

Supplementary Files

# Identification of GSN and LAMC2 as Key Prognostic Genes of Bladder Cancer by Integrated Bioinformatics Analysis

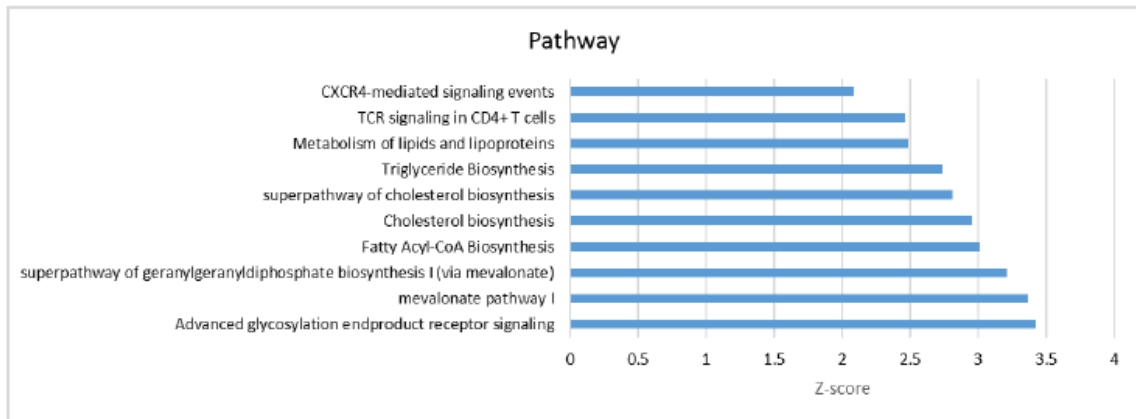
Jia-Lian Yang, Charles C.N. Wang, Jia-Hua Cai, Che-Yi Chou, Yu-Chao Lin and Chin-Chuan Hung

**Table S1.** Number of genes in each module.

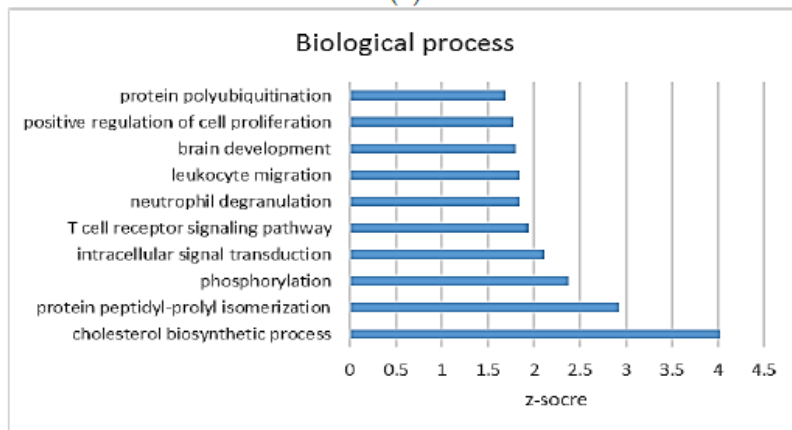
| Module         | The Number of Genes |
|----------------|---------------------|
| black          | 209                 |
| blue           | 330                 |
| brown          | 305                 |
| cyan           | 136                 |
| darkgreen      | 88                  |
| darkgrey       | 83                  |
| darkmagenta    | 46                  |
| darkolivegreen | 49                  |
| darkorange     | 78                  |
| darkred        | 90                  |
| darkturquoise  | 87                  |
| green          | 215                 |
| greenyellow    | 178                 |
| grey           | 201                 |
| grey60         | 130                 |
| lightcyan      | 134                 |
| lightgreen     | 129                 |
| lightyellow    | 105                 |
| magenta        | 207                 |
| midnightblue   | 136                 |
| orange         | 81                  |
| paleturquoise  | 61                  |
| pink           | 208                 |
| purple         | 182                 |
| red            | 209                 |
| royalblue      | 104                 |
| saddlebrown    | 65                  |
| salmon         | 141                 |
| skyblue        | 67                  |
| steelblue      | 63                  |
| tan            | 152                 |
| turquoise      | 340                 |
| violet         | 59                  |
| white          | 77                  |
| yellow         | 255                 |

**Table S2.** Hub gene list of modules with highly disease-correlated.

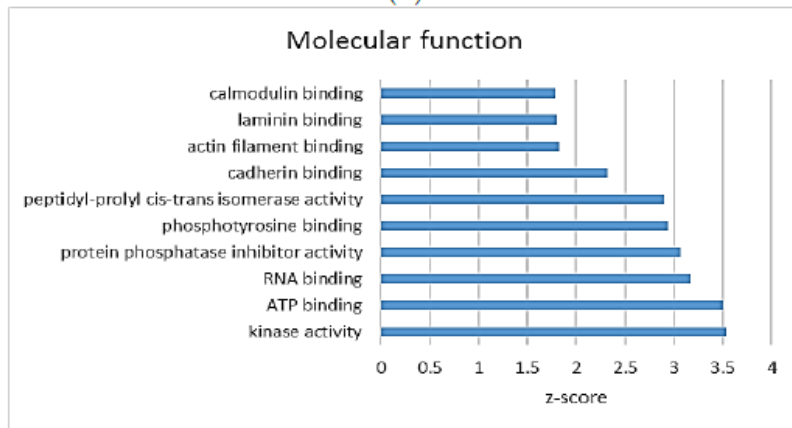
| <b>Disease type</b>                              | <b>Module</b> | <b>Gene</b>   |
|--|---------------|---|
| human adenocarcinoma lymph node metastasis       | Red           | <i>EPCAM, ACLY, ERO1L, LGALS3, MYO1D, SLC25A1, HMGCS1, CHCHD10, CRKL, EIF5B, MAPK1, GUCD1, KIAA1671, BCR, FKBP4, MVD, PPM1F, ADD3, SMARCB1, SNRPD3, SERBP1, CKB, PI4KA, LZTR1, YDJC, PPIL2, TRMT2A, UBE2L3, CABIN1, S100A6, AKR1C3, GPX4, DKK1, CD63, TRAM1, SLC12A7, FPGS, SLC35B2, CDK4, SSR4, UGDH, RAB32, JTB, UBL4A, APOA1BP, ATP6V0B, PGAM5, LAMTOR1, GPRC5B, SYNGR2, SCAMP3, NDUFB11, DCTPP1, AGPAT6, ECI1, CSF1, WDR81, SIVA1, IFRD2, RPS19BP1, STRA13, LRRC61, TMEM141, CHMP2B</i> |
| Bladder carcinoma                                | turquoise     | <i>LAMC2, PTTG1IP, LAMA3, TNIP1, TMEM132A, TNC, SETD5, CSNK1E, THBD, SEC13, TADA3, BRK1, IRAK2, VHL, TATDN2</i>   |
| Grade 2 Carcinoma                                | darkturquoise | <i>PERP, PCDH1, BCL9L, PDLIM5, PHLDB2, GSN, NDFIP2, BZW2, PSD4, ABCG2, KCTD12, RNF217, USP53, HTRA1, GNAQ, ZNF362</i>   |
| Grade 3 Carcinoma                                | lightgreen    | <i>FLNA, MYH9, ACTB, PTRF, TLN1, TIMP2, ZYX, CALD1, TRAM2, SH3BGRL3, ITGA5, PDLIM7, MAP1B, GDI1, HPCAL1, CUL4B, ACTR1A, TGFB1I1, COL5A2, CPA4, DAPK3, DAB2, SHCBBP1, STXBP1, KATNAL1</i>  |
| Grade 4 Carcinoma                                | magenta       | <i>CAV1, HIPK2, VGLL3, HSP90AA1, TRRAP, MIB1, TMEM248, SMCHD1, VKORC1L1, RBBP8, SEH1L, SS18, SSBP1, PMPCB, CAPZA2, GUSB</i>   |
| transitional cell carcinoma lymphatic metastasis | Royalblue     | <i>DTX4, ERBB3, ATP8B1, LLGL2, FOXA1, ARHGAP27, TC2N, PIK3C2B, RAB15, BCAT2, RALGAPA2, C2CD2, TBC1D8, ACSF2, ZNF320, AP1G2, AGR2, FAM59A</i>  |
| Transitional Cell papilloma                      | Salmon        | <i>AGPS</i>   |
| transitional cell carcinoma of the renal pelvis  | Grey          | <i>AGPS</i>   |
| Squamous Cell Carcinoma                          | Darlorange    | <i>EGFR, GLUL, GCLC, CAT, SLC1A3, SPG11, UFL1, KRT15</i>  |
| Transitional Cell Carcinoma                      | Greenyellow   | <i>HNRNPL</i>   |



(a)

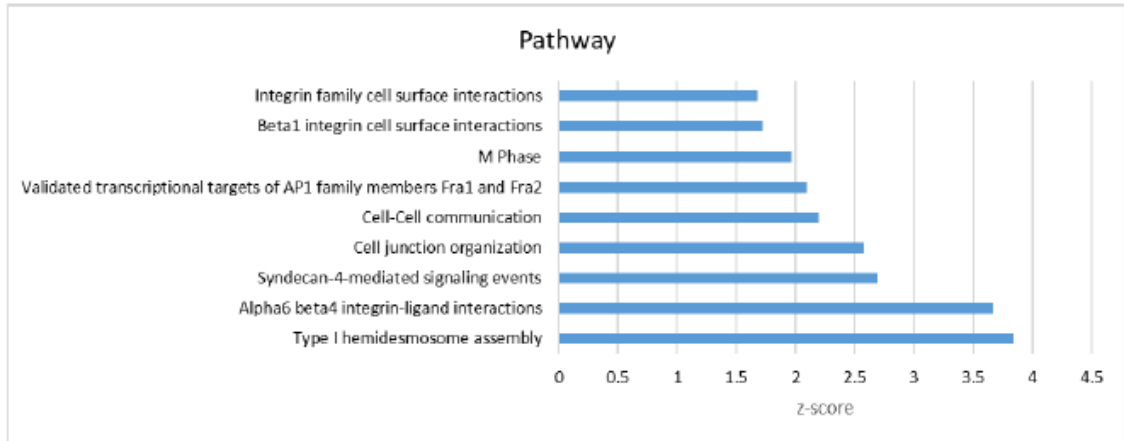


(b)

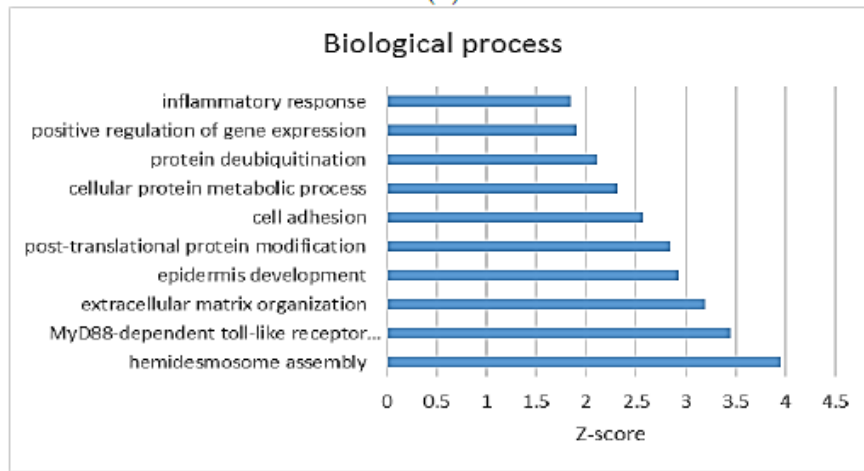


(c)

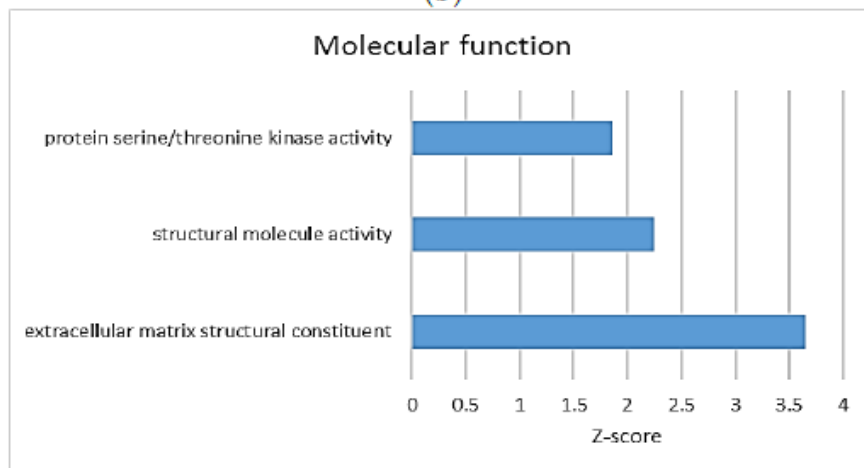
**Figure S1.** The top 10 enrichment of gene ontology and pathway for hub genes of cell lines with human adenocarcinoma lymph node metastasis. Gene ontology and pathways with z-scores greater than 1.65, which corresponds to a  $p$ -value 0.1 as statistically significant pathways. Only significant hits with overlap size  $\geq 2$  (genes that are overlapping in the same pathway) were selected. (a) Pathways (b) Biological process (c) Molecular function.



(a)

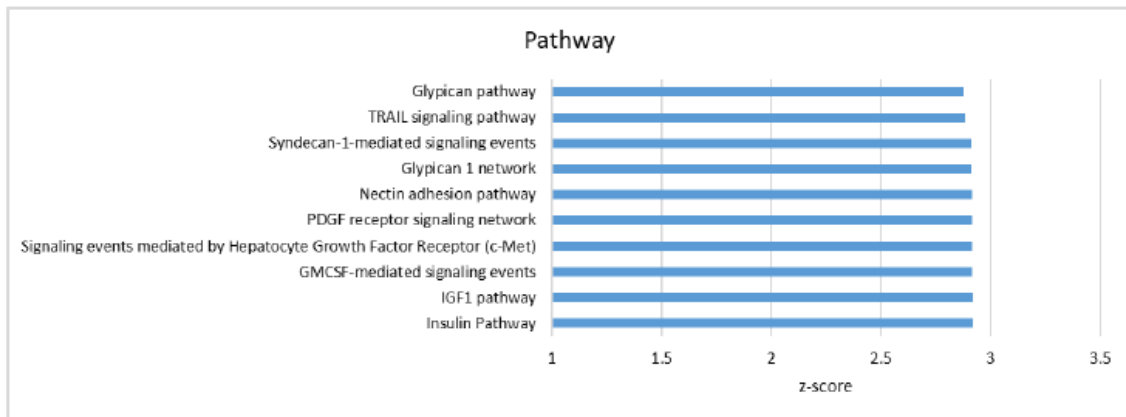


(b)

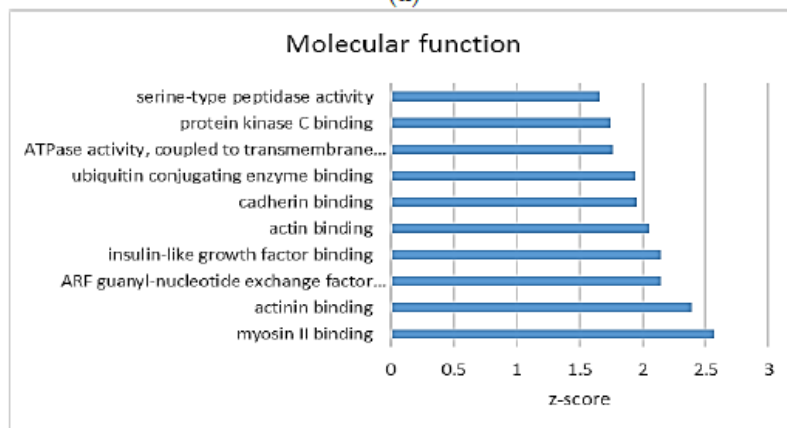


(c)

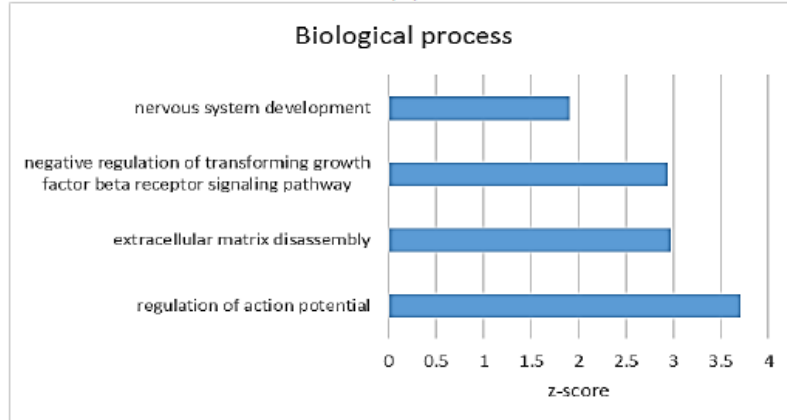
**Figure S2.** The top 10 enrichment of gene ontology and pathway for hub genes of cell lines with grade 2 carcinoma. Gene ontology and pathways with z-scores greater than 1.65, which corresponds to a *p*-value 0.1 as statistically significant pathways. Only significant hits with overlap size  $\geq 2$  (genes that are overlapping in the same pathway) were selected. (a) Pathways (b) Biological process (c) Molecular function.



(a)

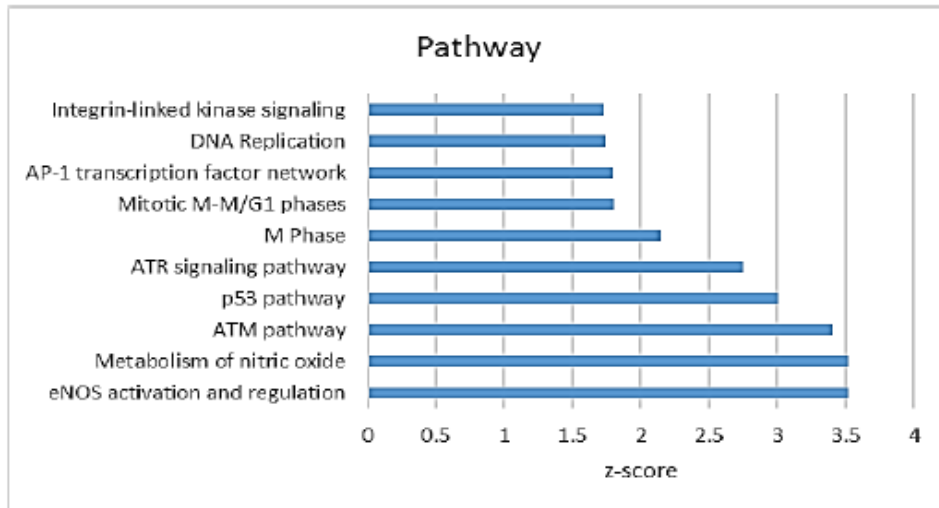


(b)

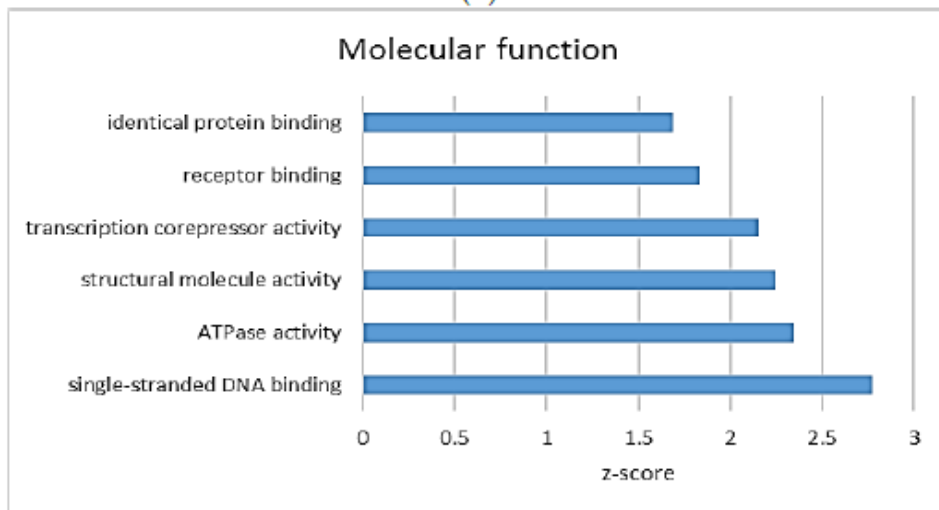


(c)

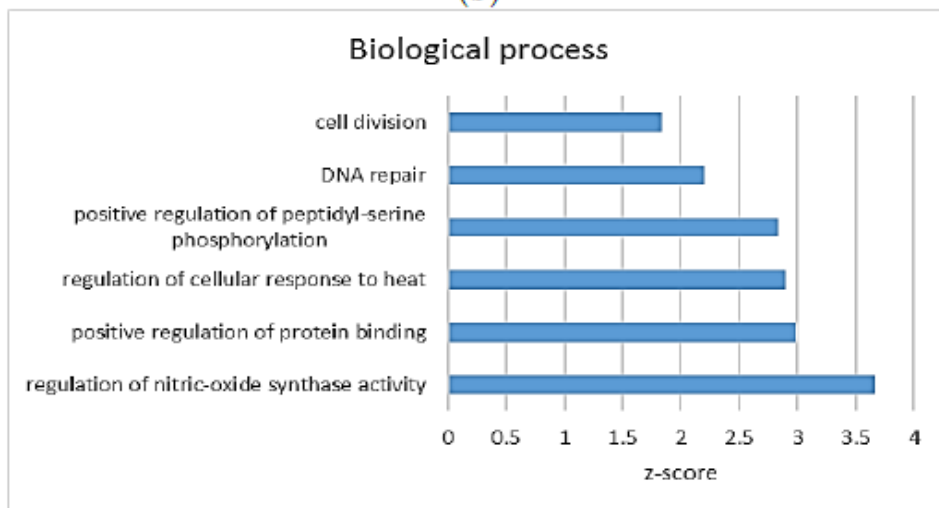
**Figure S3.** The top 10 enrichment of gene ontology and pathway for hub genes of cell lines with grade 3 carcinoma. Gene ontology and pathways with z-scores greater Table 1. 65, which corresponds to a *p*-value 0.1 as statistically significant pathways. Only significant hits with overlap size  $\geq 2$  (genes that are overlapping in the same pathway) were selected. (a) Pathways (b) Biological process (c) Molecular function.



(a)



(b)



(c)

**Figure S4.** The top 10 enrichment of gene ontology and pathway for hub genes of cell lines with transitional cell carcinoma lymphatic metastasis. Gene ontology and pathways with z-scores greater than 1.65, which corresponds to a p-value 0.1 as statistically significant pathways. Only significant hits with overlap size  $\geq 2$  (genes that are overlapping in the same pathway) was selected. (a) Pathways (b) Biological process (c) Molecular function.



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