Tissue/cell line Result average DNA methylation for each CG-dinucleotide																															
HEK293:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Leukocytes:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Hep-G2:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Fibroblast:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
trisomic_fibroblast:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Scale DNA Methylation:	0%		205	6	20%	-	4 05	4 (	)× -	- 61	0%	60%	_	805	6 81	0× ·	- 1	0.0%										_		_	_

Scale DNA Methylation: 0x - 20x | 20x - 40x | 40x - 60x | 60x - 80x | 80x - 1005

## DNA methylation level variation.

The figure shows DNA methylation level variation in amplicon 193 from 5 cell types.

The region has 31 CpG sites and methylation levels are widely different among tissues regardless of the same primer region.

The figure was captured from http://biochem.jacobs-university.de/name21/presentation/amplicon\_summaries/193\_amplicon\_summary.html.