

**Supplementary Table 1.** List of primers used for Real-Time PCR

Gene	Primer sequence
<i>THRA</i>	Forward 5'-TGG ATG ACA CGG AAG TGG CTC T-3' Reverse 5'-TAC GCC TCC TGA CTC TTC TCG A-3'
<i>THRB</i>	forward 5'-GGT TGA CTT GGA AGC CTT CAG C-3' reverse 5'-GGA TGA TCT GGT CTT CAC ATG GC-3'
<i>HIF1A</i>	forward 5'-TAT GAG CCA GAA GAA CTT TTA GGC-3' reverse 5'-CAC CTC TTT TGG CAA GCA TCC TG-3'
<i>L1CAM</i>	forward 5'-TCG CCC TAT GTC CAC TAC ACC T-3' reverse 5'-ATC CAC AGG GTT CTT CTC TGG G-3'
<i>LOX</i>	forward 5'-GAT ACG GCA CTG GCT ACT TCC A-3' reverse 5'-GCC AGA CAG TTT TCC TCC GCC-3'
<i>FN1</i>	forward 5'-ACA ACA CCG AGG TGA CTG AGA C-3' reverse 5'-GGA CAC AAC GAT GCT TCC TGA G-3'
<i>TGFB2</i>	forward 5'-AAG AAG CGT GCT TTG GAT GCG G-3' reverse 5'-GCT CCA GCA CAG AAG TTG GC-3'
<i>ERBB3</i>	forward 5'-GAT GGG GAA CCT TGA GAT TG-3' reverse 5'-GGC AAA CTT CCC ATC GTA GA-3'
<i>GAPDH</i>	forward 5'-GGA GCG AGA TCC CTC CAA AAT-3' reverse 5'-GGC TGT TGT CAT ACT TCT CAT GG-3'

**Supplementary Table 2.** Clinicopathological characteristics of TCGA THCA dataset according to the *NCOR1* expression status

Characteristic	<i>NCOR1</i>		p-value
	Low expression N=126 (%)	High expression N=126 (%)	
Age (years)	48.24±15.42	44.90±14.65	0.079*
Gender (Male:Female)	35 (27.8):91 (72.2)	29 (23.0):97 (77.0)	0.385 <sup>†</sup>
Tumor size (cm)	3.20±1.76	2.83±1.47	0.105*
MACIS score	5.44±1.51	5.00±1.30	0.023*
Histologic subtype			0.635 <sup>†</sup>
Follicular variant	31 (25.4)	26 (21.1)	
Conventional	79 (64.8)	94 (76.4)	
Tall cell variant	12 (9.8)	3 (2.4)	
Extrathyroidal extension			0.044 <sup>†</sup>
No	72 (66.7)	92 (78.6)	
Yes	36 (33.3)	25 (21.4)	
Multifocality			0.689 <sup>†</sup>
No	72 (58.1)	70 (55.6)	
Yes	52 (41.9)	56 (44.4)	
T stage			0.121 <sup>†</sup>
T1	32 (28.1)	37 (30.6)	
T2	37 (32.5)	52 (43.0)	
T3	39 (34.2)	28 (23.1)	
T4	6 (5.3)	4 (3.3)	
N stage			0.776 <sup>†</sup>
N0	58 (54.7)	57 (52.8)	
N1	48 (45.3)	51 (47.2)	
M stage			0.686 <sup>†</sup>
M0	64 (95.5)	62 (96.9)	
M1	3 (4.5)	2 (3.1)	
TNM stage			0.156 <sup>†</sup>
I	63 (54.8)	74 (61.7)	
II	10 (8.7)	16 (13.3)	
III	31 (27.0)	20 (16.7)	
IV	11 (9.6)	10 (8.3)	

\*p-values calculated using Student's t-test. Data are mean±SD.

<sup>†</sup>p-values calculated using  $\chi^2$  test or linear-by-linear association.

**Supplementary Table 3.** Clinicopathological characteristics of TCGA THCA dataset according to *SMRT* expression status

Characteristic	<i>SMRT</i>		p-value
	Low expression N=126 (%)	High expression N=126 (%)	
Age (years)	45.68±15.31	48.34±16.83	0.190*
Gender (Male:Female)	37 (29.4):89 (70.6)	30 (23.8):96 (76.2)	0.318 <sup>†</sup>
Tumor size (cm)	3.19±1.64	3.05±1.58	0.566*
MACIS score	5.14±1.40	5.66±1.70	0.016*
Histologic subtype			0.023 <sup>†</sup>
Follicular variant	36 (29.8)	19 (15.3)	
Conventional	77 (63.6)	96 (77.4)	
Tall cell variant	8 (6.6)	9 (7.3)	
Extrathyroidal extension			0.202 <sup>†</sup>
No	83 (72.2)	74 (64.3)	
Yes	32 (25.2)	41 (35.7)	
Multifocality			0.203 <sup>†</sup>
No	62 (50.0)	72 (58.1)	
Yes	62 (50.0)	52 (41.9)	
T stage			0.831 <sup>†</sup>
T1	27 (22.9)	28 (23.5)	
T2	44 (37.3)	42 (35.3)	
T3	43 (36.4)	43 (36.1)	
T4	4 (3.4)	6 (5.0)	
N stage			0.423 <sup>†</sup>
N0	53 (49.5)	61 (55.0)	
N1	54 (50.5)	50 (45.0)	
M stage			0.471 <sup>†</sup>
M0	50 (98.0)	66 (95.7)	
M1	1 (2.0)	3 (4.3)	
TNM stage			0.023 <sup>†</sup>
I	73 (62.9)	54 (45.4)	
II	8 (6.9)	18 (15.1)	
III	26 (22.4)	31 (26.1)	
IV	9 (7.8)	16 (13.4)	

\*p-values calculated using Student's t-test. Data are mean±SD.

<sup>†</sup>p-values calculated using  $\chi^2$  test or linear-by-linear association.

**Supplementary Table 4.** Molecular features of TCGA THCA dataset according to *THRA* expression status

Characteristic	<i>THRA</i>		p-value
	Low expression N=126 (%)	High expression N=126 (%)	
Ras driver mutation			0.016 <sup>†</sup>
Absent	120 (97.6)	110 (90.2)	
Present	3 (2.4)	12 (9.8)	
BRAF driver mutation			<0.0001 <sup>†</sup>
Absent	39 (31.0)	78 (62.9)	
Present	87 (69.0)	46 (37.1)	
TERT promoter mutation			0.025 <sup>†</sup>
Absent	86 (85.1)	91 (94.8)	
Present	15 (14.9)	5 (5.2)	
RAS/RAF score	-0.74±0.39	0.06±0.74	<0.0001*
ERK score	18.06±16.95	-7.59±18.73	<0.0001*
Differentiation score	-0.75±0.85	0.35±1.16	<0.0001*
Tumor status			0.017 <sup>†</sup>
Free	96 (82.8)	107 (93.0)	
With Tumor	20 (17.2)	8 (7.0)	

\*p values calculated using Student's t-test. Data are mean±SD.

<sup>†</sup>p-values calculated using  $\chi^2$  test or linear-by-linear association.

**Supplementary Table 5.** Molecular features of TCGA THCA dataset according to *THRB* expression status

Characteristic	<i>THRB</i>		p-value
	Low expression N=126 (%)	High expression N=126 (%)	
Ras driver mutation			0.005 <sup>†</sup>
Absent	108 (87.1)	119 (96.7)	
Present	16 (12.9)	4 (3.3)	
BRAF driver mutation			0.007 <sup>†</sup>
Absent	73 (57.9)	51 (40.8)	
Present	53 (42.1)	74 (59.2)	
TERT promoter mutation			0.602 <sup>†</sup>
Absent	82 (90.1)	95 (92.2)	
Present	9 (9.9)	8 (7.8)	
RAS/RAF score	-0.17±0.74	-0.44±0.66	0.008*
ERK score	0.41±20.14	10.88±21.17	<0.0001*
Differentiation score	0.09±1.02	-0.26±1.02	0.015*
Tumor status			0.583 <sup>†</sup>
Free	103 (88.8)	101 (91.0)	
With Tumor	13 (11.2)	10 (9.0)	

\*p-values calculated using Student's t-test. Data are mean±SD.

<sup>†</sup>p-values calculated using  $\chi^2$  test or linear-by-linear association.