







April 2022


## geneXplain® platform major 7.0 release


New:

-  The platform has now fully automatic pipelines for paired RNA-seq libraries 
-  New workflows for analyzing multiple BAM files 
-  Estimate DEGs from raw RNA-seq data, counts or normalized transcriptomic data in 8 new and enhanced workflows 


←

### RNA-seq





Load RNA-seq data




**RNA-seq preprocessing**


Conversion of RNAseq data

Alignment of RNAseq data


Counting reads to genomic features

From raw data to gene/transcript counts

From multiple BAM files to gene counts 

RNAseq analysis with HISAT2 (paired-end) 

RNAseq analysis with HISAT2 (single-end)


RNAseq analysis with Subread (paired-end) 

RNAseq analysis with Subread (single-end)

Quantification of RNA-seq with Cufflinks (no de-novo assembly) for FASTQ files


Quantification of RNA-seq with Cufflinks (with de-novo assembly) for FASTQ files


Discover genome variants and indels




**Detect differentially expressed genes (DEGs)**

Full RNAseq data analysis


Analyze multiple BAM files to detect DEGs 

Full RNAseq analysis with HISAT2, featureCounts and limma (paired-end) 

Full RNAseq analysis with HISAT2, featureCounts and limma (single-end)

Full RNAseq analysis with HISAT2, htseq-counts and limma (paired-end) 

Full RNAseq analysis with HISAT2, htseq-counts and limma (single-end)

Full RNAseq analysis with subread, featureCounts and limma (paired-end) 

Full RNAseq analysis with subread, featureCounts and limma (single-end)

Statistics for RNAseq data

Estimate DEGs with guided limma


Limma

Limma voom

edgeR

DESeq2

EBarrays



- Support of new species *Zebrafish* and *Arabidopsis* for analyzing RNA-seq data or genes and sequences for transcription factor binding sites in over 20 workflows



- Support of Affymetrix miRNA-4.1 microarray chip & Agilent miRNA microarray chips

- Enable multiple miRNA ID support and conversion handling

Start page mixture\_miRNA Genes E... X

First Previous Page 1 of 1 Next Last Showing 1 to 8 of 8 entries Show 50 entries

ID	miRBase ID
<a href="#">ENSG00000199121</a>	MI0000084
<a href="#">ENSG00000207547</a>	MI0000082
<a href="#">ENSG00000207757</a>	MI0000095
<a href="#">ENSG00000207808</a>	MI0000085
<a href="#">ENSG00000283736</a>	hsa-mir-484
<a href="#">ENSG00000284190</a>	MI0000077
<a href="#">ENSG00000284520</a>	hsa-let-7b
<a href="#">ENSG00000284536</a>	hsa-mir-17

- Investigate tissue- or cell-line specific miRNA promoter regions with TRANSFAC®

Start page Identify enriched motifs ... X

**Identify enriched motifs in tissue specific miRNA promoters (TRANSFAC(R))**

miRNA table (select element)

Promoter 3' most

Select tissue blood

Add Ensembl promoters blood

Profile blood vessels

Result folder brain

Run workflow Edit workflow

blood

blood vessels

brain

cartilage

cervix

choroid plexus

colon

embryonic cells

esophagus

eye

foreskin

gingiva

heart

kidney

lung

mammary gland/breast

pancreas

placenta

skin

spinal cord

Start page Identify enriched motifs ... X

**Identify enriched motifs in cell line specific miRNA promoters (TRANSFAC(R))**

miRNA table (select element)

Promoter 3' most

Select cell line GM12864

Add Ensembl promoters GM12864

Profile hESCt0

Result folder HUVEC

Run workflow Edit workflow

MCF7

AG10803

GM06990

Hela

AG04449

AG09309

CAC02

CD14

HCT116

HEEpiC

HFF\_MyC

A549

AG04450

AG09319

AoAF

BJ

CD20

Identify enriched motifs in tissue-specific miRNA promoters [ [workflow link](#) ]

Identify enriched motifs in cell-specific miRNA promoters [ [workflow link](#) ]

## Identifying miRNA binding sites in tissue-specific genes with HumanPSD™

Start page lung\_gene set X

**Genes expressed in lung tissue**

ID	Gene description	Gene symbol	Relative t.sp.	lung
ENSG00000078081	lysosomal associated membrane protein 3	LAMP3	0.41846	119.52459
ENSG00000086548	CEA cell adhesion molecule 6	CEACAM6	0.34894	118.32295
ENSG00000096088	progesterin	PGC	0.66628	102.34098
ENSG00000122852	surfactant protein A1	SFTPA1	0.95493	404.86557
ENSG00000131400	napsin A aspartic peptidase	NAPSA	0.71361	149.51803
ENSG00000133661	surfactant protein D	SFTPD	0.67854	124.13607
ENSG00000140465	cytochrome P450 family 1 subfamily A member 1	CYP1A1	0.46761	138.81639
ENSG00000142748	ficolin 3	FCN3	0.52793	147.95902
ENSG00000149021	secretoglobin family 1A member 1	SCGB1A1	0.86226	498.99836
ENSG00000157765	solute carrier family 34 member 2	SLC34A2	0.5495	251.86885
ENSG00000161055	secretoglobin family 3A member 1	SCGB3A1	0.47541	164.76721
ENSG00000164265	secretoglobin family 3A member 2	SCGB3A2	0.83947	243.23443
ENSG00000168484	surfactant protein C	SFTPC	0.97207	653.46393
ENSG00000168878	surfactant protein B	SFTPB	0.91264	
ENSG00000185303	surfactant protein A2	SFTPA2	0.96124	
ENSG00000185499	mucin 1, cell surface associated	MUC1	0.3157	
ENSG00000196260	surfactant associated 2	SFTA2	0.64514	
ENSG00000204305	advanced glycosylation end-product specific receptor	AGER	0.77179	
ENSG00000244734	hemoglobin subunit beta	HBB	0.52	

**miRNA binding sites**

ID	Sequence	miRNA	mirMap score
1122	ENST00000409383_2_85658290-85668741_-1	hsa-let-7i-5p	-0.01116
977	ENST00000428225_2_85658255-85668172_-1	hsa-let-7i-5p	-0.00645
407	ENST00000415707_6_41744479-41754109_-1	hsa-miR-103a-3p	-0.06193
413	ENST00000415707_6_41744479-41754109_-1	hsa-miR-107	-0.0557
381	ENST00000481748_1_27373530-27374805_-1	hsa-miR-10a-5p	-0.00866
75	ENST00000521315_8_22161797-22164479_1	hsa-miR-10a-5p	-0.03293
387	ENST00000481748_1_27373530-27374805_-1	hsa-miR-10b-5p	-0.00642
80	ENST00000521315_8_22161797-22164479_1	hsa-miR-10b-5p	-0.03233
110	ENST00000522109_8_22161805-22164008_1	hsa-miR-1178-3p	-0.06696
1189	ENST00000524255_8_22161807-22164479_1	hsa-miR-1178-3p	-0.0171
1376	ENST00000318561_8_22161655-22164476_1	hsa-miR-1178-3p	-0.06865
201	ENST00000679463_8_22161798-22164479_1	hsa-miR-1178-3p	-0.06273

## New pipeline to analyze SNPs with TRANSFAC® and TRANSPATH® at once

**SNP missense**

ID	#Uploaded_variation	Location	Allele	Gene	Feature	Feature_type
23	rs1046934	1:184023529	C	ENSG00000198860	ENST00000361641	Transcript
25	rs1046934	1:184023529	C	ENSG00000198860	ENST00000423085	Transcript
29	rs1046934	1:184023529	C	ENSG00000198860	ENST00000533373	Transcript
314	rs2066807	12:56740682	G	ENSG00000170581	ENST00000314128	Transcript
322	rs2066807	12:56740682	G	ENSG00000170581	ENST00000557235	Transcript
641	rs5742915	15:74336633	C	ENSG00000140464	ENST00000268058	Transcript
646	rs5742915	15:74336633	C	ENSG00000140464	ENST00000565898	Transcript
841	rs9835332	3:56667682	C	ENSG00000163946	ENST00000355628	Transcript
842	rs9835332	3:56667682	C	ENSG00000163946	ENST00000431842	Transcript
845	rs9835332	3:56667682	C	ENSG00000163946	ENST00000493960	Transcript

**SIFT analysis**

ID	#Chrom	Position	Strand	Allele	Codons	Transcript ID	Protein ID	Substitution	Region
1	chr1	184023529	+	A/C	CAA-CAC	ENST00000361641	ENSP0000035299	Q39H	EXON CDS
2	chr15	89388905	+	C/T	GTC-GTT	ENST00000268134	ENSP00000268134	V407V	EXON CDS
3	chr12	56740682	+	C/G	ATG-ATC	ENST00000314128	ENSP00000315768	M594I	EXON CDS
4	chr4	1701317	+	G/A	TAC-TAA	ENST00000318386	ENSP00000316490	Y158Y	EXON CDS
5	chr3	172165727	+	C/T	CGG-CGA	ENST00000241256	ENSP00000241256	R159R	EXON CDS
6	chr15	74336633	+	T/C	TTC-CTC	ENST00000268058	ENSP00000268058	F645L	EXON CDS
7	chr3	56667682	+	A/G	ACA-AAG	ENST00000355628	ENSP00000347845	T985R	EXON CDS
8	chr17	36922196	+	A/G	-	ENST00000269554	ENSP00000269554		3' UTR
9	chr6	109783941	+	A/G	-	ENST00000230122	ENSP00000230122		3' UTR
10	chr12	66551826	+	T/C	-	ENST00000374369	ENSP00000374369		5' UTR
11	chr20	34025756	+	A/G	-	ENST00000493223	ENSP00000493223		3' UTR
12	chr20	4101800	+	C/T	-	ENST00000505389	ENSP00000505389		5' UTR
13	chr3	141105570	+	A/G	-	ENST00000505991	ENSP00000505991		3' UTR
14	chr4	145568352	+	T/C	-	ENST00000505991	ENSP00000505991		3' UTR
15	chr16	88777242	+	C/A	-	ENST00000359985	ENSP00000359985		NON-GENIC
16	chr6	28200677	+	A/G	-	ENST00000367094	ENSP00000367094		3' UTR
17	chr6	158929442	+	T/A	-	ENST00000356061	ENSP00000356061		DOWNSTREAM
18	chr3	135974216	+	G/A	-	ENST000004459873	ENSP000004459873		5' UTR

**SNP schematic map**

ID	Gene symbol	all_SNP_track_hg19: Schematic
ENSG00000001629	ANKIB1	
ENSG000000006837	CDKL3	
ENSG000000020426	MNAT1	
ENSG000000034152	MAP2K3	
ENSG000000049323	LTBP1	
ENSG000000053918	KCNQ1	
ENSG000000067606	PRKCZ	
ENSG000000068724	TTC7A	
ENSG000000070081	NUCB2	
ENSG000000073711	PPP2R3A	
ENSG000000075420	FNDC3B	

**TFs gain & loss**

ID	Gene description	Gene symbol	TRANSFAC ID	P-value all_SNP_track_hg19_binding_sites_gain	P-value all_SNP_track_hg19_binding_sites_loss
ENSG000000006194	zinc finger protein 263	ZNF263	V\$ZNF263_04	2.6977E-4	0.04256
ENSG00000174282	zinc finger and BTB domain containing 4	ZBTB4	V\$ZBTB4_05	4.6032E-4	0.04256
ENSG00000182986	zinc finger protein 320	ZNF320	V\$ZNF320_03	8.8048E-4	0.04256
ENSG000000006704	GTF2I repeat domain containing 1	GTF2IRD1	V\$BEN_01	0.001	0.04256
ENSG00000130726	tripartite motif containing 28	TRIM28	V\$RNF96_01	0.00123	0.04256
ENSG00000116560	splicing factor proline and glutamine rich	SFPQ	V\$PSF_Q5	0.0017	0.04256

**SNP matched genes TRANSPATH® pathways**

ID	Title	Number of hits	Group size	Expected hits	P-value	Adjusted P-value	Hit names
CH0000000987	hypoxia pathways	2	21	0.13842	0.00789	0.06312	ESR1, ETS1
CH0000000651	Insulin --> AKT-1 pathway	2	39	0.25706	0.02602	0.10406	INSR, PRKCZ

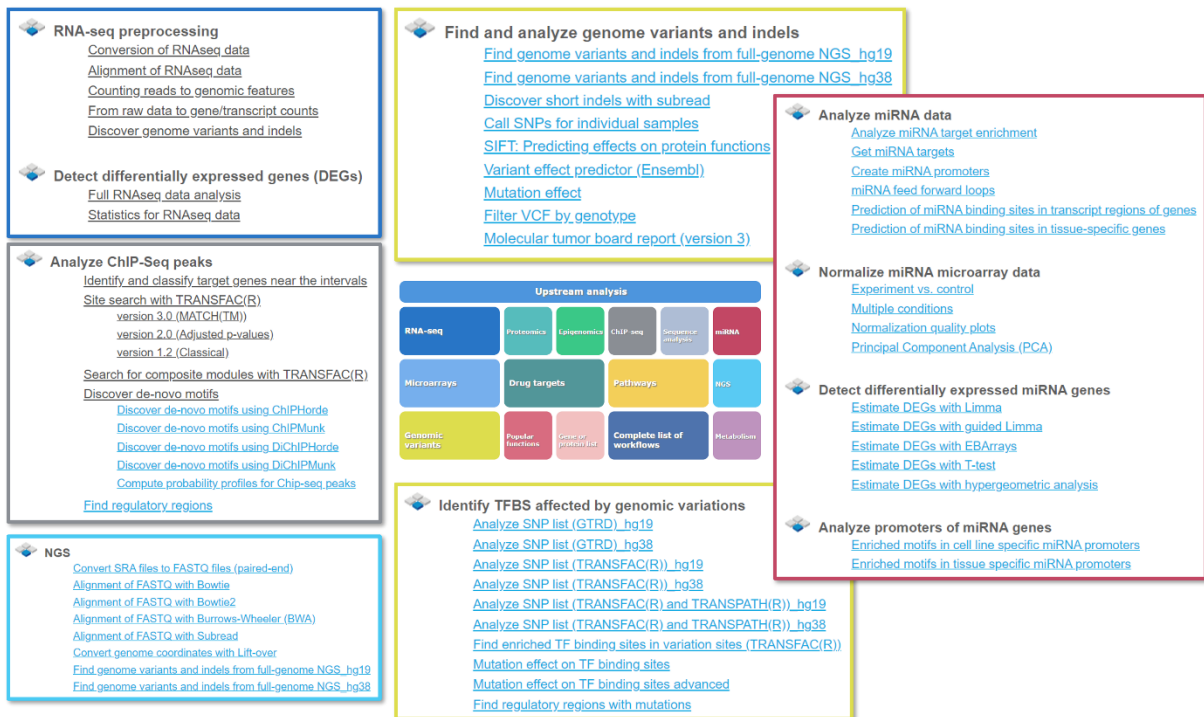
**SNP track**

Chromosome: 1 Position: 1:1-249250621 Set Find:

all\_SNP\_track\_hg19: 277 rs6699417 rs11205277 rs10863936 rs7532866 rs10874746 rs17346452 rs1325598 rs2154319 rs1046934 rs6684205 rs10799445

✂ New features: [MATCH™](#) for tracks, [Convert table to VCF track](#), [Filter VCF by genotype](#)

✂ We have updated our start page with new features and > 30 enhanced or new workflows



Database updates:

HumanPSD™ is updated to version 2022.1

TRANSFAC® is updated to version 2022.1

TRANSPATH® is updated to version 2022.1