	BAC	BES1 and BES2 (hg18)	Rearrangement	BP name	BP position	Repeat	Segmental duplication	Genes (UCSC Ac.Nr or Ref.Seq)	Putative mechanism
Sequenced BACs	CH271-224A19	chr14:32617734-32618743	t(HSA14;HSA6)	224A19_BP_Left	chr14:32656636-32657143	none	none	NPAS3 (uc001wrs.1)	
		chr6:67272170-67272901		224A19_BP_Right	chr6:67444870-67445349				
	CH271-183B5	chr8:115974044-115974755	t(HSA8;HSA5)	183B5_BP1_Left	chr8:116206959-116207470	none	none		NHEJ (GA homology)
		_		183B5_BP1_Right	chr5:20662246-20662684				
		_	Inv(HSA5)	183B5_BP2_Left	chr5:20663011-20663381		none		
		chr5:20660946-20661339		183B5_BP2_Right	chr5:20661769-20662230	L1PA4/L1			
	CH271-228C1	chr7:79789663-79790600	t(HSA7;HSA20)	228C1_BP_left	chr7:79892914-79893600	(TA)n simple repeat (318bp)flanking	none	CD36 antigen (uc003uhc.1)	Stem-Loop fragility
		chr20:16651858-16651083		228C1_BP_right	chr20:16576945-16577328				
	CH271-228N13	chr10:56218669-56219382	Inv(HSA10)	228N13_BP_left	chr10:56188874-56189350		hSD at 11Kb from BP	PCDH15 (uc001jju.1)	
		chr10:88936450-88935739		228N13_BP_right	chr10:88788971-88789386	L1PA13/L1	hSD at 17Kb from BP		
	CH271-228P23	chr3:197132159-197133169	Inv(HSA3)	228P23_BP1_left	chr3:197102596-197103088	AluSp/q		TNK2 (uc003fvs.1)	
		_		228P23_BP1_right	chr3:196942308-196943209			MUC20 (NM_152673)	
		_	t(HSA3;HSA5)	228P23_BP2_left	chr3:196989840-196990455	Tandem-SVA-(GAAA)n		MUC4 (uc003fuz.1)	
		chr5:175546939-175548355		228P23_BP2_right	chr5:175653028-175653875	L1ME4a		C5orf25 (uc003mdr.1)	
	CH271-236L11	chr2:131700083-131701676	t(HSA2;HSA8)	236L11_BP1_Left	Ambiguous mapping	L1P/L1			
		_		236L11_BP1_Right	chr8:4398611-4399410	AluSx		CSMD1 (uc003wqd.1)	
		_	t(HSA8;HSA4)	236L11_BP2_Left	chr8:4361959-4362806	Block of repeats		CSMD1 (uc003wqd.1)	
		chr4:48733170-48734080		236L11_BP2_right	chr4:48761701-48762682				
	CH271-246M2	chr2:73408992-73409723	t(HSA17;HSA2)	246M2_BP_Left	chr2:73461817-73462374	LTR -AluJ-LTR			
		chr17 Ambiguous		246M2_BP_Right	Ambiguous mapping		hSD		
	CH271-254H12	chr5:54005950-54006867	t(HSA5;HSA16)	254H12_BP_Left	chr5:54116622-54116963	AluSx-(AT)n-BP-(AT)n		SULT1A1 (uc002dqm.1)	
		chr16:16100208-16100751		254H12_BP_Right	chr16:28539672-28540248		hSD and gSD		
	CH271-263C9	chr22:32009319-32010312	Inv(HSA22)	263C9_BP1_Left	chr22:31971622-31972151	Block of repeats	hSD		
		_		263C9_BP1_Right	chr22:30928393-30928889			RFPL2 (uc003ame.1)	
		_	t(HSA22;HSA4)	263C9_BP2_Left	chr22:31046644-31047107	AluSg		AK126764 (hypothetical)	NHEJ -gggtttcaggg-filling
		chr4:140563504-140564165		263C9_BP2_Right	chr4:140587411-140587918	C HERVL-int LTR (ERVL)			
	CH271-261L1	chr1:52150331-52151147	Inv(HSA1)	261L1_BP_Left	chr1:52327906-52328412	none	gSD		NHEJ "**aaggtg**" homology
		chr1:179414362-179415103		261L1_BP_Right	chr1:179425508-179425921				
	CH271-262E11	chr17:59260052-59260792	t(HSA17;HSA2)	262E11_BP_Left	chr17:59312447-59313017	AluS	gSD and hSD	GH2(uc002jcl.1); CSH1 (uc002jck.1)	Alu-Alu recombination (Figure 1)
		chr2:27718116-27718928		262E11_BP_Right	chr2:27780363-27780861				
	CH271-267G23	chr2:99339634-99340501**	t(HSA17;HSA2)	267G23_BP_Left	chr2:99288205-99289050	Block of repeats	gSD		
		chr17:77747544-77748535		267G23_BP_Right	chr17:77869060-77870607	(CG)n-simple repeat	gSD		
	CH271-78K20	chr4:117336722-117337842	t(HSA4;HSA16)	78K20_BP_Left	chr4:117280534-117281120		gSD		NHEJ -aattccaa-filling
		chr16:1603333216034231**		78K20_BP_Right	chr16:16101960-16102505	AluSg/x	gSD	ABCC1 (uc002dee.1)	
	CH271-86M19	chr7:80017020-80017854	t(HSA7;HSA20)	86M19_BP_Left	chr7:80017020-80017854	(AT)n-simple repeat		CD36 antigen (uc003uhc.1)	NHEJ -attccaagccatatattattgg-filling
		chr20:16553059-16553552		86M19_BP_Right	chr20:16553059-16553552		gSD		
	CH271-275G5	chr7:72639276-72639991	Inv(HSA7)	275G5_BP_Left	Ambiguous mapping		hSD	BAZ1B (uc003tyc.1)	
		chr7:99624194-99625196		275G5_BP_Right	Ambiguous mapping				
	CH271-350B17	chr4:117032787-117033832	t(HSA4;HSA16)	350B17_BP1_Left	chr4:117240577-117241153				NHEJ -ctccaacctt-filling
		_		350B17_BP1_Right	chr16:16111050-16111587	L2b/LINE2	gSD		
		_	Inv(HSA16)	350B17_BP2_Left	chr16:16118590-16119249	AluSx	gSD	ABCC1 (uc002dee.1)	NAHR between ABCC1-ABCC6
		_		350B17_BP2_Right	Ambiguous mapping	L1-AluSx-L1			
		_	t(HSA16;HSA5)	350B17_BP3_Left	Ambiguous mapping	L1M2/L1-AluSx-L1M2/L1			
		chr5:54236459-54237267		350B17_BP3_Right	chr5:54203270-54203913				
	CH271-398E1	chr17:69796721-69797532	Inv(HSA17)_1	398E1_BP1_Left	chr17:69836813-69837369	AluSc		KIF19 (uc002jkj.1)	
		_		398E1_BP1_Right	chr17:64467113-64467721	L1PA16/L1-THE1B/LTR		ABCA8 (uc002jhp.1)	
		_	Inv(HSA17)_2	398E1_BP2_Left	chr17:64442878-64443431	L1P5/LINE-L1M5/L1-1AluYd8-(CA)n-AluYd8-L1M5/L1		ABCA8 (uc002jhp.1)	Alu-Alu recombination (Figure1)
		chr17:20753342-20754118		398E1_BP2_Right	chr17:20786434-20787025				
	CH271-286K22	chr7:101923026-101923857	Inv(HSA7)	286K22_BP_Left	chr7:101978533-101978861	AluJo_1-AluSx_1-AluJo_1-AluSx_2_AluJo_1-AluSx_4	hSD		NAHR of hSD
		chr7:75864301-75865131		286K22_BP_Right	chr7:75987975-75988443		hSD	UPK3B (uc003ufq.1)	
	CH271-298N13 **centromeric**	chr18:14626725-14627692	t(HSA18;HSA2)	298N13_BP1_Left	chr18:14624361-14624802		hSD		
		_		298N13_BP1_Right	chr2:130451700-130452248	(CA)n-simple repeat -AluSc-AluJb	hSD		
		_	t(HSA2;HSA8)	298N13_BP2_Left	chr2:130315436-130316178	L1PA6/L1-L1ME3A/L1			
		_		298N13_BP2_Right	chr8:4317303-4317902		gSD		
		_	t(HSA8;HSA18)	298N13_BP3_Left	chr8:4260896-4261577		gSD	CSMD1 (uc003wqd.1)	NHEJ "**CT**" homology
		chr18:72428836-72429640		298N13_BP3_Right	chr18:72396578-72397187	AluJb	hSD		
	CH271-372B11 **centromeric**	chr14:19379603-19491075	t(HSA14;HSA2)	372B11_BP1_Left	Ambiguous mapping	L1M4c /L1-L1M1/L1-CL2/L2			
		_		372B11_BP1_Right	chr2:36968096-36968623		gSD		
		_	t(HSA2;HSA9)	372B11_BP2_Left	Ambiguous mapping	BP1-**AluJ/FRAM** -BP2-MLT1G3/LTR-L1MD/L1-**AluJo**			Alu-Alu recombination
		_		372B11_BP2_Right	chr9:98027851-98028324				
		_	t(HSA9;HSA6)	372B11_BP3_Left	chr9:97415689-97416270		gSD		NAHR of gSD
		chr6:151254410-151269850		372B11_BP3_Right	chr6:151263070-151263234		gSD		
	CH271-446I8 **centromeric**	chr7:100735913-100736921	Inv(HSA7)	446I8_BP_Left	chr7:100731021-100731650	AluSx -L1P3/1			Alu-Alu recombination
		chr7:68133693-68134788		446I8_BP_Right	chr7:68241607-68242220	L1ME/L1-AluSx-L1ME/L1			
	CH271-261K6 **HSA specific**	chr3:131140276-131141065	Inv(HSA3)	261K6_BP_Left	chr3:131200116-131200598	MIR (broken in human)	hSD on other side		NAHR of hSD in human
		chr3:15040075-15040867		261K6_BP_right	chr3:15138527-15139113	MIR-LTR16B2/LTR-MLT1D/LTR	gSD, hSD on other side		
	CH271-261A22 **HSA specific**	chr7:7101310-7102318	Inv(HSA7)	261A22_BP_Left	chr7:7006371-7006881	FLAM/SINE-LTR33/ERVL	hSD		NAHR of hSD in human
		chr7:97207081-97207691		261A22_BP_right	chr7:97340602-97341177		hSD		

	BAC	BES1 and BES2 (hg18)	Rearrangement	BP name	BP position	Repeat	Segmental duplication	Genes (UCSC Ac.Nr or Ref.Seq)	Putative mechanism
Shotgun Pool	CH271-125L9	chr3:147740472-147741241	t(HSA3;HSA12)	125L9_BP_Left	chr3:147732628-147732918	none	gSD	PLSCR1 (uc003evx.1)	
		chr12:45807865-45808660		125L9_BP_Right	chr12:45890669-45891125			FAM113B (uc001rpn.1)	
	CH271-141K21	chr9:113404746-113404882	Inv(HSA9)	141K21_BP_Left	chr9:113460127-113460458			LOC552891 (uc004bfn.1)	
		chr9:22218708-22218920		141K21_BP_Right	chr9:22288734-22289442	L1M1/L1			
	CH271-185K6	chr14:30838138-30838392	Inv(HSA14)	185K6_BP_Left	chr14:30985515-31679560*	AluY			
		chr14:73124155-73124877		185K6_BP_Right	chr14:73091554-73091829	L1M1/L1		HEATR4 (uc001xoj.1)	
	CH271-18C15	chr6:9423952-9424795	t(HSA6;HSA11)	18C15_BP_Left	chr6:9375117-9375652	none	gSD		
		chr11:32321052-32321338		18C15_BP_Right	chr11:32145365-32145812	none	gSD		
	CH271-241J10	chr1:54907463-54907795	Inv(HSA1)	241J10_BP_Left	chr1:55009636-55010105	L2a/L2	gSD		NHEJ -AAAAAAAAAATTTTCT-filling
		chr1:211021684-211022133		241J10_BP_Right	chr1:211097036-211097354				
	CH271-274L1	chr17:69720630-69721057	Inv(HSA17)_1	274L1_BP1_Left	chr17:69833458-69833569				NHEJ -TGGTATGGAGCGAGCACCTCA-filling
		_		274L1_BP1_Right	chr17:70243897-70244356	Alu		RAB37 (uc002jle.1)	
		_	Inv(HSA17)_2	274L1_BP2_Left	No Breakpoint Information				
		chr17:66671503-66672271		274L1_BP2_Right					
	CH271-330D2	chr16:73591531-73592258	t(HSA16;HSA5)	330D2_BP_Left	chr16:73411618-73411924	L1			NHEJ "**CA**" homology
		chr5:132444217-132444431		330D2_BP_Right	chr5:132470668-132471176	AluJb at 210bp			
	CH271-362G10	chr6:27185623-27186149	t(HSA6;HSA9)	362G10_BP_Left	chr6:27133029-27133530		gSD		
		chr9:30805802-30806750		362G10_BP_Right	chr9:30938218-30938483	L1MEc/L1			
	CH271-405A9	chr2:27994865-27994148	t(HSA2;HSA17)_RecCH271-262E11	405A9_BP_Left	chr2:27780864-27781537	MIR3-AluSg/x			
		chr17:59333868-59333191		405A9_BP_Right	chr17:59313018-59313274		gSD and hSD		
	CH271-44A23	chr7:2700908-2701376	t(HSA7;HSA2)	44A23_BP_Left	chr7:2619384-2620096		gSD		
		chr2:150152851-150153542		44A23_BP_Right	chr2:150079919-150080449	AluS			
	CH271-171B20	chr9:32478670-32479624	Inv(HSA9)_1	171B20_BP1_Left	chr9:32478468-32478924	AluSx			NHEJ -ATACTACATATATAGA(TA)$_5$TCCT-filling
		_		171B20_BP1_Right	chr9:38261234-38261674				
		_	Inv(HSA9)_2	171B20_BP2_Left	chr9:38779194-38779598	No Breakpoint sequence			
		chr9:27166326-27166532		171B20_BP2_Right	chr9:27256349-27256935				
	CH271-185E17	chr8:62776249-62776628	Inv(HSA8)	185E17_BP_Left	chr8:62850735-62850926				
		chr8:99254477-99255380		185E17_BP_Right	chr8:99136628-99137178	AluSg/x			
	CH271-122E24	chr6:46092903-46093778	t(HSA6;HSA2)	122E24_BP_Left	chr6:46224094-46224375	AluY-(TTTA)n -AluY			
		chr2:168833875-168834096		122E24_BP_Right	chr2:168921485-168921828				
	CH271-40A18	chr6:46243705-46246528	t(HSA6;HSA2)_RecCH271-122E24	40A18_BP_Left	chr6:46244450-46244952	(TA)n			
		chr2:168943139-168960712		40A18_BP_Right	chr2:168941518-168941810	L1			
	CH271-449L10	chr12:63651232-63652094	t(HSA12;HSA19)	449L1_BP_Left	chr12:63567426-63567984	AluJo			NHEJ-AAAA-filling
		chr19:41725837-41726391		449L1_BP_Right	chr19:41824636-41824883				
	CH271-234B14	chr3:19775959-19776713	t(HSA3;HSA8)	234B14_BP_Left	chr3:19801280-19801846	Tigger3b DNA/MER2			
		chr8:20169960-20170244		234B14_BP_Right	chr8:19972153-19972405	THE1A/LTR-L1MA3/L1			
	CH271-49C12	chr17:55502427-55503122	Inv(HSA17)_1	49C12_BP1_Left	chr17:55479737-55479892			ABC1 (uc002iyk.1)	
		_		49C12_BP1_Right	chr17:27828000-27828705			PSMD11 (uc002hhm.1)	
		_	Inv(HSA17)_2	49C12_BP2_Left	Missing	AluY			
		chr17:45884382-45884620		49C12_BP2_Right	Missing				
	CH271-107F17	chr22:32050317-32050909	Inv(HSA22)	107F17_BP_Left	chr22:31971471-31971840	HSMAR2/Mariner-AluSx- HSMAR2/Mariner			
		chr22:31006873-31007483		107F17_BP_Right	chr22:30920732-30920843		hSD	RFPL2 (uc003ame.1)	
	CH271-114O8	chr5:75772933-75773648	t(HSA5;HSA16)	114O8_BP_Left	chr5:75703809-75704511				NHEJ-ATGATG-filling
		chr16:19525951-19526628		114O8_BP_Right	chr16:19419664-19419762				
	CH271-247C2	chr2:99193372-99193548	t(HSA2;HSA17)_RecCH271-267G23	247C2_BP_Left	chr2:99287211-99287966	AluY			
		chr17:77943112-77943299		247C2_BP_Right	chr17:77869210-77870732				
	CH271-438C12	chr10:52579011-52579213	t(HSA10;HSA14)	438C12_BP_Left	chr10:52595969-52596550	MSTA/LTR		PRKG1 (uc001jjm.1)	NHEJ-AAC-filling
		chr14:35365902-35366597		438C12_BP_Right	chr14:106265726-106265962			abParts (uc001yrq.1)	
	CH271-383H22	chr3:194767531-194767746	Inv(HSA3)_1	383H22_BP1_Left	chr3:194750831-194751067	AluJb	gSD		Alu-Alu recombination
		_		383H22_BP1_Right	chr3:198930706-198931429	L1MA6/L1			
		_	Inv(HSA3)_2	383H22_BP2_Left	Missing				
		chr3:196990112-196990361		383H22_BP2_Right	Missing				
Trace Archives	Trace:1744822164	_	Inv(HSA17)_RecCH271-389E1	Rec_398E1_BP_Left	chr17:64468378-64468996	Charlie			NHEJ-GAAATAGAAATAAAAAC-filling
		_		Rec_398E1_BP_Left	chr17:69838399-69838549			KIF19 (uc002jkj.1)	
	CH271-119L23	chr19:44062149-44062967	t(HSA19;HSA7)	119L13_BP_Left	chr19:44009702-44014702	**No Breakpoint sequence**		HNRNPL (uc002ojk.1); ECH1 (uc002oji.1)	**No Breakpoint sequence**
		chr7:23148716-23149425		119L13_BP_Right	chr7:23062779-23067779				
	CH271-262E15	chr4:187202780-187203261	Inv(HSA4)	262E15_BP_Left	chr4:187202337-187207337				
		chr4:185313479-185314230		262E15_BP_Right	chr4:185309892-185314892			ENPP6 (uc003iwc.1)	
	CH271-401L9	chr10:24076626-24076771	t(HSA10;HSA4)	401L9_BP_Left	chr10:23994393-23999393				
		chr4:110612050-110612158		401L9_BP_Right	chr4:110501558-110506558				
	CH271-457L13	chr22:31172669-31173346	t(HSA22;HSA4)_RecCH271-263C9	457L13_BP_Left	chr22:31042892-31047892		hSD		
		chr4:140618444-140619353		457L13_BP_Right	chr4:140586473-140591473		gSD		
	CH271-300N11	chr10:11957906-11958581	Inv(HSA10)	300N11_BP_Left	chr10:12128225-12133225				
		chr10:15049040-15049323		300N11_BP_Right	chr10:15063576-15068576		hSD		
	CH271-274K2	chr2:128217917-128218714	Inv(HSA2)	274K2_BP_Left	chr2:128110049-128115049			LIMS2 (uc002tou.1)	
		chr2:131832424-131832748		274K2_BP_Right	chr2:131905153-131910153				
	CH271-322A3	chr13:38382334-38382944	Inv(HSA13)	322A3_BP_Left	chr13:38336699-38341699			FREM2 (uc001uwv.1)	
		chr13:22312091-22312355		322A3_BP_Right	chr13:23436399-23441399				

	BAC	BES1 and BES2 (hg18)	Rearrangement	BP name	BP position	Repeat	Segmental duplication	Genes (UCSC Ac.Nr or Ref.Seq)	Putative mechanism
BES Only	CH271-212J20	chr15:28990033-28990789	Inv(HSA15)	**No Breakpoint mapping Information**					
		chr15:30748924-30749757							
	CH271-219C13/CH271-156E13	chr2:73614518-73615293	t(HSA2;HSA17)						
		chr17:61651667-61651884							
	CH271-219C17	chr17:20464920-20494920	Inv(HSA17)						
		chr17:57601971-57631971							
	CH271-186A1	chr6:57494796-57495539	Inv(HSA6)						
		chr6:62082461-62083238							
	CH271-144D7	chr17:33747350-33748174	Inv(HSA17)						
		chr17:43053145-43053947							
	CH271-144P05	chr17:43030034-43030452	Inv(HSA17)						
		chr17:45903313-45904103							
	CH271-244C18	chr6:26665529-26666210	Inv(HSA6)						
		chr6:58278082-58278396							
	CH271-133C19	chr17:27546813-27547000	Inv(HSA17)						
		chr17:26246352-26246485							
	CH271-362O01	chr2:114170325-114170537	Inv(HSA2)						
		chr2:132955805-132956199							
	CH271-314F10	chr18:10502587-10502787	Inv(HSA18)						
		chr18:12104383-12105287							
	CH271-10M04	chr11:3137758-3138457	Inv(HSA11)						
		chr11:70938138-70938965							
	CH271-316D01	chr12:50750486-50750968	t(HSA12;HSA3)						
		chr3:76165224-76165428							
	CH271-380N5	chr3:58787556-58788437	t(HSA12;HSA3)						
		chr12:120366540-120367347							
	CH271-461L14	chr13:26172852-26173025	t(HSA13;HSA1)						
		chr1:202036523-202037082							
	CH271-202N11	chr10:51751461-51752217	Inv(HSA10)						
		chr10:52229449-52229635							
	CH271-263M06	chr7:102292933-102293699	Inv(HSA7)						
		chr7:92995033-92995531							
	CH271-267G21	chr17:55284622-55285294	Inv(HSA17)						
		chr17:57642889-57643214							
	CH271-26L7	chr17:45966195-45967178	Inv(HSA17)						
		chr17:30504099-30504910							
	CH271-134D13	chrX:34418293-34418679	Inv(HSAX)						
		chrX:63295824-63296135							
	CH271-64D21	chrX:36155073-36155711	Inv(HSAX)						
		chrX:34207559-34208240							
	CH271-262O07	chr8:116011454-116012115	t(HSA8;HSA5)						
		chr5:20660956-20661663							
	CH271-30L2	chr19:5851377-5851846	Inv(HSA19)						
		chr19:51500098-51500471							
	CH271-74B2	chr17:61598754-61599496	Inv(HSA17)						
		chr17:20111039-20111836							
	CH271-216H2	chr10:52022220-52023160	Inv(HSA10)						
		chr10:89294947-89295755							
False Positives	CH271-16A10	**No Breakpoints**							
	CH271-146B14								
	CH271-188I7								