|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **Odds Ratio** | **P Value** | **% Non-Neuroendocrine** | **% Neuroendocrine** |
| RB1 | 33.4 | <0.0001 | 6.5 | 70.0 |
| MYCL | 12.6 | <0.0001 | 0.6 | 6.7 |
| TP53 | 4.98 | <0.0001 | 59.3 | 87.9 |
| CREBBP | 2.99 | <0.0001 | 1.9 | 5.4 |
| RICTOR | 2.85 | <0.0001 | 2.0 | 5.5 |
| KMT2D | 1.58 | <0.0001 | 8.4 | 12.6 |
| NOTCH3 | 1.49 | 0.01 | 1.6 | 2.3 |
| NOTCH1 | 1.44 | 0.0001 | 5.2 | 7.3 |
| LRP1B | 1.35 | 0.0002 | 7.3 | 9.6 |
| PTEN | 0.74 | <0.0001 | 14.6 | 11.2 |
| PIK3CA | 0.45 | <0.0001 | 13.8 | 6.7 |
| TERT | 0.11 | <0.0001 | 21.6 | 3.0 |
| KRAS | 0.09 | <0.0001 | 26.9 | 3.2 |
| SMAD4 | 0.08 | <0.0001 | 7.4 | 0.7 |
| CDKN2A | 0.06 | <0.0001 | 43.5 | 4.35 |
| CDKN2B | 0.05 | <0.0001 | 25.3 | 1.7 |

**Supplementary Table 3. Gene enrichment in neuroendocrine vs. non-neuroendocrine cancers.**

Frequency of alterations of selected genes in neuroendocrine vs. non-neuroendocrine cancer types listed in Figure 2B. Higher odds ratio means that gene was more likely to be altered in the neuroendocrine tumors.