

Table 1. Genes whose expression is most related to good and poor prognosis
And were combined to make the 20-gene signature

				95% CI interval		
			Average	Upper	Lower	
Poor prognosis	10855	D43950	KIAA0098	-0.004	0.027	-0.035
	19769	U96131	TRIP13	-0.039	-0.001	-0.077
	14841	NM_014865	KIAA0159	-0.007	0.029	-0.044
	15318	Contig55725_RC		-0.219	-0.150	-0.289
	12548	AF047002	ALY	-0.040	-0.008	-0.072
	3342	NM_004111	FEN1	-0.028	0.003	-0.058
	3493	NM_004153	ORC1L	0.037	0.057	0.017
	8204	NM_004631	LRP8	0.038	0.067	0.009
	3838	NM_002794	PSMB2	-0.024	0.004	-0.051
	3938	Contig55771_RC		-0.047	-0.005	-0.088
Good prognosis	6615	NM_004496	HNF3A	-0.216	-0.120	-0.312
	8786	NM_006113	VAV3	-0.170	-0.107	-0.232
	18817	AL161983		-0.015	0.007	-0.037
	17540	NM_016613	LOC51313	-0.002	0.022	-0.026
	1723	AL133074		-0.078	-0.033	-0.123
	23117	Contig14284_RC		-0.324	-0.209	-0.440
	57	Contig56678_RC		-0.205	-0.135	-0.274
	18904	NM_000125	ESR1	-0.312	-0.215	-0.409
	6709	Contig57480_RC	LOC51028	-0.021	0.009	-0.051
	6105	NM_005113	GOLGA5	-0.046	-0.024	-0.067

Table 2. Predictive ability of Aurora kinase A expression, 20-gene signature, and 70-gene signatures

Test	Aurora kinase A (NKI dataset)	20-gene (151 validation set)	70-gene (NKI dataset)
Predictive accuracy	0.64	0.67	0.61
Specificity	0.6	0.66	0.66
Positive predictive value	0.4	0.38	0.4

Table 3. Gene ontology of the 20-gene signature

Gene ID#	Systemic_name	Gene name/symbol	Biological Process
10855	D43950	KIAA0098	Protein folding / Response to virus
19769	U96131	TRIP13	Double stranded break DNA repair / Meiosis I / Spermatogonial Development / Oocyte maturation / Pachytene (cell cycle) / Meiotic recombination / Transcription from RNA Pol II promoter
14841	NM_014865	KIAA0159	N/A
15318	Contig55725_RC		N/A
12548	AF047002	ALY	Interspecies interaction between organisms / Intronless viral mRNA export from nucleus / mRNA export from nucleus / mRNA processing / Transport
3342	NM_004111	FEN1	DNA repair / DNA replication / Double stranded break DNA repair / UV protection / Phosphoinositide mediated signaling
3493	NM_004153	ORC1L	DNA replication / DNA dependent DNA replication
8204	NM_004631	LRP8	Cytokine mediated signaling pathway / Endocytosis / Hippocampus deveopment / Layer formation in the cerebral cortex / Lipid metabolic process Positive regulation of kinase activity / Proteolysis / Signal transduction
3838	NM_002794	PSMB2	Anaphase-promoting complex-dependent proteosomal ubiquitin dependent protein catabolic process / Interspecies interaction between organisms / Negative regulation of ubiquitin ligase activity involved in mitotic cell entry / Positive regulation of ubiquitin ligase activity involved in mitotic cell entry / Proteolysis involved in cellular protein catabolic process
3938	Contig55771_RC		N/A
6615	NM_004496	HNF3A	Branching morphogenesis of a tube / Chromatin remodelling / Epithelial cell differentiation / Prostate gland development / Glucose homeostasis / Hormone metabolic process / Lung development / Multicellular organismal development / Negative regulation of survival gene product / Negative regulation of transcription fro RNA pol II promoter / Neuron fate specification
8786	NM_006113	VAV3	Angiogenesis / Apoptosis / Cell Migration / Induction of apoptosis by extracellular signals / Integrin mediated signaling pathway / Lamellipodium assembly / Positive regulation of cell adhesion / Positive regulation of PI3 kinase activity / Regulation of GTPase activity / Regulation of Rho protein signal transduction / Small GTPase mediated signal transduction / Vesicle fusion
18817	AL161983		Regulation of translation / Translation initiation
17540	NM_016613	LOC51313	N/A
1723	AL133074		Apoptosis / Cell cycle arrest / Induction of apoptosis / Response to stress
23117	Contig14284_RC		N/A
57	Contig56678_RC		N/A
18904	NM_000125	ESR1	Androgen metabolic process / Antral ovarian follicle growth / Epithelial cell development / Epithelial cell proliferation involved in mammary gland duct elongation / Estrogen receptor signaling pathway / Male gonad development / Mammary gland alveolus development / Mammary gland branching involved in pregnancy / Neuroprotection / Osteoblast development
6709	Contig57480_RC	LOC51028	N/A
6105	NM_005113	GOLGAS5	Golgi organisation / Golgi vesicle transport / Protein amino acid phosphorylation / Retrograde transport, vesicle recycling within golgi