motif	gene	start	stop	strand	p.value	matched.sequence
ESR1	ENSG00000227200	266	285	-	1.51E-08	CACCCAGGTCAACATGACCC
ESR1	ENSG00000105675	20	39	-	1.30E-07	CCCCCATGTCAACCTGCCCT
ESR1	ENSG00000253302	110	129	+	1.47E-07	CTCCAAGGGCACCCAGCCCT
ESR1	ENSG00000155636	115	134	-	2.02E-07	GACGCGGGGGACCCTGACCC
ESR1	ENSG00000050426	302	321	-	2.38E-07	CGCGGAGGGCACCCTGTCCT
ESR1	ENSG00000221585	104	123	-	3.09E-07	CTGCCGGGTGACCTTGCCCT
ESR1	ENSG00000141524	270	289	-	3.53E-07	GGCCCCGGCCTCCCTGACCC
ESR1	ENSG00000258388	69	88	+	4.42E-07	CCTCCAGGCCACCCTGCCAC
ESR1	ENSG00000165182	123	142	+	6.34E-07	CGGCAGGGTCACCCCGGCCT
ESR1	ENSG00000222019	314	333	-	1.08E-06	GGGGCCGGTCACCCCGCCCC
ESR1	ENSG00000167165	233	252	-	1.12E-06	AGGGAGGGTCACACTGGCCC
ESR1	ENSG00000167635	196	215	+	1.19E-06	CGCCCAGGACTCCCAGACCC
ESR1	ENSG00000255529	217	236	+	1.30E-06	GTCCACGGTCACCCTGCTCT
ESR1	ENSG00000202031	175	194	+	1.79E-06	TGGGGAGGGCAGCCTGACTC
ESR1	ENSG00000178550	196	215	-	1.88E-06	GAGCAGGGGCAGCATGGCCT
ESR1	ENSG00000250012	155	174	+	2.02E-06	AGGCCGGGCCTCCCTGGCCC
ESR1	ENSG00000196557	1	20	+	2.27E-06	CGCCCCGGCCACGCTGGCCC
ESR1	ENSG00000257108	358	377	+	2.29E-06	GTCAGAAGTCTCCCTGACCT
ESR1	ENSG00000100934	239	258	+	2.52E-06	GGCGCATGTCACCATGCCCG
ESR1	ENSG00000107331	102	121	-	2.69E-06	GACAGAGGACAGGCTGACCC
ESR1	ENSG00000204622	219	238	-	2.74E-06	GGTTCGGGGCGCCATGACCC
ESR1	ENSG00000132849	369	388	+	2.75E-06	TTCCCGGGCCTGCCTGCCCT
ESR1	ENSG00000117632	225	244	-	3.03E-06	CCTGCAGGGCCCCCTGCCCC
ESR1	ENSG00000203896	336	355	+	3.06E-06	ACCCAGGGTGGCCCTGCCCC
ESR1	ENSG00000127022	24	43	+	3.19E-06	CCCCGAGGCCACGCAGACCT
ESR1	ENSG00000139350	299	318	-	3.46E-06	GGGCGGGGGCCCGCTGACCT
ESR1	ENSG00000185278	6	25	-	3.67E-06	TGCTAAGGTCACCCTGAATT
ESR1	ENSG00000126351	254	273	+	3.83E-06	AAGGGAGGGCAGCCTGCCAT
ESR1	ENSG00000189410	13	32	-	3.85E-06	GGAGCGGGGCACCCTGACAG
ESR1	ENSG00000100399	194	213	+	3.89E-06	AGGCGGGGACAGCCTGTCCC
ESR1	ENSG00000138442	256	275	-	3.98E-06	GCTTCAGGTCACCCCGCCCA
ESR1	ENSG00000157734	119	138	-	4.01E-06	CCCCCAGGCGACCCCGCCCC
ESR1	ENSG00000132510	134	153	-	4.08E-06	TTTCCTGGGCTCCCTGCCCC
ESR1	ENSG00000186862	260	279	-	4.10E-06	GTGCCTGGTCGGCCTCACCT
ESR1	ENSG00000247275	302	321	-	4.76E-06	GGGTTAGGTCAGCATGATCC
ESR1	ENSG00000116701	321	340	+	4.93E-06	TGCCAAGGTTACCCTGGCTC
ESR1	ENSG00000258136	127	146	-	4.93E-06	TGCTTTGGCCACTCTGACCC
ESR1	ENSG00000135709	332	351	-	5.01E-06	CTCCCGGGTCATCCTTCCCC
ESR1	ENSG00000117983	118	137	-	5.07E-06	CACGCAGGGCACCATGCTCT
ESR1	ENSG00000196372	153	172	+	5.10E-06	GGCCCAGCGCAGACTGGCCC
ESR1	ENSG00000182934	90	109	-	5.10E-06	GGGCCGGGGCCTCTTGACCC
ESR1	ENSG00000125954	30	49	+	5.91E-06	TGCCAAGGAGACTGTGCCCT
ESR1	ENSG00000004399	211	230	-	6.04E-06	GGCCCGGGTCAGCCTCGCCG
ESR1	ENSG00000202058	203	222	-	6.25E-06	CAGCCAGATCACCCTCACAT
ESR1	ENSG00000200091	203	222	-	6.25E-06	CAGCCAGATCACCCTCACAT
ESR1	ENSG00000167741	320	339	-	6.50E-06	GCTGCATGTGAGCCTGCCCC
ESR1	ENSG00000134255	338	357	-	6.61E-06	GGCTCAGCTCCCCGTGCCCT
ESR1	ENSG00000162746	267	286	-	6.61E-06	GAACCGGGGCACCTTGATCC
ESR1	ENSG00000237317	228	247	-	6.68E-06	TGACAAGGTCACTGTGGCTT

ESR1	ENSG00000143627	115	134	-	6.80E-06	CCAGTAGGCCACCCTGTCCC
ESR1	ENSG00000214597	190	209	+	6.91E-06	CTCCCTGGCCTCGCTGCCCT
ESR1	ENSG00000122778	303	322	+	7.11E-06	CGCCGGGGTCGCGCTGGCCC
ESR1	ENSG00000177731	113	132	+	7.22E-06	AGCGCAGGTGACGGTGCCTC
ESR1	ENSG00000111780	287	306	-	7.47E-06	GGCCAAGGTCACAGTCCCTC
ESR1	ENSG00000163812	4	23	-	7.47E-06	CGCCGGGTTCAGCCTGGCCC
ESR1	ENSG00000197102	188	207	-	7.55E-06	CTGCCAGGTGGCCCCGCCCC
ESR1	ENSG00000106069	320	339	-	7.55E-06	ATGTCTGATCACCCTGGCCT
ESR1	ENSG00000148814	100	119	+	7.72E-06	GCGCAGGGGCACCCACACCC
ESR1	ENSG00000185728	243	262	-	7.76E-06	GCTCCGAGCCTCCCTGACCT
ESR1	ENSG00000132010	319	338	+	7.94E-06	GCCCCGGGTCCCTCTGCCAC
ESR1	ENSG00000185507	336	355	+	7.98E-06	CCGTGGGGGCTCCGTGACCC
ESR1	ENSG00000169062	61	80	-	8.25E-06	CCGCCGGGTCAGGCGGCCCC
ESR1	ENSG00000236472	375	394	-	8.57E-06	AACCTGGGGCCTCCTGACCT
ESR1	ENSG00000165238	188	207	-	8.57E-06	GGCCAAGGACACACAGGCCC
ESR1	ENSG00000229732	345	364	-	8.62E-06	CTCTCAGGACCCCCTGTCCT
ESR1	ENSG00000130638	73	92	+	8.67E-06	AACACAGGTCCCCCTCCCCC
ESR1	ENSG00000187144	248	267	-	9.00E-06	GGCAAGGGGCTGTGTGACCT
ESR1	ENSG00000213145	43	62	-	9.00E-06	AGCCCAGGTCACTGTCAGCC
ESR1	ENSG00000161800	273	292	+	9.20E-06	TAGCCAAGCCTCCCTGCCCC
ESR1	ENSG00000115504	320	339	+	9.20E-06	ACACAAGGTTAGCATGCCCC
ESR1	ENSG00000167972	37	56	-	9.46E-06	GGCAGAGGGCGCTCTGACTT
ESR1	ENSG00000012963	97	116	-	9.61E-06	GCGCCGGGTGACGGCGACCC
ESR1	ENSG00000213689	37	56	-	9.72E-06	CTTGGGGGTCCCCCTGCCCT
ESR1	ENSG00000104529	143	162	-	9.72E-06	GGCCCCAGCCAGTCTGCCCT
ESR1	ENSG00000129810	91	110	+	9.82E-06	CCGGCGGGTCGCCGAGACCC
ESR1	ENSG00000110619	64	83	+	9.88E-06	TCGCCAGCACACCCTGTCCC
ESR1	ENSG00000178836	184	203	+	9.88E-06	GGCCCAGGTCGCCAAGCCTC
ESR1	ENSG00000168575	363	382	+	9.88E-06	GGGCCGGGTGACGCGGCCCC
ESR1	ENSG00000256500	69	88	+	1.01E-05	CGCCCGGGTCAGCCCGCGCC
ESR1	ENSG00000186106	382	401	-	1.01E-05	AAGCCCGGGCACCCTCGCCC
ESR1	ENSG00000248636	151	170	+	1.02E-05	GCACCAGGACACCACGCCCC
ESR1	ENSG00000126777	140	159	-	1.04E-05	AGGGCAAGTCACTTTGACAC
ESR1	ENSG00000254901	226	245	-	1.04E-05	CGGCCAAGGTACGCTGCCCC
ESR1	ENSG00000164142	263	282	-	1.04E-05	GGCCCAGGTCCTCCAGGCCC
ESR1	ENSG00000258545	110	129	-	1.05E-05	GGCCTGGGCCTGCCTGGCCT
ESR1	ENSG00000225187	379	398	+	1.06E-05	TGCAAGGCCCAGCCTGACCT
ESR1	ENSG00000134490	324	343	+	1.07E-05	GTCTCTGGTCGGCCTCACCT
ESR1	ENSG00000246731	7	26	+	1.08E-05	CGGCCGGGGCCCCGTGCCCG
ESR1	ENSG00000240801	32	51	-	1.09E-05	GAAGGCGGCCACCCTGCCCC
ESR1	ENSG00000139116	273	292	+	1.09E-05	GGGGCAGGGCGCACTCACCC
ESR1	ENSG00000110011	173	192	-	1.11E-05	CGGCCCGGCCACCGTGTCTC
ESR1	ENSG00000187721	224	243	-	1.13E-05	GATGCAGGCCACTTTGGCCT
ESR1	ENSG00000171169	373	392	-	1.14E-05	GAGCCGGGTGACCCCGCCCA
ESR1	ENSG00000249293	355	374	-	1.15E-05	ACCTGAGGTGACACTGGCCC
ESR1	ENSG00000226232	341	360	-	1.17E-05	GCTCAAGGGCACCAGGCCCC
ESR1	ENSG00000248423	239	258	+	1.17E-05	ACCCCTGGGGATCCTGTCCT
ESR1	ENSG00000196353	121	140	+	1.19E-05	TCCCAAGACCACCCTGGCCC
ESR1	ENSG00000103023	254	273	+	1.29E-05	GTGTCAGGCCAGCCTGAGTT
ESR1	ENSG00000099337	64	83	-	1.30E-05	AGCCCAGTGCTCCCAGACCC

ESR1	ENSG00000196923	18	37	+	1.31E-05	GGCCCGGGTCGGCGAGGCCT
ESR1	ENSG00000114503	371	390	-	1.33E-05	CGGCCCGGCCTCCCTCACCC
ESR1	ENSG00000065518	38	57	-	1.34E-05	CTCGCAGTGCGCCCTGCCCC
ESR1	ENSG00000176261	118	137	-	1.35E-05	CTCTCACGTGACCCTGACCG
ESR1	ENSG00000159214	329	348	+	1.38E-05	CGCCGAGGTGAGTCTGAACT
ESR1	ENSG00000177192	83	102	-	1.42E-05	AGGGCGGGGCACCAGGCCCT
ESR1	ENSG00000165409	293	312	+	1.44E-05	TAGCCAGGGCTGCGTGCCCG
ESR1	ENSG00000169964	87	106	-	1.45E-05	GGGCCAGGTGGCAGAGACCC
ESR1	ENSG00000207783	68	87	-	1.45E-05	GGGCCAGGTGGCAGAGACCC
ESR1	ENSG00000138434	326	345	+	1.46E-05	TCCCCGGGGCCCCCTGCCCG
ESR1	ENSG00000230165	175	194	+	1.47E-05	CACCCTGGACTACCTGCCCC
ESR1	ENSG00000145494	310	329	-	1.47E-05	CTCCCCGGTCGGCGAGACCC
ESR1	ENSG00000109452	130	149	+	1.51E-05	GGCTCTGGGCACCTTTACCT
ESR1	ENSG00000243284	88	107	+	1.54E-05	CAGGTAGGCCACCCTGTCAC
ESR1	ENSG00000169583	59	78	+	1.54E-05	GGTGGAGGTGGTCCTGACCC
ESR1	ENSG00000172819	339	358	-	1.55E-05	AGGCCAGGGCTCACAGACAT
ESR1	ENSG00000245562	11	30	+	1.55E-05	GGCACATGCCACCATGCCCA
ESR1	ENSG00000186815	240	259	-	1.59E-05	AAGAAAGGTCAGTCAGACAC
ESR1	ENSG00000108298	266	285	-	1.60E-05	AGACCAGCTCGCCCTCACCT
ESR1	ENSG00000256757	149	168	+	1.62E-05	CCTCAGGGGCATTCTGTCCC
ESR1	ENSG00000070366	363	382	+	1.64E-05	GGGCCGGGCCTGCCCGCCCC
ESR1	ENSG00000074582	246	265	-	1.66E-05	CTCCTACCTCACCCTGCCCT
ESR1	ENSG00000117419	184	203	-	1.70E-05	ACCTCCGCGCACTCTGACCC
ESR1	ENSG00000208038	354	373	+	1.70E-05	GGATGAGGTGACCCTGGCCA
ESR1	ENSG00000234751	307	326	+	1.75E-05	TCCACAGGGCTCCCCGCCCC
ESR1	ENSG00000134780	15	34	+	1.85E-05	GACTCGGCTCTCCCTGGCCT
ESR1	ENSG00000149292	245	264	+	1.85E-05	CAGGCAGGTCACTGCGCCAT
ESR1	ENSG00000142156	262	281	+	1.87E-05	GCGGCGGCCCACTCTGCCCT
ESR1	ENSG00000252974	4	23	-	1.90E-05	CGGCCGGGTGAGTGCGCCCT
ESR1	ENSG00000134333	107	126	+	1.93E-05	ACTGAAGGTCGTCCTGACTC
ESR1	ENSG00000236546	121	140	+	1.94E-05	AGGACTGGGCAGCCTCACTT
ESR1	ENSG00000215039	293	312	+	1.94E-05	CTGCCAGGTCTCACTCTCCC
ESR1	ENSG00000004766	196	215	-	1.97E-05	GACCCAGGGTATCCTGTCTT
ESR1	ENSG00000175892	41	60	-	2.00E-05	AACCGAGGCCAGAGTGTCCC
ESR1	ENSG00000003989	64	83	-	2.01E-05	GGCCCCGGCCGCGCTGACCA
ESR1	ENSG00000249199	271	290	+	2.05E-05	TAACAGGGACAGCCAGACCC
ESR1	ENSG00000088298	352	371	+	2.07E-05	TGTCCCGGCGACCCAGACCT
ESR1	ENSG00000138496	82	101	-	2.07E-05	GACCCAGTTCCAGCTGACCT
ESR1	ENSG00000155984	56	75	-	2.08E-05	GACACCTGTCACCTTGGCCC
ESR1	ENSG00000123104	43	62	+	2.10E-05	CCCGAGGGTCGCCCCGCCCC
ESR1	ENSG00000110719	146	165	-	2.12E-05	GGCCAGGGACGCCCCGCCCC
ESR1	ENSG00000149532	339	358	-	2.12E-05	CTTCCGGCCCAACCTGCCCC
ESR1	ENSG00000206567	381	400	+	2.13E-05	GCCTCAGGTGAGGGTCACCC
ESR1	ENSG00000121236	151	170	+	2.15E-05	GGGGCTGGACAATTTGACCC
ESR1	ENSG00000151006	153	172	-	2.15E-05	GTGCGAGACCAGCCTGACCA
ESR1	ENSG00000241738	114	133	-	2.15E-05	GTGCGAGACCAGCCTGACCA
ESR1	ENSG00000248127	129	148	-	2.15E-05	AGGCCAGGCGAAGCAGACCC
ESR1	ENSG00000116171	112	131	-	2.16E-05	GGACTGAGTCAACCTGTCCC
ESR1	ENSG00000121310	254	273	+	2.16E-05	GGACTGAGTCAACCTGTCCC
ESR1	ENSG00000103056	300	319	-	2.18E-05	GCCAATGGTGACCCGGACCC

ESR1	ENSG00000115239	220	239	-	2.18E-05	CGCCGAGGGCACCGCCCCCT
ESR1	ENSG00000122085	367	386	+	2.19E-05	CGGCCAGGTCGTGGAGCCCT
ESR1	ENSG00000144802	10	29	+	2.21E-05	AATCTAGGCCTCGCTGCCCC
ESR1	ENSG00000205089	380	399	+	2.21E-05	GGGGGAGGCCCCTCTGCCCC
ESR1	ENSG00000204618	22	41	+	2.21E-05	GAGCCTGGGCACCCGGCCCA
ESR1	ENSG00000226746	312	331	-	2.24E-05	AGGCCAGGACAGCGTGGGCC
ESR1	ENSG00000131435	83	102	-	2.24E-05	CCCCGCGGCCAGCCCGACCC
ESR1	ENSG00000223430	58	77	-	2.25E-05	TTCTTGGGTGGGCCTGACCT
ESR1	ENSG00000112365	299	318	-	2.25E-05	ACGCCGGGGCCCGCTGGCCC
ESR1	ENSG00000222482	97	116	-	2.29E-05	CTCCCTGGTGACTGTGAGCT
ESR1	ENSG00000133808	163	182	+	2.32E-05	GCGGAAGGGGACGCTGCCTC
ESR1	ENSG00000138111	2	21	+	2.35E-05	GAATCCAGGCAACCTGACCC
ESR1	ENSG00000240224	67	86	+	2.35E-05	GGAGGAGGGCACTCTGTCTT
ESR1	ENSG00000156508	56	75	+	2.35E-05	AGGCCAGCTCACGGTGACAA
ESR1	ENSG00000229674	308	327	-	2.36E-05	GGTGCCGGGCATGCTGACTT
ESR1	ENSG00000173137	212	231	-	2.38E-05	CTCCTGAGTCAGCTTGGCCT
ESR1	ENSG00000255152	368	387	+	2.40E-05	CCCACAGGGCCCTCAGACCC
ESR1	ENSG00000006062	180	199	-	2.42E-05	GCCCGTGGTCGCCCCGCCCC
ESR1	ENSG00000146376	126	145	-	2.45E-05	AGGGAAGGGCTTCCTGCCTC
ESR1	ENSG00000228063	13	32	+	2.46E-05	GGGGCAGGTGGCGCTGCCCG
ESR1	ENSG00000253528	100	119	-	2.46E-05	AACCCAGGGCCTTCTGGCCC
ESR1	ENSG00000250101	196	215	+	2.47E-05	CGCCCACGTCGGCCTCACCC
ESR1	ENSG00000221817	92	111	+	2.48E-05	GCTGAAGGTCTCCGAGCCCC
ESR1	ENSG00000132330	180	199	+	2.48E-05	GACCCAGCGCAGCCTCGCCT
ESR1	ENSG00000234925	373	392	-	2.57E-05	GGCCTTGGCCACGTTGGCCT
ESR1	ENSG00000227802	205	224	+	2.57E-05	GGCCCAGGTCTCCGAGCACT
ESR1	ENSG00000214535	116	135	+	2.57E-05	GTACAAGACCAGCCTGACCA
ESR1	ENSG00000256566	206	225	+	2.59E-05	GATCCCGGGCACGCTGGCTC
ESR1	ENSG00000258966	158	177	-	2.63E-05	GCTGCAGGGCACCGGGGCCT
ESR1	ENSG00000078687	26	45	-	2.68E-05	ACTGCAGGTTGCCCTGACTT
ESR1	ENSG00000125733	51	70	+	2.68E-05	CCCCCAGCTCACTCTCACCA
ESR1	ENSG00000256278	133	152	-	2.69E-05	ATCTCAGCTCACTGTAACCT
ESR1	ENSG00000231942	122	141	+	2.71E-05	ATCTGAGGTCAGCTTGCTCC
ESR1	ENSG00000240848	218	237	-	2.73E-05	GGCTCAGGTGATCCTCCCAC
ESR1	ENSG00000240776	256	275	-	2.75E-05	CTTCTTGGCCACCATGACTC
ESR1	ENSG00000214593	241	260	-	2.75E-05	CTTCTTGGCCACCATGACTC
ESR1	ENSG00000137817	52	71	-	2.76E-05	GATGGAGAGCACCCTGGCCT
ESR1	ENSG00000198417	339	358	+	2.77E-05	CGCTCAGGGGACCTTGCGCC
ESR1	ENSG00000134571	47	66	+	2.83E-05	AGCCAGGGACAATGTGGCCC
ESR1	ENSG00000181826	248	267	-	2.83E-05	CCCCCAGGGCGCCGCGTCCC
ESR1	ENSG00000187796	40	59	+	2.83E-05	TCCCCAGGACCCCCAGCCCC
ESR1	ENSG00000185885	49	68	+	2.87E-05	CGCCTAGGTCATCCAGCACT
ESR1	ENSG00000147684	77	96	+	2.87E-05	GGGACAAGTCAGAAAGACCC
ESR1	ENSG00000222489	70	89	+	2.89E-05	ACCACAGGCCACCATGCCTG
ESR1	ENSG00000130997	29	48	-	2.90E-05	CGCTGCGGGCATCCTGCCTC
ESR1	ENSG00000232748	268	287	+	2.93E-05	CTGGAGGGTCCCCCAGCCCC
ESR1	ENSG00000109625	134	153	+	2.95E-05	GGGGCGGGGCACTCCGCCCG
ESR1	ENSG00000157077	311	330	+	2.99E-05	CGGACGGGGCGTCCTGCCAC
ESR1	ENSG00000219665	146	165	-	3.01E-05	TGGATAGGGCATCCTACCCC
ESR1	ENSG00000205231	111	130	-	3.04E-05	CATCATGGACATTGTGACCC

ESR1	ENSG00000223878	159	178	-	3.04E-05	GTTCTTGGTCTCACTGACTT
ESR1	ENSG00000171056	83	102	+	3.04E-05	TCCCCAGGTTGCCCCGCCCT
ESR1	ENSG00000254093	120	139	+	3.04E-05	TCCCCAGGTTGCCCCGCCCT
ESR1	ENSG00000159337	50	69	-	3.05E-05	CTGGCAGGGCTCCAGGACCT
ESR1	ENSG00000121152	331	350	-	3.07E-05	CGCCCAGGCCAGCCCGCCAG
ESR1	ENSG00000174564	178	197	-	3.07E-05	ATGCCTGGTGACTTTGCCAT
ESR1	ENSG00000076554	247	266	+	3.07E-05	GATCCTGGTCAGCTTCACAT
ESR1	ENSG00000156150	266	285	-	3.08E-05	GGCTCAGGGCGCACAGGCCT
ESR1	ENSG00000108010	42	61	-	3.10E-05	CCGCTGGGGGGCTCTGACCC
ESR1	ENSG00000163738	126	145	+	3.11E-05	GGGCCAGATCACCGTTGCCT
ESR1	ENSG00000258959	17	36	+	3.13E-05	TGGCCGGGGCAGCGTGGGCC
ESR1	ENSG00000101082	269	288	-	3.13E-05	GGCCCAGGGCCCTTTGAGCT
ESR1	ENSG00000102312	265	284	-	3.13E-05	TCCTCCGGGCAGCCTCCCCC
ESR1	ENSG00000138495	345	364	+	3.14E-05	ATGCCGGGTCTGGTTGACTC
ESR1	ENSG00000167548	202	221	-	3.18E-05	CGGAGTGGCCACCCTCCCCC
ESR1	ENSG00000226055	325	344	-	3.21E-05	CTTCCAGGTGATTCTGACTG
ESR1	ENSG00000060656	279	298	-	3.22E-05	GGCGCGGGGGACGCCGCCCC
ESR1	ENSG00000232912	204	223	+	3.24E-05	CGGAAAGATGGCCCTGCCCT
ESR1	ENSG00000184381	69	88	-	3.25E-05	GCCCAGGGTCAGCCAGCCTG
ESR1	ENSG00000137965	366	385	+	3.30E-05	CTCTCAGGTGACAGTGTCAC
ESR1	ENSG00000114786	126	145	-	3.32E-05	GCCCCAGCGCTCTCTGGCCC
ESR1	ENSG00000248930	43	62	-	3.32E-05	CACTGAGGCCAACCTGAACT
ESR1	ENSG00000124693	326	345	+	3.32E-05	CCGCCCGGGCACTGTGGCTC
ESR1	ENSG00000150893	379	398	-	3.34E-05	TGGACAGGTCAGCCTGAGAG
ESR1	ENSG00000161179	238	257	+	3.34E-05	GACCCAGGCGGCCATGTCCC
ESR1	ENSG00000231980	15	34	+	3.39E-05	GGCCCTGGTCATCCTTCCAC
ESR1	ENSG00000140943	241	260	-	3.40E-05	CGACCGGGCCAGCGAGGCCC
ESR1	ENSG00000106608	264	283	+	3.40E-05	TGCCCGGGTTACGCTGGCCA
ESR1	ENSG00000252304	87	106	+	3.40E-05	AGCGGAAGTCACTATGACTC
ESR1	ENSG00000233246	323	342	+	3.44E-05	GCACCGGGTGAACCTGCGCT
ESR1	ENSG00000243135	85	104	+	3.45E-05	AGAGGAGGGCACTCTGTCTT
ESR1	ENSG00000236842	315	334	+	3.47E-05	CCCCGACGGCGGCCTGACCC
ESR1	ENSG00000114126	322	341	+	3.47E-05	CGCGGGGCGCGCCCTGACCC
ESR1	ENSG00000154309	5	24	+	3.49E-05	AAGCCAAGCCCCTCTGCCCT
ESR1	ENSG00000172345	91	110	+	3.49E-05	CCCCGCGGTCTCCTTGTCCT
ESR1	ENSG00000135476	47	66	+	3.51E-05	CGCGCAGAGCAGCAAGACCC
ESR1	ENSG00000240053	173	192	+	3.56E-05	GGCCCAGCCCACCCTCCCCA
ESR1	ENSG00000170421	140	159	+	3.58E-05	GCACCTGGTCACTCTGGGCC
ESR1	ENSG00000222020	55	74	-	3.65E-05	CTCATAGGGCATCCGGCCCC
ESR1	ENSG00000147642	345	364	+	3.68E-05	CACCCAGCGGTGCCTGCCCT
ESR1	ENSG00000007202	253	272	+	3.74E-05	CCCGCGGGTCCCCGAGCCCC
ESR1	ENSG00000145819	131	150	-	3.76E-05	CAATCAGCGCACCCTCCCCT
ESR1	ENSG00000198742	80	99	+	3.77E-05	GTAGCAGCGCACCCCGCCCC
ESR1	ENSG00000230798	41	60	-	3.79E-05	GGTCCCGGTCCCGCTGCCCA
ESR1	ENSG00000232536	316	335	+	3.79E-05	GTTCGGGGCGTCCCTGCCCT
ESR1	ENSG00000177868	184	203	-	3.85E-05	GACCCAGCGCTGCCTGCCCA
ESR1	ENSG00000154134	346	365	+	3.87E-05	GGGGCTGGGCCCCCAGCCCC
ESR1	ENSG00000226054	46	65	-	3.89E-05	GGCCCACGGCGGCCTCACCT
ESR1	ENSG00000255282	13	32	-	3.91E-05	GAGAATGGGCAGACTGCCTC
ESR1	ENSG00000006740	7	26	+	4.00E-05	GCTGCTGGTGACGCTGCCTT

ESR1	ENSG00000214300	139	158	+	4.04E-05	TTGCCAGGTTGGAATGACCT
ESR1	ENSG00000215450	203	222	-	4.08E-05	TCCCCAGGGCCTCCAGCCCC
ESR1	ENSG00000227848	341	360	-	4.12E-05	GGCGCTGGTCACCTTTACAT
ESR1	ENSG00000141380	77	96	-	4.12E-05	TTGGAAAGTAACCCTGACCC
ESR1	ENSG00000183773	310	329	+	4.14E-05	CGCCCCGGGGACCCTGGTCC
ESR1	ENSG00000226312	273	292	-	4.16E-05	ACTCAAAGTCACACTGTCAT
ESR1	ENSG00000104976	166	185	+	4.18E-05	CGCGCGGTTCTTTCTGACCT
ESR1	ENSG00000205424	188	207	-	4.22E-05	TGGTCATGCCTTCCTGCCCT
ESR1	ENSG00000100605	256	275	-	4.26E-05	GAGGAAGCGGACCCTGGCCC
ESR1	ENSG00000216642	230	249	+	4.26E-05	AAAAAGGGCCACTCTGCCAT
ESR1	ENSG00000219481	148	167	+	4.35E-05	GCCTTGGGTTATCCTGACAC
ESR1	ENSG00000236132	359	378	+	4.37E-05	GTTCGAGACCAGCCTGACCA
ESR1	ENSG00000251314	319	338	-	4.37E-05	TCCCCAAGCCAGCCTGGCCA
ESR1	ENSG00000258802	217	236	+	4.45E-05	TTCCAAGGGCGCCGGGCCCT
ESR1	ENSG00000214184	326	345	+	4.45E-05	GGCCCGGCTCTCCTTGCCTC
ESR1	ENSG00000232830	306	325	+	4.48E-05	CTGTGAGGACAGCCAGGCCT
ESR1	ENSG00000251705	176	195	+	4.52E-05	CGCCCTTGCCAAATTGACCT
ESR1	ENSG00000223501	253	272	-	4.54E-05	CAGCCAGGTCGCGCTGAAAC
ESR1	ENSG00000231500	167	186	+	4.54E-05	CAGCCAGGTCGCGCTGAAAC
ESR1	ENSG00000099901	4	23	+	4.56E-05	CAGCCAGGGCAGCAAGGCAC
ESR1	ENSG00000072274	53	72	-	4.56E-05	CGCGATGGGCGCACTGGCCT
ESR1	ENSG00000170873	25	44	+	4.56E-05	GGCCCAGCGCCGCCTGCCCG
ESR1	ENSG00000253773	63	82	+	4.58E-05	TATCCAGGCCTGCATGACTC
ESR1	ENSG00000215127	38	57	-	4.61E-05	GTCTCGGCTCACTGTAACCT
ESR1	ENSG00000152942	307	326	+	4.61E-05	TGCCCAGAGCACTCTGCGCC
ESR1	ENSG00000184508	106	125	-	4.65E-05	GGCCGAGTTGGGCCTGCCCC
ESR1	ENSG00000228703	132	151	-	4.67E-05	CCTCATGGTCTCCCTGTCCA
ESR1	ENSG00000250644	366	385	-	4.67E-05	GGCTGGGATCACCGAGCCCT
ESR1	ENSG00000249249	61	80	+	4.67E-05	CGGAAAGGCCTGCCCGCCCC
ESR1	ENSG00000129472	265	284	-	4.70E-05	GTTCCGGGTCCGCCCGACTT
ESR1	ENSG00000224078	18	37	+	4.70E-05	TTTCCAGGTCCACCTCCCCC
ESR1	ENSG00000135926	229	248	-	4.72E-05	CGGCTGGGGCTCCGCGCCCC
ESR1	ENSG00000173210	336	355	-	4.79E-05	GAGCCAGAGGCCCCTGCCCC
ESR1	ENSG00000075415	349	368	-	4.81E-05	AGGCCCGGCCACACTCACTC
ESR1	ENSG00000202415	203	222	-	4.83E-05	CAGCCAGGTTGCCCTCACAT
ESR1	ENSG00000256390	6	25	-	4.86E-05	TGTCCTGGTCACCAGGGCCC
ESR1	ENSG00000151465	193	212	-	4.93E-05	CCCTAAACGCACGCTGACCC
ESR1	ENSG00000157985	352	371	+	4.93E-05	CAGCGCGGCCACACTGCCCA
ESR1	ENSG00000235374	82	101	+	4.93E-05	GGCTGAGGAGACTCTGCCCG
ESR1	ENSG00000251186	225	244	+	4.93E-05	TCAGCATGTCTGCTTGACCT
ESR1	ENSG00000196712	343	362	+	5.02E-05	TCCCCGGGTCCCCTTCCCCT
ESR1	ENSG00000067182	107	126	-	5.05E-05	GTCCCAGATCTGGCTGCCTT
ESR1	ENSG00000197647	323	342	+	5.07E-05	GGTTCAGGTGCCTCTGCCAT
ESR1	ENSG00000143878	44	63	+	5.07E-05	AATCAAGCTGGCCCTGCCCC
ESR1	ENSG00000244926	106	125	-	5.10E-05	ACCACGTGTCTTCTTGACCT
ESR1	ENSG00000213204	291	310	-	5.10E-05	GGTCAAGGGCGCGGAGCCCC
ESR1	ENSG00000160957	127	146	-	5.10E-05	GCCCCTGGGCAGCCAGTCCG
ESR1	ENSG00000164051	268	287	+	5.12E-05	GAGCACGTTCGGCCTGCCCC
ESR1	ENSG00000129158	113	132	-	5.20E-05	CCTCCCAGTCAGCCCGCCCC
ESR1	ENSG00000258509	329	348	+	5.22E-05	TGAACAGATCATCGTGACCG

ESR1	ENSG00000154274	247	266	+	5.22E-05	AGCCATGGGCGCCGGGACCC
ESR1	ENSG00000163870	294	313	-	5.25E-05	GACCGAGGTCACGCAGCCAG
ESR1	ENSG00000168505	103	122	+	5.30E-05	GGCCAGAGGCGCCCAGCCCC
ESR1	ENSG00000249967	55	74	+	5.32E-05	GGGGATGGACAGCCTGTCAC
ESR1	ENSG00000102024	174	193	-	5.35E-05	AAGCCAGCGCTCCCTCCCCT
ESR1	ENSG00000110092	380	399	+	5.37E-05	CAGCCAGGACCCACAGCCCT
ESR1	ENSG00000243725	175	194	-	5.40E-05	AGCGCAGGTCCCCGCGCCTT
ESR1	ENSG00000235546	287	306	-	5.40E-05	GCCCCAGCTCATGCTGTCTC
ESR1	ENSG00000234062	189	208	+	5.48E-05	GCGACAGCTCACGATGCCCG
ESR1	ENSG00000137101	272	291	-	5.50E-05	CAGTCATGTCACCCAGTCCA
ESR1	ENSG00000023171	273	292	+	5.53E-05	TCCCAGGGTCTCCTTGGCTT
ESR1	ENSG00000103832	375	394	-	5.55E-05	GGGGCAGGGCTGACTGACAA
ESR1	ENSG00000232485	81	100	+	5.61E-05	TCACCATGTCGCCGCGACCT
ESR1	ENSG00000230753	25	44	+	5.61E-05	GCGTCAGGGCAACGCGCCAC
ESR1	ENSG00000228172	211	230	-	5.66E-05	CCTCCCGGGGACACAGACCC
ESR1	ENSG00000135916	181	200	-	5.69E-05	GTCCAAGGCCAGCATCCCCG
ESR1	ENSG00000203301	294	313	+	5.71E-05	CCCCGTGCTCCCCCTGCCCT
ESR1	ENSG00000246889	84	103	-	5.74E-05	GACCCGGGCCGGACCGACCC
ESR1	ENSG00000065361	338	357	-	5.80E-05	AGCCTCGGACCGCCTGCCCC
ESR1	ENSG00000213641	379	398	-	5.82E-05	AGAGAATGGCTCTCTGCCCT
ESR1	ENSG00000129194	262	281	-	5.82E-05	GTGGCAGGCGGGCCAGACCT
ESR1	ENSG00000168887	151	170	+	5.82E-05	GGCCGGGGCCTCCCAGACCG
ESR1	ENSG00000254827	114	133	-	5.85E-05	CCCTCTGGAGTCCCTGCCCC
ESR1	ENSG00000184669	112	131	-	5.91E-05	CCCGCCGGGCGCCCCGCCCT
ESR1	ENSG00000168291	69	88	-	5.91E-05	CGTGTGGGTGGCCGTGCCCC
ESR1	ENSG00000147687	181	200	+	5.91E-05	CTACAAGGTCTCCCGGCCAT
ESR1	ENSG00000147874	68	87	-	5.91E-05	CGCTATGCTCACTGTGACTC
ESR1	ENSG00000218739	351	370	+	5.99E-05	TAGTCAGGTGTCACTGCCTT
ESR1	ENSG00000136143	375	394	+	6.02E-05	GCAGCTGGTCACCACGACTC
ESR1	ENSG00000228501	304	323	+	6.05E-05	TCCACAGGGCTCTCCGCCCC
ESR1	ENSG00000157851	112	131	-	6.05E-05	GGCTGCGGCCGCGCTGCCCT
ESR1	ENSG00000145907	174	193	+	6.05E-05	CGCGCGGACCACCGTGCCTC
ESR1	ENSG00000176029	121	140	+	6.11E-05	CTCCCAAGGCCTCCTGTCCC
ESR1	ENSG00000083845	332	351	+	6.11E-05	GAGACGGGTCGCGCTGCTCC
ESR1	ENSG00000225611	164	183	-	6.14E-05	TGCCTGGGGCAGCCTGCTTT
ESR1	ENSG00000241550	134	153	-	6.16E-05	CGCCCAGGTCATCTTGTATT
ESR1	ENSG00000157106	86	105	-	6.19E-05	ATAGCAGGCCGCCCCGCCCC
ESR1	ENSG00000139154	202	221	+	6.25E-05	AAGCAAGGGCAACCAGCTCC
ESR1	ENSG00000126226	181	200	+	6.25E-05	GGCCGGGGGCGCCAGGACCC
ESR1	ENSG00000168883	318	337	+	6.28E-05	ATCTCGGGGCAGCCTGCATT
ESR1	ENSG00000169184	238	257	+	6.28E-05	ACCCCTCGTCTCGCTGCCCT
ESR1	ENSG00000250251	177	196	+	6.34E-05	GGCCATGCGCGCGCTGCCCT
ESR1	ENSG00000125966	250	269	-	6.34E-05	GCGCCCGGCCCGCCTGCCTT
ESR1	ENSG00000113231	266	285	+	6.43E-05	GCGGGCGGGCGCCCTGGCCC
ESR1	ENSG00000118849	222	241	-	6.46E-05	GGGCCGGGTGCTTCTGGCCC
ESR1	ENSG00000113282	304	323	-	6.55E-05	GGCCGGGGTCACCGCCGCCC
ESR1	ENSG00000130589	236	255	-	6.62E-05	CTCCTGGAGCTGCCTGCCCT
ESR1	ENSG00000008710	236	255	+	6.71E-05	CTCCCGGAGCGGCCTGGCCC
ESR1	ENSG00000176715	57	76	+	6.71E-05	CTCCCCGGTCAGCTTGCCGC
ESR1	ENSG00000255185	75	94	+	6.74E-05	TCCACCGGGCATCCTCCCCC

ESR1	ENSG00000071794	327	346	-	6.74E-05	CTTCCAGGCCCCGCAGCCCT
ESR1	ENSG00000113716	378	397	-	6.77E-05	CGCCCCGGCCGCTCAGCCCC
ESR1	ENSG00000255158	115	134	+	6.80E-05	GGCTGCAGTCACCCTGGCCA
ESR1	ENSG00000173281	211	230	-	6.80E-05	CCCCGCGGCCGCGCTGCCCC
ESR1	ENSG00000143499	365	384	-	6.90E-05	GCTCCAGGCCGCCGAGGCCC
ESR1	ENSG00000131773	195	214	-	6.90E-05	CGCCCCGCGCACTCTGAGCC
ESR1	ENSG00000236658	1	20	-	6.90E-05	GACAGAGGTCACCCTGTAAC
ESR1	ENSG00000183020	220	239	+	6.93E-05	GGAGCTGTGCAGCCTGGCCC
ESR1	ENSG00000138100	102	121	-	6.93E-05	GGAGTGAGTGACCCTGACTC
ESR1	ENSG00000163083	269	288	+	7.03E-05	CGCTGGGGGCCGCCTGCCTT
ESR1	ENSG00000127928	114	133	-	7.03E-05	AAATCGGGTCACTCCCACCC
ESR1	ENSG00000139637	88	107	+	7.06E-05	ATCGCAGGGCCCTTTGACCA
ESR1	ENSG00000100320	137	156	+	7.06E-05	GGCCCAGGGGGAGGTGGCCT
ESR1	ENSG00000100234	148	167	-	7.13E-05	GCCCCCGGGGACCCCGCCTC
ESR1	ENSG00000130560	266	285	-	7.13E-05	CGGCCGGGCCGCCGTCACTC
ESR1	ENSG00000006607	207	226	-	7.16E-05	CGCGCAGCGCGCCCCGCCCT
ESR1	ENSG00000255432	224	243	+	7.20E-05	GGGAAAGATCAACCGGCCCC
ESR1	ENSG00000189343	241	260	+	7.20E-05	GGCCCTGGTGGCCCTGAGAT
ESR1	ENSG00000176148	164	183	+	7.23E-05	GCCACTGGCCACGGAGCCCC
ESR1	ENSG00000148296	209	228	-	7.23E-05	GGGCCTGGCCTCAGTGCCTC
ESR1	ENSG00000233202	231	250	-	7.23E-05	CCTCGAGGGCAGCCTCAGCT
ESR1	ENSG00000089101	320	339	-	7.26E-05	CGCCCTGGACGCCCTGCACC
ESR1	ENSG00000233603	86	105	+	7.26E-05	TGGCTTTCCCACCCTGACCT
ESR1	ENSG00000227589	241	260	+	7.30E-05	AGCTCTCATCACTCTGACCT
ESR1	ENSG00000258930	368	387	+	7.30E-05	ATGCATGGGCTCCCTGCACT
ESR1	ENSG00000109854	156	175	-	7.37E-05	AGGCGCGGGGAAGGTGACCC
ESR1	ENSG00000124201	175	194	+	7.37E-05	ACGCCGGGCCACCCGGGCTT
ESR1	ENSG00000008988	301	320	-	7.43E-05	GCGCGCGGGCTTCCTGACCG
ESR1	ENSG00000176386	177	196	-	7.47E-05	CGCTCCGGGGGCGGTGACCC
ESR1	ENSG00000224386	201	220	+	7.54E-05	GCCTGGGGCCGGCCTGGCCC
ESR1	ENSG00000164048	56	75	-	7.61E-05	GCTGAGGCGCACTTTGACCT
ESR1	ENSG00000227328	173	192	+	7.61E-05	GGCCCAAGGGGCACTGTCCT
ESR1	ENSG00000163126	246	265	-	7.65E-05	GCCGCGCGGCAGCCTCACCC
ESR1	ENSG00000237669	20	39	+	7.65E-05	AGCCCCGCCCACCGAGCCCT
ESR1	ENSG00000258660	382	401	+	7.68E-05	CACGTTGGCCAGGCTGGCCT
ESR1	ENSG00000189269	180	199	+	7.68E-05	CAGCCAGGGCCAGCAGCCCT
ESR1	ENSG00000093167	86	105	+	7.72E-05	GTTATCAGCCACCCTGCCCC
ESR1	ENSG00000243444	326	345	-	7.72E-05	CGCCGCGGTCACCATGGCAA
ESR1	ENSG00000147036	16	35	+	7.72E-05	GGGACTGGAGACCATCACCT
ESR1	ENSG00000134824	19	38	-	7.79E-05	CTCTCATGGCAACCAGTCCC
ESR1	ENSG00000134825	186	205	+	7.79E-05	CTCTCATGGCAACCAGTCCC
ESR1	ENSG00000168496	362	381	-	7.79E-05	CTCTCATGGCAACCAGTCCC
ESR1	ENSG00000215208	337	356	+	7.79E-05	TTCCCGGATCTCCATGTCCT
ESR1	ENSG00000182909	90	109	-	7.79E-05	AGCTCTTGGGAGCCTGGCCC
ESR1	ENSG00000249915	142	161	+	7.79E-05	TGCGCGGGACCCCGTGACCA
ESR1	ENSG00000151117	174	193	+	7.82E-05	AACCCATGTTTGCCTGGCCC
ESR1	ENSG00000111252	92	111	+	7.82E-05	GCTCCTGGTGGCCCCGCCCC
ESR1	ENSG00000171345	24	43	-	7.82E-05	AGACCAGAGGCCCCTGCCCT
ESR1	ENSG00000257298	308	327	-	7.86E-05	CTGGCTGGGCACAGTGGCTC
ESR1	ENSG00000144504	87	106	-	7.86E-05	GACACGGGACAGCATGTCAC

ESR1	ENSG00000165819	336	355	-	7.90E-05	CATCCTAGTCTCCCAGCCCT
ESR1	ENSG00000231357	159	178	-	7.90E-05	AGACAATGGGACTTTGCCCC
ESR1	ENSG00000257069	304	323	-	7.93E-05	CCCTGGGGCGTCCCTGCCCC
ESR1	ENSG00000185666	375	394	-	7.93E-05	GCTCCAGGGGACGCAGCCCG
ESR1	ENSG00000152348	293	312	-	7.97E-05	GAGCCGAGCCAGCGCGCCCC
ESR1	ENSG00000111907	336	355	+	7.97E-05	TGATCAGCCCACCTTGGCCT
ESR1	ENSG00000232479	205	224	-	8.08E-05	CTTCTGGGTCACCCTGATAG
ESR1	ENSG00000170027	63	82	-	8.08E-05	TCTTCCGGGCACCCCGTCCT
ESR1	ENSG00000110171	345	364	-	8.12E-05	CTGTCTGGGCCGCCTGCCTC
ESR1	ENSG00000148344	20	39	-	8.12E-05	TCTCCGGGTGTCCCGGACCC
ESR1	ENSG00000175147	61	80	-	8.16E-05	CAAGAAGGGGACCCCGGCCT
ESR1	ENSG00000100568	183	202	+	8.27E-05	CCCGCAGGTCCCCTAGGCCC
ESR1	ENSG00000145014	238	257	+	8.27E-05	AGGAAGGGACGCCGTGCCTT
ESR1	ENSG00000109689	348	367	-	8.27E-05	CCCAGAGGCAAGCCTGCCCT
ESR1	ENSG00000125148	315	334	+	8.31E-05	CACCCGGTACACTGTGTCCT
ESR1	ENSG00000061938	19	38	+	8.42E-05	TCCCTCTGGCAGCCTGGCCC
ESR1	ENSG00000251467	124	143	-	8.46E-05	GGCACAGCTCCGCCAGCCCC
ESR1	ENSG00000212978	28	47	+	8.50E-05	GGACGACGTCAACATGTCCT
ESR1	ENSG00000226800	172	191	+	8.54E-05	CCCGGGGGTCGCCCAGACTC
ESR1	ENSG00000250174	246	265	+	8.58E-05	ATTGAAGGTCAGCTTGTTCT
ESR1	ENSG00000064763	180	199	+	8.62E-05	GCGCGCGGCCGCCCTGCCCA
ESR1	ENSG00000152503	125	144	+	8.62E-05	CGGCGCTGGCAGCCAGCCCC
ESR1	ENSG00000084676	303	322	+	8.66E-05	CCCCGACGACGCCGTGACCT
ESR1	ENSG00000066651	135	154	-	8.66E-05	TGGGAGGGGCTTCCTCACCT
ESR1	ENSG00000176444	316	335	-	8.70E-05	GGGGCGGGGGGTCCAGACCT
ESR1	ENSG00000151491	314	333	+	8.70E-05	CGGGATGGGGTCCCTGTCCC
ESR1	ENSG00000129515	145	164	-	8.74E-05	GCCTAAGGACGGCCCGCCCC
ESR1	ENSG00000249319	227	246	+	8.74E-05	AGTCCTGGGGAGCCAGTCCC
ESR1	ENSG00000143776	161	180	-	8.90E-05	CGGCCTGGCCCCCCGGCCCC
ESR1	ENSG00000090905	25	44	+	8.90E-05	GGCTGGGTGCAGCGTGACAC
ESR1	ENSG00000180385	307	326	+	8.90E-05	AGGTCAGGGGATCGAGACCA
ESR1	ENSG00000078319	290	309	-	9.03E-05	TGACAATGTCACCTTCACTC
ESR1	ENSG00000109079	1	20	-	9.11E-05	GTACCGGCTGTCGCTGACCC
ESR1	ENSG00000186868	260	279	+	9.11E-05	CGCGGAGGCCGCGCTGCCCG
ESR1	ENSG00000161642	61	80	-	9.15E-05	GCGAGGGGGCGTCCTGGCCC
ESR1	ENSG00000139988	173	192	+	9.15E-05	TGATCAGCTCATCGTAACCT
ESR1	ENSG00000175110	345	364	-	9.15E-05	CCCAGAGGTCCTCCTGAGCT
ESR1	ENSG00000257077	156	175	+	9.15E-05	GGACATGGACTGCCTCACCT
ESR1	ENSG00000080815	255	274	-	9.19E-05	ACCCCGGAGCTGCCTGTCCC
ESR1	ENSG00000258011	215	234	+	9.23E-05	CTCGAAGTCCAGCCAGCCCT
ESR1	ENSG00000234271	179	198	-	9.23E-05	TTCTCTTCTCACCCTGTCCT
ESR1	ENSG00000253172	201	220	+	9.28E-05	GGGGCGGGGCTAGCTGCCTC
ESR1	ENSG00000251447	302	321	-	9.32E-05	GAGCCACCGCACCCAGCCCT
ESR1	ENSG00000105519	196	215	+	9.36E-05	TGGCTCTGCCACCCTGCCAC
ESR1	ENSG00000244078	183	202	+	9.36E-05	CTTATCTGGCACCCTGGCCT
ESR1	ENSG00000151466	35	54	+	9.36E-05	CTACCTGGAGACACTGTCCC
ESR1	ENSG00000224680	39	58	-	9.40E-05	AGGCAGGGCCTCGCTGGCTT
ESR1	ENSG00000174791	5	24	-	9.40E-05	AGGCTCTGCCAGCCTGCCTT
ESR1	ENSG00000246982	382	401	-	9.40E-05	GGGCGGGGGCATCGGGGCCT
ESR1	ENSG00000115661	262	281	+	9.45E-05	GAGCCAGGTCAGTCCGGCAG

ESR1	ENSG00000163521	144	163	-	9.45E-05	GAGCCAGGTCAGTCCGGCAG
ESR1	ENSG00000023839	78	97	+	9.53E-05	CTGGTGAGTCTCCCTGTCCC
ESR1	ENSG00000254460	105	124	+	9.53E-05	TGCCTGGGGCTCTCTGAGCC
ESR1	ENSG00000258466	75	94	+	9.53E-05	AGGCCTGCTCACCACGACTC
ESR1	ENSG00000255329	317	336	-	9.58E-05	CGTCCAGGACTGATTGTCCT
ESR1	ENSG00000214167	96	115	-	9.58E-05	GATCAAGGCCAGGCAGCCTC
ESR1	ENSG00000145868	100	119	-	9.58E-05	AGCCATGTTCAGCGTGGCAT
ESR1	ENSG00000230870	353	372	-	9.62E-05	GTCCATGGTGATAATGACAC
ESR1	ENSG00000256813	41	60	-	9.67E-05	GCCTTCAGTGACCCTGGCCT
ESR1	ENSG00000100811	12	31	+	9.67E-05	CGCCGAGCTCGCGCCGACCC
ESR1	ENSG00000075292	4	23	+	9.67E-05	ACCTTAGGCCTCACAGACCT
ESR1	ENSG00000143158	159	178	+	9.71E-05	CAGACCCGGCAGCGTGCCCC
ESR1	ENSG00000215845	181	200	-	9.71E-05	AAGCAAGGGCACCGCCTCCC
ESR1	ENSG00000110536	201	220	+	9.71E-05	CTCCGAGGCCGCCGGGCCCT
ESR1	ENSG00000214941	214	233	+	9.71E-05	ACTCCGTCTCGCCCTGCCCC
ESR1	ENSG00000149089	279	298	+	9.75E-05	CGCCCCGTTCGCCCCGCCCC
ESR1	ENSG00000172113	239	258	+	9.75E-05	CGCCGAGGGCGCCCAGGCCG
ESR1	ENSG00000145425	35	54	-	9.75E-05	GACCAAGGCGTCGGTGGCCT
ESR1	ENSG00000109685	369	388	-	9.80E-05	CAGCCCGGCCTCCCGGCCCC
ESR1	ENSG00000198042	200	219	+	9.80E-05	AGGAGCGGGGACCCAGCCCC
ESR1	ENSG00000107201	346	365	+	9.80E-05	AGCAGAGGCCGGCATGACCA
ESR1	ENSG00000157654	54	73	+	9.80E-05	GCGCCGGGCTAGCGCGCCCT
ESR1	ENSG00000116783	139	158	-	9.84E-05	CGCCCGGTTGTTTCTGACCC
ESR1	ENSG00000130813	26	45	+	9.84E-05	GGCCCAGGTCCTCATGAGCG
ESR1	ENSG00000197128	370	389	-	9.84E-05	CGGCTAGGTCACTCAGGCAG
ESR1	ENSG00000175029	60	79	+	9.89E-05	GGCCCCTGCCACCGAGGCCC
ESR1	ENSG00000166548	322	341	-	9.89E-05	GGCGCTGGCCTGCGTGCCCA
ESR1	ENSG00000254788	18	37	+	9.89E-05	GGCGCTGGCCTGCGTGCCCA
ESR1	ENSG00000236869	271	290	-	9.89E-05	GCTACGGGGCGCCCGGCCCC
ESR1	ENSG00000257809	26	45	+	9.98E-05	TGCTCAGCTCTCCGGGACCT
ESR1	ENSG00000135414	208	227	+	0.0001	CCCCCAGTCCTCCCTCCCCT
ESR1	ENSG00000241404	156	175	+	0.0001	ATGGGAGGACTCTCTGGCCC
ESR1	ENSG00000122432	267	286	-	0.0001	GAGTCGGGTCGCGCTAGCCT
ESR1	ENSG00000174516	184	203	-	0.0001	TTCGCAGGAGACCACGCCCT
ESR1	ENSG00000171853	149	168	+	0.0001	CACCTAGGGCTCCAGGCCCC
ESR1	ENSG00000177725	253	272	-	0.0001	TTCACAGGCCACACTCCCCA
ESR1	ENSG00000168807	367	386	+	0.0001	GAGCGGGGAGAGCCTGAGCC
ESR1	ENSG00000183426	53	72	+	0.0001	CAGCCGGGCCAACCTCAGCC
ESR1	ENSG00000064489	326	345	-	0.0001	GGCCTTTGTCAGGCCGCCCC
ESR1	ENSG00000166997	157	176	-	0.0001	GCTACGGGTTTCCCTGCCTC
ESR1	ENSG00000163291	135	154	+	0.0001	GCGCCCCAGCACCCTGCCCC
ESR1	ENSG00000112079	93	112	+	0.0001	ACCCAGGTCCAGCCAGCCCT
ESR1	ENSG00000234336	271	290	+	0.0001	ATTCCGGGGCTCCCCGCCCG
ESR1	ENSG00000063177	347	366	-	0.00011	GTCGGGGGCCTCTCTGGCCC
ESR1	ENSG00000167608	29	48	+	0.00011	GCACAAAGGCATCCTGTCCG
ESR1	ENSG00000188818	123	142	+	0.00011	CCCTCTGCTCAGTGTGGCCT
ESR1	ENSG00000104325	126	145	-	0.00011	ACGCCCAGCGGCCCTGACCT
ESR1	ENSG00000224665	16	35	-	0.00011	CGGCCAGGCCTCACCCACCC
ESR1	ENSG00000228021	307	326	-	0.00011	CCCCCAAATCATCTTGTCCT
ESR1	ENSG00000174775	162	181	-	0.00011	GTGGCGCGTCACCTTCCCCT

ESR1	ENSG00000175197	102	121	+	0.00011	GGCCAATGCCGGCGTGCCAC
ESR1	ENSG00000141753	69	88	-	0.00011	GGGGGAGGGGGCGCTGTCCT
ESR1	ENSG00000205794	174	193	+	0.00011	CCGTCCGGGCAGCCGGGCCC
ESR1	ENSG00000143416	324	343	+	0.00011	TTGCCTGCTCTGTCTGCCCC
ESR1	ENSG00000175344	5	24	-	0.00011	CGCTCCGGGCACCTCCACCC
ESR1	ENSG00000179409	293	312	-	0.00011	GGGGAGAGGGACTCTGTCCT
ESR1	ENSG00000166526	95	114	+	0.00011	TCTCCAGGACACGGTCACTT
ESR1	ENSG00000247670	116	135	-	0.00011	CGCGCCGGCGACCTCGACCC
ESR1	ENSG00000111335	172	191	+	0.00011	AGTTTTGGTTTCCCTGCCCC
ESR1	ENSG00000134905	54	73	-	0.00011	CGGCCAGCGGAGCGCGCCCC
ESR1	ENSG00000114670	270	289	-	0.00011	AACTAGGGGCAACCACACCC
ESR1	ENSG00000234353	168	187	+	0.00011	GGAGCAAGTCAACTTGGCTT
ESR1	ENSG00000173402	229	248	-	0.00011	GTTTGAGACCAGCCTGACCA
ESR1	ENSG00000122565	118	137	+	0.00011	CAGCCTGGAGATCCAGCCCC
ESR1	ENSG00000084112	296	315	-	0.00011	CTGCAGGGTCACCAGGGCCA
ESR1	ENSG00000185633	7	26	+	0.00011	GCCCCAGGTGTGTCCGACTC
ESR1	ENSG00000187109	208	227	-	0.00011	AGGCCTGGCCCGCGTGCCCG
ESR1	ENSG00000102572	136	155	+	0.00011	GACCCGCTTCATCCTGACTT
ESR1	ENSG00000189050	169	188	-	0.00011	GCGCGCGCGCGCCCTGCCCC
ESR1	ENSG00000221025	135	154	+	0.00011	CCCAGAGTCCTCCCTGCCCC
ESR1	ENSG00000173585	185	204	-	0.00011	AAGCCAGGCCACCCCTGCCT
ESR1	ENSG00000010030	217	236	-	0.00011	GTCTCAGCTCCCCCTGTCTC
ESR1	ENSG00000221267	305	324	+	0.00011	CTATCAGAGCAGCCTGTCAT
ESR1	ENSG00000164542	364	383	+	0.00011	GTCTCAGCTCAGTGTGTCTC
ESR1	ENSG00000137055	34	53	-	0.00011	CTGTTAGGTCATCCTCACTG
ESR1	ENSG00000085831	127	146	-	0.00011	GACCTGCGCCTCCCTGCCCC
ESR1	ENSG00000084234	268	287	-	0.00011	CGCTTAGCACACCGCGACCC
ESR1	ENSG00000184182	226	245	-	0.00011	GCGACGGGCCTCTCGGACCT
ESR1	ENSG00000114473	214	233	-	0.00011	CTAGCGGGTGACGCTGTCCA
ESR1	ENSG00000156931	360	379	+	0.00011	GCGACAGGTCTCTGAGCCTC
ESR1	ENSG00000163743	36	55	-	0.00011	GACACACTCCACCATGACCT
ESR1	ENSG00000225721	6	25	-	0.00011	GCACCGAGTCACAGTGGCTC
ESR1	ENSG00000120805	203	222	+	0.00011	TGCTCAGGCCACCGTTCCCG
ESR1	ENSG00000144401	297	316	+	0.00011	GACTAGAGTGACCATGCCTT
ESR1	ENSG00000233436	8	27	+	0.00012	TACCAGGGTCAGTCAGGCTC
ESR1	ENSG00000151164	238	257	+	0.00012	GAAACGGAGGACCGTGCCCC
ESR1	ENSG00000103037	255	274	-	0.00012	CGCCTGGGTCGCCATGGTCT
ESR1	ENSG00000242515	277	296	+	0.00012	GCGCAGGGTGGACCAGCCCC
ESR1	ENSG00000130714	174	193	+	0.00012	CACGCGCGTCACCCTCTCCC
ESR1	ENSG00000091039	225	244	-	0.00012	CTTTCTGGGCACCCAGAACC
ESR1	ENSG00000182199	242	261	-	0.00012	ACTCCAGGAGATCTAGACCC
ESR1	ENSG00000159199	270	289	+	0.00012	CTGGGAGGTGAGTCTGTCAC
ESR1	ENSG00000112576	80	99	+	0.00012	GGGGCGGGGCGGCGTGCGCC
ESR1	ENSG00000251154	109	128	-	0.00012	CCGCCCAGAGACTGTGACCT
ESR1	ENSG00000231563	145	164	+	0.00012	GGCCAAGGTCAGAATGATTG
ESR1	ENSG00000083454	300	319	-	0.00012	CTCCCCTGACACAGTGACAC
ESR1	ENSG00000131759	83	102	+	0.00012	CGCTCTGCGCCCGCTGACCC
ESR1	ENSG00000167081	369	388	+	0.00012	GGTGCAGGGGGGCATGGCCC
ESR1	ENSG00000171097	141	160	-	0.00012	CCCCCATGTCCCCTTGTCAT
ESR1	ENSG00000171163	123	142	+	0.00012	GCCGCGGGGCTCCGCGACAC

ESR1	ENSG00000095002	308	327	+	0.00012	GGGTGTGGTCGCCGTGGCCG
ESR1	ENSG00000147813	158	177	-	0.00012	AGGACAGACCAGCCAGACTC
ESR1	ENSG00000161970	305	324	-	0.00012	GTCGGAAGCCACCATGCCCA
ESR1	ENSG00000127616	94	113	+	0.00012	CCTCCGGGCCACGCCCACCC
ESR1	ENSG00000199719	203	222	-	0.00012	CATCCAGATCGCCCTCACAT
ESR1	ENSG00000161813	134	153	+	0.00012	CGCCCAGGCTACAGTGCACT
ESR1	ENSG00000257613	281	300	-	0.00012	ATGAGTGGGCATAATGCCCT
ESR1	ENSG00000234750	237	256	+	0.00012	GGCCCTGGGGACCCTGGGAT
ESR1	ENSG00000202441	161	180	-	0.00012	CAGCAGGGTGTCTCTGAACT
ESR1	ENSG00000149485	101	120	-	0.00012	TGCCAAGAACACCCTTCCCT
ESR1	ENSG00000124279	300	319	-	0.00012	CGGCCAGGTCTTTGACACCC
ESR1	ENSG00000243350	54	73	-	0.00012	GCCCCCGCTCGCCCCGCCCC
ESR1	ENSG00000118260	217	236	+	0.00012	CGCCGGGCTCAGCCCGCCTT
ESR1	ENSG00000223725	224	243	-	0.00012	CGCCGGGCTCAGCCCGCCTT
ESR1	ENSG00000213760	281	300	-	0.00012	CGCCACGATGCCCCTGCCCT
ESR1	ENSG00000105778	301	320	-	0.00012	GGCCACGGCCGCCCTTCCCT
ESR1	ENSG00000115977	318	337	-	0.00012	TTCCTTAGGCAACCTGGCCC
ESR1	ENSG00000100316	42	61	+	0.00012	GTTCAAGACCAGCCTGGCCA
ESR1	ENSG00000163762	378	397	-	0.00012	GTTCAAGACCAGCCTGGCCA
ESR1	ENSG00000230340	128	147	+	0.00012	GTTCAAGACCAGCCTGGCCA
ESR1	ENSG00000224892	62	81	-	0.00012	GGCTCAGGTCCCCTTCAGCT
ESR1	ENSG00000236383	378	397	-	0.00012	GTTGGAGACCAGCCTGACCA
ESR1	ENSG00000248341	296	315	+	0.00012	CTTGAGGGGCCAGCTGACCC
ESR1	ENSG00000064787	163	182	+	0.00012	TCCCCAGGTCAACCCGGCAG
ESR1	ENSG00000240137	278	297	+	0.00012	GTCACCGATGTCCGTGACCT
ESR1	ENSG00000213397	253	272	+	0.00012	GGTACCAGTCACCCAGCCAC
ESR1	ENSG00000072518	137	156	-	0.00013	GTCCACGGCCATCCAGCCAC
ESR1	ENSG00000259163	71	90	+	0.00013	CCCCAAGCAGTCCCTGCCCC
ESR1	ENSG00000161980	11	30	+	0.00013	CAGCGAGGCCGCCCAGCCAC
ESR1	ENSG00000217624	226	245	-	0.00013	CTGCTCGGCCAGTTTGGCCT
ESR1	ENSG00000023191	26	45	+	0.00013	CGCCCCCGGCACCAAGCCCC
ESR1	ENSG00000207145	65	84	+	0.00013	GTGAGATGTGATCCTGCCAC
ESR1	ENSG00000221170	232	251	+	0.00013	GTGAGATGTGATCCTGCCAC
ESR1	ENSG00000258168	243	262	+	0.00013	TAGCAGAGGGACTCTGGCCT
ESR1	ENSG00000178297	323	342	+	0.00013	CAGCCTTGTCGTCCTCACCC
ESR1	ENSG00000079819	71	90	+	0.00013	CCCCCGGGTCTCCGCGGCCG
ESR1	ENSG00000204427	298	317	-	0.00013	GGCCCCGCCCTCCCTGCCTC
ESR1	ENSG00000233016	227	246	+	0.00013	GCGGGTGGGCCGCCTGACTT
ESR1	ENSG00000228838	179	198	+	0.00013	GGAGAAGGGGAGCCTAGCCC
ESR1	ENSG00000255990	300	319	-	0.00013	GAGCCAGGGCTCAGTGTGCT
ESR1	ENSG00000120159	126	145	+	0.00013	CCCCCCTGCCACCCCGGCCC
ESR1	ENSG00000249115	366	385	+	0.00013	GAGTGAGGACACCCCACCCT
ESR1	ENSG00000125848	264	283	-	0.00013	CTGCAGGCTGAGCTTGTCCT
ESR1	ENSG00000151093	365	384	-	0.00013	GGCCAGGGGCCTCGGGACCC
ESR1	ENSG00000152464	136	155	-	0.00013	GGACCGGGTCCCCCCACCCC
ESR1	ENSG00000228925	233	252	-	0.00013	TCTAGAGCTCACCGTGCCAC
ESR1	ENSG00000230194	379	398	-	0.00013	ACCACAGGCCCTGCTGACAT
ESR1	ENSG00000126217	8	27	-	0.00013	CGATGGGAACAGCCTGCCCC
ESR1	ENSG00000184635	309	328	-	0.00013	CCTGCAGGTCACAGGGCCAC
ESR1	ENSG00000144554	294	313	-	0.00013	GCCGCAGGGGAGCGGGGCCT

ESR1	ENSG00000152977	81	100	+	0.00013 AGGCCAGGTGAGGCCGCGCC
ESR1	ENSG00000251003	186	205	-	0.00013 CATCCGGTCCAGCATGACTC
ESR1	ENSG00000139626	349	368	-	0.00013 GGACCAGGTGGGCCAGAGCT
ESR1	ENSG00000105825	333	352	-	0.00013 ATGCACGGGGACTGTCACCC
ESR1	ENSG00000234695	128	147	+	0.00013 ATGCACGGGGACTGTCACCC
ESR1	ENSG00000253536	80	99	-	0.00014 GAGTTGGGGTGCACTGACCT
ESR1	ENSG00000244697	49	68	+	0.00014 GTTTGAGATCAGCCTGGCCA
ESR1	ENSG00000116213	175	194	+	0.00014 CCCCTGTGTCGCCTTGTCCC
ESR1	ENSG00000161618	36	55	-	0.00014 GTGGCCGGGCACGATGGCTC
ESR1	ENSG00000175309	92	111	-	0.00014 GTCCCGGACGACCCCGCCCC
ESR1	ENSG00000170191	354	373	+	0.00014 CTCTCTGGGCAGTCCGCCTT
ESR1	ENSG00000145040	349	368	+	0.00014 GACCCAGGGGACTCTGGGAT
ESR1	ENSG00000233509	261	280	-	0.00014 CTACCAGGTCATTCAGACGT
ESR1	ENSG00000189308	379	398	+	0.00014 GGGAAGGGGGAACCGGCCCC
ESR1	ENSG00000168394	382	401	+	0.00014 GCGCAGGATCAGCCTGTTCC
ESR1	ENSG00000228477	103	122	-	0.00014 TCCCAGGGCCACCAGGGCCT
ESR1	ENSG00000114383	335	354	+	0.00014 TGCGCCGGCGGCCCTGACAT
ESR1	ENSG00000128595	303	322	+	0.00014 CGGCCACGGCATCCTGTGCT
ESR1	ENSG00000221978	335	354	-	0.00014 CCCGGAGTACAGCCTGTCCC
ESR1	ENSG00000204311	295	314	-	0.00014 TCTTAAAGTGACCCAGCCCC
ESR1	ENSG00000212464	378	397	-	0.00014 AGCCTGTGTCAGCCTGTCTG
ESR1	ENSG00000198925	310	329	-	0.00014 GGCTCGGCTCGGCGCGACCC
ESR1	ENSG00000240950	15	34	+	0.00014 AGCTAGGGGGATACTGCCAC
ESR1	ENSG00000138794	356	375	-	0.00014 GCAGCCAGACACCTTGCCCT
ESR1	ENSG00000184205	108	127	+	0.00014 TGGCCAGGCCGAGCGGACCC
ESR1	ENSG00000021762	240	259	-	0.00014 GACCCTGCTCCGCGTGGCCT
ESR1	ENSG00000256690	150	169	+	0.00014 CTAAGGCGCCACCGTGACCC
ESR1	ENSG00000115841	342	361	-	0.00014 ATGGCAGCTGATACTGACTT
ESR1	ENSG00000258227	311	330	-	0.00014 AGGCAGGGGCCCCGTCTCCT
ESR1	ENSG00000243341	341	360	+	0.00014 CCTCAAGGGCAGTCAGACAA
ESR1	ENSG00000169991	269	288	+	0.00015 CAGCCCGGGCGGTGAGACCC
ESR1	ENSG00000180929	44	63	+	0.00015 GAGCAGGCTCTGGCTGACTC
ESR1	ENSG00000168818	103	122	-	0.00015 AGGCACGTGGACGGTGACCC
ESR1	ENSG00000241420	198	217	+	0.00015 GAGGCTGGGCGTACTGGCCT
ESR1	ENSG00000154889	345	364	-	0.00015 CTCCCGCGCCGCGCTGCCCC
ESR1	ENSG00000239737	252	271	-	0.00015 GGTTGAGATCGCTTTGACCC
ESR1	ENSG00000102893	204	223	-	0.00015 GTCCCGGGGCTGCGCGCCAC
ESR1	ENSG00000155506	331	350	-	0.00015 TGCCAAGGCCACGCTGTTTT
ESR1	ENSG00000083097	314	333	+	0.00015 GGTAAAAGCGTCCCTGCCCC
ESR1	ENSG00000198492	282	301	-	0.00015 GCTCACGGCCTCCCCGCCCC
ESR1	ENSG00000117122	245	264	+	0.00015 CCCCGGGGACACCCCCCCCC
ESR1	ENSG00000230953	324	343	-	0.00015 GGCCAAGGGCCCCTTCCCCG
ESR1	ENSG00000129084	238	257	-	0.00015 CGGCCTGGGCACGCTGGGTC
ESR1	ENSG00000080823	163	182	-	0.00015 TGCGCAGTGCAGCCCGTCCC
ESR1	ENSG00000127663	200	219	-	0.00015 GTTGCTGGCGACCGAGCCCT
ESR1	ENSG00000100412	290	309	-	0.00015 AGTAGGAGGCACCCCGCCCC
ESR1	ENSG00000172936	302	321	-	0.00015 GAGAAGCGCCGCCCTGCCCT
ESR1	ENSG00000157510	307	326	-	0.00015 GGCCCCTCTTACCCTGGCCT
ESR1	ENSG00000140961	250	269	-	0.00015 GGGCATGGTGGCGGTCACCT
ESR1	ENSG00000134508	306	325	+	0.00015 GTGTAAGGTCATTTTAGCCC

ESR1	ENSG00000237765	104	123	-	0.00015	CGCCTGGGGCCCTCTGACAA
ESR1	ENSG00000179583	281	300	+	0.00015	GAGGAGGGGCTGCCAGACTC
ESR1	ENSG00000198003	72	91	+	0.00015	AATCCTGGCCAGTCTCACTT
ESR1	ENSG00000010322	346	365	-	0.00015	GTCACTGCTCTTCCTGGCCT
ESR1	ENSG00000177685	123	142	-	0.00015	TGGCCGGCTCGCCCAGTCCC
ESR1	ENSG00000244122	207	226	-	0.00015	AGGCCAGTCCACCCTGCACG
ESR1	ENSG00000248399	124	143	+	0.00015	GTCCCGGGACTCCGTGGGCT
ESR1	ENSG00000184047	144	163	-	0.00015	GGCGCTGGCAACCCTGCCCG
ESR1	ENSG00000165792	212	231	-	0.00015	GGGCCTGGTCACCGGCCCCA
ESR1	ENSG00000112715	112	131	-	0.00015	GGGACAGGCGAGCCTCAGCC
ESR1	ENSG00000230536	148	167	-	0.00015	CTGTCATGGCAACCTGATCA
ESR1	ENSG00000143321	14	33	-	0.00016	TTTACAGATCACTTTGCCTT
ESR1	ENSG00000240210	335	354	+	0.00016	TGGACAGGATATCCAGCCCC
ESR1	ENSG00000166348	150	169	-	0.00016	GAGCCAAGGCAACCAGCTCT
ESR1	ENSG00000206535	337	356	-	0.00016	GCAAGAGGGCCATCTGCCCT
ESR1	ENSG00000258607	128	147	+	0.00016	CTATTTGGCCACCTTGCCTT
ESR1	ENSG00000168066	21	40	+	0.00016	AATCCCGGAGAAACTGCCCC
ESR1	ENSG00000182473	200	219	+	0.00016	GGCCCGGGCTCGCCTCACCT
ESR1	ENSG00000134014	139	158	+	0.00016	CTTCCAGGTCATCAGGTCAT
ESR1	ENSG00000078304	10	29	-	0.00016	CCGGCCGGCCGCCCCGCCCC
ESR1	ENSG00000136367	279	298	+	0.00016	TGGCCAGGGGAGCGAGGCCG
ESR1	ENSG00000258663	41	60	+	0.00016	TCCAAGAGCCACCCTCCCCT
ESR1	ENSG00000131876	227	246	+	0.00016	GGCGCGGGGCACGCTGGGAC
ESR1	ENSG00000244604	224	243	-	0.00016	GGCCCTTTTCAGCACGACCT
ESR1	ENSG00000130294	41	60	+	0.00016	GAGCCGGGTGTCGGTCCCCC
ESR1	ENSG00000162441	353	372	-	0.00016	CTTCCGGGCCTACCTGACAA
ESR1	ENSG00000229534	207	226	-	0.00016	TCTTTAGGAGACTCTGACTT
ESR1	ENSG00000122026	236	255	+	0.00016	CTTTCCGGGCTGTCTGACAC
ESR1	ENSG00000049883	317	336	+	0.00016	CTGTCAGCTGCCGCTGCCCT
ESR1	ENSG00000113645	37	56	-	0.00016	GGGGAAGGAGAGACCGCCCC
ESR1	ENSG00000245281	300	319	+	0.00016	CCAGCAGGAAATCCTGCCCT
ESR1	ENSG00000256682	315	334	+	0.00016	CTGAAAGGTCTCCCTGATTG
ESR1	ENSG00000088876	128	147	-	0.00016	AGGCCCGCCCTCCCTGCCTT
ESR1	ENSG00000220739	4	23	+	0.00016	GGGCAAAGACAACCTGAGAT
ESR1	ENSG00000231799	267	286	-	0.00016	TGGCAATGTCACCCCCCCAT
ESR1	ENSG00000130702	40	59	-	0.00017	CGGCCGGGCGGCCTTAACCC
ESR1	ENSG00000151743	378	397	+	0.00017	ACGGCGGGTCAGTCAGCTCC
ESR1	ENSG00000147099	339	358	-	0.00017	TTCCCAGACCAGACTCCCCT
ESR1	ENSG00000238298	325	344	-	0.00017	TATTGAGGTCTACTTGACAT
ESR1	ENSG00000258559	275	294	-	0.00017	GGCATGAGCCACCATGCCCG
ESR1	ENSG00000124208	117	136	-	0.00017	CGGCGAGATCACGCCGCCCA
ESR1	ENSG00000116652	289	308	-	0.00017	TGGATAGGTTATCCTGTCTC
ESR1	ENSG00000175773	295	314	+	0.00017	CGGTGGAGCCTGCGTGACCC
ESR1	ENSG00000227638	37	56	+	0.00017	ACAGAAGGACAGCTTGAGCC
ESR1	ENSG00000129226	173	192	+	0.00017	GACACTGTTGACTTTGCCCT
ESR1	ENSG00000154783	344	363	+	0.00017	AAGCCCAGGCTGACTGCCCC
ESR1	ENSG00000211535	354	373	+	0.00017	GGGTCGGTTCAGCCTTGCCT
ESR1	ENSG00000249144	263	282	-	0.00017	GATTCTGGTGATAGTGACTC
ESR1	ENSG00000167996	322	341	+	0.00018	TAGCCAGCCCTCCGTCACCT
ESR1	ENSG00000139163	160	179	+	0.00018	ATCGCAGGCCAACAAGCCCA

ESR1	ENSG00000258376	179	198	-	0.00018	ACTCCTGGGCTCCCTGGGCT
ESR1	ENSG00000007384	60	79	-	0.00018	GGCAGGGGCCAATCTGCTCT
ESR1	ENSG00000236939	258	277	-	0.00018	CGCCCAGGGCCGCCTCCGCC
ESR1	ENSG00000180098	163	182	+	0.00018	CGCGCGGGCCTTCGAGCCCC
ESR1	ENSG00000231365	60	79	-	0.00018	CAACGCGGTGAGCCTACCCC
ESR1	ENSG00000012048	378	397	+	0.00018	CGCTCAGGAGGCCTTCACCC
ESR1	ENSG00000218521	341	360	-	0.00018	GTAACAGTTTAGAGTGACCC
ESR1	ENSG00000173988	215	234	+	0.00018	AGGGTGTGTCTCCTTGGCCT
ESR1	ENSG00000237259	1	20	+	0.00018	AAGGCATGGCACCTTCTCCC
ESR1	ENSG00000099953	67	86	+	0.00018	TGGAAATGGGACCCTGCTCC
ESR1	ENSG00000213443	28	47	-	0.00018	TGCACAAGTCCCCCTGCCTG
ESR1	ENSG00000158092	182	201	+	0.00018	CGCGCGGATCCGCCTGCCCA
ESR1	ENSG00000151725	259	278	+	0.00018	GGAGAGCGGCACCATGGCCC
ESR1	ENSG00000066583	127	146	-	0.00018	CGGCGATGCCAGCCCGCCCG
ESR1	ENSG00000137877	43	62	-	0.00018	CTCCCAGGACGCAGAGGCCC
ESR1	ENSG00000126062	199	218	+	0.00018	AACCAAGGACTCCGTATCCC
ESR1	ENSG00000164306	193	212	+	0.00018	ACCGCAGCGCGCCCCGCCCC
ESR1	ENSG00000169762	185	204	+	0.00018	AGCCTGGGGCACCTTCGCTC
ESR1	ENSG00000167094	338	357	-	0.00018	AGCCTCGGTCTCTCTGCCTG
ESR1	ENSG00000254772	109	128	-	0.00018	GGGAAGGGGGATTATGACCA
ESR1	ENSG00000108797	111	130	-	0.00018	CGCGCCGGTTTCCCGGACCC
ESR1	ENSG00000135245	3	22	+	0.00018	ACTCCAGAACACAATGACTC
ESR1	ENSG00000233789	264	283	+	0.00018	AACCCAGGCCTATCAGACTC
ESR1	ENSG00000100522	120	139	+	0.00019	GCCCCCGCTCTCCGAGCCCC
ESR1	ENSG00000197114	206	225	-	0.00019	GCTCGAGGGTGCCGTGGCCC
ESR1	ENSG00000216895	69	88	-	0.00019	TTGTGGGGCCATCCTGACAG
ESR1	ENSG00000171346	22	41	+	0.00019	CCCAGCAGTGACCCAGACCT
ESR1	ENSG00000161960	8	27	-	0.00019	TGCGGAGGCGACAGTGCCTT
ESR1	ENSG00000115657	349	368	-	0.00019	GGACCAGGCCTCACCGCCCA
ESR1	ENSG00000251131	12	31	-	0.00019	GGGTGCTGCGACCATGACCC
ESR1	ENSG00000139173	138	157	-	0.00019	CGCGCAGGTGACCGCGATCA
ESR1	ENSG00000155957	319	338	+	0.00019	ATCATGGCTGACCCCGACCC
ESR1	ENSG00000143093	97	116	+	0.00019	CAGCAGGTTCTTTATGACCT
ESR1	ENSG00000233611	257	276	-	0.00019	CGGCAAAGGCTTCCTGGCCA
ESR1	ENSG00000126522	378	397	-	0.00019	CCCCCGGGCCGGGCTGGCTC
ESR1	ENSG00000233937	134	153	+	0.00019	GTCCGGCCCCACCCTGCCCC
ESR1	ENSG00000256175	292	311	+	0.00019	GACCCAGGCCCTTCTGTCTC
ESR1	ENSG00000182481	286	305	+	0.00019	GCCCTATGACTCCCTCCCCT
ESR1	ENSG00000255773	170	189	-	0.00019	GAGGCAGGGGACCCAGGTCT
ESR1	ENSG00000119638	53	72	+	0.00019	GGCGTGAGCCACCTTGCCCG
ESR1	ENSG00000189376	322	341	-	0.00019	GACGCGGGCGGTCCTGACCG
ESR1	ENSG00000234134	283	302	+	0.00019	TGGAAAGGCGAGCCAGCCAT
ESR1	ENSG00000116857	362	381	-	0.0002	AGGCTGGGTCCTTCTGATCC
ESR1	ENSG00000143379	120	139	+	0.0002	GGCCACGCCTACTCTGCCCT
ESR1	ENSG00000121671	333	352	-	0.0002	CGCCCGGGTGGAGCTGGCAT
ESR1	ENSG00000149564	282	301	-	0.0002	GCCGCGGGACGCACGGACCT
ESR1	ENSG00000168000	92	111	+	0.0002	CTCCAAAGGGAGCCTCTCCT
ESR1	ENSG00000243902	7	26	-	0.0002	CCGCCCGCTCCCGGTGCCCT
ESR1	ENSG00000099622	218	237	+	0.0002	GGCGAGGGCCTGCCTGCCTG
ESR1	ENSG00000163590	218	237	-	0.0002	GGCTGGGCTCTGCCTGCCTC

ESR1	ENSG00000244513	53	72	+	0.0002	GGGCCAGGGCGCGGGGCCCG
ESR1	ENSG00000226363	18	37	+	0.0002	GATCTTGGGCAAAATGTCCT
ESR1	ENSG00000151150	212	231	-	0.0002	CGCCCAGCGCGGCCTATCCT
ESR1	ENSG00000129083	328	347	+	0.0002	GTGCTAGGTGGCTGTGGCTT
ESR1	ENSG00000174483	41	60	+	2.00E-04	TGGAAAGGTGGCTCTGACTG
ESR1	ENSG00000257264	188	207	+	2.00E-04	GGCAAGAGTCACCACGCCCA
ESR1	ENSG00000112096	180	199	-	2.00E-04	GGCTGGGGTCGGGCTGTCAC
ESR1	ENSG00000204775	172	191	+	2.00E-04	AGGCCAGCACTCCTTGCCCG
ESR1	ENSG00000253502	315	334	-	2.00E-04	ATTCAATTTCAGCCTGAACT
ESR1	ENSG00000253950	105	124	-	0.0002	CTGCGGGCTCACCGTGGTCT
ESR1	ENSG00000186501	97	116	-	0.0002	GGGCCCGGCCAGCCCCGCCC
ESR1	ENSG00000119640	174	193	-	0.0002	GGGTCAAGTGACCTTGGGCT
ESR1	ENSG00000248546	235	254	-	0.0002	ATCAGAGGGCGCCCTGTTCC
ESR1	ENSG00000139351	51	70	+	0.0002	CGGCCAAAGCACCCTGGGCC
ESR1	ENSG00000240216	143	162	-	0.00021	CACCCAGAACACTGTTACCT
ESR1	ENSG00000151468	309	328	-	0.00021	ATCCGGGGGCAGCTTCCCTC
ESR1	ENSG00000124942	232	251	-	0.00021	CACCCCAGTCTCTGTGCCAT
ESR1	ENSG00000176533	263	282	-	0.00021	GTTCGCGGGCGCCCTTACCT
ESR1	ENSG00000178922	69	88	+	0.00021	GCCCTCGGGCAGCCAGCTCT
ESR1	ENSG00000152457	251	270	+	0.00021	CGGCTGGGGCCACCTGCTCT
ESR1	ENSG00000179988	10	29	+	0.00021	CAGTCAGGCCAGCCCAGCCC
ESR1	ENSG00000162174	295	314	-	0.00021	GGACGCGGACGCCGAGACCT
ESR1	ENSG00000241839	368	387	+	0.00021	GGCTGGGGTCCTCGAGCCCC
ESR1	ENSG00000095139	259	278	-	0.00021	AGCTCTGGACCTGCTGCCCC
ESR1	ENSG00000092841	152	171	-	0.00021	GGGCTGGGGCACAATGAATC
ESR1	ENSG00000244468	338	357	-	0.00021	GTTCGTGGTCTCGCTGGCTC
ESR1	ENSG00000085563	121	140	+	0.00021	CTTTCAAGCCTGCCTGCCTT
ESR1	ENSG00000000938	216	235	+	0.00021	CGTGACTGTCTCCCTGCCAC
ESR1	ENSG00000137710	264	283	+	0.00021	GGCGCCGGGCAGCCCCGCCT
ESR1	ENSG00000175175	24	43	-	0.00021	AGCTCAGCCCACGCTGCCTA
ESR1	ENSG00000105662	294	313	-	0.00021	CTCGAAGGCCGCCGTCTCCT
ESR1	ENSG00000256898	254	273	+	0.00021	GAAACATGGCACTGTTACCT
ESR1	ENSG00000258790	152	171	-	0.00021	CCGACGGACGAGACTGACCC
ESR1	ENSG00000179256	114	133	-	0.00021	CTGCTGGGTCCCTCTGCCTG
ESR1	ENSG00000133943	109	128	+	0.00021	GGCCCCGCGCCCCCAGCCCC
ESR1	ENSG00000067601	2	21	-	0.00021	CAGGCCGGGCGCCGTGGCTC
ESR1	ENSG00000077157	7	26	-	0.00021	CAGTGGGGTCACCTTTGCCC
ESR1	ENSG00000033011	233	252	+	0.00021	GGGACGGGCGGCCGTGAGCT
ESR1	ENSG00000197381	276	295	-	0.00021	CACGCGGGTCCCGCCGGCCC
ESR1	ENSG00000239775	333	352	+	0.00021	CTCCCAAGCCAGTGGGCCCC
ESR1	ENSG00000134759	155	174	+	0.00022	GGGCATGCGCAGTGCGACCC
ESR1	ENSG00000163467	332	351	-	0.00022	TCGACTGGTCACCTTTTCCT
ESR1	ENSG00000111669	50	69	-	0.00022	CGCCAGGATCATCCCAACCC
ESR1	ENSG00000213782	379	398	+	0.00022	TGCTAGGCTCAGGGAGACCC
ESR1	ENSG00000197586	267	286	-	0.00022	GGCCGGCGCCACCCCGGCCT
ESR1	ENSG00000230741	380	399	-	0.00022	AGGTTAGGTCACTCACCCAC
ESR1	ENSG00000238278	305	324	+	0.00022	GGGCCCGGTAGGCCTGCCAT
ESR1	ENSG00000203279	182	201	+	0.00022	CAGAAAAGGCTCTCTCACCT
ESR1	ENSG00000255581	110	129	-	0.00022	ATCTCGGCTCACCGCAACCT
ESR1	ENSG00000136383	31	50	-	0.00022	ATCTCGGCTCACCGCAACCT

ESR1	ENSG00000011198	212	231	+	0.00022	ATCTCGGCTCACCGCAACCT
ESR1	ENSG00000145016	101	120	+	0.00022	GGGCGGGGCCACCGACACTC
ESR1	ENSG00000143384	139	158	-	0.00022	GTTTTAGGGCGGCCAGTCCT
ESR1	ENSG00000100385	220	239	-	0.00022	GAAGCAAGGCACCTTCACAT
ESR1	ENSG00000196670	377	396	-	0.00022	GGGAGGGGGCACGCTTACTC
ESR1	ENSG00000245148	196	215	-	0.00022	GCCTGAGGACACATTGCTCT
ESR1	ENSG00000119723	353	372	-	0.00022	CGCATAGCTCTCGCTGCCAC
ESR1	ENSG00000229212	359	378	+	0.00022	GGCCGAGACCGCCGTGCCCA
ESR1	ENSG00000112305	370	389	+	0.00022	AGGTGCGTTCACTCTGCCCG
ESR1	ENSG00000229628	243	262	+	0.00022	GGGATTGGACAGCATGAGCC
ESR1	ENSG00000107371	124	143	-	0.00022	GGCCGAGGTTAGCGAGGCCG
ESR1	ENSG00000122482	162	181	+	0.00023	AGCGCTGGGGGAGGTGACCT
ESR1	ENSG00000143569	189	208	+	0.00023	AGGGCGGGTCGGCCCGACTA
ESR1	ENSG00000185736	270	289	+	0.00023	TTCCCCGCCCTCCCTGACCA
ESR1	ENSG00000234608	316	335	-	0.00023	AGGTAAGGGGGAGGTGCCCC
ESR1	ENSG00000135722	352	371	-	0.00023	AAGTCGGGTCTTCCTGCCGT
ESR1	ENSG00000185963	175	194	-	0.00023	CGCCGCCGCCGCCCTGCCCC
ESR1	ENSG00000228932	339	358	+	0.00023	CACACATGTCAGGCTGGCAA
ESR1	ENSG00000204209	197	216	-	0.00023	TTCCTCTGCCATCCTGACTC
ESR1	ENSG00000164129	14	33	-	0.00023	GCCGGGGGCGTCCCAGACCT
ESR1	ENSG00000242761	61	80	-	0.00023	GGCTCAAGTGATCCTCCCAC
ESR1	ENSG00000253729	299	318	+	0.00023	GCTGCAGGAGACCTTGTCCG
ESR1	ENSG00000197989	312	331	-	0.00023	AGGTCAGGAGATCGAGACCA
ESR1	ENSG00000185201	275	294	-	0.00023	AGGTCAGGAGATCGAGACCA
ESR1	ENSG00000252494	20	39	-	0.00023	AGGTCAGGAGATCGAGACCA
ESR1	ENSG00000242833	2	21	-	0.00023	AGGTCAGGAGATCGAGACCA
ESR1	ENSG00000215791	179	198	-	0.00023	GAACCACGTCAGGGTGAACC
ESR1	ENSG00000148303	357	376	-	0.00023	CCTCGGTGTCTCCGTGCCAC
ESR1	ENSG00000235910	26	45	-	0.00023	CGCCAAGGCCACCGAGCATC
ESR1	ENSG00000236507	353	372	-	0.00023	GGCCCAGCTCCCCTTTCCCT
ESR1	ENSG00000107771	233	252	-	0.00024	CTCCAAAGCCGCCGCGCCCC
ESR1	ENSG00000173465	250	269	+	0.00024	TGACAACGGCAACATGGCCC
ESR1	ENSG00000237416	377	396	+	0.00024	GACAAAGGTAAGTATGTCCT
ESR1	ENSG00000155269	105	124	+	0.00024	GGCCCAGCCCTCACTGGCCA
ESR1	ENSG00000213484	91	110	-	0.00024	GTTCGAGACCAGCCTGGCCA
ESR1	ENSG00000255354	345	364	+	0.00024	AGCTAAGGGCTCTCTGGCAG
ESR1	ENSG00000065923	206	225	-	0.00024	GTCCCGGGGCCCCCCGCGCC
ESR1	ENSG00000242777	107	126	+	0.00024	GACCCTGTTGAACTTGACTC
ESR1	ENSG00000222383	15	34	-	0.00024	GGGCTTGGTGGCTGTCACCT
ESR1	ENSG00000156411	196	215	-	0.00024	AGAAAGGCTCACCCTGGGCT
ESR1	ENSG00000228275	129	148	+	0.00024	CCCCACGCCCACACCGACCT
ESR1	ENSG00000256223	81	100	-	0.00024	CGTTCAGGCCACGCTCCGCC
ESR1	ENSG00000176208	129	148	-	0.00024	CGAGAGGGCCAAAATGACTC
ESR1	ENSG00000223960	165	184	-	0.00024	GGAGCAGGGCCGCGAGGCCC
ESR1	ENSG00000100926	268	287	-	0.00024	GGCCAGTCCCACCCTGGCTC
ESR1	ENSG00000003509	111	130	+	0.00024	CTCCAAAGGCTCCTTGACTG
ESR1	ENSG00000115816	354	373	-	0.00024	CTCCAAAGGCTCCTTGACTG
ESR1	ENSG00000175066	263	282	-	0.00024	GTCCCCGGGCGGCCCAACCC
ESR1	ENSG00000254732	13	32	-	0.00024	CACCCACGTCCCTCTCCCCC
ESR1	ENSG00000166598	89	108	-	0.00024	TAGCCATGGCAACGTGTTCT

ESR1	ENSG00000238111	324	343	+	0.00024	AAGAAGGGTCTGCCTCCCTC
ESR1	ENSG00000160746	308	327	-	0.00024	TGACCGGGTCTGTCAGCCTC
ESR1	ENSG00000130024	364	383	+	0.00024	CGGCCGTGCGACAGCGACCC
ESR1	ENSG00000165675	294	313	+	0.00024	CCGCGAGGGCACTACGAGCC
ESR1	ENSG00000125354	138	157	-	0.00025	CCCCTCGGTGACCACGTCCT
ESR1	ENSG00000258839	321	340	-	0.00025	GGTCTTGGTCCGAGTGGCCC
ESR1	ENSG00000242583	181	200	+	0.00025	CCCCAGGGTCCCCCTCTCCA
ESR1	ENSG00000240857	283	302	-	0.00025	GCCCGAGGGCCCACCGGCCC
ESR1	ENSG00000238650	64	83	-	0.00025	CGCCCAATTCCCCCTCCCCC
ESR1	ENSG00000213281	262	281	-	0.00025	CGCCCCGGCCACGTGGGCCT
ESR1	ENSG00000152465	170	189	-	0.00025	GAGCCCGGGCGCTACGCCCC
ESR1	ENSG00000233719	104	123	+	0.00025	CCTACTGTCCACCGTGGCCC
ESR1	ENSG00000166529	310	329	-	0.00025	CAGCCACGGCTCCCTCTCCT
ESR1	ENSG00000147804	38	57	-	0.00025	AGGGCTGGGCCCCTTCCCCT
ESR1	ENSG00000204859	315	334	-	0.00025	AGGCAGGTCCTCCCTGAGCT
ESR1	ENSG00000147677	177	196	+	0.00025	TCGCCTGACCACCTTCACCT
ESR1	ENSG00000110047	268	287	-	0.00025	CGCCGACCTCACACTCACCT
ESR1	ENSG00000249633	222	241	-	0.00025	AGGACAAAGGACCCAGACCC
ESR1	ENSG00000221656	115	134	-	0.00025	GTCCTGGGGCTCCCAGGCCG
ESR1	ENSG00000132394	40	59	+	0.00025	AACCCTGCCTACGGTGACCT
ESR1	ENSG00000237779	250	269	+	0.00025	GCACCATGGCACCCCAGCCT
ESR1	ENSG00000218014	298	317	-	0.00025	GGCCCAGTGCATGCTGAGCG
ESR1	ENSG00000139211	373	392	-	0.00025	CGCGCGGGGCGCCCCGCTCC
ESR1	ENSG00000258657	145	164	+	0.00026	TGGGCATGAGAACTTGCCCC
ESR1	ENSG00000197548	355	374	-	0.00026	AAACCGGCCCAGCAAGACCC
ESR1	ENSG00000241651	291	310	+	0.00026	TCCACAGGGCTCCCCACCCC
ESR1	ENSG00000164742	257	276	-	0.00026	CCGGAGGAGCCGCGTGACCT
ESR1	ENSG00000244005	118	137	+	0.00026	GGGCTGGGTCGCTCAGCTCT
ESR1	ENSG00000250659	340	359	-	0.00026	CAGCCTGGGCAACATGGCAA
ESR1	ENSG00000118894	128	147	+	0.00026	CACGACGTTCCTCCTGACCC
ESR1	ENSG00000142794	149	168	+	0.00026	GACGCGGCCCATCCGGACCC
ESR1	ENSG00000241635	271	290	+	0.00026	GCACAGGGTGGACCAGCCCC
ESR1	ENSG00000252150	100	119	-	0.00026	AGGCCTGCAGATCCTGGCCT
ESR1	ENSG00000227199	319	338	-	0.00026	GCGGCGAAGCCCCCTGACCC
ESR1	ENSG00000240429	214	233	-	0.00026	CTCCCGGCTCTGCGTGGCCG
ESR1	ENSG00000215301	167	186	+	0.00026	CGCCCCGGTCACCATCCTAC
ESR1	ENSG00000181222	101	120	+	0.00026	GGGCCTGCGCAGGCGGCCCC
ESR1	ENSG00000243305	16	35	-	0.00026	TGACCTGGTTAGGCTGGCTT
ESR1	ENSG00000120705	153	172	-	0.00026	TCTCATTGGCTCTCTGCCCC
ESR1	ENSG00000254872	329	348	-	0.00026	ACACATGGGCACCAGGACAC
ESR1	ENSG00000197892	94	113	+	0.00026	GGCCCCGCCCACGACGACCC
ESR1	ENSG00000159423	131	150	+	0.00026	TTGGTGTGTCACTCTGACTG
ESR1	ENSG00000236646	290	309	+	0.00026	TTGCCATGGGACCCTGTCAG
ESR1	ENSG00000166333	154	173	-	0.00026	TCCCACCGCCTCCCTGCCCT
ESR1	ENSG00000164053	69	88	-	0.00026	GACTCAGTGCGGCGCGACCC
ESR1	ENSG00000249540	355	374	+	0.00026	TACCAGGGACACTGTGAGAT
ESR1	ENSG00000113758	289	308	-	0.00027	ATTCCAGGCCATTCTCAGCC
ESR1	ENSG00000136883	284	303	-	0.00027	GTTTCCGGCCCCTCTGGCCC
ESR1	ENSG00000234741	307	326	+	0.00027	CGGGCGGGGGAGCCAGCGCT
ESR1	ENSG00000180389	269	288	-	0.00027	AGCTGAGTCCAGCCTGTCTC

ESR1	ENSG00000103021	302	321	-	0.00027	GGTGAACGCTACCCTGACTT
ESR1	ENSG00000065328	299	318	+	0.00027	GGGCCGGGGCCGCCTCGCAC
ESR1	ENSG00000196588	29	48	-	0.00027	CGAAAACGGCGGCCTGACTT
ESR1	ENSG00000225733	78	97	+	0.00027	CCGCCAGGGCTCCCGCGCCC
ESR1	ENSG00000171497	241	260	-	0.00027	CGCCCGGGCCGCCCAAACTC
ESR1	ENSG00000005022	340	359	+	0.00027	CGCCAAGGACTTCCTGGCAG
ESR1	ENSG00000142875	309	328	+	0.00027	CGGCCCGGTCTTCGCGCCCG
ESR1	ENSG00000152061	306	325	+	0.00027	CTCTCAGTTCCCTCCGCCCT
ESR1	ENSG00000233108	311	330	+	0.00027	GAGCCGGGGCTCCGTCTCTC
ESR1	ENSG00000177628	161	180	+	0.00027	GAGGAAGGGCTCTGAGTCCC
ESR1	ENSG00000075151	362	381	+	0.00027	AGGTCCGGTCTCTCCGCCTC
ESR1	ENSG00000159128	251	270	+	0.00027	CAGCCTGGTGACTCCGTCTC
ESR1	ENSG00000127364	86	105	-	0.00027	GATCAAGGGCCACCTGATTT
ESR1	ENSG00000233221	153	172	+	0.00027	CGCGCAGGGCGCCGGGAGCC
ESR1	ENSG00000255857	293	312	+	0.00028	GTCCCGGTTCCCTGTGCCAC
ESR1	ENSG00000112655	156	175	-	0.00028	CCCGCACGGCGCCCCGCCCC
ESR1	ENSG00000230042	231	250	+	0.00028	ATCATGGGGGCCCCAGACCT
ESR1	ENSG00000111229	36	55	-	0.00028	AGGGCCGGGCATAGTGGCTC
ESR1	ENSG00000160087	160	179	+	0.00028	TGCCTAGAGCGGCCAGCCCT
ESR1	ENSG00000213398	19	38	-	0.00028	GCGCCAGGGGAAACAGAGCC
ESR1	ENSG00000153993	159	178	+	0.00028	GCAGCAGCGCCCCCTGCCTC
ESR1	ENSG00000145022	382	401	+	0.00028	GACTACGGTGACAGTACCCC
ESR1	ENSG00000126368	281	300	+	0.00028	TGCGCAGAGCCCTCTGTCCC
ESR1	ENSG00000248121	296	315	+	0.00028	CGGGCCAGTCAGACTGCGCC
ESR1	ENSG00000163918	325	344	+	0.00028	TCTTCAGATGTCTCTGCCCT
ESR1	ENSG00000140009	380	399	+	0.00028	CGCTCAGGTTACAGTCATCC
ESR1	ENSG00000159079	77	96	+	0.00028	CGCCCTGGCCCCTCCGTCCT
ESR1	ENSG00000241830	12	31	-	0.00028	GGGTTTGGGCTCCCTAGCCC
ESR1	ENSG00000175206	267	286	+	0.00029	GTGTGAGGCCAGCTTGAGCA
ESR1	ENSG00000131051	124	143	-	0.00029	GGCTCCGGCGACCGTAGCCC
ESR1	ENSG00000234740	62	81	+	0.00029	GTGCGCGGGCGCCCTGGGCT
ESR1	ENSG00000241279	213	232	+	0.00029	GAGACAGGTTAGTTTTACCC
ESR1	ENSG00000254553	128	147	-	0.00029	ATCGCGGGAGCGCCTGGCCT
ESR1	ENSG00000235681	109	128	-	0.00029	ATCTCAGCTCACTGCAACCT
ESR1	ENSG00000256309	108	127	+	0.00029	GGGGAGGGGCCCAGTGAGCT
ESR1	ENSG00000236474	69	88	-	0.00029	GCTCAAAGGCACCTTGAAAT
ESR1	ENSG00000259014	52	71	+	0.00029	ATCTCAGCTCACTGCAACCT
ESR1	ENSG00000201448	49	68	-	0.00029	GTTTAAGACCAGCCTGGCCA
ESR1	ENSG00000196498	93	112	-	0.00029	TGGCTCGGCCTCCCTGCTCC
ESR1	ENSG00000134321	85	104	-	0.00029	CGCTGAGGCGCCCATGGCCT
ESR1	ENSG00000244684	280	299	-	0.00029	GACACAGCACACTATAACCC
ESR1	ENSG00000175324	233	252	-	0.00029	GACCCCAGAGTCACTGACCT
ESR1	ENSG00000257851	264	283	+	0.00029	CAGGAAGAGGGCCATGACCC
ESR1	ENSG00000167491	219	238	-	0.00029	CTCGCGGCTCAGTCTCACAC
ESR1	ENSG00000232626	309	328	-	0.00029	CTTTCAGGTCATCTTCCTCC
ESR1	ENSG00000174013	371	390	+	0.00029	GCAGCCGGTGCGTCTGCCCT
ESR1	ENSG00000078487	131	150	+	0.00029	GCGATAGGTCATTATAACTC
ESR1	ENSG00000237996	244	263	+	0.00029	CACCCAGCCCTGAGTGACAT
ESR1	ENSG00000197429	253	272	-	0.00029	AACGCAGGCCCTCCTTACCC
ESR1	ENSG00000229638	83	102	-	0.00029	AATCATGATCATTCTGCCTT

ESR1	ENSG00000047648	322	341	-	0.00029	CTCCAAAGACTGCGTGCCCA
ESR1	ENSG00000198400	324	343	+	0.0003	CTGCGGACTCAGCCTGAGCT
ESR1	ENSG00000182993	155	174	+	0.0003	CTCTTAGCGCCGCTTGACCC
ESR1	ENSG00000114735	332	351	+	0.0003	CCCAAGGGTCAACCCCACAC
ESR1	ENSG00000240793	170	189	-	0.0003	CAGCTTGGCCAGTCTCACTC
ESR1	ENSG00000109180	102	121	-	0.0003	CTGCAATGCCCTTATGACCT
ESR1	ENSG00000204498	17	36	+	0.0003	TCCCCTGCTCACTCAGCCTC
ESR1	ENSG00000256142	94	113	+	0.0003	ATCTCAGAGCACTTTGAACC
ESR1	ENSG00000238868	10	29	+	0.0003	CAGCTGTGTGAGCCTGCACT
ESR1	ENSG00000129465	308	327	+	3.00E-04	ACCCCTGCACAGACAGACCC
ESR1	ENSG00000119917	16	35	-	0.0003	TTCTAAGGCCATACTCACCA
ESR1	ENSG00000120533	180	199	-	0.0003	GGGCGGGGTCTCGCCACCCT
ESR1	ENSG00000122952	168	187	+	0.0003	CGCGAAGTCGACTGTGACTT
ESR1	ENSG00000122012	240	259	+	0.0003	TCCCCCGCGCGCCGTGACTC
ESR1	ENSG00000117523	342	361	+	0.0003	ACCCCAGCTTTCCCTCCCCC
ESR1	ENSG00000115541	217	236	+	0.00031	GTGCTAGCGCGCTCAGCCCT
ESR1	ENSG00000109189	237	256	+	0.00031	CCTCCCGGCCTCCCTCTCCC
ESR1	ENSG00000230698	6	25	-	0.00031	TGACAACGTCACAGTGGCAC
ESR1	ENSG00000142949	83	102	-	0.00031	CCTCTTGGCCTCTCTGCCTT
ESR1	ENSG00000166278	305	324	-	0.00031	GGCCCAGGCGTGTCTCGCCC
ESR1	ENSG00000235590	311	330	+	0.00031	CCGTGGGGTCACTCTTCCTC
ESR1	ENSG00000243243	53	72	+	0.00031	GACTATGGAAAGCATGACCT
ESR1	ENSG00000133112	278	297	+	0.00031	CGCGCGGCTCTTCGTGCCAC
ESR1	ENSG00000242588	101	120	+	0.00031	ATCTGCGGCCTTCGTGCCCC
ESR1	ENSG00000092470	101	120	+	0.00032	GCGCCTGGCCAAGGCGGCCT
ESR1	ENSG00000237149	194	213	+	0.00032	GAGCTGAATCACTCCGACCC
ESR1	ENSG00000182472	318	337	+	0.00032	GACCTGGGGTTTTCTGCCCC
ESR1	ENSG00000240032	262	281	-	0.00032	AGTCCATCTCACAGTGACTA
ESR1	ENSG00000137522	363	382	+	0.00032	TTGCAAGGGCACGGTACTCC
ESR1	ENSG00000245532	72	91	+	0.00032	CGCCTGGGAGACCATGCACC
ESR1	ENSG00000119922	30	49	-	0.00032	GGGTCTGGGGACATTGCTCT
ESR1	ENSG00000114395	296	315	+	0.00032	GCGCCTGCGCAGCGCGACTC
ESR1	ENSG00000249098	381	400	-	0.00032	GGCGGAGCTTACCGTGAGCC
ESR1	ENSG00000235939	26	45	-	0.00032	AAGTTAGGTCTCTGTCACTC
ESR1	ENSG00000100600	228	247	+	0.00032	TCACCGCGGCACAGTGGCCC
ESR1	ENSG00000140993	284	303	+	0.00032	TACCTCGGCCAGCTTGGCTT
ESR1	ENSG00000250893	6	25	-	0.00032	CATTCAGGTCCCCATCCCCG
ESR1	ENSG00000112339	270	289	-	0.00032	CCACCATGACGTAGTGACCC
ESR1	ENSG00000160062	96	115	-	0.00032	TCGCCCACTCCCCCTGCCCT
ESR1	ENSG00000213707	160	179	+	0.00032	GCACTGGGCGACTGTGCCTC
ESR1	ENSG00000228676	25	44	+	0.00032	AAGTCAGGAGTTCGTGACCA
ESR1	ENSG00000213703	202	221	-	0.00032	CTGCTTGGCCACAATGGCCG
ESR1	ENSG00000235706	206	225	-	0.00032	GCCCGCTGTCTCCCTGCTCC
ESR1	ENSG00000224055	171	190	+	0.00032	GTGCAGGGCCAGCTGCACCC
ESR1	ENSG00000216324	330	349	-	0.00032	CTTCCAATTCACATTGCCTT
ESR1	ENSG00000104388	145	164	-	0.00033	TGCCCGGTCCGCCCTGTCTT
ESR1	ENSG00000199916	265	284	-	0.00033	AGGTCCGGGGACTTTCCCCT
ESR1	ENSG00000124920	54	73	-	0.00033	GGCCGCGGGCACCACGCTCC
ESR1	ENSG00000184084	374	393	+	0.00033	GGACCTGCTGATACTGGCCC
ESR1	ENSG00000249921	374	393	+	0.00033	CTGTGGGGTCACTCCCACTT

ESR1	ENSG00000230116	338	357	+	0.00033	GACGCTAGTCACCAGGACTC
ESR1	ENSG00000248487	266	285	+	0.00033	AGCCTGGGCCAGCCTGTGCA
ESR1	ENSG00000238711	120	139	-	0.00033	ATCCCAGGGTTCCAAGGCCC
ESR1	ENSG00000112419	33	52	-	0.00033	AGCCCCGGGCACTGGCCCCC
ESR1	ENSG00000237806	306	325	+	0.00033	TGGGAAGATCAACCTGTGCT
ESR1	ENSG00000111845	215	234	+	0.00033	GAGATATGCCTGCTTGCCCC
ESR1	ENSG00000170289	3	22	+	0.00033	TCACAAGATCATTTTGACTC
ESR1	ENSG00000244134	152	171	+	0.00033	CACACATGTGACCATGAGTC
ESR1	ENSG00000254480	318	337	-	0.00033	GGCAAAGGGGCGTCAGCCCT
ESR1	ENSG00000231770	60	79	-	0.00033	AAGGCCGGCGTTTCTGACCT
ESR1	ENSG00000110013	98	117	+	0.00034	GGACTGAGCCATCCTGGCTT
ESR1	ENSG00000184731	263	282	-	0.00034	GTCCCCGCCCCCCCTCACCT
ESR1	ENSG00000175224	2	21	-	0.00034	TGGCCGGCGCAATCAGACTT
ESR1	ENSG00000223442	143	162	-	0.00034	GTCAGAGGTGACGCAGGCAC
ESR1	ENSG00000179195	56	75	+	0.00034	AATACAGGTCAGCATGAAAA
ESR1	ENSG00000198755	354	373	-	0.00034	CCCGCAGGCCGACCCGCCTT
ESR1	ENSG00000135114	192	211	-	0.00034	CCGTCTAGTCAATCTGTCAT
ESR1	ENSG00000235652	162	181	+	0.00034	GGGGACGCGCACGCCGCCCT
ESR1	ENSG00000258283	366	385	-	0.00034	TAGCCATGTGAACTTGGCCA
ESR1	ENSG00000120068	318	337	-	0.00034	CGGCTCGCTCGCCCTCCCCC
ESR1	ENSG00000100142	292	311	+	0.00034	AACTCAGGGGTCCCCAACCC
ESR1	ENSG00000089127	42	61	+	0.00034	CTTCCTGGTTTTTCTGACTT
ESR1	ENSG00000142330	11	30	-	0.00034	GCCCAGGGCTATCCCGGCCT
ESR1	ENSG00000147650	48	67	+	0.00034	GCGCGCGAGCTCCTTGCCCT
ESR1	ENSG00000088833	83	102	-	0.00035	TGGCAGGGCCACACTTCCTC
ESR1	ENSG00000153044	181	200	+	0.00035	GGGGCGGGGCCCTCGGGCCT
ESR1	ENSG00000138061	31	50	-	0.00035	ACACAGGGTCAGCTTAGCTT
ESR1	ENSG00000077782	255	274	+	0.00035	AGCGCCGGACAGCTCGGCCC
ESR1	ENSG00000177182	121	140	+	0.00035	AGACAAAGGCACAATTACCC
ESR1	ENSG00000248394	247	266	-	0.00035	GCGCGGGGTCGCCATACCCA
ESR1	ENSG00000156970	189	208	+	0.00035	GGGCGTGGCCACGTCGACCG
ESR1	ENSG00000024048	129	148	+	0.00035	CTCCTGGGTGTTATTGCCCC
ESR1	ENSG00000254964	229	248	+	0.00035	AGCCTGGGCCACAATCCCAT
ESR1	ENSG00000241499	325	344	-	0.00035	CACCATAGTCACTCTGCTTC
ESR1	ENSG00000137821	87	106	-	0.00035	GTCCTCAGGCACCTTGGCTC
ESR1	ENSG00000124222	255	274	-	0.00035	CAGCAGGGCCTGCCTCCCCG
ESR1	ENSG00000180398	354	373	+	0.00035	GCGCTCGGGCTGCCTCGCCT
ESR1	ENSG00000159176	52	71	-	0.00036	CGAGCTGGTCAGCAGCACCC
ESR1	ENSG00000225302	38	57	+	0.00036	CTGCCTAGGGAGGCTGCCTC
ESR1	ENSG00000250073	269	288	-	0.00036	TGCCCAGATCGCCCGAACCC
ESR1	ENSG00000179902	63	82	+	0.00036	TACCCACGTCGCCTTGACAA
ESR1	ENSG00000080573	220	239	+	0.00036	CCGAGAAGTCGCCGCGCCCC
ESR1	ENSG00000138382	115	134	+	0.00036	GGGATGGGGCAATGAGGCCC
ESR1	ENSG00000152672	138	157	-	0.00036	CTCCCAGCTCTTCCTCCCTC
ESR1	ENSG00000249055	147	166	+	0.00036	CTCCATGATTACCCTGGCTC
ESR1	ENSG00000041802	109	128	+	0.00036	CCTCCGAGTCTCCGCGTCCT
ESR1	ENSG00000085274	144	163	+	0.00036	GCGCATGCCCACTGTGCCCA
ESR1	ENSG00000233558	231	250	-	0.00036	ATGTCTGGGGTCTCTGCCAC
ESR1	ENSG00000224489	136	155	+	0.00036	GGAATGTGCCACCATGCCCG
ESR1	ENSG00000198894	162	181	-	0.00036	GGGCCAGCGCTCAGAGGCCT

ESR1	ENSG00000101230	12	31	-	0.00036	GGGCCGGGGGAGCAGGAGCT
ESR1	ENSG00000186615	111	130	-	0.00036	GTGCCGGGTCCGCCCCGCCC
ESR1	ENSG00000229863	126	145	+	0.00036	GGTTCTGGCTAAACTGACTT
ESR1	ENSG00000164404	367	386	+	0.00036	AACACTGCACAACCAGACCC
ESR1	ENSG00000182004	49	68	-	0.00036	GTGGAAGGTGGGCCGGTCCT
ESR1	ENSG00000134398	159	178	-	0.00036	AATACAGATCCGCCTGATCT
ESR1	ENSG00000232564	136	155	+	0.00036	CGATCCACCCACCTTGACCT
ESR1	ENSG00000250487	288	307	+	0.00036	CTCCGAGGCCAGCTTCACAG
ESR1	ENSG00000225374	224	243	+	0.00036	TTCCAGGGGCACACACTCCC
ESR1	ENSG00000105694	342	361	+	0.00037	GGCCCAGGTCAGTCTGCTGA
ESR1	ENSG00000000419	132	151	+	0.00037	CACACAGGTCATCCCCCGCT
ESR1	ENSG00000168350	322	341	+	0.00037	GGGCAGGGGCGGCGCGAGCC
ESR1	ENSG00000074416	243	262	+	0.00037	CGCGCAGCTCGTCCCGGCCC
ESR1	ENSG00000247828	286	305	-	0.00037	TCTCAAGGTCAGCACCGCCC
ESR1	ENSG00000255046	149	168	-	0.00037	GGCCCTGGCCAATCAGCGCC
ESR1	ENSG00000049323	211	230	-	0.00037	GGGCCCGGCGAGGGTGGCCG
ESR1	ENSG00000244580	245	264	-	0.00037	GGTTGAGATCATTTTGGCCC
ESR1	ENSG00000223505	288	307	+	0.00037	ATTGAAGGTGTTTATGCCCC
ESR1	ENSG00000153071	226	245	-	0.00037	AGTCAATCACATGCTGCCCT
ESR1	ENSG00000230955	348	367	+	0.00037	AGACGGGGTCTCCCTCTCTC
ESR1	ENSG00000244676	77	96	-	0.00037	TTTATTGGTCTCCCAGACAT
ESR1	ENSG00000186792	9	28	-	0.00037	CCTCCAGCTGGCTCTGCCTC
ESR1	ENSG00000086189	253	272	-	0.00037	CGCCCGCACCACTCTGGCCC
ESR1	ENSG00000147439	304	323	-	0.00037	CGCCTGGGCCTCACTCACCA
ESR1	ENSG00000242941	51	70	+	0.00037	GTCCAGAGGCACCCAAGCCC
ESR1	ENSG00000164855	253	272	-	0.00037	GGCCCCCGGCCTCCTGGCCT
ESR1	ENSG00000185513	302	321	+	0.00038	TCCCCTGGGCGCCGCGCCAC
ESR1	ENSG00000250604	114	133	-	0.00038	TACAGAGCTGAGGTTGACCC
ESR1	ENSG00000207556	195	214	-	0.00038	CGCCCAGGCCGCCATTATCT
ESR1	ENSG00000239783	122	141	-	0.00038	GGAGGAGGGTACCATGGCCA
ESR1	ENSG00000107165	133	152	-	0.00038	ATTTTAGGGCTTCAAGACCC
ESR1	ENSG00000207314	338	357	+	0.00038	GGACCAGGGCTGGAAGCCTT
ESR1	ENSG00000197746	103	122	+	0.00038	CTCCAAGTTCTTCCTCACTC
ESR1	ENSG00000166710	163	182	-	0.00038	GCCCGCAGGGACCGTCACCT
ESR1	ENSG00000198211	186	205	+	0.00038	CACCCAAGGCCCCCTGGCAG
ESR1	ENSG00000255730	130	149	+	0.00038	CTCCCCAGTCTCCCTCCCCA
ESR1	ENSG00000251821	245	264	+	0.00038	GAACATGGCCCCTGTGACTC
ESR1	ENSG00000153046	175	194	-	0.00038	AACAAAGGGGTCACTGAACT
ESR1	ENSG00000048828	340	359	+	0.00038	ACCCCCGGCCCCGCCGCCCC
ESR1	ENSG00000159899	10	29	+	0.00038	GCGCAGCGCCCTCCTGCCCT
ESR1	ENSG00000255276	379	398	-	0.00038	GGCCGGGCGGGGGCTGACCC
ESR1	ENSG00000039523	135	154	-	0.00038	AGTGCTGGCCAACGTGCCAG
ESR1	ENSG00000078018	17	36	-	0.00038	CGGGAGGGGGAGCACGACCG
ESR1	ENSG00000173163	60	79	+	0.00038	CGGTAAGCCCTCACTGCCTT
ESR1	ENSG00000156482	248	267	+	0.00038	TCACAAGTTCACGCTAACAC
ESR1	ENSG00000172590	178	197	+	0.00038	GCGCGTGGCCACCGAGGCCA
ESR1	ENSG00000230259	140	159	-	0.00038	CCGGCAGGCCGCGTCGCCCC
ESR1	ENSG00000136521	369	388	+	0.00038	GTGGCAGCTCTGTCTGGCCG
ESR1	ENSG00000103018	93	112	-	0.00039	AATTAGGGTCGTTCAGCCCC
ESR1	ENSG00000181789	340	359	-	0.00039	CAGGCCTGGCCCCCTCACCT

ESR1	ENSG00000171189	279	298	+	0.00039	GCACCAACTCACCCTGTACC
ESR1	ENSG00000131381	341	360	-	0.00039	CCCCAGACTGGGCCTGACCC
ESR1	ENSG00000119509	89	108	+	0.00039	GCCCCGGTCCACTGAGTCCT
ESR1	ENSG00000116750	114	133	+	0.00039	TGATAAATTCACCCTGTCTT
ESR1	ENSG00000110492	260	279	+	0.00039	GAGCCCGGGTTCTGTGGCCC
ESR1	ENSG00000254501	235	254	+	0.00039	GGGAAGGACCACCGAGACCA
ESR1	ENSG00000221182	112	131	-	0.00039	ATCCAAAGACACTCTGAATC
ESR1	ENSG00000255467	173	192	-	0.00039	TCCCCACAGCACTCAGACCC
ESR1	ENSG00000122986	284	303	-	0.00039	GGCCTAGGGTCCACTGAGCT
ESR1	ENSG00000256804	72	91	-	0.00039	CAGCAAGAGCTGCTTGCCTC
ESR1	ENSG00000234324	74	93	+	0.00039	GGCCCAAGCGATCCTCCCAC
ESR1	ENSG00000257727	347	366	-	0.00039	CGAACAGATCCACGTGACCA
ESR1	ENSG00000258830	345	364	-	0.00039	TGCAAGAGACATCCTGATCC
ESR1	ENSG00000136492	247	266	-	0.00039	GACTGGGGCCGCCGTTACCT
ESR1	ENSG00000256326	114	133	+	0.00039	TGGTCAGGTGGCTCAGATCT
ESR1	ENSG00000109971	167	186	-	0.0004	TGGTTAGGTGAACCAGGCAT
ESR1	ENSG00000110075	374	393	+	0.0004	GGCGCGGGGCCCCTCCACCT
ESR1	ENSG00000173457	133	152	-	0.0004	TCTACAGGCCCCTCTCCCCT
ESR1	ENSG00000119616	314	333	-	0.0004	GGCCACGGTCTGACTACCTC
ESR1	ENSG00000119682	40	59	+	0.0004	GGCCACGGTCTGACTACCTC
ESR1	ENSG00000129535	59	78	+	0.0004	GCCTTAGGACTCAAAGACCC
ESR1	ENSG00000113269	255	274	+	0.0004	CTCCCGTGCCGCCCTTCCCC
ESR1	ENSG00000255421	154	173	-	0.0004	TTAGCCGGGCATCGTGGCAC
ESR1	ENSG00000258212	159	178	-	0.0004	CCTGTGTGTGACACTGACAC
ESR1	ENSG00000134864	210	229	-	0.0004	AGCTATGGAGAGAGTGACAC
ESR1	ENSG00000138709	2	21	-	0.0004	GGCTGAGGCCGCCCCGACTG
ESR1	ENSG00000105640	336	355	-	4.00E-04	CCTGATGGGGCCCGTGCCCC
ESR1	ENSG00000196085	16	35	+	4.00E-04	ATCCTTGGGTACCTTGAACT
ESR1	ENSG00000113810	216	235	+	4.00E-04	CCTCTCGGCGAGCCCGCCCT
ESR1	ENSG00000244041	68	87	+	4.00E-04	GTGCCATTGCACTCTAGCCT
ESR1	ENSG00000169314	335	354	+	0.0004	TGGCCCTGGGACCCAGCCAT
ESR1	ENSG00000197958	223	242	-	0.0004	AGGAAGTTGCACCTTGGCCT
ESR1	ENSG00000224281	361	380	+	0.00041	CGCCCTTGACGCCCAGGCCC
ESR1	ENSG00000115267	292	311	-	0.00041	GCGCCTGGGGTCCCGGACCG
ESR1	ENSG00000220891	58	77	-	0.00041	GCTCCGGGACACCCCACCCG
ESR1	ENSG00000255909	59	78	+	0.00041	GGTGTGGGGTCCCCTGGCCT
ESR1	ENSG00000237813	110	129	+	0.00041	GGCGCAGGGAACCGTCCCCA
ESR1	ENSG00000170144	186	205	+	0.00041	GGCAAAGGCCCTCTTCCCCT
ESR1	ENSG00000199509	206	225	+	0.00041	CGGCCATACCACCCTGAACA
ESR1	ENSG00000054148	147	166	+	0.00041	CGCCCCGCGCCCCCTACCCC
ESR1	ENSG00000115211	98	117	-	0.00042	TGCCCAGGCGATTGCGTCCC
ESR1	ENSG00000155755	288	307	-	0.00042	CGCAGCGGCCTCCGGGACCT
ESR1	ENSG00000114270	59	78	-	0.00042	CTGAGAGGTCGCCGCCCCCC
ESR1	ENSG00000149735	67	86	-	0.00042	CACCTGGGGGATCTTGCTCT
ESR1	ENSG00000199545	66	85	+	0.00042	GAGCCAGGAGAGTGTGAAAT
ESR1	ENSG00000076321	366	385	+	0.00042	GGGACAGCGGACAGCGCCCC
ESR1	ENSG00000060339	246	265	-	0.00042	CCTAAGGGTTGCCTTGGCCT
ESR1	ENSG00000229951	320	339	+	0.00042	CTCCAGGTACCCCCAGACCC
ESR1	ENSG00000184979	17	36	+	0.00042	ACCTGAGACCAGCCTGGCCA
ESR1	ENSG00000181163	167	186	-	0.00042	GGGTGGGCCGACTCTGACTT

ESR1	ENSG00000253966	178	197	+	0.00042	CCCCCAGCTGACTATGCACC
ESR1	ENSG00000137642	22	41	+	0.00042	CCACCGGCGCTCGCTGCCTT
ESR1	ENSG00000249042	121	140	+	0.00042	CCTCCAGCGGATGCTGCCAT
ESR1	ENSG00000237380	238	257	-	0.00043	AGCCTGGGGCGCCGACCCCC
ESR1	ENSG00000102882	299	318	+	0.00043	GACCCATGGCCCCCGAACCT
ESR1	ENSG00000109046	62	81	-	0.00043	CAGGCTGGTTCCGCTGACTC
ESR1	ENSG00000093100	237	256	+	0.00043	GAGTCAGTCCAGGTTCACCT
ESR1	ENSG00000241343	80	99	-	0.00043	TCCTCTGGCCTCCCCGTCCC
ESR1	ENSG00000003056	127	146	+	0.00043	GCCCGAGGGCGAGCTGCCTG
ESR1	ENSG00000258653	77	96	-	0.00043	AGGCCTCGGCCCTCTGACCG
ESR1	ENSG00000233579	346	365	-	0.00043	CACCCAGGACACCCCGAAAG
ESR1	ENSG00000077097	156	175	+	0.00043	GGGGGCGGCCGCCGCGCCCT
ESR1	ENSG00000187741	186	205	-	0.00043	GCCCGAGCCCGCGCTGCCTT
ESR1	ENSG00000119684	165	184	-	0.00044	ATCCCAGGGTTCAGTGAACC
ESR1	ENSG00000196141	324	343	-	0.00044	ACACATGGGCATCGTGGGCT
ESR1	ENSG00000186352	362	381	+	0.00044	CACTCGGGACAGCCATCCCC
ESR1	ENSG00000106336	179	198	-	0.00044	AGTGCAGCTCATTCTCTCCC
ESR1	ENSG00000157657	27	46	-	0.00044	GCCCCCCGCCGCCCTGCCCG
ESR1	ENSG00000159409	270	289	-	0.00044	CCGCTGGGGCTGCCTGCTTT
ESR1	ENSG00000247853	341	360	-	0.00044	CTGCCCTGCCTCCCTGTCCA
ESR1	ENSG00000154146	77	96	+	0.00044	AAGCCAGGGGATTGCGCCCG
ESR1	ENSG00000234076	93	112	-	0.00044	GGGCGGGGCCACCACCTCCT
ESR1	ENSG00000133111	137	156	+	0.00044	GGCGCCGCGCTCCCTGACAG
ESR1	ENSG00000121067	227	246	-	0.00044	TCCCTGGGTTTCCCTGCTCC
ESR1	ENSG00000233547	209	228	+	0.00044	CAGAGAGGTCTCCCCAACAT
ESR1	ENSG00000258725	146	165	-	0.00044	TGGGGAGGTGTTCCTGCTCT
ESR1	ENSG00000240766	252	271	-	0.00044	AGTCAAGTTCTACCAGTCCT
ESR1	ENSG00000111291	63	82	-	0.00044	CCGGAAGGACAGAAAGACAC
ESR1	ENSG00000130717	257	276	-	0.00044	GCATCGGGTCCCCGCGCCCG
ESR1	ENSG00000253720	204	223	-	0.00045	GGTCCGCGGCGCCCTCACTT
ESR1	ENSG00000243916	236	255	-	0.00045	TCCCAGGGCCCCCGAGTCCT
ESR1	ENSG00000255905	299	318	-	0.00045	CCTCCTAGGCAGCCTCCCAC
ESR1	ENSG00000089159	155	174	-	0.00045	GTGCACGCGCGCCCCGCCCC
ESR1	ENSG00000247315	42	61	+	0.00045	GGCGCTGGCCAATATGCGCC
ESR1	ENSG00000155508	135	154	-	0.00045	GCGGCGGGCCGCCCTCAGCC
ESR1	ENSG00000236997	112	131	+	0.00045	TACACTGGTCAGAATGGTCT
ESR1	ENSG00000224985	77	96	+	0.00046	GCGCCTGCGCATCCACACCC
ESR1	ENSG00000227694	343	362	+	0.00046	AGCCGAAGACACTGCGACTC
ESR1	ENSG00000250900	8	27	-	0.00046	CGTGCGGGTGGCCCTGGACC
ESR1	ENSG00000204390	351	370	-	0.00046	AAGGCGGGTCTCCGTGACGA
ESR1	ENSG00000058091	67	86	+	0.00046	TCTCAGGCCCAGCATGTCCC
ESR1	ENSG00000198431	309	328	-	0.00046	CCCTCGGTCGTACCTGACCT
ESR1	ENSG00000235529	294	313	-	0.00046	ACAAAAGGTCTCCCAGCCTG
ESR1	ENSG00000185112	378	397	+	0.00046	CGGCCAGGCCAGCCCGGACA
ESR1	ENSG00000138400	127	146	+	0.00046	CAGCCATGACAGCTTCCCCG
ESR1	ENSG00000236256	293	312	-	0.00046	CCCAAATGCCATCATGAACT
ESR1	ENSG00000115415	353	372	-	0.00046	TGAAAAGGTCTCTTTTACCC
ESR1	ENSG00000167588	138	157	-	0.00046	GCCCCAGCCCAGCTTCCCAC
ESR1	ENSG00000204438	101	120	+	0.00046	TTGTCAGGTCCCTTTCACCG
ESR1	ENSG00000035115	98	117	+	0.00047	ATGCAAGGATACACTTCCCC

ESR1	ENSG00000114942	181	200	+	0.00047	CGGGAAGGACAACTTGGACC
ESR1	ENSG00000249715	72	91	+	0.00047	AGGCCCAGTCACCTATACCC
ESR1	ENSG00000207437	349	368	+	0.00047	TCCTGATGACAGTCTGCCTC
ESR1	ENSG00000250963	357	376	+	0.00047	TGCAACTGACATCCTCACCT
ESR1	ENSG00000242095	119	138	+	0.00047	GCGCCCGGCCAATCTTACTT
ESR1	ENSG00000096093	150	169	+	0.00047	ATGCCTGCGCCTCCTGGCCC
ESR1	ENSG00000101654	150	169	+	0.00047	GCGTCGCGGCACTCTCGCCT
ESR1	ENSG00000223522	346	365	+	0.00047	TGCCTGGTGCAGCCTGGTCT
ESR1	ENSG00000203466	337	356	-	0.00047	ATTCAAGACCAGCCTGATCA
ESR1	ENSG00000212496	355	374	-	0.00047	GGCGTGAGCCACCGTGCCTG
ESR1	ENSG00000137210	56	75	+	0.00047	GGCGCTAGCCGCGATGCCCC
ESR1	ENSG00000065150	122	141	+	0.00048	TAGCAGGAGCCAGCTGACCT
ESR1	ENSG00000148737	20	39	+	0.00048	CCCCCCGGCTTCCCCGCCCC
ESR1	ENSG00000244336	345	364	-	0.00048	AGCCCGGGAGATCCTGCATC
ESR1	ENSG00000138297	230	249	-	0.00049	CCTACTTCACACGCTGACCT
ESR1	ENSG00000172954	328	347	+	0.00049	GGCGTCGCGCGGCGTGCCCT
ESR1	ENSG00000178685	143	162	+	0.00049	GGGCACTCCCTCCATGACCT
ESR1	ENSG00000224884	345	364	-	0.00049	GAGCCACTGCACCCAGCCAT
ESR1	ENSG00000131508	214	233	+	0.00049	GACTCCGGCCAGCCTGAGTG
ESR1	ENSG00000164466	309	328	+	0.00049	ACCATACGCCACCATGCCCA
ESR1	ENSG00000116455	21	40	+	0.0005	CACCCGGGACAGCATGGTCA
ESR1	ENSG00000236439	201	220	+	0.0005	CGCACATGAGAACATGCCTC
ESR1	ENSG00000136044	95	114	+	0.0005	CGGGACTGGCACCCAGAGCC
ESR1	ENSG00000072310	1	20	+	0.0005	CGGCCAGAGGCCGCTGCCAT
ESR1	ENSG00000010404	2	21	-	0.0005	CGCTGCAGGCACCCTATCCC
ESR1	ENSG00000230371	54	73	-	0.0005	CGGCCTGGTGGCATTGCTCT
ESR1	ENSG00000112739	352	371	-	0.0005	CGCGGCGGCCATCTTGAACT
ESR1	ENSG00000255471	83	102	+	0.0005	GAAACTGGGCAGCCAGCCAG
ESR1	ENSG00000065970	92	111	-	0.0005	GAGCCGGGAGACGCCGAGCC
ESR1	ENSG00000071082	377	396	-	0.0005	TCCCAGGGTCACTAAGACGC
ESR1	ENSG00000213592	242	261	+	0.0005	GCCCCTGGGCCGCATCTCCT
ESR1	ENSG00000255729	319	338	-	0.00051	GCCGCTTGGCAGAGTGATCC
ESR1	ENSG00000255782	371	390	-	0.00051	TTTCAGGGAGATTCTCACCT
ESR1	ENSG00000061455	127	146	+	0.00051	TCTTCTGGCCTGCCTCCCCT
ESR1	ENSG00000059378	252	271	-	0.00051	AGCAAAGGACCCTCTCACAC
ESR1	ENSG00000166181	10	29	+	0.00051	TTCCCCGCCCACCCACACCC
ESR1	ENSG00000185567	282	301	+	0.00051	CGCGACGGGCCGCCAGGCCC
ESR1	ENSG00000233927	291	310	-	0.00051	GCTCCGTGTGTCCGGGACCC
ESR1	ENSG00000249825	349	368	+	0.00051	TGCCAAGGTGAGCATGGAAC
ESR1	ENSG00000142856	114	133	-	0.00051	GGCCCGCGGCGCCCTCCCTC
ESR1	ENSG00000052841	270	289	+	0.00051	GCTCCGGCCCAGGCTGGCTC
ESR1	ENSG00000136108	370	389	-	0.00051	CGGACTGCGCCCTCTGACTC
ESR1	ENSG00000244462	58	77	+	0.00051	CCGCCAGGGCCACTAGCCCA
ESR1	ENSG00000114544	29	48	+	0.00051	CAGCCAGGCCGCTCACACTC
ESR1	ENSG00000205268	214	233	-	0.00051	CCGCCGTGACTCCCTTCCCT
ESR1	ENSG00000258588	288	307	-	0.00052	AATCCAAGGCACCTTAAACT
ESR1	ENSG00000227051	282	301	+	0.00052	CTCGCTGCTCAGCCCGATCC
ESR1	ENSG00000170889	3	22	-	0.00052	ATTTCGGCTCACTGAGGCCC
ESR1	ENSG00000149716	89	108	+	0.00052	CAGCGCGGACAGACAGGCCC
ESR1	ENSG00000177981	356	375	-	0.00052	GAGCCACCGCACCCAGCCAC

ESR1	ENSG00000257894	46	65	+	0.00052	AAAGATGGTGACCCACCCCT
ESR1	ENSG00000166046	84	103	+	0.00052	GCCAGACGGCACAGAGCCCT
ESR1	ENSG00000113593	317	336	-	0.00052	CCTCCGGGTCCCGGCGCCTT
ESR1	ENSG00000139289	264	283	+	0.00052	AAATATGGCCATTTTGACAT
ESR1	ENSG00000184117	330	349	-	0.00052	CGGTCAGGTGGGCGTTTCCT
ESR1	ENSG00000182944	44	63	+	0.00052	CACACCCGGCCGCGTGACCC
ESR1	ENSG00000259118	340	359	+	0.00053	CCTCCAGGACACTCATACTT
ESR1	ENSG00000124444	284	303	-	0.00053	CCCCGTGGTTTCCGCGCCCT
ESR1	ENSG00000226763	59	78	-	0.00053	CCCCGTGGTTTCCGCGCCCT
ESR1	ENSG00000168484	65	84	-	0.00053	CACCCGGCGCGGTCAGCCCC
ESR1	ENSG00000224660	138	157	-	0.00053	AGCCCAGGAGTTCGAGACCA
ESR1	ENSG00000242257	140	159	+	0.00053	ATGGAATCTCACTCTGTCAC
ESR1	ENSG00000142541	307	326	-	0.00053	GCCCCTTGCCGCCCCGGCCC
ESR1	ENSG00000224623	174	193	-	0.00053	GTTTGAGACCAGCCTGGCCA
ESR1	ENSG00000207185	377	396	+	0.00053	ATCTCAGCTCACTGCACCCT
ESR1	ENSG00000123349	380	399	-	0.00053	CCGGGAGGCCTCGCTGCGCC
ESR1	ENSG00000254452	86	105	-	0.00054	TGGCTTGGTTTCTGTGTCCT
ESR1	ENSG00000245750	299	318	-	0.00054	GGATCTGGTGCTCGAGACCT
ESR1	ENSG00000114391	15	34	+	0.00054	AGACAGAGACAGAATGACTC
ESR1	ENSG00000242683	244	263	+	0.00054	GGGCGTGGTGGCTCTCGCCT
ESR1	ENSG00000164543	42	61	-	0.00054	GGGTGATGAGATCCTGATCT
ESR1	ENSG00000258232	159	178	-	0.00054	TTTAAATGTCGAGCTGACTT
ESR1	ENSG00000073910	249	268	+	0.00054	GGCCGGAGGCTGCCTGCACC
ESR1	ENSG00000178878	212	231	-	0.00054	CGCCCCGCGCACCCCCGCCT
ESR1	ENSG00000229127	203	222	-	0.00054	AACCTAGGAGACAATGGCCA
ESR1	ENSG00000174748	179	198	+	0.00054	ATCCCTGGGCGCTGGGGCCT
ESR1	ENSG00000139624	324	343	+	0.00054	GCCCTGGGGCCGCCTCCCCG
ESR1	ENSG00000255692	299	318	-	0.00054	CTGAAATGCCGTCGTGGCCC
ESR1	ENSG00000232739	227	246	+	0.00055	GGACCAGTGCTACCCGGCCT
ESR1	ENSG00000237827	134	153	-	0.00055	CACTCAGATTACTCTCACTT
ESR1	ENSG00000010361	64	83	-	0.00055	TTCCAAGTTGAGGACGACCT
ESR1	ENSG00000093009	163	182	-	0.00055	TCGTAAGGACAATGGGCCCT
ESR1	ENSG00000224424	188	207	-	0.00055	CCGCCGGGGCTCACGGAGCT
ESR1	ENSG00000233885	174	193	+	0.00055	ATCCACTGACAGCCTCACTC
ESR1	ENSG00000087470	221	240	-	0.00055	GCCCGCCGGCTACCTGCCCC
ESR1	ENSG00000174527	263	282	+	0.00055	AATCCAAGGTAATGTGACTT
ESR1	ENSG00000100442	109	128	-	0.00055	GGACCAGACCACGTTCACTT
ESR1	ENSG00000196542	299	318	+	0.00055	CGCCACTCTCAGCAAGCCCT
ESR1	ENSG00000133027	1	20	+	0.00056	ATCCAAGGGGATACTGCTAC
ESR1	ENSG00000148634	97	116	+	0.00056	GCCTGTGGCCAGCCACCCCC
ESR1	ENSG00000167100	291	310	+	0.00056	CCGTCAGGTCTCCTGGTCCA
ESR1	ENSG00000256885	198	217	+	0.00056	CTCCTGGGCTACAGTGATCC
ESR1	ENSG00000111249	241	260	-	0.00056	GCCGCCGGCCGCCCGGGCCC
ESR1	ENSG00000183273	85	104	+	0.00056	GTTCACGACCCCCATGACCC
ESR1	ENSG00000089775	42	61	+	0.00056	AGCCTCGGGCTCCGGGACAC
ESR1	ENSG00000198189	16	35	-	0.00056	CTCGCCTGTGATCCTGGCAC
ESR1	ENSG00000249494	300	319	-	0.00056	GTTAGATGACGCCCTAACCT
ESR1	ENSG00000104549	8	27	+	0.00056	CGCGCAGGTTGCGCCGCCTC
ESR1	ENSG00000201207	62	81	-	0.00056	ATTTCAGCTCACTGCAACCT
ESR1	ENSG00000257918	193	212	-	0.00057	TCCCCTGAGTACACTGGCCT

ESR1	ENSG00000254909	150	169	-	0.00057	TTGCTCTGTCACCCAGACTG
ESR1	ENSG00000226769	295	314	+	0.00057	TCCTCCATTGACCTTGACCT
ESR1	ENSG00000001631	52	71	+	0.00057	CGGGAAGCGCTGCGTGAGCC
ESR1	ENSG00000257755	6	25	-	0.00057	TGCCCAGGCCTGATTCACAC
ESR1	ENSG00000256029	133	152	-	0.00058	CTGTAAGCGCCCTGTGGCCT
ESR1	ENSG00000174579	340	359	-	0.00058	GTCAGAGGGCTCTAAGGCCC
ESR1	ENSG00000159082	125	144	-	0.00058	GACCACGCCCACTCTGCGCC
ESR1	ENSG00000162458	230	249	-	0.00058	AGCTCGGGTGTCGATGTCAC
ESR1	ENSG00000204856	2	21	+	0.00058	GCCCGCGGGGCCCATGACCA
ESR1	ENSG00000232021	213	232	+	0.00058	GGGCAGCGGCCCGCTCACCT
ESR1	ENSG00000197375	75	94	+	0.00058	TCGCCAGGTCCCCAGGACAG
ESR1	ENSG00000102401	335	354	+	0.00059	GCCCCAGGGGAAGATGCCGT
ESR1	ENSG00000256329	194	213	+	0.00059	AGCCCAGGGACCTTTGGCCT
ESR1	ENSG00000110108	204	223	+	0.00059	GCTCTAGAACTACATGACCC
ESR1	ENSG00000115419	45	64	+	0.00059	CTCTCCGCGCACCCAGAGCC
ESR1	ENSG00000236810	155	174	-	0.00059	ACGTCAGTTCCGCTCGACCC
ESR1	ENSG00000240695	103	122	+	0.00059	GTTGGAGACCAGCCTGGCCA
ESR1	ENSG00000230005	2	21	+	0.0006	CAGCAAAGCCACCCTGCTTG
ESR1	ENSG00000167552	27	46	-	0.0006	GGAAAATGACTGCCAGCCCC
ESR1	ENSG00000252412	88	107	-	0.0006	TGCCAGGGTCACTGGGTGCT
ESR1	ENSG00000257076	26	45	-	0.0006	GTGGCCAGGCACAGTGGCTC
ESR1	ENSG00000143256	90	109	-	0.0006	GGCCGCGGTGAATCCCACCT
ESR1	ENSG00000176973	273	292	-	0.0006	GAGAAAAGGCAACGGGACAT
ESR1	ENSG00000232633	309	328	-	0.0006	AAGGCTGGAGAATCTGCCTC
ESR1	ENSG00000214753	165	184	+	6.00E-04	TGTTTTGGGCTCCGTGAGCC
ESR1	ENSG00000224356	132	151	+	6.00E-04	TTGTTCTGTCAGCCTCACTT
ESR1	ENSG00000239688	251	270	+	6.00E-04	GTAAGAGGACCGCCTGAGCC
ESR1	ENSG00000245521	201	220	+	0.0006	AGCCCAGGACGCTAGGCCTT
ESR1	ENSG00000241762	283	302	+	0.0006	ACGTCATTTCATCTTCACCC
ESR1	ENSG00000053747	358	377	-	0.00061	CGCCTGCGCCTCCCGGACCT
ESR1	ENSG00000220378	12	31	-	0.00061	ATCTCGGCTCACTGCAACCT
ESR1	ENSG00000168092	201	220	-	0.00061	ACTTCCGGTTCCCCTGCCAC
ESR1	ENSG00000139719	193	212	-	0.00061	ACGGCAGCGCACGCCAACCC
ESR1	ENSG00000256861	95	114	-	0.00061	ACGGCAGCGCACGCCAACCC
ESR1	ENSG00000257337	93	112	+	0.00061	GCCCCCTGGCGGCCTCGCCT
ESR1	ENSG00000121749	379	398	-	0.00061	GTCCCTCGTGTCCCTCCCCC
ESR1	ENSG00000226963	371	390	-	0.00061	CTCACGGTGCACCCCGTCTC
ESR1	ENSG00000249310	38	57	+	0.00061	CTGTGATCTCGCCCTGCCTC
ESR1	ENSG00000013810	83	102	-	0.00061	GGCTCCGCCCTCCCTCCCCC
ESR1	ENSG00000234141	107	126	+	0.00061	GCGTAAGCTCAGTGTGATTC
ESR1	ENSG00000254088	194	213	+	0.00061	ACAGAAGGTCACCCCAGCTC
ESR1	ENSG00000215217	37	56	+	0.00062	ACACGTGGCCACCGAGAGCT
ESR1	ENSG00000242180	369	388	+	0.00062	TGGCAATGGCACCCTCCTTC
ESR1	ENSG00000242219	114	133	-	0.00062	GGCTCATGCGATCCTCCCAT
ESR1	ENSG00000250068	210	229	+	0.00063	GTGGATGGCGAGTAAGACCT
ESR1	ENSG00000180815	105	124	+	0.00063	GTGCCGGGACCGCCTGCGCG
ESR1	ENSG00000135473	79	98	+	0.00063	CCACCGGCGCCCCGTAACCT
ESR1	ENSG00000250656	287	306	+	0.00063	CGCCATGGTGGCCACCACCT
ESR1	ENSG00000225839	261	280	+	0.00063	GAGGCCAGGCACAGTGGCTC
ESR1	ENSG00000234233	292	311	-	0.00064	TTCGAAGGTGAGCCTTAACT

ESR1	ENSG00000173113	48	67	+	0.00064	CGCACACGCCAGCTAGTCCC
ESR1	ENSG00000128645	227	246	-	0.00064	CGGCCACGTGGCGCTGGCCG
ESR1	ENSG00000159884	155	174	-	0.00064	CGGGGAGGCCACGCCCACTC
ESR1	ENSG00000256349	376	395	+	0.00064	AAGATGTGTGGCCTTGCCCC
ESR1	ENSG00000094880	271	290	+	0.00064	GCGGCAGTGGCGCCTGTCCT
ESR1	ENSG00000133872	191	210	+	0.00064	GGCCCCGCCCACACCGCCTC
ESR1	ENSG00000140416	56	75	-	0.00065	GCGGCCGGAGAGGCCGCCCT
ESR1	ENSG00000110446	20	39	+	0.00065	AGGCTTGTTGAAAGTGCCCC
ESR1	ENSG00000089737	182	201	+	0.00065	GGGGCGGGACTTCCTCCCCA
ESR1	ENSG00000223916	173	192	-	0.00065	CTCCGCGCTCACCGCCACCC
ESR1	ENSG00000214188	11	30	+	0.00065	GGCCCGCGGCGCCCACCCCT
ESR1	ENSG00000166839	294	313	+	0.00065	GGCCGAGGCCGAGAGGACCC
ESR1	ENSG00000174374	285	304	-	0.00066	CGACAGGCTCACTGCAACCT
ESR1	ENSG00000186298	287	306	-	0.00066	CCCCCCTGCCACCCCGCTCC
ESR1	ENSG00000090006	380	399	+	0.00066	GATCCTGGACTATCCGCCCT
ESR1	ENSG00000152580	105	124	+	0.00066	AAAGAAGGTCTCCCAGATTC
ESR1	ENSG00000120306	137	156	+	0.00066	AGGACAGAAGATTCTGTCCC
ESR1	ENSG00000250234	359	378	-	0.00066	GACCCCTCTGGGCCTGCCCC
ESR1	ENSG00000183495	369	388	-	0.00066	CCGGCCGGCGAGCGGGCCCT
ESR1	ENSG00000175416	27	46	+	0.00066	AGCCCAGGTGTCCTCGACGC
ESR1	ENSG00000218186	338	357	-	0.00066	TGCCCAGGCCACCTTGGAAG
ESR1	ENSG00000197620	103	122	+	0.00066	GCCCCGCCTCTCCCAGCCCC
ESR1	ENSG00000100099	40	59	+	0.00066	CCCCCGGGGCGCCGCCTCCC
ESR1	ENSG00000162623	62	81	-	0.00067	GGAGAAGGTGTGGCAGTCCT
ESR1	ENSG00000229117	96	115	+	0.00067	GAACTAACTCAACCTACCCT
ESR1	ENSG00000227528	160	179	-	0.00067	GGAGGAAGTCAGCATGAGTC
ESR1	ENSG00000238862	2	21	-	0.00067	GCGGCCAGGCACGGTGGCTC
ESR1	ENSG00000119608	40	59	-	0.00067	ATGCCAGGGCTCATGAACCT
ESR1	ENSG00000182177	115	134	-	0.00067	TGCGGAGGGCCACCTGCCAG
ESR1	ENSG00000125991	379	398	-	0.00067	CCTCCACGCGACCCCGGCCC
ESR1	ENSG00000114302	259	278	-	0.00067	TACCACGGCCGACCTGGCAC
ESR1	ENSG00000235105	238	257	+	0.00067	AAGATGAATCACTCAGACCT
ESR1	ENSG00000118263	167	186	-	0.00067	GCCAATTGTTTGCTTGACCT
ESR1	ENSG00000232073	86	105	-	0.00067	TCTCAAGGACACTCAAGCCT
ESR1	ENSG00000254208	317	336	-	0.00067	GGTAACGGGCGCTTTGCCCG
ESR1	ENSG00000225951	361	380	+	0.00068	GGCTTGCCTCACAATGCCCT
ESR1	ENSG00000248168	74	93	+	0.00068	AGGGCAGCTGACAGCGGCCC
ESR1	ENSG00000171121	376	395	-	0.00068	CAGCGGGAGCCCCCAGCCCC
ESR1	ENSG00000189337	169	188	-	0.00068	CAAGAAGGACACCGCGCGCC
ESR1	ENSG00000241853	231	250	+	0.00068	AAGAAGGGCTATTCTGCCAT
ESR1	ENSG00000250641	28	47	+	0.00068	AGTGGTGGTCACTTTATCCC
ESR1	ENSG00000254633	122	141	-	0.00068	TGCAGGACTCTGCCTGCCCC
ESR1	ENSG00000162889	316	335	+	0.00068	CCCACGGAGCCCCGCGACCC
ESR1	ENSG00000234264	295	314	-	0.00068	AACCCTTGCCAGACTCACCG
ESR1	ENSG00000249007	39	58	+	0.00068	CACCCTGGCCTCTGTTCCCC
ESR1	ENSG00000254400	361	380	-	0.00068	AATCCAGGGGACTCGGCGCC
ESR1	ENSG00000228604	119	138	+	0.00068	AAATCAGATCATCTTCACTT
ESR1	ENSG00000163900	99	118	-	0.00068	GACTCCGCCCTCTCTGTCCT
ESR1	ENSG00000149380	154	173	-	0.00069	CGCCCCTGTCTCCGCCCCCT
ESR1	ENSG00000226677	364	383	+	0.00069	ATGTTATCGCAGCTTGACTT

ESR1	ENSG00000254140	100	119	+	0.00069	TTTCCCAGGCAACGGGACCC
ESR1	ENSG00000258395	320	339	-	0.00069	GTACAAAGACACGCGGACTC
ESR1	ENSG00000160712	195	214	-	0.00069	AACAGGGGACCGCCAGCCCC
ESR1	ENSG00000078140	378	397	-	0.00069	TCCCTCGGCGATTCAGACCT
ESR1	ENSG00000141219	29	48	+	0.00069	GGAAAGGGGGTCCCTTCCCT
ESR1	ENSG00000138433	15	34	-	0.00069	GGCGCGGCACTGCTTGACCG
ESR1	ENSG00000227617	132	151	-	0.00069	GAGCCACCACACCCGGCCCC
ESR1	ENSG00000171604	223	242	+	0.00069	GAGGAAGGTCGGCCTTGCAC
ESR1	ENSG00000105793	248	267	+	0.00069	CTTTGGGTTCATACTGCCTT
ESR1	ENSG00000230424	252	271	-	0.0007	CCCCAGACTCACCTTTACCC
ESR1	ENSG00000236404	307	326	-	0.0007	GTGCCAGGCTACTGAGTCAC
ESR1	ENSG00000155744	353	372	-	0.0007	TTTCCAGACCACCCTCGCCA
ESR1	ENSG00000127080	368	387	+	0.0007	CTGACAGGCGCTCCTCCCCC
ESR1	ENSG00000171401	303	322	+	0.00071	GGCCCAGGCCAAGCAAGCTT
ESR1	ENSG00000258974	271	290	-	0.00071	GTCCATGGCCACGTTGCTCA
ESR1	ENSG00000140525	289	308	-	0.00071	CTCTGCAGTCACCTCGGCCT
ESR1	ENSG00000135631	128	147	-	0.00071	AACCGAGGGCGCCCTCTGCT
ESR1	ENSG00000224189	285	304	-	0.00071	CGACGTGCTCAGCTTGGCAC
ESR1	ENSG00000187747	380	399	+	0.00071	AGGCAATGGCATCCTAATTT
ESR1	ENSG00000162643	316	335	-	0.00072	ACCTCAGGTCCTACTGAATC
ESR1	ENSG00000163661	234	253	+	0.00072	TATTAAGGACTCTCTGCTCC
ESR1	ENSG00000257529	12	31	-	0.00072	TGGTCCACTCACCCCGACTT
ESR1	ENSG00000177119	121	140	+	0.00072	TGCTCAGGGAACCCAGTCCA
ESR1	ENSG00000204264	279	298	-	0.00072	CACCCACAAGAGCGTGCCCT
ESR1	ENSG00000232371	22	41	+	0.00072	GGCGTGAGCCACCATGCCTG
ESR1	ENSG00000135317	160	179	-	0.00073	CCTGAGGGGCAACCGGAGCT
ESR1	ENSG00000133316	375	394	+	0.00073	GGAACGGTGCACTCTCCCTT
ESR1	ENSG00000254876	16	35	-	0.00073	GGACCCGCGCTCCCAGTCCC
ESR1	ENSG00000103550	227	246	-	0.00073	AGCCAGCTCCGCCGTGACCC
ESR1	ENSG00000167085	233	252	-	0.00074	ACCTGCTTCCACTCTGACCT
ESR1	ENSG00000198496	308	327	+	0.00074	AGAAGAGGTCCCAATCCCCC
ESR1	ENSG00000142669	204	223	-	0.00074	CTCAGATGTCCCCCTGGTCC
ESR1	ENSG00000167553	147	166	-	0.00074	GGCCGCGGGCAGCCCGTCTG
ESR1	ENSG00000250317	347	366	+	0.00074	TGCAAATTGCAAACTGACAT
ESR1	ENSG00000182575	201	220	+	0.00075	CGCGCAGGTCCCCAGCACAT
ESR1	ENSG00000242247	64	83	-	0.00075	GCAGAAGGTGCCTCTGTCAC
ESR1	ENSG00000204310	31	50	-	0.00075	TTGGCATTGCACATTGACTT
ESR1	ENSG00000254673	246	265	+	0.00075	GGCCACGTGCAGCCGGCCAC
ESR1	ENSG00000133193	156	175	-	0.00075	TGTTCAGCCCAGCGTCACAC
ESR1	ENSG00000238567	124	143	+	0.00075	GTTCCAGGCTGCAGTGAGCT
ESR1	ENSG00000100154	87	106	+	0.00075	GGCGGGGGTGGGCGAGACAC
ESR1	ENSG00000235897	102	121	+	0.00075	TCTCCAGGGCAACAGGGCCG
ESR1	ENSG00000164180	55	74	+	0.00075	CATACAGGTGTCCAGGACCG
ESR1	ENSG00000198804	319	338	+	0.00075	GAGCTGGGCCAGCCAGGCAA
ESR1	ENSG00000143164	234	253	-	0.00075	GCCGCCGGTGCCCGAGGCCT
ESR1	ENSG00000247708	305	324	+	0.00075	CGGAGAGCTCAGCGAGCTCT
ESR1	ENSG00000226059	153	172	-	0.00075	AGCGCAGGGCACAATGCATG
ESR1	ENSG00000235848	303	322	-	0.00076	CGCCAAAGTTTCAATGCCAT
ESR1	ENSG00000224502	250	269	+	0.00076	GTCCGAGGTCACACAGCGTG
ESR1	ENSG00000202314	241	260	-	0.00076	GGCCATTTTCATTCAGCCCC

ESR1	ENSG00000229759	350	369	+	0.00076	AGGCCGTATCACAGCGACTC
ESR1	ENSG00000112182	106	125	+	0.00076	CGCCGGGCGTACCGCGCCCC
ESR1	ENSG00000185684	279	298	-	0.00077	AGCCAAGGGCTCCCGGCGCG
ESR1	ENSG00000105877	313	332	-	0.00077	TCCACAGCGCCCACTGCCTC
ESR1	ENSG00000152778	50	69	-	0.00077	GCAGCTGGGCTCCTTCACTT
ESR1	ENSG00000242251	267	286	+	0.00077	GGCCCAGGAGTTCCAGACTA
ESR1	ENSG00000213741	310	329	-	0.00077	CAGACAGTTCTAAGTGCCTT
ESR1	ENSG00000214283	243	262	+	0.00077	CAGTTTGGCGACTCTGACAG
ESR1	ENSG00000224020	146	165	-	0.00077	TGCTCAGCTCGCATTGAACT
ESR1	ENSG00000226784	380	399	+	0.00078	GAAGAGAGTGATCCGGACCC
ESR1	ENSG00000223998	127	146	-	0.00078	GTTCGAGACCAGGCTGGCCA
ESR1	ENSG00000079337	4	23	-	0.00078	AGTTAAGCACACCCTGTCTA
ESR1	ENSG00000197728	49	68	-	0.00078	CCCCCCTTCCCCCCTGCCCC
ESR1	ENSG00000145741	4	23	+	0.00078	AGGACCGCGCTCTCCGACCC
ESR1	ENSG00000234084	298	317	-	0.00078	CCAAAAAGTCTCCTTGCTCT
ESR1	ENSG00000055609	75	94	+	0.00078	ACCCCGGGGGCCGGCGCCCC
ESR1	ENSG00000111237	372	391	-	0.00079	GGGCCCTGACGCCGAGGCCT
ESR1	ENSG00000010256	59	78	+	0.00079	GTTTGATATCAGCCTGGCCA
ESR1	ENSG00000219790	171	190	-	0.00079	AGCAAGGGCCATTCTCAGCC
ESR1	ENSG00000257534	194	213	+	0.00079	CAGACAGGGCTCTCCCTCCT
ESR1	ENSG00000138768	362	381	+	0.00079	AGGGCGGGGGAAGTTGTCTT
ESR1	ENSG00000169239	44	63	-	0.00079	AACCAGGTCCACGCTCTCCC
ESR1	ENSG00000171302	339	358	+	0.0008	AGCCAAGCCCAGCCAAGCCC
ESR1	ENSG00000183684	70	89	+	0.0008	TCCCCGCCTCACCCCGTCCC
ESR1	ENSG00000257355	362	381	-	0.0008	CCGCATGCTCACCATTTCCT
ESR1	ENSG00000152056	222	241	-	0.0008	CTGCCGCGCGAGTGTGTCCT
ESR1	ENSG00000240596	190	209	-	0.0008	CCTCCAGCCCTTTCTGCCAT
ESR1	ENSG00000215695	330	349	+	0.00081	GACTCAGATCGCATTGAACC
ESR1	ENSG00000012822	249	268	-	0.00081	AGCAAAGGACTTCAAGGCCC
ESR1	ENSG00000113068	38	57	-	0.00081	CGGTCAGGTCTGGCTTGCTC
ESR1	ENSG00000225251	178	197	+	0.00081	GATGCAGGTCTCTGTTCCAC
ESR1	ENSG00000207601	74	93	+	0.00081	ATCGCAGGACTACAAGTCCC
ESR1	ENSG00000207110	36	55	+	0.00081	CTTCAAGGATCCCCTGTCAT
ESR1	ENSG00000178796	17	36	+	0.00081	TCTAGAGGTGTGTCTGCCTC
ESR1	ENSG00000243364	265	284	-	0.00081	GGTCCGGTTTGGTCTGGCCT
ESR1	ENSG00000173451	123	142	+	0.00081	TACACTCGTCTCACAGACCT
ESR1	ENSG00000239607	208	227	-	0.00082	GGCATGCGCCACCACGCCCC
ESR1	ENSG00000121578	306	325	-	0.00082	GAGGCTGGTCCGCCCGGCTC
ESR1	ENSG00000127837	117	136	-	0.00082	GCCCCACCTGACTCCGCCCC
ESR1	ENSG00000127838	131	150	+	0.00082	GCCCCACCTGACTCCGCCCC
ESR1	ENSG00000183531	267	286	+	0.00082	CCCCTAGGTGAGCTAAACAC
ESR1	ENSG00000175455	357	376	+	0.00082	CTGGCGGGTCCTCGTCCCCG
ESR1	ENSG00000129484	197	216	+	0.00083	CCGCCTAGTGACACTGGGCC
ESR1	ENSG00000215424	58	77	-	0.00083	AGCCCCGCCCCTCATGCCCC
ESR1	ENSG00000108094	160	179	+	0.00083	GAAGCTTGGCTCCCTGCGCT
ESR1	ENSG00000219545	89	108	-	0.00083	TTCCGGACTCATCCAGCCCC
ESR1	ENSG00000244307	68	87	-	0.00083	GCAGCTTGTCTGCTTGCCTT
ESR1	ENSG00000124302	315	334	-	0.00083	GGCGCGGGGCGGCGTTCCTC
ESR1	ENSG00000128590	241	260	-	0.00083	GAGGAGGGCCGCCCTGCATC
ESR1	ENSG00000238300	281	300	+	0.00083	CAGCTAGGACTGAGTGTCTC

ESR1	ENSG00000243156	147	166	+	0.00084	GCGCCCGCTCGCGTTGCCAC
ESR1	ENSG00000134982	175	194	-	0.00084	GTGAGAGGTGTTGCTGGCTT
ESR1	ENSG00000073614	268	287	-	0.00084	GACGCCTGTGTGTCTGGCCT
ESR1	ENSG00000087111	83	102	-	0.00084	CTCTTAGGGTGCCCTCTCCT
ESR1	ENSG00000172543	332	351	+	0.00084	AGGTAAGTGCTCCCAAACCC
ESR1	ENSG00000196357	237	256	+	0.00084	AGACACGCGCACGCAGACAC
ESR1	ENSG00000168386	285	304	-	0.00084	GCTGCAGGATGAGGTGACCC
ESR1	ENSG00000232398	239	258	-	0.00084	GTGGAAGGCTAGCTTGCCAG
ESR1	ENSG00000106682	68	87	-	0.00085	CTGCCCGGCCTACGCGGCCC
ESR1	ENSG00000248772	311	330	+	0.00085	CCCCAAACCCAGACTGATCT
ESR1	ENSG00000253256	47	66	-	0.00086	GGCGCCTGTCACAGTGCGCG
ESR1	ENSG00000230534	85	104	+	0.00086	GGAGACGGCGAGCCCGACCG
ESR1	ENSG00000072210	303	322	-	0.00086	TTCCCTGGAGAGCTAGTCCC
ESR1	ENSG00000120738	59	78	+	0.00086	ACTCCGGGTCCTCCCGGCCG
ESR1	ENSG00000162244	83	102	-	0.00087	CGCCCCCTTCAGGCTGCCTC
ESR1	ENSG00000215472	25	44	-	0.00087	CACCAAGGGCTTGCTTTCCC
ESR1	ENSG00000249755	224	243	-	0.00087	AAGACAGGACATACTTCCAT
ESR1	ENSG00000111837	42	61	+	0.00087	AGCTCAGCCGACAGTCCCCC
ESR1	ENSG00000119711	361	380	+	0.00088	GTGCCAAGGCACCATGAAGC
ESR1	ENSG00000147316	340	359	-	0.00088	CGACGAGGGGTGCCGGTCCT
ESR1	ENSG00000172534	115	134	+	0.00089	CGGTGACGTCACCCGGCTCC
ESR1	ENSG00000251357	358	377	+	0.00089	CTGCAGGTTCAAACTGAGCA
ESR1	ENSG00000140323	33	52	-	0.0009	CCGCCAGGCCAGAGAGCCGC
ESR1	ENSG00000228093	111	130	+	0.0009	CCACCTGCTGATGCTGCCAT
ESR1	ENSG00000258813	284	303	-	9.00E-04	GAATTTTGCCATCCTGCCTC
ESR1	ENSG00000234913	357	376	-	9.00E-04	GGCGTGAGCCACCGCGCCCG
ESR1	ENSG00000109475	166	185	+	9.00E-04	TGCGCAATTCTATTTGACCT
ESR1	ENSG00000222750	139	158	+	0.00091	GATGGAGGAGGTTCTGCCCC
ESR1	ENSG00000219433	142	161	-	0.00091	GGCCAAGGCAAGCAACACCT
ESR1	ENSG00000231792	3	22	-	0.00091	GGCCTGAGCCGCAGTGCCCG
ESR1	ENSG00000176532	358	377	-	0.00092	GAGAGATGGGACCCTGGCTG
ESR1	ENSG00000155962	280	299	+	0.00092	GCTCCAGGTCTGACTCAGTC
ESR1	ENSG00000224437	234	253	-	0.00092	GAACAAGGCCACCCGCACTG
ESR1	ENSG00000227973	281	300	-	0.00092	CACCTTTGGGACCTTGAGCC
ESR1	ENSG00000115204	191	210	+	0.00093	CTGCAGACTCACAGTGACTA
ESR1	ENSG00000105397	18	37	+	0.00093	GGATCCGGCCGCGTTGCCCA
ESR1	ENSG00000240758	121	140	-	0.00093	GAGCAACGCCGCCCAGCCTC
ESR1	ENSG00000213865	103	122	-	0.00093	AAATGTGGTCTCTCAGACTC
ESR1	ENSG00000214014	65	84	+	0.00094	CTCTCATTTCCCCCAGACTT
ESR1	ENSG00000139974	207	226	-	0.00095	GGAGCGAGTCGACTTGATCT
ESR1	ENSG00000164621	162	181	+	0.00095	TGAGAAGGTTAATCTAACTT
ESR1	ENSG00000113621	206	225	-	0.00095	ACATCTGGCAACCCTAACCC
ESR1	ENSG00000172209	225	244	+	0.00095	GCGACAAGGTAGGCTGTCAT
ESR1	ENSG00000127423	83	102	+	0.00096	AGCGAAGGGGGCCAGGGCCT
ESR1	ENSG00000163468	230	249	-	0.00096	CTTCCAGATCACCTTCATAC
ESR1	ENSG00000111644	197	216	+	0.00096	GCCCGCGTGCGCCCCGCCCC
ESR1	ENSG00000187514	275	294	+	0.00097	GCGCAAGCTCTGCTGGACTT
ESR1	ENSG00000253174	36	55	-	0.00097	AAGACAGCTCTTCCTGAGAC
ESR1	ENSG00000130222	297	316	+	0.00097	GGTTGATCGCACTATGACTC
ESR1	ENSG00000168769	363	382	+	0.00097	GAGCGCGGGCAACGGGATCT

ESR1	ENSG00000005007	278	297	-	0.00098	CGCCGCTGCCGCCGAGCCCC
ESR1	ENSG00000236830	49	68	-	0.00098	AGCCCAGCCCGTCGAGGCCC
ESR1	ENSG00000233830	359	378	-	0.00098	CATCTATGTCGCCCCGAACC
ESR1	ENSG00000172375	219	238	-	0.00098	GGGCCCTTTAAGCTTGACCT
ESR1	ENSG00000177721	372	391	+	0.00098	GGCCCAGGCCGGTCTCAGCA
ESR1	ENSG00000253518	42	61	+	0.00098	TGCCAATACCACATTGCCTT
ESR1	ENSG00000257446	203	222	+	0.00099	GCGCTCGGGGGTTCTGTCCT
ESR1	ENSG00000164924	41	60	+	0.00099	TTTGCAGGTCATCCAAGCAC
ESR1	ENSG00000171863	196	215	+	0.001	TTCCTGGGACTCTCTAGCCT