**Supplemental Table S1** Relationship between expression modules with DFS within gastric cancer molecular subtypes in the training dataset

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Modules** | **Gene Count** | **MSS/TP53- (n=107)** | | | **MSS/TP53+ (n=79)** | | | **MSI (n=68)** | | | **MSS/EMT (n=46)** | | |
| **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** |
| MEblack | 43 | 0.921 | 0.549-1.544 | 0.755 | 1.353 | 0.715-2.56 | 0.353 | 0.649 | 0.284-1.483 | 0.305 | 0.806 | 0.406-1.601 | 0.539 |
| MEblue | 404 | 1.035 | 0.618-1.733 | 0.895 | 0.951 | 0.503-1.799 | 0.877 | 0.821 | 0.36-1.874 | 0.64 | 0.795 | 0.398-1.585 | 0.514 |
| MEbrown | 342 | 0.958 | 0.572-1.604 | 0.87 | 1.454 | 0.763-2.769 | 0.255 | 2.014 | 0.87-4.661 | 0.102 | 1.854 | 0.925-3.715 | 0.082 |
| MEgreen | 113 | 1.545 | 0.912-2.615 | 0.106 | 0.92 | 0.487-1.741 | 0.799 | 1.518 | 0.665-3.466 | 0.321 | 0.512 | 0.252-1.041 | 0.064 |
| MEred | 95 | 0.784 | 0.467-1.316 | 0.357 | 1.528 | 0.805-2.899 | 0.195 | 0.725 | 0.318-1.655 | 0.446 | 0.993 | 0.501-1.969 | 0.984 |
| MEturquoise | 1059 | 1.401 | 0.833-2.357 | 0.204 | 0.79 | 0.418-1.494 | 0.469 | 2.234 | 0.945-5.279 | 0.067 | 2.467 | 1.198-5.081 | 0.014\* |
| MEyellow | 236 | 0.876 | 0.523-1.469 | 0.616 | 1.227 | 0.649-2.319 | 0.529 | 0.544 | 0.235-1.258 | 0.155 | 0.661 | 0.33-1.321 | 0.241 |

\* *p* ≤ 0.05, \*\* *p* ≤ 0.01, \*\*\* *p* ≤ 0.001. Disease-free survival (DFS). Hazard ratios (HRs), 95% confidence intervals (CI), and p-values were calculated using Cox proportional hazards regression analysis after grouped the gastric cancer patients by the median of gene level.

**Supplemental Table S2** Relationships between hub genes in module brown with DFS within GC molecular subtypes in the training dataset

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **MSS/TP53- (n=107)** | | | **MSS/TP53+ (n=79)** | | | **MSI (n=68)** | | | **MSS/EMT (n=46)** | | |
| **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** | **HR** | **95%CI** | **p-value** |
| COL8A1 | 0.971 | 0.58-1.626 | 0.911 | 0.947 | 0.501-1.789 | 0.866 | 2.15 | 0.911-5.074 | 0.081 | 2.295 | 1.144-4.602 | 0.019\* |
| FRMD6 | 1.033 | 0.616-1.731 | 0.902 | 1.331 | 0.702-2.523 | 0.382 | 2.715 | 1.116-6.605 | 0.028\* | 1.726 | 0.862-3.454 | 0.123 |
| DDR2 | 1.093 | 0.652-1.831 | 0.737 | 1.106 | 0.583-2.097 | 0.758 | 1.928 | 0.833-4.462 | 0.125 | 1.951 | 0.969-3.928 | 0.061 |
| LOC100505881 | 1.119 | 0.669-1.874 | 0.668 | 1.239 | 0.65-2.362 | 0.514 | 1.224 | 0.54-2.775 | 0.629 | 1.295 | 0.652-2.572 | 0.459 |
| TIMP2 | 0.826 | 0.493-1.382 | 0.466 | 1.189 | 0.627-2.254 | 0.597 | 2.964 | 1.217-7.217 | 0.017\* | 1.568 | 0.784-3.136 | 0.204 |
| CNRIP1 | 1.03 | 0.615-1.727 | 0.911 | 1.269 | 0.669-2.406 | 0.465 | 2.942 | 1.207-7.168 | 0.018\* | 1.636 | 0.817-3.276 | 0.165 |
| CLEC11A | 1.191 | 0.71-1.996 | 0.508 | 1.313 | 0.694-2.485 | 0.402 | 1.755 | 0.759-4.058 | 0.188 | 1.304 | 0.656-2.59 | 0.449 |
| MRC2 | 0.719 | 0.429-1.204 | 0.21 | 1.544 | 0.806-2.96 | 0.191 | 2.379 | 1.007-5.62 | 0.048\* | 1.133 | 0.57-2.253 | 0.722 |
| BGN | 1.177 | 0.701-1.976 | 0.538 | 1.451 | 0.765-2.753 | 0.254 | 2.283 | 0.967-5.389 | 0.06 | 1.643 | 0.825-3.272 | 0.158 |
| GPR124 | 0.877 | 0.524-1.468 | 0.618 | 1.61 | 0.839-3.087 | 0.152 | 3.814 | 1.5-9.694 | 0.005\*\* | 1.552 | 0.777-3.102 | 0.213 |

\* *p* ≤ 0.05, \*\* *p* ≤ 0.01, \*\*\* *p* ≤ 0.001. Disease-free survival (DFS). Hazard ratios (HRs), 95% confidence intervals (CI), and p-values were calculated using Cox proportional hazards regression analysis after grouped the gastric cancer patients by the median of gene level.

**Supplemental Table S3** Gene set enriched in gastric samples with COL8A1 high expression

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG pathway | ES | NES | NOM p-val | FDR q-val |
| Focal adhesion | 0.642164 | 2.010706 | 0 | 0.013562 |
| MAPK signaling pathway | 0.486047 | 1.873360 | 0 | 0.022987 |
| Hypertrophic cardiomyopathy HCM | 0.666637 | 1.842285 | 0 | 0.029878 |
| ECM receptor interaction | 0.780677 | 1.875293 | 0 | 0.032989 |
| Dilated cardiomyopathy | 0.672196 | 1.815344 | 0 | 0.033609 |

ES, enrichment score; NES, normalized enrichment score; NOM p-val, nominal p value; FDR, false discovery rate q value.

**Supplemental Table S4** Gene set enriched in gastric samples with FRMD6 high expression

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG pathway | ES | NES | NOM p-val | FDR q-val |
| Hypertrophic cardiomyopathy HCM | 0.676538 | 1.88334 | 0 | 0.025208 |
| Focal adhesion | 0.602799 | 1.89473 | 0 | 0.034539 |
| ECM receptor interaction | 0.756069 | 1.834094 | 0 | 0.035397 |
| Arrhythmogenic right ventricular cardiomyopathy arvc | 0.675432 | 1.813331 | 0.002012 | 0.036139 |
| Dilated cardiomyopathy | 0.701614 | 1.942828 | 0 | 0.040858 |

ES, enrichment score; NES, normalized enrichment score; NOM p-val, nominal p value; FDR, false discovery rate q value.

**Supplemental Table S5** Gene set enriched in gastric samples with TIMP2 high expression

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG pathway | ES | NES | NOM p-val | FDR q-val |
| Hypertrophic cardiomyopathy HCM | 0.673980 | 1.911272 | 0 | 0.015696 |
| Dilated cardiomyopathy | 0.688504 | 1.924166 | 0 | 0.021905 |
| Acute myeloid leukemia | 0.578235 | 1.809426 | 0.003724 | 0.024328 |
| Focal adhesion | 0.627413 | 1.963339 | 0 | 0.024577 |
| Chemokine signaling pathway | 0.570614 | 1.788511 | 0 | 0.025981 |
| Arrhythmogenic right ventricular cardiomyopathy arvc | 0.667917 | 1.812366 | 0 | 0.027496 |
| MAPK signaling pathway | 0.466618 | 1.82109 | 0 | 0.029583 |
| ECM receptor interaction | 0.770251 | 1.833021 | 0 | 0.031944 |
| Regulation of actin cytoskeleton | 0.498709 | 1.76472 | 0.001946 | 0.031962 |
| Cell adhesion molecules CAMS | 0.633919 | 1.738564 | 0 | 0.037052 |
| GAP junction | 0.605841 | 1.744520 | 0.001894 | 0.037526 |
| TGF beta signaling pathway | 0.677915 | 1.727839 | 0 | 0.038904 |
| Axon guidance | 0.540830 | 1.698659 | 0.003945 | 0.049397 |

ES, enrichment score; NES, normalized enrichment score; NOM p-val, nominal p value; FDR, false discovery rate q value.

**Supplemental Table S6** Gene set enriched in gastric samples with CNRIP1 high expression

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| KEGG pathway | ES | NES | NOM  p-val | FDR  q-val |  |  |
| Focal adhesion | 0.568812 | 1.793104 | 0 | 0.105094 |  |  |
| TGF beta signaling pathway | 0.699911 | 1.776705 | 0 | 0.060615 |  |  |
| Hematopoietic cell lineage | 0.731447 | 1.757724 | 0 | 0.060004 |  |  |
| Chemokine signaling pathway | 0.548154 | 1.745753 | 0 | 0.055979 |  |  |
| MAPK signaling pathway | 0.437692 | 1.702496 | 0 | 0.064108 |  |  |
| Long term depression | 0.673645 | 1.682868 | 0 | 0.058043 |  |  |
| Regulation of actin cytoskeleton | 0.477831 | 1.671147 | 0 | 0.061342 |  |  |
| Dilated cardiomyopathy | 0.660609 | 1.814449 | 0.001961 | 0.164772 |  |  |
| Hypertrophic cardiomyopathy HCM | 0.642656 | 1.781195 | 0.001984 | 0.078367 |  |  |
| ECM receptor interaction | 0.716917 | 1.716779 | 0.002037 | 0.059999 |  |  |
| Cell adhesion molecules cams | 0.60306 | 1.694035 | 0.003914 | 0.061828 |  |  |
| Axon guidance | 0.494552 | 1.532844 | 0.00396 | 0.125964 |  |  |
| Arrhythmogenic right ventricular cardiomyopathy arvc | 0.64514 | 1.720169 | 0.003968 | 0.064665 |  |  |
| GAP junction | 0.590007 | 1.686102 | 0.003976 | 0.061453 |  |  |
| Calcium signaling pathway | 0.530217 | 1.636257 | 0.005837 | 0.083227 |  |  |
| Pathways in cancer | 0.389717 | 1.483366 | 0.010267 | 0.162581 |  |  |
| Viral myocarditis | 0.633947 | 1.589857 | 0.012766 | 0.118805 |  |  |
| Melanoma | 0.537271 | 1.548602 | 0.01581 | 0.126685 |  |  |
| Vascular smooth muscle contraction | 0.671363 | 1.589146 | 0.015842 | 0.111859 |  |  |
| FC epsilon R signaling pathway | 0.551342 | 1.584463 | 0.016667 | 0.110042 |  |  |
| Neurotrophin signaling pathway | 0.384245 | 1.541716 | 0.021611 | 0.122107 |  |  |
| FC gamma R mediated phagocytosis | 0.473051 | 1.569696 | 0.021782 | 0.11031 |  |  |
| Leukocyte transendothelial migration | 0.467239 | 1.432471 | 0.03629 | 0.203465 |  |  |
| JAK stat signaling pathway | 0.461648 | 1.502514 | 0.037182 | 0.153394 |  |  |
| Melanogenesis | 0.387778 | 1.46119 | 0.038306 | 0.174978 |  |  |
| Leishmania infection | 0.659579 | 1.581545 | 0.038697 | 0.106513 |  |  |

ES, enrichment score; NES, normalized enrichment score; NOM p-val, nominal p value; FDR, false discovery rate q value.

**Supplemental Table S7** Gene set enriched in gastric samples with GPR124 high expression

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG pathway | ES | NES | NOM p-val | FDR q-val |
| Dilated cardiomyopathy | 0.691109 | 1.912495 | 0.002024 | 0.012468 |
| Hypertrophic cardiomyopathy HCM | 0.669598 | 1.884551 | 0 | 0.015833 |
| MAPK signaling pathway | 0.485364 | 1.918648 | 0 | 0.016693 |
| Focal adhesion | 0.629513 | 1.945361 | 0 | 0.021753 |
| ECM receptor interaction | 0.766736 | 1.851674 | 0 | 0.023054 |
| Acute myeloid leukemia | 0.577098 | 1.81114 | 0.004149 | 0.033171 |
| TGF beta signaling pathway | 0.713854 | 1.797139 | 0 | 0.03375 |

ES, enrichment score; NES, normalized enrichment score; NOM p-val, nominal p value; FDR, false discovery rate q value.