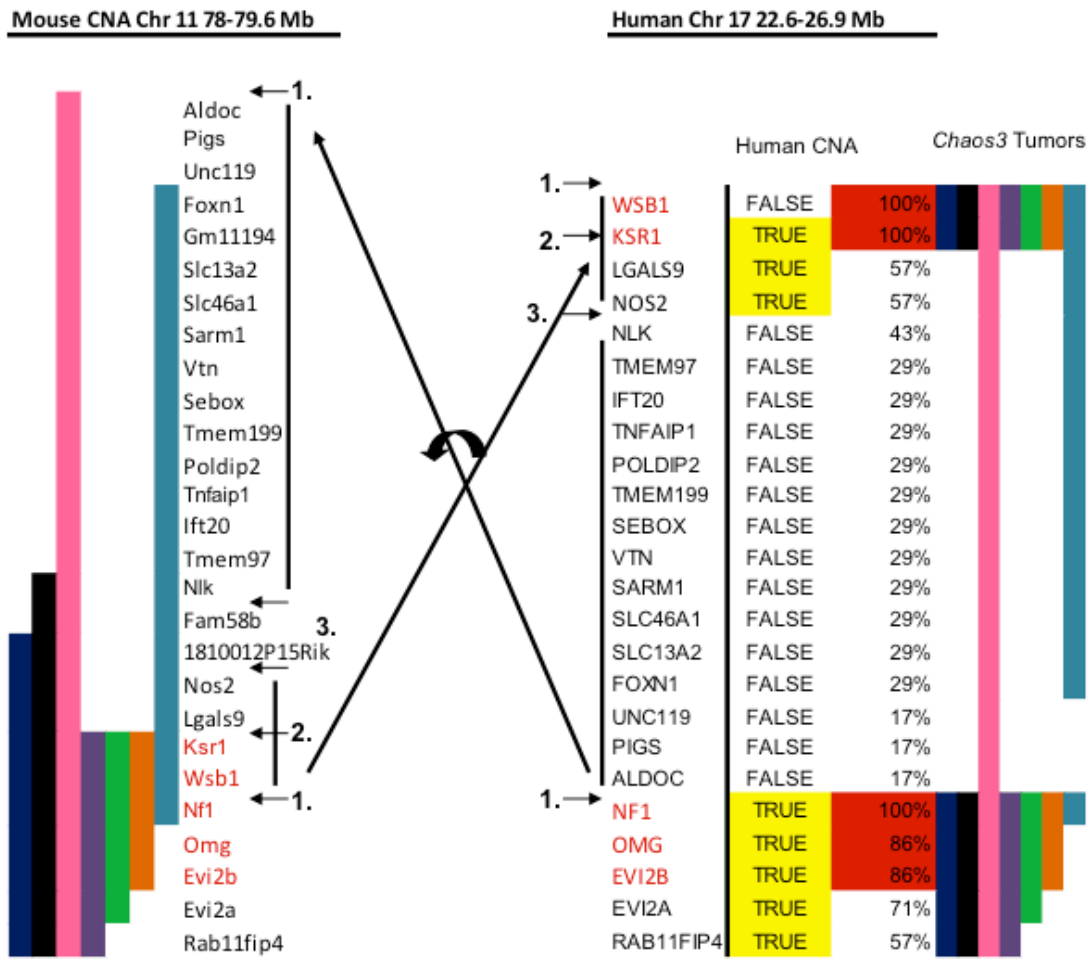

Figure S2 Genomic sequence around *Nf1* is prone to CNA and contains a genomic rearrangement. Colored vertical bars represent the deleted region in 7 *Chaos3* mammary tumors as detected by aCGH, and the percentages reflect how many of these tumors contain CNA for a given mouse gene. Gene names in red denote the *Chaos3* critical region. Mouse and human genomic orientations of the *Nf1* region are depicted. TRUE/FALSE indicates TCGA Level 4 (limited dataset) analysis of a subset of invasive breast carcinomas for segmental CNAs; it is possible that the intervals between *NOS2* and *NF1* are actually part of more inclusive deletion events. Numbers in bold with small arrows indicate positions of interest: **1.** Proximal to *Nf1*, a breakpoint of chromosomal inversion between human and mouse occurred between and including *Wsb1* to *Aldoc*. This is a site of both human and mouse tumor CNA, and the human CNA begins with *NF1*. **2.** The mouse critical CNA begins at *Ksr1*, which has flipped orientation in humans and starts/forms a second smaller CNA, with the caveats mentioned above. **3.** The mouse genome has an insertion between *Nlk* and *Nos2*, where human statistically-declared CNAs end.