

## Description of Additional Supplementary Files

**Supplementary Data 1** - Information about patient samples and oligonucleotides

**Sheet 1** – Detailed information about ovarian cancer patients

**Sheet 2** – List of experiments with ovarian cancer ascitic fluids

**Sheet 3** – List of oligonucleotides and their sequences used in this study

**Sheet 4** – Determination of cisplatin in secretomes by LC-MS/MS

**Supplementary Data 2** - Transcriptomic profiles of ovarian cancer cells isolated from paired cancer ascites before and after chemotherapy

**Sheet 1** – Analysis of differentially expressed genes in ovarian cancer cells after chemotherapy

**Sheet 2** – Results of the GSEA enrichment analysis of genes that were differentially expressed in ovarian cancer cells after chemotherapy

**Supplementary Data 3** - Transcriptomic and proteomic profiles of ovarian cancer cells incubated with autologous ascitic fluids from patients before and after chemotherapy

**Sheet 1** – Analysis of differentially expressed genes in epithelial ovarian cancer cells incubated with ascitic fluids after chemotherapy

**Sheet 2** – Analysis of differentially expressed genes in neuroendocrine ovarian cancer cells incubated with ascitic fluids after chemotherapy

**Sheet 3** – Proteins identified by LC-MS/MS analysis of ovarian cancer cells incubated with autologous ascitic fluids from patients before and after chemotherapy

**Supplementary Data 4** - Proteome profiles of ovarian cancer ascitic fluids and in vitro secretomes before and after chemotherapy

**Sheet 1** – Proteins identified by LC-MS/MS analysis of paired ovarian cancer ascitic fluids before and after chemotherapy

**Sheet 2** – Proteins identified by LC-MS/MS analysis of secretomes from cisplatin-treated or untreated SKOV3 cells and Fibroblasts

**Sheet 3** – Proteins identified by LC-MS/MS analysis of secretomes from cisplatin-treated or untreated cells

**Sheet 4** – KEGG enrichment analysis of proteins whose abundance increased in therapy-induced secretomes

**Sheet 5** – Table of spliceosomal proteins identified in ascitic fluids and secretomes after therapy

**Sheet 6** – Comparison of proteins identified in ascitic fluids and secretomes with proteins related to stress granules and senescence-associated secretory phenotype

**Supplementary Data 5** - Proteome and transcriptome profiles of SKOV3 cells in response to cisplatin treatment and incubation with secretomes before and after therapy

**Sheet 1** – Proteins identified by LC-MS/MS analysis of SKOV3 cell fractions before and after cisplatin treatment

**Sheet 2** – SILAC data analysis of unlabeled recipient SKOV3 cells after incubation with therapy-induced or control secretomes containing heavy-labeled proteins

**Sheet 3** – Analysis of differentially expressed genes in SKOV3 cells incubated with therapy-induced secretomes

**Sheet 4** – Analysis of differentially abundant proteins in SKOV3 cells incubated with therapy-induced secretomes

**Sheet 5** – Analysis of differentially expressed genes in SKOV3 cells incubated with therapy-induced secretomes

**Supplementary Data 6** - Transcriptome profiles of SKOV3 cells with overexpression of SYNCRIP or SNU13 in response to cisplatin treatment

**Sheet 1** – Analysis of differentially expressed genes in SKOV3 with overexpression of SYNCRIP or SNU13 in response to cisplatin treatment

**Supplementary Data 7** - Effect of extracellular spliceosomal snRNAs on the transcriptome and proteome of ovarian cancer cells

**Sheet 1** – Analysis of differentially expressed genes in SKOV3 cells transfected with snRNAs

**Sheet 2** – Proteins identified by LC-MS/MS analysis of SKOV3 cells transfected with snRNAs