**Supplemental Data 1: R script used to generate the median and Q1/Q3 for quantification.**

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# R script for plotting quantification from Protein Prospector

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# Inputs:

# Location of CSV file that contains the peptide sequence and protein names.

# CSV file must contain protein name and L.H.Intensities.

#Libraries required

library(tidyverse)

library(cowplot)

library(ggsci)

#Reading in csv with Proteins and L.H.Intensity

df = read.delim(file.choose(new = FALSE), header=T, sep=",", as.is=T)

#importing L.H.Intensity column as numeric

df$L.H.Intensity <- as.numeric(as.character(df$L.H.Intensity))

#Setting levels to protein column, optional

df$Protein = factor(df$Protein, levels = c("TUB2","ACT2", "SR45","PR5","PR1"))

#plot settings

g <-

 ggplot(df, aes(x = Protein , y = L.H.Intensity, color = Protein)) +

 labs(x = NULL, y = expression(paste(italic("acinus-2 pinin-1")," / Col (L/H) Intensity"))) +

 theme\_cowplot() +

 scale\_color\_lancet()+

 scale\_y\_continuous(limits = c(0.01,100),

 breaks = c(0.01,0.02,0.05,0.1,0.2,0.5,1,2,5,10,20,50,100),

 labels = c("Low",0.02,0.05,0.1,0.2,0.5,1,2,5,10,20,50,"High"),

 trans = "log2") + #Log2 transformation, before boxplot calculations

 theme(legend.position = "none",

 text = element\_text(size=7),

 axis.text = element\_text(size = 7))

#boxplot parameters

p <- g +

 geom\_boxplot(outlier.shape = NA,lwd=0.1) +

 geom\_point(position=position\_jitterdodge(

 jitter.width = 1.85,

 jitter.height = 0,

 dodge.width = NULL,

 seed = 223),

 size = .5,

 alpha=1)

#saving final plot

ggsave(plot = p, width = 8.5, height = 8.5, dpi = 300, units = "cm",filename = "plot.pdf")