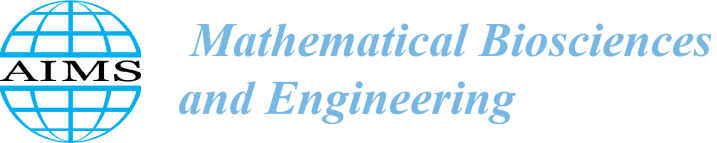
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***Research article***

**A novel defined risk signature of interferon response genes predicts the prognosis and correlates with immune infiltration in glioblastoma**

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**Supplementary**

**Table S1.** 10 interferon response gene sets.

|  |  |
| --- | --- |
| GOBP\_CELLULAR\_RESPONSE\_TO\_INTERFERON\_ALPHA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CELLULAR_RESPONSE_TO_INTERFERON_ALPHA.html> |
| GOBP\_CELLULAR\_RESPONSE\_TO\_INTERFERON\_BETA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CELLULAR_RESPONSE_TO_INTERFERON_BETA.html> |
| GOBP\_REGULATION\_OF\_RESPONSE\_TO\_INTERFERON\_GAMMA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA.html> |
| GOBP\_RESPONSE\_TO\_INTERFERON\_ALPHA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPONSE_TO_INTERFERON_ALPHA.html> |
|  | *Continued on next page* |
| GOBP\_RESPONSE\_TO\_INTERFERON\_BETA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPONSE_TO_INTERFERON_BETA.html> |
| GOBP\_RESPONSE\_TO\_INTERFERON\_GAMMA | <http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPONSE_TO_INTERFERON_GAMMA.html> |
| HALLMARK\_INTERFERON\_ALPHA\_RESPONSE | <http://www.gsea-msigdb.org/gsea/msigdb/cards/HALLMARK_INTERFERON_ALPHA_RESPONSE.html> |
| HALLMARK\_INTERFERON\_GAMMA\_RESPONSE | <http://www.gsea-msigdb.org/gsea/msigdb/cards/HALLMARK_INTERFERON_GAMMA_RESPONSE.html> |
| NATSUME\_RESPONSE\_TO\_INTERFERON\_BETA\_DN | <http://www.gsea-msigdb.org/gsea/msigdb/cards/NATSUME_RESPONSE_TO_INTERFERON_BETA_DN.html> |
| NATSUME\_RESPONSE\_TO\_INTERFERON\_BETA\_UP | <http://www.gsea-msigdb.org/gsea/msigdb/cards/NATSUME_RESPONSE_TO_INTERFERON_BETA_UP.html> |

**Table S2.** 54 interferons with uni-cox survival value.

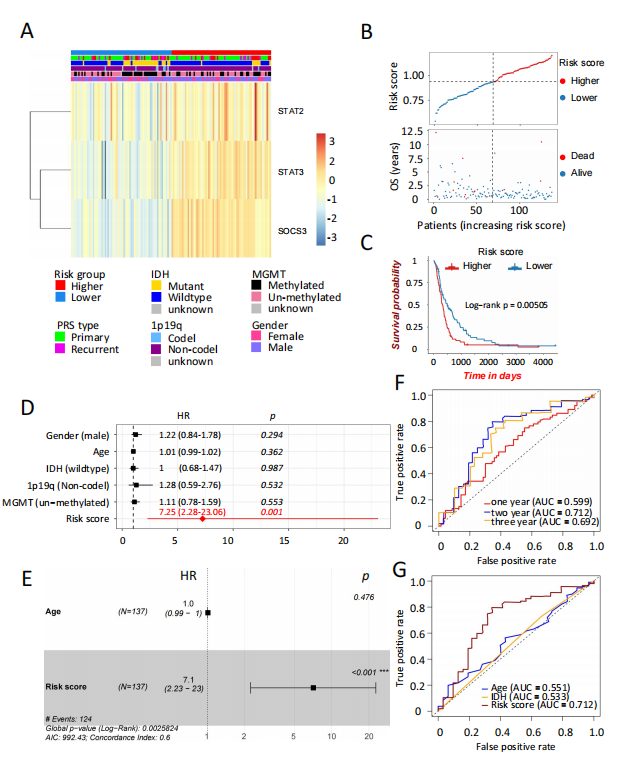
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| gene | HR | HR.95L | HR.95H | *p*-value |
| ACTR3 | 1.13461 | 1.00553 | 1.28025 | 0.04041 |
| ANXA2 | 1.1065 | 1.0309 | 1.18763 | 0.00506 |
| APOL6 | 1.21416 | 1.02795 | 1.43409 | 0.02234 |
| BANK1 | 1.40799 | 1.01334 | 1.95634 | 0.04145 |
| BCL3 | 1.12197 | 1.01465 | 1.24065 | 0.02487 |
| C1R | 1.10001 | 1.02041 | 1.18582 | 0.01287 |
| C1S | 1.10646 | 1.01575 | 1.20528 | 0.02045 |
| CCL19 | 0.85667 | 0.74548 | 0.98445 | 0.02919 |
| CCL2 | 1.0797 | 1.01292 | 1.15088 | 0.01858 |
| CD44 | 1.12817 | 1.04214 | 1.22129 | 0.00288 |
| CDK13 | 1.23636 | 1.01236 | 1.50992 | 0.03748 |
| CIITA | 1.15601 | 1.0069 | 1.3272 | 0.03963 |
| EPHB3 | 1.13317 | 1.01455 | 1.26566 | 0.02669 |
| TENT5A | 1.1665 | 1.0259 | 1.32636 | 0.01876 |
| FAS | 1.16517 | 1.02573 | 1.32355 | 0.01874 |
| GBP1 | 1.12815 | 1.03452 | 1.23026 | 0.00638 |
| GRB14 | 1.16258 | 1.04392 | 1.29474 | 0.0061 |
| HELZ2 | 1.16132 | 1.01863 | 1.32401 | 0.02535 |
| HPX | 1.18004 | 1.00063 | 1.39163 | 0.04914 |
| ICAM1 | 1.13991 | 1.03684 | 1.25323 | 0.00677 |
| IFNGR2 | 1.16758 | 1.00315 | 1.35897 | 0.04544 |
| IGFBP3 | 1.07542 | 1.00991 | 1.14518 | 0.02336 |
| IGFBP5 | 1.17496 | 1.07657 | 1.28233 | 0.0003 |
| IRF1 | 1.12727 | 1.00188 | 1.26835 | 0.04646 |
| IRF2 | 1.17427 | 1.01123 | 1.36359 | 0.03517 |
| KDM5A | 1.17292 | 1.00253 | 1.37227 | 0.04643 |
| LATS2 | 1.40644 | 1.15388 | 1.71427 | 0.00073 |
|  |  |  |  | *Continued on next page* |
| gene | HR | HR.95L | HR.95H | *p*-value |
| MAP3K14 | 1.21322 | 1.04603 | 1.40714 | 0.01063 |
| METTL7B | 1.09782 | 1.01987 | 1.18173 | 0.013 |
| MMP2 | 1.12567 | 1.02111 | 1.24095 | 0.01732 |
| MYD88 | 1.17688 | 1.03075 | 1.34373 | 0.01605 |
| NAMPT | 1.09404 | 1.01254 | 1.1821 | 0.02288 |
| NFKB1 | 1.21307 | 1.01585 | 1.44858 | 0.03287 |
| NLRC5 | 1.12868 | 1.0075 | 1.26444 | 0.03672 |
| NR1H4 | 0.39009 | 0.19755 | 0.77027 | 0.00669 |
| PARP14 | 1.1575 | 1.00178 | 1.33743 | 0.04725 |
| PARP9 | 1.15368 | 1.02454 | 1.2991 | 0.01826 |
| PDGFA | 1.15105 | 1.02447 | 1.29328 | 0.01795 |
| PTPRZ1 | 1.09817 | 1.01079 | 1.1931 | 0.02684 |
| SAMD9L | 1.16668 | 1.03761 | 1.31182 | 0.00997 |
| SELL | 0.84209 | 0.74728 | 0.94891 | 0.0048 |
| SLC11A1 | 1.13712 | 1.04531 | 1.237 | 0.00278 |
| SOCS3 | 1.12503 | 1.04765 | 1.20813 | 0.00119 |
| SOD2 | 1.11762 | 1.03075 | 1.21181 | 0.00707 |
| STAR | 0.72737 | 0.57563 | 0.91912 | 0.00767 |
| STAT2 | 1.18473 | 1.02929 | 1.36364 | 0.01816 |
| STAT3 | 1.2824 | 1.10195 | 1.49241 | 0.00131 |
| TNFAIP3 | 1.15164 | 1.02461 | 1.29441 | 0.0179 |
| TNFAIP6 | 1.1049 | 1.00411 | 1.21582 | 0.04095 |
| TNFSF14 | 1.28738 | 1.10872 | 1.49483 | 0.00092 |
| TOR1B | 1.18826 | 1.00253 | 1.40841 | 0.04669 |
| TRIM14 | 1.26632 | 1.06828 | 1.50106 | 0.0065 |
| VIM | 1.16502 | 1.0639 | 1.27574 | 0.00098 |
| XCL1 | 1.7696 | 1.00369 | 3.11998 | 0.04853 |

**Table S3.** Top 30 nodes in protein-protein interaction network based on 54 genes.

|  |  |  |
| --- | --- | --- |
| Rank | Name | Score |
| 1 | STAT3 | 20 |
| 2 | CD44 | 17 |
| 2 | CCL2 | 17 |
| 2 | ICAM1 | 17 |
| 2 | IRF1 | 17 |
| 6 | NFKB1 | 12 |
| 6 | MYD88 | 12 |
| 8 | TNFAIP3 | 11 |
| 8 | SOCS3 | 11 |
| 8 | STAT2 | 11 |
| 11 | MMP2 | 10 |
|  |  | *Continued on next page* |
| Rank | Name | Score |
| 11 | GBP1 | 10 |
| 13 | IRF2 | 9 |
| 13 | CIITA | 9 |
| 15 | SELL | 7 |
| 15 | SOD2 | 7 |
| 17 | TRIM14 | 6 |
| 17 | CCL19 | 6 |
| 17 | PARP9 | 6 |
| 20 | IFNGR2 | 5 |
| 20 | BCL3 | 5 |
| 20 | PARP14 | 5 |
| 20 | FAS | 5 |
| 24 | ANXA2 | 4 |
| 24 | VIM | 4 |
| 24 | SAMD9L | 4 |
| 24 | HELZ2 | 4 |
| 24 | MAP3K14 | 4 |
| 29 | IGFBP3 | 3 |
| 29 | XCL1 | 3 |

**Table S4.** Meta-analysis of 10 core interferon response genes prognostic value.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GENE | DATASET | CANCER TYPE | ENDPOINT | N | CUTPOINT | COX P-VALUE | HR [95% CI-low CI-upp] |
| CD44 | GSE4412-GPL97 | Glioma | Overall Survival | 74 | 0.824324 | 0.000315634 | 2.14 [1.41–3.23] |
| MYD88 | MGH-glioma | Glioma | Overall Survival | 50 | 0.72 | 0.0123751 | 1.74 [1.13–2.68] |
| STAT2 | MGH-glioma | Glioma | Overall Survival | 50 | 0.88 | 0.0178092 | 7.49 [1.42–39.59] |
| TNFAIP3 | MGH-glioma | Glioma | Overall Survival | 50 | 0.7 | 0.0183943 | 1.52 [1.07–2.16] |
| SOCS3 | GSE4412-GPL97 | Glioma | Overall Survival | 74 | 0.189189 | 0.0228091 | 1.26 [1.03–1.54] |
| NFKB1 | MGH-glioma | Glioma | Overall Survival | 50 | 0.84 | 0.0334134 | 3.54 [1.10–11.32] |
| STAT3 | GSE4412-GPL97 | Glioma | Overall Survival | 74 | 0.418919 | 0.0668225 | 2.37 [0.94–5.97] |
| ICAM1 | GSE4412-GPL96 | Glioma | Overall Survival | 74 | 0.391892 | 0.0699967 | 1.66 [0.96–2.88] |
| CCL2 | MGH-glioma | Glioma | Overall Survival | 50 | 0.22 | 0.176027 | 1.12 [0.95–1.31] |
| IRF1 | GSE4412-GPL96 | Glioma | Overall Survival | 74 | 0.459459 | 0.302895 | 1.42 [0.73–2.79] |



**Figure S1.** Validation of risk model for GBM patients in CGGA cohort 2. (A) Heatmap of 3 risk signatures expression among the higher and lower risk GBM subgroups together with clinicopathological features. Higher risk group had relative higher expression of *STAT2*, *STAT3* and *SOCS3*. (B) Risk score distribution together with survival status for GBM patients. (C) Survival analysis for the OS of GBM patients in the higher and lower risk subgroups based on risk score. Higher group confronted poor prognosis than the lower one. Uni-variate (D) and multi-variate (E) Cox regression analysis of the association between risk score, clinicopathological features and patient OS revealed the risk score was an independent factor for GBM patient survival. (F) ROC curves presented the predictive efficiency. (G) Multi-indicator ROC curves for risk score, age and IDH state. Risk score was a better predictor than others for GBM survival.

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