

Supplemental Table S1. Clinicopathological Characteristics of Patients with Papillary Thyroid Microcarcinoma Subjected to RNA Sequencing Analysis

Characteristic	CHA			TCGA		
	N0	N1b	<i>P</i> value	N0	N1b	<i>P</i> value
Number	10	10		12	6	
Age, yr	53.08±5.75	42.97±11.50	0.027	43.67±11.15	50.67±20.56	0.357
Male sex	4 (40.0)	6 (60.0)	0.371	2 (16.7)	2 (33.3)	0.569
Tumor size, cm	0.7±0.3	0.8±0.2	0.594	1.0 (0.7–1.0)	1.0 (1.0–1.0)	0.385
Multifocality	5 (50.0)	6 (60.0)	1.000	8 (66.7)	4 (66.7)	1.000
Extrathyroidal extension	1 (10.0)	5 (50.0)	0.141	1 (8.3)	1 (16.7)	1.000
Thyroiditis	3 (30.0)	2 (20.0)	1.000	4 (33.3)	1 (16.7)	0.615
Variant			1.000			1.000
Classical	9 (90.0)	9 (90.0)		10 (83.3)	5 (83.3)	
Classical+Follicular	1 (10.0)	1 (10.0)		0	0	
Follicular	0	0		1 (8.3)	0	
Tall cell	0	0		1 (8.3)	1 (16.7)	
Central node metastasis	0	8/9 (88.9)	<0.001	0	4/5 (80.0)	0.002
Number of CLNMs	0 (0–0)	3 (3–6)	<0.001	0 (0–0)	1 (0–2) ^a	0.006
Number of LLNMs	0 (0–0)	2 (2–5)	<0.001	0 (0–0)	2 (2–2) ^a	<0.001
Maximal size of tumor in metastatic LNs, mm	-	6.0 (4.0–10.0)		-	6.0 ^a	
Extranodal extension	-	8 (80.0)		-	1/2 (50.0) ^a	
<i>BRAF</i> mutation	9/9 (100.0)	9/9 (100.0)	1.000	8 (66.7)	5 (83.3)	0.615

Values are expressed as mean ± standard deviation, number (%), or median (interquartile range).

CHA, CHA Bundang Medical Center; TCGA, The Cancer Genome Atlas; CLNM, central neck lymph node metastasis; LLNM, lateral neck lymph node metastasis; LN, lymph node.

^aAmong the six patients with N1b in the TCGA dataset, the number of patients with information on the number of CLNMs and LLNMs, maximal size of metastatic lymph nodes, and extranodal extension was 5, 1, and 2, respectively.