

## SUPPLEMENTARY MATERIAL

**Table S1.** Target gene elements present in the Nanostring CodeSet

Gene symbol	Accession number	Position	Target sequence
AC015971.2.1	ENST00000426549.1	305-404	CTCCGACATTTCTCCTCCTCAGACTGGACTCCAAGACATTTAAATC GCCACATTGAGACTATACGTAACATGGACCTGGAAAAGCTTAAA AATATGAAGAGG
AC083884.8	ENST00000434256.1	679-778	AGATGGTCCCATCCTGGCATATTCTCAGGTACAATTTGGCCTCA GAATACAGAAGCCCAGCACATCCAACCTATTACCATAAAAATACCA GGAATGTTTTGG
ACTB	NM_001101.2	1011-1110	TGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAATGAAGAT CAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATC GCCGGCTCCATCCT
ADAM12	NM_003474.4	1925-2024	CAACGTGTACCTGCACGATGGGCACTCATGTCAGGATGTGGAC GGCTACTGCTACAATGGCATCTGCCAGACTCACGAGCAGCAGT GTGTCACGCTCTGG
ADAM12_b	NM_003474.5	639-738	AGCAAAGAAGTATCATAAATCTGGAAAGAAATGAAGGTCTCAT TGCCAGCAGTTTCACGGAACCCACTATCTGCAAGACGGTACT GATGTCCTCCCTCG
ADAMTS12_b	NM_030955.2	1956-2055	CAGAGGCACCAACATTTCCGGCAGATGCAGTGCAGTGAATTTGA CACTGTTCCCTACAAGAATGAACTCTACCACTGGTTTCCCATTTT TAACCCAGCACA
ADAMTS12	XM_011514147.1	3549-3648	CTGGTTACATCCCTCAGTCTCTTCTCCATCCCTGTAGGGCTCC ATATCTGGGCTGCTTAGAGTCTCCTGCCAACCTTGGGACACTA GACTAAGAGGAAA
AEBP1_b	NM_001129.4	1464-1563	CCCATTGGGATGGAGTCACACCGTATTGAGGACAACCAGATCC GAGCCTCCTCATGCTGCGCCACGGCCTGGGGGCACAGCGCG GCCGGCTCAACATGC
AEBP1_c	NM_001129.4	1724-1823	CTTCTTCGTGGGCTTTCAGCAATGACAGCCAGACATGGGTGATG TACACCAACGGCTATGAGGAAATGACCTTTTCATGGGAACGTGG ACAAGGACACACCC
AEBP1	NM_001129.4	2560-2659	AGAAGAACCCCTTCGTGCTGGGAGCAAATCTGAACGGCGGCGA GCGGCTAGTATCCTACCCCTACGATATGGCCCGCACGCTACC CAGGAGCAGCTGCT
AKT1	NM_001014432.1	1276-1375	GGACGGGCACATTAAGATCACAGACTTCGGGCTGTGCAAGGAG GGGATCAAGGACGGTGCCACCATGAAGACCTTTTGCGGCACAC CTGAGTACCTGGCC
AKT2	NM_001626.4	700-799	AGGAGATGGAAGTGGCGGTCAGCAAGGCACGGGCTAAAGTGA CCATGAATGACTTCGACTATCTCAAACCTCTTGGCAAGGGAACC TTTGGCAAAGTCAT
AKT3	NM_005465.4	288-387	GCCAGTTAATGAAAACAGAACGACCAAAGCCAAACACATTTATA ATCAGATGTCTCCAGTGGACTACTGTTATAGAGAGAACATTTCA TGATGATACTCC
ATP1A1-AS1	NR_027646.1	122-221	CCTCGTGGGCTGTGTGAGGGCCGAGTGAATCGTGCATTTGCG GTCTGAAATGCAGAAGACAGAAGATGAGCTCTGGCTCTTACC TGCATGGCTGGTGG
B2M	NM_004048.2	236-335	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTTCAGA CTTGTCTTTCAGCAAGGACTGGTCTTTCTATCTTGTACTACAC TGAATTCACCCC
BEST1	NM_004183.3	1119-1218	TGTTCTGGGTGCCCTGGGTGTGGTTTTGCCAACCTGTCAATGAA GGCGTGGCTTGGAGGTGCAATCCGGGACCCTATCCTGCTCCA GAGCCTGCTGAACGA
BICC1	NM_001080512.1	2156-2255	CACGGTCAATCATATGTCAACATGCAGGCATTTGACTATGAACAG AAGAAGCTATTAGCCACCAAAGCTATGTTAAAGAAACCAAGTGGT GACGGAGGTCAG
CALM2	NM_001743.3	869-968	TGGAGTTGTAACCTCTGCGTGGACTATGGACAGTCAACAATATGT ACTTAAAAGTTGCACTATTGCAAAACGGGTGTATTATCCAGGTA CTCGTACACTAT
CD68	NM_001251.2	1141-1240	ACCGTCCATCTTGCTGCCTCTCATCATCGGCCTGATCCTTCTT GGCCTCCTCGCCCTGGTGTATTGCTTTCTGCATCATCCGGA GACGCCATCCGC
COL10A1	NM_000493.3	136-235	AACTTGGTTTACGAGTGTGTTTACGCTGAACGATACCAAATGCC CACAGGCATAAAAGGCCCACTACCCAACCAAGACACAGTTC TTCATTCCCTACA
COL1A2	NM_000089.3	2636-2735	CCAATGGATTGCTGGTCTGCTGGTGTGCTGGTCAACCTGG TGCTAAAGGAGAAAGAGGAGCCAAAGGGCCTAAGGGTAAAAC GGTGTGTTGGTCC
COL3A1	NM_000090.3	181-280	TTGGCACAAACAGGAAGCTGTTGAAGGAGGATGTTCCCATCTTG

			GTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATG CCAAATATGTGTCT
COL3A1_b	NM_000090.3	2263-2362	CCTGGTGTCTGGTACTCCTGGTCTGCAAGGAATGCCTGGAG AAAGAGGAGGCTTGGAAAGTCTGGTCCAAGGGTGACAAGGG TGAACCAGGCGGTC
COL5A1_b	NM_000093.3	494-593	CAGCCAGCAGATCTCCTGAAGGTTCTAGATTTTCACAACCTGCC TGATGGAATAACAAAGACAACAGGCTTTTGCGCCACGCGGCGA TCTTCCAAAGGCC
COL5A1	NM_000093.3	873-972	AGTGGCACAGAATTGCTCTCAGCGTCCACAAGAAAAATGTAC CTTGATCCTCGACTGTAAAAAGAAGACCACCAATTCTCGACC GCAGCGACCACCC
COL5A2	NM_000393.3	4076-4175	GGTTCATGCTACCCTGAAGTCACTCAGTAGTCAGATTGAAACCA TGCGCAGCCCCGATGGCTCGAAAAAGCACCCAGCCCCGACGT GTGATGACCTAAAG
COL5A2_b	NM_000393.3	5761-5860	TGGAATTAGACCATTTGGCCTTTGAACTTTTCATAGGAAAAATGA CCCAACATTTCTTAGCATGAGCTACCTCATCTCTAGAAGCTGGG ATGGACTTACTA
COL6A1_b	NM_001848.2	2303-2402	CTCAGAGGGACACCACACCGCTCAACGTGCTCTGCAGCCCCG GCATCCAGGTGGTCTCCGTGGGCATCAAAGACGTGTTTGACTT CATCCAGGCTCAGA
COL6A2	NM_001849.2	1926-2025	TCGTATCAGACGCTCCGAGAGCATTGGGTACACCAACTTAC ACTGGAGAAGAACTTCGTATCAACGTGGTCAACAGGCTGGGT GCCATCGCTAAGGA
COL8A1	NM_001850.3	2141-2240	AGTGAAGTTTAAACAACTGCTGTATAACGGCAGACAGAATA ACCCGCAGACAGGCATCTTACCTGTGAGTCCCTGGTGTCTA CTACTTTGCATAC
COLEC12	NM_130386.2	901-1000	ACACAAGCCAGGCTATCCAGCGAATCAAGAACGACTTTCAAAT CTGCAGCAGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGGC TGAAGGAGAAAGT
CTSK	NM_000396.2	416-515	TCTCATTCCCGCAGTAATGACACCCTTTATATCCAGAATGGGA AGGTAGAGCCCCAGACTCTGTGACTATCGAAAGAAAGGATAT GTTACTCTGTCA
CXCL3	NM_002090.2	541-640	TCCCTGCCCTTACCAGAGCTGAAAAAGAAAAAGAGAACAGCAG CTTTCTAGGGACAGCTGGAAAGGACTTAATGTGTTTGACTATTT CTTACGAGGGTTC
ECM1	NM_004425.3	1346-1445	TGTTGCCGCCACCCTCCAGCCCTACTCGGGATGAGTGCTTTG CCCGTCGGGCTCCTACCCCAACTATGACCGGGACATCTTGAC CATTGACATCGGTC
FAP_b	NM_004460.2	1491-1590	GCATTGGAAGCTATCCTCCAAGCAAGAAGTGTGTTACTTGGCAT CTAAGGAAAGAAAGGTGCCAATATTACACAGCAAGTTTCAGCGA CTACGCCAAGTA
FN1	NM_212482.1	1777-1876	GGGAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTG CATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACA AGCGTCATGAAGA
GAPDH	NM_00125679 9.1	387-486	GAACGGGAAGCTTGTATCAATGGAATCCCATCACCATCTTCC AGGAGCGAGATCCCTCCAAAATCAAGTGGGGCGATGCTGGCG CTGAGTACGTCGTG
GUSB	NM_000181.3	1900-1999	CCGATTTTCATGACTGAACAGTCAACGACGAGAGTGCTGGGGAA TAAAAGGGGATCTTCACTCGGCAGAGACAACCAAAAAGTGCA GCGTTCCTTTTGGC
HMBS	NM_000190.3	316-415	CATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCAC TCTCTAAGATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGA CATGCCCTGGAG
HPRT1	NM_000194.1	241-340	TGTGATGAAGGAGATGGGAGGCCATCACATTGTAGCCCTCTGT GTGCTCAAGGGGGGCTATAAATTCTTGTGACCTGCTGGATTA CATCAAAGCACTG
INTS5	NM_030628.1	3026-3125	CCTCCACCGCAACATCGACCGCCTAGGTCTTTTCTCTGGCCGT TTCCAGGCACCTTACCCTCACTCTCCTTCGACAGGGGACGT AGCCTTTTCTTGCT
INTS5_b	NM_030628.1	685-784	CCTTGCTGGATACCTCTGTTTACGATTCTCCACACTTTGACTGG GTTGTGGCACATATTGGCTCCTCTTTTCTGGCACCATCATTTT CCGGTTCTCTC
ISM1	NM_080826.1	109-208	GCGGCCGCGGGCAACGCCAGCCAAGCCAGCTGCAGAATAAC CTCAACGTGGGAAGTACACCACATCAGAAACCAGCTTTTCTCT CTCCAAGAAGCAC
ITGA5_b	NM_002205.2	2629-2728	AAGGTCAGCAGCTCCTATATGTGACCAGAGTTACGGGACTCAA CTGCACCACCAATCACCCATTAAACCAAGGGCCTGGAGTTG GATCCCGAGGGTTC
ITGA5	NM_002205.2	4114-4213	GCCAGCTGCACTGATGCTGCCCTCATCTCTGCCCCAACCT TCCCTCACCTTGGCACCAGACACCCAGGACTTATTTAAACTCTG TTGCAAGTGCAAT
KDM4A-AS1	NR_033827.1	339-438	ATGGCTGAGAATCCCTTGGACCCTGGAAGCACCTACTCCATGA TGGCCCGCAGGAGGACCAAACTGGAGACAGTCTGGCTCTGA

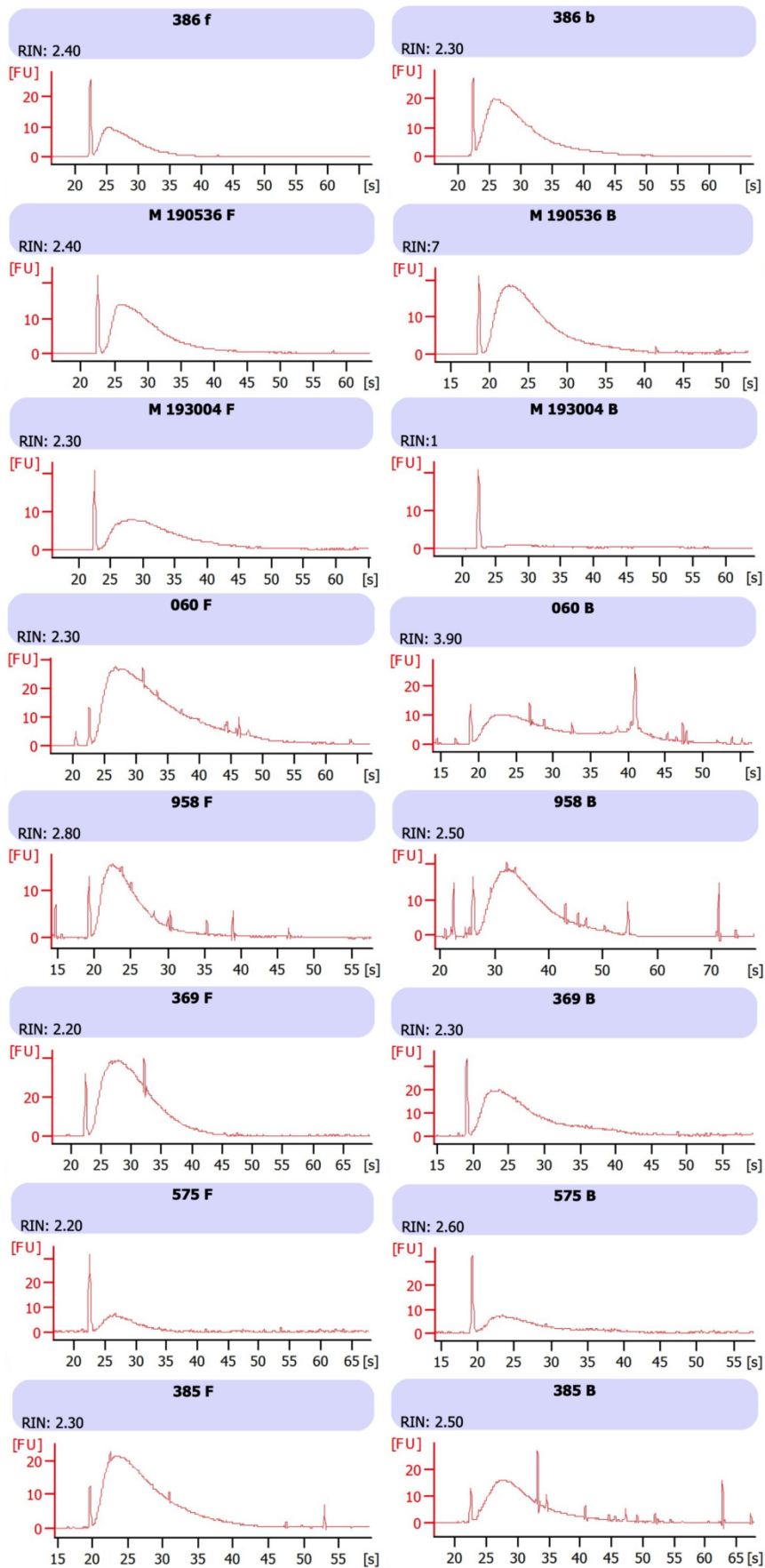
			GAAACAGGAAGGAA
KLF16	NM_031918.3	1521-1620	CTCTGGGTTCTTCCAAAGAACATTTGACTCAGTGGGGTCCGGA GGGAATCCTGGCTTATTTATTTTCTCTGTCTCGGGTGTGGGG GCCCTAGCTCGCC
KLF16_b	NM_031918.3	2298-2397	CCCCTTTTGTCCAGAACCCTGCTCCTCGCTTGGGGACAG GGGGGCTTTGGATGGCACTGGTGTGCACCTGGACCCAGCCCC GGCCTGGCAGGATCC
MAP1S_b	NM_018174.4	268-367	ACCCTGGTCTCCTGAACCCATCAGACAAGTCCCTGTATGATGA GCTCCGGAACCTTCTGTTGGACCCTGCCTCTCACAAGCTACTG GTGTTGGCTGGGC
MMP11	NM_005940.3	703-802	AGCAGCCAAGGCCCTGATGTCCGCCTTCTACACCTTTCGCTAC CCTACTGAGTCTCAGCCAGATGACTGCAGGGGCGTTCAACACC TATATGGCCAGCCC
MMP13	NM_002427.2	952-1051	CTGGCGCTGCATCCTCAGCAGTTGATGCGGAGCTGTTTTTA ACGAAATCATTTTGGCCAGAACTTCCAACCGTATTGATGCTGC ATATGAGCACCTT
MMP14	NM_004995.2	1471-1570	GACAAGATTGATGCTGCTCTTCTGGATGCCAATGGAAGAC CTACTTCTTCCGTGGAACAAGTACTACCGTTTCAACGAAGAGC TCAGGGCAGTGG
MMP14_b	NM_004995.3	2733-2832	AAACCCCTGGCAGCCCTGTGCCTCTCGAATGTTAGCCTTGGAT GGGGCTTTCACAGTTAGAAGAGCTGAAACCAGGGGTGCAGCTG TCAGGTAGGGTGGG
MMP2_b	NM_004530.5	1719-1818	AAACAGGACATTGATTTTGGTGCATCGCTCAGATCCGTGGTGA GATCTTCTTCTTCAAGGACCGGTTTCAATTTGGCGGACTGTGACGC CACGTGACAAGC
MYPOP	NM_00101264 3.3	300-399	CACGGGCCAGGAGGTGCAGAAGCGCTGGAACGACTTCAAGCG CCGCACCAAGGAGAAGCTCGCTCGCGTCCGCACTCCACGCA GGGCGCCGGGCCCGCC
NCKAP5L	NM_00103780 6.3	337-436	GGCACTTGCCAGGCCAACGAAAACCAGCGGGAGACTTATGAG CGTGTCTGGACGAGGTTGCCAACCATGTGGTACAGGCGTTGC TGAACCAGAAGGAC
PARG	NM_003631.2	2581-2680	GTGCTGGATCACAATGAATGTCTAATTATCACAGGTAAGTGC GTACAGTGAATACACAGGCTATGCTGAGACATATCGTTGGTCCC GGAGCCACGAAG
PGK1	NM_000291.2	1031-1130	GCAAGAAGTATGCTGAGGCTGTCACTCGGGCTAAGCAGATTGT GTGGAATGGTCTGTGGGGTATTTGAATGGGAAGCTTTTGCC CGGGGAACCAAAGC
PPIA	NM_021130.3	316-415	TCTATGGGGAGAAATTTGAAGATGAGAATTCATCCTAAAGCAT ACGGGTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACA CAAATGGTCCCA
PPP1CC	NM_002710.2	268-367	ACATCGACAGCATTATCCAACGGCTGCTGGAAGTGAGAGGGTC CAAGCCTGGTAAGAATGTCCAGCTTCAAGGAGAATGAAATCAGA GGACTGTGCTTAAA
PROX1	NM_002763.3	1921-2020	TCTCCTGTGCTCATAAAGTCCGAGTGCGGGGATCTTCAAGAT ATGTCTGAAATATCACCTTATTCGGGAAGTGAATGCAGGAAGG ATTGTCACCCAA
PRRX1	NM_022716.2	331-430	GAAGGAATAGGCAACCTTCAATAGCAGCCAGCTGCAGGCTTT GGAGCGTGTCTTGGAGCGGACACACTATCCTGATGCTTTTGTG CGAGAAGACCTTGC
RP11-247A12.2.1	ENST0000037 2490.1	428-527	CTCCCCATACCCGCACTCCCCATCGTGGCACTTCCCTTGTTC AGTTTTATGGAGTGTGCGTCTGGCTCTCCAAGTACTTGAACC GCTTGATGCATA
RPL19	NM_000981.3	316-415	CCAATGCCGAATGCCAGAGAAGGTCACATGGATGAGGAGAAT GAGGATTTTGCCTGGCTGCTCAGAAGATACCGTGAATCTAAG AAGATCGATCGCCA
SVEP1	NM_153366.3	5726-5825	AATGGCCACTCCTCAGGTGAGATTTATACAGTAGGTGCCGAAG TCACATTTTCTGTGAGGAGGATACAGTTGATGGGAGTAACC AAAATCACATGTT
TBP	NM_00117208 5.1	588-687	ACAGTGAATCTTGGTTGTAACCTTGACCTAAAGACCATTGCACT TCGTGCCCGAAACGCCGAATATAATCCAAGCGGTTTGTGCG GTAATCATGAGGA
TFEC	NM_012252.2	891-990	CTTCACTTGGCAGGTTGATTTAGGTGCTCATGTACCAAACAG CAGAGCCATCCTGAGCAGAATTCAGTAGACTATTGCCAACAACT GACTGTGTCTCA
TGFBR1	NM_004612.2	1256-1355	GAATCCTTCAAACGTGCTGACATCTATGCAATGGGCTTAGTATT CTGGGAAATTGCTCGACGATGTTCCATTGGTGAATTCATGAAG ATTACCAACTGC
THBS1	NM_003246.2	3466-3565	ACCCTCGTCACATAGGCTGGAAAGATTTACCGCCTACAGATG GCGTCTCAGCCACAGGCCAAAGACGGGTTTATTAGAGTGGTG ATGTATGAAGGGAA
THBS2	NM_003247.2	4461-4560	AAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTGGAT TTGGCAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGC GGTCTTTAGCTG

ZNF444	NM_00125379 2.1	1439-1538	CCACTTGGCCTCTTCCTCTCCTCCTCCCTCCCATCGTCCTCCT CCACCTGCGCCTCCCTTGTCTGAACTTCCCAACGCCTTCCTATT CCTTCCAACCTC
--------	--------------------	-----------	---

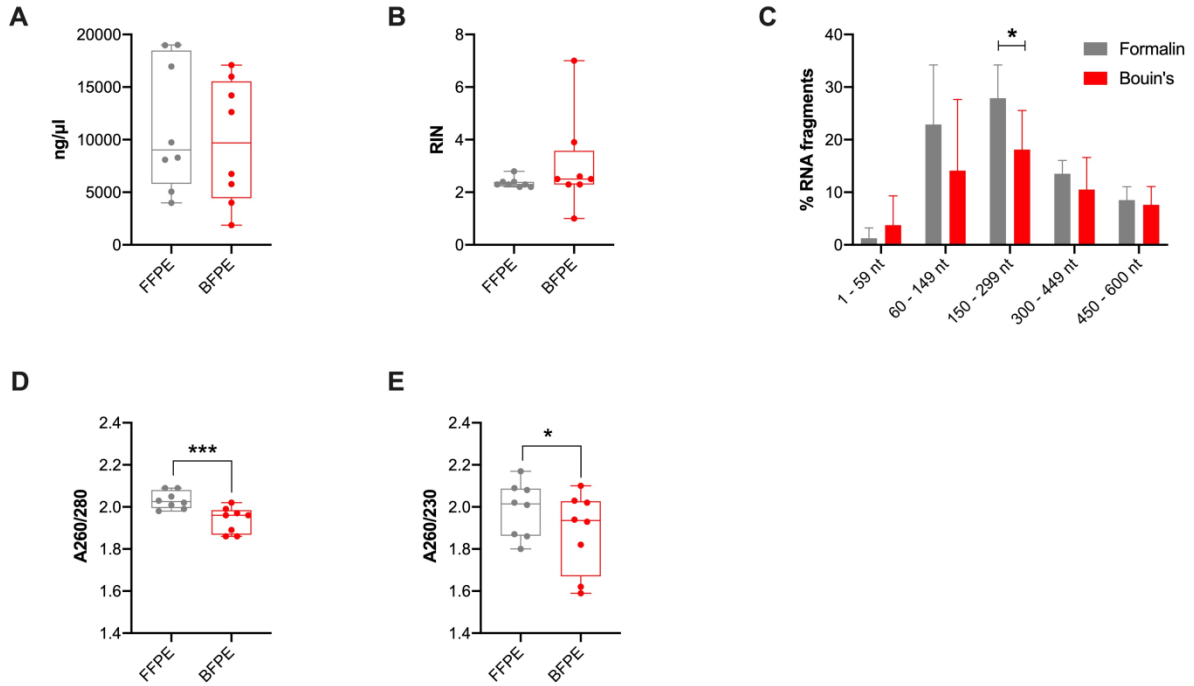
**Table S2.** Amplification primers used for ddPCR and qPCR analysis

Gene	Primer	Length
GAPDH	Fw- 5'-GCA CCG TCAA GGC TGA GAA C-3'	96
	Rev- 5'-CAT CGC CCC ACT TGA TTT TG-3'	
ACTB	Fw -5'-GTG GAT CAG CAA GCA GGA GT-3'	95
	Rev 5'-AGG GTG TAA CGC AAC TAA GTC-3'	
AKT1	Fw 5'-CCA CTG TCA TCG AAC GCA CCT-3'	77
	Rev 5'-CAC AGT CTG GAT GGC GGT TGT-3'	
AKT2	Fw 5'-AAG CAG AGG CTT GGT GGG-3'	71
	Rev 5'-TTG ATG CTG AGG AAG AAC CTG-3'	
AKT3	Fw 5'-TCG AGA GAG CGG GTG TTC T-3'	77
	Rev 5'-TGT AGA TAG TCC AAG GCA GAG A-3'	
KLF16	Fw 5'-GTC AGA CCC AGA AAG GTG GA-3'	78
	Rev 5'-GGA CGG TTC TGG AAC AAA AG-3'	
HPRT1	Fw 5'-GTG TCA TTA GTG AAA AGC A-3'	91
	Rev 5'-CGA TGT CAA TAG GAC TCC AGA TGT T-3'	

Figure S1 Agilent BioAnalyzer profiles of matched FFPE/BFPE pairs and respective RIN numbers.



**Figure S2** Results of the isolation procedure in the eight matched formalin/Bouin's samples. (A) RNA yield after isolation. (B) RNA Integrity Number (RIN). (C) Percentage of RNA fragments according to different smear regions as measured by smear analysis on Agilent BioAnalyzer. (D, E) RNA purity as measured by A260/280 and A260/230 ratios on Nanodrop.



**Figure S3** Volcano plot for differentially expressed genes on matched formalin and Bouin's tissues identified on Nanostring, ddPCR and qPCR using raw data (C).

