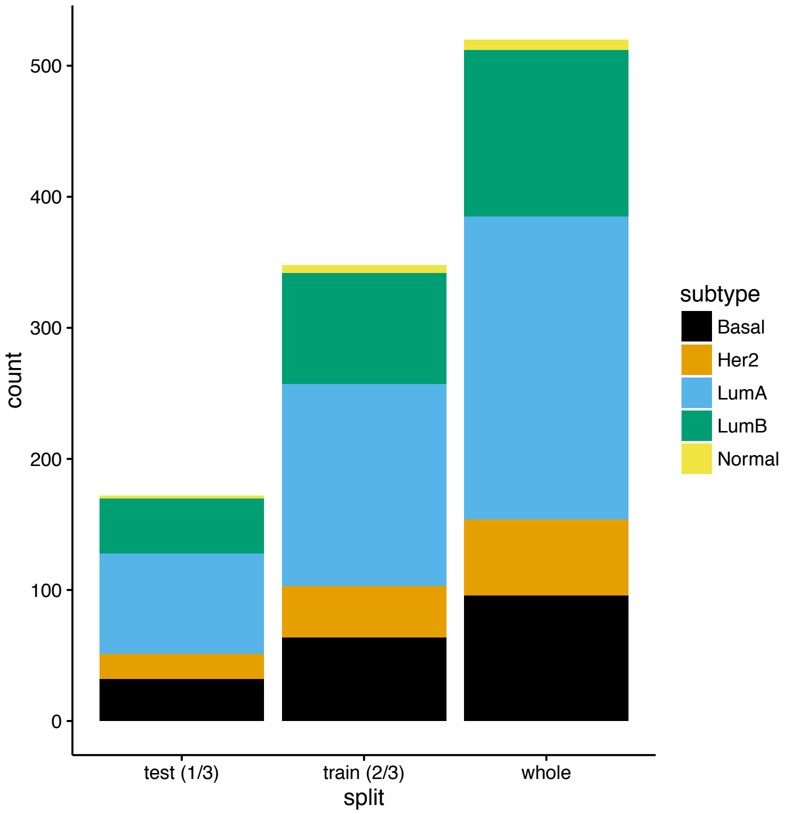


Figure S1. Representative distribution of BRCA PAM50 subtypes in training and hold-out sets.

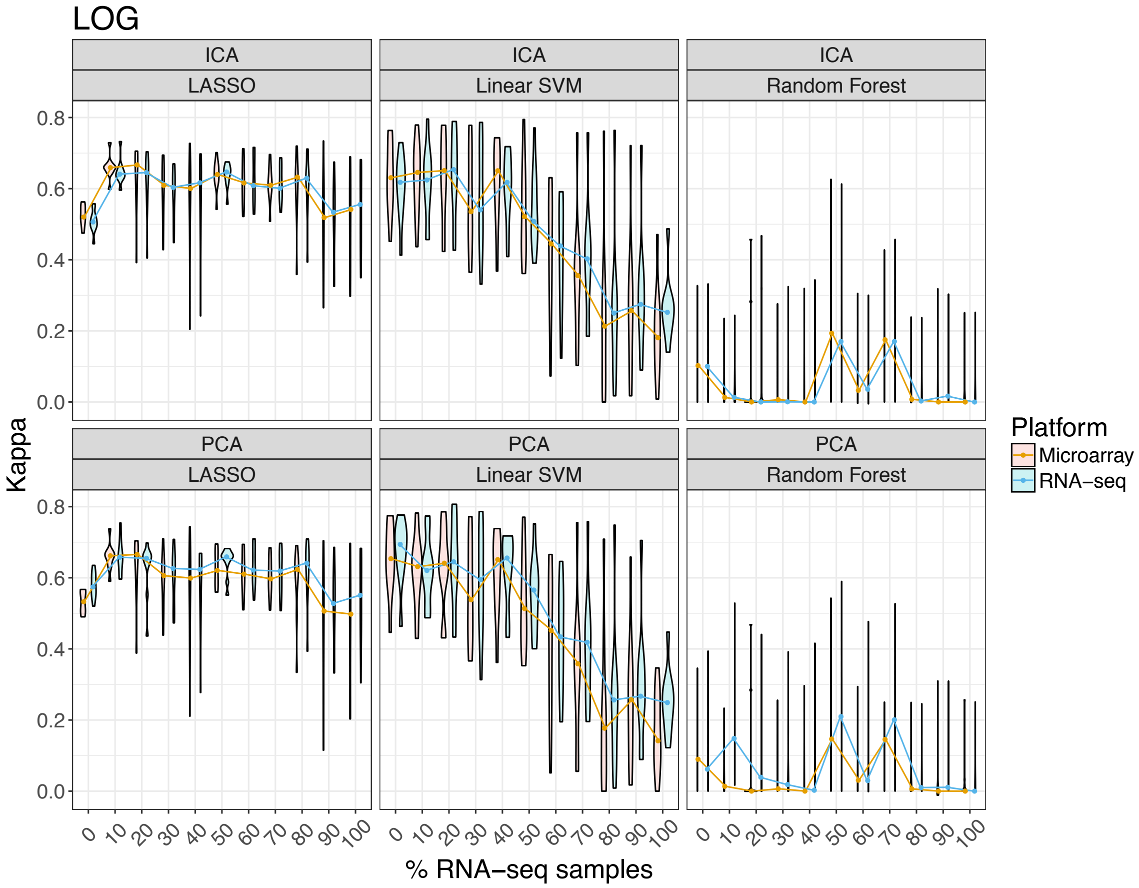
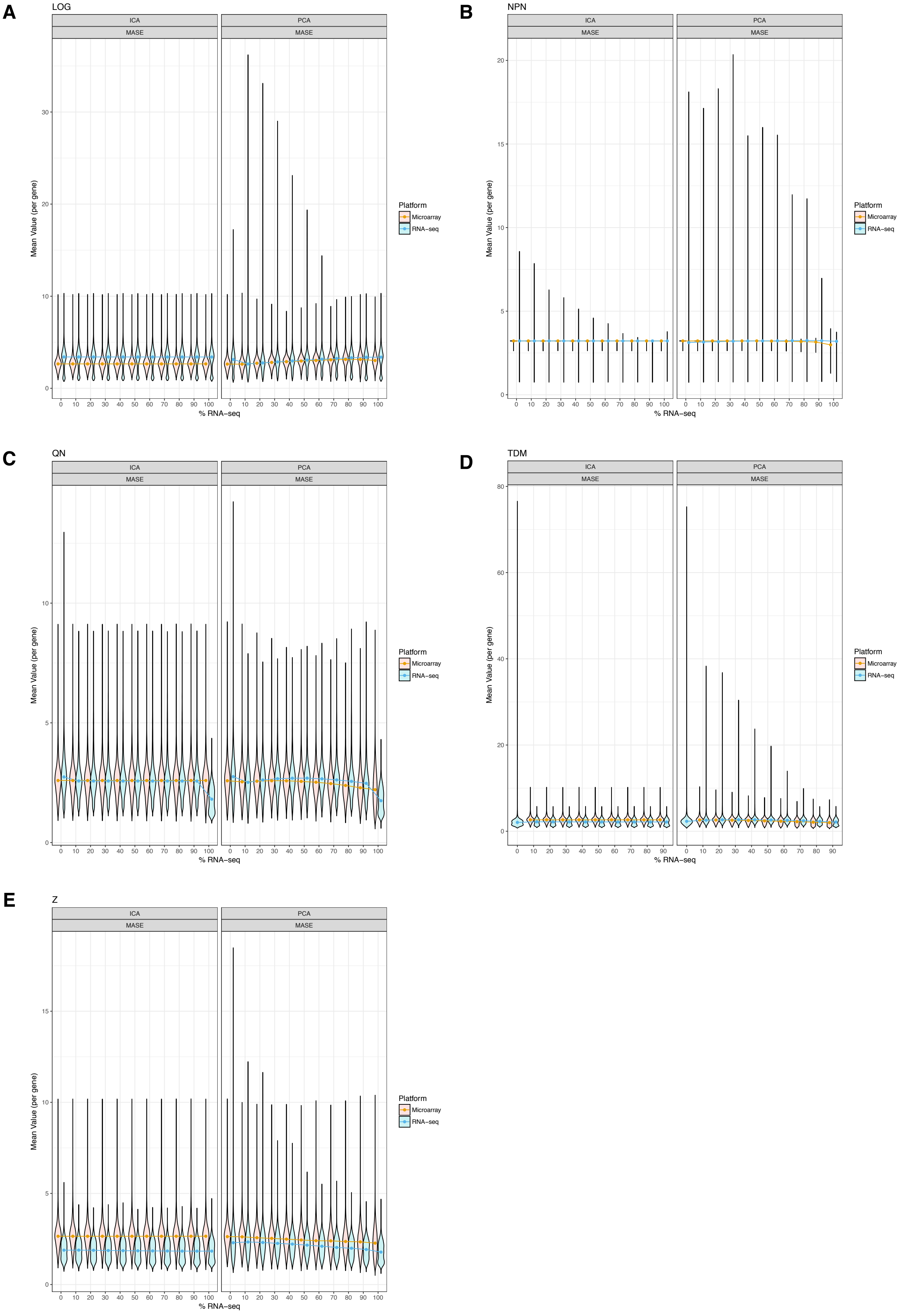


Figure S2. Reconstructed Kappa plot for LOG normalization.

Figure S3. Mean absolute scaled error (MASE) – reconstruction error. A) LOG B) NPN C) QN D) TDM E) Z


A
LOG
ICA
MASE
PCA
MASE
Mean Value (per gene)
0
10
20
30
0 10 20 30 40 50 60 70 80 90 100
% RNA−seq
Platform
Microarray
RNA−seq
B
NPN
ICA
MASE
PCA
MASE
Mean Value (per gene)
0
5
10
15
20
0 10 20 30 40 50 60 70 80 90 100
% RNA−seq
Platform
Microarray
RNA−seq
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ICA
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Mean Value (per gene)
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Microarray
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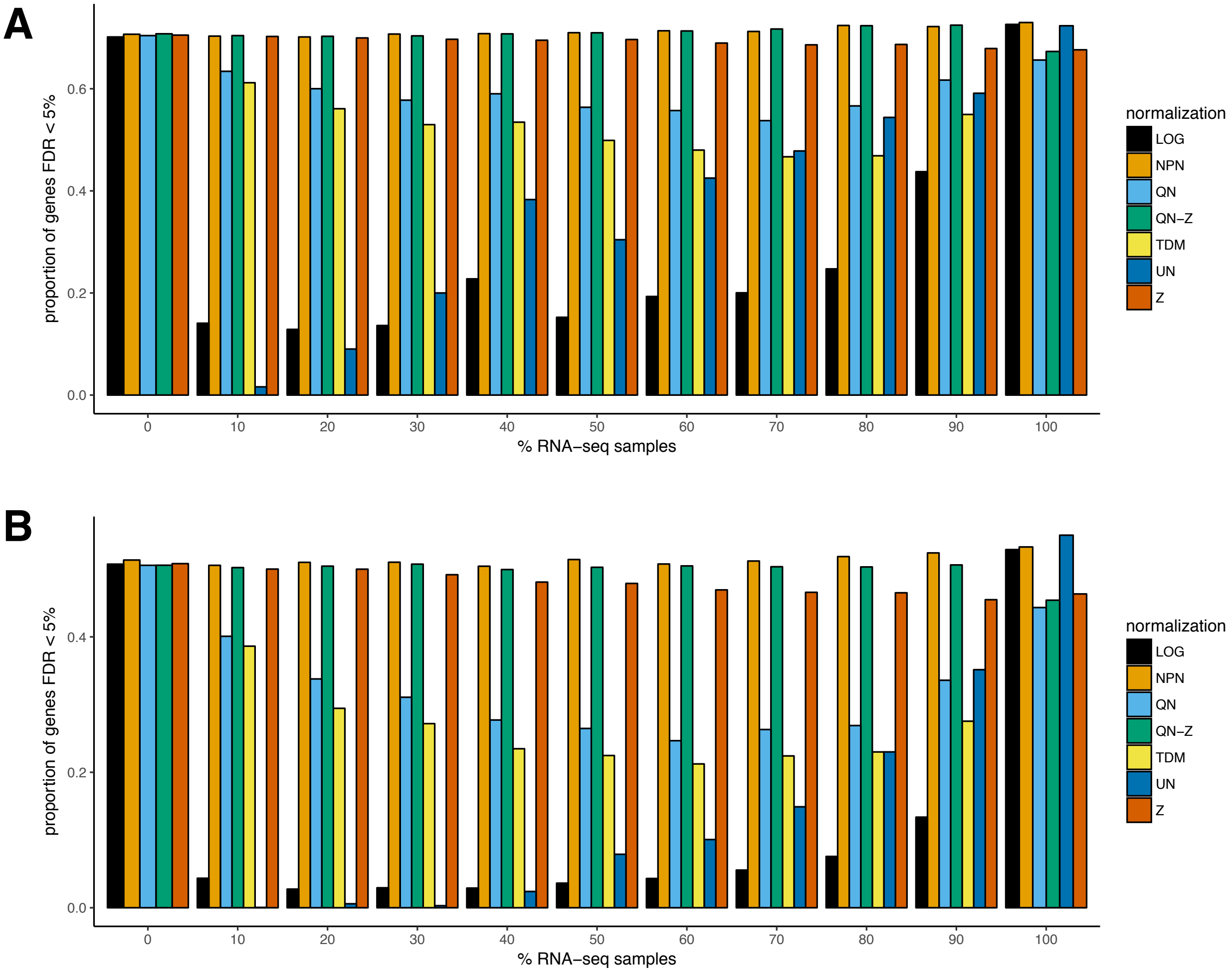

Figure S4. Proportion of tested genes that are differentially expressed at FDR < 5%. A) Basal v. Other comparison B) Her2 v. LumA comparison

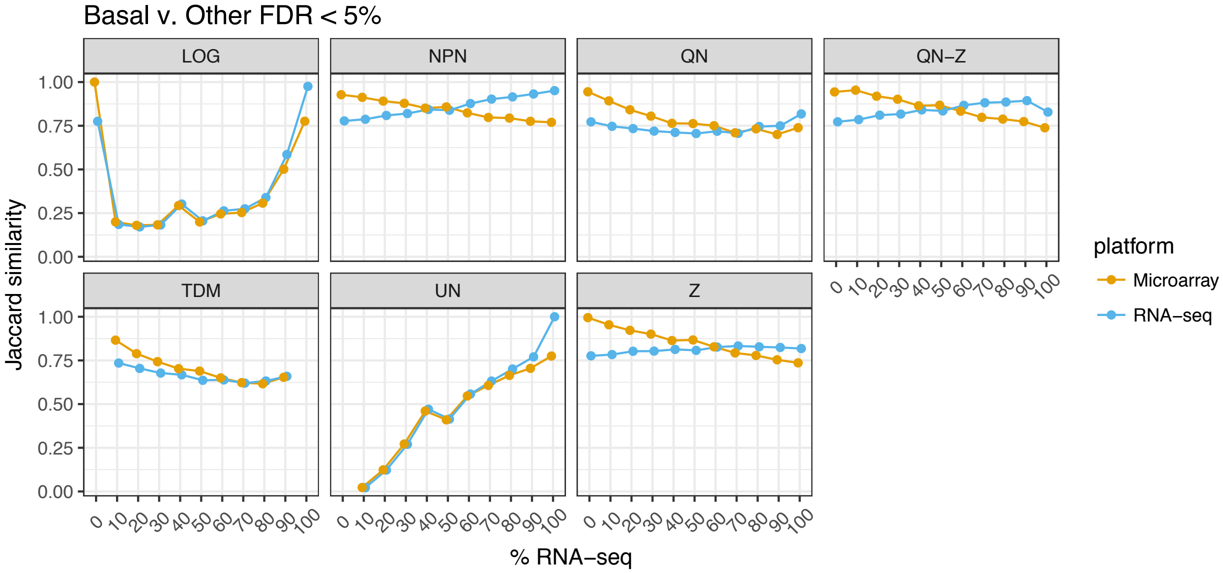

Figure S5. Overlap between platform-specific silver standard differentially expressed genes (DEGs) and experimental DEGs. Basal v. all other samples.