

Supplementary data

Table S1. Unique significant differential expression.

| Cluster | Genes |
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| A | CPSF7,ALYREF,PABPC1L,ITGA2,EFNA1,KRT23,KRT16,F3,CCL5,SIK1B,G6PD,IRF1,S100A8,CD36,ACSL1 |
| B | PPP2R2A,HK2,IGF1R,EP300,VHL,CAMK2G,EGLN3,SLC9A1,TSC2,NCOR1,TP53,ATF6B,KRT20,CREB3L2,PRKCD,HSPA1A,IRS1,CRKL,MAP3K5,RBL2,COL4A6,COL4A5,MET,IFNAR1,PRKAA1,GNG5,COL9A2,GNA15,MMP1,CAB39L,ADIPOR1,ELAVL1,ULK1,PATJ,TEAD3,FZD6,FRMD6,CAT,PGM2,PGLS,XIAP,NLRP1,ERBIN,EHMT2,SOD1,EIF4EBP2,TELO2,GNA11,GTF2I,EML4,VAV2,ELK4,MECOM,DUSP4,DUSP2,TAOK2,NF1,SGPL1,SPTLC2,ACER2,CCNG1,DBI,ACSL3,FABP4,SCP2,FABP5,ACOX1,UBC,PLIN2,HMGCS2,ACAA1,PLTP,SKIL,ZFH3,PCGF3,TBX3,ID3,TCF3 |
| C | ITGB5,TNC,FGF7,MYC,PDGFRB,VWF,ITGA1,COL6A3,ITGA7,ITGA5,CSF1R,LAMA4,THBS2,PPP2CB,FGFR1,CASC3,ICAM1,CCL2,STAT5B,CYBB,SELE,IL1B,BAX,PFKFB3,HMOX1,NOTCH2,PLN,PRKACA,RCAN1,ROCK1,ROCK2,SRF,MYLK,RGS2,MEF2D,PPP1R12A,IRAG1,GNAQ,MYL9,MMP9,HBEGF,STMN1,MAP2K3,DUSP5,DUSP3,IL1R1,CACNA1H,RAP1A,MAP3K20,CD14,FLNC,MAP4K4,GADD45B,GADD45A,NFKB2,ABL1,RAPGEF1,ITGB2,ENAH,PPP1R12B,ACTA2,SORBS1,RHOQ,CCN2,WWTR1,KLF2,APLNR,TNFAIP3,CXCL2,JUNB,DAB2IP,CFLAR,TNFRSF1B,BCL3,ANTXR2,ANTXR1,FOSL1,EGR3,LSP1,CXCL14,GRK2,CXCL12,UBE2I,PARP1,PLAU,RAB5B,RAB5C,ETS1,ETS2,RALBP1,PLA2G2A,RGL2,ARF6,DEGS1,LTBP1,DCN,GREM1,NBL1,SKP1,FBN1,CAB39,RBPJ,FHL1,STAT6,IL13RA1,IL6ST |

Table S2. Clinical characteristics of MIBC from TCGA in each cluster.

| | Cluster A | Cluster B | Cluster C | Total | p-value |
|-------------------------|---------------|---------------|---------------|-------|---------|
| | 113 | 74 | 44 | 231 | |
| Gender | | | | | |
| Male | 83 (49.1) | 57 (33.7) | 29 (17.2) | 169 | |
| Female | 30 (48.4) | 17 (27.4) | 15 (24.2) | 62 | 0.4176 |
| Age | 69.57 ± 10.52 | 68.14 ± 10.25 | 69.53 ± 11.08 | | 0.6536 |
| Follow up time | 2.40 ± 1.44 | 2.17 ± 2.07 | 2.24 ± 2.75 | | 0.8528 |
| Status | | | | | |
| Alive | 83 (49.1) | 57 (33.7) | 29 (17.2) | 169 | |
| Dead | 30 (49.2) | 17 (27.9) | 14 (23.0) | 61 | 0.4176 |
| AJCC pathological stage | | | | | |
| Stage II | 35 (53.0) | 21 (31.8) | 10 (15.2) | 66 | |

| | | | | | |
|-------------------------------|------------|-----------|-----------|-----|---------|
| Stage III | 46 (50.5) | 31 (34.1) | 14 (15.4) | 91 | 0.3255 |
| Stage IV | 32 (43.2) | 22 (29.7) | 20 (27) | 74 | |
| Pathological tumor stage | | | | | |
| T2 | 38 (50.7) | 22 (29.3) | 15 (20.0) | 75 | 0.8753 |
| T3 | 57 (46.3) | 43 (35.0) | 23 (18.7) | 123 | |
| T4 | 15 (54.5) | 9 (27.3) | 6 (18.2) | 33 | |
| Pathological lymph node stage | | | | | |
| N0 | 75 (52.4) | 46 (32.2) | 22 (15.4) | 143 | 0.4392 |
| N1 | 12 (42.9) | 9 (32.1) | 7 (25.0) | 28 | |
| N2 | 18 (42.9) | 11 (26.2) | 13 (31.0) | 42 | |
| N3 | 2 (50.0) | 2 (50.0) | 0 (0.0) | 4 | |
| Nx | 6 (42.9) | 6 (42.9) | 2 (14.3) | 14 | |
| Pathological metastasis stage | | | | | |
| M0 | 54 (46.6) | 36 (31.0) | 26 (22.4) | 116 | 0.3451 |
| M1 | 1 (20.0) | 2 (40.0) | 2 (40.0) | 5 | |
| Mx | 58 (52.7) | 36 (32.7) | 16 (14.5) | 110 | |
| mRNA clustering | | | | | |
| Basal | 49 (44.5) | 26 (37.7) | 11 (27.5) | 86 | 0.05412 |
| Luminal | 56 (50.9) | 42 (60.9) | 29 (72.5) | 127 | |
| Neuronal | 5 (4.5) | 1 (1.4) | 0 (0.0) | 6 | |
| Histological subtype | | | | | |
| Papillary | 28 (56.0) | 15 (30.0) | 7 (14.0) | 50 | 0.2016 |
| Non-papillary | 81 (48.8) | 54 (32.5) | 31 (18.7) | 166 | |
| Not determine | 1 (33.3) | 0 (0.0) | 2 (66.7) | 3 | |
| Histological grade | | | | | |
| High grade | 104 (49.5) | 67 (31.9) | 39 (18.6) | 210 | 0.822 |
| Low grade | 5 (62.5) | 2 (25.0) | 1 (12.5) | 8 | |
| Not determine | 1 (100.0) | 0 (0.0) | 0 (0.0) | 1 | |
| Lymphovascular invasion | | | | | |
| Yes | 35 (43.2) | 23 (28.4) | 23 (28.4) | 81 | 0.03155 |
| No | 46 (57.5) | 27 (33.8) | 7 (8.8) | 80 | |
| Not determine | 29 (50.0) | 19 (32.8) | 10 (17.2) | 58 | |

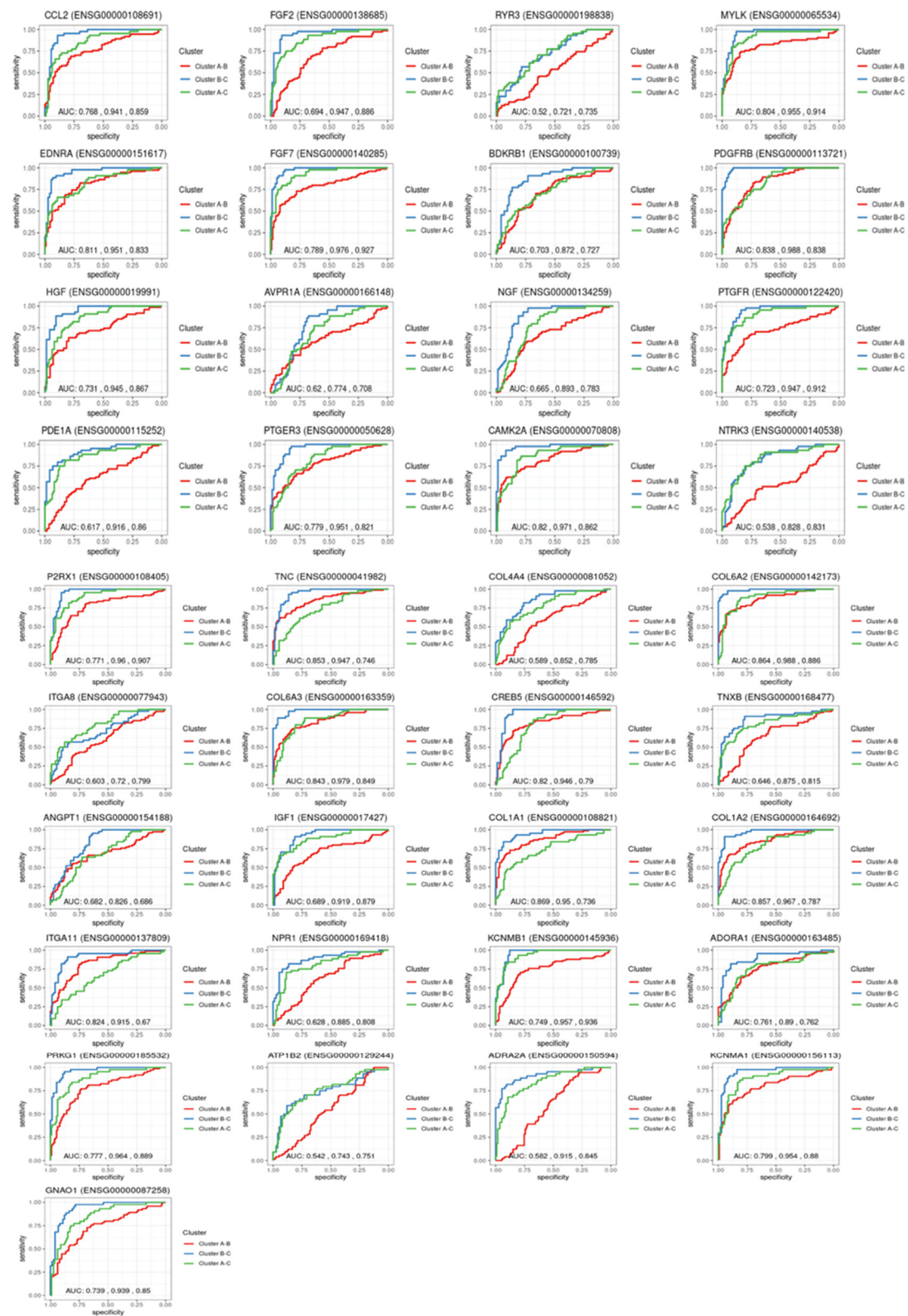


Figure S1 ROC curve analysis was performed for all 37 genes and all cluster. Interestingly, the corresponding areas under the ROC curve (AUCs) with the value more than 0.8, 0.9, and 0.95 were found in 33, 25, and 14 genes from 37 genes for cluster B.