SM Description

Figure S1. Western blotting analysis of H3K4me3 levels in MCF-7 cells incubated for 24 hours with three different concentrations of RS 3195. Shown image is representative from six independent experiments.

Figure S2. Quantification of six independent western blotting experiments, showing a slight increase in H3K4m3 levels upon RS 3195 treatment. Data are normalized to DMSO control and represented as the mean ± SD of relative H3K4me3 levels.

Figure S3. Dot plot representation of the results of Gene Ontology (Biological Process) analysis of RNA sequencing data from treated and untreated MCF7 cell samples, showing the categories of biological processes most enriched in genes upregulated or downregulated in treated MCF7 cell samples.

Figure S4. Volcano plot of log2 fold-change (x-axis) versus −log10 q-value (y-axis, representing the probability that the gene is differentially expressed) of the results of RNA sequencing analysis of treated and untreated MCF7 cell samples. 135 genes were significantly downregulated (blue dots) or upregulated (red dots), in grey are reported not significant modulated genes.

Figure S5. Scatchard plot of RS3152, RS3183, RS3195, RS4995, RS5033.

Figure S6. Flow-cytometry analysis of cell-cycle distribution of MCF-7 cells treated with two different concentrations of RS 5033. Shown image is representative from three independent experiments.

Figure S7. Quantification of three independent experiments of flow cytometry analysis, showing no significant perturbation of cell cycle dynamics by RS 5033 treatment. Data are represented as the mean ± SD of the corresponding percentage of cells in a particular cell cycle phase.

Figure S8. Transcript levels analysis by Real Time PCR of CYP1A1 and AHRR genes in MCF-7 cells treated with 10 µM RS 5033, showing a lower increase of these genes compared to RS 3195.

Figure S9. Real Time PCR analysis of genes involved in breast cancer in MCF-7 cells upon treatment with RS 5033. Analysis of BRCA1, MT1F, AKR1C2 and PCDH10 transcript levels in MCF-7 cells treated with RS 5033. Data are represented as the mean ± SD of fold change mRNA levels from at least three independent experiments using DMSO as control. Statistical significance was assessed according to two-tailed paired Student's t test. * $p<0.05$; ** $p<0.001$

Figure S10. Real Time PCR analysis of genes involved in breast cancer in MCF-7 cells upon treatment with KDOAM-25. Analysis of *BRCA1*, *MT1F, AKR1C2* and *PCDH10* transcript levels in MCF-7 cells treated with KDOAM-25 (B). Data are represented as the mean ± SD of fold change mRNA levels from at least three independent experiments using DMSO as control. Statistical significance was assessed according to two-tailed paired Student's t test. * *$p<0.05$; ** $p<0.001$*