

| Protein name | Gene symbol | Chr | Start | End | Size | Band | spectral counts | RPKM value of two gastric cancer cell lines | |
|--------------|-------------|-----|----------|----------|----------|----------|-----------------|---|---------|
| | | | | | | | | SNU16 | KATOIII |
| KHDR1 | KHDRBS1 | 1 | 3.20E+07 | 3.30E+07 | 4.70E+04 | 1p35.1 | 9 | 17.3 | 6.2 |
| P3H1 | LEPRE1 | 1 | 4.30E+07 | 4.30E+07 | 2.10E+04 | 1p34.2 | 6 | 1.9 | 1.1 |
| CEBPZ | CEBPZ | 2 | 3.70E+07 | 3.70E+07 | 3.00E+04 | 2p22.2 | 3 | 7.4 | 3.8 |
| MSH2 | MSH2 | 2 | 4.80E+07 | 4.80E+07 | 1.60E+05 | 2p21 | 6 | 7.5 | 4.8 |
| MSH6 | MSH6 | 2 | 4.80E+07 | 4.80E+07 | 2.40E+04 | 2p16.3 | 3 | 6.4 | 4.3 |
| SNUT2 | USP39 | 2 | 8.60E+07 | 8.60E+07 | 4.60E+04 | 2p11.2 | 4 | 9.7 | 3.6 |
| FHL2 | FHL2 | 2 | 1.10E+08 | 1.10E+08 | 8.10E+04 | 2q12.2 | 6 | 20.1 | 5.9 |
| RBP2 | RANBP2 | 2 | 1.10E+08 | 1.10E+08 | 6.60E+04 | 2q12.3 | 4 | 8.1 | 2.0 |
| ITAV | ITGAV | 2 | 1.90E+08 | 1.90E+08 | 9.10E+04 | 2q32.1 | 5 | 2.7 | 1.9 |
| TOP2B | TOP2B | 3 | 2.60E+07 | 2.60E+07 | 6.70E+04 | 3p24.2 | 8 | 7.3 | 2.4 |
| GBB4 | GNB4 | 3 | 1.80E+08 | 1.80E+08 | 5.60E+04 | 3q26.33 | 11 | 0.4 | 0.4 |
| ARSB | ARSB | 5 | 7.80E+07 | 7.80E+07 | 2.10E+05 | 5q14.1 | 6 | 0.5 | 0.3 |
| CSPG2 | VCAN | 5 | 8.30E+07 | 8.30E+07 | 1.10E+05 | 5q14.2 | 26 | ND | ND |
| PDLI7 | PDLIM7 | 5 | 1.80E+08 | 1.80E+08 | 1.40E+04 | 5q35.3 | 10 | 0.8 | 1.6 |
| MCM3 | MCM3 | 6 | 5.20E+07 | 5.20E+07 | 2.10E+04 | 6p12.2 | 6 | 32.6 | 12.0 |
| HDAC2 | HDAC2 | 6 | 1.10E+08 | 1.10E+08 | 7.80E+04 | 6q21 | 9 | 3.5 | 2.0 |
| IF2B3 | IGF2BP3 | 7 | 2.30E+07 | 2.40E+07 | 1.60E+05 | 7p15.3 | 9 | 8.0 | 0.8 |
| EGFR | EGFR | 7 | 5.50E+07 | 5.50E+07 | 2.40E+05 | 7p11.2 | 6 | 11.3 | 4.0 |
| CLD3 | CLDN3 | 7 | 7.30E+07 | 7.30E+07 | 1.30E+03 | 7q11.23 | 6 | 18.7 | 1.7 |
| COPG2 | COPG2 | 7 | 1.30E+08 | 1.30E+08 | 2.10E+05 | 7q32.2 | 10 | 6.5 | 2.1 |
| CD2A1 | CDKN2A | 9 | 2.20E+07 | 2.20E+07 | 2.80E+04 | 9p21.3 | 4 | ND | ND |
| TF3C4 | GTF3C4 | 9 | 1.40E+08 | 1.40E+08 | 2.50E+04 | 9q34.13 | 7 | 4.2 | 3.0 |
| VAV2* | VAV2* | 9 | 1.40E+08 | 1.40E+08 | 2.30E+05 | 9q34.2 | 5 | 1.8 | 3.6 |
| P4HA1 | P4HA1 | 10 | 7.50E+07 | 7.50E+07 | 9.00E+04 | 10q22.1 | 5 | 5.8 | 4.3 |
| BTA1F1 | BTA1F1 | 10 | 9.40E+07 | 9.40E+07 | 1.10E+05 | 10q23.32 | 4 | 4.7 | 2.3 |
| RRP5 | PDCD11 | 10 | 1.10E+08 | 1.10E+08 | 5.00E+04 | 10q24.33 | 3 | 9.0 | 2.4 |
| DDB1 | DDB1 | 11 | 6.10E+07 | 6.10E+07 | 4.30E+04 | 11q12.2 | 6 | 32.6 | 15.0 |
| DDX47 | DDX47 | 12 | 1.30E+07 | 1.30E+07 | 1.70E+04 | 12p13.1 | 7 | 4.5 | 5.4 |
| HS105 | HSPH1 | 13 | 3.20E+07 | 3.20E+07 | 2.60E+04 | 13q12.3 | 17 | 8.1 | 6.5 |
| RRP44 | DIS3 | 13 | 7.30E+07 | 7.30E+07 | 2.70E+04 | 13q22.1 | 3 | 2.8 | 1.7 |
| MP2K1* | MAP2K1* | 15 | 6.70E+07 | 6.70E+07 | 1.00E+05 | 15q22.31 | 3 | 6.0 | 3.8 |
| PML | PML | 15 | 7.40E+07 | 7.40E+07 | 5.30E+04 | 15q24.1 | 4 | 2.4 | 1.0 |
| CSK | CSK | 15 | 7.50E+07 | 7.50E+07 | 2.10E+04 | 15q24.1 | 5 | 14.7 | 4.7 |
| MMP2* | MMP2* | 16 | 5.60E+07 | 5.60E+07 | 2.80E+04 | 16q12.2 | 4 | ND | ND |
| GNAO | GNAO1 | 16 | 5.60E+07 | 5.60E+07 | 1.70E+05 | 16q12.2 | 3 | ND | ND |
| ACACA | ACACA | 17 | 3.50E+07 | 3.60E+07 | 3.20E+05 | 17q12 | 12 | 12.4 | 5.5 |
| PPR1B | PPP1R1B | 17 | 3.80E+07 | 3.80E+07 | 9.70E+03 | 17q12 | 9 | 0.6 | 21.1 |
| ERBB2* | ERBB2* | 17 | 3.80E+07 | 3.80E+07 | 4.10E+04 | 17q12 | 38 | 12.6 | 5.9 |
| GRB7* | GRB7* | 17 | 3.80E+07 | 3.80E+07 | 9.40E+03 | 17q12 | 16 | 3.0 | 1.8 |
| TOP2A | TOP2A | 17 | 3.90E+07 | 3.90E+07 | 3.00E+04 | 17q21.2 | 11 | 17.0 | 16.0 |
| U5S1 | EFTUD2 | 17 | 4.30E+07 | 4.30E+07 | 4.90E+04 | 17q21.31 | 16 | 19.2 | 2.2 |
| NMT1 | NMT1 | 17 | 4.30E+07 | 4.30E+07 | 4.80E+04 | 17q21.31 | 5 | 6.9 | 5.5 |
| IMA2 | KPNA2 | 17 | 6.60E+07 | 6.60E+07 | 1.10E+04 | 17q24.2 | 10 | 22.0 | 17.2 |
| SMCA4 | SMARCA4 | 19 | 1.10E+07 | 1.10E+07 | 1.00E+05 | 19p13.2 | 4 | 21.1 | 3.3 |
| CEAM1 | CEACAM1 | 19 | 4.30E+07 | 4.30E+07 | 2.10E+04 | 19q13.2 | 3 | 1.1 | 2.8 |
| AP2A1 | AP2A1 | 19 | 5.00E+07 | 5.00E+07 | 4.00E+04 | 19q13.33 | 14 | 9.2 | 4.0 |
| SRC* | SRC* | 20 | 3.60E+07 | 3.60E+07 | 6.10E+04 | 20q11.23 | 10 | 7.1 | 4.8 |
| ACOT8 | ACOT8 | 20 | 4.40E+07 | 4.40E+07 | 1.60E+04 | 20q13.12 | 4 | 3.1 | 2.7 |
| MMP9* | MMP9* | 20 | 4.50E+07 | 4.50E+07 | 7.70E+03 | 20q13.12 | 7 | ND | ND |

*genes are present in selected pathways for gastric cancer in Supplementary Figure S6 and S7.