Figure S1. A principal component analysis overview of proteome data related to overexpression of CBR1 in OVCAR-3 cells. Each of the indicated cell lines was cultured in three dishes and used for proteome analysis. A score scatter plot of the first two principal component scores, which account for 18.3 and 13.5% of the original variation, respectively, is shown in the left panel. There was little separation between classes along the first and second principal components. The large overlap suggests that much of the spectral variation is unrelated to class differences, meaning that there were no major outliers. The feature components of each sample can be seen from the loading plot (bottom panel), in which the positional relationship with the score plot is consistent. CBR1, carbonyl reductase 1; hCBR1, human carbonyl reductase 1; tGFP, turbo green fluorescent protein.
Figure S2. Correlation plot showing proteome data and CBR1 expression in OVCAR-3 cells overexpressing CBR1 and negative control cells. The P-values (horizontal axis) and $-\log_{10}$ (P-value) values (vertical axis) calculated using Spearman's rank correlation analysis are plotted for 938 proteins (except CBR1). The 155 proteins that met the P-value of <0.05 are presented as black circles, and those that did not meet the threshold P-value of <0.05 are presented as gray circles. CBR1, carbonyl reductase 1.
Figure S3. The 155 proteins whose expression correlated with that of hCBR1 were analyzed by IPA. The top 20 out of 65 canonical pathways that were enriched significantly are shown. The z-score indicates whether the detected signal is biased toward activation or inactivation, with positive values (orange) indicating activation and negative values (blue) indicating inactivation. It is not clear in which direction the other colors fluctuate. hCBR1, human carbonyl reductase 1; IPA, Ingenuity Pathway Analysis.