Figure S1. Acute Myelogenous Leukemia: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S2. Acute Myelogenous Leukemia: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed \(-\log(P)\) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of \(-\log(P)\) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S3. Bladder: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S4. Bladder: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log($P$) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -log($P$) for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S5. Breast: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, $PCNA$ metagene) resulted in significant gene-specific KM logrank tests.
Figure S6. Breast: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, $PCNA$ metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S7. Cervical: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S8. Cervical: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S9. Colorectal: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S10. Colorectal: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -\log(P) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -\log(P) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S11. Glioblastoma Multiforme: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S12. Glioblastoma Multiforme: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S13. Head and Neck: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S14. Head and Neck: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log($P$) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -log($P$) for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S15. Low Grade Gliomas: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S16. Low Grade Gliomas: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S17. Liver: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S18. Liver: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log($P$) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -log($P$) for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S19. Lung Sq. Cell: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, $PCNA$ metagene) resulted in significant gene-specific KM logrank tests.
Figure S20. Lung Sq. Cell: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S21. Lung: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S22. Lung: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S23. Melanoma: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S24. Melanoma: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(\( P \)) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -log(\( P \)) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S25. Ovarian: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S26. Ovarian: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed \(-\log(P)\) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of \(-\log(P)\) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S27. Renal Clear Cell: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S28. Renal Clear Cell: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed \(-\log(P)\) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of \(-\log(P)\) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S29. Renal Papillary: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S30. Renal Papillary: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed $-\log(P)$ for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of $-\log(P)$ for KM analysis of the best binarized PC using $p$ randomly selected genes $B = 1000$ times.
Figure S31. Sarcoma: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, \( PCNA \) metagene) resulted in significant gene-specific KM logrank tests.
Figure S32. Sarcoma: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, PCNA metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed \(-\log(P)\) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of \(-\log(P)\) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S33. Stomach: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S34. Stomach: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed \(-\log(P)\) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of \(-\log(P)\) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.
Figure S35. Uterine: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for $p$ genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KM logrank tests.
Figure S36. Uterine: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for \( p \) genes whose adjusted expression (via age, stage, PCNA metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed -\( \log(P) \) for the best binarized PC based on maximum likelihood analysis using KM analysis. Kernel density curves reflect the distribution of -\( \log(P) \) for KM analysis of the best binarized PC using \( p \) randomly selected genes \( B = 1000 \) times.