

Supplementary figure 1:

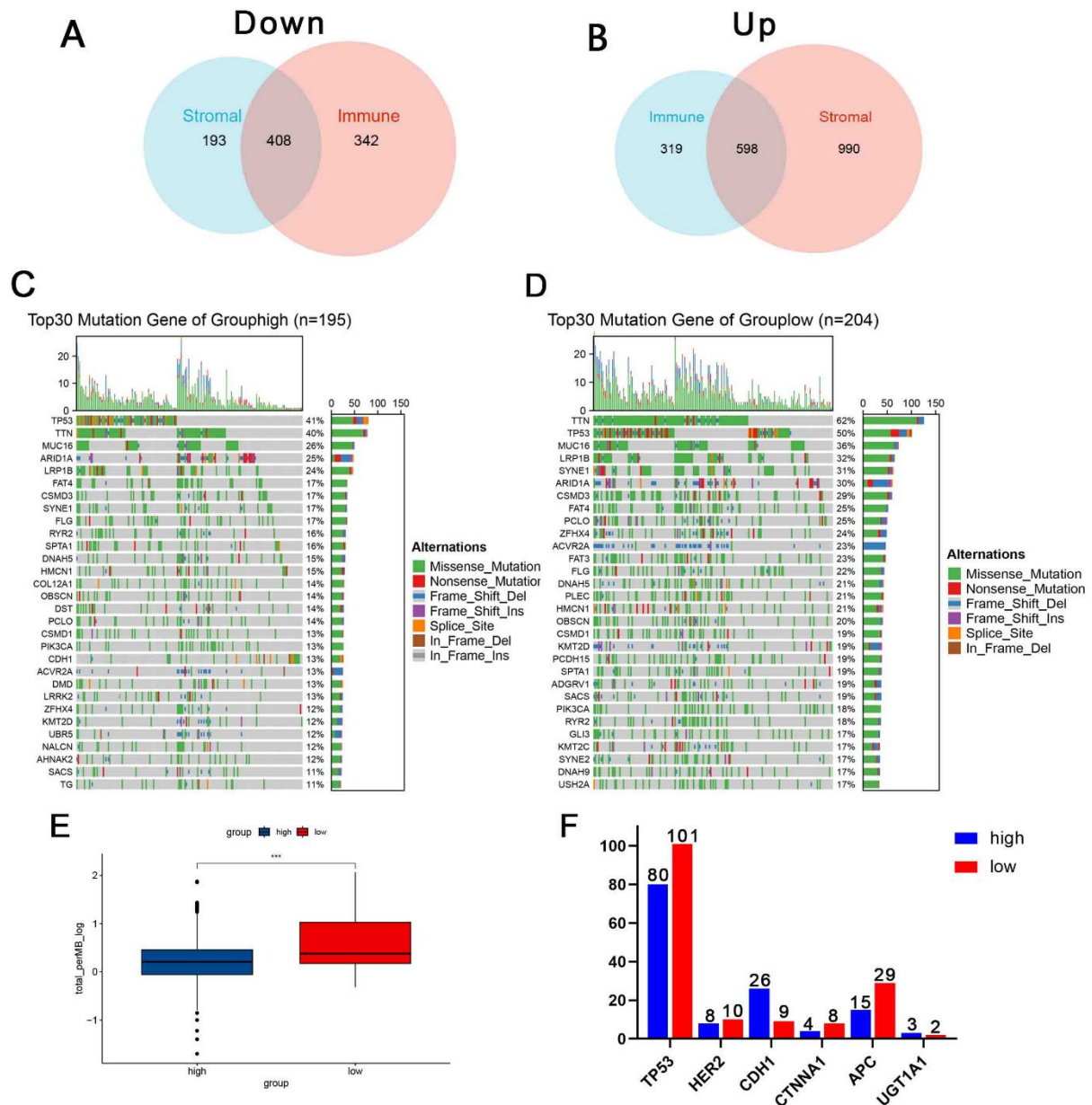


Fig. S1 The intersection is based on the DEG of StromalScore and ImmuneScore and Comparison of genetic mutations between the two groups. (A) 408 co-downregulated genes in StromalScore and ImmuneScore groups. (B) 598 co-upregulated genes in StromalScore and ImmuneScore groups. (D) SELP-high expression group's mutational landscape. (E) SELP-low expression group's mutational landscape. (F) Comparison of TMB between SELP-high expression group and SELP-low expression group. (G) Comparison of TP53, HER2, CDH1, CTNNA1, APC and UGT1A1 mutation between two groups.

Supplementary figure 2:

Figure 1 displays 20 scatter plots arranged in a 2x10 grid, showing the relationship between SELP expression (log2) and various gene expression levels (log2) for STAD (415 samples). Each plot includes a regression line and Spearman correlation statistics.

Top Row:

- CD44:** SELP_exp vs CD44_exp. Spearman Correlation Test: $\rho = 0.241$, $p = 7.51e-07$.
- CD3E:** SELP_exp vs CD3E_exp. Spearman Correlation Test: $\rho = 0.176$, $p = 0.0027$.
- BTNL2:** SELP_exp vs BTNL2_exp. Spearman Correlation Test: $\rho = 0.437$, $p < 2.2e-16$.
- CD3E:** SELP_exp vs CD3E_exp. Spearman Correlation Test: $\rho = 0.335$, $p = 3.39e-12$.
- IL1E:** SELP_exp vs IL1E_exp. Spearman Correlation Test: $\rho = 0.345$, $p = 6.19e-13$.
- FCOL1:** SELP_exp vs FCOL1_exp. Spearman Correlation Test: $\rho = 0.187$, $p = 0.00335$.
- LAO2:** SELP_exp vs LAO2_exp. Spearman Correlation Test: $\rho = 0.11$, $p = 0.054$.

Bottom Row:

- TOT:** SELP_exp vs TOT_exp. Spearman Correlation Test: $\rho = 0.478$, $p < 2.2e-16$.
- TSRSL:** SELP_exp vs TSRSL_exp. Spearman Correlation Test: $\rho = 0.114$, $p = 7.66e-11$.
- TSRSL:** SELP_exp vs TSRSL_exp. Spearman Correlation Test: $\rho = 0.364$, $p = 5.33e-08$.
- TSRSL:** SELP_exp vs TSRSL_exp. Spearman Correlation Test: $\rho = 0.394$, $p < 2.2e-16$.
- PVRSL:** SELP_exp vs PVRSL_exp. Spearman Correlation Test: $\rho = -0.234$, $p = 1.53e-06$.
- CD3E:** SELP_exp vs CD3E_exp. Spearman Correlation Test: $\rho = 0.474$, $p < 2.2e-16$.
- FCOL1:** SELP_exp vs FCOL1_exp. Spearman Correlation Test: $\rho = 0.355$, $p = 1.22e-13$.
- WDR5:** SELP_exp vs WDR5_exp. Spearman Correlation Test: $\rho = 0.243$, $p = 5.99e-07$.

Figure 1 displays 25 scatter plots arranged in a 5x5 grid, showing the Spearman correlation between SELP_exp (x-axis) and STAD (415 samples) (y-axis) for various gene expression datasets. Each plot includes a regression line and Spearman correlation statistics.

The datasets and their corresponding Spearman correlation statistics are as follows:

- Row 1:**
 - STAD (415 samples): $\rho = 0.508, p < 2.2e-16$
 - SELV_exp: $\rho = 0.468, p < 2.2e-16$
 - SELV_exp: $\rho = 0.514, p < 2.2e-16$
 - SELV_exp: $\rho = 0.257, p = 1.16e-07$
 - SELV_exp: $\rho = 0.363, p < 2.2e-16$
- Row 2:**
 - SELV_exp: $\rho = 0.492, p < 2.2e-16$
 - SELV_exp: $\rho = 0.143, p = 0.0043$
 - SELV_exp: $\rho = 0.296, p = 8.29e-10$
 - SELV_exp: $\rho = 0.374, p = 3.44e-15$
 - SELV_exp: $\rho = 0.374, p = 3.44e-15$
- Row 3:**
 - SELV_exp: $\rho = 0.301, p < 2.2e-16$
 - SELV_exp: $\rho = 0.642, p < 2.2e-16$
 - SELV_exp: $\rho = 0.294, p = 5.63e-08$
 - SELV_exp: $\rho = 0.156, p = 0.0046$
 - SELV_exp: $\rho = 0.231, p = 2.13e-06$
- Row 4:**
 - SELV_exp: $\rho = 0.441, p < 2.2e-16$
 - SELV_exp: $\rho = 0.112, p = 0.0143$
 - SELV_exp: $\rho = 0.374, p = 3.44e-15$
 - SELV_exp: $\rho = 0.171, p = 0.00459$
 - SELV_exp: $\rho = 0.117, p = 0.0274$
- Row 5:**
 - SELV_exp: $\rho = 0.397, p = 1.19e-14$
 - SELV_exp: $\rho = 0.122, p = 0.0132$
 - SELV_exp: $\rho = 0.277, p = 1.11e-08$
 - SELV_exp: $\rho = 0.153, p = 0.00208$
 - SELV_exp: $\rho = 0.424, p < 2.2e-16$

Fig. S2 Immunomodulators significantly associated with SELP. (A) 38 immunostimulators (ADORA2A, BTLA, CD160, CD244, CD96, CSF1R, HAVCR2, IL10, KDR, LAG3, PDCD1, PDCD1LG2, TGFB1, TGFB1R1, TIGIT, PVRL2, C10orf54, CD27, CD28, CD40, CD40LG, CD48, CD80, CD86, CXCL12, CXCR4, ENTPD1, ICOS, ICOSLG, IL2RA, IL6, IL6R, KLRC1, KLRK1, LTA, RAET1E, TMEM173, TMIGD2) significantly associated with SELP in STAD. (B) 16 immunoinhibitors (TNFRSF138, TNFRSF13C, TNFRSF17, TNFRSF4, TNFRSF8, TNFRSF9, TNFSF13B, TNFSF4, MICB, PVR, TNFRSF25, TNFSF13, TNFEF9, ULBP1) significantly associated with SELP in STAD.

**Supplementary figure
3:**

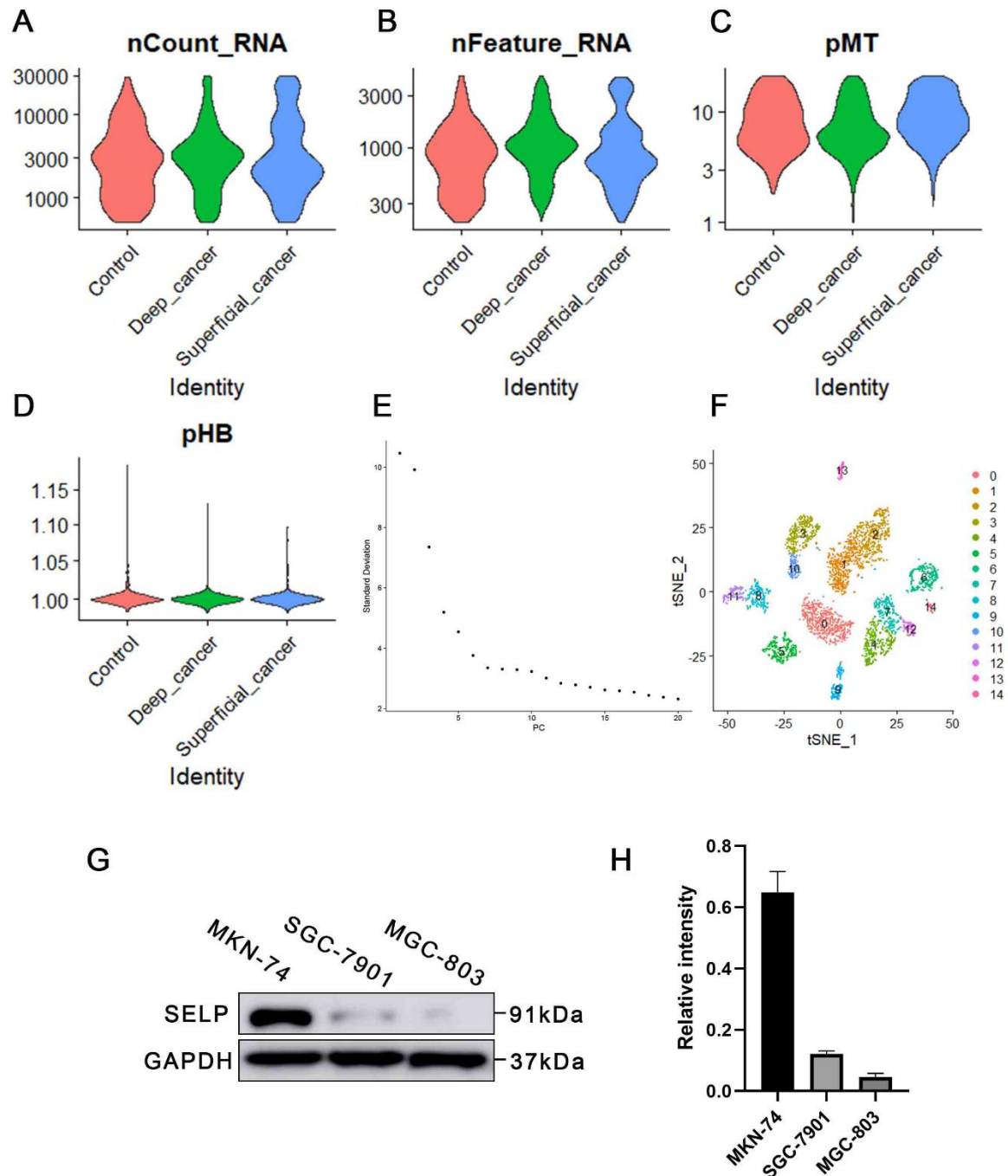


Fig. S3 Filter out non-conforming data and dimensionality reduction clustering of GSE167297 and expression of SELP in gastric cancer cell lines. (A) Filter out cells with count values less than 200 and count values greater than 30,000. (B) Filter out cells with feature values less than 200 and feature values greater than 5000. (C) Cells with mitochondrial gene expression greater than 20 are filtered out. (D) Cells with hemoglobin gene expression of more than 5 are filtered out. (E) As the PC gets bigger, the standard deviation gets smaller and smaller. (F) The cells were divided into 15 clusters. (G) SELP is

highly expressed in MKN-74 cells, but low expressed in SGC-7901 and MGC-803 cells. (H)
Grayscale values statistics in Figure G.