# MES13 Methyl-Seq Data Analysis (December 2017 Rerun)

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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
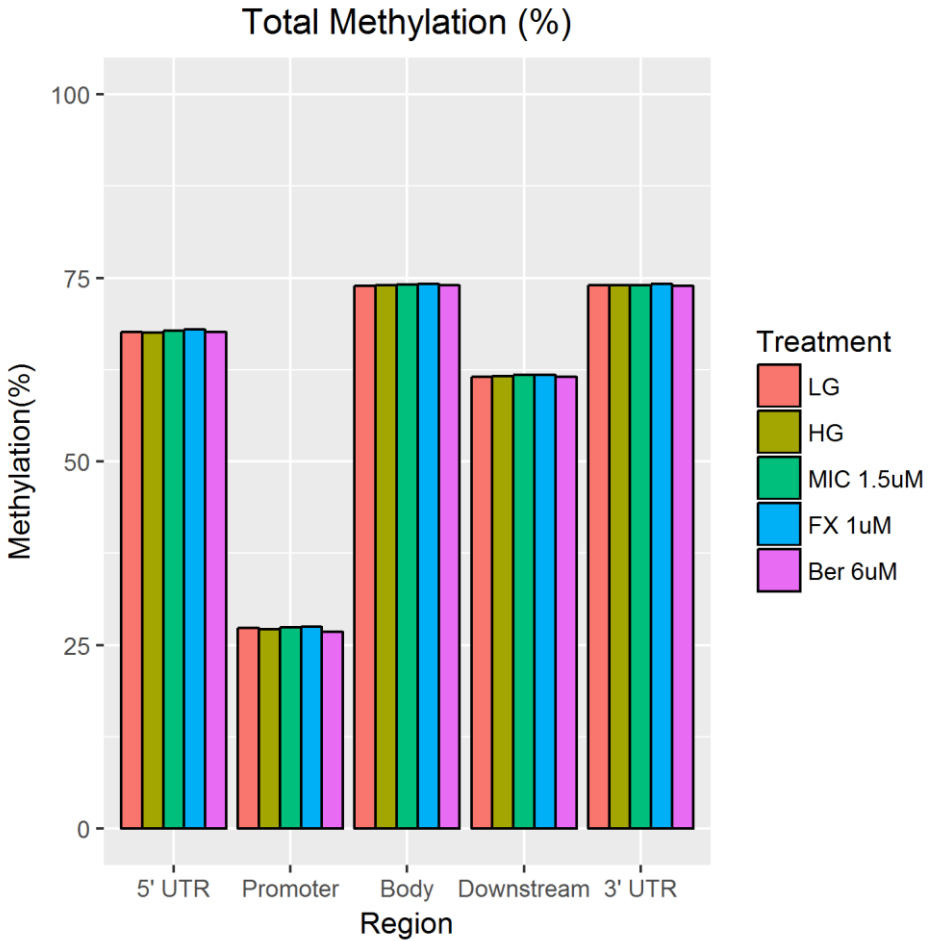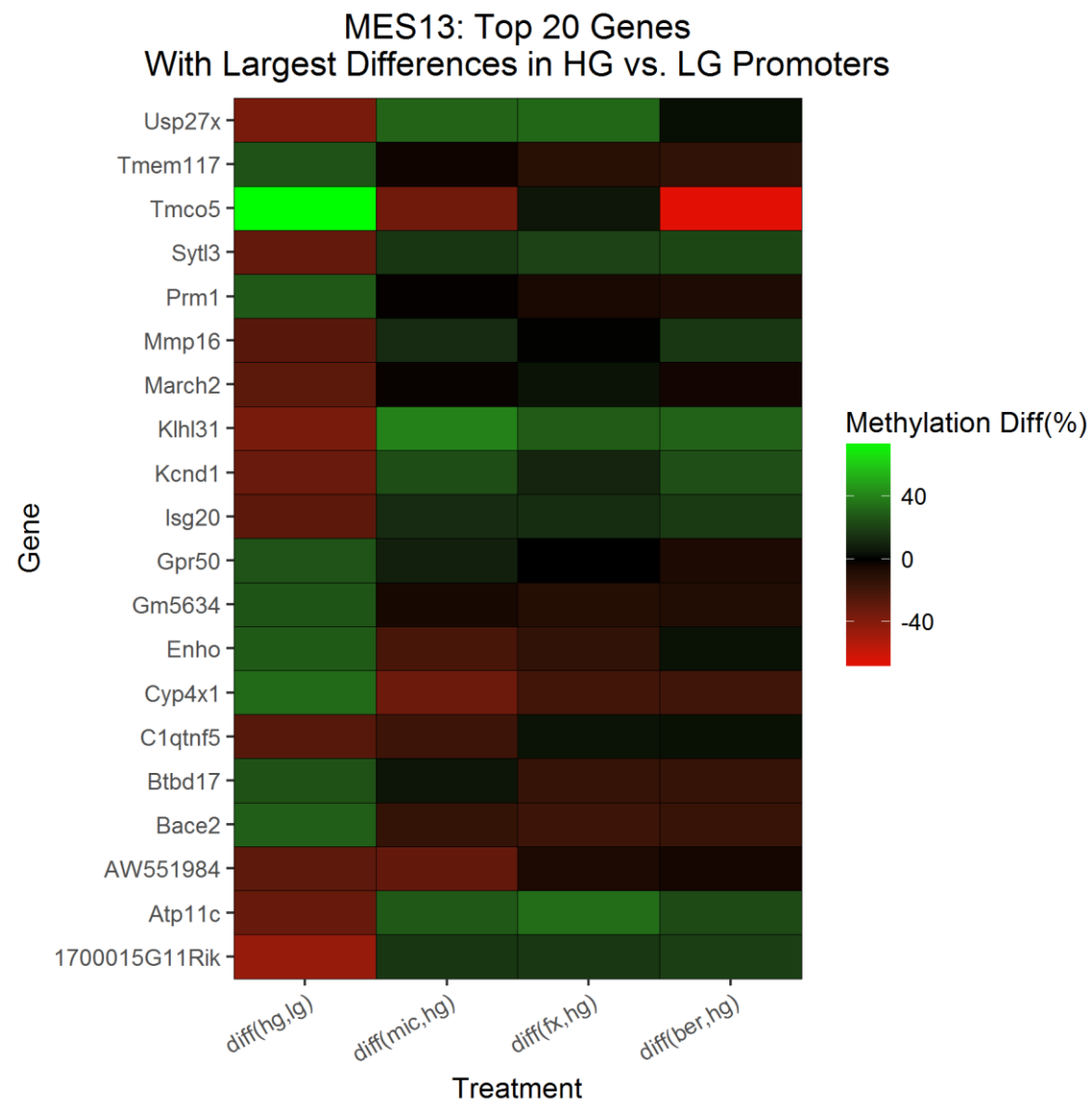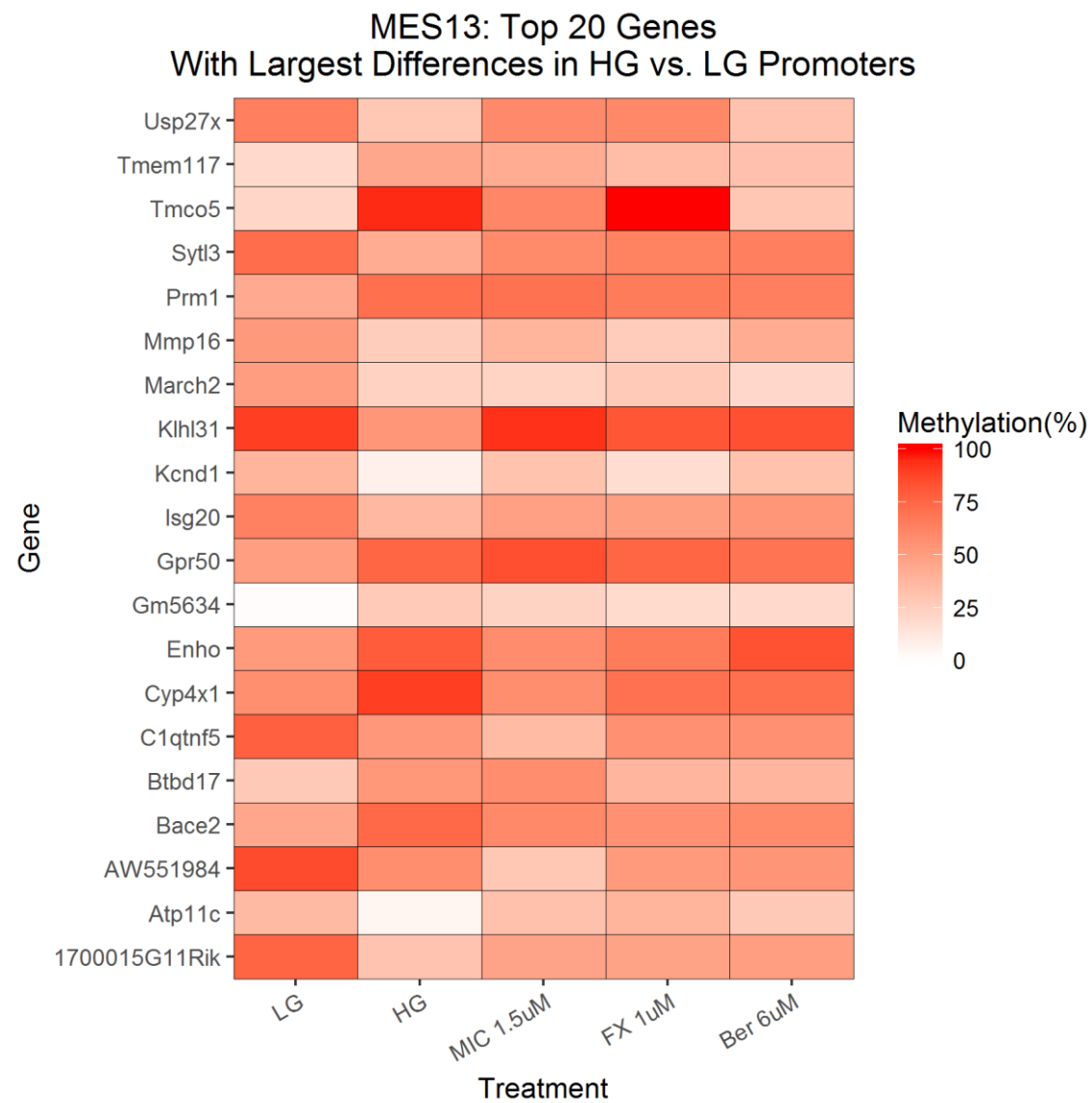
Sample correspondence: percent methylation in the promoter region between all pairs of treatment. All samples are well correlated, i.e. majority of genes have similar methylation levels in their promoter regions regardless of the treatment.
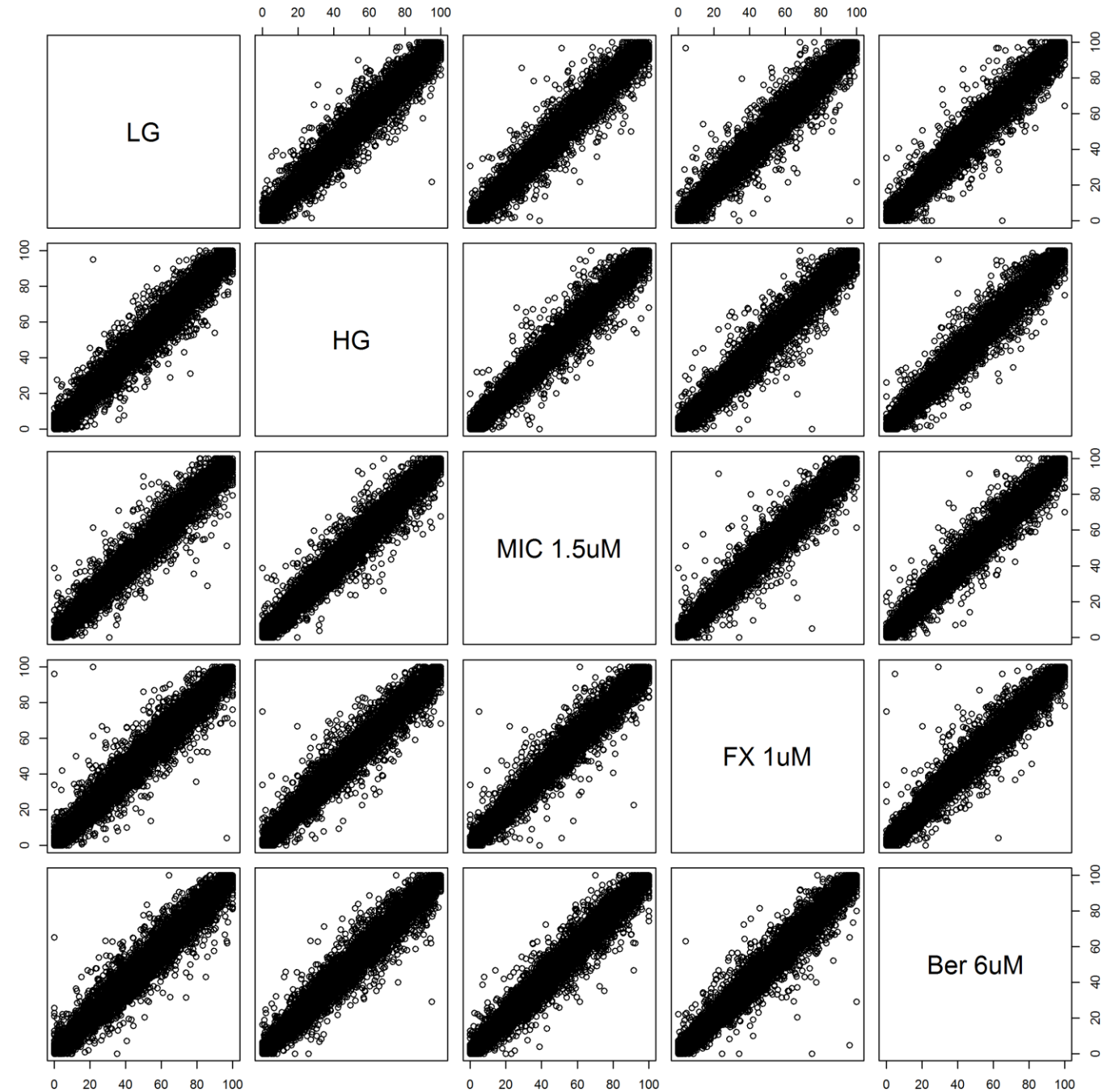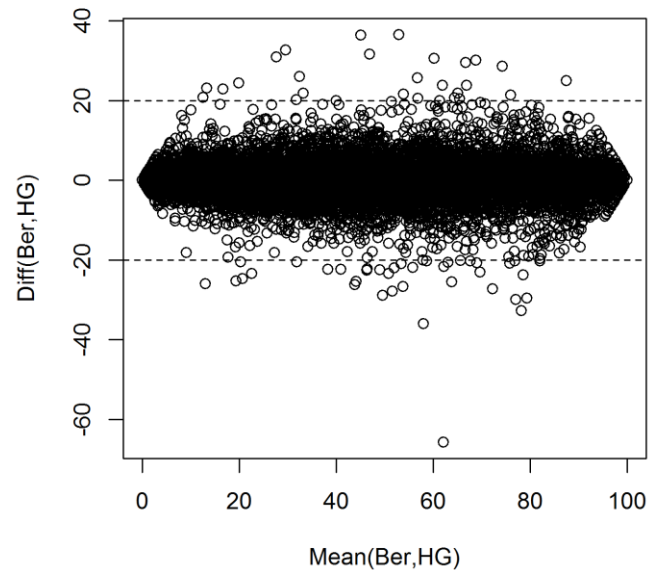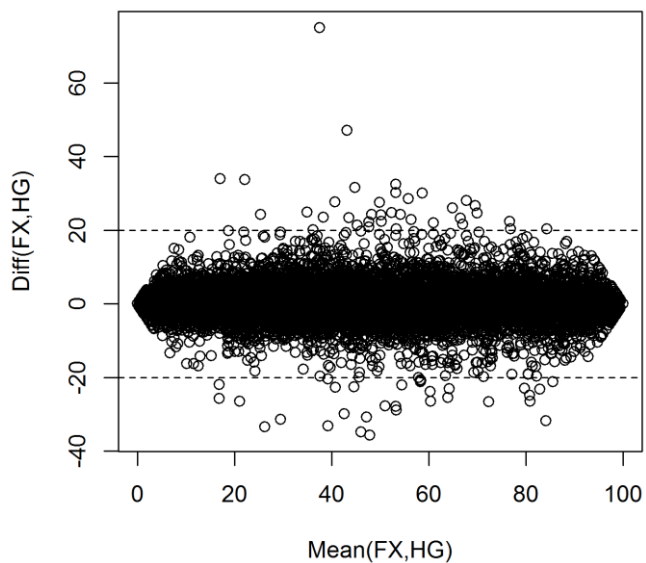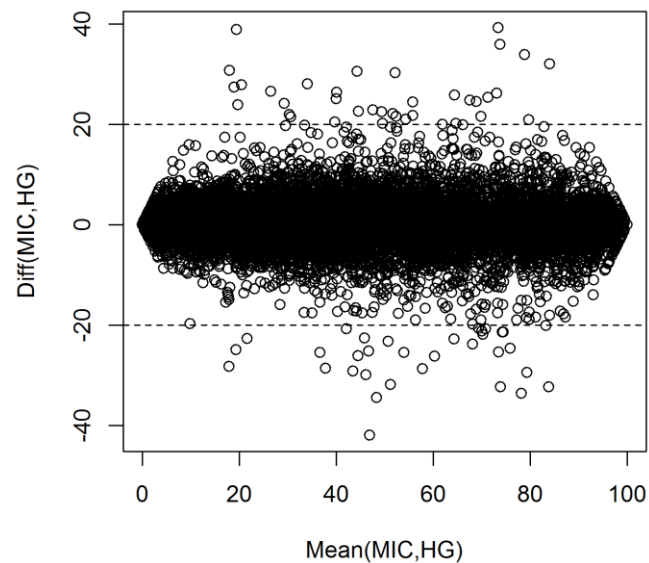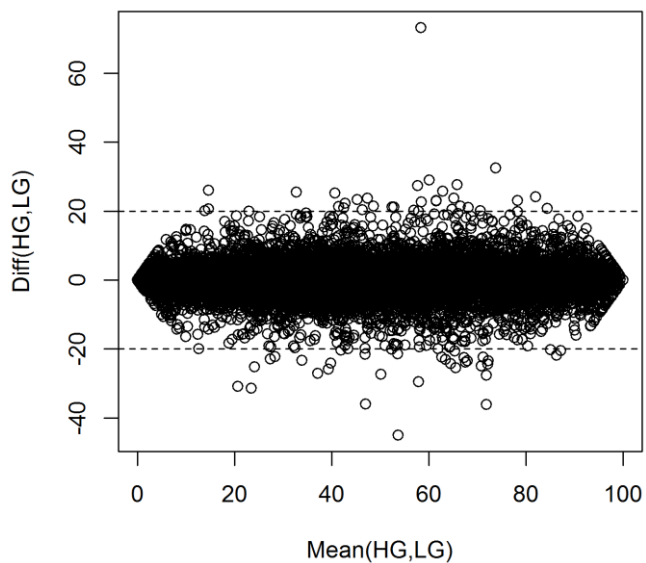
Methylation differences vs. the means in the promoter regions: no relationship between the differences and the means were observed (unlike microarray data). Majority of the genes were varying within 20% between the treatments (perhaps, we can use 20% as a cut-off).

MES13: Top 20 Genes
With Largest Differences in HG vs. LG Promoters

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MES13: Top 40 Genes With Largest Differences in (HG vs. LG) and (MIC vs. HG) Promoters
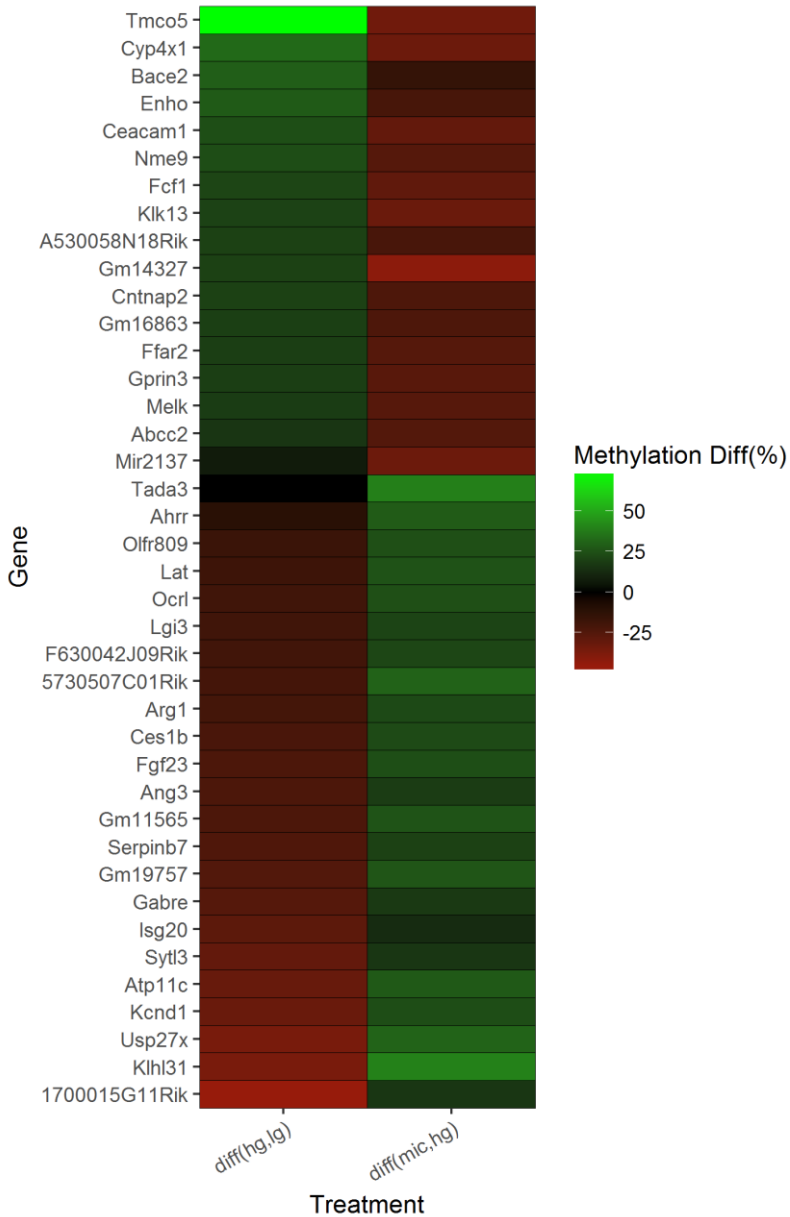
MES13: Top 40 Genes With Largest Differences in (HG vs. LG) and (FX vs. HG) Promoters
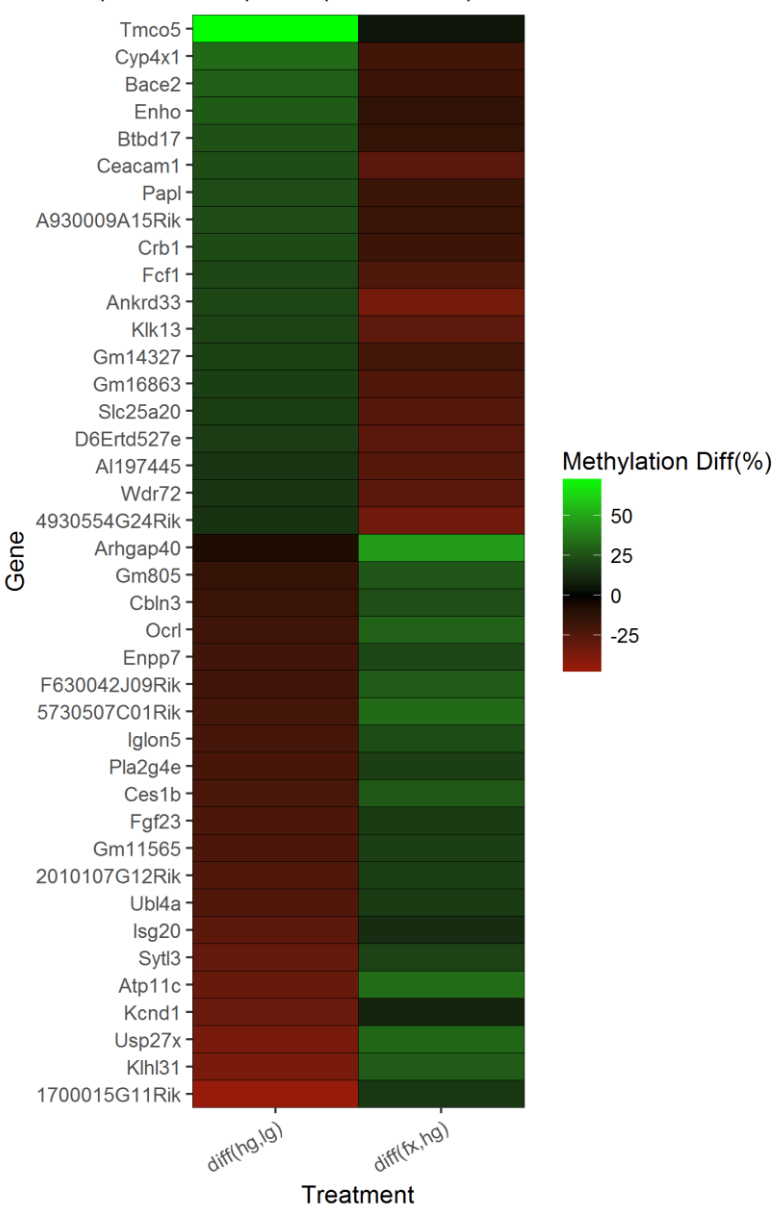
MES13: Top 40 Genes With Largest Differences in (HG vs. LG) and (Ber vs. HG) Promoters