Simple repeat
222	PBX1 intron 2	27.6	10.3	12.1	145003	145082	-	MIR	SINE/MIR
223	PBX1 intron 2	14.1	1.3	0.6	145083	145397	-	L1PA17	LINE/L1
224	PBX1 intron 2	27.6	10.3	12.1	145398	145559	-	MIR	SINE/MIR
225	PBX1 intron 2	28.8	6.3	1.5	145588	145714	-	L2b	LINE/L2
226	PBX1 intron 2	26.5	0.0	1.0	146736	146834	+	MIR	SINE/MIR
227	PBX1 intron 2	11.9	0.3	0.3	147088	147398	-	AluSx	SINE/Alu
228	PBX1 intron 2	7.7	0.0	0.0	147954	148250	-	AluY	SINE/Alu
229	PBX1 intron 2	0.0	0.0	0.0	148867	148883	+	(A)n	Simple repeat
230	PBX1 intron 2	12.5	0.0	3.7	150244	150271	+	(CCTT)n	Simple repeat
231	PBX1 intron 2	21.2	0.0	3.0	150921	150988	-	MIR3	SINE/MIR
232	PBX1 intron 2	25.0	1.8	0.0	151637	151692	+	MIR	SINE/MIR
233	PBX1 intron 2	21.4	1.6	28.8	151714	151842	+	L2d2	LINE/L2
234	PBX1 intron 2	29.5	4.8	0.0	152234	152338	+	L2a	LINE/L2
235	PBX1 intron 2	27.4	0.0	0.0	153263	153335	+	7SLRNA	srpRNA
236	PBX1 intron 2	24.1	6.4	0.9	153275	153374	-	SVA A	Retroposon/SVA

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237	PBX1 intron 2	0.0	0.0	0.0	153375	153419	+	(AC)n	Simple repeat
238	PBX1 intron 2	27.6	9.2	1.9	154617	154820	-	MIRb	SINE/MIR
239	PBX1 intron 2	32.3	3.1	1.0	155742	155838	+	AmnSINE1	SINE/5S-Deu-L2
240	PBX1 intron 2	22.1	16.1	3.2	156195	156306	+	MER5B	DNA/hAT-Charlie
241	PBX1 intron 2	0.0	0.0	3.9	158113	158139	+	(GT)n	Simple repeat
242	PBX1 intron 2	25.8	3.4	0.4	158538	158687	-	L2a	LINE/L2
243	PBX1 intron 2	12.6	8.3	0.0	159291	159326	+	(TC)n	Simple repeat
244	PBX1 intron 2	29.2	3.0	3.0	159709	159775	-	MIR3	SINE/MIR
245	PBX1 intron 2	12.0	3.7	0.5	161064	161280	-	MER30	DNA/hAT-Charlie
246	PBX1 intron 2	0.0	0.0	0.0	161360	161398	+	(T)n	Simple repeat
247	PBX1 intron 2	22.2	31.5	0.6	162435	162561	-	MIRb	SINE/MIR
248	PBX1 intron 2	30.6	0.0	1.6	163980	164042	+	L2d2	LINE/L2
249	PBX1 intron 2	14.9	2.6	2.6	164718	164731	+	GA-rich	Low complexity
250	PBX1 intron 2	16.3	3.1	0.0	164732	165020	+	AluJb	SINE/Alu
251	PBX1 intron 2	14.9	2.6	2.6	165021	165044	+	GA-rich	Low complexity
252	PBX1 intron 2	14.0	3.1	0.0	166171	166202	+	(ATATAC)n	Simple repeat
253	PBX1 intron 2	22.1	2.3	0.0	166203	166208	+	(TATA)n	Simple repeat
254	PBX1 intron 2	27.4	2.6	4.6	166211	166474	-	MIR	SINE/MIR
255	PBX1 intron 2	26.8	2.9	4.5	166484	166551	+	(ATAA)n	Simple repeat
256	PBX1 intron 2	30.0	5.1	2.2	166552	166728	-	MIRb	SINE/MIR
257	PBX1 intron 2	26.5	25.3	0.0	166823	166905	+	MamSINE1	SINE/tRNA-RTE
258	PBX1 intron 2	13.2	0.0	0.0	167748	167772	+	(GT)n	Simple repeat
259	PBX1 intron 2	37.0	10.7	0.3	168988	169243	+	L2c	LINE/L2
260	PBX1 intron 2	6.3	1.3	0.0	169244	169322	+	MADE1	DNA/TcMar-Mariner
261	PBX1 intron 2	37.0	10.7	0.3	169323	169412	+	L2c	LINE/L2
262	PBX1 intron 2	31.0	10.0	3.3	169590	169819	+	L2c	LINE/L2
263	PBX1 intron 2	20.4	4.3	5.7	169923	170027	+	L2c	LINE/L2
264	PBX1 intron 2	31.4	0.9	2.8	170322	170429	+	UCON58	DNA
265	PBX1 intron 2	28.1	1.6	0.0	171241	171304	-	L2b	LINE/L2
266	PBX1 intron 2	28.4	0.0	0.0	172148	172186	+	GA-rich	Low complexity
267	PBX1 intron 2	19.1	0.0	8.9	173978	174026	+	A-rich	Low complexity
268	PBX1 intron 2	7.8	4.6	0.6	174061	174135	-	L1ME1	LINE/L1
269	PBX1 intron 2	11.4	1.3	0.0	174160	174467	-	AluSx	SINE/Alu
270	PBX1 intron 2	21.8	3.1	7.7	174468	174985	-	L1ME1	LINE/L1
271	PBX1 intron 2	21.0	8.9	2.8	174997	175265	-	AluJb	SINE/Alu
272	PBX1 intron 2	19.2	0.0	0.0	175268	175319	-	L1ME1	LINE/L1
273	PBX1 intron 2	0.0	0.0	0.0	176443	176479	+	(TG)n	Simple repeat
274	PBX1 intron 2	20.4	4.1	0.0	177062	177110	-	L2c	LINE/L2
275	PBX1 intron 2	23.8	0.0	1.6	177283	177346	-	L2b	LINE/L2
276	PBX1 intron 2	29.3	10.2	2.8	177350	177546	-	L2c	LINE/L2
277	PBX1 intron 2	0.0	0.0	0.0	178429	178464	+	(GT)n	Simple repeat
278	PBX1 intron 2	13.5	0.0	0.0	178950	179238	+	AluSx	SINE/Alu
279	PBX1 intron 2	30.1	2.5	5.9	180429	180710	-	MLT1J	LTR/ERVL-MaLR
280	PBX1 intron 2	22.4	0.0	0.0	181289	181346	+	L2a	LINE/L2
281	PBX1 intron 2	4.9	0.0	4.5	181564	181586	+	(GTG)n	Simple repeat
282	PBX1 intron 2	26.3	3.0	1.5	181677	181811	-	MIRb	SINE/MIR
283	PBX1 intron 2	11.5	0.0	10.1	183059	183396	-	AluSx	SINE/Alu
284	PBX1 intron 2	31.8	5.1	1.1	183682	183859	-	MIRb	SINE/MIR
285	PBX1 intron 2	30.2	1.0	2.1	183973	184068	+	(TA)n	Simple repeat
286	PBX1 intron 2	26.8	2.2	4.5	184796	184932	+	LTR90A	LTR
287	PBX1 intron 2	25.2	7.4	0.0	185214	185348	+	LTR90A	LTR
288	PBX1 intron 2	30.1	3.7	3.3	185775	186045	-	L1ME4c	LINE/L1
289	PBX1 intron 2	16.9	0.0	0.0	186354	186387	+	(GGAT)n	Simple repeat
290	PBX1 intron 2	18.0	1.6	2.5	186565	186809	+	AluJb	SINE/Alu
291	PBX1 intron 2	0.0	0.0	0.0	186835	186872	+	(GT)n	Simple repeat
292	PBX1 intron 2	18.8	7.2	5.9	187647	187722	+	Charlie1b	DNA/hAT-Charlie
293	PBX1 intron 2	8.4	0.3	0.0	187723	188021	+	AluSx	SINE/Alu
294	PBX1 intron 2	18.8	7.2	5.9	188022	188270	+	Charlie1b	DNA/hAT-Charlie
295	PBX1 intron 2	10.7	0.3	0.3	188271	188570	-	AluSx	SINE/Alu
296	PBX1 intron 2	18.8	7.2	5.9	188571	188729	+	Charlie1b	DNA/hAT-Charlie

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297	PBX1 intron 2	0.0	0.0	0.0	188896	188935	+	(TG)n	Simple repeat
298	PBX1 intron 2	28.2	0.0	5.2	190093	190153	+	(TTGTTT)n	Simple repeat
299	PBX1 intron 2	22.0	0.0	0.0	191348	191392	+	(GTGTGT)n	Simple repeat
300	PBX1 intron 2	11.2	4.8	0.0	191887	192137	-	AluSx	SINE/Alu
301	PBX1 intron 2	7.4	0.0	0.0	192688	192716	+	(A)n	Simple repeat
302	PBX1 intron 2	5.5	0.0	0.0	194390	194408	+	(TAT)n	Simple repeat
303	PBX1 intron 2	21.3	0.0	0.0	195514	195574	+	L2b	LINE/L2
304	PBX1 intron 2	29.9	6.8	2.6	195632	195851	+	L1ME3A	LINE/L1
305	PBX1 intron 2	20.1	1.7	0.8	197053	197172	+	(CCTT)n	Simple repeat
306	PBX1 intron 2	7.0	10.0	0.0	197249	197279	+	A-rich	Low complexity
307	PBX1 intron 2	3.4	0.3	0.0	198137	198431	-	AluY	SINE/Alu
308	PBX1 intron 2	28.7	7.0	3.2	199618	199787	-	MIRc	SINE/MIR
309	PBX1 intron 2	29.8	3.5	4.1	199880	200222	-	MLT1J	LTR/ERVL-MaLR
310	PBX1 intron 2	25.6	8.6	5.8	201122	201341	-	UCON64	Unknown
311	PBX1 intron 2	29.2	0.8	2.4	202233	202485	-	MIRb	SINE/MIR
312	PBX1 intron 2	29.5	1.1	0.0	202620	202714	-	L2d2	LINE/L2
313	PBX1 intron 2	24.3	1.4	0.0	203233	203302	-	MIRc	SINE/MIR
314	PBX1 intron 2	9.4	3.1	1.0	203387	203702	-	AluSx	SINE/Alu
315	PBX1 intron 2	11.0	6.0	0.0	203703	203726	+	(TTTC)n	Simple repeat
316	PBX1 intron 2	23.7	2.4	0.0	203894	204062	-	MER45A	DNA/hAT-Tip100
317	PBX1 intron 2	5.3	0.0	0.0	204339	204358	+	(A)n	Simple repeat
318	PBX1 intron 2	28.2	14.2	2.0	204896	205029	-	MIRb	SINE/MIR
319	PBX1 intron 2	13.7	0.3	0.7	205477	205771	+	AluSx	SINE/Alu
320	PBX1 intron 2	30.7	8.0	0.0	206174	206261	+	MIRc	SINE/MIR
321	PBX1 intron 2	27.0	13.5	0.0	206954	207042	-	MIRc	SINE/MIR
322	PBX1 intron 2	0.0	0.0	0.0	209933	209962	+	(CA)n	Simple repeat
323	PBX1 intron 2	27.4	4.1	5.5	212684	212830	+	L2c	LINE/L2
324	PBX1 intron 2	0.0	0.0	0.0	213589	213624	+	(TG)n	Simple repeat
325	PBX1 intron 2	0.0	0.0	0.0	213632	213668	+	(GA)n	Simple repeat
326	PBX1 intron 2	14.0	4.5	0.0	213843	214128	+	AluSx	SINE/Alu
327	PBX1 intron 2	15.2	2.4	0.0	215051	215345	+	AluJb	SINE/Alu
328	PBX1 intron 2	20.8	10.2	2.2	215615	215731	+	MIR	SINE/MIR
329	PBX1 intron 2	3.6	0.0	0.0	215732	215814	-	AluY	SINE/Alu
330	PBX1 intron 2	24.8	9.2	3.4	217711	217906	-	MamSINE1	SINE/tRNA-RTE
331	PBX1 intron 2	10.6	2.1	0.0	218725	218771	-	MLT1J	LTR/ERVL-MaLR
332	PBX1 intron 2	26.0	1.8	0.0	220064	220118	+	(GTGT)n	Simple repeat
333	PBX1 intron 2	15.8	0.0	3.5	221230	221259	+	(ACAA)n	Simple repeat
334	PBX1 intron 2	10.3	0.0	2.6	221411	221450	+	MIRb	SINE/MIR
335	PBX1 intron 2	30.4	6.2	7.6	223035	223194	-	L2d2	LINE/L2
336	PBX1 intron 2	0.0	0.0	0.0	223371	223410	+	(TG)n	Simple repeat
337	PBX1 intron 2	29.2	0.0	0.0	225049	225090	+	(TTT)n	Simple repeat
338	PBX1 intron 2	7.9	3.7	0.0	225454	225480	+	(CTTTT)n	Simple repeat
339	PBX1 intron 2	32.3	1.3	0.0	227184	227262	+	(CTTC)n	Simple repeat
340	PBX1 intron 2	16.5	15.4	9.0	228473	228532	-	L1MB3	LINE/L1
341	PBX1 intron 2	10.0	0.4	2.4	228533	228789	-	AluY	SINE/Alu
342	PBX1 intron 2	16.5	15.4	9.0	228790	228981	-	L1MB3	LINE/L1

Table S5: Repeats in *TCF3* intron 16

#	query	%div.	%del.	%ins.	begin	end	orientation	repeat	class/family
1	TCF3 intron 16	28.6	14.8	0.8	337	1058	-	L2a	LINE/L2
2	TCF3 intron 16	24.7	5.1	0.0	1182	1359	+	MER20	DNA/hAT-Charlie
3	TCF3 intron 16	29.5	2.3	3.8	1979	2193	-	L1M5	LINE/L1
4	TCF3 intron 16	24.8	4.7	2.5	2312	2543	-	AluJb	SINE/Alu
5	TCF3 intron 16	20.3	7.2	0.0	2544	2612	+	U6	snRNA
6	TCF3 intron 16	10.0	0.0	0.0	2616	2904	-	AluY	SINE/Alu

Table S6: Potential cryptic recombination signal sites in *PBX1* intron 2

#	query	begin	end	type	sequence	orientation
1	PBX1 intron 2	434	472	RSS23	cacaaaaggcagcagacttagaggttctcaacagagagtgtt	+
2	PBX1 intron 2	2113	2140	RSS12	cacacacacacacacacacacacacaca	+
3	PBX1 intron 2	2115	2142	RSS12	cacacacacacacacacacacacacaca	+
4	PBX1 intron 2	2117	2155	RSS23	cacacacacacacacacacacacacacaatgtctggattaa	+
5	PBX1 intron 2	2119	2146	RSS12	cacacacacacacacacacacacacaatgc	+
6	PBX1 intron 2	2123	2161	RSS23	cacacacacacacacacacacaatgtctggattaagaggc	+
7	PBX1 intron 2	2129	2167	RSS23	cacacacacacacaatgtctggattaagaggccaccct	+
8	PBX1 intron 2	3370	3397	RSS12	cacagaataaaaaacatcaggaaatgt	-
9	PBX1 intron 2	3637	3675	RSS23	cacagagaaaaaggaaagagagagaacaaaagggttt	-
10	PBX1 intron 2	4497	4524	RSS12	cacagacactcctatttgtaaaaaaa	-
11	PBX1 intron 2	4846	4884	RSS23	cacataatttaatttggaaagacatttcatttggaaagc	+
12	PBX1 intron 2	4938	4976	RSS23	catatgtatcatccatctaaaagagatgttggaaaccatt	-
13	PBX1 intron 2	5168	5206	RSS23	cacaccatttcaggtaaaggccaatggaaaccaaaattat	-
14	PBX1 intron 2	5247	5285	RSS23	cacaggaactcaaagcacttcacaaacaactcatgaatt	-
15	PBX1 intron 2	5256	5283	RSS12	caggaactcaaagcacttcacaaacaac	-
16	PBX1 intron 2	5258	5285	RSS12	cacaggaactcaaagcacttcacaaaca	-
17	PBX1 intron 2	5509	5547	RSS23	cagagtgtccccagagggaaaaaagggtcgaggaatag	+
18	PBX1 intron 2	6733	6771	RSS23	cacaatgcctccagttgctgacgctaagaaaacaccatc	-
19	PBX1 intron 2	7054	7092	RSS23	cacccctgacaggcccagtgtgtatgttccctccc	+
20	PBX1 intron 2	7066	7104	RSS23	cacatggacacaggggagggaacatcacactggggcc	-
21	PBX1 intron 2	7193	7220	RSS12	cagtttcatttcattgtccctgtcaaaagac	+
22	PBX1 intron 2	7234	7261	RSS12	caccatggaaatctatggagccataaaaa	-
23	PBX1 intron 2	7471	7498	RSS12	cactgtttccacaatggtaataatt	+
24	PBX1 intron 2	7501	7528	RSS12	cactgtcaccacatgttggaaatcc	+
25	PBX1 intron 2	7705	7732	RSS12	cagtgggtgaaggatatacagacact	-
26	PBX1 intron 2	8855	8893	RSS23	caaagtgtggatcagggtgtggccaccgcgcagg	+
27	PBX1 intron 2	9501	9528	RSS12	cagagtgtgaccacccatcatcgt	+
28	PBX1 intron 2	9597	9635	RSS23	cactgacaaccatttaacataaaaggcagggtcaggaagc	-
29	PBX1 intron 2	9610	9637	RSS12	cacactgacaaccatttaacataaaagc	-
30	PBX1 intron 2	9683	9721	RSS23	cacagaactctagaagttaggggggggggtgtgaaagt	-
31	PBX1 intron 2	10884	10911	RSS12	cagtctattcttagggaaacacttaagatt	-
32	PBX1 intron 2	11391	11429	RSS23	caaagtgtggattatagggtgtggccaccacccag	-
33	PBX1 intron 2	11747	11785	RSS23	catagcataaaaacaacatatgcattccatcacaatgc	-
34	PBX1 intron 2	12023	12061	RSS23	cacttcttagggaaactcaaacatcttctaaatatcc	-
35	PBX1 intron 2	12089	12116	RSS12	caacctgtctcaaaggcaagacaaaatata	-
36	PBX1 intron 2	14284	14311	RSS12	cactagaatacacttaagaataataatc	-
37	PBX1 intron 2	14832	14859	RSS12	cacaaacaaatcttcatacttatacc	-
38	PBX1 intron 2	15795	15833	RSS23	cacaggttaatccacacttctctcgtactccctc	-
39	PBX1 intron 2	16134	16161	RSS12	cacagtggaaagacatcacacggaa	-
40	PBX1 intron 2	16427	16454	RSS12	catcctggatgaaaactgaacagagaat	+
41	PBX1 intron 2	17527	17565	RSS23	cagagtgtggattatagggtgtggccaccgcacccgg	+
42	PBX1 intron 2	18184	18222	RSS23	caaaaaggggggctgggtgcgggtggctatgcctgtatcc	-
43	PBX1 intron 2	18241	18279	RSS23	cactgcaatttggaaaggtagatctccctctcaaaact	-
44	PBX1 intron 2	18552	18590	RSS23	cacagccataaaggaaatgtacacaagaaaatgtaaacac	-
45	PBX1 intron 2	18563	18590	RSS12	cacagccataaaggaaatgtacacaagaaa	-
46	PBX1 intron 2	18827	18854	RSS12	cacaataaaaaggatcttatggatacc	-
47	PBX1 intron 2	19452	19479	RSS12	cattgcctcaacgcacatgataaaaaat	+
48	PBX1 intron 2	20498	20536	RSS23	cagagtggaaaataagatggaaacttgcctcaaatt	+
49	PBX1 intron 2	21832	21870	RSS23	cacattggaaagggtggggaaaggagtgaggatgtgcc	-
50	PBX1 intron 2	22222	22249	RSS12	caatgcctgactacccctcaaagact	-
51	PBX1 intron 2	23080	23118	RSS23	cacatgggcataatgtttccattccacccctggaaatgt	-
52	PBX1 intron 2	23093	23131	RSS23	cataatgtctccacatggctcagatgtttccattcc	-
53	PBX1 intron 2	23394	23432	RSS23	cacagattggcaggcatgtggggctgttggaaat	+
54	PBX1 intron 2	23748	23786	RSS23	cacacacacacaaacacccatgtgtcaatgtca	-
55	PBX1 intron 2	23765	23792	RSS12	caggcacacacacacacacac	-
56	PBX1 intron 2	24197	24224	RSS12	cacaaagatcatcaggtaacaacaaaga	-

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57	PBX1 intron 2	24428	24466	RSS23	cacacacagacacagaggcttcactgcagcagtccggc	+
58	PBX1 intron 2	24432	24459	RSS12	cacagacacagaggcttcactgcagca	+
59	PBX1 intron 2	24595	24622	RSS12	cacagtcaactgaagtccattttatat	+
60	PBX1 intron 2	25113	25151	RSS23	cacacagagatgagaaaaagagaaaagagaaatacact	+
61	PBX1 intron 2	25115	25153	RSS23	cacagagatgagaaaaagagaaaagagaaaatacactcc	+
62	PBX1 intron 2	25177	25215	RSS23	cacacttcaccatatgcgtcgaaactaaaaaaaaaaaa	-
63	PBX1 intron 2	25742	25769	RSS12	caaagtggcgcagaccttgcgtactc	+
64	PBX1 intron 2	25758	25796	RSS23	cactgagtgtgaggacaagggtagggatcaggaaaa	-
65	PBX1 intron 2	26366	26404	RSS23	catggtgacaggtggataaatctcctccaccctaaata	-
66	PBX1 intron 2	26505	26543	RSS23	caccacaacaggaaacagaataattcaactcaatca	-
67	PBX1 intron 2	27104	27142	RSS23	cacagagcacgttgttacctgaaggcacagggggccgc	-
68	PBX1 intron 2	27196	27234	RSS23	cacactgtgtccctcattaaggctcacaaaaacgg	-
69	PBX1 intron 2	27960	27998	RSS23	caaagtgtggattacaggcgtcagccaccgtcctgg	+
70	PBX1 intron 2	28579	28606	RSS12	cacagaaggccccaaacttgc当地atgc	-
71	PBX1 intron 2	28827	28865	RSS23	cacagacttgaacacaacttgtgattgaacaaaggccc	-
72	PBX1 intron 2	28913	28951	RSS23	cacaggcctcatagttgagtgtgagactgtggatgagg	+
73	PBX1 intron 2	29227	29254	RSS12	cagcaccctcagactctgtcagacact	-
74	PBX1 intron 2	29248	29275	RSS12	caaaggctctgtggccaggccagcacc	-
75	PBX1 intron 2	29483	29521	RSS23	caccaggctcccacgcgtggcgtgaggataaaga	+
76	PBX1 intron 2	29758	29796	RSS23	cacacacctgtaatgccagttactggaggctgaggca	-
77	PBX1 intron 2	29874	29912	RSS23	cacttgc当地aggccaggcaggatcacttgagccca	-
78	PBX1 intron 2	29997	30024	RSS12	caccaggagtcaaaatccaacaaaatga	-
79	PBX1 intron 2	30092	30130	RSS23	cacagtattctaaccctttggggcatagattaattct	-
80	PBX1 intron 2	30253	30280	RSS12	cacattttatagatgaaaacaaaacag	-
81	PBX1 intron 2	30393	30431	RSS23	cactgggtgaaaacacaccatgtacttctttaaaaata	+
82	PBX1 intron 2	30919	30957	RSS23	cagaatgctaaagctgcaacagagacttgggagatcatt	+
83	PBX1 intron 2	31229	31267	RSS23	caaagtgtggattacaggcatgagccactgtgcccgg	+
84	PBX1 intron 2	31513	31540	RSS12	cacagtggcttagtggcaaccttactaga	+
85	PBX1 intron 2	31583	31610	RSS12	cactgaggcccagaactgtgattaacta	+
86	PBX1 intron 2	32051	32089	RSS23	cacagccaaacttgc当地accgtggaccactactgaaaact	-
87	PBX1 intron 2	34142	34169	RSS12	caccccaaaatagctccatttcaacc	-
88	PBX1 intron 2	34735	34762	RSS12	caccatgtgtactccaccatgttac	-
89	PBX1 intron 2	34804	34831	RSS12	caaagcaattcccacagtaacaaaccca	+
90	PBX1 intron 2	34816	34854	RSS23	cacagtaacaaaaccactcttaggatagcaatgttaatc	+
91	PBX1 intron 2	35476	35503	RSS12	catttgtcatacctcgagcgtatagc	+
92	PBX1 intron 2	37313	37351	RSS23	cactgtttaaacaggcatgggctgc当地caggatcaa	-
93	PBX1 intron 2	37499	37537	RSS23	cacaccgatcaagattgtatccaggccactgaagtaatcca	+
94	PBX1 intron 2	37646	37684	RSS23	caaagtgtggattacaggcatgagccactgc当地ccag	-
95	PBX1 intron 2	38439	38466	RSS12	cacagtatccaactgtcagcatgtttaatg	-
96	PBX1 intron 2	38625	38663	RSS23	cacagagctaatccccactcttagggtgcatggctgag	-
97	PBX1 intron 2	39242	39269	RSS12	cacagactcatacagc当地ccacagacac	+
98	PBX1 intron 2	39261	39299	RSS23	cacagacacaagctctgtatcctacatgtacctgc	+
99	PBX1 intron 2	39808	39835	RSS12	cattctgactctgtcctcatgttact	-
100	PBX1 intron 2	39896	39934	RSS23	cacaaagagataaaaggaaaagcagaaaaaaaataatg	-
101	PBX1 intron 2	39905	39932	RSS12	caaagagataaaaggaaaagcagaaaa	-
102	PBX1 intron 2	40991	41018	RSS12	catagtgtgtcaagaacaacttacata	-
103	PBX1 intron 2	41063	41101	RSS23	cacagtgtcccattactctaagggttacaatctgaggt	+
104	PBX1 intron 2	41445	41472	RSS12	cacaaaagaatgactcaggatctacacca	-
105	PBX1 intron 2	41506	41533	RSS12	cacagtatttcataatgaaaaaaaaaaaa	-
106	PBX1 intron 2	41510	41548	RSS23	cacttgc当地aaaaggcacagttatcataatgaaaaaaaa	-
107	PBX1 intron 2	44620	44658	RSS23	cacagagctcacagacataggaaaacctgtatgaaaata	-
108	PBX1 intron 2	44887	44925	RSS23	cacagtactggcacatgc当地ggcactcaagtagtatct	-
109	PBX1 intron 2	46021	46048	RSS12	caccctgcttcagcatgttggccatt	+
110	PBX1 intron 2	46981	47019	RSS23	cacagacccttgc当地accggcccttctgtcaaagg	-
111	PBX1 intron 2	47317	47344	RSS12	cacagggacacagtacagaacccgatcgc	-
112	PBX1 intron 2	47888	47926	RSS23	cacagaaaatgtaaaaaggcccaaaggatgagaaaa	-
113	PBX1 intron 2	48000	48038	RSS23	cactgcaagctccgc当地ccgggttcatgc当地atttct	+
114	PBX1 intron 2	48186	48224	RSS23	caaagtgtggattacaggcgtgagccaccgc当地ccgg	+
115	PBX1 intron 2	48195	48233	RSS23	cacagaaggccgggccc当地ggctc当地ctgttaatccc	-
116	PBX1 intron 2	49378	49416	RSS23	cactgccc当地aggccggaggaagagatgc当地aaatgtgg	+

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117	PBX1 intron 2	50194	50232	RSS23	cacaatgctaggggggctcacaggagagccctggagaaaag	-
118	PBX1 intron 2	50264	50291	RSS12	cacatatacacagatcataaccgcaca	-
119	PBX1 intron 2	50687	50725	RSS23	cacagaaataccagaggaaaggcatcctggagtgtatg	-
120	PBX1 intron 2	50960	50998	RSS23	caaagtgtggtaagtgtactataccgaggacacagacct	+
121	PBX1 intron 2	51691	51729	RSS23	cactttgggaggccgaagtggcagatcacctgaggctca	-
122	PBX1 intron 2	51750	51788	RSS23	cactgtgcctggcctcagtgtaaactcttaagatttac	+
123	PBX1 intron 2	52163	52190	RSS12	cacagtataaaatcaggaatattacacc	-
124	PBX1 intron 2	52614	52652	RSS23	cacaataccctggcccccagactcctggctttaacc	-
125	PBX1 intron 2	52705	52743	RSS23	cacatagacatatcctgaattttcatctctggagaccc	-
126	PBX1 intron 2	53495	53522	RSS12	catagtctaaacccattgacatagatc	+
127	PBX1 intron 2	55789	55827	RSS23	cagggagagaaaacaaaagaaggaaactcacaggaaacca	+
128	PBX1 intron 2	55839	55866	RSS12	cactgccaggcacacccctttgaaacc	+
129	PBX1 intron 2	56070	56097	RSS12	cacttttgtggagctattacaatatct	+
130	PBX1 intron 2	56694	56721	RSS12	caacatagtgagaccctgtttctacaaa	+
131	PBX1 intron 2	57182	57220	RSS23	cacagggtgtgagggtggaaaaaaaaaaaaaaagattg	-
132	PBX1 intron 2	57193	57220	RSS12	cacagggtgtgagggtggaaaaaaaaaaag	-
133	PBX1 intron 2	57631	57669	RSS23	caaagtgtgggtacaggcgtgagccactgcgcgg	+
134	PBX1 intron 2	57738	57776	RSS23	cacagtctggctactgcAACCTCGCCTCCGGATT	+
135	PBX1 intron 2	57981	58019	RSS23	cagacagacagaaagagaaggaagactgttaagaaaata	-
136	PBX1 intron 2	58192	58230	RSS23	cagagccacccaagctaaatcagccccctgaaggagaacct	-
137	PBX1 intron 2	58537	58564	RSS12	caatttgacttccatcttcctaagaat	+
138	PBX1 intron 2	58959	58986	RSS12	cacaacagtgcggcccagagagaaaatg	-
139	PBX1 intron 2	59019	59057	RSS23	cacagagattctaggctaacctctgtggacttgacattt	-
140	PBX1 intron 2	59411	59449	RSS23	cacaccagcaaagtgttgtgggtgttcaacacag	-
141	PBX1 intron 2	59458	59496	RSS23	cacacacacacactgacacatgctgtctatacatacata	+
142	PBX1 intron 2	59466	59493	RSS12	cacactgacacatgctgtctatacatac	+
143	PBX1 intron 2	59761	59799	RSS23	caaagtgttaggattacaggcatgagccaaacacgcctgg	+
144	PBX1 intron 2	60303	60341	RSS23	cagagagacaaaggcaagcacagagaggagatgcaaggc	-
145	PBX1 intron 2	60314	60341	RSS12	cagagagacaaaggcaagcacagagagg	-
146	PBX1 intron 2	60778	60805	RSS12	cactgtcctaaaaccacaggcataactg	+
147	PBX1 intron 2	60778	60816	RSS23	cactgtcctaaaaccacaggcataactgtatctgaagaa	+
148	PBX1 intron 2	61300	61338	RSS23	catggacacacatgcagataaatatacctactaaaattc	+
149	PBX1 intron 2	61524	61551	RSS12	cacagagggtggagcttctgtctagcc	+
150	PBX1 intron 2	62371	62409	RSS23	cacacacactcacatacacaaaagatgaaagatttatga	-
151	PBX1 intron 2	62550	62577	RSS12	caccctccctctgccttctgtaaaatc	+
152	PBX1 intron 2	62761	62788	RSS12	caccttgcctctccccacccaaaact	-
153	PBX1 intron 2	64050	64077	RSS12	cacatcggtaccaacacactaaaaatc	-
154	PBX1 intron 2	64187	64225	RSS23	cacgatgtcgccgtccatctcaaatgccaccacctct	-
155	PBX1 intron 2	64312	64339	RSS12	cgcctagtcgtacttcccaaaaacatc	-
156	PBX1 intron 2	64712	64750	RSS23	cactgtctaggaacagatgtccccaaaagcaattaac	-
157	PBX1 intron 2	65548	65575	RSS12	cagcaccccttacaccgtcacatattt	+
158	PBX1 intron 2	65943	65970	RSS12	cacaaagctccatatttaactaaaatg	-
159	PBX1 intron 2	67410	67448	RSS23	caatgcaactcagagaaaagagtatggcttgaatca	-
160	PBX1 intron 2	67998	68025	RSS12	caaagtgtttctgaacaaacttaatt	+
161	PBX1 intron 2	69270	69308	RSS23	cacagtgtgaatccacgggtggcattctgcatttctca	-
162	PBX1 intron 2	69652	69679	RSS12	cactcttaggtttcttatataaaaaca	-
163	PBX1 intron 2	70098	70136	RSS23	caaagtgttaggattacaggcgtgagccacacgcacg	+
164	PBX1 intron 2	70311	70349	RSS23	cactacattacactttcccttgtatgtacaggaaatct	-
165	PBX1 intron 2	70428	70466	RSS23	cacattatttaacctcttgcatttcgtttcttaatct	+
166	PBX1 intron 2	70528	70566	RSS23	cagaaaagcaattaaaacagtcgtggcatgttaagcc	+
167	PBX1 intron 2	70723	70761	RSS23	cacagccgtggatgaacagttctccctgtgagccacg	+
168	PBX1 intron 2	71130	71157	RSS12	cactcttttcaaaagtgttcatgaaat	-
169	PBX1 intron 2	71243	71281	RSS23	cacaatgctttgggttcgtttctgaaatgaaat	+
170	PBX1 intron 2	71678	71705	RSS12	cagaatattcgcagcccttagagttaact	-
171	PBX1 intron 2	72108	72135	RSS12	cacaaattaataactctacttaaacc	+
172	PBX1 intron 2	72299	72326	RSS12	caccctccatccagcctgcctatatac	+
173	PBX1 intron 2	73032	73059	RSS12	caccttgcctcaagtcgtaaataagatc	-
174	PBX1 intron 2	74783	74821	RSS23	cacacacaggccatagcagcagtcgtacgtggcccttaactg	-
175	PBX1 intron 2	75159	75186	RSS12	cagagggccctgactttcaaaaggatt	-
176	PBX1 intron 2	75264	75302	RSS23	cacatacactcacacactcacaccatgggtaaaacg	+

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237	PBX1 intron 2	95491	95518	RSS12	cacaggtaaacagataacatgtaaag	-
238	PBX1 intron 2	97289	97316	RSS12	cactaagtgtgacctctagacaaaacca	-
239	PBX1 intron 2	97811	97849	RSS23	cacagtcaaataagaagagtggtagacagaaaaac	-
240	PBX1 intron 2	98078	98105	RSS12	cagtgaardtgcgtgatcccttagacc	-
241	PBX1 intron 2	98375	98413	RSS23	caaagtgcggattacaggcgtgagccactgtccccag	+
242	PBX1 intron 2	98445	98472	RSS12	cacattaactaatacaaaaataaaatt	-
243	PBX1 intron 2	98767	98805	RSS23	cacttgggaggcctagggtggcaggtcacctgaggta	+
244	PBX1 intron 2	99113	99140	RSS12	cacagttcaaggattctgaaaaatc	-
245	PBX1 intron 2	99526	99564	RSS23	caaagtctgcatattaaccatcactacaagaaaaaaa	-
246	PBX1 intron 2	100082	100109	RSS12	cataggagaagcaatccactaagata	-
247	PBX1 intron 2	100997	101035	RSS23	cacagacatgtactagagggacaccaactaaaaactc	-
248	PBX1 intron 2	101151	101178	RSS12	cacagtcaagggttctgaccaaaaaact	+
249	PBX1 intron 2	101263	101290	RSS12	cagaataatgcagaatgtgccaggact	-
250	PBX1 intron 2	101319	101357	RSS23	cacactgctgataaagacatacccaagaccggacaaatt	+
251	PBX1 intron 2	101746	101773	RSS12	cacagaatttattacagaattcaaactc	-
252	PBX1 intron 2	102047	102085	RSS23	cactgtAACCTTACCTCCAGGTTAAGTGATCCTCCC	+
253	PBX1 intron 2	102235	102273	RSS23	caaagtgcggattacagggtgagccactgaaccag	+
254	PBX1 intron 2	102345	102372	RSS12	cataggtagctgggtctacaaacaca	-
255	PBX1 intron 2	103214	103241	RSS12	cagaatattgtccatcagccagaatc	-
256	PBX1 intron 2	103621	103659	RSS23	cactctgtacaaagagggtccataacatcttaagcc	-
257	PBX1 intron 2	104077	104115	RSS23	cacacacacacatattatacatatgttatataaaata	-
258	PBX1 intron 2	104094	104121	RSS12	cacacacacacacacatattata	-
259	PBX1 intron 2	104299	104326	RSS12	cacagttagatcattggcattcaaagatt	+
260	PBX1 intron 2	104853	104891	RSS23	cagagtctgaaaagacaagttcaggaccatgtggccaa	-
261	PBX1 intron 2	105133	105171	RSS23	caccccccacccatgactttaggtcacctcgagagaaaaata	+
262	PBX1 intron 2	105238	105265	RSS12	caggagcccccggccatcgaaaaact	+
263	PBX1 intron 2	105265	105292	RSS12	cacttggccacagccccaaagataatatt	+
264	PBX1 intron 2	105296	105323	RSS12	cacttgacactctttagcacaagaact	-
265	PBX1 intron 2	105394	105432	RSS23	cacattggcgagggggccgtctggcagtggccaagct	-
266	PBX1 intron 2	105639	105666	RSS12	cacagtcttcattaccagactccaaagca	-
267	PBX1 intron 2	106326	106364	RSS23	cacccctacttcccttccgttcaatgcacaaaatc	+
268	PBX1 intron 2	107406	107444	RSS23	cagagagggaaaatgcagagagagggaaaaagaaatg	+
269	PBX1 intron 2	107515	107553	RSS23	cacaggcagaaaagaaaacaccccttctgatcctcccc	-
270	PBX1 intron 2	107531	107569	RSS23	cacacggggcgcaggacacaggcagaaaagaaaacacccc	-
271	PBX1 intron 2	107816	107843	RSS12	caccgacagaaaatcaaaaaaaaatata	+
272	PBX1 intron 2	108247	108285	RSS23	catactgtggggaaaagggttaacgcacaggggaaacta	-
273	PBX1 intron 2	108460	108487	RSS12	cactcacaaaaacccttattccaaagg	-
274	PBX1 intron 2	109188	109215	RSS12	cacttaagcttcagcttggcattaaa	-
275	PBX1 intron 2	109374	109401	RSS12	cacggccgtacacattatgttatcc	-
276	PBX1 intron 2	110430	110468	RSS23	cacggcattccataaaatgttcatcttagttgagaagtt	-
277	PBX1 intron 2	110681	110719	RSS23	cacagagatgaaatgactatgtggctaaaaacagacgc	+
278	PBX1 intron 2	110802	110840	RSS23	cacagacatggaggattaccaggactgtggctaaaag	-
279	PBX1 intron 2	110960	110998	RSS23	cacatggacaaaagggaggatgatgtttactaaacca	+
280	PBX1 intron 2	111236	111274	RSS23	cacagaattatccaggacattccatgcccatttagtt	-
281	PBX1 intron 2	111551	111578	RSS12	cacccaccaccaagaggatctttaact	+
282	PBX1 intron 2	111829	111856	RSS12	catcatgtcaaccaggaccaataat	-
283	PBX1 intron 2	112952	112979	RSS12	cagatcccttctgaacaaggcagacacc	+
284	PBX1 intron 2	113346	113384	RSS23	cacttagcttagcaagttggggctgcaggcttgaacc	-
285	PBX1 intron 2	114040	114078	RSS23	caaagtgcggattacaggcgtgagccaccgcggccgg	+
286	PBX1 intron 2	114067	114105	RSS23	cacccgcggccggctactgttgcattttacaaaacg	+
287	PBX1 intron 2	114401	114428	RSS12	caccatgtgtccccaccctgcacacact	-
288	PBX1 intron 2	114755	114793	RSS23	cacaatgtttccactaccaatcacatcaaggctacca	-
289	PBX1 intron 2	114995	115022	RSS12	cagagaccccttgtggataaaaaacagg	-
290	PBX1 intron 2	114997	115024	RSS12	cacagagaccccttgtggataaaaaaca	-
291	PBX1 intron 2	115273	115300	RSS12	cacagcccattagggaggctaaaccc	+
292	PBX1 intron 2	116022	116060	RSS23	cactgtgtgtccacaggcgcgttgcataact	-
293	PBX1 intron 2	116054	116092	RSS23	cacagtggggaggcgttactgggtgggggggtgttc	+
294	PBX1 intron 2	116415	116442	RSS12	cacagggtcataaaatttagaaacataact	-
295	PBX1 intron 2	116603	116641	RSS23	caaactcctgtggttttttttttgtctaaaaactg	+
296	PBX1 intron 2	117130	117157	RSS12	cacaaacccatcagcatcacacaataac	-

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357	PBX1 intron 2	144832	144870	RSS23	cagagcggaggcagagtgactaagtgactgctggaatcct	+
358	PBX1 intron 2	145189	145216	RSS12	cactctctgagtgtgtgttatttt	-
359	PBX1 intron 2	145673	145700	RSS12	cagtgcctagtcgtccagggttacaca	+
360	PBX1 intron 2	146054	146081	RSS12	caaagctgggccattgaaacagaaaagc	+
361	PBX1 intron 2	146260	146298	RSS23	caccaagacatccacgcagaccaccccactgcatttct	+
362	PBX1 intron 2	148211	148249	RSS23	caaagtgtggattacaggcgtgagccactgcggccgg	+
363	PBX1 intron 2	148385	148423	RSS23	cacaaaatcccacatgcgtggctgtccctgcaagct	+
364	PBX1 intron 2	149855	149882	RSS12	cagagaagttctgcctctggtaaaac	+
365	PBX1 intron 2	150384	150422	RSS23	cacacagattgaagtaggcacagaaggcagcagaaagca	+
366	PBX1 intron 2	150720	150747	RSS12	cacaacatttgaaccctccccagact	-
367	PBX1 intron 2	151105	151132	RSS12	cacagggtaataagtgtttcaagaact	-
368	PBX1 intron 2	152814	152841	RSS12	caagatgtttcagatcatacaaaaaca	+
369	PBX1 intron 2	152819	152846	RSS12	cacattgttttgtatgtatctgaaaaca	-
370	PBX1 intron 2	152874	152901	RSS12	cagtgggtgggtgtacagacatacaca	-
371	PBX1 intron 2	152880	152918	RSS23	cactgcctgcatacatcagtgggtgtgtacagaca	-
372	PBX1 intron 2	153376	153403	RSS12	cacacacacacacacacacacacacacaca	+
373	PBX1 intron 2	153378	153405	RSS12	cacacacacacacacacacacacacacaca	+
374	PBX1 intron 2	153380	153407	RSS12	cacacacacacacacacacacacacaca	+
375	PBX1 intron 2	153382	153409	RSS12	cacacacacacacacacacacacacaca	+
376	PBX1 intron 2	153384	153411	RSS12	cacacacacacacacacacacacacaca	+
377	PBX1 intron 2	153386	153413	RSS12	cacacacacacacacacacacacacaca	+
378	PBX1 intron 2	153386	153424	RSS23	ca	+
379	PBX1 intron 2	153388	153415	RSS12	cacacacacacacacacacacacacacaca	+
380	PBX1 intron 2	153388	153426	RSS23	ca	+
381	PBX1 intron 2	153390	153417	RSS12	cacacacacacacacacacacacacaca	+
382	PBX1 intron 2	153390	153428	RSS23	ca	+
383	PBX1 intron 2	153392	153419	RSS12	cacacacacacacacacacacacacacaca	+
384	PBX1 intron 2	153396	153434	RSS23	cacacacacacacacacacacacacacacacacacaca	+
385	PBX1 intron 2	153398	153425	RSS12	cacacacacacacacacacacacacacacacacacaca	+
386	PBX1 intron 2	153400	153427	RSS12	cacacacacacacacacacacacacacacacacacaca	+
387	PBX1 intron 2	153400	153438	RSS23	ca	+
388	PBX1 intron 2	153404	153442	RSS23	ca	+
389	PBX1 intron 2	153408	153446	RSS23	ca	+
390	PBX1 intron 2	153410	153448	RSS23	ca	+
391	PBX1 intron 2	153414	153452	RSS23	ca	+
392	PBX1 intron 2	153954	153981	RSS12	catattcttaaacaggcctcataaaac	-
393	PBX1 intron 2	153993	154031	RSS23	cacaacacaccacaggcaataaaagtctccaagaat	-
394	PBX1 intron 2	154042	154080	RSS23	caccctgtggccaagaagagacgcctctctccaaagag	-
395	PBX1 intron 2	154778	154805	RSS12	cacagagttggaaagtgcagatccaagtct	+
396	PBX1 intron 2	154778	154816	RSS23	cacagagttggaaagtgcagatccaagtctgtattctaaac	+
397	PBX1 intron 2	154782	154820	RSS23	cacatgttagaaatcagacttggatctgacttcaactc	-
398	PBX1 intron 2	155200	155238	RSS23	cacagaaccatttgaacactccattgtcacccaaatc	-
399	PBX1 intron 2	155403	155441	RSS23	cacaaagtcaaagagtcaaaagcattctgagtctccggc	-
400	PBX1 intron 2	155414	155441	RSS12	cacaaagtcaaagagtcaaaagcattct	-
401	PBX1 intron 2	155442	155480	RSS23	cacaatgataagagtcttcaatatctccaccatattca	-
402	PBX1 intron 2	155453	155480	RSS12	cacaatgataagagtcttcaatatctc	-
403	PBX1 intron 2	155825	155852	RSS12	cacagaaatgccagtctgagagagagaa	+
404	PBX1 intron 2	157123	157161	RSS23	cacagtagaaaatgtcagtcatattccaagaatctctc	-
405	PBX1 intron 2	157579	157617	RSS23	cactgtaaatacctcaggaaaggaaacccgcagaaaccc	-
406	PBX1 intron 2	158058	158085	RSS12	caccgagatttgagcagtcgtccctaaac	-
407	PBX1 intron 2	158098	158136	RSS23	cacacacacacacacactacactgcacccaaatttca	-
408	PBX1 intron 2	159508	159535	RSS12	caccctggcgactgtgtccaaagg	-
409	PBX1 intron 2	162012	162050	RSS23	cacacaggcagacagatcaagccgtatgtggggacaa	-
410	PBX1 intron 2	163405	163443	RSS23	cacagtgtgggtacagactgtgtttactagtaaaaca	-
411	PBX1 intron 2	163578	163605	RSS12	cactaagacaaaagtcggccaccaattc	-
412	PBX1 intron 2	163639	163677	RSS23	cacagaaaaccaaggcggaggttctctgcattatgg	-
413	PBX1 intron 2	164034	164061	RSS12	cactgtgtcacattaataaaactaaatc	+
414	PBX1 intron 2	164034	164072	RSS23	cactgtgtcacattaataaaactaaatcaggttataatt	+
415	PBX1 intron 2	164734	164772	RSS23	caaagtataggattacaggcatgagccaccacggccag	-
416	PBX1 intron 2	165098	165125	RSS12	cacatttgqccagaaccccttcaact	-

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417	PBX1 intron 2	165226	165264	RSS23	cacaggcagcagatgccattattcagaattataatgt	+
418	PBX1 intron 2	165523	165561	RSS23	cacagctctatgaagaaaaataacaggccattaaactg	-
419	PBX1 intron 2	166018	166045	RSS12	cacaaggataaaatgcagaaggtaattc	-
420	PBX1 intron 2	166664	166702	RSS23	cactggggcaggtttagaaactaagtcttctaaata	-
421	PBX1 intron 2	167675	167713	RSS23	catagagggtagcattcatcagaataaggctcagaaaaa	+
422	PBX1 intron 2	167728	167766	RSS23	cacacacacacataaacacggaaagcaatcgaaaaac	-
423	PBX1 intron 2	168143	168170	RSS12	cacaatatgagggagtccttcataatcc	-
424	PBX1 intron 2	168218	168245	RSS12	cactgtgaatgccgttgaagggttact	+
425	PBX1 intron 2	168819	168857	RSS23	caccaacacagaatgtggctcactagtcacaaagcc	-
426	PBX1 intron 2	169839	169877	RSS23	catgcagagccagtctgaagtcagaactcaacagaaca	-
427	PBX1 intron 2	169861	169888	RSS12	cagactggctctgcattgttatcttcttct	+
428	PBX1 intron 2	169890	169928	RSS23	caaaccacctgaggtgtatggatccctcaacaagaatg	-
429	PBX1 intron 2	169994	170032	RSS23	cacaaggacagaatgcattatcaacacaatgggtccct	+
430	PBX1 intron 2	170715	170742	RSS12	caaaaatgaatccacacttacacaacata	-
431	PBX1 intron 2	170757	170784	RSS12	cacagtcaagaaacatgttgtaaaaat	-
432	PBX1 intron 2	172051	172078	RSS12	cacatacatgttaggcacagaccaatacc	-
433	PBX1 intron 2	172644	172671	RSS12	cacaatgactcctgagcaacaaactgc	-
434	PBX1 intron 2	172650	172688	RSS23	cacatccatagacaaggccacaatgactcctgagcaaca	-
435	PBX1 intron 2	173473	173511	RSS23	cacagtactcactagcttctctacttgattctccc	-
436	PBX1 intron 2	173679	173706	RSS12	cactgaatccatatctcatctcataatcc	-
437	PBX1 intron 2	174427	174465	RSS23	caaagtgtggattacaggcgtgagccactgtacctgg	+
438	PBX1 intron 2	174780	174807	RSS12	cacaataaaaatactactcagaacaaca	-
439	PBX1 intron 2	174798	174825	RSS12	cacattgtggctattcccaataaaaa	-
440	PBX1 intron 2	175265	175292	RSS12	caaatatattaatttcataagaaacaac	+
441	PBX1 intron 2	175305	175332	RSS12	cacagtggttatgcctctaacccttct	+
442	PBX1 intron 2	176072	176110	RSS23	cacaagctgtgagagagaaccaaggccgtgtagaacac	-
443	PBX1 intron 2	176416	176454	RSS23	cacacacacacatgcacaaccacttcatgaaccctgcag	-
444	PBX1 intron 2	176422	176460	RSS23	cacacacacacacatgcacaaccacttcatgaacc	-
445	PBX1 intron 2	176428	176466	RSS23	cacacacacacacacacatgcacaaccacttca	-
446	PBX1 intron 2	176433	176460	RSS12	cacacacacacacacatgcacaacca	-
447	PBX1 intron 2	176434	176472	RSS23	cacacacacacacacacacacacacatgcacaacc	-
448	PBX1 intron 2	176437	176464	RSS12	cacacacacacacacacacatgcaca	-
449	PBX1 intron 2	176443	176470	RSS12	cacacacacacacacacacacacacacaca	-
450	PBX1 intron 2	176445	176472	RSS12	cacacacacacacacacacacacacacaca	-
451	PBX1 intron 2	176447	176474	RSS12	cacacacacacacacacacacacacacaca	-
452	PBX1 intron 2	176449	176476	RSS12	cacacacacacacacacacacacacacaca	-
453	PBX1 intron 2	176451	176478	RSS12	cacacacacacacacacacacacacacaca	-
454	PBX1 intron 2	176455	176482	RSS12	catacacacacacacacacacacacacacaca	-
455	PBX1 intron 2	176498	176525	RSS12	cacattagtgttcatttgtctgagaact	+
456	PBX1 intron 2	176744	176782	RSS23	catttagatcaaattctgtttcttcagacataaaaat	-
457	PBX1 intron 2	177567	177594	RSS12	cacatctgttaacagttgtatcaaataatc	-
458	PBX1 intron 2	177788	177815	RSS12	cacaatctataccatgcaggataggc	-
459	PBX1 intron 2	178346	178384	RSS23	cacagtggcttcatctagagatcataagtaagatgtat	-
460	PBX1 intron 2	178403	178441	RSS23	cacacacacacactcactcatacatgcactccaaacct	-
461	PBX1 intron 2	178413	178451	RSS23	cacacacacacacacacacacactcactcatacatgc	-
462	PBX1 intron 2	178416	178443	RSS12	cacacacacacacactcactcatacatgt	-
463	PBX1 intron 2	178430	178457	RSS12	cacacacacacacacacacacacacacaca	-
464	PBX1 intron 2	178432	178459	RSS12	cacacacacacacacacacacacacacaca	-
465	PBX1 intron 2	178434	178461	RSS12	cacacacacacacacacacacacacacaca	-
466	PBX1 intron 2	178436	178463	RSS12	cacacacacacacacacacacacacacaca	-
467	PBX1 intron 2	178951	178989	RSS23	caaagtgtggattacaggcgtgagccaccactcctgg	-
468	PBX1 intron 2	179748	179786	RSS23	cagggccagaaaacagtgtatgggctaaaggccagaaaaacc	+
469	PBX1 intron 2	181378	181405	RSS12	cagggacataagggtcaattcaaaaaaag	+
470	PBX1 intron 2	183200	183238	RSS23	caaaacttagccggcgtgtggcacatgcctgtatcc	-
471	PBX1 intron 2	183745	183772	RSS12	caatctgttaagcctcaattcctcacc	-
472	PBX1 intron 2	184189	184227	RSS23	cacacaaagtcaatggcttcaacctaagtctatct	-
473	PBX1 intron 2	184217	184255	RSS23	cagagagacacagttaacttccttaaggacacacaaagt	-
474	PBX1 intron 2	184254	184281	RSS12	cagtgtccccgtgttcaagattca	-
475	PBX1 intron 2	184696	184734	RSS23	cacaatggctaaactgtatcattttggagtaagaatagt	-
476	PBX1 intron 2	184901	184928	RSS12	caccataaatgtaattgtacaataacaa	+

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597	PBX1 intron 2	223371	223398	RSS12	cacacacacacacacacacacacacacaca	-
598	PBX1 intron 2	223373	223400	RSS12	cacacacacacacacacacacacacacaca	-
599	PBX1 intron 2	223375	223402	RSS12	cacacacacacacacacacacacacacaca	-
600	PBX1 intron 2	223377	223404	RSS12	cacacacacacacacacacacacacacaca	-
601	PBX1 intron 2	223379	223406	RSS12	cacacacacacacacacacacacacacaca	-
602	PBX1 intron 2	223381	223408	RSS12	cacacacacacacacacacacacacacaca	-
603	PBX1 intron 2	223383	223410	RSS12	cacacacacacacacacacacacacacaca	-
604	PBX1 intron 2	223631	223658	RSS12	cactgaattacatcaccttacaaaacat	-
605	PBX1 intron 2	223654	223681	RSS12	cagtgcgtgcaagtactttatgaacaaa	+
606	PBX1 intron 2	223818	223856	RSS23	cacaaacccatgcagagtgttatggccaggagct	-
607	PBX1 intron 2	223906	223944	RSS23	cacaccgtgggaggctacctgtgcctttccccagacc	+
608	PBX1 intron 2	224291	224318	RSS12	cacacaaggagaaaaacaaaccaaccc	-
609	PBX1 intron 2	224933	224971	RSS23	catggtgctgcagagataaaaaggagctttaaataatc	+
610	PBX1 intron 2	225472	225510	RSS23	cacataaataggatccccaaatcagagtctgaagaaaaca	-
611	PBX1 intron 2	227125	227163	RSS23	cacaacactaccacgtcatgttctcttcaaaccct	-
612	PBX1 intron 2	227612	227639	RSS12	cactgtccccctgggctcaccagatgc	+
613	PBX1 intron 2	227986	228013	RSS12	caccaagggtcctggtgtttcataaag	+
614	PBX1 intron 2	228099	228126	RSS12	caccctgtttccaacaggacagagtcc	+

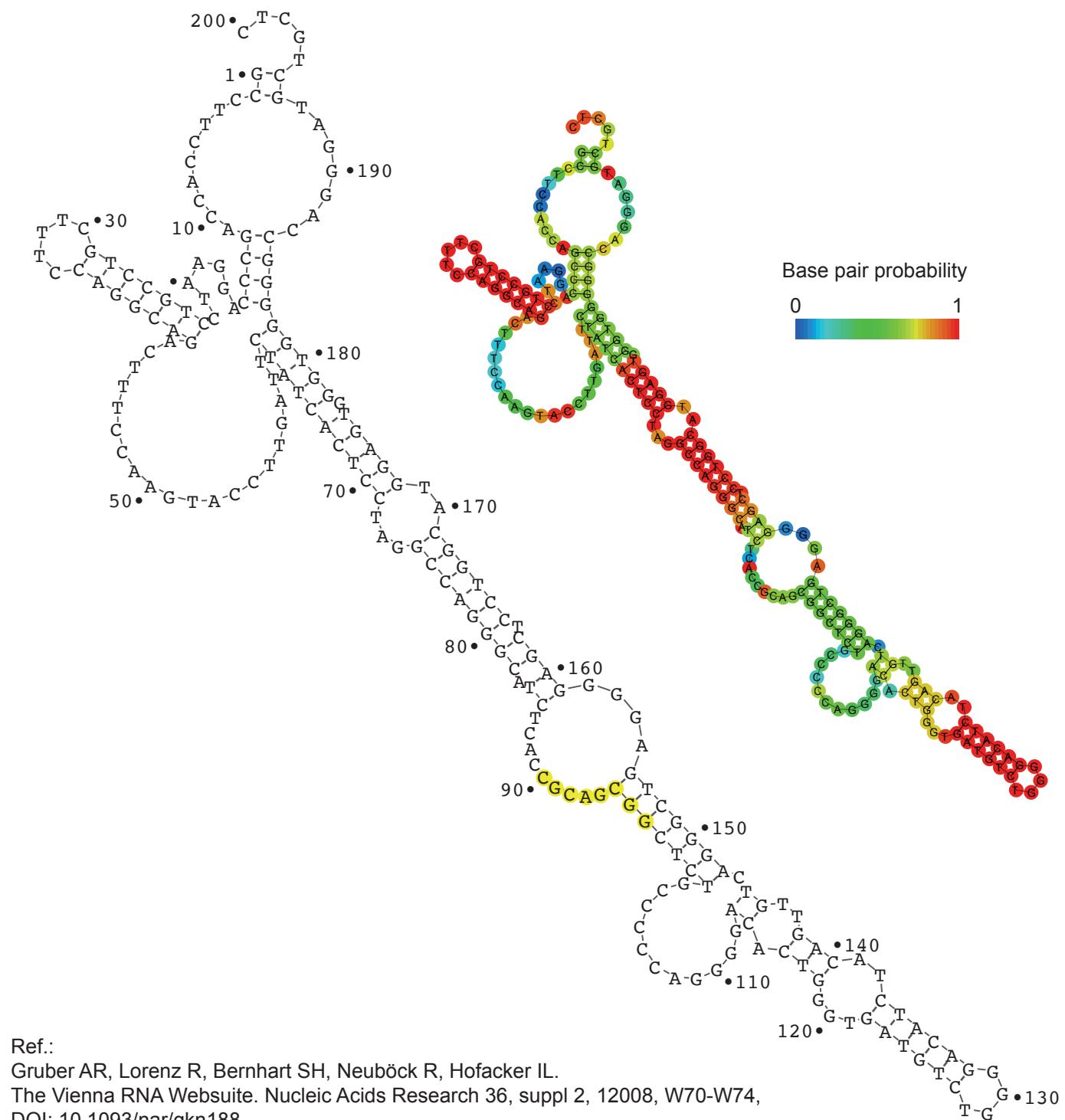
Table S7: Potential cryptic recombination signal sites in *TCF3* intron 16

#	query	begin	end	type	sequence	orientation
1	TCF3 intron 16	68	106	RSS12	cacggtgacacccatggctcccccacccgtacccca	-
2	TCF3 intron 16	391	429	RSS12	caccacccatggcctatggccaccatctcaaagcc	-
3	TCF3 intron 16	538	576	RSS12	cactctgtccaacccacgggtctctggctgttcctc	-
4	TCF3 intron 16	865	892	RSS12	caccctcaagtgttccatcacaatc	-
5	TCF3 intron 16	1051	1089	RSS12	cacagggccaggacagcgcacaaatgaccccaccc	-
6	TCF3 intron 16	1621	1659	RSS12	cacagtgcacaaatgaatgcggccactctgcattcagc	-
7	TCF3 intron 16	1689	1727	RSS12	cacgctagtggacgccgtgtcatgaagctcaagaaca	-
8	TCF3 intron 16	1766	1804	RSS12	cacaatggaccccgccgtcacaccacatgtaccc	-
9	TCF3 intron 16	2446	2484	RSS12	caaagtgtggatcacaggcgtgagtgcggccactgtgc	+
10	TCF3 intron 16	2640	2678	RSS12	cactgtactccagcctgggtgacaaagaacagactccgtc	-
11	TCF3 intron 16	2651	2678	RSS12	cactgtactccagcctgggtgacaaagc	-
12	TCF3 intron 16	2883	2921	RSS12	cacagtggctcacaccagtcacacccgtaatgccagca	-

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Figure S8: Two-dimensional DNAfold model of the *TCF3* hotspot region

1	10	20	30	40	50	60	70	80
•	•	•	•	•	•	•	•	•
GCCTTCCACCAGCCCAGGAATCCTGCCTGCTTCCAGGCAGACTTCCAAGTACCTTGATTCTATCACTCCTAGGCCAGG								
81	90	100	110	120	130	140	150	160
•	•	•	•	•	•	•	•	•
GCATCTCAC CGCAGCGG CTCTGCCCCCAGGGGACACTGGGTGATGTCTGGGGACATCTACAGTTGTCAGGGCTGAGGGGA								
161	170	180	190	200				
•	•	•	•	•				
GCTCCTGGCATGGAGTGGGTGGGGGCCAGGGATGCTGCTC								



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Figure S9: Original gel images from Figure 1

