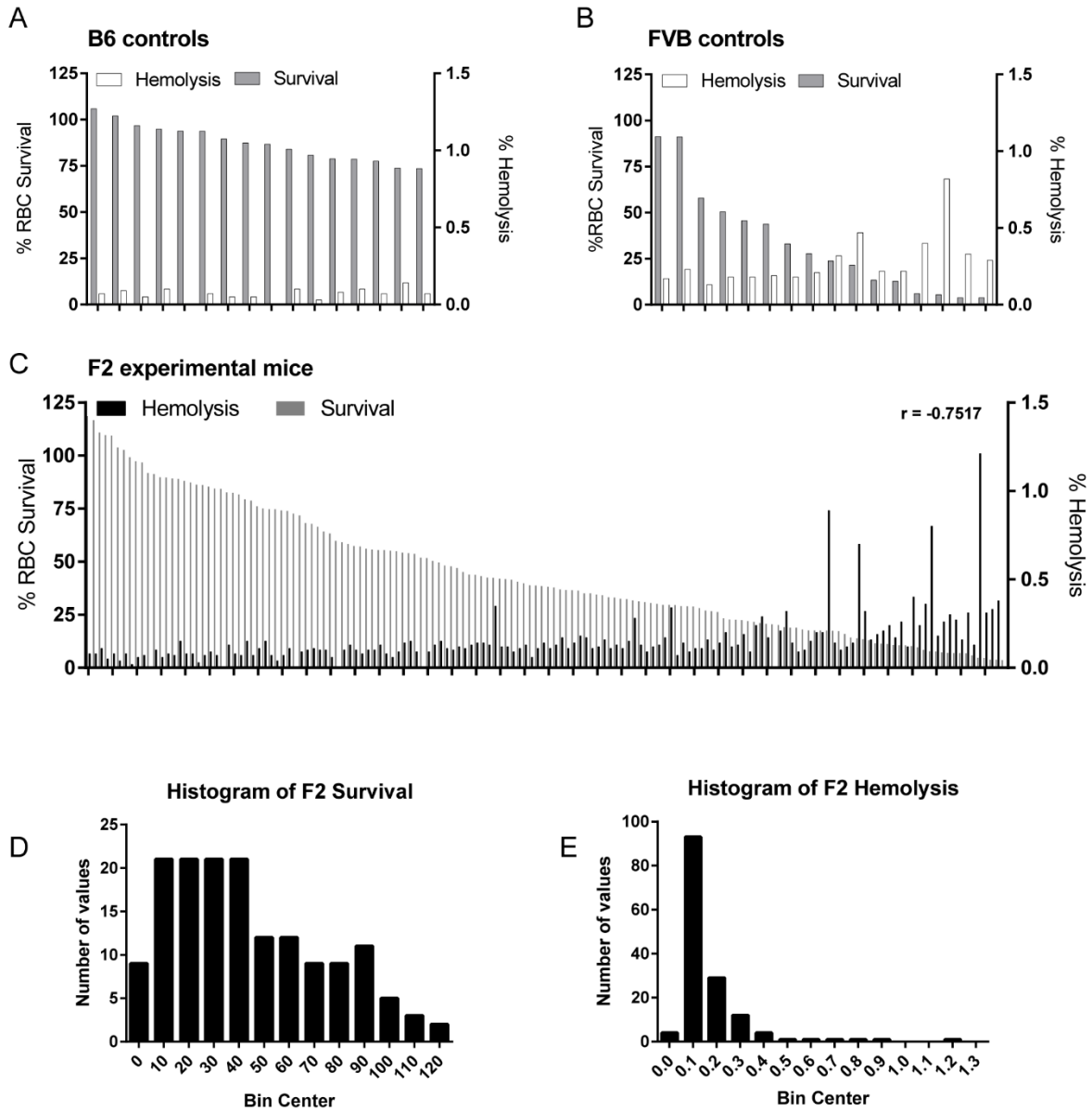
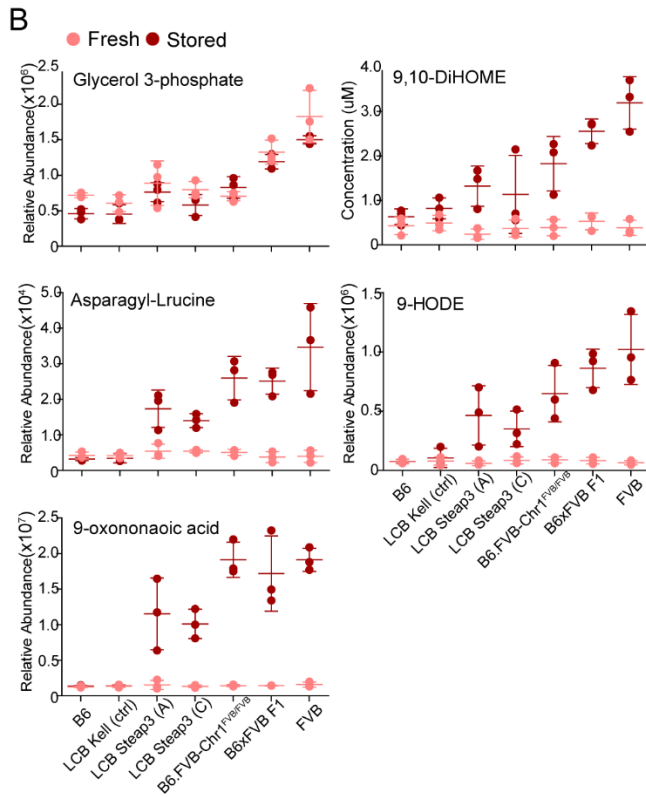
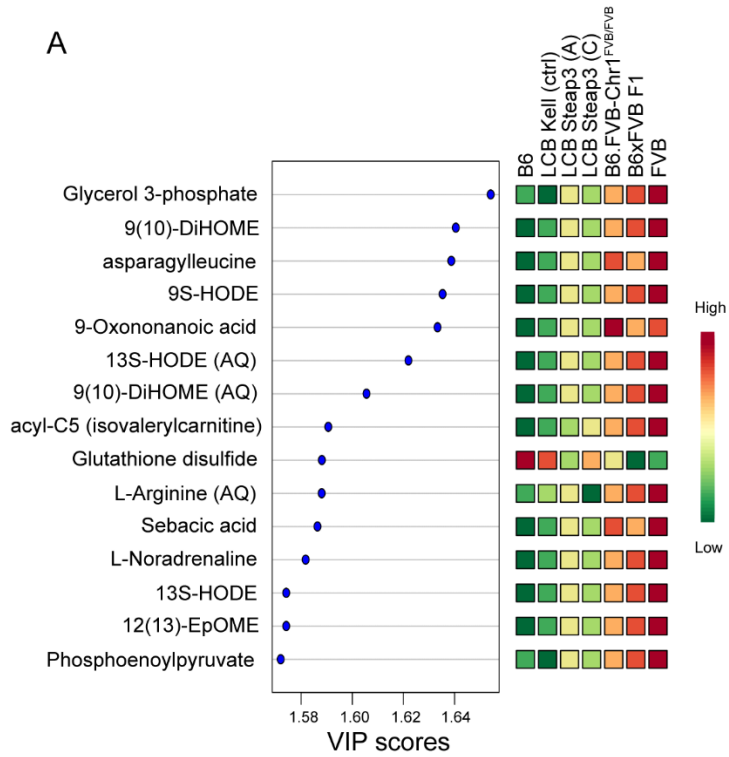


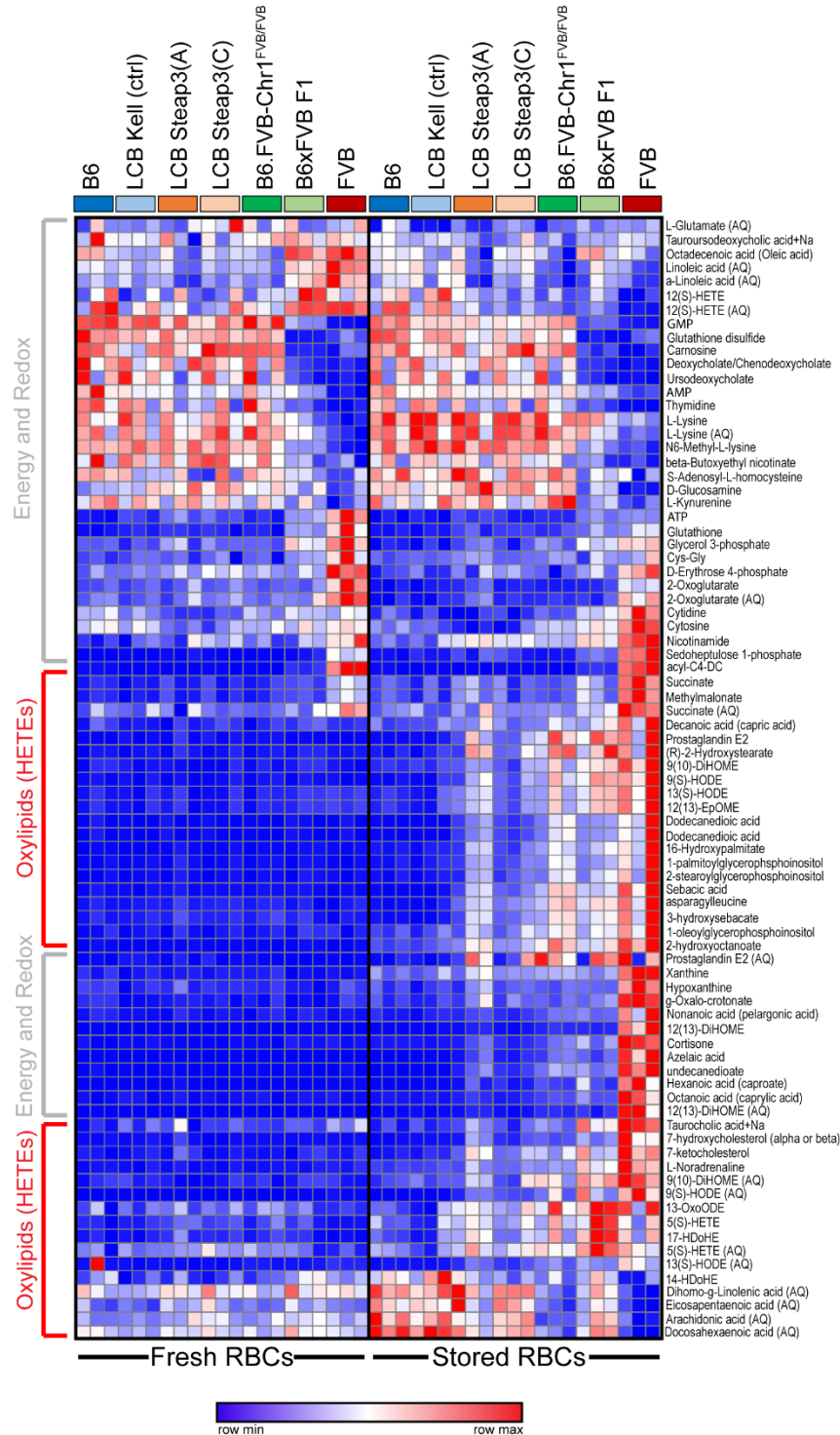
Supplemental Figure 1: Distribution of 24hr post-transfusion recoveries and spontaneous hemolysis from controls and the 156 F2 mice. 24hr recoveries (left axis; grey bars) and spontaneous hemolysis (right axis; white bars) of RBCs from 16 individual B6 mice (A), 16 individual FVB mice (B), and each of the 156 F2 experimental mice (C). (D) Frequency distributions of the 24hr survival data from the 156 experimental F2 mice. (E) Frequency distributions of the spontaneous hemolysis from the 156 experimental F2 mice.



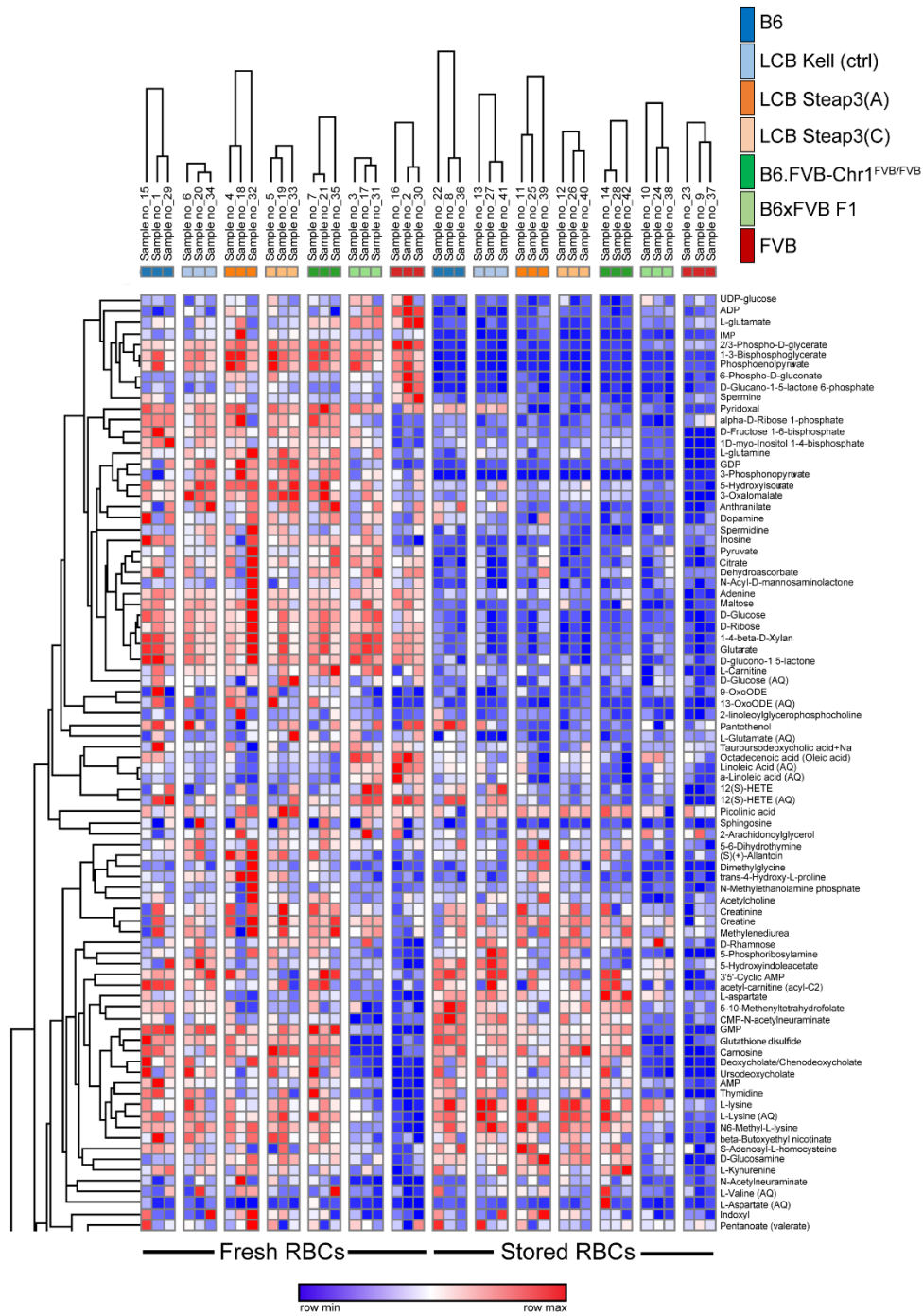
Supplemental Figure 2: VIP and top 5 metabolites: (A) Variable importance in projection analysis (VIP) was applied to the data set with a focus on which analytes carried over from FVB mice into congenic and transgenic systems. (B) The top 5 VIP identified metabolites are shown.

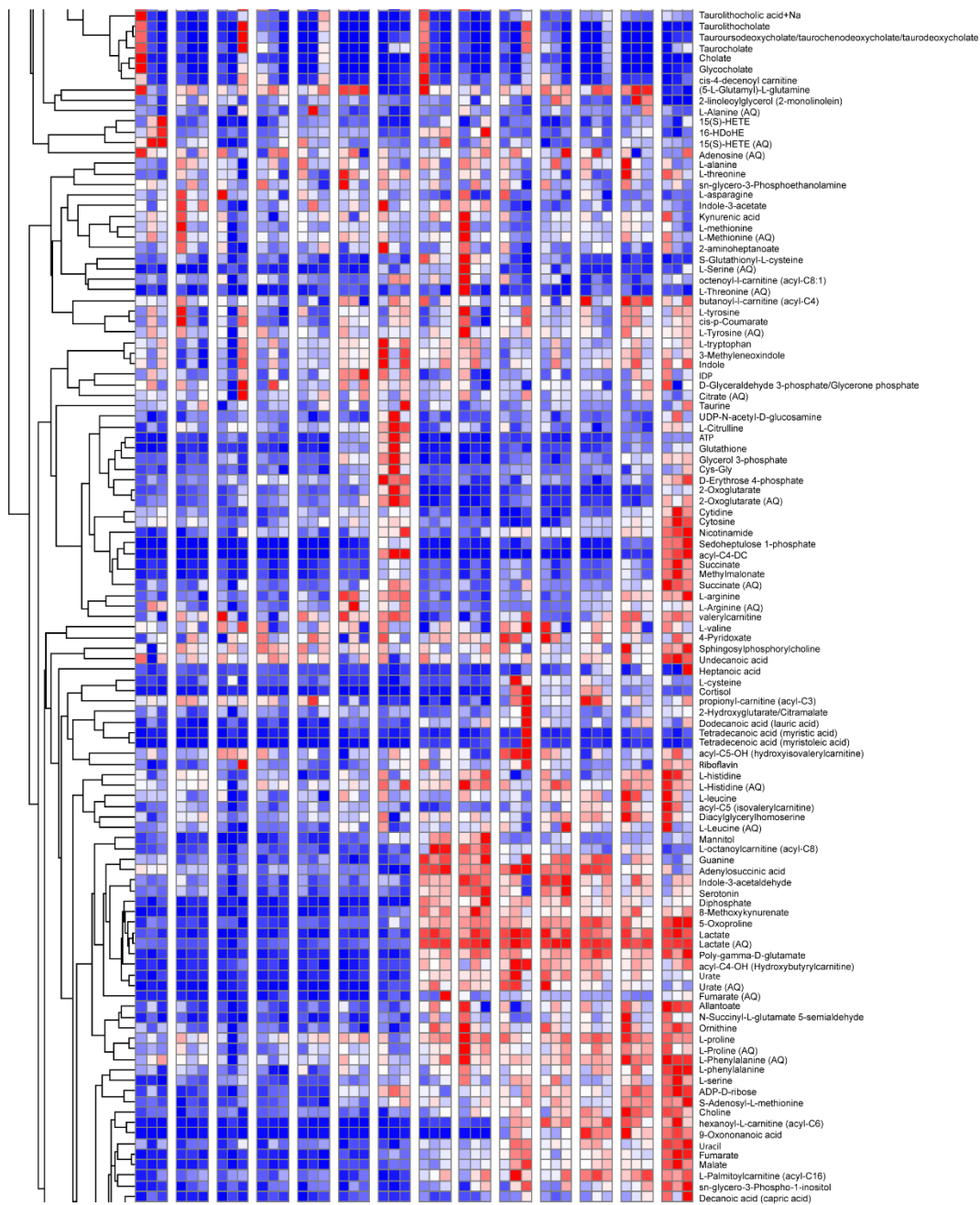


Supplemental Figure 3: Select Classes of Metabolites Carry Forward into Congenic Mice and Steap3 Transgenic Mice. A heat map depicts the relative quantitations of the indicated analytes for RBCs from each strain from each of 3 experiments. Left: fresh RBCs. Right: stored RBCs. Analytes are broken down by chemical class. Classes of compounds that generally carry forward are indicated by a red label (left), whereas those that do not carry forward are indicated by a gray label.



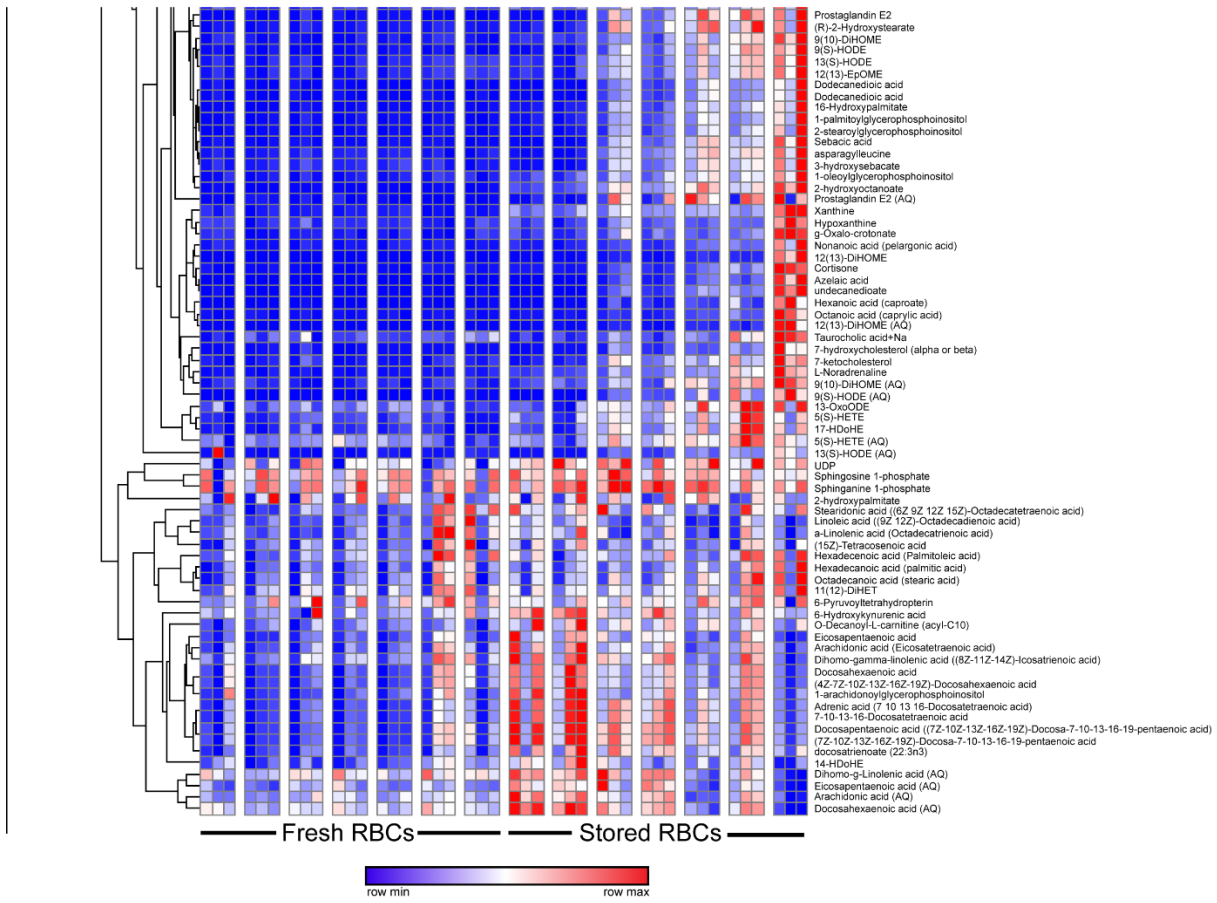
Supplemental Figure 4 (3 parts): An expanded list of compounds is presented that is too large to be included in the main text.





———— Fresh RBCs ————— ————— Stored RBCs —————





Supplemental Table 1: *SNP assays used for genotyping crossover mice.* SNP ID #s are shown along with the location of each SNP on Chromosome 1 and the predicted nucleotide at that position for both the B6 and FVB genome. Assay IDs indicate the catalog # of the Taqman SNP genotyping assay used.

Supplemental Table 2: *Genes and Genetic Elements in the 3Mb Chromosome 1 region.* The 20 open reading frames (ORFs) contained within the B6.FVB-Chr1 region, along with their respective MGI database numbers, position within the chromosome 1 region and the Taqman gene expression assay used for expression determination (Top panel). 42 additional genetic elements have been identified in the B6.FVB-Chr1 region, including rRNAs, snRNAs, miRNAs, lincRNAs and a few unclassified predicted genes (Bottom panel). Taqman gene expression assays were available for 4 of these genetic elements (in bold) however no amplification was seen for any of them (data not shown).

Supplemental Table 3: *Genes with Non-Synonymous SNPs in the 3Mb Chromosome 1 region.* The presence of non-synonymous SNPs within coding regions of genes in the B6.FVB-Chr1 region was assessed by searching the MGI database (Jackson Labs) using the coordinates delineated by the B6.FVB-Chr1 SNP genotyping. 7 non-synonymous SNPs located within 4 different ORFs were identified.

SNP ID (dbSNP Build 142)	Map Position (GRCm38)	Gene	Category	B6	FVB
rs30812533	Chr1:118,868,087	Gli2	Coding-NonSynonymous	C	T
rs30698944	Chr1:119,002044	Gli2	Coding-NonSynonymous	G	T
rs31178208	Chr1:120,063,246	Sctr	Coding-NonSynonymous; mRNA-UTR	G	T
rs31842162	Chr1:120,063,257	Sctr	Coding-NonSynonymous; mRNA-UTR	G	A
rs32405796	Chr1:120,176,728	3110009E18Rik	Coding-NonSynonymous; intron	G	A
rs30773456	Chr1:120,227,750	Steap3	Coding-NonSynonymous	T	C
rs30771292	Chr1:120,234,4378	Steap3	Coding-NonSynonymous	G	A