

Putative AREs in Autophagy related genes

ATG2A								
Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
7 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	850	868	859	(+)	0.841	0	agg tg g c acc c T GT T c taa
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	850	868	859	(+)	0.904	0	agg tg g c acc c t GT T c taa
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	850	868	859	(+)	0.896	0	agg tg g c acc c t GT T c taa
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5484	5502	5493	(+)	0.887	0	cc ag at c cc cc T GT T c cc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5484	5502	5493	(+)	0.907	0	cc ag at c cc c c t T GT T c cc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5484	5502	5493	(+)	0.926	0	cc ag at c cc c c t T GT T c cc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5484	5502	5493	(+)	0.872	0	cc ag at c cc c c t T GT T c cc
ATG2B								
Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
13 putative AREs								
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2785	2803	2794	(+)	0.873	0	t tt ca ca acca GT T c gt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3534	3552	3543	(+)	0.805	0	ca tg g ca tcc T GT T c ta c
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5870	5888	5879	(-)	0.876	0	tg c act c at a t GT T c tg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	6202	6220	6211	(-)	0.895	0	tt c at t ca tt a GT T C ct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7962	7980	7971	(+)	0.904	0	ct cact ct tg a t GT T c c t
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8012	8030	8021	(+)	0.820	0	g tt g ca ct tg c GT T ccc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	8012	8030	8021	(+)	0.947	0	g tt g ca ct tg c GT T ccc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	8012	8030	8021	(+)	0.915	0	g tt g ca ct tg c GT T ccc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	8012	8030	8021	(+)	0.930	0	g tt g ca ct tg c GT T ccc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8328	8346	8337	(-)	0.813	0	g tg cc a ag ca c T GT T c ta g
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8595	8613	8604	(-)	0.871	0	ca ag g ag tt a T GT T c taa
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	8595	8613	8604	(-)	0.886	0	ca ag g ag tt at T GT T c taa
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9160	9178	9169	(-)	0.841	0	ct gg g tg cg gg T GT T c ta t

ATG3

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
14 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	179	197	188	(+)	0.802	0	ttcaccatac TGTT ctca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	179	197	188	(+)	0.915	0	ttcaccatact GTT Ctca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	179	197	188	(+)	0.902	0	ttcaccatact GTT Ctca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2614	2632	2623	(+)	0.882	0	atgatacaaaat GTT Cctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	2614	2632	2623	(+)	0.909	0	atgatacaaaat GTT Cctt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2624	2642	2633	(+)	0.906	1	atgttcctcca GTT Ctaa
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3703	3721	3712	(-)	0.912	0	gtggaagaaag TGTT ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3703	3721	3712	(-)	0.902	0	gtggaagaaagt GTT Ctgg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	3703	3721	3712	(-)	0.855	0	gtggaagaaagt GTT Ctgg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6618	6636	6627	(+)	0.836	0	aatcagcgaag TGTT ctct
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7013	7031	7022	(+)	0.815	0	agactccattt TGTT ctgc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7013	7031	7022	(+)	0.901	0	agactccatttt GTT Ctgc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7013	7031	7022	(+)	0.891	0	agactccatttt GTT Ctgc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9845	9863	9854	(-)	0.816	0	atcgtggtttt TGTT ctgc

ATG4A

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
12 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	407	425	416	(-)	0.900	0	ggagtg cc ttt TGTT ctaa
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	407	425	416	(-)	0.928	0	ggagtg cc ttt GTT Ctaa
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	407	425	416	(-)	0.915	0	ggagtg cc ttt GTT Ctaa
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	407	425	416	(-)	0.856	0	ggag tg cc ttt GTT Ctaa
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2358	2376	2367	(+)	0.810	0	taatt tc ttt TGTT ctac
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2358	2376	2367	(+)	0.920	0	taatt tc ttt GTT Ctac
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2358	2376	2367	(+)	0.877	0	taatt tc ttt GTT Ctac
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2947	2965	2956	(-)	0.803	0	aacaag ct ag t TGTT ctgc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2947	2965	2956	(-)	0.902	0	aacaag ct ag t GTT Ctgc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2947	2965	2956	(-)	0.878	0	aacaag ct ag t GTT Ctgc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3094	3112	3103	(-)	0.819	0	act gt gag a TGTT ctac
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	4485	4503	4494	(-)	0.895	0	cttga acc agaa GTT Cgtg

ATG4B

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
8 putative AREs								
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2714	2732	2723	(-)	0.903	0	ttttt ct gta GTT Ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3353	3371	3362	(-)	0.876	0	cgggt ca agca GTT Ctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	4869	4887	4878	(-)	0.801	0	gag gt ctt tc TGTT cacg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	4869	4887	4878	(-)	0.913	0	gag gt ctt ct GTT Cacg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6613	6631	6622	(-)	0.902	0	cag g tagaaga TGTT cttt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	6613	6631	6622	(-)	0.899	0	cag g tagaagat GTT Cttt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	6613	6631	6622	(-)	0.854	0	cag g tagaagat GTT Cttt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7185	7203	7194	(-)	0.855	0	ggg ttc actct GTT Cccc

ATG4C

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
10 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	113	131	122	(+)	0.811	0	tacttccatata TGTT ctca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	113	131	122	(+)	0.906	0	tacttccatatt GTT Ctca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	113	131	122	(+)	0.898	0	tacttccatatt GTT Ctca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	826	844	835	(+)	0.821	0	tgtattcatga TGTT ctgg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	826	844	835	(+)	0.934	0	tgtattcatgat GTT Ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	826	844	835	(+)	0.901	0	tgtattcatgat GTT Ctgg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7502	7520	7511	(+)	0.887	0	agaggagagaa TGTT ctgt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7502	7520	7511	(+)	0.904	0	agaggagagaat GTT Ctgt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7502	7520	7511	(+)	0.856	0	agaggagagaat GTT Ctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9671	9689	9680	(+)	0.893	0	ctggatcttgca GTT Ccta

ATG4D

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
10 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	224	242	233	(-)	0.813	0	atgtgccccca TGTT ctgc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	224	242	233	(-)	0.871	0	atgtgcccccat GTT Ctgc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1825	1843	1834	(+)	0.828	0	gctgagagatt TGTT ctta
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5229	5247	5238	(-)	0.881	0	tgtggaagctt TGTT cttt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5229	5247	5238	(-)	0.879	0	tgtggagcttt GTT Cttt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7151	7169	7160	(-)	0.824	0	tttgacttgc TGTT ccct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7151	7169	7160	(-)	0.947	0	tttgacttgc GTT Ccct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7151	7169	7160	(-)	0.916	0	tttgacttgc GTT Ccct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7151	7169	7160	(-)	0.932	0	tttgacttgc GTT Ccct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7775	7793	7784	(+)	0.875	0	tgagccccaact GTT Cctc

ATG5

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
8 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3728	3746	3737	(+)	0.840	0	gagcatcagccTGTtctt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	3728	3746	3737	(+)	0.899	0	gagcatcagcctGTTctt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3728	3746	3737	(+)	0.901	0	gagcatcagcctGTTctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7397	7415	7406	(+)	0.858	0	ggcgggcaggTGTtctt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9960	9978	9969	(-)	0.880	0	tccgccctccgTGTtctg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9960	9978	9969	(-)	0.901	0	tccgccctccgTGTtctg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9960	9978	9969	(-)	0.926	0	tccgccctccgTGTtctg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9960	9978	9969	(-)	0.859	0	tccgccctccgTGTtctg

ATG7

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
9 putative AREs								
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	159	177	168	(+)	0.910	0	cccaaacttcttGTTcAaa
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	386	404	395	(-)	0.882	0	agctcaaatcaGTTctt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1617	1635	1626	(-)	0.891	0	gaggcagagaaTGTtctca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	1617	1635	1626	(-)	0.903	0	gaggcagagaatGTTctca
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	1617	1635	1626	(-)	0.857	0	gaggcagagaatGTTctca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3258	3276	3267	(-)	0.816	0	ggtgatagaaaTGTtctac
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	4625	4643	4634	(+)	0.824	0	agacggcgtctTGTtctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	4625	4643	4634	(+)	0.900	0	agacggcgtctTGTtctgt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9325	9343	9334	(+)	0.808	0	ttcttagattcTGTtctt

ATG9A

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
11 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1814	1832	1823	(-)	0.814	0	gagcctcccca TGTT ctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5698	5716	5707	(-)	0.890	0	ctagac cttccTGTT ctct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5698	5716	5707	(-)	0.962	0	ctagac cttccTGTT ctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5698	5716	5707	(-)	0.931	0	ctagac cttccTGTT ctct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5698	5716	5707	(-)	0.874	0	ctagac cttccTGTT ctct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	8183	8201	8192	(-)	0.910	0	ccggttc atgccGTT Ctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	8183	8201	8192	(-)	0.875	0	ccggttc atgccGTT Ctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9282	9300	9291	(-)	0.824	0	cgcg tacttccTGTT cagg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9282	9300	9291	(-)	0.934	0	cgcg tacttccTGTT cagg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9282	9300	9291	(-)	0.906	0	cgcg tacttccTGTT cagg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9282	9300	9291	(-)	0.892	0	cgcg tacttccTGTT cagg

ATG9B

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
9 putative AREs								
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	1212	1230	1221	(-)	0.893	0	acgtg ccatccaGTT Cttc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3161	3179	3170	(+)	0.841	0	g tttccactgTGTT cttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3161	3179	3170	(+)	0.900	0	g tttccactgTGTT cttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7404	7422	7413	(-)	0.823	0	agac tccattTGTT ctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7404	7422	7413	(-)	0.901	0	agac tccattTGTT ctgt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7404	7422	7413	(-)	0.892	0	agac tccattTGTT ctgt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7451	7469	7460	(-)	0.882	0	agagac agattGTT Cctg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7451	7469	7460	(-)	0.924	0	agagac agattGTT Cctg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9445	9463	9454	(+)	0.908	0	tctt ctcattctGTT Cccc

ATG10

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
19 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1049	1067	1058	(-)	0.823	0	ttgtatcctat GTT ctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	1049	1067	1058	(-)	0.910	0	ttgtatcctatt GTT Ctgt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	1049	1067	1058	(-)	0.882	0	ttgtatcctatt GTT Ctgt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3953	3971	3962	(-)	0.856	0	gtggtacagta GTT cata
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3953	3971	3962	(-)	0.920	0	gtggtacagtat GTT Cata
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	3953	3971	3962	(-)	0.948	0	gtggtacagtat GTT Cata
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	4932	4950	4941	(+)	0.872	0	caagatcagcct GTT Caac
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	4932	4950	4941	(+)	0.885	0	caagatcagcct GTT Caac
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6208	6226	6217	(+)	0.956	0	ggggaacccaa TGTT ctgc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	6208	6226	6217	(+)	0.900	0	ggggaacccaat GTT Ctgc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	6208	6226	6217	(+)	0.967	0	ggggaacccaat GTT Ctgc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	6208	6226	6217	(+)	0.931	0	ggggaacccaat GTT Ctgc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	6208	6226	6217	(-)	0.856	0	gcagaacattg GTT Cccc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6294	6312	6303	(+)	0.906	0	agagggccta TGTT citt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	6294	6312	6303	(+)	0.918	0	agagggccta TGTT citt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	6294	6312	6303	(+)	0.873	0	agagggccta TGTT citt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8890	8908	8899	(-)	0.835	0	acaagggcagt GTT ctga
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	8890	8908	8899	(-)	0.896	0	acaagggcagt GTT Ctga
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	8890	8908	8899	(-)	0.902	0	acaagggcagt GTT Ctga

ATG12

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
10 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2253	2271	2262	(-)	0.873	0	catgcccagca TGTTctcc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2253	2271	2262	(-)	0.893	0	catgcccagcat GTTctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2253	2271	2262	(-)	0.938	0	catgcccagcat GTTctcc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	2253	2271	2262	(-)	0.899	0	catgcccagcat GTTctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7133	7151	7142	(-)	0.857	0	attcaaccct TGTTctag
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7133	7151	7142	(-)	0.911	0	attcaaccct GTTctag
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9169	9187	9178	(-)	0.890	0	tgataactgcac GTTctgt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9254	9272	9263	(-)	0.826	0	ggacttctt TGTTcttt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9254	9272	9263	(-)	0.946	0	ggacttctt GTTcttt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9254	9272	9263	(-)	0.888	0	ggacttctt GTTcttt

ATG13

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
1 putative ARE								
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	661	679	670	(+)	0.874	0	ggctcacagcta GTTctag

ATG14

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
6 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8	26	17	(+)	0.835	0	tctgtttaag TGTTcttt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2251	2269	2260	(+)	0.885	0	agaggccctg TGTTctac
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2251	2269	2260	(+)	0.921	0	agaggccctg GTTctac
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2251	2269	2260	(+)	0.915	0	agaggccctg GTTctac
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	2251	2269	2260	(+)	0.864	0	agaggccctg GTTctac
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2307	2325	2316	(+)	0.831	0	ccagcttacac TGTTctgg

ATG16L1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
11 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	50	68	59	(-)	0.912	0	g ttgaccagg g TGT ctg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	50	68	59	(-)	0.891	0	g ttgaccagg g TGT Cttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	50	68	59	(-)	0.942	0	gttgaccagg g TGT Cttg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	50	68	59	(-)	0.904	0	gttgaccagg g TGT Cttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	591	609	600	(-)	0.871	0	ccagag catggg GTT Ctcc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	1160	1178	1169	(-)	0.873	0	t caaaccg ca ctGTT Caa
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5636	5654	5645	(+)	0.833	0	tt tgacttta TGT Cctt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5636	5654	5645	(+)	0.946	0	tt gtacttta TGT Cctt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5636	5654	5645	(+)	0.915	0	tt gtacttta TGT Cctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5636	5654	5645	(+)	0.931	0	tt gtacttta TGT Cctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	8131	8149	8140	(-)	0.851	0	ta gaccactg TGT Ccag

ATG16L2

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
7 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1524	1542	1533	(-)	0.815	0	ggaggga ta ctGTT ctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1931	1949	1940	(+)	0.814	0	ga ataatatt TGT Tctat
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2597	2615	2606	(+)	0.891	0	tt aaacaat ca GTT Ctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2597	2615	2606	(+)	0.883	0	tt aaacaat ca GTT Ctct
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	4932	4950	4941	(+)	0.806	0	t ctagcc acca TGT Tctga
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	4932	4950	4941	(+)	0.896	0	t ctagcc accat GTT Ctga
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6580	6598	6589	(+)	0.827	0	tg agacagt ct TGT ctgt

ATG101

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
6 putative AREs								
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	277	295	286	(+)	0.913	0	cccaaaccttca GTT Ctag
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3976	3994	3985	(-)	0.888	0	tg tg ctgtc TGT Tctcc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	3976	3994	3985	(-)	0.932	0	tg tg ctgtc GTT Ctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3976	3994	3985	(-)	0.931	0	tg tg ctgtc GTT Ctcc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	3976	3994	3985	(-)	0.864	0	tg tg ctgtc GTT Ctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9124	9142	9133	(-)	0.870	0	ggagcgcatt gGTT Ctcc

BECN1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
13 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2760	2778	2769	(-)	0.801	0	atagagcatga TGT Tatat
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2960	2978	2969	(+)	0.817	0	aaa at gctt TGT Tctca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3899	3917	3908	(+)	0.821	0	aca ca gcaacc TGT Tctga
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	3899	3917	3908	(+)	0.894	0	acacag ca acct GTT Ctga
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3899	3917	3908	(+)	0.890	0	acacag ca acct GTT Ctga
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5151	5169	5160	(+)	0.876	0	ctg ca cattc TGT Tctc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5151	5169	5160	(+)	0.965	0	ctg ca cattc GTT Ctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5151	5169	5160	(+)	0.955	0	ctg ca cattc GTT Ctcc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5151	5169	5160	(+)	0.907	0	ctg ca cattc GTT Ctcc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9092	9110	9101	(+)	0.928	0	tg tg ctct gGTT Ccct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9092	9110	9101	(+)	0.871	0	tg tg ctct gGTT Ccct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9092	9110	9101	(+)	0.871	0	tg tg ctct gGTT Ccct
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9520	9538	9529	(+)	0.812	0	g ttg ctgt gTGT Tctga

GABARAP

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
7 putative AREs								
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5396	5414	5405	(+)	0.877	0	atggttccatctGTTcctc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5548	5566	5557	(+)	0.891	0	ccagcccatcttGTTcctc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5548	5566	5557	(+)	0.875	0	ccagcccatcttGTTcctc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	5548	5566	5557	(+)	0.916	0	ccagcccatcttGTTcctc
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	6978	6996	6987	(+)	0.856	0	gggtctcactctGTTccta
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	8447	8465	8456	(+)	0.913	0	tcttaacttctgGTTcaca
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9642	9660	9651	(+)	0.862	0	attgtccctgctGTTcctc

GABARAPL1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
5 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	471	489	480	(+)	0.801	0	tttctctaaaTGTtctt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	471	489	480	(+)	0.897	0	tttctctaaatGTTctt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	471	489	480	(+)	0.885	0	tttctctaaatGTTctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	2026	2044	2035	(+)	0.864	0	gaggaagaatctGTTcat
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6408	6426	6417	(+)	0.848	0	atggaggaacaTGTtcta

GABARAPL2

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
12 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2490	2508	2499	(-)	0.871	0	cattacaatcTGTtctct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2490	2508	2499	(-)	0.930	0	cattacaatctGTTctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2490	2508	2499	(-)	0.952	0	cattacaatctGTTctct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	2490	2508	2499	(-)	0.891	0	cattacaatctGTTctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	3467	3485	3476	(+)	0.903	0	gagggaccctcaGTTctgg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	4100	4118	4109	(+)	0.864	0	tcaatactactTGTtcttg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	4100	4118	4109	(+)	0.932	0	tcaatactactGTTcttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	4100	4118	4109	(+)	0.930	0	tcaatactactGTTcttg
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	4100	4118	4109	(+)	0.855	0	tcaatactactGTTcttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5439	5457	5448	(+)	0.819	0	cactccacaaTGTtcttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5439	5457	5448	(+)	0.895	0	cactccacaatGTTcttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6587	6605	6596	(-)	0.814	0	tagctatggaaTGTtctaa

MAP1LC3A

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
7 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7868	7886	7877	(+)	0.815	0	atttctccttgTGTtctta
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7868	7886	7877	(+)	0.918	0	atttctcctgtGTTctta
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7868	7886	7877	(+)	0.885	0	atttctcctgtGTTctta
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8751	8769	8760	(+)	0.829	0	tcagcttccaTGTtcttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9576	9594	9585	(+)	0.820	0	ttctagcatccTGTtctat
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9576	9594	9585	(+)	0.951	0	ttctagcatcctGTTctat
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9576	9594	9585	(+)	0.898	0	ttctagcatcctGTTctat

MAP1LC3B2

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
7 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1758	1776	1767	(+)	0.816	0	cctg tt atct TGTT ctgc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2323	2341	2332	(+)	0.908	1	taaatt ctt ggt GTT Ccat
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9535	9553	9544	(+)	0.801	0	tcc a ccc acca TGTT ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9535	9553	9544	(+)	0.895	0	tcc acc c accat GTT Ctgg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9971	9989	9980	(+)	0.809	0	c ctt t ccatt TGTT ctct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9971	9989	9980	(+)	0.918	0	c ctt t ccatt t GTT Ctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9971	9989	9980	(+)	0.900	0	c ctt t ccatt t GTT Ctct

MAP1LC3C

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
10 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	137	155	146	(-)	0.874	0	tt g gag agga TGTT ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	137	155	146	(-)	0.901	0	tt g gag aggat GTT Ctgg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	876	894	885	(-)	0.892	0	tcatt a cag cca GTT Ctgg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	876	894	885	(-)	0.883	0	tcatt a cag cca GTT Ctgg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2779	2797	2788	(-)	0.807	0	a att ct ctc ct TGTT ctct
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2779	2797	2788	(-)	0.904	0	a att ct ctc ctt GTT Ctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2779	2797	2788	(-)	0.888	0	a att ct ctc ctt GTT Ctct
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7131	7149	7140	(+)	0.878	0	tt g tc a ctt t GTT Catt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7131	7149	7140	(+)	0.870	0	tt g tc a ctt t GTT Catt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7290	7308	7299	(-)	0.895	0	acag ct ct cca GTT Ccca

MAP1LC3B

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
3 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6674	6692	6683	(+)	0.894	0	aatgaaagatgTGTtcttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	6674	6692	6683	(+)	0.877	0	aatgaaagatgtGTTcttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8853	8871	8862	(-)	0.832	0	ttggctgtttTGTtctt

RB1CC1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
5 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	3615	3633	3624	(-)	0.805	0	cttctagttagTGTtctta
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7285	7303	7294	(-)	0.892	0	atcttccttcaGTTctca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9054	9072	9063	(+)	0.894	0	acctaacattttGTTcagt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9054	9072	9063	(+)	0.878	0	acctaacattttGTTcagt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9054	9072	9063	(+)	0.851	0	acctaacattttGTTcagt

SNX4

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
11 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1132	1150	1141	(+)	0.830	0	ctgataaattgTGTtctgt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2266	2284	2275	(-)	0.805	0	tttcccatacTGTtctcg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2266	2284	2275	(-)	0.898	0	tttcccatactGTTctcg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2266	2284	2275	(-)	0.892	0	tttcccatactGTTctcg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5877	5895	5886	(-)	0.823	0	aatttctgtgTGTtctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5877	5895	5886	(-)	0.894	0	aatttctgtgtGTTctgt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5877	5895	5886	(-)	0.888	0	aatttctgtgtGTTctgt
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	6391	6409	6400	(+)	0.908	0	atatttctgggTTCcca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7259	7277	7268	(+)	0.908	0	cagtctcattctGTTcct
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7259	7277	7268	(+)	0.855	0	cagtctcattctGTTcct
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8231	8249	8240	(-)	0.803	0	gccgagcatggTGTtgtgt

SNX30

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
8 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2905	2923	2914	(-)	0.811	0	gtgagccttta TGTT ctac
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	2905	2923	2914	(-)	0.933	0	gtgagcctttat GTT Ctac
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2905	2923	2914	(-)	0.879	0	gtgagcctttat GTT Ctac
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5840	5858	5849	(-)	0.820	0	ttgagaaacac TGTT ctct
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	6738	6756	6747	(+)	0.812	0	gctccatgctg TGTT cttg
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9294	9312	9303	(+)	0.815	0	ctcatgctcg TGTT ctga
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9294	9312	9303	(+)	0.908	0	ctcatgctcgct GTT Ctga
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9294	9312	9303	(+)	0.886	0	ctcatgctcgct GTT Ctga

ULK1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
10 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5142	5160	5151	(-)	0.827	0	actgagtatga TGTT ctcc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7267	7285	7276	(+)	0.852	0	caaacactaca TGTT ctca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7267	7285	7276	(+)	0.931	0	caaacactacat GTT Ctca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7267	7285	7276	(+)	0.929	0	caaacactacat GTT Ctca
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7267	7285	7276	(+)	0.858	0	caaacactacat GTT Ctca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8202	8220	8211	(+)	0.838	0	caggcgggtct TGTT ctca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	8855	8873	8864	(-)	0.847	0	gaggcacttgc TGTT atgt
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	9446	9464	9455	(-)	0.831	0	ccccactgcc TGTT ctcc
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9446	9464	9455	(-)	0.924	0	ccccactgcct GTT Ctcc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9446	9464	9455	(-)	0.929	0	ccccactgcct GTT Ctcc

ULK2

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
4 putative AREs								
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	388	406	397	(+)	0.853	0	aaag tacagca G TT C cca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	9292	9310	9301	(+)	0.892	0	acctgac aatct G TT C ctt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	9292	9310	9301	(+)	0.888	0	acctgac aatct G TT C ctt
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	9292	9310	9301	(+)	0.898	0	acctgac aatct G TT C ctt

WIPI1

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
15 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	248	266	257	(+)	0.922	0	ggag ttcagag T GTT c tca
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	248	266	257	(+)	0.901	0	ggag ttcagagt G TT C tca
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	248	266	257	(+)	0.950	1	ggag ttcagagt G TT C tca
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	248	266	257	(+)	0.917	0	ggag ttcagagt G TT C tca
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	1349	1367	1358	(+)	0.907	0	agg gagctgta T GTT c tat
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	1349	1367	1358	(+)	0.924	0	agg gagctgta T GTT C tat
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	1349	1367	1358	(+)	0.923	0	agg gagctgta T GTT C tat
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	1349	1367	1358	(+)	0.875	0	agg gagctgta T GTT C tat
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2708	2726	2717	(+)	0.803	0	ttt gtccagc T GTT c tta
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2708	2726	2717	(+)	0.880	0	ttt gtccagct G TT C tta
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	2721	2739	2730	(+)	0.871	0	ttc ttcacctc G TT C tat
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	5101	5119	5110	(+)	0.817	0	acc cgctctgt T GTT c ttg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	5101	5119	5110	(+)	0.891	0	acc cgctctgt G TT C ttg
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	5101	5119	5110	(+)	0.883	0	acc cgctctgt G TT C ttg
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7069	7087	7078	(+)	0.900	0	ag taagcatgca G TT C gca

WIPI2

Matrix	Detailed Matrix Information	from	to	anchor	Strand	Matrix sim.	#	Sequence
8 putative AREs								
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	519	537	528	(+)	0.875	0	agaggaaact TGTTcttc
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	519	537	528	(+)	0.895	0	agaggaaact GTTCttc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	2779	2797	2788	(+)	0.821	0	ttgatagag TGTTctgc
V\$GREF/ARE.01	Androgene receptor binding site, IR3 sites	7668	7686	7677	(-)	0.840	0	aaagaactcta TGTTcaga
V\$GREF/ARE.02	Androgene receptor binding site, IR3 sites	7668	7686	7677	(+)	0.920	0	tctgaacataga GTTCttt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7668	7686	7677	(+)	0.928	0	tctgaacataga GTTCttt
V\$GREF/ARE.03	Androgene receptor binding site, IR3 sites	7668	7686	7677	(-)	0.905	0	aaagaactctat GTTCaga
V\$GREF/ARE.04	Androgene receptor binding site, IR3 sites	7668	7686	7677	(-)	0.910	0	aaagaactctat GTTCaga