Legends for Supplementary Figures and Tables:

Fig. S1. Venn diagram representation of sex-specific gene expression profiles in sets of livers representing three mixed or outbred strains of mice. Diagram is based on a total of 4104 genes showing sex-specificity (M-WT:F-WT >1.5 or < 0.66 at $p<0.05$) for any one of three independent microarray data sets, 129 x BALB/c from the STAT5b-KO study (upper left), 129J x Black Swiss from the present STAT5a-KO study (upper right), and ICR mice (bottom). 523 genes were found to be sex-specific in all three data sets (center).

Table S1. Mouse qPCR primer sets and GenBank accession numbers. qPCR primer pairs were designed as described in "Materials and Methods." Nucleotide numbering indicating the position of the resultant PCR amplicon is based on the indicated GenBank accession numbers.

Table S2. Average expression ratios for all 3905 genes of interest.

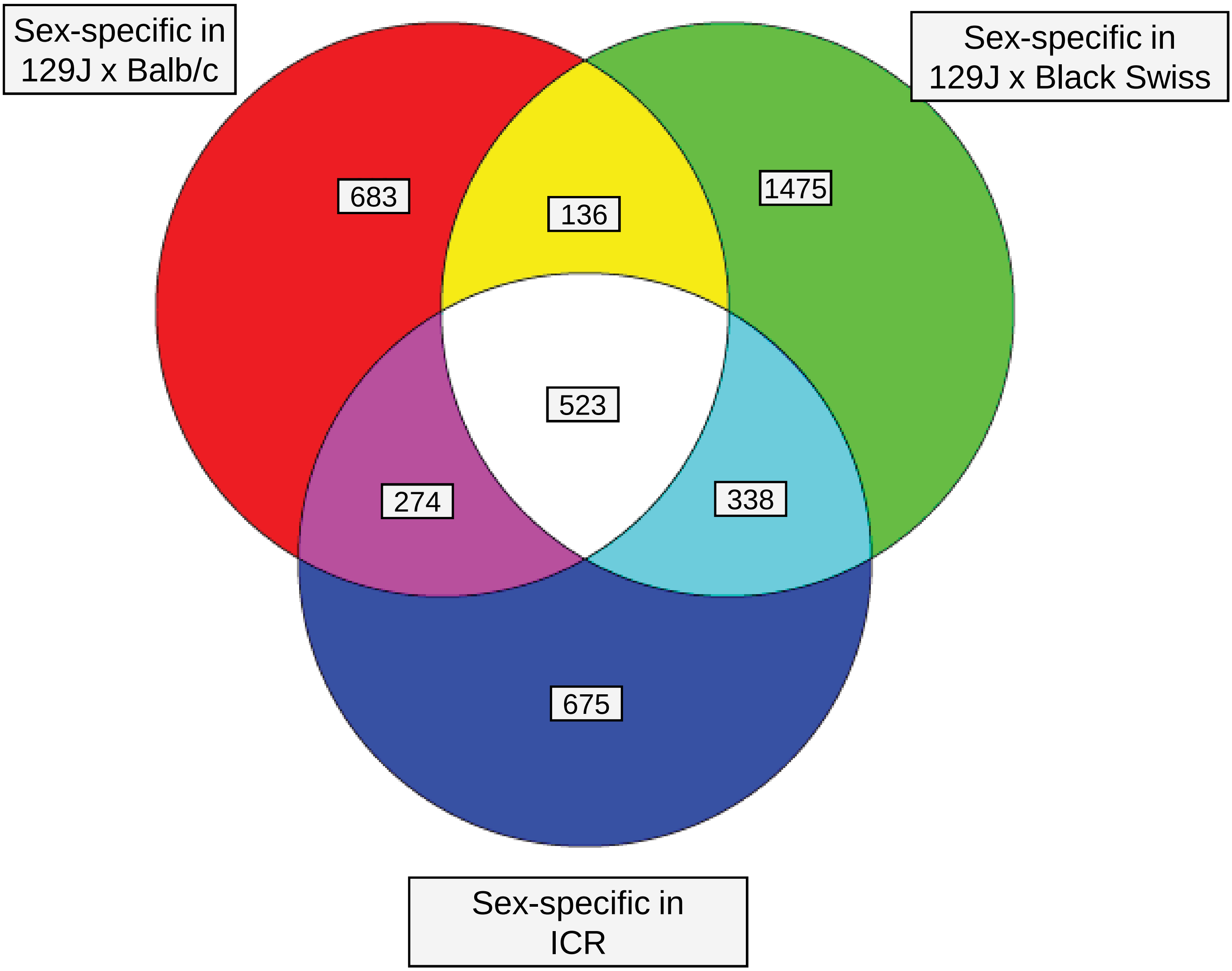
Table S3. Expression ratios determined by qPCR and microarray analysis for select genes - Ratios shown for each of the four comparisons indicated were determined by microarray analysis or by qPCR, as indicated for select genes from groups 13 and 14 (c.f., Tables 4 and 5. Values shown in bold are significant by P-value, as indicated in Tables 4 and 5 (microarray data) or as indicated at the bottom of this Table. Results were in good agreement for the two methods, although in some cases ratios determined by qPCR were substantially greater than those determined by microarray (e.g., AB056442 and Acot3), reflecting the much greater dynamic range of the qPCR assay. Significant values are shown in Bold.

Table S4. 1028 sex-specific genes based on 10 independent replicate microarrays from three mixed or outbred mouse strains treated as a single data set with thresholds of 1.5-fold differential expression and $P < 0.01$. Group assignemnt and TFS numbers are based on the present STAT5a-KO microarray study (Table 3 and Supplemental Table 1).

Table S5. 523 sex-specific genes where the M-WT:F-WT ratio met the 1.5-fold and $P<0.05$ thresholds in each of three independent data sets, based on three mixed or outbred mouse strains.

Table S6. Lists of genes that showed sex-specificity in only one of the three mixed or outbred mouse strains by ANOVA (FDR < 0.001). Table is comprised of three separate sections, marked A, B and C.

Fig. S1


Sex-specific in
129J x Balb/c
Sex-specific in
129J x Black Swiss
683
136
1475
523
274
338
675
Sex-specific in
ICR