Figure S9: Oncomine examination of *NR2F2* expression in breast tumors. Data mining in Oncomine microarray data sets for NR2F2 in breast cancer identified that: A, *NR2F2* expression is significantly higher in ERα+ breast tumors ($p < 0.007$). B. *NR2F2* is significantly lower in metastatic breast tumors ($p < 0.05$). Data are from (van de Vijver MJ, He YD, van't Veer LJ, et al. A gene-expression signature as a predictor of survival in breast cancer. N Engl J Med 2002; 347: 1999-2009).