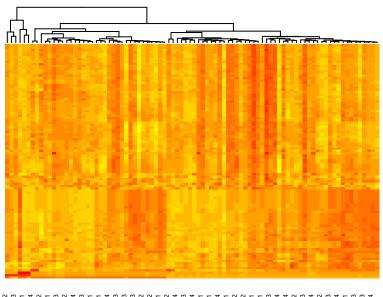
Differential expresion and GO terms analysis with HiSat2

Section 1 - Limma

Heatmap raw data

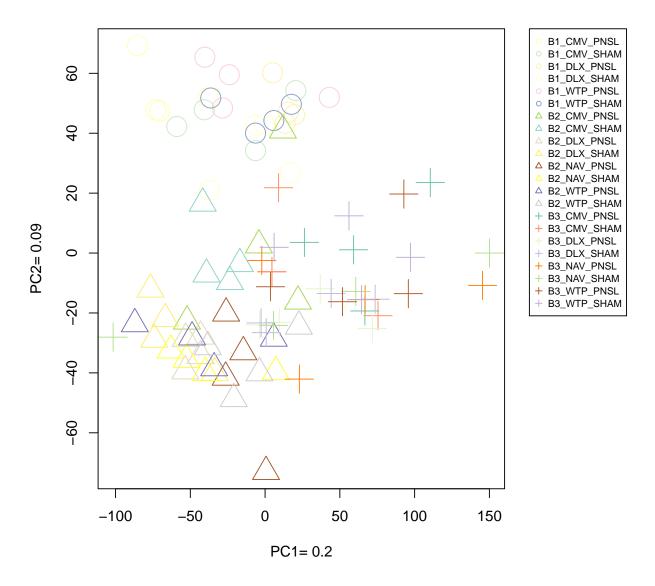
atmap for 100 most varible samples raw data



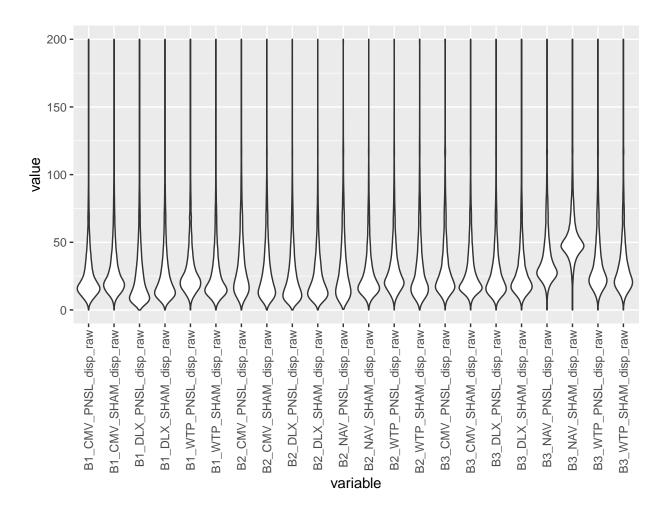
82. CMV_SHAM Z B2. AMV_SHAM Z B2. WTP_PUNEL, Z B2. NAV_PUNEL, Z B2. NAV_PUNEL, Z B2. NAV_PUNEL, Z B3. DLX_SHAM J B3. DLX_SHAM Z B4. WTP_PUNEL, Z B2. WTP_PUNEL, Z B2. WTP_PUNEL, Z B3. DLX_SHAM Z B4. WTP_PUNEL, Z B4. WTP_PUNEL, Z B4. WTP_PUNEL, Z B5. DLX_SHAM Z B7. WTP_SHAM Z B1. CMV_SHAM Z B1. CMV_SHAM Z B2. DLX_SHAM Z B2. DLX_SHAM Z B3. DLX_SHAM Z B2. DLX_SHAM Z B3. DLX_SHAM Z B3. DLX_SHAM Z B4. WTP_SHAM Z B4. WTP_SHAM Z B5. DLX_SHAM Z B6. DLX_SHAM Z B7. NNSL Z B7. NNSL Z B7. NNSL Z B8. DLX_PUNEL, Z B9. DLX_SHAM Z B9. WTP_SHAM Z B9. CMV_SHAM Z B9. DLX_SHAM Z B9. DLX_SHAM Z B9. DLX_SHAM Z B9. CMV_SHAM Z B9. DLX_SHAM Z B9. DLX_SHA

PCA raw data

PCA before SVA

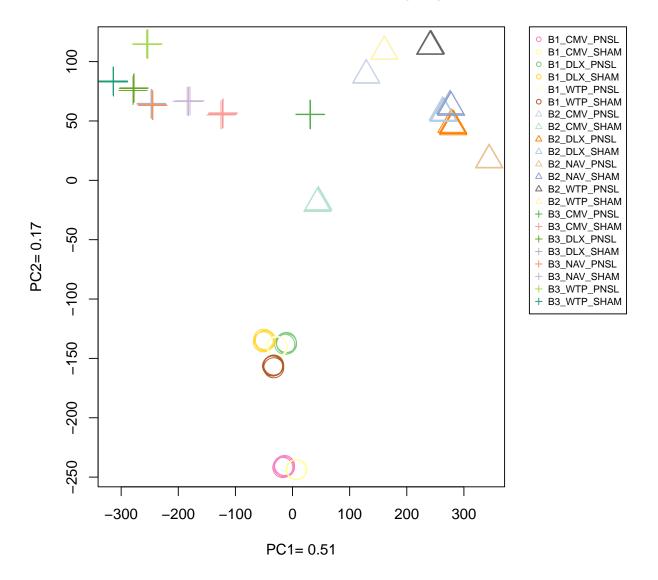


Violinplot raw data



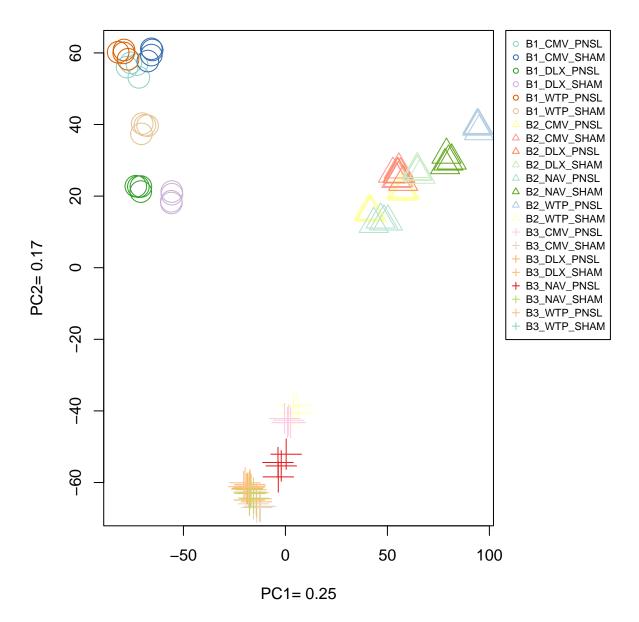
PCA with all factors removed 58'

PCA with all factors removed (58)



Final PCA with 32 factors removed





Number of differentially expressed genes with adjusted p-value < 0.05: 9703

Section 2 -EdgeR

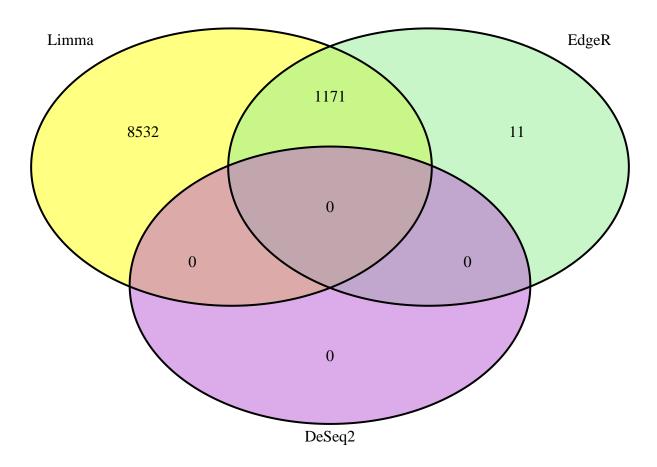
Number of differentially expressed genes with adjusted p-value < 0.05: 1182

Section 3 -DeSeq

Number of differentially expressed genes with adjusted p-value < 0.05: 0

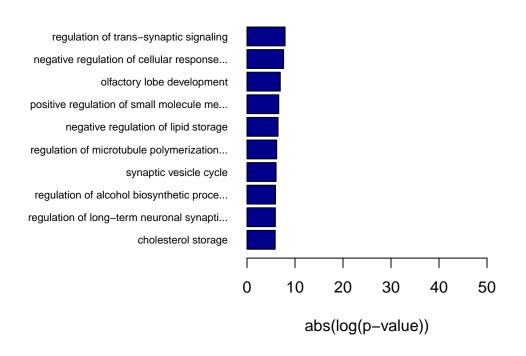
Ven diagram for all three methods

NULL

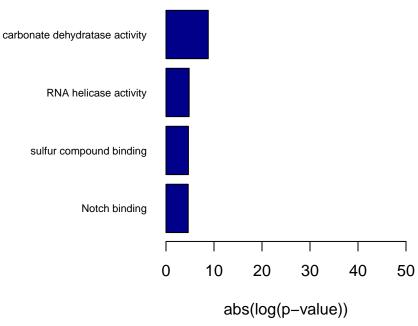


Barplots for top 10 terms for given GO term

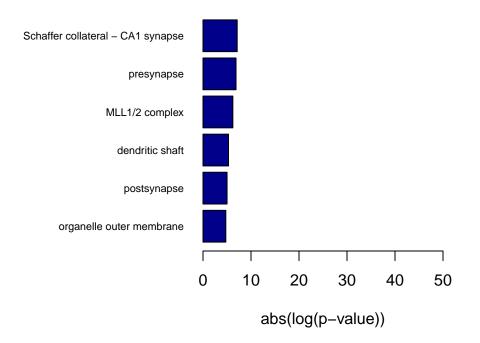
Top 10 BP for limma



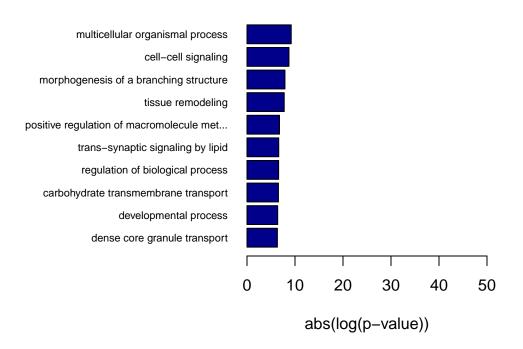
Top 4 MF for limma



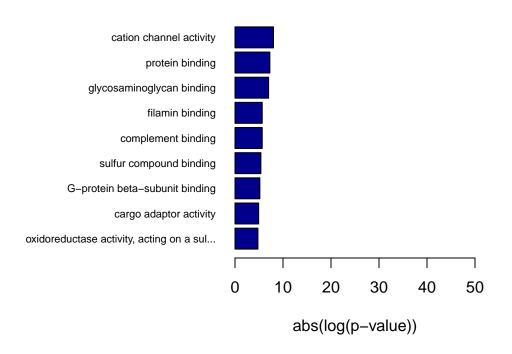
Top 6 CC for limma



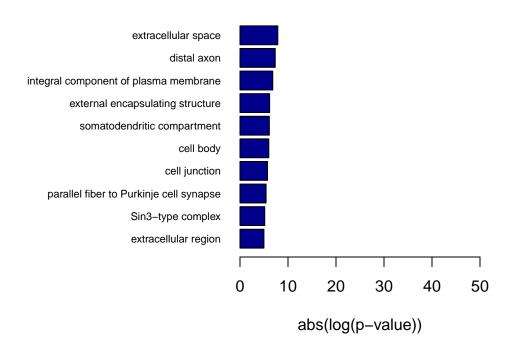
Top 10 BP for edgeR



Top 9 MF for edgeR



Top 10 CC for edgeR



Biological Process

