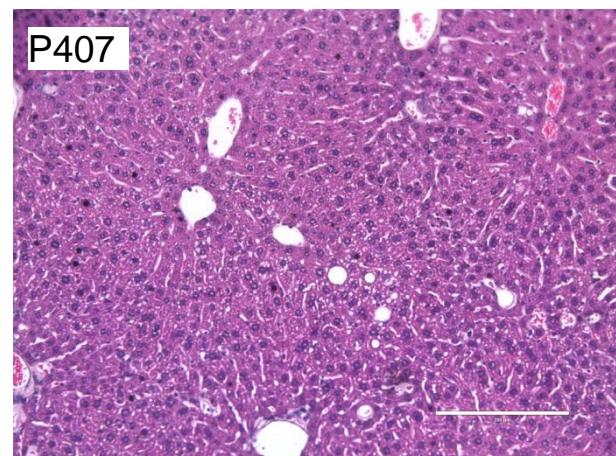
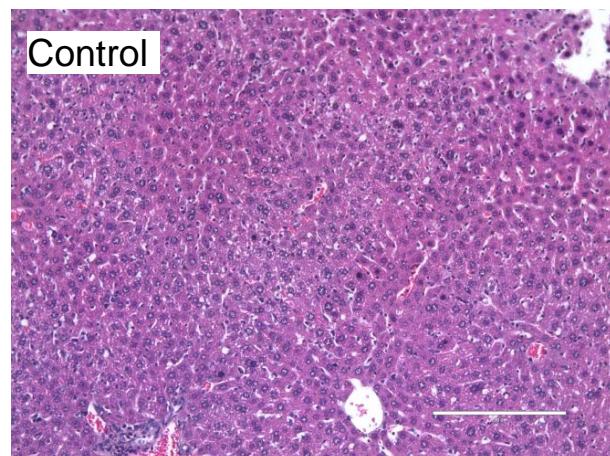
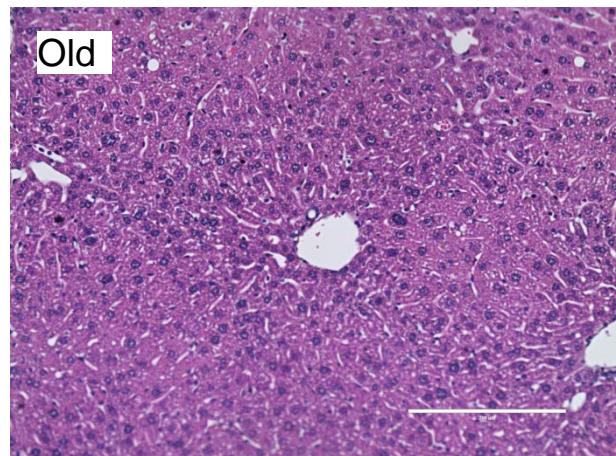
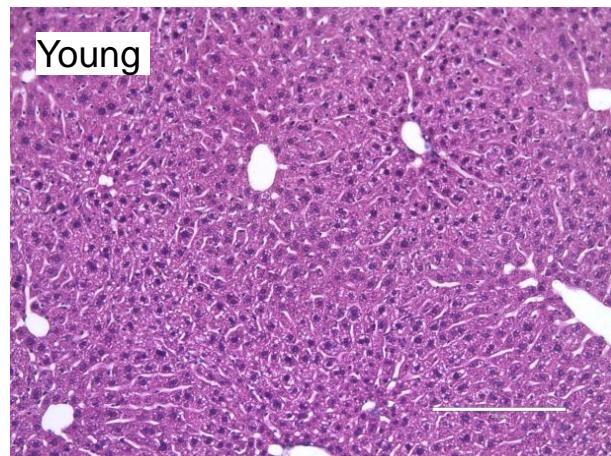
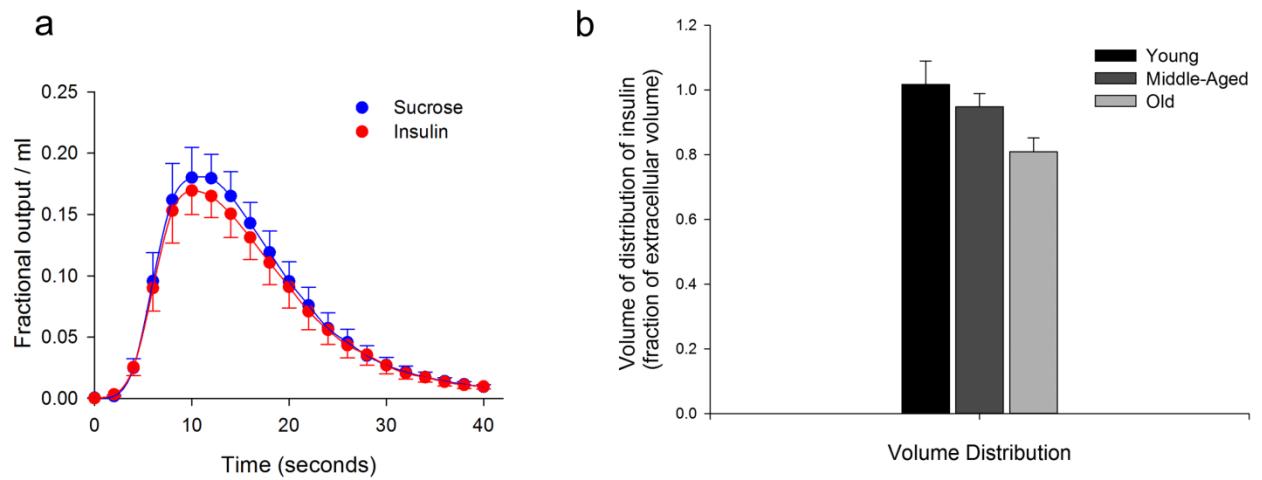


**S1 H&E Staining of liver tissue from the young and old rats and control and P07 treated rats.**

There was no evidence of liver pathology in any of the animal groups (Scale bar = 1 micron)



**S2 Multiple Indicator Dilution experiments in middle aged F344 rats.** There was an intermediate loss of insulin transfer in the middle aged rats.

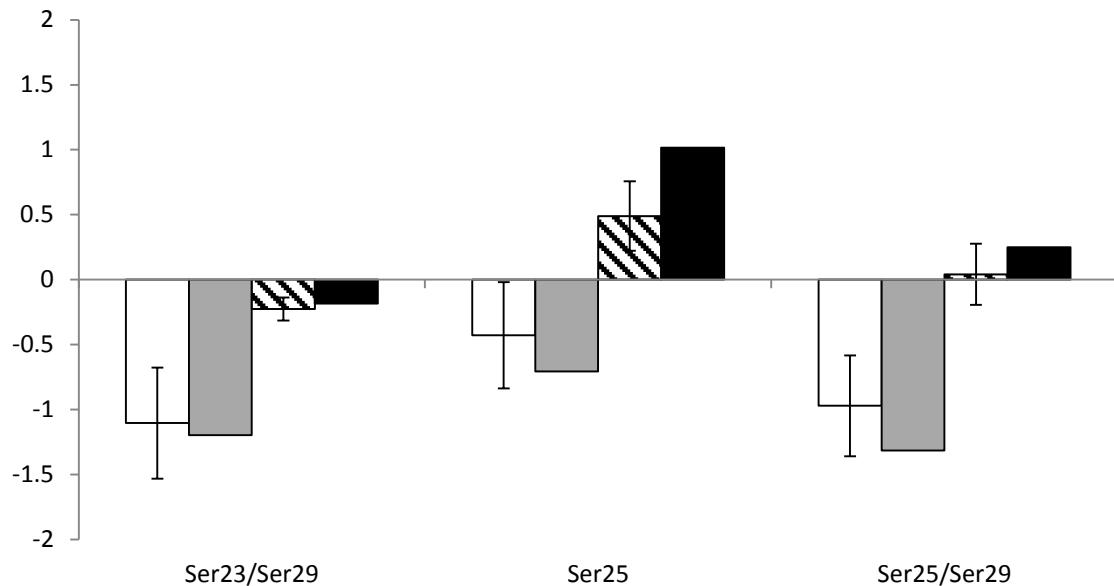


### S3 Supplementary information for Phosphoproteomics

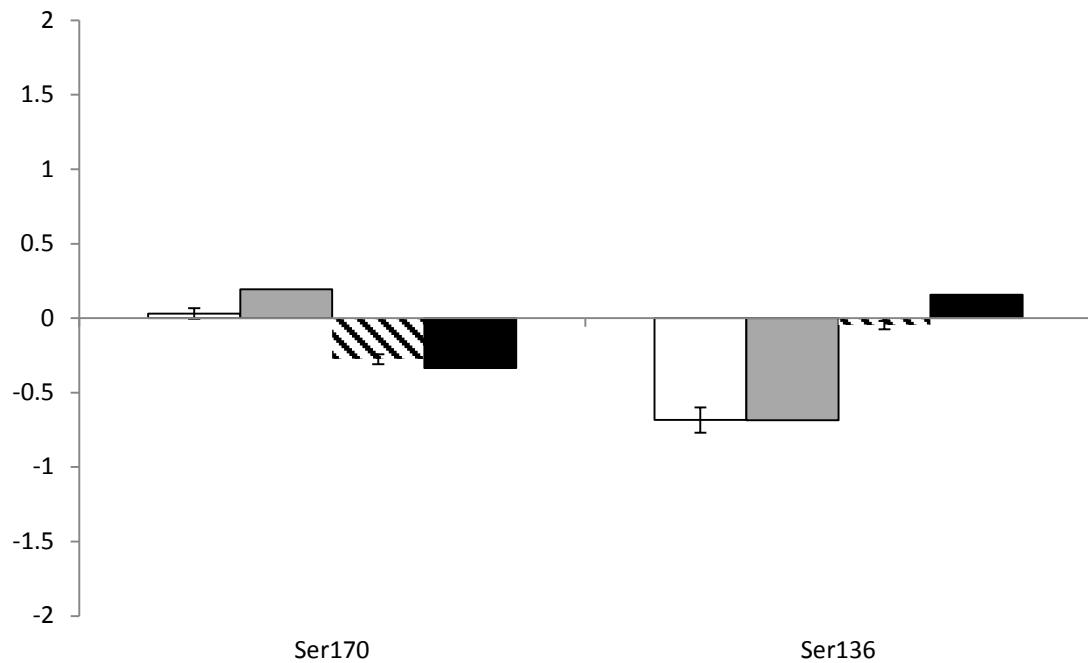
Quantitative phosphoproteomics of 47 peptides containing insulin-regulated sites from the KEGG insulin signaling pathway. Z-scores of  $>+/-1.0$  were considered significant. Log2 values are provided to show statistical variation.



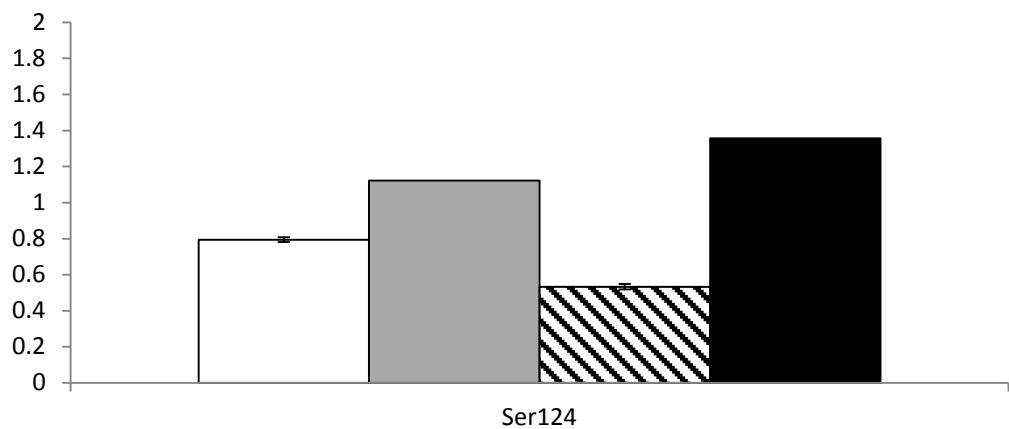
### Acaca



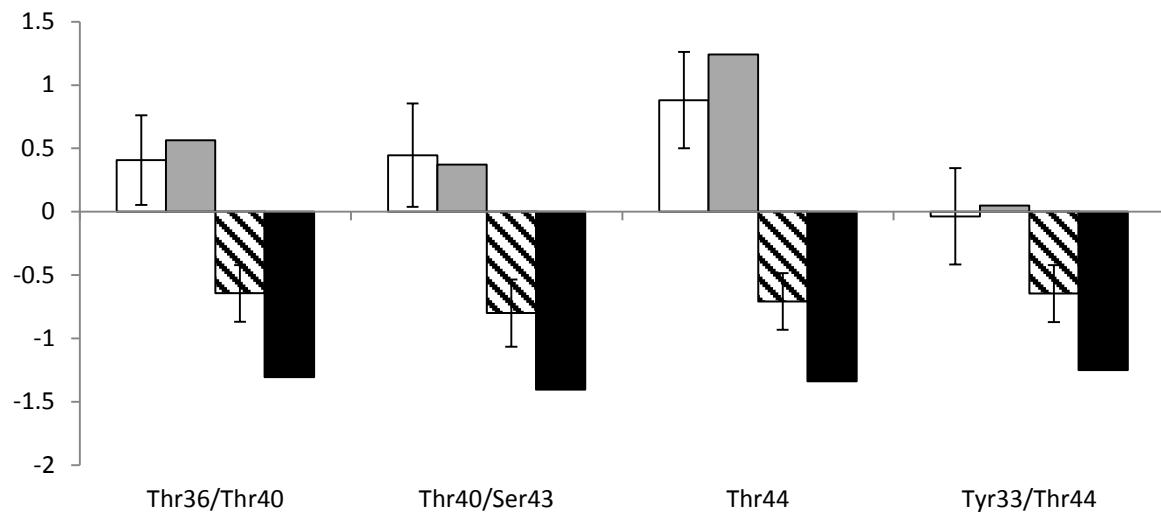
### Bad



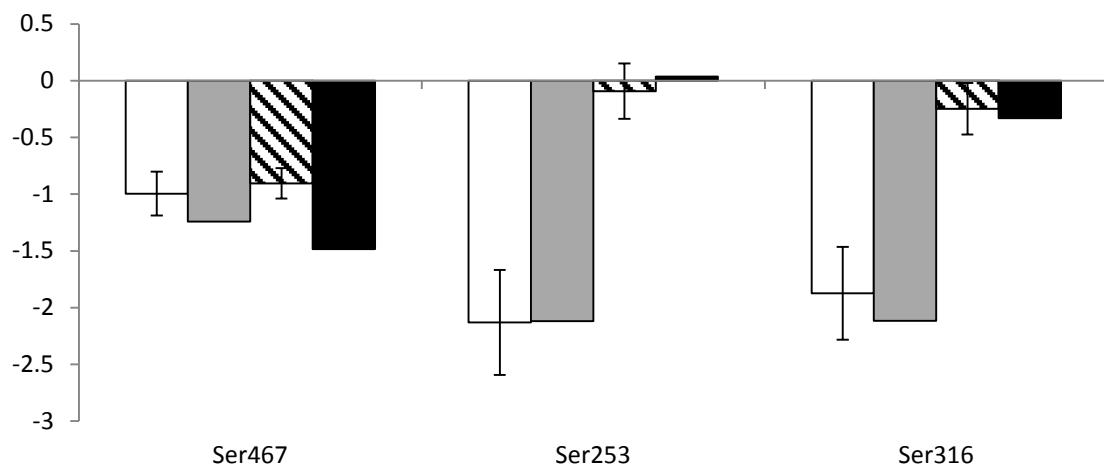
### Akt1



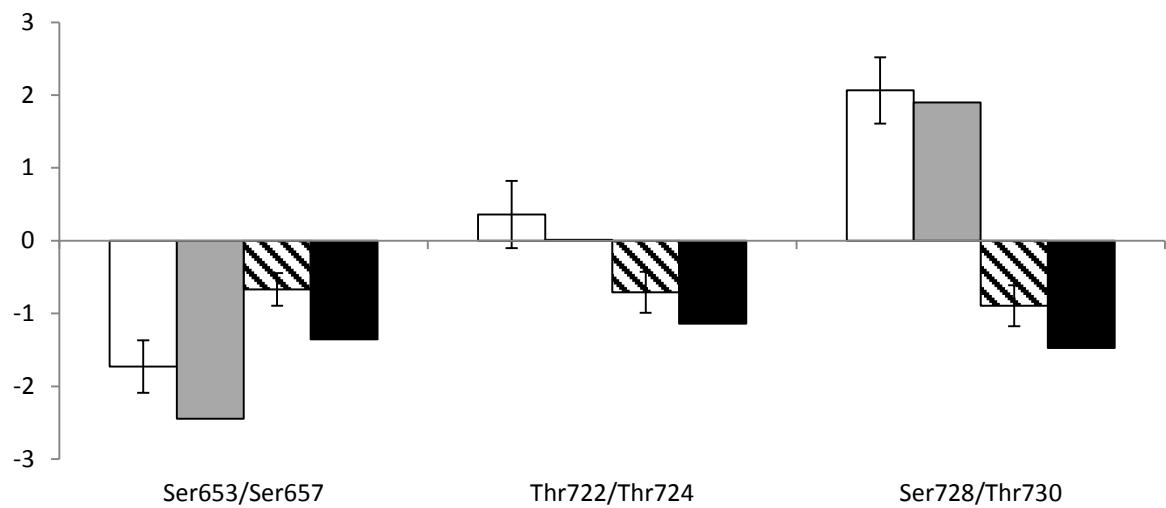
### Eif4ebp1



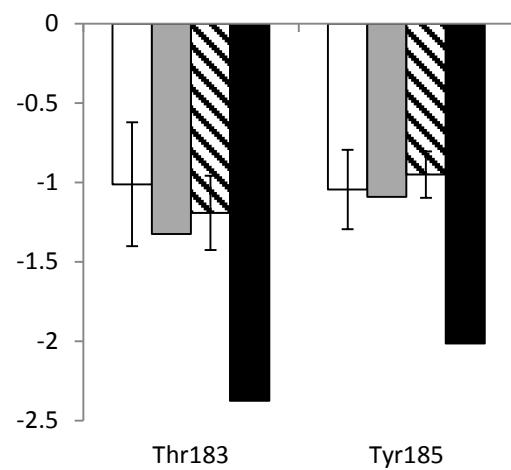
### Foxo1



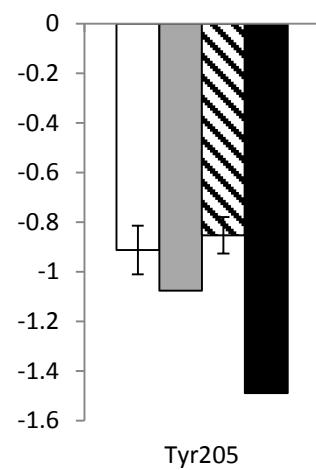
### Gys1



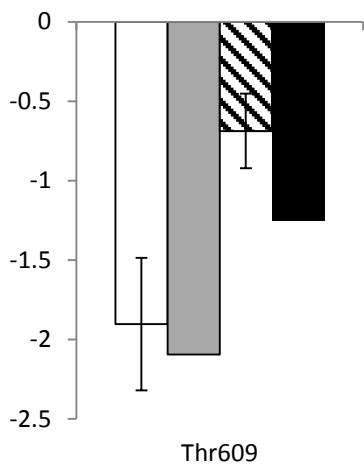
### Mapk1



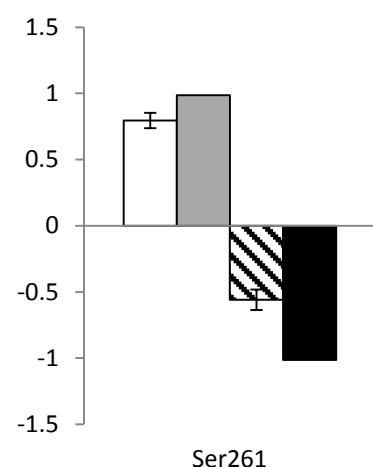
### Mapk3



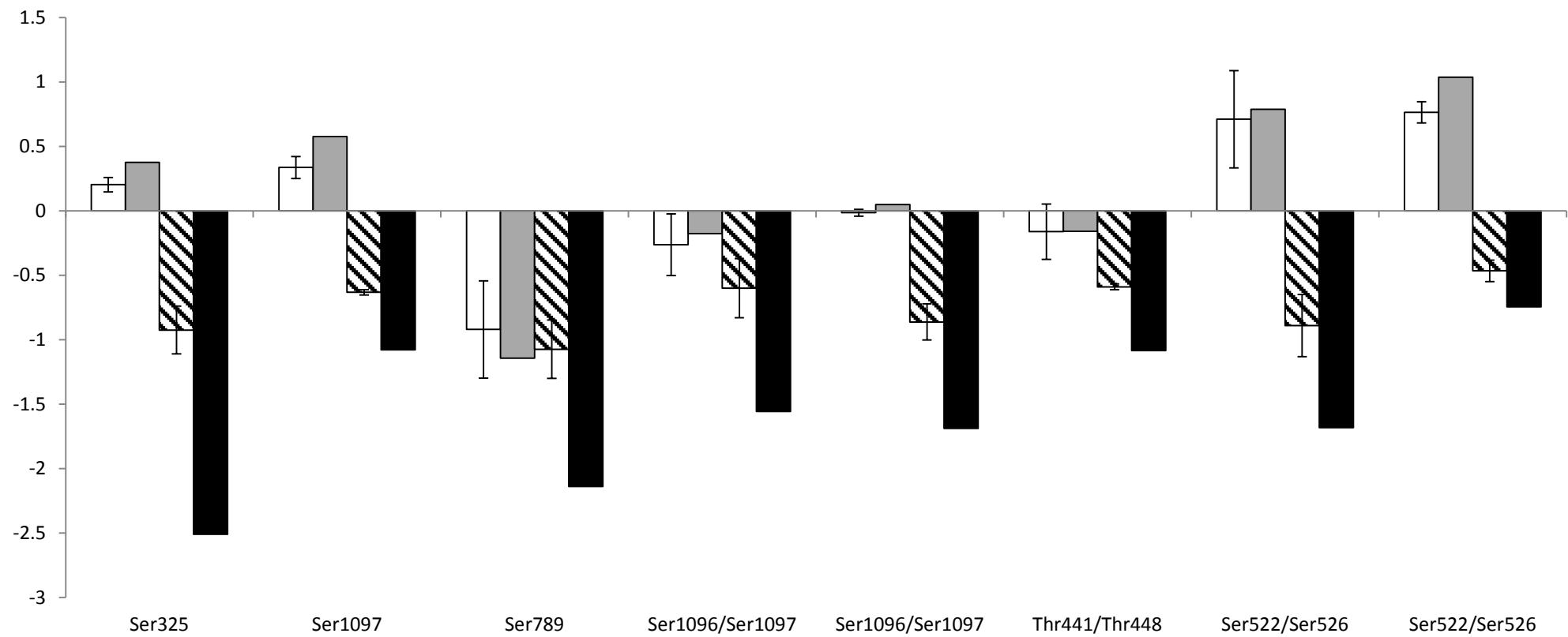
### Pik3r6



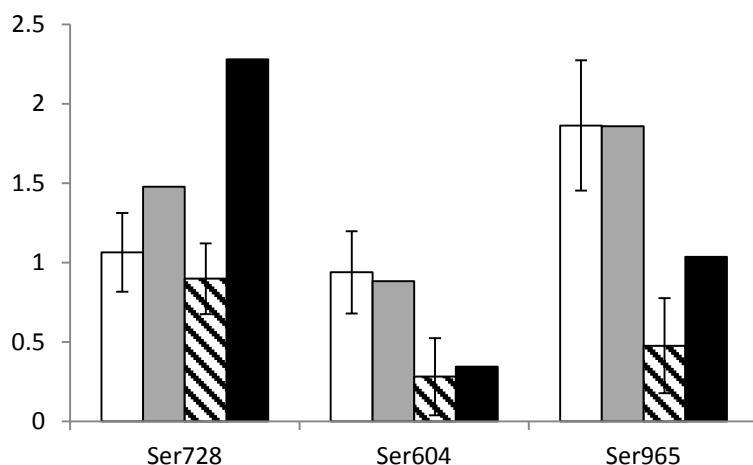
### Pik3c2a



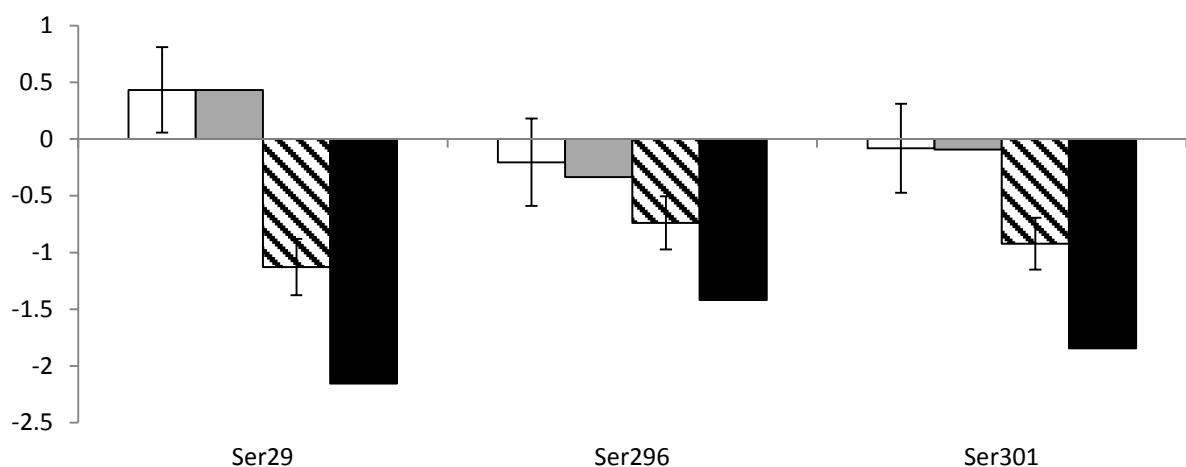
# Irs1



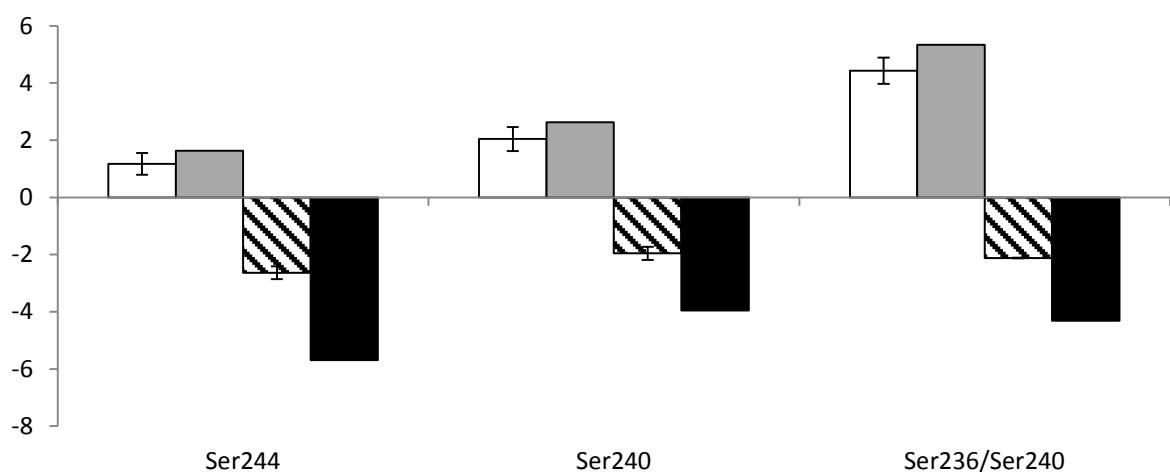
### Irs2

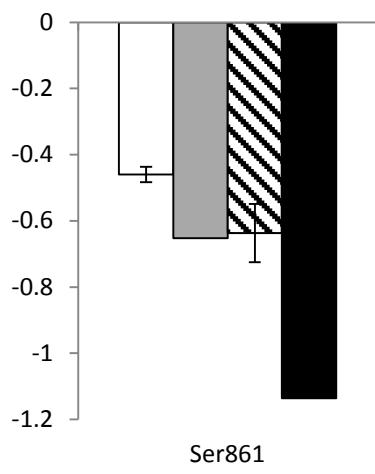
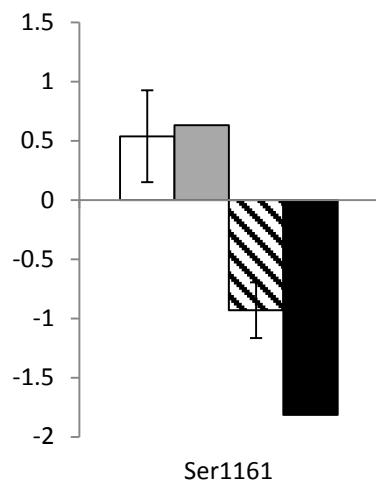
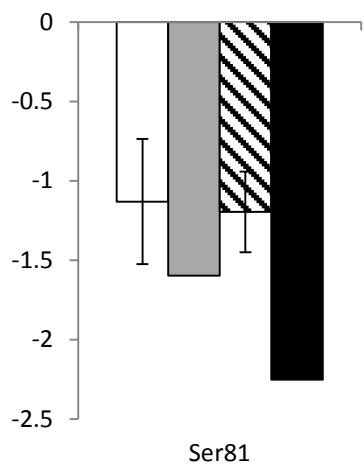
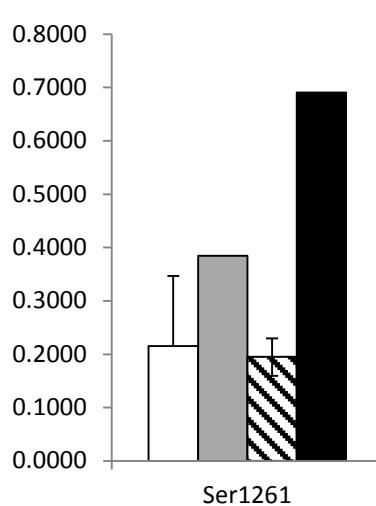
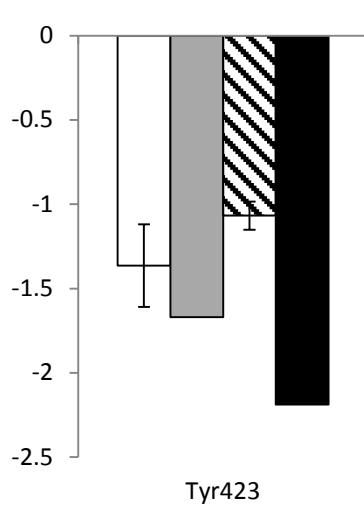
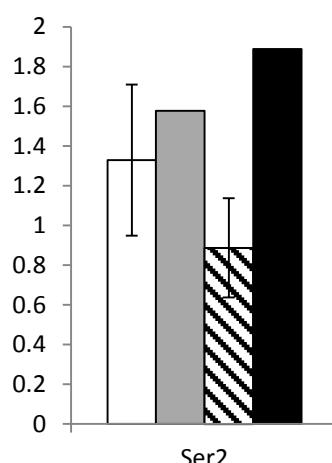


### Raf1

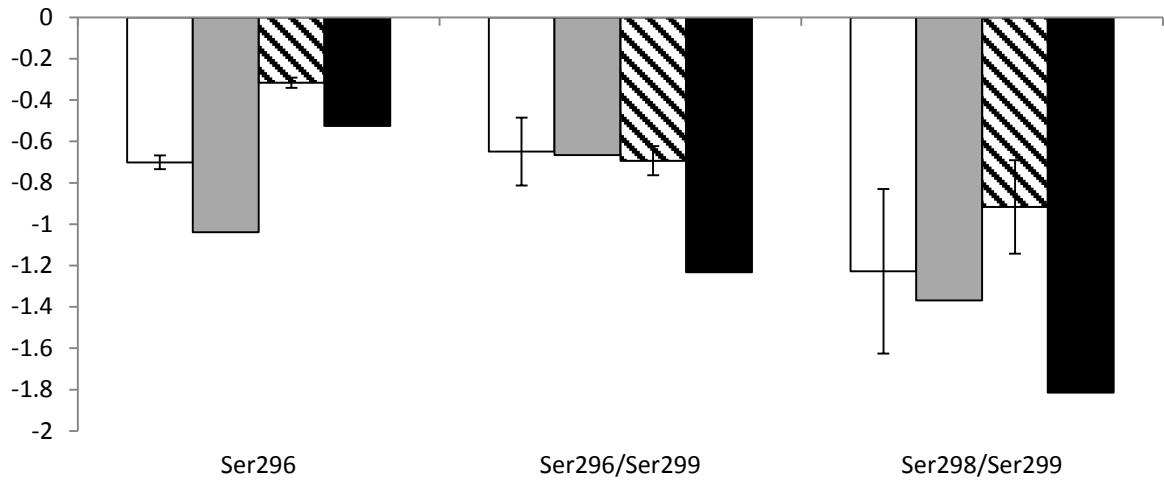


### Rps6

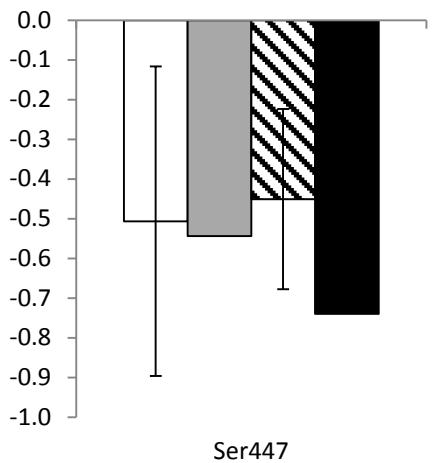


**Ppp1r12a****Sos1****Ppp1r3g****mTOR****Shc1****Ppp1ca**

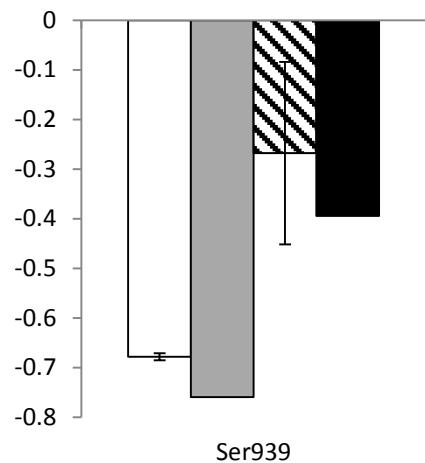
### **Trip10**



### **Rps6kb1**



### **Tsc2**



#### S4- RTPCR data for Insulin signalling pathway in Young versus Old livers and Control versus P407 livers

##### **Legend:**

**Fold-Change** ( $2^{(-\Delta\Delta Ct)}$ ) is the normalized gene expression ( $2^{(-\Delta\Delta Ct)}$ ) in the Test Sample divided by the normalized gene expression ( $2^{(-\Delta\Delta Ct)}$ ) in the Control Sample.

**Fold-Regulation** represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicate a positive- or an up-regulation, and the fold-regulation is equal to the fold-change.

Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change.

Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than -2 are indicated in blue.

**p-values:** The p values are calculated based on a Student's t-test of the replicate  $2^{(-\Delta\Delta Ct)}$  values for each gene in the control group and treatment groups, and p values less than 0.05 are indicated in red.

##### **Comments:**

A: This gene's average threshold cycle is relatively high (> 30) in either the control or the test sample, and is reasonably low in the other sample (< 30).

These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.

This fold-change result may also have greater variations if p value > 0.05; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

B: This gene's average threshold cycle is relatively high (> 30), meaning that its relative expression level is low, in both control and test samples, and the p-value for the fold-change is either unavailable or relatively high (p > 0.05).

This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

C: This gene's average threshold cycle is either not determined or greater than the defined cut-off (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.





| Symbol  | Well | AVG $\Delta C_t$<br>(Ct(GOI) - Ave Ct<br>(HKG)) |       | 2 <sup>^-</sup> $\Delta C_t$ |         | Fold<br>Change | T-TEST   | Fold Up-<br>or Down-<br>Regulation |
|---------|------|---|-------|------------------------------|---------|----------------|----------|------------------------------------|
|         |      | OLD   | YOUNG | OLD                          | YOUNG   |                |          |                                    |
| Slc27a4 | G05  | 7.29  | 8.70  | 6.4E-03                      | 2.4E-03 | 2.66           | 0.899783 | 2.66                               |
| Slc2a1  | G06  | 7.26  | 8.72  | 6.5E-03                      | 2.4E-03 | 2.76           | 0.835286 | 2.76                               |
| Slc2a4  | G07  | 6.46  | 7.41  | 1.1E-02                      | 5.9E-03 | 1.93           | 0.922519 | 1.93                               |
| Sos1    | G08  | 6.28  | 5.85  | 1.3E-02                      | 1.7E-02 | 0.74           | 0.568297 | -1.34                              |
| Srebf1  | G09  | 1.82  | 1.09  | 2.8E-01                      | 4.7E-01 | 0.60           | 0.291791 | -1.66                              |
| Tg      | G10  | 9.45  | 10.21 | 1.4E-03                      | 8.4E-04 | 1.70           | 0.355179 | 1.70                               |
| Ucp1    | G11  | 9.26  | 10.32 | 1.6E-03                      | 7.8E-04 | 2.08           | 0.333236 | 2.08                               |
| Vegfa   | G12  | 6.48  | 7.75  | 1.1E-02                      | 4.6E-03 | 2.42           | 0.782530 | 2.42                               |
| Actb    | H01  | -1.03   | -1.43 | 2.0E+00                      | 2.7E+00 | 0.76           | 0.658113 | -1.31                              |
| B2m     | H02  | 2.82  | 1.90  | 1.4E-01                      | 2.7E-01 | 0.53           | 0.769787 | -1.89                              |
| Hprt1   | H03  | -0.84   | 0.20  | 1.8E+00                      | 8.7E-01 | 2.06           | 0.922424 | 2.06                               |
| Ldha    | H04  | 0.42  | 0.03  | 7.5E-01                      | 9.8E-01 | 0.77           | 0.809575 | -1.30                              |
| Rplp1   | H05  | -1.36   | -0.71 | 2.6E+00                      | 1.6E+00 | 1.57           | 0.388136 | 1.57                               |





| Symbol  | Well | AVG ΔC <sub>t</sub><br>(Ct(GOI) - Ave Ct<br>(HKG)) |         | 2 <sup>ΔC<sub>t</sub></sup> |         | Fold<br>Change | T-TEST          | Fold Up-<br>or Down-<br>Regulation |
|---------|------|--|---------|-----------------------------|---------|----------------|-----------------|------------------------------------|
|         |      | P407   | CONTROL | P407                        | CONTROL |                |                 |                                    |
| Slc27a4 | G05  | 7.79   | 7.78    | 4.5E-03                     | 4.6E-03 | 0.99           | 0.956394        | -1.01                              |
| Slc2a1  | G06  | 11.55  | 10.78   | 3.3E-04                     | 5.7E-04 | 0.59           | 0.262772        | -1.70                              |
| Slc2a4  | G07  | 12.79  | 13.16   | 1.4E-04                     | 1.1E-04 | 1.29           | N/A             | 1.29                               |
| Sos1    | G08  | 6.78   | 6.66    | 9.1E-03                     | 9.9E-03 | 0.92           | 0.898960        | -1.09                              |
| Srebf1  | G09  | 9.09   | 9.58    | 1.8E-03                     | 1.3E-03 | 1.41           | N/A             | 1.41                               |
| Tg      | G10  | 11.90  | 10.99   | 2.6E-04                     | 4.9E-04 | 0.53           | <b>0.010198</b> | -1.88                              |
| Ucp1    | G11  | 13.22  | 12.14   | 1.1E-04                     | 2.2E-04 | 0.47           | N/A             | -2.11                              |
| Vegfa   | G12  | 4.95   | 4.90    | 3.2E-02                     | 3.4E-02 | 0.96           | 0.857308        | -1.04                              |
| Actb    | H01  | 0.68   | 0.92    | 6.3E-01                     | 5.3E-01 | 1.19           | 0.551329        | 1.19                               |
| B2m     | H02  | -2.55  | -2.89   | 5.8E+00                     | 7.4E+00 | 0.79           | 0.059386        | -1.27                              |
| Hprt1   | H03  | 1.68   | 0.98    | 3.1E-01                     | 5.1E-01 | 0.62           | 0.239562        | -1.63                              |
| Ldha    | H04  | 0.34   | 0.88    | 7.9E-01                     | 5.4E-01 | 1.46           | 0.108750        | 1.46                               |
| Rplp1   | H05  | -0.15  | 0.10    | 1.1E+00                     | 9.3E-01 | 1.19           | 0.175467        | 1.19                               |

**S5 Increased blood levels of cholesterol and triglycerides following P407 treatment**

