



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.