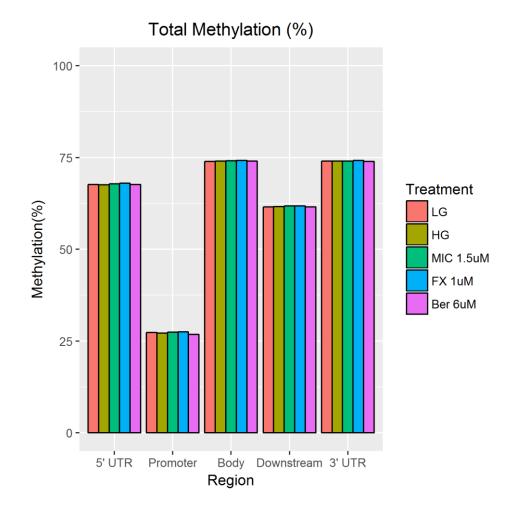
MES13 Methyl-Seq Data Analysis (December 2017 Rerun)

Davit Sargsyan

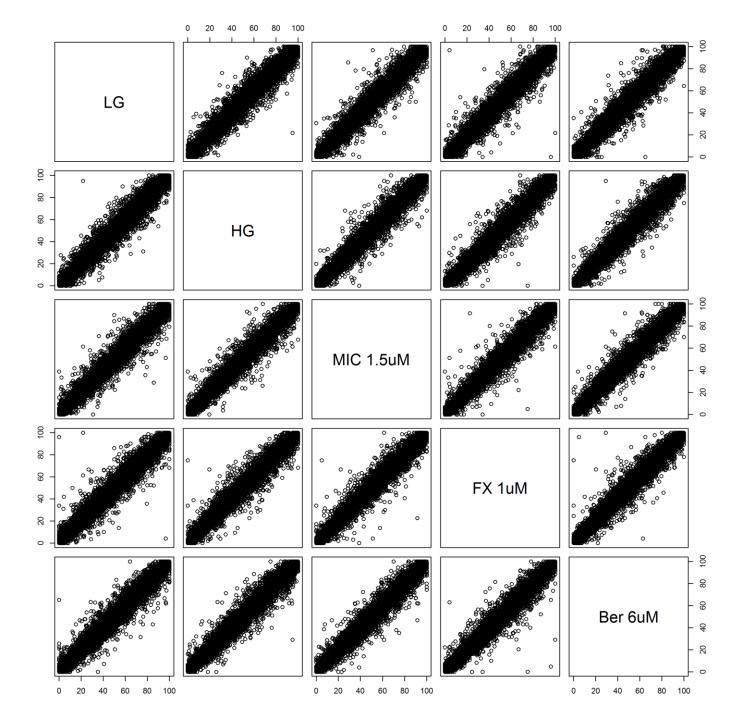
Table1: Average Number of Hits per CpG

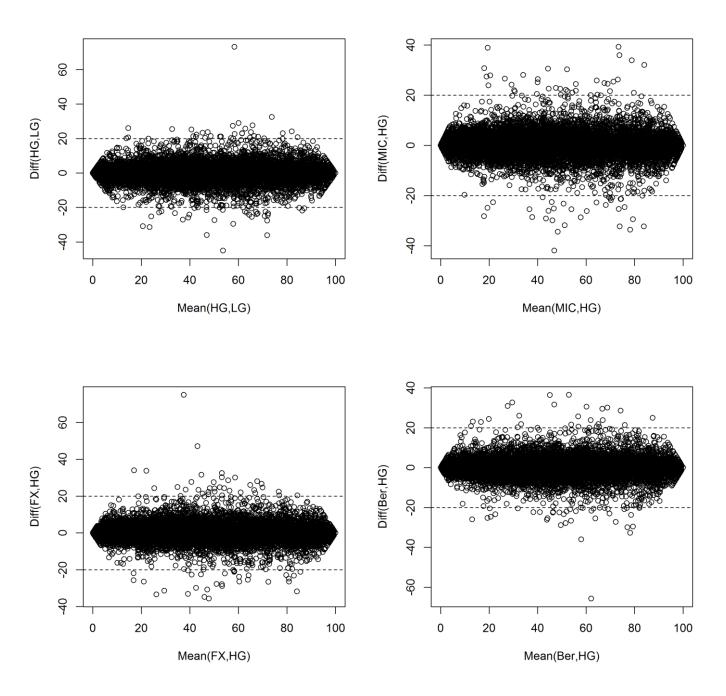
Gene Region	Total CpG Count	LG	HG	MIC 1.5uM	FX 1uM	Ber 6uM
5' UTR	6423	9	9.6	11.1	11	11.6
Promoter	1229957	8.8	9.4	10.8	10.8	11.5
Body	472884	10.5	11.2	13	13.1	13.5
Downstream	489164	10.8	11.5	13.3	13.5	13.9
3' UTR	34952	9.4	10.1	11.8	11.7	12.2

NOTE: much better coverage compared to the previous results with vertical coverage between 0.6 and 4.1 hits/CpG



Sample correspondence: percent methylation in the promoter region between all pairs of treatment. All samples are well correlated, i.e. majority of genes have similar methylation levels in their promoter regions regardless of the treatment.





Methylation differences vs. the means in the promoter regions: no relationship between the differences and the means were observed (unlike microarray data). Majority of the genes were varying within 20% between the treatments (perhaps, we can use 20% as a cutoff).

MES13: Top 20 Genes With Largest Differences in HG vs. LG Promoters MES13: Top 20 Genes With Largest Differences in HG vs. LG Promoters Usp27x -Usp27x -Tmem117 -Tmem117 Tmco5 -Tmco5 -Sytl3 -Sytl3 -Prm1 -Prm1 -Mmp16 -Mmp16 -March2 -March2 -Methylation(%) Methylation Diff(%) Klhl31 -Klhl31 -100 Kcnd1 -Kcnd1 -40 75 lsg20 lsg20 -50 Gpr50 -Gpr50 -Gm5634 -Gm5634 -25 -40 Enho-Enho -0 Cyp4x1 -Cyp4x1 -C1qtnf5 -C1qtnf5 -Btbd17 -Btbd17 -Bace2 -Bace2 -AW551984 -AW551984 -Atp11c -Atp11c -1700015G11Rik -1700015G11Rik -MIC 1.5UM EX JUM BerGuM diff(K,hg) LG HG Treatment Treatment

