### Supplementary Table 1. Cox regression analysis.

|                      | Univariate |              |          | Multivariate |              |          |
|----------------------|------------|--------------|----------|--------------|--------------|----------|
|                      | Hazard_ratio | CI95  | p_values | Hazard_ratio | CI95  | p_values |
| Age                  | 1.01        | 1.01-1.03    | 0.066    |              |              |          |
| Gender               | 0.82        | 0.58-1.17    | 0.284    |              |              |          |
| Race                 | 1.14        | 0.95-1.37    | 0.166    |              |              |          |
| Family_History       | 1.16        | 0.81-1.68    | 0.418    |              |              |          |
| BMI                  | 1.00        | 0.97-1.03    | 0.995    |              |              |          |
| Ethnicity            | 1.11        | 0.49-2.52    | 0.811    |              |              |          |
| Fibrosis_Stage       | 1.18        | 0.87-1.6     | 0.287    |              |              |          |
| Child_Pugh_Classification | 1.52 | 0.84-2.77    | 0.17     |              |              |          |
| Tumor_Stage          | 1.64        | 1.34-2.01    | 0        | 0.8          | 0.34-1.87   | 0.611    |
| Pathologic_T         | 1.63        | 1.37-1.97    | 0        | 1.95         | 0.87-4.34   | 0.103    |
| Pathologic_N         | 1.22        | 1.01-1.46    | 0.037    | 1.07         | 0.81-1.4    | 0.637    |
| Pathologic_M         | 1.26        | 1.05-1.52    | 0.012    | 1.24         | 0.95-1.63   | 0.11     |
| Radiation_Therapy    | 0.84        | 0.21-3.42    | 0.808    |              |              |          |
| Vascular_Invasion    | 0.74        | 0.53-1.02    | 0.069    |              |              |          |
| BMS1P1               | 1.19        | 0.59-2.4     | 0.622    |              |              |          |
| C2orf27A             | 2.13        | 1.51-2.99    | 0        | 1.5          | 0.99-2.27   | 0.057    |
| CFB                  | 0.85        | 0.75-0.97    | 0.017    | 1            | 0.85-1.18   | 0.979    |
| COL1A2               | 1.06        | 0.95-1.17    | 0.291    |              |              |          |
| CST3                 | 1.2         | 0.97-1.48    | 0.091    |              |              |          |
| CYP4F30P             | 11680.6     | 0-4.11e13    | 0.245    |              |              |          |
| DEFB122              | 2384.77     | 0.03-2.03e8  | 0.179    |              |              |          |
| GPER1                | 0.96        | 0.81-1.13    | 0.6      |              |              |          |
| IGF2R                | 1.28        | 1.01-1.63    | 0.041    | 1.08         | 0.83-1.4    | 0.565    |
| OR2A20P              | 5.13        | 0.3-86.48    | 0.256    |              |              |          |
| PON1                 | 0.33        | 0.07-1.45    | 0.141    |              |              |          |
| ZNF826P              | 1.35        | 0.99-1.83    | 0.057    |              |              |          |
| ZSCAN12P1            | 0.94        | 0.58-1.5     | 0.784    |              |              |          |
### Table 2. Correlation between selected genes and infiltrating immune cells in GSE109211.

| Activated.CD4.T.cell | CFB  | IGF2R | PON1 | C2orf27A |
|----------------------|------|-------|------|----------|
|                      | r    | p     | r    | p        | r    | p     | r    | p     |
| Activated.CD8.T.cell | 0.51 | 0.00  | 0.33 | 0.01    | 0.09 | 0.45  | 0.40 | 0.00  |
| Activated.dendritic.cell | 0.43 | 0.00  | 0.34 | 0.00    | 0.20 | 0.11  | 0.09 | 0.46  |
| CD56bright.natural.killer.cell | 0.68 | 0.00  | 0.56 | 0.00    | 0.33 | 0.01  | 0.35 | 0.00  |
| Central.memory.CD4.T.cell | 0.65 | 0.00  | 0.59 | 0.00    | 0.41 | 0.00  | 0.48 | 0.00  |
| Central.memory.CD8.T.cell | 0.44 | 0.00  | 0.50 | 0.00    | 0.48 | 0.00  | 0.09 | 0.46  |
| Effector.memory.CD4.T.cell | -0.18 | 0.13  | -0.22 | 0.07   | -0.48 | 0.00  | 0.02 | 0.89  |
| Effector.memory.CD8.T.cell | 0.70 | 0.00  | 0.16 | 0.20    | 0.02 | 0.86  | 0.35 | 0.00  |
| Natural.killer.cell | 0.70 | 0.00  | 0.14 | 0.27    | 0.04 | 0.75  | 0.35 | 0.00  |
| Natural.killer.T.cell | -0.40 | 0.00  | -0.11 | 0.36   | -0.06 | 0.96  | -0.23 | 0.06  |
| Type.1.T.helper.cell | 0.56 | 0.00  | 0.26 | 0.03    | 0.21 | 0.08  | 0.44 | 0.00  |
| Type.17.T.helper.cell | -0.52 | 0.00  | -0.33 | 0.01   | -0.30 | 0.01  | -0.44 | 0.00  |
| CD56dim.natural.killer.cell | 0.61 | 0.00  | 0.13 | 0.28    | 0.14 | 0.26  | 0.23 | 0.06  |
| Immature.dendritic.cell | 0.24 | 0.05  | 0.50 | 0.00    | 0.48 | 0.00  | 0.30 | 0.01  |
| Macrophage | -0.35 | 0.00  | -0.30 | 0.01   | -0.09 | 0.46  | -0.06 | 0.62  |
| MDSC | 0.53 | 0.00  | 0.56 | 0.00    | 0.30 | 0.01  | 0.28 | 0.02  |
| Neutrophil | -0.50 | 0.00  | -0.33 | 0.01   | -0.16 | 0.19  | -0.21 | 0.09  |
| Plasmacytoid.dendritic.cell | 0.68 | 0.00  | 0.66 | 0.00    | 0.47 | 0.00  | 0.32 | 0.01  |
| Regulatory.T.cell | 0.56 | 0.00  | 0.13 | 0.31    | 0.01 | 0.95  | 0.38 | 0.00  |
| Type.2.T.helper.cell | -0.46 | 0.00  | -0.17 | 0.17   | -0.15 | 0.22  | 0.02 | 0.86  |
| Activated.B.cell | -0.42 | 0.00  | -0.67 | 0.00    | -0.60 | 0.00  | -0.10 | 0.41  |
| Eosinophil | 0.16 | 0.18  | 0.34 | 0.00    | 0.34 | 0.01  | 0.12 | 0.33  |
| Gamma.delta.T.cell | 0.65 | 0.00  | 0.57 | 0.00    | 0.46 | 0.00  | 0.38 | 0.00  |
| Immature.B.cell | -0.27 | 0.03  | -0.27 | 0.03   | -0.38 | 0.00  | -0.04 | 0.74  |
| Mast.cell | -0.16 | 0.20  | 0.02 | 0.86    | 0.02 | 0.85  | 0.00 | 0.99  |
| Memory.B.cell | 0.24 | 0.05  | -0.00 | 0.97   | -0.10 | 0.41  | 0.19 | 0.13  |
| Monocyte | 0.75 | 0.00  | 0.57 | 0.00    | 0.43 | 0.00  | 0.38 | 0.00  |
| T.follicular.helper.cell | -0.22 | 0.08  | 0.32 | 0.01    | 0.16 | 0.19  | -0.21 | 0.09  |
**Supplementary Table 3. qRT-PCR primers.**

| Genes       | Primers | Sequences (5’ to 3’)               |
|-------------|---------|------------------------------------|
| Homo β-actin| Forward | CACCAACTGGGAGCGACAT                |
|             | Reverse | ACAGCCTGGATAGCAACG                 |
| Homo C2orf27a| Forward | TCACGCTGCTGATGGAATAGAA             |
|             | Reverse | ATCAGAGCTGCTGAGGGA                 |
| Homo IGF2R   | Forward | CACCAAGCGTGGATGTTGG                |
|             | Reverse | TTTGGGAATGGTGCCCTTC                |
| Homo CFB     | Forward | TCTCTGTGCGATGTTGGG                 |
|             | Reverse | CCATAAGCTCGTATGGTTCCC              |
| Homo PON1    | Forward | AGCGTGGTCGATGTTGTCT                |
|             | Reverse | TGAGCCAGCAACTCAGCTAT               |

**Supplementary Table 4. Target sequences of siRNAs and lncRNA smart silencer.**

| siRNAs          | Target sequences              |
|-----------------|-------------------------------|
| siR-IGF2R       | GCATCAAGATATCGACTCT             |
| siR-CFB         | GTGGCAAGTGTTATGGTGTGA           |
| siR-PON1        | GTCGTATGTTGCTACTAT             |
| SmartSiliencer-C2orf27A (mix) |                               |
| ASO-h-C2orf27A_001 | CCAAGGTTATGCTGCA              |
| ASO-h-C2orf27A_001 | GAGAGTAACTTTGTACCCAT          |
| ASO-h-C2orf27A_001 | ACCACAGTTACTTATCCCT          |
| si-h-C2orf27A_001 | TCTCTGTGCTGCTCTCAA             |
| si-h-C2orf27A_002 | CCTCCAGGTCCAACGAT             |
| si-h-C2orf27A_003 | ACTGATCCCTCCGAGACT           |