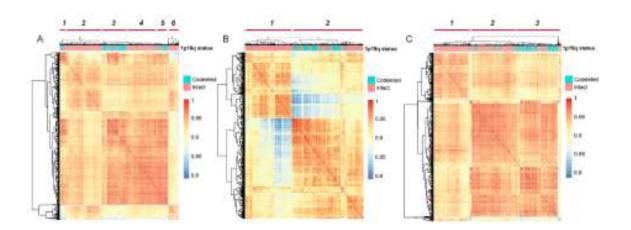
## **SUPPLEMENTARY FIGURE**



Supplementary Figure 1. Expression profile revealed a distinct gene expression between Chromosome 1p19q codeleted and intact patients. (A) Hierarchical clustering based on whole genome expression profiling (20501 genes), there were 92.4% (159/172) 1p/19q co-deleted patients in group1, 3 and 5 and 85.7% (446/520) 1p/19q intact patients in the rest of groups. (B) Hierarchical clustering based on highly variable expression genes (MAD >2, 886 genes), there were 96.5% (166/172) 1p/19q co-deleted patients in group2. (C) Hierarchical clustering based on genes on chromosome 1p and 19q (1775 genes), there were 75% (129/172) 1p/19q co-deleted patients in group3