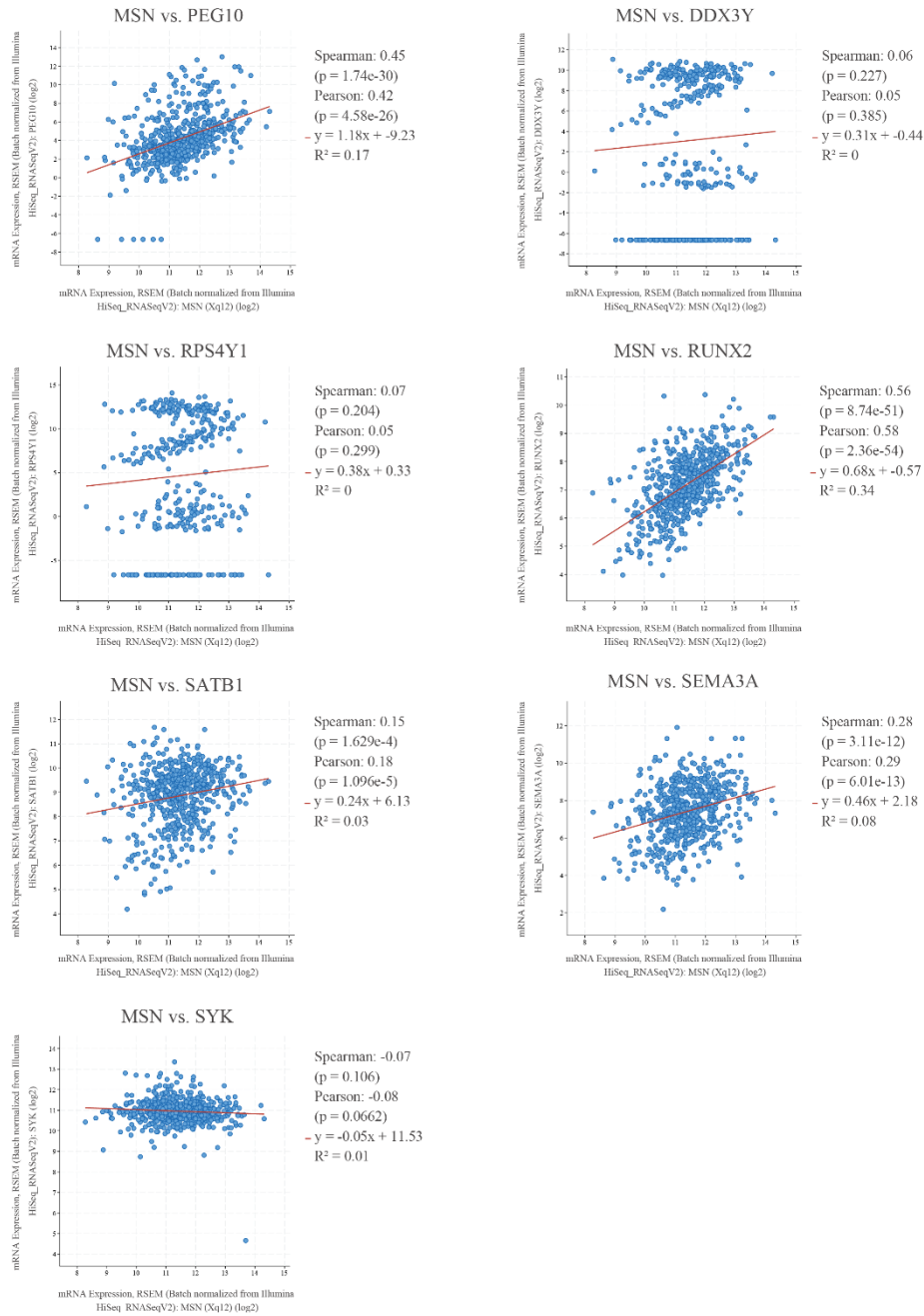


Supplemental Table S1. Differentially expressed genes.

| No | Symbol | Log2fold | padj |
|----|---------|----------|----------|
| 1 | SAT1 | -2.269 | 3.1E-135 |
| 2 | MSN | -2.828 | 6.85E-44 |
| 3 | ACSL5 | -2.542 | 8.59E-39 |
| 4 | CNDP2 | -2.941 | 2.07E-17 |
| 5 | PEG10 | -2.903 | 1.25E-14 |
| 6 | DHRS3 | 2.300 | 1.95E-11 |
| 7 | SEMA3A | -3.984 | 9.86E-06 |
| 8 | RPS4Y1 | -5.613 | 1.94E-05 |
| 9 | NFIB | -6.721 | 3.87E-05 |
| 10 | FER1L4 | -2.457 | 0.000556 |
| 11 | SYK | -3.699 | 0.001409 |
| 12 | TAGLN | 2.685 | 0.001856 |
| 13 | SATB1 | -6.533 | 0.004604 |
| 14 | DPP4 | -2.605 | 0.007916 |
| 15 | DDX3Y | -4.681 | 0.008699 |
| 16 | PRKAA2 | -4.541 | 0.015905 |
| 17 | CHAC1 | 2.155 | 0.016749 |
| 18 | RUNX2 | -3.061 | 0.0239 |
| 19 | CNTNAP2 | -3.440 | 0.026913 |
| 20 | LIMCH1 | -2.127 | 0.030347 |



Supplemental Figure S1. RUNX2 was the most significantly positively correlated with MSN expression in CRC patients. The expression correlation of the seven key genes (PEG10, SEMA3A, RPS4Y1, SYK, SATB1, DDX3Y, and RUNX2) with MSN was analyzed by the cBioPortal database.