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## **DATA SUPPLEMENT**

**Binding Sites for Ets Family of Transcription Factors Dominate the Promoter Regions of Differentially Expressed Genes in Abdominal Aortic Aneurysms**

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**Table S1. Tissue Samples Used in Immunohistochemical Analyses**

Sample Code	Sample Origin	Sample Type	Donor Sex	Donor Age (years)	Diagnosis
WSU037	Aneurysmal sac	Operation	Male	79	AAA
WSU038	Aneurysmal sac	Operation	Male	67	AAA
WSU039	Aneurysmal sac	Operation	Male	64	AAA
WSU048	Aneurysmal sac	Operation	Female	87	AAA
WSU050	Aneurysmal sac	Operation	NA*	87	AAA
WSU064	Aneurysmal sac	Operation	Male	63	AAA
A07-83	Aortic wall	Autopsy	Female	87	
A07-84	Aortic wall	Autopsy	Male	58	
A07-87	Aortic wall	Autopsy	Male	62	
A07-88	Aortic wall	Autopsy	Female	58	
A07-90	Aortic wall	Autopsy	Male	68	

Control aorta samples were obtained at autopsy. Patient samples were tissues removed from the aneurysmal sac during surgical repair operations to trim the area for fitting the prosthesis.

\*Not available

**Table S2. 144 Overrepresented TFBSs in Promoters of Genes Downregulated in AAA**

TFBS*	Hits in Gene Set	Hits on Genome	$-\log_{10} P$	TF Class	TransFac Class ID
SOX5	3923	44277	91.5	HMG	C0015
LEF1/TCF1	3771	42880	84.3	HMG	C0015
FOXO1	3811	43570	82.5	fork head	C0023
POU1F1	3523	40305	76.1	POU	C0007
FOXP3	3630	42427	68.7	fork head	C0023
FOXO4	2992	34073	66.6	fork head	C0023
TFIIA <sup>‡</sup>	3547	41523	66.5		
RFX1	4087	48905	66.1	fork head	C0023
AP4	3565	41839	65.8	bHLH-ZIP	C0012
HNF4ALPHA	3899	46399	65.5	CC (rec)	C0002
POU6F1	3327	38731	64.7	POU	C0007
PITX2	4030	48560	62.1	homeo	C0006
RBPJK <sup>‡</sup>	4050	49039	60.2		
E2F1/DP2 <sup>‡</sup>	2972	34433	59.7		
BARBIE <sup>‡</sup>	3092	36071	59.5		
GATA3	3393	40302	57.9	CC (g)	C0003
IRF1	2522	28928	54.0	trp	C0022
TEF	2573	29679	53.3	bZIP	C0008
E2F1/DP1	3189	38173	51.7	fork head	C0023
SOX9	2349	27130	48.4	HMG	C0015
CART1	2092	23736	48.0	homeo	C0006
DR3	3318	40723	44.9	CC (rec)	C0002
STAF	2308	27302	40.9	CH	C0001
CEBP	1680	18937	40.2	bZIP	C0008
GATA	1791	20534	38.8	CC (g)	C0003
S8	1482	16494	38.2	homeo	C0006
LHX3	1849	21421	37.6	LIM-homeo	C0025
AMEF2	1793	20711	37.2	MADS	C0014
HP1/SITEFACTOR <sup>‡</sup>	1566	17707	36.9		
IK1	1938	22989	33.9	CH	C0001
MINI20 <sup>‡</sup>	3053	38710	31.8		
GATA2	1521	17575	31.7	CC (g)	C0003
NKX61	960	10209	31.5	NK-2/Nkx	C0053
VBP	1464	16840	31.4	bZIP	C0008
LBP1	1687	19854	31.2	Grainyhead	C0051
HFH8	1389	15852	31.2	fork head	C0023
TITF1	1705	20286	29.4	NK-2/Nkx <sup>†</sup>	C0053
				homeo <sup>†</sup>	C0006
TEF1	1125	12520	29.3	TEA	C0024
ERR1	3309	42698	29.3	CC (rec)	C0002
MEIS1	2219	27385	29.2	homeo	C0006
TFIII <sup>‡</sup>	1992	24258	29.0		
CMYB	2113	25955	28.8	trp	C0022
GLI	3401	44154	28.3	CH	C0001
AR	1561	18467	28.0	CC (rec)	C0002
NANOG	1816	22062	27.0	homeo	C0006
ETS1	1847	22501	26.9	ETS	C0016
SMAD3	2343	29403	26.9	SMAD	C0041
SP3	2308	28919	26.9	CH	C0001
LFA1 <sup>‡</sup>	2267	28678	24.4		
ZID	2321	29502	23.9	CH	C0001

TFBS*	Hits in Gene Set	Hits on Genome	$-\log_{10} P$	TF Class	TransFac Class ID
LMO2COM	1833	22717	23.5	LIM	C0028
NRF2	2530	32616	22.9	ETS <sup>†</sup>	C0016
				bZIP <sup>†</sup>	C0008
MYOGENIN	1479	18024	21.8	bHLH	C0010
ARP1	1412	17149	21.3	CC (rec)	C0002
HFH3	3117	41393	20.6	fork head	C0023
IK3	778	8744	19.6	CH	C0001
CHX10	859	9846	19.3	homeo	C0006
TCF4	1025	12126	18.8	HMG	C0015
CIZ	862	9945	18.6	CH	C0001
CREBATF	1425	17756	17.8	bZIP	C0008
NKX25	1528	19198	17.8	NK-2/Nkx	C0053
ATF4	2025	26282	17.4	bZIP	C0008
ZNF219	822	9536	17.2	CH	C0001
HFH4	787	9096	16.9	fork head	C0023
SMAD3	2343	29403	26.9	SMAD	C0041
HFH1	774	8925	16.9	fork head	C0023
CDP	618	6892	16.4	homeo	C0006
SOX	587	6496	16.3	HMG	C0015
AP2ALPHA	1103	13468	16.3	bHSH	C0032
AML	1439	18339	14.9	runt	C0029
NFKAPPAB	1829	23956	14.5	Rel	C0020
ELF1	944	11549	13.9	Grainyhead <sup>†</sup>	C0051
				ETS <sup>†</sup>	C0016
NFE2	914	11215	13.2	bZIP	C0008
E47	1168	14763	13.2	bHLH	C0010
ATF3	1238	15751	13.2	bZIP	C0008
TGIF	729	8716	12.8	homeo	C0006
XFD1	512	5806	12.6	fork head	C0023
PEA3	1662	21887	12.5	ETS	C0016
R <sup>‡</sup>	733	8819	12.3		
FOXO3	319	3332	12.1	fork head	C0023
HES1	1920	25756	11.7	bHLH	C0010
ETS2	953	11968	11.5	ETS	C0016
RSRFC4	324	3454	11.2	MADS	C0014
NKX22	526	6138	11.0	NK-2/Nkx	C0053
OCT	500	5806	10.8	POU	C0007
MEIS1AHOXA9	423	4781	10.8	homeo	C0006
AFP1 <sup>‡</sup>	353	3869	10.7		
RREB1	1292	16902	10.6	CH	C0001
GFI1B	472	5477	10.3	CH	C0001
FREAC2	284	3014	10.1	fork head	C0023
TAL1ALPHA47	495	5814	10.0	bHLH	C0010
MYC	1754	23703	9.9	bHLH-ZIP	C0012
PEBP	1286	16969	9.7	runt	C0029
E2 <sup>‡</sup>	614	7487	9.6		
PADS <sup>‡</sup>	493	5913	8.8		
XFD2	383	4440	8.6	fork head	C0023
EGR1	300	3338	8.6	CH	C0001
NMYC	1329	17846	8.3	bHLH-ZIP	C0012
OSF2	795	10228	8.0	runt	C0029
HNF6	151	1479	7.9	homeo	C0006
NGFIC	252	2780	7.6	CH	C0001
BLIMP1	169	1716	7.6	CH	C0001
MEIS1BHOXA9	207	2213	7.4	homeo	C0006
RORA	549	6870	7.2	CC (rec)	C0002
DEC	787	10307	6.8	bHLH	C0010
ZTA	568	7222	6.6	bZIP	C0008
CLOX	100	930	6.5	homeo	C0006
GCM	355	4276	6.4	GCM	C0031
RP58	117	1148	6.3	CH+BTB/POZ	C0058
ATF1	491	6207	6.1	bZIP	C0008
YY1	578	7443	6.0	CH	C0001
CETS168	955	12878	6.0	ETS	C0016
E12	647	8453	5.9	bHLH	C0010
TAL1BETAITF2	244	2849	5.6	bHLH	C0010
E2F4DP2 <sup>‡</sup>	365	4525	5.4		
STAT5A	238	2785	5.4	STAT	C0039
ICSBP	175	1947	5.4	trp	C0022
POU3F2	91	878	5.3	POU	C0007

TFBS*	Hits in Gene Set	Hits on Genome	$-\log_{10} P$	TF Class	TransFac Class ID
TALIBETAE47	263	3131	5.3	bHLH	C0010
TFE	1014	13897	5.2	bHLH-ZIP	C0012
PBX1	115	1186	5.2	homeo	C0006
GRE	230	2709	5.0	CC (rec)	C0002
CDPCR3	200	2306	5.0	homeo	C0006
HIF1	650	8663	4.9	bHLH	C0010
PTF1BETA <sup>‡</sup>	166	1879	4.7		
SREBP	395	5049	4.6	bHLH-ZIP	C0012
HSF1	193	2261	4.5	HSF	C0050
AREB6	1710	24574	4.0	CH+homeo	C0021
E4BP4	92	970	3.9	bZIP	C0008
ATF	269	3416	3.6	bZIP	C0008
E2F1DP1RB <sup>‡</sup>	124	1419	3.5		
FREAC4	69	704	3.5	fork head	C0023
FXR	179	2174	3.5	CC (rec)	C0002
CREBP1CJUN	251	3183	3.4	bZIP	C0008
AHRARNT	389	5199	3.1	bHLH	C0010
XFD3	138	1647	3.1	fork head	C0023
ATATA <sup>‡</sup>	29	242	3.1		
SREBP1	584	8106	2.9	bHLH-ZIP	C0012
UF1H3BETA <sup>‡</sup>	89	1008	2.9		
STAT5B	86	970	2.8	STAT	C0039
AHR	131	1580	2.8	bHLH	C0010
RORA1	287	3791	2.8	CC (rec)	C0002
ISRE <sup>‡</sup>	48	485	2.7		
BACH1	38	376	2.4	bZIP	C0008
HOXA7	67	749	2.4	homeo	C0006

The downregulated gene set of 1,603 genes was analyzed in Whole Genome rVISTA<sup>1</sup> to search for human sequences (UCSC version hg18, NCBI Build 36.1) conserved in alignment with mouse (UCSC version mm8, NCBI Build 36). The 5 kb region upstream from the transcription start site of each gene was examined for transcription factor binding site (TFBS) enrichment using a p-value cutoff of 0.006. Of the 1,603 downregulated genes, 23 (1.4%) were not found in the database resulting in an analysis of 1,580 genes. The 1,580 genes contained 144 overrepresented TFBSs when compared to the entire genome. Out of these 1,580 genes, 1,550 (98%) contain at least one binding site for one of the 144 overrepresented TFBSs with a range of one (16 genes) to 128 (2 genes) enriched TFBSs and an average of 52 TFBSs per gene. The TRANSFAC<sup>®</sup> Professional library<sup>2</sup> was then used to obtain further information about the TFBSs and the transcription factors binding to them.

\*Transcription factor binding site

<sup>†</sup>Three TFBSs each mapped to two transcription factor classes.

<sup>‡</sup>No transcription factor had been assigned to this TFBS in TRANSFAC<sup>®</sup> and thus no TF Class nor TransFac Class ID is shown here.

**Table S3. Summary of Transcription Factor Classes for 144 TFBSs for Genes with Decreased Expression (N=1,550)**

TF Class	TransFac CLASS ID	N	Duplicate*	N <sub>2</sub> *	Proportion	Cumulative
fork head	C0023	15		15	0.122	0.122
homeo	C0006	16	1	15	0.122	0.244
CH	C0001	14		14	0.114	0.358
bZIP	C0008	14	1	13	0.106	0.463
bHLH	C0010	11		11	0.089	0.553
CC (rec)	C0002	9		9	0.073	0.626
bHLH-ZIP	C0012	6		6	0.049	0.675
HMG	C0015	5		5	0.041	0.715
ETS	C0016	6	2	4	0.033	0.748
POU	C0007	4		4	0.033	0.780
CC (g)	C0003	3		3	0.024	0.805
NK-2/Nkx	C0053	4	1	3	0.024	0.829
runt	C0029	3		3	0.024	0.854
trp	C0022	3		3	0.024	0.878
MADS	C0014	2		2	0.016	0.894
STAT	C0039	2		2	0.016	0.911
bHSH	C0032	1		1	0.008	0.919
CH+BTB/POZ	C0058	1		1	0.008	0.927
CH+homeo	C0021	1		1	0.008	0.935
GCM	C0031	1		1	0.008	0.943
Grainyhead	C0051	2	1	1	0.008	0.951
HSF	C0050	1		1	0.008	0.959
LIM	C0028	1		1	0.008	0.967
LIM-homeo	C0025	1		1	0.008	0.976
Rel	C0020	1		1	0.008	0.984
SMAD	C0041	1		1	0.008	0.992
TEA	C0024	1		1	0.008	1.000

\*Three binding sites mapped to more than 1 TF class.

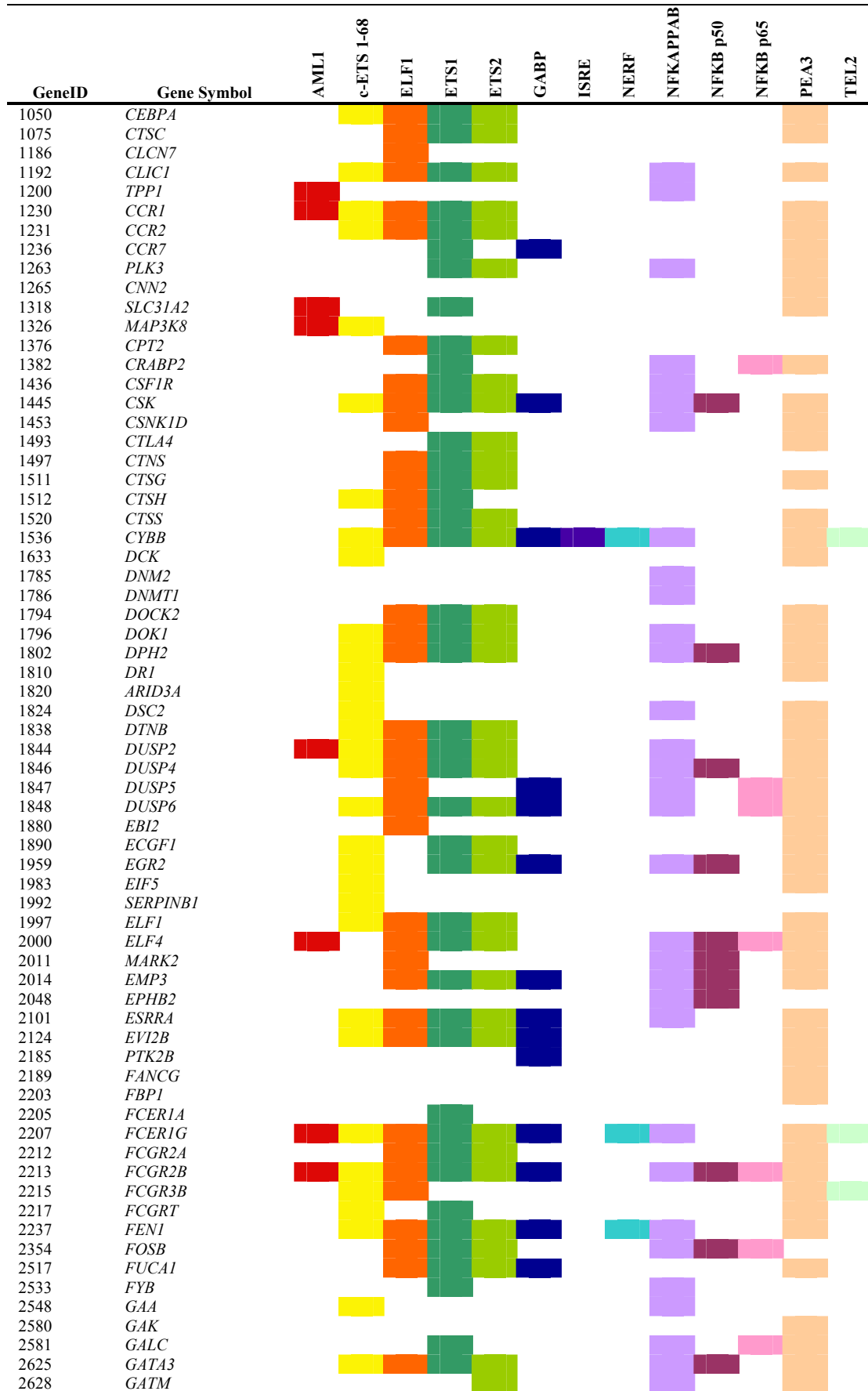
**Table S4. Enriched Gene Ontology (GO) Categories for Genes with Decreased Expression (N=1,242\*)**

GO Term	GO ID	GO Size	Expect. Count	Count	Odds Ratio	P-value
cell adhesion	0007155	690	67.16	124	2.15	5.15E-12
cell morphogenesis	0000902	496	48.27	87	2.05	3.01E-08
muscle development	0007517	64	6.15	22	5.00	5.32E-08
negative regulation of biological process	0048519	1338	130.22	187	1.60	8.33E-08
localization of cell	0051674	432	42.05	77	2.08	9.68E-08
regulation of locomotion	0040012	127	12.36	33	3.32	1.01E-07
cell-matrix adhesion	0007160	89	8.66	25	3.68	7.32E-07
anatomical structure development	0048856	330	30.28	58	2.18	8.48E-07
cell motility	0048870	286	27.84	54	2.21	1.34E-06
regulation of cell motion	0051270	81	7.82	23	3.76	1.43E-06
embryonic development	0009790	356	34.65	62	2.01	3.82E-06
regulation of anatomical structure morphogenesis	0022603	307	29.88	55	2.07	5.67E-06
regulation of cell growth	0001558	124	12.07	29	2.87	5.94E-06
heart development	0007507	144	14.02	32	2.69	6.34E-06
regulation of cell size	0008361	163	15.86	34	2.49	1.41E-05
regulation of cellular component organization	0051128	420	40.66	68	1.85	1.41E-05
striated muscle development	0014706	128	12.46	28	2.63	3.20E-05
cellular developmental process	0048869	1459	142.00	186	1.42	3.93E-05
circulatory system process	0003013	188	18.30	36	2.23	5.55E-05
regulation of blood vessel size	0050880	56	5.45	16	3.75	5.70E-05
negative regulation of RNA metabolic process	0051253	254	24.72	44	1.98	0.00011
positive regulation of cell migration	0030335	53	5.16	15	3.69	0.00011
pattern specification process	0007389	180	17.52	34	2.19	0.00012
negative regulation of transcription	0016481	333	32.41	54	1.83	0.00012
actin cytoskeleton organization	0030036	113	10.90	24	2.56	0.00016
negative regulation of cellular metabolic process	0031324	506	49.25	74	1.63	0.00022
regulation of vasoconstriction	0019229	15	1.46	7	8.17	0.00026
kidney development	0001822	51	4.96	14	3.54	0.00026
skeletal system development	0001501	264	25.69	44	1.89	0.00026
smooth muscle contraction	0006939	35	3.41	11	4.28	0.00033
negative regulation of biosynthetic process	0009890	406	39.52	61	1.67	0.00038
chordate embryonic development	0043009	184	17.91	33	2.05	0.00040
negative regulation of transcription from RNA polymerase II promoter	0000122	178	17.32	32	2.06	0.00046
regulation of cell shape	0008360	42	4.09	12	3.74	0.00048
growth	0040007	322	31.34	50	1.73	0.00059
response to heat	0009408	27	2.63	9	4.66	0.00070
integrin-mediated signaling pathway	0007229	51	4.96	13	3.20	0.00093
homophilic cell adhesion	0007156	126	12.26	24	2.21	0.00099
cell junction organization	0034330	23	2.24	8	4.97	0.00102
actin filament organization	0007015	98	9.54	20	2.40	0.00105
BMP signaling pathway	0030509	52	5.06	13	3.11	0.00113
organ morphogenesis	0009887	509	49.54	71	1.53	0.00114
transmembrane receptor protein serine/threonine kinase signaling pathway	0007178	120	11.68	23	2.22	0.00114
neural tube formation	0001841	19	1.85	7	5.44	0.00143
glycogen metabolic process	0005977	41	3.99	11	3.42	0.00144
limb development	0060173	60	5.84	14	2.84	0.00153
oxidation reduction	0055114	567	55.18	77	1.49	0.00154
gastrulation	0007369	54	5.26	13	2.96	0.00164
nervous system development	0007399	773	75.23	100	1.41	0.00168
negative regulation of cell migration	0030336	42	4.09	11	3.31	0.00178
glucan metabolic process	0044042	42	4.09	11	3.31	0.00178
system development	0048731	814	76.50	101	1.40	0.00194
regulation of signal transduction	0009966	599	58.30	80	1.46	0.0020
extracellular structure organization	0043062	96	9.34	19	2.31	0.0020
negative regulation of cell differentiation	0045596	126	12.26	23	2.09	0.0022
germ cell migration	0008354	7	0.68	4	12.40	0.0025
regulation of protein complex disassembly	0043244	44	4.28	11	3.11	0.0027
oxygen and reactive oxygen species metabolic process	0006800	57	5.55	13	2.76	0.0028
cellular polysaccharide metabolic process	0044264	57	5.55	13	2.76	0.0028
muscle cell differentiation	0042692	51	4.95	12	2.88	0.0029
Notch signaling pathway	0007219	51	4.96	12	2.87	0.0030
regulation of muscle contraction	0006937	45	4.38	11	3.02	0.0032
mesoderm formation	0001707	27	2.63	8	3.92	0.0032
appendage morphogenesis	0035107	58	5.65	13	2.70	0.0032
negative regulation of cell motion	0051271	4	0.39	3	28.06	0.0034

GO Term	GO ID	GO Size	Expect.		Odds	
			Count	Count	Ratio	P-value
regulation of amyloid precursor protein biosynthetic process	0042984	4	0.39	3	27.89	0.0034
cytoskeleton organization	0007010	156	14.89	26	1.92	0.0034
ureteric bud development	0001657	22	2.14	7	4.35	0.0037
neural tube closure	0001843	12	1.17	5	6.65	0.0038
embryonic skeletal system morphogenesis	0048704	40	3.89	10	3.11	0.0041
anterior/posterior pattern formation	0009952	95	9.25	18	2.19	0.0043
enzyme linked receptor protein signaling pathway	0007167	238	22.95	36	1.69	0.0043
positive regulation of mesenchymal cell proliferation	0002053	8	0.78	4	9.30	0.0045
regulation of smooth muscle cell migration	0014910	8	0.78	4	9.30	0.0045
platelet-derived growth factor receptor signaling pathway	0048008	8	0.78	4	9.30	0.0045
negative regulation of cell proliferation	0008285	271	26.38	40	1.63	0.0049
protein depolymerization	0051261	41	3.99	10	3.01	0.0050
multicellular organismal process	0032501	3433	334.13	373	1.19	0.0052
myofibril assembly	0030239	18	1.75	6	4.65	0.0056
positive regulation of fibroblast proliferation	0048146	18	1.75	6	4.65	0.0056
negative regulation of microtubule depolymerization	0007026	13	1.27	5	5.82	0.0057
cell-cell junction assembly	0007043	13	1.27	5	5.82	0.0057
mesoderm development	0007498	55	5.35	12	2.60	0.0058
positive regulation of epithelial cell proliferation	0050679	24	2.34	7	3.83	0.0064
response to calcium ion	0051592	30	2.92	8	3.39	0.0066
cell projection assembly	0030031	63	6.13	13	2.43	0.0068
tube morphogenesis	0035239	63	6.13	13	2.43	0.0068
negative regulation of cell communication	0010648	146	14.21	24	1.84	0.0073
regulation of systemic arterial blood pressure by renin-angiotensin	0003081	9	0.88	4	7.44	0.0075
middle ear morphogenesis	0042474	9	0.88	4	7.44	0.0075
artery morphogenesis	0048844	9	0.88	4	7.44	0.0075
cytokinesis	0000910	37	3.60	9	3.00	0.0077
muscle cell proliferation	0033002	37	3.60	9	3.00	0.0077
Golgi to plasma membrane transport	0006893	5	0.49	3	13.94	0.0079
cilium morphogenesis	0060271	5	0.49	3	13.94	0.0079
ossification	0001503	116	11.29	20	1.95	0.0081
regulation of cellular protein metabolic process	0032268	331	32.22	46	1.52	0.0084
muscle contraction	0006936	102	9.85	18	2.02	0.0084
embryonic limb morphogenesis	0030326	51	4.96	11	2.56	0.0088
muscle cell development	0055001	20	1.95	6	3.99	0.0098

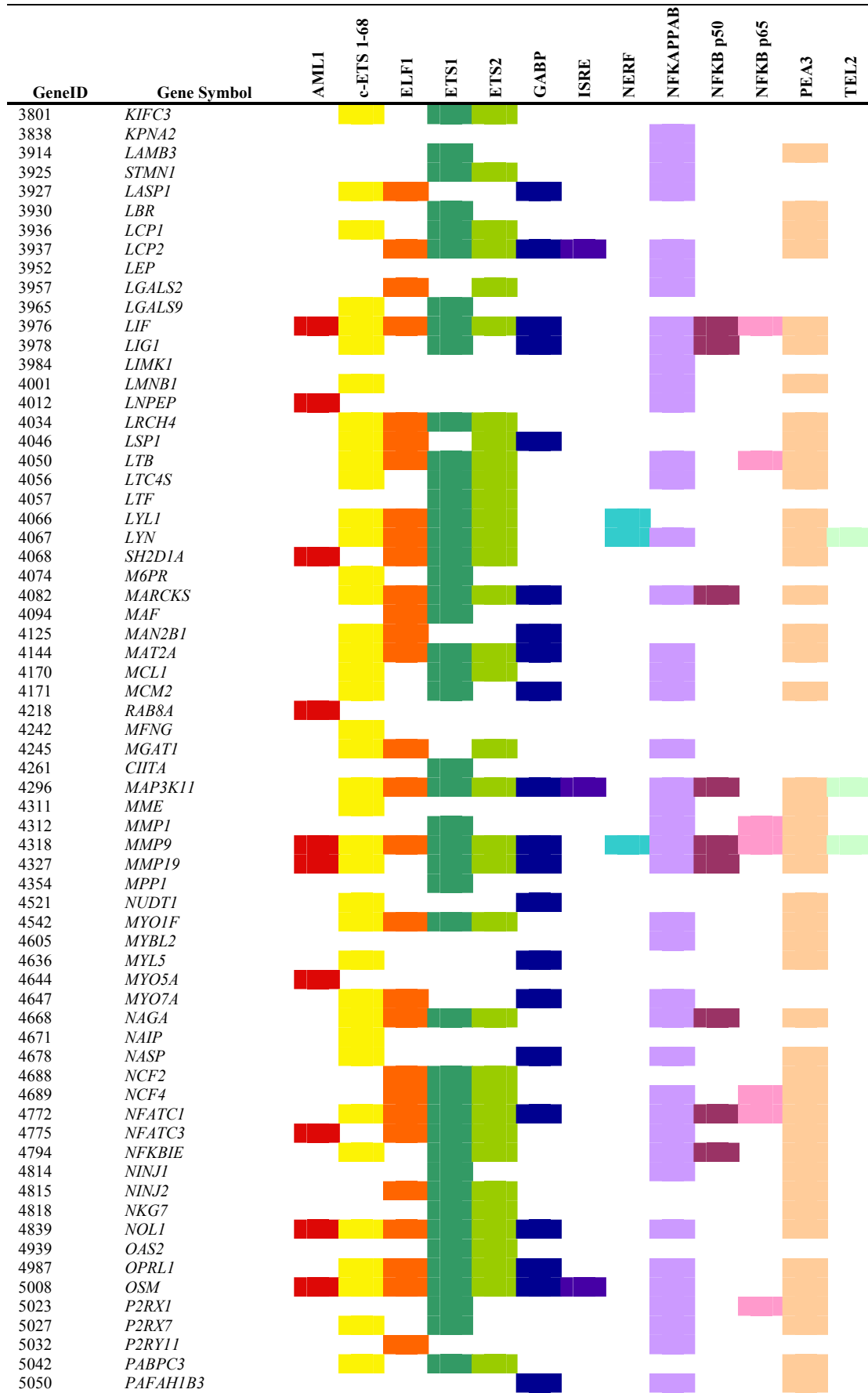
\*The downregulated gene list was used to identify enriched GO biological process categories with a software package available using R and Bioconductor.<sup>3,4</sup> A total of 1,242 genes with GO annotations were included into the analysis. This represents 77.5% of the total number of 1,603 genes with decreased expression in AAA tissue samples and analyzed with Whole Genome rVISTA. The remaining 22.5% did not have functional annotations as of June 6, 2009. The reference gene set was the 18,057 distinct genes represented on both Affymetrix and Illumina arrays based on our initial microarray studies.<sup>5</sup> Only GO categories with more than 2 genes and a nominal  $P < 0.01$  using the hypergeometric test for enrichment are listed here..



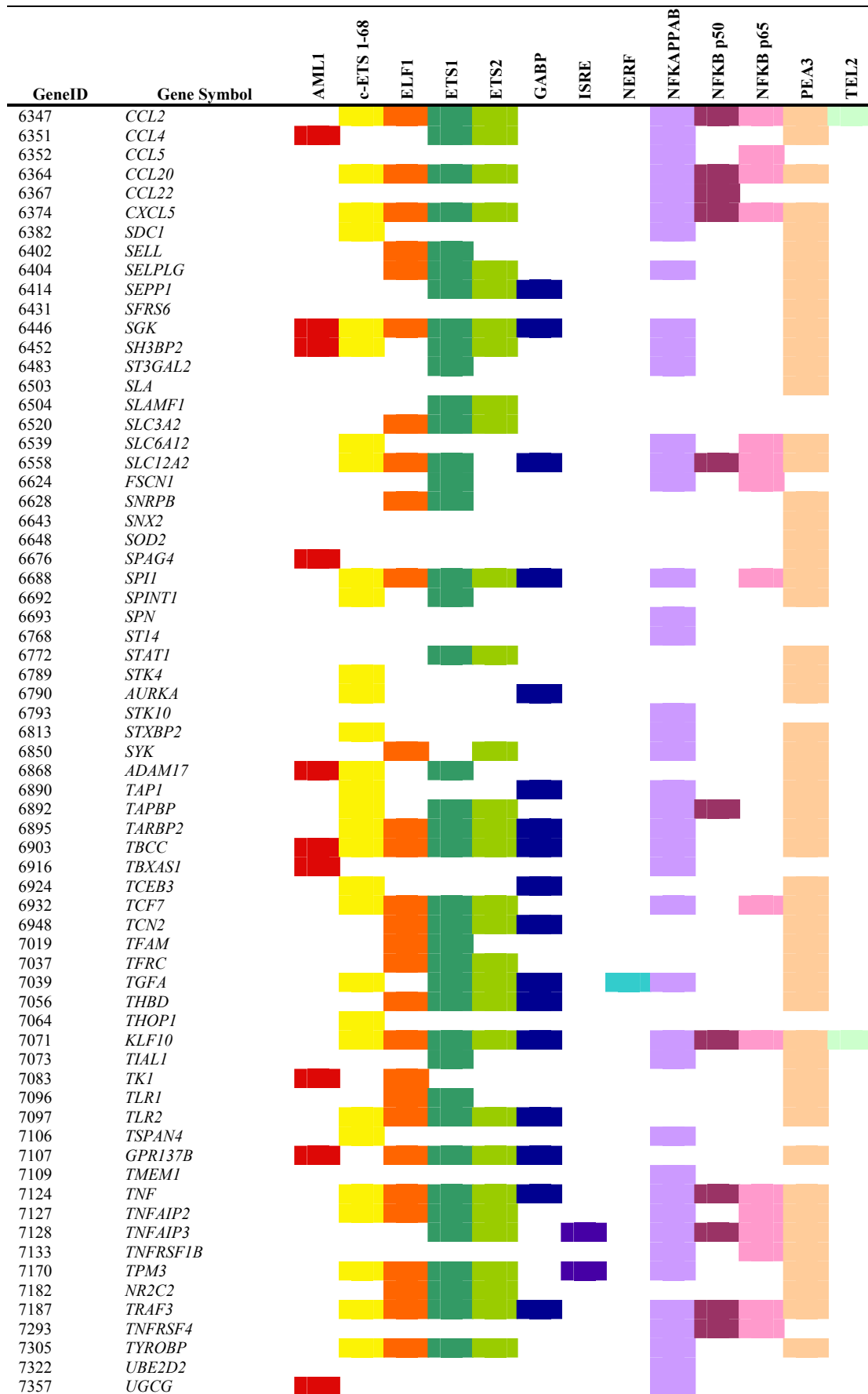


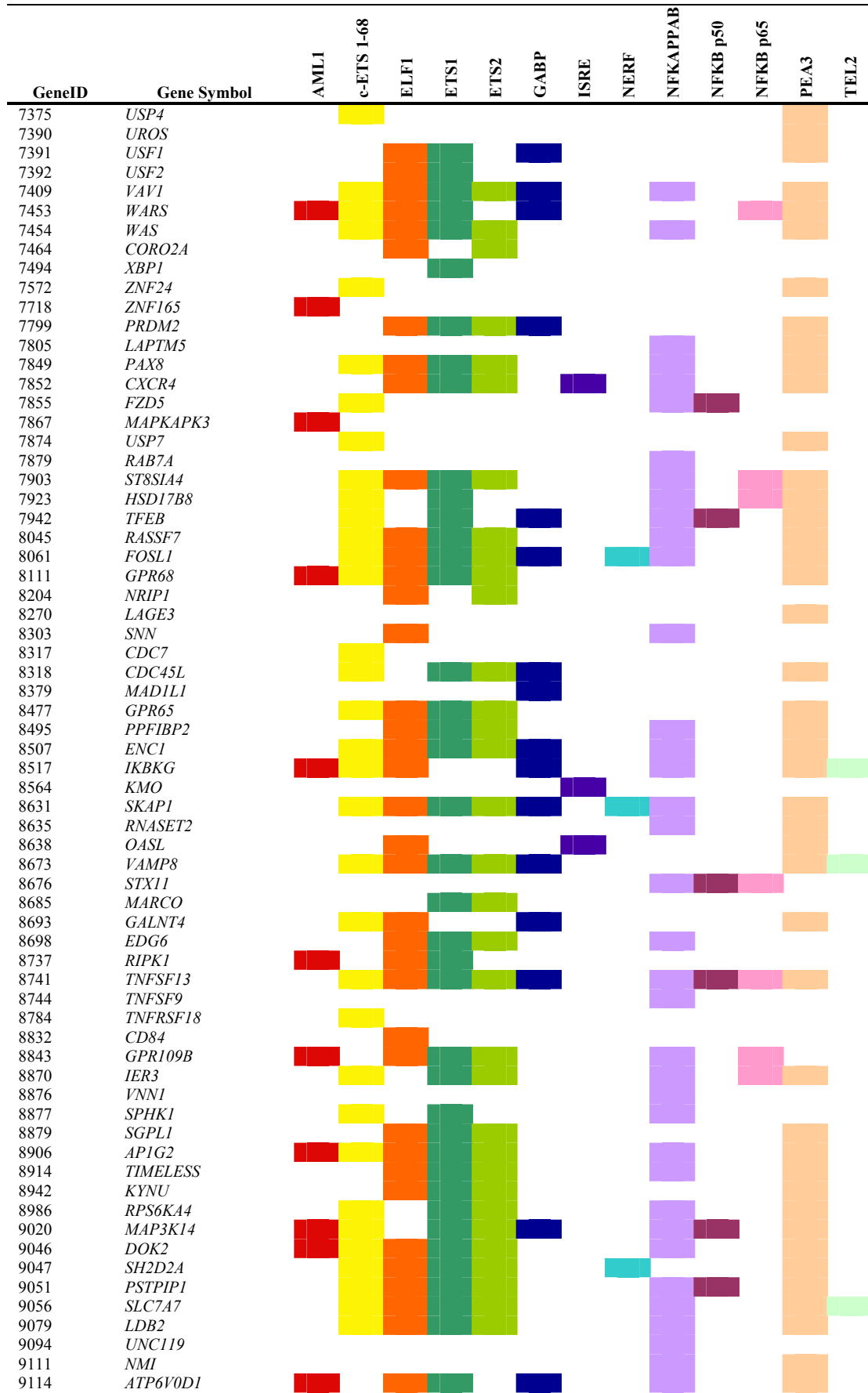


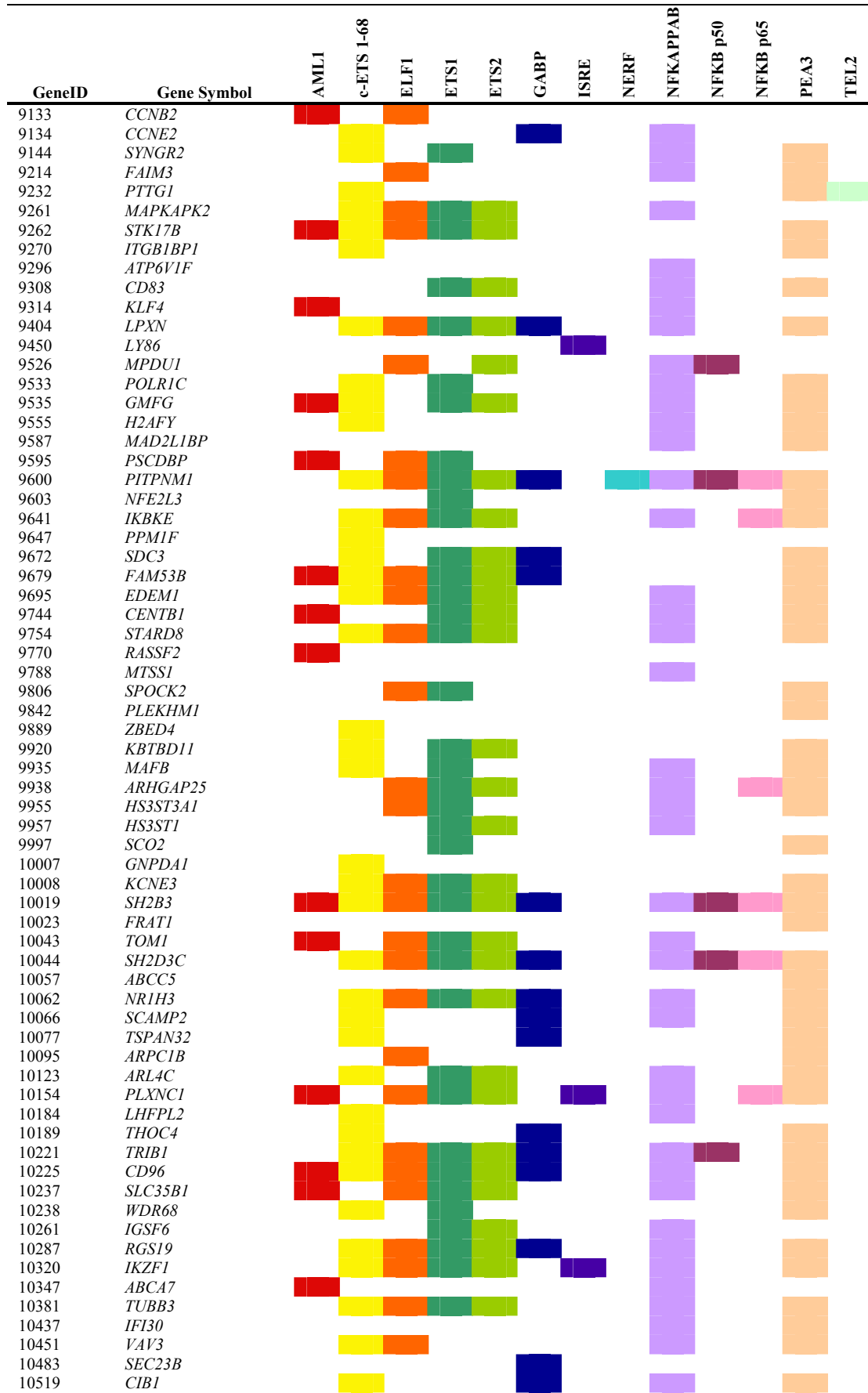


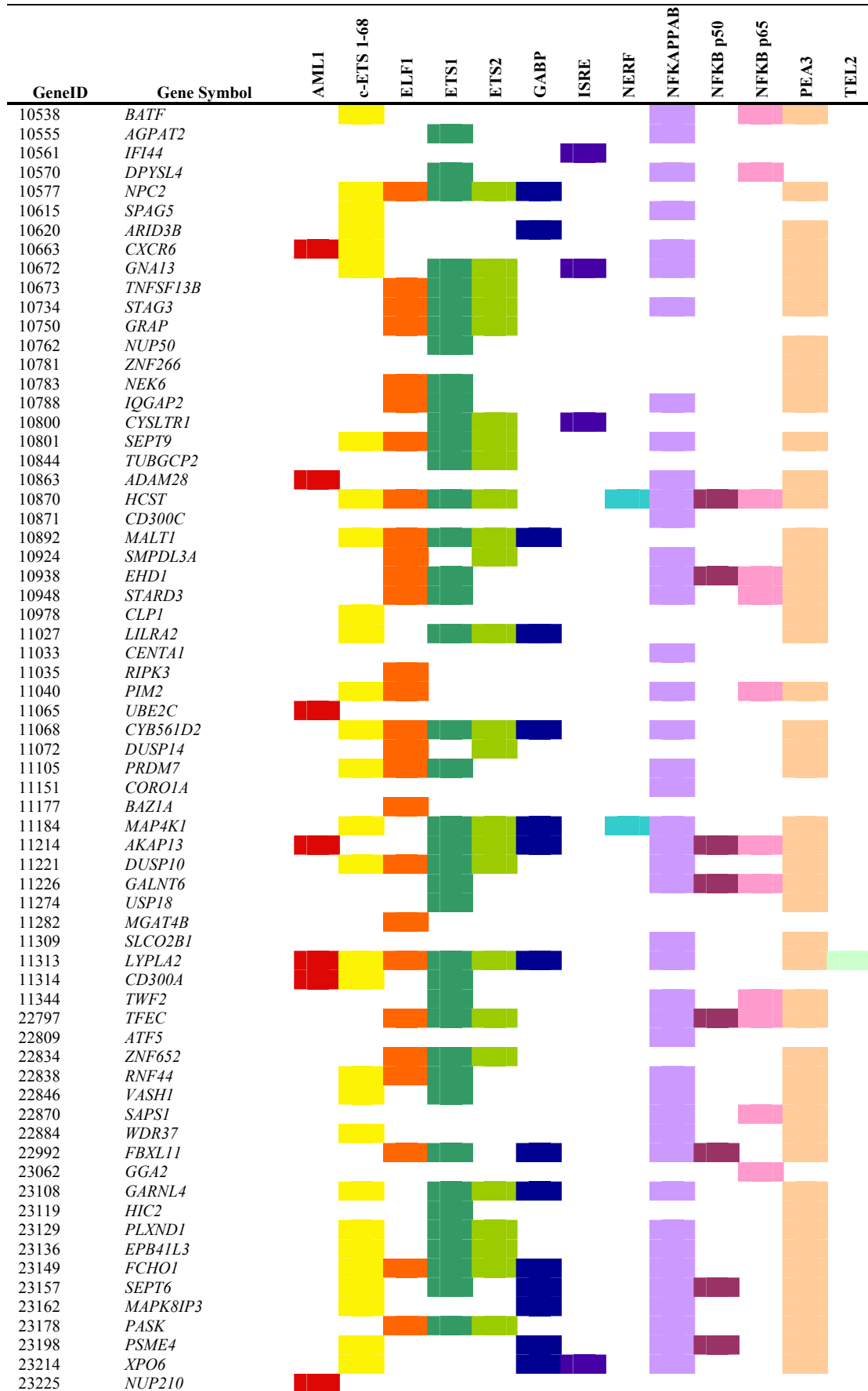








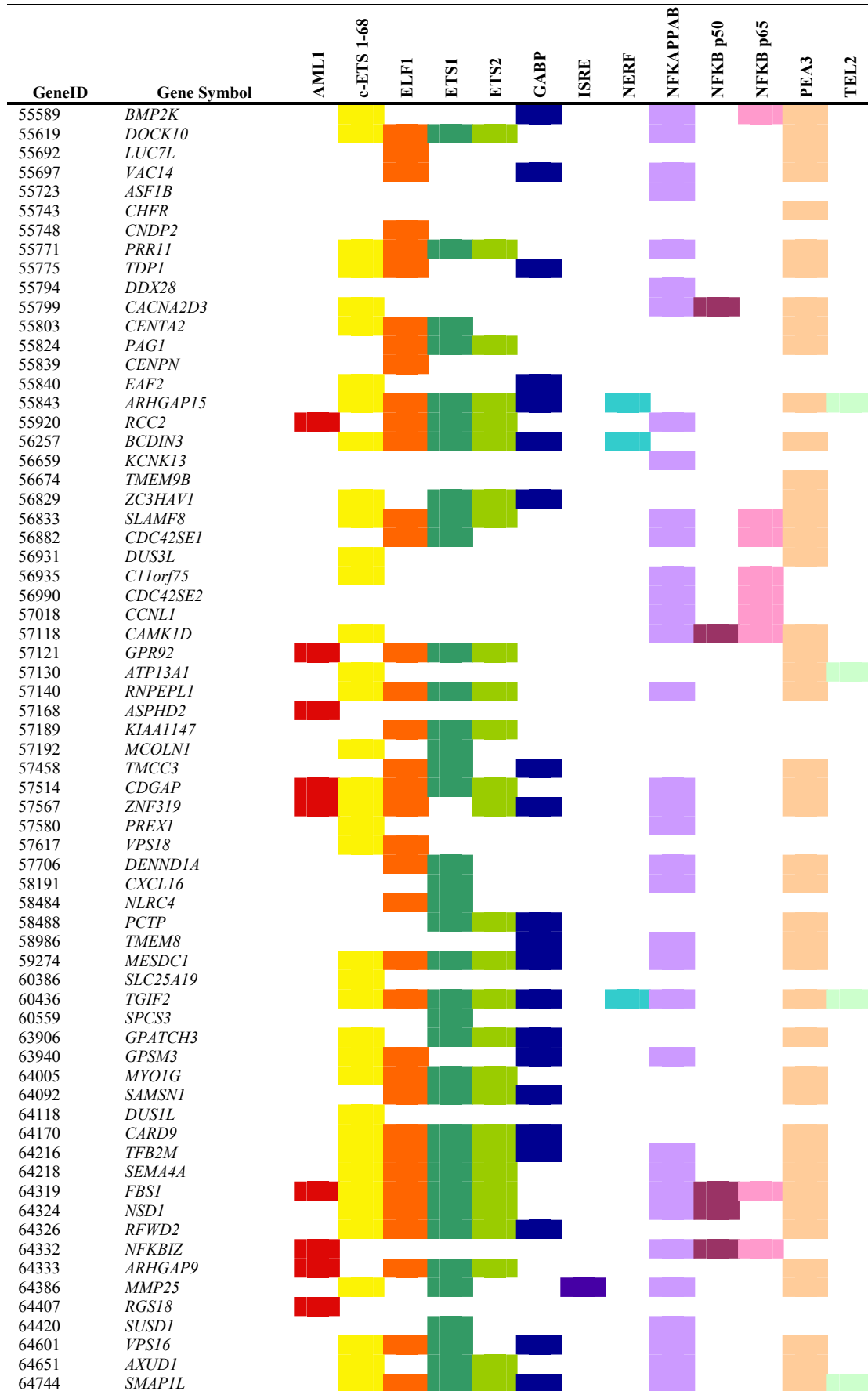
















GeneID	Gene Symbol	AML1	c-ETS 1-68	ELF1	ETS1	ETS2	GABP	ISRE	NERF	NFKAPPAB	NFKB p50	NFKB p65	PEA3	TEL2
144108	<i>SPTY2D1</i>			■								■		
147138	<i>TMC8</i>			■	■	■							■	
150094	<i>SNF1LK</i>		■							■				
150290	<i>DUSP18</i>	■	■							■				
160364	<i>CLEC12A</i>			■	■	■							■	
160760	<i>PPTC7</i>			■	■	■							■	
162979	<i>ZNF342</i>		■	■	■	■		■					■	
162989	<i>DEDD2</i>		■	■	■	■		■		■			■	
163702	<i>IL28RA</i>	■	■	■	■	■		■					■	
165530	<i>CLEC4F</i>				■	■		■						
166012	<i>CHST13</i>		■							■			■	
170394	<i>PWWP2</i>			■						■			■	
201176	<i>ARHGAP27</i>			■	■	■				■			■	
201255	<i>LRRC45</i>		■		■	■							■	
201294	<i>UNC13D</i>	■	■		■	■				■			■	
219855	<i>SLC37A2</i>		■	■	■	■							■	
219931	<i>TPCN2</i>		■											
220002	<i>CYBASC3</i>		■							■			■	■
221002	<i>RASGEF1A</i>	■	■		■	■								
221178	<i>SPATA13</i>				■	■								
221692	<i>PHACTR1</i>									■				
223082	<i>ZNRF2</i>				■	■				■				
253943	<i>YTHDF3</i>			■										
254359	<i>ZDHHC24</i>				■	■	■			■	■	■		
255231	<i>MCOLN2</i>	■	■							■	■	■		
255877	<i>BCL6B</i>	■	■	■	■	■	■	■		■	■	■	■	
257106	<i>ARHGAP30</i>	■	■		■	■	■	■		■	■	■	■	
261734	<i>NPHP4</i>	■	■		■	■	■	■		■	■	■	■	
282991	<i>BLOC1S2</i>	■	■		■	■	■	■		■	■	■	■	
283234	<i>CCDC88</i>		■	■	■	■	■	■		■	■	■	■	
283991	<i>FAM100B</i>	■	■	■	■	■	■	■		■	■	■	■	
284013	<i>VMO1</i>	■	■	■	■	■	■	■				■	■	
284098	<i>PIGW</i>		■	■			■			■			■	
284996	<i>RNF149</i>		■	■			■			■			■	
286336	<i>FAM78A</i>		■	■	■	■				■	■		■	
333929	<i>SNAI3</i>									■				
340348	<i>TSPAN33</i>				■	■				■			■	
353514	<i>LILRA5</i>												■	
374403	<i>TBC1D10C</i>	■	■	■	■	■	■	■	■	■	■	■	■	
374659	<i>HDDC3</i>	■	■	■	■	■	■	■	■	■	■	■	■	
375387	<i>LRRC33</i>									■	■	■	■	
375593	<i>TRIM73</i>		■										■	
387521	<i>Kua</i>		■										■	
388325	<i>UNQ5783</i>	■	■	■	■	■	■	■					■	

\*Transcription factor binding site

†Data compiled from Whole Genome rVISTA.<sup>1</sup> Color in a box denotes the presence of at least one TFBS in the 5 kb promoter region of the respective gene.

**Table S6. mRNA Expression of Transcription Factors Based on Microarray Analyses\***

Transcription Factor	Gene Symbol	GeneID	Expression		Fold Change	FDR P <sup>†</sup>	Detection Score <sup>‡</sup>	
			Control	AAA			Control	AAA
PEA3	<i>ETV4</i>	2118	3.84	3.62	-2.44	NA <sup>§</sup>	0.367	0.258
ELF1	<i>ELF1</i>	1997	9.64	10.44	1.76	2.63e-02	1	1
ETS2	<i>ETS2</i>	2114	8.58	8.08	1.44	NA	1	1
ETS1	<i>ETS1</i>	2113	4.87	5.69	2.59	NA	0.956	0.996
NFKB p65	<i>RELA</i>	5970	9.44	9.46	1.01	NA	1	1
NFKB p50	<i>NFKB1</i>	4790	10.29	10.83	1.46	NA	1	1
GABPA	<i>GABPA</i>	2551	7.51	6.98	1.51	NA	1	1
GABPB2	<i>GABPB</i>	2553	6.67	7.32	1.68	NA	0.999	1
TEL2	<i>ETV7</i>	51513	5.70	5.44	1.32	NA	0.993	0.993
AML1	<i>RUNX1</i>	861	6.80	8.00	2.5	5.78e-03	0.999	1
NERF	<i>ELF2</i>	1998	8.69	8.18	1.45	NA	1	1
ISGF-3	<i>STAT1</i>	6772	8.63	10.08	2.80	3.38e-04	1	1

\*Data based on Lenk et al. (2007) analysis.<sup>5</sup>

<sup>†</sup>FDR= False Discovery Rate. P-value for AAA compared to control after correction for multiple testing.

<sup>‡</sup>Based on Illumina platform in which a *Detection Score* ≥ 0.99 was used as the criteria for a gene to be considered expressed.

<sup>§</sup>Not applicable as the gene was not expressed or did not show significant differential expression between AAA and control.

**Table S7. Enriched Gene Ontology (GO) Categories for Genes with Increased Expression (N=1,222\*)**

GO Term	GO ID	GO Size	Expect.		Odds Ratio	P value
			Count	Count		
immune response	0006955	383	32.27	112	4.91	1.22e-33
response to external stimulus	0009605	718	63.13	122	2.26	3.56e-13
inflammatory response	0006954	291	25.40	62	2.94	2.31e-11
locomotory behavior	0007626	219	19.26	51	3.25	6.34e-11
chemotaxis	0006935	121	10.55	34	4.19	4.43e-10
response to bacterium	0009617	25	2.18	14	13.46	2.47e-09
cellular defense response	0006968	56	4.92	21	6.32	3.76e-09
cell death	0008219	871	76.25	126	1.86	6.16e-09
cytokine production	0001816	146	12.84	36	3.47	8.34e-09
response to biotic stimulus	0009607	282	24.75	55	2.60	1.13e-08
positive regulation of cell activation	0050867	72	6.33	23	4.95	2.42e-08
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	0002504	18	1.58	11	16.45	4.13e-08
multi-organism process	0051704	252	21.68	49	2.64	4.17e-08
regulation of leukocyte activation	0002694	75	6.54	23	4.70	4.94e-08
positive regulation of lymphocyte activation	0051251	62	5.45	20	5.01	1.64e-07
immune response-regulating signal transduction	0002764	29	2.55	13	8.52	3.12e-07
immune response-activating cell surface receptor signaling pathway	0002429	25	2.20	12	9.67	3.55e-07
cell communication	0007154	3436	298.94	370	1.40	4.34e-07
immune system development	0002520	252	22.16	47	2.44	5.44e-07
leukocyte activation	0045321	99	8.47	25	3.67	5.80e-07
myeloid leukocyte activation	0002274	46	4.04	16	5.60	8.99e-07
regulation of defense response	0031347	83	7.30	22	3.80	1.79e-06
protein kinase cascade	0007243	212	18.32	40	2.51	1.81e-06
lymphocyte differentiation	0030098	49	4.29	16	5.12	2.21e-06
hemopoiesis	0030097	218	19.17	41	2.46	2.29e-06
phosphate metabolic process	0006796	910	80.01	120	1.64	2.85e-06
locomotion	0040011	408	35.87	64	1.99	3.26e-06
T cell activation	0042110	46	3.96	15	5.20	3.78e-06
interspecies interaction between organisms	0044419	239	21.01	42	2.26	1.03e-05
response to lipopolysaccharide	0032496	19	1.67	9	9.40	1.25e-05
regulated secretory pathway	0045055	15	1.32	8	11.93	1.28e-05
positive regulation of immune system process	0002684	56	4.84	16	4.28	1.30e-05
defense response	0006952	78	6.45	19	3.62	1.40e-05
regulation of response to stimulus	0048583	137	11.88	28	2.75	1.45e-05
regulation of cytokine biosynthetic process	0042035	56	4.91	16	4.21	1.58e-05
cell chemotaxis	0060326	34	2.99	12	5.71	1.77e-05
regulation of catalytic activity	0050790	637	56.01	87	1.69	1.93e-05
positive regulation of mononuclear cell proliferation	0032946	35	3.08	12	5.46	2.48e-05
response to virus	0009615	77	6.74	19	3.46	2.53e-05
membrane protein ectodomain proteolysis	0006509	25	2.20	10	6.97	2.54e-05
antigen processing and presentation	0019882	31	2.69	11	5.82	3.38e-05
activation of immune response	0002253	66	5.80	17	3.64	3.94e-05

regulation of apoptosis	0042981	309	26.81	48	1.98	5.01e-05
regulation of lymphocyte proliferation	0050670	49	4.31	14	4.19	5.46e-05
regulation of adaptive immune response	0002819	38	3.34	12	4.83	6.29e-05
positive regulation of cytokine secretion	0050715	18	1.58	8	8.35	6.83e-05
positive regulation of immune response	0050778	14	1.22	7	10.58	7.25e-05
regulation of JUN kinase activity	0043506	23	2.02	9	6.71	7.98e-05
positive regulation of protein kinase activity	0045860	149	13.10	28	2.44	9.05e-05
regulation of kinase activity	0043549	247	21.72	40	2.04	0.00011
positive regulation of T cell proliferation	0042102	29	2.55	10	5.50	0.00011
regulation of T cell activation	0050863	35	3.04	11	4.85	0.00012
protein modification process	0006464	1345	118.26	156	1.42	0.00013
positive regulation of developmental process	0051094	432	37.98	61	1.75	0.00014
lymphocyte activation during immune response	0002285	15	1.32	7	9.13	0.00014
viral infectious cycle	0019058	53	4.66	14	3.76	0.00014
ARF protein signal transduction	0032011	41	3.60	12	4.33	0.00014
protein amino acid phosphorylation	0006468	567	49.35	75	1.64	0.00015
lysosome organization	0007040	20	1.76	8	6.96	0.00017
leukocyte migration	0050900	42	3.68	12	4.20	0.00018
innate immune response	0045087	118	10.34	23	2.55	0.00020
positive regulation of transferase activity	0051347	156	13.72	28	2.30	0.00020
leukocyte mediated immunity	0002443	82	7.17	18	2.97	0.00020
positive regulation of I-kappaB kinase/NF-kappaB cascade	0043123	89	7.83	19	2.85	0.00022
cytokine metabolic process	0042107	62	5.43	15	3.36	0.00023
adaptive immune response	0002250	56	4.89	14	3.52	0.00024
positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0002824	21	1.85	8	6.42	0.00025
leukocyte adhesion	0007159	21	1.85	8	6.42	0.00025
T cell selection	0045058	5	0.44	4	41.78	0.00027
chronic inflammatory response	0002544	5	0.44	4	41.64	0.00028
antigen processing and presentation of exogenous peptide antigen via MHC class II	0019886	5	0.44	4	41.64	0.00028
regulation of leukocyte degranulation	0043300	5	0.44	4	41.64	0.00028
ceramide metabolic process	0006672	32	2.81	10	4.75	0.00028
stress-activated protein kinase signaling pathway	0031098	63	5.54	15	3.27	0.00029
I-kappaB kinase/NF-kappaB cascade	0007249	51	4.44	13	3.62	0.00032
intracellular signaling cascade	0007242	914	76.85	106	1.48	0.00033
apoptosis	0006915	243	20.61	37	1.97	0.00034
cell activation during immune response	0002263	17	1.49	7	7.30	0.00035
antigen processing and presentation of peptide antigen via MHC class I	0002474	17	1.49	7	7.30	0.00035
regulation of B cell activation	0050864	33	2.90	10	4.54	0.00037
regulation of immune effector process	0002697	34	2.97	10	4.38	0.00047
positive regulation of calcium-mediated signaling	0050850	9	0.79	5	13.02	0.00049
cellular alkene metabolic process	0043449	23	2.02	8	5.57	0.00051
positive regulation of mast cell degranulation	0043306	3	0.26	3	Inf	0.00068
regulation of ARF GTPase activity	0032312	24	2.11	8	5.22	0.00071
negative regulation of programmed cell death	0043069	270	23.74	40	1.83	0.00072
T cell receptor signaling pathway	0050852	14	1.23	6	7.82	0.00074
regulation of inflammatory response to antigenic stimulus	0002861	6	0.53	4	20.82	0.00077
regulation of myeloid leukocyte mediated immunity	0002886	6	0.53	4	20.82	0.00077
antigen processing and presentation of exogenous antigen	0019884	6	0.53	4	20.82	0.00077
regulation of mast cell activation	0033003	6	0.53	4	20.82	0.00077
positive regulation of exocytosis	0045921	6	0.53	4	20.82	0.00077
lymphocyte chemotaxis	0048247	6	0.53	4	20.82	0.00077
activation of JUN kinase activity	0007257	19	1.67	7	6.08	0.00078
leukotriene biosynthetic process	0019370	19	1.67	7	6.08	0.00078
phospholipid efflux	0033700	10	0.88	5	10.42	0.00090
T-helper 2 type immune response	0042092	10	0.88	5	10.42	0.00090
positive regulation of interleukin-1 beta secretion	0050718	10	0.88	5	10.42	0.00090
chemokine metabolic process	0050755	10	0.88	5	10.42	0.00090
apoptotic program	0008632	100	8.79	19	2.46	0.00102
regulation of lymphocyte mediated immunity	0002706	37	3.25	10	3.87	0.00102
membrane invagination	0010324	214	18.82	33	1.92	0.00103
regulation of protein kinase cascade	0010627	165	14.51	27	2.05	0.00117
regulation of small GTPase mediated signal transduction	0051056	216	18.99	33	1.90	0.00121
icosanoid metabolic process	0006690	38	3.34	10	3.73	0.00128
positive regulation of interleukin-2 biosynthetic process	0045086	11	0.97	5	8.68	0.00153
induction of apoptosis by extracellular signals	0008624	39	3.43	10	3.60	0.00158

response to ATP	0033198	7	0.62	4	13.88	0.00167
thymic T cell selection	0045061	7	0.62	4	13.88	0.00167
positive regulation of chemokine biosynthetic process	0045080	7	0.62	4	13.88	0.00167
di-, tri-valent inorganic cation homeostasis	0055066	169	14.86	27	2.00	0.00168
neutrophil chemotaxis	0030593	16	1.41	6	6.25	0.00169
positive regulation of T cell differentiation	0045582	16	1.41	6	6.25	0.00169
negative regulation of inflammatory response	0050728	16	1.41	6	6.25	0.00169
glycolipid metabolic process	0006664	27	2.37	8	4.39	0.00169
defense response to virus	0051607	27	2.37	8	4.39	0.00169
sphingolipid metabolic process	0006665	60	5.28	13	2.89	0.00181
elevation of cytosolic calcium ion concentration	0007204	82	7.21	16	2.54	0.00185
anti-apoptosis	0006916	179	15.74	28	1.95	0.00192
regulation of MAP kinase activity	0043405	83	7.25	16	2.52	0.00198
cell cycle	0007049	830	72.98	97	1.41	0.0020
T cell proliferation	0042098	22	1.92	7	4.90	0.0020
regulation of interleukin-6 production	0032675	22	1.93	7	4.87	0.0021
calcium-mediated signaling	0019722	28	2.45	8	4.19	0.0021
positive regulation of apoptosis	0043065	269	23.65	38	1.73	0.0023
regulation of interleukin-1 secretion	0050704	12	1.06	5	7.44	0.0024
mast cell degranulation	0043303	4	0.35	3	31.28	0.0025
acute inflammatory response to antigenic stimulus	0002438	4	0.35	3	31.20	0.0025
regulation of hypersensitivity	0002883	4	0.35	3	31.20	0.0025
smooth muscle adaptation	0014805	4	0.35	3	31.20	0.0025
regulation of retroviral genome replication	0045091	4	0.35	3	31.20	0.0025
positive regulation of interleukin-6 biosynthetic process	0045410	4	0.35	3	31.20	0.0025
regulation of defense response to virus by host	0050691	4	0.35	3	31.20	0.0025
cell cycle phase	0022403	382	33.59	50	1.59	0.0028
myeloid leukocyte mediated immunity	0002444	8	0.70	4	10.44	0.0031
antigen processing and presentation of endogenous antigen	0019883	8	0.70	4	10.41	0.0031
intracellular lipid transport	0032365	8	0.70	4	10.41	0.0031
Cdc42 protein signal transduction	0032488	8	0.70	4	10.41	0.0031
type I interferon biosynthetic process	0045351	8	0.70	4	10.41	0.0031
humoral immune response	0006959	71	6.24	14	2.57	0.0031
alcohol biosynthetic process	0046165	36	3.17	9	3.48	0.0032
induction of programmed cell death	0012502	212	18.64	31	1.80	0.0033
superoxide metabolic process	0006801	18	1.58	6	5.21	0.0034
negative regulation of intracellular transport	0032387	18	1.58	6	5.21	0.0034
cytolysis	0019835	24	2.11	7	4.29	0.0036
regulation of chemokine production	0032642	13	1.14	5	6.51	0.0037
negative regulation of protein import into nucleus	0042308	13	1.14	5	6.51	0.0037
cellular calcium ion homeostasis	0006874	128	11.25	21	2.06	0.0038
pyridine nucleotide metabolic process	0019362	31	2.73	8	3.63	0.0044
leukocyte homeostasis	0001776	25	2.20	7	4.05	0.0047
positive regulation of secretion	0051047	52	4.56	11	2.81	0.0047
activation of MAPK activity	0000187	45	3.94	10	3.00	0.0047
negative regulation of response to stimulus	0048585	38	3.34	9	3.24	0.0048
cellular cation homeostasis	0030003	182	16.00	27	1.83	0.0049
regulation of cell cycle process	0010564	67	5.89	13	2.51	0.005
regulation of T cell differentiation	0045580	14	1.23	5	5.81	0.005
germinal center formation	0002467	9	0.79	4	8.32	0.005
positive regulation of B cell proliferation	0030890	9	0.79	4	8.32	0.005
amyloid precursor protein catabolic process	0042987	9	0.79	4	8.32	0.005
cellular extravasation	0045123	9	0.79	4	8.32	0.005
vesicle-mediated transport	0016192	500	43.96	61	1.47	0.005
metal ion homeostasis	0055065	140	12.31	22	1.95	0.005
release of cytochrome c from mitochondria	0001836	14	1.23	5	5.78	0.005
response to osmotic stress	0006970	14	1.23	5	5.78	0.005
respiratory burst	0045730	14	1.23	5	5.78	0.005
negative regulation of leukocyte activation	0002695	32	2.81	8	3.48	0.005
regulation of protein secretion	0050708	39	3.43	9	3.13	0.006
positive regulation of protein transport	0051222	46	4.04	10	2.90	0.006
tryptophan catabolic process	0006569	5	0.44	3	15.60	0.006
cellular response to nutrient	0031670	5	0.44	3	15.60	0.006
intracellular cholesterol transport	0032367	5	0.44	3	15.60	0.006
granulocyte macrophage colony-stimulating factor biosynthetic process	0042253	5	0.44	3	15.60	0.006
indole derivative catabolic process	0042436	5	0.44	3	15.60	0.006
negative regulation of viral genome replication	0045071	5	0.44	3	15.60	0.006



regulation of interferon-alpha biosynthetic process	0045354	5	0.44	3	15.60	0.006
sphingoid catabolic process	0046521	5	0.44	3	15.60	0.006
defense response to bacterium	0042742	76	6.68	14	2.36	0.006
glutathione metabolic process	0006749	20	1.76	6	4.46	0.006
B cell mediated immunity	0019724	61	5.36	12	2.56	0.006
positive regulation of cell communication	0010647	221	19.43	31	1.71	0.006
nucleobase, nucleoside and nucleotide metabolic process	0055086	332	29.19	43	1.57	0.006
nuclear division	0000280	222	19.52	31	1.70	0.007
positive regulation of immune effector process	0002699	27	2.37	7	3.65	0.007
regulation of cytokine production during immune response	0002718	15	1.32	5	5.21	0.007
NAD metabolic process	0019674	15	1.32	5	5.21	0.007
positive regulation of nitric oxide biosynthetic process	0045429	15	1.32	5	5.21	0.007
positive regulation of proteolysis	0045862	15	1.32	5	5.21	0.007
regulation of viral reproduction	0050792	15	1.32	5	5.21	0.007
regulation of cell proliferation	0042127	567	49.85	67	1.41	0.007
regulation of establishment of protein localization	0070201	78	6.86	14	2.29	0.008
vitamin biosynthetic process	0009110	21	1.85	6	4.17	0.008
regulation of interleukin-2 production	0032663	21	1.85	6	4.17	0.008
regulation of tumor necrosis factor production	0032680	21	1.85	6	4.17	0.008
regulation of multi-organism process	0043900	21	1.85	6	4.17	0.008
alpha-beta T cell differentiation	0046632	21	1.85	6	4.17	0.008
negative regulation of T cell activation	0050868	21	1.85	6	4.17	0.008
phagocytosis	0006909	48	4.22	10	2.75	0.008
M phase of mitotic cell cycle	0000087	225	19.78	31	1.68	0.008
production of molecular mediator of immune response	0002440	41	3.60	9	2.93	0.008
B cell differentiation	0030183	41	3.60	9	2.93	0.008
regulation of acute inflammatory response	0002673	10	0.88	4	6.94	0.008
positive regulation of JNK cascade	0046330	10	0.88	4	6.94	0.008
spindle organization	0007051	28	2.46	7	3.47	0.009
membrane lipid catabolic process	0046466	28	2.46	7	3.47	0.009
purine ribonucleotide metabolic process	0009150	121	10.64	19	1.95	0.009
biological regulation	0065007	6657	585.31	623	1.16	0.010
positive regulation of innate immune response	0045089	22	1.93	6	3.91	0.010
positive regulation of mitosis	0045840	22	1.93	6	3.91	0.010
T cell mediated immunity	0002456	16	1.41	5	4.73	0.010

\*The entire set of upregulated genes was used to identify enriched GO biological process categories with a software package available using R and Bioconductor.<sup>3,4</sup> A total of 1,222 genes with GO annotations were included into the analysis. This represents 91.8% of the total number of 1,331 genes with increased expression in AAA tissue samples and analyzed with Whole Genome rVISTA. The remaining 8.2% did not have functional annotations as of June 6, 2009. The reference gene set was the 18,057 distinct genes represented on both Affymetrix and Illumina arrays based on our initial microarray studies.<sup>5</sup> Only GO categories with more than 2 genes and a nominal  $P < 0.01$  using the hypergeometric test for enrichment are listed here. Tables S8 and S9 contain the results of GO analyses carried out with upregulated target genes for each transcription factor separately.



Positive regulation of cellular process	45		48			
Positive regulation of cellular process		41				
Positive regulation of JAK-STAT cascade				2	2	
Positive regulation of JNK activity				4		
Positive regulation of physiological process	43					
Positive regulation of tyrosine phosphorylation of STAT protein				2	2	
Programmed cell death			44			
Protein amino acid dephosphorylation	14					
Protein amino acid phosphorylation		37			42	15
Protein kinase cascade	27	26	31		29	12
Protein modification						24
Regulation of apoptosis		28				
Regulation of catalytic activity	23		28			
Regulation of programmed cell death		28				
Response to biotic stimulus			29			
Response to external stimulus	38		50			
Response to other organism			26			
Response to wounding	28		35			
Signal transduction	155	164	191		154	44
Stress-activated protein kinase signaling pathway				6		43
T-cell activation	9		10			
Taxis			20			

\*The target gene lists were used to identify enriched GO biological process categories using WebGestalt (Web-based Gene Set Analysis Toolkit; <http://bioinfo.vanderbilt.edu/webgestalt>).<sup>6,7</sup> The reference gene set was the 18,057 distinct genes represented on both Affymetrix and Illumina arrays based on our initial microarray studies.<sup>5</sup> PEA3 was excluded from the GO analysis since it was not expressed on mRNA nor protein level in aortic tissues. C-ETS 1-68 was excluded from GO analysis since no human protein binding to the TFBS has been identified. GO Biological Process categories with a nominal P<0.0001 using the hypergeometric test for enrichment are listed for all TFs except ISGF-3, for which the nominal P was <0.001. Cell entries indicate the number of target genes for each TF having the specific GO annotation. N, total number of target genes with the TFBS among the gene set upregulated in AAA; n, number of target genes for which the GO category was available.

†GO categories listed for ISGF-3 have significance of P<0.001

**Table S9. Functional Classification of Upregulated Target Genes for each Transcription Factor Using GO Biological Process Terms**

<b>GO Biological Process Category*</b>	<b>Number of Genes<sup>†</sup></b>	<b>P<sup>‡</sup></b>	<b>Annotation Level</b>
<b>ELF1 (377/483)</b>			
Immune system process	74	2.14e-23	4
Immune response	60	2.83e-19	4
Physiological response to stimulus	91	5.91e-15	3
Signal transduction	155	5.43e-14	4
Cell communication	162	1.07e-12	3
Positive regulation of biological process	54	3.78e-08	3
Intracellular signaling cascade	71	4.75e-08	5
Positive regulation of cellular process	45	1.48e-07	4
Positive regulation of cellular physiological process	40	2.42e-07	5
Positive regulation of physiological process	43	2.66e-07	4
Organismal physiological process	98	2.85e-07	3
Response to external stimulus	38	2.92e-07	3
Defense response	36	4.08e-07	3
Protein kinase cascade	27	1.07e-06	6
Phosphate metabolism	52	1.18e-06	6
Phosphorus metabolism	52	1.18e-06	5
Physiological defense response	31	1.99e-06	4
Response to wounding	28	6.62e-06	4
Physiological response to wounding	27	1.07e-05	4
Lymphocyte activation	12	3.38e-05	6
T-cell activation	9	4.25e-05	7
Leukocyte activation	13	4.28e-05	5
Cell activation	14	4.46e-05	4
Cytokine production	9	5.00e-05	4
Regulation of catalytic activity	23	5.96e-05	3
Cellular defense response	10	6.55e-05	5
Protein amino acid dephosphorylation	14	7.11e-05	8
Defense response to virus	4	8.49e-05	5
<b>ETS2 (370/481)</b>			
Signal transduction	164	2.02e-18	4
Cell communication	170	1.61e-16	3
Intracellular signaling cascade	73	3.94e-09	5
Phosphate metabolism	52	6.59e-07	6
Phosphorus metabolism	52	6.59e-07	5
Protein kinase cascade	26	2.44e-06	6
Positive regulation of cellular process	41	3.70e-06	4
Positive regulation of cellular physiological process	36	7.38e-06	5
Protein amino acid phosphorylation	37	1.74e-05	8
Cell surface receptor linked signal transduction	64	1.74e-05	5
Immune system development	13	1.82e-05	5
Regulation of apoptosis	28	2.67e-05	6
Regulation of programmed cell death	28	3.27e-05	5
Hemopoiesis	12	4.47e-05	7
Hemopoietic or lymphoid organ development	12	5.00e-05	6
<b>ETS1 (483/635)</b>			
Immune system process	94	2.10e-29	4

<b>GO Biological Process Category*</b>	<b>Number of Genes<sup>†</sup></b>	<b>P<sup>‡</sup></b>	<b>Annotation Level</b>
Immune response	77	1.06e-24	4
Physiological response to stimulus	112	8.08e-17	3
Signal transduction	191	5.77e-15	4
Cell communication	198	7.30e-13	3
Organismal physiological process	128	1.11e-09	3
Response to external stimulus	50	1.37e-09	3
Defense response	44	7.77e-08	3
Chemotaxis	20	2.35e-07	4
Taxis	20	2.35e-07	4
Locomotor behavior	20	4.65e-07	4
Intracellular signaling cascade	82	4.70e-07	5
Response to wounding	35	7.79e-07	4
Physiological response to wounding	34	1.07e-06	4
Protein kinase cascade	31	1.74e-06	6
Response to other organism	26	1.77e-06	4
Physiological defense response	36	2.94e-06	4
Positive regulation of biological process	58	4.81e-06	3
Response to biotic stimulus	29	5.11e-06	3
Antimicrobial humoral response (sensu Vertebrata)	14	6.26e-06	6
Antimicrobial humoral response	14	8.51e-06	5
Humoral immune response	19	8.91e-06	5
Positive regulation of cellular process	48	1.14e-05	4
Inflammatory response	26	1.30e-05	4
Behavior	23	1.45e-05	3
Immune system development	15	1.70e-05	5
Lymphocyte activation	14	2.01e-05	6
Regulation of catalytic activity	28	2.34e-05	3
Hemopoiesis	14	3.41e-05	7
Leukocyte activation	15	3.56e-05	5
Hemopoietic or lymphoid organ development	14	3.87e-05	6
Cell activation	16	4.92e-05	4
T-cell activation	10	5.08e-05	7
Cell death	46	6.79e-05	4
Death	46	6.79e-05	3
Apoptosis	44	8.77e-05	6
Positive regulation of cellular physiological process	40	9.79e-05	5
Programmed cell death	44	9.93e-05	5
<b>GABP (179/224)</b>			
Immune response	23	2.17e-06	4
Immune system process	26	2.94e-06	4
Activation of JNK activity	4	5.95e-05	8
Positive regulation of JNK activity	4	5.95e-05	8
JNK cascade	6	7.18e-05	7
Stress-activated protein kinase signaling pathway	6	8.17e-05	6
<b>TEL2 (33/39)</b>			
Immune system process	13	5.38e-09	4
Positive regulation of JAK-STAT cascade	2	5.21e-05	6
Positive regulation of tyrosine phosphorylation of STAT protein	2	5.21e-05	7
Immune response	8	5.61e-05	4

<b>GO Biological Process Category*</b>	<b>Number of Genes<sup>†</sup></b>	<b>P<sup>‡</sup></b>	<b>Annotation Level</b>
JAK-STAT cascade	3	9.43e-05	7
<b>NERF (25/34)</b>			
Hemopoiesis	5	1.52e-06	7
Hemopoietic or lymphoid organ development	5	1.61e-06	6
Immune system development	5	2.10e-06	5
Immune system process	9	3.14e-06	4
Positive regulation of JAK-STAT cascade	2	2.96e-05	6
Positive regulation of tyrosine phosphorylation of STAT protein	2	2.96e-05	7
Myeloid cell differentiation	3	7.64e-05	4
<b>NFKB (421/536)</b>			
Immune system process	65	4.17e-15	4
Immune response	50	3.56e-11	4
Signal transduction	154	2.45e-09	4
Cell communication	165	3.57e-09	3
Phosphate metabolism	59	1.26e-07	6
Phosphorus metabolism	59	1.26e-07	5
Intracellular signaling cascade	74	4.42e-07	5
Protein kinase cascade	29	9.32e-07	6
Immune system development	15	3.26e-06	5
Physiological response to stimulus	74	4.00e-06	3
Protein amino acid phosphorylation	42	4.95e-06	8
Hemopoiesis	14	7.30e-06	7
Hemopoietic or lymphoid organ development	14	8.33e-06	6
Phosphorylation	45	2.10e-05	7
<b>NFKB p65 (99/127)</b>			
Immune system process	21	4.26e-08	4
Immune response	17	8.41e-07	4
Signal transduction	44	5.84e-06	4
Negative regulation of biological process	20	1.66e-05	3
Negative regulation of apoptosis	8	3.62e-05	7
Negative regulation of programmed cell death	8	4.00e-05	6
Cell communication	44	7.60e-05	3
<b>NFKB p50 (89/116)</b>			
Signal transduction	43	4.68e-07	4
Immune system process	18	8.34e-07	4
Protein kinase cascade	12	2.31e-06	6
Cell communication	43	7.28e-06	3
Protein amino acid phosphorylation	15	1.91e-05	8
Immune response	14	2.22e-05	4
Behavior	9	2.67e-05	3
Phosphate metabolism	18	3.09e-05	6
Phosphorus metabolism	18	3.09e-05	5
Protein modification	24	4.45e-05	7
Biopolymer modification	24	7.72e-05	6
<b>ISRE (37/43)</b>			
Immune system process	9	1.08e-04	4

GO Biological Process Category*	Number of Genes <sup>†</sup>	P <sup>‡</sup>	Annotation Level
Immune response	7	8.35e-04	5
<b>AML1 (128/162)</b>			
Immune system process	26	2.79e-09	4
Immune response	20	4.47e-07	4
Physiological response to stimulus	29	4.18e-05	3

\*Using Whole Genome rVISTA,<sup>1</sup> genes in the upregulated gene set were sub-categorized according to the overrepresented TFBSs they contain for ELF1, ETS2, ETS1, NFKB, NFKB p65, NFKB p50, GABP, TEL2, ISRE, AML1 and NERF. PEA3 was excluded from the GO analysis since it was not expressed on mRNA nor protein level in aortic tissues. C-ETS 1-68 was excluded from GO analysis since no human protein binding to the TFBS has been identified. These gene lists were then used to identify enriched GO biological process categories they have in common using WebGestalt (Web-based Gene Set Analysis Toolkit; <http://bioinfo.vanderbilt.edu/webgestalt>).<sup>6,7</sup> The reference gene set for each analysis was comprised of the 18,057 distinct genes represented on both Affymetrix and Illumina arrays based on our initial microarray studies.<sup>5</sup> The numbers in parentheses indicate for each TFBS the number of genes with information on their GO Biological Process and the total number of target genes among the significantly upregulated genes in AAA for the TF in question.

<sup>†</sup>The number of genes in the indicated GO category belonging to the target gene list of the TFBS in question.

<sup>‡</sup>GO Biological Process categories with a nominal P<0.0001 using the hypergeometric test are listed for all other TFBSs, except for ISRE for which the nominal P was <0.001.

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