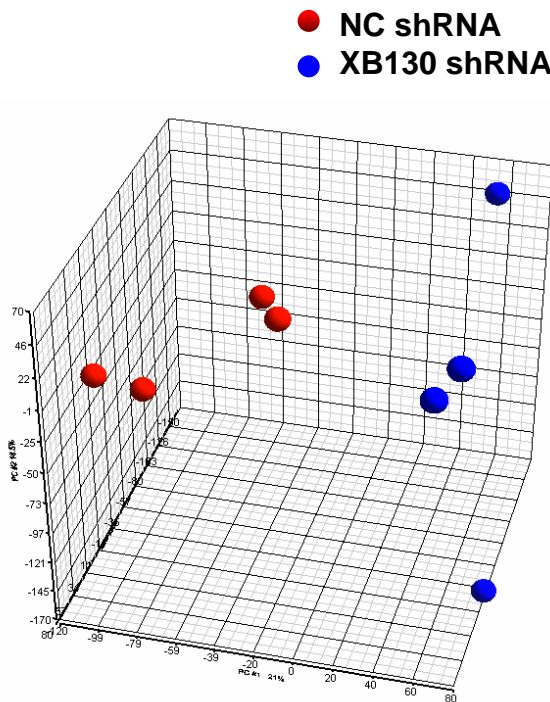
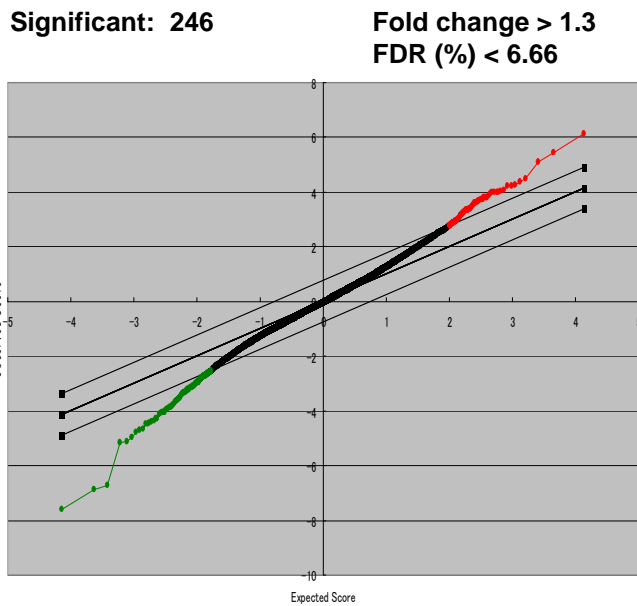


## Supplementary Figure 2 *Shiozaki A, et al.*

**A**



**B**



### Supplementary Figure 2. *Principle Component Analysis (PCA) and Significance Analysis of Microarray (SAM).*

(A) Principle Component Analysis (PCA) was performed using Partek software. PCA results indicated a significant separation of samples based on the expression of XB130. (B) Differential expression analysis was performed using Significance Analysis of Microarray (SAM). SAM analysis showed that 246 genes were significantly changed by the stable knock down of XB130 in WRO cells with criteria Fold Discovery Rate (FDR)  $q$  value < 6.66% and fold change > 1.3.