RNAseq viewer report

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Contents

Biological context

- Samples background: CE1502 - Astrocytes WT with two different AAV (GFP vs SOCS3) extracted from the Kelly AD project.
- Raw data (Fasta files): /local/aa_SideProject_ComparisonWT/FASTAfiles
- Bam files
  - Aligned Genosplice (STAR 2.4): /home/Pactivastro/Genosplice-BAMfiles (All) or /local/aa_SideProject_ComparisonWT/BAMstar (subset)

–outSAMstrandField intronMotif –outFilterMismatchNmax 2 –outFilterMultimapNmax 10 –outSAMunmapped Within –outSAMtype BAM SortedByCoordinate –outStd BAM_SortedByCoordinate –genomeLoad NoSharedMemory –chimSegmentMin 15

- Aligned myself (STAR with customed genome adding GFPV5): /local/aa_SideProject_ComparisonWT/CUSTOM
- Aligned myself (HISAT2): /local/aa_SideProject_ComparisonWT/BAMhisat2
- Folder routes for the whole project
  - Local linux: /local/aa_SideProject_ComparisonWT (Full data files)
  - Pactivastro: /home/Pactivastro/Resultats-manip/Miriam/aa_SideProject_ComparisonWT (Only reports)

Metata experiment

code	name	type	AAV
Astro_GFP_AD_63694	63694	WT	GFP
Astro_GFP_WT_63702	63702	WT	GFP
Astro_GFP_WT_63703	63703	WT	GFP
Astro_GFP_WT_63746	63746	WT	GFP
Astro_GFP_WT_63747	63747	WT	GFP
Astro_GFP_WT_63765	63765	WT	GFP
Astro_GFP_WT_63778	63778	WT	GFP
Astro_SOCS3_WT_63704	63704	WT	SOCS3
Astro_SOCS3_WT_63750	63750	WT	SOCS3
Astro_SOCS3_WT_63780	63780	WT	SOCS3
Astro_SOCS3_WT_63796	63796	WT	SOCS3
Astro_SOCS3_WT_63799	63799	WT	SOCS3

DEseq result

Gene name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Col3a1	37.9402	-7.9855	1.7999	-4.4367	0e+00	0.0009
Slc40a1	1386.5615	-1.5181	0.2624	-5.7857	0e+00	0.0000
Fn1	793.8706	-2.9630	0.5910	-5.0132	0e+00	0.0001
Sgpp2	314.5429	-3.7740	0.6167	-6.1200	0e+00	0.0000
Sp100	257.6586	-3.0534	0.5781	-5.2820	0e+00	0.0000
A630001G21Rik	33.8002	-8.3987	2.1373	-3.9296	1e-04	0.0058
Bok	448.2461	-2.0216	0.5429	-3.7238	2e-04	0.0113
Mgat5	1876.3098	0.8007	0.2353	3.4025	7e-04	0.0309
Btg2	3073.3391	-0.9387	0.2134	-4.3984	0e+00	0.0010
Ppfia4	243.4574	-3.2151	0.9663	-3.3272	9e-04	0.0386

PCA samples plot