

FIGURE LEGENDS

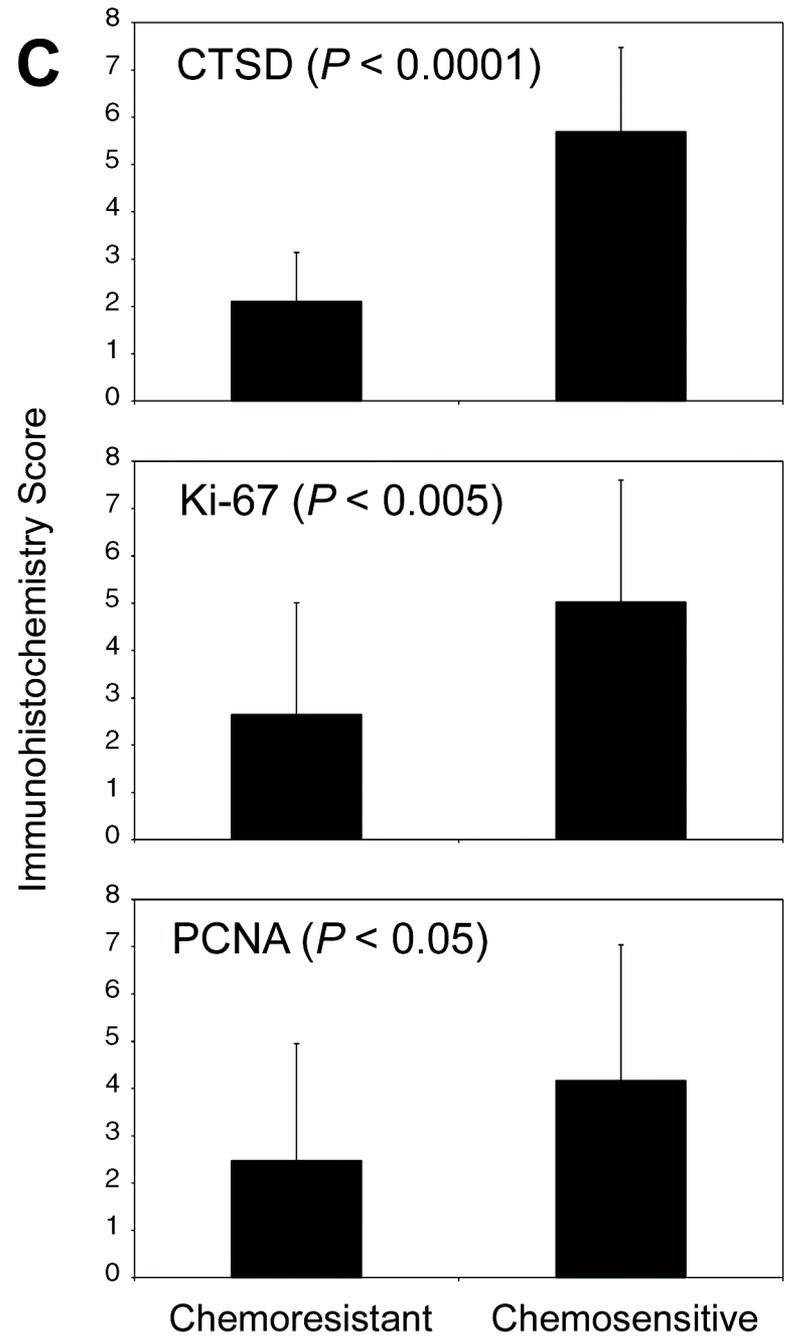
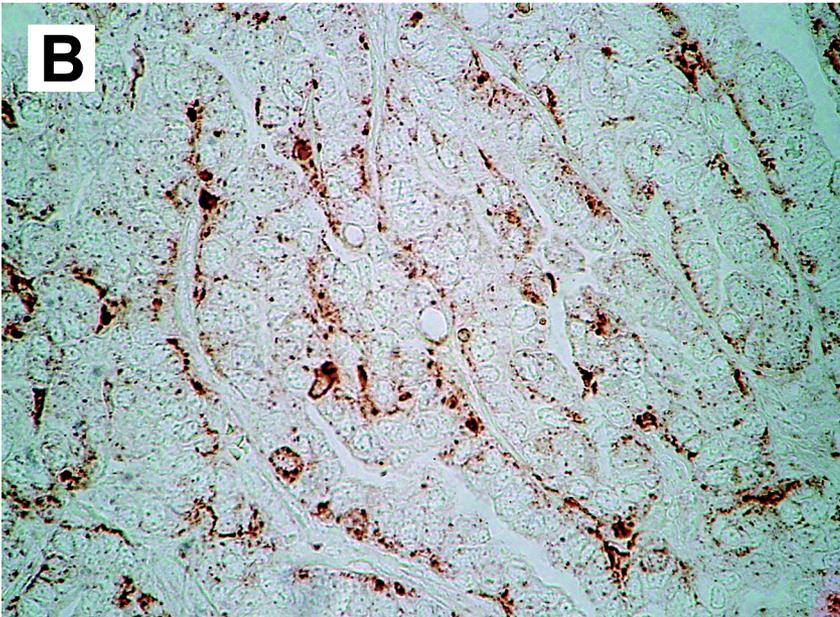
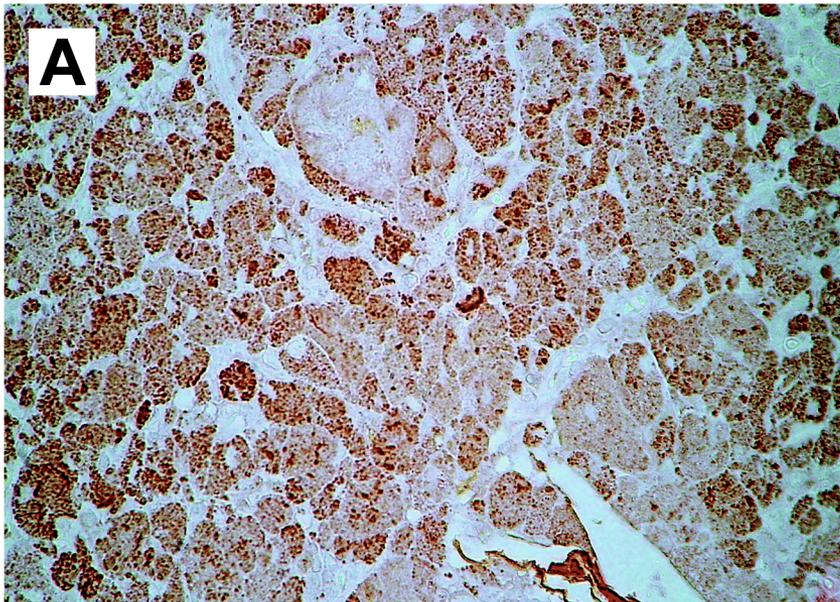
Fig. 1. Semi-quantitative immunohistochemical analyses of CTSD, Ki-67, and PCNA expression. Shown to the left are representative photomicrographs of primary chemosensitive (A) and primary chemoresistant (B) ovarian cancers immunostained for CTSD at 40X magnification. To the right are results of immunohistochemical scoring for CTSD (C), Ki-67 (D), and PCNA (E). Histograms represent mean score and error bars represent standard deviation.

Fig. 2. Gene expression differences between post-chemo and primary chemosensitive or primary chemoresistant tumors. A, An overview of the number of differentially expressed genes ($P < 0.001$), with the top circle representing post-chemo vs. primary chemosensitive samples, the bottom circle representing post-chemo vs. primary chemoresistant samples, and the overlap region representing genes differentially expressed between post-chemo samples and primary tumors irrespective of intrinsic chemosensitivity. B, Changes in the magnitude and direction of the 178 genes that discriminated the post-chemo samples from all primary tumors ($P < 0.001$). For each gene, the fold-difference between the post-chemo and the primary chemoresistant tumors (x-axis), is plotted against the fold-difference between the post-chemo and primary chemosensitive tumors (y-axis). Values less than 1.0 reflect higher expression in the primary tumors. r , Pearson correlation coefficient.

Fig. 3. Specific genes with statistically significant differential expression between post-chemo and primary tumors ($P < 0.001$). The corresponding expression values from normal postmenopausal ovaries are shown for comparison. A, Genes that were differentially expressed between the post-chemo tumors and both groups of primary tumors. The top 50 genes are shown; the full list may be found in supplemental data. B, Genes that were differentially higher expressed by two-fold or greater ($n = 41$) in the post-chemo compared to primary

chemosensitive tumors. Genes encoding extracellular matrix-related proteins are shown in bold type. *C*, Genes that were differentially higher expressed by two-fold or greater ($n = 10$) in primary chemosensitive compared to post-chemo tumors. *D*, Genes differentially expressed between the post-chemo tumors and the primary chemoresistant tumors.

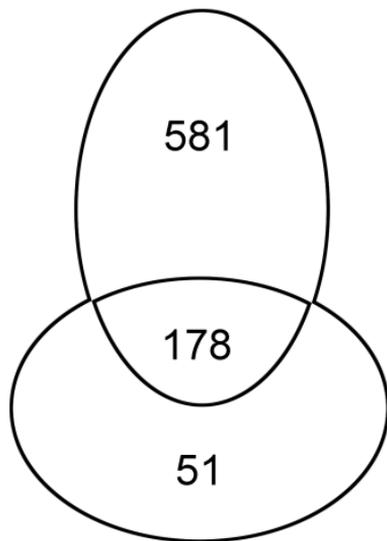
Fig. 4. Diagrammatic depiction of chemoresistance in primary and post-chemo samples. Smaller differences in gene expression observed between primary chemosensitive and chemoresistant tumors are likely the result of low relative abundance of intrinsically chemoresistant clones as predicted by the Goldie-Coleman hypothesis. Chemotherapy results in a reduction in the number of chemosensitive and an enrichment of chemoresistant clones in the post-chemo samples. In addition, chemotherapy is likely to induce additional genetic changes contributing to acquired chemoresistance. The combination of these effects is likely to be responsible for the robust differences in gene expression observed between the primary and post-chemo samples.



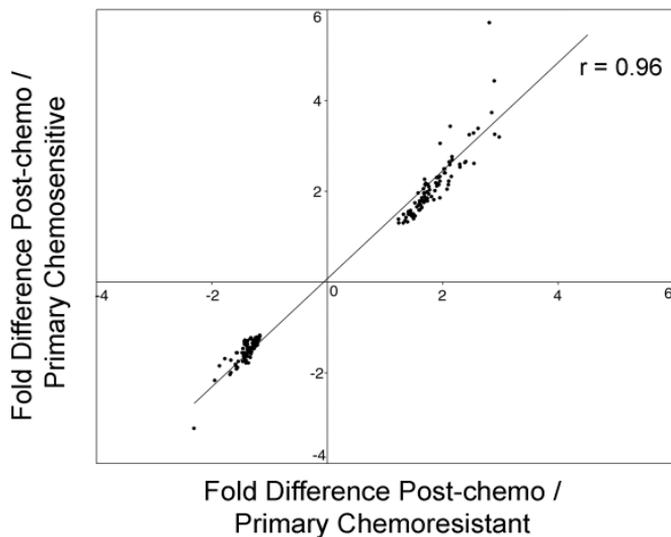
A

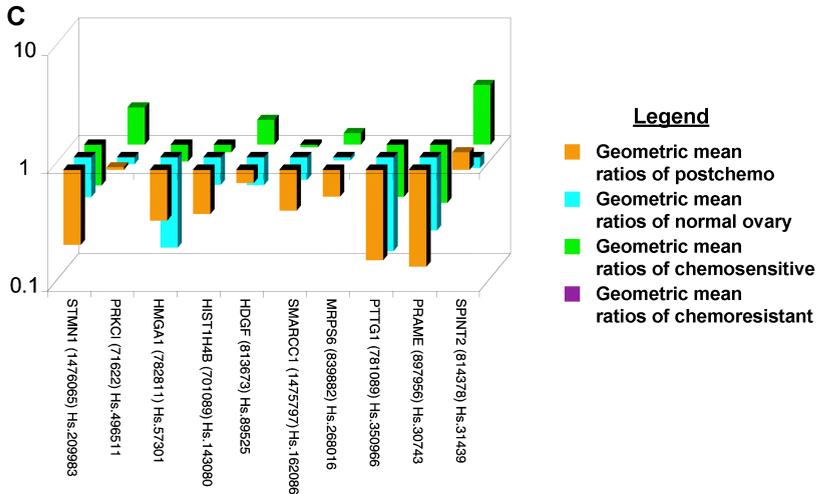
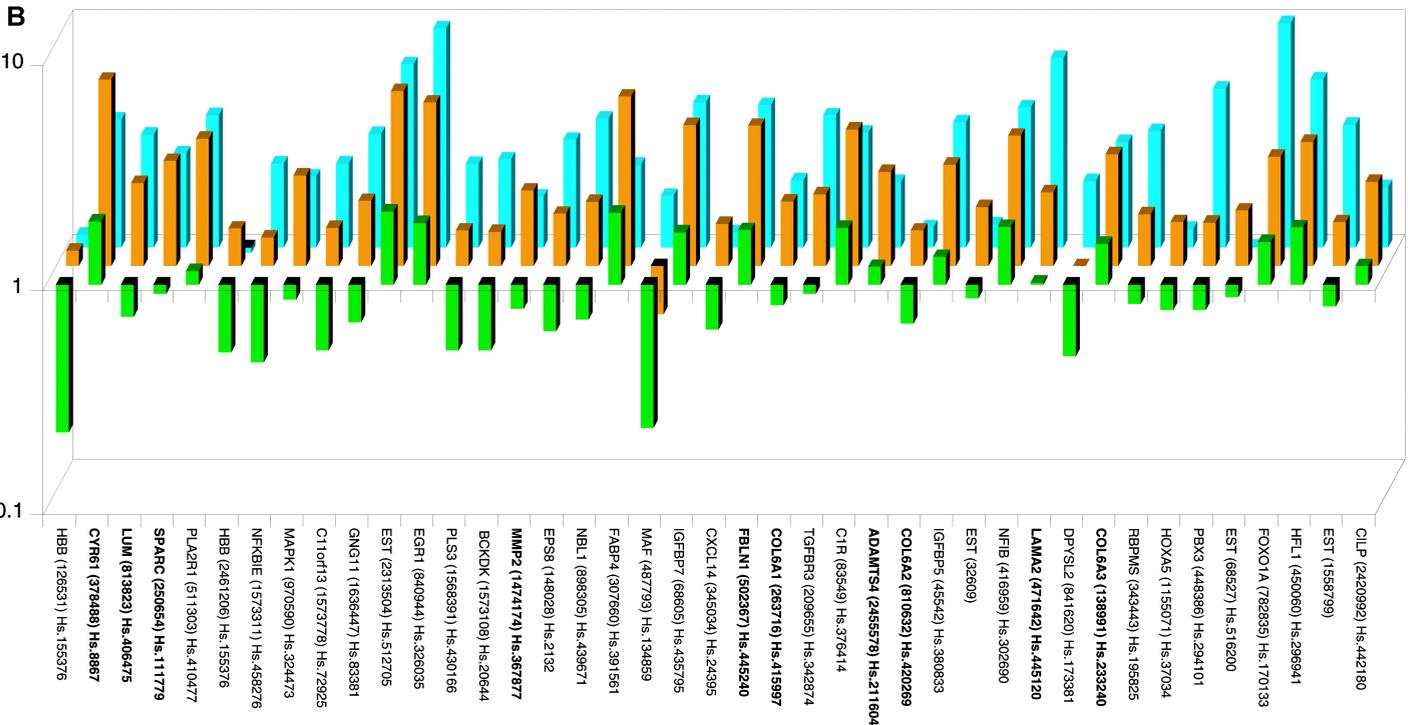
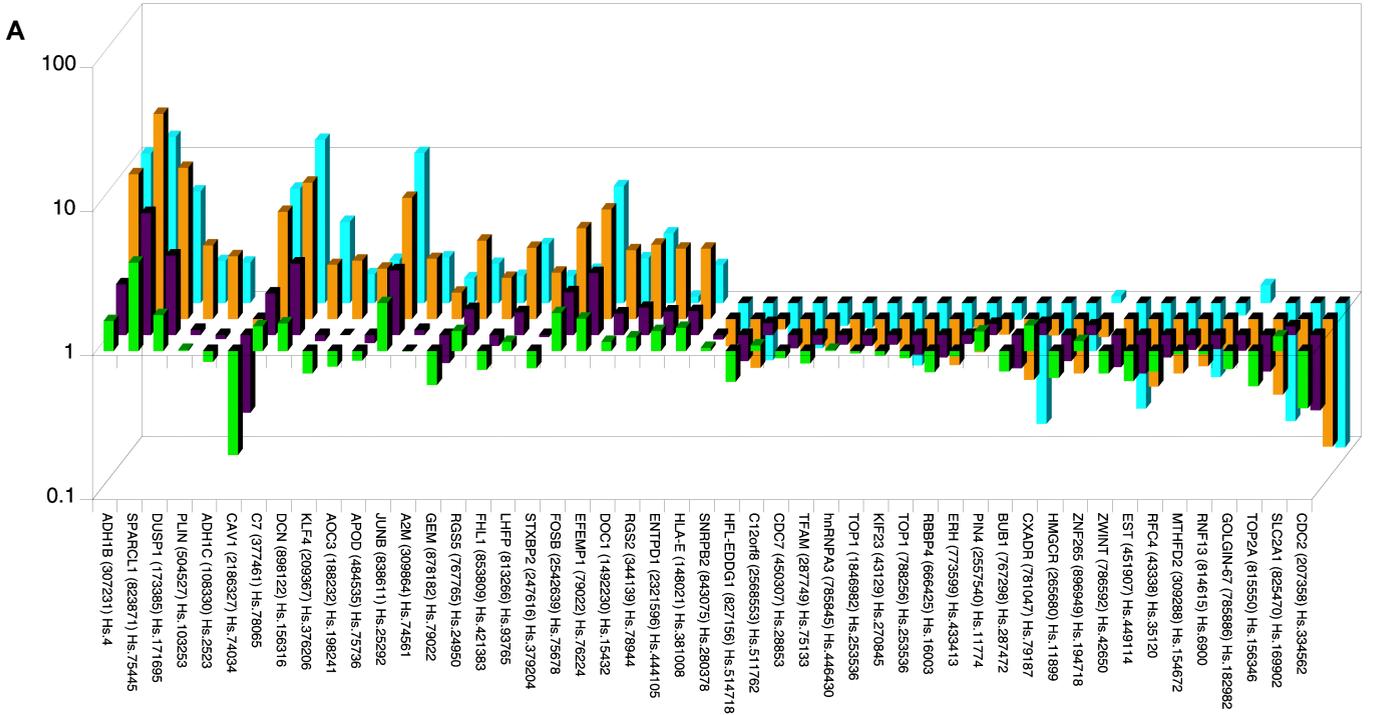
Primary chemosensitive
vs.
Post-chemo samples

Primary chemoresistant
vs.
Post-chemo samples



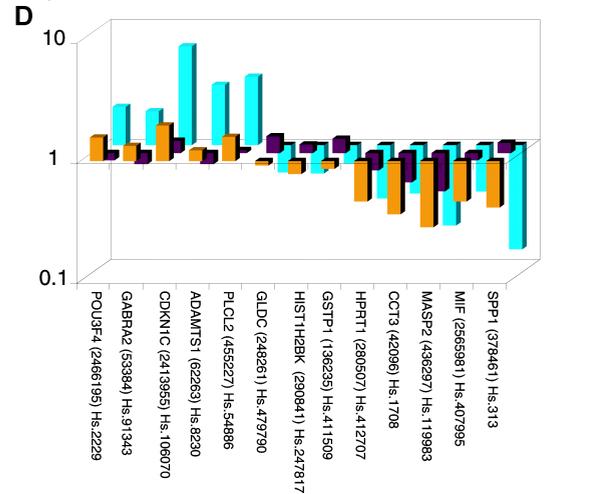
B



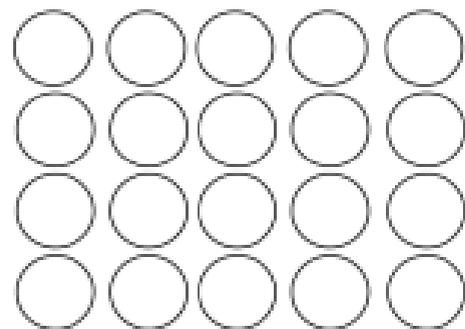


Legend

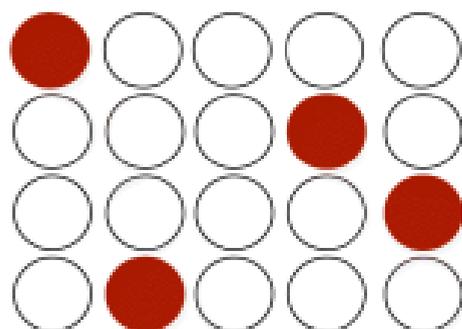
- Geometric mean ratios of postchemo
- Geometric mean ratios of normal ovary
- Geometric mean ratios of chemosensitive
- Geometric mean ratios of chemoresistant



Primary Tumors

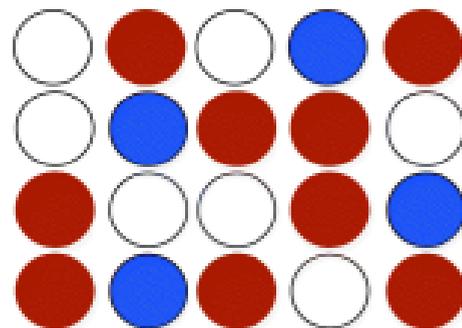


chemosensitive



chemoresistant

Post-chemo Tumors



○ chemosensitive

● chemoresistant-intrinsic

● chemoresistant-acquired