

Additional file 2. DIFFERENTIALLY EXPRESSION GENES AND THEIR CORRESPONDS CpGsDM BETWEEN MRD+/+ PATIENTS AND MRD-/-

GENE/CpG	FC	METHYLATION STATUS	RELATION TO CpGs ISLAND	p-value	Rho
CDH5	5,7				
cg05410910		Hypermethylated	N_Shelf	0,94	0,022
CNKSR3	5,7				
cg00460149		Hypomethylated		0,0003	-0,85
PROM1	5,7				
cg22867816		Hypomethylated	N_Shelf	0,1	-0,47
CTHRC1	5,5				
cg01224234		Hypomethylated		0,003	-0,76
CDH13	5,4				
cg01935413		Hypermethylated	OpenSea	0,75	-0,09
cg10249243		Hypomethylated			-0,09
CHRNA7	4,5				
cg03222361		Hypermethylated		0,42	0,24
NPDC1	4,4				
cg14190761		Hypomethylated	Island	0,003	-0,74
DAPK1	3,9				
cg08719486		Hypomethylated	N_Shore	0,14	-0,42
cg11518830		Hypomethylated		0,000009	-0,91
RAB31	3,9				
cg16346414		Hypomethylated		0,74	-0,09
SLC45A3	3,9				
cg01455178		Hypomethylated	N_Shore	0,03	-0,59
cg04896348		Hypomethylated		0,04	-0,57
RBFOX2	3,3				
cg07521199		Hypermethylated		0,03	0,86
ITGA6	3,8				
cg13586889		Hypomethylated		0,02	-0,63
cg07592198		Hypomethylated		0,1	-0,46
CXCR4	-1,1				
cg07784959		Hypermethylated	N_Shore	0,09	-0,48
cg23374992		Hypermethylated	N_Shelf	0,3	-0,29
CYTH3	-1,7				
cg08687948		Hypermethylated	S_Shore	0,008	-0,69
CDC42EP2	-2,3				
cg13338240		Hypomethylated		0,002	0,75
TMEM178B	-3,2				
cg23018598		Hypomethylated		0,12	0,45
cg24278165		Hypomethylated	S_Shore	0,26	0,33
INSC	-3,5				
cg01223673		Hypermethylated	N_Shelf	0,07	-0,51
cg19115017		Hypomethylated	OpenSea	0,09	0,68
cg02175489		Hypermethylated		0,05	-0,54
PCDHB9	-3,8				

cg01274907		Hypermethylated	N_Shore	0,25	-0,34
TIFAB	-4,4				
cg09288778		Hypermethylated		0,02	-0,62
cg12738534		Hypermethylated		0,04	-0,55
Whitespaces indicate that no differentially methylated CpGs were identified in this comparison group. MRD, minimal residual disease. FC, fold change. CpGs with the highest inverse correlation and significant p-value are highlighted in bold					