

**Additional file 9: Lists of the cell cycle related transcripts among the selection according to the value of the index calculated either under the crossing hazard effect or the PH model.**

Table 1: Cell-cycle related genes selected according to  $D_0^{(NPH)}$

AffyID	Gene Symbol	UniGene Name	Cytoband	$D_0^{(NPH)}$
221326-s-at	<i>TUBD1</i>	tubulin, delta 1	chr17q23.1	37.9%
209661-at	<i>KIFC3</i>	kinesin family member C3	chr16q13-q21	35.9%
208228-s-at	<i>FGFR2</i>	fibroblast growth factor receptor 2	chr10q26	34.5%
206003-at	<i>CEP135</i>	centrosomal protein 135kDa	chr4q12	34.4%
225237-s-at	<i>MSI2</i>	musashi homolog 2 (Drosophila)	chr17q22	34.1%
1562139-a-at	<i>FOXP2</i>	forkhead box P2	chr7q31	34.0%
206113-s-at	<i>RAB5A</i>	RAB5A, member RAS oncogene family	chr3p24-p22	33.7%
200796-s-at	<i>MCL1</i>	myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	32.9%
221281-at	<i>SRC</i>	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	32.7%
207319-s-at	<i>CDC2L5</i>	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	32.5%
213023-at	<i>UTRN</i>	utrophin	chr6q24	32.1%
214908-s-at	<i>TRRAP</i>	transformation/transcription domain-associated protein	chr7q21.2-q22.1	32.1%
222563-s-at	<i>TNKS2</i>	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	chr10q23.3	32.1%
1555346-at	<i>CDC20B</i>	cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	31.9%
219944-at	<i>CLIP4</i>	CAP-GLY domain containing linker protein family, member 4	chr2p23.2	31.8%
239223-s-at	<i>FBXL20</i>	F-box and leucine-rich repeat protein 20	chr17q12	31.6%
222540-s-at	<i>RSF1</i>	remodeling and spacing factor 1	chr11q14.1	31.1%
203639-s-at	<i>FGFR2</i>	fibroblast growth factor receptor 2	chr10q26	31.0%
224010-at	<i>ANAPC11</i>	anaphase promoting complex subunit 11	chr17q25.3	31.0%
215739-s-at	<i>TUBGCP3</i>	tubulin, gamma complex associated protein 3	chr13q34	30.9%
206235-at	<i>LIG4</i>	ligase IV, DNA, ATP-dependent	chr13q33-q34	30.8%
243999-at	<i>SLFN5</i>	schlafen family member 5	chr17q12	30.5%
211103-at	<i>MYO7A</i>	myosin VIIA	chr11q13.5	30.4%
211401-s-at	<i>FGFR2</i>	fibroblast growth factor receptor 2	chr10q26	30.1%
212308-at	<i>CLASP2</i>	cytoplasmic linker associated protein 2	chr3p22.3	29.8%

Table 2: Cell-cycle related genes selected according to  $D_0^{(PH)}$ 

AffyID	Gene Symbol	UniGene Name	Cytoband	$D_0^{(PH)}$
226765-at	<i>SPTBN1</i>	CDNA clone IMAGE:3897439	chr2p21	41.0%
1566851-at	<i>TRIM42</i>	tripartite motif-containing 42	chr3q23	37.1%
202257-s-at	<i>CD2BP2</i>	CD2 (cytoplasmic tail) binding protein 2	chr16p11.2	36.3%
203348-s-at	<i>ETV5</i>	ets variant 5	chr3q28	35.8%
210356-x-at	<i>MS4A1</i>	membrane-spanning 4-domains, subfamily A, member 1	chr11q12	34.3%
205861-at	<i>SPIB</i>	Spi-B transcription factor (Spi-1/PU.1 related)	chr19q13.3-q13.4	34.2%
233251-at	<i>STRBP</i>	Chromosome 9 open reading frame 45, mRNA	chr9q33.3	31.5%
216609-at	<i>TXN</i>	Full length insert cDNA clone YI46D09	chr9q31	31.4%
214114-x-at	<i>FASTK</i>	Fas-activated serine/threonine kinase	chr7q35	30.9%
202252-at	<i>RAB13</i>	RAB13, member RAS oncogene family	chr1q21.2	30.9%
202810-at	<i>DRG1</i>	developmentally regulated GTP binding protein 1	chr22q12.2	30.7%
202676-x-at	<i>FASTK</i>	Fas-activated serine/threonine kinase	chr7q35	30.7%
229664-at	<i>MAPK8</i>	mitogen-activated protein kinase 8	chr10q11.22	30.5%
224434-s-at	<i>MORG1</i>	mitogen-activated protein kinase organizer 1	chr19p13.13	30.3%
210187-at	<i>FKBP1A</i>	FK506 binding protein 1A, 12kDa	chr20p13	29.9%
210111-s-at	<i>KLHDC10</i>	KIAA0265 gene	chr7q32.2	29.7%