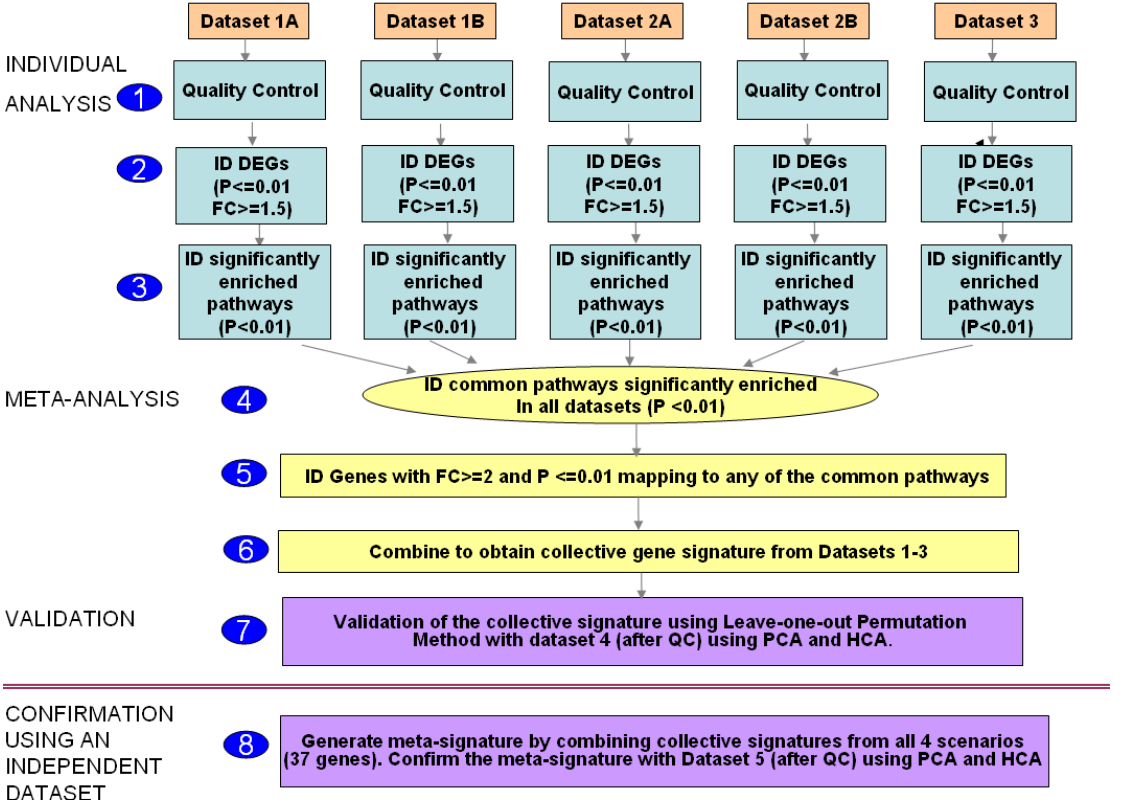
Dataset 1A
Dataset 1B
Dataset 2A
Dataset 2B
Dataset 3
INDIVIDUAL ANALYSIS
1
Quality Control
2
ID DEGs (P<=0.01 FC>=1.5)
3
ID significantly enriched pathways (P<0.01)
META-ANALYSIS
4
ID common pathways significantly enriched In all datasets (P <0.01)
5
ID Genes with FC>=2 and P <=0.01 mapping to any of the common pathways
6
Combine to obtain collective gene signature from Datasets 1-3
VALIDATION
7
Validation of the collective signature using Leave-one-out Permutation Method with dataset 4 (after QC) using PCA and HCA.
CONFIRMATION USING AN INDEPENDENT DATASET
8
Generate meta-signature by combining collective signatures from all 4 scenarios (37 genes). Confirm the meta-signature with Dataset 5 (after QC) using PCA and HCA