

### Additional file 3

#### 10 CpG sites in 850K BeadChip and replication stage.

Target	Gene Name	Group difference	<i>P</i> value	Methylation type in IS
850K array				
cg08931687	<i>PCDHB16</i>	-0.1711	<i>P</i> =0.0307*	Hypomethylated
cg09150559	<i>PCDHB10</i>	-0.2068	<i>P</i> =0.0390*	Hypomethylated
cg09319843	<i>CDH2</i>	-0.1519	<i>P</i> =0.0438*	Hypomethylated
cg13464915	<i>CDH2</i>	-0.1600	<i>P</i> =0.0357*	Hypomethylated
cg18417245	<i>PCDHB11</i>	-0.1026	<i>P</i> =0.0451*	Hypomethylated
cg16049600	<i>PCDHB11</i>	-0.1999	<i>P</i> =0.0182*	Hypomethylated
cg21522026	<i>PCDHB14</i>	-0.1275	<i>P</i> =0.0059*	Hypomethylated
cg22879458	<i>PCDHB9</i>	-0.1314	<i>P</i> =0.0344*	Hypomethylated
cg24586758	<i>PCDHB3</i>	-0.1300	<i>P</i> =0.0186*	Hypomethylated
cg26866168	<i>PCDHB6</i>	-0.1397	<i>P</i> =0.0470*	Hypomethylated
Replication in 20 paired samples				
cg08931687	<i>PCDHB16</i>	-0.0970	<i>P</i> =0.0280*	Hypomethylated
cg09150559	<i>PCDHB10</i>	-0.1121	<i>P</i> =0.0042*	Hypomethylated
cg09319843	<i>CDH2</i>	-0.0183	<i>P</i> =0.1222	Hypomethylated
cg13464915	<i>CDH2</i>	-0.0244	<i>P</i> =0.0374*	Hypomethylated
cg18417245	<i>PCDHB11</i>	-0.0687	<i>P</i> =0.0683	Hypomethylated
cg16049600	<i>PCDHB11</i>	-0.1226	<i>P</i> =0.0175*	Hypomethylated
cg21522026	<i>PCDHB14</i>	-0.0257	<i>P</i> =0.1509	Hypomethylated
cg22879458	<i>PCDHB9</i>	-0.1043	<i>P</i> =0.0035*	Hypomethylated
cg24586758	<i>PCDHB3</i>	-0.0499	<i>P</i> =0.0570	Hypomethylated
cg26866168	<i>PCDHB6</i>	-0.0556	<i>P</i> =0.0636	Hypomethylated

AS the sample size is small and the samples are matched, we did not correct for confounding factors.

\*Statistically significant difference ( $P < 0.05$ ). *CpG* cytosine phosphate guanine; *IS* ischemic stroke