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| R functions name | R package | Application |
| readIDAT | illuminaio | Analyze the Illumina gene chip data |
| calcNormFactors | edgeR | Calculate the normalization factor |
| voom | Limma | Normalization and correction of batch effects |
| makeContrasts | Limma | Difference analysis |
| ggplot | ggplot2 | Drawing |
| enrichKEGG/ enrichGO | clusterProfiler | Perform enrichment analysis |