Hassan et al Supplementary data
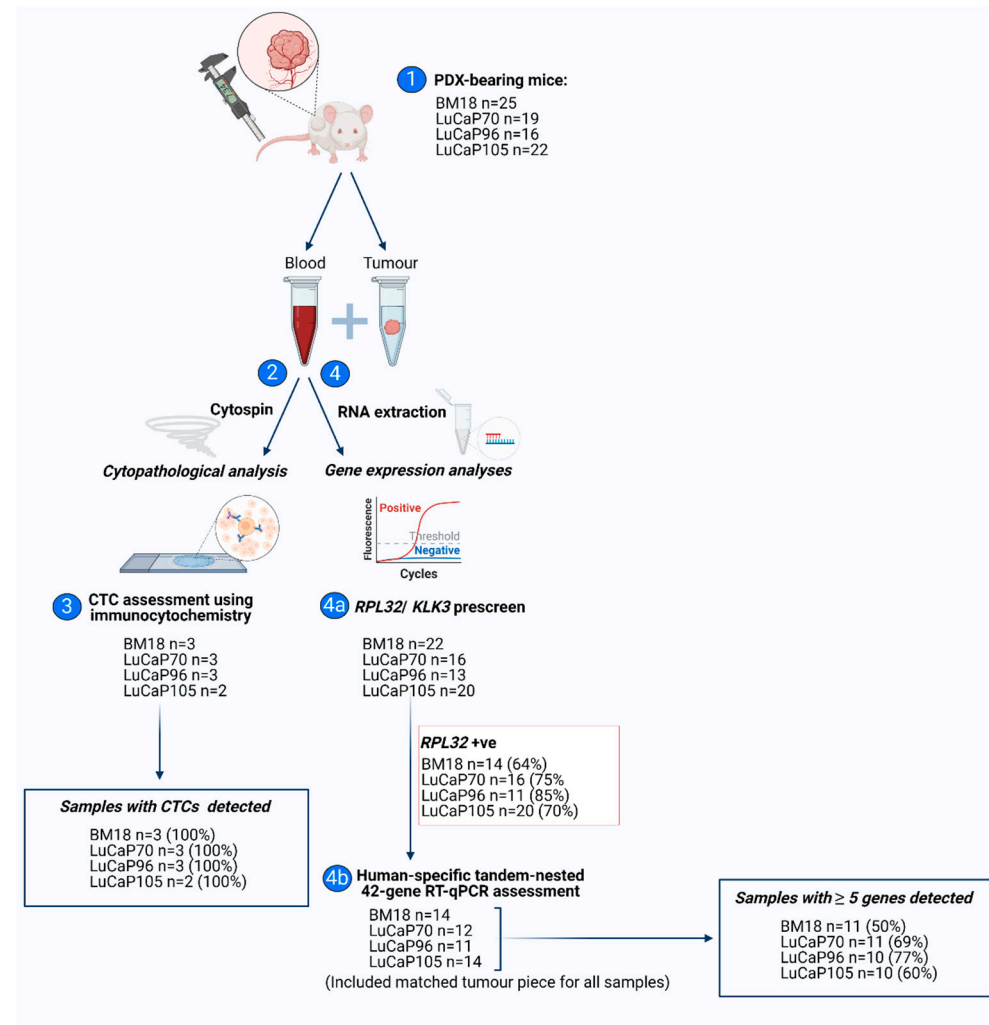
Figure S1. Schematic of experimental workflow, including number of samples at each stage. This study comprised of 4 prostate cancer PDX models (BM18, LuCaP70, LuCaP96, Lu-CaP105) that were grown as subcutaneous tumours in male severe combined immune-deficient (SCID) mice (1). Blood was collected at terminal draw using cardiac puncture. Matched tumours were collected and stored in RNAlater™ Stabilization Solution overnight and then stored briefly at -80°C until further processing. Following red blood cell (RBC) lysis, blood samples were used for either cytopathological (2) or gene expression (4) analyses. For cytopathological analysis (3), samples were cytospun onto slides and then stained for VIM, KRT, KLK3 and SERPINE1. For gene expression analysis, RNA was extracted from blood and tumour samples and assessed using a 42-gene human-specific tandem-nested RT-qPCR approach. Prior to complete 42-gene analysis, RNA extracted from blood samples was screened for CTCs using RPL32/KLK3 expression (4a). RPL32-positive blood samples and their paired tumour tissues were then assessed for the remainder of the 42 gene panel using a tandem-nested RT-qPCR assay (4b). Samples with less than 5 genes detected were excluded from further analysis. *n* denotes number of samples. CTC circulating tumour cell; SCID severe combined immune-deficient; PDX patient derived xenograft.
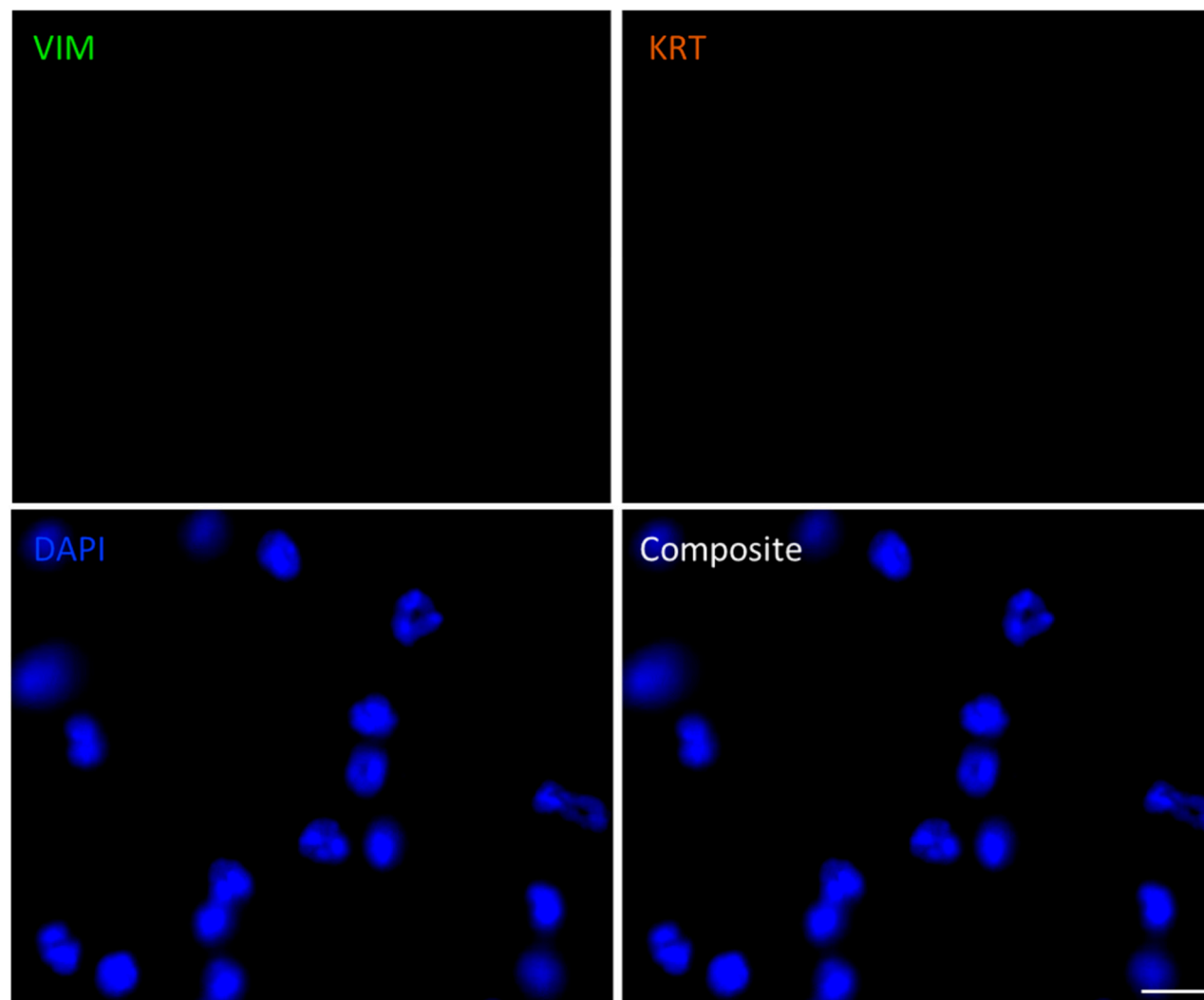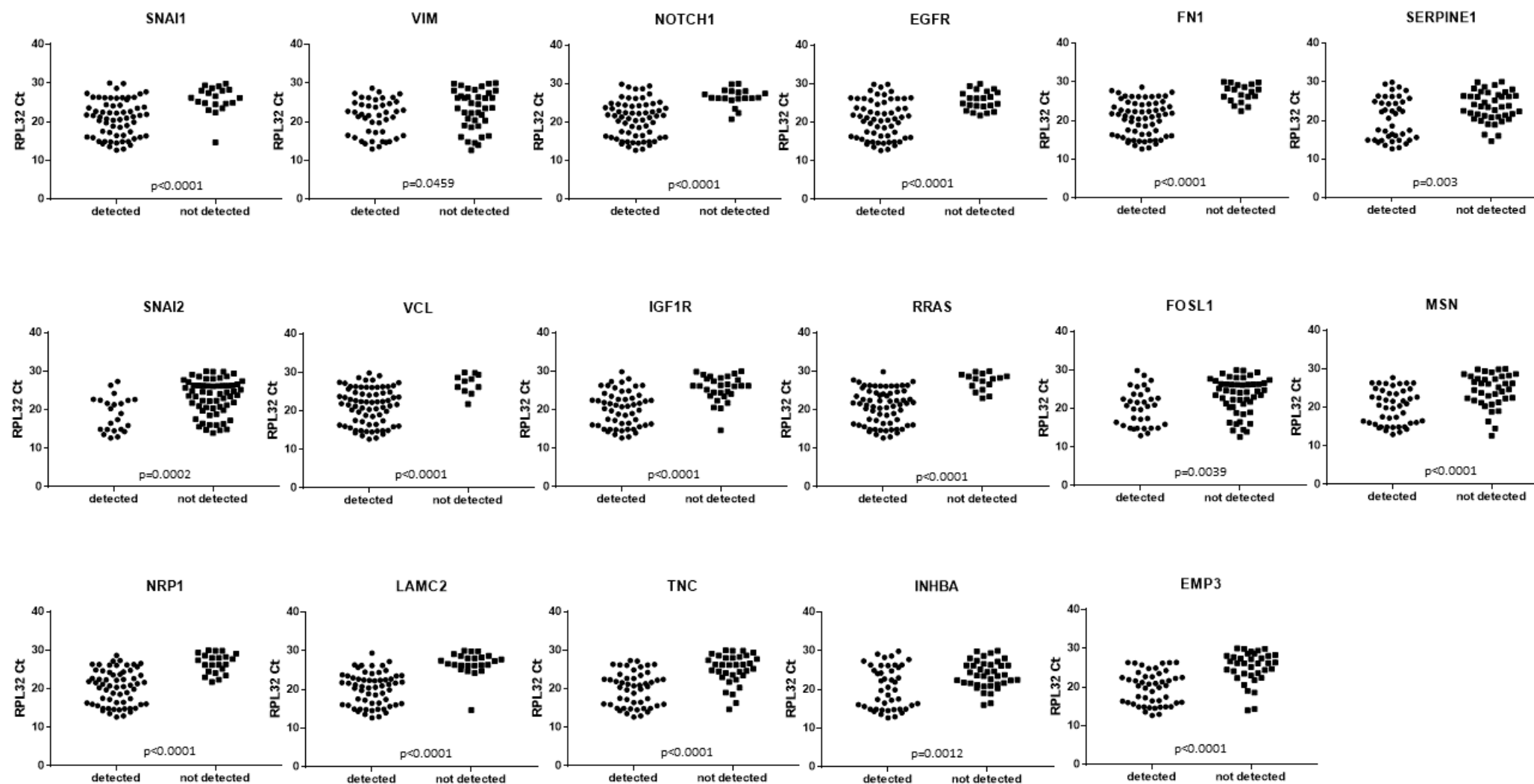
Figure S2. Representative images for immunofluorescent staining for VIM and KRT in negative control sample. Negative staining was observed for both VIM and KRT. Scale bar denotes 5 µm.

Mesenchymal

Epithelial
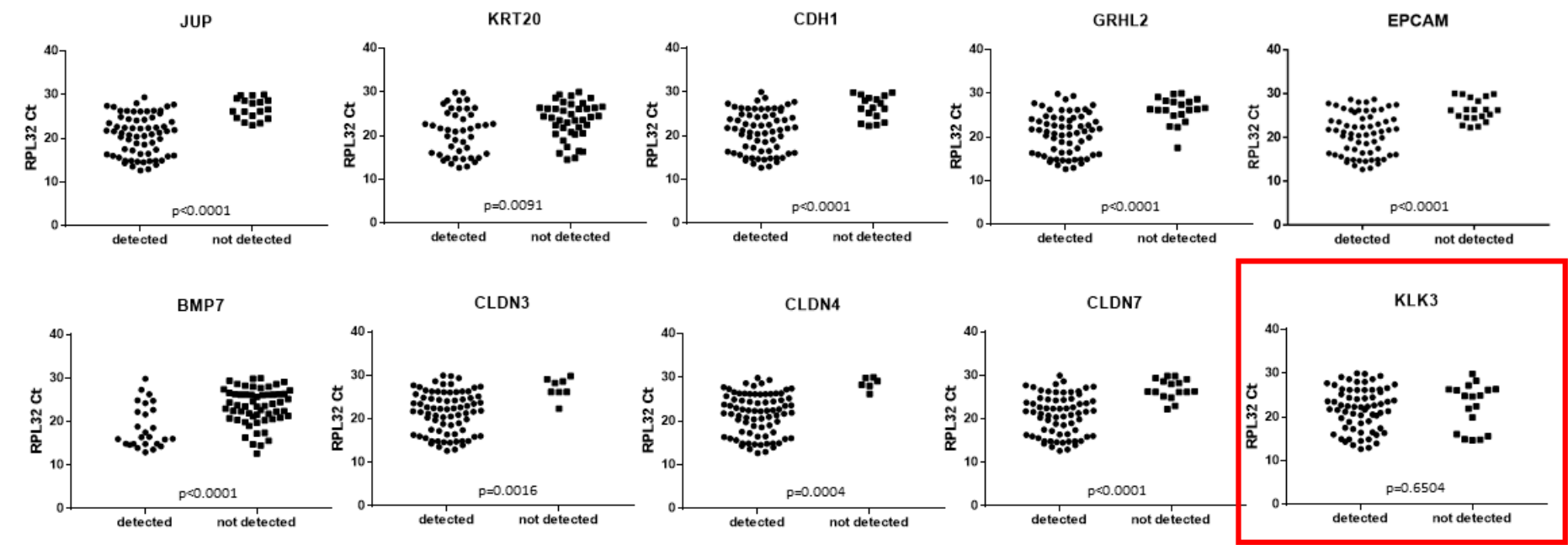
Other
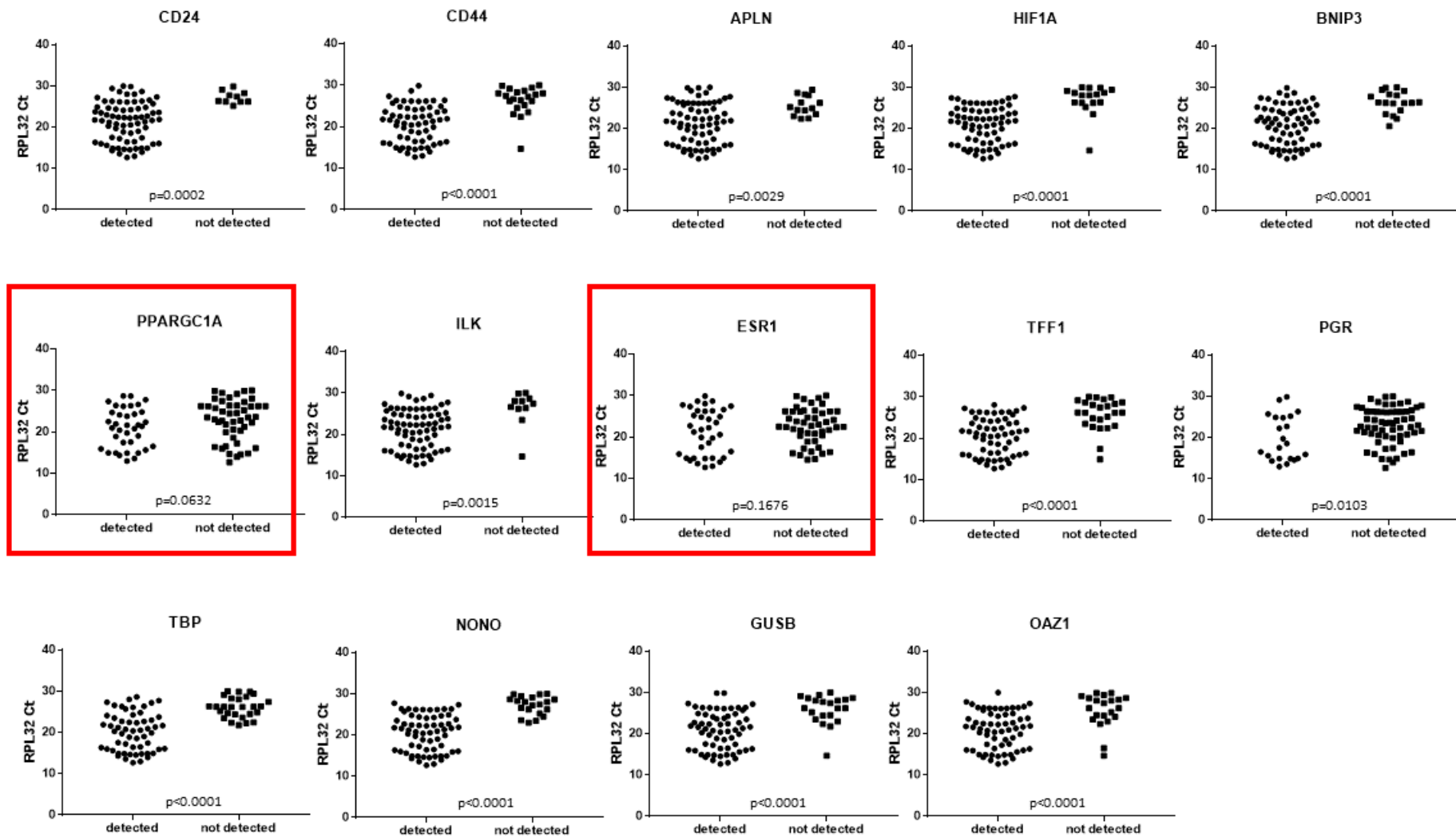
Figure S3. Gene expression in the context of *RPL32* expression. Each circle/square represents an individual CTC sample from a different mouse. Statistical significance determined using an unpaired t-test. *p* < 0.05 was considered significant.
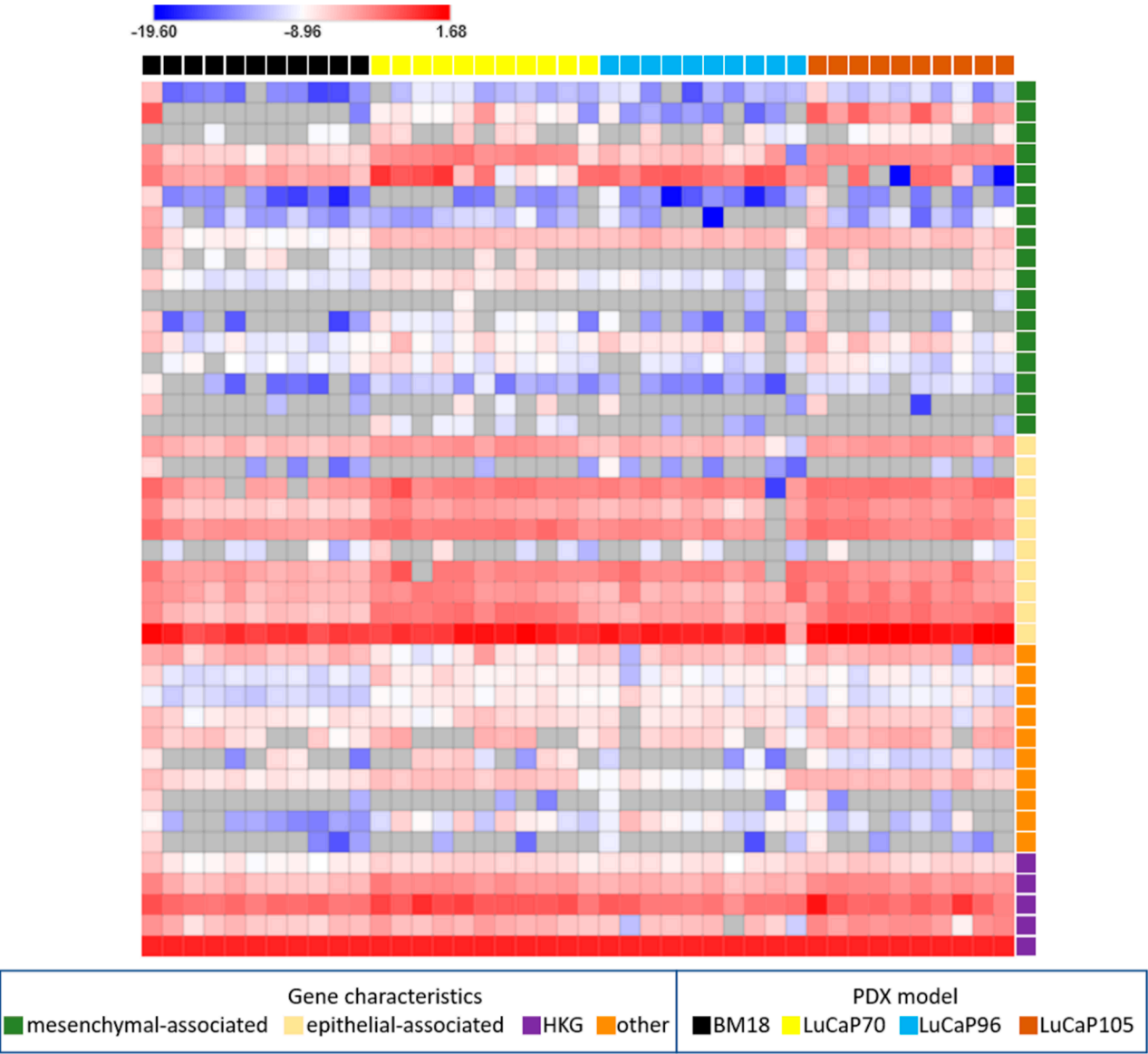
Figure S4. Heat map showing 42 gene panel expression profiles in tumour samples from 4 PDX models as Ct values normalised to RPL32, with global normalisation. For each sample, the PDX model is shown above the heat map. Genes are categorised as mesenchymal-associated, epithelial-associated, potential HKG (GUSB, TBP, OAZ1 and NONO), and others

(which includes HR (ESR1, PGR and TFF1), CSC (CD24 and CD44), hypoxia (APLN, HIF1A and BNIP3), metabolism (PPARGCIA), and anoikis (ILK) - associated genes). HR hormone receptor; CSC cancer stem cell; HKG housekeeper gene.
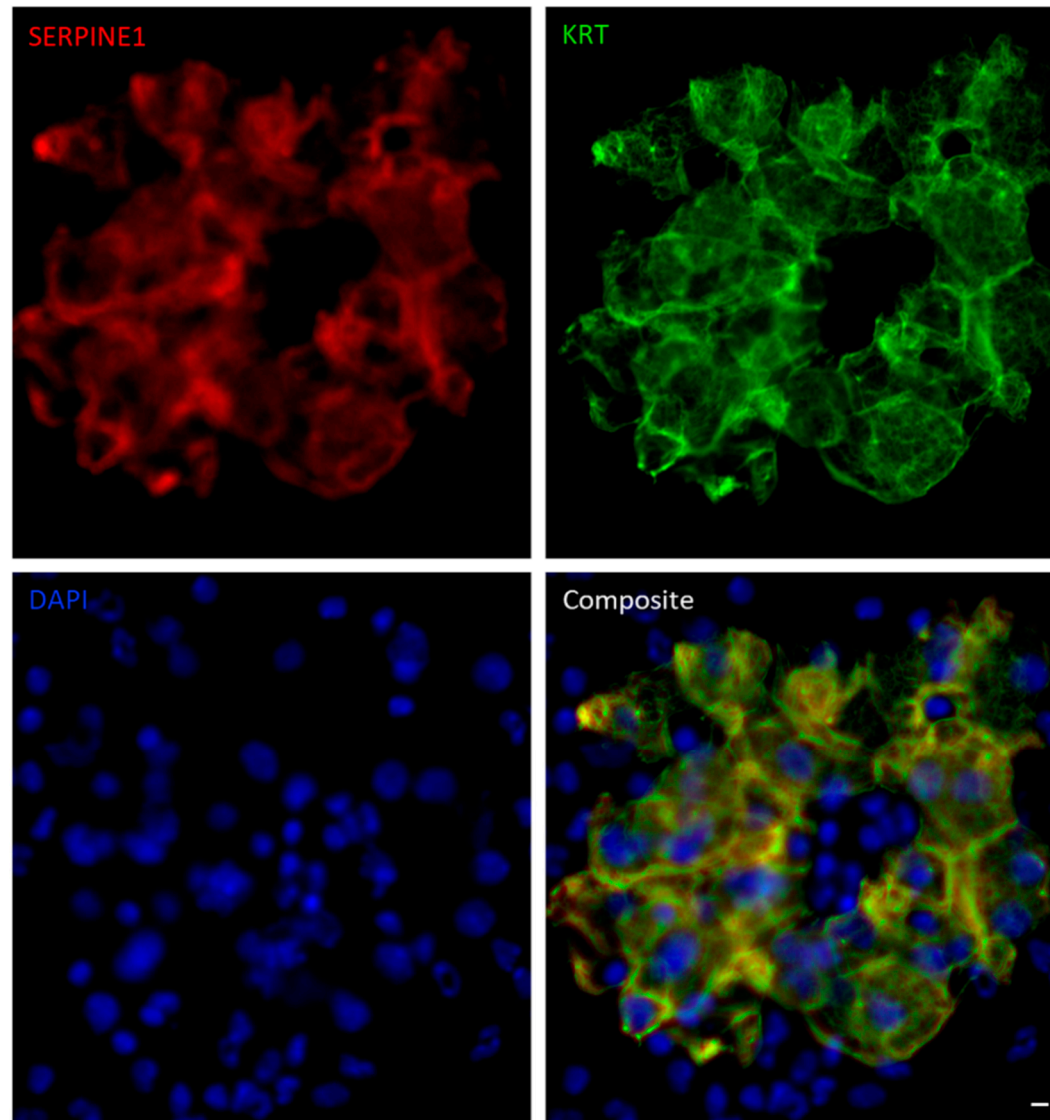
Figure S5. Representative images for immunofluorescent staining for SERPINE1 and KRT in negative control sample. Negative staining was observed for both SERPINE1 and KRT. Scale bar denotes 5 μm.
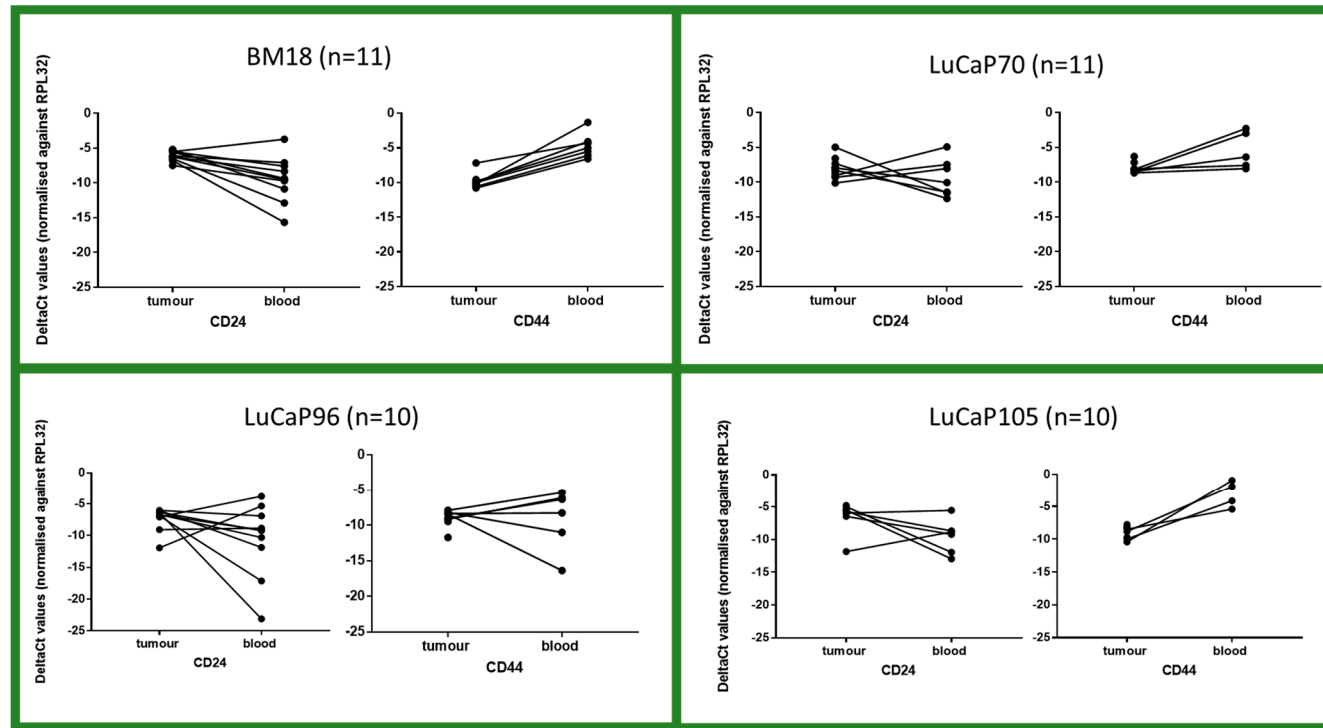
Figure S6: Gene expression for CSC markers, *CD24* and *CD44*, normalised to housekeeper gene *RPL32*. Downregulation of *CD24* and upregulation of *CD44* was observed in BM18 and LuCaP105 while only upregulation of *CD44* was observed in CTCs in LuCaP70. There was no change in expression in the LuCaP96 model.

Table S1. Summary of RT-qPCR results for *RPL32* gene in 4T1 (murine) and MDA-MB-231 (human) cell line.

sample	ct value
4T1 cell line (murine)	not detected
MDA-MB-231 cell line (human)	34.14
no template control	not detected

Table 2. Summary of the estimated number of CTCs present in total mouse blood and compared to tumour weight for each mouse in this study.

PDX ID	tumour weight (g)	estimated CTCs (total number per mouse)
BM18: 18-142	1.07	19
BM18: 19-14	3.05	174
BM18: 18-133	1.89	52
BM18: 19-15	2.42	269
BM18: 17-174	0.69	21
BM18: 18-162	0.98	3
BM18: 19-37	1.91	296
BM18: 17-147	0.66	14
BM18: 19-30	1.37	246
BM18: 18-193	2.1	5
BM18: 18-254	1.69	7
LuCaP96: 18-99	1.42	4758
LuCaP96: 18-192	1.19	15
LuCaP96: 18-257	0.99	5
LuCaP96: 19-93	1.34	85
LuCaP96: 17-132	0.8	31
LuCaP96: 18-138	1.44	147
LuCaP96: 18-164	1.25	1958
LuCaP96: 17-176	0.9	31
LuCaP96: 17-208	0.64	12
LuCaP96: 17-175	0.9	2
LuCaP70: 19-101	0.98	16
LuCaP70: 18-214	0.48	1
LuCaP70: 19-42	0.59	49
LuCaP70: 17-146	1.16	3
LuCaP70: 17-182	0.92	29
LuCaP70: 17-140	1.19	137
LuCaP70: 19-50	0.21	2
LuCaP70: 18-159	0.14	278
LuCaP70: 18-261	1.33	277
LuCaP70: 18-238	1.1	4

LuCaP70: 19-133	0.97	3
LuCaP105: 19-39	0.91	13
LuCaP105: 18-179	0.88	308
LuCaP105: 19-90	0.31	3
LuCaP105: 17-158	1.07	2
LuCaP105: 19-121	0.67	2
LuCaP105: 19-41	1.26	4
LuCaP105: 17-165	0.87	7
LuCaP105: 17-166	0.84	4
LuCaP105: 18-265	1.31	183
LuCaP105: 19-60	0.9	45

Table S3: List of genes analysed in the study and the primer sequences used for qRT-PCR analysis.

Gene Name	RT primer name	RT Sequence	5' primer name	5' Sequence	3' primer name	3' Sequence	5 i	5' Sequence	3 i	3' Sequence
Hs RPL32	Hs L 32 RT	CAGAAAACGTGCACATGAGCTGC	5o' Hs L 32	CAGGGTTCGTAGAA-GATTCAAGGG	3o' Hs L 32	CTTGGAGGAAACATT-GTGAGCGATC	5 i Hs L 32	GATCTT-GATGCCCAACATT-GGTTATG	3 i Hs L 32	GCACTTCCAGCTCCTTGACG
Hs CD24	Hs CD24 RTb	GGGCGACAAAGTGA-GACTGTCTAAAA	5o' Hs CD24	CTGTTCTCTTGG-GAACTGAACTCACTTT	3o' Hs CD24	GTCGTGGTCAATGCAAT TCTACTCTTT	5 i Hs CD24	CTGAGCAACTCTTGAT-TATCCATATTGAGTCAAA	3 i Hs CD24	CTCTTGTT-GAATGGAAACAGGTGA-TAGGAAA
Hs VIM	Hs VIM RT	CTAAATCTTGTAGGAG-TGTCGGTTGTT	5o' Hs VIM	CTAGA-GATGGACAGGTTATCAACGAA	3' Hs VIM	CTTGTAGGAG-TGTCGGTTGTTAAGAA	5 i Hs VIM	GCACACACTCAGTGCAG-CAATATAT	3 i Hs VIM	GCAGAAAGGCACTTGAAA-GCTGTTTCTT
Hs CDH1	Hs CDH1 RT	CTCTGTCTTTGGCTGCAGCAC-TTTA	5o' Hs CDH1	CTGTGCCCAGCCTCCAT GTTTT	3o' Hs CDH1	CTGGATAGCTGCCCATT-GCAAGTTA	5 i Hs CDH1	CAACTCTCAC-TCCTGAATTCAGTTGCTTT	3 i Hs CDH1	CAAGATGTGGCCAGA-CAAAGACACAAA
Hs ILK	Hs ILK RTb	GCTGGGGTAGTACCATGACTG	5o' Hs ILK	GATGCAG-GACAAGTAGGACTG-GAA	3o' Hs ILK	CAAC-CAGAGGCCTGCTGCTTT	5 i Hs ILK	CTCCAGAGGTGTCGG-GACA	3 i Hs ILK	GGGAGGTGCATTCCCCCAA
Hs EGFR	Hs EGFR RTb	CAGTTCCTGTGGATCCAGAGGAG-GAGTATGT	5o' Hs EGFR	GGACTGAAGGAGCTGC CCATGAGAAAT	3o' Hs EGFR	CTTGCAC-GTGGCTTCGTCTCG-GAATTT	5 i Hs EGFR	CAGTGGCGG-GACATAGTCAGCAGTGA	3 i Hs EGFR	CCCATTGGGACAGCTT-GGATCACACTTTT
Hs CD44	Hs CD44 RTb	CAACACATAGTGGCCTAATGTCC AGTTTCTTT	5o' Hs CD44	GGTATCTCCTTTCTGAG GCTCCTACTAAAA	3o' Hs CD44	GCAGAGGCTGGGAA-TAGTGCAGAAA	5 i Hs CD44	CAGGCAATGCTTCTCAGAC CACAAA	3 i Hs CD44	CTCTGTCTAA-GCCCAGCCCTGATTTA
Hs ESR1	Hs ESR1 RT	CCAGGGCCACGCTGG-GAAATGAA	5o' Hs ESR1	GTTCCAGTGGGCACTG-TACTTGGATCTT	3o' Hs ESR1	CAGCTCCATGCCCCAGG GCTAAAT	5 i Hs ESR1	GTGCCTTACACAGGGGTG AACTGTT	3 i Hs ESR1	GCCCCTGCTCCTTTCAAC-TACCATTT
Hs PGR	Hs PGR RT	GGGAGAGATCTCACAAAGTAG-GAAGCAAA	5o' Hs PGR	GGAG-GAGGGAGGTATCAATT CACATACCTTT	3o' Hs PGR	GGCAGGTAAACTCTAG-GAGAAGGCAAATT	5 i Hs PGR	CGA-GACTCAGCCAAATGTCATT TCTGTAA	3 i Hs PGR	CTGCTTGGAA-GACTCAGGGAAGATT

Hs TFF1	Hs TFF1 RT	GGCAGCCGAGCTCTGGGACTAAT	5o' Hs TFF1	CCCCCCGTGAAAGA-CAGAATTGTGGTTTT	3o' Hs TFF1	GGCAGATCCCTG-CAGAAGTGTCTAAA	5 i Hs TFF1	GTCACGCCCTCCCAG-TGTGCAA	3 i Hs TFF1	GTCGTCGAAACAG-CAGCCCTTAT
Hs EP-CAM	Hs EP-CAM RT b	GTTTTGCTCTTCTCCCAAGTTTT-GAGCCATT	5o' Hs EPCAM	CTCGCGTTCGGGCTTCT GCTT	3o' Hs EPCAM	CAACTGAAGTACAC-TGGCATTGACGATTATT	5 i Hs EPCAM	CGC GGC GAC GGC GAC TTT T	3 i Hs EPCAM	GCAGTTTACGGCCAGCTT-GTAGTTTT
Hs OAZ1	Hs OAZ1 RT	GGCTTTTGGAGAG-CAATGGAGGGGATTAA	5o' Hs OAZ1	GGCCTACACGTTCGA-GAGAGAGTCTT	3o' Hs OAZ1	CTCCTCAAAGTACAAGG ATAATCTGAATCAT	5 i Hs OAZ1	CCTTGTCAGCCGGGTGGG-TAGGAA	3 i Hs OAZ1	CAGGCGAGATGAGCGAG-TCTA
Hs CK20	Hs CK20 RT	GGACTCCCAAAGGGGGTTTTACA ATTCAGAAA	5o' Hs CK20	GCTCCCTGCAA-GAAATCAGCCATAA	3o' Hs CK20	CAGCTTGTAATT-GATGTGCTTCATGA-TAAA	5 i Hs CK20	CGGGAATCC-TATTTATCAGACTCTG-TAATT	3 i Hs CK20	GGCAATTT-GCAGCTCCTCTGAGTA
Hs SNAI1	Hs SNAI1 RT	CGCAGACAGGCCAGCTCAG-GAAT	5o' Hs SNAI1	CACATCCTTCTCAC-TGCCATGGAATT	3o' Hs SNAI1	GCTGCCCTCCCTCCACA GAAAT	5 i Hs SNAI1	GCCCCACAGGACTTT-GATGAAGACCAT	3 i Hs SNAI1	GAGCCCAGGCAGAG-GACACAGAA
Hs NOTCH 1	Hs NOTCH 1 RT	GCAAGTGCCACAG-TCCACACATCTCAT	5o' Hs NOTCH 1	GCATCAC-CTGCCTGTTAGGAGAA	3o' Hs NOTCH 1	GGCATACACACTCCGA-GAACACATTT	5 i Hs NOTCH 1	GCACGCGGATTAATTTG CATCTGAAA	3 i Hs NOTCH 1	GGCAACATCTAACCCATATG CTTTCACTT
Hs CLDN3	Hs CLDN3 RT	CGTGCTCCAGAAGGGTGAGGTTT CA	5o' Hs CLDN3	GCCCACCCCCAGAA-GCCAGGAA	3o' Hs CLDN3	GGTT-GGTCCCTGGGCCCCGAA GT	5 i Hs CLDN3	CGCTGGACTGGGGCAGCTT	3 i Hs CLDN3	CGACTGCCCGGCCCGCAAA
Hs CLDN4	Hs CLDN4 RT	GCAAGGCACAG-TCCCAGAGGTGATAT	5o' Hs CLDN4	GGCCAGGA-TAGCTTAACCCTGACTT T	3o' Hs CLDN4	CAAGGCCTACCCG-GAACAGAGGAGAT	5 i Hs CLDN4	GGCGTTGGCCAC-TGTCCCCATTTA	3 i Hs CLDN4	GCAGGCAGACAGAGTGGG-GAAAAT
Hs CLDN7	Hs CLDN7 RT	CCCTTTCAGGCATCTAGACAC-TCCCATA	5o' Hs CLDN7	GCCTTGGTAGCTT-GCTCCTGGTAT	3o' Hs CLDN7	GTCAGGCTGGGG-CAAGGAGAT	5 i Hs CLDN7	CCCTTTGATCCCTAC-CAACATTAAGTATGA	3 i Hs CLDN7	CGGTACCCAGCCTT-GCTCTCATT
Hs FOSL1	Hs FOSL1 RT	CTGGTGCCACTGG-TACTGCCTGTGT	5o' Hs FOSL1	GAGTCAGAACCCAG-CAGCCGTGTA	3o' Hs FOSL1	GTCAGAGGCCTGGGG-TAACTGCT	5i' Hs FOSL1	GCAGGCAGCCCAG-CAGAAGTT	3i' Hs FOSL1	GCAGCTCCTGACTGCCAC-TCAT

Hs PPARG C1A	Hs PPARG C1A RT	CCTGCCAATCAGAGGAGA-CATCTTTATTTT	5o' Hs PPARG C1A	CAGTGAGTCTTCTGG-TACACAAGGCAATAA	3o' Hs PPARG C1A	TGACTGGCAA-TAGTCATGGTCAC-CAAACA	5i' Hs PPARG C1A	CAGCAAGTCCTCAG-TCCTCACTGGT	3i' Hs PPARG C1A	GACTGGGCCGCTT-GGTCTTCCTTT
Hs VCL	Hs VCL RT	CATGGGCTAGAAACCCAG-TCTGCCTATT	5o' Hs VCL	CTGAGCCTGGCTGG-CACAGAAA	3o' Hs VCL	GATAGAGGGTG-CACAAGTG-TAACTGTGTTT	5i' Hs VCL	GTCCCAG-GAGCTGCCCAGAGTT	3i' Hs VCL	GAA-GAGGCCCCCATTCCTTTCTGA TGT
Hs IGF1R	Hs IGF1R RT	CTGGAT-TCCTGGCCGAGGGAAAGT	5o' Hs IGF1R	CGACTGACCTGTCTTT-GGAACCAGAACAT	3o' Hs IGF1R	CCTGGTCCCCCAGCAA-GAAGCAAA	5i' Hs IGF1R	CTCCTTCGCACTGGCGTT-GAGT	3i' Hs IGF1R	GCGTCTGTGCTGCCTCCAC-CTA
Hs RRAS	Hs RRAS RT	GCACACAGTGGCAG-TAGCCCAGAA	5o' Hs RRAS	GTAGCCCAGGCAAGA-GAGAAGCAA	3o' Hs RRAS	GGCCAG-GAAGTAAGGGTGGG-TATGTGA	5i' Hs RRAS	CGCACCTTGCTGTGTGAC-CTGA	3i' Hs RRAS	GTCCTGGGA-GACCCAGATGAGGAAATT
Hs GRHL2	Hs GRHL2 RT	CTGGTTTCACAG-GAGCCAGGTATCTT	5o' Hs GRHL2	GCTGCCATGTGA-GAGCTGTGAACA	3o' Hs GRHL2	GGCACATTCTTTCTCAC-TCACTTCCTTAAA	5i' Hs GRHL2	CCT CCT GGG CCA CCA GAT GGA AA	3i' Hs GRHL2	CAGCATCCAGGAG-TGAGGCAAACAATA
Hs EMP 3	Hs EMP 3 RT	CTGCAGGCCCATGTTTT-GGTGTCGT	5o' Hs EMP 3	GCCCGAGCGAGGGACA AGACT	3o' Hs EMP 3	GTCCAAAGTGGCCAC-GAAAAGCAGTAT	5i' Hs EMP 3	GACTCCGACTCCAGCTCTG ACTTTTTT	3i' Hs EMP 3	GAGGAGTGACATGGCTG-CAGTGGAA
Hs MSN	Hs MSN RT	GAGCCTACTGGCATCAAGCTCTA-GAT	5o' Hs MSN	CCAGCCCCATCAG-GACTCTTGTGAAAA	3o' Hs MSN	GATGGCTGTGGAGCAG-GAGCTAT	5i' Hs MSN	GAGGATATGTTCACAC-CTAGCGTCAGTATT	3i' Hs MSN	GTAGCTCTGAGAGGGGAA-GAGACCTAAAA
Hs TBP	Hs TBP RT	CAC-TTAAAGTTTTCTCCCTCAAAC-CAACTTGT	5o' Hs TBP	GGTGGTGTTGTGAGAA-GATGGATGTTGAGTT	3o' Hs TBP	CTGCCCAGATAGCAG-CACGGTAT	5i' Hs TBP	GGCAC-CAGGTGATGCCCTTCTG-TAA	3i' Hs TBP	CGCGGTGTTCTCAGTG-CACAAATAAT
Hs GUSB	Hs GUSB RT	GTGTTCCCTGCTAGAA-TAGATGACCACAAAA	5o' Hs GUSB	GATACTGGAA-GATTGCCAATGAAAC-CAGGTAT	3o' Hs GUSB	CGTGAACAGTCCAG-GAGGCACTTGTT	5i' Hs GUSB	CCCACTCAG-TAGCCAAGTCACAATGTTT	3i' Hs GUSB	GCAGGTGGTATCAGTCTT-GCTCAAGTAAA
Hs NONO	NONO RT	GAGTGG-CATATTGTCCAGCTCCACTTT	5o' Hs NONO	GACCTTCACCCAAC-GAAGCCGTCTTTT	3o' Hs NONO	CTAGGGTTCGGGTTTCCA AGCGGATAAA	5i' Hs NONO	CCTCCCGACATCACTGAG-GAAGAAAT	3i' Hs NONO	GAA-GACTTCGCCTGCCTTTCCATA TTT
Hs FN1	Hs FN1 RT	GAACGTCCTGCCATT-GTAGGTGAATGGTAA	5o' Hs FN1	CTAGAAA-TAGATGCAACGATCAG-GACACAA	3o' Hs FN1	GCGGTTGG-TAAACAGCTGCACGAA	5i' Hs FN1	GGAAGTGTGA-GAGGCACACCTCTGT	3i' Hs FN1	GGGGCCAGATCCGCTCGATG T

Hs HIF1A	Hs HIF1A RT	CTACCACGTACTGCTGGCAAA-GCATTAT	5o' Hs HIF1A	GCTACAATACTG-CACAAACTTGGTTAG-TTCAA	3o' Hs HIF1A	CGAAAAAGGGA-TAAACTCCCTAGCCAAAAA	5i' Hs HIF1A	GCTGGATCACAGA-CAGCTCATTTTCT	3i' Hs HIF1A	GCTACTG-CAATGCAATGGTTTAAATAC-CAAAAA
Hs NRP1	Hs NRP1 RT	GAGCCTGAATCAGCCATTCG-CATTTT	5o' Hs NRP1	GGCATT-GCCTCGCTGCTTTCTT	3o' Hs NRP1	CAGGCAGACGCGGGA-GAACGA	5i' Hs NRP1	CTCCAAGACGGGCTGAG-GATTGTACA	3i' Hs NRP1	GAA-GAGCCCCAACTCCGCCTAGA
Hs SNAI2	Hs SNAI2 RT	CATGCGCCAGGAATGTTCAAA-GCTAAT	5o' Hs SNAI2	CTGATGGCTAGATTGA-GAGAATAAAAGACAG-TAA	3o' Hs SNAI2	CTCCTCCCCCAAGGCAC ATACTGTTAAT	5i' Hs SNAI2	GAAGAGATCTGCCAGAC-GCGAACT	3i' Hs SNAI	CAATGGCAACCAGACAAC-CGACATGTAAT
Hs BMP7	Hs BMP7 RT	GCTAGGTTTTGCCTGCACAGCTT-GTA	5o' Hs BMP7	GAATTCAGACCCTTT-GGGGCCAAGTTTTT	3o' Hs BMP7	CTTGTTCATT-GGATGCTGCCAC-TGAAAAA	5i' Hs BMP7	GGAACCAGCAGAC-CAACTGCCTTTT	3i' Hs BMP7	GATCAAAA-GCCATATGCTGCTCATGTTT
Hs SERPINE1	Hs SERPINE1 RT	GAGTGATGGCAATGTGACTG-GAACAGAAATA	5o' Hs SERPINE1	CTTGGCCTCTCCTT-GGAGGACCTTTA	3o' Hs SERPINE1	GTAAGCCCCGTAG-TTCCATCCTGCAAA	5i' Hs SERPINE1	CACCTGAGACCCTGGGA-GAGAAGTTT	3i' Hs SERPINE1	CGTCACCGTCTGGTTTGGA-GACCTTAA
Hs LAMC2	Hs LAMC2 RT	CAGTCACACTTGGAGTCTAGCAG-TCT	5o' Hs LAMC2	GCATTCACTGCGA-GAAGTGCAAGAAT	3o' Hs LAMC2	CATCTGGCTCCTGTCACA CCTGGTTTA	5i' Hs LAMC2	GGCACAGAGAAAGGGAC-CGCTGTTT	3i' Hs LAMC2	CGAGCACTAAGAGAACCTTT-GGAGTTACAA
Hs TNC	Hs TNC RT	GCTCTAGGGCTCTAGGG-TATCTCACTTT	5o' Hs TNC	CCACAC-TCCAGGTACTTCTTCCAAGGA	3o' Hs TNC	GAATTGGGGATTTAGAA-GCACAGAGTAGACTT	5i' Hs TNC	GGT CTC TCG CCC ATC GGA AAG AAA	3i' Hs TNC	CAAATCAGTT-GTCCCTGATCTTCTTGAAA-GAATT
Hs BNIP3	Hs BNIP3 RT	CCAGGGTGATCACCTAATAATCG-GAGACTTAAT	5o' Hs BNIP3	CTCCACCAGCAC-CTTTTGATGAAGAACT	3o' Hs BNIP3	GATCCCATAGGTG-TAATTATA-GATCAACATGATTTT	5i' Hs BNIP3	GTTAGTGGAT-TACTTCTGAGCTT-GCAACATA	3i' Hs BNIP3	GTGACGTGGCCACCCCAG-GATCTAA
Hs APLN	Hs APLN RT	GAAGGGAAGGCCATGGAG-TCCAGTGATT	5o' Hs APLN	CCAGCTGGGCTG-GAAGGTTCCATAA	3o' Hs APLN	CTGGGGTTGAGCGGTAG-TCTCAGT	5i' Hs APLN	CTGGCCAGCTGCCCCCA-TAACT	3i' Hs APLN	GCCTGAGCCGCCCCTATTAG AGTA
Hs INHBA	Hs INHBA RT	GTAG-GAAAGTGCCTGTGATGGGCCCTT T	5o' Hs INHBA	GTGAAAGAGACAG-GAATTGGGAGGGAAA	3o' Hs INHBA	CTAGTCCACACTACTG-CAGACTAGATTG	5i' Hs INHBA	GGGAGAATGGTG-TACCCTTTATTTCTTCTGAA AT	3i' Hs INHBA	CAAGGGGGGAAAGGACAA-TACCCCGTTTAA

Hs JUP	Hs JUP RT	CAGTTGGTCGGTGGAGTTCAG-TGAGAAAAT	5o' Hs JUP	GCTGGGGAA-GCCGGGGTGTAACTT	3o' Hs JUP	CTGGAGA-CAGGGAGGCTG-GAGGTTT	5i' Hs JUP	CAGAGGTCCTC CGTAGGGTCTTTCTT	3i' Hs JUP	CAGAATGGGTACTTGAG-TCTGAAGCTTTA
Hs KLK3	KLK3 RT	GGGGGTCCAG-TCCCTCTCCTTACTTCAT	5o' KLK3	CCAAGACTCAA-GCCTCCCCAGTTCT	3o' KLK3	CAGTGCCTCCAG-GACAGAGTGGGTTAT	5i' KLK3	GTCCTTAGGTGTGAGGTCC AGGGTTGCT	3i' KLK3	CACCCCTCTTTCATCTCTG-TACCCCAC AA