

Supplementary Materials for

Identification and validation of a metabolism-related gene signature for predicting the prognosis of paediatric medulloblastoma

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This PDF file includes:

Supplementary figure 1

Figure-S1

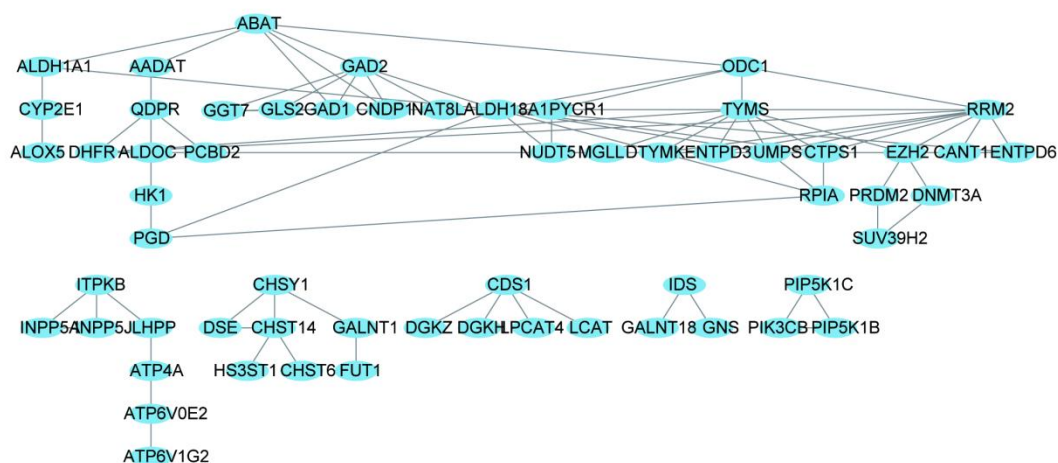


Figure. S1: The PPI network of 71 DE-MRGs in MB

Supplementary figure 2

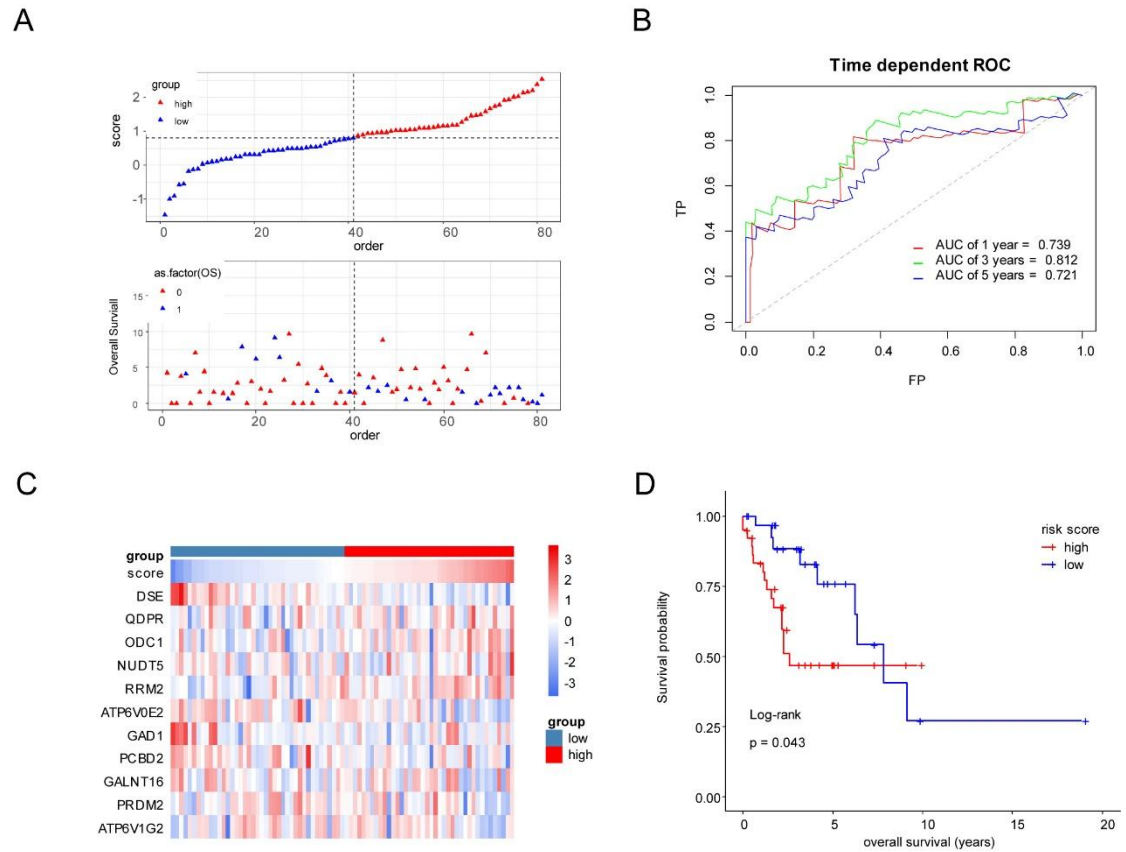


Figure. S2 Validation of prognostic risk model for pediatric MB in testing cohort

- A The distribution of risk score, OS, and survival status in the CBTTC MB cohort.
- B The time dependent ROC curves of OS time based on the in the CBTTC MB cohort.
- C The heatmap shows the relationship between risk score and expression of 12 MRGs in this risk model.
- D The K-M curves of OS time in high-risk and low-risk patients.

Supplementary figure 3

Figure-S3

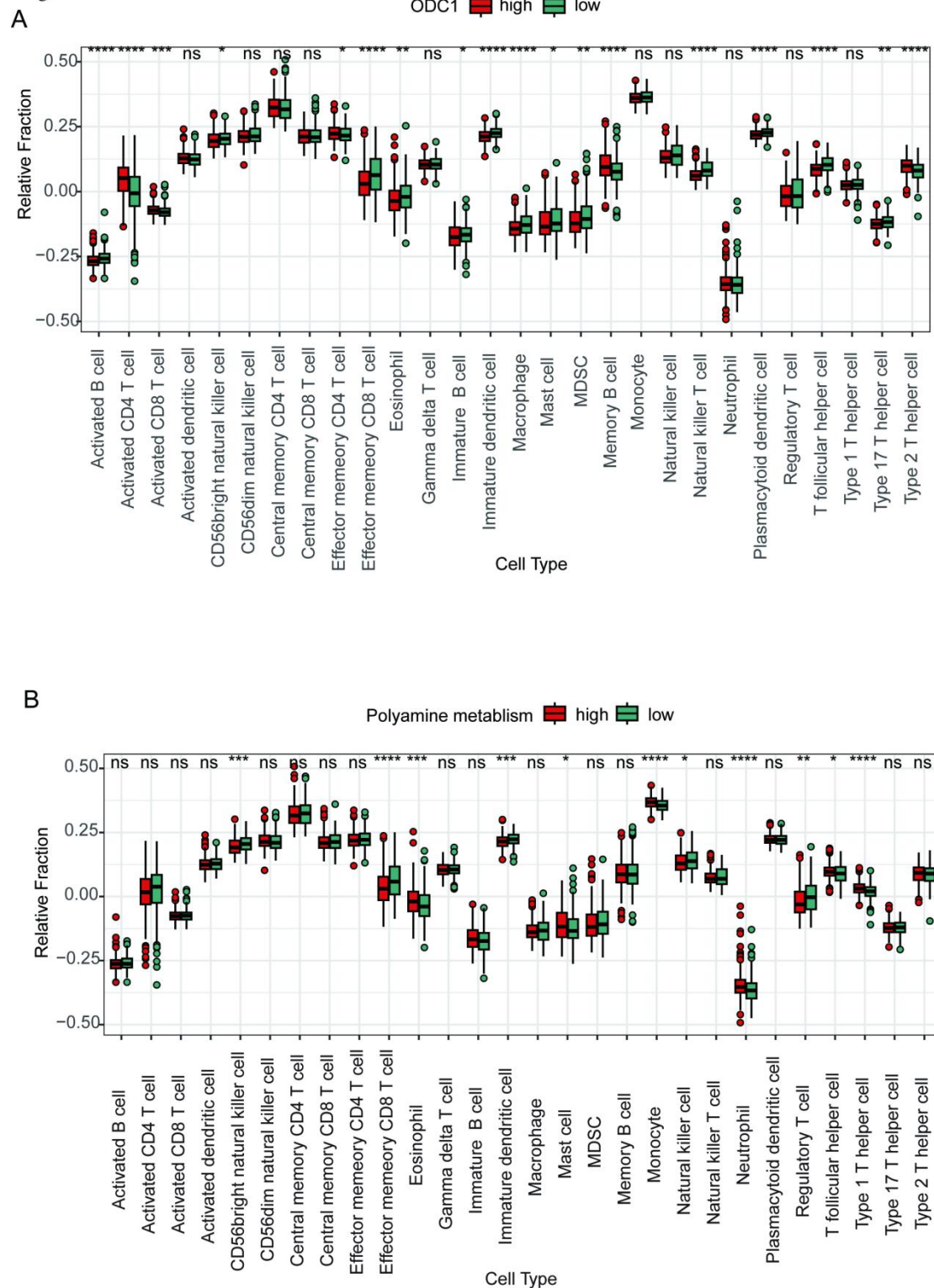


Figure. S3 The ODC1 expression and polyamine metabolism activity associated with the infiltration level of immune cells in MB.

A The box plot shows the difference in infiltration level of 28 immune cells between ODC1 high expression group and ODC1 low expression risk group.

B The box plot shows the difference in infiltration level of 28 immune cells between

polyamine metabolism high activity group and polyamine metabolism low activity group.

Supplementary figure 4

Figure-S4

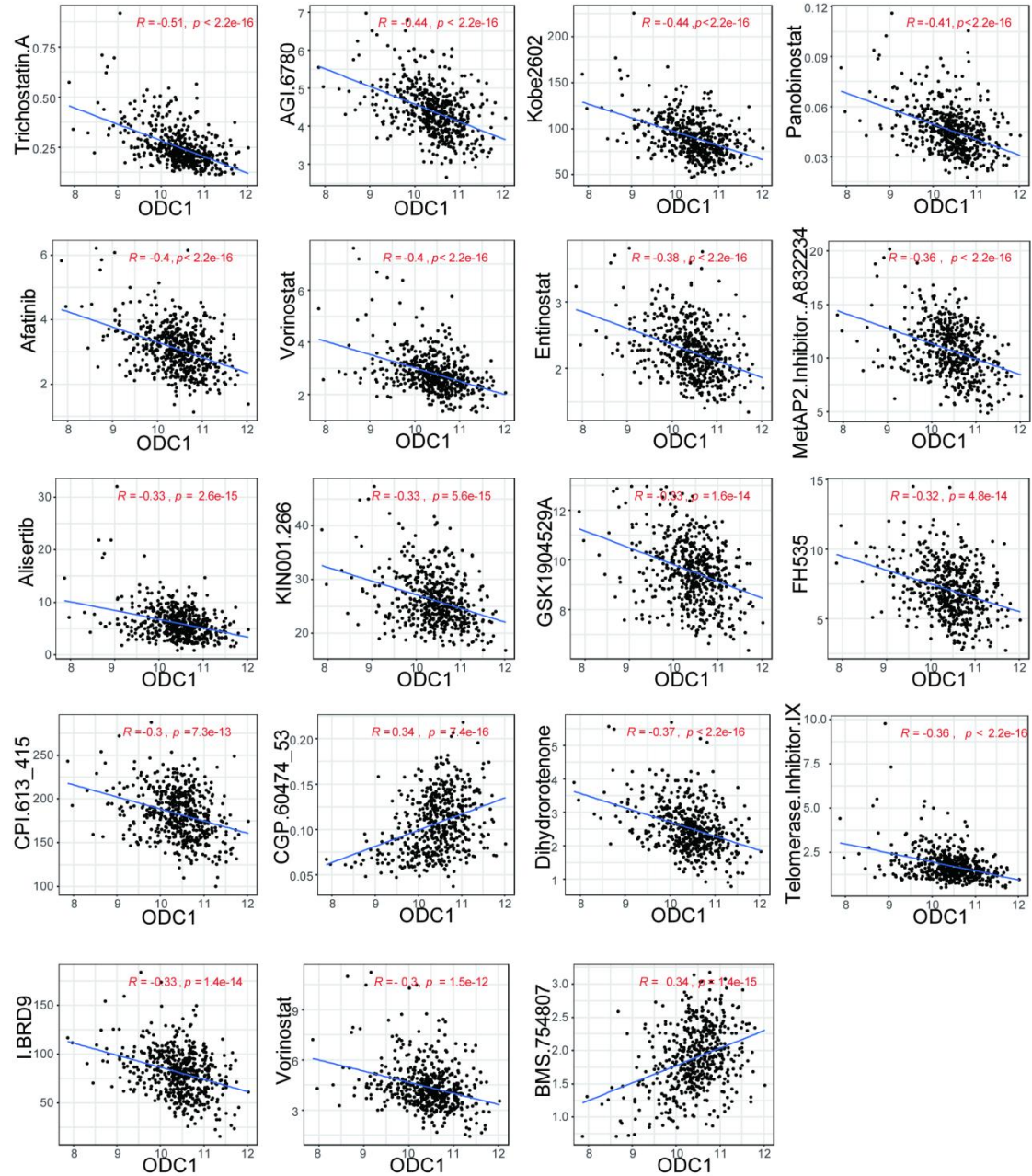


Figure. S4 ODC1 expression correlated with sensitivity of some drugs.