

**Supp. Table S1. Prediction score for each SNP in putative transcription regulatory regions**

This table is available online as a separate .csv file.

**Supp. Table S2. Performance of individual feature sets and data sets**

	SNP-based features only	SNP-based features+ Expression-based features	SNP-based features+ Function-based features	All features excluding the feature of Distance to TSS	All features
All	0.784767309	0.775183171	0.869331415	0.894740215	0.903141
Monogenic	0.884655859	0.884135727	0.931412506	0.949788056	0.958155
Complex	0.773923689	0.757378152	0.840505764	0.872722426	0.889062
Functional	0.77124755	0.767426622	0.886756535	0.906049016	0.905175

**Supp. Table S3. List of predicted functional SNPs**

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs35203747	NM_000518	91	1	YES
rs36208385	NM_001025366	49	0.999013889	
rs6053	NM_005141	28	0.9986	YES
rs4341800	NM_000515	208	0.998425	
rs3122011	NM_000567	100	0.998225	YES
rs11545077	NM_003878	150	0.998117063	YES
rs2069904	NM_000312	238	0.998099206	YES
rs71640268	NM_000515	292	0.998091667	
rs2854700	NM_000312	178	0.998089286	
rs72481825	NM_000515	128	0.998047619	
rs16991480	NM_001819	54	0.99795	YES
rs11099960	NM_005141	103	0.997875	YES
rs59260042	NM_001025366	179	0.997722222	
rs2001345	NM_000515	69	0.997522222	
rs61761358	NM_000515	260	0.997522222	
rs12210204	NM_001025366	662	0.997388889	
rs1799982	NM_000041	440	0.99734246	YES
rs36203394	NM_005141	19	0.997125	YES
rs41311442	NM_000953	120	0.99702381	
rs2227395	NM_005141	365	0.997	YES
rs10399931	NM_001276	157	0.996963095	YES
rs61761357	NM_000515	359	0.99667619	
rs72654467	NM_000041	51	0.996663492	YES
rs9282609	NM_000041	74	0.996614683	YES
rs41280570	NM_000312	213	0.996599206	
rs73598766	NM_001819	384	0.996446429	YES
rs877973	NM_000041	244	0.996307143	YES

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs2070010	NM_000508	69	0.99628373	
rs2001344	NM_000515	192	0.996230952	
rs36006214	NM_000518	104	0.996222222	YES
rs55809110	NM_015837	241	0.996193651	
rs1800909	NM_003878	75	0.996132143	YES
rs2069712	NM_000619	332	0.996032143	YES
rs41311440	NM_000953	29	0.99602381	
rs61762496	NM_000515	343	0.996009524	
rs2736677	NM_003878	423	0.995886905	YES
rs56077270	NM_000600	523	0.995880952	
rs56947728	NM_000312	294	0.995755952	
rs1800788	NM_005141	232	0.995740079	YES
rs71640267	NM_000515	351	0.995714286	
rs34260214	NM_000567	225	0.995671032	YES
rs35500644	NM_000567	495	0.995610317	YES
rs6039	NM_000131	123	0.995593254	YES
rs7219235	NM_000515	226	0.995485317	
rs3813727	NM_000519	53	0.995472222	YES
rs28913904	NM_000668	609	0.995372222	
rs10482844	NM_000131	122	0.995357937	YES
rs9332097	NM_000771	1514	0.995279762	
rs2774030	NM_000131	310	0.995232937	YES
rs439382	NM_000041	564	0.99515	YES
rs17152845	NM_005746	504	0.995126587	
rs35125951	NM_000360	344	0.995032937	YES
rs41495052	NM_000953	514	0.994986905	
rs7865453	NM_015837	54	0.994956349	
rs9282659	NM_000567	213	0.994947619	YES
rs34680782	NM_000078	225	0.99492619	YES

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs3758147	NM_003878	619	0.994917063	YES
rs11558195	NM_001819	122	0.994810714	YES
rs72654466	NM_000041	253	0.994767857	YES
rs34236606	NM_000953	511	0.994447619	
rs41269713	NM_173353	608	0.994391667	
rs7032741	NM_015837	279	0.994343254	
rs11575010	NM_002982	357	0.994236508	
rs33935445	NM_000518	94	0.994222222	YES
rs72551336	NM_007120	45	0.994200397	
rs41360251	NM_002986	771	0.994111111	
rs72551121	NM_015837	59	0.994087302	
rs36208049	NM_001025366	1274	0.994043254	
rs33933811	NM_000078	183	0.993997619	YES
rs769447	NM_000041	487	0.993881349	YES
rs769445	NM_000041	727	0.993878968	YES
rs11575011	NM_002982	49	0.993793651	
rs17735961	NM_002986	347	0.993561508	
rs72551117	NM_015837	839	0.993555952	
rs13306748	NM_002982	482	0.993536508	
rs648272	NM_002422	261	0.993511508	YES
rs35382661	NM_000518	106	0.993458333	YES
rs72551118	NM_015837	810	0.993288095	
rs72551119	NM_015837	543	0.993276587	
rs2736678	NM_003878	14	0.993251984	YES
rs28913907	NM_000668	237	0.993213492	
rs36215461	NM_000600	501	0.993202381	
rs2736676	NM_003878	589	0.993190476	YES
rs1860184	NM_002986	445	0.993155556	
rs45621441	NM_007120	230	0.993045635	

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs3917465	NM_000446	674	0.993017857	
rs16966671	NM_000101	817	0.992802381	
rs35634210	NM_000078	96	0.99278254	YES
rs41269707	NM_173353	378	0.992777381	
rs13306296	NM_000101	499	0.992682143	
rs34514827	NM_000863	45	0.992604365	YES
rs41454744	NM_002985	243	0.992594048	YES
rs2069711	NM_000619	312	0.992552778	YES
rs16966669	NM_000101	796	0.992534127	
rs4783962	NM_000078	797	0.992504762	YES
rs33970907	NM_000559	121	0.992496032	YES
rs41272325	NM_001063	142	0.992484127	
rs56120942	NM_002986	153	0.99241746	
rs11575012	NM_002982	46	0.992398413	
rs3025091	NM_002422	285	0.992309921	YES
rs62191899	NM_007120	70	0.992206349	
rs33955330	NM_000559	117	0.992162698	YES
rs28365060	NM_003878	545	0.992046032	YES
rs55701929	NM_002423	68	0.991972619	
rs5884	NM_000078	122	0.991947619	YES
rs130059	NM_000863	276	0.991861111	YES
rs36208414	NM_000131	419	0.991835714	YES
rs72503766	NM_000668	234	0.991834921	
rs61733934	NM_018242	172	0.991819444	YES
rs11574981	NM_001872	251	0.991815079	
rs63751196	NM_000559	115	0.991634921	YES
rs711752	NM_000078	376	0.991620238	YES
rs1800249	NM_001063	441	0.991587302	
rs464138	NM_002462	19	0.991562302	

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs55972053	NM_000559	210	0.991527778	YES
rs7941835	NM_000559	15	0.991527778	YES
rs17245715	NM_000078	845	0.991449206	YES
rs58849201	NM_001004056	54	0.991444444	
rs35802118	NM_000518	105	0.991440476	YES
rs2860470	NM_000184	306	0.991430556	YES
rs36208384	NM_001025366	44	0.991346825	
rs2069830	NM_000600	319	0.991328175	
rs7598133	NM_000312	261	0.991236111	YES
rs41311354	NM_000953	529	0.991164683	
rs17844147	NM_001872	182	0.991123413	
rs1130459	NM_001063	48	0.991123016	
rs35086834	NM_000567	78	0.991115476	YES
rs2280789	NM_002985	375	0.99107381	YES
rs45510694	NM_007120	178	0.991039683	
rs45571233	NM_007120	193	0.991039683	
rs34389944	NM_000519	272	0.991027778	YES
rs34410778	NM_000542	277	0.991017857	
rs3024488	NM_000572	507	0.99099246	
rs35549891	NM_000078	385	0.990957143	YES
rs41311352	NM_000953	709	0.990864286	
rs6827826	NM_001729	133	0.990796032	YES
rs3816117	NM_000078	323	0.990727381	YES
rs3742266	NM_001872	173	0.990688492	
rs34018799	NM_000559	113	0.990634921	YES
rs61757167	NM_000029	118	0.99063373	
rs9658639	NM_001275	341	0.99062381	
rs33924825	NM_000559	72	0.990611111	YES
rs17231534	NM_000078	269	0.990471429	YES

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs10411464	NM_004708	162	0.990455952	YES
rs34432567	NM_000559	73	0.990369048	YES
rs34263826	NM_000559	70	0.990293651	YES
rs41298273	NM_001063	85	0.99025873	
rs57946219	NM_000101	403	0.990250794	
rs71351177	NM_004708	210	0.990181349	YES
rs36215459	NM_000600	255	0.99014127	
rs140313	NM_000853	331	0.990130159	
rs35157665	NM_001729	69	0.990086111	YES
rs34460332	NM_000519	269	0.990075397	YES
rs12828954	NM_004064	569	0.990038492	
rs11564712	NM_000360	257	0.990026984	YES
rs522616	NM_002422	705	0.990025794	YES
rs41559012	NM_001983	128	0.989972619	
rs6684919	NM_001276	260	0.989966667	
rs10142136	NM_001007023	284	0.989960317	
rs34866629	NM_000518	108	0.989890476	YES
rs17847006	NM_001275	404	0.98987381	
rs35621390	NM_000559	107	0.989829365	YES
rs34197986	NM_000542	238	0.989726587	
rs61757165	NM_000029	206	0.989688095	
rs36215817	NM_000600	773	0.98954127	
rs28730833	NM_002982	198	0.98948373	
rs41507946	NM_002982	245	0.98948373	
rs3024793	NM_000542	51	0.989442063	
rs3212935	NM_001983	403	0.98938373	
rs4108129	NM_000766	1246	0.989279762	
rs16840275	NM_001037631	231	0.989275794	YES
rs41540513	NM_001983	55	0.989210714	

RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs16843684	NM_001004056	333	0.989162698	
rs231775	NM_001037631	205	0.989150794	YES
rs6298	NM_000863	129	0.989069048	YES
rs28399435	NM_000762	95	0.98906746	
rs8178901	NM_000042	131	0.989060317	
rs56283800	NM_000762	153	0.989055159	
rs10482839	NM_000131	512	0.989032143	YES
rs2222202	NM_000572	459	0.98899246	YES
rs72546660	NM_005266	196	0.988966667	YES
rs28399438	NM_000762	422	0.988955159	
rs56360274	NM_000762	417	0.988955159	
rs3024489	NM_000572	404	0.98886746	
rs3783610	NM_001078	106	0.988861111	YES
rs41432444	NM_002986	295	0.988784921	
rs8177185	NM_001063	617	0.988762302	
rs1894397	NM_000184	25	0.988701587	YES
rs10465885	NM_181703	25	0.988683333	YES
rs9658637	NM_001275	13	0.98862381	
rs28399437	NM_000762	397	0.98859127	
rs17132982	NM_001101648	326	0.988486111	YES
rs11872023	NM_002986	81	0.988479365	
rs34504099	NM_002875	99	0.98846746	YES
rs521018	NM_000868	643	0.988464286	
rs41385751	NM_002198	481	0.988431349	YES
rs33973337	NM_000767	82	0.988319444	YES
rs3212933	NM_001983	42	0.988210714	
rs9658635	NM_001275	368	0.98813373	
rs3811698	NM_000581	641	0.988133333	YES
rs34093840	NM_000519	257	0.988071429	YES



RefSNP id	Associated transcript	Distance to transcription start site	Prediction Score	In LD with reported GWAS ?
rs8192722	NM_000762	218	0.987900794	
rs1800508	NM_000623	16	0.987896429	YES
rs3797219	NM_000762	610	0.987871825	
rs4147582	NM_000853	78	0.987836508	
rs3794624	NM_000101	384	0.987829365	
rs11574982	NM_001872	252	0.987796825	
rs72546658	NM_005266	188	0.987763492	YES
rs12290216	NM_000184	270	0.987706349	YES
rs57655006	NM_001276	291	0.987633333	YES
rs4459901	NM_001063	464	0.987554762	
rs28399436	NM_000762	246	0.987539286	
rs28399416	NM_000761	155	0.987528968	YES
rs8177184	NM_001063	739	0.987484127	
rs1129844	NM_002986	207	0.987411508	
rs248743	NM_004064	522	0.987350794	
rs13447446	NM_000600	110	0.987236111	
rs34844625	NM_000184	355	0.987222222	YES
rs34289459	NM_000519	276	0.987202778	YES
rs62626349	NM_001042599	168	0.98717381	
rs8176073	NM_007294	364	0.987096825	YES
rs58554624	NM_007120	170	0.987090873	
rs8179169	NM_000581	94	0.987073016	YES
rs7159215	NM_001275	325	0.987070238	
rs2302990	NM_000762	492	0.987055159	

**Supp. Table S4. Description statistics for all investigated features**

FEATURE	ITEM	ALL	MS	CS	FS	BACKGROUND
Coefficient of variation for expression level	N	168182	48	208	172	167754
Coefficient of variation for expression level	MEDIAN	11.06329972	17.80061	12.17694	11.26883	11.06176899
Coefficient of variation for expression level	MEAN	12.24058306	19.26055	13.6566	13.38164	12.23564875
Coefficient of variation for expression level	MIN	2.546574035	5.802231	4.396191	4.487093	2.546574035
Coefficient of variation for expression level	MAX	53.70137252	31.02476	44.15748	31.24862	53.70137252
Coefficient of variation for expression level	STD	5.745930076	5.076439	6.50731	6.165525	5.743150696
Coefficient of variation for expression level	CV	46.94163706	26.35667	47.64955	46.07452	46.93785197
Derived allele frequency	N	45235	2	106	71	45056
Derived allele frequency	MEDIAN	0.7944444444	0.957158	0.710037	0.693309	0.794776119
Derived allele frequency	MEAN	0.702134134	0.957158	0.66044	0.647022	0.702307751
Derived allele frequency	MIN	0	0.955056	0.17037	0.005725	0
Derived allele frequency	MAX	1	0.959259	0.976471	0.997191	1
Derived allele frequency	STD	0.277817006	0.002972	0.219572	0.270432	0.277940917
Derived allele frequency	CV	39.56751173	0.310505	33.24629	41.79636	39.57537373
Distance to transcription start site	N	241910	48	214	183	241465
Distance to transcription start site	MEDIAN	965	109.5	344	261	967
Distance to transcription start site	MEAN	1062.03054	169.8333	481.4206	459.377	1063.179202
Distance to transcription start site	MIN	0	1	1	1	0
Distance to transcription start site	MAX	2499	1257	2306	2313	2499
Distance to transcription start site	STD	761.4792122	216.6322	455.1627	515.9776	761.4414484
Distance to transcription start site	CV	71.70031212	127.5558	94.54575	112.3212	71.61929495
Effective number of codons	N	240848	48	213	179	240408
Effective number of codons	MEDIAN	49.48	40.22	48.33	50.06	49.48
Effective number of codons	MEAN	48.12359816	41.63313	47.89085	48.3157	48.12495724
Effective number of codons	MIN	23.35	34.01	26.65	29.87	23.35
Effective number of codons	MAX	61	59.44	61	61	61
Effective number of codons	STD	6.908323254	7.657274	7.119066	6.668819	6.907583189

FEATURE	ITEM	ALL	MS	CS	FS	BACKGROUND
Effective number of codons	CV	14.35537557	18.39226	14.86519	13.80259	14.35343237
Frequency of optimal codons	N	241125	48	213	179	240685
Frequency of optimal codons	MEDIAN	0.453	0.49	0.469	0.452	0.453
Frequency of optimal codons	MEAN	0.457502623	0.47625	0.474113	0.462615	0.457480383
Frequency of optimal codons	MIN	0.212	0.386	0.345	0.355	0.212
Frequency of optimal codons	MAX	0.797	0.593	0.718	0.594	0.797
Frequency of optimal codons	STD	0.062147284	0.035613	0.060003	0.057858	0.062153977
Frequency of optimal codons	CV	13.58402796	7.477894	12.65591	12.50664	13.58615126
GC content	N	239918	47	214	181	239476
GC content	MEDIAN	10	12	11	11	10
GC content	MEAN	10.20417393	11.2766	11.14019	11.06077	10.20247958
GC content	MIN	0	7	4	2	0
GC content	MAX	20	15	20	18	20
GC content	STD	3.625532451	2.113128	3.268712	3.335276	3.626080246
GC content	CV	35.52989666	18.73906	29.34163	30.15409	35.54116641
In conserved non-coding sequences	N	241910	48	214	183	241465
In conserved non-coding sequences	MEDIAN	0	0	0	0	0
In conserved non-coding sequences	MEAN	0.121888306	0.125	0.21028	0.202186	0.121748494
In conserved non-coding sequences	MIN	0	0	0	0	0
In conserved non-coding sequences	MAX	1	1	1	1	1
In conserved non-coding sequences	STD	0.327157438	0.334219	0.408463	0.402732	0.326995781
In conserved non-coding sequences	CV	268.4075688	267.3749	194.2469	199.189	268.58302
In CpG island	N	241910	48	214	183	241465
In CpG island	MEDIAN	0	0	0	0	0
In CpG island	MEAN	0.17554049	0.0625	0.252336	0.273224	0.175420868
In CpG island	MIN	0	0	0	0	0
In CpG island	MAX	1	1	1	1	1
In CpG island	STD	0.380429527	0.244623	0.435372	0.446837	0.380327473
In CpG island	CV	216.7189611	391.3968	172.5362	163.5425	216.8085679

FEATURE	ITEM	ALL	MS	CS	FS	BACKGROUND
In enhancer	N	241910	48	214	183	241465
In enhancer	MEDIAN	0	0	0	0	0
In enhancer	MEAN	0.017200612	0.416667	0.084112	0.136612	0.016971404
In enhancer	MIN	0	0	0	0	0
In enhancer	MAX	1	1	1	1	1
In enhancer	STD	0.13001854	0.498224	0.278207	0.34438	0.129164408
In enhancer	CV	755.8948548	119.5737	330.7569	252.0858	761.0708579
In insulator	N	241910	48	214	183	241465
In insulator	MEDIAN	0	0	0	0	0
In insulator	MEAN	0.106415609	0.020833	0.135514	0.136612	0.106383948
In insulator	MIN	0	0	0	0	0
In insulator	MAX	1	1	1	1	1
In insulator	STD	0.308369454	0.144338	0.343074	0.34438	0.308329041
In insulator	CV	289.7784046	692.8203	253.1652	252.0858	289.8266576
In nuclease hypersensitive site	N	241910	48	214	183	241465
In nuclease hypersensitive site	MEDIAN	0	0	0	0	0
In nuclease hypersensitive site	MEAN	0.275060973	0.0625	0.378505	0.322404	0.274975669
In nuclease hypersensitive site	MIN	0	0	0	0	0
In nuclease hypersensitive site	MAX	1	1	1	1	1
In nuclease hypersensitive site	STD	0.44654592	0.244623	0.486152	0.468679	0.446502941
In nuclease hypersensitive site	CV	162.3443394	391.3968	128.44	145.37	162.3790723
In RNA polymerase II enriched region	N	241910	48	214	183	241465
In RNA polymerase II enriched region	MEDIAN	0	0	0	0	0
In RNA polymerase II enriched region	MEAN	0.269124881	0.020833	0.285047	0.245902	0.269177728
In RNA polymerase II enriched region	MIN	0	0	0	0	0
In RNA polymerase II enriched region	MAX	1	1	1	1	1
In RNA polymerase II enriched region	STD	0.44350591	0.144338	0.452495	0.431802	0.443533418
In RNA polymerase II enriched region	CV	164.7955806	692.8203	158.7442	175.5994	164.7734463
In transcription factor binding site	N	241910	48	214	183	241465

FEATURE	ITEM	ALL	MS	CS	FS	BACKGROUND
In transcription factor binding site	MEDIAN	0	0	0	0	0
In transcription factor binding site	MEAN	0.031763879	0.145833	0.056075	0.032787	0.031718883
In transcription factor binding site	MIN	0	0	0	0	0
In transcription factor binding site	MAX	1	1	1	1	1
In transcription factor binding site	STD	0.175371213	0.356674	0.230605	0.178567	0.175251027
In transcription factor binding site	CV	552.1089285	244.5764	411.2464	544.6291	552.5132412
Maximum expression level	N	168182	48	208	172	167754
Maximum expression level	MEDIAN	10.89746734	16.51697	11.29692	11.81984	10.89595389
Maximum expression level	MEAN	11.10662289	15.23264	11.64668	11.96963	11.10388782
Maximum expression level	MIN	5.50779464	9.744203	7.257388	7.812712	5.50779464
Maximum expression level	MAX	17.52835185	17.43634	16.68701	17.04871	17.52835185
Maximum expression level	STD	1.91455089	2.781005	2.187364	2.059736	1.912186659
Maximum expression level	CV	17.2379211	18.25688	18.78101	17.20801	17.22087515
Mean expression level	N	168182	48	208	172	167754
Mean expression level	MEDIAN	8.344517751	9.816024	8.130068	8.239046	8.344517751
Mean expression level	MEAN	8.348121378	9.958372	8.209925	8.203246	8.347980525
Mean expression level	MIN	2.716359169	5.062283	5.146559	5.461743	2.716359169
Mean expression level	MAX	15.1416688	12.64329	13.51322	12.97615	15.1416688
Mean expression level	STD	1.503725761	2.167975	1.4113	1.371667	1.503489497
Mean expression level	CV	18.01274435	21.77037	17.19016	16.72102	18.01021808
Minimum expression level	N	168182	48	208	172	167754
Minimum expression level	MEDIAN	6.14974712	6.375039	5.748052	6.228819	6.14974712
Minimum expression level	MEAN	6.179215217	6.600146	5.982155	6.195733	6.179322176
Minimum expression level	MIN	-1	3.392317	1.807355	2.906891	-1
Minimum expression level	MAX	13.30972502	8.304541	11.09002	10.74908	13.30972502
Minimum expression level	STD	1.645747463	1.472888	1.577413	1.45615	1.646042626
Minimum expression level	CV	26.63359999	22.31599	26.36864	23.50246	26.6379156
Protein-protein interaction complexity	N	129749	40	201	149	129359
Protein-protein interaction complexity	MEDIAN	5	7	8	5	5

FEATURE	ITEM	ALL	MS	CS	FS	BACKGROUND
Protein-protein interaction complexity	MEAN	14.27493854	8.1	17.79602	14.87919	14.27068082
Protein-protein interaction complexity	MIN	1	1	1	1	1
Protein-protein interaction complexity	MAX	251	62	173	173	251
Protein-protein interaction complexity	STD	26.586524	9.994357	25.40813	28.00577	26.58979564
Protein-protein interaction complexity	CV	186.246154	123.3871	142.7742	188.221	186.3246469
Sequence conservation	N	240012	48	214	182	239568
Sequence conservation	MEDIAN	0.004428571	0.172286	0.007024	0.004762	0.004428571
Sequence conservation	MEAN	0.104558197	0.240896	0.130101	0.11593	0.104499424
Sequence conservation	MIN	0	0	0	0	0
Sequence conservation	MAX	1	0.993714	0.999952	0.998667	1
Sequence conservation	STD	0.241781198	0.260133	0.259074	0.239628	0.241755551
Sequence conservation	CV	231.2407876	107.9856	199.1335	206.6995	231.3462995
SNP diversity	N	45235	2	106	71	45056
SNP diversity	MEDIAN	0.270048884	0.082005	0.367295	0.340813	0.268619779
SNP diversity	MEAN	0.263922419	0.082005	0.353004	0.312562	0.26364427
SNP diversity	MIN	0	0.078162	0.045952	0.005602	0
SNP diversity	MAX	0.5	0.085848	0.499929	0.499971	0.5
SNP diversity	STD	0.168101556	0.005435	0.127662	0.159541	0.168133663
SNP diversity	CV	63.69354954	6.627341	36.16446	51.04291	63.77292505
Standard deviation for expression level	N	168182	48	208	172	167754
Standard deviation for expression level	MEDIAN	0.916624714	2.250583	0.964512	0.924345	0.91632799
Standard deviation for expression level	MEAN	0.979989378	1.908862	1.084335	1.057783	0.979514454
Standard deviation for expression level	MIN	0.262302324	0.53493	0.389662	0.391889	0.262302324
Standard deviation for expression level	MAX	3.517978462	2.856553	2.31765	2.877258	3.517978462
Standard deviation for expression level	STD	0.391533256	0.57041	0.443843	0.428915	0.391025356
Standard deviation for expression level	CV	39.95280614	29.88222	40.93225	40.54844	39.92032522