1: QQ Normalization and RMA summation from RMA express → Cyber-T (not paired) applied at N=3 → statistics level normalization [12] → generation of p-values by scheme 4 [12] → BH-FDR applied at 10% → list of expressed genes

2: Quantile-Quantile from DChip → Cyber-T paired comparing probes of the first array to the probes of the second array → statistics level normalization [12] → generation of p-values by PINC → BH FDR applied at 10% → list of expressed genes