Supplementary Figure 8 Hybrid male-identity trait in mice that map to the X chromosome. Based upon the mouse genome information phenotype database, three loci (Phef2, Pwef, Phef1) are flanked and map within or adjacent to independently acquired genes. Phef2 (peak hybrid identity QTL2; Elliott et al., 2004) is genetically linked to chromosomal position 29.5 Mb — within the Skal enhancer — and is associated with low sperm production in hybrids. Pwef (peak hybrid identity QTL1; Elliott et al., 2001) is genetically linked to chromosomal position 10.1 Mb (the map position of the GS3 marker) — 600 kb proximal to the Skal enhancer — and is associated with reduced levels of male fertility and reduced testis weight in hybrids. Phef1 (hybrid identity, X chromosome Y; Stanchina et al., 2006) is genetically linked to chromosomal position 9.3 Mb (the map position of the GSK1 marker) — flanked by the RGSX6TEN10cR5 marker (27.3 Mb) and the Rgsx1c marker (25.6 Mb) — and is associated with increased levels of male fertility, increased testis weight, reduced sperm count and increased abnormal sperm head morphology in hybrids. A fourth locus, Hef7, maps to the X chromosome (peak hybrid identity region) but is not linked to differences in the Skal enhancer. Hef7 shows a strong and consistent effect on male fertility in both inbred and hybrid male mice. The most proximal peak hybrid identity (Hef7, X chromosome) is mapped to chromosome 17 near the centromere, and the remaining loci (Hef1, Hef2, Hef4, and Hef5) all map within close linkage at the proximal end of chromosome 17, near the centromere, and the remaining loci (Hef1, Hef2, Hef4, and Hef5) all map within close linkage at the proximal end of chromosome 17, near the centromere, and the remaining loci (Hef1, Hef2, Hef4, and Hef5) all map within close linkage at the proximal end of chromosome 17, near the centromere.