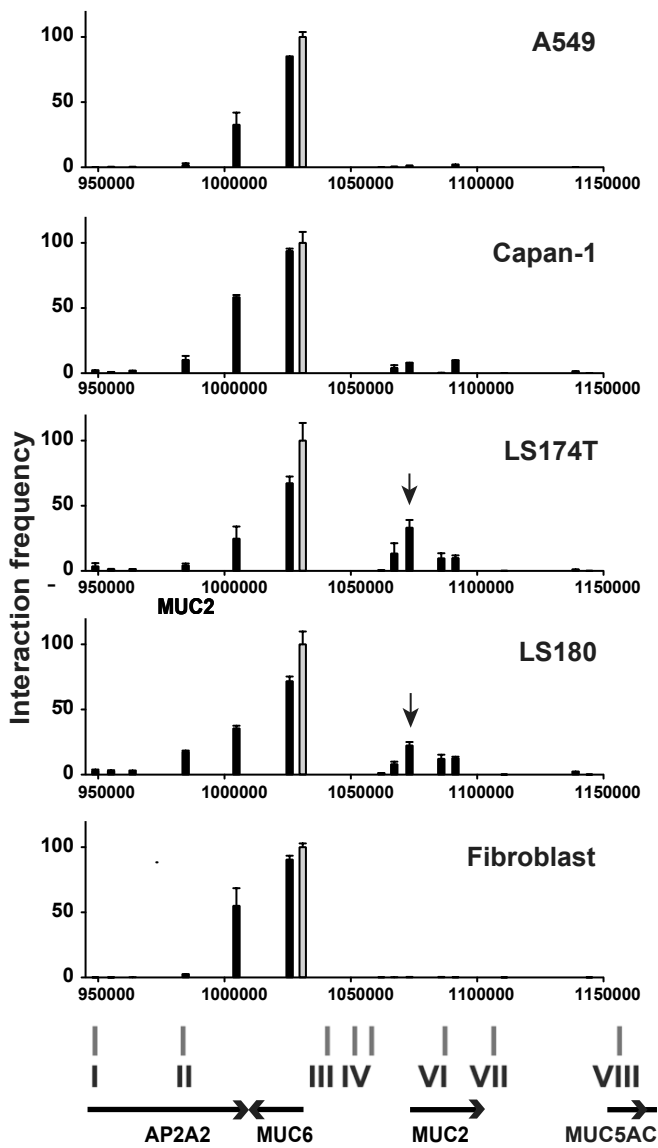


Supplementary Figure 1 The four mucin genes on 11p15.5 are shown on UCSC genome browser (<http://genome.ucsc.edu>). The top track shows the location of CTCF sites across the region used in ChIP experiments. Below are histone modification peaks determined by ChIP-seq from ENCODE/Broad Institute (H3K4Me1, H3K9Ac, H3K27Ac, H3K9Me3, H3K27Me3) in human lung carcinoma cells (A549) and normal human lung fibroblasts (Fibrobl). H3K4Me1, H3K9Ac, and H3K27Ac active histone modifications, while H3K9Me3 and H3K27Me3 are repressive histone modifications.



Supplementary Figure 2. Long-range interactions are evident across the 11p15.5 mucin gene cluster. 3C (q3C) interactions are shown in A549, Capan-1, LS180 and LS174T cell lines and fibroblasts. A fixed forward primer and a Taqman probe were designed within a *Bgl* II fragment at the *MUC6* promoter (bait, grey bar), and multiple reverse primers were generated within *AP2A2*, *MUC2* and the 5' end of the 11p15.5 mucin gene cluster (black bars). The x-axis represents the genomic location on chromosome 11; the y-axis represents the interaction frequency relative to a control fragment adjacent to the bait. Experiments were performed at least twice for each cell type and data shown are from a single representative 3C experiment. Error bars represent the SEM of at least two qPCR reactions for each fragment. Arrows denote *Bgl*II fragments interacting with the bait.