**SUPPLEMENTARY TABLE AND FIGURE LEGEND**

**SUPPLEMENTARY TABLES:**

**Supplementary Table S1:** Whole genome regions with copy number gain/loss were included.

**Supplementary Table S2:** All genes with CNA affecting candidate pathway genes and statistically significant positive correlation (p-value <10-4, qFDR <10-4) with gene expression are represented (N = 2,364).

**Supplementary Table S3:** Gene expression signature predictive of complete response (CR) versus incomplete response (IR) using the CNA-Correlated-Pathway (CCP) gene subset.

**Supplementary Table S4:** Differentially methylated genes between the CR and IR groups.

**Supplementary Table S5:** Differentially expressed miRNA between the CR and IR groups.

**Supplementary Table S6:** Differentially expressed genes (CR versus IR) from the 1,772 genes identified to have TF binding sites within the CNA-Correlated-Pathway (CCP) gene subset.

**Supplementary Table S7:** 422 significant genes included in the final model or signature.

**Supplementary Table S8:** Pathways and biological processes identified with the software for enrichment analysis GeneGo. These pathways were overrepresented in cluster #1 of the NMF consensus clustering.

**Supplementary Table S9:** Pathways and biological processes identified with the software for enrichment analysis GeneGo. These pathways overrepresented in cluster #2 of the NMF consensus clustering.

**SUPPLEMENTARY FIGURES:**

**Supplementary Figure S1:** Multivariate analysis of clinical factors affecting survival in TCGA database. Kaplan-Meier curve representing survival of patients with CR versus patients with IR (above). Table with independent clinical variables for survival in TCGA: chemo-response is the most significant of all of them with a p-value <10-15 (below)

**Supplementary Figure S2:** Differentially expressed genes between patients with complete response (CR) and patients with incomplete response (IR) in the 3 clinical databases (GSE9891, TCGA, GSE23554); and in OVCA cell lines after *in vitro* chemo-sensitivity analysis. Only common significant genes between analyses, marked with colored arrows, were included in the enrichment analysis with GeneGo (MetaCore TM, Carlsbad, CA).

**Supplementary Figure S3:** Representation of genomic somatic gains and losses determined by the genomic identification of significant targets in cancer (GISTIC) analysis. Losses (blue) and gains (red) are represented with respect to their position in each chromosome. Depiction of X and Y chromosomes are the result of all individuals being female.

**Supplementary Figure S4:** TCGA analyses of gene expression, mutations, DNA methylation and miRNA expression between CR samples and IR samples.

**Panel A.** Heat map of a 69 gene expression signature predictive of CR versus IR in the correlated CNA-gene expression (CCP) subset of genes.

**Panel B.** Mutated genes associated with chemo-response, CR versus IR (in the first column) and their significant correlation with expressed genes (second column) in the CCP gene subset, p-value <10-4.

**Panel C.** Heat map of the 69 genes differentially methylated between the CR and IR groups at 0.001 level of the univariate test.

**Panel D:** Heat map of the 38 miRNA differentially expressed between the CR and IR groups (p-value <0.05, as there were only 619 unique miRNA entering the analysis).

**Supplementary Figure S5:** Validation of TCGA gene expression signature in independent available databases. Same study design (definitions of variables, normalization procedures, statistics), same software and analysis tools (BRB ArrayTools) were used for validation.

Above: GEO# GSE9891[15](#_ENREF_15), with a p-value < 0.001. Below: GSE23554[12](#_ENREF_12), with a p-value of 0.02 (left); GSE28739[16](#_ENREF_16), with a p-value of 0.01 (right).

**Supplementary Figure S6:** Transcription factor (TF) binding site analysis.

**Panel A.** Heat map of the 59 differentially expressed genes between CR and IR that were identified to have TF binding sites at the CCP gene subset (p-value <0.01).

**Panel B.** UCSC Genome Browser of one of the significant genes, *RHOT1*, with representation of its TF binding sites (above) and conserved gene structure across species (below).

**Supplementary Figure S7:** Detail of level of agreement (kappa coefficient) for placement of an individual gene in the same cluster than in TCGA analysis represented in contingency tables.

**Panel A.** GSE9891 database[15](#_ENREF_15).

**Panel B.** GSE3149 database[14](#_ENREF_14).

**Panel C.** GSE26712 database[18](#_ENREF_18).

**Panel D.** GSE23554 database[12](#_ENREF_12).

**Panel E.** GSE17260 database[17](#_ENREF_17).