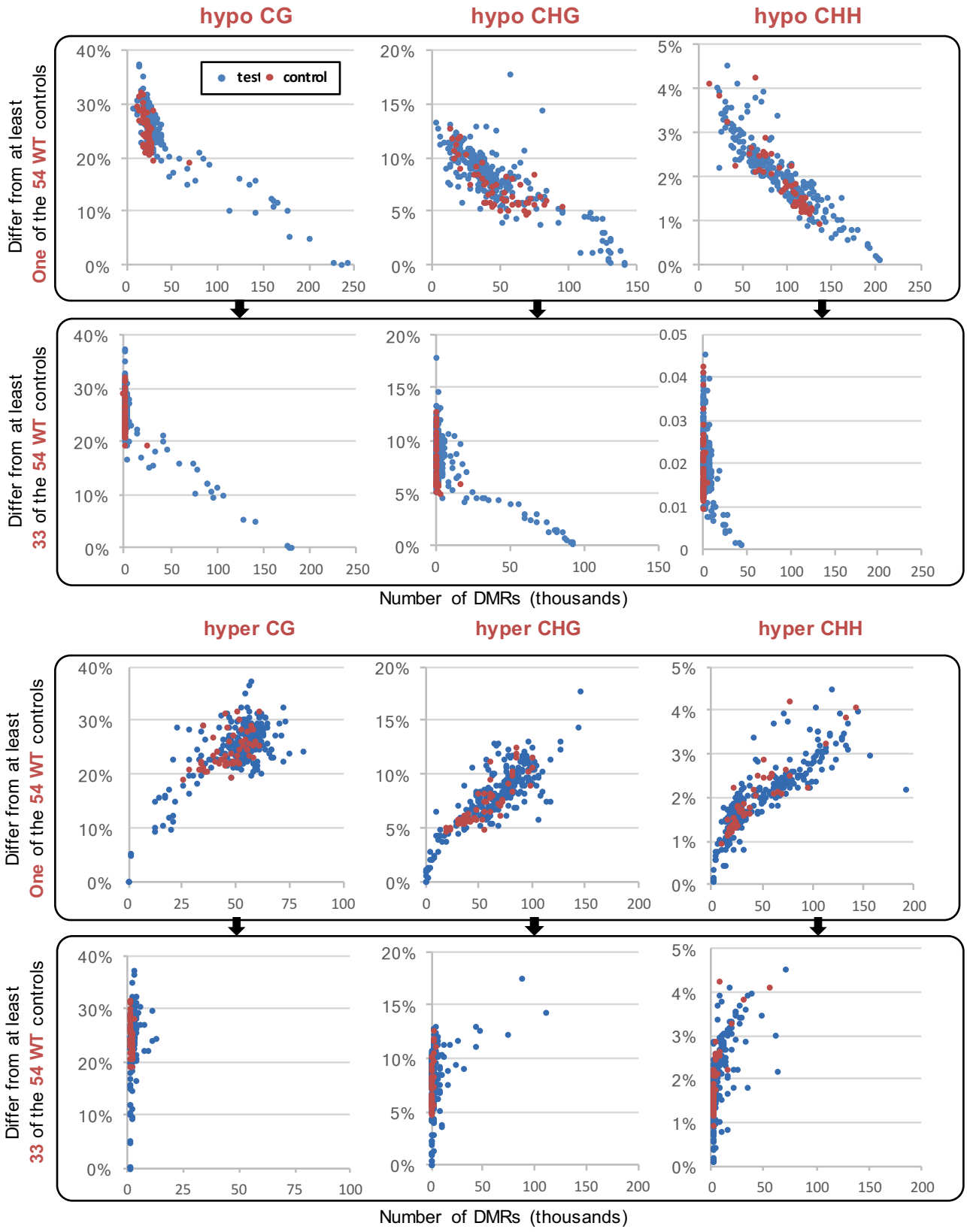


Figure S1. Distribution of the number of DMRs of each control (red dots) and test (blue dots) library compared to all the other control libraries.

The vertical and horizontal axes represent the methylation level of the genome and the number of hypo/hyper-DMRs defined in each library, respectively. The top panel indicates DMRs that have at least one supporting control library, while the bottom panel indicates DMRs that have at least 33 out of 54 supporting control libraries.

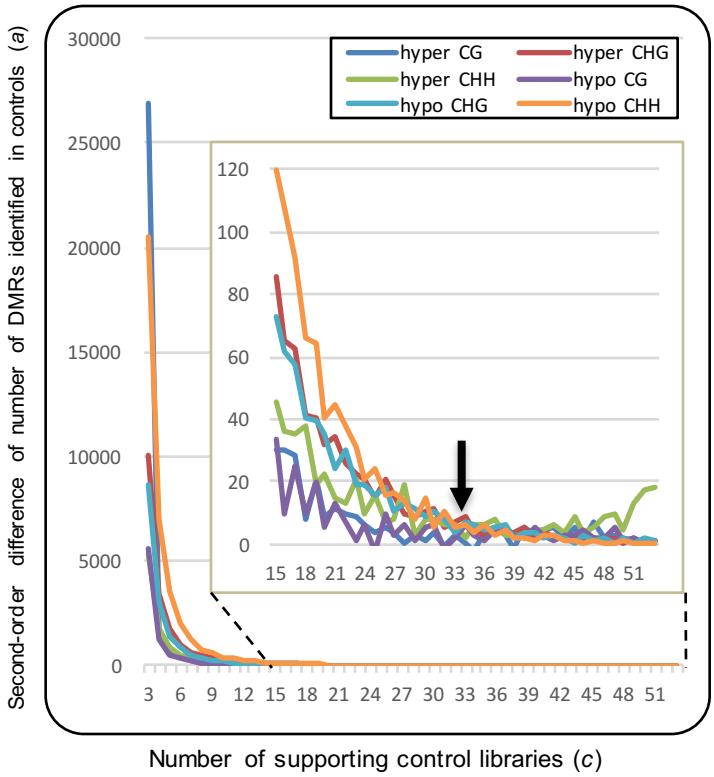


Figure S2. Selection of high-confidence Differentially Methylated Regions.
Correlation between deceleration of number of DMRs identified in control libraries with number of supporting control libraries. The inner plot is the zooming in of subset (c = 15-53) of the whole plot, while the black arrow point the inflexion where the deceleration of number of DMRs becomes flat (c = 33).

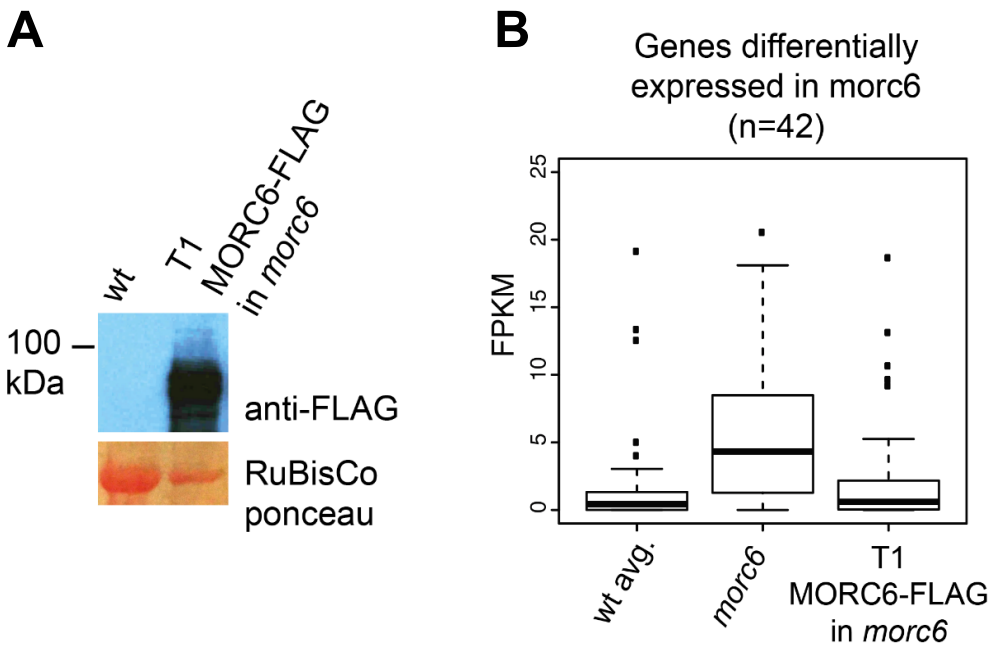


Figure S3. genomic MORC6-FLAG complementation of *morc6.*
A. Western blot of T1 (transgenic generation 1) *gMORC6pro::*gMORC6-9xFLAG tagged line in the *morc6-3* mutant background (genomic construct as described in Moissiard *et al.,* 2012).
B. Boxplot of RNAseq from the T1 MORC6 plant, showing complementation by re-silencing of genes differentially expressed in the *morc6* mutant background.

Figure S4. Hyper-CG

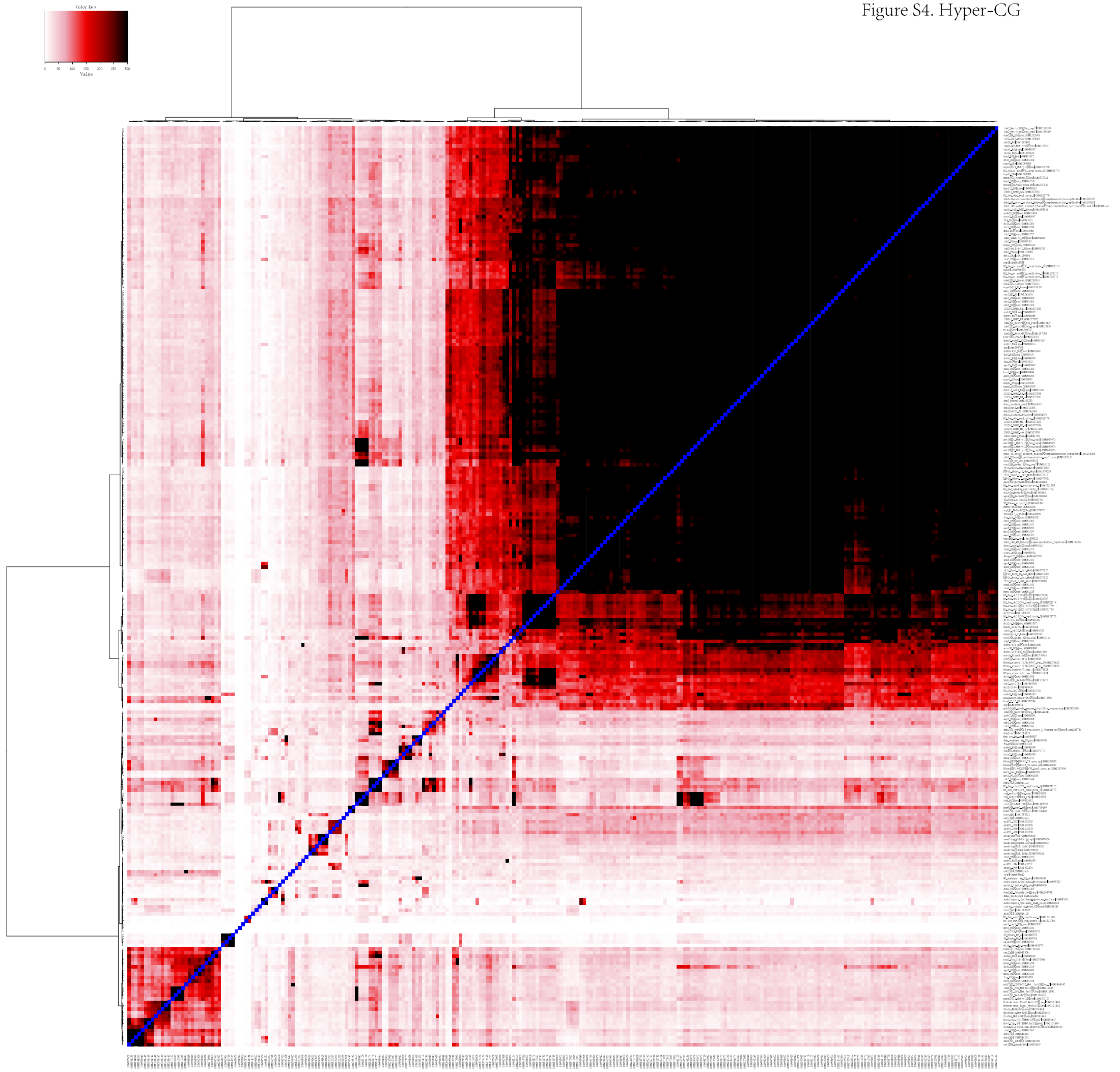


Figure S5. Hyper-CHG

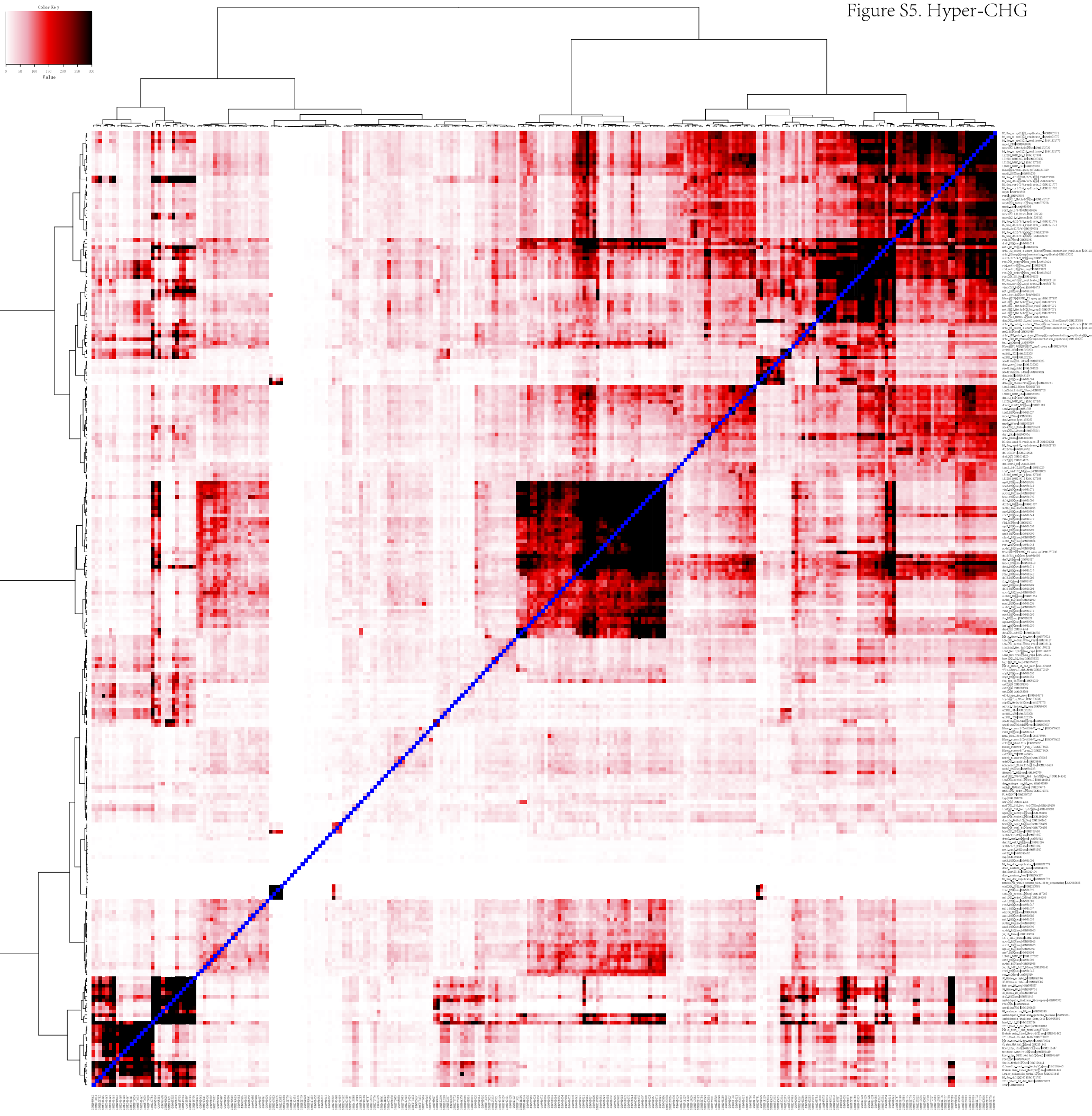


Figure S6. Hyper-CHH

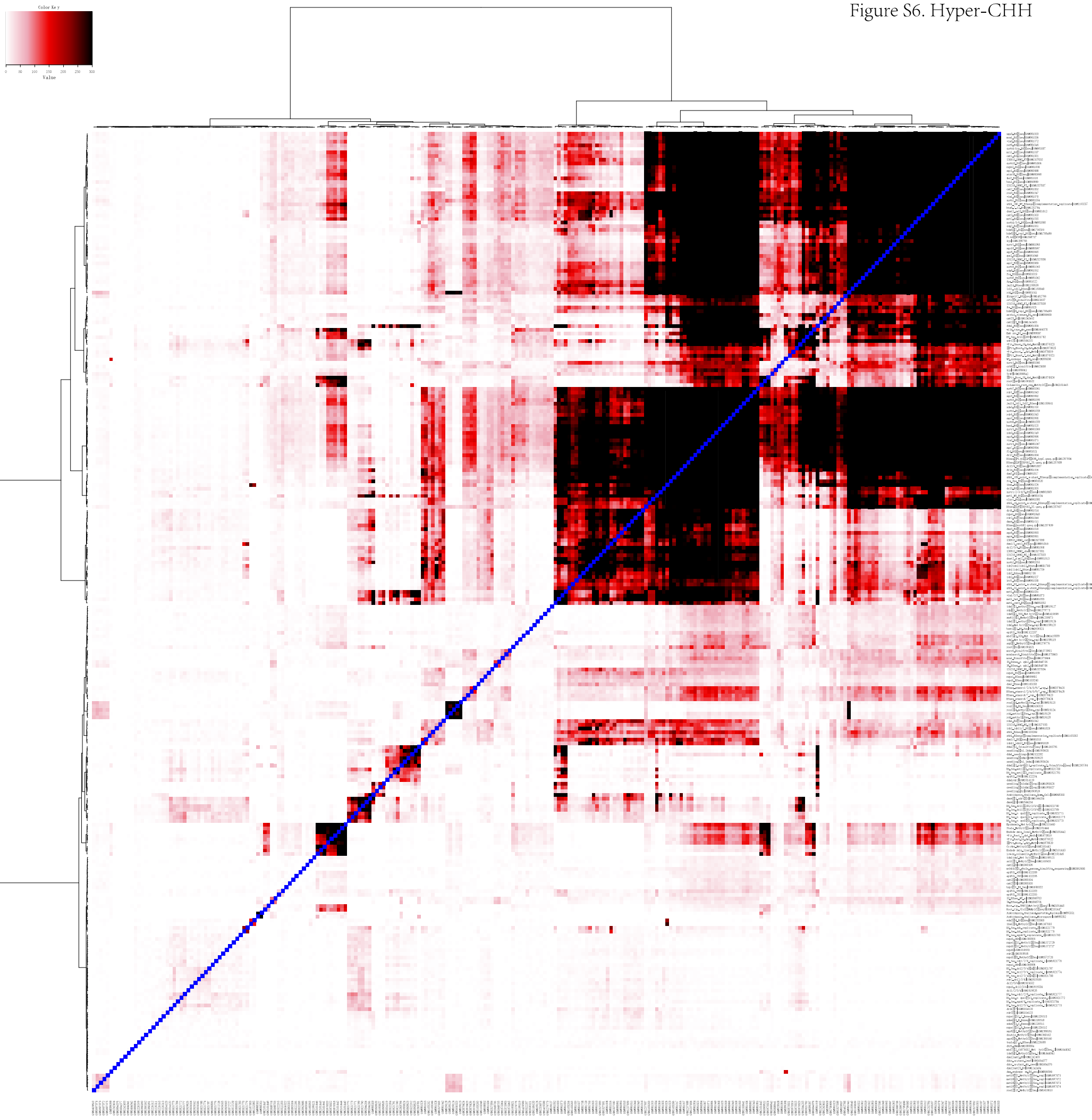


Figure S7. Hypo-CG

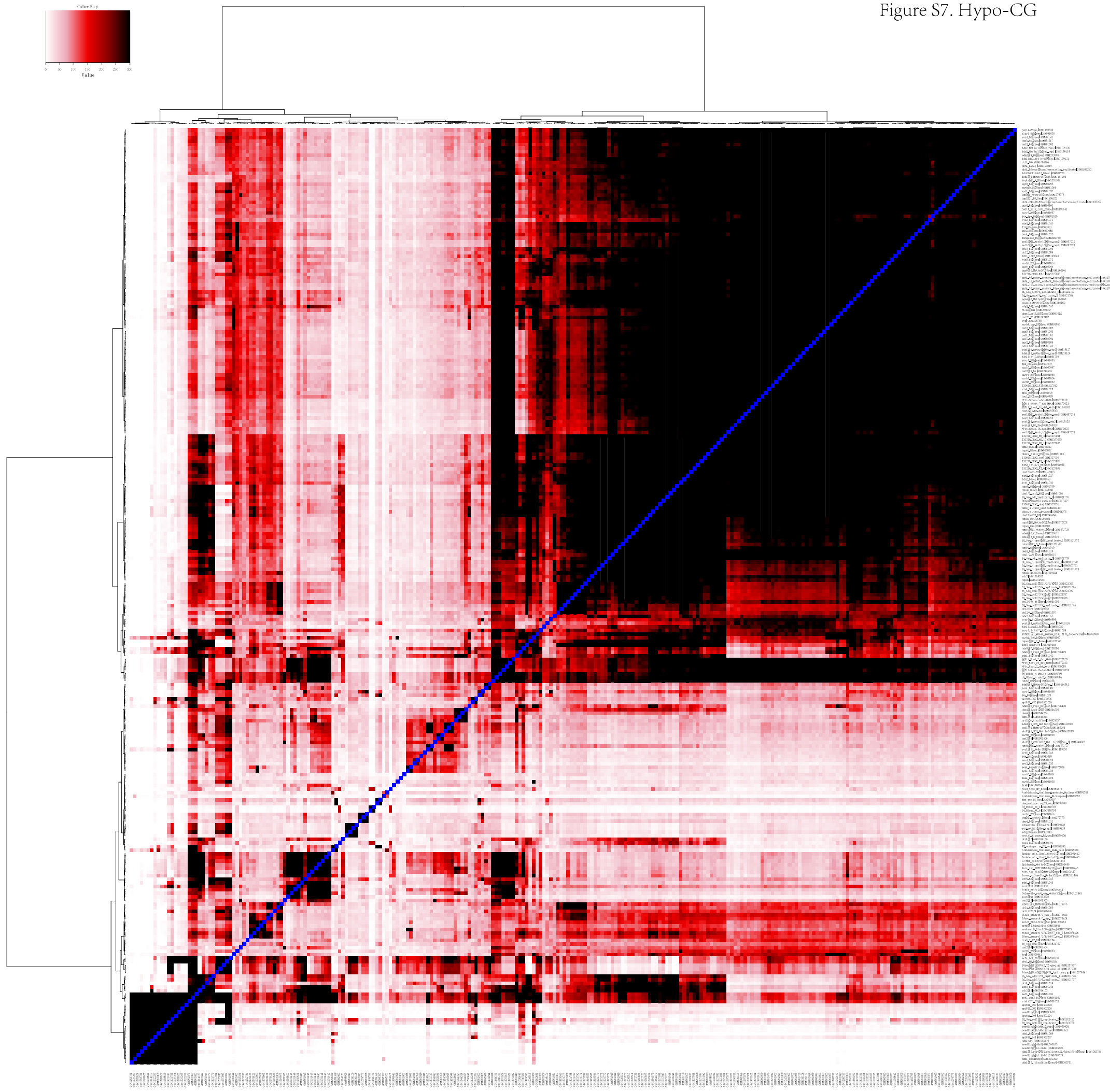


Figure S8. Hypo-CHG

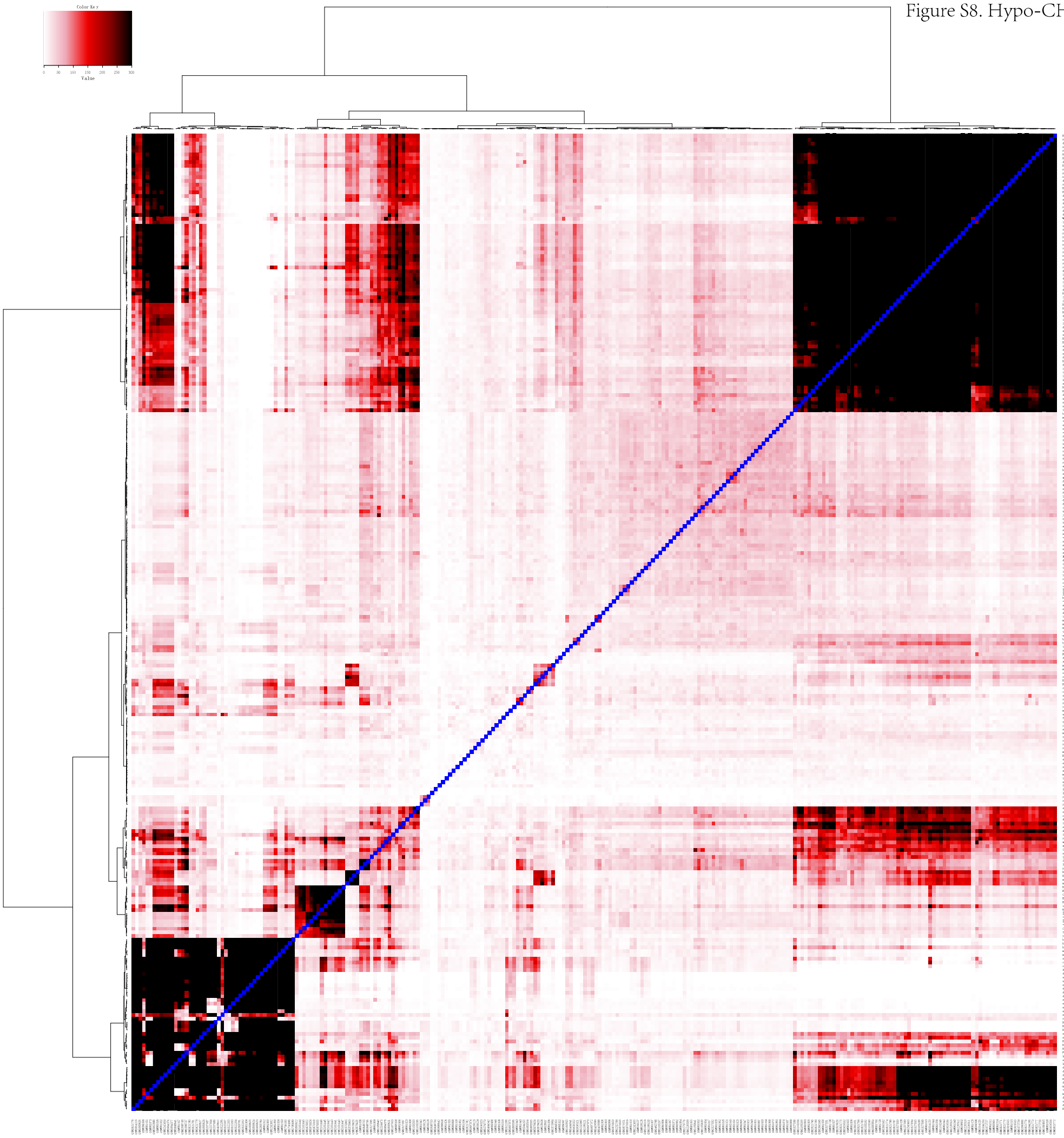


Figure S9. Hypo-CHH

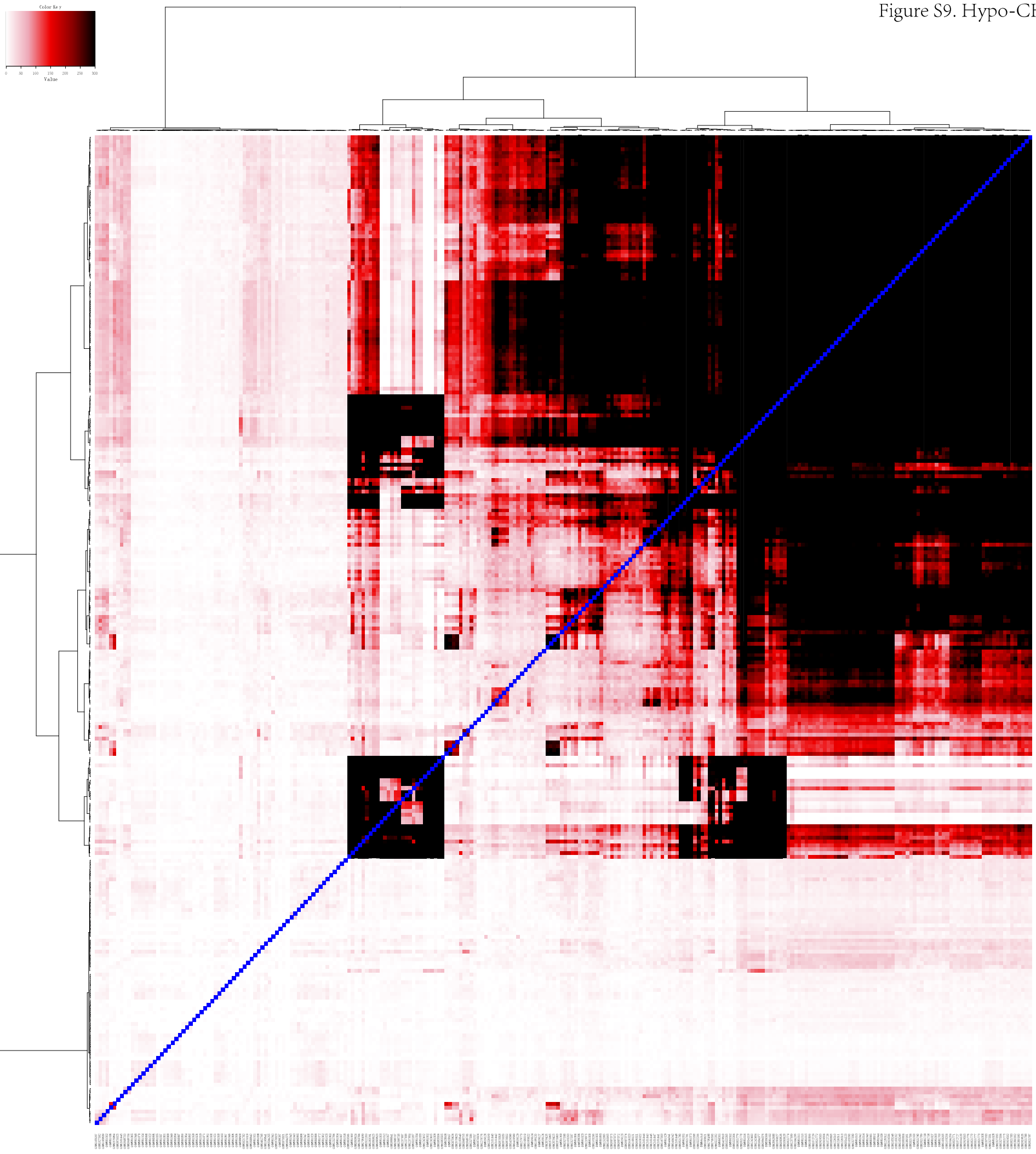


Figure S4-9. Clustering of tests with overlapping DMRs using the S-MOD method.
The S-MOD score was calculated based on the overlapping hyper/hypo- CG/CHG/CHH DMRs between pairs of 260 test libraries (see Fig. 3a). The S-MOD matrix was clustered in R. The order of libraries from left to right is the same as from top to bottom. The color scale represents the S-MOD value (0-300).

Figure S10. Hyper-CG

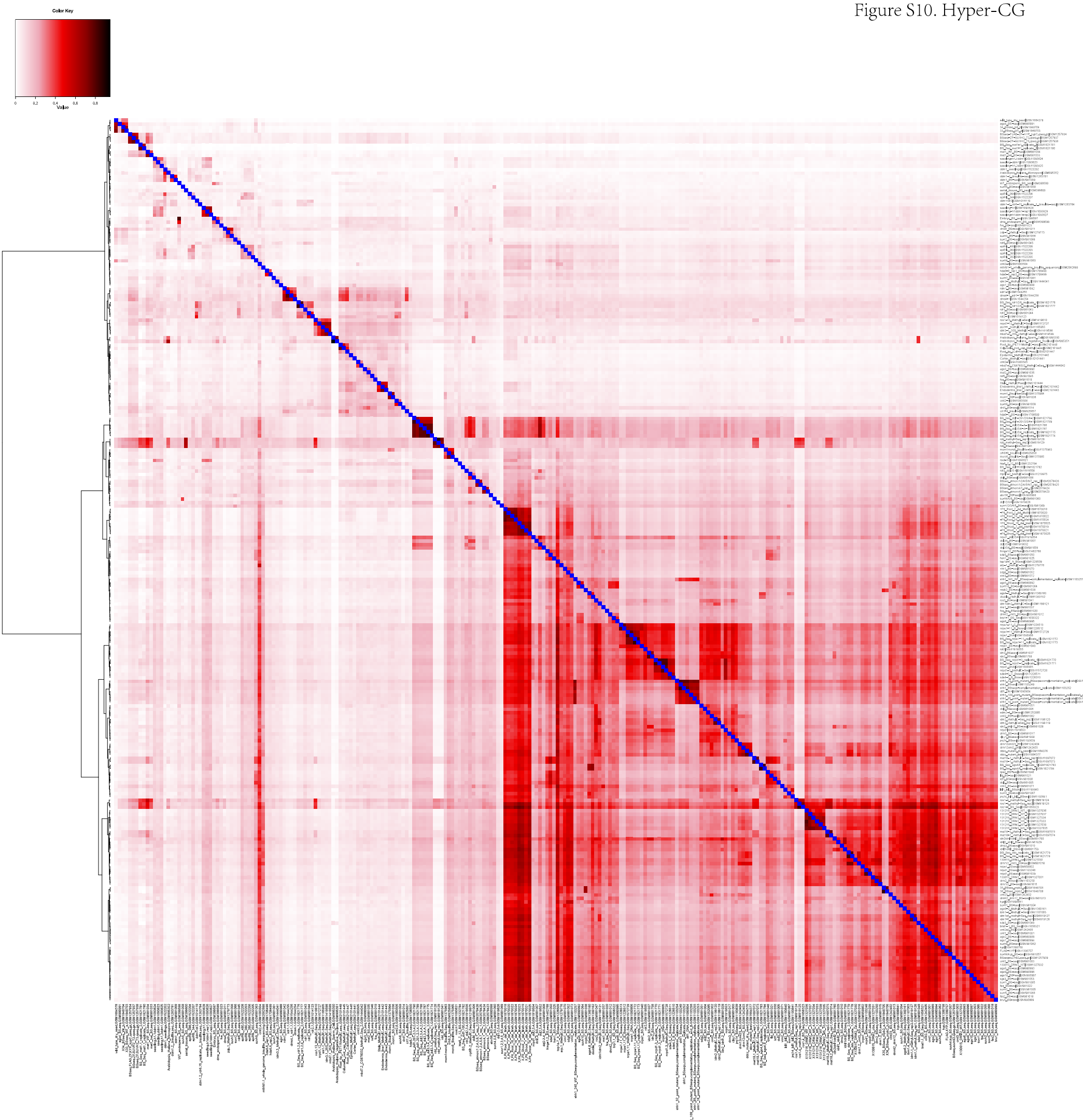


Figure S11. Hyper-CHG

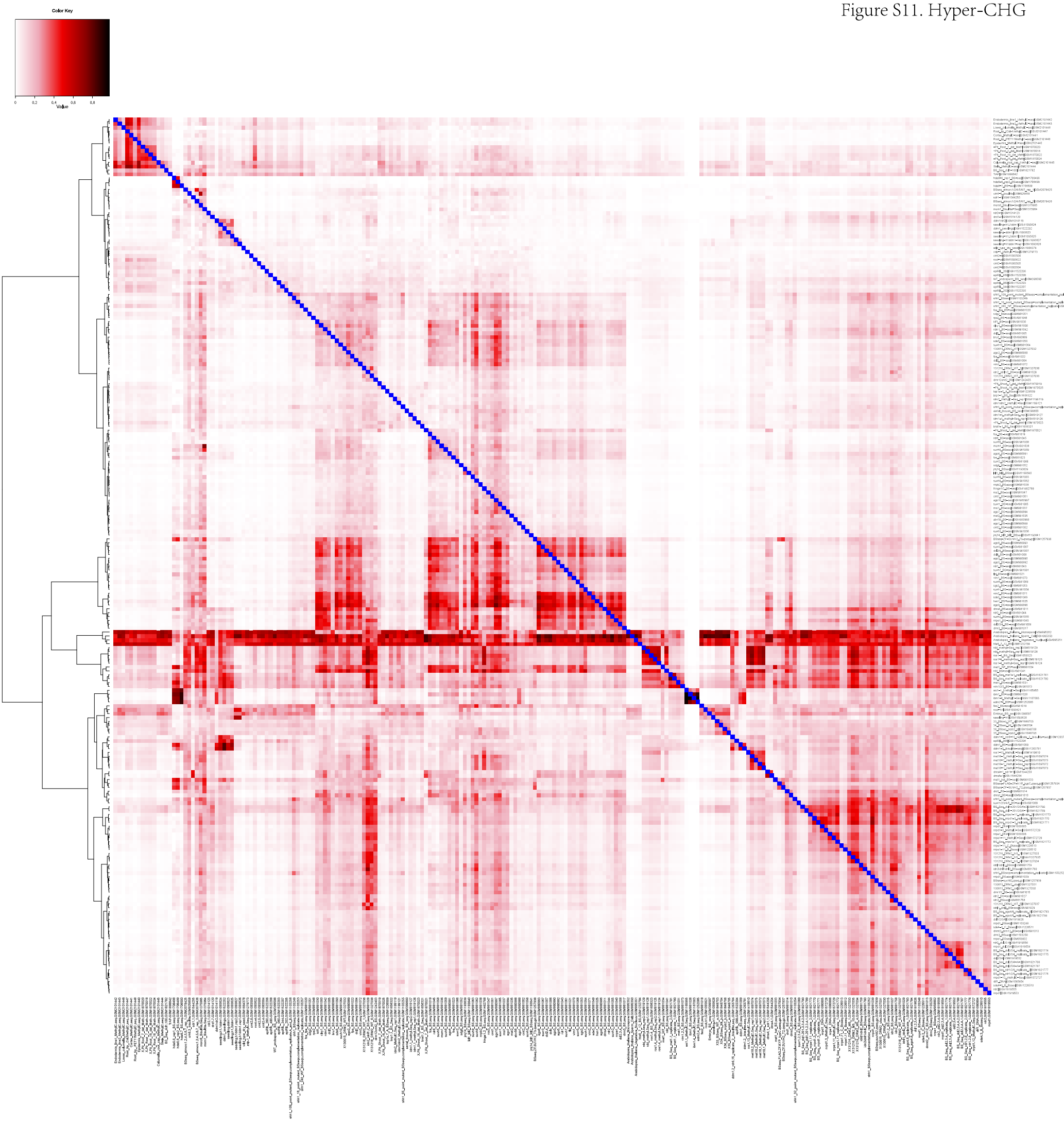


Figure S12. Hyper-CHH

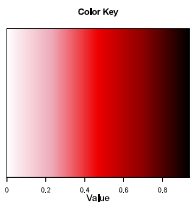


Figure S13. Hypo-CG

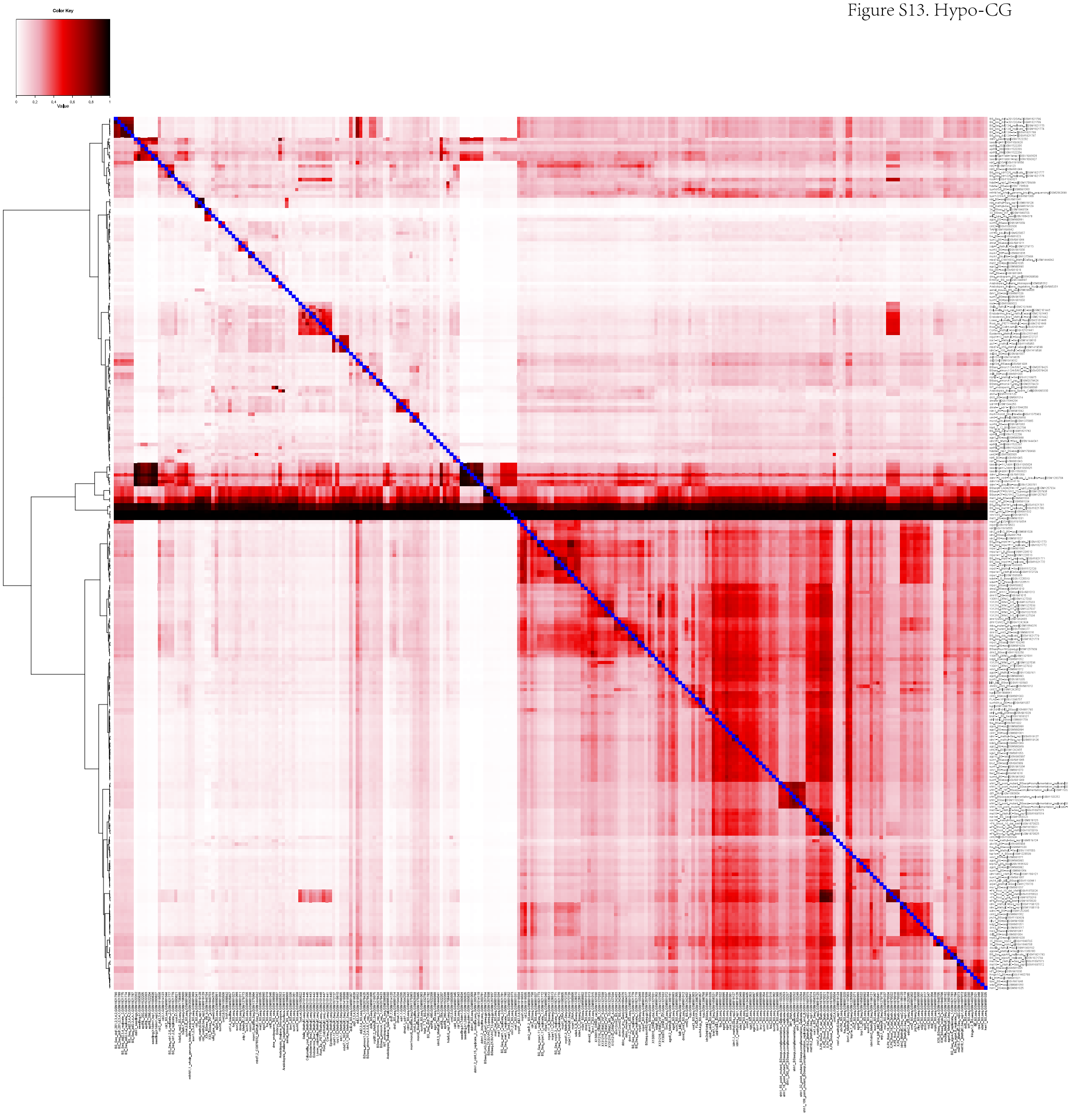


Figure S14. Hypo-CHG

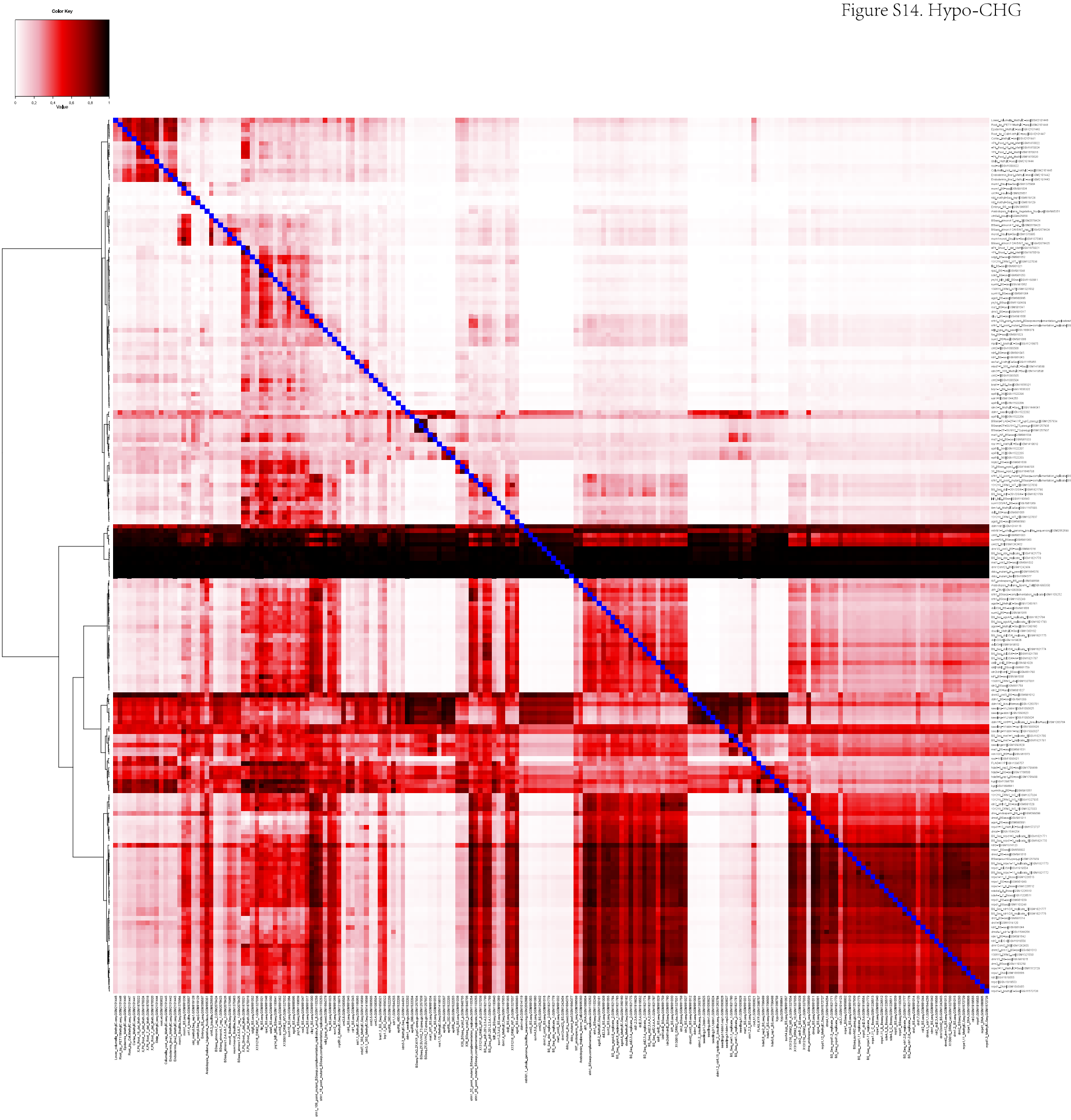


Figure S15. Hypo-CHH

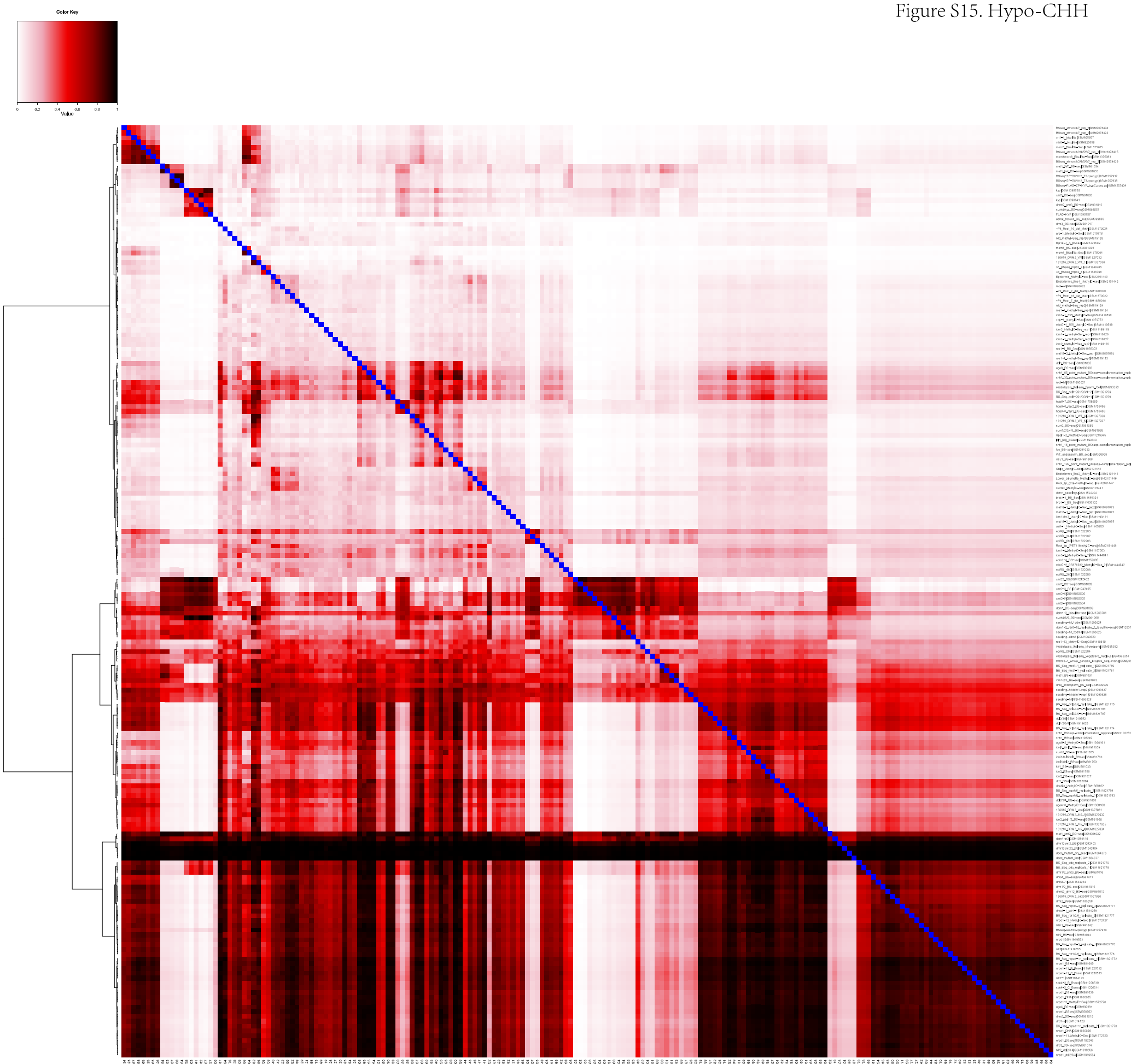
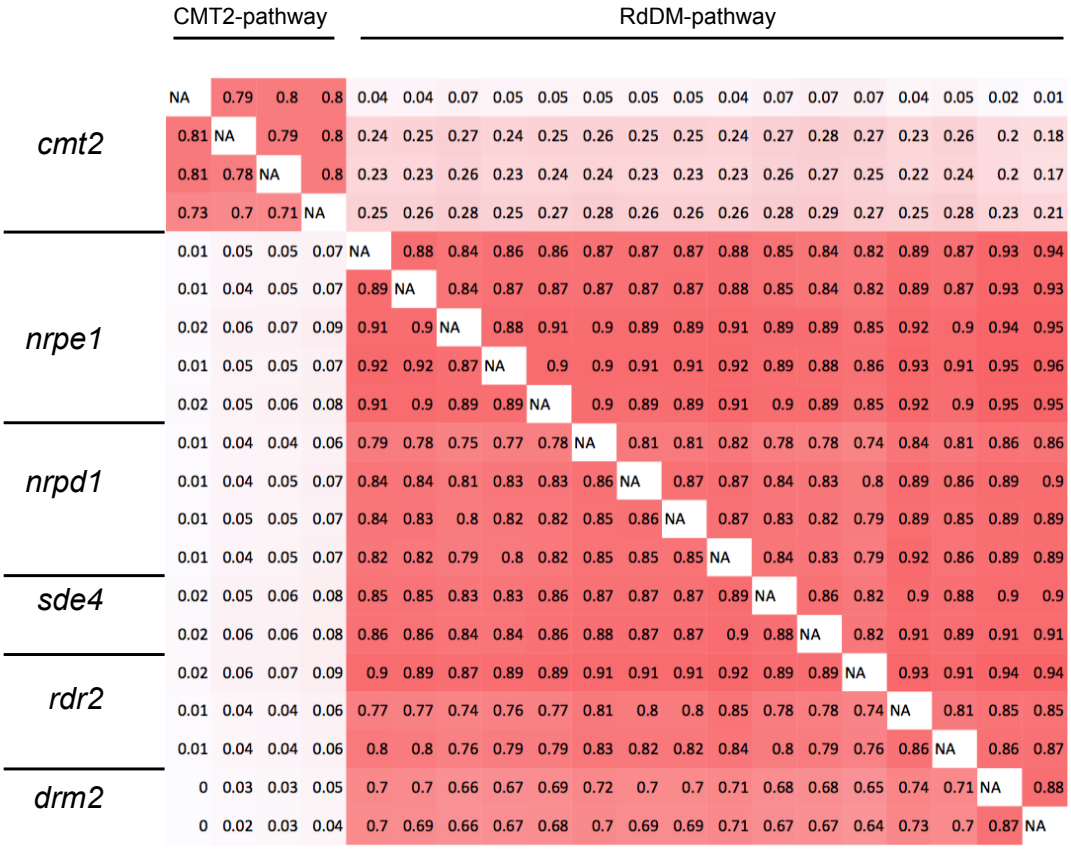


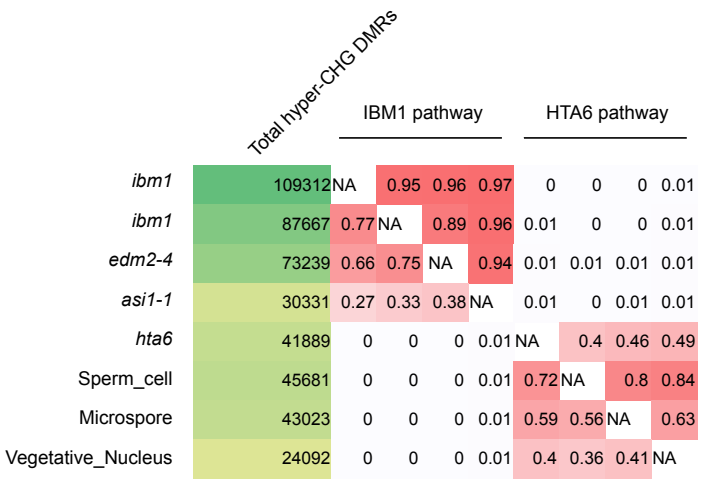
Figure S10-15. Clustering of tests with overlapping DMRs using the Q-MOD method. The Q-MOD score was calculated based on the overlapping hyper/hypo- CG/CHG/CHH DMRs between pairs of test libraries (see Fig. 3c) that pass the S-MOD filter of requiring a maximum S-MOD score of >100. The Q-MOD matrix was clustered in R. The order of libraries from left to right is the same as from top to bottom. The color scale represents the Q-MOD value (0-1).

A



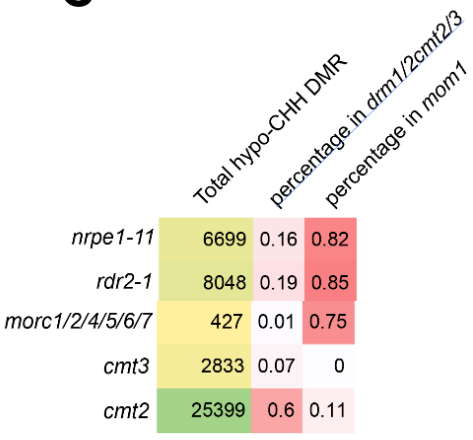
	cmt2				nrpe1				nrpd1				sde4		rdr2		drm2	
cmt2	NA	0.79	0.8	0.8	0.04	0.04	0.07	0.05	0.05	0.05	0.05	0.05	0.04	0.07	0.07	0.07	0.04	0.05	0.02	0.01
	0.81	NA	0.79	0.8	0.24	0.25	0.27	0.24	0.25	0.26	0.25	0.25	0.24	0.27	0.28	0.27	0.23	0.26	0.2	0.18
	0.81	0.78	NA	0.8	0.23	0.23	0.26	0.23	0.24	0.24	0.23	0.23	0.23	0.26	0.27	0.25	0.22	0.24	0.2	0.17
	0.73	0.7	0.71	NA	0.25	0.26	0.28	0.25	0.27	0.28	0.26	0.26	0.26	0.28	0.29	0.27	0.25	0.28	0.23	0.21
nrpe1	0.01	0.05	0.05	0.07	NA	0.88	0.84	0.86	0.86	0.87	0.87	0.87	0.88	0.85	0.84	0.82	0.89	0.87	0.93	0.94
	0.01	0.04	0.05	0.07	0.89	NA	0.84	0.87	0.87	0.87	0.87	0.87	0.88	0.85	0.84	0.82	0.89	0.87	0.93	0.93
	0.02	0.06	0.07	0.09	0.91	0.9	NA	0.88	0.91	0.9	0.89	0.89	0.91	0.89	0.89	0.85	0.92	0.9	0.94	0.95
	0.01	0.05	0.05	0.07	0.92	0.92	0.87	NA	0.9	0.9	0.91	0.91	0.92	0.89	0.88	0.86	0.93	0.91	0.95	0.96
	0.02	0.05	0.06	0.08	0.91	0.9	0.89	0.89	NA	0.9	0.89	0.89	0.91	0.9	0.89	0.85	0.92	0.9	0.95	0.95
nrpd1	0.01	0.04	0.04	0.06	0.79	0.78	0.75	0.77	0.78	NA	0.81	0.81	0.82	0.78	0.78	0.74	0.84	0.81	0.86	0.86
	0.01	0.04	0.05	0.07	0.84	0.84	0.81	0.83	0.83	0.86	NA	0.87	0.87	0.84	0.83	0.8	0.89	0.86	0.89	0.9
	0.01	0.05	0.05	0.07	0.84	0.83	0.8	0.82	0.82	0.85	0.86	NA	0.87	0.83	0.82	0.79	0.89	0.85	0.89	0.89
	0.01	0.04	0.05	0.07	0.82	0.82	0.79	0.8	0.82	0.85	0.85	0.85	NA	0.84	0.83	0.79	0.92	0.86	0.89	0.89
sde4	0.02	0.05	0.06	0.08	0.85	0.85	0.83	0.83	0.86	0.87	0.87	0.87	0.89	NA	0.86	0.82	0.9	0.88	0.9	0.9
	0.02	0.06	0.06	0.08	0.86	0.86	0.84	0.84	0.86	0.88	0.87	0.87	0.9	0.88	NA	0.82	0.91	0.89	0.91	0.91
rdr2	0.02	0.06	0.07	0.09	0.9	0.89	0.87	0.89	0.89	0.91	0.91	0.91	0.92	0.89	0.89	NA	0.93	0.91	0.94	0.94
	0.01	0.04	0.04	0.06	0.77	0.77	0.74	0.76	0.77	0.81	0.8	0.8	0.85	0.78	0.78	0.74	NA	0.81	0.85	0.85
	0.01	0.04	0.04	0.06	0.8	0.8	0.76	0.79	0.79	0.83	0.82	0.82	0.84	0.8	0.79	0.76	0.86	NA	0.86	0.87
drm2	0	0.03	0.03	0.05	0.7	0.7	0.66	0.67	0.69	0.72	0.7	0.7	0.71	0.68	0.68	0.65	0.74	0.71	NA	0.88
	0	0.02	0.03	0.04	0.7	0.69	0.66	0.67	0.68	0.7	0.69	0.69	0.71	0.67	0.67	0.64	0.73	0.7	0.87	NA

B



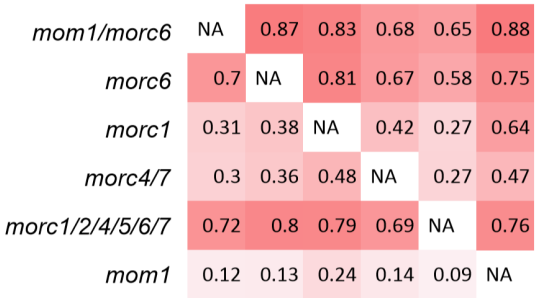
	Total hyper-CHG DMRs	IBM1 pathway				HTA6 pathway			
ibm1	109312	NA	0.95	0.96	0.97	0	0	0	0.01
ibm1	87667	0.77	NA	0.89	0.96	0.01	0	0	0.01
edm2-4	73239	0.66	0.75	NA	0.94	0.01	0.01	0.01	0.01
asi1-1	30331	0.27	0.33	0.38	NA	0.01	0	0.01	0.01
hta6	41889	0	0	0	0.01	NA	0.4	0.46	0.49
Sperm_cell	45681	0	0	0	0.01	0.72	NA	0.8	0.84
Microspore	43023	0	0	0	0.01	0.59	0.56	NA	0.63
Vegetative_Nucleus	24092	0	0	0	0.01	0.4	0.36	0.41	NA

C



	Total hypo-CHH DMR	percentage in *drm1/2cmt2/3*	percentage in *mom1*
nrpe1-11	6699	0.16	0.82
rdr2-1	8048	0.19	0.85
morc1/2/4/5/6/7	427	0.01	0.75
cmt3	2833	0.07	0
cmt2	25399	0.6	0.11

D



mom1/morc6	NA	0.87	0.83	0.68	0.65	0.88
morc6	0.7	NA	0.81	0.67	0.58	0.75
morc1	0.31	0.38	NA	0.42	0.27	0.64
morc4/7	0.3	0.36	0.48	NA	0.27	0.47
morc1/2/4/5/6/7	0.72	0.8	0.79	0.69	NA	0.76
mom1	0.12	0.13	0.24	0.14	0.09	NA

Figure S16. Clustering of mutants with overlapping DMRs by Q-MOD method.

A. The overlapping percentage of hypo-CHH DMRs between *cmt2* and RdDM mutants.
B. The overlapping percentage of hyper-CHG DMRs between IBM1 and HTA6 pathways
C. The overlaps of hypo-CHH methylation between *mom1* and other mutants.
D. The overlaps of hypo-CHH methylation between *mom1* and *morc* mutants.

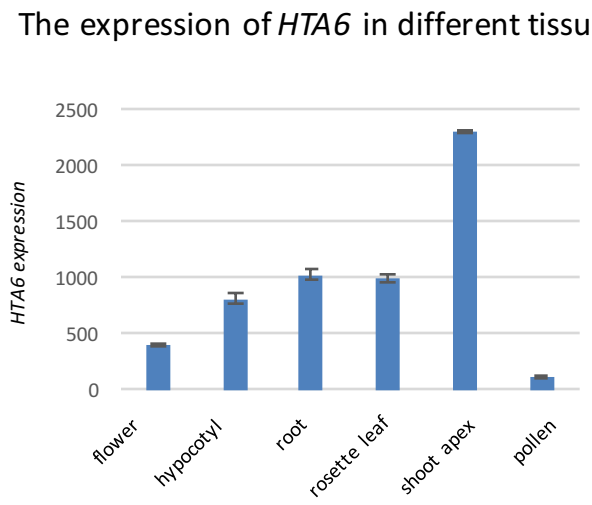


Figure S17. The expression of *HTA6* in different tissues.
Barplot of microarray values showing *HTA6* expression levels in different Arabidopsis tissues. Error bars show standard deviation. Figure is derived from the Arabidopsis eFP Browser by B. Vinegar, J. Alls and N. Provart. Data originate from Schmid et al., 2005, Nat. Gen. 37:501.

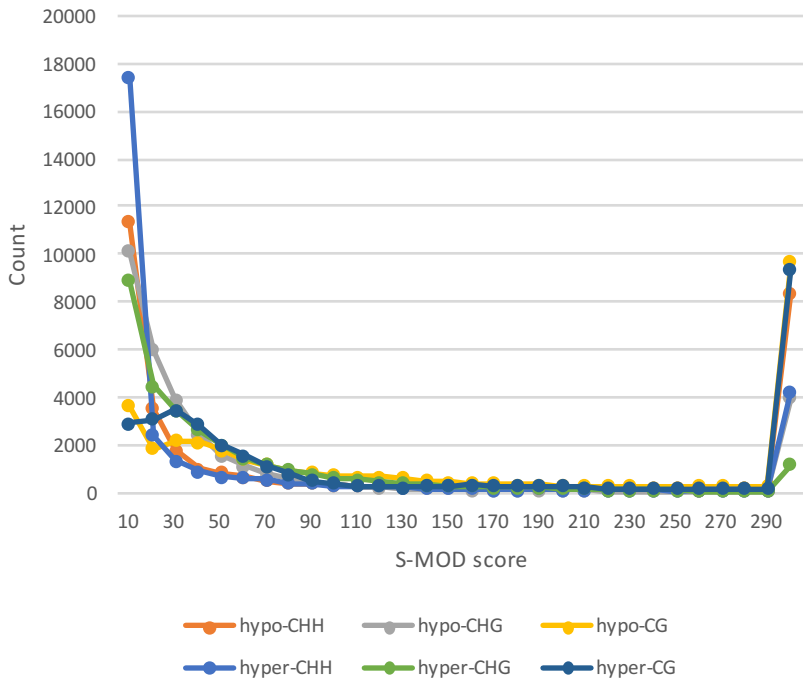


Figure S18. Distribution of all S-MOD scores across libraries.
The figure summarizes the distribution of all S-MOD scores from each of the 260×260 pairwise comparisons (so in total (260×260 – 260)/2 = 33670 comparisons), which are grouped into 10 points score window (0-10, 10-20, 20-30, ... , 290-300) shown on the x-axis. The counts of S-MOD scores within each window are shown on the y-axis. The maximum of S-MOD score is 300, because 10^{-300} is the smallest P-value that R software can store, which transform into 300 in S-MOD score. We observe a bimodal distribution with most pairwise comparisons either having a high S-MOD relatedness score (>290) or a low S-MOD relatedness score (<90).

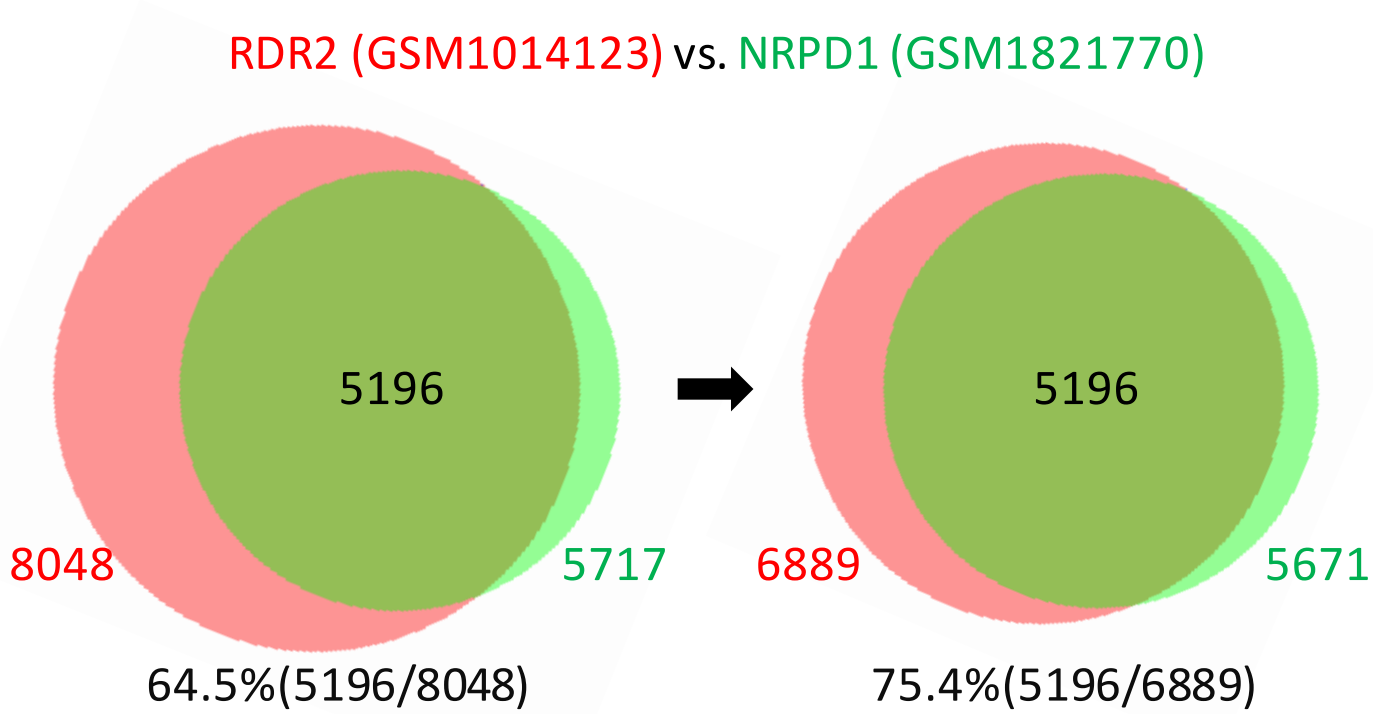


Figure S19. Improved overlapping ratio of hcDMRs between two mutant libraries when using bins of sufficient coverage in both libraries.
Left, the overlapping of hcDMRs between *rdr2* mutant library (GSM1014123) and *nrpd1* (GSM1821770) without filtering out low-coverage binds; right, the overlapping of hcDMRs between *rdr2* mutant library (GSM1014123) and *nrpd1* (GSM1821770) using bins with sufficient coverage in both libraries.

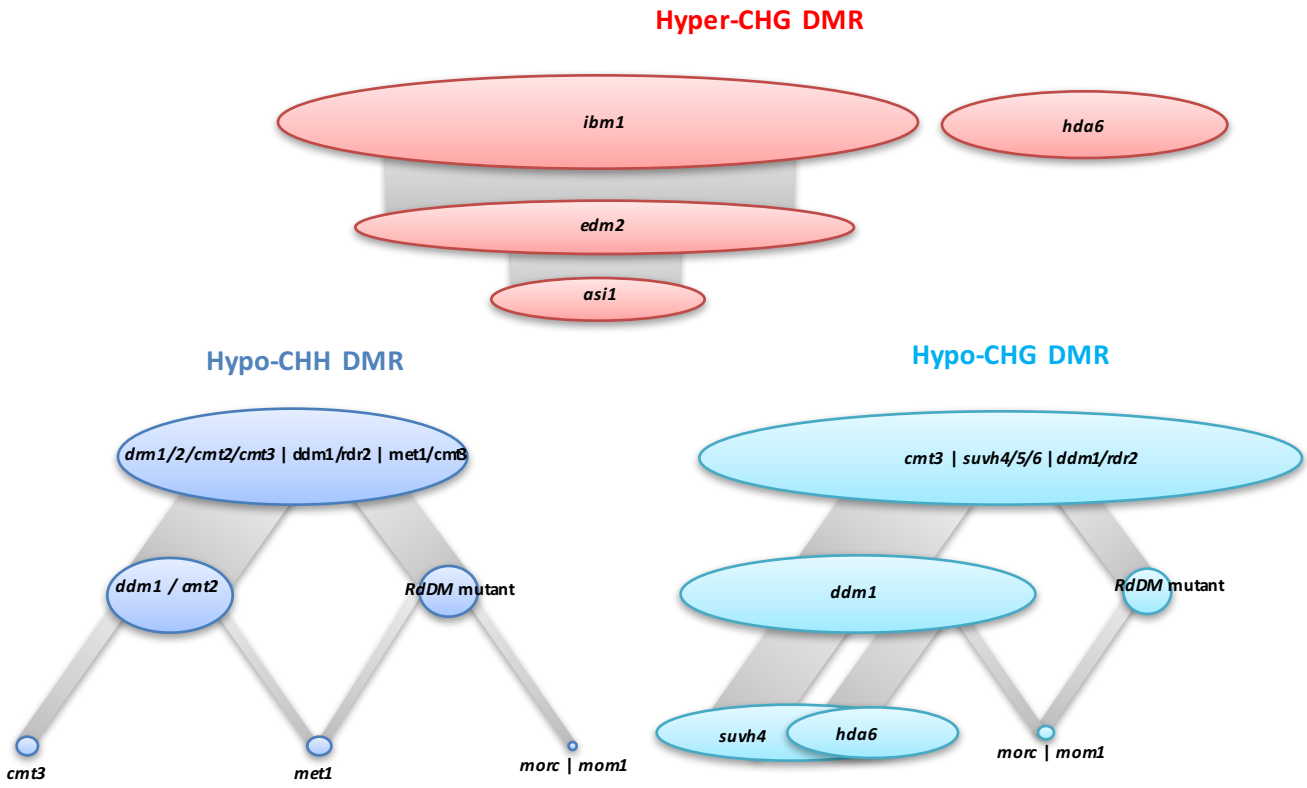


Figure S20. A hierarchical network for regulating DNA methylation in Arabidopsis.
A schematic diagram to summarize the network and major players controlling each type of DNA methylation. The length of ellipse is approximately proportional to the number of loci controlled by each gene. Different genetic backgrounds of comparable functional importance are separated by a vertical line.

References

1. Schmid M, et al. (2005) A gene expression map of Arabidopsis thaliana development. Nat Genet 37(5):501-506.

2. Winter D, et al. (2007) An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. PLoS One 2(8):e718.