

Table S1: List of putative TFBS in pGTH1 predicted by Matinspector.

Colour code	Matrix Family	Detailed Family Informator	Matrix	Detailed Matrix Informator	Opt.	Start	End	Position	Anchor	Position	Strand	Core sim.	Matrix sim.	Mat. sim. - opt.	Sequence	Deletion
	FSTEAF	TEA/ATTS DNA binding domain factors	FSBAA0.01	Aspergillus spore/developmental regulator	0.93	-985	-969	-977	-	1	0.94	0.01	0.01	0.01	acctcaCATTTctactg	
	FSNRGF	NRG zinc finger factors	FSNRG1.01	Transcriptional repressor Nrg1	0.89	-976	-964	-970	+	1	0.922	0.032	0.032	0.032	tgtAGGtccc	
	FSYSTR	Yeast stress response elements	FMSNZ2.01	Transcriptional activator for genes in multistress response	1	-956	-942	-949	-	1	1	0	0	0	gaactaGGGGGagcc	
	FSPDRE	Pleiotropic drug resistance responsive elements	FSPDRE.01	Pleiotropic drug resistance responsive element (yeast)	0.87	-944	-936	-940	-	0.773	1	0.007	0.007	0.007	TCCGtgag	
	FSYMAT	Yeast mating factors	FSHMR2.01	Hidden Mat Right A2, a2 is one of two genes encoded by the a mating type cassette in S. cerevisiae	0.94	-939	-927	-933	+	1	0.947	0.007	0.007	0.007	ggaaatGTGAaaa	
	FSMADS	Yeast MADS-Box factors	FSRLM1.01	Yeast MADS-Box RLM1 transcription factor	0.78	-926	-908	-917	-	1	0.873	0.003	0.003	0.003	gtttTCtAGtaagata	
	OSINRE	Core promoter initiator elements	OSDINR.01	Drosophila initiator motifs	0.94	-899	-889	-894	+	1	0.974	0.034	0.034	0.034	gcTCAgTgct	
	FSRFXP	Regulatory factor X protein, homologous to mammalian RFX1-5	FSRFX1.02	RFX1 (CRT1), acts by recruiting Ssn6 and Tup1, general repressors to the promoters of damage-inducible genes	0.77	-896	-882	-889	-	1	0.811	0.041	0.041	0.041	ttatctcaGAAcct	
	FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.02	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.96	-889	-875	-882	-	1	0.968	0.008	0.008	0.008	aacgtaAATTctctg	
	FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.02	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.96	-888	-874	-881	+	1	0.992	0.032	0.032	0.032	aggataATTAcctc	
	OSMTEN	Core promoter motif ten elements	OSDMTE.01	Drosophila motif ten element	0.77	-888	-868	-878	-	0.938	0.79	0.02	0.02	0.02	acagtcgAACGtaattact	
	FSBZIP	Fungal basic leucine zipper family	FSCS16.01	Chromosome stability, bZIP transcription factor of the ATF/CREB family (ACA2)	0.95	-865	-865	-875	-	1	0.965	0.015	0.015	0.015	actaccggaACGtattact	
	FSMADS	Yeast MADS-Box factors	FSRLM1.01	Yeast MADS-Box RLM1 transcription factor	0.78	-855	-837	-846	-	1	0.822	0.042	0.042	0.042	lcttCTCAacataagat	
	FSYMAT	Yeast mating factors	FSMATALPHA2	Homeodomain transcriptional repressor Mata1pha2	0.86	-853	-841	-847	+	1	0.918	0.058	0.058	0.058	ctgtaTTGtag	
	FSMMAT	M-box interacting with Mat1-Mc	FSMAT1MC.01	HMG-BOX protein interacts with M-box site, cooperativity with HMG-Box STE11 protein	0.87	-852	-842	-847	+	1	0.895	0.025	0.025	0.025	tgtATTGTgag	
	FSSTPF	STP gene family	FSSTP2.01	Proteolytically activated transcription factor	0.87	-828	-814	-821	-	1	0.966	0.096	0.096	0.096	cgccgCCGtaaaaa	
	FSSTPF	STP gene family	FSSTP2.01	Proteolytically activated transcription factor	0.87	-823	-809	-816	+	1	0.912	0.042	0.042	0.042	acgcccGCCccat	
	FSYADR	Yeast metabolic regulator	FSADR1.01	Alcohol Dehydrogenase Regulator, carbon source-responsive zinc-finger transcription factor	0.94	-785	-777	-781	+	1	0.984	0.044	0.044	0.044	aaCCCact	-785 to -777
	FSRFXP	Regulatory factor X protein, homologous to mammalian RFX1-5	FSRFX1.02	RFX1 (CRT1) is a DNA-binding protein that acts by recruiting Ssn6 and Tup1, general repressors to the promoters of damage-inducible genes	0.92	-763	-749	-756	-	1	0.992	0.072	0.072	0.072	cgglataGCCAacg	
	FSYMCB	Yeast Mlu I cell cycle box	FSMW4.01	DNA binding component of the SBF/SCB binding factor complex (Swi4p-Swi6p)	0.84	-756	-744	-750	+	1	0.88	0.04	0.04	0.04	latacaCGCAc	
	FSCYTO	Activator of cytochrome C	FSHAP1.01	HAP1, S. cerevisiae member of GAL family, regulates heme dependent cytochrome expression	0.76	-715	-701	-708	+	1	0.773	0.013	0.013	0.013	ctgaagCATCGgtt	
	FSFKHD	Fungal fork head transcription factors	FSFKH1.01	Fork head transcription factor Fkh1	0.81	-709	-693	-701	+	0.755	0.818	0.008	0.008	0.008	lcatccgTTAAacatac	
	FSROX1	Repressor of hypoxic genes	FSROX1.01	Heme-dependent transcriptional repressor of hypoxic genes	0.82	-704	-692	-698	-	1	0.846	0.026	0.026	0.026	ltgaTTGTtaacc	
	FSYMAT	Yeast mating factors	FSMATALPHA2	Homeodomain transcriptional repressor Mata1pha2	0.86	-703	-691	-697	-	1	0.863	0.003	0.003	0.003	ctgtaTTGtaacc	
	FSMMAT	M-box interacting with Mat1-Mc	FSMAT1MC.01	HMG-BOX protein interacts with M-box site, cooperativity with HMG-Box STE11 protein	0.87	-702	-692	-697	-	1	0.931	0.061	0.061	0.061	ltgATTGTtaacc	
	FSYHSF	Yeast heat shock factors	FSHSF1.01	Trimeric heat shock transcription factor	0.95	-678	-646	-662	-	1	0.958	0.008	0.008	0.008	aacacactacgaatatGGAaaggaacaccgag	
	FSPHD1	Pseudoh yphal determinant 1	FSPHD1.03	Transcription factor involved in regulation of filamentous growth	0.98	-635	-623	-629	-	1	0.994	0.014	0.014	0.014	lcaCATGCaacaa	
	FSMCGM	Monomeric Gal4-class motifs	FSRG1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-628	-612	-620	+	1	0.944	0.074	0.074	0.074	caactcGGCAaagattag	-628 to -612
	FSCSRE	Carbon source-responsive element	FSCSRE.01	Carbon source-responsive element (yeast)	0.79	-626	-612	-619	-	1	0.842	0.052	0.052	0.052	ctaattCTCCGag	
	FSYRSC	Yeast transcription factors remodeling chromatin structure	FSRSC3.01	Component of the RSC chromatin remodeling complex	0.82	-614	-594	-604	+	1	0.826	0.006	0.006	0.006	tagcaatgCCGGttcata	
	FSYMCB	Yeast Mlu I cell cycle box	FSTUAP.01	Aspergillus Stunted protein, (bHLH)-like structure, regulates multicellular complexity during asexual reproduction	0.95	-609	-597	-603	-	1	0.951	0.001	0.001	0.001	gaaaCGCCgtatt	
	FSYMCB	Yeast Mlu I cell cycle box	FSMCSB.01	Mlu I cell cycle box, activates G1/S-specific transcription (yeast)	0.84	-608	-596	-602	+	1	0.903	0.063	0.063	0.063	atacCGCCttca	
	FSDUIS	DAL upstream induction sequence	FSDAL82.01	Transcriptional activator for allantoin catabolic genes	0.92	-597	-589	-593	+	1	0.966	0.046	0.046	0.046	cataTGCCgc	
	FSPHD1	Pseudoh yphal determinant 1	FSPHD1.02	Transcription factor involved in regulation of filamentous growth	0.97	-597	-585	-591	+	1	0.978	0.008	0.008	0.008	cataTGCCgttt	
	FSRDN	RDNA binding factor	FSREB1.02	DNA enhancer/ binding protein I, termination factor for RNA polymerase I and transcription factor for RNA polymerase II	0.85	-589	-577	-583	+	1	0.915	0.065	0.065	0.065	chlTTACcccc	
	FSYMG	Yeast GC-Box Proteins	FSMG1.02	MG1, zinc finger protein mediates glucose repression	0.83	-568	-568	-577	-	1	0.839	0.009	0.009	0.009	ttgacaaaGGGGGgtaa	-568 to -568
	FSYSTR	Yeast stress response elements	FMSNZ2.01	Transcriptional activator for genes in multistress response	1	-566	-572	-579	-	1	1	0	0	0	caaaaGGGGgtaa	
	FSBZIP	Fungal basic leucine zipper family	FSYAP1.02	Yeast activator protein of the basic leucine zipper (bZIP) family	0.93	-565	-565	-575	+	0.967	0.974	0.044	0.044	0.044	taccocctcttTCTCAagcg	
	FSTALE	Fungal TALE homeodomain class	FSTOS8.01	Homeodomain-containing transcription factor	0.96	-579	-567	-573	+	1	0.962	0.002	0.002	0.002	ctctttTCTCAag	
	FSDUIS	DAL upstream induction sequence	FSDAL82.01	Transcriptional activator for allantoin catabolic genes	0.92	-567	-559	-563	-	1	0.975	0.055	0.055	0.055	atattTGCgc	
	FSYMG	Yeast GC-Box Proteins	FSMG1.01	MG1, zinc finger protein mediates glucose repression	0.84	-553	-535	-544	+	1	0.852	0.012	0.012	0.012	taagatttggGGGGgtgt	-553 to -535
	FSYRAP	Yeast activator of glycolysis genes / repressor of mating type I	FSRAP1.06	RAP1 (TUF1), activator or repressor depending on context	0.94	-546	-524	-535	-	1	0.967	0.027	0.027	0.027	actaacgctcacCACccccca	
	FSIRT	Iron-responsive transcriptional activators	FSAFT2.01	Activator of Fe (iron) transcription 2, iron-regulated transcriptional activator	0.98	-543	-529	-536	-	1	1	0.02	0.02	0.02	cgccatCACCCca	
	OSVTP	Vertebrate TATA binding protein factor	OSATA0.01	Avian C-type LTR TATA box	0.78	-530	-514	-522	-	0.75	0.782	0.002	0.002	0.002	tttttCACGtaaacg	
	FSRPE	Ribosomal RNA processing element	FSTB3.01	Ribosomal RNA processing element (RPE)-binding protein	0.82	-504	-488	-496	-	1	0.875	0.055	0.055	0.055	ttgacttTTTcaggga	
	FSMCGM	Monomeric Gal4-class motifs	FSRG1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-442	-426	-434	-	0.793	0.893	0.023	0.023	0.023	atataCGGAaaacatac	-442 to -426
	FSGATA	Fungal GATA binding factors	FSGZF3.01	GATA zinc finger protein Gz3	0.81	-434	-420	-427	+	1	0.817	0.007	0.007	0.007	tcttGATatgatac	
	FSPHD1	Pseudoh yphal determinant 1	FSPHD1.01	Transcription factor involved in regulation of filamentous growth	0.89	-430	-418	-424	+	1	0.926	0.036	0.036	0.036	gataTGCAtaaa	
	FSYMAT	Yeast mating factors	FSMATA1.01	Homeodomain protein mating factor a1	0.92	-429	-417	-423	-	1	0.921	0.001	0.001	0.001	tttttTGCatac	
	FSICGG	Inverted CGG triplets spaced preferentially by 10 bp	FSCH4.01	Fungal zinc cluster transcription factor Cha4, single triplet	0.92	-408	-398	-398	+	1	0.922	0.002	0.002	0.002	taaacacttattCTCCGctat	
	FSMCGM	Monomeric Gal4-class motifs	FSYRR1.01	Zinc cluster transcription factor, activates genes involved in multidrug resistance (PDR2)	0.76	-403	-387	-395	-	1	0.807	0.047	0.047	0.047	aatagCGGAagattcag	
	FSRDR1	Repressor of Drug Resistance 1	FSRDR1.01	Repressor of Drug Resistance 1 (transcriptional repressor involved in the control of multidrug resistance)	0.89	-399	-389	-394	-	1	0.915	0.025	0.025	0.025	taqCGAagat	
	FSRFXP	Regulatory factor X protein, homologous to mammalian RFX1-5	FSRFX1.02	RFX1 (CRT1), acts by recruiting Ssn6 and Tup1, general repressors to the promoters of damage-inducible genes	0.77	-366	-352	-359	-	0.78	0.782	0.012	0.012	0.012	ttgtcacgaAAcGg	
	FSYMCB	Yeast Mlu I cell cycle box	FSSW4.01	DNA binding component of the SBF/SCB binding factor complex (Swi4p-Swi6p)	0.84	-364	-352	-358	-	1	0.887	0.047	0.047	0.047	tttgcaCGAAac	
	FSBZIP	Fungal basic leucine zipper family	FSYAP1.02	Yeast activator protein of the basic leucine zipper (bZIP) family	0.93	-361	-345	-353	-	0.967	0.974	0.044	0.044	0.044	ltgaaaattaaattGTCACgaa	
	FSRPE	Ribosomal RNA processing element	FSTB3.01	Ribosomal RNA processing element (RPE)-binding protein	0.82	-359	-347	-353	-	0.752	0.823	0.003	0.003	0.003	aaattattTGTCTCagca	
	FSRTALE	Fungal TALE homeodomain class	FSCS16.01	Homeodomain transcriptional repressor Cup9	0.98	-341	-341	-351	-	1	0.989	0.019	0.019	0.019	ttatTTGCaac	
	FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.01	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.86	-358	-344	-351	-	1	0.886	0.026	0.026	0.026	aaattAATTgtcac	
	FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.01	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.86	-357	-343	-350	+	1	0.879	0.019	0.019	0.019	tgacaAATTAatttc	
	FSICGG	Inverted CGG triplets spaced preferentially by 10 bp	FSTEA1.01	Ty1 enhancer activator, zinc cluster DNA-binding protein	0.75	-357	-337	-347	+	1	0.789	0.039	0.039	0.039	tgacaAAATTAattccaag	
	FSMCGM	Monomeric Gal4-class motifs	FSYRR1.01	Zinc cluster transcription factor, activates genes involved in multidrug resistance (PDR2)	0.76	-352	-336	-344	-	0.753	0.763	0.003	0.003	0.003	ccogTTGAaattaat	
	FSASG1	Activator of stress genes	FSASG1.01	Fungal zinc cluster transcription factor Asg1	0.79	-340	-324	-332	-	1	0.835	0.045	0.045	0.045	lCCGGCaagaccocgt	
	FSMCGM	Monomeric Gal4-class motifs	FSRG1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-335	-321	-329	-	1	0.88	0.01	0.01	0.01	ttatcCGGAaagacc	-337 to -316
	FSMCGM	Monomeric Gal4-class motifs	FSRG1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-330	-320	-325	+	1	0.885	0.015	0.015	0.015	ttgtcCGAataagaaa	
	FSRDR1	Repressor of Drug Resistance 1	FSRDR1.01	Repressor of Drug Resistance 1 (transcriptional repressor involved in the control of multidrug resistance)	0.89	-332	-316	-324	+	1	0.9	0.01	0.01	0.01	gtCCGAlaag	
	FSGATA	Fungal GATA binding factors	FSGATA.01	GATA binding factor (yeast)	0.89	-329	-315	-322	+	1	0.974	0.084	0.084	0.084	ttccGATAAaggaat	
	FSP															

FSCSRE	Carbon source-responsive elements	FSCSRE.01	Carbon source-responsive element (yeast)	0.79	-276	-260	-268	+	1	0.81	0.02	catatttTCCGgtt	
FMSGCM	Monomeric Gal4-class motifs	FSGRT1.01	Glucose-responsive transcription factor involved in regulation of glucose transport	0.82	-275	-259	-267	-	1	0.982	0.162	ataacCGAaaaatg	-275 to -261
FICGG	Inverted CGG triplets spaced preferentially by 10 bp	FSTEA1.01	Ty1 enhancer activator, zinc cluster DNA-binding protein	0.75	-269	-249	-259	-	0.752	0.772	0.022	aggtgggGTAAtaacggaaa	
FSDNA	rDNA binding factor	FSREB1.02	rDNA enhancer binding protein 1, termination factor for RNA polymerase I and transcription factor for RNA polymerase II	0.85	-262	-250	-256	+	1	0.823	0.073	htaTACcccacc	
FSYNCM	Yeast cell cycle and metabolic regulator	FSMCM1.02	Yeast factor MCM1 cooperating with MATalpha factors	0.75	-258	-250	-254	-	1	0.776	0.026	ctTCGagagaggaat	
FSYMG	Yeast GC-Box Proteins	FSMIG1.01	MIG1, zinc finger protein mediates glucose repression	0.84	-260	-244	-252	-	1	0.843	0.003	cacttccaggtGGGtaat	-268 to -242
FSYADR	Yeast metabolic regulator	FSADR1.01	Alcohol Dehydrogenase Regulator, carbon source-responsive zinc-finger transcription factor	0.94	-260	-242	-251	+	1	1	0.06	taCCCacc	
FMSGCM	Monomeric Gal4-class motifs	FSGRT1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-239	-223	-231	-	1	0.956	0.086	atcccCGGAaattctg	-239 to -221
FSYMG	Yeast GC-Box Proteins	FSMIG1.01	MIG1, zinc finger protein mediates glucose repression	0.84	-239	-221	-230	+	1	0.854	0.014	cagaatttccGGGatta	
FICGG	Inverted CGG triplets spaced preferentially by 10 bp	FSTEA1.01	Ty1 enhancer activator, zinc cluster DNA-binding protein	0.75	-232	-224	-228	-	0.752	0.774	0.024	attatccGTAAtcccggaaa	
FSARPU	Regulator of pyrimidine and purine utilization pathway	FSPPR1.01	Pyrimidine pathway regulator 1	0.73	-231	-223	-227	-	0.75	0.739	0.009	atccgtaatccCGGaa	
FSPDRE	Pleiotropic drug resistance responsive elements	FSPDRE.01	Pleiotropic drug resistance responsive element (yeast)	0.87	-232	-216	-224	-	0.773	0.904	0.034	TCCcgaaa	
FSARPU	Regulator of pyrimidine and purine utilization pathway	FSPPR1.01	Pyrimidine pathway regulator 1	0.73	-231	-215	-223	+	0.75	0.798	0.068	tcgggggattaCGGata	
FSPDRE	Pleiotropic drug resistance responsive elements	FSPDRE.01	Pleiotropic drug resistance responsive element (yeast)	0.87	-230	-216	-223	+	1	0.942	0.072	TCCGgggat	
FSCYTO	Activator of cytochrome C	FSHAP1.01	HAP1, S. cerevisiae member of GAL family, regulates heme dependent cytochrome expression	0.76	-233	-213	-223	+	0.75	0.892	0.132	ccgggaatTACGaat	
FSYQA1	Neurospora crassa QA1 gene activator	FSQA1F.01	qa-1F, required for quinic acid induction of transcription in the qa gene cluster	0.75	-228	-208	-218	+	0.794	0.753	0.003	ggggattaccgataAATacggt	
FMSGCM	Monomeric Gal4-class motifs	FSGRT1.02	Glucose-responsive transcription factor involved in regulation of glucose transport	0.87	-225	-209	-217	+	1	0.906	0.036	gattaCGGataatcgg	-220 to -209
FSCYTO	Activator of cytochrome C	FSHAP1.01	HAP1, S. cerevisiae member of GAL family, regulates heme dependent cytochrome expression	0.76	-221	-207	-214	+	0.75	0.793	0.033	acggataatTACGgtg	
FSBZIP	Fungal basic leucine zipper family	FSCIN5.01	bZIP transcriptional factor of the yAP-1 family that mediates pleiotropic drug resistance and salt tolerance	0.89	-208	-188	-198	+	1	0.901	0.011	tggtctgattaatTAATacg	
FSBZIP	Fungal basic leucine zipper family	FSCIN5.01	bZIP transcriptional factor of the yAP-1 family that mediates pleiotropic drug resistance and salt tolerance	0.89	-203	-189	-196	-	1	0.945	0.055	ctggcgattaatTAAATcca	
FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.02	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.96	-202	-188	-195	-	1	0.979	0.019	gtataATTaatcc	
FSHOMD	Homeodomain-containing transcriptional regulators	FSYOX1.02	Yeast homeobox 1, homeodomain-containing transcriptional repressor	0.96	-203	-183	-193	+	1	0.979	0.019	ggattaATTaatcc	
FSYABF	Yeast ABF factors	FSABF1.04	ARS (autonomously replicating sequence)-binding factor I	0.77	-202	-184	-193	+	0.755	0.794	0.024	ggATTAAaataccgcaa	
FSPHRR	pH responsive regulators	FSRIM101.01	Transcriptional repressor involved in response to pH and in cell wall construction	0.99	-192	-176	-184	+	1	1	0.01	atacGCCAagttctaca	
FSPRES	Pheromone response elements	FSSTE12.01	Transcription factor activated by a MAP kinase signaling cascade, activates genes involved in mating of pseudohyphal/invasive growth pathways	0.86	-175	-163	-169	-	1	0.89	0.03	gactgCAACAaa	
FSFKHD	Fungal fork head transcription factors	FSFKH2.01	Fork head transcription factor Fkh2	0.86	-148	-132	-140	+	1	0.877	0.017	gcaataaTAAcaaat	
FSYCAT	Yeast CCAAT binding factors	FSHAP234.01	Yeast factor complex HAP2/3/5, homolog to vertebrate NF-Y/CP1/CBF	0.86	-124	-112	-118	-	1	0.937	0.077	ctaatCCAATAaa	
FSYORE	Yeast olate response elements	FSORE.01	Olate response element, binding motif of Oaf1 homodimers or Oaf1/Pip2 heterodimers	0.72	-120	-96	-108	-	0.86	0.745	0.025	CGAGGtcaagctgcaactatccaa	
FSAAAU	A. nidulans activator of acetate utilization genes	FSFACBCB.01	FACB, activator of acetate utilization genes with a GAL4-type Zn(II)2Cys6 zinc binuclear cluster	0.8	-109	-93	-101	+	1	0.816	0.016	CGAGGtaccgcccga	
FSYMG	Yeast GC-Box Proteins	FSMIG3.01	Zinc finger transcriptional repressor MIG3	0.81	-104	-86	-95	-	1	0.86	0.05	ctagctatggcGGGtcaa	
FSYRAP	Yeast activator of glycolysis genes / repressor of mating type I	FSRAP1.06	RAP1 (TUF1), activator or repressor depending on context	0.94	-74	-52	-63	-	1	0.972	0.032	tgcatcatctaaCACcctagca	
FSPHD1	Pseudoh yphal determinant 1	FSPHD1.03	Transcription factor involved in regulation of filamentous growth	0.98	-60	-48	-54	-	1	0.994	0.014	caaGTGCatcatc	
OSVTBP	Vertebrate TATA binding protein factor	OSVTATA.01	Cellular and viral TATA box elements	0.9	-31	-15	-23	+	1	0.974	0.074	gaataTAAaagatcct	
FMSGCM	Monomeric Gal4-class motifs	FSLYS14.01	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway	0.8	-17	-1	-9	-	1	0.838	0.038	aaaggtGGAAttaag	