

**Supplementary Table S1.** Top 20 significantly enriched genes on transcriptome analysis in *TERT* promoter mutated vs *TERT* wild type (*TERT* mut/*TERT* WT) samples

<b>Gene</b>	<b>Gene Name</b>	<b>Log2 fold change</b>
<b>SST</b>	somatostatin	7.31
<b>CYSLTR2</b>	cysteinyl leukotriene receptor 2	4.15
<b>WNK2</b>	WNK lysine deficient protein kinase 2	3.67
<b>PTGES</b>	prostaglandin E synthase	3.53
<b>C4orf48</b>	chromosome 4 open reading frame 48	3.39
<b>RPS21</b>	ribosomal protein S21	3.35
<b>JPT1</b>	Jupiter microtubule associated homolog 1	3.29
<b>CLDN4</b>	claudin 4	3.09
<b>MIR1915HG</b>	MIR1915 host gene	3.08
<b>MTLN</b>	mitoregulin	3.08
<b>CDR2L</b>	cerebellar degeneration related protein 2 like	3.07
<b>NME2</b>	NME/NM23 nucleoside diphosphate kinase 2	3.02
<b>RPL38</b>	ribosomal protein L38	3.0
<b>TMEM54</b>	transmembrane protein 54	2.92
<b>RPL29</b>	ribosomal protein L29	2.87
<b>RPL32</b>	ribosomal protein L32	2.75
<b>MTCO1P12</b>	MT-CO1 pseudogene 12	2.69
<b>RPL31</b>	ribosomal protein L31	2.67
<b>SCARNA13</b>	small Cajal body-specific RNA 13	2.65
<b>ITGB3</b>	integrin subunit beta 3	2.58

Significance was defined as adjusted p-values < 0.05.