Supplementary Figure 1. Unsupervised clustering carried out with the most frequent aberrations found in our series. The unsupervised analysis was able to segregate H-MM and NH-MM in different branches. The H-MM was characterized by gains in chromosomes 19, 15, 11, 9. 7, 5 and 3 that were not in NH-MM. Chr 13 deletions and 1q duplications are distributed along both groups.