

Table S1. List of 28 genes validated by qPCR. No significant gene was found (data not shown).

Gene	Full gene name
<i>ACACA</i>	acetyl-Coenzyme A carboxylase alpha
<i>AMACR</i>	alpha-methylacyl-CoA racemase
<i>ARHGEF2</i>	rho/rac guanine nucleotide exchange factor (GEF) 2
<i>BLVRA</i>	biliverdin reductase A
<i>CASK</i>	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
<i>CCT5</i>	chaperonin containing TCP1, subunit 5 (epsilon)
<i>CDC2</i>	cell division cycle 2, G1 to S and G2 to M
<i>CIB1</i>	calcium and integrin binding 1 (calmyrin)
<i>CRELD2</i>	homo sapiens cysteine rich with EGF like domains 2
<i>GALNT10</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10
<i>GUSB</i>	glucuronidase, beta
<i>HMMR</i>	hyaluronan-mediated motility receptor
<i>IGFBP3</i>	insulin-like growth factor binding protein 3
<i>ITPR3</i>	inositol 1,4,5-triphosphate receptor, type 3
<i>KLK10</i>	kallikrein-related peptidase 10
<i>KPNA6</i>	karyopherin alpha 6 (importin alpha 7)
<i>LAMP1</i>	lysosomal-associated membrane protein 1
<i>P4HB</i>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide
<i>PARP8</i>	poly (ADP-ribose) polymerase family, member 8
<i>PLCH1</i>	phospholipase C, eta 1
<i>RPN2</i>	ribophorin II
<i>SERTAD2</i>	SERTA domain containing 2
<i>SLC2A8</i>	solute carrier family 2, (facilitated glucose transporter) member 8
<i>SMOX</i>	spermine oxidase
<i>SNCA</i>	synuclein, alpha (non A4 component of amyloid precursor)
<i>SRI</i>	Sorcin
<i>TRPS1</i>	trichorhinophalangeal syndrome I
<i>TXNRD3</i>	thioredoxin reductase 3

Table S2. Clinical characteristic of the qPCR group. .

	All QPCR patients	M1 patients	M0 patients	<i>p</i> -value
Patients number	63	9	54	
Median age at diagnosis [years] (range)	50 (12-75)	29 (12-66)	53 (12-75)	0.091
Median follow-up [months] (range)	148.3 (18.0-238.4)	135.1 (40.6-238.4)	148.9 (18.0-184.0)	0.875
Sex:				
- male	14 (22.2%)	5 (55.6%)	9 (16.7%)	0.020
- female	49 (77.8%)	4 (44.4%)	45 (83.3%)	
PTC histological subtype				
- classic	51 (81.0%)	6 (66.7%)	45 (83.3%)	0.158
- follicular	9 (14.3%)	3 (33.3%)	6 (11.1%)	
- other	3 (4.8%)	0 (0%)	3 (5.6%)	
T feature (primary tumor):				
- T1	39 (61.9%)	1 (11.1%)	38 (70.4%)	< 0.001
- T2	11 (17.5%)	2 (22.2%)	9 (16.7%)	
- T3	8 (12.7%)	2 (22.2%)	6 (11.1%)	
- T4	3 (4.8%)	2 (22.2%)	1 (1.9%)	
- Tx	2 (3.2%)	2 (22.2%)	0 (0%)	
Lymph node metastases:				
- central neck compartment and upper mediastinum (N1a)	24 (38.1%)	7 (77.8%)	17 (31.5%)	0.003
- lateral neck compartment and retropharyngeal lymph nodes (N1b)	21 (33.3%)	7 (77.8%)	14 (25.9%)	0.001
Recurrence after primary treatment	6 (9.5%)	1 (11.1%)	5 (9.3%)	> 0.999
PTC-related death	3 (4.8%)	3 (33.3%)	0 (0%)	0.002

The patients were staged according to the 8th UICC/AJCC TNM Edition (2016). PTC – papillary thyroid cancer; M1 – distant metastases present; M0 - distant metastases absent

Table S3. List of primers used in qPCR.

Gene	Primers sequence (5'-3')		Lenght (bp)
<i>ACACA</i>	F	gatgtggatgatgggctaca	63
	R	tgaggccttgatcattactgg	
<i>AMACR</i>	F	tagtgctggacctgaagcag	112
	R	agctggagtttctccatgaca	
<i>ARHGEF2</i>	F	gtgctatgcctgtaacaagagc	72
	R	tggatagtcacattgcaggtg	
<i>BLVRA</i>	F	aggtcgctatatctgcagtg	71
	R	cttgccagcattaaggaactg	
<i>CASK</i>	F	caattaggggagtctggactg	63
	R	tggtgccataaaatgaggtg	
<i>CCT5</i>	F	attggagatggaaccacagg	66
	R	caattgctccgcttctctaa	
<i>CDC2</i>	F	tggatctgaagaaacttgattcta	96
	R	caatccctgtaggatttg	
<i>CIB1</i>	F	acaggcggtttgtgagc	123
	R	gctcctgaaggggttg	
<i>CRELD2</i>	F	gcttcgaaggaaacggaagat	72
	R	gtgtcgggcttctcctct	
<i>GALNT10</i>	F	ggaagtatgtgcctacaaggt	64
	R	gccaccgcttaaggttc	
<i>GUSB</i>	F	cgccctgcctatctgtattc	91
	R	tccccacaggagtgtag	
<i>HMMR</i>	F	cgattcaatgaccttctgg	85
	R	aggatactggtccttcaatacttct	
<i>IGFBP3</i>	F	aacgctagtgccgtcagc	86
	R	cggcttctccgactcac	
<i>ITPR3</i>	F	tgtgctggacacatcaac	94
	R	cagcagctgcaccacaac	
<i>KLK10</i>	F	ttccctaccgctgtgctc	95
	R	ggtcaggcccttgtgtact	
<i>KPNA6</i>	F	tcagactttgaggatgttcagg	73
	R	ggcaaacagagctatctccag	
<i>LAMP1</i>	F	gtgggtccaggcttcaa	78
	R	agcatgctgttctcgcca	
<i>P4HB</i>	F	gcttcccccaaggaatataca	61
	R	tcttcagccagttcacgatg	
<i>PARP8</i>	F	agggtttgaaaagcaaacaca	71

Gene	Primers sequence (5'-3')		Lenght (bp)
<i>PLCH1</i>	R	agggttgaaaagcaaacaca	74
	F	aactgtggaagaactggctca	
	R	caagacaatagtcggtgtcacat	
<i>RPN2</i>	F	ggcagtgtgacgtttctgg	76
	R	tctggaactaatgtgctgttctct	
<i>SERTAD2</i>	F	ccctcctgatgcggttagttc	66
	R	cgtttctcctttaccaac	
<i>SLC2A8</i>	F	ggcctttctcgtgaccaa	71
	R	caagccagaaggctccatag	
<i>SMOX</i>	F	gatgctgcgtcagttcacag	95
	R	aggagccgcggaagtaag	
<i>SNCA</i>	F	caaacaggggtgtggcaga	72
	R	tccttggtttggagcctac	
<i>SRI</i>	F	aaagatcaccttcgacgactaca	86
	R	gctgagcagtatcccgtctt	
<i>TRPS1</i>	F	cggtggcctctaccagaag	109
	R	gggtaaggcgctttcttg	
<i>TXNRD3</i>	F	aaggaaattggctgggaat	74
	R	ggttctgaatcgctttgtca	