



**Figure 2- Supplemental 1.** Examples of genomic localization of the genes hypermethylated in the most aggressive cell lines. Promoter methylation scores correspond to the average methylation values at CpG positions located in the promoter regions showing an increased methylation above 20% in WM266-4 compared to WM115 cells. The genes are indicated on the “band giemsa-related” representation (arrows). The graph shows genes with at least two CpGs in the promoter region with DNA methylation differences over 40% between WM266-4 and WM115 cells (grey squares).

- A) Localization and promoter methylation score of nine hypermethylated genes found on chromosome 5. The PCDH $\beta$  genes cluster is magnified in the insert.
- B) Localization and promoter methylation score of 15 hypermethylated genes found on chromosome 17; five of them belong to the MYH1 cluster (insert).