Neoadjuvant chemotherapy with Gemcitabine and Carboplatin for invasive bladder cancer can improve the radicality for a subset of patients, but some patients suffer from severe adverse drug reactions without any benefit. To establish a method for predicting responses to the Gemcitabine and Carboplatin therapy, we analyzed gene expression profiles of biopsy materials from 18 invasive bladder cancers using an oligoDNA microarray consisting of 38,500 genes or ESTs, after enrichment of cancer cell population with laser microbeam microdissection. Analyzing nine responders (60% tumor reduction) and nine non-responders, we identified 20 of genes that were expressed differently between the 'responder' and 'non-responder' groups. We further selected 14 genes showing the most significant differences and established a numerical prediction scoring system that clearly separated the responder group from the non-responder group. This system accurately predicted the drug response of seven of eight additional test cases that were reserved from the original 26 cases. When we compared a set of predictive genes for Gemcitabine and Carboplatin therapy with those for Methotrexate, Vinblastine, Doxorubicin and Cisplatin (M-VAC) therapy reported previously, no common gene was detected. Our results suggest that the sensitivity of an invasive bladder cancer to the neoadjuvant chemotherapy with GC could be predicted by expression patterns in this set of genes.