Tissue Expression of MANE-Select Transcripts

Gene Symbol: e.g. TACR2

START with Gene Search

MST V1.0 (19,062)	MST = V9 TRP-Tx (13,245)	MST ≠ V9 TRP-Tx (3,153)	MST ∉ V9 Tx (1,685)	MST Unique Gene ID (979)

Previously, the RefSeq and GENCODE projects are the principal keystones for genome analysis and annotation. A new reference gene transcript dataset (MANE-select) was released by NCBI and EMBL-EBI to bring new unified representative transcript for human protein-coding genes. Since there are far more numbers of alternative spliced mRNA transcripts due to the rapid accumulation of NGS transcriptome data, it is essential to learn more about the thorough tissue expression profiles of alternative transcripts in order to obtain the molecular modulations and functional significance of these MANE-select transcripts. There is no dedicated database to display the tissue expression information on the MANE-select transcripts. Therefore, this TEx-MST database is aimed to deliver tissue expression profiles of MANE-select transcripts in various normal human tissues. We have utilized the GTEx (Genotype-Tissue Expression) transcriptome datasets to construct an easy to use web interface in visualization among alternative transcripts of human protein-coding genes. This TEx-MST database is primarily based on the new GTEx V9 expression information using the third generation long-read sequencing platform. Therefore, TEx-MST is a novel bioinformatic database for providing the valuable expression of MANE-select transcripts in normal human tissues. Users can initiate the expression interrogation by search the gene symbols or browse the MANE genes in various criteria (such as genome locations or expression rankings).

Or browsing by chromosome locations

MANE-select transcripts (19,062)

Listed by chromosome locations:

chr 1	chr 2	chr 3	chr 4	chr 5	chr 6
1,984	1,211	1,029	736	843	996

This Tex-MST (Tissue Expression of MANE-Select Transcripts) bioinformatic tool provides the MANE-select transcript expression information in human normal tissues utilizing the GTEx V9 long-read transcript expression information as well as V8 short-read datasets.

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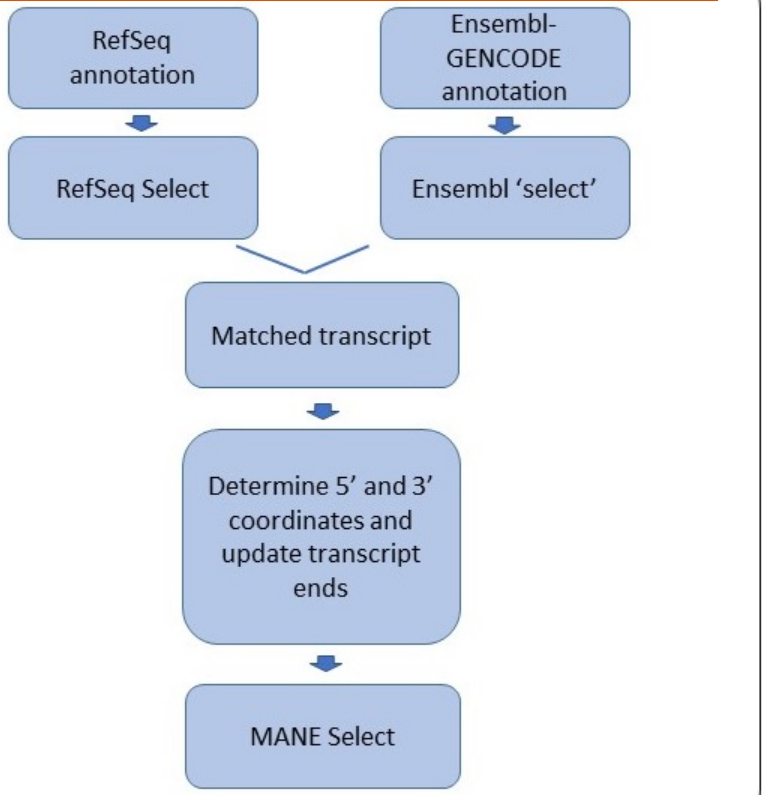
MANE–select transcr … ng transcripts (3,153)

Different t… …cal gene ID.

18,083 records with matched gene IDs

MANE V1.0
19,062 human protein-coding genes



https://www.ncbi.nlm.nih.gov/refseq/MANE/

There are 19,062 human protein-coding gene records in MANE dataset; and one MANE-select transcript assigned for each protein-coding genes. For comparison, we utilized the GTEx V9 dataset, and assigned the Top-Ranked Protein-coding transcript (TRP-Tx) expressed for all protein-coding genes (GENCODE V26).
There are 18,083 genes (gene ID) matched between MANE and GTEx datasets. Among them, 13,245 MANE-select transcripts matched with the TRP-Tx in GTEx V9; and 3,153 MANE-select transcripts are different from GTEx TRP-Tx records. For 1,685 genes, the MANE-select transcripts were not found in the GTEx V9 dataset in those protein-coding genes.

chr 4 125 | chr 5 152 | chr 6 147

300 | 225 | 170

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MANE-select transcripts matched with GTEx V9 Top-Ranked protein-coding transcripts (13,245)

The same transcript was chosen by MANE-select transcript and our V9 TRP-Tx under identical gene ID.

Listed by expression percentages:

%=100	90≤%<100	80≤%<90
2,433	5,106	1,488

40≤%	%<30
52	93

Click any block to show the gene list table

Listed by expression Ranks:

Rank=1	Rank=2	Rank=3
12,370	639	150

We further classified the MANE-select transcripts by their expression percentages in respective protein-coding genes; by their expression Ranks; by their transcript expression TPMs; and the location of the protein-coding genes.

Listed by expression TPM values:

100≤TPM	10≤TPM<100	1≤TPM<10	0.1≤TPM<1	0<TPM<0.1	TPM=0
856	3,898	4,681	2,369	1,403	38

Listed by chromosome locations:

chr 1	chr 2	chr 3	chr 4	chr 5	chr 6
1,400	859	730	506	622	705

Tissue Expression of MANE-Select Transcripts

MANE-select transcript matched with the Top-Ranked Protein-coding transcripts in GTEx

Gene List : 90≤TPM%<100

Show 10 entries

Chromosome	Gene Symbol	Gene ID	Start	End	Strand	MANE-Select	V9 TRP-Tx	V8 TRP-Tx
1	KLHL17	ENSG00000187961	960584	965719	+	ENST00000338591	⊙	⊙
1	PLEKHN1	ENSG00000187583	966482	975865	+	ENST00000379410	⊙	
1	TNFRSF18	ENSG00000186891	1203508	1206592	-	ENST00000379268	⊙	⊙
1	SDF4	ENSG00000078808	1216931	1232001	-	ENST00000360001	⊙	⊙
1	PUSL1	ENSG00000169972	1308597	1311677	+	ENST00000379031	⊙	⊙
1	CPTP	ENSG00000224051	1324802	1328896	+	ENST00000343938	⊙	⊙
1	MRPL20	ENSG00000242485	1401909	1407293	-	ENST00000344843	⊙	⊙
1	VWA1	ENSG00000179403	1435690	1442882	+	ENST00000476993	⊙	
1	ATAD3C	ENSG00000215915	1449689	1470163	+	ENST00000378785	⊙	⊙
1	GABRD	ENSG00000187730	2019345	2030758	+	ENST00000378585	⊙	⊙

Showing 1 to 10 of 5,106 entries

Previous 1 2 3 4 5 ... 511 Next

ATAD3C

GTEx V9

Gene Name : ATPase family AAA domain containing 3C

GTEx V8

NCBI GeneID : 219293

NCBI : NM_001039211.3

NCBI : NP_001034300.2

Chromosome : 1

Strand : +

MANE Select : ENST00000378785

MANE Plus Clinical :

Basic gene information from MANE dataset

	Gene Symbol	Ensembl Gene ID	Start	End
MANE	ATAD3C	ENSG00000215915	1449689	1470163
GTEx V9	ATAD3C	ENSG00000215915	1449688	1470158
Gencode v40	ATAD3C	ENSG00000215915	1449688	1470163

Expression information from GTEx V9 transcript dataset

Show 10 entries

Gencode v26 (GTEx V9)											Gencode v40							
V9 TRP-Tx	Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	Exp Tx%	Exp Rank	MANE Match	APPRIS	Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	MANE Match	APPRIS
⊙	ENST00000378785	12	3859	1	1236	1	96.94	1	☀	P:1	ENST00000378785	12	3864	1	1236	1	☀	P:1
	ENST00000484537	2	506	2	0	2	3.06	2			ENST00000484537	2	506	3	0	3		

Showing 1 to 2 of 2 entries

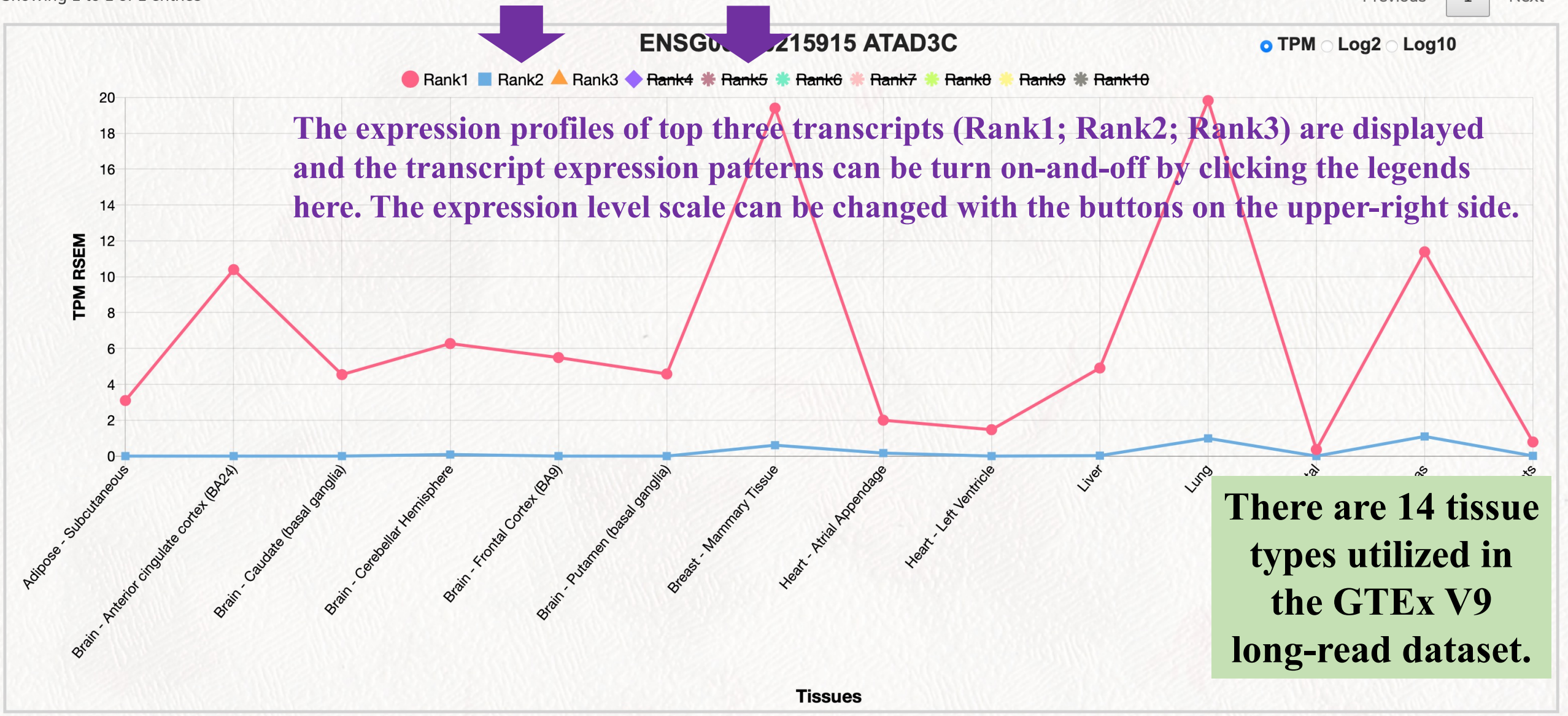
Previous 1 Next

Show 5 entries

Gencode v26 (GTEx V9)										Gencode v40							
V9 TRP-Tx	No Match Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	Exp Tx%	Exp Rank	MANE Match	APPRIS	No Match Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	MANE Match	APPRIS
											ENST00000475091	6	525	2	394	2		

Showing 1 to 1 of 1 entries

Previous 1 Next



The expression profiles of top three transcripts (Rank1; Rank2; Rank3) are displayed and the transcript expression patterns can be turn on-and-off by clicking the legends here. The expression level scale can be changed with the buttons on the upper-right side.

There are 14 tissue types utilized in the GTEx V9 long-read dataset.

ATAD3C

GTEx V8

Gene Name : ATPase family AAA domain containing 3C

GTEx V9

NCBI GeneID : 219293

NCBI : NM_001039211.3

NCBI : NP_001034300.2

Chromosome : 1

Strand : +

MANE Select : ENST00000378785

MANE Plus Clinical :

Basic gene information from MANE dataset

	Gene Symbol	Ensembl Gene ID	Start	End
MANE	ATAD3C	ENSG00000215915	1449689	1470163
GTEx V8	ATAD3C	ENSG00000215915	1449688	1470158
Gencode v40	ATAD3C	ENSG00000215915	1449688	1470163

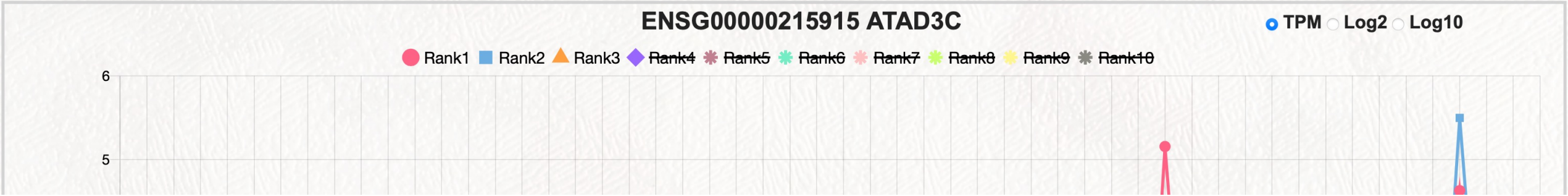
Show 10 entries

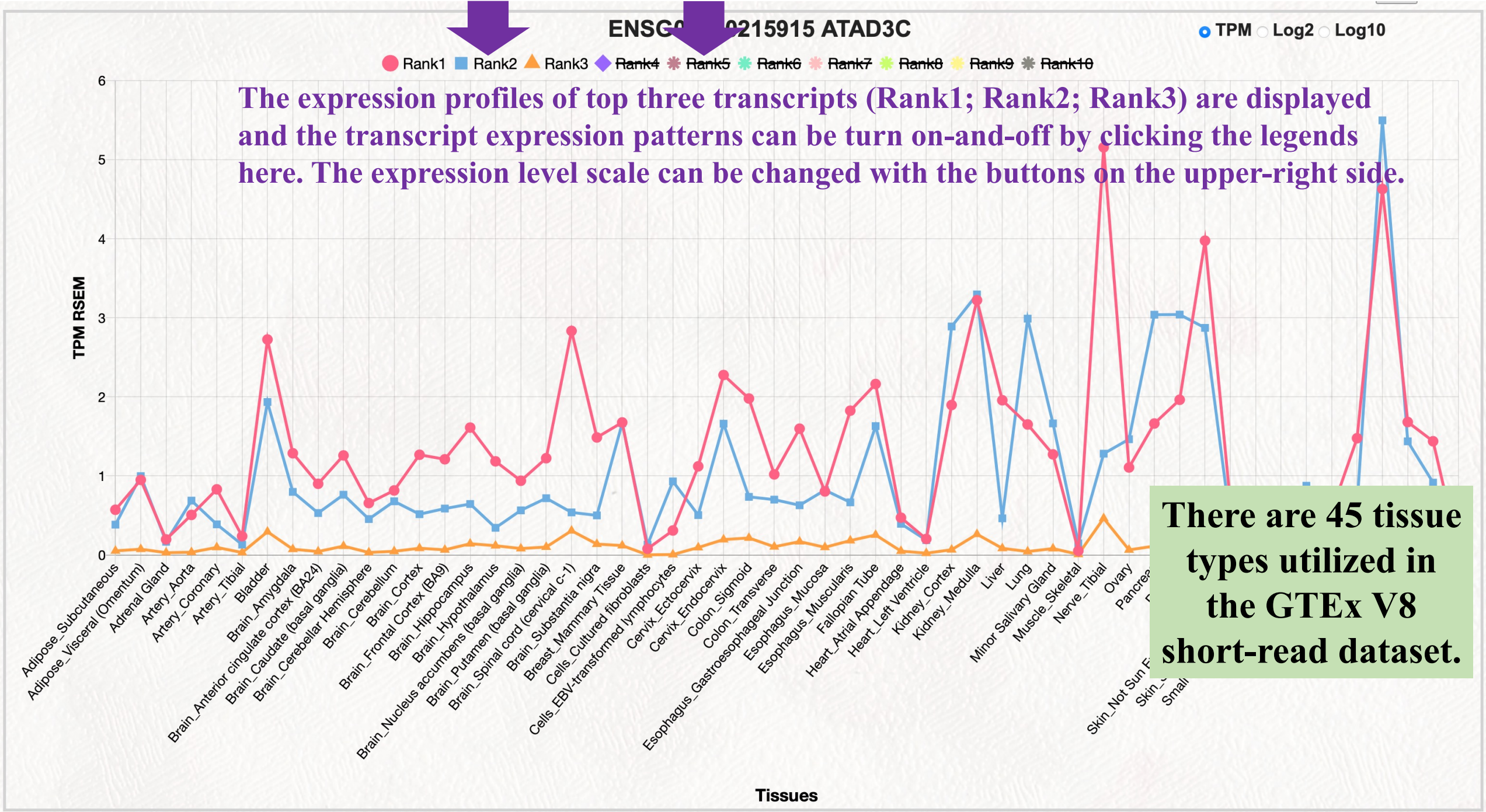
Expression information from GTEx V8 transcript dataset

Gencode v26 (GTEx V8)										Gencode v40							
V8 TRP-Tx	Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	Exp Tx%	Exp Rank	MANE Match	APPRIS	Transcript ID	Exon Count	Transcript Length	Tx Length Rank	CDS Length	CDS Rank	MANE Match	APPRIS
⊙	ENST00000378785	12	3859	1	1236	1	54.07	1	☀	P:1	ENST00000378785	12	3864	1	1236	1	☀	P:1
	ENST00000484537	2	506	3	0	3	41.77	2			ENST00000484537	2	506	3	0	3		
	ENST00000475091	6	525	2	394	2	4.16	3			ENST00000475091	6	525	2	394	2		

Showing 1 to 3 of 3 entries

Previous 1 Next





There are 45 tissue types utilized in the GTEx V8 short-read dataset.