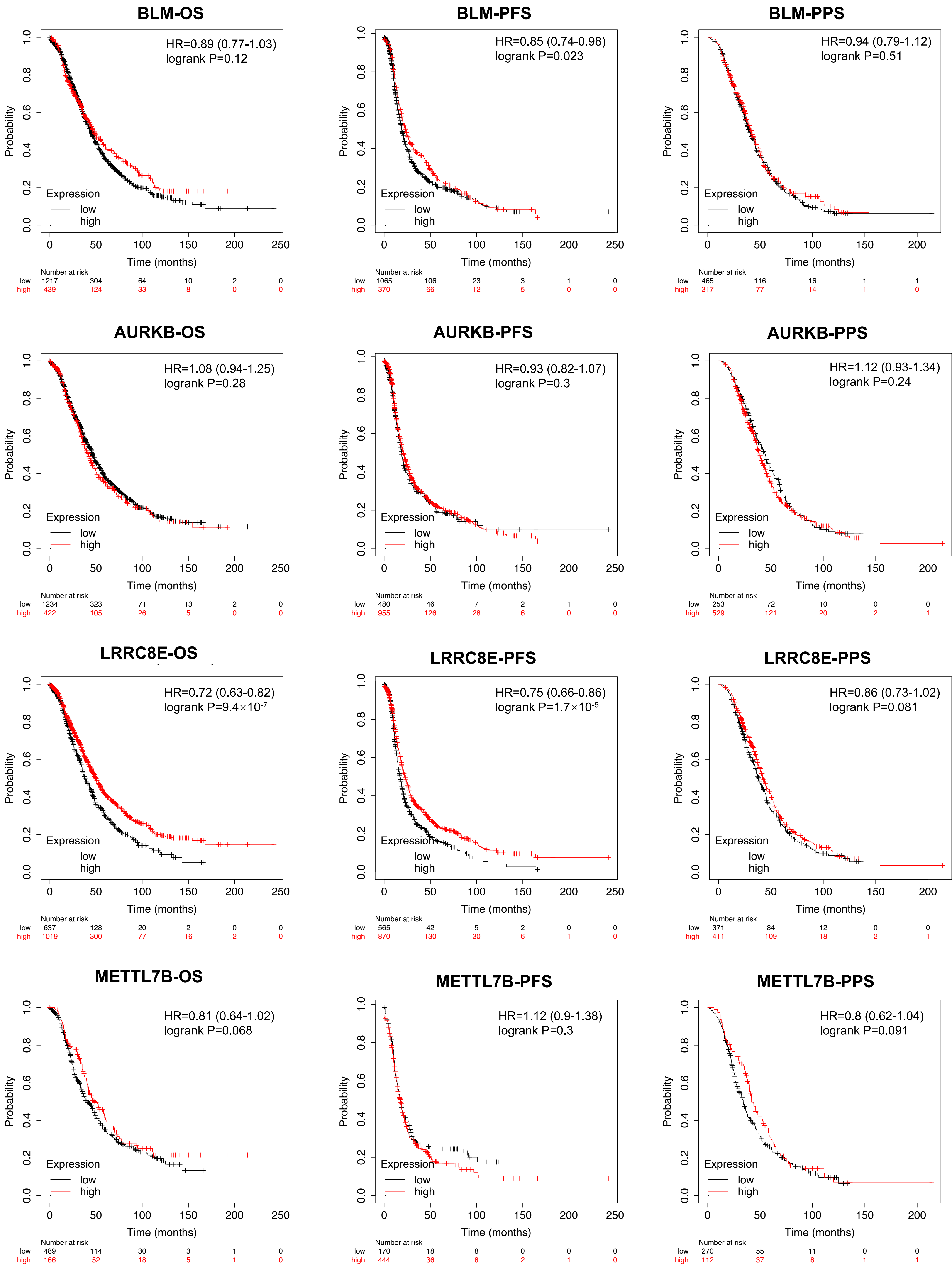
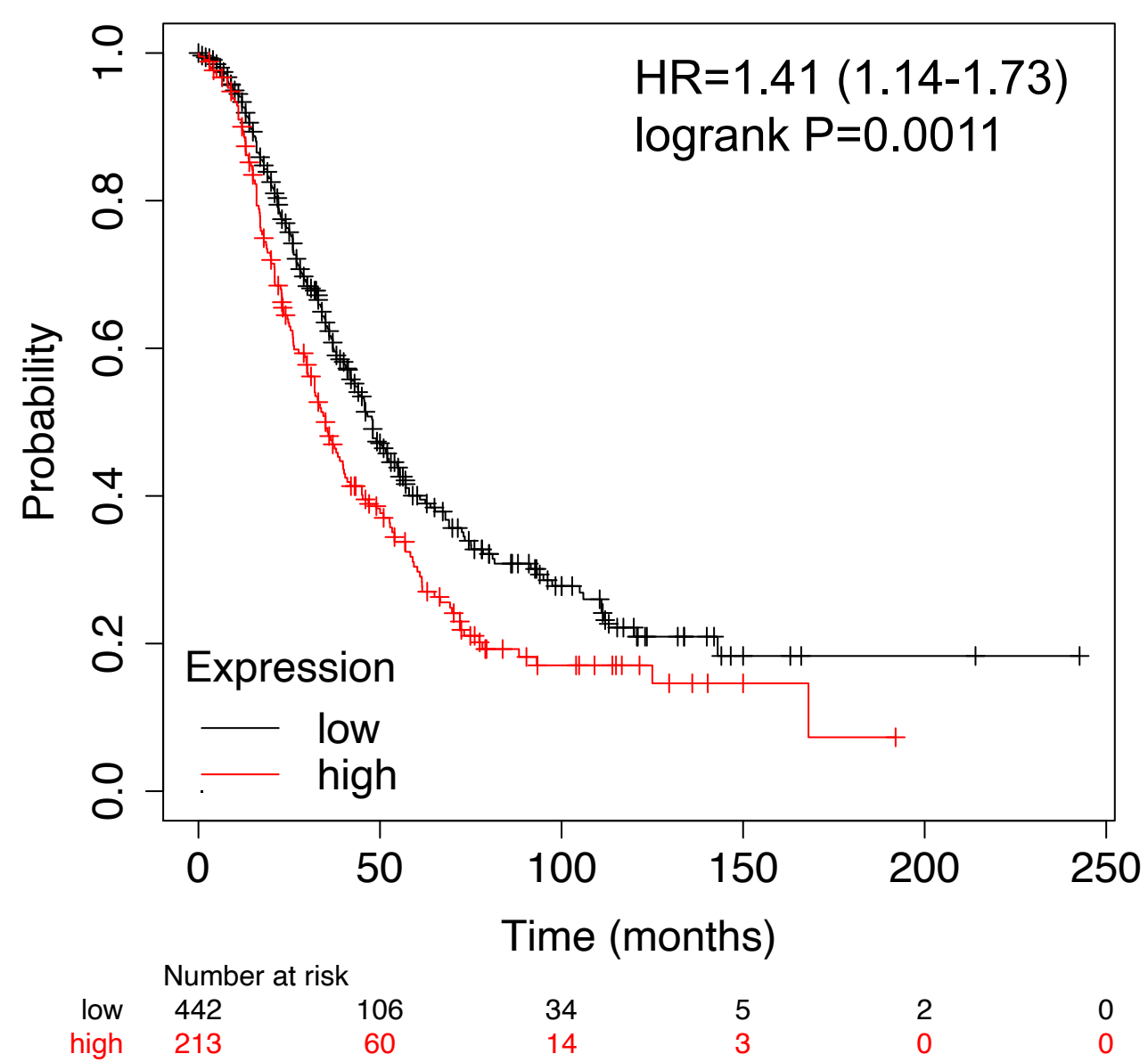


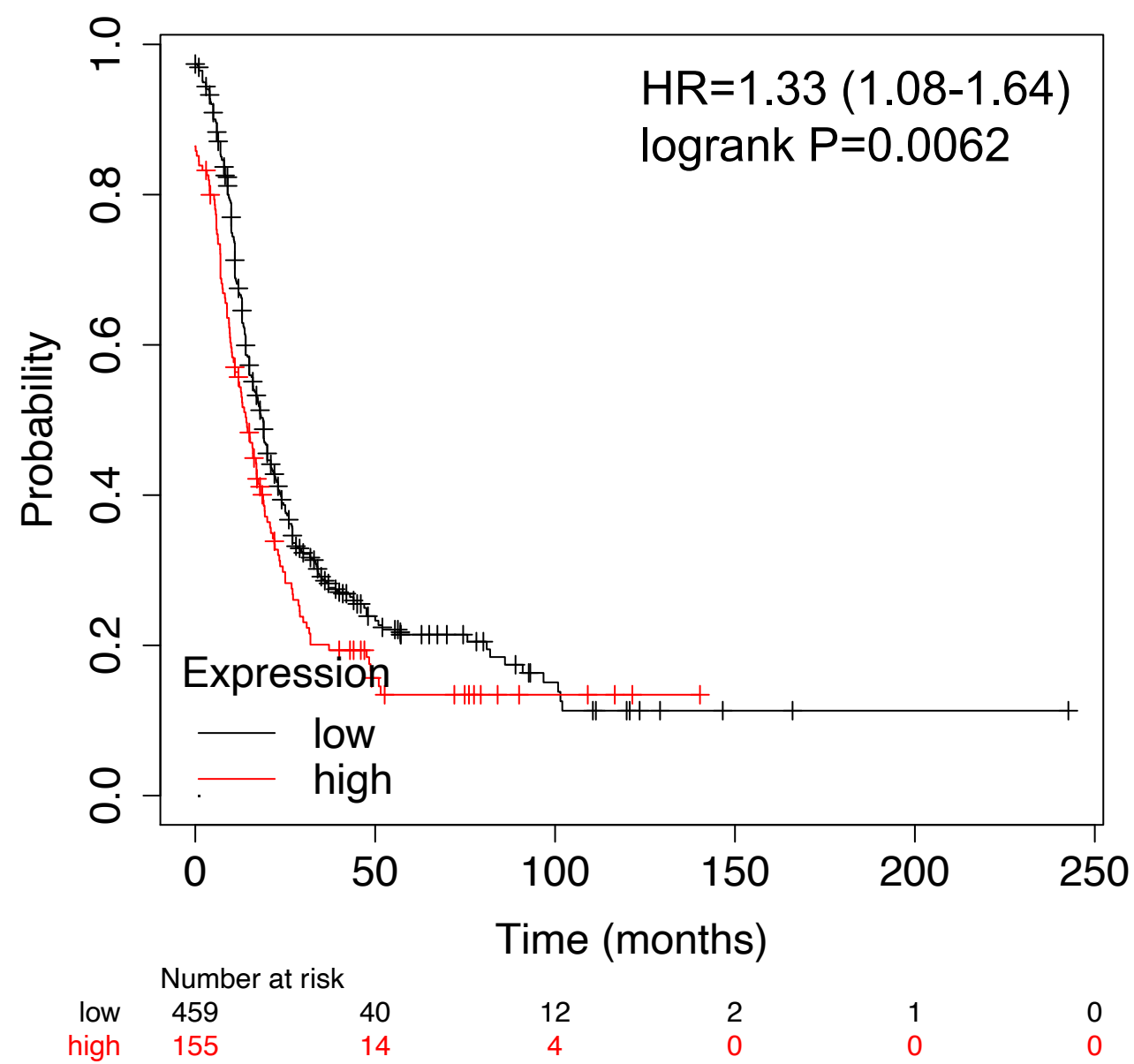
Figure S1



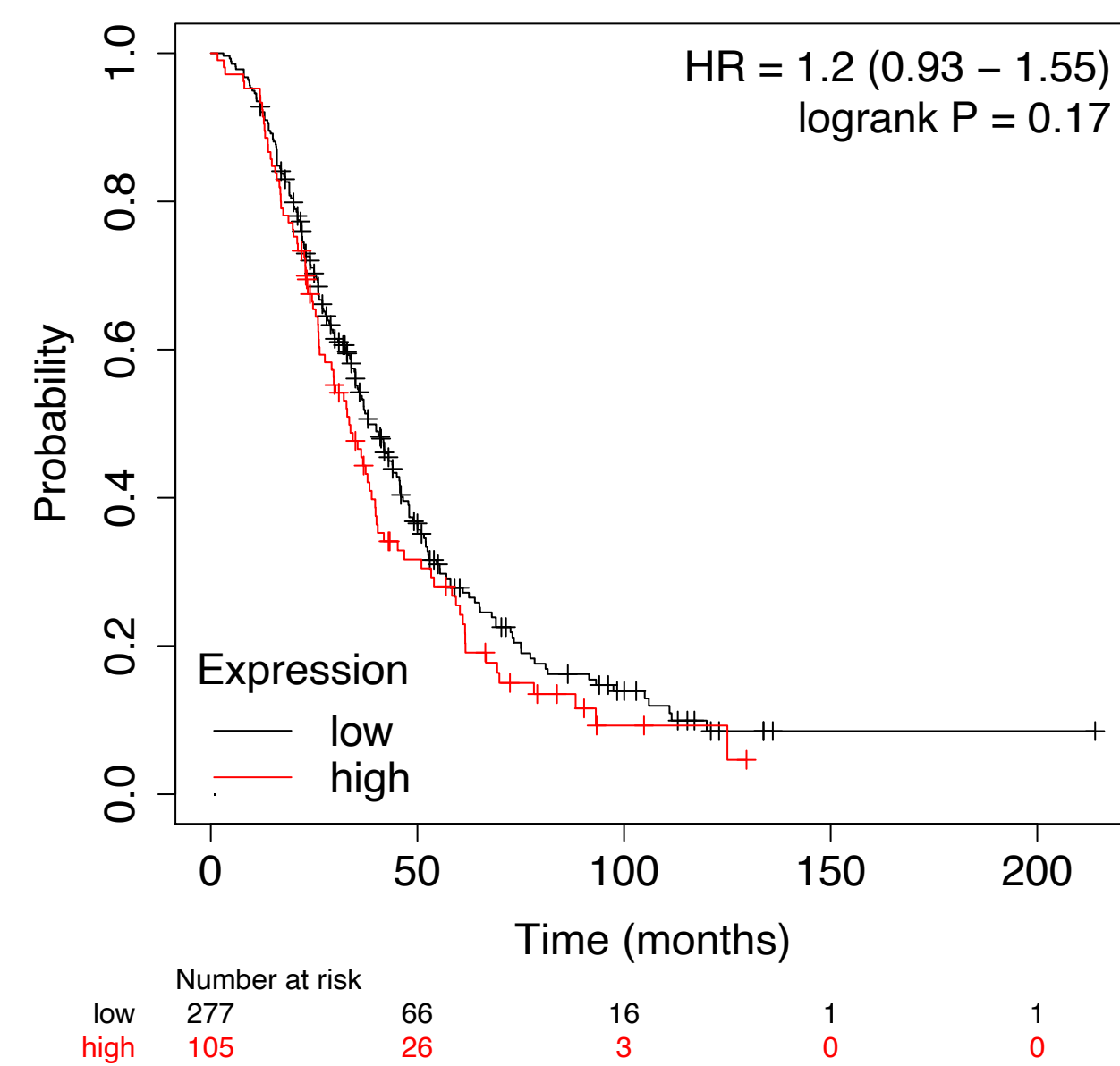
GPRIN1-OS



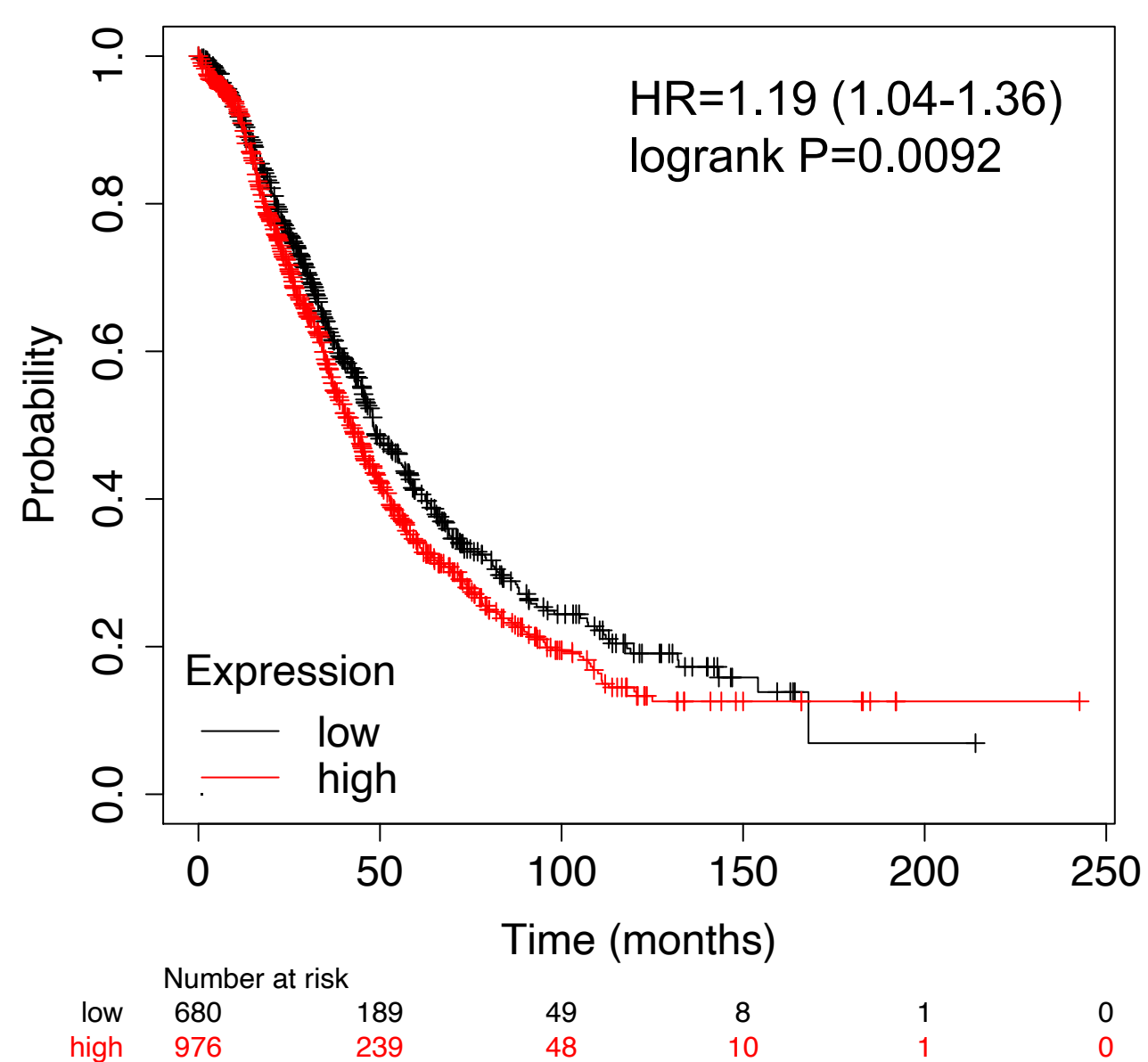
GPRIN1-PFS



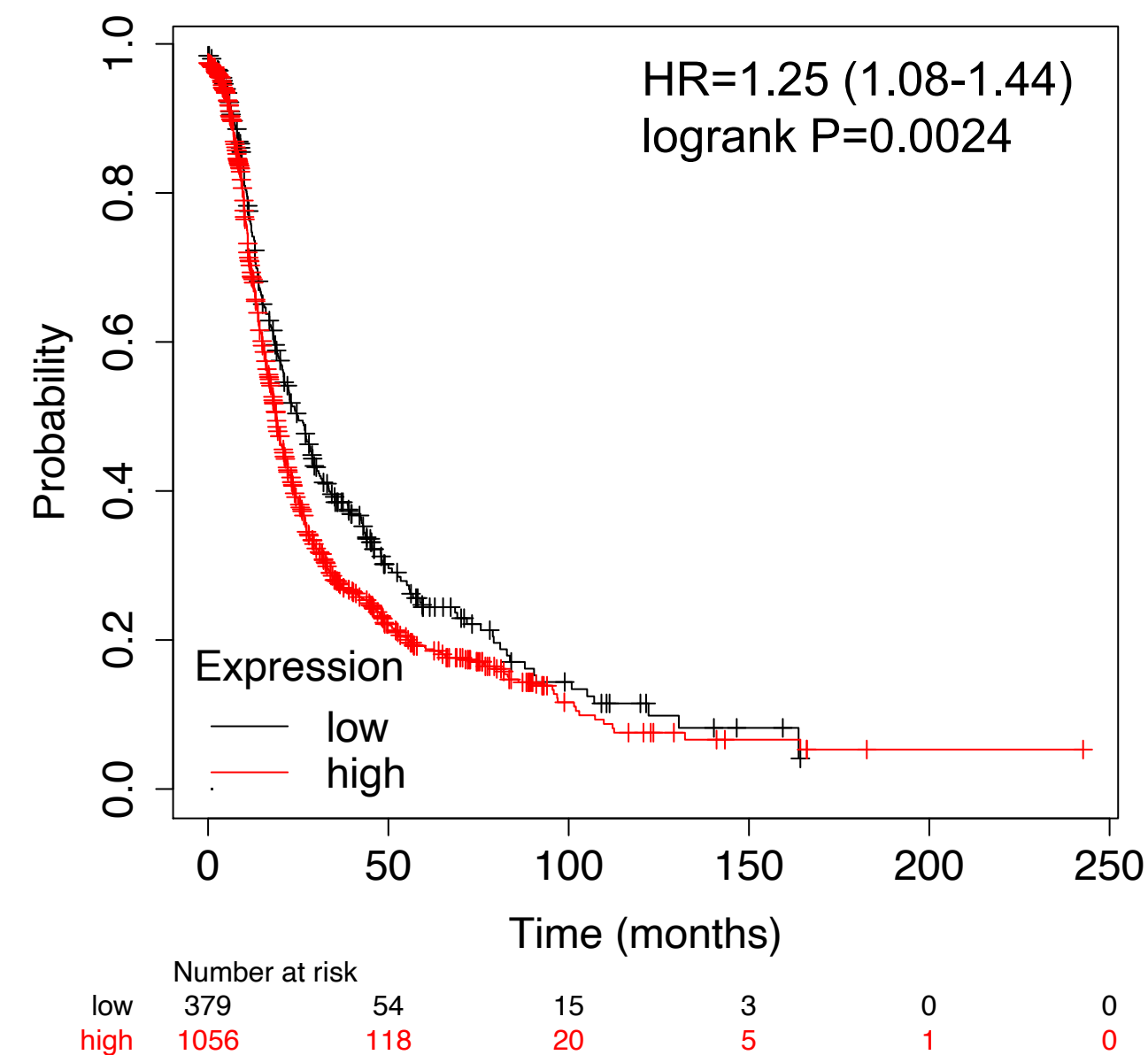
GPRIN1-PPS



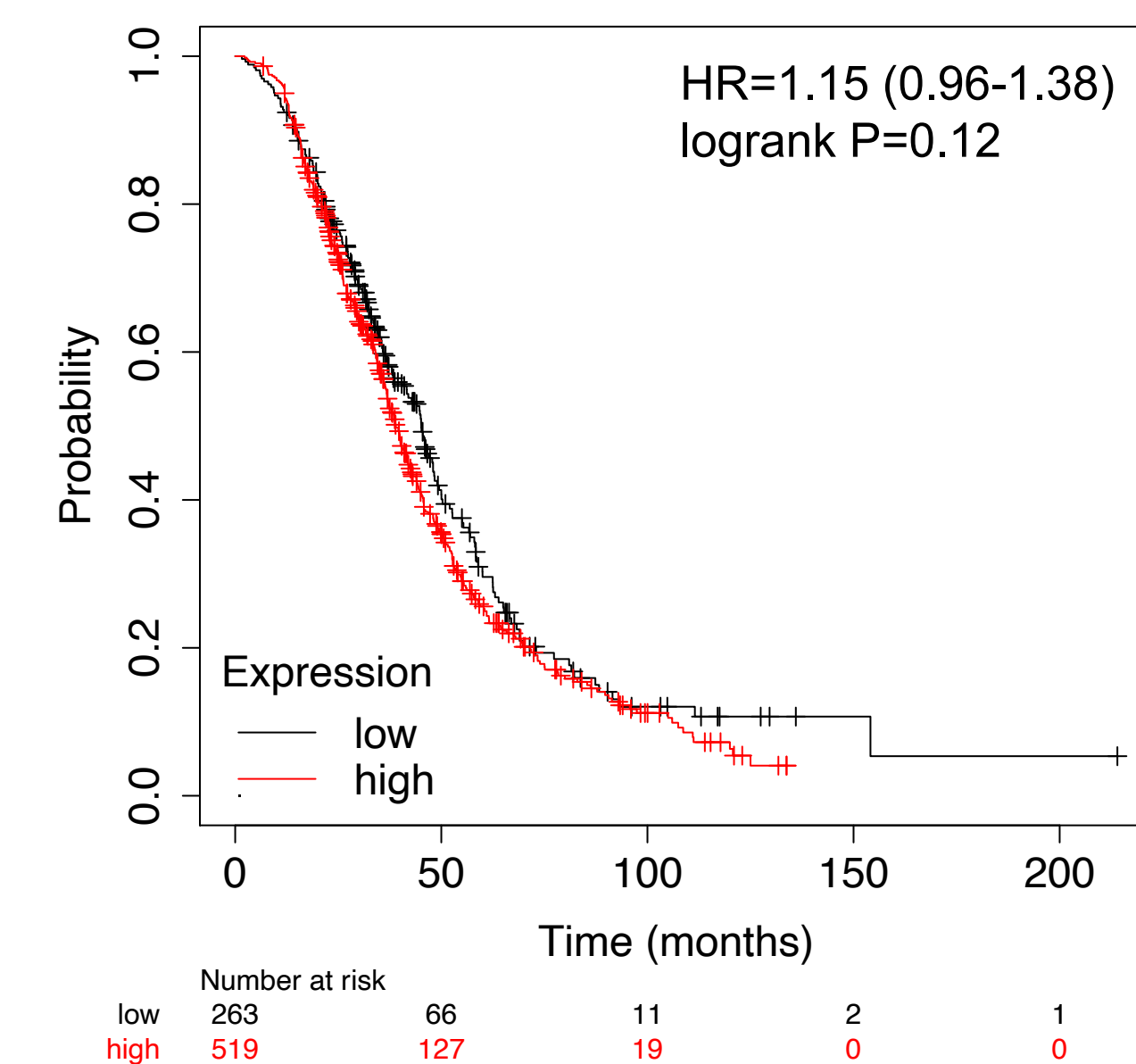
E2F8-OS



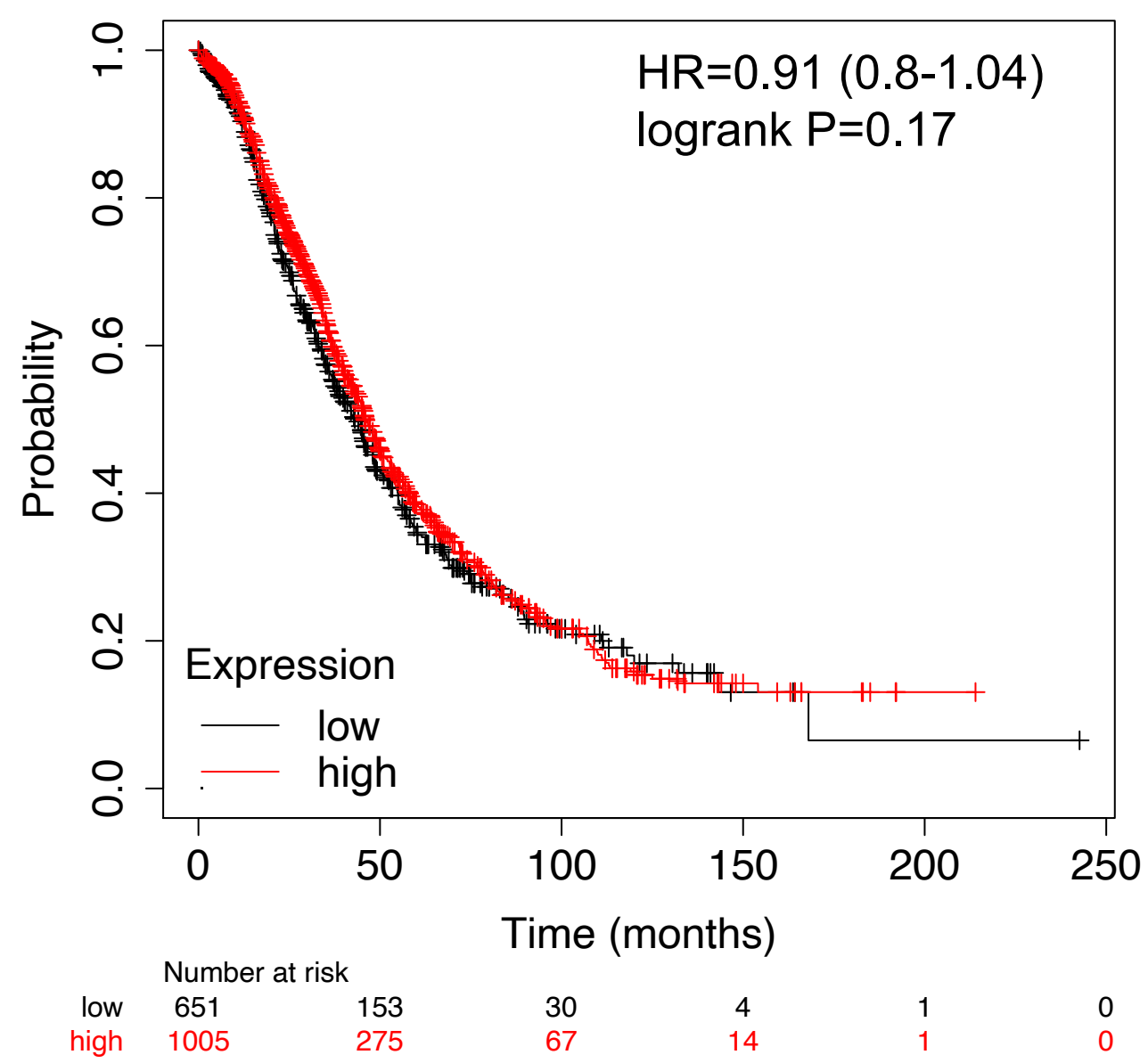
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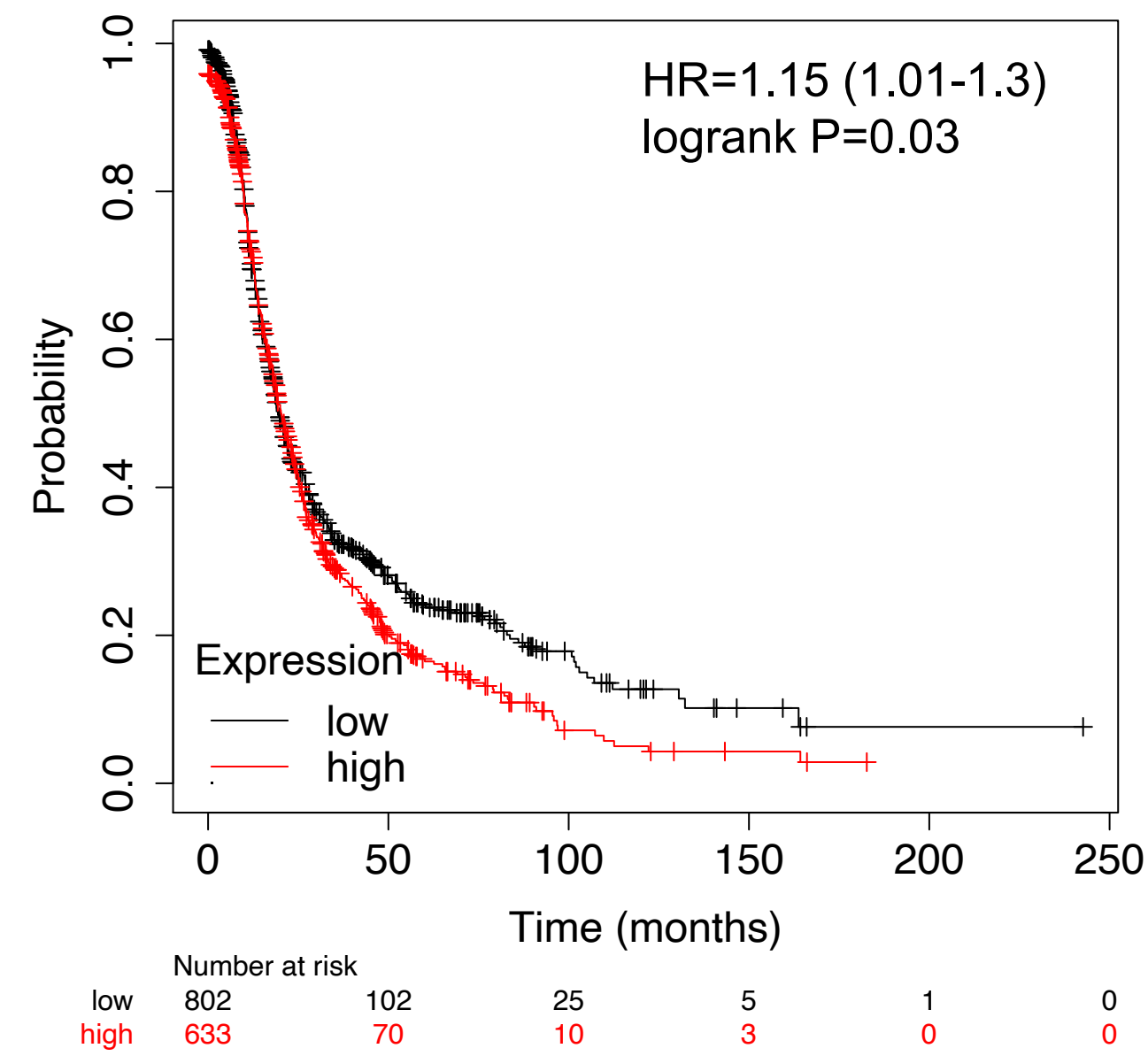
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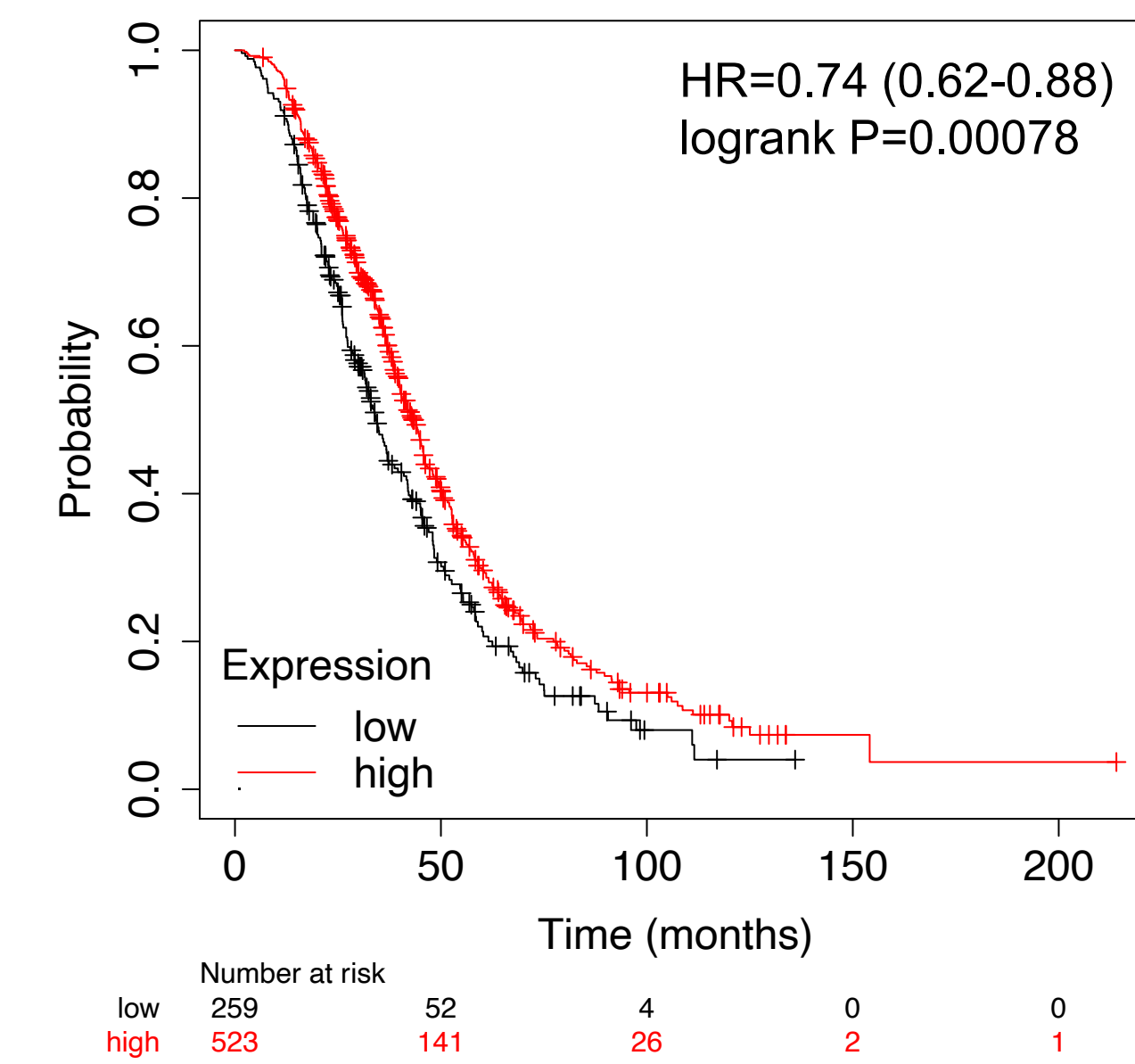
MYCL-OS



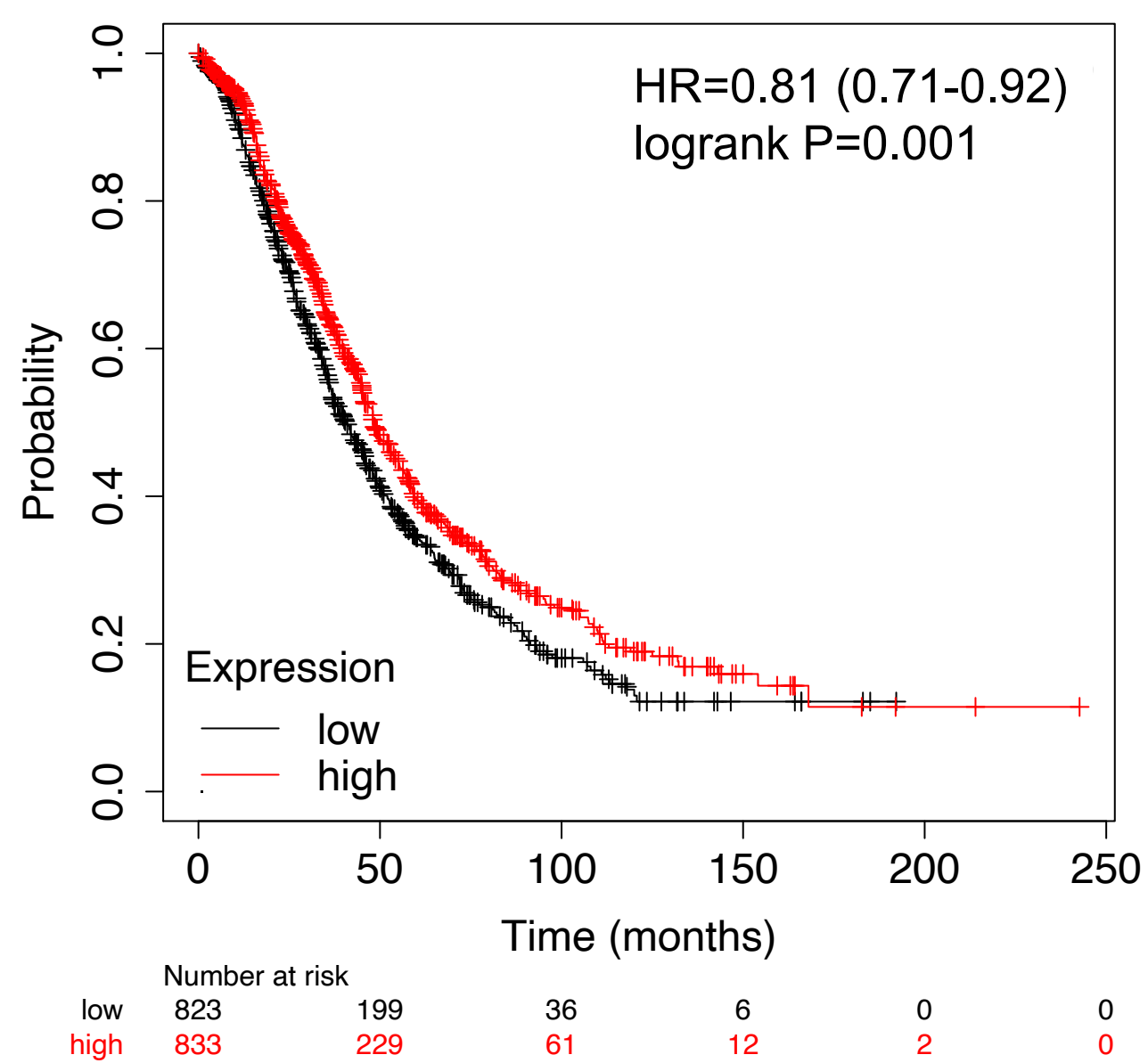
MYCL-PFS



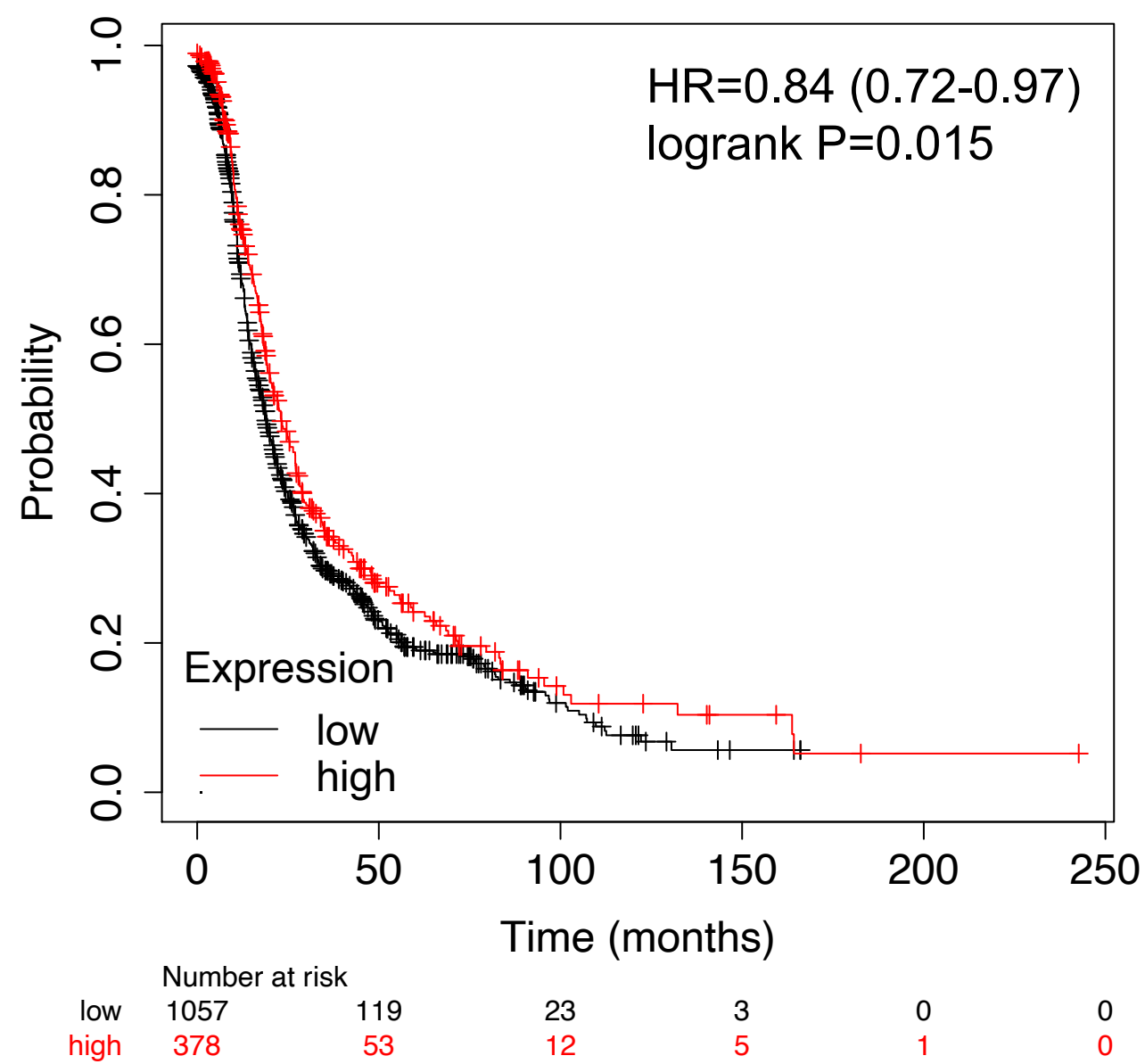
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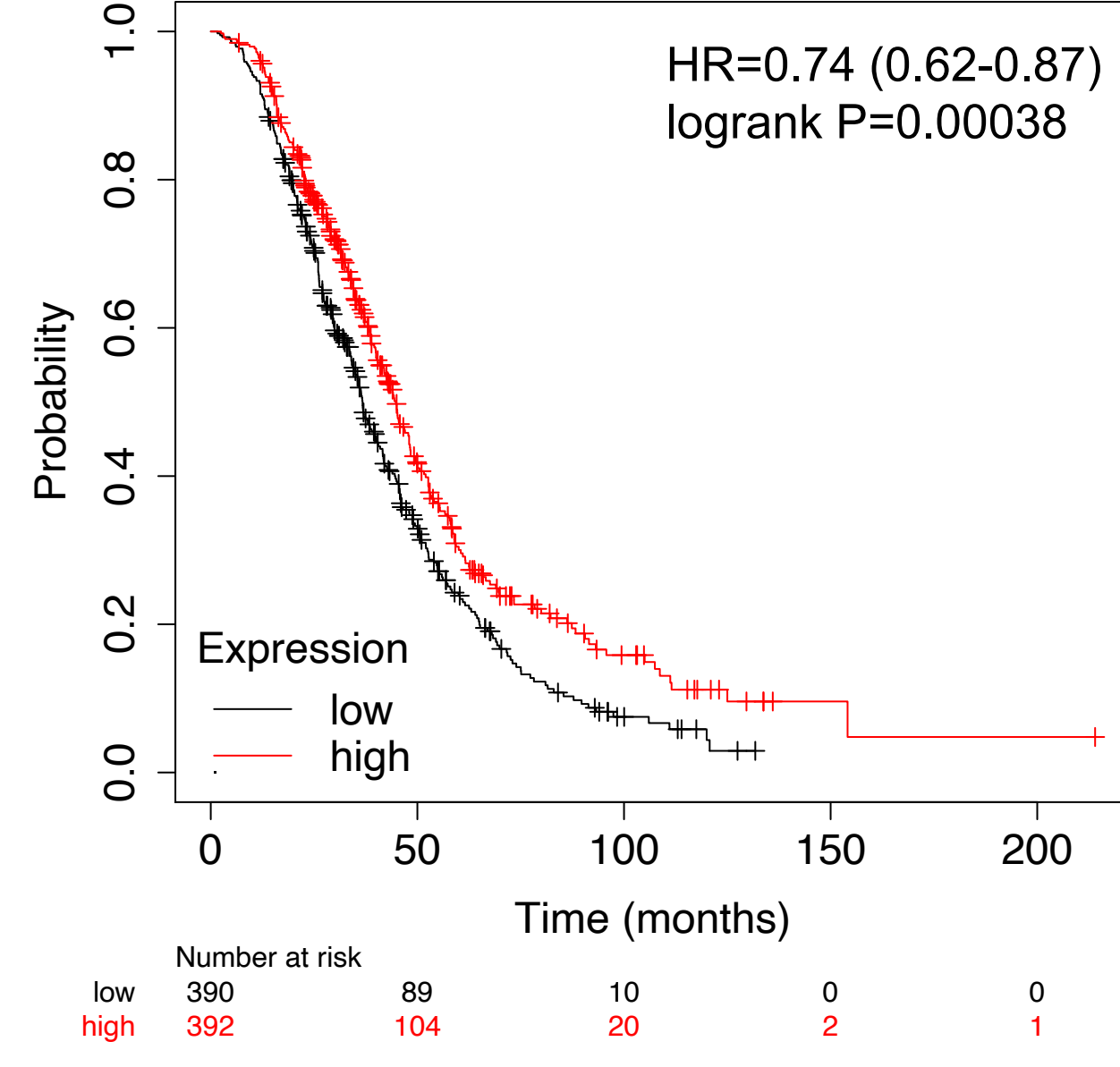
ICAM3-OS



ICAM3-PFS



ICAM3-PPS



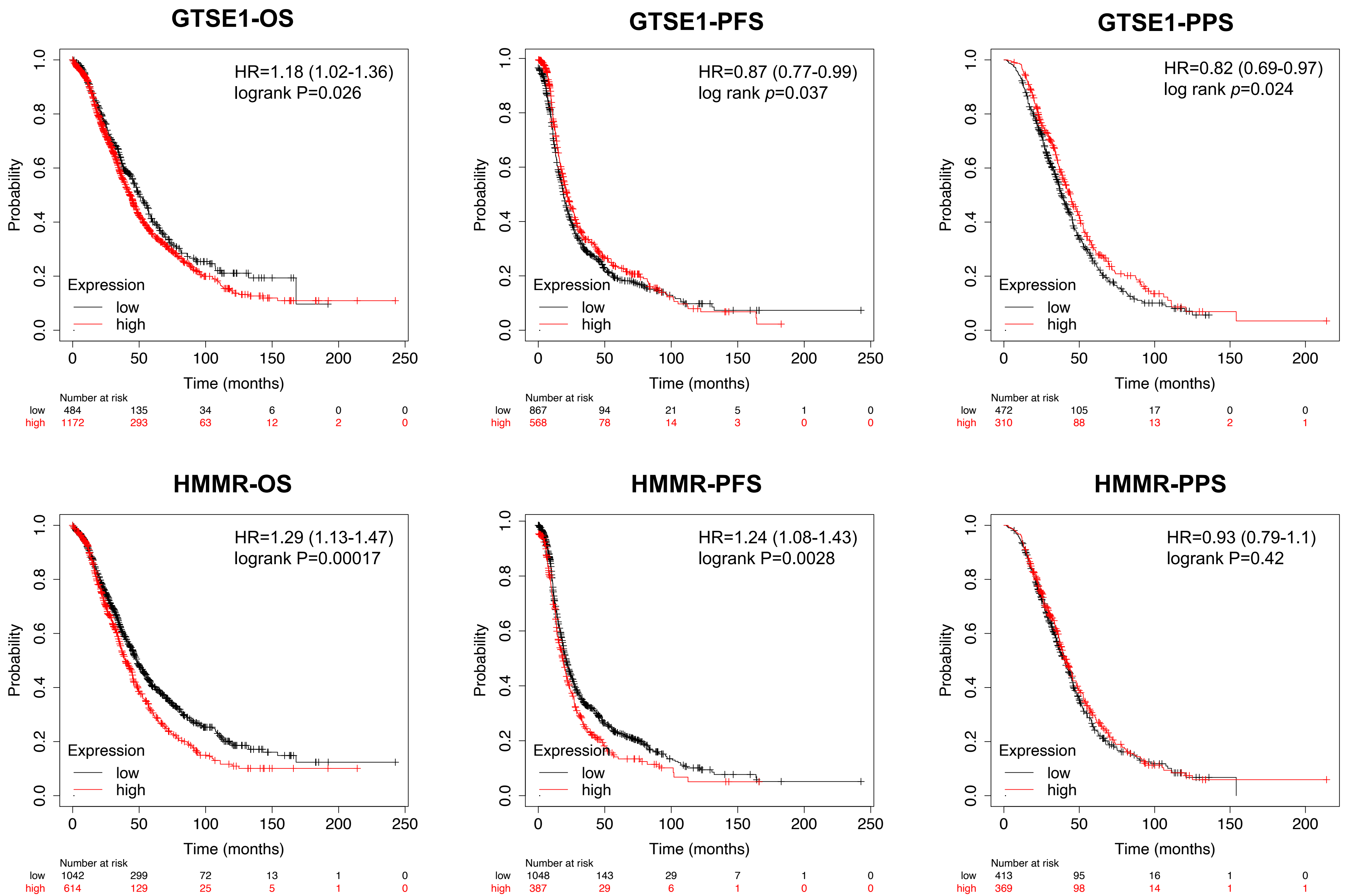


Figure S1. Survival analysis of DEGs regarding OS (overall survival), PFS (post-free survival), and PPS (post-progression survival) using TCGA-OV dataset. Red, high-expression group; Black, low-expression group. p -value is log-ranked. Auto-selected best cutoff was used

Figure S2

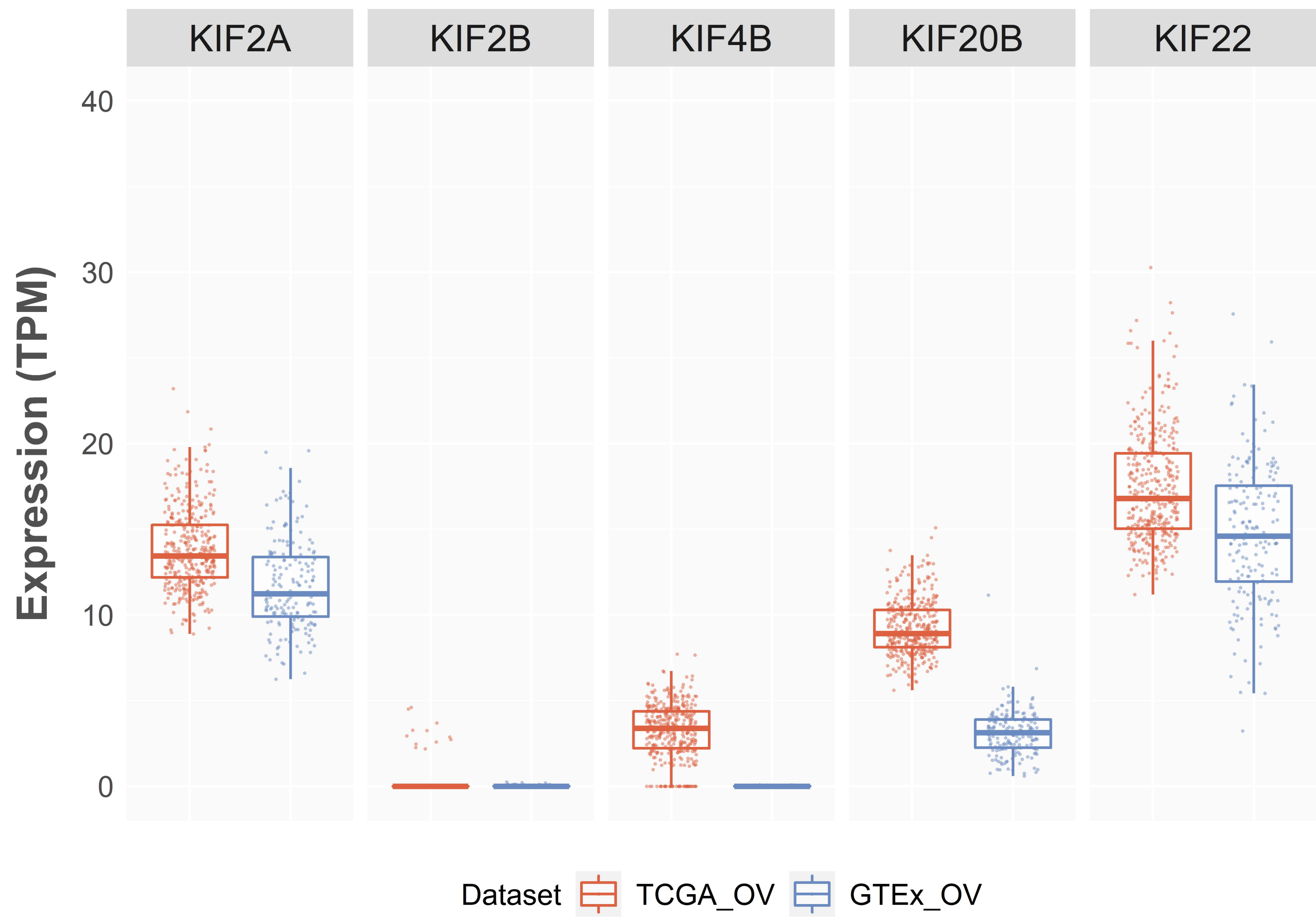


Figure S2. Expression profiles of mitotic KIFs in OC. No significant difference was obtained of mitotic KIFs (2A, 2B, 4B, 20B, and 22) between ovarian cancer and normal ovarian tissues from TCGA-OV (n=426) and GTEx-OV (n=88) dataset, respectively; TPM, transcripts per million; Expression of KIF10 was not detected in either ovarian cancer nor normal ovarian tissues.

Figure S3

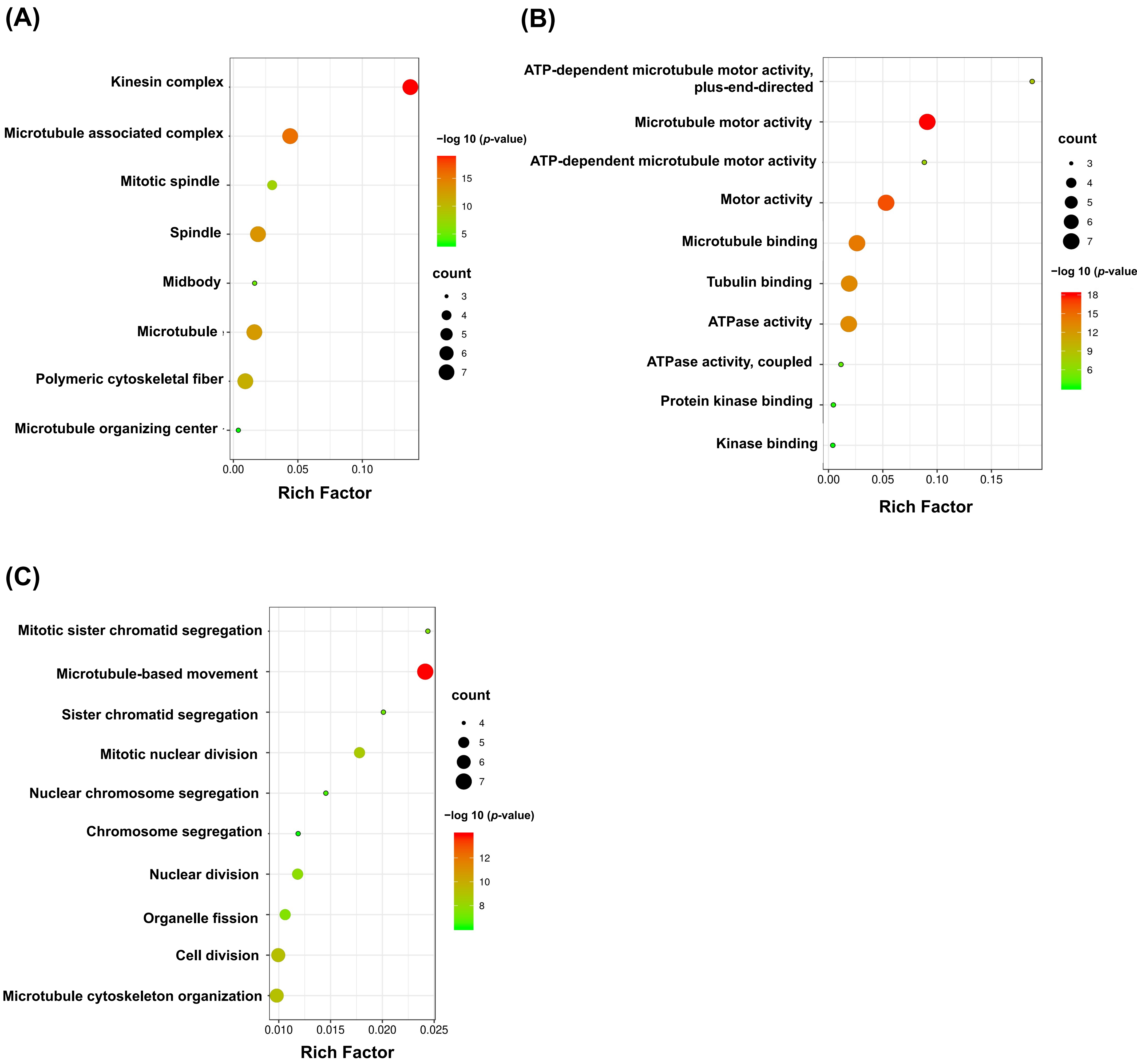
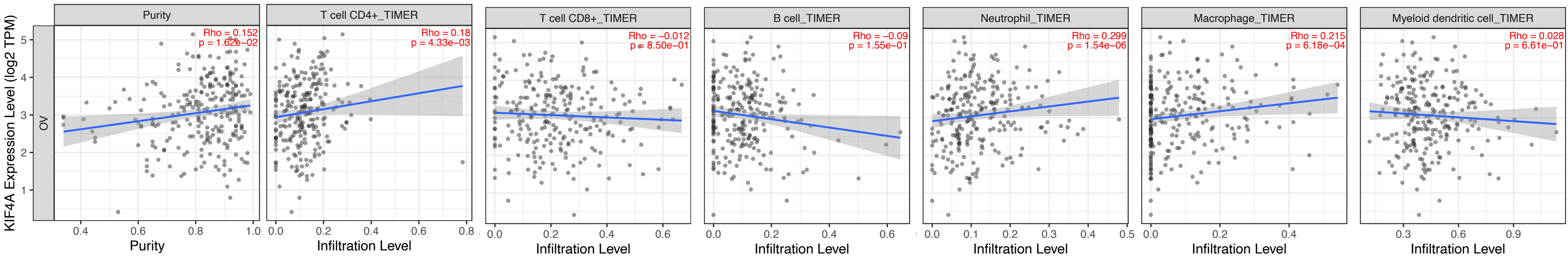


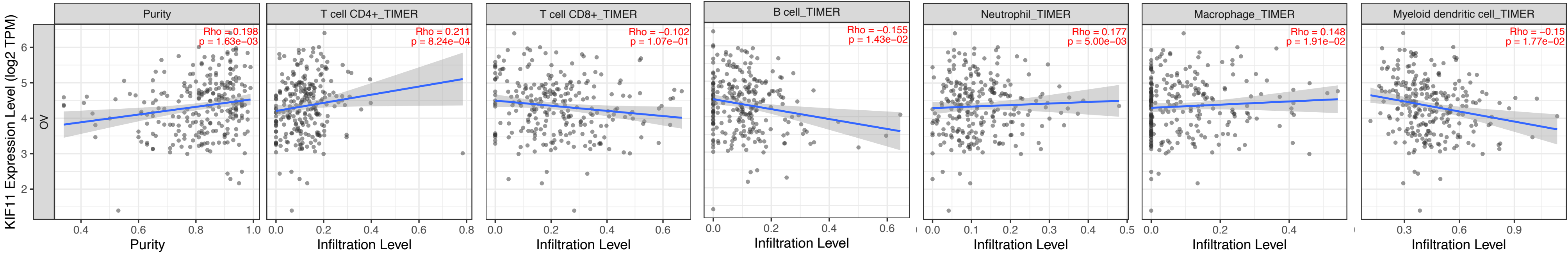
Figure S3. Top 10 GO functional enrichment analysis of overexpressed mitotic KIFs. (A) Cellular components; (B) Molecular function; (C) Biological pathways. Rich factor is the ratio of the DEGs number to the total gene numbers in a certain pathway. The color and size of the dots represent the range of *p*-value (hypergeometric test and Benjamini–Hochberg methods) and the number of DEGs mapped to the indicated results.

Figure S4

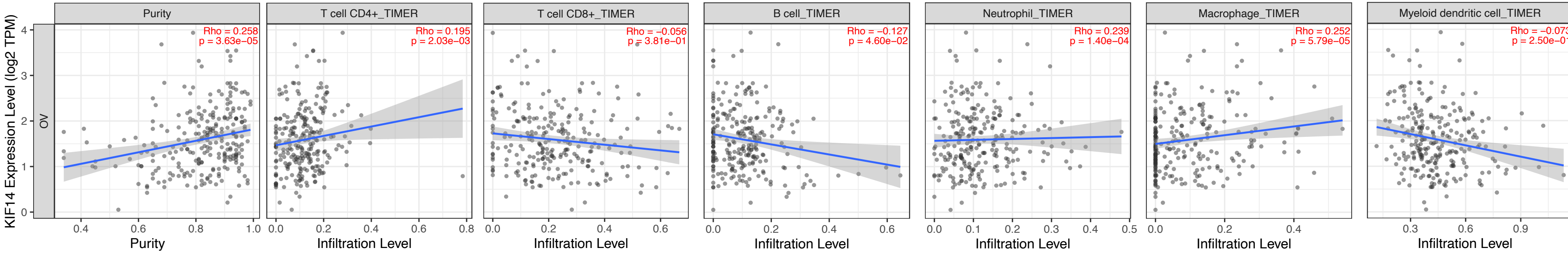
KIF4A



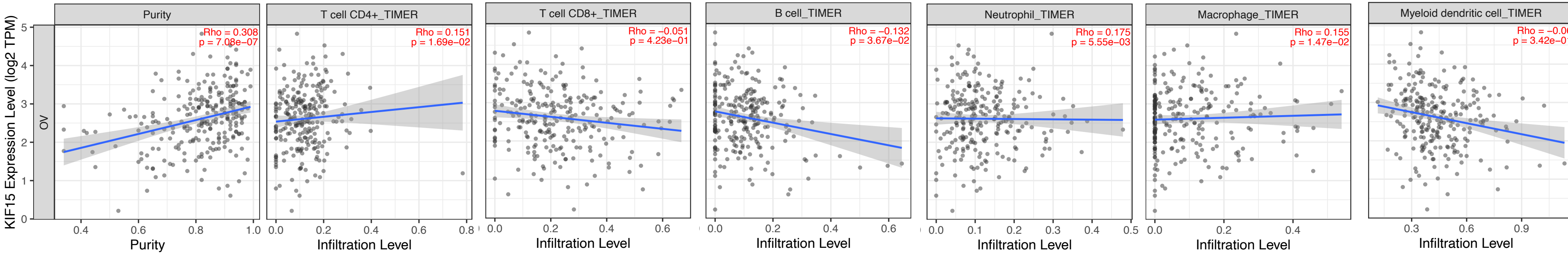
KIF11



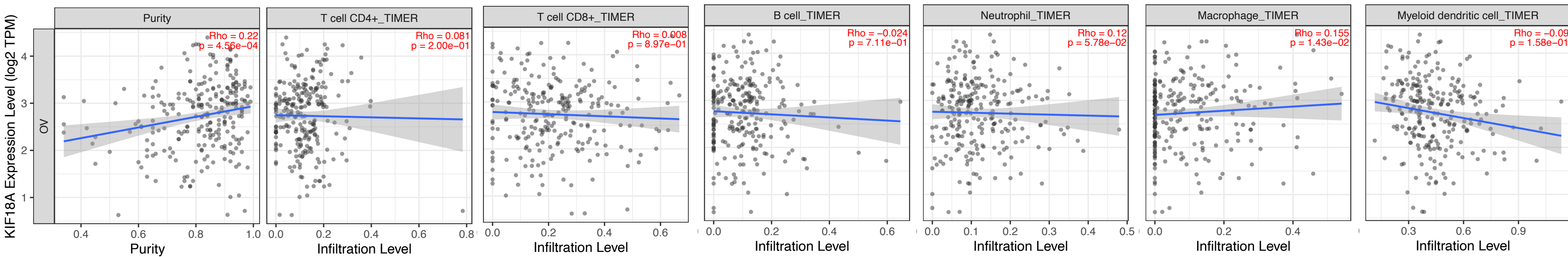
KIF14



KIF15



KIF18A



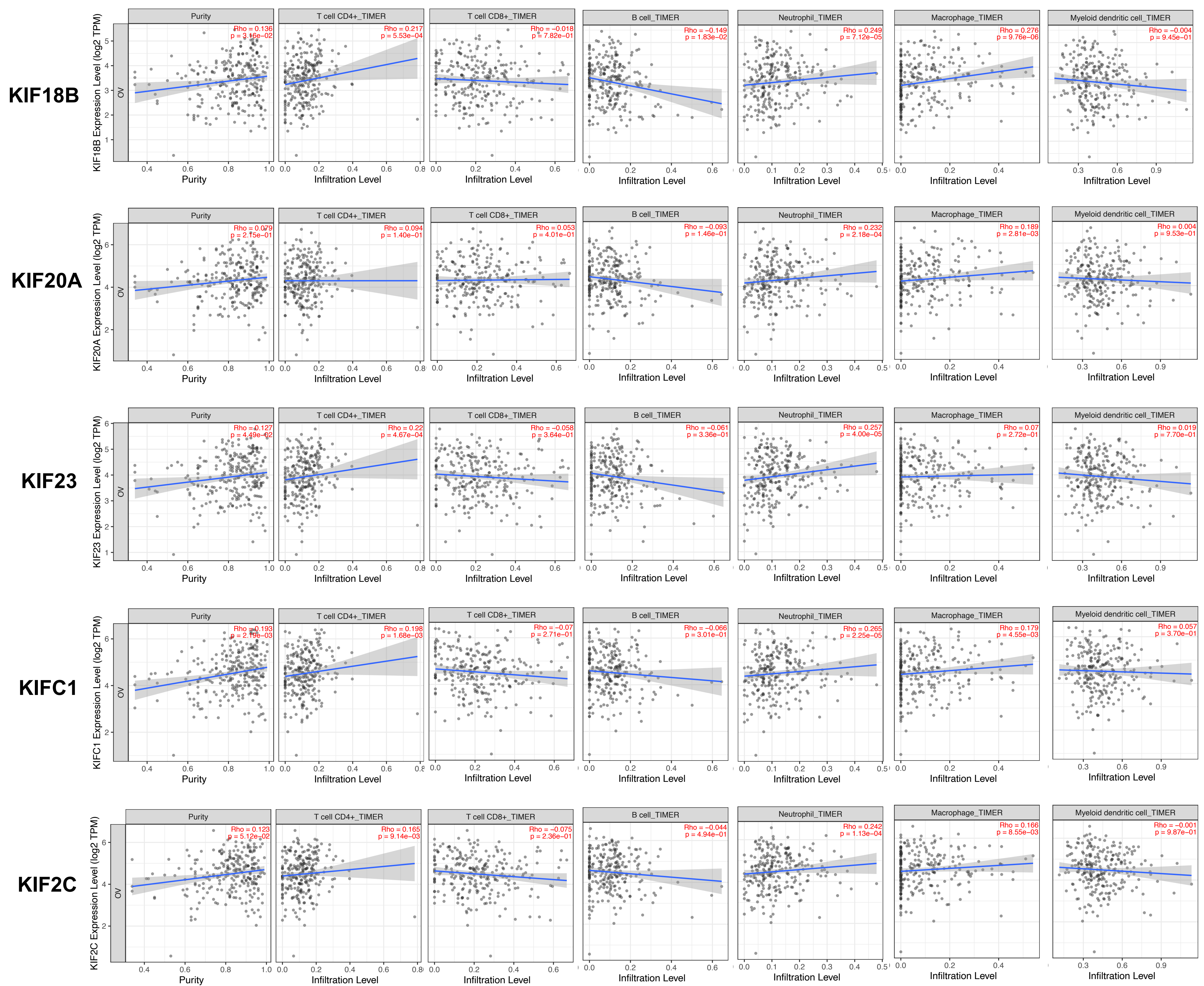


Figure S4. Correlation analysis between the overexpressed mitotic KIFs and common immune cells in OC using TIMER2.0 database.

Figure S5

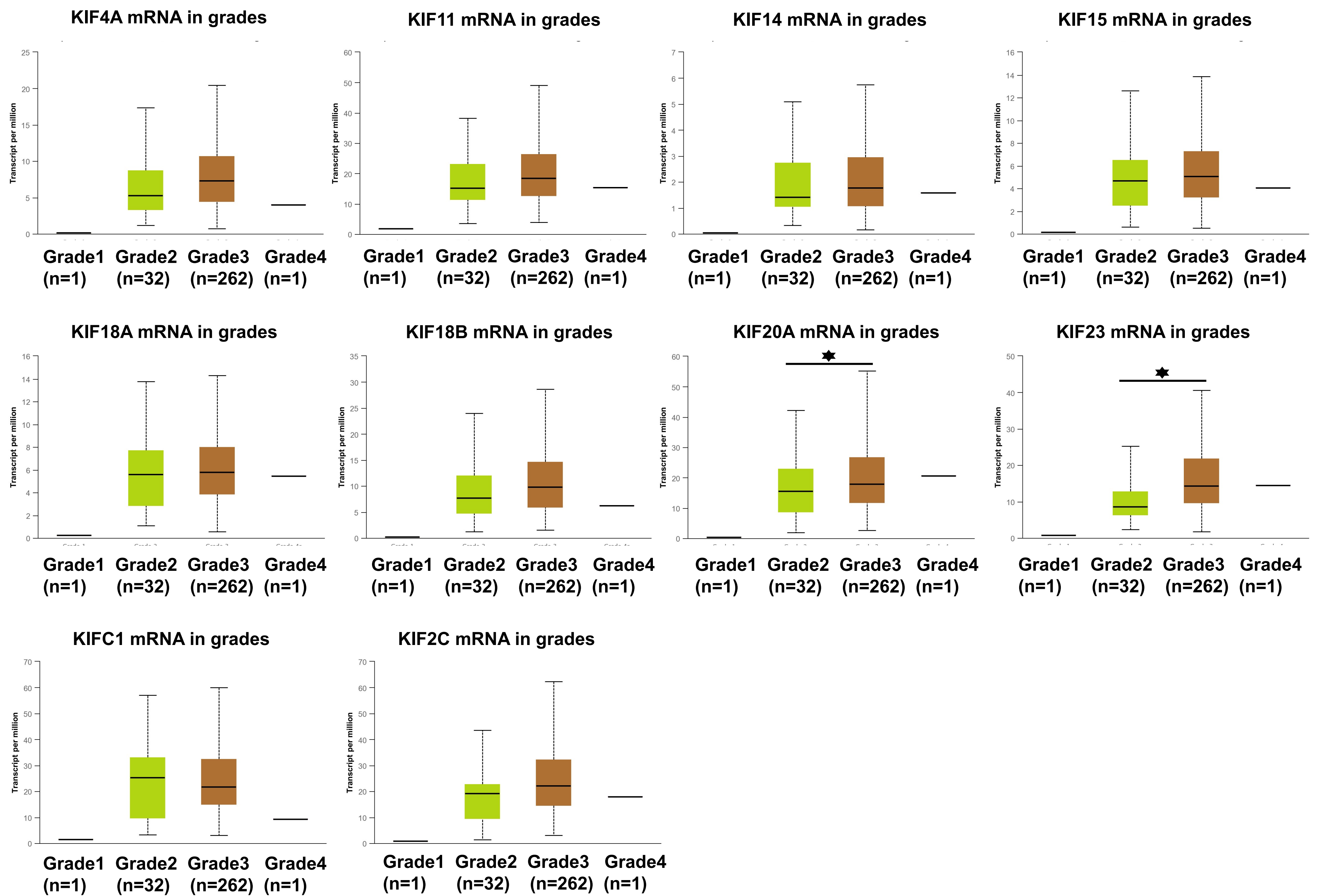
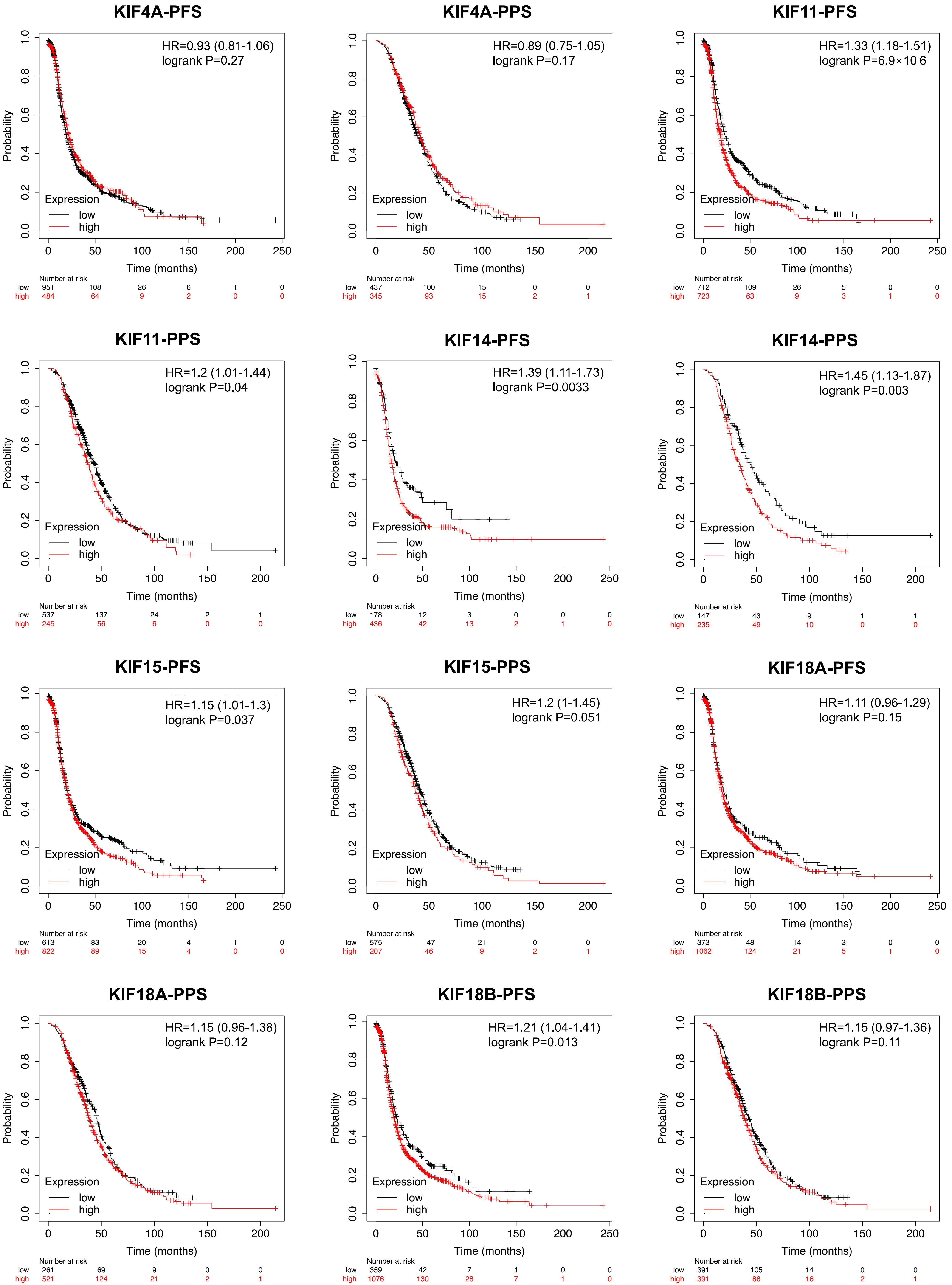


Figure S5. Transcription profiles of ten overexpressed mitotic KIFs in OC clinicopathological subgroup analysis (UALCAN). Sample numbers of each grade: grade 1 (n=1); grade 2 (n=32); grade 3 (n=262); grade 4 (n=1). * $p < 0.05$.

Figure S6



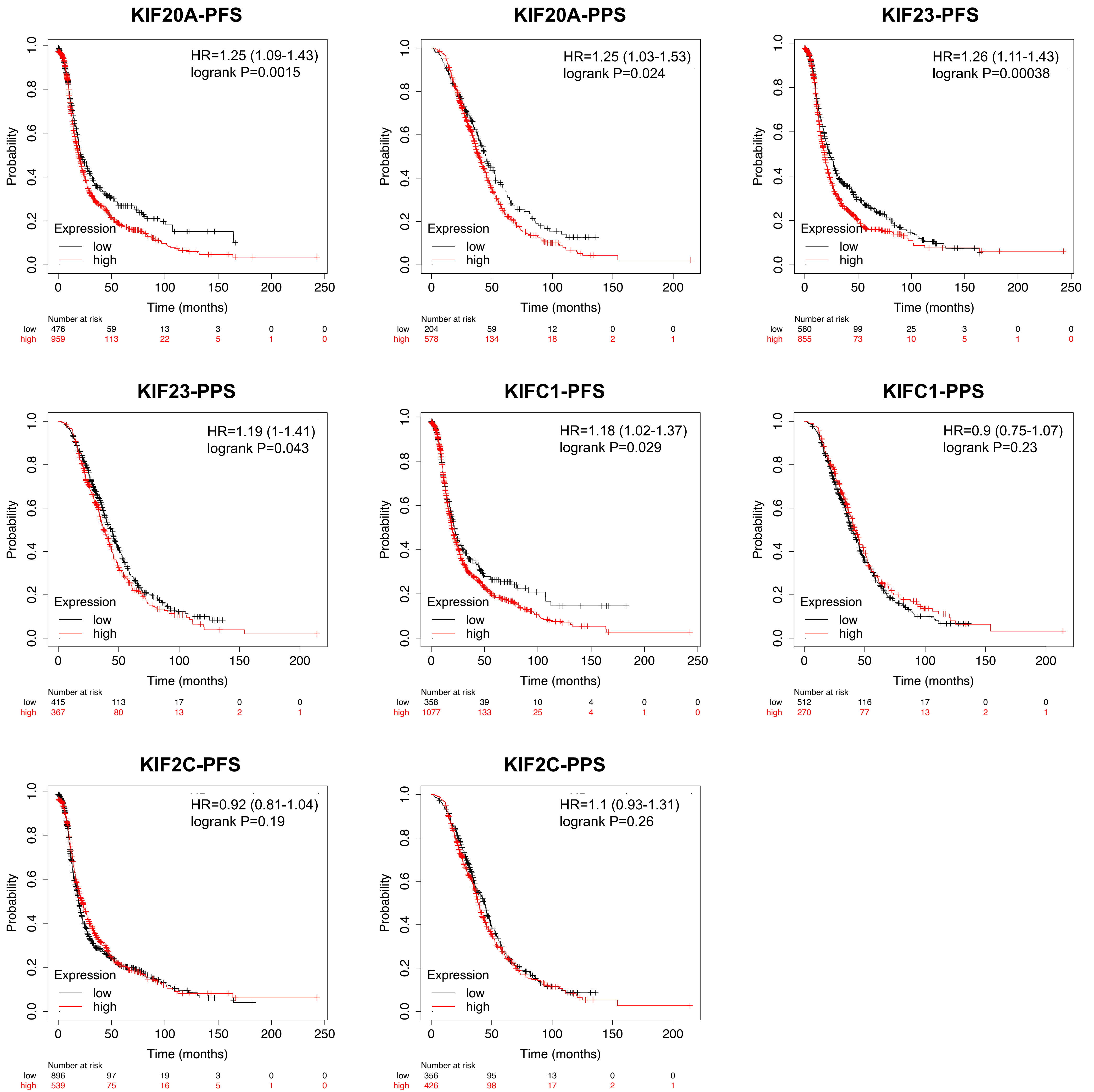


Figure S6.
 Survival analysis of mitotic KIFs regarding PFS (post-free survival) and PPS (post-progression survival) using TCGA-OV dataset. Red, high-expression group; Black, low-expression group. *p*-value is log-ranked. Auto-selected best cutoff was used