



Figure S2

An unsupervised hierarchical clustering was performed by combining telomere length (TL) and *TERT*, *TRF2*, *RAP1* and *TIN2* gene expression as dichotomic parameters relative to best cutoff values used for survival analysis. Negative prognostic factors (short TL, high *TERT* and *TRF2*, low *RAP1* and *TIN2*) are shown in red and their absence is indicated in green. The different color intensities of dichotomic parameters reflect normalized values and not original binary (0/1) values.