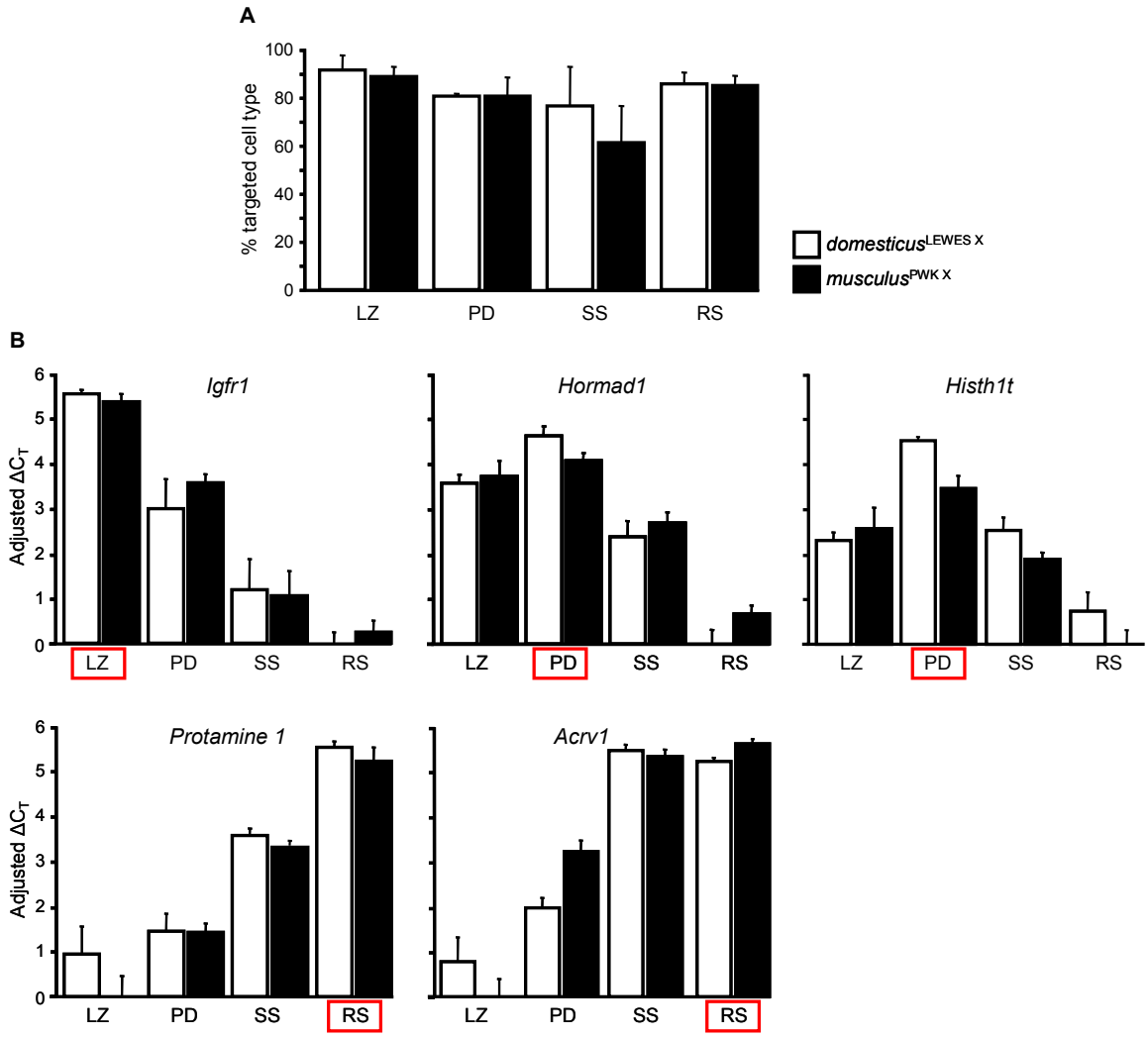

Figure S1 Validations of germ cell population purity. (A) Percentage of targeted cell types based on Giemsa staining for spermatogonia/early prophase I (LZ), pachytene/diplotene (PD), secondary spermatocyte (SS), and round spermatid (RS) populations from reciprocal F_1 males (white bars, *domesticus*^{LEWES} X chromosome; black bars, *musculus*^{PWK} X chromosome). Data are presented as genotype means + 1 SE. (B) Autosomal genes that are expressed in different germ cell types are enriched in the correct germ cell populations from reciprocal F_1 males. The cell population in which each gene should be most highly expressed is indicated with a red box. All genes were enriched in the expected cell populations with the exception of *Acrv1*, which was equally enriched in the SS and RS populations. Expression was normalized relative to *Ubc* (ΔC_T) and adjusted to produce positive values by setting the lowest expression level to zero. Data are presented as genotype means + 1 SE.

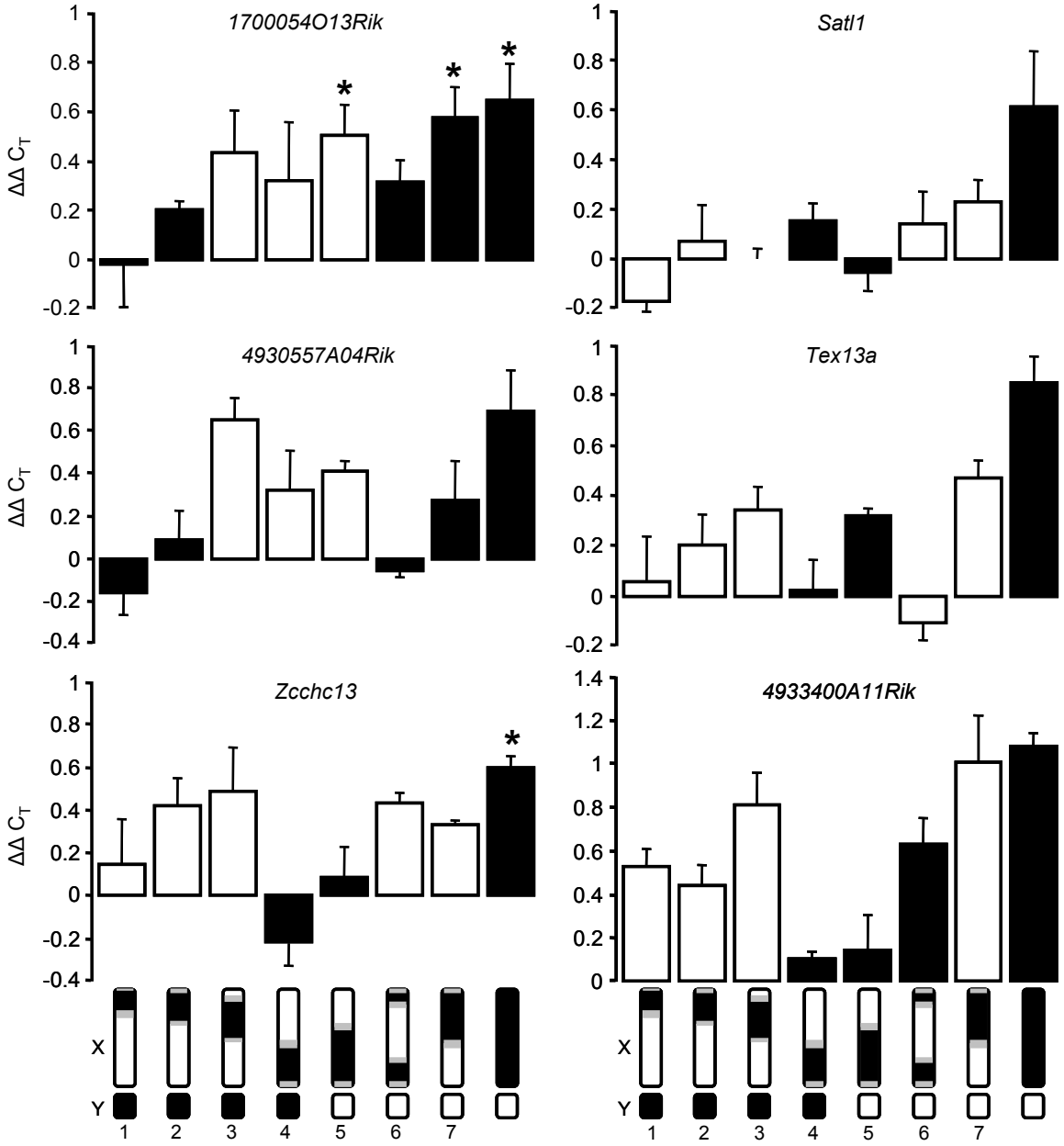

Figure S2 Relative expression of six X-linked genes in the testes of F_1 males. $\Delta\Delta C_T$ is the normalized difference in expression between experimental genotypes (shown on the X axis) and the fertile F_1. X introgression genotypes are numbered 1-7; black bars denote the *musculus*^{PWK} allele at a given locus, white bars denote the *domesticus*^{LEWES} allele. Error bars are +/- 1 SE. Tests for significant differences between experimental and control genotypes were performed on ΔC_T values with ANOVA followed by Dunnett *post hoc* tests, * $P \leq 0.05$.

Table S1 Primers used in this study

Gene	Chr.	Primer name	Primer sequence	Amplicon size (bp)	Reference
4930557A04Rik	X	A04Rik F	KGCTGATGAGACTCCAGGAT	163	*a*
		A04Rik R	TCCACCAACAAGGGAGTCAT		
Efhc2	X	Efhc2 F	CATCCTGGGTTGCTTTTGAT	136	*a*
		Efhc2 R	TGAATGGTGTCATCTTCAAGG		
Actrt1	X	Actrt1 F	CTCAAAAATGGTCTGCAACAGC	164	*b*
		Actrt1 R	TCTTGATAGGGGTTCCCTCAAA		
1700013H16Rik	X	H16Rik F	GCAATGGCACAGCTTAATGA	68	*a*
		H16Rik R	TCCTCATTCCATTGCTCAAA		
Fmr1	X	Fmr1 F	GGAAAAGCCAGACAGCGTAG	165	*a*
		Fmr1 R	CCTGTGCCATCTTGCCTACT		
4930468A15Rik	X	A15Rik F	CACTGGCAATGGCAACTCTA	162	*a*
		A15Rik R	GCCTGCGATAACTCCTGGTA		
Dmrtc1a	X	Dmrtc1a F	GAGACGCCTGGTTGAGAGAC	104	*a*
		Dmrtc1a R	TCTTTCCAGTGCGAACTCCT		
Zcchc13	X	Zcchc13 F	GTGAACTGCAGCAAGACGAG	100	*a*
		Zcchc13 R	GGGGTTACTAAGCGGTAGCC		
Rps6ka6	X	Rps6ka6 F	AAGAACGCAGCAACGGTTAT	94	*a*
		Rps6ka6 R	AAACTGGCTCTCCCTCTTCC		
Satl1	X	Satl1 F	AACCATTGGATTTGCCATGT	153	*a*
		Satl1 R	TCGGTGTTGATGGCTATCTG		
1700008I05Rik	X	I05Rik F	AAAGCCAATTCGTGGAGACAAT	192	*b*
		I05Rik R	TGGGAGAGATGCAGAATATCCA		
Tex13a (*1700025D03Rik*)	X	Tex13a F	TGTCACCAGACCTGAAGCAG	169	*a*
		Tex13a R	CTTACTGCATTCGGGAGAGC		
Ammecr1	X	Ammecr1 F	GCTTTTCTGCTCGGTGTCTC	143	*a*
		Ammecr1 R	CAACCTCCGGTAGGTAGGTG		
4933400A11Rik	X	A11Rik F	AAATGGGTATCAGGCAGCAC	170	*a*
		A11Rik R	CAGTGGGCCATTAAGCATGT		
Acrv1	9	Acrv1 F	TGAGTACACCACTTCCAAGCA	60	*c*
		Acrv1 R	AAGCACATGTGTGGCAATTT		
Protamine 1 (Prm1)	16	Prot1 F	ACAAAATTCCACCTGCTCACA	129	*d*
		Prot1 R	CATCTGCTCCTGCTTTTGCT		*a*

Gene	Chr.	Primer name	Primer sequence	Amplicon size (bp)	Reference
Hormad1	3	Hormad1 F	CTGCTGACACCAAGAAAGCA	148	*a*
		Hormad1 R	CCTGGTGGTTGGTAATCTGG		
Hist1h1t (H1t)	13	Hist1h1t F	GTTGGCTCTCCTTTAGTTTTCACTT	128	*a*
		Hist1h1t R	GCCTTTTAGATGAAGGTTTCTCCT		
Igf1r	7	Igf1r F	CGGTGACTTCTGCTCAAATG	150	*a*
		Igf1r R	AATGGCGGATCTTCACGTAG		
Ubc	5	Ubc F	AGCCCAGTGTTACCACCAAG	118	*a*
		Ubc R	CTAAGACACCTCCCCCATCA		
beta-actin (actb1)	5	B-actin F	CTGTATTCCCCTCCATCGTG	167	*a*
		B-actin R	CTTCTCCATGTCGTCCCAGT		

a, this study; *b*, Coquet *et al*. 2009; *c*, Åkerfelt *et al.* 2008; *d*, Okada *et al*. 2007

Supporting Literature Cited

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