

# Expression and prognostic significance of TCTN1 in human glioblastoma

Delong Meng<sup>1\*</sup>, Yuanyuan Chen<sup>1\*</sup>, Yingjie Zhao<sup>1</sup>, Jingkun Wang<sup>1</sup>, Dapeng Yun<sup>1</sup>, Song Yang<sup>2</sup>, Juxiang Chen<sup>3</sup>, Hongyan Chen<sup>1</sup>, Daru Lu<sup>1§</sup>

<sup>1</sup>State Key Laboratory of Genetic Engineering and MOE Key Laboratory of Contemporary Anthropology, School of Life Sciences, Fudan University, No. 220 Handan Road, Shanghai, 200433, PR China

<sup>2</sup>The Eighth Department of General Surgery and Department of Pathology, the First Affiliated Hospital of Anhui Medical University, No. 218 Jixi Road, Hefei, 230022, PR China

<sup>3</sup>Department of Neurosurgery, Shanghai Institute of Neurosurgery, Changzheng Hospital, Second Military Medical University, No. 415 Fengyang Road, Shanghai, 200003, PR China

\*These authors contributed equally to this work.

§Corresponding author

## Additional files

### Additional file 1 as PDF

Additional file 1 Figure S1. TCTN1 protein expression was analysed by immunohistochemistry staining and positive staining rate of TCTN1 in normal brain samples and GBMs was indicated as a scatter plot. *P* value was determined by Student's t-test.

Additional file 1 Figure S2. *TCTN1* mRNA expression was significantly different in subgroups of GBMs in the TCGA cohort according to status of *IDH1* mutation (A), *ATRX* mutation (B), *MYCN* amplification (C) or *PDGFRA* amplification (D) as indicated. A single spot represents the *TCTN1* expression value (in log<sub>2</sub> scale) of an individual patient, with a line in the middle representing the mean expression value. *P* values were determined by Student's t-test.

Additional file 1 Figure S3. Correlations between *TCTN1* with *GLII*(A) and *PTCHI*(B) levels in TCGA cohort.

Additional file 1 Figure S4. Kaplan-Meier curves were plotted according to different *TCTN1* gene expression for overall survival of GBM patients in the TCGA cohort stratified by the status of EGFR amplification (A, B), PDGFRA amplification (C, D), MYCN amplification (E, F), PARK2 deletion (G, H), CDKN2A deletion (I, J) and CDKN2B deletion (K, L) as indicated. *P* values were obtained from log-rank test.

Figure S1

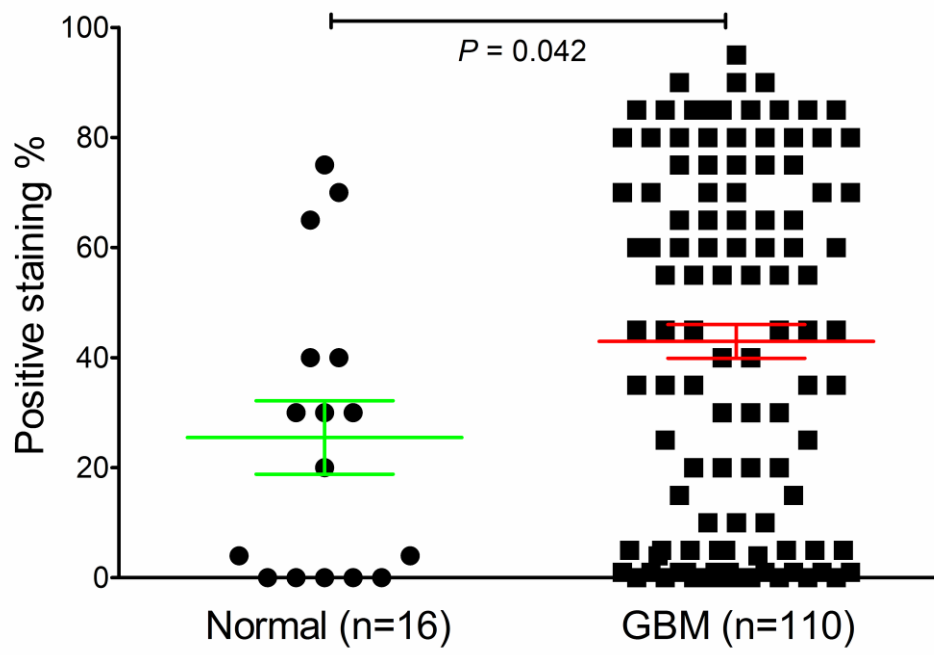


Figure S2

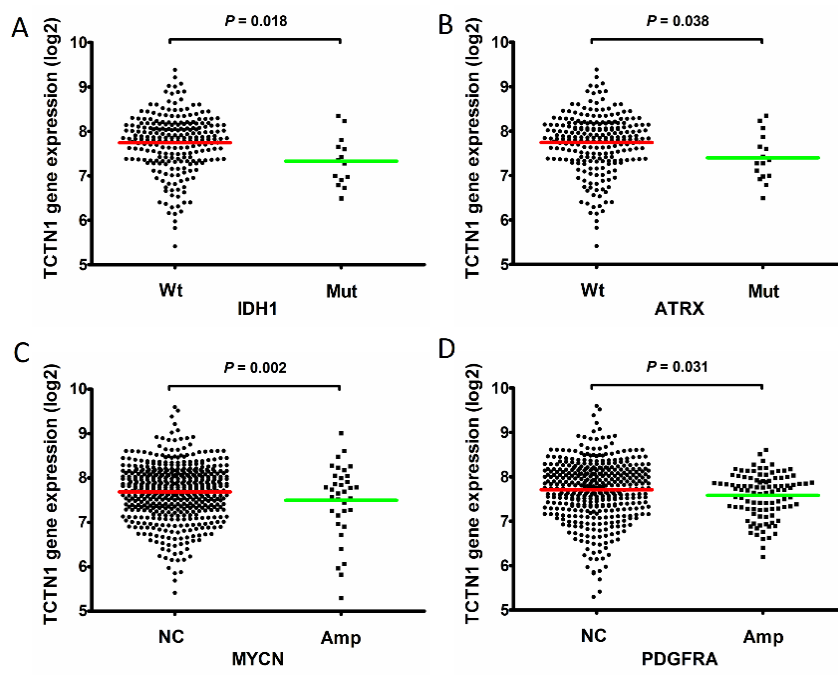


Figure S3

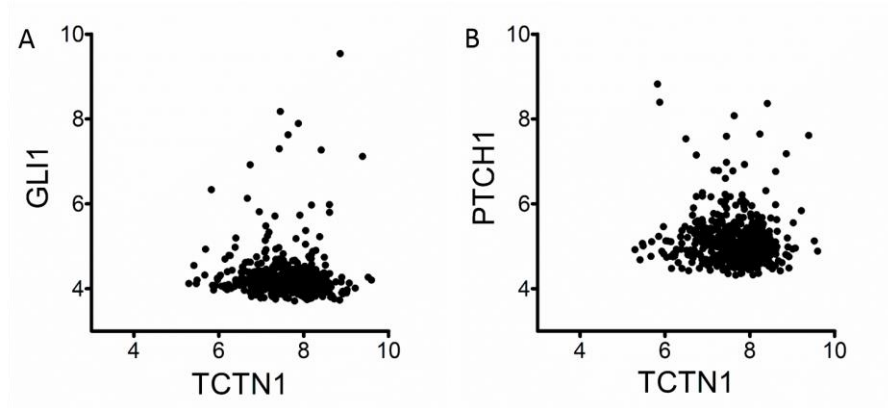


Figure S4

