Prostate Cell Transcriptomes Database Manual v1.0

The default search window is pictured below.

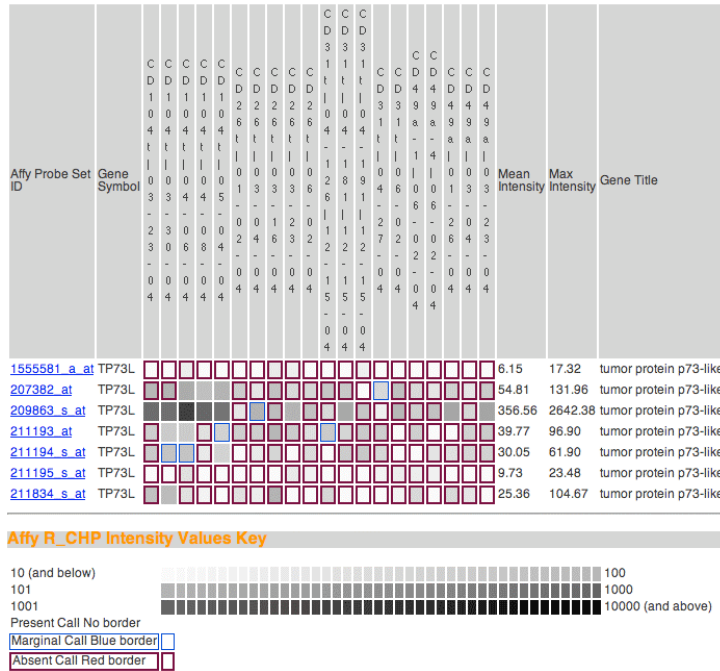
Genes may be searched by Affymetrix Probeset ID, HUGO gene name, or Genbank Accession number. The tick box "Coalesce probesets" combines all probesets that are annotated as targeting the gene searched. The tick box "Coalesce replicates" averages the signal for each of the 5 biological replicates that make up a sort. The use of a semicolon ";" in a search string will search all the components of the list, for example: "TP73L;THY1" would retrieve expression data for the HUGO gene names TP73L and THY1. The default search results for TP73L (p63) are pictured below.
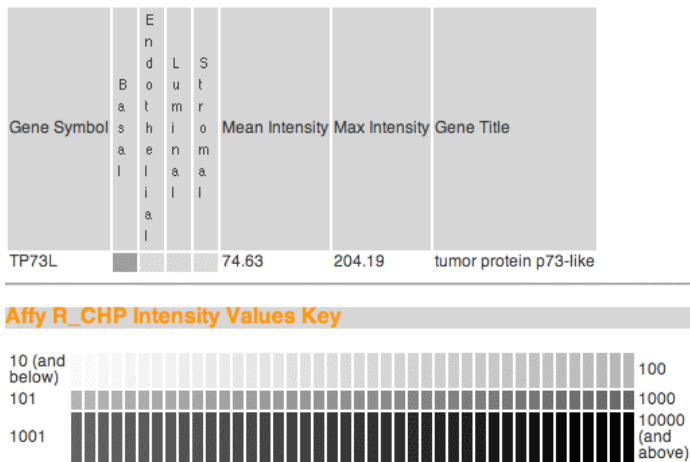
The greyscale gradient indicates RMA normalized Affymetrix signal intensity. Signals less than 10 are represented as 10 (white) and signals greater than 10,000 are represented as 10,000 (black). Higher Affymetrix signal (more black) indicates greater levels of gene expression. The column "Basal" is CD104 sorted cells, the column "Endothelial" is CD31 sorted cells, the column "Luminal" is CD26 sorted cells, and the column "Stromal" is CD49a sorted cells. The column "Mean Intensity" is the average intensity of the gene searched across the four cell types. The column "Max Intensity" is the highest signal for the gene searched in the 4 cell types. The signal for a gene in any of the cell types can be inspected by mousing over the greyscale block that indicates its intensity.

Performing the search for TP73L with the "Coalesce probesets" and "Coalesce replicates" tick boxes unchecked (expanding the probesets and replicates) will return the results pictured below.

Affy Probe Set ID	Gene Symbol	Mean Intensity	Max Intensity	Gene Title
1555581_a_at	TP73L	6.15	17.32	tumor protein p73-like
207382_at	TP73L	54.81	131.96	tumor protein p73-like
209863_s_at	TP73L	356.56	2642.38	tumor protein p73-like
211193_at	TP73L	39.77	96.90	tumor protein p73-like
211194_s_at	TP73L	30.05	61.90	tumor protein p73-like
211195_s_at	TP73L	9.73	23.48	tumor protein p73-like
211834_s_at	TP73L	25.36	104.67	tumor protein p73-like

Affy R_CHP Intensity Values Key

10 (and below) — 100
101 — 1000
1001 — 10000 (and above)
Present Call No border
Marginal Call Blue border
Absent Call Red border

In the expanded view all 5 biological replicates for each sort are listed in columns. The columns starting with CD104, CD26, CD31, and CD49a are the replicates for basal, luminal, endothelial, and stromal prostate cells respectively. Affymetrix arrays may contain numerous probesets that target the same gene some of which are more effective than others. In the TP73L example probeset 209863_s_at is the most effective probeset and shows high expression of the gene in CD104$^+$ (Basal) cells and negligible expression in other cell types. Each greyscale block indicates the expression of a gene for a specific probeset in one sample. Blocks outlined in red have been called "absent", blocks outlined in blue have been called "marginal", and blocks that are not outlined have been called "present" by the Affymetrix GCOS software. Previous work in out lab [1] has indicated that Affymetrix "present" calls are approximately 90% accurate, however, "absent" calls are approximately 40% accurate. Therefore, as with any microarray data, the expression of a gene should be verified by other means at the RNA and protein levels.

1.   Oudes, A.J., et al., *Application of affymetrix array and massively parallel signature sequencing for identification of genes involved in prostate cancer progression.* BMC Cancer, 2005. **5**(1): p. 86.