**Table S1. Signatures summary.**

A summary of 33 signatures about the platforms derived from, the subtypes used for, the gene number included, and the function terms involved.

| classes | | Signatures number (n) |
|---|---|---|
| **Subtype used for** | | 33 |
| | ER-positive | 10 |
| | ER-negative | 2 |
| | HER2-enriched | 3 |
| | Triple negative/basal | 6 |
| | mix subtypes | 12 |
| **Platform derived from** | | 33 |
| | Affymetrix microarray | 18 |
| | Agilent microarray | 6 |
| | RT-PCR/qRT-PCR/ATAC-PCR | 7 |
| | - FISH | 1 |
| | Immunohistochemistry | 1 |
| | other microarray | 2 |
| **Number of genes included** | | 33 |
| | < 10 | 9 |
| | 10~50 | 11 |
| | 50~100 | 7 |
| | > 100 | 6 |
| **Number of function terms included** | | 29 |
| | < 10 | 5 |
| | 10~50 | 11 |
| | 50~100 | 5 |
| | > 100 | 8 |

**Table S8. The number of function terms in each signature.**

| signature_union | number_of_term |
|---|---|
| Tcell | 199 |
| HDPP | 187 |
| MBC | 187 |
| Robust | 177 |
| PAM50 | 163 |
| Novel2 | 159 |
| GGI97 | 143 |
| CCPS | 111 |
| Olaf | 94 |
| Iwao | 74 |
| LM | 65 |
| Pawitan | 59 |
| RS | 55 |
| Chang | 50 |
| IGS | 41 |
| GCN | 31 |
| SDPP | 31 |
| Wang | 27 |
| Mamma | 23 |
| Endo | 21 |
| MS14 | 21 |
| Bcell | 12 |
| BCI | 12 |
| Vegran | 11 |
| IR7 | 8 |
| Novel1 | 7 |
| p53 | 6 |
| GGI8 | 4 |
| SMS | 1 |

The number of significant function terms of each signature generated by DAVID is listed in this table. We selected GO term Biological process and KEGG pathways to define the functions enrichment with the default settings (EASE p-value less than 0.1). No significantly enriched function terms were found for four signatures (HI, IHC4, Multigene and MAGEA).