

# Gene Functional Analysis Using ENCODE Data

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# Activator/Repressor Assignment for 119 TFs Using DAVID

- Background: all homo sapiens genes
- 52 Activators with GO Term “Positive regulation of gene expression”,  $P = 7.2E-39$  ( $1.4E-36$ )
- 33 Repressors with GO Term “Negative regulation of gene expression”,  $P = 1.9E-19$  ( $9.4E-18$ )
- 20 TFs are both activators and repressors
- Distribution of Activator/Repressor in Levels:
  - Activator Only: Top(14) Mid(5) Bottom(11)
  - Repressor Only: Top(6) Mid(5) Bottom(2)
  - Both: Top(7) Mid(7) Bottom(5)
- With all homo sapiens genes as background, TFs in all three levels are significantly enriched for positive regulation of gene expression and negative regulation of gene expression, respectively.
- Using the 119 TFs as background, top-level TFs are enriched for Chromatin Organization ( $P=0.0070$ ) and Chromatin Modification ( $P=0.0076$ ), Chromatin Regulators

















# Functional Enrichment of Coding Gene Targets of TF Out-Degree Hubs (1)

- All Homo Sapiens Genes as Background
- CTCF: ribosomal protein (corrected  $P=9.3E-3$ ), organelle lumen ( $P=0.030$ ), intracellular organelle lumen ( $P=0.036$ ) and membrane-enclosed lumen ( $P=0.033$ )
- RAD21: blood vessel development ( $P=4.4E-08$ ), blood vessel morphogenesis ( $P=4.8E-7$ ), regulation of cell migration ( $P=9.2E-3$ ), regulation of cell motion ( $P=0.013$ ), regulation of locomotion ( $P=0.028$ ), negative regulation of apoptosis ( $P=0.039$ ), negative regulation of programmed cell death (0.044), neural crest cell differentiation (0.036), mesenchyme development (0.028), regulation of phosphorylation ( $P=0.059$ )
- MYC: ribosomal protein ( $P=1.8E-25$ ), structural constituent of ribosome ( $P=6.5E-22$ ), organelle lumen ( $P=1.3E-22$ ), intracellular organelle lumen ( $P=5.5E-23$ ), membrane-enclosed lumen ( $P=7.4E-22$ ), and nuclear lumen ( $7.9E-15$ ), RNA Recognition Motif ( $P=4.7E-6$ ), RNA Splicing ( $P=4.3E-6$ ), mRNA processing ( $P=4.7E-4$ ), helicase activity (0.018), tRNA aminoacylation ( $P=4.5E-4$ ), amino acid activation ( $P=4.5E-4$ ), ATP binding (0.014), nucleoside binding (0.013), ribonucleotide binding(0.0097), [RNA splicing, via transesterification reactions](#)
- MAX: ribosomal biogenesis ( $P=1.1E-7$ ), structural constituent of ribosome ( $P=1.5E-3$ ), organelle lumen ( $P=1.4E-16$ ), intracellular organelle lumen ( $P=6.8E-17$ ), membrane-enclosed lumen ( $P=3.7E-17$ ), and nuclear lumen ( $7.9E-15$ ), RNA Recognition Motif ( $P=6.4E-5$ ), ATP binding (0.026), nucleoside binding (0.054) [RNA splicing, via transesterification reactions](#) (0.017)




































# Functional Enrichment of Coding Gene Targets of TF Out-Degree Hubs (2)

- TAF1: translational elongation (P=1.4E-55), ribosome (P=2.6E-46), structural constituent of ribosome (P=1.5E-44), structural molecule activity (P=8.3E-19), intracellular organelle (P=2.3E-21), organelle lumen (P=5.2E-21), membrane-enclosed lumen (P=2.8E-20), nuclear lumen (P=2.9E-18), RNA splicing (P=4.7E-8), mRNA metabolic process (P=6.5E-8), mRNA processing (P=6.0E-8), nucleosome organization (P=6.5E-6), nucleosome (9.7E-6), chromatin assembly (1.5E-5), protein-DNA complex assembly (2.6E-5), chromatin assembly or disassembly (7.5E-5), protein-DNA complex (3.3E-5), DNA packaging (4.9E-4), cellular protein localization (4.0E-3), cellular macromolecule localization (4.4E-3), regulation of endopeptidase activity (2.1E-4), regulation of peptidase activity (3.4E-4), regulation of caspase activity (6.3E-4), activation of caspase (3.1E-3), regulation of apoptosis (5.3E-4), regulation of programmed cell death (6.5E-4), regulation of cell death (6.7E-4)



























# Function Enrichment of CTCF's 1406 Targets (~9000 genes as background) (Bottom)

Annotation Cluster 1		Enrichment Score: 3.2	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like fold</a>	RT		42	4.4E-4	1.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Immunoglobulin domain</a>	RT		37	6.1E-4	8.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like</a>	RT		37	9.1E-4	2.2E-1
Annotation Cluster 2		Enrichment Score: 2.6	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Cadherin, N-terminal</a>	RT		9	7.9E-5	6.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 6	RT		9	7.1E-4	5.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 5	RT		10	2.4E-3	7.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">homophilic cell adhesion</a>	RT		13	2.9E-3	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 3	RT		10	3.5E-3	7.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 4	RT		10	3.5E-3	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cadherin</a>	RT		10	6.4E-3	6.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 2	RT		10	6.8E-3	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 1	RT		10	6.8E-3	9.3E-1
<input type="checkbox"/>	SMART	<a href="#">CA</a>	RT		10	7.7E-3	3.8E-1
Annotation Cluster 3		Enrichment Score: 1.82	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">reproductive process in a multicellular organism</a>	RT		46	6.0E-3	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">multicellular organism reproduction</a>	RT		46	6.0E-3	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">gamete generation</a>	RT		35	3.5E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">sexual reproduction</a>	RT		38	4.0E-2	9.9E-1

# Function Enrichment of FOS's 490 Targets (Homo Sapiens genes as background) (Bottom)

Annotation Cluster 1		Enrichment Score: 6.45	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	RT		12	6.8E-9	5.7E-6
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	RT		12	1.4E-8	1.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		13	1.8E-8	6.9E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	RT		15	7.0E-8	6.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	RT		14	1.5E-7	9.7E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	RT		14	2.3E-7	1.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	RT		14	3.9E-7	1.3E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Histone-fold</a>	RT		11	5.6E-7	2.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	RT		13	6.3E-7	8.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	RT		15	1.3E-6	3.6E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">chromosomal protein</a>	RT		15	1.1E-5	9.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	RT		11	5.4E-4	6.9E-2
Annotation Cluster 2		Enrichment Score: 3.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">angiogenesis</a>	RT		15	2.0E-5	3.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel morphogenesis</a>	RT		16	2.7E-4	3.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel development</a>	RT		16	1.3E-3	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vasculature development</a>	RT		16	1.6E-3	1.3E-1
Annotation Cluster 3		Enrichment Score: 3.42	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Transcription</a>	RT		75	3.1E-4	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transcription</a>	RT		77	4.1E-4	4.2E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transcription regulation</a>	RT		73	4.4E-4	1.8E-2
Annotation Cluster 4		Enrichment Score: 3.06	G		Count	P_Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		5	6.9E-4	1.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		5	7.8E-4	2.0E-1
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		5	1.2E-3	2.0E-1
Annotation Cluster 5		Enrichment Score: 3	G		Count	P_Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002048:histone H2A	RT		5	6.9E-4	1.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2A</a>	RT		5	9.7E-4	1.8E-1
<input type="checkbox"/>	SMART	<a href="#">H2A</a>	RT		5	1.5E-3	1.3E-1
Annotation Cluster 6		Enrichment Score: 2.82	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		52	1.5E-3	5.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		61	1.5E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		63	1.6E-3	4.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		62	1.6E-3	4.6E-2

# Functions of MYC's 683 Targets (1) (Mid)




















Annotation Cluster 1		Enrichment Score: 17.99	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	RT		53	2.5E-20	8.9E-18
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	RT		47	1.5E-18	1.6E-16
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	RT		43	2.8E-17	9.9E-15
Annotation Cluster 2		Enrichment Score: 14.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	RT		34	8.2E-17	1.6E-14
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	RT		30	4.8E-16	3.8E-14
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	RT		28	2.6E-13	1.8E-11
Annotation Cluster 3		Enrichment Score: 9.1	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		144	1.1E-10	5.8E-9
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		145	1.8E-10	8.2E-9
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		145	7.2E-10	2.9E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		118	2.5E-8	7.5E-7
Annotation Cluster 4		Enrichment Score: 4.92	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotide-binding, alpha-beta plait</a>	RT		27	4.4E-6	4.8E-3
<input type="checkbox"/>	SMART	<a href="#">RRM</a>	RT		25	7.5E-6	1.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">RNA recognition motif, RNP-1</a>	RT		25	5.2E-5	2.8E-2
Annotation Cluster 5		Enrichment Score: 3.85	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing, via transesterification reactions</a>	RT		25	9.1E-6	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nuclear mRNA splicing, via spliceosome</a>	RT		25	9.1E-6	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing, via transesterification reactions with bulged adenosine as nucleophile</a>	RT		25	9.1E-6	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing</a>	RT		32	9.3E-5	1.5E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">mRNA splicing</a>	RT		24	5.2E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mRNA metabolic process</a>	RT		34	1.1E-3	1.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">mRNA processing</a>	RT		26	1.4E-3	3.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mRNA processing</a>	RT		30	2.6E-3	2.1E-1

# Functions of MYC's 683 Targets (2)





























Annotation Cluster 6		Enrichment Score: 3.49			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">tRNA aminoacylation</a>	RT		11	1.4E-4	1.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">amino acid activation</a>	RT		11	1.4E-4	1.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">tRNA aminoacylation for protein translation</a>	RT		11	1.4E-4	1.9E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ligase activity, forming carbon-oxygen bonds</a>	RT		11	2.7E-4	3.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">aminoacyl-tRNA ligase activity</a>	RT		11	2.7E-4	3.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ligase activity, forming aminoacyl-tRNA and related compounds</a>	RT		11	2.7E-4	3.1E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Aminoacyl-tRNA synthetase</a>	RT		9	8.4E-4	2.3E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Aminoacyl-tRNA biosynthesis</a>	RT		9	2.7E-3	1.2E-1
Annotation Cluster 7		Enrichment Score: 3.06			Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">UBQ</a>	RT		8	3.9E-4	3.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin</a>	RT		8	7.6E-4	2.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin supergroup</a>	RT		8	1.4E-3	3.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin conserved site</a>	RT		7	1.4E-3	2.6E-1
Annotation Cluster 8		Enrichment Score: 2.34			Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">atp-binding</a>	RT		71	3.0E-3	7.2E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleotide-binding</a>	RT		86	3.1E-3	7.0E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">adenyl ribonucleotide binding</a>	RT		80	3.6E-3	2.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">purine ribonucleotide binding</a>	RT		94	4.2E-3	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ribonucleotide binding</a>	RT		94	4.2E-3	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">nucleoside binding</a>	RT		84	5.2E-3	2.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">adenyl nucleotide binding</a>	RT		82	5.7E-3	2.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ATP binding</a>	RT		78	6.1E-3	2.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">purine nucleoside binding</a>	RT		83	6.1E-3	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">purine nucleotide binding</a>	RT		96	6.8E-3	2.5E-1

















# Functions of MYC's 683 Targets (3)

Annotation Cluster 9		Enrichment Score: 2.3	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside monophosphate metabolic process</a>	RT		7	1.1E-4	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside monophosphate biosynthetic process</a>	RT		7	1.1E-4	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">IMP biosynthetic process</a>	RT		5	4.3E-4	5.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">'de novo' IMP biosynthetic process</a>	RT		5	4.3E-4	5.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">IMP metabolic process</a>	RT		5	4.3E-4	5.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside monophosphate metabolic process</a>	RT		6	4.4E-4	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	RT		6	4.4E-4	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	RT		6	4.4E-4	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside monophosphate biosynthetic process</a>	RT		6	4.4E-4	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside monophosphate metabolic process</a>	RT		8	4.0E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside monophosphate biosynthetic process</a>	RT		7	4.7E-3	2.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">purine biosynthesis</a>	RT		4	1.1E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleotide biosynthetic process</a>	RT		8	8.7E-2	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleotide metabolic process</a>	RT		9	1.1E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleotide biosynthetic process</a>	RT		7	1.5E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleotide biosynthetic process</a>	RT		8	1.6E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleotide metabolic process</a>	RT		8	1.7E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleotide metabolic process</a>	RT		9	2.6E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleotide biosynthetic process</a>	RT		9	2.7E-1	9.9E-1































# Functional Enrichment of MAX's 597 Targets (Mid)

Annotation Cluster 1		Enrichment Score: 6.95	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		120	4.6E-8	8.3E-6
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		117	4.8E-8	5.7E-6
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		117	1.2E-7	1.1E-5
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		98	6.1E-7	4.3E-5
Annotation Cluster 2		Enrichment Score: 5.61	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribosome biogenesis</a>	RT		21	2.7E-7	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">rRNA processing</a>	RT		16	6.1E-6	1.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">rRNA metabolic process</a>	RT		16	9.1E-6	2.1E-3
Annotation Cluster 3		Enrichment Score: 3.92	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">RRM</a>	RT		21	5.5E-5	7.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotide-binding, alpha-beta plait</a>	RT		23	5.7E-5	4.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">RNA recognition motif, RNP-1</a>	RT		21	5.6E-4	2.2E-1
Annotation Cluster 4		Enrichment Score: 2.91	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">WD40</a>	RT		22	6.8E-5	4.6E-3
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat</a>	RT		22	7.3E-4	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	RT		21	8.1E-4	6.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	RT		20	8.1E-4	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	RT		22	8.7E-4	3.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat 2</a>	RT		19	1.2E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	RT		22	1.2E-3	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	RT		22	1.2E-3	2.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">wd repeat</a>	RT		22	1.3E-3	6.1E-2
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, conserved site</a>	RT		22	1.3E-3	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, subgroup</a>	RT		20	1.7E-3	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, region</a>	RT		19	2.5E-3	2.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">WD40/YVTN repeat-like</a>	RT		21	5.1E-3	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	RT		15	9.3E-3	8.5E-1

# Functional Enrichment of RAD21's 762 Targets (~9000 genes as background) (Top)

Annotation Cluster 1		Enrichment Score: 8.18	G		Count	P_Value	BenjamInl
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel development</a>	RT		36	1.8E-9	2.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vasculature development</a>	RT		36	2.7E-9	2.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel morphogenesis</a>	RT		31	6.2E-8	4.4E-5
Annotation Cluster 2		Enrichment Score: 3.51	G		Count	P_Value	BenjamInl
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell migration</a>	RT		20	1.6E-4	4.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell motion</a>	RT		21	2.9E-4	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>	RT		20	6.2E-4	9.8E-2
Annotation Cluster 3		Enrichment Score: 3.01	G		Count	P_Value	BenjamInl
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchyme development</a>	RT		10	4.8E-4	8.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neural crest cell differentiation</a>	RT		8	7.3E-4	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neural crest cell development</a>	RT		8	7.3E-4	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchymal cell differentiation</a>	RT		9	1.8E-3	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchymal cell development</a>	RT		9	1.8E-3	1.8E-1

# Functional Enrichment of TAF1's 595 Targets (1) (Top)

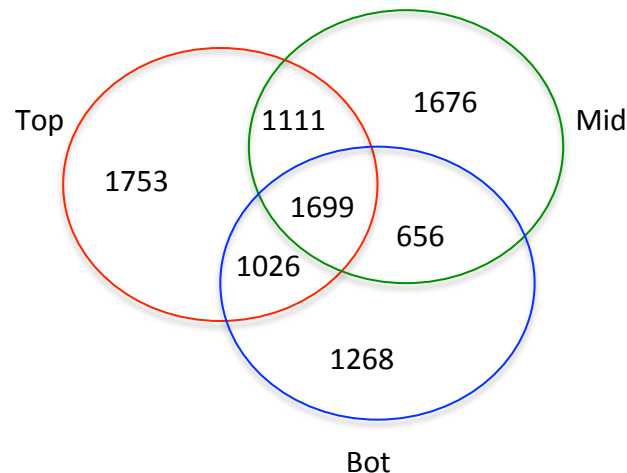
Annotation Cluster 1		Enrichment Score: 35.83	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translational elongation</a>	RT		58	1.2E-44	2.7E-41
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	RT		54	8.3E-41	1.2E-38
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	RT		47	1.7E-39	6.6E-37
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribonucleoprotein</a>	RT		77	1.4E-38	2.9E-36
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	RT		64	9.6E-38	1.3E-35
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	RT		61	4.1E-37	2.7E-34
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	RT		67	7.1E-36	2.9E-33
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	RT		45	9.2E-35	1.9E-32
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosomal subunit</a>	RT		53	2.0E-34	2.7E-32
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural molecule activity</a>	RT		72	3.7E-22	7.9E-20
Annotation Cluster 2		Enrichment Score: 8.62	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		130	6.6E-10	2.3E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		131	9.4E-10	3.0E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		131	3.2E-9	9.5E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		109	1.7E-8	4.6E-7
Annotation Cluster 3		Enrichment Score: 5.7	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nuclear mRNA splicing, via spliceosome</a>	RT		25	2.0E-6	4.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing, via transesterification reactions with bulged adenosine as nucleophile</a>	RT		25	2.0E-6	4.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing, via transesterification reactions</a>	RT		25	2.0E-6	4.8E-4
Annotation Cluster 4		Enrichment Score: 5.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotide-binding, alpha-beta plait</a>	RT		27	5.8E-7	2.7E-4
<input type="checkbox"/>	SMART	<a href="#">RRM</a>	RT		24	2.3E-6	3.8E-4
<input type="checkbox"/>	INTERPRO	<a href="#">RNA recognition motif, RNP-1</a>	RT		24	2.8E-5	6.5E-3
Annotation Cluster 5		Enrichment Score: 5.46	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA splicing</a>	RT		34	2.3E-6	4.5E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">mrna splicing</a>	RT		27	2.4E-6	8.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mRNA metabolic process</a>	RT		39	3.0E-6	5.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mRNA processing</a>	RT		36	3.2E-6	5.1E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">mrna processing</a>	RT		29	9.7E-6	3.0E-4

# Functional Enrichment of TAF1's 595 Targets (2)




























Annotation Cluster 6		Enrichment Score: 5.07			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	RT		13	2.9E-7	2.7E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	RT		13	5.9E-7	2.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	RT		17	1.9E-6	5.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	RT		16	2.2E-6	4.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	RT		16	2.9E-6	5.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	RT		16	3.7E-6	5.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		14	9.0E-6	2.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly or disassembly</a>	RT		18	1.4E-5	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	RT		16	1.1E-4	1.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	RT		14	1.9E-4	4.0E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">chromosomal protein</a>	RT		16	9.1E-4	1.9E-2
Annotation Cluster 7		Enrichment Score: 3			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of endopeptidase activity</a>	RT		14	1.0E-4	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of peptidase activity</a>	RT		14	1.5E-4	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of caspase activity</a>	RT		13	3.6E-4	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of caspase activity</a>	RT		11	3.7E-4	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of peptidase activity</a>	RT		11	3.7E-4	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of caspase activity</a>	RT		10	5.9E-4	4.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of hydrolase activity</a>	RT		14	2.0E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of hydrolase activity</a>	RT		18	1.2E-1	9.3E-1
Annotation Cluster 8		Enrichment Score: 2.98			Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		6	5.6E-4	4.5E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		6	1.1E-3	1.8E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		6	2.0E-3	4.3E-1
Annotation Cluster 9		Enrichment Score: 2.62			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>	RT		51	2.1E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>	RT		51	2.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell death</a>	RT		51	2.8E-3	1.5E-1
Annotation Cluster 10		Enrichment Score: 2.12			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular protein localization</a>	RT		30	6.1E-3	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular macromolecule localization</a>	RT		30	6.5E-3	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">intracellular protein transport</a>	RT		27	1.1E-2	4.1E-1

# Functional Enrichment of TF Targets in Different Levels




























- Top level TFs have 5589 coding gene targets
- Middle level TFs have 5142 coding gene targets
- Bottom level TFs have 4649 coding gene targets



# Only Targets of Top-Level TFs (1)





























Annotation Cluster 1		Enrichment Score: 41.85	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Homeobox</a>	RT		113	4.9E-45	3.0E-42
<input type="checkbox"/>	INTERPRO	<a href="#">Homeobox, conserved site</a>	RT		112	1.4E-44	2.6E-41
<input type="checkbox"/>	INTERPRO	<a href="#">Homeobox</a>	RT		111	5.4E-44	4.9E-41
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Homeobox	RT		102	1.2E-42	4.4E-39
<input type="checkbox"/>	SMART	<a href="#">HOX</a>	RT		111	4.7E-40	1.5E-37
<input type="checkbox"/>	INTERPRO	<a href="#">Homeodomain-related</a>	RT		109	3.4E-39	2.1E-36
Annotation Cluster 2		Enrichment Score: 28.96	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of RNA metabolic process</a>	RT		357	1.1E-33	4.0E-30
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transcription, DNA-dependent</a>	RT		349	3.5E-33	6.4E-30
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transcription</a>	RT		427	3.7E-22	4.6E-19
Annotation Cluster 3		Enrichment Score: 19.37	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transcription</a>	RT		427	3.7E-22	4.6E-19
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transcription regulation</a>	RT		349	2.4E-21	3.7E-19
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Transcription</a>	RT		349	2.2E-19	2.6E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transcription</a>	RT		351	1.7E-17	1.5E-14
Annotation Cluster 4		Enrichment Score: 8	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Krueppel-associated box</a>	RT		64	2.1E-9	9.4E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KRAB	RT		62	4.1E-9	4.9E-6
<input type="checkbox"/>	SMART	<a href="#">KRAB</a>	RT		64	1.2E-7	2.0E-5
Annotation Cluster 5		Enrichment Score: 7.9	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">limb development</a>	RT		36	3.0E-9	7.0E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">appendage development</a>	RT		36	3.0E-9	7.0E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">appendage morphogenesis</a>	RT		34	1.3E-8	2.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">limb morphogenesis</a>	RT		34	1.3E-8	2.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">embryonic appendage morphogenesis</a>	RT		30	5.2E-8	7.2E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">embryonic limb morphogenesis</a>	RT		30	5.2E-8	7.2E-6

# Only Targets of Top-Level TFs (2)
























Annotation Cluster 6		Enrichment Score: 6.61	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	RT		81	1.2E-8	2.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription, DNA-dependent</a>	RT		98	2.0E-8	3.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of RNA metabolic process</a>	RT		98	4.4E-8	6.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription</a>	RT		109	6.9E-8	9.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of gene expression</a>	RT		109	2.2E-7	2.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nitrogen compound metabolic process</a>	RT		117	2.8E-7	2.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule biosynthetic process</a>	RT		118	3.2E-7	3.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT		114	3.4E-7	3.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of biosynthetic process</a>	RT		123	3.9E-7	3.7E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular biosynthetic process</a>	RT		121	4.7E-7	4.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule metabolic process</a>	RT		134	2.1E-4	9.4E-3
Annotation Cluster 7		Enrichment Score: 5.96	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell morphogenesis involved in differentiation</a>	RT		51	2.4E-7	2.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell morphogenesis</a>	RT		67	3.2E-7	3.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular component morphogenesis</a>	RT		68	1.8E-5	1.2E-3
Annotation Cluster 8		Enrichment Score: 5.63	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 5</a>	RT		88	8.9E-8	5.3E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 6</a>	RT		81	1.2E-7	6.1E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C2H2-type/integrase, DNA-binding</a>	RT		97	2.0E-7	7.3E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 7</a>	RT		73	1.1E-6	4.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 3</a>	RT		95	2.9E-6	8.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 8</a>	RT		66	4.0E-6	8.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 2</a>	RT		93	4.1E-6	8.6E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C2H2-type</a>	RT		112	4.1E-6	1.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C2H2-like</a>	RT		114	6.6E-6	1.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 4</a>	RT		85	6.7E-6	1.3E-3





# Only Targets of Top-Level TFs (3)

Annotation Cluster 9		Enrichment Score: 5.35	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	<a href="#">RT</a>		55	2.4E-6	7.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	<a href="#">RT</a>		60	2.9E-6	7.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	<a href="#">RT</a>		66	4.0E-6	8.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	<a href="#">RT</a>		48	1.3E-5	2.5E-3
Annotation Cluster 10		Enrichment Score: 5.31	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell morphogenesis involved in differentiation</a>	<a href="#">RT</a>		51	2.4E-7	2.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell projection morphogenesis</a>	<a href="#">RT</a>		48	4.3E-6	3.6E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell morphogenesis involved in neuron differentiation</a>	<a href="#">RT</a>		42	4.9E-6	4.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neuron projection development</a>	<a href="#">RT</a>		48	7.1E-6	5.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neuron projection morphogenesis</a>	<a href="#">RT</a>		41	9.9E-6	7.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">axonogenesis</a>	<a href="#">RT</a>		39	1.0E-5	7.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell part morphogenesis</a>	<a href="#">RT</a>		49	1.9E-5	1.2E-3
Annotation Cluster 11		Enrichment Score: 4.9	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intrinsic to membrane</a>	<a href="#">RT</a>		447	1.5E-7	4.1E-5
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">integral to membrane</a>	<a href="#">RT</a>		422	6.4E-6	6.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	<a href="#">RT</a>		396	1.4E-4	2.1E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transmembrane</a>	<a href="#">RT</a>		397	1.9E-4	6.4E-3
Annotation Cluster 12		Enrichment Score: 4.26	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell migration</a>	<a href="#">RT</a>		51	3.2E-5	2.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell motility</a>	<a href="#">RT</a>		52	7.3E-5	4.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">localization of cell</a>	<a href="#">RT</a>		52	7.3E-5	4.0E-3
Annotation Cluster 13		Enrichment Score: 3.92	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neural crest cell development</a>	<a href="#">RT</a>		13	9.1E-5	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neural crest cell differentiation</a>	<a href="#">RT</a>		13	9.1E-5	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchymal cell development</a>	<a href="#">RT</a>		16	1.2E-4	6.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchymal cell differentiation</a>	<a href="#">RT</a>		16	1.2E-4	6.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mesenchyme development</a>	<a href="#">RT</a>		16	2.0E-4	9.2E-3






















# Only Targets of Top-Level TFs (4)

Annotation Cluster 14		Enrichment Score: 3.75	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Basic helix-loop-helix dimerisation region</a> <a href="#">bHLH</a>	RT		26	5.3E-5	9.6E-3
<input type="checkbox"/>	SMART	<a href="#">HLH</a>	RT		26	3.2E-4	3.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		24	3.4E-4	4.9E-2
Annotation Cluster 15		Enrichment Score: 3.63	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of neurological system process</a>	RT		28	1.6E-4	7.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transmission of nerve impulse</a>	RT		27	2.5E-4	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of synaptic transmission</a>	RT		25	3.3E-4	1.3E-2
Annotation Cluster 16		Enrichment Score: 3.62	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">g-protein coupled receptor</a>	RT		42	1.2E-4	4.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">GPCR, rhodopsin-like superfamily</a>	RT		35	1.7E-4	2.7E-2
<input type="checkbox"/>	INTERPRO	<a href="#">7TM GPCR, rhodopsin-like</a>	RT		35	3.3E-4	4.2E-2
<input type="checkbox"/>	PIRSUPERFAMILY	PIRSF800006:rhodopsin-like G protein-coupled receptors	RT		32	5.0E-4	1.5E-1
Annotation Cluster 17		Enrichment Score: 3.53	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT		16	8.8E-5	1.5E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor, fork head</a>	RT		15	3.1E-4	4.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor, fork head, conserved site</a>	RT		15	3.1E-4	4.2E-2
<input type="checkbox"/>	SMART	<a href="#">FH</a>	RT		15	9.6E-4	6.0E-2
Annotation Cluster 18		Enrichment Score: 3.28	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of neurogenesis</a>	RT		33	2.1E-4	9.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nervous system development</a>	RT		36	4.0E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of neuron differentiation</a>	RT		27	4.3E-4	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell development</a>	RT		37	2.2E-3	6.5E-2




















# Only Targets of Top-Level TFs (5)

Annotation Cluster 19		Enrichment Score: 3.11	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclase activity</a>	RT		18	1.9E-4	8.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of lyase activity</a>	RT		18	2.9E-4	1.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of adenylate cyclase activity</a>	RT		17	3.1E-4	1.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cAMP biosynthetic process</a>	RT		17	6.8E-4	2.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cAMP metabolic process</a>	RT		17	6.8E-4	2.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide metabolic process</a>	RT		18	1.7E-3	5.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide biosynthetic process</a>	RT		18	1.7E-3	5.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide biosynthetic process</a>	RT		18	1.7E-3	5.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide metabolic process</a>	RT		18	3.0E-3	8.3E-2
Annotation Cluster 20		Enrichment Score: 2.84	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of lyase activity</a>	RT		12	1.5E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of adenylate cyclase activity</a>	RT		12	1.5E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cyclase activity</a>	RT		12	1.5E-3	4.7E-2






























# Only Targets of Mid-Level TFs

Annotation Cluster 1		Enrichment Score: 3.14		G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PCI	<a href="#">RT</a>			10	4.0E-4	5.0E-1
<input type="checkbox"/>	SMART	<a href="#">PINT</a>	<a href="#">RT</a>			9	7.2E-4	1.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome component region PCI</a>	<a href="#">RT</a>			9	1.3E-3	9.1E-1
Annotation Cluster 2		Enrichment Score: 1.91		G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 13	<a href="#">RT</a>			5	4.9E-3	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 14	<a href="#">RT</a>			5	4.9E-3	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 12	<a href="#">RT</a>			5	1.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 15	<a href="#">RT</a>			4	2.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 16	<a href="#">RT</a>			4	2.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 11	<a href="#">RT</a>			5	2.5E-2	1.0E0
Annotation Cluster 3		Enrichment Score: 1.6		G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside monophosphate metabolic process</a>	<a href="#">RT</a>			7	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside monophosphate biosynthetic process</a>	<a href="#">RT</a>			7	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">'de novo' IMP biosynthetic process</a>	<a href="#">RT</a>			5	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">IMP biosynthetic process</a>	<a href="#">RT</a>			5	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">IMP metabolic process</a>	<a href="#">RT</a>			5	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	<a href="#">RT</a>			6	2.0E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	<a href="#">RT</a>			6	2.0E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside monophosphate metabolic process</a>	<a href="#">RT</a>			6	2.0E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside monophosphate biosynthetic process</a>	<a href="#">RT</a>			6	2.0E-2	1.0E0

# Only Targets of Bottom-Level TFs

Annotation Cluster 1		Enrichment Score: 4.94	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Immunoglobulin domain</a>	RT		42	1.1E-6	1.6E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like</a>	RT		40	1.1E-5	6.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like fold</a>	RT		41	1.3E-4	3.4E-2
Annotation Cluster 2		Enrichment Score: 4.51	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transmembrane</a>	RT		313	1.7E-6	2.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		311	2.0E-6	1.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">integral to membrane</a>	RT		335	2.9E-4	7.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intrinsic to membrane</a>	RT		342	9.5E-4	1.5E-1
Annotation Cluster 3		Enrichment Score: 2.74	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">LRR_TYP</a>	RT		15	5.8E-4	5.5E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Leucine-rich repeat, typical subtype</a>	RT		15	8.2E-4	1.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Leucine-rich repeat</a>	RT		19	1.3E-2	7.5E-1
Annotation Cluster 4		Enrichment Score: 2.56	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ion channel activity</a>	RT		29	1.6E-3	5.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">substrate specific channel activity</a>	RT		29	1.8E-3	4.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">channel activity</a>	RT		29	3.5E-3	5.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">passive transmembrane transporter activity</a>	RT		29	3.5E-3	5.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ionic channel</a>	RT		22	4.5E-3	2.3E-1








































# Common Targets of Top and Mid-Level TFs (1)

Annotation Cluster 1		Enrichment Score: 9.84	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	RT		48	3.1E-11	5.7E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translational elongation</a>	RT		59	3.4E-11	7.5E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	RT		47	2.2E-10	7.7E-8
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	RT		52	1.8E-9	3.4E-7
Annotation Cluster 2		Enrichment Score: 9.25	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	RT		74	7.1E-11	1.0E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	RT		85	1.5E-9	3.4E-7
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	RT		79	1.7E-9	2.1E-7
Annotation Cluster 3		Enrichment Score: 8.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		430	1.8E-9	2.5E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		436	2.5E-9	2.9E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		420	1.1E-8	9.1E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		351	8.7E-8	5.5E-6
Annotation Cluster 4		Enrichment Score: 6	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	RT		28	3.8E-9	3.9E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		34	4.7E-9	4.6E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	RT		25	7.1E-8	1.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	RT		38	6.7E-7	7.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	RT		34	3.6E-6	3.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	RT		36	3.7E-6	1.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	RT		34	6.4E-6	3.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	RT		34	1.1E-5	5.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly or disassembly</a>	RT		42	3.0E-5	1.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	RT		40	4.2E-5	1.5E-2
Annotation Cluster 5		Enrichment Score: 4.08	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		12	6.4E-5	1.3E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		12	7.5E-5	6.4E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		12	1.2E-4	1.2E-1

# Common Targets of Top and Mid-Level TFs (2)





































Annotation Cluster 6		Enrichment Score: 3.94			G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">BRLZ</a>	<a href="#">RT</a>				25	1.8E-5	7.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Basic-leucine zipper (bZIP) transcription factor</a>	<a href="#">RT</a>				25	2.5E-5	3.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper	<a href="#">RT</a>				34	3.4E-3	9.9E-1
Annotation Cluster 7		Enrichment Score: 3.52			G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotide-binding, alpha-beta plait</a>	<a href="#">RT</a>				62	1.1E-4	6.8E-2
<input type="checkbox"/>	SMART	<a href="#">RRM</a>	<a href="#">RT</a>				60	4.0E-4	5.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">RNA recognition motif, RNP-1</a>	<a href="#">RT</a>				60	6.5E-4	2.5E-1

# Common Targets of Middle and Bottom-Level TFs




































Annotation Cluster 1		Enrichment Score: 6.53			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		31	1.2E-8	7.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly or disassembly</a>	RT		43	7.8E-8	3.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	RT		36	1.0E-7	2.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	RT		33	2.2E-7	1.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	RT		33	3.9E-7	2.6E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	RT		33	6.9E-7	3.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	RT		34	7.6E-7	2.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	RT		37	1.4E-5	4.8E-3
Annotation Cluster 2		Enrichment Score: 6.13			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		31	1.2E-8	7.5E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	RT		24	1.7E-8	4.2E-5
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	RT		24	2.7E-7	6.1E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	RT		28	5.4E-3	6.4E-1
Annotation Cluster 3		Enrichment Score: 3.31			Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">H2A</a>	RT		11	3.5E-4	1.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2A</a>	RT		11	4.0E-4	3.9E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002048:histone H2A	RT		10	8.6E-4	5.6E-1
Annotation Cluster 4		Enrichment Score: 3.04			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	RT		346	2.8E-4	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	RT		332	7.4E-4	3.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	RT		336	8.8E-4	4.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	RT		273	3.7E-3	1.4E-1
Annotation Cluster 5		Enrichment Score: 2.87			Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		10	1.0E-3	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		10	1.1E-3	5.0E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		10	2.1E-3	6.3E-1
Annotation Cluster 6		Enrichment Score: 2.86			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	RT		61	4.2E-4	2.7E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	RT		54	1.8E-3	1.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	RT		48	3.3E-3	5.3E-1
Annotation Cluster 7		Enrichment Score: 2.57			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">nucleotide binding</a>	RT		360	3.7E-5	4.8E-2



# Common Targets of Top and Bottom-Level TFs

Annotation Cluster 1		Enrichment Score: 5.76	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	RT		25	4.8E-8	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly or disassembly</a>	RT		47	8.7E-8	3.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	RT		37	1.7E-7	3.6E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	RT		36	1.8E-7	2.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	RT		36	3.6E-7	3.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	RT		38	5.2E-7	4.6E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	RT		25	8.9E-7	6.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	RT		30	1.6E-6	1.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	RT		41	1.2E-5	8.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	RT		32	1.8E-4	1.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	RT		30	6.6E-3	3.4E-1
Annotation Cluster 2		Enrichment Score: 3.23	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	RT		36	1.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translational elongation</a>	RT		45	1.7E-4	6.2E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	RT		38	1.8E-3	2.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	RT		32	3.6E-3	1.2E-1
Annotation Cluster 3		Enrichment Score: 3.17	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		11	5.7E-4	5.3E-1
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		11	6.7E-4	2.4E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		11	8.1E-4	3.5E-1
Annotation Cluster 4		Enrichment Score: 3.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	RT		56	5.5E-4	2.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	RT		62	8.2E-4	5.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	RT		66	1.2E-3	6.1E-2
Annotation Cluster 5		Enrichment Score: 3.06	G		Count	P_Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002048:histone H2A	RT		11	2.6E-4	2.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2A</a>	RT		11	1.5E-3	7.2E-1
<input type="checkbox"/>	SMART	<a href="#">H2A</a>	RT		11	1.7E-3	2.9E-1
Annotation Cluster 6		Enrichment Score: 2.96	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">nucleotide binding</a>	RT		408	1.3E-5	1.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ribonucleotide binding</a>	RT		326	2.5E-4	1.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">purine ribonucleotide binding</a>	RT		326	2.5E-4	1.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ATP binding</a>	RT		265	1.2E-3	3.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">purine nucleotide binding</a>	RT		332	1.3E-3	3.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">adenyl ribonucleotide binding</a>	RT		266	1.6E-3	3.1E-1

# Common Targets of Top, Middle, and Bottom-Level TFs

Annotation Cluster 1		Enrichment Score: 7.28	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	<a href="#">RT</a>		23	2.0E-10	3.8E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nucleosome</a>	<a href="#">RT</a>		28	6.7E-10	4.1E-7
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">nucleosome core</a>	<a href="#">RT</a>		23	2.8E-9	8.9E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly or disassembly</a>	<a href="#">RT</a>		38	5.7E-9	2.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome assembly</a>	<a href="#">RT</a>		30	1.1E-8	1.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleosome organization</a>	<a href="#">RT</a>		32	1.1E-8	1.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chromatin assembly</a>	<a href="#">RT</a>		30	1.8E-8	1.7E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein-DNA complex assembly</a>	<a href="#">RT</a>		30	3.1E-8	2.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">protein-DNA complex</a>	<a href="#">RT</a>		30	6.2E-8	1.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA packaging</a>	<a href="#">RT</a>		33	8.6E-7	5.2E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Histone-fold</a>	<a href="#">RT</a>		19	6.1E-5	5.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	<a href="#">RT</a>		25	8.7E-4	1.5E-1
Annotation Cluster 2		Enrichment Score: 3.97	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	<a href="#">RT</a>		10	8.1E-5	5.0E-2
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	<a href="#">RT</a>		10	8.3E-5	2.7E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002050:histone H2B	<a href="#">RT</a>		10	1.9E-4	6.3E-2
Annotation Cluster 3		Enrichment Score: 3.94	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translational elongation</a>	<a href="#">RT</a>		35	2.1E-5	7.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	<a href="#">RT</a>		28	2.6E-5	2.3E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	<a href="#">RT</a>		26	2.3E-4	1.2E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	<a href="#">RT</a>		29	1.4E-3	1.2E-1
Annotation Cluster 4		Enrichment Score: 3.86	G		Count	P_Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002048:histone H2A	<a href="#">RT</a>		10	7.0E-5	4.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2A</a>	<a href="#">RT</a>		10	1.9E-4	8.6E-2
<input type="checkbox"/>	SMART	<a href="#">H2A</a>	<a href="#">RT</a>		10	2.0E-4	3.2E-2
Annotation Cluster 5		Enrichment Score: 3.78	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	<a href="#">RT</a>		49	1.3E-4	7.3E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	<a href="#">RT</a>		42	1.4E-4	7.5E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	<a href="#">RT</a>		45	2.5E-4	1.2E-2
Annotation Cluster 6		Enrichment Score: 3.23	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	<a href="#">RT</a>		254	3.2E-4	1.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle lumen</a>	<a href="#">RT</a>		249	4.3E-4	2.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	<a href="#">RT</a>		245	5.0E-4	2.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	<a href="#">RT</a>		203	1.7E-3	5.4E-2