

Supplementary file 1: the sequence of KCNJ16-CDS

ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATACCCAGGCTACCCGCC
AGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAAGACGATTACTTCACAAAGATGGCAGCTG
TAATGTCTACTTCAAGCACATTTTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTC
TTGTGGACACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCTCGTGGTTGAT
ATTTGGCTCTGTCTTTTGGCTCATAGCCTTTTCATCATGGCGATCTATTAAATGATCCAGACATCACA
CCTTGTGTTGACAACGTCCATTCTTTACAGGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCAC
CATAGGATATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTGATCCTCCA
GTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGCTGCCTTGGCCAAAATGGCAACTGC
TCGAAAGAGAGCCCAAACCATTCGTTTCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAG
CTTTGCCTCATGTGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAGAG
CCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGGCATTAAAGACCTCAA
ATTAGTCAACGACCAAATCATCCTGGTCACCCCGGTAACCTATTGTCCATGAAATTGACCATGAGA
GCCCTCTGTATGCCCTTGACCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTT
ATCTATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTTCCCCGAGAAATT
CTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAAGAGGAAGTATTACAAAGTGAAGTGCTT
ACAGTTTGAAGGAAGTGTGGAAGTATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAA
GACCAGCAGCTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACACCAAG
GCGAGACGAAGGTCATTTAGTGCAGTTGCCATTGTCAGCAGCTGTGAAAACCCTGAGGAGACC
ACCACTTCCGCCACACATGAATATAGGGAAACACCTTATCAGAAAGCTCTCCTGACTTTAAACAG
AATCTCTGTAGAATCCCAAATGTAG

Supplementary table 1: The information of 4 GEO datasets and the sequence of primers

4 GEO datasets from GEO database

GEO dataset	Platform	ATC	PTC	PDTC	N
GSE29265	Affymetrix Human Genome U133 Plus 2.0 Array	9	20	-	20
GSE33630	Affymetrix Human Genome U133 Plus 2.0 Array	11	49	-	45
GSE65144	Affymetrix Human Genome U133 Plus 2.0 Array	12	-	-	13
GSE76039	Affymetrix Human Genome U133 Plus 2.0 Array	20	-	17	-

ATC: Anaplastic thyroid cancer; PTC: Papillary thyroid cancer; PDTC: Poorly differentiated thyroid cancer; N: Normal thyroid

The primer sequences of Real-Time PCR

Gene	sequence	length
TSHR	5'-GGAATGGGGTGTTTCGTCTCC-3'(sense)	78bp
	5'- GCGTTGAATATCCTTGCAGGT-3'(antisense)	
KCNJ16	5'-TATCAATGCGGACGCAAAATACC-3'(sense)	147bp
	5'- ACCACATAGCTTCCCCATTCT-3'(antisense)	
SYT1	5'- GCTGCTGGTAGGGATCATTCA-3'(sense)	132bp
	5'- GTTTTTCGGTGGACTTTTGTCTC-3'(antisense)	
GAPDH	5'- GGAGCGAGATCCCTCCAAAAT-3'(sense)	197bp
	5'- GGCTGTTGTCATACTTCTCATGG-3'(antisense)	



