SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure S1. The expression distribution of each of the 13 immune metagenes is shown for the (A) ER positive, (B) TNBC and (C) HER2 positive cancers.

Supplementary Figure S2. Correlation between the LCK metagene expression and infiltrating lymphocyte (TIL) count.

Supplementary Figure S3. The distribution of genomic features and LCK metagene expression within breast cancer subtypes in the TCGA.

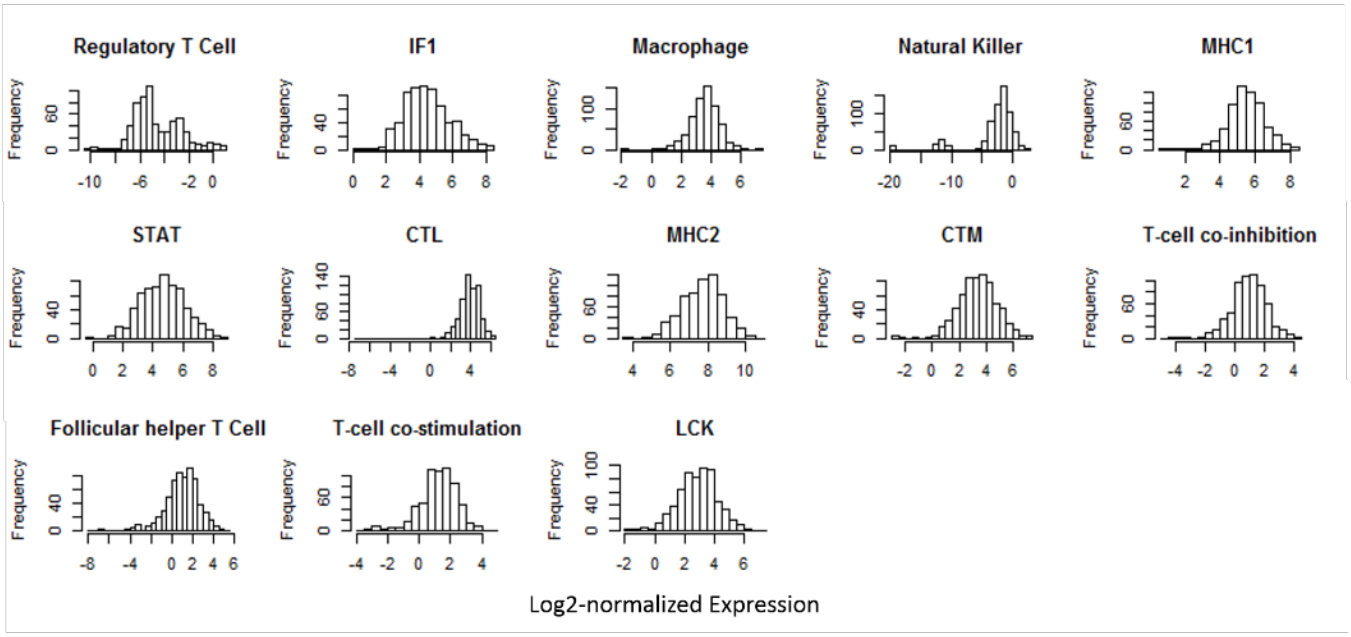
Supplementary Figure S4. Correlations between 13 immune metagene expressions and 5 exome-wide genomic features including all breast cancers combined in TCGA.

Supplementary Figure S5. Correlations between the LCK immune metagene expression and five different genomic features within each breast cancer subtype in the TCGA.

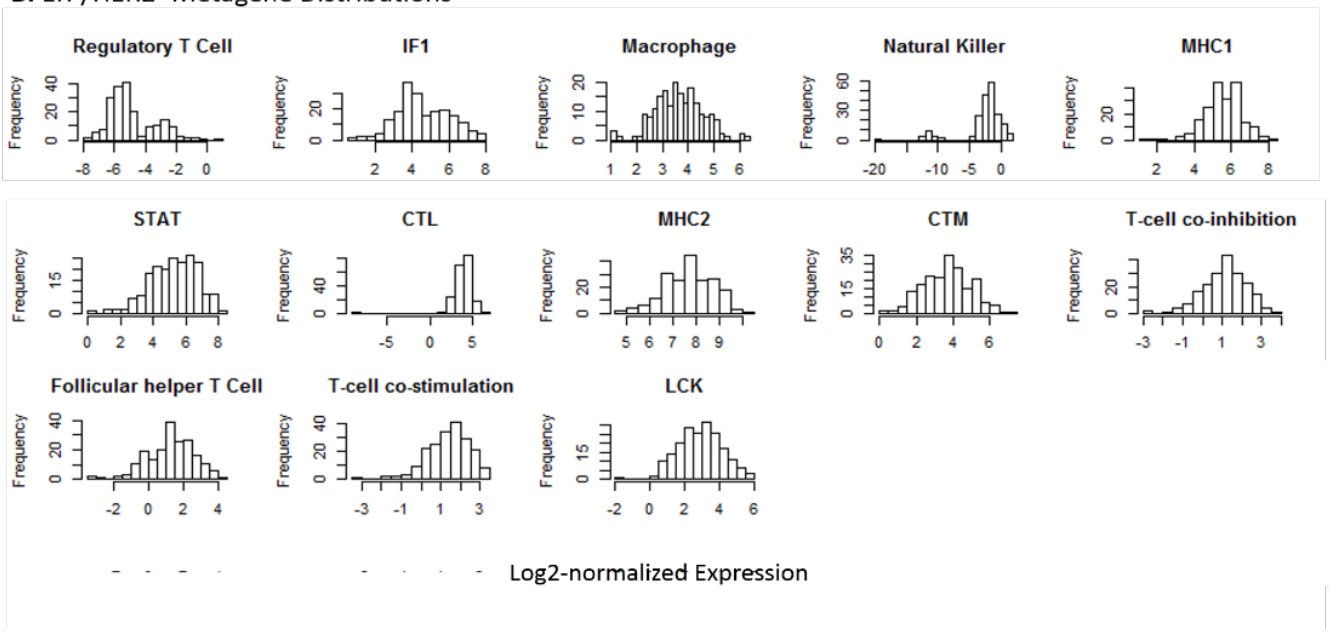
Supplementary Figure S6. Distribution of genomic features and their correlation with an immune metagene in the breast cancer subtypes from TCGA data.

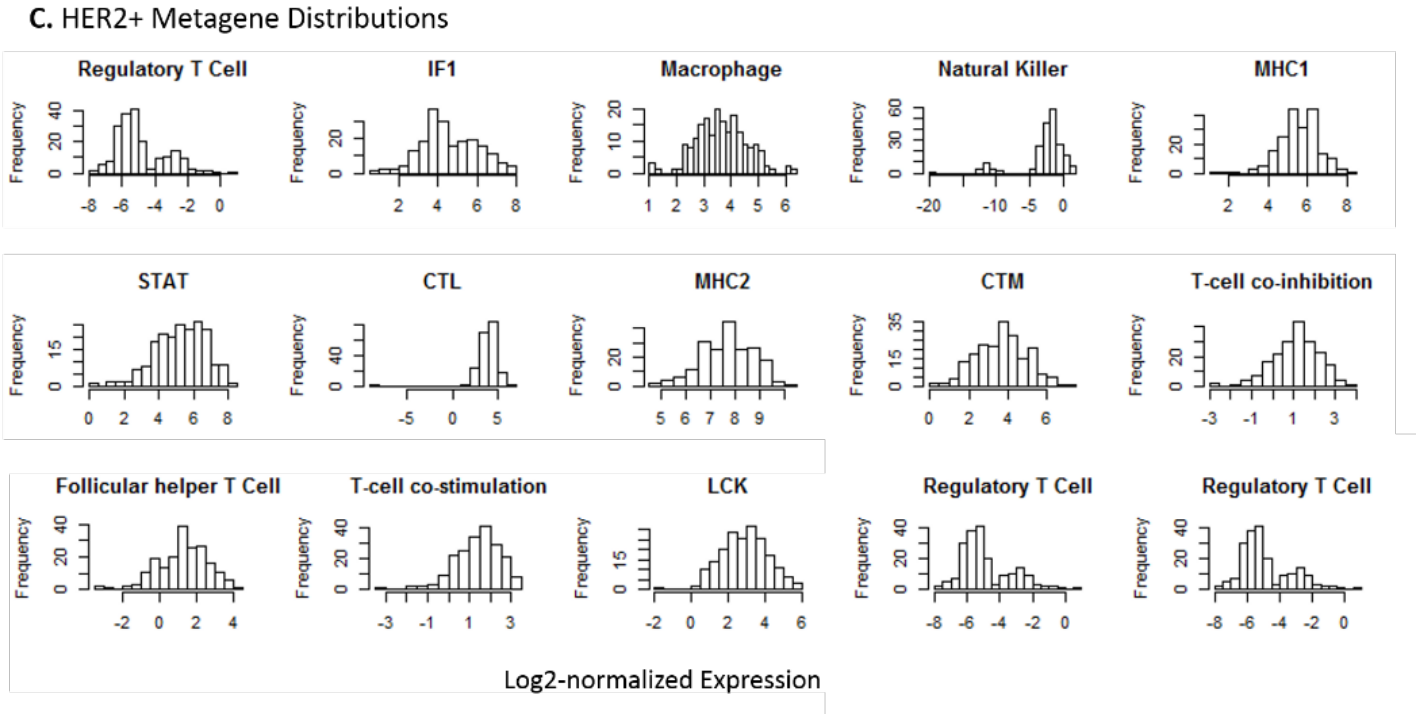
Supplementary Figure S1

A. ER+/HER2- Metagene Distributions

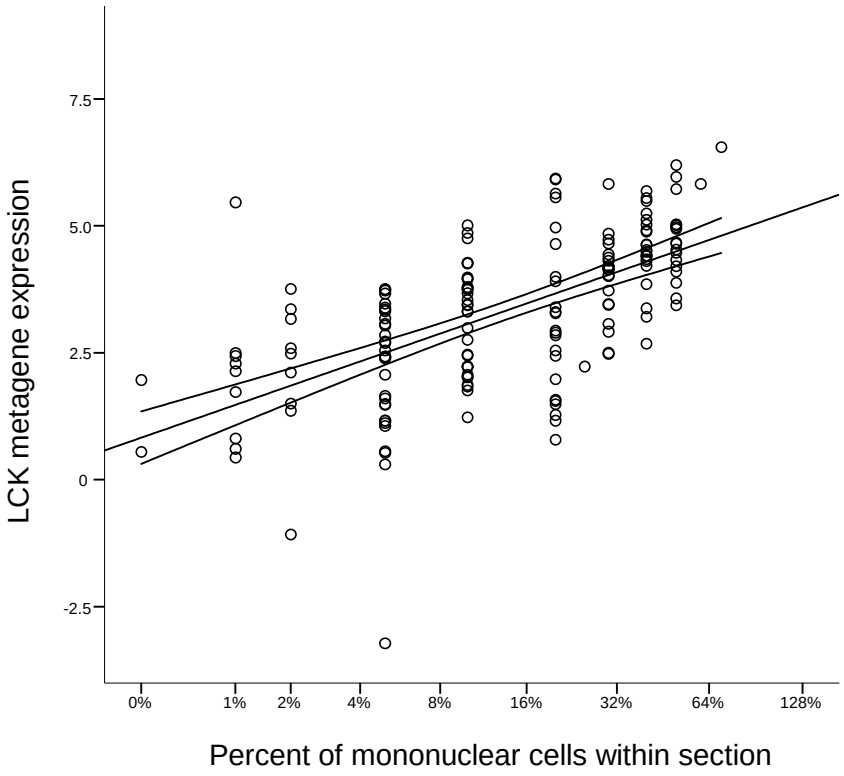


B. ER-/HER2- Metagene Distributions

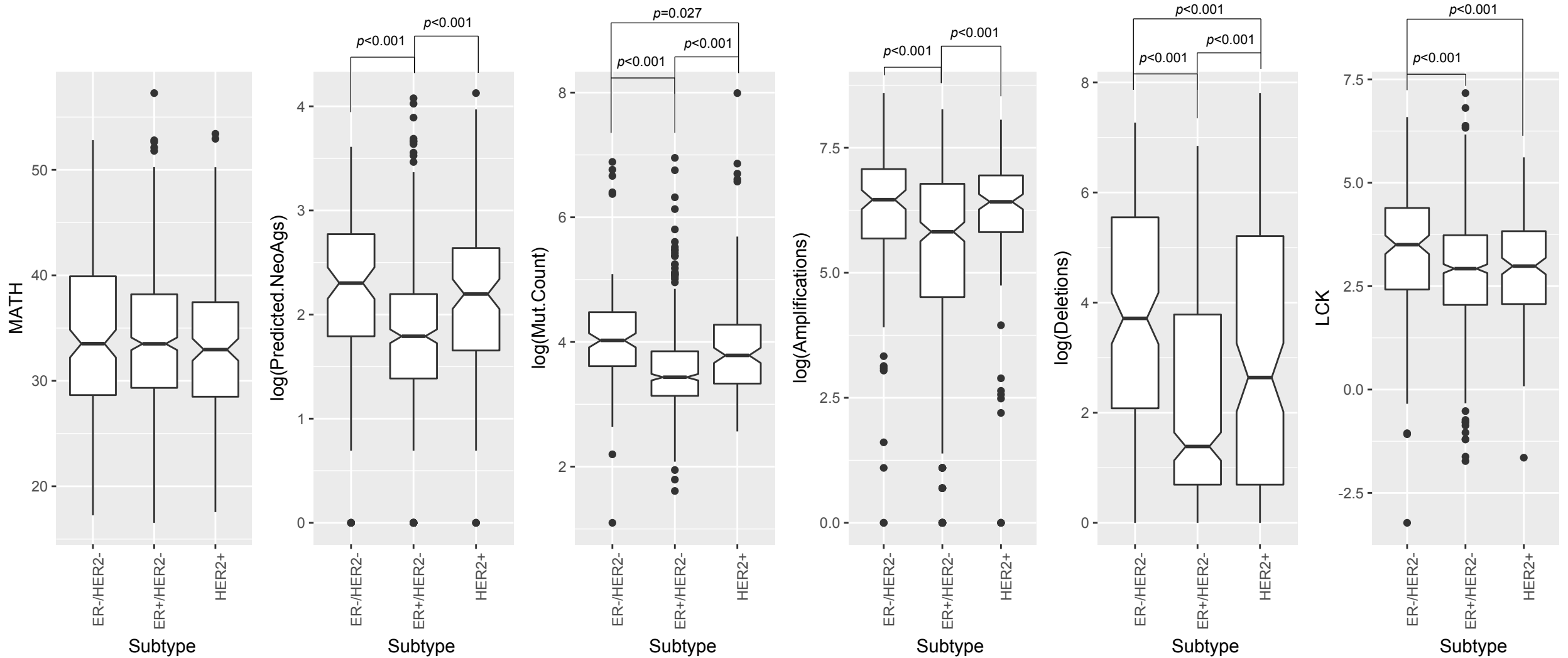




Supplementary Figure 1. The expression distribution of each of the 13 immune metagenes is shown for the (A) ER positive, (B) TNBC and (C) HER2 positive cancers. Metagenes describing IF1, macrophage, MHC1, MHC2, STAT1, T follicular cells, T cell inhibitory and stimulatory activity, as well as lymphocyte-specific kinase (LCK), cytolytic activity (CTL), and consensus T-cell metagene (CTM) show unimodal normal distributions. Metagenes describing natural killer (NK) cells, and regulatory T-cells (T-regs) show bimodal distributions.

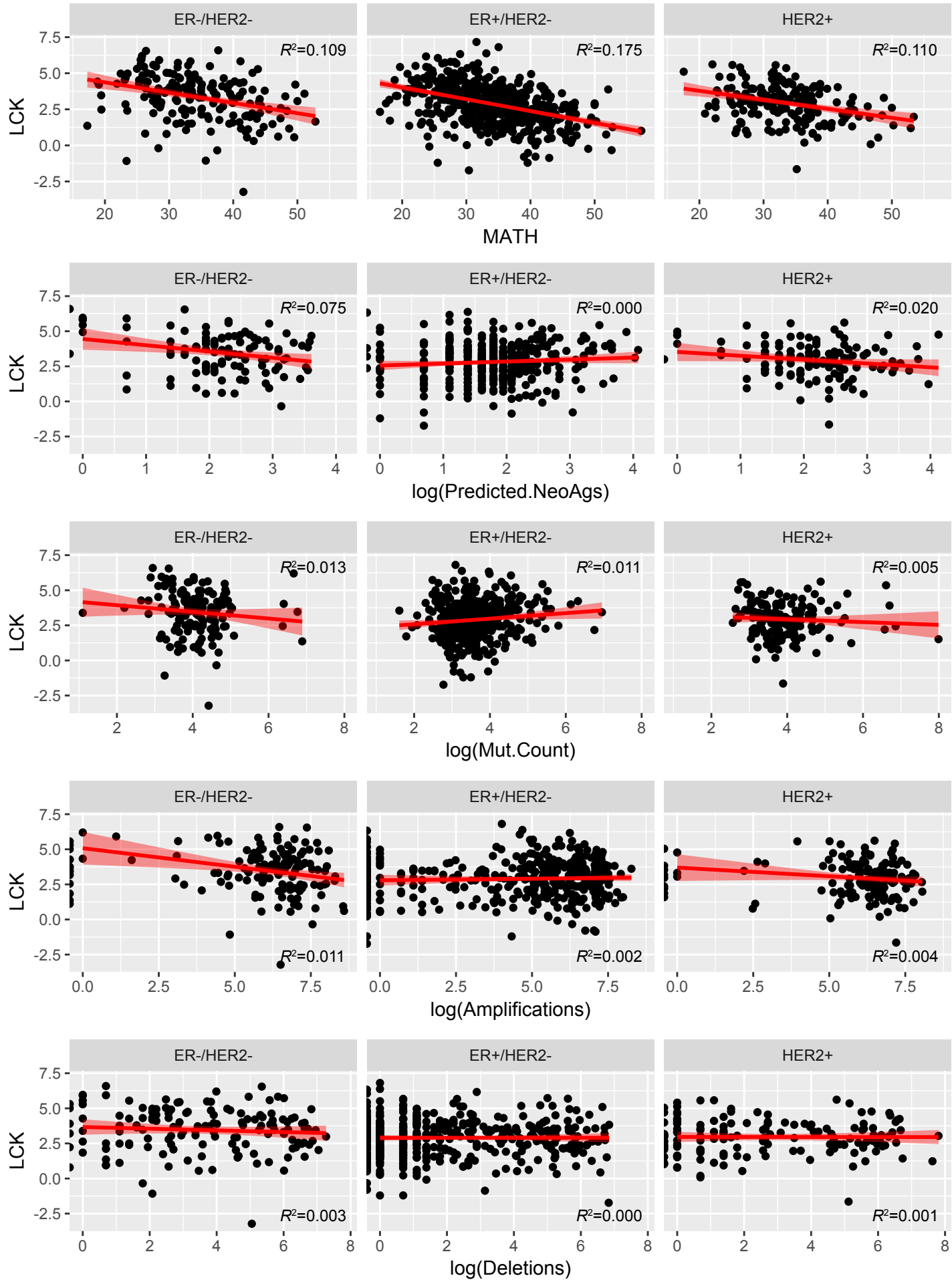

LCK metagene expression
7.5
5.0
2.5
0
-2.5
0%
1%
2%
4%
8%
16%
32%
64%
128%
Percent of mononuclear cells within section

Supplementary Figure S2. Correlation between the LCK metagene expression and infiltrating lymphocyte (TIL) count. TILs were quantified histologically, and the data were obtained from Lehman BD et al (*PLoS One* 11.6 (2016): e0157368). The percent mononuclear cells are plotted on a log scale (n=171 triple negative breast cancers), Spearman rho=0.64 (P<0.001).


MATH
log(Predicted.NeoAgs)
log(Mut.Count)
log(Amplifications)
log(Deletions)
LCK
p<0.001
p=0.027
ER-/HER2-
ER+/HER2-
HER2+
Subtype

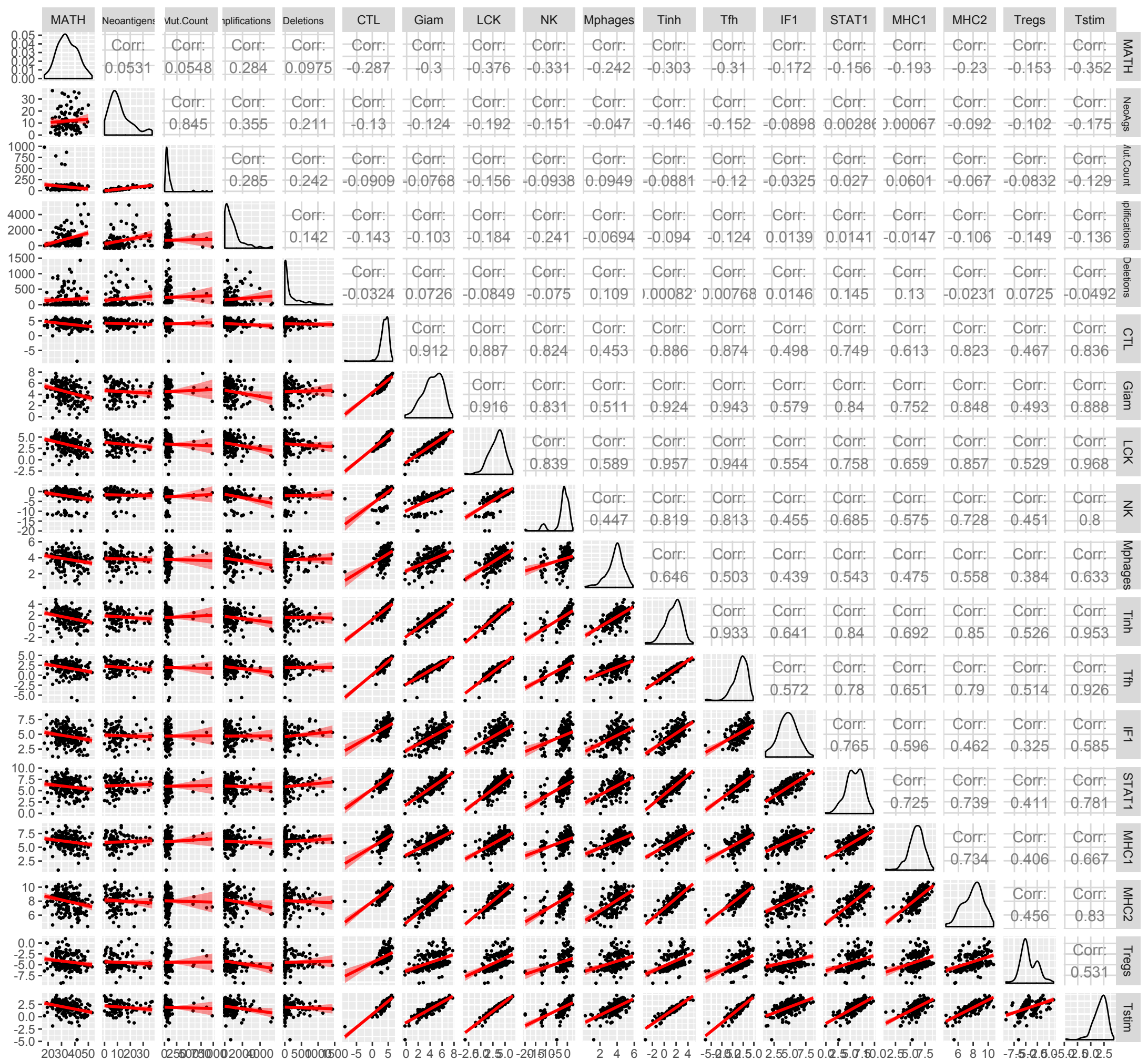
Suppl. Fig S3

Supplementary Figure S3. The distribution of genomic features and LCK metagene expression within breast cancer subtypes in the TCGA. The medians of the distribution of each molecular feature were compared using the Wilcoxon test. P-values < 0.05 are shown on the plot.


ER-/HER2-
ER+/HER2-
HER2+
LCK
MATH
R^2=0.109
R^2=0.175
R^2=0.110
log(Predicted.NeoAgs)
R^2=0.075
R^2=0.000
R^2=0.020
log(Mut.Count)
R^2=0.013
R^2=0.011
R^2=0.005
log(Amplifications)
R^2=0.011
R^2=0.002
R^2=0.004
log(Deletions)
R^2=0.003
R^2=0.000
R^2=0.001

Suppl. Fig S4

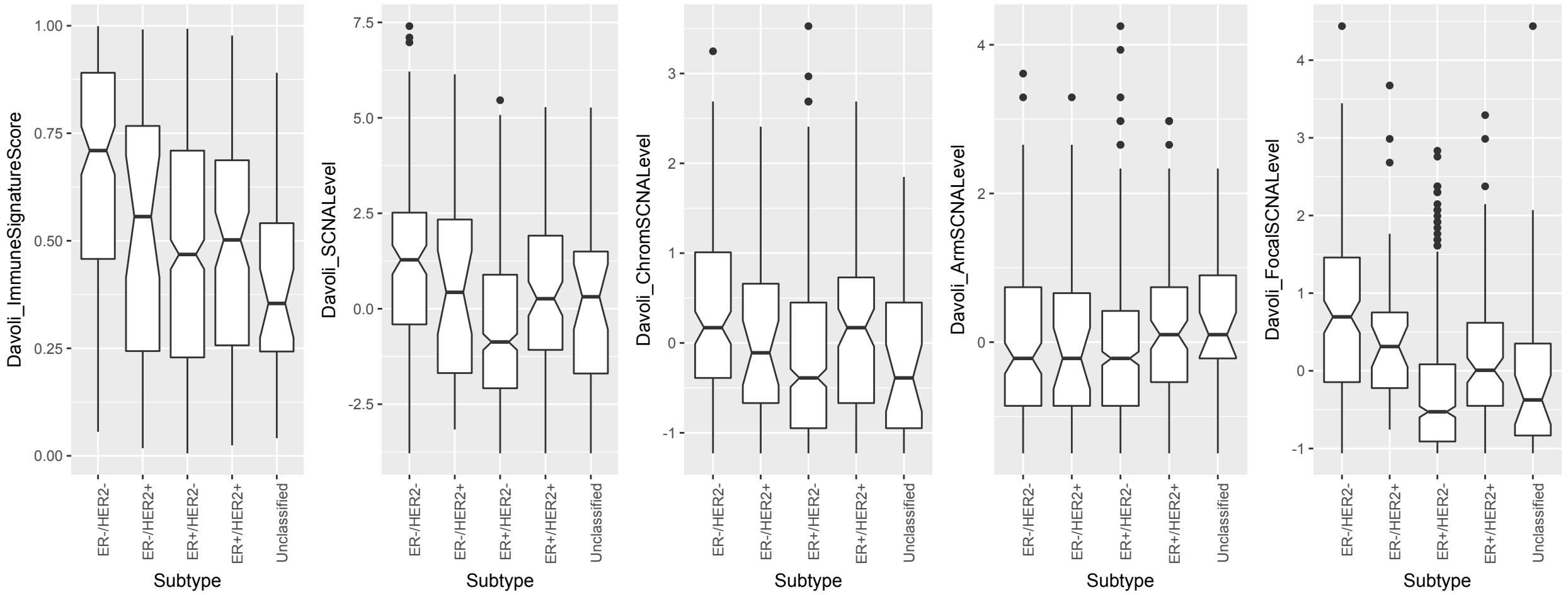
Supplementary Figure S4. Correlations between 13 immune metagene expressions and 5 exome-wide genomic features including all breast cancers combined in TCGA. Linear regression lines are shown in the scatterplots (left lower half) along with the Spearman rank correlation coefficients (right upper half) and the kernel density estimates of each feature (distribution curves in the diagonal).


MATH
Neoantigens
Mut.Count
plifications
Deletions
CTL
Giam
LCK
NK
Mphages
Tinh
Tfh
IF1
STAT1
MHC1
MHC2
Tregs
Tstim
NeoAgs
Corr: 0.0531
Corr: 0.0548
Corr: 0.284
Corr: 0.0975
Corr: -0.287
Corr: -0.3
Corr: -0.376
Corr: -0.331
Corr: -0.242
Corr: -0.303
Corr: -0.31
Corr: -0.172
Corr: -0.156
Corr: -0.193
Corr: -0.23
Corr: -0.153
Corr: -0.352
Corr: 0.845
Corr: 0.355
Corr: 0.211
Corr: -0.13
Corr: -0.124
Corr: -0.192
Corr: -0.151
Corr: -0.047
Corr: -0.146
Corr: -0.152
Corr: -0.0898
Corr: 0.00286
Corr: 0.00067
Corr: -0.092
Corr: -0.102
Corr: -0.175
Corr: 0.285
Corr: 0.242
Corr: -0.0909
Corr: -0.0768
Corr: -0.156
Corr: -0.0938
Corr: 0.0949
Corr: -0.0881
Corr: -0.12
Corr: -0.0325
Corr: 0.027
Corr: 0.0601
Corr: -0.067
Corr: -0.0832
Corr: -0.129
Corr: 0.142
Corr: -0.143
Corr: -0.103
Corr: -0.184
Corr: -0.241
Corr: -0.0694
Corr: -0.094
Corr: -0.124
Corr: 0.0139
Corr: 0.0141
Corr: -0.0147
Corr: -0.106
Corr: -0.149
Corr: -0.136
Corr: -0.0324
Corr: 0.0726
Corr: -0.0849
Corr: -0.075
Corr: 0.109
Corr: 0.00082
Corr: 0.00768
Corr: 0.0146
Corr: 0.145
Corr: 0.13
Corr: -0.0231
Corr: 0.0725
Corr: -0.0492
Corr: 0.912
Corr: 0.887
Corr: 0.824
Corr: 0.453
Corr: 0.886
Corr: 0.874
Corr: 0.498
Corr: 0.749
Corr: 0.613
Corr: 0.823
Corr: 0.467
Corr: 0.836
Corr: 0.916
Corr: 0.831
Corr: 0.511
Corr: 0.924
Corr: 0.943
Corr: 0.579
Corr: 0.84
Corr: 0.752
Corr: 0.848
Corr: 0.493
Corr: 0.888
Corr: 0.839
Corr: 0.589
Corr: 0.957
Corr: 0.944
Corr: 0.554
Corr: 0.758
Corr: 0.659
Corr: 0.857
Corr: 0.529
Corr: 0.968
Corr: 0.447
Corr: 0.819
Corr: 0.813
Corr: 0.455
Corr: 0.685
Corr: 0.575
Corr: 0.728
Corr: 0.451
Corr: 0.8
Corr: 0.646
Corr: 0.503
Corr: 0.439
Corr: 0.543
Corr: 0.475
Corr: 0.558
Corr: 0.384
Corr: 0.633
Corr: 0.933
Corr: 0.641
Corr: 0.84
Corr: 0.692
Corr: 0.85
Corr: 0.526
Corr: 0.953
Corr: 0.572
Corr: 0.78
Corr: 0.651
Corr: 0.79
Corr: 0.514
Corr: 0.926
Corr: 0.765
Corr: 0.596
Corr: 0.462
Corr: 0.325
Corr: 0.585
Corr: 0.725
Corr: 0.739
Corr: 0.411
Corr: 0.781
Corr: 0.734
Corr: 0.406
Corr: 0.667
Corr: 0.456
Corr: 0.83
Corr: 0.531

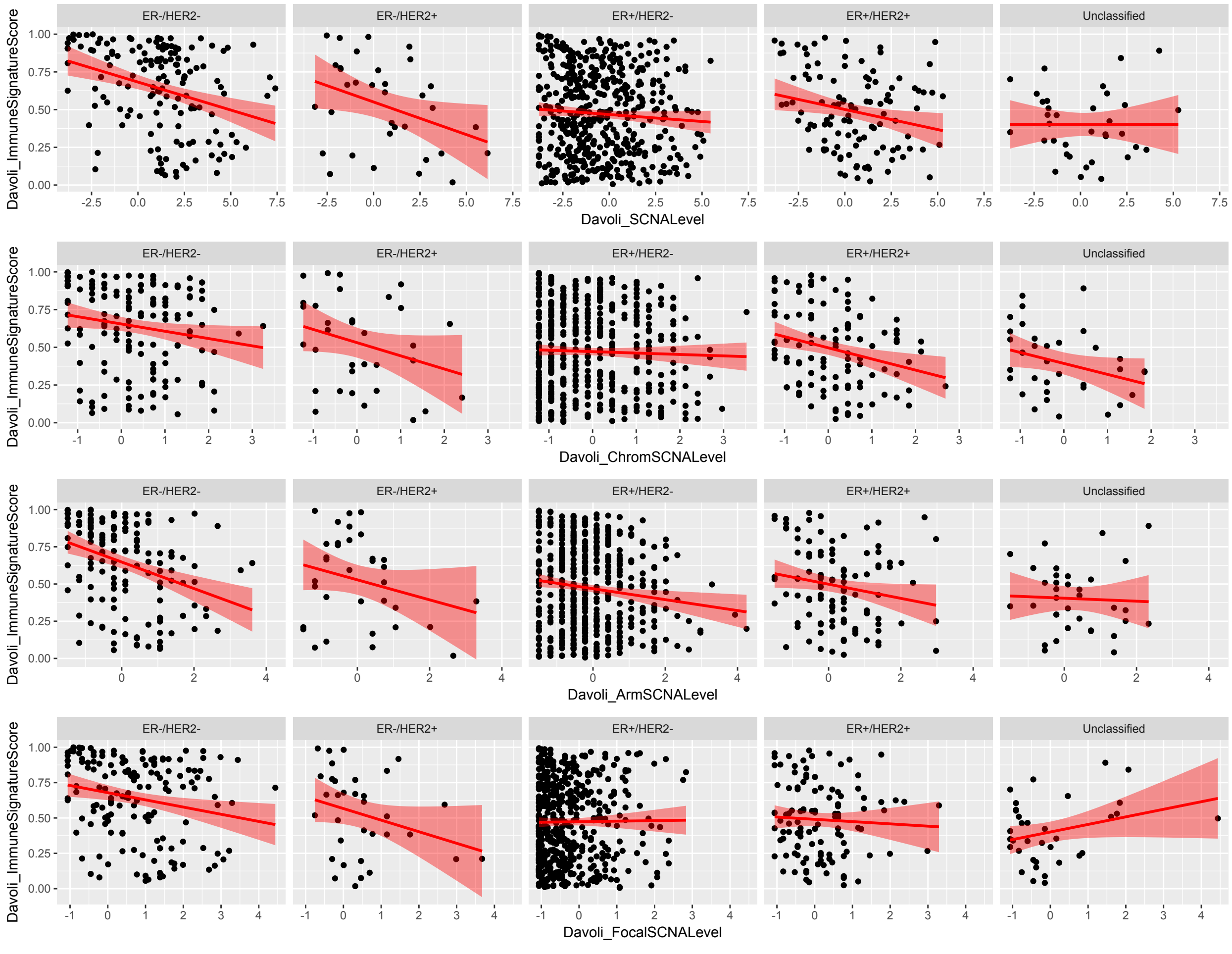
Suppl. Fig S5

Supplementary Figure S5. Correlations between the LCK immune metagene expression and five different genomic features within each breast cancer subtype in the TCGA. The linear regression line is shown (red) along with the corresponding R^2 values for each subtype.

a



b



Suppl Fig S6

Supplementary Figure S6. Distribution of genomic features and their correlation with an immune metagene in the breast cancer subtypes from TCGA data. Plots were generated by using published data from Davoli et al (ref 34). Somatic copy number alteration (SCNA) levels were calculated with adjustment for estimated tumor cellularity as described in the manuscript.