Figure S7

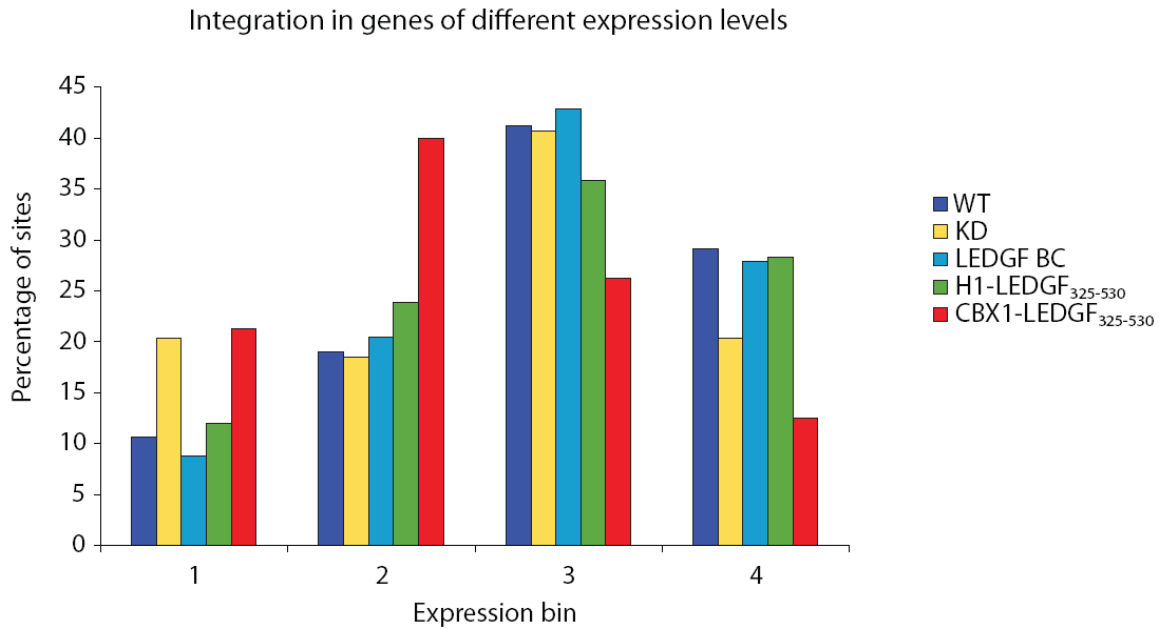Integration in genes of different expression levels

Figure S7. Distribution of integration sites relative to gene expression level. Transcriptional profiling data from WT HeLa cells analyzed on the HU133 Affymetrix microarray was used to classify the expression of genes harboring EIAV integration sites. Genes represented on the microarray were ranked by expression level and divided into 4 bins. For each cell line, integration sites found within genes were sorted into the 4 bins. The percentages shown are the proportions of sites in each bin out of sites falling in all expression bins.