**Supplementary Table S3. Relapse-free survival of gene signature and single genes according to intrinsic subtype.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **RFS (Not****censored)** | **Subtypeχ** | ***n*** | **Low-expression****cohort (months)** | **High-expression****cohort (months)** | ***P* value****(¥ Log-rank)** |
| **Signature** | Basal | 360 | 33 | 14 | **1.3E-7 ¥\*** |
| *ATF4* | 618 | 22 | 17 | **0.0153 ¥** |
| *TGFBR1* | 360 | 22 | 18 | 0.1436 |
| *SMAD4* | 360 | 21 | 16 | **0.0182 ¥** |
| *PIK3CA* | 618 | 23 | 16 | **0.0041 ¥\*** |
| *RICTOR* | 360 | 15 | 20 | **0.0054 ¥\*** |
| *RPTOR* | 360 | 14 | 19 | 0.0562 |
| *EIF4EBP1* | 618 | 24 | 16 | 0.1548 |
| *NDRG1* | 618 | 38 | 17 | **1.3E-5 ¥\*** |
| **Signature** | Luminal A | 841 | 70 | 40 | **0.044 ¥**† |
| *ATF4* | 1933 | 71 | 84 | 0.1394 |
| *TGFBR1* | 841 | 52 | 68 | **0.0111 ¥** |
| *SMAD4* | 841 | 37 | 85 | **3.7E-7 ¥\*** |
| *PIK3CA* | 1933 | 217 | 185 | **1.2E-5 ¥\*** |
| *RICTOR* | 841 | 42 | 68 | **0.0029 ¥\*** |
| *RPTOR* | 841 | 46 | 66 | 0.0507 |
| †*EIF4EBP1* | 1933 | 214 | 152 | **1.8E-10 ¥\***† |
| *NDRG1* | 1933 | 217 | 184 | **0.0005 ¥\*** |
| **Signature** | Luminal B | 407 | 41 | 28 | **0.0081 ¥\***† |
| *ATF4* | 1149 | 43 | 37 | 0.1003 |
| *TGFBR1* | 407 | 36 | 40 | 0.3899 |
| *SMAD4* | 407 | 26 | 41 | **0.0015 ¥\*** |
| *PIK3CA* | 1149 | 54 | 37 | **0.0004 ¥\*** |
| *RICTOR* | 407 | 28 | 43 | **0.0002 ¥\*** |
| *RPTOR* | 407 | 106 | 171 | **0.0289 ¥** |
| †*EIF4EBP1* | 1149 | 79 | 35 | **2.2E-7 ¥\***† |
| *NDRG1* | 1149 | 48 | 36 | **0.005 ¥\*** |
| **Signature** | HER2 | 156 | 98 | 32 | 0.0718 |
| *ATF4* | 251 | 23 | 16 | **0.013 ¥\*** |
| *TGFBR1* | 156 | 40 | 123 | 0.1254 |
| *SMAD4* | 156 | 15 | 19 | 0.1249 |
| *PIK3CA* | 251 | 15 | 23 | 0.2276 |
| *RICTOR* | 156 | 23 | 15 | 0.1506 |
| *RPTOR* | 156 | 13 | 18 | **0.0256 ¥** |
| *EIF4EBP1* | 251 | 25 | 18 | 0.1713 |
| *NDRG1* | 251 | 15 | 24 | 0.0673 |
| **RFS:** relapse free survival. **\*** Significant with multivariate analysis. **†** Does not meet leave-one-out cross-validation. **χ** Intrinsic subtype according to StGallen criteria (2013). |