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Prosaposin activates the androgen receptor and potentiates resistance to endocrine treatment in breast cancer.

AUTHOR(S)

Azlena Ali, Laura Creevey, Yuan Hao, Damian McCartan, Peadar O'Gaora, Arnold DK Hill, Leonie Young, Marie McIlroy

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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