



Supplementary Figure 3: Analysis of nischarin expression using bioinformatics. **A)** Oncomine analysis of three independent gene microarray studies. The Oncomine data-mining tool (www.oncomine.org) was used with data from three analyses of breast cancer markers by stage (14–16). Mean nischarin mRNA levels in normal tissue (**blue**) and in breast cancer tissue (**red**) are shown with 95% confidence intervals. In each case, nischarin expression was lower in breast cancer tissue compared with normal tissue. Student t-tests were performed for each study to evaluate statistical significance. **B)** Oncomine analyses of eight additional independent gene microarray studies. In eight additional studies (16-23) nischarin expression decreased with increasing breast cancer grade. Mean nischarin expression, with 95% confidence interval, is shown for low grade breast cancers (**blue**), intermediate grade breast cancers (**red**), and high grade breast cancers (**green**). ANOVA was performed for each study to evaluate statistical significance.