Supplemental Figure 1: Representative sample of output smoothing using Hidden Markov Models in R. Top panel in each pair shows Affymetrix's Chromosome Copy Number Tool (CCNT) output without modification. Lower panel shows same data after smoothing transformation. Y-axis represents number of copies calculated for a given SNP. Numbers under each panel correspond to the basepair position of SNP in Mb, counting from the p telomere. A) Trisomic Chromosome 7, B) Heterozygous and homozygous deletion in Chromosome 9, C) Homozygous loss of short arm of Chromosome 15, coupled with heterozygous loss of proximal q arm, D) Normal copy number. Vertical red lines show the centromere's position.

Supplemental Figure 2: Representative microphotographs of the EGFR staining in tissue microarrays. Primary antibody was detected with the EnVision system and Permanent Red chromogen. A) High expression sample, 200x; B) Low expression sample, 200x; C) High expression sample, 200x; D) Low expression sample, 400x.