**Supplementary table 4: Pathway analysis of concordantly hypermethylated DMCs in AML subtypes.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Term Name | Binomial FDR  Q-Val | Binomial Fold Enrichment | Binomial Observed Region Hits | Hypergeometric  FDR Q-Val | Hypergeometric  Fold Enrichment | Hypergeometric Observed Gene Hits | Hypergeometric  Total Genes |
| Cadherin signaling pathway | 2.56E-52 | 4.12 | 181 | 5.85E-06 | 2.27 | 44 | 124 |
| Wnt signaling pathway | 6.68E-40 | 2.72 | 243 | 0.0005 | 1.67 | 69 | 264 |
| Notch signaling pathway | 5.03E-13 | 3.93 | 46 | 0.04 | 2.42 | 14 | 37 |