**Table S9**. Functional analysis of the melanoma mutation network: top significant GO terms (*p*Bonferroni <10-6).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **GO ID (BP)** | **GO term** | **Count** | ***p*-value** | ***p*Bonferroni** |
| GO:0007167 | Enzyme linked receptor protein signaling pathway | 38 | 3.49×10-15 | 9.01×10-12 |
| GO:0070271 | Protein complex biogenesis | 45 | 2.05×10-14 | 5.38×10-11 |
| GO:0006461 | Protein complex assembly | 45 | 2.05×10-14 | 5.38×10-11 |
| GO:0010033 | Response to organic substance | 54 | 3.83×10-14 | 1.00×10-10 |
| GO:0007242 | Intracellular signaling cascade | 74 | 5.88×10-14 | 1.54×10-10 |
| GO:0042127 | Regulation of cell proliferation | 56 | 9.64×10-14 | 2.52×10-10 |
| GO:0051174 | Regulation of phosphorus metabolic process | 43 | 1.05×10-13 | 2.75×10-10 |
| GO:0019220 | Regulation of phosphate metabolic process | 43 | 1.05×10-13 | 2.75×10-10 |
| GO:0042325 | Regulation of phosphorylation | 42 | 1.26×10-13 | 3.30×10-10 |
| GO:0007169 | Transmembrane receptor protein tyrosine kinase signaling pathway | 29 | 2.72×10-13 | 7.13×10-10 |
| GO:0043549 | Regulation of kinase activity | 36 | 3.96×10-13 | 1.04×10-9 |
| GO:0009719 | Response to endogenous stimulus | 38 | 7.03×10-13 | 1.84×10-9 |
| GO:0051338 | Regulation of transferase activity | 36 | 1.32×10-12 | 3.45×10-9 |
| GO:0006468 | Protein amino acid phosphorylation | 49 | 1.57×10-12 | 4.12×10-9 |
| GO:0010604 | Positive regulation of macromolecule metabolic process | 55 | 1.02×10-11 | 2.66×10-8 |
| GO:0044093 | Positive regulation of molecular function | 44 | 1.40×10-11 | 3.68×10-8 |
| GO:0006796 | Phosphate metabolic process | 59 | 1.45×10-11 | 3.80×10-8 |
| GO:0006793 | Phosphorus metabolic process | 59 | 1.45×10-11 | 3.80×10-8 |
| GO:0043933 | Macromolecular complex subunit organization | 49 | 1.48×10-11 | 3.88×10-8 |
| GO:0009725 | Response to hormone stimulus | 34 | 2.07×10-11 | 5.42×10-8 |
| GO:0007610 | Behavior | 38 | 5.48×10-11 | 1.44×10-7 |
| GO:0007268 | Synaptic transmission | 30 | 5.52×10-11 | 1.45×10-7 |
| GO:0065003 | Macromolecular complex assembly | 46 | 6.78×10-11 | 1.78×10-7 |
| GO:0016310 | Phosphorylation | 51 | 8.94×10-11 | 2.34×10-7 |
| GO:0042981 | Regulation of apoptosis | 51 | 1.07×10-10 | 2.80×10-7 |
| GO:0007267 | Cell-cell signaling | 43 | 1.11×10-10 | 2.91×10-7 |
| GO:0060341 | Regulation of cellular localization | 27 | 1.11×10-10 | 2.91×10-7 |
| GO:0010557 | Positive regulation of macromolecule biosynthetic process | 45 | 1.37×10-10 | 3.60×10-7 |
| GO:0043067 | Regulation of programmed cell death | 51 | 1.52×10-10 | 3.98×10-7 |
| GO:0010941 | Regulation of cell death | 51 | 1.73×10-10 | 4.52×10-7 |
| GO:0031328 | Positive regulation of cellular biosynthetic process | 46 | 1.80×10-10 | 4.71×10-7 |
| GO:0016477 | Cell migration | 28 | 2.34×10-10 | 6.11×10-7 |
| GO:0009891 | Positive regulation of biosynthetic process | 46 | 2.89×10-10 | 7.56×10-7 |
| GO:0019899 | Enzyme binding | 39 | 3.58×10-10 | 2.06×10-7 |