**Additional file 5: Table. S1** Univariate Cox regression analysis for 48 mRNAs

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| Gene symbol | HR (95%CI) | *P* value |
| PIP4K2A | 1.23 (0.96-1.58) | 0.107 |
| ANKRD29 | 1.09 (0.79-1.51) | 0.596 |
| GPD1L | 0.87 (0.75-1.01) | 0.073 |
| PCGF3 | 0.6 (0.43-0.83) | 0.002 |
| FGF2 | 0.98 (0.74-1.28) | 0.867 |
| HOXB5 | 0.76 (0.64-0.9) | 0.002 |
| FASN | 1.22 (1.01-1.49) | 0.044 |
| PPP1R37 | 0.68 (0.53-0.87) | 0.002 |
| ORMDL3 | 0.69 (0.54-0.89) | 0.004 |
| EGR2 | 1.2 (0.99-1.45) | 0.065 |
| HEG1 | 1.3 (1.07-1.59) | 0.009 |
| MSANTD2 | 0.76 (0.52-1.1) | 0.151 |
| THBS1 | 1.17 (1.02-1.34) | 0.029 |
| AIFM3 | 0.74 (0.58-0.96) | 0.022 |
| RGS2 | 1.14 (0.99-1.3) | 0.063 |
| BCAT2 | 0.85 (0.72-0.99) | 0.038 |
| BLCAP | 0.85 (0.68-1.06) | 0.151 |
| ZNF606 | 0.69 (0.46-1.02) | 0.062 |
| ACOX1 | 0.86 (0.72-1.03) | 0.101 |
| OGT | 0.73 (0.55-0.95) | 0.021 |
| VIM | 1.16 (1.01-1.32) | 0.031 |
| GOLGA8A | 0.82 (0.69-0.99) | 0.035 |
| BTG2 | 0.92 (0.8-1.05) | 0.196 |
| ITGB3 | 1.21 (0.88-1.66) | 0.243 |
| CFL2 | 1.22 (0.98-1.5) | 0.071 |
| SGTB | 1.88 (1.26-2.79) | 0.002 |
| NR3C1 | 1.1 (0.88-1.37) | 0.411 |
| RS1 | 0.36 (0.08-1.68) | 0.192 |
| S1PR1 | 1.09 (0.9-1.33) | 0.375 |
| IGF2BP2 | 1.18 (1.05-1.33) | 0.005 |
| SATB1 | 0.79 (0.63-0.99) | 0.04 |
| KATNAL1 | 1.5 (1.14-1.98) | 0.004 |
| ITGA5 | 1.2 (1.04-1.38) | 0.011 |
| KLHL23 | 0.78 (0.59-1.02) | 0.067 |
| DPYSL2 | 1.33 (1.11-1.6) | 0.002 |
| SFRP1 | 1.08 (0.95-1.22) | 0.261 |
| CYBRD1 | 1.17 (1.01-1.37) | 0.04 |
| LEFTY1 | 1.2 (0.92-1.57) | 0.176 |
| CLIC4 | 1.28 (1.08-1.51) | 0.004 |
| GOLGA8B | 0.84 (0.68-1.06) | 0.138 |
| KLF9 | 1.22 (1.01-1.48) | 0.041 |
| TGFBI | 1.18 (1.06-1.31) | 0.003 |
| CHRDL1 | 1.07 (0.91-1.26) | 0.389 |
| FAM129A | 1.24 (1.07-1.44) | 0.004 |
| SHISA6 | 1.79 (0.75-4.24) | 0.188 |
| PCDH7 | 1.11 (0.94-1.29) | 0.211 |
| NTF3 | 0.55 (0.31-1) | 0.049 |
| PRUNE2 | 1.15 (0.95-1.4) | 0.141 |

HR, hazard ratio; CI, confidence interval;