**Table S5: Gene ontology and pathway analysis of prakriti methylated genes.**

| **Prakriti/Cluster/Category and Term** | **Count** | **%** | **P-Value** | **Fold Enrichment** |
|---|---|---|---|---|
| **Kapha Prakriti** | | | | |
| **Annotation Cluster 1:Enrichment Score: 1.83; Biological Process** | | | | |
| GO:0046907~intracellular transport | 5 | 25.00 | 9.78E-03 | 5.41 |
| GO:0006913~nucleocytoplasmic transport | 3 | 15.00 | 1.79E-02 | 13.69 |
| GO:0051169~nuclear transport | 3 | 15.00 | 1.83E-02 | 13.51 |
| **Annotation Cluster 2:Enrichment Score: 1.65; Biological Process** | | | | |
| GO:0006605~protein targeting | 4 | 20.00 | 2.71E-03 | 13.25 |
| GO:0046907~intracellular transport | 5 | 25.00 | 9.78E-03 | 5.42 |
| GO:0006886~intracellular protein transport | 4 | 20.00 | 1.26E-02 | 7.61 |
| GO:0034613~cellular protein localization | 4 | 20.00 | 1.62E-02 | 6.93 |
| GO:0070727~cellular macromolecule localization | 4 | 20.00 | 1.65E-02 | 6.88 |
| GO:0015031~protein transport | 4 | 20.00 | 7.73E-02 | 3.74 |
| GO:0045184~establishment of protein localization | 4 | 20.00 | 7.90E-02 | 3.70 |
| GO:0008104~protein localization | 4 | 20.00 | 1.09E-01 | 3.23 |
| **Annotation Cluster 3:Enrichment Score: 1.07; Cellular Component** | | | | |
| GO:0044427~chromosomal part | 3 | 15.00 | 5.70E-02 | 7.10 |
| GO:0005694~chromosome | 3 | 15.00 | 7.76E-02 | 5.95 |
| GO:0043228~non-membrane-bounded organelle | 6 | 30.00 | 1.04E-01 | 2.11 |
| GO:0043232~intracellular non-membrane-bounded organelle | 6 | 30.00 | 1.04E-01 | 2.11 |
| **Annotation Cluster 4: Enrichment Score: 0.87; Cellular Component** | | | | |
| GO:0005578~proteinaceous extracellular matrix | 3 | 15.00 | 4.06E-02 | 8.56 |
| GO:0031012~extracellular matrix | 3 | 15.00 | 4.66E-02 | 7.94 |
| GO:0044421~extracellular region part | 3 | 15.00 | 2.55E-01 | 2.85 |
| GO:0005576~extracellular region | 3 | 15.00 | 6.30E-01 | 1.36 |
| Annotation Cluster 5: Enrichment Score: 0.84; Cellular Component | | | | |
| GO:0016337~cell-cell adhesion | 3 | 15.00 | 5.12E-02 | 7.74 |
| GO:0007155~cell adhesion | 3 | 15.00 | 2.38E-01 | 3.05 |
| GO:0022610~biological adhesion | 3 | 15.00 | 2.39E-01 | 3.05 |
| **Pitta Prakriti** | | | | |
| **Annotation Cluster 1: Enrichment Score: 3.09; Cellular Component** | | | | |
| GO:0044459~plasma membrane part | 49 | 21.49 | 4.46E-06 | 1.91 |
| GO:0031226~intrinsic to plasma membrane | 25 | 10.96 | 6.47E-03 | 1.77 |

| **Prakriti/Cluster/Category and Term** | **Count** | **%** | **P-Value** | **Fold Enrichment** |
|---|---|---|---|---|
| GO:0005887~integral to plasma membrane | 23 | 10.09 | 1.83E-02 | 1.66 |
| **Annotation Cluster 2: Enrichment Score: 2.44; Biological Process** | | | | |
| GO:0030182~neuron differentiation | 19 | 8.33 | 9.28E-06 | 3.45 |
| GO:0048666~neuron development | 15 | 6.58 | 9.07E-05 | 3.52 |
| GO:0000904~cell morphogenesis involved in differentiation | 11 | 4.82 | 9.80E-04 | 3.59 |
| GO:0000902~cell morphogenesis | 13 | 5.70 | 1.72E-03 | 2.91 |
| GO:0030030~cell projection organization | 13 | 5.70 | 2.27E-03 | 2.81 |
| GO:0032989~cellular component morphogenesis | 13 | 5.70 | 4.19E-03 | 2.61 |
| GO:0007409~axonogenesis | 8 | 3.51 | 1.07E-02 | 3.30 |
| GO:0048858~cell projection morphogenesis | 9 | 3.95 | 1.19E-02 | 2.92 |
| GO:0032990~cell part morphogenesis | 9 | 3.95 | 1.52E-02 | 2.80 |
| GO:0031175~neuron projection development | 9 | 3.95 | 1.52E-02 | 2.80 |
| GO:0048667~cell morphogenesis involved in neuron differentiation | 8 | 3.51 | 1.60E-02 | 3.05 |
| GO:0048812~neuron projection morphogenesis | 8 | 3.51 | 1.76E-02 | 2.99 |
| GO:0007411~axon guidance | 4 | 1.75 | 1.50E-01 | 2.97 |
| **Annotation Cluster 3: Enrichment Score: 2.15; Biological Process** | | | | |
| GO:0021537~telencephalon development | 6 | 2.63 | 1.29E-03 | 7.35 |
| GO:0030900~forebrain development | 8 | 3.51 | 2.98E-03 | 4.19 |
| GO:0021761~limbic system development | 4 | 1.75 | 7.28E-03 | 9.95 |
| GO:0021543~pallium development | 4 | 1.75 | 1.96E-02 | 6.92 |
| GO:0021766~hippocampus development | 3 | 1.32 | 3.04E-02 | 10.85 |
| **Annotation Cluster 4: Enrichment Score: 1.78; Molecular Function** | | | | |
| GO:0046872~metal ion binding | 70 | 30.70 | 4.38E-03 | 1.32 |
| GO:0043167~ion binding | 71 | 31.14 | 5.21E-03 | 1.31 |
| GO:0043169~cation binding | 70 | 30.70 | 5.61E-03 | 1.31 |
| GO:0008270~zinc ion binding | 38 | 16.67 | 7.50E-02 | 1.29 |
| GO:0046914~transition metal ion binding | 43 | 18.86 | 1.23E-01 | 1.21 |
| **Annotation Cluster 5: Enrichment Score: 1.57; Biological process** | | | | |
| GO:0045665~negative regulation of neuron differentiation | 4 | 1.75 | 7.94E-03 | 9.65 |
| GO:0051960~regulation of nervous system development | 8 | 3.51 | 1.04E-02 | 3.32 |
| GO:0060284~regulation of cell development | 8 | 3.51 | 1.45E-02 | 3.11 |
| GO:0050767~regulation of neurogenesis | 7 | 3.07 | 1.79E-02 | 3.36 |
| GO:0045596~negative regulation of cell differentiation | 7 | 3.07 | 5.40E-02 | 2.58 |
| GO:0045664~regulation of neuron differentiation | 5 | 2.19 | 8.53E-02 | 2.99 |

| **Prakriti/Cluster/Category and Term** | **Count** | **%** | **P-Value** | **Fold Enrichment** |
|---|---|---|---|---|
| GO:0045165~cell fate commitment | 5 | 2.19 | 9.65E-02 | 2.86 |
| **Annotation Cluster 6: Enrichment Score: 1.38; KEGG_Pathway** | | | | |
| hsa04660:T cell receptor signaling pathway | 7 | 3.07 | 1.20E-03 | 5.68 |
| hsa04662:B cell receptor signaling pathway | 5 | 2.19 | 9.56E-03 | 5.84 |
| hsa04650:Natural killer cell mediated cytotoxicity | 5 | 2.19 | 6.09E-02 | 3.30 |
| hsa04722:Neurotrophin signaling pathway | 4 | 1.75 | 1.61E-01 | 2.83 |
| hsa04370:VEGF signaling pathway | 3 | 1.32 | 2.05E-01 | 3.51 |
| hsa04664:Fc epsilon RI signaling pathway | 3 | 1.32 | 2.17E-01 | 3.37 |
| Annotation Cluster 7:Enrichment Score: 1.37; Molecular function | | | | |
| GO:0003700~transcription factor activity | 24 | 10.53 | 2.88E-03 | 1.93 |
| GO:0030528~transcription regulator activity | 29 | 12.72 | 2.58E-02 | 1.50 |
| GO:0003677~DNA binding | 40 | 17.54 | 3.83E-02 | 1.34 |
| GO:0043565~sequence-specific DNA binding | 14 | 6.14 | 4.57E-02 | 1.80 |
| GO:0006350~transcription | 35 | 15.35 | 6.41E-02 | 1.33 |
| GO:0006355~regulation of transcription, DNA-dependent | 30 | 13.16 | 7.63E-02 | 1.35 |
| GO:0051252~regulation of RNA metabolic process | 30 | 13.16 | 9.47E-02 | 1.32 |
| GO:0045449~regulation of transcription | 39 | 17.11 | 1.62E-01 | 1.19 |
| **Vata Prakriti** | | | | |
| **Annotation Cluster 1:Enrichment Score: 2.57; Molecular Function** | | | | |
| GO:0043565~sequence-specific DNA binding | 17 | 11.64 | 4.45E-05 | 3.31 |
| GO:0003700~transcription factor activity | 21 | 14.38 | 1.57E-04 | 2.54 |
| GO:0003677~DNA binding | 35 | 23.97 | 5.37E-04 | 1.77 |
| GO:0006355~regulation of transcription, DNA-dependent | 27 | 18.49 | 3.41E-03 | 1.78 |
| GO:0051252~regulation of RNA metabolic process | 27 | 18.49 | 4.61E-03 | 1.74 |
| GO:0030528~transcription regulator activity | 23 | 15.75 | 6.77E-03 | 1.80 |
| GO:0006357~regulation of transcription from RNA polymerase II promoter | 13 | 8.90 | 2.06E-02 | 2.09 |
| GO:0045449~regulation of transcription | 32 | 21.92 | 2.65E-02 | 1.43 |
| GO:0006350~transcription | 27 | 18.49 | 2.83E-02 | 1.50 |
| **Annotation Cluster 2:Enrichment Score: 1.44; Biological Process** | | | | |
| GO:0031571~G1 DNA damage checkpoint | 3 | 2.05 | 3.75E-03 | 31.81 |
| GO:0007093~mitotic cell cycle checkpoint | 4 | 2.74 | 5.77E-03 | 10.85 |
| GO:0031575~G1/S transition checkpoint | 3 | 2.05 | 8.96E-03 | 20.58 |
| GO:0007346~regulation of mitotic cell cycle | 5 | 3.42 | 4.06E-02 | 3.84 |
| GO:0000075~cell cycle checkpoint | 4 | 2.74 | 4.24E-02 | 5.13 |
| GO:0000077~DNA damage checkpoint | 3 | 2.05 | 6.27E-02 | 7.29 |
| GO:0031570~DNA integrity checkpoint | 3 | 2.05 | 7.22E-02 | 6.73 |

| Prakriti/Cluster/Category and Term | Count | % | P-Value | Fold Enrichment |
|---|---|---|---|---|
| GO:0006974~response to DNA damage stimulus | 7 | 4.79 | 9.83E-02 | 2.19 |
| GO:0042770~DNA damage response, signal transduction | 3 | 2.05 | 1.48E-01 | 4.37 |
| GO:0051726~regulation of cell cycle | 6 | 4.11 | 1.51E-01 | 2.11 |
| **Annotation Cluster 3:Enrichment Score 1.40 Cellular component and KEGG Pathway** | | | | |
| GO:0005891~voltage-gated calcium channel complex | 3 | 2.05 | 1.19E-02 | 17.79 |
| GO:0034704~calcium channel complex | 3 | 2.05 | 1.77E-02 | 14.49 |
| GO:0034702~ion channel complex | 5 | 3.42 | 7.05E-02 | 3.18 |
| hsa04010:MAPK signaling pathway | 6 | 4.11 | 7.87E-02 | 2.54 |
| GO:0034703~cation channel complex | 4 | 2.74 | 7.90E-02 | 3.95 |
| **Annotation Cluster 4:Enrichment Score: 1.37; Cellular component** | | | | |
| GO:0030182~neuron differentiation | 13 | 8.90 | 3.45E-04 | 3.46 |
| GO:0048666~neuron development | 9 | 6.16 | 8.32E-03 | 3.10 |
| GO:0046658~anchored to plasma membrane | 3 | 2.05 | 1.19E-02 | 17.79 |
| GO:0007409~axonogenesis | 6 | 4.11 | 2.44E-02 | 3.63 |
| GO:0000902~cell morphogenesis | 8 | 5.48 | 3.22E-02 | 2.62 |
| GO:0048667~cell morphogenesis involved in neuron differentiation | 6 | 4.11 | 3.29E-02 | 3.35 |
| GO:0048812~neuron projection morphogenesis | 6 | 4.11 | 3.52E-02 | 3.29 |
| GO:0051301~cell division | 7 | 4.79 | 4.00E-02 | 2.77 |
| GO:0032989~cellular component morphogenesis | 8 | 5.48 | 5.26E-02 | 2.35 |
| GO:0000904~cell morphogenesis involved in differentiation | 6 | 4.11 | 5.71E-02 | 2.87 |
| GO:0048858~cell projection morphogenesis | 6 | 4.11 | 5.79E-02 | 2.86 |
| GO:0007163~establishment or maintenance of cell polarity | 3 | 2.05 | 6.51E-02 | 7.14 |
| GO:0032990~cell part morphogenesis | 6 | 4.11 | 6.73E-02 | 2.73 |
| GO:0031175~neuron projection development | 6 | 4.11 | 6.73E-02 | 2.73 |
| GO:0048729~tissue morphogenesis | 5 | 3.42 | 6.74E-02 | 3.24 |
| GO:0030030~cell projection organization | 7 | 4.79 | 9.37E-02 | 2.22 |
| GO:0031225~anchored to membrane | 3 | 2.05 | 5.00E-01 | 1.78 |
| GO:0031226~intrinsic to plasma membrane | 8 | 5.48 | 8.27E-01 | 0.86 |
| **Annotation Cluster 5:Enrichment Score: 1.35; Biological Process** | | | | |
| GO:0006355~regulation of transcription, DNA-dependent | 27 | 18.49 | 3.41E-03 | 1.78 |
| GO:0051252~regulation of RNA metabolic process | 27 | 18.49 | 4.61E-03 | 1.74 |
| GO:0032583~regulation of gene-specific transcription | 6 | 4.11 | 5.69E-03 | 5.22 |
| GO:0045893~positive regulation of transcription, DNA-dependent | 11 | 7.53 | 7.41E-03 | 2.69 |
| GO:0051254~positive regulation of RNA metabolic process | 11 | 7.53 | 7.84E-03 | 2.67 |

| Prakriti/Cluster/Category and Term | Count | % | P-Value | Fold Enrichment |
|---|---|---|---|---|
| GO:0006357~regulation of transcription from RNA polymerase II promoter | 13 | 8.90 | 2.06E-02 | 2.09 |
| GO:0045941~positive regulation of transcription | 11 | 7.53 | 2.18E-02 | 2.27 |
| GO:0035239~tube morphogenesis | 5 | 3.42 | 2.30E-02 | 4.59 |
| GO:0010628~positive regulation of gene expression | 11 | 7.53 | 2.61E-02 | 2.21 |
| GO:0035295~tube development | 6 | 4.11 | 3.96E-02 | 3.18 |
| GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 11 | 7.53 | 3.97E-02 | 2.06 |
| GO:0051173~positive regulation of nitrogen compound metabolic process | 11 | 7.53 | 4.74E-02 | 1.99 |
| GO:0010557~positive regulation of macromolecule biosynthetic process | 11 | 7.53 | 5.16E-02 | 1.96 |
| GO:0031328~positive regulation of cellular biosynthetic process | 11 | 7.53 | 6.63E-02 | 1.87 |
| GO:0009891~positive regulation of biosynthetic process | 11 | 7.53 | 7.15E-02 | 1.85 |
| GO:0010604~positive regulation of macromolecule metabolic process | 12 | 8.22 | 1.12E-01 | 1.63 |
| GO:0043193~positive regulation of gene-specific transcription | 3 | 2.05 | 1.69E-01 | 4.02 |
| GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 6 | 4.11 | 2.08E-01 | 1.89 |