**Supplementary Table S1. Source, clone, and dilution of used antibodies**

|  |  |  |  |
| --- | --- | --- | --- |
| Antibody | Clone | Dilution | Company |
| *Glycolysis-related* | | | |
| GLUT1 | Polyclonal | 1:50 | Abcam, Cambridge, UK |
| CAIX | Polyclonal | 1:100 | Abcam, Cambridge, UK |
| Hexokinase II | Polyclonal | 1:100 | Abcam, Cambridge, UK |
| *Pentose phosphate pathway related* | | | |
| G6PDH | Polyclonal | 1:100 | Abcam, Cambridge, UK |
| *Serine/glycine metabolism related* | | | |
| PHGDH | Polyclonal | 1:100 | Abcam, Cambridge, UK |
| SHMT1 | Polyclonal | 1:100 | Abcam, Cambridge, UK |

**Supplementary Table S2. Basal characteristics of adrenal cortical neoplasm**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameters | Total  N=132 (%) | Adrenal cortical adenoma  n=115 (%) | Adrenal cortical carcinoma  n=17 (%) | p-value |
| Age  (year, mean±SD) | 47.5±14.5 | 48.4±12.2 | 41.0±25.1 | 0.048 |
| Sex |  |  |  | 0.107 |
| Male | 40 (30.3) | 32 (27.8) | 8 (47.1) |  |
| Female | 92 (69.7) | 83 (72.2) | 9 (52.9) |  |
| Tumor size  (cm, mean±SD) | 3.6±3.7 | 2.5±1.3 | 10.9±5.8 | <0.001 |
| Fuhrman grade |  |  |  | <0.001 |
| 1, 2 | 106 (80.3) | 102 (88.7) | 4 (23.5) |  |
| 3, 4 | 26 (19.7) | 13 (11.3) | 13 (76.5) |  |
| Mitosis |  |  |  | <0.001 |
| ≤5/50HFPs | 122 (92.4) | 115 (100.0) | 7 (41.2) |  |
| >5/50HFPs | 10 (7.6) | 0 (0.0) | 10 (58.8) |  |
| Atypical mitosis |  |  |  | <0.001 |
| Absent | 121 (91.7) | 114 (99.1) | 7 (41.2) |  |
| Present | 11 (8.3) | 1 (0.9) | 10 (58.8) |  |
| Clear cell proportion |  |  |  | <0.001 |
| ≥25% | 96 (72.7) | 95 (82.6) | 1 (5.9) |  |
| <25% | 36 (27.3) | 20 (17.4) | 16 (94.1) |  |
| Diffuse architecture |  |  |  | <0.001 |
| Absent | 117 (88.6) | 111 (96.5) | 6 (35.3) |  |
| Present | 15 (11.4) | 4 (3.5) | 11 (64.7) |  |
| Necrosis |  |  |  | <0.001 |
| Absent | 113 (85.6) | 113 (98.3) | 0 (0.0) |  |
| Present | 19 (14.4) | 2 (1.7) | 17 (100.0) |  |
| Venous invasion |  |  |  | <0.001 |
| Absent | 126 (95.5) | 115 (100.0) | 11 (64.7) |  |
| Present | 6 (4.5) | 0 (0.0) | 6 (35.3) |  |
| Sinusoidal invasion |  |  |  | <0.001 |
| Absent | 126 (95.5) | 115 (100.0) | 11 (64.7) |  |
| Present | 6 (4.5) | 0 (0.0) | 6 (35.3) |  |
| Capsular invasion |  |  |  | <0.001 |
| Absent | 117 (88.6) | 111 (96.5) | 6 (35.3) |  |
| Present | 15 (11.4) | 4 (3.5) | 11 (64.7) |  |
| Weiss total score |  |  |  | <0.001 |
| < 4 | 117 (88.6) | 115 (100.0) | 2 (11.8)\* |  |
| ≥ 4 | 15 (11.4) | 0 (0.0) | 15 (88.2) |  |
| Recurrence | 3 (2.3) | 0 (0.0) | 3 (17.6) | <0.001 |
| Distant metastasis | 7 (5.3) | 0 (0.0) | 7 (41.2) | <0.001 |
| Patient death | 9 (6.8) | 0 (0.0) | 9 (52.9) | <0.001 |

**Supplementary Table S3. Basal characteristics of pheochromocytoma**

|  |  |
| --- | --- |
| Parameters | Total, N=189 (%) |
| Age (year, mean±SD) | 48.1±13.7 |
| Sex |  |
| Male | 73 (38.6) |
| Female | 116 (61.4) |
| Tumor size (cm, mean±SD) | 5.0±3.4 |
| Histologic pattern |  |
| Zellballen | 165 (87.3) |
| Non-Zellballen | 24 (12.7) |
| Cellularity |  |
| Low | 11 (5.8) |
| Moderate | 162 (85.7) |
| High | 16 (8.5) |
| Comedo necrosis |  |
| Absent | 189 (100.0) |
| Present | 0 (0.0) |
| Vascular or capsular invasion |  |
| Absent | 129 (68.3) |
| Present | 60 (31.7) |
| Ki-67 labeling index (%) |  |
| <1 | 139 (73.5) |
| 1-3 | 38 (20.1) |
| >3 | 12 (6.3) |
| Catecholamine type |  |
| Non-norepinephrine type | 154 (81.5) |
| Norepinephrine type | 35 (18.5) |
| GAPP score |  |
| 0-2 (well-differentiated type) | 138 (73.0) |
| 3-6 (moderately differentiated type) | 50 (26.5) |
| 7-10 (poorly differentiated type) | 1 (0.5) |
| Tumor recurrence | 5 (2.6) |
| Distant metastasis | 7 (3.7) |
| Patient death | 11 (5.8) |

**Supplementary Table S4. Univariate analysis of the impact of expression of glycolysis-related proteins in adrenal cortical neoplasm on disease-free survival and overall survival by the log-rank test**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Parameter | Number  of patients  /recurrence/death | Disease-free survival | | Overall survival | | |
| Mean survival months  (95% CI) | p-value | Mean survival months  (95% CI) | p-value | |
| GLUT1 (T) |  |  | 0.150 |  | | **0.017** |
| Negative | 90/1/3 | 117 (115-120) |  | 115 (111-119) | |  |
| Positive | 42/2/6 | 91 (85-97) |  | 83 (73-92) | |  |
| GLUT1 (S) |  |  | - |  | | - |
| Negative | 115/3/9 | - |  | - | |  |
| Positive | 17/0/0 | - |  | - | |  |
| CAIX (T) |  |  | 0.321 |  | | 0.466 |
| Negative | 113/2/7 | 117 (114-119) |  | 112 (107-117) | |  |
| Positive | 19/1/2 | 103 (93-113) |  | 98 (85-112) | |  |
| CAIX (S) |  |  | - |  | | **0.003** |
| Negative | 126/3/7 | - |  | 112 (108-117) | |  |
| Positive | 6/0/2 | - |  | 64 (29-99) | |  |
| Hexokinase II |  |  | - |  | | - |
| Negative | 131/3/9 | - |  | - | |  |
| Positive | 1/0/0 | - |  | - | |  |
| G6PDH |  |  | - |  | | - |
| Negative | 9/0/0 | - |  | - | |  |
| Positive | 123/3/9 | - |  | - | |  |
| PHGDH |  |  | - |  | | **0.009** |
| Negative | 119/3/6 | - |  | 104 (100-107) | |  |
| Positive | 13/0/3 | - |  | 92 (66-118) | |  |
| SHMT1 |  |  | 0.552 |  | | 0.834 |
| Negative | 25/1/2 | 94 (88-100) |  | 91 (82-100) | |  |
| Positive | 107/2/7 | 116 (114-119) |  | 111 (106-116) | |  |

**Supplementary Table S5. Univariate analysis of the impact of expression of glycolysis-related proteins in pheochromocytoma on disease-free survival and overall survival by the log-rank test**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Parameter | Number  of patients  /recurrence/death | | Disease-free survival | | Overall survival | | |
| Mean survival months  (95% CI) | p-value | Mean survival months  (95% CI) | p-value | |
| GLUT1 (T) |  |  | | 0.302 |  | | **0.001** |
| Negative | 173/4/7 | 154 (147-161) | |  | 157 (150-164) | |  |
| Positive | 15/1/4 | 95 (78-111) | |  | 75 (53-97) | |  |
| CAIX (T) |  |  | | 0.852 |  | | 0.084 |
| Negative | 153/4/7 | 154 (146-161) | |  | 155 (146-163) | |  |
| Positive | 35/1/4 | 100 (92-107) | |  | 88 (74-102) | |  |
| CAIX (S) |  |  | | - |  | | 0.681 |
| Negative | 176/5/10 | - | |  | 152 (143-161) | |  |
| Positive | 12/0/1 | - | |  | 87 (75-99) | |  |
| Hexokinase II |  |  | | - |  | | - |
| Negative | 187/5/11 | - | |  | - | |  |
| Positive | 1/0/0 | - | |  | - | |  |
| G6PDH |  |  | | 0.226 |  | | 0.087 |
| Negative | 102/4/3 | 117 (111-124) | |  | 159 (151-168) | |  |
| Positive | 86/1/8 | 158 (154-163) | |  | 136 (120-152) | |  |
| PHGDH |  |  | | - |  | | **<0.001** |
| Negative | 178/5/8 | - | |  | 153 (144-162) | |  |
| Positive | 10/0/3 | - | |  | 69 (37-102) | |  |
| SHMT1 |  |  | | 0.519 |  | | 0.051 |
| Negative | 66/1/7 | 155 (150-160) | |  | 132 (114-150) | |  |
| Positive | 122/4/4 | 151 (142-161) | |  | 158 (149-166) | |  |