Deseq2 and heatmap

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1 RNAseq data loading

2 Batch effect

2.1 Raw data batch effect

2.2 Batch effect was removed by normalization

3 14 MPNST vs 30 PN (normalized counts, DEseq2)

3.1 Top 20 exprssed genes

4 GSEA analysis

5 Significant pathways

Table 1: Significant pathways in MPNST (vs PN)

pathway	padj	NES
FISCHER_G2_M_CELL_CYCLE	0.0014132	1.890361
MEISSNER_BRAIN_HCP_WITH_H3K27ME3	0.0000000	2.627215
WINNEPENNINCKX_MELANOMA_METASTASIS_UP	0.0089315	1.829773
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.0002778	2.001783

5.1 MPNST markers

S100B, CNP,PMP22,ngfr ,Expression of Schwann cell differentiation markers Downregulaed in MPNST **TWIST1,SOX9,SOX10 ,stem cell marker, upregulated in MPNST" E-cadherin (CDH1) was downregulated in both neurofibroma and MPNSTs GAS1 (Growth Arrest Specific 1) is a Protein Coding gene. IFG2, PTK7, FGFR1, TWIST1, GAS1, and EGFR.upregulated in MPNST**

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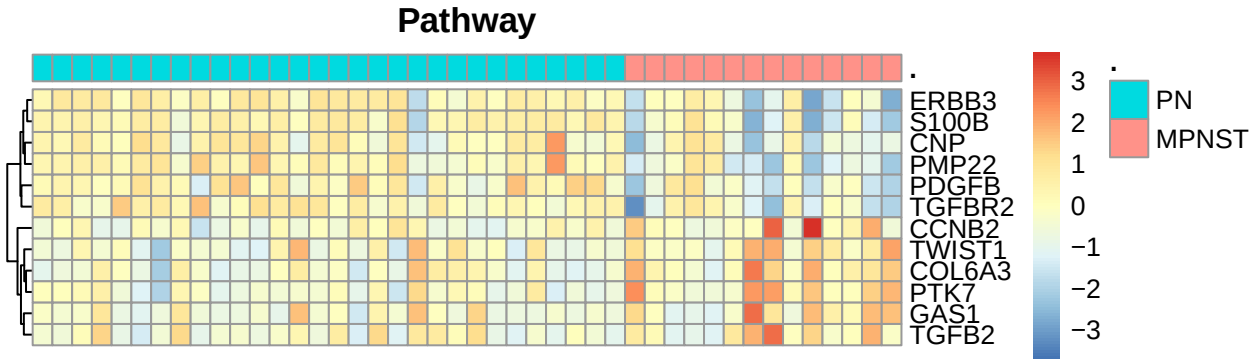
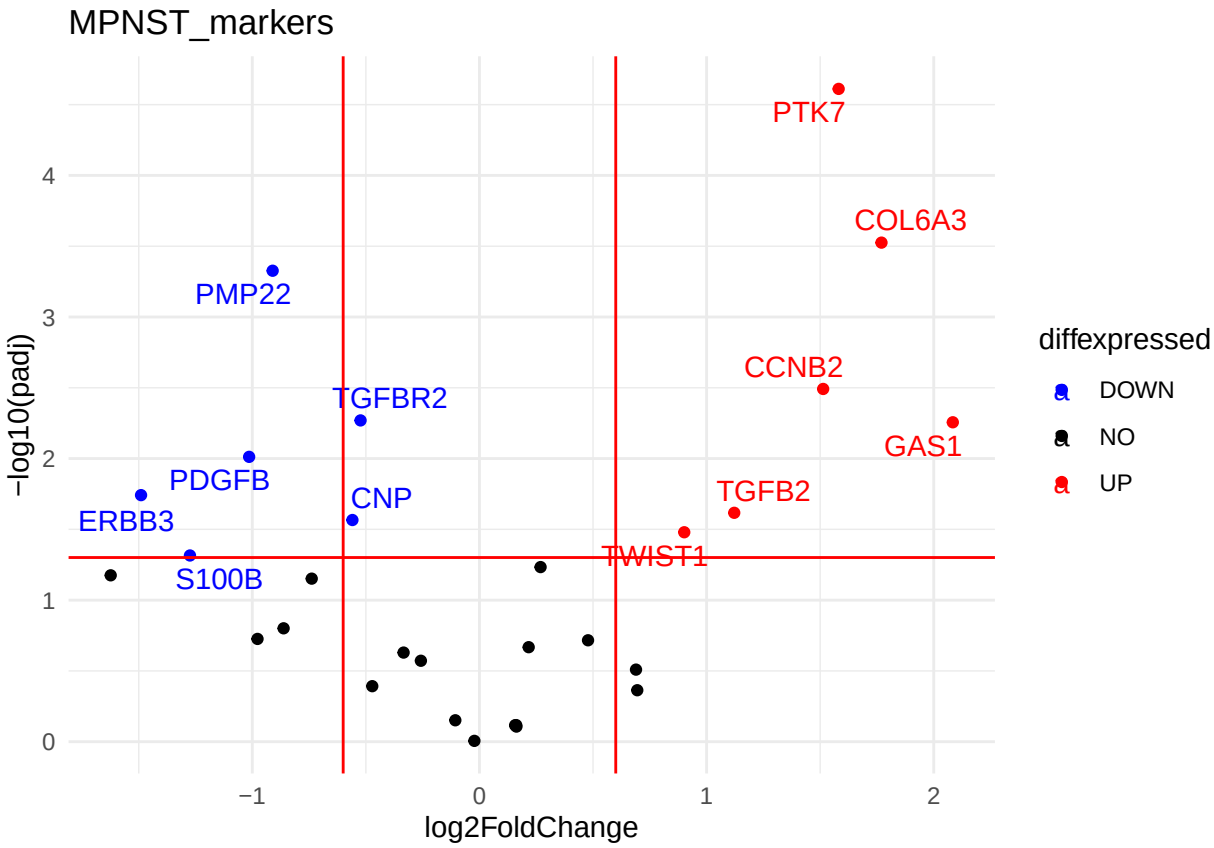
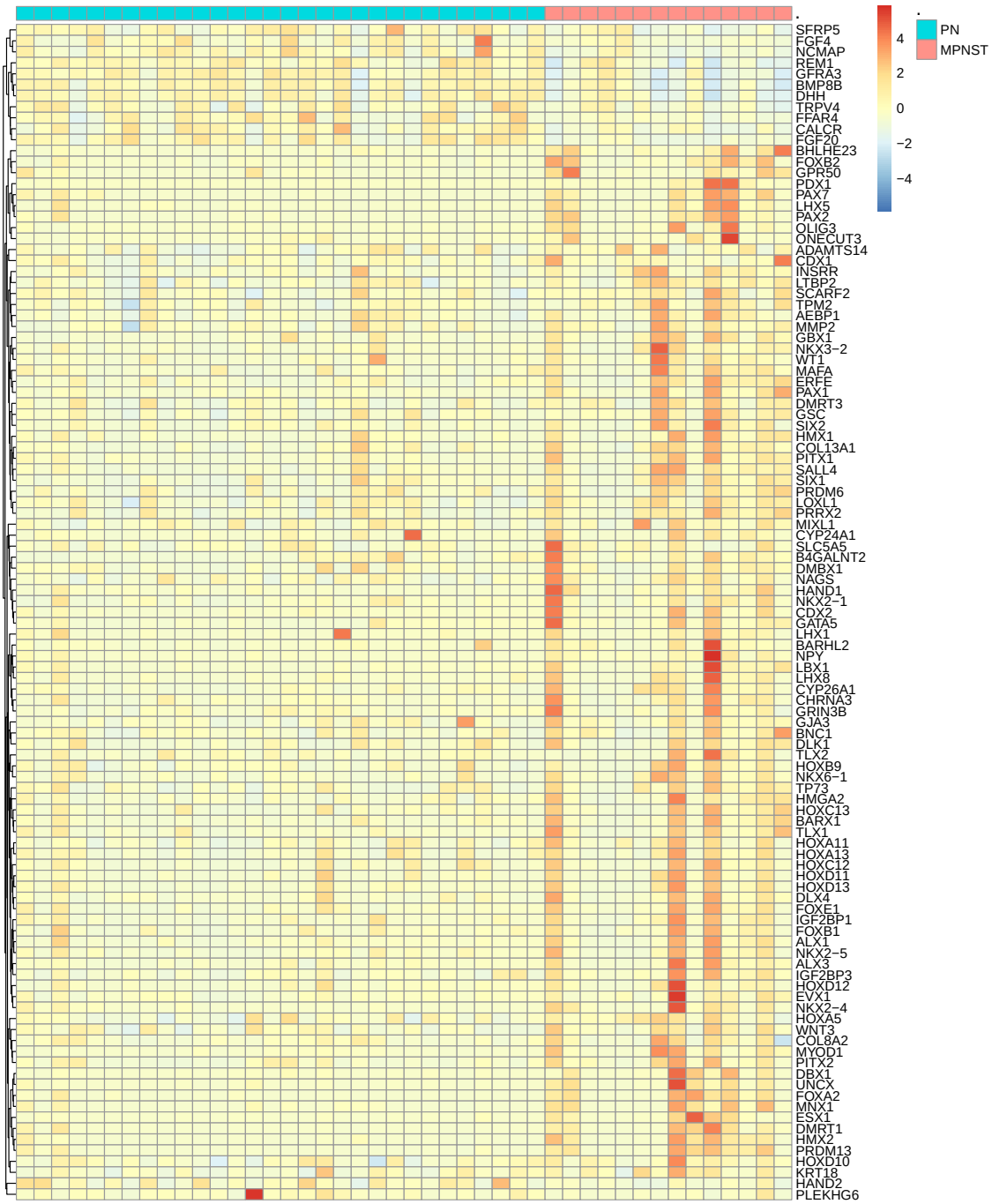
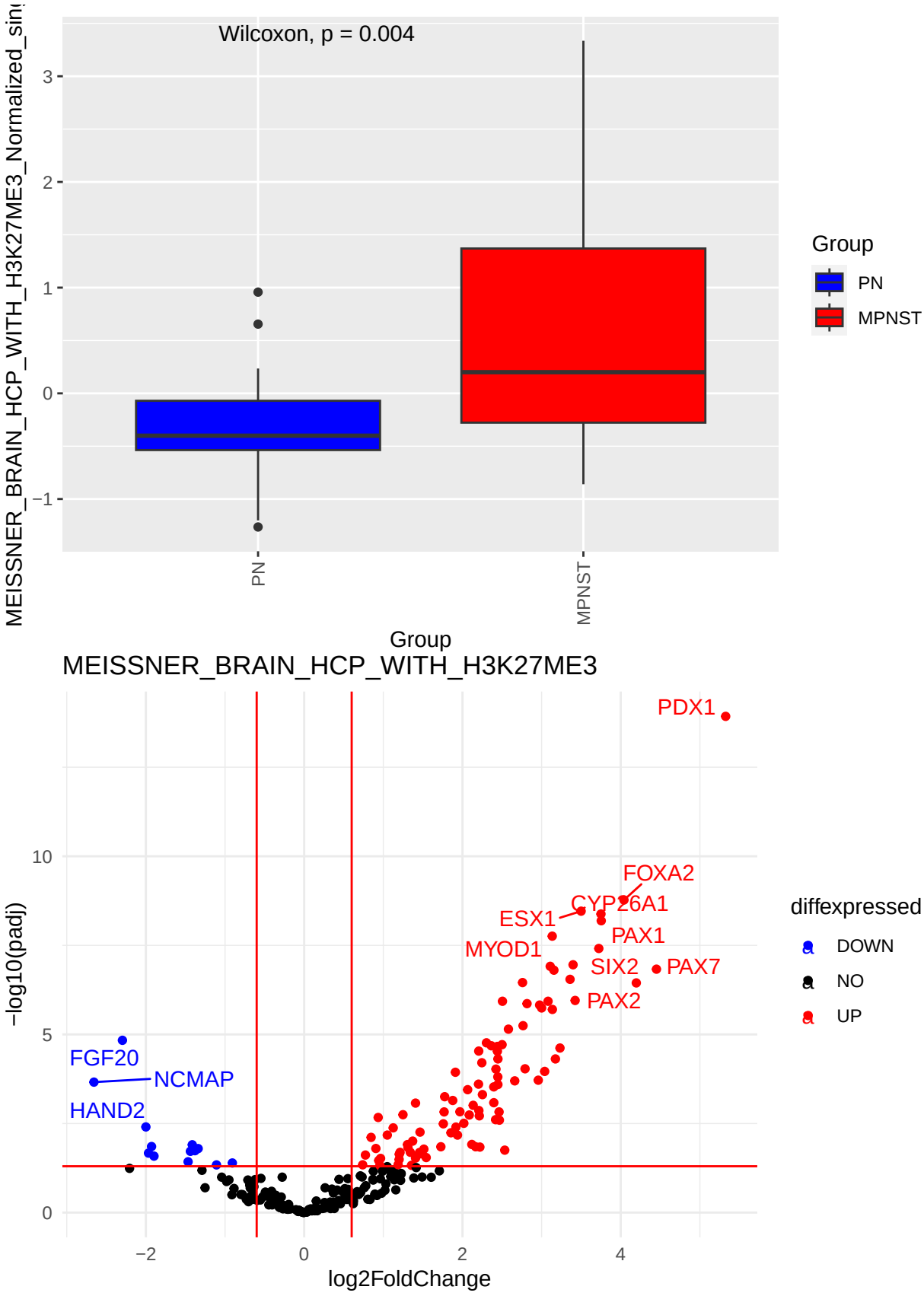
##  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [16] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [31] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```



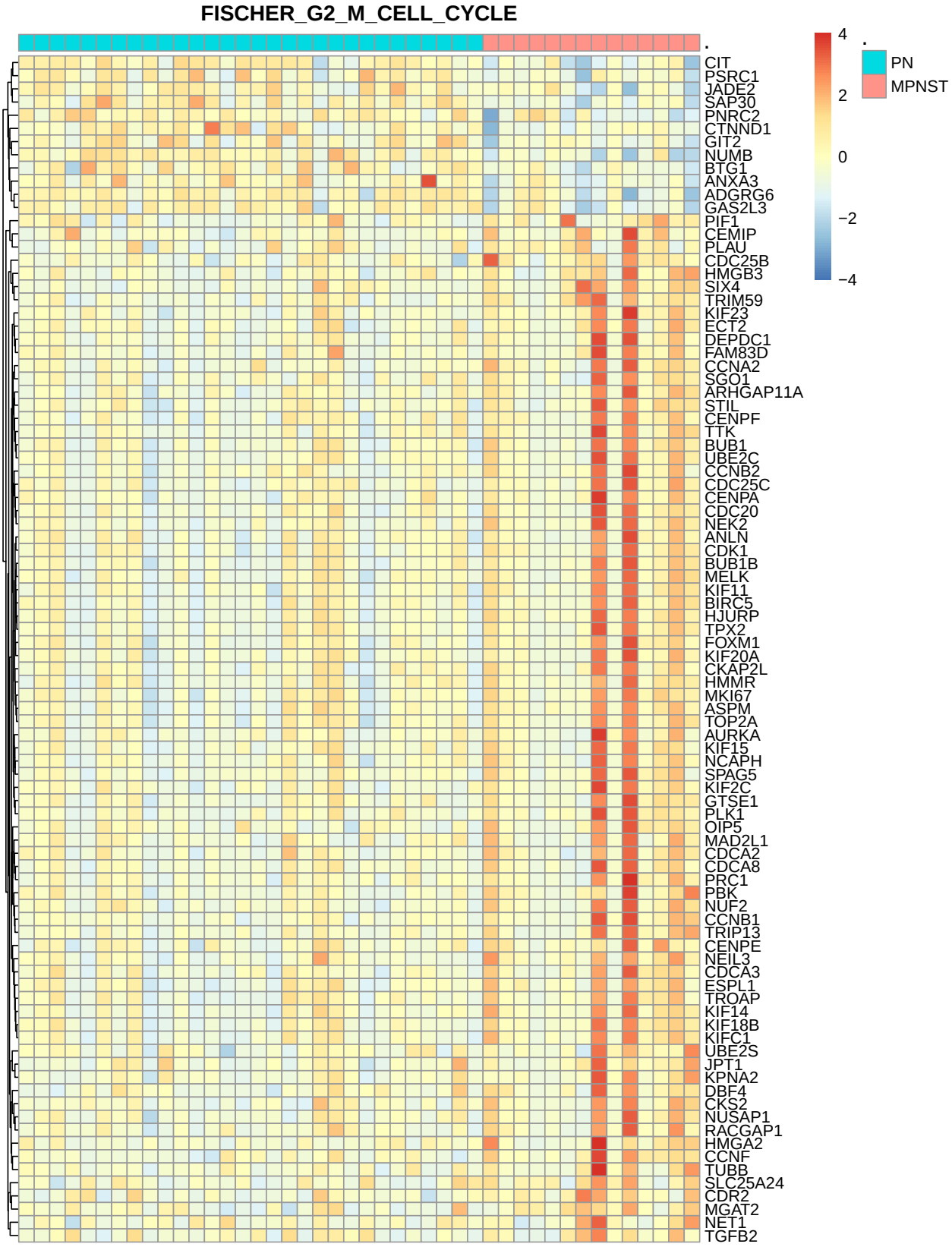


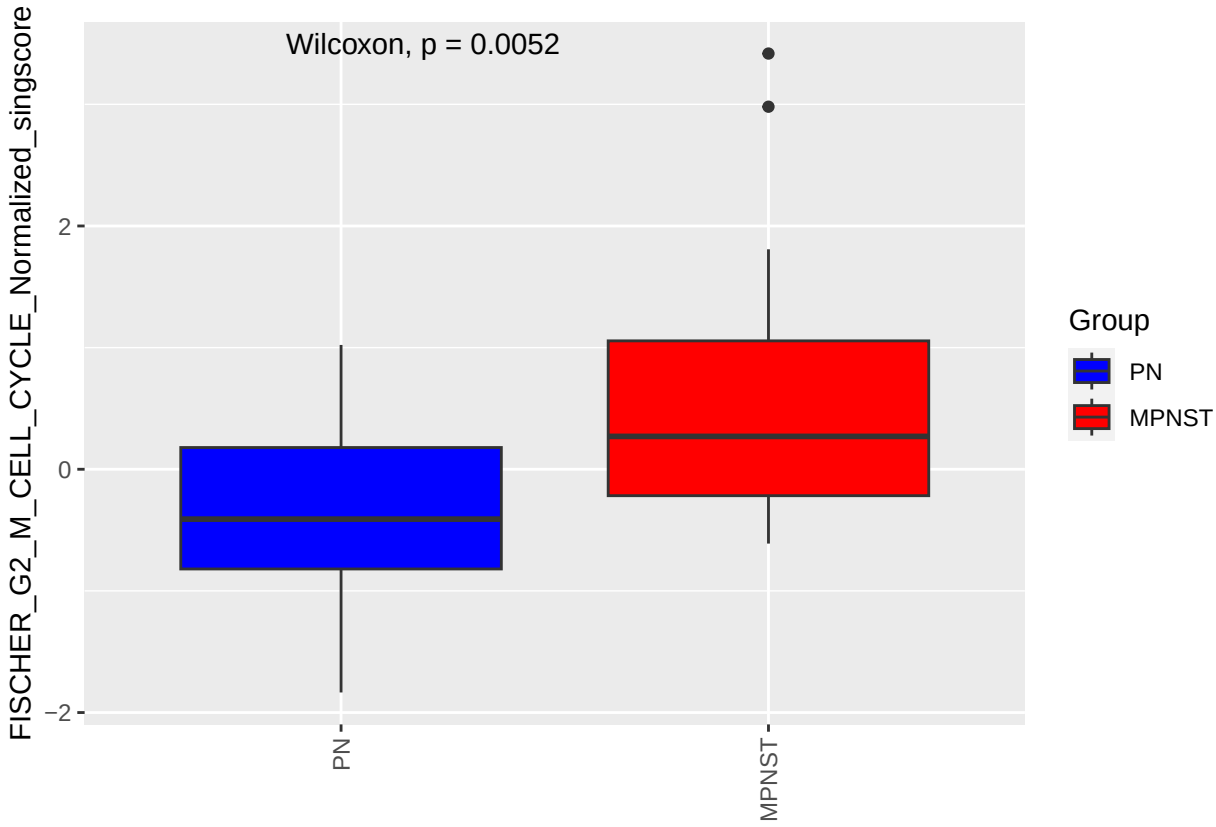
5.2 MEISSNER BRAIN HCP WITH H3K27ME3

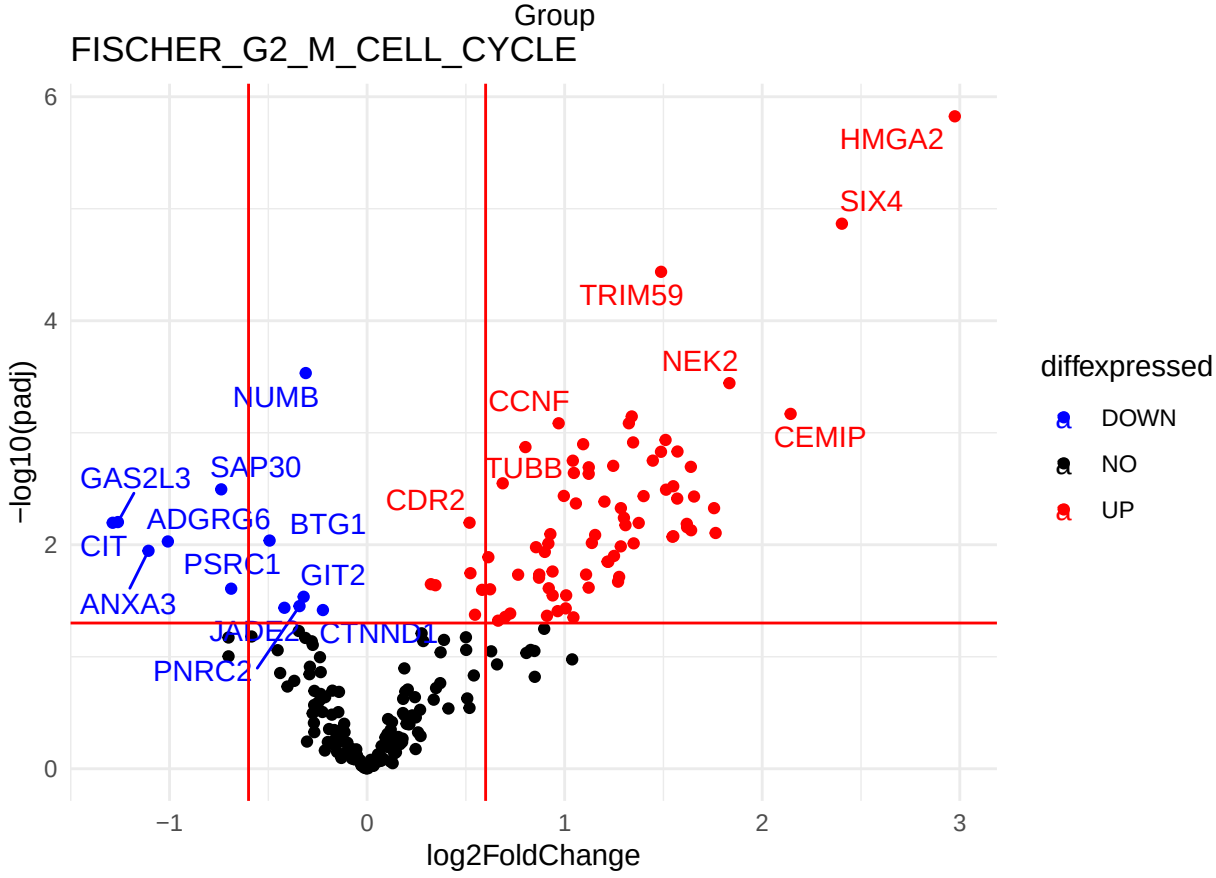



Wilcoxon, p = 0.004
MEISSNER_BRAIN_HCP_WITH_H3K27ME3_Normalized_sin
3
2
1
0
−1
PN
MPNST
Group
Group
PN
MPNST
MEISSNER_BRAIN_HCP_WITH_H3K27ME3
−log10(padj)
10
5
0
−2
0
2
4
log2FoldChange
PDX1
FOXA2
CYP26A1
ESX1
PAX1
MYOD1
SIX2
PAX7
PAX2
FGF20
NCMAP
HAND2
diffexpressed
DOWN
NO
UP

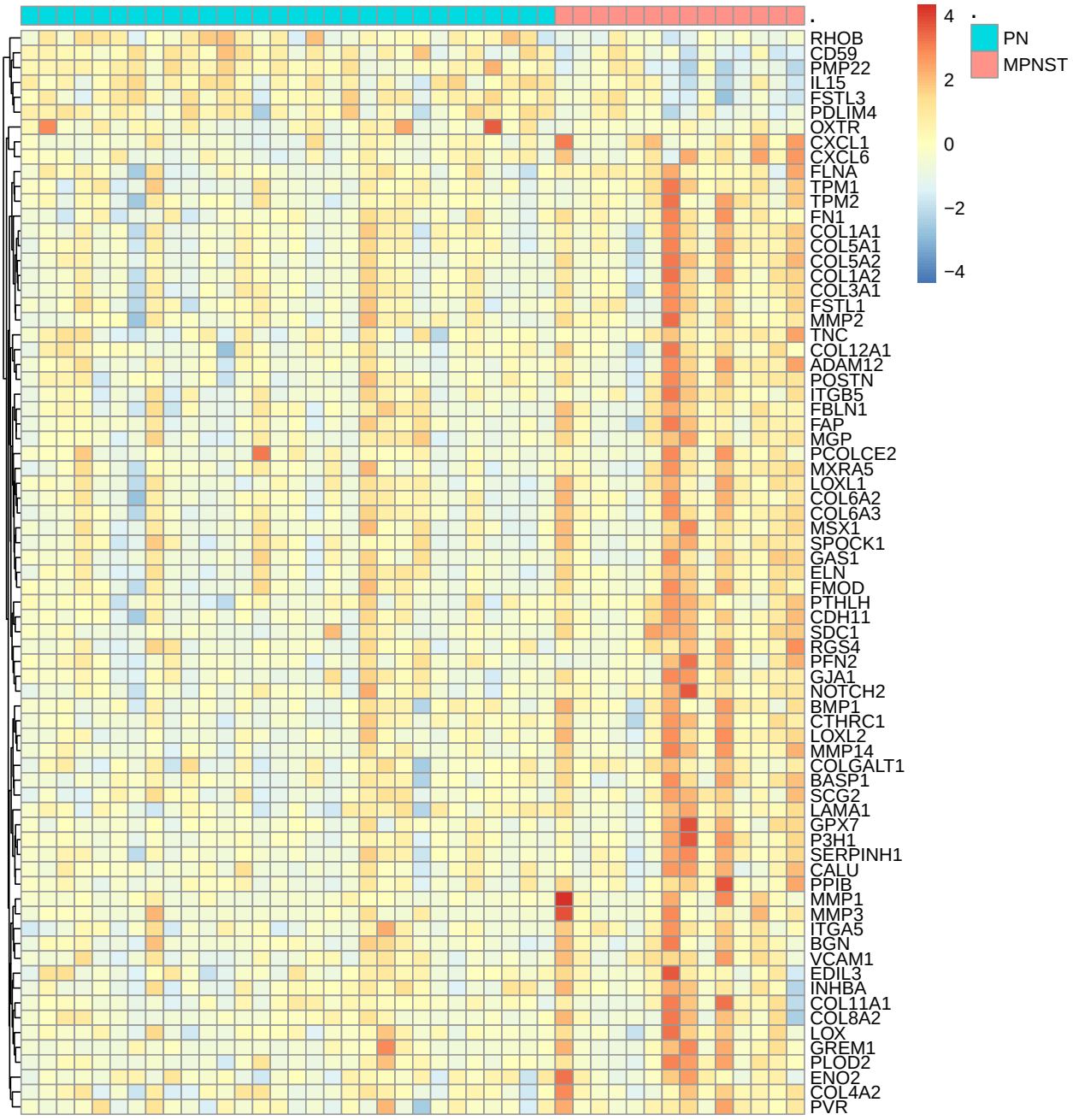
5.3 FISCHER G2 M CELL CYCLE

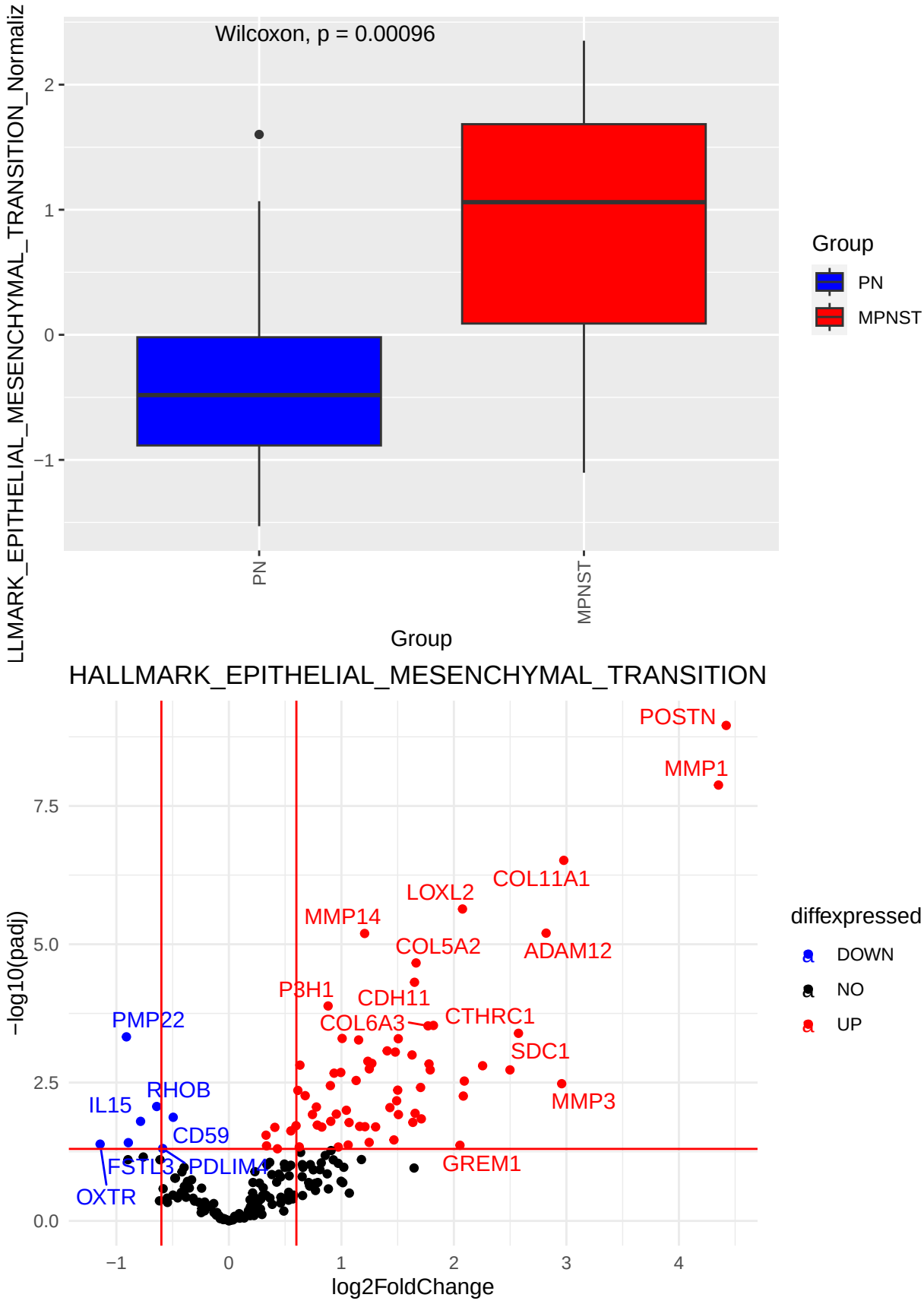



Wilcoxon, p = 0.0052
FISCHER_G2_M_CELL_CYCLE_Normalized_singscore
2
0
−2
PN
MPNST
Group
Group
PN
MPNST


FISCHER_G2_M_CELL_CYCLE
−log10(padj)
6
4
2
0
−1
0
1
2
3
log2FoldChange
HMGA2
SIX4
TRIM59
NEK2
CEMIP
CCNF
TUBB
CDR2
NUMB
SAP30
GAS2L3
ADGRG6
BTG1
CIT
PSRC1
GIT2
ANXA3
JADE2
CTNND1
PNRC2
diffexpressed
DOWN
NO
UP

5.4 HALLMARK EPITHELIAL MESENCHYMAL TRANSITION




Wilcoxon, p = 0.00096
LLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION_Normaliz
2
1
0
−1
PN
MPNST
Group
Group
PN
MPNST
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
−log10(padj)
7.5
5.0
2.5
0.0
−1
0
1
2
3
4
log2FoldChange
POSTN
MMP1
COL11A1
LOXL2
MMP14
COL5A2
ADAM12
P3H1
CDH11
CTHRC1
COL6A3
SDC1
MMP3
PMP22
RHOB
IL15
CD59
FSTL3
PDLIM4
OXTR
GREM1
diffexpressed
DOWN
NO
UP

5.5 WINNEPENNINCKX MELANOMA METASTASIS UP

5.6 MAPK/AKT PATHWAY

5.6.1 WP_PI3KAKT_SIGNALING_PATHWAY

5.6.2 REACTOME_PI3K_AKT_SIGNALING_IN_CANCER

5.6.3 WP_MAPK_SIGNALING_PATHWAY

5.6.4 HALLMARK_MTORC1_SIGNALING