

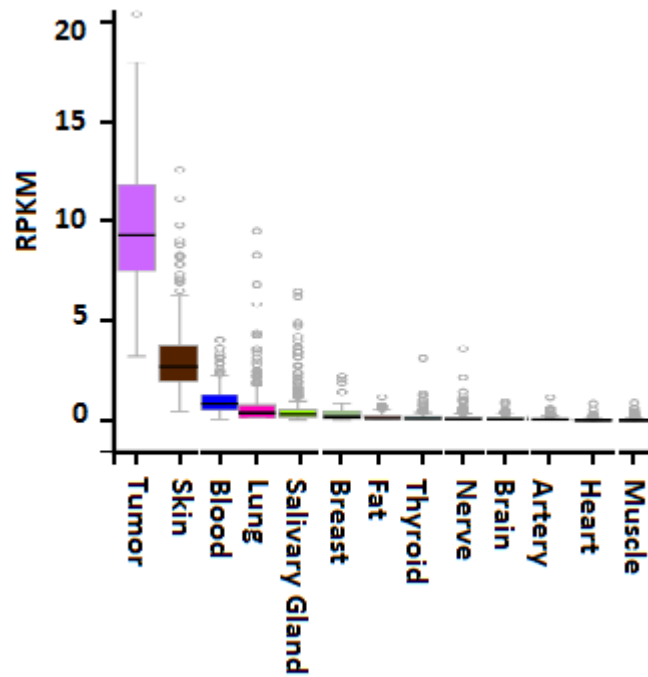
OMTO, Volume 12

Supplemental Information

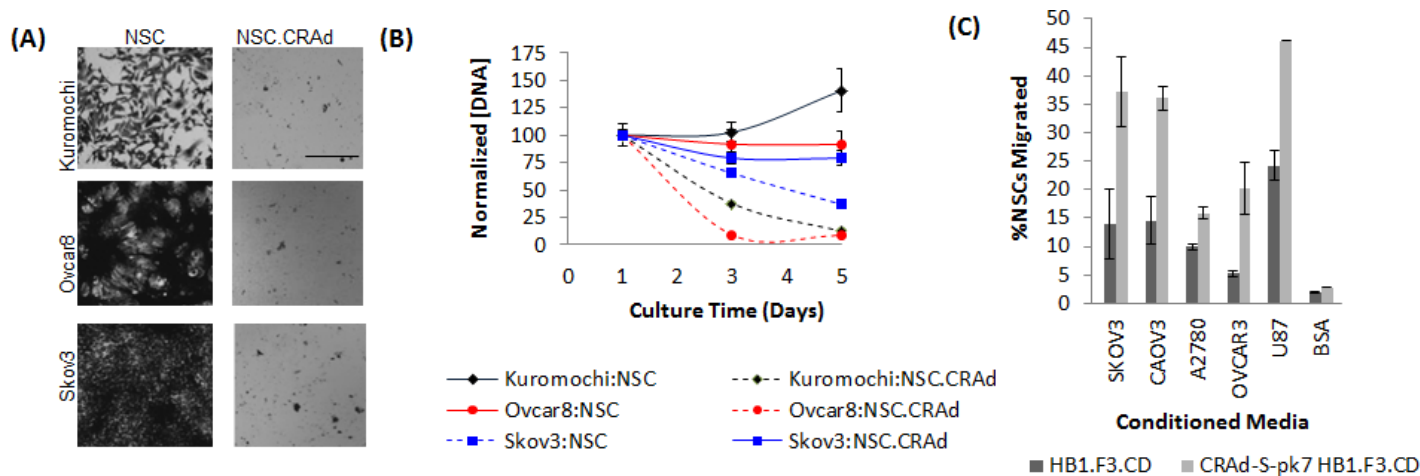
Enhanced Delivery of Oncolytic Adenovirus by Neural Stem Cells for Treatment of Metastatic Ovarian Cancer

Rachael Mooney, Asma Abdul Majid, Jennifer Batalla-Covello, Diana Machado, Xueli Liu, Joanna Gonzaga, Revathiswari Tirughana, Mohamed Hammad, Thanh H. Dellinger, Maciej S. Lesniak, David T. Curiel, and Karen S. Aboody

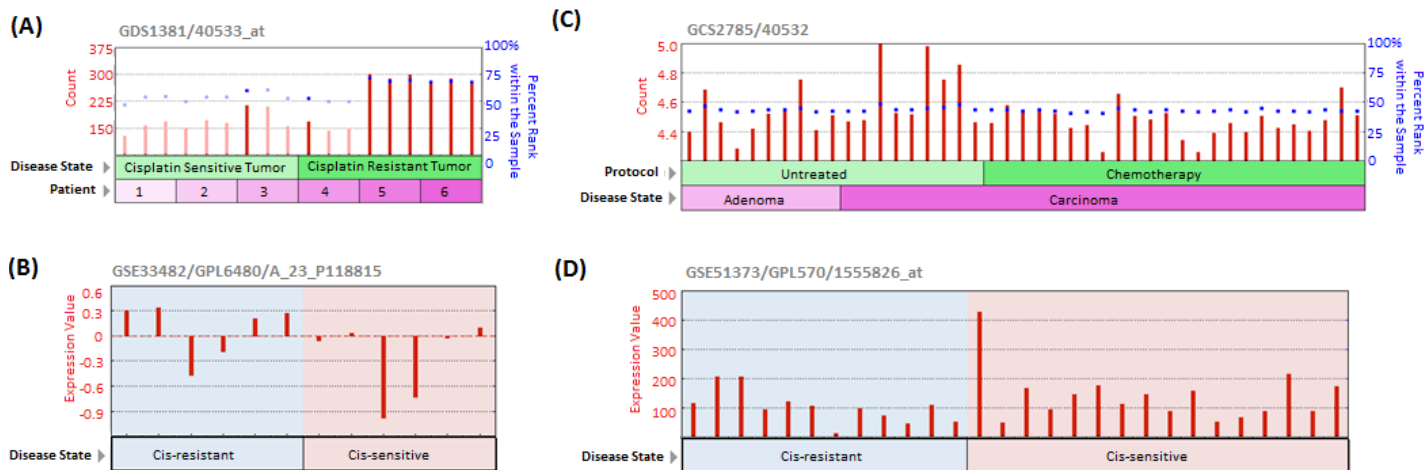
Supplemental Information



Supplementary Figure 1. Analysis of GTExPortal data showing survivin expression in various organs and tissues from outside the peritoneum. Expression values are shown in RPKM (reads per kilobase of transcript per million mapped reads), calculated from a gene model in which isoforms were collapsed to a single gene. No other normalization steps were applied. Box plots are shown as median and 25th and 75th; points are displayed as outliers if they are greater than or less than 1.5 times the interquartile range.



Supplementary Figure 2. Ovarian cancer lysis by CRAd-s-pk7 NSCs. (A-B) CRAd-S-pk7 NSCs co-cultured in a 1:1 seeding ratio with 3 different cisplatin-resistant ovarian tumor cell lines shows elimination of tumor cells within 7 days as indicated by crystal violet stained culture wells (A); and a decrease in total DNA content in culture over 5 days (B). (C) Boyden migration assay comparing tropism of NSC-CRAd-S-pk7 and NSCs to ovarian cancer conditioned media vs. U87 (+,"100") and BSA (-) control media.



Supplementary Figure 3. Comparison of *survivin* expression levels in response to cisplatin treatment. Gene Expression Omnibus Accession Viewer data showing *survivin* (BIRC5, gene ID: 202095_s_at) expression in: (A) cancer cells prepared from primary cultures of ovarian papillary serous adenocarcinomas in response to cisplatin; (B) A2780 ovarian cancer cells in response to cisplatin; (C) malignant ovarian cancer tumors obtained from 43 patients receiving neo-adjuvant cisplatin therapy or not; and (D) 12 cisplatin-resistant and 16 cisplatin-sensitive high-grade serous epithelial ovarian cancer samples. For all samples, total RNA was analyzed by whole transcriptome profiling using Affymetrix U133 Plus 2.0 arrays.⁴⁸