**Figure S1.** Upregulation of ISG15, IFI27, and OASL gene expression by KU55933 (KU) in parent (CAL27) and cisplatin-resistant (CDDP-R, CAL-A8) oral cancer cells was demonstrated by RT-qPCR. *, $p < 0.05$ versus control (Ctrl). **, $p < 0.001$ versus control (Ctrl).
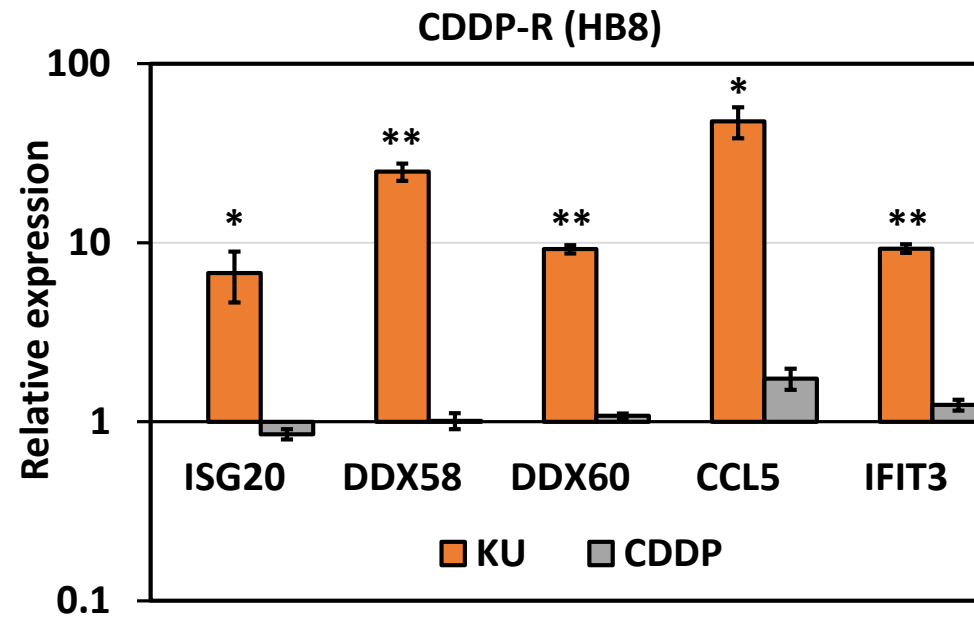
**Figure S2.** Upregulation of interferon-stimulated genes by KU55933 in cisplatin-resistant cancer cells was demonstrated by RT-qPCR. CDDP-R, cisplatin-resistant. KU, KU55933. CDDP, cisplatin. *, $p < 0.05$ versus control. **, $p < 0.001$ versus control.
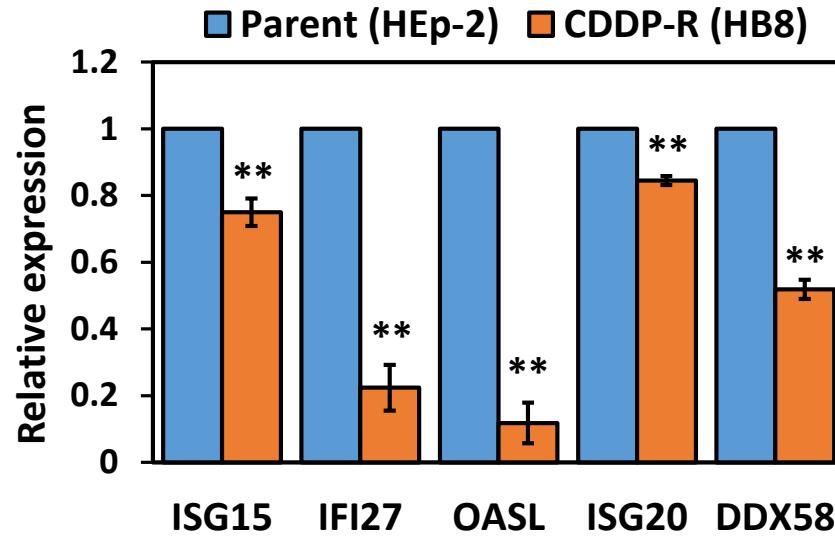
**Figure S3.** Downregulation of interferon-stimulated genes in cisplatin-resistant cancer cells compared to parent cancer cells. The gene expression levels were determined by RT-qPCR. CDDP-R, cisplatin-resistant. **, $p < 0.001$ versus parent cells (HEp-2).
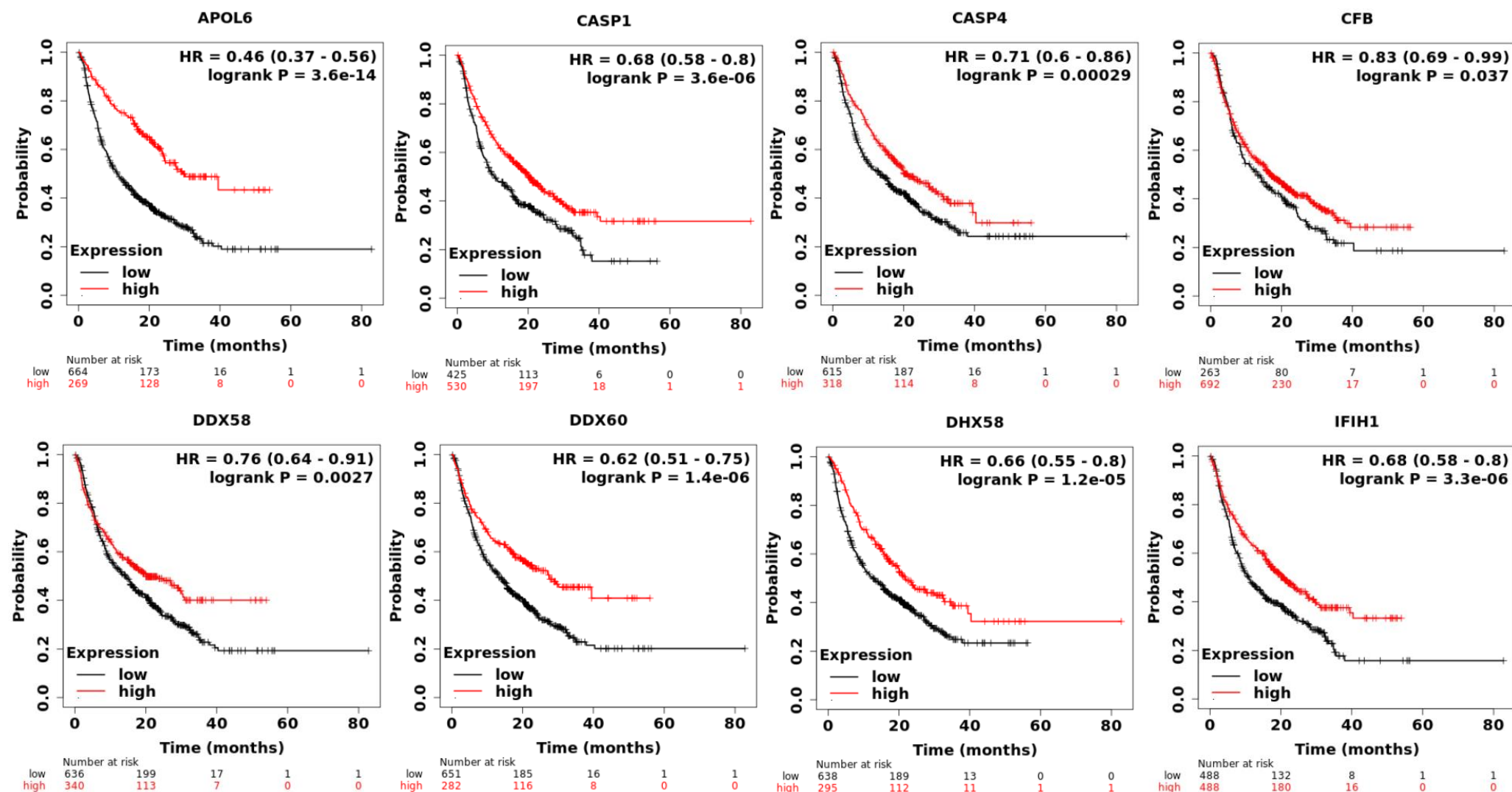
**Figure S4.** Kaplan-Meier plots of overall survival of cancer patients who received immune checkpoint blockade therapy. The best cut-off values were determined by ROC curve analysis.

**Figure S4.** (Cont.) Kaplan-Meier plots of overall survival of cancer patients who received immune checkpoint blockade therapy. The best cut-off values were determined by ROC curve analysis.

**Figure S4.** (Cont.) Kaplan-Meier plots of overall survival of cancer patients who received immune checkpoint blockade therapy. The best cut-off values were determined by ROC curve analysis.
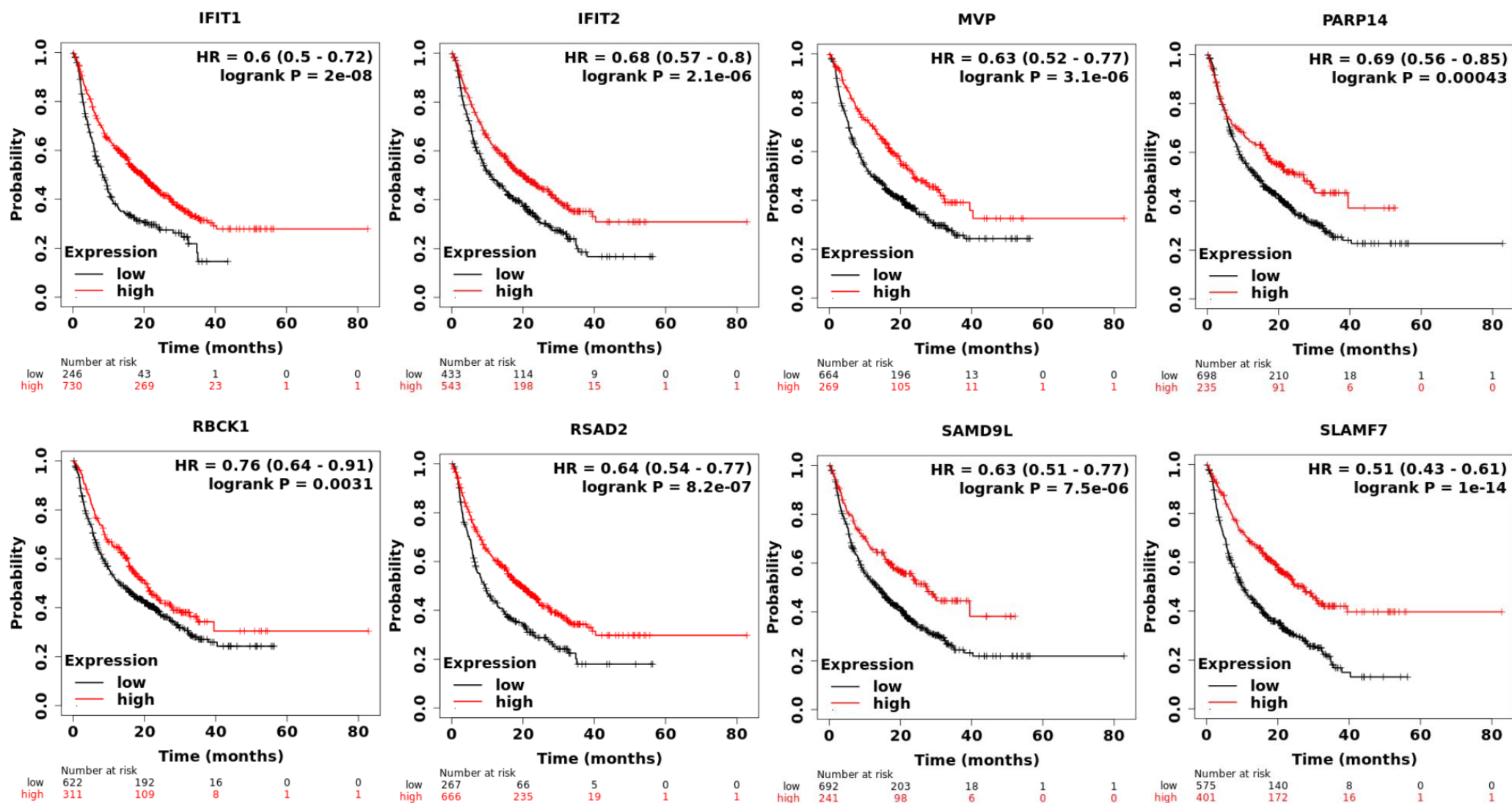
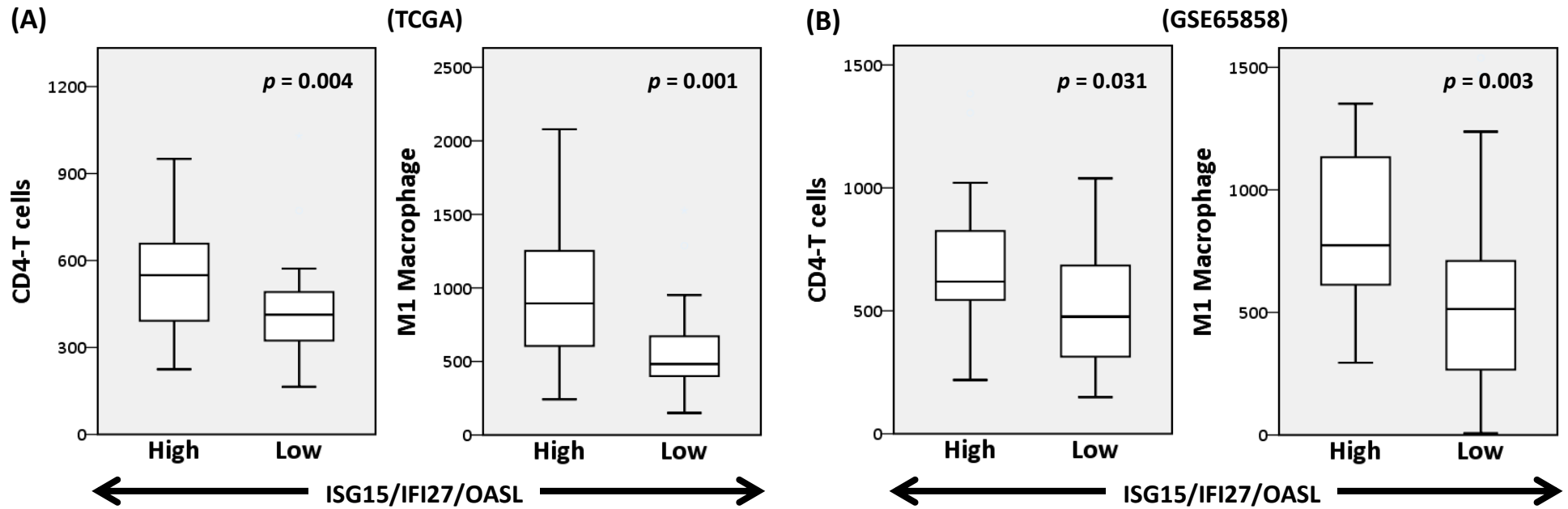**Figure S5.** Enrichment of CD4+ T cells and M1 macrophages in oral cancer with high expression of ISG15/IFI27/OASL. Cell type enrichment scores in ISG15/IFI27/OASL-High (n=30) and ISG15/IFI27/OASL–Low (n=30) subgroups of TCGA (A) and GSE65858 (B) oral cancer data sets were analyzed using xCell algorithm.

**Table S1.** The patient demographics of TCGA cohort based on ATM expression.

| Characteristics | ATM-High (n=30) | ATM-Low (n=30) | p |
|---|---|---|---|
| Age (Years) [a] | 58 (49, 66) | 58 (53, 65) | 0.981 |
| Male (%) | 20 (66.6) | 20 (66.6) | 0.695 |
| Survival status: Living (%) | 16 (53.3) | 16 (57.1) | 0.771 |
| OS [b] (Days) [a] | 593 (375, 873) | 527 (295, 1079) | 0.950 |
| PFS [c] (Days) [a] | 568 (431, 662) | 546 (219, 1370) | 0.941 |
| Tumor stage (2 missing) | | | |
| Stage I (%) | 3 (10.0) | 0 (0) | 0.084 |
| Stage II (%) | 3 (10.0) | 4 (13.3) | |
| Stage III (%) | 10 (33.3) | 4 (13.3) | |
| Stage VI (%) | 12 (40.0) | 14 (46.7) | |
| ATM [a] | 10.3 (10.2, 10.8) | 7.6 (7.3, 7.8) | <0.001 |
| OASL [a] | 8.8 (7.7, 10.4) | 10.5 (9.88, 11.5) | <0.001 |
| IFI27 [a] | 13.1 (12.3, 13.4) | 15.0 (14.5, 15.8) | <0.001 |
| ISG15 [a] | 11.4 (9.9, 12.2) | 14.2 (12.6, 15.3) | <0.001 |

[a] median (interquartile range). [b] overall survival. [c] progression free survival.

**Table S2.** The patient demographics of GSE65858 cohort based on ATM expression.

| Characteristics | ATM-High (n=30) | ATM-Low (n=30) | *p* |
|---|---|---|---|
| Age (Years) [a] | 56 (48, 70) | 57 (52, 68) | 0.701 |
| Male (%) | 24 (80) | 24 (80) | >0.999 |
| Survival status: Living (%) | 21 (70) | 21 (70) | >0.999 |
| OS [b] (Days) [a] | 849 (667, 1016) | 787 (581, 982) | 0.589 |
| PFS [c] (Days) [a] | 806 (380, 1011) | 691 (334, 957) | 0.482 |
| Tumor stage | | | |
| Stage I (%) | 4 (13.3) | 4 (13.3) | 0.534 |
| Stage II (%) | 4 (13.3) | 4 (13.3) | |
| Stage III (%) | 0 (0) | 3 (10.0) | |
| Stage VI (%) | 22 (73.3) | 19 (63.3) | |
| ATM [a] | 7.9 (7.8, 8.1) | 7.4 (7.3, 7.5) | <0.001 |
| OASL [a] | 7.8 (6.9, 8.4) | 8.3 (7.6, 8.9) | 0.001 |
| IFI27 [a] | 11.6 (10.5, 12.2) | 12.3 (11.6, 12.5) | 0.003 |
| ISG15 [a] | 9.8 (8.7, 11.0) | 10.7 (9.8, 11.6) | 0.028 |

[a] median (interquartile range). [b] overall survival. [c] progression free survival.

**Table S3.** The patient demographics of TCGA cohort based on ISG [a] expression.

| Characteristics | ISG-Low (n=30) | ISG-High (n=30) | p |
|---|---|---|---|
| Age (Years) [b] | 66 (54, 72) | 56 (50, 69) | 0.071 |
| Male (%) | 25 (86.2) | 17 (59.0) | 0.019 |
| Survival status: Living (%) | 16 (57.1) | 20 (69.0) | 0.355 |
| OS [c] (Days) [b] | 518.5 (385, 939) | 428 (225, 1043) | 0.508 |
| PFS [d] (Days) [b] | 394 (185, 783) | 342 (210, 698) | 0.920 |
| Tumor stage (2 missing) | | | |
|     Stage I (%) | 2 (8.3) | 2 (8.3) | 0.495 |
|     Stage II (%) | 5 (20.8) | 2 (8.3) | |
|     Stage III (%) | 4 (16.7) | 9 (37.5) | |
|     Stage VI (%) | 13 (54.2) | 11 (45.9) | |
| ATM [b] | 9.53 (8.9, 9.8) | 8.85 (7.8, 9.2) | <0.001 |
| OASL [b] | 6.55 (5.2, 6.9) | 10.48 (10.3, 10.8) | <0.001 |
| IFI27 [b] | 11.17 (9.5, 12.0) | 14.48 (13.4, 14.9) | <0.001 |
| ISG15 [b] | 9.06 (8.4, 10.1) | 13.13 (12.5, 13.8) | <0.001 |

[a] ISG15/IFI27/OASL. [b] median (interquartile range). [c] overall survival. [d] progression free survival.

**Table S4.** The patient demographics of GSE65858 cohort based on ISG [a] expression.

| Characteristics | ISG-Low (n=30) | ISG-High (n=30) | *p* |
|---|---|---|---|
| Age (Years) [b] | 54 (48, 71) | 58 (51, 71) | 0.220 |
| Male (%) | 25 (83.3) | 23 (76.7) | 0.519 |
| Survival status: Living (%) | 21 (70) | 20 (66.7) | 0.780 |
| OS [c] (Days) [b] | 825 (596, 967) | 845 (664, 1064) | 0.340 |
| PFS [d] (Days) [b] | 757.5 (372, 967) | 790 (563, 1027) | 0.370 |
| Tumor stage (2 missing) | | | |
|     Stage I (%) | 5 (16.7) | 4 (13.3) | 0.717 |
|     Stage II (%) | 5 (16.7) | 4 (13.3) | |
|     Stage III (%) | 2 (6.7) | 4 (13.3) | |
|     Stage VI (%) | 18 (60.0) | 18 (60.0) | |
| ATM [b] | 7.7 (7.5, 8.0) | 7.5 (7.4, 7.7) | <0.001 |
| OASL [b] | 7.1 (6.8, 7.4) | 8.8 (8.4, 9.2) | 0.008 |
| IFI27 [b] | 10.8 (10.0, 11.3) | 12.5 (12.3, 12.7) | 0.005 |
| ISG15 [b] | 9.0 (8.3, 9.4) | 11.4 (10.8, 11.7) | 0.023 |

[a] ISG15/IFI27/OASL. [b] median (interquartile range). [c] overall survival. [d] progression free survival.

**Table S5.** The significantly downregulated immune pathways in ATM-High subgroup of TCGA cohort.

| TCGA_ATM (High vs. Low) | SIZE | NES | NOM-p | FDR-q |
|---|---|---|---|---|
| GOBP_INTERFERON_GAMMA_PRODUCTION | 116 | -1.468 | 0.001 | 0.098 |
| GOBP_INTERFERON_BETA_PRODUCTION | 56 | -1.413 | 0.021 | 0.126 |
| GOBP_POSITIVE_REGULATION_OF_CELL_KILLING | 65 | -1.637 | <0.001 | 0.039 |
| GOBP_REGULATION_OF_CELL_KILLING | 104 | -1.592 | <0.001 | 0.049 |
| GOBP_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 26 | -1.555 | 0.012 | 0.061 |
| GOBP_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY | 50 | -1.436 | 0.019 | 0.113 |
| GOBP_ALPHA_BETA_T_CELL_ACTIVATION | 169 | -1.585 | <0.001 | 0.051 |
| GOBP_ALPHA_BETA_T_CELL_DIFFERENTIATION | 116 | -1.597 | <0.001 | 0.048 |
| GOBP_DENDRITIC_CELL_CHEMOTAXIS | 27 | -1.773 | <0.001 | 0.013 |
| GOBP_DENDRITIC_CELL_MIGRATION | 34 | -1.871 | 0.001 | 0.004 |
| GOBP_B_CELL_PROLIFERATION | 103 | -1.845 | <0.001 | 0.005 |
| GOBP_B_CELL_ACTIVATION | 275 | -1.620 | <0.001 | 0.042 |

**Table S6.** The significantly downregulated immune pathways in ATM-High subgroup of GSE65858 cohort.

| GSE65858_ATM (High vs. Low) | SIZE | NES | NOM-p | FDR-q |
|---|---|---|---|---|
| GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA | 104 | -1.767 | <0.001 | 0.020 |
| GOBP_INTERFERON_GAMMA_PRODUCTION | 105 | -1.524 | 0.005 | 0.137 |
| GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY | 77 | -1.846 | <0.001 | 0.008 |
| GOBP_REGULATION_OF_CELL_KILLING | 91 | -1.826 | <0.001 | 0.010 |
| GOBP_NATURAL_KILLER_CELL_ACTIVATION | 77 | -1.777 | <0.001 | 0.018 |
| GOBP_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY | 68 | -1.578 | 0.005 | 0.102 |
| GOBP_ALPHA_BETA_T_CELL_ACTIVATION | 157 | -2.192 | <0.001 | <0.001 |
| GOBP_ALPHA_BETA_T_CELL_PROLIFERATION | 43 | -2.133 | <0.001 | <0.001 |
| GOBP_DENDRITIC_CELL_ANTIGEN_PROCESSING_AND_PRESENTATION | 15 | -2.047 | <0.001 | <0.001 |
| GOBP_DENDRITIC_CELL_CHEMOTAXIS | 26 | -1.860 | 0.002 | 0.006 |
| GOBP_B_CELL_ACTIVATION | 82 | -2.422 | <0.001 | <0.001 |
| GOBP_B_CELL_PROLIFERATION | 19 | -2.420 | <0.001 | <0.001 |

**Table S7.** Expression of interferon-stimulated genes in cervical cancer patients with or without cisplatin therapy.

| | | PD/SD [a] [mean (S.D.)] [b] | CR [c] [mean (S.D.)] | p [d] |
|---|---|---|---|---|
| ISG15 | w CDDP [e] | 10.744 (1.447) | 12.560 (1.354) | 0.002 |
| | wo CDDP [f] | 11.086 (2.001) | 11.296 (1.568) | 0.522 |
| IFI27 | w CDDP | 12.875 (0.944) | 13.720 (0.876) | 0.010 |
| | wo CDDP | 12.588 (2.088) | 12.916 (1.394) | 0.944 |
| OASL | w CDDP | 8.274 (1.261) | 10.022 (1.271) | 0.001 |
| | wo CDDP | 8.726 (2.324) | 8.703 (1.617) | 0.912 |

[a] progression disease/stable disease. [b] Gene expression (RSEM) shown as mean and standard deviation (S.D.). [c] complete remission. [d] Mann-Whitney U test. [e] with cisplatin therapy (11 PD, 42 CR). [f] without cisplatin therapy (11 PD/SD, 96 CR).

**Table S8.** The patient demographics of TCGA CESC [a] cohort.

| | With Cisplatin Therapy | | Without Cisplatin Therapy | |
|---|---|---|---|---|
| | PD [b] (n=11) | CR [c] (n=42) | PD/SD [d] (n=11) | CR (n=96) |
| Age (Years) [e] | 46 (37, 51) | 43 (37, 54) | 45 (32, 56) | 45 (37, 53) |
| Survival status: Living (%) | 2 (18.2) | 39 (92.9) | 3 (27.3) | 91 (94.8) |
| Overall survival (Days) [e] | 370 (292, 581) | 949 (601, 1669) | 634 (359, 1048) | 799 (491, 1376) |
| Clinical stage | | | | |
|   Stage I (%) | 1 (9.1) | 15 (36.6) | 5 (45.5) | 66 (68.8) |
|   Stage II (%) | 4 (36.4) | 17 (41.5) | 3 (27.3) | 17 (17.7) |
|   Stage III (%) | 2 (18.2) | 7 (17.1) | 2 (18.2) | 12 (12.5) |
|   Stage VI (%) | 4 (36.4) | 2 (4.9) | 1 (9.1) | 1 (1.0) |

[a] cervical squamous cell carcinoma and endocervical adenocarcinoma. [b] progression disease. [c] complete remission. [d] progression disease/stable disease. [e] median (interquartile range).