

# How to search for gene expression

## GENE SEARCH

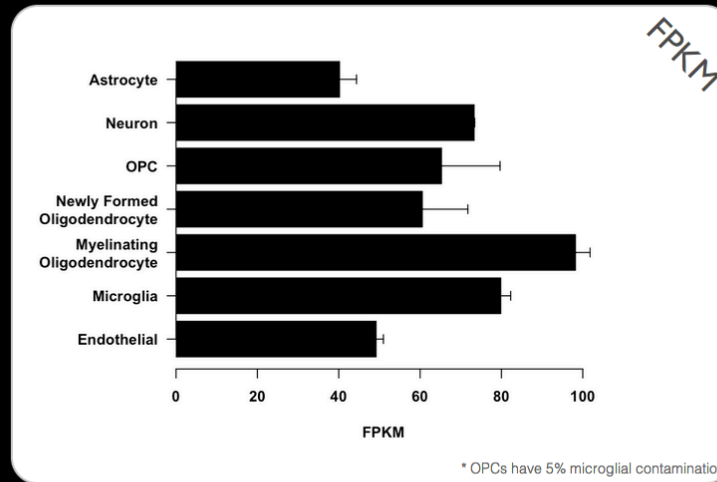
Step 1: Enter a gene of interest

Gapdh

Search

Step 2: Graph displays the expression (FPKM) of the gene in various CNS cell types

### Gapdh



Note: FPKM is a normalized expression value that considers the total reads in the library as well as the coding length of the gene

# Using official gene symbols

## GENE SEARCH

*Enter Gene*

Search

Oops! Gene not found. Make sure to use the official gene name

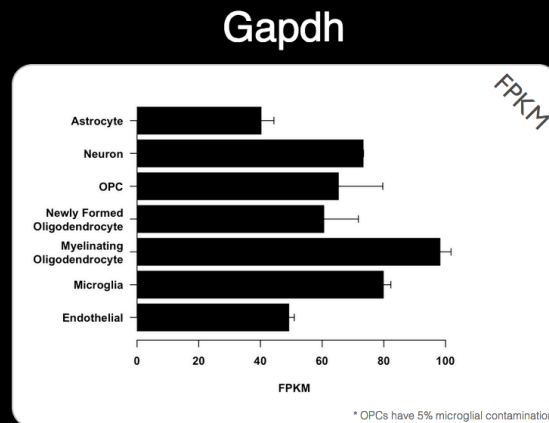
Please be aware that only official gene symbols will work here. Many databases will search for common aliases and provide the official symbols for various genes.

# Interactive Splicing Browser

Click here to view the  
INTERACTIVE SPLICING BROWSER

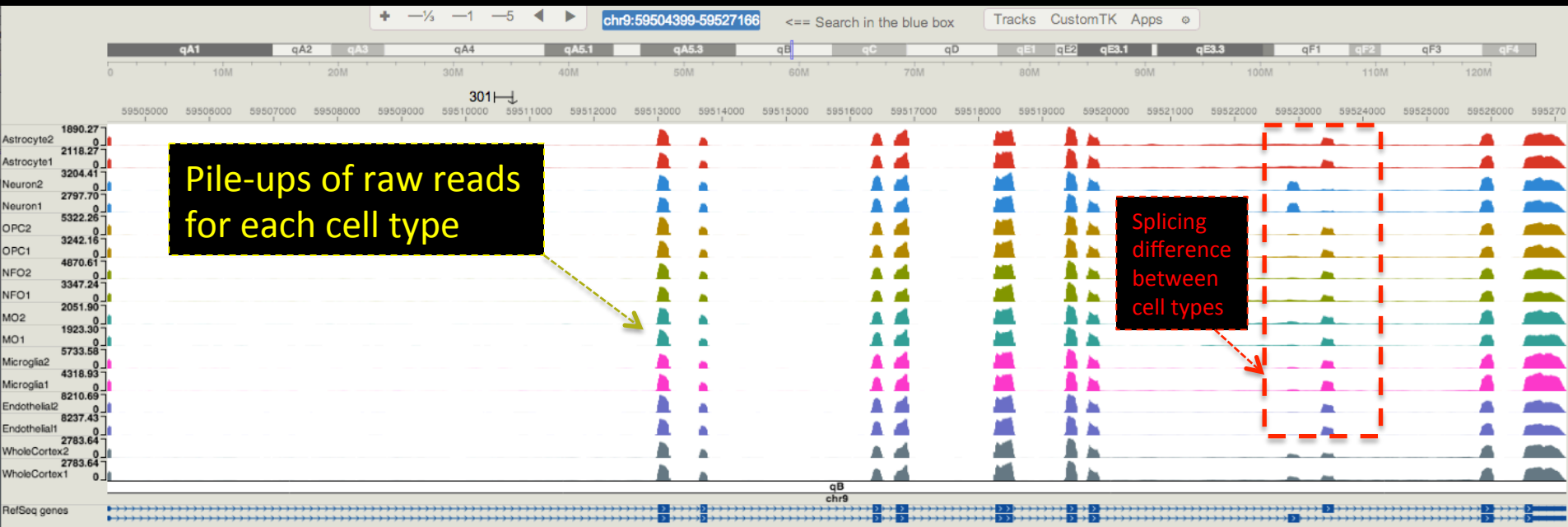
Click to enter a *searchable browser* that allows you to look carefully at potential splicing differences between cell types.

You can also enter the same browser for a specific gene locus by using the gene search feature and then clicking the link under the FPKM graph



Click here to view the  
Interactive Splicing Browser  
for Gapdh

# Using the interactive splicing browser

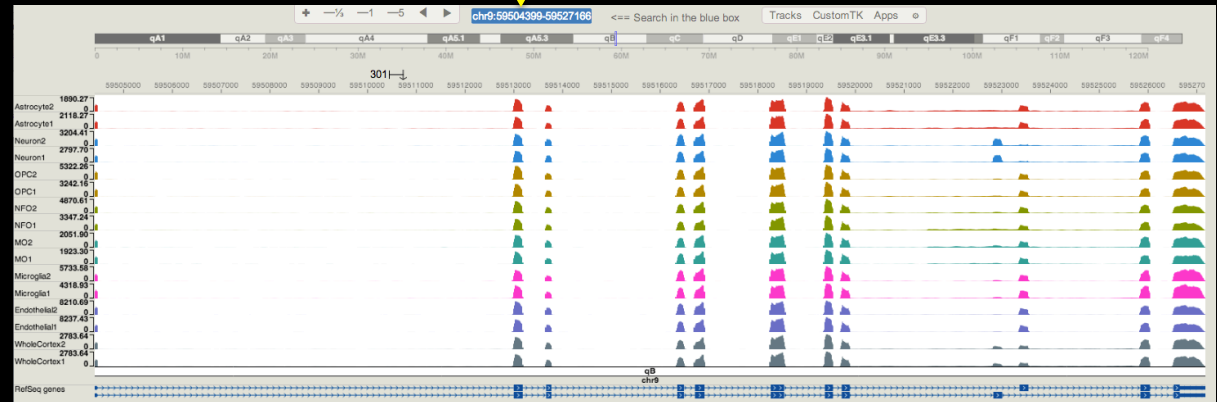
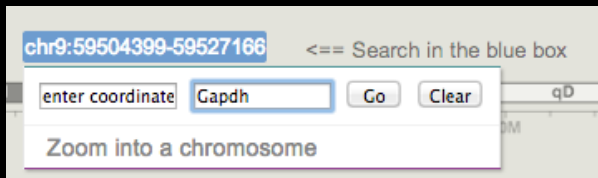


The reference genome is depicted on the bottom. Solid blue boxes = exons. Thin lines = introns. Arrows depict gene direction.

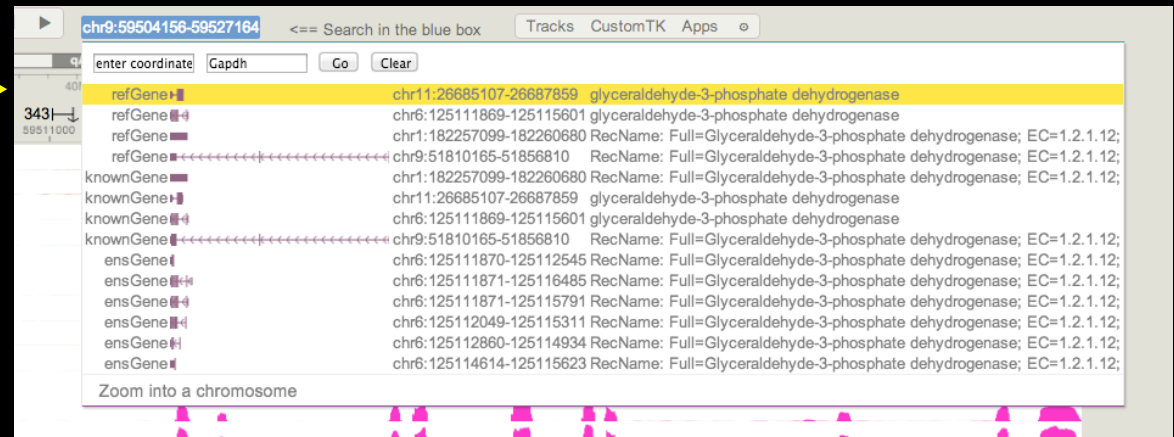
Note: The scales on this database are AUTOSCALED. This allows the user to visualize splicing differences among genes that are lowly expressed in a given cell type. These numbers should not be compared to the FPKM values, though the trends should be identical.

# Searching the interactive splicing browser

Step 1: Enter a gene of interest in blue box to search within this browser



Step 2: Select the top refGene model for your gene of interest. It doesn't matter which transcript you select; each will take you to the same chromosomal location



# Creating custom lists of enriched genes

## CELL TYPE(S) ENRICHMENT

- find genes enriched in cell type(s) 1 relative to cell type(s) 2

1

- Astrocyte
- Neuron
- OPC
- Newly Formed Oligodendrocyte
- Myelinating Oligodendrocyte
- Microglia
- Endothelial

Select All

2

- Astrocyte
- Neuron
- OPC
- Newly Formed Oligodendrocyte
- Myelinating Oligodendrocyte
- Microglia
- Endothelial

Select All

Option to remove low expressing genes in Type(s) 1  
Default: No threshold

20

Submit

As an example, this query will find genes that are expressed in astrocytes and NOT in all other cell types.

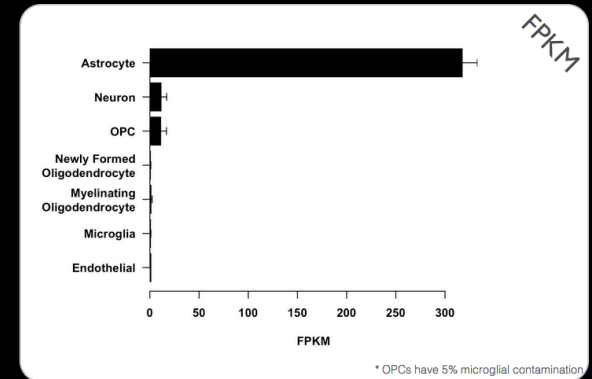
You can choose as many cell types as you desire for either column

To avoid ratio inflation, you may choose an FPKM cutoff to select only those enriched genes that are more highly expressed. An FPKM of 20 is a reasonable starting point for highly expressed genes.

Top 500 genes enriched in type(s) 1 relative to type(s) 2

GENE	TYPE(S) 1 (Mean FPKM)	TYPE(S) 2 (Mean FPKM)	FOLD CHANGE (Type(s) 1 / Type(s) 2)
Hgf	28.338	0.2978	95.150
Aqp4	317.63	4.5109	70.415
Bmpr1b	29.887	0.4414	67.705
Plcd4	33.970	0.5314	63.920
Ppp1r3c	104.65	1.6505	63.406
Tnc	118.15	1.9750	59.820
Pla2g3	47.764	0.8277	57.707
Slc30a10	64.690	1.1771	54.953
Itih3	68.640	1.3056	52.572
Slc14a1	53.171	1.0301	51.615
Atp13a4	76.301	1.4882	51.269
Grm3	158.36	3.3015	47.967
Paqr6	22.317	0.4846	46.044
Fgfr3	295.65	6.4864	45.580
Egfr	38.625	0.8643	44.687
Gdpd2	71.550	1.6040	44.605
Nwd1	53.629	1.2135	44.193
Slc4a4	266.26	6.0994	43.654

Aqp4



The top 500 genes that match the search criteria will be displayed along with their mean FPKM values. Click on any gene to view its expression pattern.

# Download raw excel data

Click to download

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## Excel FPKM Data

Click to download the raw data for further investigation.

Sheet 1 lists average FPKM values for all genes in all cell types

Sheet 2 includes co-expression modules

Enjoy!

Please contact with any questions