**Table S1: Gene ontology enrichment of methylated-differentially expressed genes related with Alzheimer's disease (Top 10)**

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| Class | Category | Term | Adjusted P-value | Genes |
| HyperLGs | Biological Process | positive regulation of potassium ion transport (GO:0043268) | 0.016 | ANK2;ADRA2A |
|   |   | regulation of steroid metabolic process (GO:0019218) | 0.016 | DGKQ;RORA |
|   |   | regulation of calcium ion transmembrane transporter activity (GO:1901019) | 0.022 | ANK2;ADRA2A |
|   |   | regulation of glucose metabolic process (GO:0010906) | 0.022 | DGKQ;RORA |
|   |   | regulation of potassium ion transport (GO:0043266) | 0.031 | ANK2;ADRA2A |
| Hypo-HGs | Biological Process | positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus (GO:1901522) | 0.003 | CREB3;BMP2 |
|   |   | endocardial cushion development (GO:0003197) | 0.003 | BMP2;GATA4 |
|   |   | mesenchyme development (GO:0060485) | 0.003 | BMP2;GATA4 |
|   |   | anterior/posterior pattern specification (GO:0009952) | 0.006 | BMP2;GATA4 |
|   |   | positive regulation of cytokine production (GO:0001819) | 0.006 | POLR3E;CYBA;GATA4 |
|   |   | regulation of toll-like receptor 2 signaling pathway (GO:0034135) | 0.037 | CYBA |
|   |   | nucleoplasm part (GO:0044451) | 0.088 | POLR3E;GATA4 |
|   |   | nuclear DNA-directed RNA polymerase complex (GO:0055029) | 0.088 | POLR3E |
|   |   | phagocytic vesicle membrane (GO:0030670) | 0.088 | CYBA |