Supplementary Table 1 Variants of *TUBB8* reported in previous studies.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| variant | Amino acid alteration | exon | DOMAIN | Inheritance pattern | PPH2 | PROVEAN | Hetero-/Homo-/Compound heterozygote | Variant type | reference |
| c.10A>C | p.(I4L) | 1 | 1 | Unknown | Benign | N | Hetero- | Missense | [1] |
| c.181C>A | p.(P61T) | 3 | 1 | Unknown | PB | D | Hetero- | Missense |  |
| c.322G>A | p.(E108K) | 4 | 1 | AD | PB | D | Hetero- | Missense |  |
| c.426dupG | p.(T143Dfs\*12) | 4 | 1 | AR | / | / | Hetero- | Frameshift insertion | |
| c.292G>A | p.(G98R) | 4 | 1 | Unknown | PB | D | Hetero- | Missense |  |
| c.527C>T | p.(S176L) | 4 | 1 | Unknown | PB | D | Hetero- | Missense |  |
| c.523G>A | p.(V175M) | 4 | 1 | Unknown | PB | N | Hetero- | Missense |  |
| c.600T>G | p.(F200L) | 4 | 1 | Unknown | Benign | D | Hetero- | Missense |  |
| c.763G>A | p.(V255M) | 4 | 1.5 | AD | PB | N | Hetero- | Missense |  |
| c.721C>T | p.(R241C) | 4 | 1.5 | AR | PB | D | Homo- | Missense |  |
| c.735G>C | p.(Q245H) | 4 | 1.5 | Unknown | PB | D | Hetero- | Missense |  |
| c.722G>A | p.(R241H) | 4 | 1.5 | Unknown | PB | D | Hetero- | Missense |  |
| c.1073C>T | p.(P358L) | 4 | 2 | AD | PB | D | Hetero- | Missense |  |
| c.1000C>G | p.(Q334E) | 4 | 2 | AD | PB | N | Hetero- | Missense |  |
| c.883G>C | p.(D295H) | 4 | 2 | Incomplete dominance | PB | D | Hetero- | Missense |  |
| c.1099T>C | p.(F367L) | 4 | 2 | AD | PB | D | Hetero- | Missense |  |
| c.1072C>G | p.(P358A) | 4 | 2 | Unknown | PB | D | Hetero- | Missense |  |
| c.1061G>A | p.(C354Y) | 4 | 2 | Unknown | PB | D | Hetero- | Missense |  |
| c.1057G>A | p.(V353I) | 4 | 2 | Unknown | Benign | N | Hetero- | Missense |  |
| c.1270C>T | p.(Q424\*) | 4 | 2.5 | AR | / | / | Homo- | Non-sense |  |
| c.1286C>T | p.(T429M) | 4 | 2.5 | Incomplete dominance | PB | N | Compound heterozygote | Missense |  |
| c.1301\_1327del | p.(434\_442del) | 4 | 2.5 | Incomplete dominance | / | D | Compound heterozygote | In-frame deletion | |
| c.1205dupG | p.(M403Hfs\*3) | 4 | 2.5 | AR | / | / | Homo- | Frameshift insertion | |
| c.1249G>T | p.(D417Y) | 4 | 2.5 | Unknown | PB | D | Hetero- | Missense |  |
| c.1171C>T | p.(R391C) | 4 | 2.5 | Unknown | PB | D | Hetero- | Missense |  |
| c.1228G>A | p.(E410K) | 4 | 2.5 | Unknown | PB | N | Hetero- | Missense |  |
| c. 80\_100del | p.E27\_A33del | 2 | 1 | AR |  |  | Homo- | In-frame deletion | [2] |
| c. 527C>T | p.S176L | 4 | 1 | Unknown |  |  | Hetero- | Missense |  |
| c. 628A>G | p.I210V | 4 | 1 | Unknown |  |  | Hetero- | Missense |  |
| c. 853A>C | p.T285P | 4 | 1 | Unknown |  |  | Hetero- | Missense |  |
| c. 1043A>G | p.N348S | 4 | 1 | Unknown |  |  | Hetero- | Missense |  |
| c. 426\_427insG | p.T143Dfs\*12 | 4 | 1 | AR |  |  | Homo- | Frameshift insertion | |
| c. 713C>T | p.T238M | 4 | 1.5 | AD |  |  | Hetero- | Missense |  |
| c. 763G>A | p.V255M | 4 | 1.5 | Unknown |  |  | Hetero- | Missense |  |
| c. 784C>T | p.R262Q | 4 | 2 | Unknown |  |  | Hetero- | Missense |  |
| c. 5G>A | p.R2K | 1 | "-1" | AD |  |  | Hetero- | Missense | [3] |
| c. 527C>T | p.S176L | 4 | 1 | Unknown |  |  | Hetero- | De novo |  |
| c. 686T>C | p.V229A | 4 | 1 | AD |  |  | Hetero- | Missense |  |
| c. 785G>A | p.R262Q | 4 | 2 | Unknown |  |  | Hetero- | Missense |  |
| c. 900G>A | p.M300I | 4 | 2 | AD |  |  | Hetero- | Missense |  |
| c. 1088T>C | p.M363T | 4 | 2 | AD |  |  | Hetero- | Missense |  |
| c. 1249G>A | p.D417N | 4 | 2 | AD |  |  | Hetero- | Missense |  |
| c. 5G>T | p.R2M | 1 | 1 | AD | PB | N | Hetero- | Missense | [4] |
| c. 10A>C | p.I4L | 1 | 1 | AD | benign | N | Hetero- | Missense |  |
| c. 35G>A | p.C12Y | 1 | 1 | AR | benign | D | Homo- | Missense |  |
| c. 209C>T | p.P70L | 3 | 1 | AR | PB | D | Homo- | Missense |  |
| c. 580G>A | p.E194K | 4 | 1 | Unknown | PB | D | Hetero- | Missense |  |
| c. 613G>A | p.E205K | 4 | 1 | Unknown | PD | D | Hetero- | Missense |  |
| c. 990G>A | p.M330I | 4 | 2 | AD | benign | D | Hetero- | Missense |  |
| c. 1057G>A | p.V353I | 4 | 2 | Unknown | benign | N | Hetero- | Missense |  |
| c. 1245G>A | p.M415I | 4 | 2 | Unknown | benign | N | Hetero- | Missense |  |
| Exon 1–4 deletion | NA | 1–4 |  | AR | NA | NA | Homo- | Whole deletion | |
| c. 5G>T | p.R2M | 1 | 1 | AD | D | D(SIFT) | Hetero- | Missense | [5] |
| c. 535G>A | p.V179M | 4 | 1 | AD | D | D(SIFT) | Hetero- | Missense |  |
| c. 292G>A | p.G98R | 4 | 1 | Unknown | D | D(SIFT) | Hetero- | Missense | [6] |
| c.322G > A | p.Glu108Lys | 4 | 1 | Unknown | PD | D(SIFT) | Hetero- | Missense | [7] |
| c.1054G>T | p.A352S | 4 | 2 | AD | PD | disease-causing(Mutation Taster) | Hetero- | Missense | [8] |
| c.161C>T | p.A54V | 2 | 1 | AR | benign | N | Homo- | Missense | this study |

PB, Probably damaging; D, Deleterious; N, Neutral;

Domain "-1"：Location in front of GTPase domain;

Domain 1：Tubulin FtsZ family, GTPase domain;

Domain 1.5: Location between GTPase domain and Tubulin C-terminal domain;

Domain 2: Tubulin C-terminal domain;

Domain 2.5: Location behind Tubulin C-terminal domain.

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