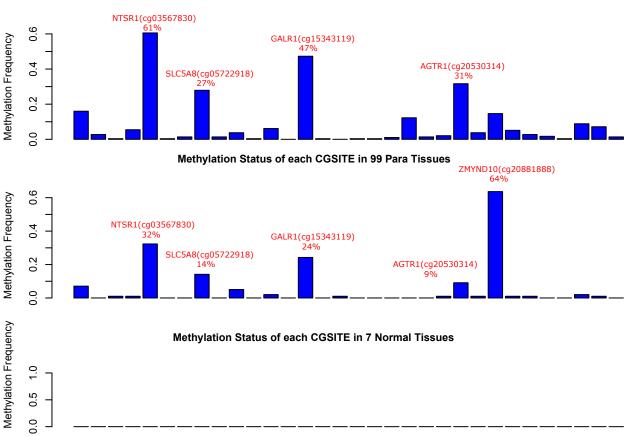
Methylation Status of each CGSITE in 294 NSCLC Tissues



In shared 99 probes by GoldenGate and Methylation 27K array, 32 probes are hypomethylated (beta<0.25) in all 7 normal lung tissues. Meanwhile, NTSR1,GALR1 are hypermethylated in at least 24% NSCLC and para-tumors. Interestingly, NTSR1, SLC5A8, GALR1, AGTR1 show higher methylation level than that of para-tumors but ZMYND10 show lower methylation level in para-tumors than NSCLC.