**PTM ANALYSIS RESULT-BDNF GENE**

**1.Wild Type**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Position** | **Residue (Code)** | **Kinase** | **Motif (PSP)** | **Score** | **Cutoff** |
| Wild Type | 130 | S | AGC | SMRVRRHSDPARRGE | 0.1345 | 0.0478 |
| Wild Type | 39 | T | CK1 | LAYPGVRTHGTLESV | 0.2032 | 0.0996 |
| Wild Type | 123 | S | CK1 | YLDAANMSMRVRRHS | 0.1833 | 0.0996 |
| Wild Type | 130 | S | CK1 | SMRVRRHSDPARRGE | 0.1758 | 0.0996 |
| Wild Type | 145 | S | CK1 | LSVCDSISEWVTAAD | 0.116 | 0.0996 |

**2.MUTANT-rs6265**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Position** | **Residue (Code)** | **Kinase** | **Motif (PSP)** | **Score** | **Cutoff** |
| rs6265 | 130 | S | AGC | SMRVRRHSDPARRGE | 0.1345 | 0.0478 |
| rs6265 | 39 | T | CK1 | LAYPGVRTHGTLESV | 0.2044 | 0.0996 |
| rs6265 | 123 | S | CK1 | YLDAANMSMRVRRHS | 0.1833 | 0.0996 |
| rs6265 | 130 | S | CK1 | SMRVRRHSDPARRGE | 0.1758 | 0.0996 |
| rs6265 | 145 | S | CK1 | LSVCDSISEWVTAAD | 0.116 | 0.0996 |

**3. MUTANT rs1048218**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Position** | **Residue (Code)** | **Kinase** | **Motif (PSP)** | **Score** | **Cutoff** |
| rs1048218 | 130 | S | AGC | SMRVRRHSDPARRGE | 0.1345 | 0.0478 |
| rs1048218 | 39 | T | CK1 | LAYPGVRTHGTLESV | 0.2032 | 0.0996 |
| rs1048218 | 123 | S | CK1 | YLDAANMSMRVRRHS | 0.1833 | 0.0996 |
| rs1048218 | 130 | S | CK1 | SMRVRRHSDPARRGE | 0.1758 | 0.0996 |
| rs1048218 | 145 | S | CK1 | LSVCDSISEWVTAAD | 0.116 | 0.0996 |

**4. Mutant rs8192466-T>I**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Position** | **Residue (Code)** | **Kinase** | **Motif (PSP)** | **Score** | **Cutoff** |
| rs8192466-T>I | 130 | S | AGC | SMRVRRHSDPARRGE | 0.1345 | 0.0478 |
| rs8192466-T>I | 39 | T | CK1 | LAYPGVRTHGTLESV | 0.2032 | 0.0996 |
| rs8192466-T>I | 123 | S | CK1 | YLDAANMSMRVRRHS | 0.1833 | 0.0996 |
| rs8192466-T>I | 130 | S | CK1 | SMRVRRHSDPARRGE | 0.1758 | 0.0996 |
| rs8192466-T>I | 145 | S | CK1 | LSVCDSISEWVTAAD | 0.116 | 0.0996 |

**5. Mutant rs8192466-T>N**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Position** | **Residue (Code)** | **Kinase** | **Motif (PSP)** | **Score** | **Cutoff** |
| rs8192466T>N | 130 | S | AGC | SMRVRRHSDPARRGE | 0.1345 | 0.0197 |
| rs8192466T>N | 39 | T | CK1 | LAYPGVRTHGTLESV | 0.2032 | 0.0532 |
| rs8192466T>N | 123 | S | CK1 | YLDAANMSMRVRRHS | 0.1833 | 0.0532 |
| rs8192466T>N | 130 | S | CK1 | SMRVRRHSDPARRGE | 0.1758 | 0.0532 |
| rs8192466T>N | 145 | S | CK1 | LSVCDSISEWVTAAD | 0.116 | 0.0532 |
| rs8192466T>N | 192 | T | CK1 | KCNPMGYTKEGCRGI | 0.0872 | 0.0532 |
| rs8192466T>N | 206 | S | CK1 | IDKRHWNSQCRTTQS | 0.0553 | 0.0532 |
| rs8192466T>N | 213 | S | CK1 | SQCRTTQSYVRALTM | 0.0727 | 0.0532 |
| rs8192466T>N | 222 | S | CK1 | VRALTMDSKKRIGWR | 0.0726 | 0.0532 |
| rs8192466T>N | 34 | Y | TK | RGQGGLAYPGVRTHG | 0.839 | 0.7641 |
| rs8192466T>N | 90 | Y | TK | NNKDADLYTSRVMLS | 0.8788 | 0.7641 |
| rs8192466T>N | 116 | Y | TK | LLEEYKNYLDAANMS | 0.8758 | 0.7641 |
| rs8192466T>N | 163 | T | CMGC | AVDMSGGTVTVLEKV | 0.0566 | 0.0403 |
| rs8192466T>N | 173 | S | CMGC | VLEKVPVSKGQLKQY | 0.041 | 0.0403 |
| rs8192466T>N | 214 | Y | TK | QCRTTQSYVRALTMD | 0.8333 | 0.7641 |

**CONCLUSION:**

The predicted phosphorylation sites at positions 39 (Threonine), 123 (Serine), 130 (Serine), and 145 (Serine) are conserved across the wild-type and mutant protein sequences (**rs6265, rs1048218, and rs8192466-T>I**).

* The mutations introduced by **rs6265, rs1048218, and rs8192466-T>** did not alter any predicted phosphorylation sites or disrupt the corresponding kinase recognition motif.
* This suggests that the post-translational regulation of the protein at these sites is likely maintained in these mutants, and the structural integrity required for kinase-mediated phosphorylation is preserved.

In another case, the **rs8192466-T>N** mutant exhibited multiple additional predicted phosphorylation sites, including new Serine, Threonine, and Tyrosine residues targeted by CK1, CMGC, and Tyrosine Kinases (TK).

* These newly predicted sites suggest that the mutation introduced by **rs8192466-T>N** may create novel kinase recognition motifs.
* This could potentially alter the protein’s post-translational regulation of protein, potentially influencing its stability, activity, and interactions within cellular signalling pathways.