Supplementary table 1.Correlation between MHCII expression and clinicopathological factors in PTC patients

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Variables | Low expression | | High expression | | X2 | *P* |
| Age |  |  |  |  |  |  |
| <55 | 36 | | 33 | | 0.028 | 0.867 |
| >=55 | 62 | | 54 | |  |  |
| Sex |  |  |  |  |  |  |
| Female | 74 | | 58 | | 1.763 | 0.184 |
| Male | 24 | | 29 | |  |  |
| CD4 T cell infiltration | | | | |  |  |
| Present | 17 | | 28 | | 5.511 | 0.019 |
| Absent | 81 | | 59 | |  |  |
| BRAF V600E mutation | | | |  |  |  |
| Present | 59 | | 34 | | 8.226 | 0.004 |
| Absent | 39 | | 53 | |  |  |
| Multifocality | | |  |  |  |  |
| Present | 30 | | 28 | | 0.053 | 0.818 |
| Absent | 68 | | 59 | |  |  |
| Tumour stage | |  |  |  |  |  |
| T1/2 | 82 | | 85 | | 10.325 | 0.001 |
| T3/4 | 16 | | 2 | |  |  |
| Lymph node metastasis | | | | |  |  |
| N0 | 37 | | 52 | | 8.947 | 0.003 |
| N1a/b | 51 | | 35 | |  |  |
| AJCC stage | | |  |  |  |  |
| I+II | 86 | | 86 | | 8.684 | 0.003 |
| III+IV | 12 | | 1 | |  |  |
| Recurrence | | |  |  |  |  |
| Absent | 70 | | 85 | | 23.414 | <0.001 |
| Present | 28 | | 2 | |  |  |

Supplementary table 2.Hazard Ratios of DSS and OS acording to the expression of tsMHCII in Patients with PTC

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variables | Disease-speciﬁc Survival | | Overall Survival | |
|  | P-value | HR（95%CI） | P-value | HR（95%CI） |
| Female | 0.608 | 1.311(0.466-3.690) | 0.392 | 1.501(0.592-3.807) |
| Stage III+IV | <0.001 | 15.305(4.578-51.166) | <0.001 | 18.201(6.381-51.917) |
| Multifocality | 0.820 | 0.885(0.307-2.549) | 0.613 | 0.783(0.302-2.025) |
| BRAF mutation | 0.012 | 4.612(1.405-15.141) | 0.001 | 5.524(1.942-15.719) |
| MHC II expression | 0.038 | 0.205(0.046-0.917) | 0.024 | 0.240(0.070-0.827) |
| CD4 T cell infiltration | 0.872 | 0.903(0.258-3.154) | 0.904 | 0.935(0.315-2.774) |

Supplementary table 3. Hazard Ratios of OS acording to the mRNA levels of CIITA using TIMER webtool

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | 95%CI | |  |
|  | HR | Lower | Uper | *P* |
| CIITA | 0.504 | 0.27 | 0.938 | 0.031 |
| Purity | 14.540 | 1.286 | >100 | 0.031 |
| Stage I | Ref. | - | - | - |
| Stage II | 6.304 | 0.738 | 53.849 | 0.093 |
| Stage III | 11.326 | 1.883 | 68.117 | 0.008 |
| Stage IV | 41.385 | 5.495 | >100 | <0.001 |
| mate | 1.109 | 0.312 | 3.930 | 0.874 |
| B cell | 0.006 | <0.001 | >100 | 0.312 |
| CD8 T cell | <0.001 | <0.001 | 0.500 | 0.041 |
| CD4 T cell | 0.021 | <0.001 | >100 | 0.046 |
| Marcrophage | <0.001 | <0.001 | >100 | 0.211 |
| Neutrophage | 0.050 | <0.001 | >100 | 0.983 |
| Dendritic | >100 | >100 | >100 | 0.007 |

Supplementary table 4. Clinicopathologic Characteristics of 185 PTC Patients for IHC assay.

|  |  |
| --- | --- |
| Patient characteristics | N=185 |
| Age |  |
| ≥55 | 116(62.7%) |
| Sex |  |
| Female | 132(71.4%) |
| Tumour stage |  |
| T3/4 | 18(9.7%) |
| Lymph node metastasis |  |
| N1a/b | 96(51.9%) |
| Multifocality |  |
| Present | 58(31.4%) |
| AJCC stage |  |
| III+IV | 13(7.0%) |
| BRAF mutation |  |
| Present | 93(50.3%) |
| CD4 T cell infiltration |  |
| Present | 45(24.3%) |
| Recurrence |  |
| Present | 30(16.2%) |
| Overall mortality | 28(15.1%) |
| Disease-specific mortality | 21(11.4%) |
| Follow-up years, median (range) | 68(20-72) |

Supplementary table 5. Clinicopathologic Characteristics of 30 PTC Patients for iTRAQ assay.

|  |  |  |
| --- | --- | --- |
| Patient characteristics | BRAFV600E (N=15) | BRAF wildtype (N=15) |
| Age |  |  |
| ≥55 | 10 | 8 |
| Sex |  |  |
| Female | 12 | 10 |
| Tumour stage |  |  |
| T3/4 | 3 | 1 |
| Lymph node metastasis |  |  |
| N1a/b | 7 | 8 |
| Multifocality |  |  |
| Present | 9 | 7 |
| AJCC stage |  |  |
| III+IV | 1 | 1 |
| Thyroidectomy |  |  |
| Total | 15 | 15 |
| Lymphadenectomy |  |  |
| Central | 6 | 6 |
| Central+lateral | 9 | 9 |

Supplementary table 6. List of Real-time PCR Probes in 5′→3′orientation.

|  |  |  |
| --- | --- | --- |
|  | FORWARD | REVERSE |
| CIITA | GAAGAAGCTGCTCCGAGGTTGC | GCTCTGTCTTGGTGCTCTGTCATC |
| HLA-DPA1 | GACCGTCTGGCATCTGGAGGAG | GAGTGTGGTTGGAACGCTGGATC |
| HLA-DQA1 | GTGGACCTGGAGAGGAAGGAGAC | CATTGGTAGCAGCGGTAGAGTTGTAG |
| HLA-DRA | GCCGAGTTCTATCTGAATCCTGACC | AAGCCGCCAGACCGTCTCC |