Journal of the American Heart Association

ORIGINAL RESEARCH

CD4+ T Cell-Specific Proteomic Pathways Identified in Progression of Hypertension Across Postmenopausal Transition

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BACKGROUND: Menopause is associated with an increase in the prevalence and severity of hypertension in women. Although premenopausal females are protected against T cell-dependent immune activation and development of angiotensin II (Ang II) hypertension, this protection is lost in postmenopausal females. Therefore, the current study hypothesized that specific CD4+ T cell pathways are regulated by sex hormones and Ang II to mediate progression from premenopausal protection to postmenopausal hypertension.

METHODS AND RESULTS: Menopause was induced in C57BL/6 mice via repeated 4-vinylcyclohexene diepoxide injections, while premenopausal females received sesame oil vehicle. A subset of premenopausal mice and all menopausal mice were infused with Ang II for 14 days (Control, Ang II, Meno/Ang II). Proteomic and phosphoproteomic profiles of CD4+ T cells isolated from spleens were examined. Ang II markedly increased CD4+ T cell protein abundance and phosphorylation associated with DNA and histone methylation in both premenopausal and postmenopausal females. Compared with premenopausal T cells, Ang II infusion in menopausal mice increased T cell phosphorylation of MP2K2, an upstream regulator of ERK, and was associated with upregulated phosphorylation at ERK targeted sites. Additionally, Ang II infusion in menopausal mice decreased T cell phosphorylation of TLN1, a key regulator of IL-2Rα and FOXP3 expression.

CONCLUSIONS: These findings identify novel, distinct T cell pathways that influence T cell-mediated inflammation during postmenopausal hypertension.

Key Words: 4-vinylcyclohexene diepoxide ■ Ang II ■ menopause ■ phosphoproteomics ■ proteomics ■ T cells

Hypertension is the leading risk factor for global disease burden.[1] While premenopausal females are protected from hypertension,[2] about 40% of a woman's lifespan is spent in a postmenopausal state that is associated with increased hypertension and cardiovascular disease risk.[3–5] Mechanistic understanding of this shift in blood pressure regulation is inadequate and correlates to greater uncontrolled hypertension in postmenopausal women compared with age matched men, despite greater medication adherence.[6,7] Using the VCD-menopause model (VCD, 4-vinylcyclohexene diepoxide), a novel estrogen-deplete, ovary-intact menopause model,[8,9] we have shown that premenopausal and perimenopausal females are protected from angiotensin II (Ang II)-induced hypertension, whereas postmenopausal females are susceptible and respond to Ang II with a significant increase in blood pressure. Estrogen treatment during the transition into menopause prevents postmenopausal Ang II-induced hypertension.[8,9] However, the underlying protective mechanisms of estrogen against hypertension development remain unclear.

Inflammation plays an essential role in the genesis and maintenance of hypertension.[10,11] Genetic ablation

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Supplementary Material for this article is available at https://www.ahajournals.org/doi/suppl/10.1161/JAHA.120.018038

For Sources of Funding and Disclosures, see page 14.

JAHA is available at: www.ahajournals.org/journal/jaha

CLINICAL PERSPECTIVE

What Is New?

- To our knowledge, this is the first proteomic study of T-cell specific pathways in pre and postmenopausal females to establish that Ang II infusion and a menopausal increase in blood pressure have distinct effects on the CD4+ T cell proteome and phosphoproteome.
- The identified T cell molecular pathways are hypothesized to be involved in premenopausal protection against hypertension and menopausal susceptibility to hypertension development.

What Are the Clinical Implications?

- The differentiation of CD4+ T cells has previously been implicated in sex differences in hypertension development; thus far the effect of sex hormones on CD4+ T cell pathways has not been studied.
- The current study used a proteomic and phopshoproteomic approach to identify novel regulated CD4+ T cell pathways which are altered following Ang II infusion.
- We found that in the context of Ang II infusion, menopause is associated with an increased ERK activity and reduced activity and expression of Treg associated pathways, suggesting an increased Th17/Treg ratio.
- Treg associated pathways, such as TLN1 phosphorylation, are potential therapeutic targets for postmenopausal hypertension.

Nonstandard Abbreviations and Acronyms

Ang II	angiotensin II
CDK	cyclin-dependent kinase
ERK	mitogen-activated protein kinase
EZH	enhancer of zeste homolog
GATA3	trans-acting T-cell-specific transcription factor GATA-3
GSK3	glycogen synthase kinase 3
H3K27me3	histone 3 trimethylation of the 27th lysine
HINFP	histone H4 transcription factor
HS	high salthigh salt
KLF14	Krueppel-like factor 14
MP2K2	dual specificity mitogen-activated protein kinase kinase 2 (aka MEK2)
MPEG1	macrophage-expressed gene 1 protein
Rag-1	recombination activating gene-1
TLN1	talin-1
Treg	T regulatory cell
VCD	4-vinylcyclohexene diepoxide

of the recombination activating gene-1 (Rag-1), which results in the absence of mature T and B cells, mitigates Ang II and salt-induced hypertension in males.[12,13] The adoptive transfer of T cells into Rag-1$^{-/-}$ male mice restores the magnitude of blood pressure elevation to wild-type levels.[12]

However, we have demonstrated that premenopausal females are protected from this T cell-mediated hypertension. Compared with male mice, the adoptive transfer of T cells into premenopausal Rag-1$^{-/-}$ mice results in attenuated blood pressure, renal T cell infiltration, and renal T cell-dependent inflammatory cytokine expression.[14] In contrast, the adoptive transfer of T cells into estrogen-deplete, menopausal Rag-1$^{-/-}$ mice causes a significant increase in Ang II-induced blood pressure accompanied by an increase in renal T cell-dependent inflammatory cytokine expression and a reduced renal T regulatory cell (Treg) population.[15] Thus, females are protected from T cell-mediated hypertension until the onset of menopause. Moreover, we have demonstrated that female protection is dependent on the anti-inflammatory CD4+ Treg population.[15]

Therefore, the current study hypothesized that specific CD4+ T cell pathways are regulated by sex hormones and Ang II to mediate progression from premenopausal protection to postmenopausal hypertension. Splenic T cell numbers do not increase or decrease with Ang II infusion studies, unlike those in the kidney, therefore splenic populations were chosen for this analysis of Ang II activation of signaling, in the presence and absence of estrogen. Using quantitative proteomic and phosphoproteomic approaches, we identified and profiled alterations in CD4+ T cell protein abundance and phosphorylation associated with menopausal susceptibility to Ang II hypertension.

METHODS

The authors declare that all supporting data are available within the article and its online supplementary files (Data S1). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the data set identifier PXD021233 and 10.6019/PXD021233.

Experimental Animals

Eight-week-old, female C57BL/6J mice were purchased from the Jackson Laboratory. Mice were housed in the University Animal Care Keating/BIO5 Clean Animal Facility in standard cages, given access to water and standard mouse chow (0.25% NaCl; Harlan Teklan, 7013) ad libitum, and maintained on 12/12-hour light/dark cycles. All protocols were approved by the Institutional Animal Care and Use Committee at the University of Arizona.

To induce ovarian failure (menopause), a subset (n=4) of female mice received daily intraperitoneal injections of VCD (160 mg/kg i.p., Sigma V3630) for 20 consecutive days. Control (n=4) and Ang II (n=4) mice received intraperitoneal injections of vehicle (sesame oil). Vaginal cytology was measured daily to determine the onset of menopause, defined as 10 consecutive days of diestrus. VCD treated mice demonstrated confirmed ovarian failure 53±2 days from the first day of VCD injections.

Ang was infused into both premenopausal and postmenopausal mice at 800 ng/kg per minute for 14 days (Ang II and Meno/Ang II) via subcutaneous implantation of osmotic minipumps (Alzet, model 1004). The goal of the study was to identify T cell changes associated with progression into hypertension susceptibility in the VCD model of menopause (ie premenopause and postmenopausal mice +/– Ang II). We have previously shown that VCD treated mice do not have an increase in blood pressure, in the absence of Ang II, and therefore did not include for proteomic analyses. Blood pressure responses for the current study are shown in Figure S1.

Splenic CD4$^+$ T Cell Isolation for Protein Collection

Upon euthanasia, spleens were isolated and mechanically disrupted through a 70 µm Nylon tissue separation filter (Fisher Scientific, cat. # 07-201-431) to create a single- cell suspension in 2% FBS in PBS. Splenic CD4$^+$ cells were isolated via negative immunomagnetic separation using the EasySep™ Mouse CD4$^+$ T Cell Isolation Kit (StemCell Technologies, cat. # 19852) according to the manufacturer's protocol. Purity for CD4$^+$ cells was assessed via flow cytometry by staining with surface antibodies for CD4 overnight as previously described.[14] All samples were >88% pure and average sample purity was not different between groups (P=0.34).

Isolated CD4$^+$ T-cells were incubated in lysis buffer (50 mmol/L HEPES pH 7.6, 1% Triton X-100, 50 mmol/L sodium chloride, 20 mmol/L sodium pyrophosphate, 20 mmol/L B- glycerophosphate disodium salt hydrate, 10 mmol/L sodium fluoride, 1.0 mmol/L sodium orthovanadate, 1.0 mmol/L phenylmethylsulfonyl fluoride, 0.017 mg/mL aprotinin, 0.01 mg/mL leupeptin) on ice for 20 minutes followed by centrifugation (18 626*g*, 20 minutes, 4°C). The supernatant was collected, and protein concentration was quantified using the Pierce™ BCA Protein Assay Kit.

Gene Ontology Overrepresentation and Transcription Factor Identification

For 2 pairwise comparisons (Control versus Ang II and Ang II versus Meno/Ang II), the differentially expressed proteins and phosphosites were separated into 2 groups of expression: upregulated or downregulated. The protein/phosphorylated protein groups were entered into the PANTHER Classification System (Thomas Lab at the University of Southern California, version 14.0) to identify overrepresented molecular functions and biological processes.

Differentially expressed proteins were also subject to transcription factor binding site motif analysis using Pscan[16] (version 1.5). The default promoter region of −450 to +50 was used to identify transcriptional regulators of the differentially expressed proteins.

Phosphorylation Motif Determination and Kinase Prediction

Kinase motif analysis was conducted by input of significantly downregulated or upregulated phosphosites ±6 amino acids into iceLogo,[17] which determines significantly overrepresented or underrepresented amino acids in a site-specific manner within the experimental peptide sequences. Scansite 4.0[18] was used to predict the kinase(s) specific to each significantly downregulated or upregulated phosphosite.

Volcano Plot Visualization

Volcano plot visualization was used to identify major protein abundance and phosphorylation changes between Control and Ang II, and Ang II and Meno/Ang II samples, as defined by a log2 fold change > |1| and $P \leq 0.05$. A pseudo-count of 1 was added to all protein abundance and phosphosite intensities to avoid a logarithm of zero. From this reduced list of proteins or phosphosites, identified from the volcano plot proteins, Euclidean distance from the origin (log2 fold change, –log10 P value from the origin [0,0]) was used to further identify an arbitrary number (4) of proteins of interest for further analysis into their functional role in T cells. These proteins had a large fold change between groups and high statical significance between groups. All figures were generated using the statistical software R (v3.3.3) (R Core Team [2017]. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/).

Data Analysis and Statistics

All statistical analyses presented were performed using GraphPad Prism software, the Perseus software platform,[19,20] the PANTHER Classification System, or Pscan. A Student t test was used for analyses conducted between 2 groups and one-way ANOVA was performed in instances when all 3 experimental groups were compared. A P<0.05 with no multiple testing correction was considered significant.

RESULTS

Ang II and Menopause Exert Distinct Effects on CD4+ T-Cell Protein Profiles

Premenopausal females are protected against T cell-mediated Ang II hypertension, whereas menopausal females are susceptible to T cell-mediated Ang II hypertension.[14,15] Anti-inflammatory CD4+FOXP3+ Tregs are part of the protective mechanism for blood pressure control in premenopausal females.[15] To determine CD4+ T cell molecular changes associated with premenopausal resistance and menopausal susceptibility to Ang II-induced hypertension, we subjected splenic CD4+ T cells from premenopausal mice (Control and Ang II) and menopausal mice (Meno/Ang II) to proteomic quantification (Figure 1A). Of the 7085 proteins identified, 546 were significantly different among the 3 groups (Figure 1B).

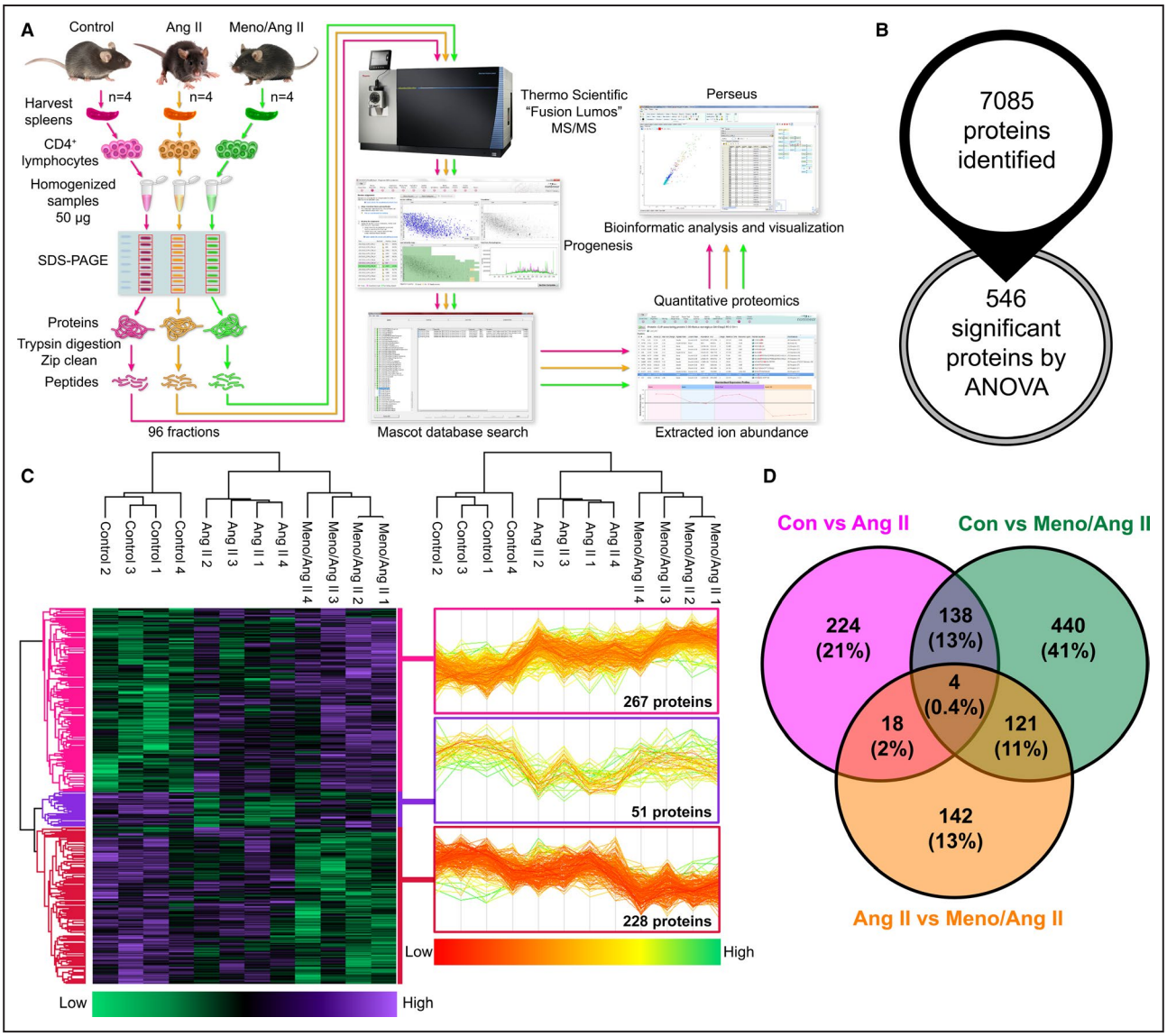


Figure 1. Ang II and Menopause exert distinct effects on CD4+ T cell protein profiles.
A, Splenic CD4+ T cells were isolated from Control, Ang II (800 ng/kg per minute, 14 days), and Meno/Ang II (VCD, 160 mg/kg, 20 days) female animals (n=4). CD4+ protein homogenates were separated into 8 lanes by SDS-PAGE. Protein in each lane was excised and digested and the resulting peptides were analyzed by tandem mass spectrometry. Raw data processing for quantification was completed in Progenesis and peptide/protein identification was performed via alignment with Mascot database. Resulting Mascot peptide/protein identifications were imported into Progenesis for protein abundance quantification via extracted ion abundance. **B**, A total of 7085 proteins were identified and quantified, of which 546 were differentially expressed between the 3 groups (ANOVA, $P \leq 0.05$). **C**, Hierarchical protein clustering, heatmap visualization and protein cluster profiles of the 546 proteins were also performed in Perseus. This revealed 3 patterns of protein abundance in CD4+ T cell protein expression. **D**, Venn diagram of the pairwise (Student *t* test, $P \leq 0.05$) protein abundance differences between groups. A majority of protein abundance differences were observed between Control and Meno/Ang II CD4+ T cells. Ang II indicates angiotensin II; Meno, menopause; and VCD, 4-vinylcyclohexene diepoxide.

Hierarchical clustering of the 546 proteins confirmed distinct CD4+ T cell proteomic differences amongst groups. The clustering results from the pattern in changes of protein abundance, which is unbiased. Ang II and Meno/Ang II groups clustered within the same dendrogram node (Figure 1C). A total of 3 principal patterns of expression were observed. *Cluster 1*: When compared with Control, Ang II infusion induced a stepwise increase in the expression of 267 proteins that were further induced when menopause was superimposed. *Cluster 2*: Conversely, Ang II infusion resulted in a stepwise decrease in the expression of 228 proteins that were further reduced with menopause. *Cluster 3*: The remaining 51 proteins decreased in expression in Ang II CD4+ T cells compared with Control, and this effect was reversed in menopause (Figure 1C). Pairwise comparisons revealed the largest percent of differentially expressed protein abundance changes were between Control and Meno/Ang II CD4+ T cells (41%; Figure 1D).

In Premenopausal T Cells, Ang II Increases Abundance of Proteins Associated With Transcription

To identify CD4+ T cell protein abundance changes associated with premenopausal resistance to T cell-mediated Ang II hypertension, we analyzed the 384 differentially expressed proteins between Control and Ang II. The majority (263, 68%) were upregulated in Ang II CD4+ T cells (Figure 2A; Table S1).

To provide cellular context, differentially expressed proteins were analyzed in PANTHER. Proteins upregulated in Ang II CD4+ T cells associated with biological processes involved in DNA replication and transcription (Figure 2B; Table S2) and molecular functions associated with histone modification and RNA polymerase binding (Figure 2C; Table S3). A smaller proportion of proteins were downregulated in Ang II CD4+ T cells and these associated with biological processes related to metabolic activity, including cellular respiration (Figure 2B; Table S4).

From the volcano plot, BRNP3, DAXX, CDK12, and SENP8 were the highest upregulated Ang II proteins (Figure 2D). These proteins are collectively involved in transcription regulation and ubiquitination-like processes.[21–23] Proteins downregulated by Ang II infusion included MPEG1, OXLA, CATR, and SERC1, and are known to be involved in regulating innate and adaptive immune function.[24,25]

The promoter regions (−450 to +50) were analyzed by the Pscan Web Interface to identify transcription factors predicted to transcriptionally regulate differentially expressed proteins. The ZBTB family of transcription factors, which have a role in T cell lineage commitment and the formation of memory T cells,[26] were amongst the transcription factors associated with upregulated proteins from Ang II CD4+ T cells (Figure 2E; Table S5). ZBTB7A maintains the size and function of peripheral Treg pools.[27] The ELF family of transcription factors, that control proliferation and homing of T cells,[28] were amongst the transcription factors associated with downregulated proteins from Ang II CD4+ T cells (Figure 2E; Table S6).

In Menopausal T Cells, Ang II Differentially Regulates KLF14 Transcription

Premenopausal females are resistant to blood pressure changes following Ang II infusion. In contrast, using the VCD model, we have shown that menopausal females respond to Ang II with a significant increase in blood pressure.[9] To identify T cell proteins associated with the divergent blood pressure phenotype,[9] we directly compared CD4+ T cell protein abundance from premenopausal and menopausal Ang II infused females (Ang II versus Meno/Ang II). Of the 285 differentially expressed proteins identified between the 2 groups, the majority (189, 66%) were downregulated in Meno/Ang II CD4+ T cells (Figure 3A; Table S7).

Via PANTHER we classified the biological processes and molecular functions represented by differentially expressed proteins in Meno/Ang II CD4+ T cells. Proteins upregulated in Meno/Ang II CD4+ T cells were enriched in metabolic processes (Figure 3B; Table S8) and functions associated with binding and metallochaperone activity (Figure 3C; Table S9). Downregulated proteins associated with processes involved in immune responses, in particular innate T cell processes (Figure 3B; Table S10) associated with functions related to viral RNA binding (Figure 3C; Table S11).

Volcano plot visualization identified MYCN, OASL2, GPAA1, and COR2A as proteins with the greatest downregulation in Meno/Ang II CD4+ T cells compared with Ang II alone (Figure 3D). OASL2 is involved in anti-viral responses,[29] and COR2A regulates TLR4 induced transcription.[30] The proteins with the greatest upregulation in Meno/Ang II CD4+ T cells were COX17, OXLA, RRP36, and EZH1 (Figure 3D). Of interest, OXLA and EZH1 regulate CD4+ T cell differentiation, proliferation, and cytokine release.[31,32] Overall the results indicate that menopause amplifies the T cell mediated inflammatory response to Ang II.

Pscan analysis of promoter binding motifs within the 189 downregulated proteins in Meno/Ang II CD4+ T cells showed transcriptional regulation by HINFP, TFDP1, KLF14, and SP4 (Figure 3E; Table S12). Promoter binding motifs within the 96 upregulated proteins specify KLF14, GABPA, GMEB1, and ZBTB7A transcriptional activity (Figure 3E; Table S13). The presence of KLF14 binding motifs in Meno/Ang II CD4+ T

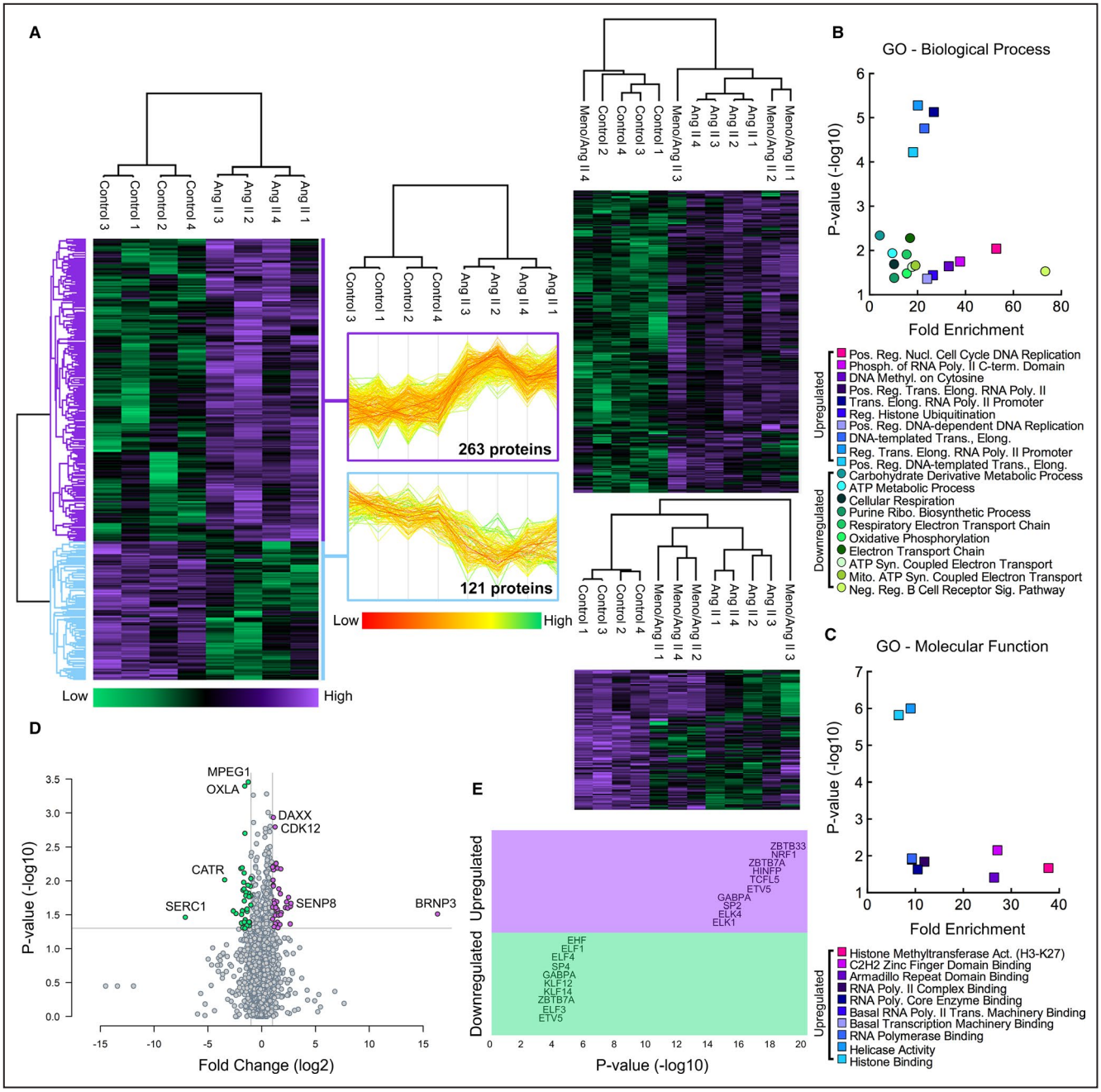


Figure 2. In premenopausal T cells, Ang II increased abundance of proteins associated with transcription.
A, Heatmap visualization of the 384 (Student *t* test $P \leq 0.05$) significantly different proteins between Control and Ang II CD4+ T cells. The majority of proteins, 263, were upregulated with Ang II treatment. When Meno/Ang II protein abundance of the 384 proteins was observed, Meno/Ang II samples clustered more tightly with Ang II than Control samples. **B**, PANTHER classification of significantly overrepresented biological processes associated with upregulated (squares) and downregulated (circles) proteins in Ang II CD4+ T cells. **C**, PANTHER classification of significantly overrepresented molecular functions associated with upregulated (squares) proteins in Ang II CD4+ T cells. No molecular functions were significantly overrepresented amongst downregulated proteins. **D**, Volcano plot identification of upregulated (purple) and downregulated (green) proteins in Ang II CD4+ T cells, $P \leq 0.05$, log2 fold change > |1|. The 4 proteins with the greatest upregulation and downregulation, as determined by Euclidean distance from the origin (0,0), were BRNP3, DAXX, CDK12, SENP8 and MPEG1, OXLA, CATR, SERC1 respectively. **E**, Pscan identification of transcription factors significantly associated with promoter regions (−450 to +50) of upregulated (purple) and downregulated (green) proteins in Ang II CD4+ T cells. Ang II indicates angiotensin II; BRNP3, BMP/retinoic acid-inducible neural-specific protein 3; CATR, cathepsin R; CDK12, cyclin-dependent kinase 12; DAXX, death domain-associated protein 6; Meno, menopause; MPEG1, macrophage-expressed gene 1 protein; OXLA, L-amino-acid oxidase; SENP8, sentrin-specific protease 8; and SERC1, serine incorporator 1.

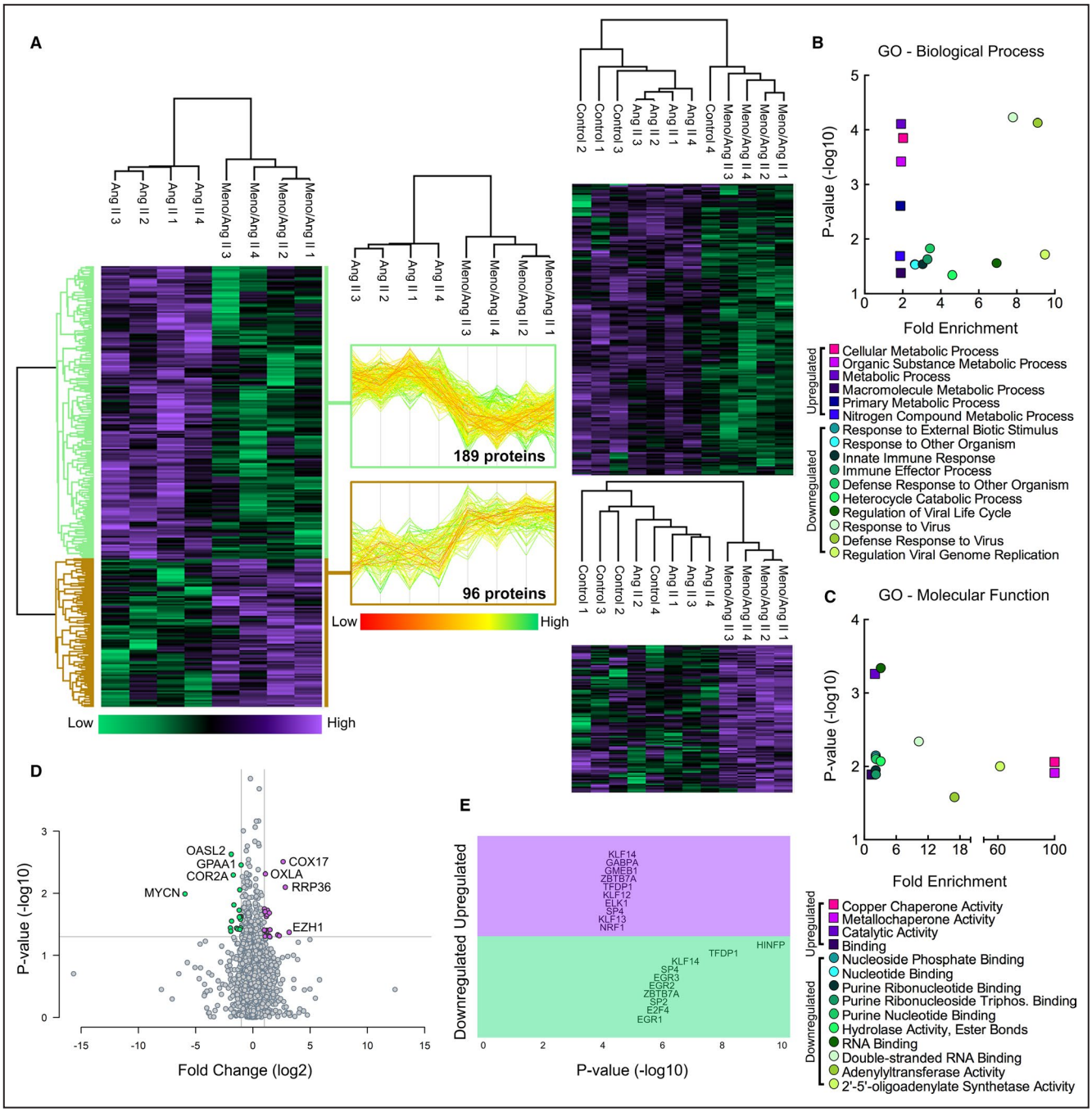


Figure 3. In menopausal T cells, Ang II differentially regulated KLF14 transcription.
A, Heatmap visualization of the 285 (Student *t* test $P \leq 0.05$) significantly different proteins between Ang II and Meno/Ang II CD4$^+$ T cells. The majority of proteins, 189, were downregulated in Meno/Ang II. When Control protein abundance of the 285 proteins was observed, Ang II and Control samples clustered. **B**, PANTHER classification of overrepresented biological processes associated with upregulated (squares) and downregulated (circles) proteins in Meno/Ang II CD4$^+$ T cells. **C**, PANTHER classification of significantly overrepresented molecular functions associated with upregulated (squares) and downregulated (circles) proteins in Meno/Ang II CD4$^+$ T cells. **D**, Volcano plot identification of upregulated and downregulated proteins in Meno/Ang II CD4$^+$ T cells: the 4 proteins with the greatest upregulation and downregulation were COX17, OXLA, RRP36, EZH1 and MYCN, OASL2, GPAA1, COR2A, respectively. **E**, Pscan promoter region analysis of upregulated and downregulated proteins predicted KLF14 binding in both subsets of proteins. Ang II indicates angiotensin II; COR2A, Coronin-2A; COX17, Cyctochrome c oxidase copper chaperone; EZH1, Histone-lysine N-methyltransferase 1; GPAA1, glycosylphosphatidylinositol anchor attachment 1 protein; KLF14, Krueppel-like factor 14; Meno, menopause; MYCN, N-myc proto-oncogene protein; OASL2, 2'-5'-oligoadenylate synthase-like protein 2; OXLA, L-amino-acid oxidase; and RRP36, ribosomal RNA processing protein 36 homolog.

cell differentially expressed proteins is particularly interesting considering the inverse association of KLF14 expression with Treg function.[33] Overall, the proteomic evaluation reveals that Ang II superimposed on menopause amplifies inflammatory pathways while potentially suppressing T regulatory responses.

Phosphoproteome Analysis of CD4+ T Cells Uncovers Distinct Effects of Both Ang II and Menopause

Using peptide residue modification readouts, we quantified the CD4+ T cell phosphoproteome from premenopausal mice (Control) and Ang II treated premenopausal (Ang II) and menopausal mice (Meno/Ang II). Mass spectrometry enabled the detection of 6059 phosphorylated sites (phosphosites), of which 466 were differentially phosphorylated among the 3 groups (Figure 4A).

Distinct treatment effect was confirmed by hierarchical clustering (Figure 4B). Similar to protein abundance, clustering of Ang II and Meno/Ang II samples within the same dendrogram node was noted (Figure 4B).

Three principal patterns of peptide phosphorylation were observed across the 3 groups (Figure 4B). *Pattern 1*: The majority of phosphosites (248, 53%) increased from Control to Ang II to Meno/Ang II such that maximal phosphorylation was seen in Meno/Ang II CD4+ T cells. *Pattern 2*: 189 phosphosites (41%) linearly decreased from Control, to Ang II to Meno/Ang II. *Pattern 3*: 29 phosphosites (6%) increased in Ang II compared with both Control and Meno/Ang II groups. By pairwise comparisons, the majority of phosphorylation differences (43%) were uniquely different between Control and Meno/Ang II CD4+ T cells (Figure 4C).

Ang II Increases Proline-Directed Protein Phosphorylation Linked to Chromatin Regulation by Methylation

To identify signaling cascades involved in premenopausal protection from T cell-mediated Ang II hypertension, we analyzed the 226 differentially regulated phosphosites between Control and Ang II CD4+ T cells. Peptide phosphosites were normalized to protein abundance to account for the positive relationship

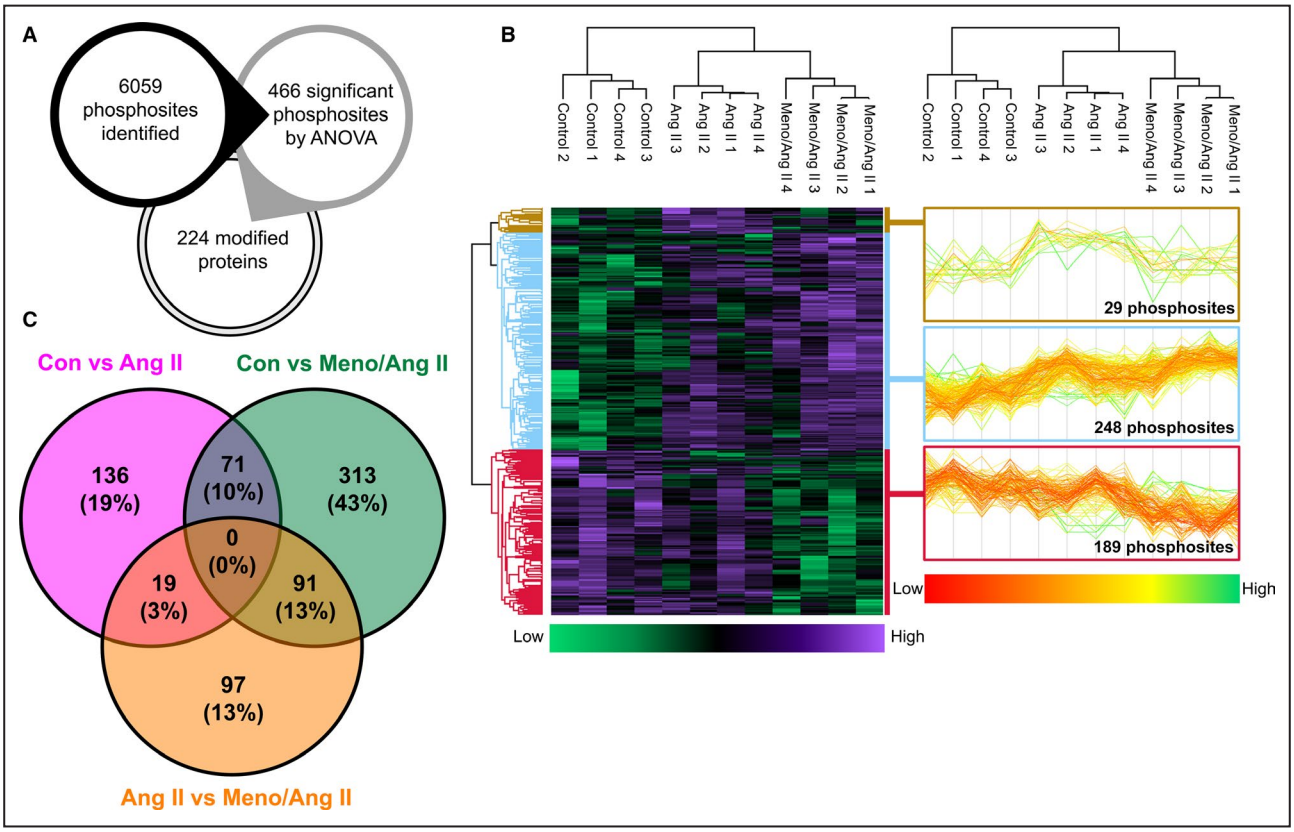


Figure 4. Phosphoproteome analysis of CD4+ T cells uncovered distinct effects of both Ang II and menopause.
A, Progenesis was used to identify peptide ion modifications and quantify extracted phosphopeptide ion abundance. In total, 6059 phosphosites within CD4+ T cell proteins were identified, of which 466 phosphosites on 224 proteins were differentially phosphorylated (ANOVA, $P \leq 0.05$) between the 3 groups. **B**, Hierarchical clustering confirmed distinct treatment effect on CD4+ T cell protein phosphorylation. Heatmap and cluster profile visualization identified 3 patterns of phosphorylation. **C**, Venn diagram of the pairwise (Student *t* test, $P \leq 0.05$) peptide phosphorylation differences between groups. A majority of differences were observed between Control and Meno/Ang II CD4+ T cells. Ang II indicates angiotensin II; and Meno, menopause.

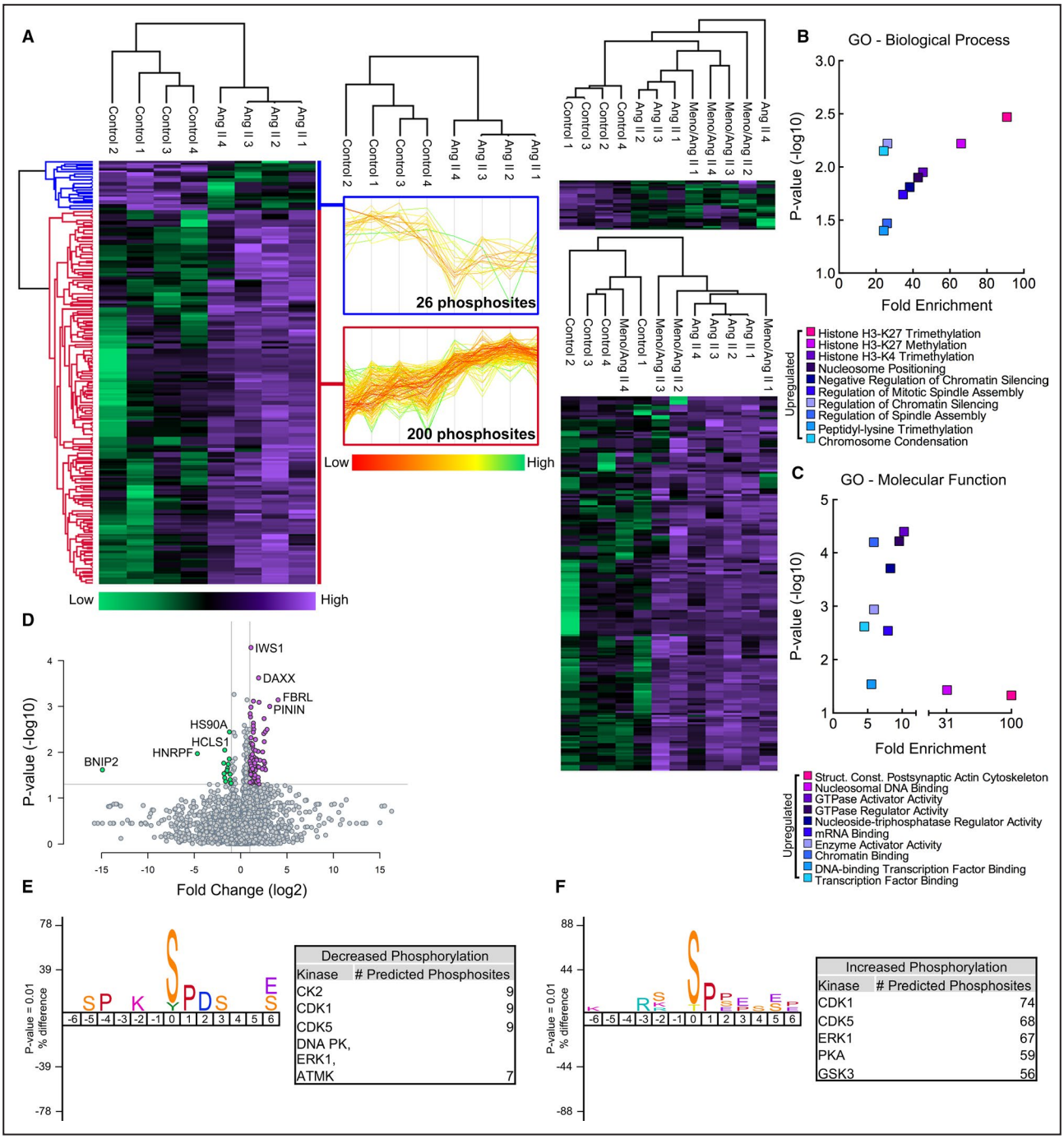


Figure 5. Ang II increased proline-directed protein phosphorylation linked to chromatin regulation by methylation.
A, Heatmap visualization of the 226 (Student *t* test $P \leq 0.05$) significantly different phosphosites between Control and Ang II CD4$^+$ T cells. Phosphorylation of the majority of phosphosites, 200, was upregulated with Ang II treatment. When Meno/Ang II phosphorylation was observed, Meno/Ang II samples clustered more tightly with Ang II than Control samples. **B**, PANTHER classification of significantly overrepresented biological processes associated with proteins with upregulated phosphorylation in Ang II CD4$^+$ T cells. **C**, PANTHER classification of significantly overrepresented molecular functions associated with proteins with upregulated phosphorylation in Ang II CD4$^+$ T cells. No significantly overrepresented biological processes or molecular functions were associated with proteins with downregulated phosphorylation. **D**, Volcano plot identification of upregulated (purple) and downregulated (green) phosphosites of interest in Ang II CD4$^+$ T cells. The 4 phosphosites with the greatest upregulation and downregulation were FBRL S130, IWS1 S666, PININ S346, DAXX S515 and BNIP2 S114, HNRPF Y276, HS90A S252, HCLS1 S333, respectively. **E**, IceLogo determination of overrepresented amino acid residues surrounding (±6 AAs) significantly downregulated phosphosites. Kinases predicted (Scansite ver. 4.0) to phosphorylate downregulated phosphosites. **F**, IceLogo determination of overrepresented amino acid residues surrounding significantly upregulated phosphosites along with kinases predicted to regulate upregulated phosphosites. Ang II indicates angiotensin II; BNIP2, BCL2/adenovirus E1B 19 kDa protein-interacting protein 2; DAXX, death domain-associated protein 6; FBRL, rRNA 2'-O-methyltransferase fibrillarin; HCLS1, hematopoietic lineage cell-specific protein; HNRPF, heterogeneous nuclear ribonucleoprotein F; HS90A, heat shock protein HSP 90-alpha; IWS1, protein IWS1 homolog; Meno, menopause; and PININ, Pinin.

between protein abundance and peptide modification frequency. Ang II increased phosphorylation at 200 phosphosites and decreased phosphorylation at 26 phosphosites (Figure 5A; Table S14). Classification of proteins associated with differentially regulated phosphosites between Control and Ang II was performed with PANTHER. Proteins with upregulated phosphorylation were enriched for histone methylation, chromatin regulation, enzyme activity, and DNA binding (Figure 5B and 5C; Tables S15 and S16). No known annotated biological processes were enriched within the 26 downregulated phosphosites.

Phosphosites with greatest phosphorylation upregulation in Ang II CD4+ T cells included FBRL S130, IWS1 S666, PININ S346, and DAXX S515 (Figure 5D). Of note, DAXX decreases TCR-induced proliferation and is a critical regulator of T cell homeostasis.[34] Conversely, Ang II resulted in the downregulation of 26 phosphosites, of which BNIP2 S114, HNRPF Y276, HS90A S252, and HCLS1 S333 were phosphorylated the least compared with Control CD4+ T cells. Overexpression of HNRPF has been shown to reduce Treg suppressive function in vitro, through direct interaction with FOXP3.[35] Whereas, upon T cell activation, HCLS1 interacts with actin at immunological synapses and promotes chemokine induced T cell migration.[36,37]

Differentially regulated phosphosites (±6 amino acids) were uploaded into iceLogo to determine putative phosphorylation motifs within modified proteins. In downregulated phosphosites (Figure 5E), serine and tyrosine were significantly overrepresented as the site of modification. Moreover, the phosphorylation motif (Figure 5E) indicated inactivity of proline directed kinases, as well as some acidophilic (residues D/E) and basophilic kinases (K). Scansite 4.0 was used to determine specific kinases associated with each downregulated phosphosite. Scansite identified kinases included CK2, CDK1, and CDK5, which were predicted to interact with amino acid motifs surrounding 9 of the 26 downregulated phosphosites (Figure 5E). It is important to note that increased phosphatase activity, rather than reduced kinase activity likely explains the decreased phosphorylation.

This analysis was repeated for upregulated phosphosites where serine and threonine residues were found to be overrepresented at the site of modification (Figure 5F). Additionally, the phosphorylation motif suggested increased activity of proline directed and acidophilic kinases, and the possibility of phosphorylation induced phosphorylation. Kinases predicted to have increased activity in Ang II CD4+ T cells include CDK1, CDK5, ERK1, PKA, and GSK3.

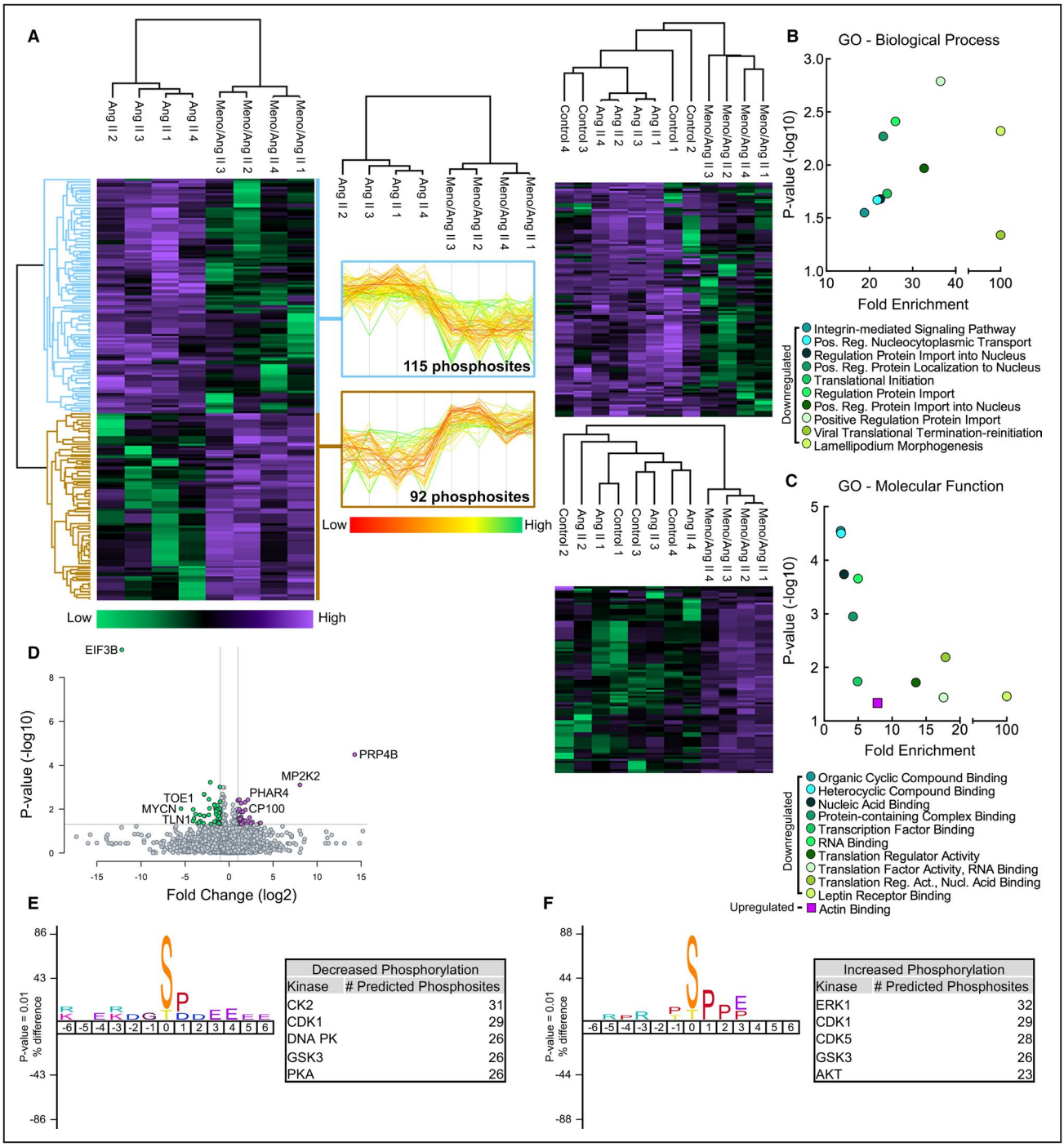
Meno/Ang II Results in Decreased Proline-Directed Protein Phosphorylation, Notably S405 Within TLN1, a Positive Regulator of Treg Maintenance

To identify phosphorylation activity and protein signaling associated with menopausal susceptibility to Ang II hypertension, we focused on differentially expressed phosphosites between Ang II and Meno/Ang II CD4+ T cells. After peptide phosphorylation normalization to protein abundance, 115 of 207 phosphosites (56%) were downregulated in Meno/Ang II CD4+ T cells (Figure 6A; Table S17). As a collective group, Meno/Ang II CD4+ T cell proteins with significantly upregulated phosphorylation associated with one molecular function, actin binding (Figure 6C; Table S18). Whereas, proteins with significantly downregulated phosphorylation associated with protein localization to the nucleus, translation initiation, and nucleic acid binding (Figure 6B and 6C; Tables S19 and S20).

Downregulated phosphosites included EIF3B S120, MYCN S350, TOE1 S349, and TLN1 S405 (Figure 6D). Of interest, TLN1 is necessary for the maintenance and survival of Tregs through positive regulation of Treg IL-2Rα (CD25) expression.[38] Further, 92 phosphosites were upregulated in Meno/Ang II CD4+ T cells. Phosphosites with the greatest phosphorylation

Figure 6. Meno/Ang II resulted in decreased proline-directed protein phosphorylation, notably S405 within TLN1, a positive regulator of Treg maintenance.

A, Heatmap visualization of the 207 (Student *t* test $P \leq 0.05$) significantly different phosphosites between Ang II and Meno/Ang II CD4+ T cells. Phosphorylation of the majority of phosphosites, 115, was downregulated after menopause induction. When Control phosphorylation was observed, Control and Ang II samples clustered. **B**, PANTHER classification of significantly overrepresented biological processes associated with proteins with downregulated phosphorylation in Meno/Ang II CD4+ T cells. No significantly overrepresented biological processes were associated with proteins with upregulated phosphorylation. **C**, PANTHER classification of significantly overrepresented molecular functions associated with proteins with downregulated and upregulated phosphorylation in Meno/Ang II CD4+ T cells. **D**, Volcano plot identification of upregulated (purple) and downregulated (green) phosphosites in Meno/Ang II CD4+ T cells. The 4 phosphosites with the greatest upregulation and downregulation were PRP4B S278, MP2K2 S23, PHAR4 S118, CP100 S244 and EIF3B S120, MYCN S350, TOE1 S349, and TLN1 S405, respectively. **E**, IceLogo determination of overrepresented amino acid residues surrounding (±6 AAs) significantly downregulated phosphosites. Kinases predicted (Scansite ver. 4.0) to phosphorylate downregulated phosphosites. **F**, IceLogo determination of overrepresented amino acid residues surrounding significantly upregulated phosphosites along with kinases predicted to regulate upregulated phosphosites. Ang II indicates angiotensin II; CP100, cilia- and flagella-associated protein 100; EIF3B, eukaryotic translation initiation factor 3 subunit B; Meno, menopause; MP2K2, dual specificity mitogen-activated protein kinase kinase 2; MYCN, N-myc proto-oncogene protein; PHAR4, phosphatase and actin regulator 4; PRP4B, serine/threonine-protein kinase PRP4 homolog; TLN1, talin-1; and TOE1, target of EGR1 protein 1.



upregulation in Meno/Ang II CD4+ T cells included PRP4B S278, MP2K2 S23, PHAR4 S118, CP100 S244 (Figure 6D). Of note, MP2K2 stimulates ERK1/2 activity, which influences the polarization of CD4+ T cells to a Th17 lineage.[39]

Downregulated and upregulated phosphosites (±6 amino acids) in Meno/Ang II CD4+ T cells were uploaded into iceLogo. Decreased phosphosites predominantly consisted of a modified serine with neighboring acidophilic amino acid residues (Figure 6E). Analysis of kinase specificity for this motif suggested that CK2, CDK1, DNA PK, GSK3, and PKA had decreased activity at the identified phosphosites in Meno/Ang II CD4+ T cells compared with Ang II CD4+ T cells (Figure 6E). Motif analysis of upregulated phosphosites identified an overrepresentation of proline directed serine phosphorylation in Meno/Ang II CD4+ T cells (Figure 6F). Kinases responsible

for increased phosphorylation at the identified sites were predicted to be ERK1, CDK1, CDK5, GSK3, and AKT (Figure 6F).

DISCUSSION

The goal of this study was to identify molecular targets responsible for the loss of female protection against Ang II-induced T cell-mediated hypertension following menopause. The major findings of this study were: (1) Ang II infusion in both premenopausal and menopausal mice increased CD4+ T cell protein abundance and phosphorylation associated with DNA and histone methylation; (2) in menopausal T cells, Ang II infusion increased phosphorylation of MP2K2, an upstream regulator of ERK; and (3) in menopausal T cells, Ang II infusion decreased phosphorylation of TLN1, a key regulator of IL-2Rα and FOXP3 expression. These findings identify novel T cell pathways that suggest increased T cell-mediated inflammation during postmenopausal hypertension (Figure 7).

Several studies support the role of epigenomic regulation in the development of hypertension.[40] A well characterized epigenetic modification known to influence hypertension development is DNA methylation, which within the gene promoter, is generally associated with gene repression.[41,42] In the Dahl salt-sensitive rat, increased blood pressure caused by a high salt (HS) diet is associated with increased DNA methylation in the renal outer medulla[43] and in renal T cells.[44] Inhibition of HS-induced methylation and demethylation within the renal outer medulla significantly reduced MAP by HS day 7.[43] Global inhibition of DNA methyltransferase activity in non-terminally differentiated cells via decitabine administration significantly blunted HS-induced MAP and proteinuria.[44] Together these studies suggest a causal contribution of DNA methylation and demethylation in hypertension development.

Another epigenetic modification known to be associated with hypertension is histone methylation.[40] Histone 3 trimethylation of the fourth lysine (H3K4me3) is a hallmark of active DNA transcription whereas histone 3 trimethylation of the twenty-seventh lysine (H3K27me3) and trimethylation of the ninth lysine (H3K9me3) are associated with transcription repression.[45,46] Spontaneously hypertensive rats (SHRs) have been shown to express increased recruitment of H3K4me3 to the ACE promoter within aortic, heart, and kidney tissue, that corresponded to local increased ACE expression.[47] Valsartan treatment of SHRs significantly reduced enrichment of H3K4me3 to the ACE promoter in heart and kidney tissue, reduced ACE expression in heart and kidney, and reduced blood pressure.[47]

The current study found that in premenopausal mice, Ang II infusion increased CD4+ T cell protein abundance and phosphorylation associated with the following processes/functions: DNA methylation, H3K4me3, H3K27me3, negative regulation of chromatin silencing, and histone methyltransferase activity. However, as seen in Figures 2A and 5A proteins with increased abundance and phosphorylation in Ang II compared with Control were similarly upregulated in Meno/Ang II, suggesting that similar to other hypertension models, Ang II stimulates DNA and histone methylation.

When protein abundance changes between Meno/Ang II and Ang II were analyzed, differentially expressed proteins consistent with increased KLF14 transcription factor activity were identified. KLF14

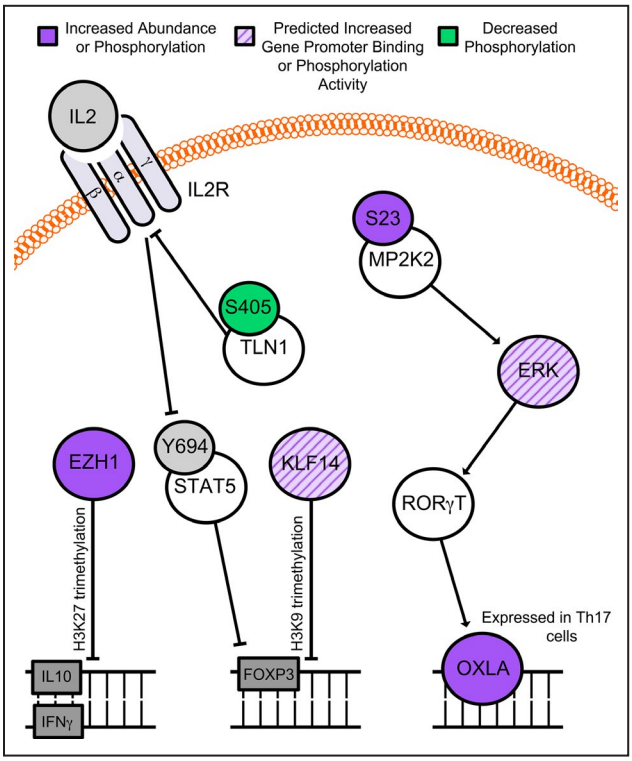


Figure 7. Proposed T cell mechanisms involved in postmenopausal hypertension.
Compared with CD4+ T cells from Ang II infused premenopausal females, CD4+ T cells from Ang II infused menopausal mice demonstrated increased expression or phosphorylation (solid purple) and predicted activity (striped purple) of proteins associated with decreased FOXP3 and IL-10 transcription and increased Th17 cell development. Further, CD4+ T cells from Ang II infused menopausal mice demonstrated decreased (green) S405 phosphorylation of TLN1, a positive regulator of Treg function. Ang II indicates angiotensin II; ERK, mitogen-activated protein kinase; EZH1, histone-lysine N-methyltransferase 1; FOXP3, foxhead box protein P3; IFNγ, interferon gamma; IL-10, interleukin-10; IL-2R, interleukin-2 receptor; KLF14, Krueppel-like factor 14; MP2K2, dual specificity mitogen-activated protein kinase kinase 2; OXLA, L-amino-acid oxidase; RORγT, retinoic acid receptor-related orphan nuclear receptor gamma-thymic; STAT5, signal transducer and activator of transcription 5; and TLN1, talin-1.

expression is inversely associated with FOXP3 expression and is thought to repress FOXP3 transcription via recruitment of repressive H3K9me3 to the FOXP3 promoter.[33] Furthermore, protein abundance of EZH1, a methyltransferase, was increased in Meno/Ang II $CD4^+$ T cells. EZH1, along with EZH2, is associated with the repressive H3K27me3, and is known to silence IFNγ, GATA3, and IL-10 loci in naïve $CD4^+$ T cells.[32] As seen in Figure 7, the increase in KLF14 activity and EZH1 expression are 2 pathways that may contribute to the susceptibility of menopausal mice to T cell-mediated hypertension.[15]

In T cells sustained ERK activation, downstream of TCR signaling, is known to correlate with T cell differentiation and proliferation, whereas transient ERK activation correlates with T cell unresponsiveness and apoptosis.[48] Activation of ERK via phosphorylation mediates the degradation of NF-κB inhibitory protein IkBα, leading to NF-κB nuclear translocation and increased pro-inflammatory gene transcription, specifically mediating Th17 cell development.[49] In splenocytes isolated from asthmatic mice, in vitro inhibition of ERK activation, via PD98059, reduced secretion of pro-inflammatory Th17 associated cytokine, IL-17, and increased secretion of Treg associated cytokine, IL-10.[49] Furthermore, treatment of asthmatic mice with a voltage gated potassium channel antagonist reduced lung expression of phosphorylated ERK and nuclear NF-κB, reduced serum and bronchoalveolar lavage fluid IL-17 concentration and reduced the splenic percentage of $CD4^+IL17A^+$ T cells. This reduction in Th17 associated response was accompanied by increased serum and bronchoalveolar lavage fluid IL-10 concentration and increased splenic percentage of $CD4^+FOXP3^+CD25^+$ T cells.[49]

Further evidence supports ERK activation as a mediator of Th17 cell development. Inhibition of ERK activation in isolated murine $CD4^+$ T cells cultured under Th17 polarization conditions led to less IL-17 secretion, but more IL-10 and TGFβ. Additionally, ERK inhibitor treated T cells under Th17 polarization conditions suppressed naïve T cell proliferation at levels comparable with that of purified Tregs. Moreover, adoptive transfer of ERK inhibitor treated T cells, after 5 days under Th17 polarization culture, into Rag-$1^{-/-}$ mice, resulted in reduced colitis pathological scores as compared with transfer of unpolarized and Th17 polarized T cells.[39]

The current study found that compared with premenopausal mice, Ang II infusion in menopausal mice increased phosphorylation of phosphosites associated with ERK activity, increased phosphorylation of MP2K2 (also known as MEK2), and increased $CD4^+$ T cell protein abundance of OXLA (Figure 7). Of the 92 identified phosphosites with increased phosphorylation in T cells from Meno/Ang II treated females, 35% were predicted to be targeted by ERK. Increased MP2K2 activity is consistent with the increased predicted ERK activity at proline-directed phosphosites in Meno/Ang II. Furthermore, OXLA expression is dependent on retinoic acid orphan receptor (RORγt) expression, the main transcription factor associated with Th17 cell development.[25,50] Consistent with this, OXLA expression is upregulated in Th17 cells.[50] As seen in Figure 7 increased ERK activation and increased Th17 differentiation in menopausal $CD4^+$ T cells is a pathway to consider in the development of menopausal hypertension.

In addition to a role for Th17 cells in hypertension development[51–53] several studies support a role for Tregs in hypertension prevention.[15,54,55] Recently TLN1, a cytoskeletal protein essential in mediating integrin activation, has been shown to be essential for Treg proliferation and function.[38] $CD4^+$ T-cell specific TLN1 deletion in $TLN1^{fl/fl}CD4^{Cre}$ mice resulted in spontaneous lymphocyte activation. This spontaneous lymphocyte activation was accompanied by a depletion of splenic $CD4^+FOXP3^+$ Tregs. Further, splenic $CD4^+FOXP3^+$ Tregs from $TLN1^{fl/fl}CD4^{Cre}$ mice have decreased p-STAT5, IL-10, and IL-2Rα expression and decreased FOXP3 median fluorescence intensity on a per cell basis.[38] This suggests an important role for TLN1 in regulating Treg survival through maintenance of increased IL-2Rα expression (also known as CD25) and downstream p-STAT5 signaling. STAT5 phosphorylation occurs directly downstream of the IL-2R[56] and is known to block Th17 cell development and promote Treg differentiation and maintenance of function by targeting the FOXP3 promoter.[57]

The importance of TLN1 in Treg function was further confirmed in Treg specific TLN1 depleted ($TLN1^{fl/fl}FOXP3^{Cre}$) hemizygous mice.[58] $TLN1^{fl/fl}FOXP3^{Cre}$ hemizygous mice developed systemic autoimmunity that ultimately resulted in death by 2 to 3 months of age. These mice exhibited increased splenic percentages of activated ($CD62L^{lo}CD44^{hi}$) $CD4^+$ and $CD8^+$ cells that were highly proliferative and expressed increased levels of IFNγ and TNFα. This increase in inflammation was accompanied by reduced IL-2Rα and FOXP3 expression in TLN1 deficient Tregs, again suggesting an important role for TLN1 in mediating Treg suppressive function.

The current study found that compared with premenopausal mice, Ang II infusion in menopausal mice decreased $CD4^+$ T cell phosphorylation of TLN1 at S405, however little is known about the role of phosphorylation at S405 in TLN1 function. TLN1 phosphorylation by CDK5 at S425 has been shown to activate β1 integrins in metastatic prostate cancer cells.[59] Given the proximity of our identified phosphosite to a known activating phosphosite and the major integrin binding domain of TLN1 (AAs 86–403), phosphorylation at S405 may regulate TLN1-integrin binding. Therefore,

decreased phosphorylation of TLN1 at S405 and downstream IL-2R signaling in CD4+ T cells may contribute to reduced Treg function and increased hypertension susceptibility in menopausal females (Figure 7).

In conclusion, this proteomic study of T cells from premenopausal and postmenopausal females identifies Ang II regulated T cell pathways. In postmenopausal females, Ang II signaling and an increase in blood pressure potentially regulate the T cell proteome. Taken together we identify novel T cell pathways that contribute to enhanced T cell inflammation leading to hypertension in postmenopausal females.

CONCLUSIONS

The present study identifies T cell function and signaling during the progression of hypertension across the postmenopausal transition. CD4+ T cell proteomic and phosphoproteomic analyses revealed 285 differentially regulated proteins and 207 differentially regulated phosphorylation sites between Ang II infused menopausal and premenopausal mice. Pathways including ERK, TLN1, EZH1, and KLF14 were identified as potential regulators of CD4+ T cell function during menopausal hypertension. These data identify novel T cell pathways that are dysregulated in postmenopausal females, contributing to greater T cell-mediated inflammation and an increased incidence and severity of hypertension. Selective manipulation of the identified T cell molecular targets may prove to be an effective strategy to inhibit the inflammation and renal damage associated with severe postmenopausal hypertension.

ARTICLE INFORMATION

Received June 16, 2020; accepted September 29, 2020.

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Acknowledgments

We acknowledge excellent technical support from Jennifer L. Uhrlaub for the determination of CD4+ T cell purity via flow cytometry and Kevin Doubleday for assistance in producing the volcano plots.

Author contributions: Brooks, Lindsey, and Langlais conceived and designed research; Husband, Uhlorn, Moffett, and Romero-Aleshire performed experiments; Uhlorn, Husband, Langlais, and Brooks analyzed data; Uhlorn, Husband, Langlais, Lindsey, and Brooks interpreted results of experiments; Uhlorn, Langlais, and Brooks prepared figures; Uhlorn, Husband, and Brooks drafted manuscript; Uhlorn, Husband, Langlais, Romero-Aleshire, Moffett, Lindsey, and Brooks edited and revised manuscript; Uhlorn, Husband, Langlais, Romero-Aleshire, Moffett, Lindsey, and Brooks approved final version of manuscript.

Sources of Funding

This work was funded by grants from the National Heart, Lung, and Blood Institute, RO1HL131834, T32HL007249 and National Institute of Diabetes and Digestive and Kidney Diseases RO1DK098493.

Disclosures

None.

Supplementary Material

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REFERENCES

1. Lim SS, Vos T, Flaxman AD, Danaei G. A comparative risk assessment of burden of disease and injury attributable to 67 risk factors and risk factor clusters in 21 regions, 1990–2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet*. 2012;380:2224–2260.
2. Dubey R, Oparil S, Imthurn B, Jackson E. Sex hormones and hypertension. *Cardiovasc Res*. 2002;53:688–708.
3. Murphy SL, Xu J, Kochanek KD, Arias E. Mortality in the United States, 2017. *NCHS Data Brief*. 2018;328:1–8.
4. Rosano G, Vitale C, Marazzi G, Volterrani M. Menopause and cardiovascular disease: the evidence. *Climacteric*. 2007;10:19–24.
5. Lima R, Wofford M, Reckelhoff JF. Hypertension in postmenopausal women. *Curr Hypertens Rep*. 2012;14:254–260.
6. Wang J, Jiang W, Sharma M, Wu Y, Li J, You N, Ding Z, Zhao X, Chen H, Tang H, et al. Sex differences in antihypertensive drug use and blood pressure control. *Postgrad Med J*. 2019;95:295–299.
7. Nwankwo T, Yoon SS, Burt V, Gu Q. Hypertension among adults in the United States: National Health and Nutrition Examination Survey, 2011–2012. *NCHS Data Brief*. 2013;133:1–8.
8. Brooks HL, Pollow DP, Hoyer PB. The VCD mouse model of menopause and perimenopause for the study of sex differences in cardiovascular disease and the metabolic syndrome. *Physiology (Bethesda)*. 2016;31:250–257.
9. Pollow DP, Romero-Aleshire MJ, Sanchez JN, Konhilas JP, Brooks HL. ANG II-induced hypertension in the VCD mouse model of menopause is prevented by estrogen replacement during perimenopause. *Am J Physiol Regul Integr Comp Physiol*. 2015;309:R1546–R1552.
10. Rodriguez-Iturbe B, Pons H, Johnson RJ. Role of the immune system in hypertension. *Physiol Rev*. 2017;97:1127–1164.
11. Sylvester MA, Brooks HL. Sex-specific mechanisms in inflammation and hypertension. *Curr Hypertens Rep*. 2019;21:53.
12. Guzik TJ, Hoch NE, Brown KA, McCann LA, Rahman A, Dikalov S, Goronzy J, Weyand C, Harrison DG. Role of the T cell in the genesis of angiotensin II-induced hypertension and vascular dysfunction. *J Exp Med*. 2007;204:2449–2460.
13. Mattson DL, Lund H, Guo C, Rudemiller N, Geurts AM, Jacob H. Genetic mutation of recombination activating gene 1 in Dahl salt-sensitive rats attenuates hypertension and renal damage. *Am J Physiol Regul Integr Comp Physiol*. 2013;304:R407–R414.
14. Pollow DP, Uhrlaub J, Romero-Aleshire M, Sandberg K, Nikolich-Zugich J, Brooks HL, Hay M. Sex differences in T-lymphocyte tissue infiltration and development of angiotensin II hypertension. *Hypertension*. 2014;64:384–390.
15. Pollow DP, Uhlorn JA, Sylvester MA, Romero-Aleshire MJ, Uhrlaub JL, Lindsey ML, Nikolich-Zugich J, Brooks HL. Menopause and FOXP3+ Treg cell depletion eliminate female protection against T cell-mediated angiotensin II hypertension. *Am J Physiol Heart Circ Physiol*. 2019;317:H415–H423.
16. Zambelli F, Pesole G, Pavesi G. Pscan: finding over-represented transcription factor binding site motifs in sequences from co-regulated or co-expressed genes. *Nucleic Acids Res*. 2009;37:W247–W252.
17. Colaert N, Helsens K, Martens L, Vandekerckhove J, Gevaert K. Improved visualization of protein consensus sequences by iceLogo. *Nat Methods*. 2009;6:786–787.
18. Obenauer JC, Cantley LC, Yaffe MB. Scansite 2.0: proteome-wide prediction of cell signalling interactions using short sequence motifs. *Nucleic Acids Res*. 2003;31:3635–3641.
19. Tyanova S, Temu T, Sinitcyn P, Carlson A, Hein MY, Geiger T, Mann M, Cox J. The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nat Methods*. 2016;13:731–740.
20. Tyanova S, Cox J. Perseus: a bioinformatics platform for integrative analysis of proteomics data in cancer research. *Methods Mol Biol*. 2018;1711:133–148.

21. Kawano H, Nakatani T, Mori T, Ueno S, Fukaya M, Abe A, Kobayashi M, Toda F, Watanabe M, Matsuoka I. Identification and characterization of novel developmentally regulated neural-specific proteins, BRINP family. *Brain Res Mol Brain Res*. 2004;125:60–75.
22. Peiffer DS, Wyatt D, Zlobin A, Piracha A, Ng J, Dingwall AK, Albain KS, Osipo C. DaXX suppresses tumor-initiating cells in estrogen receptor–positive breast cancer following endocrine therapy. *Cancer Res*. 2019;79:4965–4977.
23. Chen JJ, Schmucker LN, Visco DP. Identifying de-NEDDylation inhibitors: virtual high-throughput screens targeting SENP8. *Chem Biol Drug Des*. 2019;93:590–604.
24. McCormack R, Podack ER. Perforin-2/Mpeg1 and other pore-forming proteins throughout evolution. *J Leukoc Biol*. 2015;98:761–768.
25. Romagnani S. IL4I1: key immunoregulator at a crossroads of divergent T-cell functions. *Eur J Immunol*. 2016;46:2302–2305.
26. Ellmeier W, Taniuchi I. The role of BTB-zinc finger transcription factors during T cell development and in the regulation of T cell-mediated immunity. *Curr Top Microbiol Immunol*. 2014;381:21–49.
27. Carpenter AC, Wohlfert E, Chopp LB, Vacchio MS, Nie J, Zhao Y, Shetty J, Xiao Q, Deng C, Tran B, et al. Control of regulatory T cell differentiation by the transcription factors Thpok and LRF. *J Immunol*. 2017;199:1716–1728.
28. Yamada T, Park CS, Mamonkin M, Lacorazza HD. Transcription factor ELF4 controls the proliferation and homing of CD8+ T cells via the Krüppel-like factors KLF4 and KLF2. *Nat Immunol*. 2009;10:618–626.
29. Malilas W, Koh SS, Srisuttee R, Boonying W, Cho IR, Jeong CS, Johnston RN, Chung YH. Cancer upregulated gene 2, a novel oncogene, confers resistance to oncolytic vesicular stomatitis virus through STAT1-OASL2 signaling. *Cancer Gene Ther*. 2013;20:125–132.
30. Huang W, Ghisletti S, Saijo K, Gandhi M, Aouadi M, Tesz GJ, Zhang DX, Yao J, Czech MP, Goode BL, et al. Coronin 2A mediates actin-dependent de-repression of inflammatory response genes. *Nature*. 2011;470:414–418.
31. Molinier-Frenkel V, Prévost-Blondel A, Castellano F. The IL4I1 enzyme: a new player in the immunosuppressive tumor microenvironment. *Cells*. 2019;8:757.
32. Zhang Y, Kinkel S, Maksimovic J, Bandala-Sanchez E, Tanzer MC, Naselli G, Zhang JG, Zhan Y, Lew AM, Silke J, et al. The polycomb repressive complex 2 governs life and death of peripheral T cells. *Blood*. 2014;124:737–749.
33. Sarmento OF, Svingen PA, Xiong Y, Xavier RJ, McGovern D, Smyrk TC, Papadakis KA, Urrutia RA, Faubion WA. A novel role for Kruppel-like factor 14 (KLF14) in T-regulatory cell differentiation. *Cell Mol Gastroenterol Hepatol*. 2015;1:188–202.e4.
34. Leal-Sanchez J, Couzinet A, Rossin A, Abdel-Sater F, Chakrabandhu K, Luci C, Anjuere F, Stebe E, Hancock D, Hueber AO. Requirement for Daxx in mature T-cell proliferation and activation. *Cell Death Differ*. 2007;14:795–806.
35. Du J, Wang Q, Ziegler SF, Zhou B. FOXP3 interacts with hnRNPF to modulate pre-mRNA alternative splicing. *J Biol Chem*. 2018;293:10235–10244.
36. Gomez TS, McCarney SD, Carrizosa E, Labno CM, Comiskey EO, Nolz JC, Zhu P, Freedman BD, Clark MR, Rawlings DJ, et al. HS1 functions as an essential actin-regulatory adaptor protein at the immune synapse. *Immunity*. 2006;24:741–752.
37. Lettau M, Kabelitz D, Janssen O. SDF1α-induced interaction of the adapter proteins Nck and HS1 facilitates actin polymerization and migration in T cells. *Eur J Immunol*. 2015;45:551–561.
38. Klann JE, Remedios KA, Kim SH, Metz PJ, Lopez J, Mack LA, Zheng Y, Ginsberg MH, Petrich BG, Chang JT. Talin plays a critical role in the maintenance of the regulatory T cell pool. *J Immunol*. 2017;198:4639–4651.
39. Liu H, Yao S, Dann SM, Qin H, Elson CO, Cong Y. ERK differentially regulates Th17- and Treg-cell development and contributes to the pathogenesis of colitis. *Eur J Immunol*. 2013;43:1716–1726.
40. Stoll S, Wang C, Qiu H. DNA methylation and histone modification in hypertension. *Int J Mol Sci*. 2018;19:1174.
41. Laird PW. Principles and challenges of genome-wide DNA methylation analysis. *Nat Rev Genet*. 2010;11:191–203.
42. Branco MR, Ficz G, Reik W. Uncovering the role of 5-hydroxymethylcytosine in the epigenome. *Nat Rev Genet*. 2012;13:7–13.
43. Liu P, Liu Y, Liu H, Pan X, Li Y, Usa K, Mishra MK, Nie J, Liang M. Role of DNA de novo (De)methylation in the kidney in salt-induced hypertension. *Hypertension*. 2018;72:1160–1171.
44. Dasinger JH, Alsheikh AJ, Abais-Battad JM, Pan X, Fehrenbach DJ, Lund H, Roberts ML, Cowley AW Jr, Kidambi S, Kotchen TA, et al. Epigenetic modifications in T cells: the role of DNA methylation in salt-sensitive hypertension. *Hypertension*. 2020;75:372–382.
45. Zegerman P, Canas B, Pappin D, Kouzarides T. Histone H3 lysine 4 methylation disrupts binding of nucleosome remodeling and deacetylase (NuRD) repressor complex. *J Biol Chem*. 2002;277:11621–11624.
46. Greer EL, Shi Y. Histone methylation: a dynamic mark in health, disease and inheritance. *Nat Rev Genet*. 2012;13:343–357.
47. Lee H-A, Cho H-M, Lee D-Y, Kim K-C, Han HS, Kim IK. Tissue-specific upregulation of angiotensin-converting enzyme 1 in spontaneously hypertensive rats through histone code modifications. *Hypertension*. 2012;59:621–626.
48. Poltorak M, Meinert I, Stone JC, Schraven B, Simeoni L. Sos1 regulates sustained TCR-mediated Erk activation. *Eur J Immunol*. 2014;44:1535–1540.
49. Zhou Q-L, Wang T-Y, Li M, Shang Y-X. Alleviating airway inflammation by inhibiting ERK-NF-κB signaling pathway by blocking Kv1.3 channels. *Int Immunopharmacol*. 2018;63:110–118.
50. Santarlasci V, Maggi L, Capone M, Querci V, Beltrame L, Cavalieri D, D'Aiuto E, Cimaz R, Nebbioso A, Liotta F, et al. Rarity of human T helper 17 cells is due to retinoic acid orphan receptor-dependent mechanisms that limit their expansion. *Immunity*. 2012;36:201–214.
51. Du YN, Tang XF, Xu L, Chen WD, Gao PJ, Han WQ. SGK1-FoxO1 signaling pathway mediates Th17/Treg imbalance and target organ inflammation in angiotensin II-induced hypertension. *Front Physiol*. 2018;9:1581.
52. Ji Q, Cheng G, Ma N, Huang Y, Lin Y, Zhou Q, Que B, Dong J, Zhou Y, Nie S. Circulating Th1, Th2, and Th17 levels in hypertensive patients. *Dis Markers*. 2017;2017:7146290.
53. Orejudo M, Rodrigues-Diez RR, Rodrigues-Diez R, Garcia-Redondo A, Santos-Sanchez L, Randez-Garbayo J, Cannata-Ortiz P, Ramos AM, Ortiz A, Selgas R, et al. Interleukin 17A participates in renal inflammation associated to experimental and human hypertension. *Front Pharmacol*. 2019;10:1015.
54. Harmon A, Cornelius D, Amaral L, Paige A, Herse F, Ibrahim T, Wallukat G, Faulkner J, Moseley J, Dechend R, et al. IL-10 supplementation increases Tregs and decreases hypertension in the RUPP rat model of preeclampsia. *Hypertens Pregnancy*. 2015;34:291–306.
55. Barhoumi T, Kasal DA, Li MW, Shbat L, Laurant P, Neves MF, Paradis P, Schiffrin EL. T regulatory lymphocytes prevent angiotensin II-induced hypertension and vascular injury. *Hypertension*. 2011;57:469–476.
56. Boyman O, Sprent J. The role of interleukin-2 during homeostasis and activation of the immune system. *Nat Rev Immunol*. 2012;12:180–190.
57. Farrar MA, Owen DL. STAT5 and CD4+ T cell immunity. *F1000Res*. 2017;6:32.
58. Klann JE, Kim SH, Remedios KA, He Z, Metz PJ, Lopez J, Tysl T, Olvera JG, Ablack JN, Cantor JM, et al. Integrin activation controls regulatory T cell-mediated peripheral tolerance. *J Immunol*. 2018;200:4012–4023.
59. Jin JK, Tien PC, Cheng CJ, Song JH, Huang C, Lin SH, Gallick GE. Talin1 phosphorylation activates β1 integrins: a novel mechanism to promote prostate cancer bone metastasis. *Oncogene*. 2015;34:1811–1821.
60. Kruse R, Krantz J, Barker N, Coletta RL, Rafikov R, Luo M, Hojlund K, Mandarino LJ, Langlais PR. Characterization of the CLASP2 protein interaction network identifies SOGA1 as a microtubule-associated protein. *Mol Cell Proteomics*. 2017;16:1718–1735.
61. Campbell LE, Langlais PR, Day SE, Coletta RL, Benjamin TR, De Filippis EA, Madura JA II, Mandarino LJ, Roust LR, Coletta DK. Identification of novel changes in human skeletal muscle proteome after Roux-en-Y gastric bypass surgery. *Diabetes*. 2016;65:2724–2731.
62. Parker SS, Krantz J, Kwak EA, Barker NK, Deer CG, Lee NY, Mouneimne G, Langlais PR. Insulin induces microtubule stabilization and regulates the microtubule plus-end tracking protein network in adipocytes. *Mol Cell Proteomics*. 2019;18:1363–1381.
63. Chambers MC, Maclean B, Burke R, Amodei D, Ruderman DL, Neumann S, Gatto L, Fischer B, Pratt B, Egertson J, et al. A cross-platform toolkit for mass spectrometry and proteomics. *Nat Biotechnol*. 2012;30:918–920.

SUPPLEMENTAL MATERIAL

Data S1.

Supplemental Methods

Protein Separation and In-Gel Digestion for Mass Spectrometry Analysis

Protein samples from isolated $CD4^+$ cells were processed in triplicate batches with one sample from each group in each batch [60,61]. Total protein, (50 μg) per sample, was denatured in 10 μL of SDS sample loading buffer (4% SDS, 0.0625 M Tris-HCl, 10% glycerol, 0.02% bromophenol blue, 8 M Urea) at 95°C prior to protein separation by SDS-PAGE and staining with BioRad Bio-Safe Coomassie Stain (cat. # 1610786). Each lane was cut into eight sections, de-stained, and dehydrated for in-gel trypsin digestion. The resulting peptides were extracted and washed on a solid phase C18 ZipTip [60,62]. Eluted peptides were completely dehydrated by vacuum centrifugation and stored at -80°C until use.

Mass Spectrometry and Database Search

HPLC-ESI-MS/MS was performed in positive ion mode on a Thermo Scientific Orbitrap Fusion Lumos tribrid mass spectrometer fitted with an EASY-Spray Source (Thermo Scientific, San Jose, CA). NanoLC was performed using a Thermo Scientific UltiMate 3000 RSLCnano System with an EASY Spray C18 LC column (Thermo Scientific, 50cm x 75 µm inner diameter, packed with PepMap RSLC C18 material, 2 µm, cat. # ES803); loading phase for 15 min at 0.300 μL/min; mobile phase, linear gradient of 1–34% Buffer B in 119 min at 0.220 μL/min, followed by a step to 95% Buffer B over 4 min at 0.220 μL/min, hold 5 min at 0.250 μL/min, and then a step to 1% Buffer B over 5 min at 0.250 μL/min and a final hold for 10 min (total run 159 min); Buffer A = 0.1% FA/H_2O, and Buffer B = 0.1% FA in 80% ACN.

All solvents were liquid chromatography mass spectrometry grade. Spectra were acquired using XCalibur, version 2.3 (Thermo Scientific). A top speed data-dependent MS/MS analysis was performed. Dynamic exclusion was enabled with a repeat count of 1, a repeat duration of 30 sec, and an exclusion duration of 60 sec. Tandem mass spectra were extracted from Xcalibur RAW files and charge states were assigned using the ProteoWizard 2.1.xmsConvert script using the default parameters [63]. The fragment mass spectra were then searched against the mouse SwissProt_2016_10 database (16,838 entries) using Mascot (Matrix Science, London, UK; version 2.6.0) using the default probability cut-off score. The search variables that were used were: 10 ppm mass tolerance for precursor ion masses and 0.5 Da for product ion masses; digestion with trypsin; a maximum of two missed tryptic cleavages; variable modifications of oxidation of methionine and phosphorylation of serine, threonine, and tyrosine. Cross-correlation of Mascot search results with X! Tandem was accomplished with Scaffold (version Scaffold_4.8.4; Proteome Software, Portland, OR, USA). Probability assessment of peptide assignments and protein identifications were made through the use of Scaffold. Only peptides with ≥ 95% probability were considered.

Label-Free Peptide/Protein Quantification and Identification

Progenesis QI proteomics software (version 2.4, Nonlinear Dynamics Ltd., Newcastle upon Tyne, UK) was used to perform ion-intensity based label-free quantification. In brief, in an automated format, RAW files were imported and converted into two- dimensional maps (y-axis = time, x-axis =m/z) followed by

selection of a reference run for alignment purposes. An aggregate data set containing all peak information from all samples was created from the aligned runs, which was further narrowed down by selecting only +2, +3, and +4 charged ions for further analysis. The samples were grouped as Control, Ang II, or Meno/Ang II. A peak list of fragment ion spectra from the top eight most intense precursors of a feature was exported in Mascot generic file (.mgf) format and searched against the murine SwissProt_2016_10 database (16,838 entries) using Mascot (Matrix Science, London, UK; version 2.6). The search variables that were used were: 10 ppm mass tolerance for precursor ion masses and 0.5 Da for product ion masses; digestion with trypsin; a maximum of two missed tryptic cleavages; variable modifications of oxidation of methionine and phosphorylation of serine, threonine, and tyrosine; 13C=1. The resulting Mascot .xml file was then imported into Progenesis, allowing for peptide/protein assignment, while peptides with a Mascot Ion Score of <25 were not considered for further analysis. Protein quantification and logarithmic transformation was performed using only non-conflicting peptides and precursor ion- abundance values were normalized in a run to those in a reference run (not necessarily the same as the alignment reference run). Progenesis identified differentially expressed peptides and phosphosites were used for gene ontology, transcription factor, phosphorylation motif, and kinase identification downstream analyses.

Table S1. Differentially Expressed Proteins Between Ang II and Control.

Accession	Control 1	Control 2	Control 3	Control 4	Ang II 1	Ang II 2	Ang II 3	Ang II 4	P Value	Fold change
SERC1_MOUSE	465	88689	130669	135465	1	832	1744	1	0.03	0.01
DHSD_MOUSE	546537	218496	1095007	948243	12281	90163	251754	95066	0.03	0.16
CJ035_MOUSE	72807	131892	111129	27416	23188	33032	6903	2622	0.03	0.19
ARHG3_MOUSE	85333	113560	73204	83093	11578	19692	51248	9836	0.00	0.26
LYZ2_MOUSE	109024630	69896303	182726495	77461506	52196581	18556253	29595195	24551226	0.03	0.28
ATPK_MOUSE	16047586	6094899	24332346	10957959	5711746	3092834	3727656	4653711	0.04	0.30
ALG6_MOUSE	279442	139727	209846	135365	74454	40746	27224	97089	0.01	0.31
VMA21_MOUSE	6906698	7879939	14262146	4894248	4910968	1995611	1540546	2420177	0.04	0.32
VPS8_MOUSE	38385	35526	48561	30382	25208	10493	6729	6822	0.00	0.32
QCR9_MOUSE	6411688	2762055	3798445	2397734	2562813	1105578	717159	643003	0.04	0.33
PTRD1_MOUSE	806069	252474	684853	720273	406353	60278	134418	205679	0.03	0.33
OXLA_MOUSE	6123033	5206659	7502733	5266404	1493189	1936051	2808020	1869351	0.00	0.34
KV6A9_MOUSE	8558453	6418455	5756524	7908297	3060040	1413018	3241664	1986926	0.00	0.34
B2MG_MOUSE	39158117	17453231	60334760	44989340	21125476	5829611	8825870	20540402	0.03	0.35
QCR8_MOUSE	30060836	14657556	33074180	24271459	17647821	5730522	5956635	7848888	0.02	0.36
NDUA5_MOUSE	10993112	3468862	10078622	5597331	4091547	1086280	2419537	3540005	0.05	0.37
EMC6_MOUSE	2388938	1326013	3297873	1890039	1532894	710689	340456	771581	0.03	0.38
TM256_MOUSE	933067	560107	1559210	704997	517236	218420	227637	497293	0.05	0.39
GOGA7_MOUSE	1490403	834724	1601635	1472532	879158	215609	303193	723823	0.01	0.39
DPM3_MOUSE	1710722	743218	2567010	2036567	858785	344952	706561	867316	0.04	0.39
USMG5_MOUSE	10551490	10534854	24203768	13998051	8654429	5085799	4811044	6020140	0.04	0.41
MPEG1_MOUSE	42129537	35826725	44634277	40835180	13743040	14920476	22980836	16980204	0.00	0.42
NDUB3_MOUSE	12317315	5851510	16265359	13267929	6415131	1869230	4883086	6934124	0.03	0.42
FCRL5_MOUSE	145082	216780	209159	182046	41446	106154	54548	122732	0.01	0.43
THIO_MOUSE	153502491	88068812	173690732	105707513	91382244	52196529	34727607	54573853	0.02	0.45
ATP5I_MOUSE	44344838	25635047	38649342	24533482	29906416	11876006	12799269	6254464	0.04	0.46
COCH_MOUSE	1525188	792365	873469	878571	667511	680801	201972	320463	0.04	0.46
NDUC2_MOUSE	27998342	12840257	24392769	17030658	17103838	4654206	5168537	11229543	0.05	0.46
FABP5_MOUSE	10481284	6381704	10027580	9440624	7761981	2195134	1624705	5581263	0.03	0.47
ISCA2_MOUSE	657918	633771	532043	333997	326638	241977	180988	292472	0.01	0.48
LSM6_MOUSE	3122427	1871017	4170077	2301461	1916788	566716	1405865	1688772	0.05	0.49
SQSTM_MOUSE	5211406	2603133	4168648	3337907	1548592	1591774	2912801	1528723	0.03	0.49
CTNB1_MOUSE	149748	154997	216129	170412	109353	53021	70629	109114	0.01	0.49
RL37A_MOUSE	5226766	5073127	10588295	7443016	4869045	3165114	2472129	3620208	0.04	0.50
SACS_MOUSE	12574097	14894412	17981580	13634090	6749947	7723368	10066759	5151426	0.00	0.50
DYLT1_MOUSE	6988308	4523340	9360556	8557091	4680878	2103663	2484221	5524950	0.04	0.50
MPC2_MOUSE	989358	914503	1096301	995089	780481	363108	262520	629377	0.01	0.51
CHIL3_MOUSE	476699567	315458064	450897674	529788270	217819287	186955347	281871287	236782037	0.01	0.52
SPA3K_MOUSE	2285893	1755370	3032836	1384379	1262368	632940	1378303	1162524	0.04	0.52
FCGR2_MOUSE	1197092	1426017	1998293	1286509	834289	960013	861307	459557	0.02	0.53
CATD_MOUSE	1102664844	979062563	1375070830	904557247	470647611	495352619	873454145	467147257	0.01	0.53
CK016_MOUSE	98433	101666	118365	136716	37893	57137	74004	71966	0.00	0.53
FBP1L_MOUSE	480725	511422	408169	541450	414665	13513	284626	337357	0.05	0.54
CBPQ_MOUSE	54590753	39066210	28805507	48309750	14737128	28816563	30888915	19515531	0.03	0.55
H4_MOUSE	152515587	108566169	134078185	123077797	98273019	52167231	54763983	83842728	0.01	0.56
A1AT1_MOUSE	7520235	8834284	9465497	5684361	5829227	3743981	4109555	4074565	0.01	0.56
SCIMP_MOUSE	413656	515741	658351	385457	351710	277927	335993	146818	0.03	0.56
GABT_MOUSE	986901	816440	696180	1376284	581114	400352	662540	569794	0.04	0.57
S35F6_MOUSE	4543817	4132515	4035727	3540633	2083574	2181042	2358631	2789756	0.00	0.58
FA26F_MOUSE	7396036	5835959	7007615	4552243	3003057	3131631	5079560	3345676	0.02	0.59
SO2B1_MOUSE	1080782	996354	1371178	1071109	732871	551049	684094	698660	0.00	0.59
FLOT2_MOUSE	13690773	10589211	12861370	10680063	6333834	4991923	9471739	7476332	0.01	0.59
BGAL_MOUSE	186814315	208559904	217159845	220203064	93897990	109807903	192457671	98120338	0.01	0.59
COX41_MOUSE	324921768	209308785	399828130	372805775	256605236	142116643	145605694	238755858	0.04	0.60
TPPC1_MOUSE	4717356	3563608	3568047	2841362	3534627	1731914	1372592	2165022	0.05	0.60
PSMG4_MOUSE	3795131	3011950	4486916	2874089	2769287	1368800	1795025	2613261	0.03	0.60
HA2B_MOUSE	93842524	58349584	104831154	74599537	46196097	51377801	62136235	40563893	0.03	0.60
S29A3_MOUSE	1943404	1174149	1943249	1494522	933066	907299	1325041	799179	0.03	0.60
CD68_MOUSE	15264544	19316646	19897931	19494266	8101970	10368724	16826265	10140121	0.02	0.61
PPAL_MOUSE	17820537	14216183	17627494	17422384	8176907	9436802	15820663	7917577	0.02	0.62
NDUB4_MOUSE	58711058	43390974	63684042	58990517	49317259	22926775	29134829	37377508	0.02	0.62
COTL1_MOUSE	681174051	436042153	809498766	697734159	534713078	282142993	316255462	503622011	0.05	0.62
FUCO_MOUSE	4203682	3520587	3135341	2871534	1937066	1825134	3418147	1517755	0.05	0.63
TM1L2_MOUSE	889561	936041	1427985	829164	740773	753848	580109	559712	0.05	0.65
MFGM_MOUSE	14011731	13419763	15105491	16989652	10286116	8792355	12746986	7887995	0.01	0.67
GLCM_MOUSE	8443196	7134359	9291316	7206724	4283599	5163738	8170279	3847586	0.05	0.67
METL2_MOUSE	206424	230659	227841	160016	126697	135799	142910	151638	0.01	0.68
CD22_MOUSE	6070973	6779937	5594304	5520955	4410798	4384763	4469544	2955115	0.01	0.68
OARD1_MOUSE	7397349	7420083	6839596	7900800	5471091	5753217	3797645	5052023	0.00	0.68
FTM_MOUSE	14239144	11717708	19136244	14177957	8187669	8844968	12672136	10579750	0.04	0.68
PTPS_MOUSE	16980039	16937518	19398508	24414128	16505673	10886114	11837398	14384340	0.03	0.69
FRRS1_MOUSE	4031593	3886343	3842964	4240909	2826634	2665815	3705960	1911541	0.02	0.69
PHLD_MOUSE	30690950	23862992	28777292	24341503	16359600	17447806	20707412	20246505	0.01	0.69
CSF1R_MOUSE	2750387	3886804	4760304	3923500	2699827	2134796	2900259	2911138	0.04	0.69
SMD2_MOUSE	151123976	123315524	163787712	161810421	127423218	68671320	90891731	130023187	0.04	0.69
T106B_MOUSE	1594344	1321948	1549201	1771725	803056	1271080	1173706	1094282	0.01	0.70
LG3BP_MOUSE	158244349	144030091	211411459	156013843	100148079	98279291	154562828	114891728	0.04	0.70
MIC1_MOUSE	3156167	2871487	3153548	2105506	2287978	1454509	2185623	1957794	0.03	0.70
VATC1_MOUSE	58410564	52442801	55991593	42025242	46102087	29017493	35408497	36807256	0.02	0.71
P2RX4_MOUSE	14691583	15661473	13985277	11030939	8551000	8914138	12502989	9280579	0.02	0.71
ITAX_MOUSE	9190022	8452383	8156486	10061656	6543742	7178793	6147487	5574022	0.00	0.71
UFO_MOUSE	5984764	5617035	7824527	5259009	4605163	4563015	4976715	3505520	0.04	0.72
CTNA1_MOUSE	1389579	1263923	1354742	1463538	1202798	685470	1194099	875603	0.03	0.72
SPTB1_MOUSE	86437105	100405055	75925090	64473889	73180779	52135397	50075485	62358679	0.05	0.73
LAMP1_MOUSE	185595069	218613101	180250260	174344229	120001854	137136712	174030159	122677770	0.02	0.73
VIME_MOUSE	87431446	67028603	100735983	92441327	57783376	55964910	71080932	69645153	0.03	0.73

UBE2N_MOUSE	300882002	251358454	308512448	353004962	258095303	165985444	201823078	263219691	0.04	0.73
LMBD1_MOUSE	8685761	8130583	6509883	6664280	4559109	4731396	5813831	7061906	0.05	0.74
MYO1C_MOUSE	35770597	36996402	32863709	24525262	26710741	24122504	22659391	22717747	0.03	0.74
MSPD2_MOUSE	5174060	4925650	6209205	4313833	3778312	4357028	3613473	3519693	0.02	0.74
CD44_MOUSE	53242855	49480881	69424600	50624956	41465372	35493322	46730284	42215275	0.03	0.74
CD226_MOUSE	8927893	8777187	11207862	8756264	7353691	7328655	6669531	6703558	0.01	0.74
RAB9A_MOUSE	19654781	19363162	17381791	18755468	17589423	11260807	11408420	15818658	0.03	0.75
NCF2_MOUSE	2711083	3500965	3255203	2647557	2812994	2196846	1924801	2190080	0.04	0.75
ANM3_MOUSE	6355774	6872240	8287796	6615599	6397233	5250661	5589626	3999749	0.04	0.75
EHD1_MOUSE	204836277	207245420	185184042	147008833	132031429	175671159	127432176	127288171	0.05	0.76
PLXB2_MOUSE	22863679	26925022	24663825	19086913	19212387	14512052	17850765	19424818	0.03	0.76
HB2A_MOUSE	311720880	334335250	342335656	268816278	272996843	260552921	236419800	186971308	0.02	0.76
2AAB_MOUSE	20501133	14655789	19400098	16484561	14455664	14598745	11597186	13931175	0.03	0.77
PTRF_MOUSE	22587357	23540851	22632662	25520805	19935124	17856314	18634924	16370215	0.00	0.77
TGM1_MOUSE	9411134	10392927	12355630	10399037	10263456	6470557	7617401	8523902	0.05	0.77
LAMP2_MOUSE	42389735	47159817	49136119	43268945	27861293	32526578	42805487	37393332	0.03	0.77
ACS2L_MOUSE	24611022	24341862	27889171	22994264	17288613	20778658	22456438	17453465	0.02	0.78
XXLT1_MOUSE	608255	697434	660321	617955	402007	447134	624997	560591	0.05	0.79
ICAM1_MOUSE	24349111	24668625	28673181	27644388	17735272	18776726	25323937	21129412	0.03	0.79
KRIT1_MOUSE	1038256	873418	964046	938958	889629	816641	569376	790734	0.05	0.80
SLAF1_MOUSE	30685821	31035067	37299342	29074286	29710305	23323028	25971623	24035577	0.03	0.80
STX8_MOUSE	18890712	19327158	16187184	17046595	15140993	12037050	14448851	16236089	0.03	0.81
KTN1_MOUSE	9379770	10018177	8573785	8253738	7641065	7106997	7804755	7112906	0.01	0.82
LACTB_MOUSE	31363777	35740753	33726840	31994484	23671818	27035341	30474586	27831622	0.01	0.82
ODP2_MOUSE	113282739	90702254	95590610	86202692	79387999	87602630	81602074	69424043	0.05	0.82
SEPP1_MOUSE	5123538	4868483	5076376	5164457	4874312	4237653	3742466	4177170	0.02	0.84
TAXB1_MOUSE	6668156	6424427	6042256	6451962	5293145	5182088	6052039	5021966	0.01	0.84
GPDM_MOUSE	170236722	145445996	171253105	145488061	151371865	123584905	129083263	128927820	0.04	0.84
FIBP_MOUSE	5915589	5198663	5888577	4821115	4655583	4345744	4655545	4959511	0.04	0.85
ATAD3_MOUSE	40700417	45661283	43347589	42466598	34982838	38683342	40955943	33105653	0.02	0.86
RUFY3_MOUSE	1565235	1530554	1776498	1366088	1353247	1379965	1307935	1359709	0.05	0.87
RASA2_MOUSE	3368197	3640233	3258867	3494088	3026712	2539089	3012091	3345864	0.05	0.87
CH60_MOUSE	1631707038	1666037237	1610040078	1648750587	1377692537	1624531997	1449440895	1375261847	0.02	0.89
CUX1_MOUSE	1864107	2092577	1870401	1908250	1834538	1648886	1782404	1777633	0.04	0.91
ATPB_MOUSE	5542451666	5967222019	5457459740	5340178680	4825562315	5478299288	5183744016	4833179074	0.05	0.91
UBE2Z_MOUSE	10078142	9983250	9631385	10480358	11010495	11231031	10426326	11424460	0.01	1.10
BAG3_MOUSE	2067902	1740260	1968436	1802744	2052282	2102223	2121605	2216157	0.03	1.12
ZFN2B_MOUSE	3366674	3080285	3095674	3380951	4027803	3600347	3657669	3317947	0.05	1.13
MITD1_MOUSE	5246318	5400155	4734623	4856787	5500510	5746344	5645580	6011808	0.01	1.13
SF01_MOUSE	82825667	76830784	83699424	93297890	100371537	96246560	86526435	98097670	0.05	1.13
LAP2B_MOUSE	245283117	242154628	237503813	256561897	263355023	296668040	300980293	261477349	0.02	1.14
LEO1_MOUSE	9613331	10979637	8748643	9887480	11370991	11758794	11833109	10200358	0.05	1.15
HCD2_MOUSE	199497184	234888677	199736522	212686073	268693143	251500060	217267532	240064262	0.05	1.15
KC1A_MOUSE	30633301	32024842	28091549	32489988	36936140	37484647	32973880	35492930	0.01	1.16
RANG_MOUSE	191544981	218630240	247096185	225015514	239225692	259262497	266421973	258561034	0.03	1.16
EXOSX_MOUSE	20674810	21675554	19514233	20898531	21157428	24323961	24430610	26268301	0.03	1.16
SGTA_MOUSE	15727110	13533527	16311929	14929571	15644503	17787908	18916902	18256790	0.03	1.17
EI3JA_MOUSE	70623422	55084850	69520505	58961935	78697193	73991193	72320833	72177120	0.04	1.17
MOGS_MOUSE	64734343	71264187	63114963	58000201	73823119	71704998	73238189	82479358	0.02	1.17
DHX34_MOUSE	1962492	1590847	1881617	1802064	1944502	2345014	1952746	2263286	0.05	1.18
U2AF2_MOUSE	158319273	187908669	155616933	196991219	196873279	223405879	198537533	202789712	0.04	1.18
IP3KA_MOUSE	731897	801888	821282	849585	947204	963381	1037788	819650	0.03	1.18
PBDC1_MOUSE	24229966	29717518	24938480	29125705	29399305	34264078	35261570	30647959	0.04	1.20
RP25L_MOUSE	1747267	2157184	2326536	1860464	2338814	2621216	2362290	2397424	0.03	1.20
RU2B_MOUSE	37294147	41736551	37669920	44741327	43642067	49193537	49852314	51636937	0.02	1.20
RAVR1_MOUSE	178360712	147318989	143303189	127478926	176351965	179657078	172118396	189916420	0.04	1.20
NUP98_MOUSE	8351671	7868158	8247489	7591324	7782570	9939169	10665594	10282247	0.05	1.21
PRDX6_MOUSE	791877691	810191353	651724713	749250394	934857441	896918854	933142542	864214636	0.01	1.21
DYR_MOUSE	22482648	25638170	21645937	23416027	27878578	26592432	29431408	28741190	0.00	1.21
RCD1_MOUSE	10410766	8719306	8363376	10909958	11972614	11657183	11387878	11577003	0.02	1.21
UBAP2_MOUSE	7363304	5816668	5943887	6187524	7746047	8520824	7056388	7485962	0.03	1.22
RBP10_MOUSE	1931742	1656547	1513361	1472576	1944421	2280804	1767873	2010459	0.05	1.22
EXOS5_MOUSE	10379836	14131594	11084957	11310020	12872756	14384851	14921509	15013802	0.04	1.22
IGJ_MOUSE	15742420	17398307	13104537	18259789	19449390	20334744	20676665	18536087	0.03	1.22
MA7D1_MOUSE	7212120	7903110	7750837	7428911	9824720	9593730	10292685	7529746	0.03	1.23
SRRM2_MOUSE	52194780	45872521	43755410	54530168	58263233	60284851	66595792	56268382	0.02	1.23
SLAI2_MOUSE	9694737	10840759	10315924	9053202	12908323	12082709	10306210	13771632	0.03	1.23
SYNM_MOUSE	649278	532455	502277	535704	612184	681906	652139	793447	0.04	1.23
ICLN_MOUSE	15635134	14207060	15947446	13981581	17853485	19236141	19240246	17466054	0.00	1.23
UNK_MOUSE	3449167	3072044	3429020	2929850	3738204	4057355	4189672	3929255	0.00	1.24
RASF1_MOUSE	686750	636456	756868	619134	839497	938048	789543	771139	0.02	1.24
RYBP_MOUSE	6579946	5712981	6004851	5652475	8701897	7279023	6176774	7463500	0.04	1.24
IN35_MOUSE	64798268	53049243	53227196	58437632	83430050	72894808	59371685	68958769	0.05	1.24
TYW4_MOUSE	5171213	4959931	4337549	5480288	6732719	6443559	4955634	6731508	0.05	1.25
TAF9B_MOUSE	1330375	987001	1144545	1119344	1334960	1565485	1257961	1584231	0.04	1.25
CAPR1_MOUSE	41303417	45681927	54724633	51373120	52876029	70515481	58425174	60496340	0.04	1.25
PERQ2_MOUSE	20543113	15795975	18551453	17537968	21545121	25860910	24308891	19383331	0.04	1.26
GMEB1_MOUSE	3003946	2678042	2887611	2975956	3326100	3656312	3669780	3938018	0.00	1.26
RUNX3_MOUSE	3581523	4440813	4175137	4000981	5135171	4378645	6078575	4991311	0.03	1.27
TSSC4_MOUSE	1860732	2280103	2325066	1820536	2404545	2778117	2936459	2420354	0.02	1.27
WBP11_MOUSE	29590927	31518347	28609727	30778244	39275847	39340921	43789247	30937579	0.02	1.27
MB12A_MOUSE	7786743	8427283	7208863	9912450	11356318	11626335	9786103	9700821	0.03	1.27
HEXI1_MOUSE	6753840	6869325	6625606	7797174	9682749	9953048	8801865	7359933	0.02	1.28
CWC27_MOUSE	6589901	6184526	5941201	5583136	8260449	8032286	7187325	7560801	0.00	1.28
NFRKB_MOUSE	6905625	5532486	5716487	5928616	8369217	8177734	8185467	6106141	0.03	1.28
SNX19_MOUSE	140337	93241	130793	111157	164900	157734	140451	146388	0.03	1.28
SARNP_MOUSE	205482333	216382097	182861293	208949307	214824335	310410035	258916939	259463599	0.03	1.28
ANR17_MOUSE	11428990	8083869	11301243	10522128	14818356	14322251	11317338	12605187	0.04	1.28
WDR33_MOUSE	16391661	14978905	13837482	16275541	19357142	23101648	20423848	16093254	0.03	1.28
YLPM1_MOUSE	26693664	23879277	25311467	26196026	30234505	41024875	29303863	30636995	0.04	1.29
FAM21_MOUSE	71758554	71702581	76423853	67306271	89139187	101797215	99285420	79295351	0.01	1.29

KIN17_MOUSE	2254638	2261216	2076351	2719167	2797885	3709956	2601598	2912847	0.05	1.29
RPGF2_MOUSE	4617668	3559462	3757727	3211075	4992576	5683617	4474871	4409843	0.04	1.29
APOA1_MOUSE	65060202	45620314	54717573	63453618	60128589	73027781	76865558	86293243	0.05	1.29
KDM3B_MOUSE	22788599	18735645	18617836	17215120	26321006	28809047	23223429	21960845	0.03	1.30
STMN1_MOUSE	55786298	46218356	51936644	58345839	65480043	83302499	58862961	68830711	0.03	1.30
AKTS1_MOUSE	1705608	1390424	2065023	1842072	1934563	2237121	2239783	2713085	0.05	1.30
MLXIP_MOUSE	1367506	1161945	1063472	1111880	1448258	1753508	1701044	1232133	0.04	1.30
ELF4_MOUSE	3300317	3258397	4088422	4608292	4776856	5888677	4954441	4318678	0.05	1.31
DJB12_MOUSE	1273072	1412137	1577695	1369890	1429675	1896634	1988973	2055808	0.03	1.31
LIN54_MOUSE	236044	151999	212029	205622	278818	286299	281438	213115	0.04	1.32
EMC8_MOUSE	17003665	17398057	16006408	12708066	17335751	20016184	24094467	21887310	0.03	1.32
ZEP2_MOUSE	2054788	1212823	1577583	1884256	2358759	2302877	2125520	2113300	0.03	1.32
SSXT_MOUSE	978302	1031026	1117230	1087495	1227453	1607966	1550531	1190567	0.02	1.32
FKBP3_MOUSE	149429720	174854765	196263497	154351491	192751137	217482336	203208332	281167341	0.05	1.33
SSRP1_MOUSE	55438136	66644171	58632143	68138764	72699398	91960617	89697711	75851468	0.01	1.33
PMM2_MOUSE	106743166	104363498	96233217	118132111	117241550	125248326	175869775	146209227	0.05	1.33
TRIPC_MOUSE	57138896	38801976	52952476	43187940	69699377	65910377	65742398	53550964	0.03	1.33
OTUD4_MOUSE	3454353	4137006	3116168	3249684	5264175	5059279	3866191	4333933	0.03	1.33
ATRX_MOUSE	19022822	10986224	13841906	15716051	18592354	20290064	18754516	21443023	0.04	1.33
JUND_MOUSE	599297	703706	726662	648461	1051233	1009094	775897	729234	0.04	1.33
CHMP5_MOUSE	15452051	16820958	13488992	14828421	24486971	19799298	19843527	17206508	0.02	1.34
CRTC3_MOUSE	3188573	2895672	3258644	3627155	4137488	4725147	3934145	4669511	0.00	1.35
ZN574_MOUSE	1812777	1430098	1598287	1478067	2161886	2406111	2217101	1728108	0.02	1.35
YIPF4_MOUSE	2640265	2861340	1972664	1906125	3180821	2595330	3442875	3528894	0.04	1.36
IPP2_MOUSE	14561934	14126731	18207088	11236203	15148270	20231790	20662126	23147199	0.05	1.36
UBR5_MOUSE	8738753	6886941	7227891	6749589	10977699	10701463	7644878	11015632	0.03	1.36
CTF8A_MOUSE	3152568	5988865	5542071	5746804	6463198	7946331	6418899	7045245	0.05	1.36
RRBP1_MOUSE	132167938	197244919	142760852	132246689	227925273	212689604	222111226	161995434	0.04	1.36
IF4H_MOUSE	105189527	99507687	107475736	116640557	126892998	134273302	156103539	169035091	0.01	1.37
SIAT1_MOUSE	729845	520912	806975	735506	962364	992089	942071	923429	0.01	1.37
TF3C2_MOUSE	901725	858625	969457	833447	1202920	1324450	1218079	1128813	0.00	1.37
CDK9_MOUSE	2898538	3658690	3354956	3852189	4134504	5932465	4392634	4387573	0.03	1.37
RPB4_MOUSE	7769978	7514274	6376925	6884194	9098265	11634735	9766776	8627070	0.01	1.37
NCOR1_MOUSE	18626818	9564726	13924486	14218061	19596363	21461284	18072765	18119748	0.04	1.37
CP131_MOUSE	125666	66213	112306	105274	137980	129960	155140	139687	0.03	1.37
TPR_MOUSE	202225974	117198241	164373074	160658698	232295114	246386077	219336793	188381367	0.03	1.38
ALS2_MOUSE	1011176	760409	1421147	974418	1468864	1380373	1290365	1608231	0.04	1.38
SMAL1_MOUSE	526243	522102	828546	570173	737694	870367	930720	855373	0.03	1.39
DIDO1_MOUSE	63198615	43095075	45284668	46086365	77288805	75933839	60284631	61634990	0.02	1.39
SP2_MOUSE	4492252	5067331	3950126	4949514	6783467	7689577	4628654	6623952	0.04	1.39
RBM19_MOUSE	1538388	1794557	1809354	1708021	2109573	2711642	2684226	2055642	0.01	1.40
CA198_MOUSE	217836	117514	230009	217386	254422	270433	272142	296371	0.03	1.40
CREB1_MOUSE	9495183	14741881	13452276	14333991	16343683	17430281	21000251	17901853	0.02	1.40
KANL1_MOUSE	1529280	1063710	1075705	1306916	1673258	2081575	1720281	1510421	0.02	1.40
PDIP3_MOUSE	15804719	22982615	19995886	23667555	27215196	31981337	25759664	30867971	0.01	1.40
DNMT1_MOUSE	102222583	83544205	108517736	83539173	150987861	144446210	115255536	120141332	0.01	1.40
LZIC_MOUSE	39389392	36345151	26125135	35351269	41742880	57602490	48846983	44988502	0.02	1.41
MAZ_MOUSE	375394	565890	457587	363633	589216	789204	587781	520879	0.05	1.41
THYN1_MOUSE	12092146	16128703	13003476	18150213	19510513	22615029	23643298	18366403	0.02	1.42
CREL2_MOUSE	4468228	5475597	5355378	5179169	6923631	9145089	7544958	5409532	0.04	1.42
EHMT1_MOUSE	2905717	4201795	4160645	2573790	5202610	5586743	5033597	3798780	0.04	1.42
RHG30_MOUSE	74934410	38009417	66763680	61070183	94623159	91873977	74387522	82269033	0.03	1.43
GID8_MOUSE	8318546	10125652	8542271	8512822	9549235	13877436	16074907	11209895	0.04	1.43
TAGL2_MOUSE	2205838276	2458386672	2475488769	2858307589	2842610725	3302843252	3889172469	4252575645	0.02	1.43
ABL1_MOUSE	726762	413885	514618	487097	923893	784683	589495	766150	0.05	1.43
SEC20_MOUSE	7042525	7091043	5445276	6954291	9498417	8139186	9972642	10422498	0.00	1.43
DNJC8_MOUSE	104541498	141749371	111231931	107365428	157580164	194894680	157402969	156610335	0.01	1.43
COPZ1_MOUSE	62644172	46639699	41862076	52085191	60618980	66394696	87060521	77390901	0.02	1.43
ISY1_MOUSE	2530041	2823508	3317234	3732798	3306567	5129562	4478623	4881493	0.03	1.43
ZN148_MOUSE	3121270	3678348	3057214	3914105	3865265	5471631	4820642	5619586	0.02	1.44
NDUS4_MOUSE	44383325	48874098	41100228	45376391	58361106	54784044	83480867	61780282	0.03	1.44
GPAM1_MOUSE	1518007	1782402	1786279	1717900	1986970	2841479	2419901	2545563	0.01	1.44
IFT22_MOUSE	447839	566888	289968	381796	579693	591775	672341	586694	0.02	1.44
BAZ1A_MOUSE	4651896	5016695	6586411	4449813	6659585	8626322	8530077	6047226	0.03	1.44
B3GT4_MOUSE	241185	260581	183675	163228	352947	359740	261408	254469	0.04	1.45
RBM39_MOUSE	14800112	15795754	10615048	15158217	21495286	20776747	20507533	18876940	0.00	1.45
CE170_MOUSE	7706212	5171401	8352482	6534982	12187837	10830194	8231682	9095713	0.03	1.45
ABLM1_MOUSE	9861268	9258567	8268450	10594507	10738635	16839528	12906905	14748897	0.02	1.45
HIRP3_MOUSE	933386	665037	642140	967548	1190311	1148803	1435306	897783	0.04	1.46
HN1L_MOUSE	19673165	14446546	15599093	13760882	18974477	23268310	27436362	23056956	0.02	1.46
LUC7L_MOUSE	5719019	5876199	5544880	9362392	8416975	11765445	8773127	9890427	0.04	1.47
WIZ_MOUSE	2572686	1863850	2287004	2081954	3334115	4059680	2798230	2725250	0.02	1.47
OAS3_MOUSE	8086368	13857411	13014914	9583617	14714835	19933658	14954774	15788280	0.03	1.47
TYSY_MOUSE	1506540	2840171	1306512	2414927	3229040	2951705	3033874	2632828	0.05	1.47
RTF1_MOUSE	12572097	17707346	12580103	15495347	19915064	21700098	23338595	21021130	0.00	1.47
BT3L4_MOUSE	37245863	49642003	49318246	41876939	58488845	78218665	64216072	61831406	0.01	1.48
CBX5_MOUSE	1904517	1722791	1555681	2372733	2214067	3004443	2794758	3139707	0.02	1.48
RM40_MOUSE	5869560	6654717	8255482	5524719	7997141	8883201	12270102	9799304	0.03	1.48
PAF1_MOUSE	5787088	8846189	8399650	8929220	11254662	13383444	11741495	10979695	0.01	1.48
ACINU_MOUSE	192651345	187133631	194951577	225933054	311310950	355405801	291130719	229504396	0.01	1.48
GON4L_MOUSE	3075077	1495462	2790825	2942320	3853076	4599013	3864699	3057604	0.04	1.49
KMT2E_MOUSE	1150439	583617	763088	975082	1260839	1371496	1358901	1191105	0.02	1.49
HDGR3_MOUSE	11133908	12575001	9511304	9599247	14126669	15886669	18518048	15805886	0.00	1.50
TR30A_MOUSE	1026280	1110866	978919	1210597	1547101	1870693	1600213	1491102	0.00	1.50
RPRD2_MOUSE	23315092	16301357	18299940	18876356	32423058	35135817	23779290	24340281	0.02	1.51
F107B_MOUSE	88169003	56281607	50661265	72686318	111379983	70865438	117218736	104074213	0.04	1.51
SC11C_MOUSE	23846102	30776555	19534923	26661023	44661430	32237497	35204000	39882293	0.01	1.51
UIMC1_MOUSE	2082258	2504618	2987905	2818542	4079797	4801293	3775844	3016788	0.02	1.51
SPT6H_MOUSE	59406668	27831367	50282796	39696636	68694598	78268442	64365544	56010324	0.03	1.51
AN32A_MOUSE	672269343	759351566	490949294	655937170	982134311	994029499	980722902	954231362	0.00	1.52
CCD43_MOUSE	7401756	13956698	12437481	10639044	14831791	18035262	17594138	17038635	0.01	1.52

ADNP2_MOUSE	444146	349292	315899	283193	666524	472365	411440	568050	0.03	1.52
PNO1_MOUSE	2650452	6149523	4289491	3742573	7791217	6233583	5504363	6076833	0.05	1.52
PRC2A_MOUSE	41742128	22941449	35668871	36373965	62531977	55015208	42305345	48499492	0.02	1.52
GAR1_MOUSE	12916480	15828563	13195024	15661365	20754055	28391533	23084163	15675351	0.03	1.53
UVSSA_MOUSE	114532	243136	258505	259062	327839	376572	326345	305118	0.02	1.53
THY1_MOUSE	134208123	224864180	189287427	195374471	325797433	264750291	284635713	260681986	0.01	1.53
PQBP1_MOUSE	34615590	26426541	30634570	30116339	45527948	58616597	45751406	36154406	0.02	1.53
F221A_MOUSE	529912	451866	346665	525954	925533	662353	481742	767039	0.05	1.53
PRP4B_MOUSE	2626920	3071742	1684194	1931721	3762012	4193168	2998861	3356100	0.02	1.54
IWS1_MOUSE	3595153	5813325	3767100	3432352	6009699	8018992	6592325	4947570	0.04	1.54
SPN1_MOUSE	256620	237606	316882	208975	300134	458426	382306	429634	0.02	1.54
CE152_MOUSE	226248	137380	242788	238305	310071	382354	366065	242093	0.03	1.54
CHD4_MOUSE	174050736	138458118	121616605	143991099	279046623	236340328	149970392	228492679	0.03	1.55
ATF1_MOUSE	673077	719808	679706	849124	815922	1568716	1094832	1047402	0.05	1.55
UBN1_MOUSE	513812	699380	570406	483989	933563	1111230	828751	646560	0.03	1.55
PRR12_MOUSE	5120033	3387403	4133874	5256573	7145319	9062379	5759853	5826556	0.03	1.55
JHD2C_MOUSE	963532	519722	732895	660117	1196230	1232134	1052226	987594	0.01	1.55
SRRM1_MOUSE	21068741	23249828	16799173	23707759	34434781	36400770	36778244	24175973	0.01	1.55
MOC2B_MOUSE	353557	437538	290568	368655	505272	692460	539018	524872	0.01	1.56
DDX3X_MOUSE	23829287	26090051	28442206	21905865	48584100	43290328	28184419	36506403	0.02	1.56
SET1B_MOUSE	6401288	6058590	4343142	3696927	8673524	9682805	6753182	7051838	0.02	1.57
LMBL3_MOUSE	584806	421042	501682	533432	675183	1023237	827041	694084	0.01	1.58
PSIP1_MOUSE	26276113	50932058	41420465	41798887	60985405	70104777	77273435	45251958	0.04	1.58
NOP58_MOUSE	37726287	72861386	57255439	62779253	98255781	105908163	96452444	64411858	0.03	1.58
CHD2_MOUSE	1762239	805460	1043896	1221544	2144184	1862680	1938717	1719113	0.02	1.59
PHF8_MOUSE	355043	589196	448867	491844	929024	891521	703297	493886	0.04	1.60
RU1C_MOUSE	20733611	21376628	24469059	28303541	28020101	49460690	39708184	34801502	0.03	1.60
CCD12_MOUSE	13706327	23906229	14551259	15508869	25639447	25169754	29367349	28273198	0.01	1.60
CWC22_MOUSE	4045622	5233232	3603896	4642203	7238293	8152494	5950336	6758153	0.00	1.60
HELZ_MOUSE	1653920	893460	1653860	1599077	2988565	2277222	1736170	2306031	0.03	1.60
PON3_MOUSE	12874435	16702173	20274600	9642735	17767502	28864112	26624157	23031475	0.03	1.62
FNBP4_MOUSE	11006978	5690065	11276161	10227087	18686587	16434540	14016384	12755169	0.02	1.62
CA052_MOUSE	1150728	2218776	1898532	2526872	2149676	3378929	3994205	3168890	0.04	1.63
IF3M_MOUSE	1400219	1153281	643531	1249225	2260531	1414036	1780026	1786941	0.03	1.63
PTMS_MOUSE	20906028	27579766	36314744	30715480	36709374	54136357	53487686	44029474	0.01	1.63
DNM3A_MOUSE	170844	52092	132786	110810	218943	162672	208340	171753	0.04	1.63
ZN638_MOUSE	21303788	15500774	19142904	20214618	31415590	42407263	21342276	29196397	0.04	1.63
RM12_MOUSE	59832124	47674868	32543411	35933460	62073256	70898517	72023441	83812804	0.01	1.64
PCNP_MOUSE	24937498	38224582	42628320	53526297	41495251	78387940	81270944	64882451	0.05	1.67
GPAA1_MOUSE	1530539	1422986	1968979	1605287	3576510	2386991	2674240	2319291	0.01	1.68
CO2A1_MOUSE	140263	224216	212950	245214	410459	325101	275477	370946	0.01	1.68
CDK13_MOUSE	13884378	11861608	13078418	12917792	22313168	27108859	20339918	17508041	0.01	1.69
NSD3_MOUSE	1579259	3107652	3004840	3102560	4422181	5083872	5316004	3388073	0.02	1.69
INO80_MOUSE	3716365	2553141	3065981	1943589	5650133	5365211	4009787	4182315	0.01	1.70
BAD_MOUSE	2499136	2230741	2579192	2701469	3938341	3496461	3856552	5765047	0.01	1.70
EHMT2_MOUSE	671006	639051	888328	637657	1327171	1695922	914074	908740	0.04	1.71
LNEBL_MOUSE	559457	392935	239017	356297	555357	632770	710523	752662	0.01	1.71
PYM1_MOUSE	54708947	77102459	60646949	54604022	96462707	128143305	110445455	89113317	0.00	1.72
SREK1_MOUSE	194627	181243	183095	240857	419416	343961	298882	316087	0.00	1.72
CHD8_MOUSE	21405951	6524441	13658761	10970642	27576952	23977794	15671765	23664211	0.05	1.73
F168B_MOUSE	1338769	1139870	1421804	1729607	1735415	3184630	2222102	2631378	0.02	1.74
CGBP1_MOUSE	11533227	24109908	14799256	25977543	26032425	38901026	33770922	34034680	0.02	1.74
ST18_MOUSE	49015	21895	43323	62778	78329	83443	70852	75255	0.01	1.74
DHX8_MOUSE	2169151	4593341	3257355	4110552	6349939	8419987	5100700	4753023	0.04	1.74
KLF13_MOUSE	2122677	3799191	2520005	2952493	5354911	6577683	4243194	3858270	0.02	1.76
SUMF1_MOUSE	349435	607672	681733	586714	1188768	782147	1176358	810787	0.02	1.78
SZT2_MOUSE	1480334	1021058	1534006	1426320	2345729	3486841	1918450	2096630	0.03	1.80
S35A1_MOUSE	286332	219884	244585	201918	466803	454883	214001	582966	0.05	1.80
SHPRH_MOUSE	1081457	325563	1077712	884065	1730522	1368107	1391526	1604264	0.01	1.81
ZN526_MOUSE	35503	44826	33623	33173	41894	87052	61076	76172	0.03	1.81
ZFP62_MOUSE	128024	170353	121940	74948	211567	238795	207503	239381	0.00	1.81
DAZP2_MOUSE	231905	260001	459796	397625	352978	766379	611214	724657	0.04	1.82
BRD2_MOUSE	2826427	6628011	2277500	3702331	8420815	7880967	5148746	6790756	0.04	1.83
AXIN1_MOUSE	45157	45677	30955	45029	79289	90967	53947	81677	0.01	1.83
LEF1_MOUSE	1446655	1948832	1805925	1268408	3113045	4034825	2375445	2345400	0.02	1.83
SETX_MOUSE	2526596	1720505	1837995	2104111	5005207	3555116	1999278	4728838	0.05	1.87
CDK4_MOUSE	1725199	2695745	1402374	2369748	4955409	3611544	3796474	2970792	0.01	1.87
BCL7B_MOUSE	3389598	1802596	3018497	3077024	2751843	7379257	5250892	5753829	0.05	1.87
ENSA_MOUSE	9790774	13578016	16240322	13719637	18521624	29789435	33006970	18608542	0.03	1.87
RNPS1_MOUSE	11099488	19608077	7174061	7453990	27208361	24261134	18418317	15357708	0.05	1.88
AFF4_MOUSE	97018	94323	121505	108062	234708	175092	222660	161315	0.00	1.89
F102B_MOUSE	25092	34964	5587	30671	46729	56944	44051	34700	0.04	1.89
HMGN2_MOUSE	23103077	25446990	41635436	33051293	46740802	47366773	66225961	73162304	0.01	1.89
POLK_MOUSE	77777	54653	81442	51337	119574	164488	110209	110032	0.01	1.90
PININ_MOUSE	13689729	33034903	18327905	27924289	42453799	56805658	45881614	32062104	0.02	1.91
DEK_MOUSE	26675596	84484884	47382266	80359240	100255799	150575347	130863375	74500130	0.05	1.91
THOC4_MOUSE	97572087	144408030	83014520	74697789	248956542	247503610	153189770	124958645	0.04	1.94
SZRD1_MOUSE	7112479	6627502	7216041	9321480	10938790	11833887	22414975	14765770	0.03	1.98
RUSD4_MOUSE	119072	228449	222770	205055	456310	438425	334024	333436	0.00	2.01
CDN2D_MOUSE	86879	111315	143326	104087	131671	186871	327648	259175	0.04	2.03
PED1B_MOUSE	24532	51601	22770	30022	68184	76712	50201	73176	0.01	2.08
LSG1_MOUSE	31915	42864	25993	73541	97093	108256	45537	112646	0.05	2.09
SMBT1_MOUSE	5433	3697	10118	4324	12230	14257	12562	10671	0.01	2.11
DAXX_MOUSE	2026604	2750660	2804768	2533360	4569127	6438083	6148400	4252493	0.00	2.12
SPF30_MOUSE	12409294	9244288	6301459	7775730	23559346	19657942	21213756	11671143	0.01	2.13
NEIL1_MOUSE	104389	146366	117208	220875	270901	343185	395255	251340	0.01	2.14
GFOD1_MOUSE	62112	92842	54350	51784	95080	173835	150438	140660	0.01	2.14
TMA16_MOUSE	318869	770281	270404	499748	1288911	1290278	1018439	498718	0.04	2.20
CS025_MOUSE	1657278	1645011	2480008	1506769	2547727	4909979	5993342	2766390	0.04	2.22
MUM1_MOUSE	255296	595472	363751	330312	1211179	1096935	605729	578666	0.04	2.26
CDK12_MOUSE	3105881	2783878	3767201	4212643	10405387	9469173	6368477	6551584	0.00	2.36

CA174_MOUSE	69751	207619	208336	240735	339590	675048	424381	309586	0.03	2.41
DDX49_MOUSE	26793	96782	26274	55551	110291	182540	99244	114980	0.02	2.47
PHF12_MOUSE	209405	12138	193308	5770	292836	294333	277160	175807	0.05	2.47
STK16_MOUSE	501424	1042820	980829	589806	2909960	2417582	1082680	1355104	0.04	2.49
GRAM3_MOUSE	38665	88483	69329	103851	220949	196678	148662	192397	0.00	2.53
HMGA1_MOUSE	16276284	35577536	26204560	46902668	45793941	55505255	119974970	95891033	0.04	2.54
FA76B_MOUSE	59383	122289	73590	105578	187523	380351	264250	120406	0.04	2.64
SPAS2_MOUSE	210079	329054	151027	376396	815891	954407	215166	887231	0.04	2.69
NDE1_MOUSE	78468	69758	125465	25242	195981	304285	181118	133829	0.02	2.73
CC124_MOUSE	372835	2377783	339368	790274	3952704	2739017	2531933	1469739	0.05	2.76
NRDE2_MOUSE	210579	473203	182123	327541	916610	1125588	651724	615451	0.01	2.77
SCNM1_MOUSE	112571	396342	470474	476403	871389	1149201	1109650	1262524	0.00	3.02
NEPRO_MOUSE	1	16976	25926	23885	39231	69236	42662	56267	0.01	3.11
PHRF1_MOUSE	103554	25216	52452	180957	277664	485875	289495	119250	0.05	3.24
S39A8_MOUSE	512	401	486	160	1403	2039	1088	649	0.02	3.32
ZN524_MOUSE	7420	20553	6684	23303	42920	65563	18357	70637	0.03	3.41
SNIP1_MOUSE	28442	40668	43764	66047	227846	187572	78085	119913	0.02	3.43
CHD1_MOUSE	40534	5344	32938	15607	135580	67964	47014	83536	0.03	3.54
OZF_MOUSE	1	2476	1	33844	34905	66007	34524	22197	0.05	4.34
CBX8_MOUSE	4939	26270	10576	87469	175044	243070	95078	83971	0.03	4.62
JUNB_MOUSE	132711	258543	136661	134623	949228	1202020	943949	185232	0.03	4.95
CX040_MOUSE	1561	1387	17789	12217	22316	28785	73330	52549	0.03	5.37
CE112_MOUSE	55585	39587	12584	76595	319900	107668	129245	481240	0.05	5.63
ARL5A_MOUSE	8685	1	1	36804	31039	76037	46063	128963	0.04	6.20
SENP8_MOUSE	4810	52413	15763	154115	144414	510795	341140	504920	0.01	6.61

Table S2. Biological Processes Associated with Upregulated Proteins in Ang II vs. Control.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190308)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (253)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
positive regulation of nuclear cell cycle DNA replication (GO:0010571)	5	3	0.06	+	52.88	7.50E-05	9.12E-03
phosphorylation of RNA polymerase II C-terminal domain (GO:0070816)	7	3	0.08	+	37.77	1.58E-04	1.78E-02
DNA methylation on cytosine (GO:0032776)	8	3	0.09	+	33.05	2.15E-04	2.31E-02
transcription elongation from RNA polymerase II promoter (GO:0006368)	23	7	0.26	+	26.82	3.37E-08	7.33E-06
positive regulation of transcription elongation from RNA polymerase II promoter (GO:0032968)	23	7	0.26	+	26.82	3.37E-08	7.43E-06
regulation of histone ubiquitination (GO:0033182)	10	3	0.11	+	26.44	3.67E-04	3.60E-02
positive regulation of DNA-dependent DNA replication (GO:2000105)	11	3	0.12	+	24.03	4.64E-04	4.41E-02
DNA-templated transcription, elongation (GO:0006354)	27	7	0.31	+	22.85	8.56E-08	1.74E-05
regulation of transcription elongation from RNA polymerase II promoter (GO:0034243)	35	8	0.40	+	20.14	2.32E-08	5.20E-06
positive regulation of DNA-templated transcription, elongation (GO:0032786)	34	7	0.39	+	18.14	3.35E-07	5.96E-05
mRNA splice site selection (GO:0006376)	28	5	0.32	+	15.74	3.14E-05	4.17E-03
regulation of DNA-templated transcription, elongation (GO:0032784)	49	8	0.56	+	14.39	2.31E-07	4.32E-05
regulation of histone H3-K4 methylation (GO:0051569)	29	4	0.33	+	12.16	4.90E-04	4.60E-02
mRNA cis splicing, via spliceosome (GO:0045292)	29	4	0.33	+	12.16	4.90E-04	4.63E-02
regulation of histone methylation (GO:0031060)	70	9	0.79	+	11.33	2.54E-07	4.68E-05
positive regulation of histone methylation (GO:0031062)	41	5	0.47	+	10.75	1.61E-04	1.80E-02
mRNA 3'-end processing (GO:0031124)	43	5	0.49	+	10.25	1.97E-04	2.13E-02
DNA alkylation (GO:0006305)	45	5	0.51	+	9.75	2.40E-04	2.49E-02
DNA methylation (GO:0006306)	45	5	0.51	+	9.75	2.40E-04	2.51E-02
spliceosomal complex assembly (GO:0000245)	46	5	0.52	+	9.58	2.63E-04	2.68E-02
RNA splicing (GO:0008380)	310	30	3.52	+	8.53	2.38E-18	2.87E-15
RNA splicing, via transesterification reactions (GO:0000375)	187	18	2.12	+	8.48	1.99E-11	7.79E-09
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)	187	18	2.12	+	8.48	1.99E-11	7.99E-09
mRNA splicing, via spliceosome (GO:0000398)	187	18	2.12	+	8.48	1.99E-11	8.20E-09
regulation of histone modification (GO:0031056)	149	14	1.69	+	8.28	4.79E-09	1.23E-06
mRNA processing (GO:0006397)	395	36	4.48	+	8.03	4.63E-21	6.60E-18
transcription by RNA polymerase II (GO:0006366)	201	18	2.28	+	7.89	5.97E-11	2.23E-08
regulation of mRNA processing (GO:0050684)	143	12	1.62	+	7.40	1.93E-07	3.69E-05
regulation of chromatin organization (GO:1902275)	192	16	2.18	+	7.34	1.88E-09	5.07E-07
RNA 3'-end processing (GO:0031123)	84	7	0.95	+	7.34	7.48E-05	9.16E-03
DNA modification (GO:0006304)	72	6	0.82	+	7.34	2.46E-04	2.54E-02
positive regulation of histone modification (GO:0031058)	97	8	1.10	+	7.27	2.45E-05	3.29E-03
positive regulation of chromatin organization (GO:1905269)	111	9	1.26	+	7.15	8.65E-06	1.26E-03
mRNA metabolic process (GO:0016071)	509	41	5.78	+	7.10	4.80E-22	8.36E-19
mRNA transport (GO:0051028)	103	8	1.17	+	6.84	3.67E-05	4.80E-03
regulation of RNA splicing (GO:0043484)	139	10	1.58	+	6.34	7.38E-06	1.08E-03
nucleosome organization (GO:0034728)	112	8	1.27	+	6.29	6.40E-05	7.91E-03
RNA localization (GO:0006403)	159	11	1.80	+	6.10	3.67E-06	5.58E-04
transcription, DNA-templated (GO:0006351)	350	24	3.97	+	6.04	7.04E-12	3.68E-09
nucleic acid-templated transcription (GO:0097659)	351	24	3.98	+	6.03	7.44E-12	3.77E-09
RNA biosynthetic process (GO:0032774)	356	24	4.04	+	5.94	9.83E-12	4.67E-09
regulation of mRNA splicing, via spliceosome (GO:0048024)	105	7	1.19	+	5.88	2.74E-04	2.76E-02
regulation of DNA replication (GO:0006275)	107	7	1.21	+	5.77	3.06E-04	3.05E-02
nucleic acid transport (GO:0050657)	139	9	1.58	+	5.71	4.62E-05	5.84E-03
RNA transport (GO:0050658)	139	9	1.58	+	5.71	4.62E-05	5.89E-03
establishment of RNA localization (GO:0051236)	141	9	1.60	+	5.63	5.13E-05	6.44E-03
chromatin assembly or disassembly (GO:0006333)	112	7	1.27	+	5.51	3.97E-04	3.82E-02
negative regulation of chromosome organization (GO:2001251)	129	8	1.46	+	5.47	1.62E-04	1.80E-02
RNA processing (GO:0006396)	734	45	8.33	+	5.40	1.00E-19	1.31E-16
chromatin organization (GO:0006325)	614	37	6.97	+	5.31	4.36E-16	4.89E-13
nucleobase-containing compound transport (GO:0015931)	169	10	1.92	+	5.21	3.63E-05	4.79E-03
covalent chromatin modification (GO:0016569)	323	18	3.67	+	4.91	6.66E-08	1.37E-05
positive regulation of chromosome organization (GO:2001252)	180	10	2.04	+	4.90	6.01E-05	7.49E-03
ribonucleoprotein complex subunit organization (GO:0071826)	219	12	2.49	+	4.83	1.26E-05	1.77E-03
RNA metabolic process (GO:0016070)	1211	64	13.74	+	4.66	8.15E-25	2.56E-21
regulation of mRNA metabolic process (GO:1903311)	249	13	2.83	+	4.60	9.01E-06	1.30E-03
regulation of chromosome organization (GO:0033044)	347	18	3.94	+	4.57	1.84E-07	3.60E-05
histone modification (GO:0016570)	314	16	3.56	+	4.49	1.12E-06	1.83E-04
DNA conformation change (GO:0071103)	178	9	2.02	+	4.46	2.74E-04	2.77E-02
nuclear transport (GO:0051169)	198	10	2.25	+	4.45	1.27E-04	1.46E-02
nucleocytoplasmic transport (GO:0006913)	198	10	2.25	+	4.45	1.27E-04	1.47E-02
ribonucleoprotein complex assembly (GO:0022618)	206	10	2.34	+	4.28	1.73E-04	1.91E-02
nucleic acid metabolic process (GO:0090304)	1725	83	19.57	+	4.24	4.89E-30	7.67E-26
macromolecule methylation (GO:0043414)	214	10	2.43	+	4.12	2.33E-04	2.45E-02
chromosome organization (GO:0051276)	905	42	10.27	+	4.09	2.14E-14	1.86E-11
positive regulation of cell cycle process (GO:0090068)	248	11	2.81	+	3.91	1.76E-04	1.93E-02
gene expression (GO:0010467)	1585	69	17.99	+	3.84	3.13E-22	6.14E-19
DNA repair (GO:0006281)	417	18	4.73	+	3.80	2.31E-06	3.62E-04
nucleobase-containing compound biosynthetic process (GO:0034654)	649	27	7.36	+	3.67	1.29E-08	3.10E-06
DNA metabolic process (GO:0006259)	607	25	6.89	+	3.63	5.53E-08	1.16E-05
nucleobase-containing compound metabolic process (GO:0006139)	2141	87	24.29	+	3.58	1.45E-28	7.60E-23
heterocycle biosynthetic process (GO:0018130)	713	29	8.09	+	3.58	5.79E-09	1.47E-06
methylation (GO:0032259)	272	11	3.09	+	3.56	3.77E-04	3.65E-02
regulation of DNA metabolic process (GO:0051052)	354	14	4.02	+	3.49	7.74E-05	9.34E-03
heterocycle metabolic process (GO:0046483)	2278	90	25.85	+	3.48	9.65E-27	7.57E-23
positive regulation of cell cycle (GO:0045787)	357	14	4.05	+	3.46	8.44E-05	1.00E-02
aromatic compound biosynthetic process (GO:0019438)	729	28	8.27	+	3.38	3.49E-08	7.50E-06
cellular aromatic compound metabolic process (GO:0006725)	2344	89	26.60	+	3.35	3.23E-25	1.27E-21
ribonucleoprotein complex biogenesis (GO:0022613)	404	15	4.58	+	3.27	8.52E-05	1.00E-02
negative regulation of transcription by RNA polymerase II (GO:0000122)	839	31	9.52	+	3.26	1.44E-08	3.32E-06
organic cyclic compound metabolic process (GO:1901360)	2545	91	28.88	+	3.15	4.76E-24	1.24E-20
organic cyclic compound biosynthetic process (GO:1901362)	839	30	9.52	+	3.15	5.05E-08	1.07E-05
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1323	46	15.01	+	3.06	1.97E-11	8.35E-09
negative regulation of RNA metabolic process (GO:0051253)	1224	42	13.89	+	3.02	2.52E-10	8.59E-08

cellular macromolecule biosynthetic process (GO:0034645)	1197	41	13.58	+	3.02	4.48E-10	1.43E-07
posttranscriptional regulation of gene expression (GO:0010608)	408	14	4.63	+	3.02	3.19E-04	3.16E-02
cellular nitrogen compound metabolic process (GO:0034641)	2720	92	30.86	+	2.98	1.11E-22	2.48E-19
cellular protein-containing complex assembly (GO:0034622)	681	23	7.73	+	2.98	5.03E-06	7.51E-04
negative regulation of gene expression (GO:0010629)	1570	53	17.82	+	2.97	1.26E-12	7.31E-10
cellular response to DNA damage stimulus (GO:0006974)	656	22	7.44	+	2.96	9.05E-06	1.29E-03
macromolecule biosynthetic process (GO:0009059)	1229	41	13.95	+	2.94	9.52E-10	2.72E-07
negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	1325	44	15.04	+	2.93	2.40E-10	8.37E-08
negative regulation of transcription, DNA-templated (GO:0045892)	1133	37	12.86	+	2.88	1.21E-08	2.96E-06
negative regulation of nucleic acid-templated transcription (GO:1903507)	1137	37	12.90	+	2.87	1.32E-08	3.13E-06
negative regulation of RNA biosynthetic process (GO:1902679)	1138	37	12.91	+	2.87	1.35E-08	3.16E-06
negative regulation of macromolecule biosynthetic process (GO:0010558)	1360	44	15.43	+	2.85	5.31E-10	1.63E-07
negative regulation of cellular biosynthetic process (GO:0031327)	1409	45	15.99	+	2.81	4.85E-10	1.52E-07
negative regulation of biosynthetic process (GO:0009890)	1446	45	16.41	+	2.74	1.07E-09	3.00E-07
cellular nitrogen compound biosynthetic process (GO:0044271)	1108	33	12.57	+	2.62	6.18E-07	1.08E-04
regulation of transcription by RNA polymerase II (GO:0006357)	1942	56	22.04	+	2.54	1.61E-10	5.87E-08
positive regulation of transcription by RNA polymerase II (GO:0045944)	1203	34	13.65	+	2.49	1.88E-06	2.97E-04
positive regulation of gene expression (GO:0010628)	1931	52	21.91	+	2.37	7.45E-09	1.85E-06
regulation of nucleobase-containing compound metabolic process (GO:0019219)	3220	86	36.54	+	2.35	1.15E-14	1.21E-11
regulation of RNA metabolic process (GO:0051252)	2995	80	33.99	+	2.35	1.68E-13	1.20E-10
positive regulation of RNA metabolic process (GO:0051254)	1612	43	18.29	+	2.35	2.78E-07	5.08E-05
positive regulation of transcription, DNA-templated (GO:0045893)	1512	40	17.16	+	2.33	9.57E-07	1.61E-04
positive regulation of nucleic acid-templated transcription (GO:1903508)	1515	40	17.19	+	2.33	9.83E-07	1.64E-04
positive regulation of RNA biosynthetic process (GO:1902680)	1516	40	17.20	+	2.33	9.92E-07	1.64E-04
negative regulation of macromolecule metabolic process (GO:0010605)	2404	63	27.28	+	2.31	3.33E-10	1.11E-07
negative regulation of nitrogen compound metabolic process (GO:0051172)	2181	57	24.75	+	2.30	3.73E-09	9.76E-07
positive regulation of macromolecule biosynthetic process (GO:0010557)	1768	46	20.06	+	2.29	1.52E-07	3.06E-05
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1770	46	20.08	+	2.29	1.56E-07	3.10E-05
protein-containing complex subunit organization (GO:0043933)	1502	39	17.04	+	2.29	1.82E-06	2.92E-04
negative regulation of cellular metabolic process (GO:0031324)	2386	61	27.07	+	2.25	1.47E-09	4.04E-07
regulation of gene expression (GO:0010468)	3616	92	41.03	+	2.24	1.51E-14	1.40E-11
macromolecule metabolic process (GO:0043170)	5049	127	57.29	+	2.22	2.36E-21	3.70E-18
negative regulation of metabolic process (GO:0009892)	2663	67	30.22	+	2.22	3.50E-10	1.15E-07
positive regulation of biosynthetic process (GO:0009891)	1903	48	21.59	+	2.22	2.06E-07	3.90E-05
regulation of RNA biosynthetic process (GO:2001141)	2752	69	31.23	+	2.21	1.90E-10	6.76E-08
regulation of cellular macromolecule biosynthetic process (GO:2000112)	3159	79	35.85	+	2.20	6.19E-12	3.35E-09
regulation of transcription, DNA-templated (GO:0006355)	2737	68	31.06	+	2.19	5.32E-10	1.61E-07
regulation of nucleic acid-templated transcription (GO:1903506)	2744	68	31.14	+	2.18	5.61E-10	1.66E-07
positive regulation of cellular biosynthetic process (GO:0031328)	1862	46	21.13	+	2.18	6.41E-07	1.10E-04
regulation of macromolecule biosynthetic process (GO:0010556)	3246	80	36.83	+	2.17	1.08E-11	4.99E-09
regulation of organelle organization (GO:0033043)	1227	30	13.92	+	2.15	8.87E-05	1.04E-02
cellular response to stress (GO:0033554)	1398	34	15.86	+	2.14	3.85E-05	4.99E-03
regulation of biosynthetic process (GO:0009889)	3453	83	39.18	+	2.12	1.13E-11	4.90E-09
organelle organization (GO:0006996)	2957	71	33.55	+	2.12	6.72E-10	1.95E-07
regulation of cellular biosynthetic process (GO:0031326)	3383	81	38.39	+	2.11	2.73E-11	1.04E-08
protein-containing complex assembly (GO:0065003)	1318	31	14.96	+	2.07	1.45E-04	1.65E-02
cellular macromolecule metabolic process (GO:0044260)	3963	91	44.97	+	2.02	8.31E-12	4.07E-09
cellular biosynthetic process (GO:0044249)	1962	44	22.26	+	1.98	1.73E-05	2.38E-03
organic substance biosynthetic process (GO:1901576)	2070	46	23.49	+	1.96	1.12E-05	1.59E-03
regulation of nitrogen compound metabolic process (GO:0051171)	4952	109	56.19	+	1.94	2.90E-13	1.98E-10
regulation of macromolecule metabolic process (GO:0060255)	5232	114	59.37	+	1.92	8.38E-14	6.91E-11
macromolecule modification (GO:0043412)	2441	53	27.70	+	1.91	4.20E-06	6.33E-04
nitrogen compound metabolic process (GO:0006807)	5669	122	64.33	+	1.90	1.20E-14	1.18E-11
regulation of primary metabolic process (GO:0080090)	5098	110	57.85	+	1.90	5.82E-13	3.65E-10
biosynthetic process (GO:0009058)	2134	46	24.22	+	1.90	2.45E-05	3.31E-03
regulation of cellular metabolic process (GO:0031323)	5288	113	60.00	+	1.88	3.93E-13	2.57E-10
regulation of metabolic process (GO:0019222)	5688	118	64.54	+	1.83	7.81E-13	4.71E-10
positive regulation of nitrogen compound metabolic process (GO:0051173)	2986	62	33.88	+	1.83	2.71E-06	4.20E-04
positive regulation of macromolecule metabolic process (GO:0010604)	3147	65	35.71	+	1.82	1.26E-06	2.03E-04
cellular metabolic process (GO:0044237)	6280	128	71.26	+	1.80	9.49E-14	7.44E-11
positive regulation of metabolic process (GO:0009893)	3419	70	38.80	+	1.80	6.83E-07	1.16E-04
cellular component biogenesis (GO:0044085)	2352	48	26.69	+	1.80	7.91E-05	9.47E-03
positive regulation of cellular metabolic process (GO:0031325)	3144	64	35.68	+	1.79	2.93E-06	4.50E-04
cellular component assembly (GO:0022607)	2144	43	24.33	+	1.77	2.51E-04	2.57E-02
organic substance metabolic process (GO:0071704)	6644	132	75.39	+	1.75	1.64E-13	1.22E-10
primary metabolic process (GO:0044238)	6235	124	70.75	+	1.75	2.28E-12	1.28E-09
protein modification process (GO:0036211)	2268	45	25.74	+	1.75	2.32E-04	2.46E-02
cellular protein modification process (GO:0006464)	2268	45	25.74	+	1.75	2.32E-04	2.48E-02
cellular component organization or biogenesis (GO:0071840)	5262	103	59.71	+	1.73	2.59E-09	6.89E-07
cellular protein metabolic process (GO:0044267)	2859	56	32.44	+	1.73	4.35E-05	5.60E-03
cellular component organization (GO:0016043)	5086	98	57.71	+	1.70	1.76E-08	4.01E-06
negative regulation of cellular process (GO:0048523)	4482	86	50.86	+	1.69	3.45E-07	6.08E-05
regulation of cellular protein metabolic process (GO:0032268)	2445	47	27.74	+	1.69	3.66E-04	3.61E-02
metabolic process (GO:0008152)	7166	134	81.31	+	1.65	1.13E-11	5.04E-09
negative regulation of biological process (GO:0048519)	5005	93	56.79	+	1.64	3.10E-07	5.60E-05
protein metabolic process (GO:0019538)	3450	61	39.15	+	1.56	4.42E-04	4.22E-02
positive regulation of cellular process (GO:0048522)	5244	86	59.51	+	1.45	1.84E-04	2.00E-02

Table S3. Molecular Functions Associated with Upregulated Proteins in Ang II vs. Control.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190701)**						
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**						
Analyzed List:	**Client Text Box Input (Mus musculus)**						
Reference List:	**Mus musculus (all genes in database)**						
Test Type:	**FISHER**						
Correction:	**FDR**						
GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (253)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
histone methyltransferase activity (H3-K27 specific) (GO:0046976)	7	3	0.08	+	37.77	1.58E-04	2.13E-02
C2H2 zinc finger domain binding (GO:0070742)	13	4	0.15	+	27.12	3.28E-05	7.15E-03
armadillo repeat domain binding (GO:0070016)	10	3	0.11	+	26.44	3.67E-04	3.91E-02
RNA polymerase II complex binding (GO:0000993)	37	5	0.42	+	11.91	1.04E-04	1.44E-02
RNA polymerase core enzyme binding (GO:0043175)	42	5	0.48	+	10.49	1.78E-04	2.33E-02
RNA polymerase binding (GO:0070063)	57	6	0.65	+	9.28	7.48E-05	1.18E-02
basal transcription machinery binding (GO:0001098)	57	6	0.65	+	9.28	7.48E-05	1.22E-02
basal RNA polymerase II transcription machinery binding (GO:0001099)	57	6	0.65	+	9.28	7.48E-05	1.27E-02
helicase activity (GO:0004386)	137	14	1.55	+	9.01	1.76E-09	1.01E-06
histone binding (GO:0042393)	229	17	2.60	+	6.54	2.97E-09	1.51E-06
nuclear receptor binding (GO:0016922)	113	8	1.28	+	6.24	6.79E-05	1.24E-02
methylated histone binding (GO:0035064)	106	7	1.20	+	5.82	2.90E-04	3.40E-02
methylation-dependent protein binding (GO:0140034)	106	7	1.20	+	5.82	2.90E-04	3.49E-02
ribonucleoprotein complex binding (GO:0043021)	144	9	1.63	+	5.51	5.99E-05	1.19E-02
nuclear hormone receptor binding (GO:0035257)	150	9	1.70	+	5.29	8.06E-05	1.23E-02
catalytic activity, acting on DNA (GO:0140097)	171	10	1.94	+	5.15	3.99E-05	8.30E-03
modification-dependent protein binding (GO:0140030)	188	10	2.13	+	4.69	8.49E-05	1.21E-02
hormone receptor binding (GO:0051427)	178	9	2.02	+	4.46	2.74E-04	3.39E-02
RNA binding (GO:0003723)	1032	47	11.71	+	4.01	9.29E-16	1.06E-12
chromatin binding (GO:0003682)	575	25	6.52	+	3.83	2.02E-08	9.24E-06
RNA polymerase II-specific DNA-binding transcription factor binding (GO:0061629)	271	11	3.08	+	3.58	3.66E-04	3.98E-02
DNA-binding transcription factor binding (GO:0140297)	350	14	3.97	+	3.53	6.89E-05	1.21E-02
nucleic acid binding (GO:0003676)	3055	113	34.67	+	3.26	2.14E-32	9.77E-29
transcription factor binding (GO:0008134)	699	24	7.93	+	3.03	2.36E-06	6.75E-04
DNA binding (GO:0003677)	2038	67	23.13	+	2.9	1.89E-15	1.73E-12
transcription coregulator activity (GO:0003712)	457	15	5.19	+	2.89	3.10E-04	3.45E-02
double-stranded DNA binding (GO:0003690)	984	31	11.17	+	2.78	4.42E-07	1.56E-04
transcription regulatory region DNA binding (GO:0044212)	965	30	10.95	+	2.74	9.00E-07	2.94E-04
regulatory region nucleic acid binding (GO:0001067)	969	30	11.00	+	2.73	9.77E-07	2.98E-04
transcription regulatory region sequence-specific DNA binding (GO:0000976)	855	26	9.70	+	2.68	7.39E-06	1.78E-03
sequence-specific double-stranded DNA binding (GO:1990837)	895	27	10.16	+	2.66	5.62E-06	1.43E-03
RNA polymerase II regulatory region DNA binding (GO:0001012)	819	23	9.29	+	2.47	8.28E-05	1.22E-02
RNA polymerase II regulatory region sequence-specific DNA binding (GO:0000977)	811	22	9.20	+	2.39	2.60E-04	3.30E-02
protein domain specific binding (GO:0019904)	782	21	8.87	+	2.37	4.03E-04	4.10E-02
sequence-specific DNA binding (GO:0043565)	1120	29	12.71	+	2.28	6.47E-05	1.23E-02
transcription regulator activity (GO:0140110)	1343	34	15.24	+	2.23	1.50E-05	3.42E-03
heterocyclic compound binding (GO:1901363)	4950	124	56.17	+	2.21	1.50E-20	3.42E-17
organic cyclic compound binding (GO:0097159)	5053	125	57.34	+	2.18	2.85E-20	4.35E-17
ion binding (GO:0043167)	5414	87	61.43	+	1.42	3.82E-04	3.97E-02
binding (GO:0005488)	13135	191	149.05	+	1.28	4.99E-08	2.07E-05

Table S4. Biological Processes Associated with Downregulated Proteins in Ang II vs. Control.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190308)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (114)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
negative regulation of B cell receptor signaling pathway (GO:0050859)	8	3	0.04	+	73.34	2.05E-05	2.93E-02
mitochondrial ATP synthesis coupled electron transport (GO:0042775)	51	5	0.26	+	19.17	9.69E-06	2.17E-02
ATP synthesis coupled electron transport (GO:0042773)	55	5	0.28	+	17.78	1.36E-05	2.37E-02
electron transport chain (GO:0022900)	81	7	0.41	+	16.90	3.31E-07	5.19E-03
oxidative phosphorylation (GO:0006119)	63	5	0.32	+	15.52	2.52E-05	3.29E-02
respiratory electron transport chain (GO:0022904)	76	6	0.39	+	15.44	3.88E-06	1.22E-02
purine ribonucleotide biosynthetic process (GO:0009152)	114	6	0.58	+	10.29	3.46E-05	4.18E-02
cellular respiration (GO:0045333)	134	7	0.69	+	10.22	7.89E-06	2.06E-02
ATP metabolic process (GO:0046034)	165	8	0.84	+	9.48	2.94E-06	1.15E-02
carbohydrate derivative metabolic process (GO:1901135)	781	17	3.99	+	4.26	5.89E-07	4.62E-03
regulation of immune system process (GO:0002682)	1479	21	7.56	+	2.78	2.00E-05	3.13E-02
regulation of transport (GO:0051049)	1911	25	9.77	+	2.56	1.13E-05	2.22E-02
regulation of localization (GO:0032879)	2785	33	14.24	+	2.32	2.77E-06	1.45E-02

Table S5. Transcription Factors Associated with Upregulated Proteins in Ang II vs. Control.

TF_NAME	MATRIX_ID	Z_SCORE	P_VALUE	SAMPLE_AVERAGE	BACKGROUND_AVERAGE	SAMPLE_DEVSTD	SAMPLE_SIZE
ZBTB33	MA0527.1	9.02	6.22E-20	0.80	0.77	0.06	262
NRF1	MA0506.1	8.96	1.18E-19	0.87	0.83	0.07	262
ZBTB7A	MA0750.2	8.68	1.44E-18	0.86	0.83	0.06	262
HINFP	MA0131.2	8.69	1.46E-18	0.84	0.81	0.05	262
Tcfl5	MA0632.1	8.64	2.08E-18	0.92	0.88	0.05	262
ETV5	MA0765.1	8.54	4.83E-18	0.89	0.86	0.05	262
Gabpa	MA0062.2	8.10	1.87E-16	0.87	0.84	0.06	262
SP2	MA0516.1	8.09	2.51E-16	0.90	0.87	0.05	262
ELK4	MA0076.2	8.03	3.46E-16	0.88	0.85	0.06	262
ELK1	MA0028.2	7.92	8.34E-16	0.83	0.80	0.07	262
ELK3	MA0759.1	7.79	2.34E-15	0.86	0.83	0.06	262
ETV1	MA0761.1	7.79	2.43E-15	0.87	0.84	0.06	262
E2F4	MA0470.1	7.64	9.04E-15	0.89	0.86	0.05	262
ETV4	MA0764.1	7.55	1.57E-14	0.87	0.85	0.05	262
TFDP1	MA1122.1	7.52	2.19E-14	0.87	0.84	0.05	262
SP1	MA0079.3	7.17	3.19E-13	0.93	0.90	0.05	262
FEV	MA0156.2	7.03	7.74E-13	0.87	0.84	0.06	262
Gmeb1	MA0615.1	6.96	1.39E-12	0.83	0.81	0.04	262
GLIS2	MA0736.1	6.74	6.60E-12	0.80	0.78	0.04	262
FLI1	MA0475.2	6.71	7.65E-12	0.85	0.83	0.06	262
ETV6	MA0645.1	6.58	1.88E-11	0.87	0.85	0.06	262
KLF14	MA0740.1	6.54	2.59E-11	0.84	0.82	0.06	262
ERG	MA0474.2	6.35	8.38E-11	0.87	0.85	0.06	262
ETS1	MA0098.3	6.32	1.06E-10	0.87	0.85	0.06	262
YY1	MA0095.2	6.25	1.41E-10	0.82	0.80	0.08	262
KLF5	MA0599.1	6.26	1.65E-10	0.95	0.92	0.05	262
ETV3	MA0763.1	6.14	3.24E-10	0.86	0.84	0.05	262
ERF	MA0760.1	6.00	8.08E-10	0.85	0.83	0.05	262
Hes1	MA1099.1	5.99	8.75E-10	0.88	0.86	0.05	262
SP4	MA0685.1	5.92	1.40E-09	0.81	0.79	0.06	262
GLIS1	MA0735.1	5.85	2.07E-09	0.71	0.70	0.05	262
Atf1	MA0604.1	5.82	2.34E-09	0.86	0.84	0.07	262
EGR3	MA0732.1	5.70	5.31E-09	0.80	0.77	0.06	262
EGR1	MA0162.3	5.67	6.38E-09	0.77	0.75	0.05	262
HIF1A	MA1106.1	5.63	7.50E-09	0.85	0.83	0.06	262
KLF16	MA0741.1	5.57	1.15E-08	0.89	0.87	0.06	262
ELF1	MA0473.2	5.49	1.65E-08	0.80	0.78	0.06	262
EGR2	MA0472.2	5.46	2.09E-08	0.82	0.80	0.05	262
CENPB	MA0637.1	5.36	3.54E-08	0.79	0.78	0.04	262
SP3	MA0746.1	5.31	4.90E-08	0.90	0.88	0.06	262
ARNT::HIF1A	MA0259.1	5.24	7.32E-08	0.90	0.88	0.06	262
ZIC3	MA0697.1	5.20	9.09E-08	0.79	0.78	0.04	262
ELF4	MA0641.1	5.18	9.22E-08	0.80	0.78	0.06	262
SP8	MA0747.1	5.16	1.12E-07	0.89	0.87	0.05	262
YY2	MA0748.1	5.11	1.37E-07	0.82	0.80	0.05	262
Zfx	MA0146.2	5.11	1.43E-07	0.86	0.84	0.05	262
EHF	MA0598.2	5.03	2.09E-07	0.80	0.78	0.06	262
E2F1	MA0024.3	5.02	2.36E-07	0.78	0.76	0.04	262
CTCFL	MA1102.1	4.99	2.70E-07	0.81	0.79	0.06	262
TFAP2C(var.3)	MA0815.1	4.98	2.89E-07	0.82	0.80	0.05	262
HEY1	MA0823.1	4.92	3.87E-07	0.82	0.80	0.06	262
TFAP2A	MA0003.3	4.88	4.85E-07	0.88	0.86	0.04	262
HEY2	MA0649.1	4.82	6.34E-07	0.83	0.81	0.06	262
TFAP2A(var.3)	MA0872.1	4.79	7.62E-07	0.81	0.79	0.05	262
ZIC4	MA0751.1	4.77	8.23E-07	0.81	0.80	0.04	262
GMEB2	MA0862.1	4.76	8.36E-07	0.83	0.81	0.06	262
E2F6	MA0471.1	4.77	8.51E-07	0.90	0.88	0.05	262
BHLHE41	MA0636.1	4.72	9.86E-07	0.79	0.77	0.07	262
GLIS3	MA0737.1	4.71	1.12E-06	0.75	0.74	0.04	262
TFAP2B(var.3)	MA0813.1	4.68	1.31E-06	0.82	0.81	0.05	262
TFAP2A(var.2)	MA0810.1	4.67	1.37E-06	0.88	0.86	0.04	262
SPDEF	MA0686.1	4.62	1.72E-06	0.82	0.80	0.05	262
EGR4	MA0733.1	4.63	1.73E-06	0.79	0.78	0.04	262
ZBTB7B	MA0694.1	4.61	1.83E-06	0.80	0.79	0.05	262
Arntl	MA0603.1	4.52	2.69E-06	0.83	0.82	0.07	262
Arnt	MA0004.1	4.51	2.83E-06	0.88	0.86	0.08	262
BHLHE40	MA0464.2	4.44	3.91E-06	0.82	0.81	0.07	262
Creb3l2	MA0608.1	4.41	4.54E-06	0.85	0.83	0.06	262
PLAG1	MA0163.1	4.38	5.50E-06	0.80	0.79	0.05	262
ELF5	MA0136.2	4.35	6.06E-06	0.88	0.87	0.05	262
KLF13	MA0657.1	4.35	6.12E-06	0.75	0.74	0.04	262
ZIC1	MA0696.1	4.30	8.08E-06	0.78	0.77	0.04	262
USF2	MA0526.2	4.27	8.61E-06	0.78	0.77	0.07	262
Ahr::Arnt	MA0006.1	4.27	8.76E-06	0.93	0.91	0.06	262
ZNF740	MA0753.1	4.26	9.44E-06	0.86	0.84	0.06	262
ELF3	MA0640.1	4.18	1.30E-05	0.78	0.77	0.06	262
TFAP2C(var.2)	MA0814.1	4.17	1.41E-05	0.86	0.85	0.04	262
ZBTB7C	MA0695.1	4.09	2.00E-05	0.83	0.82	0.04	262
MLX	MA0663.1	4.07	2.13E-05	0.79	0.77	0.07	262
MYCN	MA0104.4	4.04	2.39E-05	0.80	0.78	0.06	262
TFAP2B(var.2)	MA0812.1	4.03	2.61E-05	0.86	0.84	0.05	262
HES7	MA0822.1	3.96	3.53E-05	0.74	0.72	0.05	262
TFAP2B	MA0811.1	3.92	4.24E-05	0.86	0.85	0.04	262
ETV2	MA0762.1	3.85	5.35E-05	0.82	0.81	0.05	262
TFAP2C	MA0524.2	3.84	5.86E-05	0.86	0.85	0.04	262
PAX5	MA0014.3	3.82	6.33E-05	0.82	0.81	0.04	262
HES5	MA0821.1	3.70	9.97E-05	0.75	0.74	0.05	262
MXI1	MA1108.1	3.65	1.23E-04	0.82	0.80	0.06	262
SREBF2(var.2)	MA0828.1	3.33	4.04E-04	0.79	0.78	0.06	262
IRF5	MA1420.1	3.12	8.44E-04	0.76	0.75	0.04	262
CTCF	MA0139.1	3.02	1.20E-03	0.78	0.78	0.04	262
Atf3	MA0605.1	3.00	1.26E-03	0.85	0.84	0.06	262
NFYB	MA0502.1	2.95	1.48E-03	0.81	0.80	0.06	262
Klf12	MA0742.1	2.92	1.66E-03	0.82	0.81	0.05	262

Crem	MA0609.1	2.92	1.66E-03	0.79	0.78	0.07	262
MAX::MYC	MA0059.1	2.85	2.10E-03	0.81	0.80	0.06	262
Srebf1(var.2)	MA0829.1	2.84	2.15E-03	0.79	0.78	0.06	262
MLXIPL	MA0664.1	2.79	2.52E-03	0.81	0.80	0.07	262
Id2	MA0617.1	2.72	3.07E-03	0.83	0.82	0.08	262
TFE3	MA0831.2	2.71	3.20E-03	0.86	0.85	0.07	262
GLI2	MA0734.1	2.69	3.47E-03	0.78	0.77	0.05	262
CREB3	MA0638.1	2.65	3.79E-03	0.77	0.76	0.05	262
MYC	MA0147.3	2.61	4.33E-03	0.81	0.80	0.06	262
CREB3L1	MA0839.1	2.61	4.38E-03	0.74	0.74	0.05	262
MNT	MA0825.1	2.51	5.69E-03	0.84	0.83	0.07	262
BATF3	MA0835.1	2.39	8.07E-03	0.67	0.67	0.06	262
NFKB2	MA0778.1	2.39	8.23E-03	0.75	0.74	0.05	262
Mlxip	MA0622.1	2.37	8.62E-03	0.83	0.82	0.08	262
ATF7	MA0834.1	2.33	9.42E-03	0.74	0.73	0.07	262
Klf1	MA0493.1	2.30	1.05E-02	0.87	0.87	0.05	262
JDP2(var.2)	MA0656.1	2.22	1.28E-02	0.75	0.74	0.07	262
NFKB1	MA0105.4	2.21	1.32E-02	0.72	0.71	0.05	262
MZF1(var.2)	MA0057.1	2.20	1.37E-02	0.91	0.91	0.04	262
NFYA	MA0060.3	2.14	1.55E-02	0.83	0.83	0.07	262
MZF1	MA0056.1	2.12	1.68E-02	0.97	0.96	0.04	262
MAX	MA0058.3	2.11	1.69E-02	0.83	0.82	0.07	262
XBP1	MA0844.1	2.10	1.75E-02	0.76	0.75	0.05	262
TFEB	MA0692.1	2.08	1.82E-02	0.83	0.82	0.07	262
ZNF263	MA0528.1	2.02	2.13E-02	0.83	0.82	0.05	262
NR2C2	MA0504.1	1.94	2.58E-02	0.83	0.82	0.04	262
E2F8	MA0865.1	1.94	2.58E-02	0.74	0.73	0.05	262
KLF9	MA1107.1	1.93	2.61E-02	0.83	0.82	0.05	262
FOSB::JUN	MA1127.1	1.84	3.21E-02	0.76	0.76	0.07	262
CREB1	MA0018.3	1.79	3.57E-02	0.78	0.77	0.07	262
FOSL2::JUN(var.2)	MA1131.1	1.75	3.89E-02	0.79	0.78	0.07	262
FOSL2::JUND(var.2)	MA1145.1	1.75	3.90E-02	0.77	0.76	0.06	262
USF1	MA0093.2	1.71	4.21E-02	0.82	0.82	0.07	262
TFEC	MA0871.1	1.70	4.31E-02	0.87	0.86	0.05	262
E2F7	MA0758.1	1.70	4.39E-02	0.70	0.69	0.05	262
FOSB::JUNB(var.2)	MA1136.1	1.68	4.55E-02	0.79	0.78	0.06	262
FOSL2::JUNB(var.2)	MA1139.1	1.64	4.91E-02	0.76	0.75	0.07	262

Table S6. Transcription Factors Associated with Downregulated Proteins in Ang II vs. Control.

TF_NAME	MATRIX_ID	Z_SCORE	P_VALUE	SAMPLE_AVERAGE	BACKGROUND_AVERAGE	SAMPLE_DEVSTD	SAMPLE_SIZE
EHF	MA0598.2	4.56	2.47E-06	0.81	0.78	0.06	120
ELF1	MA0473.2	4.42	4.61E-06	0.80	0.78	0.06	120
ELF4	MA0641.1	4.11	1.90E-05	0.80	0.78	0.06	120
SP4	MA0685.1	4.04	2.63E-05	0.81	0.79	0.07	120
Gabpa	MA0062.2	3.98	3.35E-05	0.86	0.84	0.06	120
Klf12	MA0742.1	3.94	3.89E-05	0.83	0.81	0.06	120
KLF14	MA0740.1	3.93	4.08E-05	0.84	0.82	0.06	120
ZBTB7A	MA0750.2	3.87	5.18E-05	0.85	0.83	0.06	120
ELF3	MA0640.1	3.80	7.04E-05	0.79	0.77	0.05	120
ETV5	MA0765.1	3.67	1.20E-04	0.88	0.86	0.05	120
ELF5	MA0136.2	3.64	1.31E-04	0.88	0.87	0.05	120
ETV6	MA0645.1	3.63	1.35E-04	0.87	0.85	0.06	120
ELK4	MA0076.2	3.62	1.41E-04	0.87	0.85	0.06	120
ELK1	MA0028.2	3.51	2.14E-04	0.82	0.80	0.06	120
NRF1	MA0506.1	3.47	2.50E-04	0.86	0.83	0.07	120
ELK3	MA0759.1	3.47	2.56E-04	0.85	0.83	0.06	120
PAX5	MA0014.3	3.46	2.65E-04	0.82	0.81	0.05	120
Zfx	MA0146.2	3.42	3.02E-04	0.86	0.84	0.06	120
ETV1	MA0761.1	3.33	4.23E-04	0.86	0.84	0.05	120
SP8	MA0747.1	3.33	4.29E-04	0.89	0.87	0.05	120
Tcfl5	MA0632.1	3.27	5.30E-04	0.90	0.88	0.06	120
SP3	MA0746.1	3.24	5.82E-04	0.90	0.88	0.06	120
SP2	MA0516.1	3.20	6.78E-04	0.89	0.87	0.06	120
ETV4	MA0764.1	3.19	7.01E-04	0.86	0.85	0.05	120
TFAP2C(var.2)	MA0814.1	3.18	7.26E-04	0.87	0.85	0.05	120
TFAP2A	MA0003.3	3.15	7.90E-04	0.88	0.86	0.05	120
KLF13	MA0657.1	3.13	8.60E-04	0.75	0.74	0.05	120
ETV3	MA0763.1	3.07	1.06E-03	0.85	0.84	0.05	120
ETS1	MA0098.3	3.02	1.22E-03	0.86	0.85	0.05	120
FEV	MA0156.2	2.99	1.38E-03	0.86	0.84	0.05	120
KLF16	MA0741.1	2.98	1.41E-03	0.89	0.87	0.06	120
SPDEF	MA0686.1	2.96	1.48E-03	0.82	0.80	0.05	120
KLF4	MA0039.3	2.95	1.55E-03	0.86	0.85	0.05	120
Srebf1(var.2)	MA0829.1	2.92	1.71E-03	0.80	0.78	0.06	120
Klf1	MA0493.1	2.91	1.78E-03	0.88	0.87	0.05	120
SP1	MA0079.3	2.84	2.22E-03	0.92	0.90	0.06	120
TFEC	MA0871.1	2.82	2.33E-03	0.87	0.86	0.05	120
TFAP2A(var.2)	MA0810.1	2.74	3.02E-03	0.88	0.86	0.04	120
NFKB2	MA0778.1	2.74	3.02E-03	0.76	0.74	0.05	120
CENPB	MA0637.1	2.71	3.26E-03	0.79	0.78	0.04	120
TFDP1	MA1122.1	2.71	3.32E-03	0.86	0.84	0.06	120
TFAP2B(var.2)	MA0812.1	2.70	3.45E-03	0.86	0.84	0.05	120
KLF5	MA0599.1	2.69	3.54E-03	0.94	0.92	0.06	120
TFEB	MA0692.1	2.68	3.58E-03	0.84	0.82	0.06	120
Hes1	MA1099.1	2.66	3.85E-03	0.87	0.86	0.06	120
SREBF2(var.2)	MA0828.1	2.64	4.10E-03	0.79	0.78	0.06	120
ERG	MA0474.2	2.64	4.12E-03	0.86	0.85	0.05	120
FLI1	MA0475.2	2.59	4.74E-03	0.84	0.83	0.05	120
MITF	MA0620.2	2.57	4.91E-03	0.76	0.74	0.06	120
ERF	MA0760.1	2.54	5.43E-03	0.84	0.83	0.05	120
Bach1::Mafk	MA0591.1	2.53	5.68E-03	0.78	0.77	0.05	120
NHLH1	MA0048.2	2.52	5.84E-03	0.84	0.82	0.05	120
EGR2	MA0472.2	2.45	7.11E-03	0.81	0.80	0.06	120
RELB	MA1117.1	2.38	8.65E-03	0.83	0.82	0.05	120
ZBTB7B	MA0694.1	2.37	8.83E-03	0.80	0.79	0.05	120
Znf423	MA0116.1	2.31	1.03E-02	0.83	0.82	0.05	120
E2F4	MA0470.1	2.29	1.08E-02	0.87	0.86	0.06	120
TFAP2C	MA0524.2	2.28	1.10E-02	0.86	0.85	0.04	120
KLF9	MA1107.1	2.27	1.15E-02	0.83	0.82	0.05	120
TFAP2B	MA0811.1	2.26	1.18E-02	0.86	0.85	0.04	120
YY1	MA0095.2	2.26	1.19E-02	0.81	0.80	0.06	120
RELA	MA0107.1	2.24	1.25E-02	0.83	0.82	0.05	120
GLIS1	MA0735.1	2.20	1.39E-02	0.71	0.70	0.04	120
MLX	MA0663.1	2.19	1.42E-02	0.78	0.77	0.06	120
ASCL1	MA1100.1	2.17	1.50E-02	0.83	0.82	0.06	120
SREBF1	MA0595.1	2.14	1.58E-02	0.86	0.85	0.05	120
MZF1(var.2)	MA0057.1	2.14	1.60E-02	0.91	0.91	0.03	120
EGR1	MA0162.3	2.13	1.65E-02	0.76	0.75	0.05	120
NKX2-8	MA0673.1	2.10	1.78E-02	0.91	0.90	0.04	120
HEY1	MA0823.1	2.05	2.02E-02	0.81	0.80	0.06	120
PLAG1	MA0163.1	2.03	2.11E-02	0.80	0.79	0.05	120
Myog	MA0500.1	2.01	2.18E-02	0.88	0.87	0.06	120
Nr2e3	MA0164.1	2.00	2.23E-02	0.86	0.84	0.07	120
Tcf12	MA0521.1	2.00	2.25E-02	0.87	0.86	0.06	120
MAX	MA0058.3	1.98	2.37E-02	0.83	0.82	0.06	120
E2F6	MA0471.1	1.94	2.57E-02	0.89	0.88	0.06	120
BACH2	MA1101.1	1.94	2.58E-02	0.77	0.76	0.06	120
Ascl2	MA0816.1	1.93	2.67E-02	0.84	0.84	0.06	120
Myod1	MA0499.1	1.92	2.73E-02	0.87	0.86	0.05	120
EGR3	MA0732.1	1.91	2.79E-02	0.78	0.77	0.06	120
Gmeb1	MA0615.1	1.90	2.83E-02	0.82	0.81	0.04	120
MYC	MA0147.3	1.90	2.86E-02	0.81	0.80	0.06	120
GLIS2	MA0736.1	1.88	2.97E-02	0.79	0.78	0.04	120
USF2	MA0526.2	1.87	3.01E-02	0.78	0.77	0.07	120
TFE3	MA0831.2	1.85	3.21E-02	0.86	0.85	0.06	120
GLIS3	MA0737.1	1.84	3.29E-02	0.75	0.74	0.04	120
SPI1	MA0080.4	1.83	3.34E-02	0.75	0.74	0.06	120
THAP1	MA0597.1	1.82	3.38E-02	0.92	0.92	0.03	120
MXI1	MA1108.1	1.80	3.57E-02	0.81	0.80	0.06	120
ZIC1	MA0696.1	1.79	3.63E-02	0.77	0.77	0.04	120
Arnt	MA0004.1	1.79	3.64E-02	0.87	0.86	0.07	120
BHLHE40	MA0464.2	1.74	4.05E-02	0.82	0.81	0.07	120
MYCN	MA0104.4	1.72	4.20E-02	0.79	0.78	0.05	120

Table S7. Differentially Expressed Proteins Between Meno/Ang II and Ang II.

Accession	Ang II 1	Ang II 2	Ang II 3	Ang II 4	Meno/Ang II 1	Meno/Ang II 2	Meno/Ang II 3	Meno/Ang II 4	P Value	Fold Change
MYCN_MOUSE	4752	243177	180995	172830	2570	2309	2294	2743	0.03	0.02
OASL2_MOUSE	43634	45252	38334	19116	12695	11697	6339	8883	0.00	0.27
NOC3L_MOUSE	32729	44664	48451	21993	2596	18669	2950	16515	0.01	0.28
COR2A_MOUSE	165470	124980	68995	158453	50392	48942	36632	22769	0.01	0.31
AP4B1_MOUSE	561460	444494	1186157	597725	262852	108957	377996	136742	0.04	0.32
MIB2_MOUSE	61353	27003	28081	68325	28258	9997	2682	17409	0.04	0.32
I17RA_MOUSE	53163	29208	48849	64303	11760	22683	7145	37081	0.03	0.40
IFIT3_MOUSE	2730206	6034409	5615614	5086854	1792077	2255711	1383974	3450530	0.02	0.46
INT9_MOUSE	3885999	3073845	5862796	2678590	2008311	2021016	1697404	1328050	0.03	0.46
MTMRA_MOUSE	46659	43821	46811	26926	3507	30071	19437	21715	0.02	0.46
CL004_MOUSE	1659773	1746954	1729780	1202728	601521	1400611	716946	307426	0.02	0.48
OX2G_MOUSE	76109	159059	155392	118435	38890	46860	64024	92557	0.03	0.48
THNS1_MOUSE	1568443	1102370	1755938	1510942	419862	408083	1289043	704680	0.02	0.48
DHX58_MOUSE	3769322	1903761	4306837	3574338	1400826	2015288	1164610	2089181	0.02	0.49
GPAA1_MOUSE	3576510	2386991	2674240	2319291	1240545	1802717	1016866	1317774	0.01	0.49
RNF32_MOUSE	852128	551855	763698	576556	254230	546794	465228	146460	0.03	0.51
JKIP3_MOUSE	690161	337387	762552	648458	319015	120413	442085	351942	0.04	0.51
CNTLN_MOUSE	596434	447693	795819	709730	225217	164471	598876	330960	0.05	0.52
GFOD1_MOUSE	95080	173835	150438	140660	94039	76555	82170	35730	0.02	0.52
TLR7_MOUSE	1751241	1662030	3038969	2265468	983006	943080	1246642	1454240	0.02	0.53
EIF2D_MOUSE	6935721	11354726	10708146	7485145	4758185	4014848	5825417	4764331	0.01	0.53
HVM51_MOUSE	32854223	22962041	18954286	18498366	9539927	7080914	13628350	19142255	0.04	0.53
LIPA2_MOUSE	7248842	4437377	10026907	6915100	3343377	2371584	5086106	4308859	0.04	0.53
RPC3_MOUSE	1923386	2014109	2444921	1176008	1213172	992692	1267747	619803	0.03	0.54
VWF_MOUSE	900946634	548020968	407233337	764140204	409636683	328160074	271766222	403510181	0.04	0.54
HS71A_MOUSE	1415833	1234977	1422155	570645	655050	571180	821168	569673	0.05	0.56
ZN239_MOUSE	263041	257565	252185	256774	221830	149585	53630	155027	0.02	0.56
CAF1A_MOUSE	118634	137727	101046	87448	54180	63284	30687	102289	0.04	0.56
AKT3_MOUSE	787914	1055975	582737	893523	520797	389994	610815	346657	0.02	0.56
DNJA4_MOUSE	3208269	3352412	3270499	3126166	1795612	1402032	2259966	1825722	0.00	0.56
TM163_MOUSE	1682931	1269707	1588348	2217191	722271	814557	1383652	836983	0.02	0.56
IFT22_MOUSE	579693	591775	672341	586694	474910	133443	244428	539500	0.04	0.57
SYDM_MOUSE	5054394	3114985	5041657	3412204	1570145	1903437	3728097	2316026	0.04	0.57
PLPL2_MOUSE	54646	89037	66057	88022	55777	20547	44305	49528	0.03	0.57
ZC12A_MOUSE	787885	721593	646348	356779	430058	319534	456694	226125	0.05	0.57
RUSD4_MOUSE	456310	438425	334024	333436	210846	336810	198570	136706	0.02	0.57
OGFD1_MOUSE	3544929	2814127	2944866	2128469	2352188	1288428	1318030	1699289	0.02	0.58
ANR11_MOUSE	6415665	5710728	6187377	3794762	3528204	2610097	4162840	2563121	0.02	0.58
CHIL4_MOUSE	176604986	108757298	113350207	148250933	74394250	68375692	109874484	61865726	0.02	0.58
MTMRE_MOUSE	3991887	4623142	4596621	5823869	3772785	2691623	2583383	2192113	0.01	0.59
TRM2A_MOUSE	3409135	3296794	4474744	2172465	1875412	1861467	1971762	2148708	0.03	0.59
PEX6_MOUSE	1947430	1635564	1826415	1316603	1270780	995280	891019	795971	0.01	0.59
GSTA2_MOUSE	142869	274541	185515	211429	81619	94132	154786	147888	0.04	0.59
GCYB1_MOUSE	20021703	12213093	10434334	12713880	10195036	8619513	5370096	8246530	0.05	0.59
R12BA_MOUSE	632203	488207	464193	551337	387354	266392	412354	184269	0.01	0.59
T11L1_MOUSE	631444	643236	726931	474966	485974	320403	305072	383042	0.01	0.60
SNTB2_MOUSE	566475	392668	562912	444675	251779	416980	334155	182863	0.03	0.60
PO2F2_MOUSE	201251	251482	202570	160267	140892	166951	83844	99260	0.02	0.60
EST2C_MOUSE	3280689	4728808	2724440	2649185	2018919	1998373	1943570	2041132	0.03	0.60
TRI25_MOUSE	3513854	3234855	2551559	4032829	2783661	2320049	1475084	1615224	0.03	0.61
COG6_MOUSE	1829828	928525	1566739	1236104	1002422	873327	769955	749302	0.04	0.61
IREB2_MOUSE	59352	35434	39023	45085	37318	21638	21031	28456	0.03	0.61
PON3_MOUSE	17767502	28864112	26624157	23031475	10083614	19505684	18751498	11470060	0.04	0.62
FKB11_MOUSE	1299792	1105875	784675	784762	432158	831968	538224	654706	0.05	0.62
MTO1_MOUSE	438042	332739	567601	332913	303378	265234	255072	231142	0.04	0.63
PCTL_MOUSE	3376685	3293446	2994665	2674305	1383608	1881798	2655517	1822038	0.01	0.63
ATX1_MOUSE	131911	107868	134225	174980	74047	81334	129882	68460	0.05	0.64
SRC_MOUSE	23550869	18161042	11709712	17827685	12224168	11775564	12167502	9672631	0.04	0.64
RBM47_MOUSE	157151	119575	123696	140263	98226	112196	56770	79542	0.02	0.64
PPIP2_MOUSE	1923515	1431041	1830592	1186526	835452	1056475	1207000	974748	0.02	0.64
SORC2_MOUSE	236818	173029	183397	158404	150105	155022	78492	94455	0.04	0.64
EGLN_MOUSE	969364	635752	919380	1201546	691805	631022	542559	573393	0.04	0.65
MICU1_MOUSE	1883970	2421202	2723358	1488918	1306530	1361092	1776364	1122689	0.05	0.65
PDE2A_MOUSE	13468087	17050654	21828505	17634312	11348053	11703710	12947821	9653096	0.02	0.65
FA46C_MOUSE	2211450	1652005	1281698	1881949	1268435	1113637	1024550	1174071	0.02	0.65
ZN800_MOUSE	1366929	1213886	1415189	1550044	1022715	1091808	826540	669710	0.01	0.65
TMCC2_MOUSE	1522029	1013458	1691407	1154483	749821	1130468	813888	804840	0.04	0.65
MMRN1_MOUSE	410991694	308545214	193423313	330523582	221875837	195132750	206722718	181813698	0.05	0.65
HTRA2_MOUSE	39962802	31190007	39081608	25145941	18272219	18286898	31767531	19229079	0.05	0.65
HIRP3_MOUSE	1190311	1148803	1435306	897783	787032	540315	968504	801340	0.03	0.66
CREL2_MOUSE	6923631	9145089	7544958	5409532	3138270	4441107	5709935	5914096	0.05	0.66
ITAX_MOUSE	6543742	7178793	6147487	5574022	4069283	4788274	3128239	4693680	0.01	0.66
APBA3_MOUSE	221878	164985	201376	210748	141614	120660	142887	133323	0.00	0.67
VAV3_MOUSE	10597434	7306099	10465654	12919883	8764577	5809972	7156448	6018853	0.04	0.67
CAH12_MOUSE	286339	295754	188601	234827	195043	145844	218694	115942	0.05	0.67
DDX41_MOUSE	3360254	2948592	3558512	2645887	1890984	1718214	3137608	1655975	0.04	0.67
GUAA_MOUSE	104452386	111668766	122494748	79193974	69300306	71113809	74313157	63177135	0.01	0.67
STK3_MOUSE	1310949	980866	1144134	1094890	969001	804528	572230	742225	0.01	0.68
MET16_MOUSE	6450842	6644002	5716932	4155789	4861288	3803847	3847060	3082035	0.03	0.68
VWA9_MOUSE	6115790	6740617	6247170	5780590	4184123	5602701	4429429	2637422	0.02	0.68
PRSR2_MOUSE	57618	42162	39854	63909	29146	34622	42664	31327	0.05	0.68
LZTR1_MOUSE	336666	238347	295530	274946	268292	175535	148291	182321	0.03	0.68
LOX12_MOUSE	494518085	356526702	361781502	503206038	376490299	314652485	207765855	261169500	0.04	0.68
KIFA3_MOUSE	577166	479654	657332	784926	456782	463065	451994	364868	0.03	0.69
IGHM_MOUSE	398395722	428614063	418430525	366696929	177155149	313511700	366961733	257014832	0.03	0.69
SLAF6_MOUSE	912613	857803	859682	648486	519105	561633	744624	429945	0.03	0.69
PGM2L_MOUSE	10318750	9403005	11954845	12514643	8481629	8049345	7078841	6681266	0.01	0.69
CPT2_MOUSE	83050361	72605749	78000939	66012965	61638838	53444992	51833502	43904382	0.01	0.70
CTGE5_MOUSE	4212133	3036021	4073122	2786191	2251376	1875148	3002971	2743872	0.05	0.70
AIDA_MOUSE	9497016	8158643	6059789	6049178	5064162	5384303	5882259	4497993	0.05	0.70
OAS3_MOUSE	14714835	19933658	14954774	15788280	12697930	13068438	9313834	10600639	0.02	0.70
GPKOW_MOUSE	5222236	6225771	6905403	4951046	4555086	3196606	5333889	3186462	0.05	0.70
ENDD1_MOUSE	9812490	10481149	6282988	9948957	5917540	6430435	7538688	5581666	0.04	0.70
KI13A_MOUSE	3080631	2717398	2240237	3202592	2036304	1949701	1603072	2436184	0.03	0.71

DPH7_MOUSE	406820	438743	378568	575116	373480	314936	309914	284920	0.03	0.71
LONP2_MOUSE	809572	722391	970511	826448	596714	634726	694141	439446	0.02	0.71
TAF1_MOUSE	10186593	11433778	9900658	10184008	8143603	8224822	7319009	5812827	0.00	0.71
SHIP2_MOUSE	4694615	4262795	3155440	4302881	3358883	2983777	2181110	3083714	0.03	0.71
SDPR_MOUSE	363351470	281045842	257501140	289733159	239559493	211408268	222781372	168635641	0.02	0.71
LDAH_MOUSE	14590418	9987819	12059884	11017497	7368053	9846656	9094229	7339810	0.02	0.71
OAS1A_MOUSE	11622768	10408556	10424354	13009198	6124649	8049316	9370628	9338940	0.02	0.72
MYOME_MOUSE	377858	392889	334392	311522	248394	282191	180684	312640	0.03	0.72
ALG11_MOUSE	1378050	1261862	1107945	1132405	906191	1223839	673231	722906	0.05	0.72
EPC2_MOUSE	276809	249895	344326	323633	225502	168244	264658	201467	0.03	0.72
TPR_MOUSE	232295114	246386077	219336793	188381367	150858609	162212591	165780575	157241050	0.00	0.72
DCAF6_MOUSE	421818	330591	351236	306230	270929	239232	176569	324994	0.05	0.72
CMC2_MOUSE	21367640	14694259	15406888	14925193	12927733	12263060	11939619	10440278	0.03	0.72
EMIL1_MOUSE	41297610	35922635	27565998	32099256	28005121	21112242	23681355	25160681	0.02	0.72
RAB7L_MOUSE	6027555	4710735	4130986	4670729	3509406	3673097	3172330	4003668	0.03	0.73
LRRF2_MOUSE	15678086	16028239	12609361	13982978	11473623	8378341	12861747	10037433	0.02	0.73
SETD3_MOUSE	8748948	11547984	9398427	8397910	8262302	7171329	5457099	7025664	0.03	0.73
PEAR1_MOUSE	5805786	5018606	4147823	4629022	3851147	3504758	3646246	3349030	0.01	0.73
PRDX4_MOUSE	73294410	55809027	62719335	50562545	43445876	34459354	50390995	48483778	0.04	0.73
FAN_MOUSE	2077836	1630036	2152463	1832523	1628657	1606205	1052012	1319076	0.03	0.73
TRPC5_MOUSE	1329693	1559056	1275957	1496752	1136288	673425	1156817	1141654	0.03	0.73
PCKGM_MOUSE	112892571	104073008	83339168	78560255	71654069	66260846	73838389	69931776	0.03	0.74
ATLA2_MOUSE	1972725	2109586	2470297	1788351	1831812	1704311	1566872	1091368	0.05	0.74
TAF6L_MOUSE	3961510	4424837	5023275	3519014	3469943	2853070	3400424	2782520	0.02	0.74
LTBP1_MOUSE	69416866	53522990	54381365	75397975	49938577	36735081	51647267	47634865	0.04	0.74
LPIN2_MOUSE	521392	464783	404727	504155	374837	359569	374356	316587	0.01	0.75
GLGB_MOUSE	14488195	11083173	15257775	11297218	11738095	9726769	9843417	7845477	0.05	0.75
HCK_MOUSE	19037799	19448894	22158630	19094481	13218326	11623468	16386030	18620293	0.03	0.75
MSPD2_MOUSE	3778312	4357028	3613473	3519693	2609911	2679791	3175092	2993891	0.01	0.75
NOP14_MOUSE	218641	195258	196820	164112	135948	103483	160615	181137	0.05	0.75
QSOX1_MOUSE	5478151	4819757	4343223	5232676	3833576	3726160	3359023	3935038	0.00	0.75
STRP1_MOUSE	8308511	5603093	7646114	6230715	5541448	4461167	4890653	5835320	0.04	0.75
RM01_MOUSE	19595109	17163328	18012341	13706319	11749471	13312172	14984683	12273854	0.03	0.76
PDIP2_MOUSE	18537013	13792655	14553961	13484728	10114801	10995219	13344533	11360196	0.04	0.76
PDE12_MOUSE	17109250	13014589	13753086	12488070	12283156	12394379	9079297	8969863	0.05	0.76
WDR11_MOUSE	2820457	2332993	2336258	3101767	2352886	2081869	1490299	2081434	0.05	0.76
TMC5_MOUSE	2423708	1816320	1822448	2249617	1745727	1657017	1421611	1457456	0.03	0.76
ERLN2_MOUSE	19826642	14873721	14220873	15624089	12257268	12417648	10594187	14716175	0.05	0.77
TREX1_MOUSE	10136884	7818036	9416125	9808637	6372522	9068533	6729498	6520906	0.04	0.77
PTN9_MOUSE	1572939	1582373	1829034	1544354	1433425	1411531	1147433	1042034	0.02	0.77
UH1BL_MOUSE	7231141	5621502	5135837	7214461	5258097	5049564	4750090	4351137	0.05	0.77
SYG_MOUSE	143878143	119435391	126229037	115751743	100879424	90564690	99618810	97296027	0.00	0.77
ECM1_MOUSE	14439670	12108854	14247392	16728531	9418115	9737138	12926829	12085034	0.04	0.77
UBS3B_MOUSE	44063699	40109758	40219310	40392369	34975135	34266060	32115329	25078100	0.01	0.77
CAN2_MOUSE	170380807	156684725	175453992	152634243	140795496	121085847	137647826	114399754	0.01	0.78
GDPD1_MOUSE	2351515	2067737	2723728	2325490	1770407	1899501	1823617	1927651	0.01	0.78
LCP2_MOUSE	267987921	231153198	249335985	213547851	209551788	182439280	200063676	159132226	0.02	0.78
SRPRA_MOUSE	7956315	6069766	6111363	6119219	5412787	5317092	4794542	4951786	0.03	0.78
NUP37_MOUSE	611527	542903	583283	494557	393257	537675	439255	368248	0.03	0.78
GPDM_MOUSE	151371865	123584905	129083263	128927820	117722315	103540187	109623693	84056739	0.02	0.78
CAZA2_MOUSE	437773123	363014096	414387767	333021614	236688953	314168620	363521764	289401185	0.05	0.78
GRP78_MOUSE	2852679029	2575793439	3220316755	2508891095	1841999495	1968533657	2672602038	2175150922	0.04	0.78
ATRX_MOUSE	18592354	20290064	18754516	21443023	12109659	16903893	15540830	18258894	0.03	0.79
RHG26_MOUSE	3438748	3682496	3527319	3852254	2632713	2993304	3376761	2485494	0.01	0.79
SMG9_MOUSE	3735857	3668466	3816838	3348452	2896119	3566360	2358751	2677148	0.03	0.79
PCCA_MOUSE	60553114	50522375	61713833	47254501	46130713	42781641	46173638	38119492	0.03	0.79
SNTB1_MOUSE	12652954	11839060	9207809	11946387	10055107	10075537	8303699	7438366	0.05	0.79
PGTA_MOUSE	10633339	10870600	10800871	12470177	10097643	7250650	10438490	8221679	0.05	0.80
CNPY3_MOUSE	6668087	5314612	6234990	5191668	4695652	4585895	5301570	4181743	0.03	0.80
PLCB3_MOUSE	8313005	6861210	6594002	7302717	5651328	5424433	6411718	5771413	0.02	0.80
BIR1B_MOUSE	1301811	1509855	1280222	1306866	1023578	1310511	977524	996454	0.03	0.80
NOMO1_MOUSE	30367333	25029004	25944511	28854993	23138327	22621187	18199220	23860696	0.02	0.80
LIMA1_MOUSE	3016209	2382699	2545594	2284378	2160250	1882589	2350499	1933677	0.05	0.81
EHD4_MOUSE	206036720	178095233	169576381	186208137	169666748	150467607	157463802	124593169	0.03	0.81
EF1D_MOUSE	591061805	613348887	607960615	505959172	432961375	455213136	538876494	459737267	0.02	0.81
IFIH1_MOUSE	12690456	15194722	13641472	12438656	10660689	11373615	10954488	10917488	0.01	0.81
PAR14_MOUSE	56865172	59661241	51610304	46658635	47457788	47741280	37928174	41515062	0.04	0.81
K1468_MOUSE	12377998	12178479	12135436	11259695	10860533	10598699	8159730	9355806	0.02	0.81
NCOR2_MOUSE	4596843	5789602	5753171	5671890	3853153	4419548	4599659	4825258	0.03	0.81
XDH_MOUSE	20942232	19239979	21338817	22665576	17547527	18001451	13010686	19401685	0.04	0.81
LYAM3_MOUSE	57513883	45943975	43099552	45100468	41731710	33262707	40226987	39297780	0.05	0.81
NDUV2_MOUSE	102638567	108091244	106193727	94974941	84429793	78429537	94722784	81471970	0.01	0.82
DNM1L_MOUSE	84481554	85491700	95262471	93088380	79395339	72212774	84082355	58516665	0.04	0.82
PAOX_MOUSE	24891191	27286043	29425890	27349082	23542870	23493479	20212656	22198690	0.01	0.82
XPP1_MOUSE	69398660	63442515	60628971	54884675	61046502	50612926	46175450	45953907	0.05	0.82
ELP3_MOUSE	10654091	9973972	9305068	10143051	9150624	9410340	6654310	7627391	0.04	0.82
ITSN1_MOUSE	13862938	11986052	12640554	11716376	10040401	9191167	10251891	11582075	0.02	0.82
FYCO1_MOUSE	37187320	31514153	28853419	30929336	29747591	25463723	25819072	24010632	0.04	0.82
KTN1_MOUSE	7641065	7106997	7804755	7112906	6745816	5523527	4943897	6998564	0.04	0.82
CPSF3_MOUSE	26349340	23282564	22079155	24916238	19874786	23390388	19074235	18146912	0.03	0.83
STAT2_MOUSE	15333242	16813379	17352630	15574022	12748283	14511204	13395117	13473828	0.00	0.83
AAAT_MOUSE	2435715	2380000	2873866	2227216	1954109	2126373	1990558	2171595	0.03	0.83
MCM5_MOUSE	69598893	67682584	73632673	88155807	63940300	64899782	58677718	60441151	0.04	0.83
PRUNE_MOUSE	15268980	14344039	16306505	17722415	14954906	12904896	12252599	13577031	0.04	0.84
EFHD2_MOUSE	101048133	97850904	93973232	85153997	83734035	80080261	87343099	66336754	0.04	0.84
PREX1_MOUSE	65049244	65189432	58781973	59787939	53231549	56450840	47966482	50479889	0.01	0.84
EXOC1_MOUSE	15974577	15606476	18424597	17369390	13882448	12295778	16042110	14094270	0.03	0.84
MIA3_MOUSE	35136240	31698302	33401513	27344088	26693820	26779913	28471656	26482817	0.03	0.85
PABP1_MOUSE	526074252	493058805	545854984	467514722	444947427	404963335	471651021	402247434	0.02	0.85
NMD3_MOUSE	921170	965074	897244	914327	805900	791197	785100	810418	0.00	0.86
AP1G1_MOUSE	54257363	49879437	53333608	63218123	49607706	49667436	46935653	43829990	0.05	0.86
EXOS7_MOUSE	20761154	18607836	20381475	19559675	17014021	19526348	17099605	15724864	0.04	0.87
WDHD1_MOUSE	762100	648549	719890	692999	574282	655330	599157	659649	0.04	0.88
WNK1_MOUSE	65682913	64901987	62054251	59073842	56043085	58874180	59523894	53362231	0.03	0.91
DDB1_MOUSE	122798934	127195956	117421590	123395177	114537409	117195642	114431062	111272607	0.01	0.93
QCR2_MOUSE	562517814	512993256	539645101	519196811	610920468	543741294	591527511	611138310	0.03	1.10
RUVB2_MOUSE	142727915	173761026	178360382	168469740	191432785	195866729	189433222	176026843	0.05	1.13
ACY1_MOUSE	8804078	9004577	9300502	9363296	10750458	9016885	10840259	10500571	0.04	1.13

SYCC_MOUSE	16746128	16573803	15750569	16286347	17130915	17993145	20674330	18921538	0.03	1.14
EIF3E_MOUSE	145242631	131030376	124110495	145910644	164679790	161742971	145225893	150448558	0.04	1.14
SYWC_MOUSE	99450701	95260162	91226112	95620675	111010421	110426930	103866369	108540792	0.00	1.14
CUX1_MOUSE	1834538	1648886	1782404	1777633	1936909	1895172	2242261	1928199	0.04	1.14
QCR1_MOUSE	445517698	470784268	453102426	428771404	530818659	525510305	519765134	499741004	0.00	1.15
TOIP2_MOUSE	1662160	1826040	1997189	1553104	1969385	1927555	2081390	2082995	0.05	1.15
RU2A_MOUSE	179140308	209006948	180664878	172043861	234186754	224954100	204726429	197755795	0.04	1.16
WAC_MOUSE	4883977	5340656	4905451	4656778	5790625	5840584	6191266	5054142	0.03	1.16
PSD12_MOUSE	97024109	115212596	95039084	105935618	123527111	126527259	115662634	118709697	0.01	1.17
RUSD2_MOUSE	2293493	2032350	2204773	1899988	2472109	2469740	2338370	2554148	0.01	1.17
PRS6B_MOUSE	143830389	132479308	120628233	124463578	149014309	168882772	163683342	133613145	0.05	1.18
METK2_MOUSE	79219016	74220474	77429768	83549864	95115480	93750022	102792779	83665189	0.01	1.19
CSN2_MOUSE	56120667	54829354	58932237	51785708	57170796	69466069	74312031	63203232	0.04	1.19
EVL_MOUSE	295041109	411171244	342554597	337759845	408703475	440576488	393950725	408029460	0.04	1.19
NANP_MOUSE	2465020	2299205	2140222	2079891	2845112	2563222	2616927	2656885	0.01	1.19
PHB_MOUSE	631886324	620580255	525807675	598639719	810575723	677525238	632913960	699271392	0.05	1.19
CCS_MOUSE	14070810	15295328	14484531	15362765	20307741	18036957	16743263	15160813	0.05	1.19
PEF1_MOUSE	10614221	10500606	10008653	10958455	13035916	13624222	11319640	12617825	0.01	1.20
IF4E2_MOUSE	8560278	8729283	7871273	9077314	11745356	10059631	8967180	10754068	0.03	1.21
CP4F3_MOUSE	161865	148553	163016	174265	176272	201800	211432	194699	0.01	1.21
EXTL3_MOUSE	87598	104921	100199	91012	118833	104179	114985	131010	0.02	1.22
CRTC1_MOUSE	1565950	1680254	1668053	1647053	1676705	1948963	2285146	2062849	0.03	1.22
NHSL2_MOUSE	1937000	2038636	1785522	1853199	2362580	2422337	2254410	2316666	0.00	1.23
RS24_MOUSE	123627136	129874690	115860462	147317189	168262105	152106962	163549654	150560096	0.01	1.23
CCD86_MOUSE	414473	413991	455892	415716	527295	443912	570927	590015	0.02	1.25
TRM5_MOUSE	7065977	8753346	7706945	6190552	9110906	10631791	9251804	8401659	0.04	1.26
ECSIT_MOUSE	2671653	2745898	2717611	2426303	3377145	3887343	3466861	2675033	0.03	1.27
TATD1_MOUSE	4287519	4449406	3438630	4054525	5666733	5810327	4799511	4564451	0.02	1.28
PI42B_MOUSE	4657112	4974330	3702708	5660780	6491968	6967850	6282023	4950888	0.05	1.30
SSH1_MOUSE	715332	495035	754745	681003	914449	904078	905697	709842	0.04	1.30
KCMF1_MOUSE	4765657	4537426	5134789	5605908	6635762	5629923	6662049	7302980	0.01	1.31
CD11B_MOUSE	2578011	3178942	2632067	2183099	3327809	3418937	3882641	3338545	0.01	1.32
RBM38_MOUSE	19500562	17669129	17179368	24486229	26779378	23813493	31216708	22058464	0.05	1.32
VNN1_MOUSE	1453102	1149340	1435720	875688	1471855	1589288	1621636	1779031	0.04	1.32
MET23_MOUSE	199852	172567	179266	240260	297241	208890	244605	300631	0.05	1.33
SNX15_MOUSE	5014069	6066548	4108685	4592176	7426503	6422633	6109278	6271262	0.02	1.33
SARAF_MOUSE	8422590	10074284	7332937	7467998	12407751	13024351	9810600	9539501	0.04	1.34
PEPL1_MOUSE	23274345	32070060	22961260	23901707	33983918	40760327	28531444	34100414	0.04	1.34
MTMR1_MOUSE	9315905	15308810	10810034	14430602	18121153	14691442	17163912	17234869	0.04	1.35
CNO11_MOUSE	7692606	8899318	5994216	6458948	10210350	9764241	9865371	9625584	0.01	1.36
YRDC_MOUSE	2599557	4006364	4381327	5256605	5347615	5489873	5676430	5536994	0.04	1.36
PHLD_MOUSE	16359600	17447806	20707412	20246505	24709570	24742648	24194296	29060887	0.00	1.37
VIME_MOUSE	57783376	55964910	71080932	69645153	76303407	79898977	111459701	80520868	0.04	1.37
TRAD1_MOUSE	1515556	1646126	1083154	1486978	2032720	2328992	1570805	2058818	0.03	1.39
SFT2C_MOUSE	534825	804520	740610	462006	755995	834813	900749	1041968	0.05	1.39
RAD18_MOUSE	209955	219944	179354	174498	281806	278936	254478	284639	0.00	1.40
AMPE_MOUSE	624234	603668	587353	726910	934663	900108	945913	834146	0.00	1.42
ENOB_MOUSE	11460509	9076801	8168782	8686817	14978503	16354441	11891376	10202066	0.04	1.43
LX12B_MOUSE	607715	831764	885275	794410	1437189	1142966	877341	989737	0.05	1.43
RFC3_MOUSE	1682460	2874448	2902114	3005116	3580958	3489316	4499491	3629755	0.02	1.45
CP2S1_MOUSE	8011241	8448153	10250070	8156724	12287815	14134136	13001846	11547806	0.00	1.46
C295L_MOUSE	1707187	952900	1091317	1490942	2034493	1676475	1614048	2439679	0.05	1.48
SLN14_MOUSE	43686638	38635871	36229707	35244611	57410831	56674376	58063780	54883158	0.00	1.48
NXN_MOUSE	2013470	2376020	1527154	1309897	2819848	2925883	2985369	2053921	0.03	1.49
MTDC_MOUSE	10415146	3922911	7136413	8759723	10595785	12339421	10023013	12430690	0.05	1.50
LRIQ4_MOUSE	285330	342069	220185	217815	420001	501796	295041	378686	0.04	1.50
GIMA6_MOUSE	424116	269211	426183	404462	474341	807584	580378	532603	0.04	1.57
CHIL3_MOUSE	217819287	186955347	281871287	236782037	271165871	438993759	336857440	415602811	0.02	1.58
ERG28_MOUSE	4518458	1874086	3977556	5534385	7111788	5304810	5768340	6921915	0.04	1.58
HAUS7_MOUSE	1028777	1054822	1213121	809890	1675706	2032711	1574395	1291165	0.01	1.60
CATD_MOUSE	470647611	495352619	873454145	467147257	754189218	847958874	1027934953	1092550394	0.03	1.61
DIRC2_MOUSE	509017	438984	780115	728641	797737	935137	898683	1457698	0.05	1.66
MMAA_MOUSE	221840	235966	153453	361503	397749	361475	413770	445565	0.01	1.66
RCL1_MOUSE	287129	155332	108755	139188	296504	212872	293591	342729	0.05	1.66
ELK4_MOUSE	177997	78622	144366	161718	246308	327634	186137	196547	0.04	1.70
SEP10_MOUSE	100044	81701	84737	122334	166386	221770	127941	152793	0.02	1.72
KMT2A_MOUSE	522623	619781	389125	329705	897012	1002399	742811	593473	0.02	1.74
KLDC4_MOUSE	4727922	7281597	4411293	3050389	8462304	12170635	7110140	7288029	0.04	1.80
CK084_MOUSE	34795	24512	9533	38607	42237	64086	60656	45046	0.02	1.97
NLRC4_MOUSE	11066	14302	30671	28342	37197	52225	43989	34277	0.02	1.99
RNF12_MOUSE	149314	198161	83520	71046	255013	270521	236633	248792	0.01	2.01
SNX24_MOUSE	31206	42704	60430	28160	104156	106305	46010	69970	0.04	2.01
SAP_MOUSE	34664028	27048731	71922657	28501192	87481402	91155536	59765248	94160781	0.02	2.05
SGK3_MOUSE	76951	149740	46891	133946	267173	254303	179980	143552	0.03	2.07
TLR3_MOUSE	422771	1172741	966516	1039371	2363287	1538640	1616810	2053313	0.01	2.10
MTL5_MOUSE	129964	226029	78040	274058	309184	572199	261144	349063	0.05	2.11
OXLA_MOUSE	1493189	1936051	2808020	1869351	3502109	5265453	5204842	3424661	0.01	2.15
ATOX1_MOUSE	283591	162261	480362	500171	678527	1004945	592659	942874	0.01	2.26
ANS1B_MOUSE	249836	401031	112661	607649	873162	1029593	564961	749715	0.02	2.35
REV1_MOUSE	258640	712322	553040	1149845	1203319	1777317	1690366	1714247	0.01	2.39
PPR37_MOUSE	7901	27599	23873	13835	41980	59563	36319	39111	0.01	2.42
DPM3_MOUSE	858785	344952	706561	867316	1658437	2660882	698644	2327132	0.04	2.64
FIZ1_MOUSE	179745	43928	7351	66843	208141	182998	277704	122962	0.05	2.66
SBNO2_MOUSE	44750	66959	23614	26424	81403	170988	125781	63283	0.04	2.73
TRCG1_MOUSE	189614	170982	542531	626702	803403	1586720	1377342	468507	0.05	2.77
SLIRP_MOUSE	218796	95322	109447	181699	456007	543784	149670	558014	0.03	2.82
H4_MOUSE	98273019	52167231	54763983	83842728	283949902	304859021	52190752	220029419	0.05	2.98
PP16B_MOUSE	26514	465	14582	33760	79442	61601	51300	33535	0.02	3.00
COX17_MOUSE	33985	42586	59026	108187	230607	402522	198903	688228	0.03	6.24
RRP36_MOUSE	27295	39642	5082	30689	326338	91140	167945	144910	0.02	7.11
EZH1_MOUSE	5261	786	9206	30	25625	64569	29946	17080	0.03	8.98
T2AG_MOUSE	74	90137	137364	11348	852414	979917	36428	920403	0.03	11.67
CATR_MOUSE	9679	4313	8152	29583	159852	355032	6588	289091	0.05	15.67

Table S8. Biological Processes Associated with Upregulated Proteins in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190308)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (93)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
cellular metabolic process	6280	53	26.19	+	2.02	8.99E-09	1.41E-04
organic substance metabolic process	6644	53	27.71	+	1.91	7.28E-08	3.81E-04
metabolic process	7166	57	29.89	+	1.91	9.88E-09	7.74E-05
macromolecule metabolic process	5049	40	21.06	+	1.90	1.60E-05	4.17E-02
primary metabolic process	6235	49	26.01	+	1.88	6.25E-07	2.45E-03
nitrogen compound metabolic process	5669	44	23.65	+	1.86	6.45E-06	2.02E-02

Table S9. Molecular Functions Associated with Upregulated Proteins in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190701)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (93)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
copper chaperone activity (GO:0016531)	5	3	0.02	+	> 100	3.83E-06	8.75E-03
metallochaperone activity (GO:0016530)	7	3	0.03	+	> 100	8.15E-06	1.24E-02
catalytic activity (GO:0003824)	5692	48	23.74	+	2.02	1.21E-07	5.55E-04
binding (GO:0005488)	13135	75	54.79	+	1.37	1.12E-05	1.28E-02

Table S10. Biological Processes Associated with Downregulated Proteins in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190308)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (181)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
regulation of viral genome replication (GO:0045069)	91	7	0.74	+	9.48	1.46E-05	1.91E-02
defense response to virus (GO:0051607)	176	13	1.43	+	9.10	4.68E-09	7.35E-05
response to virus (GO:0009615)	221	14	1.79	+	7.80	7.50E-09	5.88E-05
regulation of viral life cycle (GO:1903900)	142	8	1.15	+	6.94	3.01E-05	2.78E-02
heterocycle catabolic process (GO:0046700)	267	10	2.17	+	4.61	8.74E-05	4.57E-02
defense response to other organism (GO:0098542)	646	18	5.24	+	3.43	7.48E-06	1.47E-02
immune effector process (GO:0002252)	635	17	5.15	+	3.30	2.23E-05	2.33E-02
innate immune response (GO:0045087)	728	18	5.91	+	3.05	3.52E-05	2.91E-02
response to other organism (GO:0051707)	1024	22	8.31	+	2.65	3.77E-05	2.96E-02
response to external biotic stimulus (GO:0043207)	1026	22	8.33	+	2.64	3.88E-05	2.90E-02
response to biotic stimulus (GO:0009607)	1049	22	8.52	+	2.58	5.35E-05	3.36E-02
defense response (GO:0006952)	1304	26	10.59	+	2.46	4.01E-05	2.86E-02
organic substance catabolic process (GO:1901575)	1394	27	11.32	+	2.39	3.49E-05	3.04E-02
cellular catabolic process (GO:0044248)	1450	27	11.77	+	2.29	5.86E-05	3.54E-02
nucleic acid metabolic process (GO:0090304)	1725	30	14.00	+	2.14	7.49E-05	4.20E-02
nucleobase-containing compound metabolic process (GO:0006139)	2141	37	17.38	+	2.13	1.14E-05	1.78E-02
heterocycle metabolic process (GO:0046483)	2278	39	18.49	+	2.11	6.99E-06	1.57E-02
cellular aromatic compound metabolic process (GO:0006725)	2344	39	19.03	+	2.05	1.50E-05	1.81E-02
organic cyclic compound metabolic process (GO:1901360)	2545	41	20.66	+	1.98	1.83E-05	2.05E-02
response to stress (GO:0006950)	3064	49	24.87	+	1.97	2.35E-06	9.20E-03
immune system process (GO:0002376)	2249	36	18.26	+	1.97	9.48E-05	4.79E-02
cellular nitrogen compound metabolic process (GO:0034641)	2720	42	22.08	+	1.90	5.17E-05	3.53E-02
cellular metabolic process (GO:0044237)	6280	80	50.98	+	1.57	6.09E-06	1.59E-02
primary metabolic process (GO:0044238)	6235	78	50.62	+	1.54	1.38E-05	1.97E-02
regulation of metabolic process (GO:0019222)	5688	71	46.18	+	1.54	5.29E-05	3.46E-02
positive regulation of biological process (GO:0048518)	5947	73	48.28	+	1.51	6.81E-05	3.96E-02
metabolic process (GO:0008152)	7166	87	58.17	+	1.50	9.66E-06	1.68E-02
organic substance metabolic process (GO:0071704)	6644	81	53.94	+	1.50	2.75E-05	2.69E-02

Table S11. Molecular Functions Associated with Downregulated Proteins in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190701)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (181)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
2'-5'-oligoadenylate synthetase activity (GO:0001730)	6	3	0.05	+	61.59	4.16E-05	1.00E-02
adenylyltransferase activity (GO:0070566)	29	4	0.24	+	16.99	1.39E-04	2.64E-02
double-stranded RNA binding (GO:0003725)	84	7	0.68	+	10.27	8.95E-06	4.55E-03
RNA binding (GO:0003723)	1032	26	8.38	+	3.10	3.97E-07	4.53E-04
hydrolase activity, acting on ester bonds (GO:0016788)	718	18	5.83	+	3.09	2.96E-05	8.45E-03
purine nucleotide binding (GO:0017076)	1781	32	14.46	+	2.21	2.41E-05	7.87E-03
purine ribonucleoside triphosphate binding (GO:0035639)	1697	30	13.78	+	2.18	5.91E-05	1.29E-02
purine ribonucleotide binding (GO:0032555)	1769	31	14.36	+	2.16	4.86E-05	1.11E-02
nucleoside phosphate binding (GO:1901265)	2008	35	16.30	+	2.15	2.01E-05	7.07E-03
nucleotide binding (GO:0000166)	2008	35	16.30	+	2.15	2.01E-05	7.66E-03
ribonucleotide binding (GO:0032553)	1784	31	14.48	+	2.14	8.45E-05	1.76E-02
carbohydrate derivative binding (GO:0097367)	2085	36	16.93	+	2.13	1.61E-05	6.69E-03
small molecule binding (GO:0036094)	2390	40	19.40	+	2.06	9.94E-06	4.55E-03
anion binding (GO:0043168)	2659	44	21.59	+	2.04	4.73E-06	2.71E-03
hydrolase activity (GO:0016787)	2488	40	20.20	+	1.98	2.57E-05	7.84E-03
metal ion binding (GO:0046872)	3463	53	28.11	+	1.89	4.21E-06	2.75E-03
cation binding (GO:0043169)	3560	54	28.90	+	1.87	3.35E-06	2.55E-03
ion binding (GO:0043167)	5414	80	43.95	+	1.82	5.45E-09	1.25E-05
catalytic activity (GO:0003824)	5692	82	46.21	+	1.77	1.01E-08	1.55E-05
heterocyclic compound binding (GO:1901363)	4950	65	40.18	+	1.62	3.11E-05	8.36E-03
organic cyclic compound binding (GO:0097159)	5053	66	41.02	+	1.61	3.52E-05	8.94E-03
protein binding (GO:0005515)	9011	107	73.15	+	1.46	5.85E-07	5.35E-04
binding (GO:0005488)	13135	151	106.63	+	1.42	2.71E-12	1.24E-08
signaling receptor activity (GO:0038023)	2305	5	18.71	-	0.27	1.92E-04	3.38E-02
molecular transducer activity (GO:0060089)	2354	5	19.11	-	0.26	1.35E-04	2.68E-02
transmembrane signaling receptor activity (GO:0004888)	2120	4	17.21	-	0.23	1.74E-04	3.19E-02

Table S12. Transcription Factors Associated with Downregulated Proteins in Meno/Ang II vs. Ang II.

TF_NAME	MATRIX_ID	Z_SCORE	P_VALUE	SAMPLE_AVERAGE	BACKGROUND_AVERAGE	SAMPLE_DEVSTD	SAMPLE_SIZE
HINFP	MA0131.2	6.21	2.34E-10	0.83	0.81	0.05	184
TFDP1	MA1122.1	5.62	8.93E-09	0.87	0.84	0.06	184
KLF14	MA0740.1	5.09	1.68E-07	0.84	0.82	0.06	184
SP4	MA0685.1	4.85	5.60E-07	0.81	0.79	0.06	184
EGR3	MA0732.1	4.80	7.35E-07	0.80	0.77	0.05	184
EGR2	MA0472.2	4.73	1.05E-06	0.82	0.80	0.05	184
ZBTB7A	MA0750.2	4.72	1.09E-06	0.85	0.83	0.06	184
SP2	MA0516.1	4.68	1.33E-06	0.89	0.87	0.05	184
E2F4	MA0470.1	4.67	1.41E-06	0.88	0.86	0.05	184
EGR1	MA0162.3	4.54	2.64E-06	0.77	0.75	0.05	184
Tcfl5	MA0632.1	4.53	2.73E-06	0.91	0.88	0.06	184
ELK4	MA0076.2	4.46	3.83E-06	0.87	0.85	0.06	184
Gabpa	MA0062.2	4.39	5.16E-06	0.86	0.84	0.06	184
SP1	MA0079.3	4.23	1.15E-05	0.92	0.90	0.05	184
ZBTB33	MA0527.1	4.18	1.34E-05	0.78	0.77	0.06	184
Klf12	MA0742.1	4.15	1.54E-05	0.83	0.81	0.06	184
CTCF	MA0139.1	4.11	1.84E-05	0.79	0.78	0.05	184
NRF1	MA0506.1	4.07	2.24E-05	0.86	0.83	0.07	184
KLF5	MA0599.1	4.03	2.70E-05	0.94	0.92	0.05	184
TFAP2A(var.2)	MA0810.1	4.01	2.95E-05	0.88	0.86	0.04	184
SP8	MA0747.1	3.95	3.81E-05	0.89	0.87	0.05	184
SP3	MA0746.1	3.84	5.90E-05	0.90	0.88	0.05	184
ETV6	MA0645.1	3.73	9.05E-05	0.87	0.85	0.05	184
Zfx	MA0146.2	3.71	1.02E-04	0.86	0.84	0.05	184
ELF1	MA0473.2	3.68	1.12E-04	0.80	0.78	0.06	184
KLF13	MA0657.1	3.64	1.30E-04	0.75	0.74	0.05	184
KLF16	MA0741.1	3.64	1.30E-04	0.89	0.87	0.06	184
CTCFL	MA1102.1	3.63	1.33E-04	0.81	0.79	0.06	184
ETV5	MA0765.1	3.63	1.35E-04	0.88	0.86	0.05	184
ZIC4	MA0751.1	3.61	1.45E-04	0.81	0.80	0.04	184
ELF4	MA0641.1	3.60	1.54E-04	0.79	0.78	0.06	184
E2F1	MA0024.3	3.58	1.65E-04	0.78	0.76	0.05	184
EGR4	MA0733.1	3.53	1.97E-04	0.79	0.78	0.05	184
ELF5	MA0136.2	3.35	3.82E-04	0.88	0.87	0.05	184
Hes1	MA1099.1	3.18	7.24E-04	0.87	0.86	0.05	184
ETV4	MA0764.1	3.15	7.77E-04	0.86	0.85	0.05	184
TFAP2C	MA0524.2	3.13	8.57E-04	0.86	0.85	0.04	184
Klf1	MA0493.1	3.12	8.91E-04	0.88	0.87	0.05	184
NFKB1	MA0105.4	3.08	1.00E-03	0.72	0.71	0.06	184
TFAP2B	MA0811.1	3.08	1.02E-03	0.86	0.85	0.04	184
ETS1	MA0098.3	3.06	1.07E-03	0.86	0.85	0.05	184
EHF	MA0598.2	3.05	1.11E-03	0.80	0.78	0.05	184
ZIC3	MA0697.1	3.01	1.27E-03	0.79	0.78	0.04	184
TFAP2C(var.3)	MA0815.1	2.99	1.34E-03	0.81	0.80	0.05	184
ERG	MA0474.2	2.99	1.37E-03	0.86	0.85	0.05	184
ETV1	MA0761.1	2.96	1.51E-03	0.85	0.84	0.05	184
FEV	MA0156.2	2.94	1.59E-03	0.85	0.84	0.05	184
ELK3	MA0759.1	2.92	1.71E-03	0.84	0.83	0.06	184
ELK1	MA0028.2	2.86	2.06E-03	0.82	0.80	0.07	184
GLIS2	MA0736.1	2.86	2.07E-03	0.79	0.78	0.04	184
TFAP2B(var.3)	MA0813.1	2.83	2.30E-03	0.82	0.81	0.05	184
TFAP2A(var.3)	MA0872.1	2.79	2.56E-03	0.80	0.79	0.05	184
FLI1	MA0475.2	2.79	2.59E-03	0.84	0.83	0.05	184
MZF1	MA0056.1	2.78	2.66E-03	0.97	0.96	0.04	184
ELF3	MA0640.1	2.73	3.04E-03	0.78	0.77	0.05	184
NFKB2	MA0778.1	2.72	3.19E-03	0.76	0.74	0.06	184
HIF1A	MA1106.1	2.66	3.83E-03	0.84	0.83	0.05	184
TFAP2B(var.2)	MA0812.1	2.61	4.46E-03	0.85	0.84	0.05	184
TFAP2A	MA0003.3	2.61	4.50E-03	0.87	0.86	0.05	184
IRF3	MA1418.1	2.59	4.69E-03	0.72	0.71	0.05	184
KLF9	MA1107.1	2.57	5.01E-03	0.83	0.82	0.06	184
THAP1	MA0597.1	2.52	5.80E-03	0.92	0.92	0.03	184
PLAG1	MA0163.1	2.51	5.92E-03	0.80	0.79	0.04	184
ZNF740	MA0753.1	2.51	5.93E-03	0.85	0.84	0.06	184
Ahr::Arnt	MA0006.1	2.49	6.19E-03	0.92	0.91	0.06	184
KLF4	MA0039.3	2.48	6.49E-03	0.86	0.85	0.06	184
ZBED1	MA0749.1	2.47	6.58E-03	0.71	0.70	0.05	184
ARNT::HIF1A	MA0259.1	2.44	7.13E-03	0.90	0.88	0.06	184
TFAP2C(var.2)	MA0814.1	2.44	7.18E-03	0.86	0.85	0.05	184
ETV3	MA0763.1	2.41	7.70E-03	0.85	0.84	0.05	184
ZIC1	MA0696.1	2.35	9.20E-03	0.77	0.77	0.04	184
Znf423	MA0116.1	2.33	9.61E-03	0.83	0.82	0.04	184
E2F6	MA0471.1	2.31	1.03E-02	0.89	0.88	0.05	184
PAX5	MA0014.3	2.26	1.17E-02	0.82	0.81	0.04	184
Gmeb1	MA0615.1	2.18	1.44E-02	0.82	0.81	0.04	184
IRF8	MA0652.1	2.17	1.48E-02	0.73	0.72	0.05	184
HES7	MA0822.1	2.14	1.59E-02	0.73	0.72	0.05	184
ERF	MA0760.1	2.10	1.76E-02	0.84	0.83	0.05	184
Atf1	MA0604.1	2.08	1.83E-02	0.85	0.84	0.06	184
HEY1	MA0823.1	2.08	1.84E-02	0.81	0.80	0.06	184
IRF9	MA0653.1	2.07	1.90E-02	0.70	0.70	0.06	184
HEY2	MA0649.1	2.06	1.95E-02	0.82	0.81	0.05	184
SPDEF	MA0686.1	2.05	2.00E-02	0.81	0.80	0.05	184
MTF1	MA0863.1	2.01	2.17E-02	0.73	0.73	0.04	184
Bach1::Mafk	MA0591.1	1.85	3.20E-02	0.77	0.77	0.04	184
RELA	MA0107.1	1.84	3.24E-02	0.83	0.82	0.05	184
EWSR1-FLI1	MA0149.1	1.84	3.26E-02	0.70	0.69	0.06	184
CENPB	MA0637.1	1.83	3.30E-02	0.78	0.78	0.04	184
IRF4	MA1419.1	1.80	3.55E-02	0.71	0.70	0.05	184
NR2C2	MA0504.1	1.79	3.65E-02	0.83	0.82	0.04	184
Creb3l2	MA0608.1	1.74	4.01E-02	0.84	0.83	0.06	184
TFCP2	MA0145.3	1.70	4.40E-02	0.82	0.81	0.05	184

Table S13. Transcription Factors Associated with Upregulated Proteins in Meno/Ang I.

TF_NAME	MATRIX_ID	Z_SCORE	P_VALUE	SAMPLE_AVERAGE	BACKGROUND_AVERAGE	SAMPLE_DEVSTD	SAMPLE_SIZE
KLF14	MA0740.1	4.08	2.21E-05	0.84	0.82	0.06	95
Gabpa	MA0062.2	4.07	2.22E-05	0.86	0.84	0.06	95
Gmeb1	MA0615.1	4.06	2.39E-05	0.83	0.81	0.05	95
ZBTB7A	MA0750.2	4.01	2.94E-05	0.85	0.83	0.06	95
TFDP1	MA1122.1	4.00	3.10E-05	0.87	0.84	0.06	95
Klf12	MA0742.1	3.98	3.38E-05	0.83	0.81	0.06	95
ELK1	MA0028.2	3.97	3.43E-05	0.83	0.80	0.07	95
SP4	MA0685.1	3.95	3.88E-05	0.82	0.79	0.06	95
KLF13	MA0657.1	3.89	4.79E-05	0.76	0.74	0.05	95
NRF1	MA0506.1	3.89	4.80E-05	0.86	0.83	0.07	95
SP2	MA0516.1	3.82	6.44E-05	0.89	0.87	0.06	95
ELK3	MA0759.1	3.73	9.37E-05	0.85	0.83	0.06	95
Klf1	MA0493.1	3.67	1.20E-04	0.89	0.87	0.05	95
GMEB2	MA0862.1	3.56	1.80E-04	0.83	0.81	0.06	95
E2F4	MA0470.1	3.54	1.93E-04	0.88	0.86	0.06	95
Zfx	MA0146.2	3.44	2.87E-04	0.86	0.84	0.05	95
ETV4	MA0764.1	3.41	3.22E-04	0.87	0.85	0.06	95
ELF4	MA0641.1	3.38	3.56E-04	0.80	0.78	0.06	95
ELK4	MA0076.2	3.36	3.76E-04	0.87	0.85	0.06	95
ETV5	MA0765.1	3.36	3.78E-04	0.88	0.86	0.06	95
Tcfl5	MA0632.1	3.36	3.82E-04	0.91	0.88	0.06	95
ETV3	MA0763.1	3.36	3.82E-04	0.85	0.84	0.06	95
KLF5	MA0599.1	3.27	5.28E-04	0.94	0.92	0.06	95
ZBTB33	MA0527.1	3.26	5.56E-04	0.78	0.77	0.05	95
HINFP	MA0131.2	3.23	6.02E-04	0.83	0.81	0.04	95
FEV	MA0156.2	3.18	7.16E-04	0.86	0.84	0.06	95
ERF	MA0760.1	3.14	8.18E-04	0.85	0.83	0.06	95
ETV1	MA0761.1	3.13	8.55E-04	0.86	0.84	0.06	95
ETV6	MA0645.1	3.10	9.34E-04	0.87	0.85	0.06	95
Ahr::Arnt	MA0006.1	3.00	1.31E-03	0.93	0.91	0.06	95
SP1	MA0079.3	2.97	1.48E-03	0.92	0.90	0.06	95
EGR1	MA0162.3	2.91	1.81E-03	0.77	0.75	0.05	95
HIF1A	MA1106.1	2.90	1.86E-03	0.85	0.83	0.06	95
TFAP2B(var.3)	MA0813.1	2.86	2.11E-03	0.82	0.81	0.05	95
FLI1	MA0475.2	2.77	2.78E-03	0.85	0.83	0.06	95
ELF1	MA0473.2	2.76	2.82E-03	0.80	0.78	0.06	95
KLF16	MA0741.1	2.69	3.50E-03	0.89	0.87	0.06	95
EGR2	MA0472.2	2.69	3.56E-03	0.82	0.80	0.05	95
ETS1	MA0098.3	2.68	3.63E-03	0.86	0.85	0.06	95
TFAP2C(var.3)	MA0815.1	2.68	3.67E-03	0.81	0.80	0.05	95
SP3	MA0746.1	2.67	3.78E-03	0.90	0.88	0.06	95
ZIC1	MA0696.1	2.65	3.93E-03	0.78	0.77	0.04	95
SP8	MA0747.1	2.62	4.37E-03	0.88	0.87	0.05	95
TFAP2A(var.2)	MA0810.1	2.60	4.60E-03	0.88	0.86	0.05	95
GLIS1	MA0735.1	2.57	5.07E-03	0.71	0.70	0.04	95
ERG	MA0474.2	2.56	5.17E-03	0.86	0.85	0.06	95
CENPB	MA0637.1	2.56	5.24E-03	0.79	0.78	0.03	95
EGR3	MA0732.1	2.54	5.43E-03	0.79	0.77	0.06	95
EGR4	MA0733.1	2.52	5.80E-03	0.79	0.78	0.05	95
ARNT::HIF1A	MA0259.1	2.47	6.76E-03	0.90	0.88	0.06	95
E2F1	MA0024.3	2.46	6.85E-03	0.78	0.76	0.05	95
ZIC3	MA0697.1	2.45	7.13E-03	0.79	0.78	0.04	95
TFAP2C	MA0524.2	2.44	7.20E-03	0.86	0.85	0.05	95
TFAP2B	MA0811.1	2.44	7.35E-03	0.86	0.85	0.05	95
PAX5	MA0014.3	2.34	9.67E-03	0.82	0.81	0.05	95
ZNF740	MA0753.1	2.31	1.02E-02	0.85	0.84	0.06	95
TFAP2A(var.3)	MA0872.1	2.30	1.06E-02	0.81	0.79	0.05	95
EHF	MA0598.2	2.28	1.11E-02	0.80	0.78	0.06	95
PAX1	MA0779.1	2.28	1.12E-02	0.76	0.75	0.04	95
ELF3	MA0640.1	2.25	1.21E-02	0.78	0.77	0.06	95
REL	MA0101.1	2.16	1.54E-02	0.88	0.87	0.05	95
GLIS3	MA0737.1	2.15	1.55E-02	0.75	0.74	0.04	95
ETV2	MA0762.1	2.15	1.55E-02	0.82	0.81	0.06	95
E2F3	MA0469.2	2.08	1.87E-02	0.71	0.70	0.05	95
ZIC4	MA0751.1	2.05	1.99E-02	0.81	0.80	0.04	95
Atf1	MA0604.1	2.01	2.22E-02	0.85	0.84	0.06	95
Crem	MA0609.1	1.97	2.41E-02	0.79	0.78	0.07	95
ZNF354C	MA0130.1	1.97	2.42E-02	0.97	0.96	0.03	95
Hes1	MA1099.1	1.90	2.83E-02	0.87	0.86	0.05	95
ELF5	MA0136.2	1.88	2.99E-02	0.87	0.87	0.05	95
YY2	MA0748.1	1.88	3.01E-02	0.81	0.80	0.06	95
MZF1(var.2)	MA0057.1	1.82	3.42E-02	0.91	0.91	0.03	95
E2F6	MA0471.1	1.77	3.84E-02	0.89	0.88	0.06	95
GLIS2	MA0736.1	1.69	4.49E-02	0.79	0.78	0.04	95
Arnt	MA0004.1	1.64	4.98E-02	0.87	0.86	0.07	95

Table S14. Differentially Expressed Phosphorylation Between Ang II and Control.

Accession	Sequence	Modifications	Control 1	Control 2	Control 3	Control 4	Ang II 1	Ang II 2	Ang II 3	Ang II 4	P Value	Fold Change
BNIP2_MOUSE	KGSITEYTATEEK	[3] Phospho (ST)	91535	1	109431	44813	1	1	1	1	0.05	0.00
HNRPF_MOUSE	YGDSEFTVQSTTGHCVHMR	[1] Phospho (Y)|[18] Oxidation (M)	1079	461	1322	64	1	1	108	1	0.05	0.04
CALX_MOUSE	SDAEEDGVTGSQDEEDSKPKAEEDEILNRSPR	[9] Phospho (ST)|[30] Phospho (ST)	99488	182085	17893	133444	4315	20462	19672	1	0.03	0.10
CALX_MOUSE	SDAEEDGVTGSQDEEDSKPKAEEDEILNRSPR	[11] Phospho (ST)|[30] Phospho (ST)	99488	182085	17893	133444	4315	20462	19672	1	0.03	0.10
ALDR_MOUSE	YKPAVNQIECHPYLTQEK	[1] Phospho (Y)	18231	15618	47973	51848	7818	7363	7382	15188	0.05	0.28
HCLS1_MOUSE	EYPVPSLPTRQSPLQNHLEDNEEPPALPPR	[12] Phospho (ST)	238725	763353	302900	512644	170950	167406	103517	111709	0.04	0.30
SDPR_MOUSE	SSPFKVSPLSFGR	[7] Phospho (ST)	89057	90445	121928	29783	35548	12627	46410	12450	0.04	0.32
IL16_MOUSE	NHCSSQAGQSVISLLSAEELEK	[10] Phospho (ST)	3321	2820	3750	5355	2565	1	639	2373	0.03	0.37
ALBU_MOUSE	AADKDTCFSTEGPNLVTR	[6] Phospho (ST)	606022	376437	595890	241291	152089	145318	131780	291613	0.03	0.40
HS90A_MOUSE	ESDDKPEIEDVGSDEEEEEKKDGDK	[2] Phospho (ST)	570396	675457	477587	321882	259379	205181	233562	182350	0.01	0.43
LAT_MOUSE	SPQPLGGSHR	[1] Phospho (ST)	217285	126699	135317	144310	65668	95970	113553	28956	0.03	0.49
SDPR_MOUSE	SSPFKVSPLSFGR	[1] Phospho (ST)	375729	329729	406279	222720	290916	152264	129973	125937	0.03	0.52
SDPR_MOUSE	SSPFKVSPLSFGR	[2] Phospho (ST)	375729	329729	406279	222720	290916	152264	129973	125937	0.03	0.52
SMRC2_MOUSE	GHREEEQEDLTKDMDEPSPVPNVEEVTLPK	[18] Phospho (ST)	296931	225761	236156	158244	209313	98324	57519	136692	0.05	0.55
SCRIB_MOUSE	LAEAPSPAPTPSPTPLEDFGLQTSASPGRLSPDFVEELR	[31] Phospho (ST)	416891	462717	341325	307102	232932	234542	252555	190205	0.01	0.60
FYB_MOUSE	HTFGQKPSLSTEDSQEENTSK	[10] Phospho (ST)	1048683	601112	892072	863177	630362	378159	604187	417382	0.02	0.60
FYB_MOUSE	HTFGQKPSLSTEDSQEENTSK	[11] Phospho (ST)	1048683	601112	892072	863177	630362	378159	604187	417382	0.02	0.60
GP1BA_MOUSE	RPSALSQGRGQDLLGTVGIR	[3] Phospho (ST)|[16] Phospho (ST)	15276368	11798969	18957316	8892488	8840086	9150614	8804017	6135079	0.05	0.60
RAE1_MOUSE	FNIDLVSKLLYSR	[11] Phospho (Y)	15407766	13289138	12246868	15934433	7864331	8372545	8934716	9460984	0.00	0.61
FAM21_MOUSE	GLFSDEEDSEDLFSSQSSSKPK	[9] Phospho (ST)	935607	680665	554526	596367	590864	450922	293119	386232	0.05	0.62
FAM21_MOUSE	GLFSDEEDSEDLFSSQSSSKPK	[4] Phospho (ST)	935607	680665	554526	596367	590864	450922	293119	386232	0.05	0.62
HCLS1_MOUSE	EYPVPSLPTRQSPLQNHLEDNEEPPALPPR	[12] Phospho (ST)	1196727	1205882	1342246	1309890	663965	921129	1065571	521266	0.01	0.63
RAE1_MOUSE	FNIDLVSKLLYSR	[11] Phospho (Y)	52495260	50227919	40977529	47453875	27982376	31880090	27804040	38714444	0.00	0.66
SH3K1_MOUSE	SIEVENDFLPVEK	[1] Phospho (ST)	646095	593026	640275	465167	422361	438742	402083	293135	0.01	0.66
EP15R_MOUSE	STPSHGSVSSLNSTGSLSPK	[18] Phospho (ST)	736870	571503	562670	718679	531634	448461	567281	297124	0.05	0.71
EP15R_MOUSE	STPSHGSVSSLNSTGSLSPK	[16] Phospho (ST)	736870	571503	562670	718679	531634	448461	567281	297124	0.05	0.71
FYB_MOUSE	TTAVEIDYDSLKR	[10] Phospho (ST)	3840613	3077474	3894168	3272525	4988379	4112181	4257235	3904690	0.04	1.23
MCM2_MOUSE	RISDPLTSSPGR	[3] Phospho (ST)	1479059	1189157	1294288	1175461	1610233	1779093	1647230	1378986	0.03	1.25
FYB_MOUSE	VAGQSSPSGIQSR	[5] Phospho (ST)	3726145	3530520	3567236	3668819	4790267	5216752	5009122	4084108	0.00	1.32
FYB_MOUSE	VAGQSSPSGIQSR	[6] Phospho (ST)	3726145	3530520	3567236	3668819	4790267	5216752	5009122	4084108	0.00	1.32
MCM2_MOUSE	RADALTSSPGR	[8] Phospho (ST)	945965	716385	781187	759925	1005918	1143952	987277	1178251	0.01	1.35
HCFC1_MOUSE	YDIPATAATATSPTPNPVPSVPANPPK	[14] Phospho (ST)	912098	988290	663554	690437	1119039	1207132	969882	1091335	0.02	1.35
HNRL2_MOUSE	SKSPPPPEEEAK	[3] Phospho (ST)	4730770	2598139	3867628	4422776	4876239	5483541	5914096	4899478	0.04	1.36
SP3_MOUSE	IGPPSPGDDDEEAAVAAAAGVPAAAAGATGDLASAQLGGAPNR	[5] Phospho (ST)	1249497	1478067	1058212	1040820	1660420	1947158	1702184	1351398	0.03	1.38
RBL2_MOUSE	AQPAGSPSHQIQQR	[6] Phospho (ST)	167686	91687	146681	99072	184061	196006	180280	153349	0.04	1.41
SASH3_MOUSE	SSSFKDFAK	[3] Phospho (ST)	406099	463489	694896	637422	940341	675157	841265	667835	0.05	1.42
SASH3_MOUSE	SSSFKDFAK	[1] Phospho (ST)	406099	463489	694896	637422	940341	675157	841265	667835	0.05	1.42
HNRL2_MOUSE	AVEEQGDDQDSEKSKPAGSDGERR	[11] Phospho (ST)|[14] Phospho (ST)	138781	124451	121859	109827	174873	221147	189175	122748	0.05	1.43
AB1IP_MOUSE	QGLGNHSPGATR	[7] Phospho (ST)	551041	529749	802903	585752	893944	1047158	879085	725968	0.03	1.44
ZN592_MOUSE	VLHSSNPVPLYAPNLSPPADSR	[16] Phospho (ST)	350957	218383	278803	164309	410802	354348	362210	333490	0.04	1.44
DC1L1_MOUSE	KPASVSPTTPTSPTEGEAS	[14] Phospho (ST)	832501	1321544	751496	855914	1213552	1522802	1326192	1374137	0.03	1.45
RHG01_MOUSE	SSSPEPVTHLK	[3] Phospho (ST)	1304085	2132527	1794500	1391444	2009005	2980945	2172861	2468694	0.04	1.45
PP6R1_MOUSE	NTVDLVNTHHLHSSSDDEDDRLK	[15] Phospho (ST)	1862514	1539206	1925743	1328080	2437431	2850732	2807015	1664841	0.05	1.47
HNRL2_MOUSE	AVEEQGDDQDSEKSKPAGSDGER	[11] Phospho (ST)	542432	481573	437459	413079	690406	827806	778690	454450	0.05	1.47
SP3_MOUSE	IGPPSPGDDDEEAAVAAAAGVPAAAAGATGDLASAQLGGAPNR	[5] Phospho (ST)	513460	607052	375988	325094	697340	782663	654419	557431	0.03	1.48
TIF1B_MOUSE	SGEGEVSGLLR	[1] Phospho (ST)	366788	443575	535945	379973	531386	784964	736117	503502	0.04	1.48
NFAC2_MOUSE	SLSPGLLGYQQPSLLAAPLGLADAHR	[1] Phospho (ST)	673717	637074	540776	532882	895414	943390	979381	722605	0.00	1.48
NFAC2_MOUSE	SLSPGLLGYQQPSLLAAPLGLADAHR	[3] Phospho (ST)	673717	637074	540776	532882	895414	943390	979381	722605	0.00	1.48
NFAC2_MOUSE	DAGLSPEQPALALAGVAASPR	[5] Phospho (ST)	599678	560710	484455	501820	817769	958443	770627	642408	0.01	1.49
RGS18_MOUSE	SRSFTYNDFQDVK	[3] Phospho (ST)	1381966	945252	1381657	1427170	2096462	2006908	1738011	1813668	0.00	1.49
RGS18_MOUSE	SRSFTYNDFQDVK	[5] Phospho (ST)	1381966	945252	1381657	1427170	2096462	2006908	1738011	1813668	0.00	1.49
RGS18_MOUSE	SRSFTYNDFQDVK	[1] Phospho (ST)	1381966	945252	1381657	1427170	2096462	2006908	1738011	1813668	0.00	1.49
41_MOUSE	SLDGAAAAESTDRSPRPTSAPAIAQSQVTEGPGAPIKK	[1] Phospho (ST)	377412	344025	303201	364676	553180	607752	583123	327800	0.04	1.49
41_MOUSE	SLDGAAAAESTDRSPRPTSAPAIAQSQVTEGPGAPIKK	[10] Phospho (ST)	377412	344025	303201	364676	553180	607752	583123	327800	0.04	1.49
TIF1B_MOUSE	SRSGEGEVSGLLR	[3] Phospho (ST)	2632107	3553011	4025842	2797819	3956864	5930257	5377119	4189782	0.03	1.50
TIF1B_MOUSE	SRSGEGEVSGLLR	[1] Phospho (ST)	2632107	3553011	4025842	2797819	3956864	5930257	5377119	4189782	0.03	1.50
MILK1_MOUSE	KPSPSASPTVR	[3] Phospho (ST)	164614	76730	132914	140592	179075	189858	198417	203275	0.02	1.50
REPS1_MOUSE	RQSSSYEDPWK	[3] Phospho (ST)	423940	322874	463508	477653	590959	626295	751212	576390	0.01	1.51
HCFC1_MOUSE	TITLVKSPISVPGGSALISNLGK	[7] Phospho (ST)	1327944	1215292	908271	789607	1498162	2048676	1454365	1397917	0.03	1.51
HCFC1_MOUSE	TITLVKSPISVPGGSALISNLGK	[3] Phospho (ST)	1327944	1215292	908271	789607	1498162	2048676	1454365	1397917	0.03	1.51
PACS1_MOUSE	ADLQGSASPSKVEGTHTPR	[8] Phospho (ST)	125766	81131	77085	71986	140884	146096	143943	113412	0.02	1.53
PACS1_MOUSE	ADLQGSASPSKVEGTHTPR	[6] Phospho (ST)	125766	81131	77085	71986	140884	146096	143943	113412	0.02	1.53

BIN2_MOUSE	ASPDASSNPEPAETR	[2] Phospho (ST)	550159	652455	775773	755305	1114173	933474	1292575	842792	0.02	1.53
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAERSPSQEPSAPGK	[23] Phospho (ST)	161934	199719	272675	127202	314323	258961	329392	266863	0.03	1.54
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAERSPSQEPSAPGK	[29] Phospho (ST)	161934	199719	272675	127202	314323	258961	329392	266863	0.03	1.54
ZCCHV_MOUSE	LPPSPLSSSTSHR	[4] Phospho (ST)	124465	85817	95511	76090	151767	142242	139524	156494	0.00	1.55
RGS18_MOUSE	SRSFTYNDFQDVK	[3] Phospho (ST)	1269875	745493	1160136	1068756	1669645	1814769	1444470	1694007	0.00	1.56
RGS18_MOUSE	SRSFTYNDFQDVK	[5] Phospho (ST)	1269875	745493	1160136	1068756	1669645	1814769	1444470	1694007	0.00	1.56
RGS18_MOUSE	SRSFTYNDFQDVK	[1] Phospho (ST)	1269875	745493	1160136	1068756	1669645	1814769	1444470	1694007	0.00	1.56
EDC4_MOUSE	DSQDTSAEQSDHDDEVASLASASGGFGSK	[10] Phospho (ST)	807283	670725	1262933	628552	1390167	1606359	1309821	992336	0.05	1.57
EDC4_MOUSE	DSQDTSAEQSDHDDEVASLASASGGFGSK	[6] Phospho (ST)	807283	670725	1262933	628552	1390167	1606359	1309821	992336	0.05	1.57
EDC4_MOUSE	DSQDTSAEQSDHDDEVASLASASGGFGSK	[2] Phospho (ST)	807283	670725	1262933	628552	1390167	1606359	1309821	992336	0.05	1.57
ARHG2_MOUSE	LQDSSDPDTGSEEEVSSRLSPPHSPR	[20] Phospho (ST)	474981	292297	565964	353331	812074	616172	685732	541167	0.03	1.57
ARHG2_MOUSE	LQDSSDPDTGSEEEVSSRLSPPHSPR	[16] Phospho (ST)	474981	292297	565964	353331	812074	616172	685732	541167	0.03	1.57
ERCC5_MOUSE	VKPEREPEAAPPSPR	[13] Phospho (ST)	376329	418639	398297	321739	597297	585144	734397	471463	0.01	1.58
ASAP1_MOUSE	SHTGDLSPNVQSR	[7] Phospho (ST)	211665	73663	181128	132889	268886	241106	229434	206240	0.04	1.58
CHAP1_MOUSE	EQPSKDTESGKSPSPPER	[12] Phospho (ST)	225208	171092	183386	207863	339335	317265	350083	250315	0.00	1.60
CHAP1_MOUSE	EQPSKDTESGKSPSPPER	[7] Phospho (ST)	225208	171092	183386	207863	339335	317265	350083	250315	0.00	1.60
BC11B_MOUSE	ELAGNSSTPPPVSPGR	[13] Phospho (ST)	142932	104493	168620	180150	256377	287850	229097	180521	0.02	1.60
AP3B1_MOUSE	NFYESEEEEEEKEK	[5] Phospho (ST)	186104	255957	211502	168880	350053	373711	297760	303549	0.00	1.61
LS14A_MOUSE	SSPQLDPLRKSPTMEQAVQTASAHLPAPAPVGR	[2] Phospho (ST)|[11] Phospho (ST)|[14] Oxidation (M)	715355	880338	942721	726834	1205688	1309765	1406905	1341287	0.00	1.61
LS14A_MOUSE	SSPQLDPLRKSPTMEQAVQTASAHLPAPAPVGR	[11] Phospho (ST)|[13] Phospho (ST)|[14] Oxidation (M)	715355	880338	942721	726834	1205688	1309765	1406905	1341287	0.00	1.61
ACTB_MOUSE	EKLCYVALDFEQEMATAASSSSLEK	[14] Oxidation (M)|[16] Phospho (ST)	1199985	975415	1053352	1762257	2349069	2484632	1515898	1706044	0.04	1.61
MCM3_MOUSE	RYSDLTTLVAFPSSSVYPTKDEENNPLETEYGLSVYK	[3] Phospho (ST)	314021	451052	610064	318573	611088	862101	598614	668651	0.03	1.62
MAP1S_MOUSE	KPPPPASPGSSDSSAR	[7] Phospho (ST)	226119	134328	183743	149442	278439	291334	325111	259267	0.00	1.66
FA65B_MOUSE	SQSFAGFSGLQER	[3] Phospho (ST)	191765	200082	125959	148388	350224	279618	218434	279878	0.01	1.69
FA65B_MOUSE	SQSFAGFSGLQER	[1] Phospho (ST)	191765	200082	125959	148388	350224	279618	218434	279878	0.01	1.69
CORO7_MOUSE	ADTDLSEGFSSPSSLMSPSTPSSLGPSLSSTSGIGTSPSQR	[11] Phospho (ST)|[16] Oxidation (M)	120983	66130	83204	90499	116241	140907	182878	185367	0.02	1.73
CORO7_MOUSE	ADTDLSEGFSSPSSLMSPSTPSSLGPSLSSTSGIGTSPSQR	[16] Oxidation (M)|[23] Phospho (ST)	120983	66130	83204	90499	116241	140907	182878	185367	0.02	1.73
BC11B_MOUSE	VLDKSSPPPSSR	[5] Phospho (ST)	293504	198810	311146	343029	483889	623935	504598	376331	0.01	1.73
BC11B_MOUSE	VLDKSSPPPSSR	[6] Phospho (ST)	293504	198810	311146	343029	483889	623935	504598	376331	0.01	1.73
GMIP_MOUSE	DLSPEGPAPLTEEELDLR	[3] Phospho (ST)	136870	104898	113154	87753	172626	240136	212486	144115	0.01	1.74
HMHA1_MOUSE	ESHAASNDSDSELEDASDPLSSSDASALHR	[9] Phospho (ST)	308117	271807	288291	270374	496503	461576	701122	366207	0.02	1.78
HMHA1_MOUSE	ESHAASNDSDSELEDASDPLSSSDASALHR	[11] Phospho (ST)	308117	271807	288291	270374	496503	461576	701122	366207	0.02	1.78
HMHA1_MOUSE	ESHAASNDSDSELEDASDPLSSSDASALHR	[6] Phospho (ST)	308117	271807	288291	270374	496503	461576	701122	366207	0.02	1.78
ARHG2_MOUSE	SLPAGDALYLSFNPPQPSR	[1] Phospho (ST)	32634	48040	54230	54388	67259	97016	87687	86202	0.00	1.79
SRRT_MOUSE	TQLWASEPGTPPVPTSLPSQNPILK	[10] Phospho (ST)	577143	129466	555729	448960	673834	1001129	878004	571554	0.05	1.83
SRRT_MOUSE	TQLWASEPGTPPVPTSLPSQNPILK	[6] Phospho (ST)	577143	129466	555729	448960	673834	1001129	878004	571554	0.05	1.83
CHAP1_MOUSE	EQPSKDTESGKSPSPPER	[12] Phospho (ST)	16277	7306	13480	6606	16325	23514	19951	20446	0.02	1.84
CHAP1_MOUSE	EQPSKDTESGKSPSPPER	[7] Phospho (ST)	16277	7306	13480	6606	16325	23514	19951	20446	0.02	1.84
PACS1_MOUSE	VGLVEDSPSTAGDGDDSPVVSLTVPSTSPPSSSGLSR	[28] Phospho (ST)	308614	132006	235462	152367	411620	436102	396324	278819	0.02	1.84
GDIB_MOUSE	AYDATTHFETTCDDIKDIYKR	[6] Phospho (ST)	257582	376955	591956	405299	1112767	752239	610429	547887	0.05	1.85
GDIB_MOUSE	AYDATTHFETTCDDIKDIYKR	[5] Phospho (ST)	257582	376955	591956	405299	1112767	752239	610429	547887	0.05	1.85
RU17_MOUSE	YDERPGPSPLPHR	[8] Phospho (ST)	2293412	1868696	1791183	135741	2464789	3186084	3360991	2278554	0.05	1.85
ACINU_MOUSE	SLSPLSGTTDTKAESPAGR	[1] Phospho (ST)|[15] Phospho (ST)	572228	421102	780044	1005303	1214205	1453881	1228048	1269807	0.01	1.86
RBM25_MOUSE	LGASNSPGQPNSVKR	[6] Phospho (ST)	170478	72937	217782	236126	342250	367620	371795	222891	0.02	1.87
RBM25_MOUSE	LGASNSPGQPNSVKR	[4] Phospho (ST)	170478	72937	217782	236126	342250	367620	371795	222891	0.02	1.87
CLIP1_MOUSE	TASESISNLSEAGSVK	[5] Phospho (ST)	645604	331696	812562	834044	1240972	1380459	1470387	857581	0.02	1.89
AP3B1_MOUSE	EDGGLEDNEKNFYESEEEEEEKEK	[15] Phospho (ST)	202504	287536	359915	235224	577951	607044	591641	292921	0.02	1.91
AP3B1_MOUSE	EDGGLEDNEKNFYESEEEEEEKEK	[15] Phospho (ST)	281633	364554	431963	209822	552981	886118	631957	400675	0.04	1.92
XRN2_MOUSE	KAEDSDSEPEPEDNVR	[5] Phospho (ST)|[7] Phospho (ST)	212479	212594	535321	341989	557883	861977	660535	437265	0.04	1.93
HDGR2_MOUSE	GGSSEELHDSPR	[10] Phospho (ST)	85191	47078	83994	82617	142033	150885	140084	147165	0.00	1.94
HDGR2_MOUSE	GGSSEELHDSPR	[4] Phospho (ST)	85191	47078	83994	82617	142033	150885	140084	147165	0.00	1.94
GP1BB_MOUSE	ARSIQEFSLTAPLVAESAR	[3] Phospho (ST)	9340792	13798070	5289588	10352312	11448724	20302365	18081696	26874093	0.04	1.98
HMHA1_MOUSE	KGSFNPGDASGPEAAGSPPEEGGTSEAAPNKDHR	[17] Phospho (ST)	610215	461691	475145	428220	968395	939542	1289983	799051	0.00	2.02
AGFG1_MOUSE	GTPSQSPVVGR	[6] Phospho (ST)	36794	65525	57689	140792	157423	131826	188491	148687	0.02	2.08
ACINU_MOUSE	KISVVSATK	[3] Phospho (ST)	737401	578226	718418	896996	1619175	1928930	1191878	1396806	0.00	2.09
HNRPU_MOUSE	EKPYFPIPEDCTFIQNVPLEDR	[12] Phospho (ST)	215006	202810	280220	392292	393042	875536	488425	531748	0.04	2.10
HNRPU_MOUSE	EKPYFPIPEDCTFIQNVPLEDR	[4] Phospho (Y)	215006	202810	280220	392292	393042	875536	488425	531748	0.04	2.10
H12_MOUSE	KASGPPVSELITK	[3] Phospho (ST)	5471508	8127800	7531184	5451158	16734577	13451970	8225974	18370664	0.02	2.14
H13_MOUSE	KASGPPVSELITK	[3] Phospho (ST)	5471508	8127800	7531184	5451158	16734577	13451970	8225974	18370664	0.02	2.14
MA7D1_MOUSE	RSSQPSPTTVPASDSPPAK	[3] Phospho (ST)	33054	7047	18977	12297	43988	21487	47844	39737	0.05	2.14
PDS5A_MOUSE	AAGSQESLEAGNAK	[4] Phospho (ST)	94861	23146	45848	28778	102821	125382	102473	83573	0.02	2.15
MK14_MOUSE	DLKPSNLAVNEDCELK	[5] Phospho (ST)	15866	80198	103062	77841	186304	183200	107975	120174	0.03	2.16
IWS1_MOUSE	RLSSTGGQTPR	[3] Phospho (ST)	233778	199531	206158	240541	443816	565086	445624	445896	0.00	2.16
CPZIP_MOUSE	LQANLAFDPAALLPGASPK	[17] Phospho (ST)	19361	24985	18296	20429	29908	64355	43513	42068	0.02	2.16
FLNA_MOUSE	LTVSSLQESGLK	[5] Phospho (ST)	430376	56967	214401	271052	720822	456971	332616	596481	0.05	2.17
TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[3] Phospho (ST)	1661473	51763	814761	917455	1876765	2523934	1696395	1377146	0.05	2.17

TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[2] Phospho (ST)	1661473	51763	814761	917455	1876765	2523934	1696395	1377146	0.05	2.17
TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[4] Phospho (ST)	1661473	51763	814761	917455	1876765	2523934	1696395	1377146	0.05	2.17
SET_MOUSE	SASPGLPKGEK	[3] Phospho (ST)	102343	95534	137156	131392	130891	390342	240231	255045	0.04	2.18
H12_MOUSE	RKASGPPVSELITK	[4] Phospho (ST)	2629170	4552797	2504055	2635847	8019657	7373851	4453985	7354013	0.01	2.21
H13_MOUSE	RKASGPPVSELITK	[4] Phospho (ST)	2629170	4552797	2504055	2635847	8019657	7373851	4453985	7354013	0.01	2.21
PP1RA_MOUSE	VLSPTAAKPSPFEGK	[3] Phospho (ST)	72621	100706	200063	122018	203526	406783	271235	216719	0.03	2.22
HDGR2_MOUSE	GGSSGEELEDEEPVK	[3] Phospho (ST)|[4] Phospho (ST)	220978	212457	525196	338282	611838	964472	852282	464590	0.03	2.23
EF1A1_MOUSE	SGDAAIVDMVPGKPMCVESFSDYPPLGR	[1] Phospho (ST)|[9] Oxidation (M)|[15] Oxidation (M)	1338928	685877	1334070	1127072	3425391	3035221	901435	2672403	0.05	2.24
IWS1_MOUSE	RLSSTGGQTPR	[3] Phospho (ST)|[4] Phospho (ST)	66690	4789	60220	58654	120223	87687	111410	109542	0.01	2.25
IWS1_MOUSE	RLSSTGGQTPR	[3] Phospho (ST)|[9] Phospho (ST)	66690	4789	60220	58654	120223	87687	111410	109542	0.01	2.25
ACTB_MOUSE	EKLCYVALDFEQEMATAASSSSLEK	[14] Oxidation (M)|[16] Phospho (ST)	103740	38787	34614	112900	198834	172956	113943	168509	0.02	2.26
ACTB_MOUSE	EKLCYVALDFEQEMATAASSSSLEK	[5] Phospho (Y)|[14] Oxidation (M)	103740	38787	34614	112900	198834	172956	113943	168509	0.02	2.26
ACTG_MOUSE	EKLCYVALDFEQEMATAASSSSLEK	[14] Oxidation (M)|[16] Phospho (ST)	103740	38787	34614	112900	198834	172956	113943	168509	0.02	2.26
ACTG_MOUSE	EKLCYVALDFEQEMATAASSSSLEK	[5] Phospho (Y)|[14] Oxidation (M)	103740	38787	34614	112900	198834	172956	113943	168509	0.02	2.26
RHG25_MOUSE	SKDAPISPPAQK	[7] Phospho (ST)	64058	98324	72590	42768	201780	166358	212736	57623	0.05	2.30
GMIP_MOUSE	DLSPEGPAPLTEEELDLR	[3] Phospho (ST)	51778	14504	45787	33894	72574	103343	113360	47824	0.03	2.31
EH1L1_MOUSE	GQGSEPAAITGGQVGPETPEPPPSPPETR	[24] Phospho (ST)	656795	2348079	3917679	1969783	6916341	5256341	4784222	3622845	0.02	2.31
KRI1_MOUSE	YVDEDNSDGETVDHR	[7] Phospho (ST)	137994	3313	146140	141146	277117	302398	258973	155332	0.02	2.32
H14_MOUSE	KTSGPPVSELITK	[3] Phospho (ST)	584391	1012525	651087	581250	2001553	1790211	865890	1910754	0.02	2.32
FA65B_MOUSE	GHLSEALTEDTGVGTSVAGSPLPLTTGNESLDITIVK	[15] Phospho (ST)|[16] Phospho (ST)	11541	9139	48917	59826	83937	66270	77523	75445	0.02	2.34
EF1A1_MOUSE	SGDAAIVDMVPGKPMCVESFSDYPPLGR	[1] Phospho (ST)|[9] Oxidation (M)	434721	332104	571184	410623	1463360	1455566	536042	798747	0.04	2.43
XRN2_MOUSE	NSPGCQVASNPR	[2] Phospho (ST)	4601	3468	6553	3239	9047	16355	9580	8493	0.02	2.43
TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENREEK	[7] Phospho (ST)|[18] Phospho (ST)	222172	145321	395355	522199	925620	1024778	735706	496522	0.02	2.48
TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENREEK	[7] Phospho (ST)|[20] Phospho (ST)	222172	145321	395355	522199	925620	1024778	735706	496522	0.02	2.48
LS14A_MOUSE	SSPQLDPLRKSPTMEQAVQTASAHLPAPAPVGR	[2] Phospho (ST)|[13] Phospho (ST)|[14] Oxidation (M)	131560	360630	370694	96663	732273	271162	613244	802118	0.04	2.52
LS14A_MOUSE	SSPQLDPLRKSPTMEQAVQTASAHLPAPAPVGR	[2] Phospho (ST)|[11] Phospho (ST)|[14] Oxidation (M)	131560	360630	370694	96663	732273	271162	613244	802118	0.04	2.52
LS14A_MOUSE	SSPQLDPLRKSPTMEQAVQTASAHLPAPAPVGR	[11] Phospho (ST)|[13] Phospho (ST)|[14] Oxidation (M)	131560	360630	370694	96663	732273	271162	613244	802118	0.04	2.52
ARHG2_MOUSE	EAQELGSPEDR	[7] Phospho (ST)	57454	82484	60831	7938	140686	109788	132595	143362	0.00	2.52
ACINU_MOUSE	SLSPLSGTTDTKAESPAGR	[1] Phospho (ST)|[15] Phospho (ST)	199280	35487	408347	403970	802123	723532	679229	443419	0.01	2.53
TWF1_MOUSE	YLLSQSSPAPLTAAEEELR	[7] Phospho (ST)	2533	137677	163475	97170	391586	133346	226920	264783	0.05	2.54
TWF1_MOUSE	YLLSQSSPAPLTAAEEELR	[1] Phospho (Y)	2533	137677	163475	97170	391586	133346	226920	264783	0.05	2.54
SIPA1_MOUSE	SGSDAGEVRPPTPASPR	[15] Phospho (ST)	24437	16944	23872	32494	56186	78131	62355	56125	0.00	2.59
H14_MOUSE	RKTSGPPVSELITK	[4] Phospho (ST)	1034953	2082815	834938	1042016	4147915	3549797	1971154	3260323	0.01	2.59
XRN2_MOUSE	NSSPSISPNTSFASDGSPSPLGGIK	[2] Phospho (ST)	4946	11043	8657	9254	23788	34292	7850	23230	0.05	2.63
ATX2L_MOUSE	LSLTPTDVK	[4] Phospho (ST)	28818	7685	27837	11843	46753	45575	56694	54420	0.00	2.67
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[23] Phospho (ST)|[24] Phospho (ST)	36578	42158	78112	61511	138225	166160	178955	102888	0.00	2.68
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[15] Phospho (ST)|[18] Phospho (ST)	36578	42158	78112	61511	138225	166160	178955	102888	0.00	2.68
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[18] Phospho (ST)|[23] Phospho (ST)	36578	42158	78112	61511	138225	166160	178955	102888	0.00	2.68
SET_MOUSE	SASPGLPKGEK	[3] Phospho (ST)	16337	29573	28634	39684	40784	119752	75945	70731	0.03	2.69
CD11B_MOUSE	AYTPVVVTLWYR	[3] Phospho (ST)	13937	35837	33680	59843	121497	88514	93727	81778	0.00	2.69
RANB3_MOUSE	SPSESAEETHTLEEK	[3] Phospho (ST)	8004	17691	26313	13776	31481	68898	43135	33699	0.03	2.69
RANB3_MOUSE	SPSESAEETHTLEEK	[1] Phospho (ST)	8004	17691	26313	13776	31481	68898	43135	33699	0.03	2.69
ICAL_MOUSE	KEQKPFTPASPVQSTPSKPSDK	[10] Phospho (ST)	23961	2910	33805	7967	51572	54692	53052	26921	0.02	2.71
PML_MOUSE	ATSPPHLDGTSNPESTVPEKK	[3] Phospho (ST)	106054	6752	81623	19767	198664	147470	169075	67194	0.05	2.72
FA65B_MOUSE	GHLSEALTEDTGVGTSVAGSPLPLTTGNESLDITIVK	[16] Phospho (ST)|[20] Phospho (ST)	13581	24232	92562	78924	177363	143723	108459	146005	0.01	2.75
AN32A_MOUSE	SLDLFNCEVTNLNAYR	[1] Phospho (ST)	56936	587212	335605	385590	726707	1393333	851681	822006	0.02	2.78
CCD43_MOUSE	AALLAQYADVTDEEDEADKKDDAGASTANVSSDR	[11] Phospho (ST)	120925	34474	439110	156702	379626	520121	669000	538342	0.02	2.80
CCD43_MOUSE	AALLAQYADVTDEEDEADKKDDAGASTANVSSDR	[7] Phospho (Y)	120925	34474	439110	156702	379626	520121	669000	538342	0.02	2.80
FAM21_MOUSE	ARPAQAPVSEELPPSPKPGK	[15] Phospho (ST)	108780	203308	1088433	773400	1129616	1595119	2469819	1009614	0.05	2.85
TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENREEK	[7] Phospho (ST)	83206	10038	140198	204556	326987	449179	295445	180682	0.03	2.86
IF4G1_MOUSE	SFSKEVEER	[3] Phospho (ST)	9004	1572	288292	217475	447150	387375	271183	387917	0.02	2.89
PTPRC_MOUSE	RSSNLDEQQELVERDDEK	[3] Phospho (ST)	3960	9544	421446	244206	574414	588271	474883	352304	0.03	2.93
H12_MOUSE	RKASGPPVSELITK	[4] Phospho (ST)	67105	159051	27399	96799	331249	362267	166705	167634	0.03	2.93
H13_MOUSE	RKASGPPVSELITK	[4] Phospho (ST)	67105	159051	27399	96799	331249	362267	166705	167634	0.03	2.93
PSIP1_MOUSE	ETNVSKEDTDQEEKASNEDVTK	[2] Phospho (ST)|[16] Phospho (ST)	24532	40822	48511	84826	89501	186538	177367	143098	0.01	3.00
USO1_MOUSE	LKDLGHPVEEEDESGDQEDDDDEIDDGDKDQDI	[14] Phospho (ST)	90800	44890	1300661	1081588	2513531	2044951	1587363	1513870	0.02	3.04
TR150_MOUSE	KSPVGKSPPATGSAYGSSQK	[7] Phospho (ST)	129541	11324	154347	245264	544999	540029	333271	270448	0.02	3.12
TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENR	[7] Phospho (ST)	32408	40346	108563	124341	350612	263851	246100	145378	0.01	3.29
KRI1_MOUSE	YVDEDNSDGETVDHR	[7] Phospho (ST)	28419	1	32852	32494	112290	98802	71878	51667	0.01	3.57
XPC_MOUSE	KSSKETSVEGPGGSSELSSNSPESHNKPTTSR	[6] Phospho (ST)	33658	1	32782	19074	70549	106419	89695	42254	0.01	3.61
XPC_MOUSE	KSSKETSVEGPGGSSELSSNSPESHNKPTTSR	[2] Phospho (ST)	33658	1	32782	19074	70549	106419	89695	42254	0.01	3.61
XPC_MOUSE	KSSKETSVEGPGGSSELSSNSPESHNKPTTSR	[3] Phospho (ST)	33658	1	32782	19074	70549	106419	89695	42254	0.01	3.61
HN1_MOUSE	SNSSEASSGDFLDLK	[3] Phospho (ST)	247201	321018	164967	106608	626459	1012662	1078311	368838	0.02	3.68
HN1_MOUSE	SNSSEASSGDFLDLK	[4] Phospho (ST)	247201	321018	164967	106608	626459	1012662	1078311	368838	0.02	3.68
PININ_MOUSE	RGFSDSGGGPPAK	[4] Phospho (ST)	80341	14584	120301	217541	371211	613417	361123	267511	0.01	3.73
TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENREEK	[7] Phospho (ST)|[18] Phospho (ST)	46213	8868	130463	136515	381415	384720	255303	185643	0.01	3.75

TR150_MOUSE	WAHDKFSGEEGEIEDDESGTENREEK	[7] Phospho (ST)|[20] Phospho (ST)	46213	8868	130463	136515	381415	384720	255303	185643	0.01	3.75
DAXX_MOUSE	RNSEPAEGLR	[3] Phospho (ST)	49712	58732	85332	104634	259175	320056	298429	262922	0.00	3.82
NFRKB_MOUSE	KGSLAALYDLAVLK	[3] Phospho (ST)	9671	1826	8043	13990	25253	51141	34463	19954	0.02	3.90
PININ_MOUSE	SLSPGKENINSQEVEK	[3] Phospho (ST)	120460	131402	171206	291022	643942	959181	656205	565193	0.00	3.96
PININ_MOUSE	SLSPGKENINSQEVEK	[1] Phospho (ST)	120460	131402	171206	291022	643942	959181	656205	565193	0.00	3.96
HACD3_MOUSE	WLDESDAEMELR	[5] Phospho (ST)|[9] Oxidation (M)	64169	24133	61437	88947	248909	273686	53508	370267	0.04	3.96
CRTC1_MOUSE	TNSDSALHQSTMTPSQAESFTGGSQDAHQK	[5] Phospho (ST)|[12] Oxidation (M)	18416	1640	15340	1	42924	51344	39896	8430	0.04	4.03
CRTC1_MOUSE	TNSDSALHQSTMTPSQAESFTGGSQDAHQK	[12] Oxidation (M)|[13] Phospho (ST)	18416	1640	15340	1	42924	51344	39896	8430	0.04	4.03
CHAP1_MOUSE	KTSPASLDFPEPQK	[3] Phospho (ST)	5058	26532	56112	28849	144132	125244	123580	103220	0.00	4.26
PRP4B_MOUSE	EVIEASDKEGLSPAKR	[12] Phospho (ST)	7376	5338	86145	76602	232916	266853	190332	190154	0.00	5.02
SPT5H_MOUSE	SAAGSEKEEEPEEEEEEEEEYDEEEEEEDDDRPPKKPR	[1] Phospho (ST)|[5] Phospho (ST)	206925	1	187742	227695	1336255	411129	883102	519683	0.03	5.06
SMC3_MOUSE	KGDVEGSQSQDEGEGSGESER	[9] Phospho (ST)	3631	4053	16149	18887	54845	65301	74833	26710	0.01	5.19
SMC3_MOUSE	KGDVEGSQSQDEGEGSGESER	[7] Phospho (ST)	3631	4053	16149	18887	54845	65301	74833	26710	0.01	5.19
PININ_MOUSE	EAGIVHSDAEKEQEEEEQK	[7] Phospho (ST)	19135	0	43666	65806	188010	137292	236204	116586	0.00	5.27
CDK12_MOUSE	LYNSEESRPYTNK	[11] Phospho (ST)	23867	54135	66973	15718	222018	345488	122402	215292	0.01	5.63
TR150_MOUSE	SPVGKSPPATGSAYGSSQK	[6] Phospho (ST)	5042	6875	20481	48195	147291	192302	65159	55580	0.03	5.71
TR150_MOUSE	SPVGKSPPATGSAYGSSQK	[1] Phospho (ST)	5042	6875	20481	48195	147291	192302	65159	55580	0.03	5.71
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[15] Phospho (ST)|[18] Phospho (ST)	3899	13046	12686	19606	70746	67552	87354	58949	0.00	5.78
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[18] Phospho (ST)|[23] Phospho (ST)	3899	13046	12686	19606	70746	67552	87354	58949	0.00	5.78
CHAP1_MOUSE	HSSFADTGAAPSALSPESPVLATSPEPWGPSLSASPESR	[12] Phospho (ST)|[15] Phospho (ST)	3899	13046	12686	19606	70746	67552	87354	58949	0.00	5.78
AN32B_MOUSE	SLDLFGCEVTNR	[1] Phospho (ST)	2891	54253	19096	58062	167711	258189	127326	225461	0.00	5.80
ABCF1_MOUSE	SKPAAADSEGEEEEEDTAK	[8] Phospho (ST)	17672	44713	63271	82346	347449	365911	382840	121230	0.01	5.85
CD11B_MOUSE	GTSPRPPEGGLGYSQLGDDDLKETGFHLTTTNQGASAAGPGFSLK	[3] Phospho (ST)	14724	7233	93264	54588	169029	501735	191745	156446	0.05	6.00
EVL_MOUSE	SPEAKSPLQSQPHSR	[6] Phospho (ST)	2623	15313	2911	10668	41573	43383	57836	58205	0.00	6.38
ABCF1_MOUSE	SKPAAADSEGEEEEEDTAKEKEPPQQGK	[8] Phospho (ST)	14323	535	94616	86150	374902	456513	488332	58798	0.03	7.05
TR150_MOUSE	ERSPALKSPLQSVVVR	[3] Phospho (ST)|[8] Phospho (ST)	13010	5333	23525	29985	143420	207624	86209	83548	0.01	7.25
PININ_MOUSE	EAGIVHSDAEKEQEEEEQKQEMEVK	[7] Phospho (ST)|[22] Oxidation (M)	1	1	15794	48112	197663	69906	105653	139356	0.01	8.02
PININ_MOUSE	EAGIVHSDAEKEQEEEEQKQEMEVK	[7] Phospho (ST)	21806	19814	52906	50543	348168	410249	381676	137152	0.00	8.80
LA_MOUSE	SPSRPLPEVTDEYKNDVK	[3] Phospho (ST)	804	1	24194	152	82535	1301	87902	86506	0.04	10.27
PININ_MOUSE	SLSPGKENINSQEVEKESEEK	[3] Phospho (ST)	1450	1	6660	16667	98457	34508	97795	60122	0.01	11.74
PININ_MOUSE	SLSPGKENINSQEVEKESEEK	[1] Phospho (ST)	1450	1	6660	16667	98457	34508	97795	60122	0.01	11.74
FBRL_MOUSE	RVSISEGDDKIEYR	[3] Phospho (ST)	500	640	2711	831	15364	30229	22531	8589	0.01	16.38

Table S15. Biological Processes Associated with Proteins with Upregulated Phosphorylation in Ang II vs. Control.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190429)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (92)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
histone H3-K27 trimethylation (GO:0098532)	8	3	0.03	+	90.88	1.08E-05	3.39E-03
histone H3-K27 methylation (GO:0070734)	11	3	0.05	+	66.09	2.37E-05	6.08E-03
histone H3-K4 trimethylation (GO:0080182)	16	3	0.07	+	45.44	6.20E-05	1.12E-02
nucleosome positioning (GO:0016584)	17	3	0.07	+	42.77	7.28E-05	1.25E-02
negative regulation of chromatin silencing (GO:0031936)	19	3	0.08	+	38.27	9.77E-05	1.55E-02
regulation of mitotic spindle assembly (GO:1901673)	21	3	0.09	+	34.62	1.28E-04	1.82E-02
regulation of chromatin silencing (GO:0031935)	37	4	0.15	+	26.20	2.41E-05	6.09E-03
regulation of spindle assembly (GO:0090169)	28	3	0.12	+	25.97	2.78E-04	3.40E-02
chromosome condensation (GO:0030261)	40	4	0.17	+	24.23	3.20E-05	7.06E-03
peptidyl-lysine trimethylation (GO:0018023)	30	3	0.12	+	24.23	3.35E-04	3.98E-02
histone H3-K4 methylation (GO:0051568)	31	3	0.13	+	23.45	3.66E-04	4.19E-02
positive regulation of protein import into nucleus (GO:0042307)	42	4	0.17	+	23.08	3.82E-05	7.98E-03
positive regulation of gene expression, epigenetic (GO:0045815)	32	3	0.13	+	22.72	4.00E-04	4.35E-02
cellular response to virus (GO:0098586)	32	3	0.13	+	22.72	4.00E-04	4.38E-02
regulation of viral release from host cell (GO:1902186)	32	3	0.13	+	22.72	4.00E-04	4.41E-02
regulation of cell cycle checkpoint (GO:1901976)	32	3	0.13	+	22.72	4.00E-04	4.44E-02
positive regulation of protein import (GO:1904591)	47	4	0.19	+	20.63	5.76E-05	1.06E-02
nucleosome assembly (GO:0006334)	75	6	0.31	+	19.39	1.03E-06	6.24E-04
regulation of protein import into nucleus (GO:0042306)	61	4	0.25	+	15.89	1.49E-04	2.07E-02
chromatin assembly (GO:0031497)	94	6	0.39	+	15.47	3.57E-06	1.43E-03
positive regulation of nucleocytoplasmic transport (GO:0046824)	63	4	0.26	+	15.39	1.68E-04	2.29E-02
regulation of gene silencing (GO:0060968)	82	5	0.34	+	14.78	2.97E-05	7.07E-03
regulation of protein import (GO:1904589)	66	4	0.27	+	14.69	1.99E-04	2.67E-02
regulation of mRNA processing (GO:0050684)	143	8	0.59	+	13.56	2.05E-07	2.14E-04
negative regulation of chromosome organization (GO:2001251)	129	7	0.53	+	13.15	1.49E-06	7.79E-04
positive regulation of protein localization to nucleus (GO:1900182)	74	4	0.31	+	13.10	3.02E-04	3.61E-02
nucleosome organization (GO:0034728)	112	6	0.46	+	12.98	9.30E-06	2.98E-03
chromatin assembly or disassembly (GO:0006333)	112	6	0.46	+	12.98	9.30E-06	3.04E-03
regulation of chromatin organization (GO:1902275)	192	10	0.79	+	12.62	1.08E-08	2.43E-05
DNA packaging (GO:0006323)	137	7	0.57	+	12.38	2.18E-06	1.04E-03
negative regulation of mRNA metabolic process (GO:1903312)	80	4	0.33	+	12.12	4.01E-04	4.34E-02
negative regulation of DNA metabolic process (GO:0051053)	121	6	0.50	+	12.02	1.42E-05	4.11E-03
histone methylation (GO:0016571)	83	4	0.34	+	11.68	4.58E-04	4.85E-02
regulation of mRNA splicing, via spliceosome (GO:0048024)	105	5	0.43	+	11.54	9.15E-05	1.48E-02
protein-DNA complex assembly (GO:0065004)	129	6	0.53	+	11.27	2.00E-05	5.51E-03
regulation of nucleocytoplasmic transport (GO:0046822)	110	5	0.45	+	11.02	1.13E-04	1.69E-02
regulation of RNA splicing (GO:0043484)	139	6	0.57	+	10.46	3.00E-05	6.92E-03
DNA conformation change (GO:0071103)	178	7	0.73	+	9.53	1.14E-05	3.43E-03
regulation of chromosome organization (GO:0033044)	347	13	1.43	+	9.08	2.75E-09	1.44E-05
positive regulation of mitotic cell cycle (GO:0045931)	165	6	0.68	+	8.81	7.53E-05	1.27E-02
regulation of mRNA metabolic process (GO:1903311)	249	9	1.03	+	8.76	1.18E-06	6.60E-04
regulation of microtubule cytoskeleton organization (GO:0070507)	196	7	0.81	+	8.66	2.07E-05	5.61E-03
protein-DNA complex subunit organization (GO:0071824)	169	6	0.70	+	8.60	8.56E-05	1.41E-02
regulation of viral life cycle (GO:1903900)	142	5	0.59	+	8.53	3.54E-04	4.12E-02
positive regulation of chromosome organization (GO:2001252)	180	6	0.74	+	8.08	1.20E-04	1.74E-02
RNA splicing (GO:0008380)	310	10	1.28	+	7.82	7.92E-07	5.17E-04
regulation of microtubule-based process (GO:0032886)	230	7	0.95	+	7.38	5.56E-05	1.04E-02
mRNA processing (GO:0006397)	395	12	1.63	+	7.36	1.09E-07	1.22E-04
regulation of organelle assembly (GO:1902115)	200	6	0.83	+	7.27	2.08E-04	2.75E-02
mRNA metabolic process (GO:0016071)	509	15	2.10	+	7.14	3.55E-09	1.39E-05
negative regulation of cell cycle process (GO:0010948)	210	6	0.87	+	6.92	2.69E-04	3.32E-02
regulation of mitotic cell cycle phase transition (GO:1901990)	254	7	1.05	+	6.68	1.02E-04	1.58E-02
actin filament organization (GO:0007015)	223	6	0.92	+	6.52	3.68E-04	4.18E-02
negative regulation of organelle organization (GO:0010639)	373	10	1.54	+	6.50	3.96E-06	1.55E-03
regulation of cell cycle phase transition (GO:1901987)	286	7	1.18	+	5.93	2.08E-04	2.76E-02
regulation of DNA metabolic process (GO:0051052)	354	8	1.46	+	5.48	1.24E-04	1.78E-02
positive regulation of cell cycle (GO:0045787)	357	8	1.47	+	5.43	1.31E-04	1.85E-02
posttranscriptional regulation of gene expression (GO:0010608)	408	9	1.68	+	5.35	5.50E-05	1.04E-02
regulation of mitotic cell cycle (GO:0007346)	500	11	2.06	+	5.33	7.99E-06	2.78E-03
mitotic cell cycle process (GO:1903047)	413	9	1.70	+	5.28	6.02E-05	1.10E-02
regulation of cell cycle process (GO:0010564)	586	12	2.42	+	4.96	6.12E-06	2.23E-03
RNA processing (GO:0006396)	734	15	3.03	+	4.95	3.83E-07	3.00E-04
negative regulation of cell cycle (GO:0045786)	402	8	1.66	+	4.82	2.88E-04	3.50E-02
actin cytoskeleton organization (GO:0030036)	465	9	1.92	+	4.69	1.45E-04	2.04E-02
regulation of protein complex assembly (GO:0043254)	418	8	1.72	+	4.64	3.71E-04	4.19E-02
regulation of cytoskeleton organization (GO:0051493)	532	10	2.20	+	4.56	7.75E-05	1.29E-02
mitotic cell cycle (GO:0000278)	495	9	2.04	+	4.41	2.30E-04	2.97E-02
regulation of organelle organization (GO:0033043)	1227	22	5.06	+	4.35	4.77E-09	1.50E-05
chromatin organization (GO:0006325)	614	11	2.53	+	4.34	5.09E-05	9.74E-03
chromosome organization (GO:0051276)	905	16	3.73	+	4.28	9.91E-07	6.22E-04
positive regulation of organelle organization (GO:0010638)	580	10	2.39	+	4.18	1.55E-04	2.14E-02
actin filament-based process (GO:0030029)	523	9	2.16	+	4.17	3.41E-04	4.02E-02
negative regulation of cellular component organization (GO:0051129)	704	12	2.90	+	4.13	3.65E-05	7.73E-03
regulation of cell cycle (GO:0051726)	942	16	3.89	+	4.12	1.66E-06	8.38E-04
DNA metabolic process (GO:0006259)	607	10	2.50	+	3.99	2.23E-04	2.91E-02
cell cycle (GO:0007049)	1170	19	4.83	+	3.94	2.94E-07	2.71E-04
nucleic acid metabolic process (GO:0090304)	1725	27	7.12	+	3.79	1.02E-09	8.01E-06
cellular response to DNA damage stimulus (GO:0006974)	656	10	2.71	+	3.69	4.08E-04	4.35E-02
RNA metabolic process (GO:0016070)	1211	18	5.00	+	3.60	2.21E-06	1.02E-03
cell cycle process (GO:0022402)	742	11	3.06	+	3.59	2.61E-04	3.25E-02
cytoskeleton organization (GO:0007010)	1007	14	4.16	+	3.37	7.02E-05	1.22E-02

gene expression (GO:0010467)	1585	22	6.54	+	3.36	4.11E-07	2.93E-04
negative regulation of gene expression (GO:0010629)	1570	21	6.48	+	3.24	1.44E-06	7.81E-04
response to abiotic stimulus (GO:0009628)	903	12	3.73	+	3.22	3.62E-04	4.18E-02
positive regulation of cellular component organization (GO:0051130)	1210	16	4.99	+	3.20	3.64E-05	7.82E-03
regulation of cellular component biogenesis (GO:0044087)	914	12	3.77	+	3.18	4.04E-04	4.33E-02
negative regulation of RNA metabolic process (GO:0051253)	1224	16	5.05	+	3.17	4.17E-05	8.39E-03
protein-containing complex assembly (GO:0065003)	1318	17	5.44	+	3.13	2.74E-05	6.71E-03
organelle organization (GO:0006996)	2957	38	12.20	+	3.11	3.14E-11	4.92E-07
nucleobase-containing compound metabolic process (GO:0006139)	2141	27	8.83	+	3.06	9.47E-08	1.14E-04
negative regulation of macromolecule biosynthetic process (GO:0010558)	1360	17	5.61	+	3.03	4.05E-05	8.25E-03
negative regulation of biosynthetic process (GO:0009890)	1446	18	5.97	+	3.02	2.44E-05	6.08E-03
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1770	22	7.30	+	3.01	2.55E-06	1.14E-03
positive regulation of RNA metabolic process (GO:0051254)	1612	20	6.65	+	3.01	8.28E-06	2.76E-03
negative regulation of transcription, DNA-templated (GO:0045892)	1133	14	4.68	+	2.99	2.37E-04	3.02E-02
negative regulation of nucleic acid-templated transcription (GO:1903507)	1137	14	4.69	+	2.98	2.46E-04	3.11E-02
negative regulation of RNA biosynthetic process (GO:1902679)	1138	14	4.70	+	2.98	2.48E-04	3.11E-02
regulation of cellular component organization (GO:0051128)	2451	30	10.11	+	2.97	2.71E-08	4.73E-05
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1323	16	5.46	+	2.93	1.03E-04	1.59E-02
negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	1325	16	5.47	+	2.93	1.05E-04	1.60E-02
negative regulation of cellular biosynthetic process (GO:0031327)	1409	17	5.81	+	2.92	6.26E-05	1.12E-02
protein-containing complex subunit organization (GO:0043933)	1502	18	6.20	+	2.90	4.01E-05	8.27E-03
positive regulation of transcription, DNA-templated (GO:0045893)	1512	18	6.24	+	2.89	4.37E-05	8.67E-03
positive regulation of RNA biosynthetic process (GO:1902680)	1516	18	6.26	+	2.88	4.52E-05	8.75E-03
positive regulation of nucleic acid-templated transcription (GO:1903508)	1515	18	6.25	+	2.88	4.48E-05	8.78E-03
establishment of localization in cell (GO:0051649)	1430	17	5.90	+	2.88	7.50E-05	1.28E-02
heterocycle metabolic process (GO:0046483)	2278	27	9.40	+	2.87	3.28E-07	2.86E-04
cellular aromatic compound metabolic process (GO:0006725)	2344	27	9.67	+	2.79	5.77E-07	3.93E-04
cellular nitrogen compound metabolic process (GO:0034641)	2720	31	11.22	+	2.76	7.46E-08	9.75E-05
positive regulation of macromolecule biosynthetic process (GO:0010557)	1768	20	7.30	+	2.74	3.13E-05	7.00E-03
negative regulation of macromolecule metabolic process (GO:0010605)	2404	26	9.92	+	2.62	3.24E-06	1.37E-03
positive regulation of cellular biosynthetic process (GO:0031328)	1862	20	7.68	+	2.60	6.44E-05	1.14E-02
organic cyclic compound metabolic process (GO:1901360)	2545	27	10.50	+	2.57	2.82E-06	1.23E-03
regulation of gene expression (GO:0010468)	3616	38	14.92	+	2.55	1.04E-08	2.71E-05
positive regulation of biosynthetic process (GO:0009891)	1903	20	7.85	+	2.55	8.69E-05	1.42E-02
positive regulation of gene expression (GO:0010628)	1931	20	7.97	+	2.51	1.06E-04	1.60E-02
regulation of transcription by RNA polymerase II (GO:0006357)	1942	20	8.01	+	2.50	1.14E-04	1.68E-02
negative regulation of metabolic process (GO:0009892)	2663	27	10.99	+	2.46	6.60E-06	2.35E-03
cellular localization (GO:0051641)	2014	20	8.31	+	2.41	1.87E-04	2.52E-02
cellular component biogenesis (GO:0044085)	2352	23	9.71	+	2.37	1.01E-04	1.58E-02
cellular component assembly (GO:0022607)	2144	21	8.85	+	2.37	2.35E-04	3.02E-02
regulation of RNA metabolic process (GO:0051252)	2995	29	12.36	+	2.35	8.05E-06	2.74E-03
negative regulation of cellular metabolic process (GO:0031324)	2386	23	9.85	+	2.34	1.13E-04	1.67E-02
regulation of nucleobase-containing compound metabolic process (GO:0019219)	3220	31	13.29	+	2.33	3.55E-06	1.47E-03
regulation of macromolecule biosynthetic process (GO:0010556)	3246	30	13.39	+	2.24	1.12E-05	3.43E-03
regulation of cellular macromolecule biosynthetic process (GO:2000112)	3159	29	13.03	+	2.22	2.98E-05	6.97E-03
negative regulation of biological process (GO:0048519)	5005	45	20.65	+	2.18	2.69E-08	5.26E-05
regulation of biosynthetic process (GO:0009889)	3453	31	14.25	+	2.18	1.59E-05	4.45E-03
negative regulation of cellular process (GO:0048523)	4482	40	18.49	+	2.16	3.62E-07	2.99E-04
regulation of cellular biosynthetic process (GO:0031326)	3383	30	13.96	+	2.15	2.83E-05	6.83E-03
cellular component organization (GO:0016043)	5086	45	20.99	+	2.14	5.70E-08	8.13E-05
cellular component organization or biogenesis (GO:0071840)	5262	46	21.71	+	2.12	4.41E-08	6.92E-05
response to stress (GO:0006950)	3064	26	12.64	+	2.06	3.53E-04	4.13E-02
regulation of macromolecule metabolic process (GO:0060255)	5232	44	21.59	+	2.04	3.86E-07	2.88E-04
macromolecule metabolic process (GO:0043170)	5049	42	20.83	+	2.02	1.17E-06	6.79E-04
regulation of metabolic process (GO:0019222)	5688	45	23.47	+	1.92	1.68E-06	8.22E-04
regulation of cellular metabolic process (GO:0031323)	5288	42	21.82	+	1.92	5.90E-06	2.20E-03
regulation of nitrogen compound metabolic process (GO:0051171)	4952	39	20.43	+	1.91	2.24E-05	5.86E-03
cellular macromolecule metabolic process (GO:0044260)	3963	31	16.35	+	1.90	2.93E-04	3.53E-02
regulation of primary metabolic process (GO:0080090)	5098	39	21.04	+	1.85	3.13E-05	7.10E-03
positive regulation of cellular process (GO:0048522)	5244	40	21.64	+	1.85	3.36E-05	7.32E-03
positive regulation of biological process (GO:0048518)	5947	44	24.54	+	1.79	1.55E-05	4.41E-03
nitrogen compound metabolic process (GO:0006807)	5669	41	23.39	+	1.75	9.47E-05	1.52E-02
regulation of cellular process (GO:0050794)	10472	65	43.21	+	1.50	5.10E-06	1.95E-03
regulation of biological process (GO:0050789)	11171	67	46.09	+	1.45	1.35E-05	3.98E-03
biological regulation (GO:0065007)	11782	69	48.62	+	1.42	2.11E-05	5.61E-03
cellular process (GO:0009987)	13888	80	57.31	+	1.40	2.19E-07	2.15E-04
system process (GO:0003008)	2526	1	10.42	-	0.10	3.80E-04	4.26E-02

Table S16. Molecular Functions Associated with Proteins with Upregulated Phosphorylation in Ang II vs. Control.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190429)**
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**
Analyzed List:	**Client Text Box Input (Mus musculus)**
Reference List:	**Mus musculus (all genes in database)**
Test Type:	**FISHER**
Correction:	**FDR**

GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (92)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
structural constituent of postsynaptic actin cytoskeleton (GO:0098973)	4	2	0.02	+	> 100	2.48E-04	4.72E-02
nucleosomal DNA binding (GO:0031492)	23	3	0.09	+	31.61	1.63E-04	3.73E-02
GTPase activator activity (GO:0005096)	236	10	0.97	+	10.27	7.00E-08	4.00E-05
GTPase regulator activity (GO:0030695)	253	10	1.04	+	9.58	1.31E-07	5.97E-05
nucleoside-triphosphatase regulator activity (GO:0060589)	292	10	1.20	+	8.30	4.67E-07	1.94E-04
mRNA binding (GO:0003729)	244	8	1.01	+	7.95	9.50E-06	2.90E-03
enzyme activator activity (GO:0008047)	450	11	1.86	+	5.92	3.01E-06	1.15E-03
chromatin binding (GO:0003682)	575	14	2.37	+	5.90	1.25E-07	6.34E-05
DNA-binding transcription factor binding (GO:0140297)	350	8	1.44	+	5.54	1.14E-04	2.91E-02
transcription factor binding (GO:0008134)	699	13	2.88	+	4.51	6.76E-06	2.38E-03
cytoskeletal protein binding (GO:0008092)	943	15	3.89	+	3.85	7.94E-06	2.59E-03
double-stranded DNA binding (GO:0003690)	984	14	4.06	+	3.45	5.49E-05	1.57E-02
DNA binding (GO:0003677)	2038	28	8.41	+	3.33	8.04E-09	6.12E-06
enzyme regulator activity (GO:0030234)	962	13	3.97	+	3.27	1.72E-04	3.58E-02
nucleic acid binding (GO:0003676)	3055	41	12.61	+	3.25	7.66E-13	3.50E-09
enzyme binding (GO:0019899)	2306	29	9.52	+	3.05	2.81E-08	1.84E-05
protein-containing complex binding (GO:0044877)	1210	15	4.99	+	3.00	1.34E-04	3.22E-02
ATP binding (GO:0005524)	1382	16	5.70	+	2.81	1.70E-04	3.70E-02
heterocyclic compound binding (GO:1901363)	4950	49	20.43	+	2.40	9.59E-11	1.46E-07
organic cyclic compound binding (GO:0097159)	5053	49	20.85	+	2.35	2.48E-10	2.84E-07
protein binding (GO:0005515)	9011	66	37.18	+	1.78	1.57E-09	1.43E-06
binding (GO:0005488)	13135	83	54.20	+	1.53	6.35E-11	1.45E-07

Table S17. Differentially Expressed Phosphorylation Between Meno/Ang II and Ang II.

Accession	Sequence	Modifications	Ang II 1	Ang II 2	Ang II 3	Ang II 4	Meno/Ang II 1	Meno/Ang II 2	Meno/Ang II 3	Meno/Ang II 4	P Value	Fold Change
MYCN_MOUSE	IKSEASPRPLK	[3] Phospho (ST)	1	80328	46634	38767	1	1	1	1	0.05	0.00
EIF3B_MOUSE	GHPSAGAEEEGGSDGSAAEAEPR	[13] Phospho (ST)|[16] Phospho (ST)	11690	7868	10376	6965	1	1	1	1	0.00	0.00
MYCN_MOUSE	IKSEASPRPLK	[3] Phospho (ST)	4752	162849	134361	134064	2570	2309	2294	2743	0.02	0.02
TLN1_MOUSE	SKDHFGLEGDEESTMLEDSVSPK	[1] Phospho (ST)|[15] Oxidation (M)	26515	5820	6787	23603	151	1	692	2826	0.04	0.06
TOE1_MOUSE	KRSLQSQPGTQTLAEAEDGPPTK	[10] Phospho (ST)	152071	23453	213918	171251	18489	1663	1228	12172	0.02	0.06
TOE1_MOUSE	KRSLQSQPGTQTLAEAEDGPPTK	[3] Phospho (ST)	152071	23453	213918	171251	18489	1663	1228	12172	0.02	0.06
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAER	[13] Phospho (ST)	4279	4332	1	4311	1	1	1137	149	0.04	0.10
EH1L1_MOUSE	RSSVNGEAGPVPPPR	[3] Phospho (ST)	7536	2153	1851	4525	1595	1	22	1	0.04	0.10
DI3L2_MOUSE	RPGLEKASDEEPED	[8] Phospho (ST)	2224	1312	51	1404	514	1	1	1	0.05	0.10
TBB1_MOUSE	AGLEDSEEDVEEAEVEAEDKDH	[6] Phospho (ST)	104201	143426	318439	120938	1	39334	44230	4735	0.03	0.13
GCFC2_MOUSE	SNEEDPESDPDDHEKR	[8] Phospho (ST)	11698	51819	65343	33710	1	1	1	22848	0.04	0.14
FBRL_MOUSE	RVSISEGDDKIEYR	[3] Phospho (ST)	15364	30229	22531	8589	3498	3379	2794	1144	0.01	0.14
FYN_MOUSE	DGSLNQSSGYR	[3] Phospho (ST)	38761	25961	41735	7601	16527	1	1	1	0.03	0.14
USO1_MOUSE	LKDLGHPVEEEDESGDQEDDDDEIDDGDKDQDI	[14] Phospho (ST)	2513531	2044951	1587363	1513870	7238	585775	3	615673	0.00	0.16
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAER	[14] Phospho (ST)	151961	82106	65909	49878	1	15923	7535	42571	0.03	0.19
USO1_MOUSE	LKDLGHPVEEEDESGDQEDDDDEIDDGDKDQDI	[14] Phospho (ST)	3108648	2193677	2359583	1518504	3110	751366	11443	1041726	0.00	0.20
TBB1_MOUSE	AGLEDSEEDVEEAEVEAEDKDH	[6] Phospho (ST)	71730	118036	130456	56623	14857	27043	34101	1	0.01	0.20
SMCA4_MOUSE	KAENAEGQTPAIGPDGEPLDETSQMSDLPVK	[23] Phospho (ST)	246772	203415	82788	104179	24137	77855	21728	6152	0.02	0.20
URP2_MOUSE	TASGDYIDSSWELR	[3] Phospho (ST)	296249	88168	182235	186858	65337	21943	30920	36823	0.01	0.21
URP2_MOUSE	TASGDYIDSSWELR	[1] Phospho (ST)	296249	88168	182235	186858	65337	21943	30920	36823	0.01	0.21
MCM3_MOUSE	KASEDESDLEDEEEKSQEDTEQK	[7] Phospho (ST)	174075	107824	89061	40430	13993	14240	43260	17331	0.03	0.22
SDPR_MOUSE	SLEETLHNVDLSSDDELPR	[12] Phospho (ST)|[13] Phospho (ST)	255556	192549	134040	44767	18348	1356	23706	93775	0.05	0.22
EIF3C_MOUSE	QPLLLSEDEEDTKR	[6] Phospho (ST)	882267	438706	388765	363318	127019	136081	111373	101238	0.02	0.23
STK4_MOUSE	NVSGSLKNSSDWK	[5] Phospho (ST)	14680	28095	9176	13046	7297	2656	5782	1	0.03	0.24
SMC3_MOUSE	KGDVEGSQSQDEGEGSGESER	[9] Phospho (ST)	54845	65301	74833	26710	31272	1	13229	12568	0.02	0.26
SMC3_MOUSE	KGDVEGSQSQDEGEGSGESER	[7] Phospho (ST)	54845	65301	74833	26710	31272	1	13229	12568	0.02	0.26
TBB1_MOUSE	AGLEDSEEDVEEAEVEAEDKDH	[6] Phospho (ST)	673514	783477	562161	272820	18088	264483	310580	62326	0.02	0.29
YBOX1_MOUSE	NYQQNYQNSESGEKNEGSESAPEGQAQQR	[11] Phospho (ST)	757849	2082483	1554923	1185391	414934	697684	15178	527250	0.02	0.30
YBOX1_MOUSE	NYQQNYQNSESGEKNEGSESAPEGQAQQR	[9] Phospho (ST)	757849	2082483	1554923	1185391	414934	697684	15178	527250	0.02	0.30
LEUK_MOUSE	QGSLVLEELKPGSGPNLK	[3] Phospho (ST)	280236	218637	150103	416896	108011	58661	109894	59167	0.02	0.31
FAK2_MOUSE	RNSLPQIPTLNLEAR	[3] Phospho (ST)	606304	434353	403968	1158315	236098	242770	159442	184630	0.04	0.32
EIF3B_MOUSE	GHPSAGAEEEGGSDGSAAEAEPR	[13] Phospho (ST)|[16] Phospho (ST)	76887	24894	78453	49648	12155	18813	2060	39656	0.04	0.32
TBB1_MOUSE	AGLEDSEEDVEEAEVEAEDKDH	[6] Phospho (ST)	8264892	18511692	10966392	5347814	1192059	5570627	5145969	2011773	0.05	0.32
DDX24_MOUSE	KAQAVSEEEEEEEGQSSSPK	[6] Phospho (ST)	80752	60664	70898	42698	21165	9443	24994	32130	0.00	0.34
ITAD_MOUSE	SSSCSINHPIFR	[2] Phospho (ST)	55127	30284	40839	91883	13424	21825	23244	19171	0.04	0.36
TPC12_MOUSE	LSSLTAPVGEKSPDSTSPSYSTR	[12] Phospho (ST)	140785	78190	135458	112164	33650	18372	71769	44612	0.01	0.36
TBB1_MOUSE	AGLEDSEEDVEEAEVEAEDKDH	[6] Phospho (ST)	5405164	10730733	7318600	4156168	1245254	2482450	4132059	2107452	0.03	0.36
DOK1_MOUSE	VGQAQDILRTDSHDGETEGK	[12] Phospho (ST)	307472	186416	197141	110278	108689	6135	146326	28605	0.05	0.36
SDPR_MOUSE	SLEETLHNVDLSSDDELPR	[12] Phospho (ST)|[13] Phospho (ST)	839450	720532	747032	774538	240698	40479	489442	372410	0.00	0.37
ABI1_MOUSE	TNPPTQKPPSPPVSGR	[10] Phospho (ST)	209770	374923	422835	215109	228414	135193	22272	70660	0.03	0.37
GNL1_MOUSE	EEQTDTSDGESVTHHIR	[7] Phospho (ST)	121599	112199	134878	40650	13157	23351	81466	36263	0.05	0.38
GNL1_MOUSE	EEQTDTSDGESVTHHIR	[6] Phospho (ST)	121599	112199	134878	40650	13157	23351	81466	36263	0.05	0.38
ABCF1_MOUSE	SKPAAADSEGEEEEEDTAKEKEPPQQGK	[8] Phospho (ST)	108682	45555	85330	42450	8542	24664	38042	37686	0.05	0.39
CATA_MOUSE	SALEHSVQCAVDVKR	[1] Phospho (ST)	67715	68744	40253	106539	35139	29169	29072	16246	0.02	0.39
KPCD_MOUSE	SPSDYSNFDPEFLNEKPQLSFSDK	[20] Phospho (ST)	816815	412679	785858	420240	217912	161459	357558	232358	0.02	0.40
HS105_MOUSE	IESPKLER	[3] Phospho (ST)	728190	429957	477389	273231	216632	165822	204903	186396	0.02	0.41
RGS18_MOUSE	SFTYNDFQDVK	[1] Phospho (ST)	1286509	826886	762463	810983	5678	601179	646643	300549	0.03	0.42
RGS18_MOUSE	SFTYNDFQDVK	[3] Phospho (ST)	1286509	826886	762463	810983	5678	601179	646643	300549	0.03	0.42
STXB5_MOUSE	LLYEINDVDTPEGEQPPPLSTPVGSSNPQPIPPQSHPSTSSSSSDGLR	[10] Phospho (ST)	740348	359742	293629	535356	253876	213976	129570	239565	0.04	0.43
STXB5_MOUSE	LLYEINDVDTPEGEQPPPLSTPVGSSNPQPIPPQSHPSTSSSSSDGLR	[26] Phospho (ST)	740348	359742	293629	535356	253876	213976	129570	239565	0.04	0.43
SNTB1_MOUSE	GSPVSEIGWETPPPESPR	[16] Phospho (ST)	99244	70172	97175	63963	32580	61150	42408	8519	0.02	0.44
EIF3B_MOUSE	GHPSAGAEEEGGSDGSAAEAEPR	[13] Phospho (ST)	161970	87868	138385	151773	63004	26219	28810	120095	0.03	0.44
ARP10_MOUSE	AGMSKPIK	[4] Phospho (ST)|[5] Acetyl (K)	311975	440761	467814	190702	87202	168841	248056	125427	0.04	0.45
EIF3C_MOUSE	QPLLLSEDEEDTKR	[6] Phospho (ST)	2088503	1027926	1256203	848988	704177	474707	706747	478660	0.04	0.45
TOM70_MOUSE	ASPALGSGHHDGSGDSLEMSSLDR	[2] Phospho (ST)|[19] Oxidation (M)	150043	68096	83698	111566	56621	17898	62816	50208	0.03	0.45
TOM70_MOUSE	ASPALGSGHHDGSGDSLEMSSLDR	[7] Phospho (ST)|[19] Oxidation (M)	150043	68096	83698	111566	56621	17898	62816	50208	0.03	0.45
CD11B_MOUSE	AYTPVVVTLWYR	[3] Phospho (ST)	121497	88514	93727	81778	75196	64215	18220	17684	0.02	0.45
EIF3B_MOUSE	GHPSAGAEEEGGSDGSAAEAEPR	[13] Phospho (ST)|[16] Phospho (ST)	1581129	766569	1146970	696484	567585	360143	402572	598109	0.04	0.46
AB1IP_MOUSE	QGLGNHSPGATR	[7] Phospho (ST)	378393	206576	300600	156994	180524	86252	113380	115279	0.04	0.48
CALU_MOUSE	VHNDAQNFDYDHDAFLGAEEAK	[10] Phospho (Y)	3126425	6272491	6774780	3951259	1385886	2483490	4120009	1594947	0.05	0.48
CPZIP_MOUSE	AIVSPFHSPPSTPSSPGIR	[8] Phospho (ST)	875308	663165	1147993	533973	468653	303145	389674	381535	0.02	0.48
NHSL2_MOUSE	GSKATPR	[5] Phospho (ST)	872972	586387	989839	860628	488259	370106	25769	720078	0.04	0.48
FAK2_MOUSE	RNSLPQIPTLNLEAR	[3] Phospho (ST)	1287101	854967	1041203	965591	632776	444282	499750	438650	0.00	0.49
RBM39_MOUSE	DKSPVREPIDNLTPEER	[3] Phospho (ST)	2400661	2329272	2188991	1882123	596840	317261	2034279	1401821	0.03	0.49
TIF1B_MOUSE	SRSGEGEVSGLLR	[3] Phospho (ST)	820242	549522	973688	857385	418961	296865	393655	474077	0.01	0.49
TIF1B_MOUSE	SRSGEGEVSGLLR	[1] Phospho (ST)	820242	549522	973688	857385	418961	296865	393655	474077	0.01	0.49
EF1D_MOUSE	GATPAEDDEDKDIDLFGSDEEEEDK	[18] Phospho (ST)	9247891	6609280	7218066	4029777	1892318	4052089	4877686	2768880	0.04	0.50
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAER	[13] Phospho (ST)	2052573	1083756	1620651	1148393	850145	467328	605022	1044396	0.03	0.50

EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAER	[14] Phospho (ST)	2052573	1083756	1620651	1148393	850145	467328	605022	1044396	0.03	0.50
PDS5A_MOUSE	AAGSQESLEAGNAK	[4] Phospho (ST)	102821	125382	102473	83573	89463	74301	11205	33577	0.04	0.50
TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[3] Phospho (ST)	1876765	2523934	1696395	1377146	981603	1072506	1157587	586949	0.02	0.51
TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[2] Phospho (ST)	1876765	2523934	1696395	1377146	981603	1072506	1157587	586949	0.02	0.51
TPR_MOUSE	RSSTSQTVSTPAPEPVIDSTEAIEAK	[4] Phospho (ST)	1876765	2523934	1696395	1377146	981603	1072506	1157587	586949	0.02	0.51
LEUK_MOUSE	VPDEEATTTSGAGGNKGSEVLETEGSGQRPTLTTFFSR	[18] Phospho (ST)	575140	387687	719290	691912	361600	162259	300977	384959	0.02	0.51
SNX1_MOUSE	RFSDFLGLYEK	[3] Phospho (ST)	110308	121810	145079	169422	67031	40378	110271	62661	0.01	0.51
GP1BA_MOUSE	RPSALSQGR	[6] Phospho (ST)	1335370	861989	896155	1088765	622651	505587	257790	804747	0.02	0.52
TOM70_MOUSE	ASPALGSGHHDGSGDSLEMSSLDR	[2] Phospho (ST)|[19] Oxidation (M)	1372665	1089433	1186525	1054341	532109	354988	822434	754651	0.00	0.52
TOM70_MOUSE	ASPALGSGHHDGSGDSLEMSSLDR	[7] Phospho (ST)|[19] Oxidation (M)	1372665	1089433	1186525	1054341	532109	354988	822434	754651	0.00	0.52
ZC3H4_MOUSE	DYSPPYAPSHQQYSSSHNAPLPK	[3] Phospho (ST)	976422	1187671	843384	985672	730499	506404	508112	354293	0.00	0.53
ZC3H4_MOUSE	DYSPPYAPSHQQYSSSHNAPLPK	[6] Phospho (Y)	976422	1187671	843384	985672	730499	506404	508112	354293	0.00	0.53
FLNA_MOUSE	LTVSSLQESGLK	[5] Phospho (ST)	720822	456971	332616	596481	290588	270886	322922	245262	0.03	0.54
EF1D_MOUSE	GATPAEDDEDKDIDLFGSDEEEEDKEAAR	[18] Phospho (ST)	35480772	40980828	47343864	20274816	13562453	22817845	26594435	14654356	0.05	0.54
EIF3B_MOUSE	AKPAAQSEEETATSPAASPTPQSAER	[14] Phospho (ST)|[18] Phospho (ST)	4045059	2423632	3279872	2216215	2169235	1026635	1377378	1912937	0.03	0.54
TIF1B_MOUSE	SRSGEGEVSGLLR	[3] Phospho (ST)	1803691	1221037	1794485	1436076	917246	673403	874762	974889	0.00	0.55
TIF1B_MOUSE	SRSGEGEVSGLLR	[1] Phospho (ST)	1803691	1221037	1794485	1436076	917246	673403	874762	974889	0.00	0.55
PSD4_MOUSE	KSHSSPSLHQEEAPTTAK	[4] Phospho (ST)	177456	285403	233586	275084	143604	205633	118929	99417	0.02	0.58
RERE_MOUSE	EKVASDTEDTDRITSK	[5] Phospho (ST)	170386	111985	98662	108396	97776	59872	47723	82907	0.04	0.59
FYB_MOUSE	VAGQSSPSGIQSR	[6] Phospho (ST)	812263	441973	591953	478552	336291	330452	301058	413451	0.03	0.59
FAM21_MOUSE	VPLLFSDEEDSEVPSGVKPEDLK	[6] Phospho (ST)	703434	526365	335844	501660	281348	277398	260059	412847	0.05	0.60
SNX2_MOUSE	ELILSSEPSPAVTPVTPTTLIAPR	[13] Phospho (ST)	2842712	1313957	2385245	1805429	1283582	1049016	1429374	1234528	0.05	0.60
SNX2_MOUSE	ELILSSEPSPAVTPVTPTTLIAPR	[16] Phospho (ST)	2842712	1313957	2385245	1805429	1283582	1049016	1429374	1234528	0.05	0.60
ASAP1_MOUSE	SHTGDLSPNVQSR	[7] Phospho (ST)	268886	241106	229434	206240	154100	156747	110004	147306	0.00	0.60
TCRG1_MOUSE	AKPVATTPIPGTPWCVVWTGDER	[12] Phospho (ST)	82640	108890	76883	93135	59484	78068	38019	43170	0.02	0.61
MTMR3_MOUSE	RSSDPSLNEK	[6] Phospho (ST)	224902	183311	125996	222425	134344	110938	70519	150172	0.05	0.62
DIEXF_MOUSE	RYTIKGIR	[2] Phospho (Y)	219454	237388	178537	241523	146774	108531	80798	204932	0.03	0.62
PDCD4_MOUSE	SGVAVPTSPK	[8] Phospho (ST)	1394062	1223898	1996508	1415716	872163	960673	1337900	638194	0.05	0.63
CLASR_MOUSE	ITFITSFGGSDEEAAAAAAAAAASGAAPGKPPAPPQTGGPAPGR	[10] Phospho (ST)	592993	425005	465613	323866	334193	199742	358626	250926	0.05	0.63
CLASR_MOUSE	ITFITSFGGSDEEAAAAAAAAAASGAAPGKPPAPPQTGGPAPGR	[5] Phospho (ST)	592993	425005	465613	323866	334193	199742	358626	250926	0.05	0.63
NFRKB_MOUSE	KGSLAALYDLAVLK	[3] Phospho (ST)	63023	57181	52086	51109	40188	34622	27531	39940	0.00	0.64
AGFG1_MOUSE	GTPSQSPVVGR	[6] Phospho (ST)	157423	131826	188491	148687	114993	136036	101149	57296	0.04	0.65
ASAP1_MOUSE	SHTGDLSPNVQSR	[7] Phospho (ST)	164277	173294	193935	140808	115560	123617	104713	96197	0.00	0.65
PDCD4_MOUSE	SGVAVPTSPKGR	[8] Phospho (ST)	83888	86732	89767	83539	57049	76125	68022	29661	0.03	0.67
MAP1S_MOUSE	KPPPPASPGSSDSSAR	[7] Phospho (ST)	278439	291334	325111	259267	169802	208742	206863	190273	0.00	0.67
SK2L2_MOUSE	MSPTIGKQLLK	[1] Oxidation (M)|[4] Phospho (ST)	1548565	1806347	1507923	1620408	929135	1038048	1304777	1112750	0.00	0.68
CREB1_MOUSE	TAPTSTIAPGVVMASSPALPTQPAEEAAR	[6] Phospho (ST)|[13] Oxidation (M)	130656	147111	111718	151857	79651	78099	103700	112563	0.02	0.69
MAP4_MOUSE	AAVGVTGNDITTPPNKEPPPSPEKK	[21] Phospho (ST)	1496729	1495479	944097	1282557	904217	976845	932443	809790	0.03	0.69
RGS18_MOUSE	SRSFTYNDFQDVK	[3] Phospho (ST)	1669645	1814769	1444470	1694007	793444	1334654	1457443	1107740	0.03	0.71
RGS18_MOUSE	SRSFTYNDFQDVK	[5] Phospho (ST)	1669645	1814769	1444470	1694007	793444	1334654	1457443	1107740	0.03	0.71
RGS18_MOUSE	SRSFTYNDFQDVK	[1] Phospho (ST)	1669645	1814769	1444470	1694007	793444	1334654	1457443	1107740	0.03	0.71
TISD_MOUSE	NQQQGLTGPAPPPAQPPAAPAPPSPPFGFQLPR	[24] Phospho (ST)	190009	128889	186238	168182	98494	127488	155196	105953	0.05	0.72
RGS18_MOUSE	SRSFTYNDFQDVK	[3] Phospho (ST)	2096462	2006908	1738011	1813668	1061152	1447661	1738749	1552852	0.03	0.76
RGS18_MOUSE	SRSFTYNDFQDVK	[5] Phospho (ST)	2096462	2006908	1738011	1813668	1061152	1447661	1738749	1552852	0.03	0.76
RGS18_MOUSE	SRSFTYNDFQDVK	[1] Phospho (ST)	2096462	2006908	1738011	1813668	1061152	1447661	1738749	1552852	0.03	0.76
EIF3G_MOUSE	GIPLPTGDTSPEPELLPGDPLPPPK	[10] Phospho (ST)	3990489	5401824	4055824	3935804	3303315	3842292	3386950	2754148	0.05	0.76
EIF3G_MOUSE	GIPLPTGDTSPEPELLPGDPLPPPK	[6] Phospho (ST)	3990489	5401824	4055824	3935804	3303315	3842292	3386950	2754148	0.05	0.76
LRCH1_MOUSE	ENSPSVSPTANITAPFGLKPR	[3] Phospho (ST)|[5] Phospho (ST)	328188	310192	289102	336560	363367	329256	426654	430777	0.04	1.23
SP100_MOUSE	DRGGDTSDTESSIIIR	[6] Phospho (ST)	1097072	989667	1057667	1007338	1340124	1624663	1182856	1532093	0.01	1.37
SP100_MOUSE	DRGGDTSDTESSIIIR	[7] Phospho (ST)	1097072	989667	1057667	1007338	1340124	1624663	1182856	1532093	0.01	1.37
SP100_MOUSE	DRGGDTSDTESSIIIR	[11] Phospho (ST)	1097072	989667	1057667	1007338	1340124	1624663	1182856	1532093	0.01	1.37
EP15R_MOUSE	STPSHGSVSSLNSTGSLSPK	[18] Phospho (ST)	128074	136960	153446	109906	176102	188791	206142	158663	0.01	1.38
ZRAB2_MOUSE	EVEDKESEGEEEDEDEDLSK	[7] Phospho (ST)	1528056	2248632	1398980	2418066	3095772	2708643	2849284	2317835	0.03	1.44
DI3L2_MOUSE	RPGLEKASDEEPED	[8] Phospho (ST)	298483	513754	554945	393110	663561	795358	689940	491776	0.04	1.50
3BP1_MOUSE	SSPPAPSLPPGSVSPGTPQALPR	[7] Phospho (ST)	633790	824755	565265	395240	973547	902463	967158	789868	0.02	1.50
3BP1_MOUSE	ERTEADLPKPTSPK	[12] Phospho (ST)	4810270	5515651	4659481	2932618	7537088	6798896	7090471	5859202	0.01	1.52
3BP1_MOUSE	ERTEADLPKPTSPK	[11] Phospho (ST)	4810270	5515651	4659481	2932618	7537088	6798896	7090471	5859202	0.01	1.52
KBTBB_MOUSE	ASAAEGSEASPPSLR	[10] Phospho (ST)	159882	132021	149327	102918	265463	213112	167170	187275	0.03	1.53
CAPZB_MOUSE	GCWDSIHVVEVQEK	[5] Phospho (ST)	357871	237561	224184	347311	472821	336955	444994	544322	0.03	1.54
NHSL2_MOUSE	GSKATPR	[5] Phospho (ST)	676203	940833	553735	744554	1281714	1286804	839871	1216926	0.02	1.59
RHG17_MOUSE	NSNQMTTVPNQAQTGGNSHQLSVSTPHSAAGPSPHTLR	[5] Oxidation (M)|[33] Phospho (ST)	205432	244864	155039	329313	458536	308633	324964	409214	0.03	1.61
SMRC2_MOUSE	DMDEPSPVPNVEEVTLPK	[6] Phospho (ST)	21775	25843	7489	23058	35081	31102	26707	33490	0.04	1.62
SAMH1_MOUSE	TPPSTPPATANLSADDDFQNTDLR	[1] Phospho (ST)	2934438	4069381	2461621	1351814	4380075	4892509	4970587	3382524	0.04	1.63
SAMH1_MOUSE	TPPSTPPATANLSADDDFQNTDLR	[5] Phospho (ST)	2934438	4069381	2461621	1351814	4380075	4892509	4970587	3382524	0.04	1.63
SAMH1_MOUSE	TPPSTPPATANLSADDDFQNTDLR	[4] Phospho (ST)	2934438	4069381	2461621	1351814	4380075	4892509	4970587	3382524	0.04	1.63
3BP1_MOUSE	ERTEADLPKPTSPK	[12] Phospho (ST)	470023	641889	375639	259645	702603	923369	621308	641000	0.04	1.65
3BP1_MOUSE	ERTEADLPKPTSPK	[11] Phospho (ST)	470023	641889	375639	259645	702603	923369	621308	641000	0.04	1.65
HDGF_MOUSE	NSTPSEPDSGQGPPAEEEEGEEEAAKEEAEAQGVR	[9] Phospho (ST)	138016	212741	112646	181375	306521	307908	275044	199734	0.02	1.69
HDGF_MOUSE	NSTPSEPDSGQGPPAEEEEGEEEAAKEEAEAQGVR	[3] Phospho (ST)	138016	212741	112646	181375	306521	307908	275044	199734	0.02	1.69
HDGF_MOUSE	NSTPSEPDSGQGPPAEEEEGEEEAAKEEAEAQGVR	[5] Phospho (ST)	138016	212741	112646	181375	306521	307908	275044	199734	0.02	1.69
SMRC2_MOUSE	GHREEEQEDLTKDMDEPSPVPNVEEVTLPK	[14] Oxidation (M)|[18] Phospho (ST)	1268536	405664	1411763	831291	2218319	2005662	1471146	1328803	0.05	1.79
RANB3_MOUSE	VLSPPKLNEANSDTSR	[3] Phospho (ST)	503626	737957	506139	319806	1227290	1081058	821458	595988	0.04	1.80

PAK2_MOUSE	YLSFTPPEKDGFPSGTPALNTK	[3] Phospho (ST)	601095	2025633	731731	1458690	2333065	2410483	2278849	1877138	0.03	1.85
PAK2_MOUSE	YLSFTPPEKDGFPSGTPALNTK	[5] Phospho (ST)	601095	2025633	731731	1458690	2333065	2410483	2278849	1877138	0.03	1.85
CP062_MOUSE	KGSTSSTSSSSSSSSVIDPLSSVLDGTDPLSMFAATSDPAATGTVTDSSR	[26] Phospho (ST)|[31] Oxidation (M)	79831	165390	157723	174189	286778	311275	261341	256454	0.00	1.93
LRC8C_MOUSE	SQSLKSIPEK	[3] Phospho (ST)|[6] Phospho (ST)	166367	211957	263308	277287	459534	554899	493548	279619	0.01	1.95
KAP0_MOUSE	TDSREDEISPPPPNPVVK	[9] Phospho (ST)	7962783	8621420	5414372	6474050	13129824	17413281	14916415	10472677	0.01	1.96
KAP0_MOUSE	TDSREDEISPPPPNPVVK	[3] Phospho (ST)	7962783	8621420	5414372	6474050	13129824	17413281	14916415	10472677	0.01	1.96
HDAC1_MOUSE	MLPHAPGVQMQAIPEDAIPEESGDEDEEDPDKR	[1] Oxidation (M)|[10] Oxidation (M)|[22] Phospho (ST)	770782	922484	683460	1407011	1797641	1795067	1947131	2147836	0.00	2.03
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[34] Phospho (ST)	134785	219909	326286	183695	440064	469412	607157	263946	0.03	2.06
KPCD2_MOUSE	RLSSTSLASGHSVR	[3] Phospho (ST)	867481	2899711	3162408	1860642	4003133	5614634	5929111	2654176	0.04	2.07
KPCD2_MOUSE	RLSSTSLASGHSVR	[5] Phospho (ST)	867481	2899711	3162408	1860642	4003133	5614634	5929111	2654176	0.04	2.07
KPCD2_MOUSE	RLSSTSLASGHSVR	[4] Phospho (ST)	867481	2899711	3162408	1860642	4003133	5614634	5929111	2654176	0.04	2.07
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[34] Phospho (ST)	1826657	5365060	6839618	3621185	7935778	10622606	12829880	5172936	0.05	2.07
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[31] Phospho (ST)	1826657	5365060	6839618	3621185	7935778	10622606	12829880	5172936	0.05	2.07
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[10] Phospho (ST)	1826657	5365060	6839618	3621185	7935778	10622606	12829880	5172936	0.05	2.07
BUD13_MOUSE	RGHHGSLGTSSPR	[11] Phospho (ST)	38642	36294	5535	39395	39625	54616	89152	70035	0.05	2.11
BUD13_MOUSE	RGHHGSLGTSSPR	[10] Phospho (ST)	38642	36294	5535	39395	39625	54616	89152	70035	0.05	2.11
PAK2_MOUSE	YLSFTPPEK	[3] Phospho (ST)	93494	690411	116524	365005	782832	670663	689474	562831	0.05	2.14
DDX21_MOUSE	EIITEEPSEEEADMPKPK	[8] Phospho (ST)|[14] Oxidation (M)	182873	545781	527372	727186	1093364	1124920	968166	1154105	0.00	2.19
RHG17_MOUSE	SPSPPQQQQQQQQQQQQQQQQQQQTPGMR	[1] Phospho (ST)|[26] Oxidation (M)	68795	90290	162487	75959	167209	187159	281692	254249	0.01	2.24
KAP0_MOUSE	TDSREDEISPPPPNPVVK	[9] Phospho (ST)	1813605	1741847	938245	1531255	3834883	4215686	2853318	2828733	0.00	2.28
KAP0_MOUSE	TDSREDEISPPPPNPVVK	[3] Phospho (ST)	1813605	1741847	938245	1531255	3834883	4215686	2853318	2828733	0.00	2.28
HSP74_MOUSE	KPVVDCVVSVPSFYTDAER	[9] Phospho (ST)	5770	493	10357	5256	14447	13417	12744	10029	0.02	2.31
ADDG_MOUSE	TEEVLSPDGSPSKSPSKK	[16] Phospho (ST)	26336	88071	122872	41198	136909	201652	193888	114595	0.02	2.32
ADDG_MOUSE	TEEVLSPDGSPSKSPSKK	[14] Phospho (ST)	26336	88071	122872	41198	136909	201652	193888	114595	0.02	2.32
TOM70_MOUSE	ASPALGSGHHDGSGDSLEMSSLDR	[2] Phospho (ST)|[19] Oxidation (M)	509182	677789	117247	361214	1157851	1198182	504337	1025405	0.03	2.33
KPCD2_MOUSE	RLSSTSLASGHSVR	[3] Phospho (ST)	108707	253873	304845	181150	416607	609138	665551	291096	0.03	2.34
KPCD2_MOUSE	RLSSTSLASGHSVR	[5] Phospho (ST)	108707	253873	304845	181150	416607	609138	665551	291096	0.03	2.34
KPCD2_MOUSE	RLSSTSLASGHSVR	[4] Phospho (ST)	108707	253873	304845	181150	416607	609138	665551	291096	0.03	2.34
ACINU_MOUSE	SSSFSEEKGESDDEKPR	[11] Phospho (ST)	13293	21714	14530	1	16331	34696	31879	33870	0.04	2.36
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[34] Phospho (ST)	185621	705581	964413	502596	1469286	1599103	1786682	712730	0.03	2.36
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[31] Phospho (ST)	185621	705581	964413	502596	1469286	1599103	1786682	712730	0.03	2.36
DYN2_MOUSE	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	[10] Phospho (ST)	185621	705581	964413	502596	1469286	1599103	1786682	712730	0.03	2.36
RHG27_MOUSE	LSPVWETHTDTGTGRPYYYNPDTGVTTWESPFETPEGTTSPATSR	[40] Phospho (ST)	70779	180249	115668	52537	175266	347962	305131	177821	0.03	2.40
SEPT2_MOUSE	IYHLPDAESDEDEDFKEQTR	[9] Phospho (ST)	118697	402250	212536	300266	791667	668552	252829	814025	0.04	2.44
FOXK1_MOUSE	EGSPIPHDPDLGSK	[3] Phospho (ST)	93390	328818	289483	172640	388867	726329	744493	326372	0.04	2.47
PAK2_MOUSE	YLSFTPPEKDGFPSGTPALNTK	[3] Phospho (ST)	46469	257706	54210	132954	331102	339968	286235	263097	0.01	2.48
PAK2_MOUSE	YLSFTPPEKDGFPSGTPALNTK	[5] Phospho (ST)	46469	257706	54210	132954	331102	339968	286235	263097	0.01	2.48
FHOD1_MOUSE	APEPGSTGSASPVGSTPSTGSAPPTNPAFSSTGPASGLLR	[21] Phospho (ST)	79722	136554	686613	252430	786017	601493	1012852	506919	0.05	2.52
FHOD1_MOUSE	APEPGSTGSASPVGSTPSTGSAPPTNPAFSSTGPASGLLR	[19] Phospho (ST)	79722	136554	686613	252430	786017	601493	1012852	506919	0.05	2.52
FHOD1_MOUSE	APEPGSTGSASPVGSTPSTGSAPPTNPAFSSTGPASGLLR	[9] Phospho (ST)	79722	136554	686613	252430	786017	601493	1012852	506919	0.05	2.52
FHOD1_MOUSE	APEPGSTGSASPVGSTPSTGSAPPTNPAFSSTGPASGLLR	[15] Phospho (ST)	79722	136554	686613	252430	786017	601493	1012852	506919	0.05	2.52
FHOD1_MOUSE	APEPGSTGSASPVGSTPSTGSAPPTNPAFSSTGPASGLLR	[11] Phospho (ST)	79722	136554	686613	252430	786017	601493	1012852	506919	0.05	2.52
DDX21_MOUSE	EIITEEPSEEEADMPKPK	[8] Phospho (ST)|[14] Oxidation (M)	2528	47029	23041	57674	93353	75413	56546	106223	0.02	2.54
GNL1_MOUSE	EEQTDTSDGESVTHHIR	[7] Phospho (ST)	43861	94214	21549	24987	141904	177844	77809	78053	0.05	2.58
LCP2_MOUSE	NLPLPVPNRPQPPSPGEEETPLDEEWYVSYITRPEAEAALR	[14] Phospho (ST)	450199	247195	413837	564235	626186	1571748	1227882	903726	0.02	2.58
EIF3G_MOUSE	GIPLPTGDTSPEPELLPGDPLPPPK	[10] Phospho (ST)	559412	888228	310074	270818	2101129	1246893	964820	955052	0.04	2.60
NSF1C_MOUSE	KKSPNELVDDLFK	[3] Phospho (ST)	102248	183513	76698	232870	488992	408873	245125	411742	0.01	2.61
FLNA_MOUSE	LQVEPAVDTSGVQCYGPGIEGQGVFR	[9] Phospho (ST)	91539	33085	126346	220505	311331	578540	257390	248030	0.04	2.96
FLNA_MOUSE	LQVEPAVDTSGVQCYGPGIEGQGVFR	[10] Phospho (ST)	91539	33085	126346	220505	311331	578540	257390	248030	0.04	2.96
PURA1_MOUSE	LDILDVLSEIK	[8] Phospho (ST)	89058	190424	59794	189881	328216	616950	294076	333209	0.02	2.97
MDC1_MOUSE	GRPSKSPNKTPEPLISTGPELQPPTSIEQPVIPKPTSR	[17] Phospho (ST)	2321	1	71978	81815	184019	137431	125945	67246	0.03	3.30
CP100_MOUSE	ELTAQITSIK	[8] Phospho (ST)	57706	50790	69067	66864	237649	359239	112375	146630	0.03	3.50
DEN1C_MOUSE	VPTRHSPPESPQLLVSTEPNSDAVQR	[6] Phospho (ST)	49797	136224	100306	103579	199106	568200	434867	205337	0.03	3.61
DEN1C_MOUSE	VPTRHSPPESPQLLVSTEPNSDAVQR	[10] Phospho (ST)	49797	136224	100306	103579	199106	568200	434867	205337	0.03	3.61
SDPR_MOUSE	DEEALEDSAEEK	[8] Phospho (ST)	102640	206060	87677	15828	244042	476377	280972	489039	0.01	3.62
SRRM1_MOUSE	KVELSESEEDKGSK	[5] Phospho (ST)	44463	1	63752	12858	151856	199986	149612	22652	0.05	4.33
SRRM1_MOUSE	KVELSESEEDKGSK	[7] Phospho (ST)	44463	1	63752	12858	151856	199986	149612	22652	0.05	4.33
PHAR4_MOUSE	SSSPVLVEEEPER	[3] Phospho (ST)	13700	37494	31872	17143	87558	156819	137462	60067	0.01	4.41
CR025_MOUSE	RDSSESQLASTESDKPTTGR	[4] Phospho (ST)	21098	778	14756	10029	65199	77879	24740	42500	0.02	4.51
CR025_MOUSE	RDSSESQLASTESDKPTTGR	[6] Phospho (ST)	21098	778	14756	10029	65199	77879	24740	42500	0.02	4.51
CR025_MOUSE	RDSSESQLASTESDKPTTGR	[3] Phospho (ST)	21098	778	14756	10029	65199	77879	24740	42500	0.02	4.51
HDAC1_MOUSE	MLPHAPGVQMQAIPEDAIPEESGDEDEEDPDKR	[22] Phospho (ST)	170175	122111	193795	27105	608235	790426	769587	154938	0.02	4.53
NP1L4_MOUSE	EFITGDVEPTDAESAWHSENEEEDKLAGDMK	[18] Phospho (ST)	41181	568580	87604	181289	800218	1993336	1212840	429859	0.05	5.05
SATB1_MOUSE	QPTVASSAESDEENRQK	[10] Phospho (ST)	3722	39194	33887	978	79627	191656	123885	38889	0.04	5.58
CAP1_MOUSE	LEAVSHTSDMHCGYGDSPSK	[5] Phospho (ST)	19123	3702	1	141364	324502	578663	38280	491931	0.04	8.73
MP2K2_MOUSE	RKPVLPALTINPTIAEGPSPTSEGASEANLVDLQK	[19] Phospho (ST)	1	1	186	1	10440	8889	4574	27289	0.04	271.42
PRP4B_MOUSE	KKSPIVNER	[3] Phospho (ST)	1	1	1	1	28676	48414	79276	1845	0.05	39552.71

Table S18. Molecular Functions Associated with Proteins with Upregulated Phosphorylation in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190429)**						
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**						
Analyzed List:	**Client Text Box Input (Mus musculus)**						
Reference List:	**Mus musculus (all genes in database)**						
Test Type:	**FISHER**						
Correction:	**FDR**						
GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (48)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
actin binding (GO:0003779)	414	7	0.89	+	7.85	3.03E-05	4.62E-02

Table S19. Biological Processes Associated with Proteins with Downregulated Phosphorylation in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190429)**						
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**						
Analyzed List:	**Client Text Box Input (Mus musculus)**						
Reference List:	**Mus musculus (all genes in database)**						
Test Type:	**FISHER**						
Correction:	**FDR**						
GO biological process complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (65)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
lamellipodium morphogenesis (GO:0072673)	7	3	0.02	+	> 100	2.77E-06	4.83E-03
viral translational termination-reinitiation (GO:0075525)	5	2	0.01	+	> 100	1.73E-04	4.60E-02
positive regulation of protein import (GO:1904591)	47	5	0.14	+	36.49	4.15E-07	1.63E-03
positive regulation of protein import into nucleus (GO:0042307)	42	4	0.12	+	32.67	9.68E-06	1.08E-02
regulation of protein import (GO:1904589)	66	5	0.19	+	25.99	1.99E-06	3.91E-03
translational initiation (GO:0006413)	57	4	0.17	+	24.07	3.00E-05	1.88E-02
positive regulation of protein localization to nucleus (GO:1900182)	74	5	0.22	+	23.18	3.39E-06	5.31E-03
regulation of protein import into nucleus (GO:0042306)	61	4	0.18	+	22.49	3.85E-05	2.08E-02
positive regulation of nucleocytoplasmic transport (GO:0046824)	63	4	0.18	+	21.78	4.34E-05	2.13E-02
integrin-mediated signaling pathway (GO:0007229)	73	4	0.21	+	18.80	7.50E-05	2.80E-02
regulation of protein localization to nucleus (GO:1900180)	114	5	0.33	+	15.04	2.51E-05	1.88E-02
response to hydrogen peroxide (GO:0042542)	94	4	0.27	+	14.60	1.91E-04	4.92E-02
positive regulation of intracellular protein transport (GO:0090316)	129	5	0.38	+	13.30	4.44E-05	2.11E-02
regulation of organelle assembly (GO:1902115)	200	6	0.58	+	10.29	2.99E-05	1.95E-02
regulation of cellular amide metabolic process (GO:0034248)	356	7	1.04	+	6.74	8.70E-05	3.10E-02
cell morphogenesis (GO:0000902)	709	13	2.07	+	6.29	1.30E-07	1.02E-03
plasma membrane bounded cell projection morphogenesis (GO:0120039)	455	8	1.33	+	6.03	5.71E-05	2.42E-02
cell projection morphogenesis (GO:0048858)	459	8	1.34	+	5.98	6.06E-05	2.44E-02
cellular component morphogenesis (GO:0032989)	810	14	2.36	+	5.93	8.11E-08	1.27E-03
posttranscriptional regulation of gene expression (GO:0010608)	408	7	1.19	+	5.89	1.99E-04	4.95E-02
cell part morphogenesis (GO:0032990)	484	8	1.41	+	5.67	8.72E-05	3.04E-02
mRNA metabolic process (GO:0016071)	509	8	1.48	+	5.39	1.23E-04	3.85E-02
cell activation (GO:0001775)	583	9	1.70	+	5.30	5.13E-05	2.23E-02
cell morphogenesis involved in differentiation (GO:0000904)	545	8	1.59	+	5.04	1.95E-04	4.92E-02
neuron projection development (GO:0031175)	667	9	1.94	+	4.63	1.41E-04	4.25E-02
regulation of cellular component biogenesis (GO:0044087)	914	11	2.66	+	4.13	6.61E-05	2.53E-02
plasma membrane bounded cell projection organization (GO:0120036)	1018	12	2.97	+	4.04	3.60E-05	2.02E-02
cell projection organization (GO:0030030)	1069	12	3.12	+	3.85	5.75E-05	2.37E-02
nucleic acid metabolic process (GO:0090304)	1725	19	5.03	+	3.78	3.05E-07	1.60E-03
RNA metabolic process (GO:0016070)	1211	13	3.53	+	3.68	4.26E-05	2.15E-02
negative regulation of cell death (GO:0060548)	1029	11	3.00	+	3.67	1.86E-04	4.87E-02
regulation of organelle organization (GO:0033043)	1227	13	3.58	+	3.63	4.87E-05	2.18E-02
gene expression (GO:0010467)	1585	16	4.62	+	3.46	9.95E-06	9.76E-03
negative regulation of cellular biosynthetic process (GO:0031327)	1409	14	4.11	+	3.41	4.76E-05	2.19E-02
negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	1325	13	3.86	+	3.37	1.05E-04	3.45E-02
negative regulation of biosynthetic process (GO:0009890)	1446	14	4.22	+	3.32	6.28E-05	2.46E-02
negative regulation of macromolecule biosynthetic process (GO:0010558)	1360	13	3.96	+	3.28	1.37E-04	4.20E-02
negative regulation of gene expression (GO:0010629)	1570	14	4.58	+	3.06	1.50E-04	4.20E-02
nucleobase-containing compound metabolic process (GO:0006139)	2141	19	6.24	+	3.04	7.55E-06	1.08E-02
anatomical structure morphogenesis (GO:0009653)	2148	19	6.26	+	3.03	7.91E-06	9.55E-03
cellular nitrogen compound metabolic process (GO:0034641)	2720	23	7.93	+	2.90	1.29E-06	3.36E-03
heterocycle metabolic process (GO:0046483)	2278	19	6.64	+	2.86	1.82E-05	1.59E-02
cellular aromatic compound metabolic process (GO:0006725)	2344	19	6.83	+	2.78	2.72E-05	1.85E-02
negative regulation of macromolecule metabolic process (GO:0010605)	2404	19	7.01	+	2.71	3.86E-05	2.02E-02
organic cyclic compound metabolic process (GO:1901360)	2545	20	7.42	+	2.70	2.43E-05	1.91E-02
negative regulation of cellular metabolic process (GO:0031324)	2386	18	6.96	+	2.59	1.20E-04	3.84E-02
regulation of cellular component organization (GO:0051128)	2451	18	7.15	+	2.52	1.68E-04	4.56E-02
negative regulation of metabolic process (GO:0009892)	2663	19	7.76	+	2.45	1.53E-04	4.22E-02
regulation of cellular biosynthetic process (GO:0031326)	3383	24	9.86	+	2.43	1.51E-05	1.39E-02
regulation of macromolecule biosynthetic process (GO:0010556)	3246	23	9.46	+	2.43	2.53E-05	1.80E-02
regulation of biosynthetic process (GO:0009889)	3453	24	10.07	+	2.38	2.13E-05	1.76E-02
cellular macromolecule metabolic process (GO:0044260)	3963	27	11.55	+	2.34	9.68E-06	1.01E-02
macromolecule metabolic process (GO:0043170)	5049	33	14.72	+	2.24	7.75E-07	2.43E-03
negative regulation of cellular process (GO:0048523)	4482	29	13.07	+	2.22	7.55E-06	9.87E-03
cellular developmental process (GO:0048869)	3715	24	10.83	+	2.22	7.84E-05	2.86E-02
regulation of gene expression (GO:0010468)	3616	23	10.54	+	2.18	1.49E-04	4.24E-02
negative regulation of biological process (GO:0048519)	5005	30	14.59	+	2.06	3.34E-05	2.02E-02
developmental process (GO:0032502)	5369	31	15.65	+	1.98	3.38E-05	1.97E-02
regulation of macromolecule metabolic process (GO:0060255)	5232	30	15.25	+	1.97	9.12E-05	3.11E-02
cellular component organization or biogenesis (GO:0071840)	5262	30	15.34	+	1.96	9.40E-05	3.14E-02
cellular component organization (GO:0016043)	5086	29	14.83	+	1.96	1.47E-04	4.27E-02
nitrogen compound metabolic process (GO:0006807)	5669	31	16.53	+	1.88	1.46E-04	4.33E-02
cellular process (GO:0009987)	13888	58	40.49	+	1.43	1.99E-06	4.45E-03

Table S20. Molecular Functions Associated with Proteins with Downregulated Phosphorylation in Meno/Ang II vs. Ang II.

Analysis Type:	**PANTHER Overrepresentation Test (Released 20190429)**						
Annotation Version and Release Date:	**GO Ontology database Released 2019-02-02**						
Analyzed List:	**Client Text Box Input (Mus musculus)**						
Reference List:	**Mus musculus (all genes in database)**						
Test Type:	**FISHER**						
Correction:	**FDR**						
GO molecular function complete	**Mus musculus - REFLIST (22296)**	**Client Text Box Input (65)**	**Client Text Box Input (expected)**	**Client Text Box Input (over/under)**	**Client Text Box Input (fold Enrichment)**	**Client Text Box Input (raw P-value)**	**Client Text Box Input (FDR)**
leptin receptor binding (GO:1990460)	3	2	0.01	+	> 100	8.27E-05	3.44E-02
translation regulator activity, nucleic acid binding (GO:0090079)	96	5	0.28	+	17.87	1.13E-05	6.48E-03
translation factor activity, RNA binding (GO:0008135)	78	4	0.23	+	17.59	9.59E-05	3.66E-02
translation regulator activity (GO:0045182)	127	5	0.37	+	13.50	4.13E-05	1.89E-02
RNA binding (GO:0003723)	1032	15	3.01	+	4.99	2.37E-07	2.17E-04
transcription factor binding (GO:0008134)	699	10	2.04	+	4.91	3.57E-05	1.81E-02
protein-containing complex binding (GO:0044877)	1210	15	3.53	+	4.25	1.72E-06	1.12E-03
nucleic acid binding (GO:0003676)	3055	26	8.91	+	2.92	1.58E-07	1.80E-04
heterocyclic compound binding (GO:1901363)	4950	36	14.43	+	2.49	6.96E-09	3.18E-05
organic cyclic compound binding (GO:0097159)	5053	36	14.73	+	2.44	1.23E-08	2.82E-05
protein binding (GO:0005515)	9011	46	26.27	+	1.75	1.36E-06	1.04E-03
binding (GO:0005488)	13135	58	38.29	+	1.51	1.58E-07	2.40E-04

Figure S1A and S1B.

Blood pressures were measured via tail cuff as previously published [9] in all animals used for the proteomic analysis (n=4). 14 day SBP and MAP are shown in Control, Ang II and Menopause Ang II treated mice.