Table S1. Comparison of mutation frequency between ex-GCC and pure GCC

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Ex-GCC (N = 26) | | | Pure GCC (N = 27) | | | *P*-value  (Ex-GCC vs pure GCC) |
| MT | Total | Mutation  rate (%) | MT | Total | Mutation  rate (%) |
| *APC* | 1 | 26 | 3.8 | 0 | 27 | 0.0 | 0.30 |
| *ARID1A* | 2 | 7 | 28.6 | 0 | 6 | 0.0 | 0.15 |
| *ATM* | 1 | 26 | 3.8 | 0 | 27 | 0.0 | 0.30 |
| *BCOR* | 0 | 24 | 0.0 | 1 | 27 | 3.7 | 0.34 |
| *BRAF* | 1 | 26 | 3.8 | 1 | 27 | 3.7 | 0.98 |
| *CDC73* | 0 | 26 | 0.0 | 1 | 25 | 4.0 | 0.30 |
| *CDH1* | 0 | 25 | 0.0 | 2 | 27 | 7.4 | 0.17 |
| *CHEK2* | 2 | 25 | 8.0 | 0 | 25 | 0.0 | 0.15 |
| *CIC* | 0 | 22 | 0.0 | 1 | 21 | 4.8 | 0.30 |
| *ERBB2* | 0 | 26 | 0.0 | 1 | 27 | 3.7 | 0.32 |
| *ERCC2* | 1 | 25 | 4.0 | 0 | 25 | 0.0 | 0.31 |
| *FBXW7* | 1 | 26 | 3.8 | 1 | 27 | 3.7 | 0.98 |
| *FGFR2* | 0 | 26 | 0.0 | 1 | 27 | 3.7 | 0.32 |
| *GNAS* | 0 | 26 | 0.0 | 2 | 27 | 7.4 | 0.16 |
| *KDM6A* | 0 | 24 | 0.0 | 1 | 23 | 4.3 | 0.30 |
| *KMT2D* | 1 | 25 | 4.0 | 0 | 23 | 0.0 | 0.33 |
| *KRAS* | 2 | 26 | 7.7 | 2 | 27 | 7.4 | 0.97 |
| *NF1* | 0 | 25 | 0.0 | 1 | 22 | 4.5 | 0.28 |
| *PIK3CA* | 1 | 26 | 3.8 | 0 | 27 | 0.0 | 0.30 |
| *RNF43* | 0 | 26 | 0.0 | 1 | 27 | 3.7 | 0.32 |
| *SMAD2* | 0 | 26 | 0.0 | 1 | 27 | 3.7 | 0.32 |
| *SMAD4* | 2 | 26 | 7.7 | 3 | 27 | 11.1 | 0.67 |
| *SMARCA4* | 1 | 26 | 3.8 | 0 | 27 | 0.0 | 0.30 |
| *STK11* | 1 | 26 | 3.8 | 0 | 27 | 0.0 | 0.30 |
| *TP53* | 6 | 25 | 24.0 | 6 | 25 | 24.0 | 1.00 |