Supporting Information

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SI Methods

Gene Expression in Normal Prostate Tissue. Gene expression of transcript at chr8: 128,168,145–128,168,232 in 105 normal prostate tissue from men of European-American ancestry (Fig. S1) was determined using the Quantitative Gene Expression application of the Sequenom platform. Briefly, this is a competitive PCR strategy where primers are designed to amplify cDNA in a region of interest, in the presence of differing amounts of competitor oligonucleotide. The competitor sequence differs from the expected amplicon by a single base. The assay uses this single base difference to determine the quantity of each product (cDNA or competitor oligonucleotide) and calculates an EC_{50}—the concentration at which the two products are equal. Further details on the gene-expression assay and statistical analysis used can be found at Pomerantz et al. (1).

1. Pomerantz MM, et al. (2009) Evaluation of the 8q24 prostate cancer risk locus and MYC expression. *Cancer Res* 69:5568–5574.

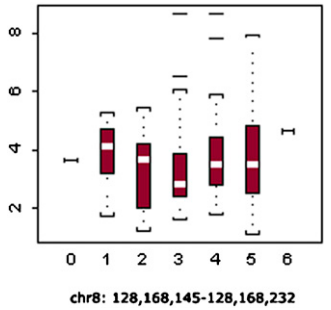

Fig. S1. Box-plots demonstrating the lack of association between the total number of prostate cancer risk alleles an individual possesses at 8q24 and the expression of a transcript at chr8: 128,168,145–128,168,232 in 105 normal prostate tissue from men of European-American ancestry. The number of 8q24 risk alleles is shown on the *x* axis and normalized gene expression (EC_{50}) on the *y* axis. When broken down by number of risk alleles within each risk region, there was still no significant association found.

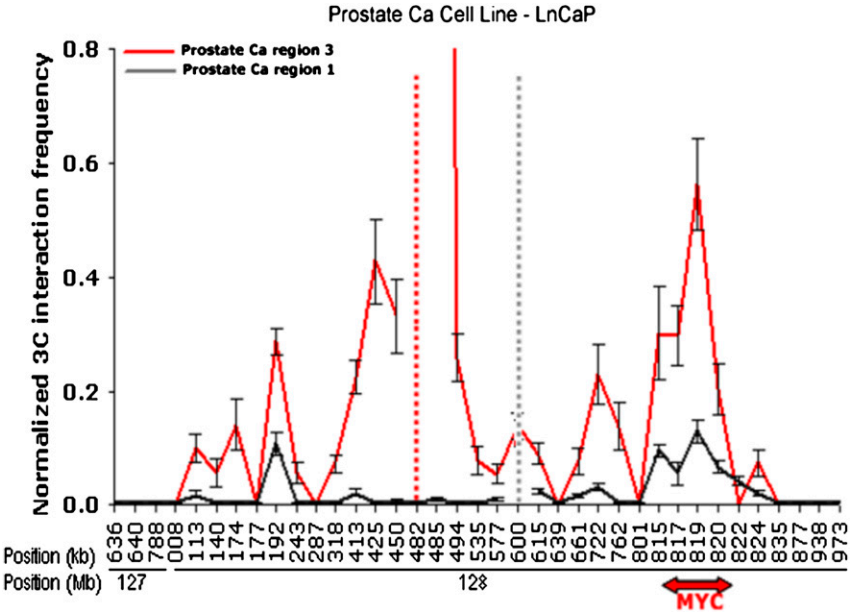

Fig. S2. Normalized 3C interaction frequency of prostate cancer region 3 (red lines) and region 1 (gray lines) in a prostate cancer cell line (LNCaP). *x* axis: genomic position of target fragments (not drawn to scale); 3C interaction frequency (±1 SEM) of the constant fragment with each of the target fragments including *MYC*, normalized to a 3C interaction within a housekeeping gene, FAM32A. Hatched lines denote position of respective constant fragments (color-coded).

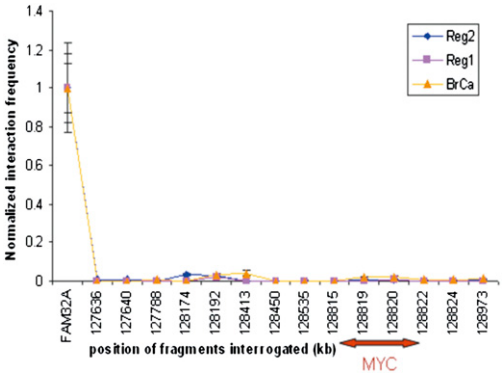

Fig. S3. Normalized 3C interaction frequency of the prostate cancer risk regions 1 (Reg1) and 2 (Reg2), and the breast cancer risk region (BrCa) in a fibroblast cell line (LL24). The interaction frequency of shared prostate cancer and colon cancer risk region 3 in fibroblast line LL24, showing no interaction with *MYC*, as previously reported (1). *x* axis: genomic position; *y* axis: 3C interaction frequency (±1 SEM) normalized to a housekeeping gene, FAM32A, demonstrating no interaction of risk regions with *MYC* in fibroblast cell line LL24.

1. Pomerantz MM, et al. (2009) The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. *Nat Genet* 41:882–884.

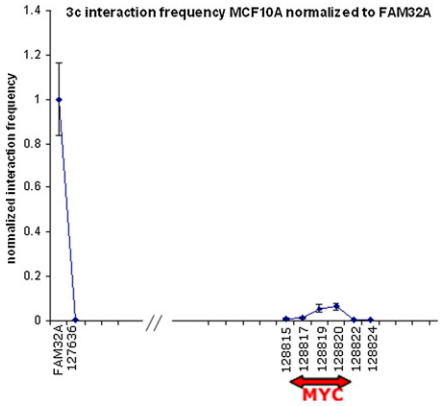

Fig. S4. Normalized 3C interaction frequency of the breast cancer risk locus with *MYC* in a normal breast epithelial line, MCF10A, normalized to a housekeeping gene FAM32A. x-axis, genomic position in kb (not drawn to scale); y-axis, 3C interaction frequency, ±1 SEM.

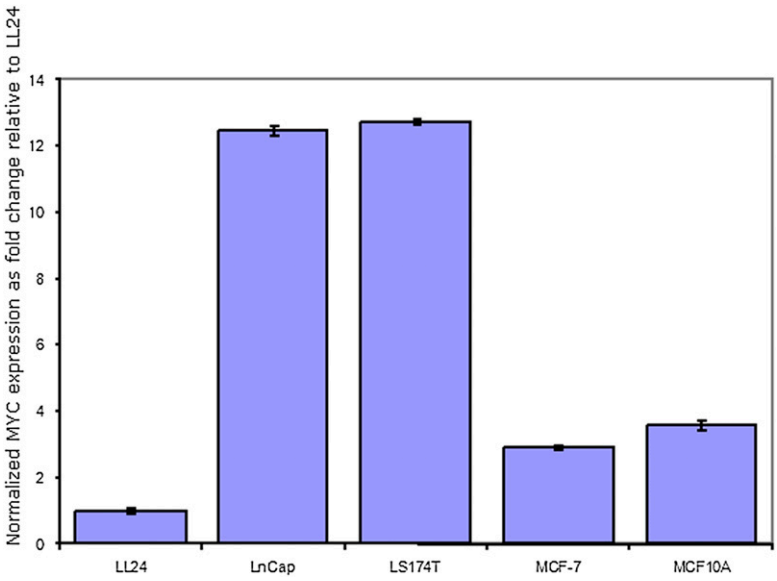

Fig. S5. Normalized *MYC* expression in various cell lines shown as fold change relative to normalized *MYC* expression of LL24. *MYC* expression normalized to two housekeeping genes, geometric mean taken ±1 SD of three technical replicates.