Supplementary Figure 1: X chromosome inactivation. This figure demonstrated the random LOH (denoted with grey bars) in 10 female DNA samples (each sample is represented horizontally, above the ideogram), and the complete "LOH" seen in the paired cDNA samples (represented below the ideogram).

Supplementary Table 1: SNPs/genes that were analyzed for MAE/DAE by Sequenom.

Supplementary Table 2: PCR/sequencing primers for TP53 and IDH1.

Supplementary Table 3: A list of oncogenes and tumor suppressors used in the comparison of gene functional groups. Compiled from the CancerGenes website (http://cbio.mskcc.org/CancerGenes/Select.action). Where a gene was listed as both an oncogene and tumor suppressor, a literature search was performed to determine the role of the specific gene in tumor development. Any genes whose role as an oncogene or tumor suppressor was still questionable were excluded from the final list.

Supplementary Table 4: The percentage of genes displaying MAE for all samples.

Supplementary Table 5: 56 genes shortlisted from the genome-wide analysis. This table also shows the number of informative samples for each gene, and the % of informative samples that demonstrated MAE.