

Table ST2. Region pairs that were detected as differentially interacting when comparing (corrected) replicates of IMR90 and ESC cell lines. The regions' coordinates are given (chromosome name, start and end positions) along with the associated BF value (the maximal value across all cross comparisons). In addition we provide the number of cross comparisons (between the different replicates) in which the change was detected as significant (Votes). The top 2 differentially interacting regions are highlighted (in bold). BF, Bayes Factor.

Chr1	Start1	End1	Chr2	Start2	End2	BF	Votes
<b>chr11</b>	<b>84000000</b>	<b>84999999</b>	<b>chr17</b>	<b>30000000</b>	<b>30999999</b>	<b>46.36672</b>	<b>1</b>
<b>chr1</b>	<b>91000000</b>	<b>91999999</b>	<b>chrX</b>	<b>1.08E+08</b>	<b>1.09E+08</b>	<b>41.13984</b>	<b>2</b>
chr1	1.62E+08	1.63E+08	chr16	69000000	69999999	17.59863	2
chr1	91000000	91999999	chr12	34000000	34999999	15.17791	2
chr13	26000000	26999999	chr14	87000000	87999999	13.9271	2
chr16	7000000	7999999	chr6	1	999999	12.37341	3
chr1	1.74E+08	1.75E+08	chr16	69000000	69999999	11.27555	2
chr19	24000000	24999999	chr5	62000000	62999999	10.9823	2
chr19	24000000	24999999	chr5	63000000	63999999	10.44883	2
chr21	18000000	18999999	chr4	1.9E+08	1.91E+08	10.33765	1
chr19	24000000	24999999	chr5	61000000	61999999	10.20545	2
chr1	1.72E+08	1.73E+08	chr16	69000000	69999999	10.15263	1
chr1	1.66E+08	1.67E+08	chr16	69000000	69999999	10.12206	2
chr1	1.67E+08	1.68E+08	chr16	69000000	69999999	10.12206	3
chr19	24000000	24999999	chr5	59000000	59999999	10.03875	1
chr19	24000000	24999999	chr5	60000000	60999999	10.03875	2
chr19	24000000	24999999	chr5	67000000	67999999	9.912153	2
chr21	19000000	19999999	chr4	1.9E+08	1.91E+08	9.772827	2
chr1	1.75E+08	1.76E+08	chr16	69000000	69999999	9.622689	3
chr15	19000000	19999999	chr21	9000000	9999999	9.414303	1
chr4	67000000	67999999	chr7	61000000	61999999	9.359272	1
chr1	1.69E+08	1.7E+08	chr16	69000000	69999999	9.241399	2
chr6	62000000	62999999	chr7	61000000	61999999	9.172505	1
chr1	1.63E+08	1.64E+08	chr16	69000000	69999999	9.057243	1
chr1	1.56E+08	1.57E+08	chr16	69000000	69999999	9.015332	1
chr1	1.21E+08	1.22E+08	chr5	45000000	45999999	8.935408	2
chr3	77000000	77999999	chr6	57000000	57999999	8.924011	1
chr15	19000000	19999999	chr16	33000000	33999999	8.873315	1
chr12	13000000	13999999	chr4	67000000	67999999	8.627406	2
chr21	20000000	20999999	chr4	1.9E+08	1.91E+08	8.528016	3
chr16	6000000	6999999	chr6	1	999999	8.435892	2
chr16	13000000	13999999	chr6	1	999999	8.330147	2
chr19	24000000	24999999	chr5	58000000	58999999	8.208523	2
chr20	53000000	53999999	chr9	67000000	67999999	8.201227	1
chr21	30000000	30999999	chr4	1.9E+08	1.91E+08	8.112089	2
chr1	1.68E+08	1.69E+08	chr16	69000000	69999999	8.064983	3
chr21	19000000	19999999	chr9	67000000	67999999	8.04476	2
chr19	24000000	24999999	chr5	66000000	66999999	8.024014	1
chr16	33000000	33999999	chr20	53000000	53999999	7.98145	1
chr3	1.18E+08	1.19E+08	chr6	57000000	57999999	7.758112	1
chr16	5000000	5999999	chr6	1	999999	7.623317	2
chr13	53000000	53999999	chr21	10000000	10999999	7.588509	1
chr16	33000000	33999999	chr17	42000000	42999999	7.507705	1
chr1	1.41E+08	1.42E+08	chr4	45000000	45999999	7.484834	1
chr12	17000000	17999999	chr4	67000000	67999999	7.45981	2
chr14	25000000	25999999	chr4	1.9E+08	1.91E+08	7.430886	1

chr21	40000000	40999999	chr4	1.9E+08	1.91E+08	7.3916	2
chr1	1.64E+08	1.65E+08	chr16	69000000	69999999	7.389136	1
chr1	1.41E+08	1.42E+08	chr4	47000000	47999999	7.379373	1
chr19	24000000	24999999	chr5	57000000	57999999	7.327549	1
chr1	1.21E+08	1.22E+08	chr19	34000000	34999999	7.272698	1
chr21	31000000	31999999	chr4	1.9E+08	1.91E+08	7.208303	1
chr13	34000000	34999999	chr21	10000000	10999999	7.148562	1
chr3	1.46E+08	1.47E+08	chr6	57000000	57999999	7.131365	1
chr16	33000000	33999999	chr20	40000000	40999999	7.126427	1
chr12	69000000	69999999	chr4	67000000	67999999	6.978656	2
chr13	69000000	69999999	chr4	1.9E+08	1.91E+08	6.89874	1
chr3	1.19E+08	1.2E+08	chr6	57000000	57999999	6.867292	2
chr4	1.9E+08	1.91E+08	chr5	46000000	46999999	6.862155	1
chr15	19000000	19999999	chr9	67000000	67999999	6.842531	1
chr2	1.32E+08	1.33E+08	chr20	40000000	40999999	6.837236	2
chr19	32000000	32999999	chr21	19000000	19999999	6.833563	2
chr16	25000000	25999999	chr6	1	999999	6.810314	1
chr3	1	999999	chr7	61000000	61999999	6.663006	1
chr12	16000000	16999999	chr4	67000000	67999999	6.616876	1
chr3	1.32E+08	1.33E+08	chr6	57000000	57999999	6.609255	2
chr17	22000000	22999999	chr7	61000000	61999999	6.525028	1
chr12	41000000	41999999	chr4	67000000	67999999	6.512667	1
chr12	31000000	31999999	chr4	67000000	67999999	6.506781	1
chr1	1.61E+08	1.62E+08	chr16	69000000	69999999	6.481288	1
chr12	61000000	61999999	chr4	67000000	67999999	6.447913	2
chr6	57000000	57999999	chr7	61000000	61999999	6.427203	1
chr1	1.73E+08	1.74E+08	chr16	69000000	69999999	6.424035	2
chr21	18000000	18999999	chr9	67000000	67999999	6.418103	1
chr21	22000000	22999999	chr4	1.9E+08	1.91E+08	6.400423	1
chr15	25000000	25999999	chr21	9000000	9999999	6.375954	1
chr15	18000000	18999999	chr21	9000000	9999999	6.350599	1
chr19	24000000	24999999	chr5	65000000	65999999	6.227969	1
chr3	1.17E+08	1.18E+08	chr6	57000000	57999999	6.209266	1
chr12	14000000	14999999	chr4	67000000	67999999	6.202226	1
chr13	53000000	53999999	chr4	1.9E+08	1.91E+08	6.198277	1
chr3	1.41E+08	1.42E+08	chr6	57000000	57999999	6.18264	1
chr13	25000000	25999999	chr21	10000000	10999999	6.179253	1
chr12	53000000	53999999	chr4	67000000	67999999	6.12365	1
chr3	1.22E+08	1.23E+08	chr6	57000000	57999999	6.104072	1