

Supplementary Material

Supplementary Figure 1: Unsupervised clustering of the RNA-seq data obtained from grade-specific tumor samples only.

a) Cluster dendrogram for all the grade I meningioma samples.

b) Cluster dendrogram for all the grade II meningioma samples.

Supplementary Figure 2: GSEA analysis shows the significant correlation of the genes up-regulated in grade IP vs INP tumors with those gene sets associated with 'Hypoxia,' 'EGF signaling,' 'HRAS oncogenic,' 'Tumor angiogenesis' and 'TGF β signaling Down.'

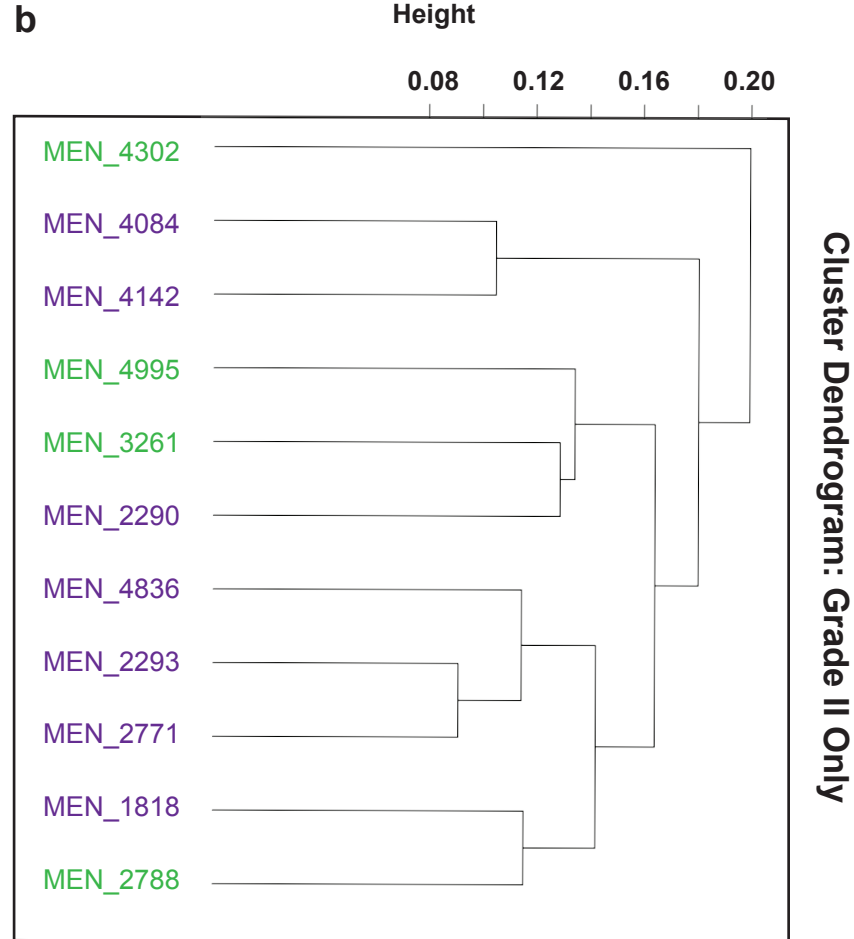
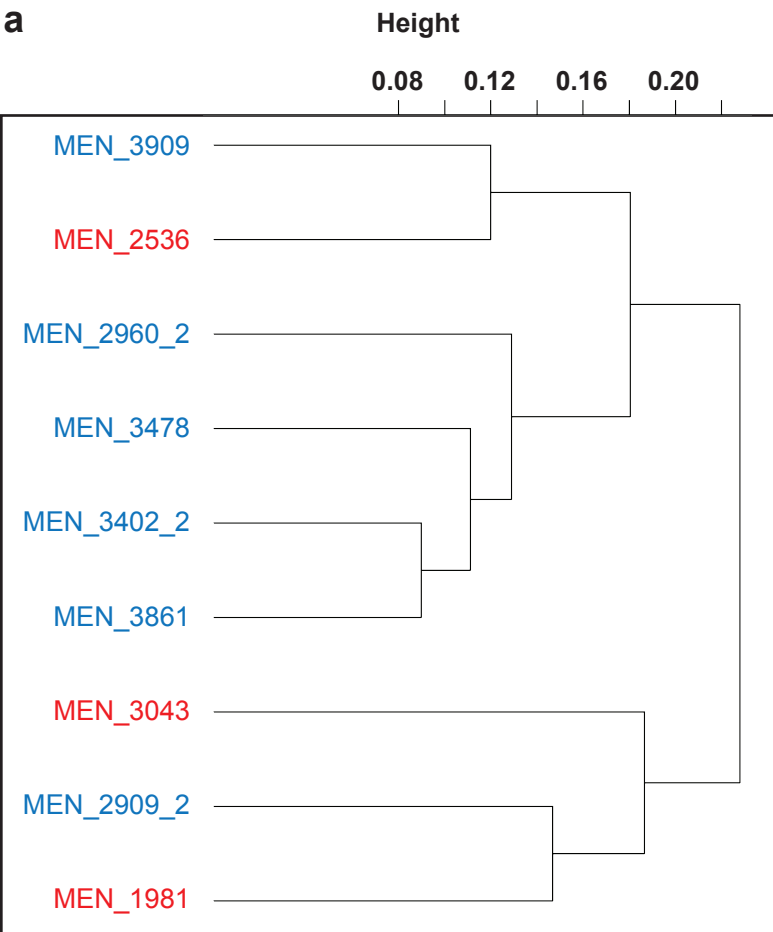
Supplementary Table 1: List of significantly differentially expressed genes between grade INP and IP meningiomas, as identified by RNA-seq.

Supplementary Table 2: List of significantly differentially expressed genes between all grade I and all grade II meningiomas, as identified by RNA-seq.

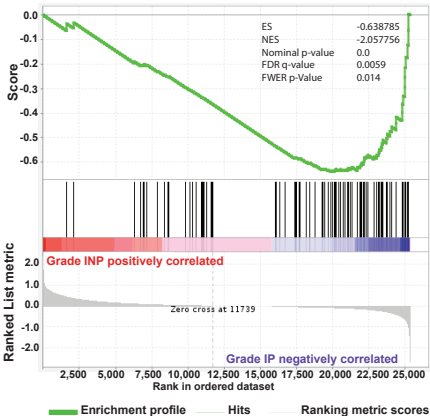
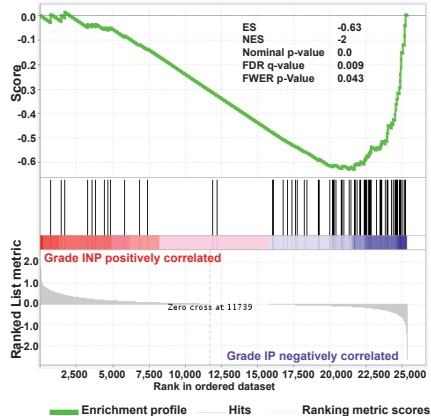
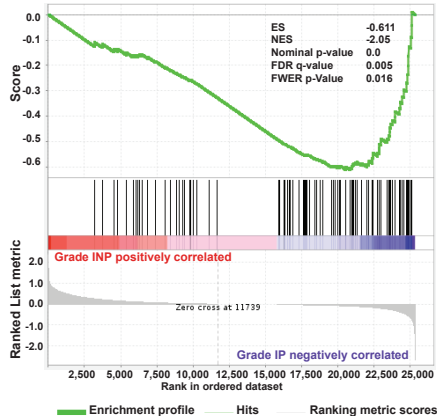
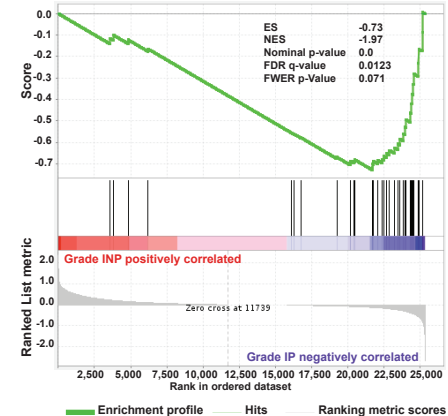
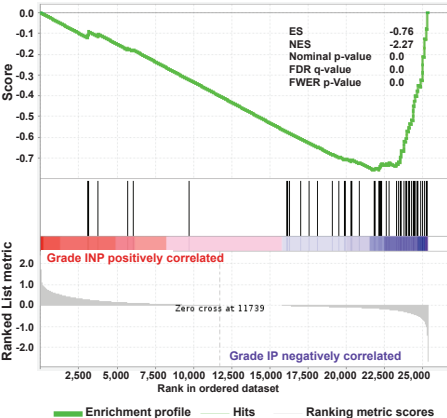
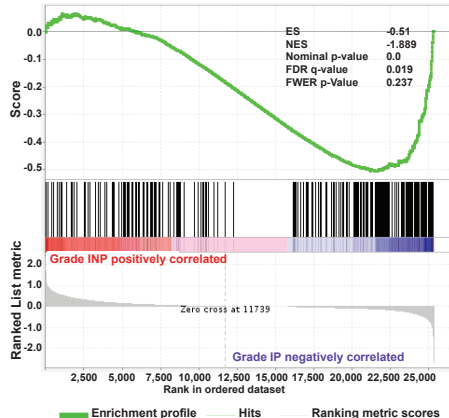
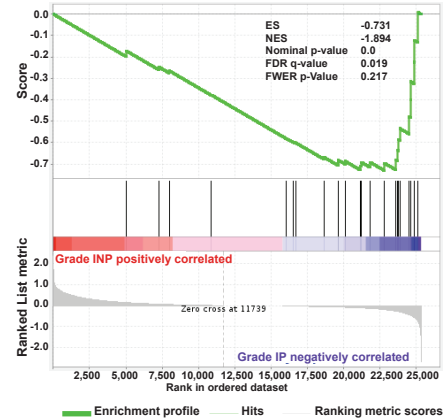
Supplementary Table 3: List of significantly differentially expressed genes between all grade I and all grade III meningiomas, as identified by RNA-seq.

Supplementary Table 4: List of significantly differentially expressed genes between all grade I and grade II and III meningiomas, as identified by RNA-seq.

Supplementary Table 5: List of significantly differentially expressed genes between grade II S. and II DN meningiomas, as identified by RNA-seq.



- Grade INP (never progressed)
- Grade IP (progressed)
- Grade II S. ("secondary" grade II)
- Grade II DN ("de novo" grade II)

WINTER HYPOXIA UP**HARRIS HYPOXIA****MENSE HYPOXIA_UP****SEMENZA HIF1 TARGETS****NAGASHIMA EGF SIGNALING UP****BILD HRAS ONCOGENIC SIGNATURE****LU TUMOR ANGIOGENESIS UP****JAZAG TGFB1 SIGNALING DN**