## Corrigendum

## Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis

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The authors regret that the below figures in this manuscript should have been published in colour.

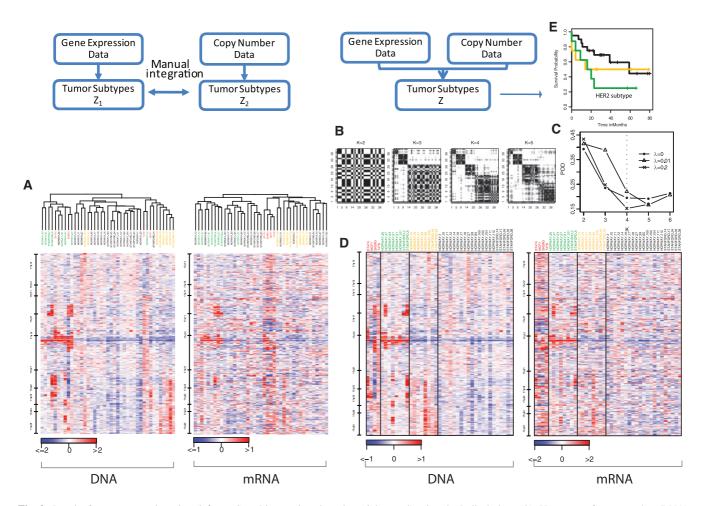


Fig. 2. Results from separate clustering (left panel) and integrative clustering (right panel) using the Pollack data. (A). Heatmaps of copy number (DNA) and gene expression (mRNA) on chromosome 17. Samples are arranged by separate hierarchical clustering on each data type. (B) Cluster separability plots. (C) Model selection based on POD measure. A four-cluster sparse solution ( $\lambda = 0.2$ ) was chosen. (D) Heatmaps on the same data as in A with samples arranged by the integrated cluster assignment under the sparse iCluster model. (E) Kaplan–Meier plots of the subclasses identified via the integrative clustering. The HER2/ERBB2 subtype showed poor survival.

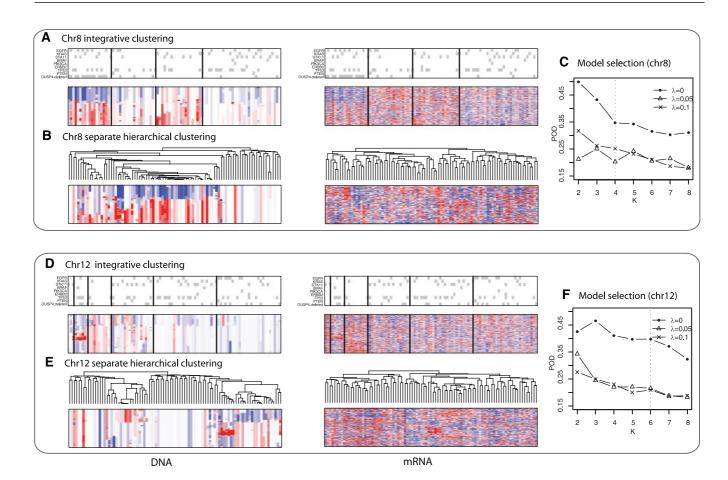


Fig. 3. Lung cancer subtypes for chromosomes 8 and 12. (A) Heatmap of DNA copy number (left) and mRNA expression (right) on chromosome 8. Columns are tumors arranged by the three subclasses obtained by iCluster. Rows are genes ordered by genomic position. On top of the heatmaps are gray-dot panels indicating mutation status of several well-known lung cancer genes. (B) Separate hierarchical clustering of the same data on chromosome 8 used in (A). (C) Model selection based on the POD measure. A four-cluster sparse solution ( $\lambda$  = 0.05) was chosen that selected 301 mRNA probes and 126 DNA probes from a total of 642 probes. (D) iCluster output on chromosome 12. Tumor samples are arranged by the six subclasses obtained by iCluster.(E) Separate hierarchical clustering of the same data on chromosome 12 used in (D). (F) Model selection based on the POD statistic. A six-cluster sparse solution ( $\lambda$  = 0.1) was chosen that selected 408 mRNA probes and 24 DNA probes from a total of 1038 probes.