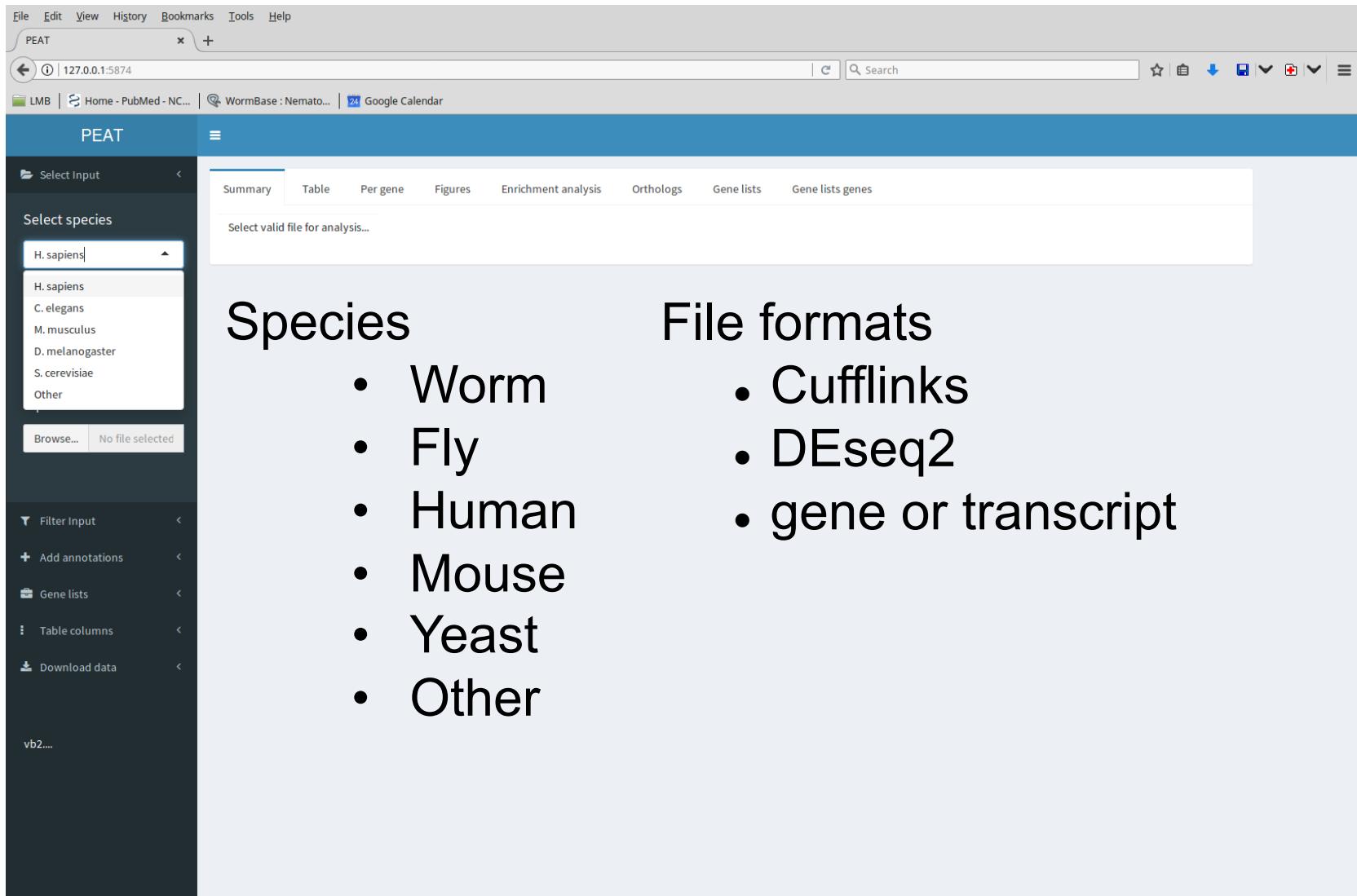


# PEAT – PRAGUI Exploratory Analysis Tool



The screenshot shows the PEAT web application interface. At the top, there is a navigation bar with links for File, Edit, View, History, Bookmarks, Tools, and Help. Below the navigation bar is a browser-style header with a back button, forward button, address bar (127.0.0.1:5874), search bar, and various browser icons. The main content area has a blue header bar with the text "PEAT". Below the header, there are two main sections: "Select species" on the left and "Analysis tabs" on the right.

**Select species:** A dropdown menu is open, showing "H. sapiens" as the selected option. Other options listed include H. sapiens, C. elegans, M. musculus, D. melanogaster, S. cerevisiae, and Other. Below the dropdown are buttons for "Browse..." and "No file selected".

**Analysis tabs:** A horizontal navigation bar with tabs: Summary (selected), Table, Per gene, Figures, Enrichment analysis, Orthologs, Gene lists, and Gene lists genes. Below this bar is a message: "Select valid file for analysis...".

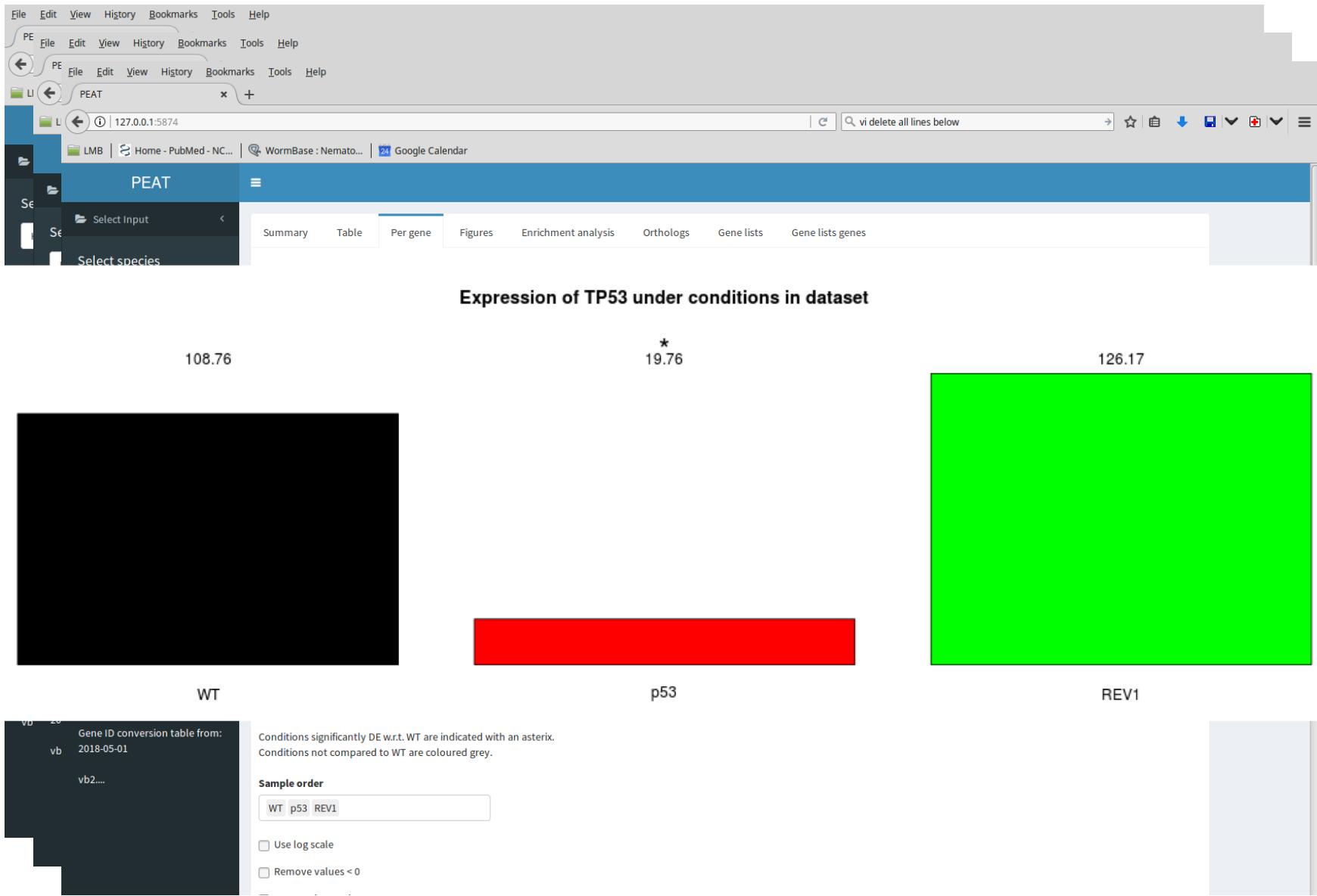
**Species:** A list of supported species:

- Worm
- Fly
- Human
- Mouse
- Yeast
- Other

**File formats:**

- Cufflinks
- DEseq2
- gene or transcript

# Different views



# Table

File Edit View History Bookmarks Tools Help

PEAT Gene: ZNF806 (ENSG0000018607) +

Gene: ZNF806 (ENSG0000018607);r=2;132309309-132318736;t=ENST00000438300

LMB | Home - PubMed - NC... | WormBase : Nemat... | Google Calendar

**eEnsembl** BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Login/Register

Human (GRCh38.p12) ▾

Location: 2:132,309,309-132,318,736 Gene: ZNF806 Transcript: ZNF806-201

**Gene-based displays**

- Summary
  - Splice variants
  - Transcript comparison
  - Gene alleles
- Sequence
  - Secondary Structure
- Comparative Genomics
  - Genomic alignments
  - Gene tree
  - Gene gain/loss tree
  - Orthologues
  - Paralogues
  - Ensembl protein families
- Ontologies
  - GO: Cellular component
  - GO: Molecular function
  - GO: Biological process
- Phenotypes
- Genetic Variation
  - Variant table
  - Variant image
  - Structural variants
- Gene expression
- Pathway
- Regulation
- External references
- Supporting evidence
- ID History
  - Gene history

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

**Gene: ZNF806 ENSG0000018607**

Description zinc finger protein 806 [Source:HGNC Symbol;Acc:[HGNC:33228](#)]

Location Chromosome 2: 132,309,309-132,318,736 forward strand.  
GRCh38:CM000664.2

About this gene This gene has 1 transcript ([splice variant](#)).

Transcripts Hide transcript table

Name	Transcript ID	bp	Protein	Biotype	CCDS	Flags
ZNF806-201	<a href="#">ENST00000438300.1</a>	1774	No protein	Unprocessed pseudogene	-	TSL:NA GENCODE basic

**Summary** ⓘ

Name [ZNF806](#) (HGNC Symbol)

RefSeq Overlapping RefSeq annotation not matched

Ensembl version ENSG0000018607.6

Other assemblies This gene maps to [133,066,882-133,076,309](#) in GRCh37 coordinates.  
View this locus in the GRCh37 archive: [ENSG0000018607](#)

Gene type Unprocessed pseudogene

Annotation method Manual annotation (determined on a case-by-case basis) from the [Havana](#) project.

Go to Region In Detail for more tracks and navigation options (e.g. zooming)

Drag>Select:

Genes (Comprehensive set...)

Contigs

Regulatory Build

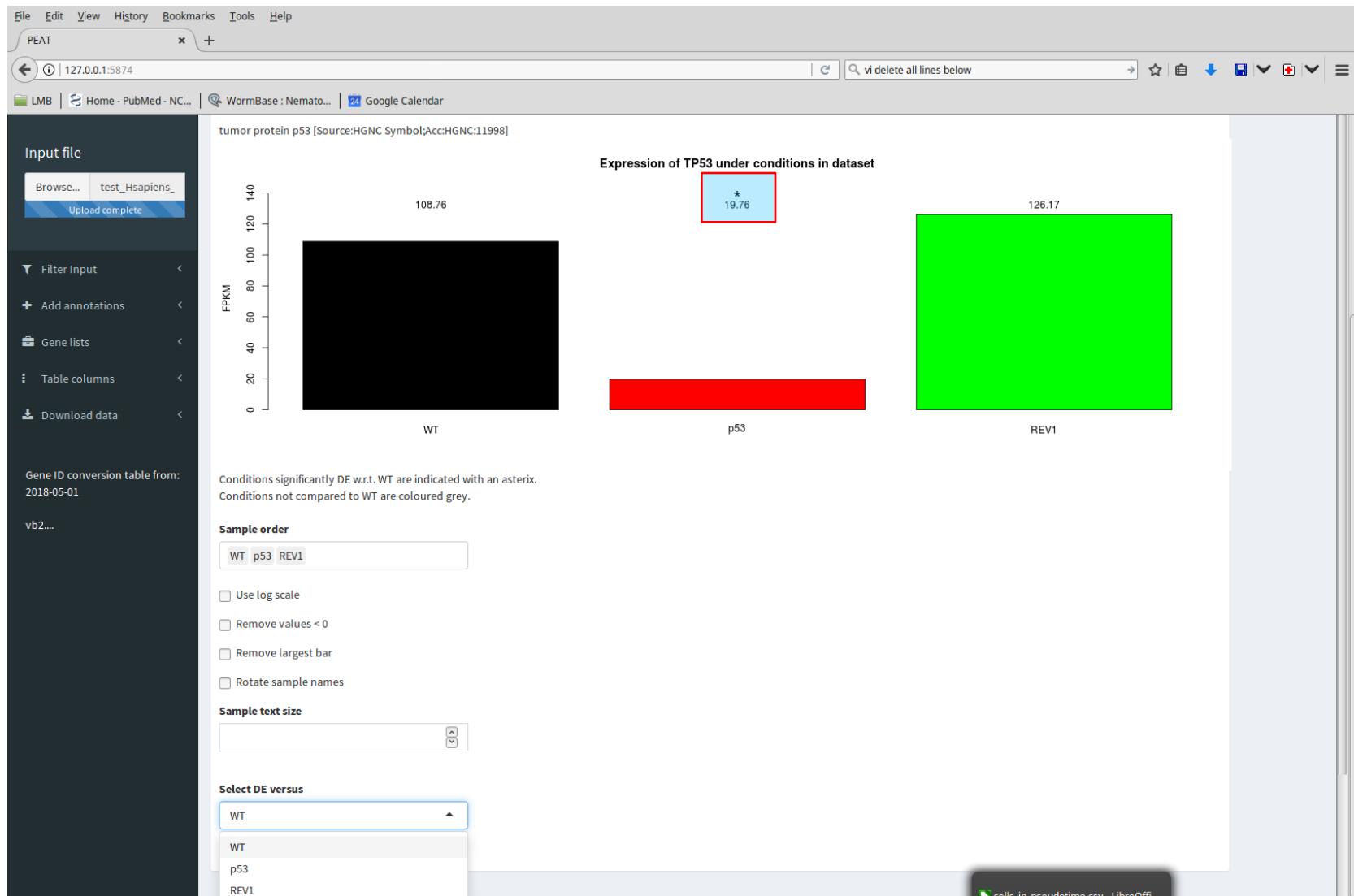
Regulation Legend

Open Chromatin Promoter Plank

This website requires cookies, and the limited processing of your personal data in order to function. By using the site you are agreeing to this as outlined in our [Privacy Policy](#) and [Terms of Use](#)

I Agree

# Per gene



# Filtering

The screenshot shows the PEAT software interface. On the left, the 'Filter Input' panel is open, displaying various filtering options:

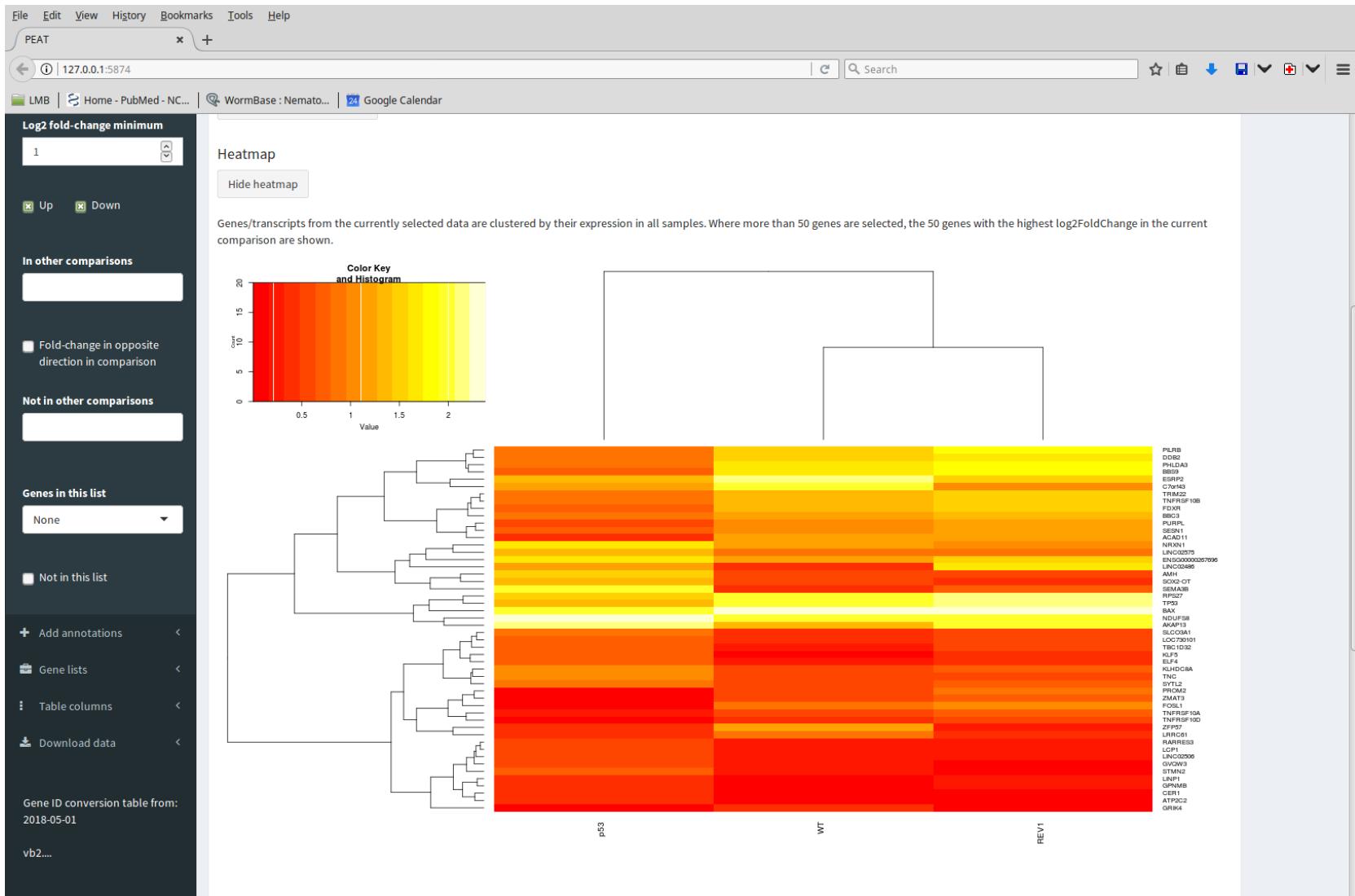
- Select comparison:** WT vs p53
- Sample 1 FPKM at least:** 0
- Sample 2 FPKM at least:** 0
- Log2 fold-change minimum:** 0
- In other comparisons:** WT vs REV1, p53 vs REV1
- Not in other comparisons:** (empty)
- Genes in this list:** Create a gene list to filter by, Not in this list
- Add annotations:** Gene lists, Table columns

The main window displays a summary table with the following data:

	Sample 1 (WT) FPKM	Sample 2 (p53) FPKM
mean value	13.79	14.23
median value	0.02	0
max value	26967	35361.2
min value	0	0
log2(fold change)	NAN	
mean value	NAN	
median value	0	
max value	Inf	
min value	-Inf	
Significantly DE		
yes	212	
no	59904	

- Choose comparison
- Filter for DE
- Expression level
- Fold-change of expression
- In multiple comparisons
- In list of genes

# Multigene plots



# Gene lists

File Edit View History Bookmarks Tools Help

PEAT x +

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LMB | Home - PubMed - NC... | WormBase : Nemato... | Google Calendar

List name: All genes

All genes

p53\_DE\_genes

REV1\_DE\_genes

Showing 1 to 25 of 25

Gene lists genes

Show data for genes in this list: p53\_DE\_genes

Show 25 entries

Search:

x.gene_id	x.Other.gene.IDs	x.found.in.filtered.data	x.WT.FPKM	x.p53.FPKM	x.REV1.FPKM
ENSG00000240303	ACAD11	TRUE	12.96	2.49	15.66
ENSG00000170776	AKAP13	TRUE	25.45	117.13	104.98
ENSG00000104899	AMH	TRUE	3.05	37.76	4.12
ENSG00000064270	ATP2C2	TRUE	1.01	2.79	1.01
ENSG00000087088	BAX	TRUE	211.82	92.51	237.06
ENSG00000105327	BBC3	TRUE	16.99	6.5	24.46
ENSG00000122507	BBS9	TRUE	38.55	4.44	59.72
ENSG00000146826	C7orf43	TRUE	84.51	13.34	11.42
ENSG00000147869	CER1	TRUE	1.15	3	1.32
ENSG00000134574	DDB2	TRUE	36.13	7.71	48.73
ENSG00000102034	ELF4	TRUE	1.89	4.71	2.18
ENSG00000267696	ENSG00000267696	TRUE	17.29	43.27	29.51
ENSG00000103067	ESRP2	TRUE	136.23	22.57	26.85

# Annotations

PEAT

File Edit View History Bookmarks Tools Help

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LMB | Home - PubMed - NC... | WormBase : Nemato... | Google Calendar

PEAT

Select input

Filter Input

+ Add annotations

Add brief description

Add GO terms

Annotation file

Browse... No file selected

Hide annotation(s) from file(s)

Gene lists

Table columns

Download data

Summary Table Per gene Figures Enrichment analysis Orthologs Gene lists Gene lists genes

Show 25 entries

Search:

x.gene_id	x.gene	x.locus	x.sample_1	x.sample_2	x.value_1	x.value_2	x.log2.fold_change.	x.significant
ENSG00000018607	ENSG00000018607	2:132309308-132318736	WT	p53	5.22247e-9	0	-0.368728	no
ENSG00000060303	ENSG00000060303	6:50857254-50857662	WT	p53	1.17005	0.906164	-0.460665	no
ENSG00000078319	ENSG00000078319	7:100307701-100400099	WT	p53	0.0404977	0.055732	-0.441682	no
ENSG00000082929	LINC01587	4:5524568-5527801	WT	p53	0.109395	0.0805446	-0.460665	no
ENSG00000093100	ENSG00000093100	22:17787648-18024559	WT	p53	0.0374362	0.0385016	-0.441682	no
ENSG00000100101	ENSG00000100101	22:37681672-37776556	WT	p53	0.0374362	0.0385016	-0.441682	no
ENSG00000101898	ENSG00000101898	20:31514427-31577923	WT	p53	0.0374362	0.0385016	-0.441682	no
ENSG00000103200	ENSG00000103200	7:140435315-140435787	WT	p53	0	0	-0.441682	no
ENSG00000103832	ENSG00000103832	15:30791572-30801859	WT	p53	0.00689062	7.99861e-9	-19.7165	no

now 25 entries

Search:

x.gene_id	x.gene	x.locus	x.sample_1	x.sample_2	x.value_1	x.value_2	x.log2.fold_change.	x.significant	x.GO.ID	x.GO.names
ENSG00000000003	TSPAN6	X:100627108-100639991	WT	p53	39.4141	37.3635	-0.0770824	no	GO:000515, GO:0005887, GO:0007166, GO:0039532, GO:0043123, GO:0007062, GO:1901223	protein binding, integral component of plasma membrane, cell surface receptor signaling pathway, negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway, positive regulation of I-kappaB kinase/NF-kappaB signaling
ENSG00000000005	TNMD	X:100584801-100599885	WT	p53	3.91841	4.95482	0.338564	no	GO:0001886, GO:0001937, GO:0005515, GO:0005634, GO:0005731, GO:0016021, GO:001625, GO:0035990, GO:0071773	endothelial cell morphogenesis, negative regulation of endothelial cell proliferation, protein binding, nuclear envelope, cytoplasm, integral component of membrane, negative regulation of angiogenesis, tendon cell differentiation, cellular response to BMP stimulus
ENSG000000000419	DPM1	20:5088818-50958555	WT	p53	62.2364	66.2105	0.0893029	no	GO:0004169, GO:0004582, GO:0005515, GO:0005634, GO:0005783, GO:0005789, GO:0006506, GO:0016020, GO:0019348, GO:0033185, GO:0035268, GO:0035269	dolichyl-phosphate-mannose-protein mannosyltransferase activity, dolichyl-phosphate beta-D-mannosyltransferase activity, protein binding, nucleus, endoplasmic reticulum, endoplasmic reticulum membrane, GPI anchor biosynthetic process, membrane, dolichol metabolic process, dolichyl-phosphate-mannose synthase complex, protein mannosylation, protein O-linked mannosylation
ENSG000000000457	SCYL3	1:169662006-169894267	WT	p53	2.12921	2.37713	0.158903	no	GO:0005515, GO:0005524, GO:0005737, GO:0005794, GO:0006468, GO:0016301, GO:0016477, GO:0030027	protein binding, ATP binding, cytoplasm, Golgi apparatus, protein phosphorylation, kinase activity, cell migration, lamellipodium
ENSG000000000460	C1orf112	1:169662006-169894267	WT	p53	14.2563	13.2189	-0.108998	no	GO:0001784, GO:0002768, GO:0004713,	

InterMine Annotations

User-defined annotations

# Enrichment analysis

File Edit View History Bookmarks Tools Help

PEAT +/-

127.0.0.1:5874 | vi delete all lines below | C | S | D | F | V | R | E | M

LMB | Home - PubMed - NC... | WormBase : Nemato... | Google Calendar

**PEAT**

Select input | Filter Input | Select comparison | Significantly DE | Sample 1 FPKM at least | Sample 2 FPKM at least | Log2 fold-change minimum | Up | Down | In other comparisons | Fold-change in opposite direction in comparison | Not in other comparisons | Genes in this list

WT vs p53

Summary Table Per gene Figures Enrichment analysis Orthologs Gene lists Gene lists genes

Enrichment calculation is slow. We recommend hiding all but one enrichment before changing filters.  
All enrichments use Benjamini Hochberg multiple testing correction for their probabilities.  
Please note that query size for enrichment may be (much) smaller than the selected number of genes, as query size is only the number of genes with that type of annotation.

**gProfile enrichment**

Select data source: Reactome

	adjusted p-value	count in selected genes	count in all genes	genes with annotation
TP53 Regulates Transcription of Cell Death Genes REAC:R-HSA-5633008	4.39e-7	6	44	ENSG0000087088,ENSG0000104689,ENSG0000105327,ENSG0000120889,ENSG0000141510,ENSG0000173530
TP53 Regulates Transcription of Death Receptors and Ligands REAC:R-HSA-6803211	0.0000028	4	12	ENSG0000104689,ENSG0000120889,ENSG0000141510,ENSG0000173530
TRAIL signaling REAC:R-HSA-75158	0.0000834	3	8	ENSG0000104689,ENSG0000120889,ENSG0000173530
Transcriptional Regulation by TP53 REAC:R-HSA-3700989	0.000306	8	365	ENSG0000080546,ENSG0000087088,ENSG0000104689,ENSG0000105327,ENSG0000120889,ENSG0000134574,ET
TP53 Regulates				

# Modular

- New species
- New annotations
- New enrichments
- Anything with an API
- Single cell analysis version for those interested

Practical (full):

Thursday 17th January 3-4pm in the Milstein  
Seminar room  
Laptops required

Files (and Manuals) at:

<https://github.com/lmb-seq/PRAGUI>

<https://github.com/lmb-seq/PEAT>

Questions?