

Figure 2 – figure supplement 3. Significantly imprinted genes. (a) Magnification of the clusters close to points (1,0) and (0,1) in the context of the same plot shown in Fig. 1i, where BAF is plotted as a function of the direction of the cross. Mother's strain is listed first according to convention. (b) Plot of the average difference in BAF between the two reciprocal crosses, for each of the F1 and N2 crosses. Each gene is a point. For each gene, for F1 embryos, average BAF of embryos from CastxB6 cross was subtracted from average BAF of embryos from B6xCast cross. For N2 embryos, only embryos heterozygous at the assayed gene are considered; for each gene, average BAF of embryos from F1xB6 cross is subtracted from average BAF of embryos from B6xF1 cross. Significantly imprinted genes, where the two crosses give a large difference, are in red near (1,1) or (−1,−1). If imprinting were not usually Boolean (either fully on or off) but rather a quantitative phenomenon in which different tissues respond differently to the imprint or change the imprint, the significant genes would reside in the tails of a continuous distribution and not be so clearly separated from the bulk of the non-imprinted genes.

