Figure S1

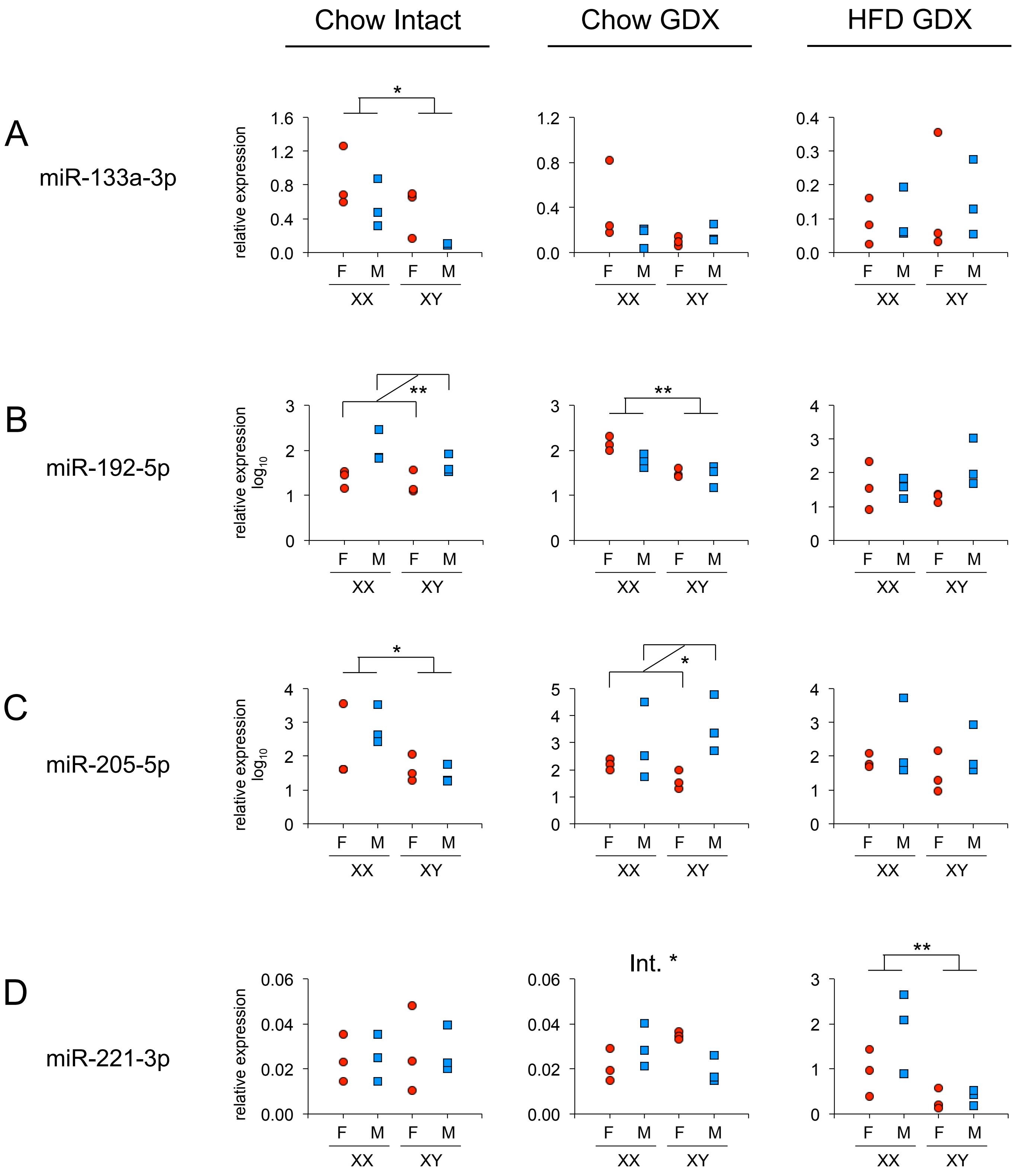

Figure S1. Expression of select miRNAs with distinct sex- and sex-chromosome-biased patterns. Levels of expression for miR-133a-3p (A), miR-192-5p (B), miR-205-5p (C), and miR-221-3p (D) were measured by TaqMan qPCR in chow-fed gonadally intact and gonadectomized mice, and in high fat diet-fed gonadectomized mice. Each point represents an individual mouse. Note that for miR-192-5p and miR-205-5p, values are plotted on logarithmic scale. Groups were compared using two-way ANOVA. HFD, high fat diet; GDX, gonadectomized; F, female; M, male; *, $p<0.05$; **, $p<0.01$.

Table S1. Enrichment of specific pathways in predicted targets of sex-influenced miRNAs

KEGG Pathway	Fold Enrichment	Bonferroni-corrected *P*-value
Chow-fed, gonadally intact male–female differences		
mmu04150: mTOR signaling pathway	7.41	0.003
Chow-fed, gonadally intact XX–XY differences		
mmu04144: Endocytosis	4.29	0.004
Chow-fed, gonadectomized male–female differences		
no significant KEGG pathways		
Chow-fed, gonadectomized XX–XY differences		
mmu04120: Ubiquitin mediated proteolysis	7.67	0.03
High fat diet-fed, gonadectomized male–female differences		
no significant KEGG pathways		
High fat diet-fed, gonadectomized XX–XY differences		
mmu04720: Long-term potentiation	6.19	0.03
mmu04070: Phosphatidylinositol signaling system	5.77	0.05

Table S1.Predicted targets of sex-biased miRNAs were enriched for specific cellular pathways. miRNAs with exclusively male–female or XX–XY $\log_2$ fold changes greater than 0.5 were selected for target prediction. Targets for miRNAs were predicted by mirdb.org, version 5.0. All targets with a prediction score of 95 or above were included in subsequent functional analysis using DAVID, version 6.7. The functional annotation tool was used to identify enriched annotation terms in the KEGG Pathway. Unique KEGG pathways with a Bonferroni-corrected *p*-value < 0.05 were included in this table.