

Table S2. The characteristics of 5 regions selected for DNA bisulfite pyrosequencing

Region	CG name (GRCh37/hg19)	Chromosome (GRCh37/hg19)	Position (GRCh37/hg19)	Region length (bp)	Fast-growing tumors						Slow-growing tumors						MMD (FGT- SGT)
					FGT-1	FGT-2	FGT-3	FGT-4	MMV in FGT	SD (FGT)	SGT-1	SGT-2	SGT-3	SGT-4	MMV in SGT	SD (SGT)	
1	cg06748470	chr1	65467980	38	0.74	0.79	0.95	0.88	0.84	0.09	0.52	0.27	0.41	0.47	0.42	0.11	0.42
	cg09774749		65467991		0.61	0.6	0.79	0.71	0.68	0.09	0.45	0.32	0.4	0.42	0.4	0.06	0.28
	cg15208832		65467997		0.64	0.6	0.83	0.76	0.71	0.1	0.46	0.32	0.38	0.41	0.39	0.06	0.32
	cg00600454		65468017		0.46	0.46	0.63	0.61	0.54	0.09	0.31	0.21	0.31	0.29	0.28	0.05	0.26
2	cg18413218	chr14	77371470	55	0.41	0.56	0.6	0.61	0.54	0.09	0.2	0.16	0.21	0.21	0.19	0.02	0.35
	cg09310348		77371524		0.62	0.61	0.71	0.67	0.66	0.05	0.18	0.16	0.23	0.21	0.2	0.03	0.46
3	cg10121788	chr16	77469583	128	0.5	0.57	0.77	0.65	0.62	0.12	0.15	0.09	0.13	0.11	0.12	0.03	0.5
	cg08249296		77469710		0.57	0.71	0.8	0.77	0.71	0.1	0.03	0.13	0.19	0.42	0.19	0.17	0.52
4	cg18455472	chr17	17311855	12	0.78	0.86	0.8	0.84	0.82	0.04	0.42	0.45	0.35	0.17	0.35	0.12	0.47
	cg14066163		17311866		0.85	0.85	0.85	0.87	0.86	0.01	0.57	0.7	0.54	0.25	0.52	0.19	0.34
5	cg14000730	chr3	171529077	534	0.49	0.43	0.55	0.65	0.53	0.09	0.28	0.22	0.2	0.28	0.24	0.04	0.29
	cg26752773		171529090		0.79	0.69	0.71	0.76	0.74	0.05	0.61	0.22	0.23	0.32	0.34	0.19	0.39
	cg19930657		171529610		0.83	0.81	0.81	0.83	0.82	0.01	0.49	0.23	0.13	0.38	0.31	0.16	0.51

Primarily selected six CpGs are bolded. The remaining CpGs are located in close proximity. MMV - mean methylation value; SD - standard deviation; MMD - mean methylation difference