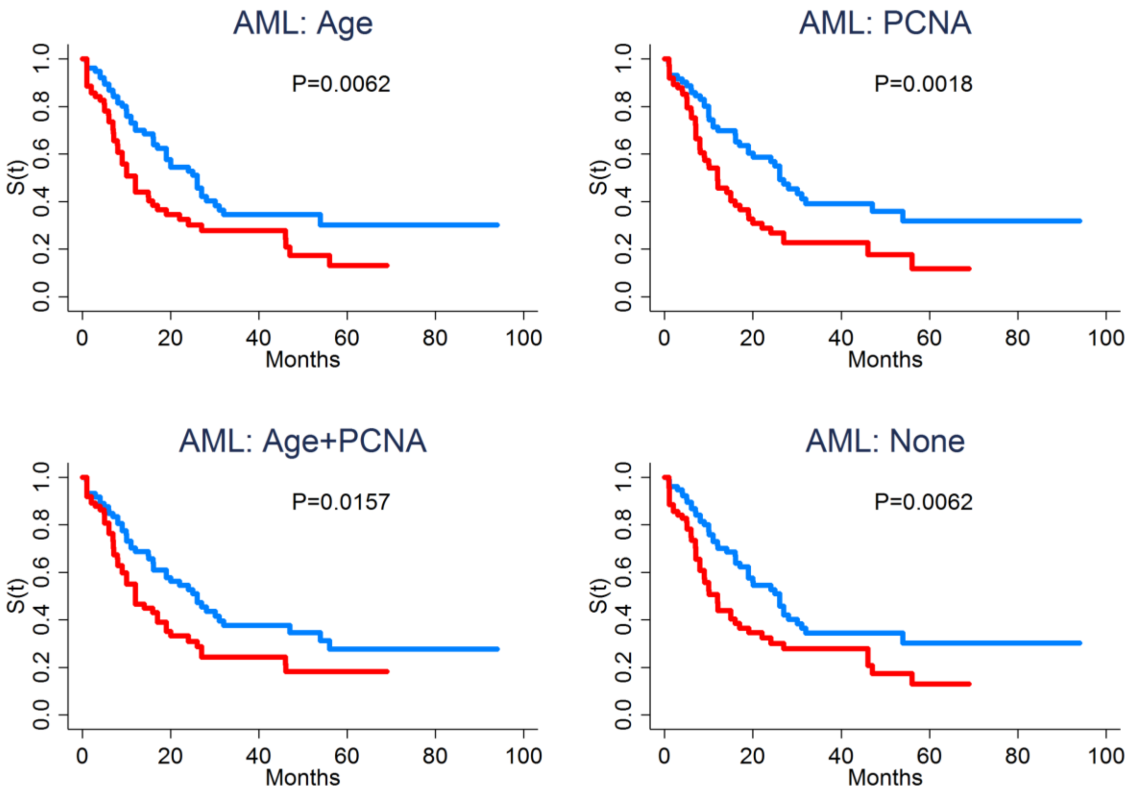


Figure S1. Acute Myelogenous Leukemia: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for *p* genes whose adjusted expression (via age, *PCNA* metagene) resulted in significantgene-specific KM logrank tests.

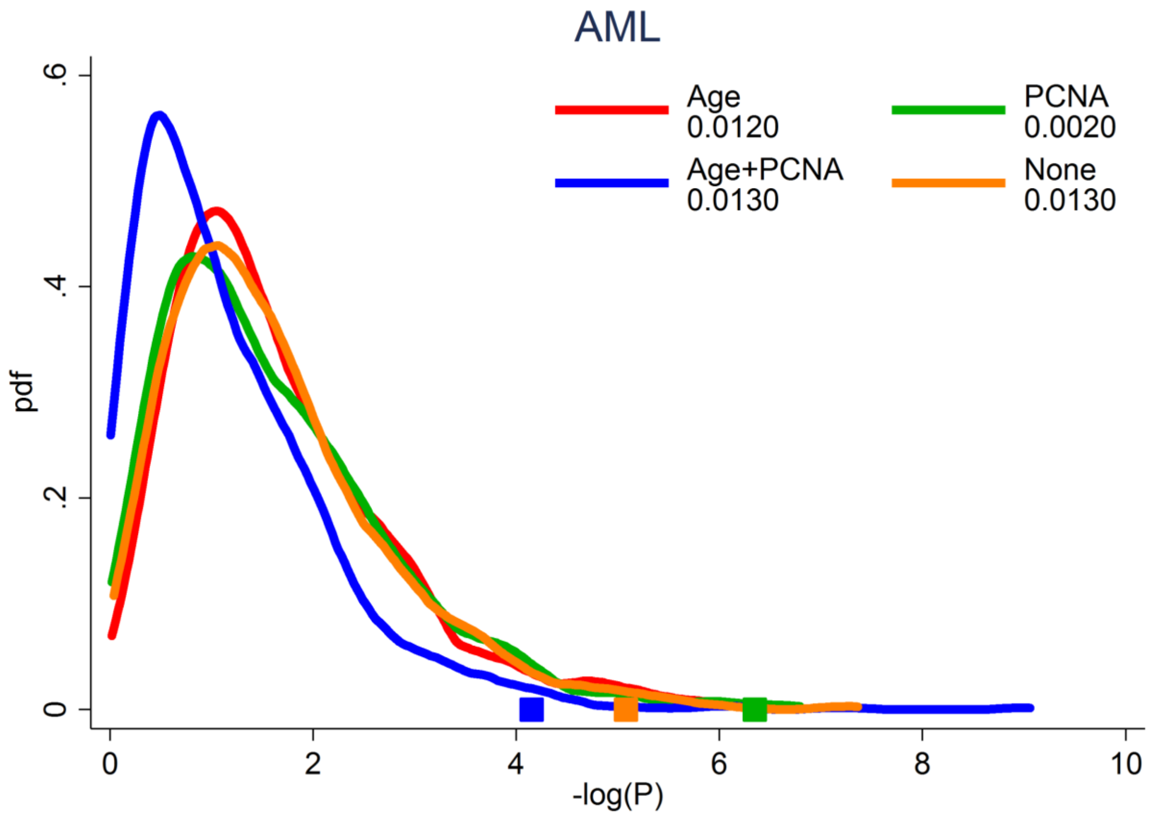


Figure S2. Acute Myelogenous Leukemia: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the 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.

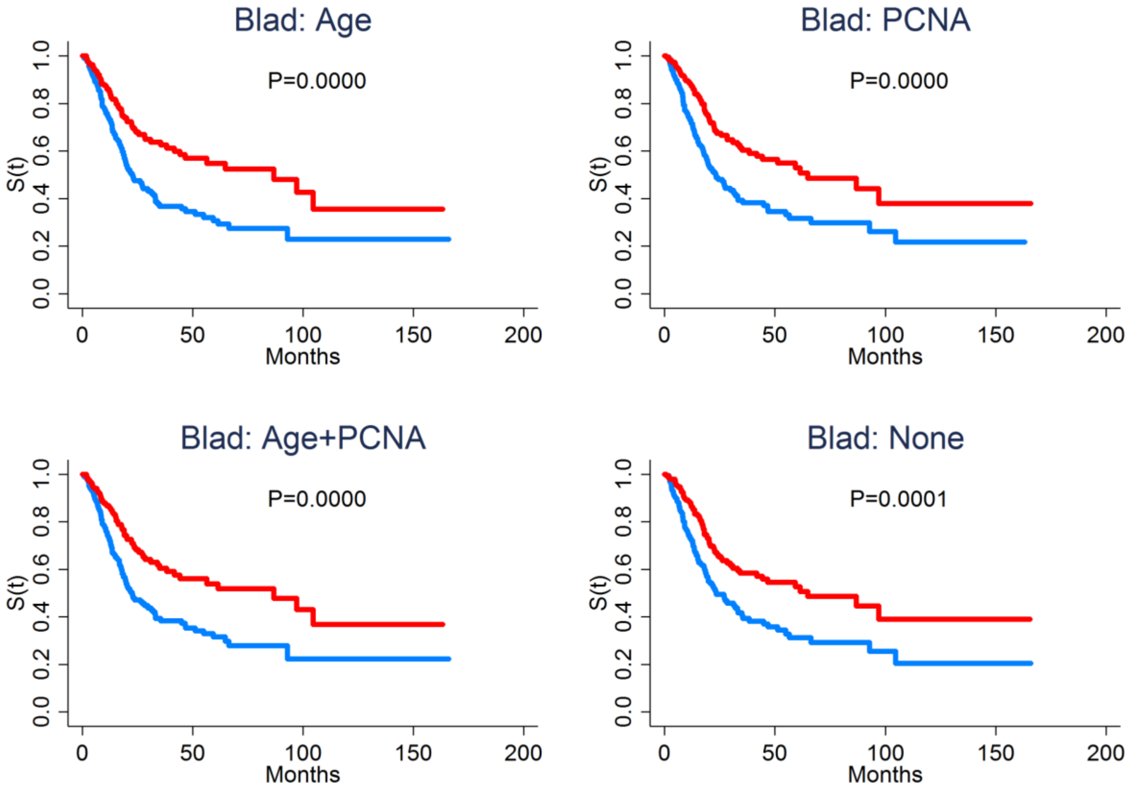


Figure S3. Bladder: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

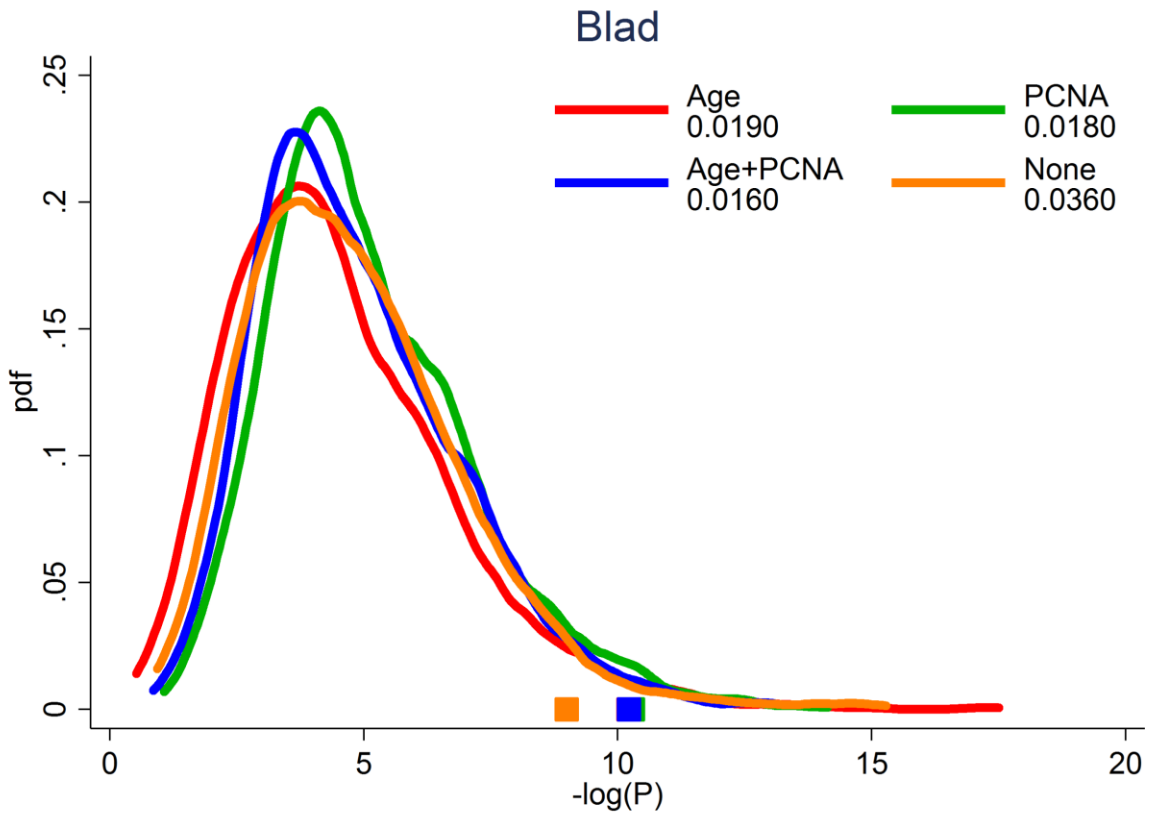


Figure S4. Bladder: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.

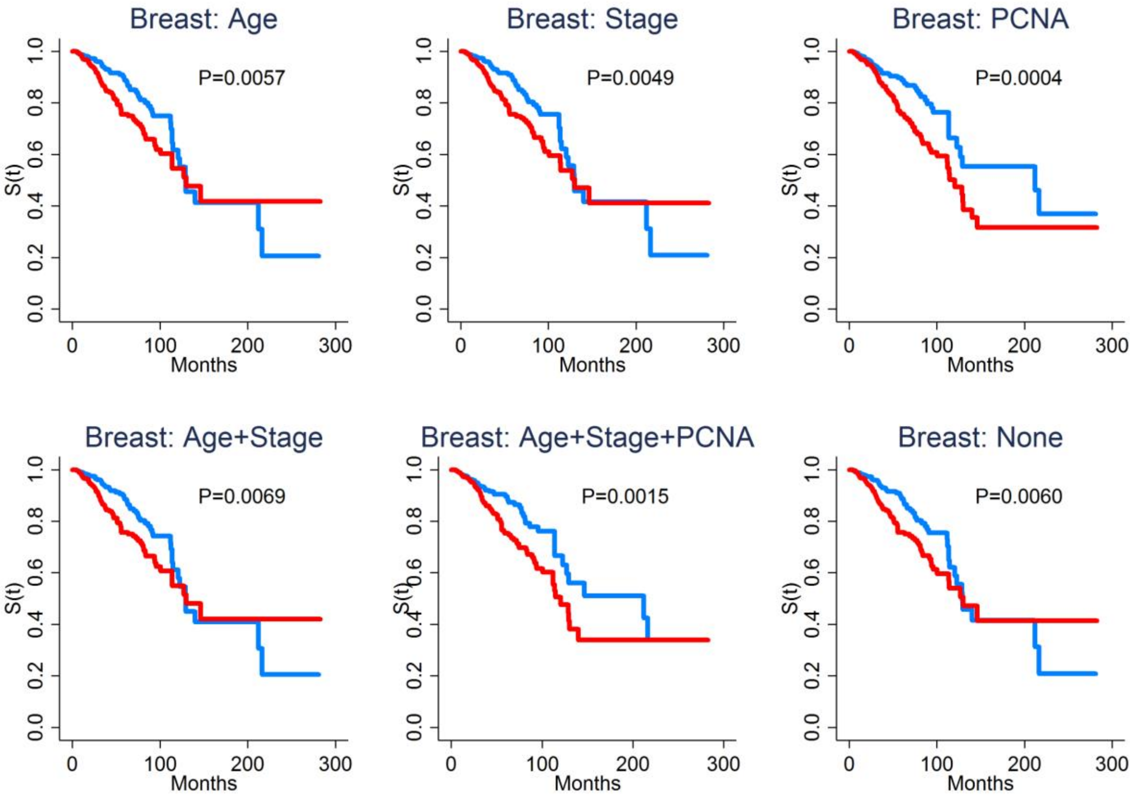


Figure S5. Breast: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

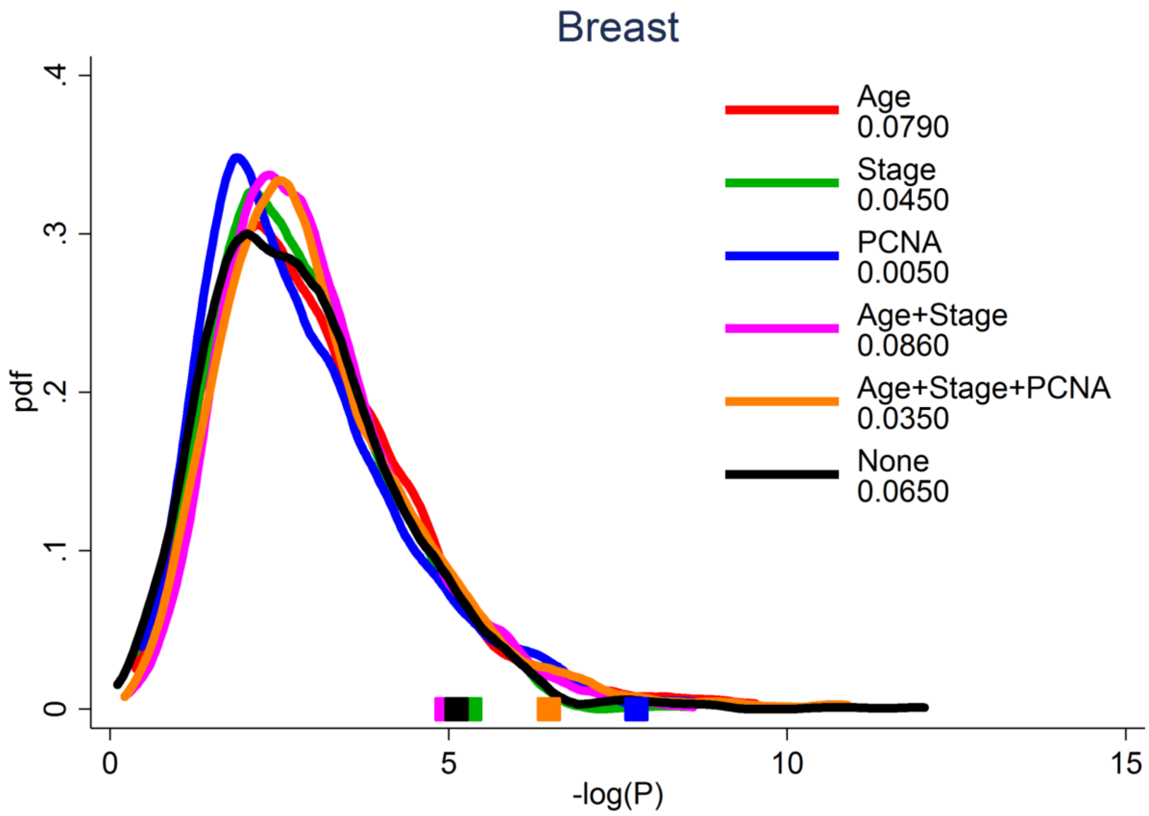


Figure S6. Breast: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.

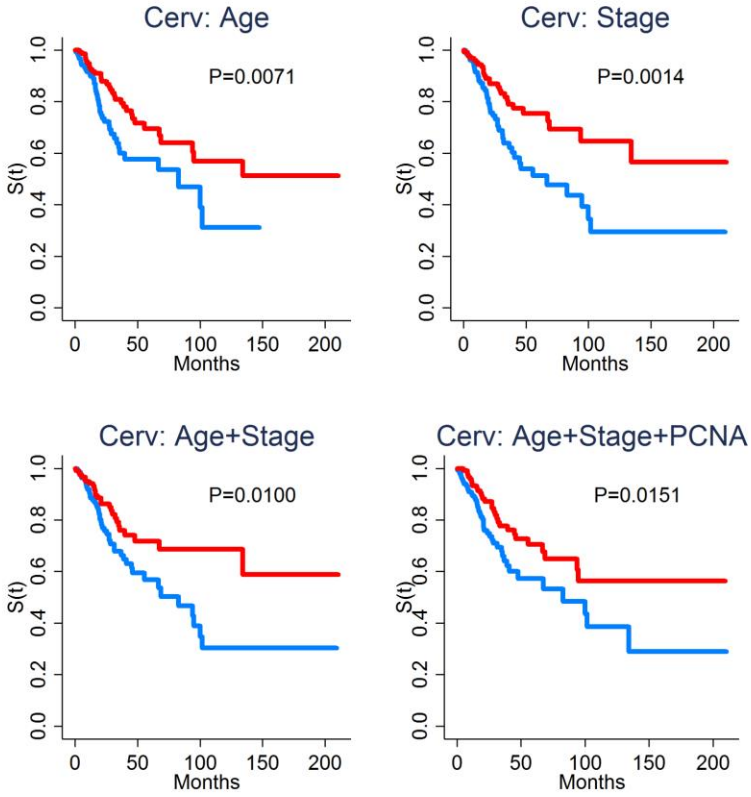


Figure S7. Cervical: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

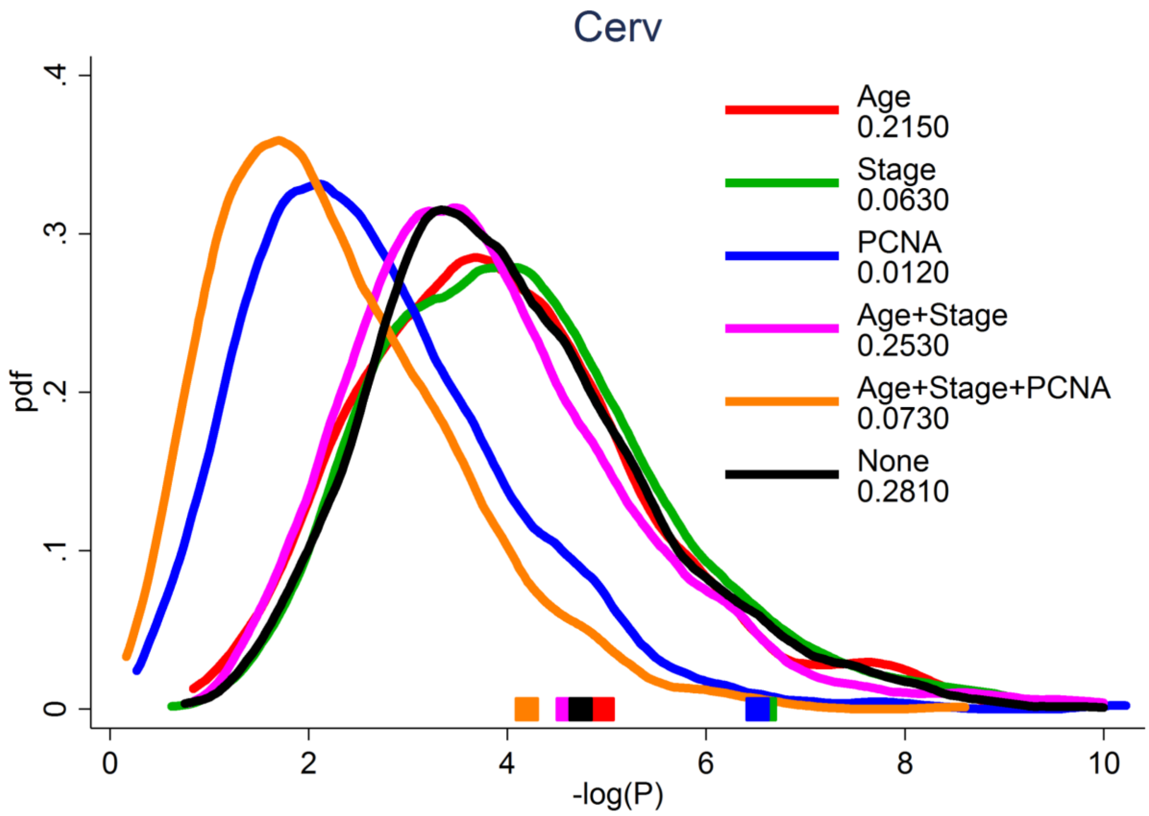


Figure S8. **Cervical: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specificKM logrank tests. Square symbols denote the observed -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.**

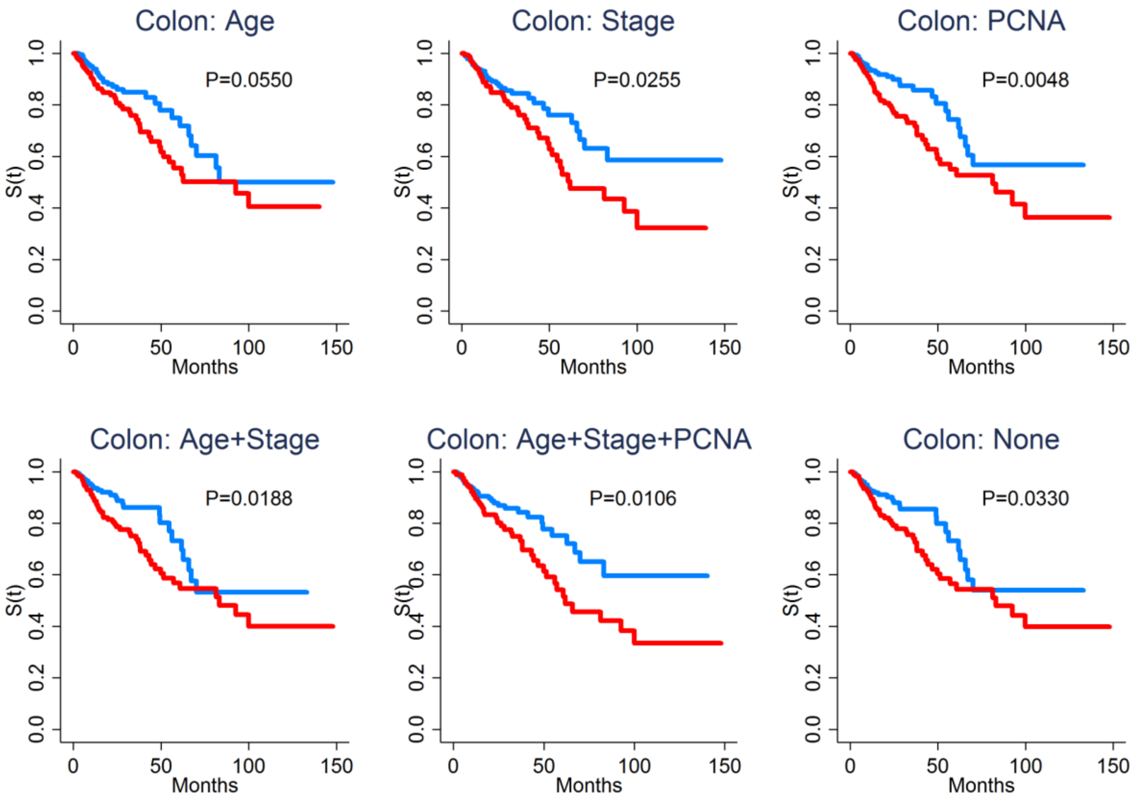


Figure S9. Colorectal: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

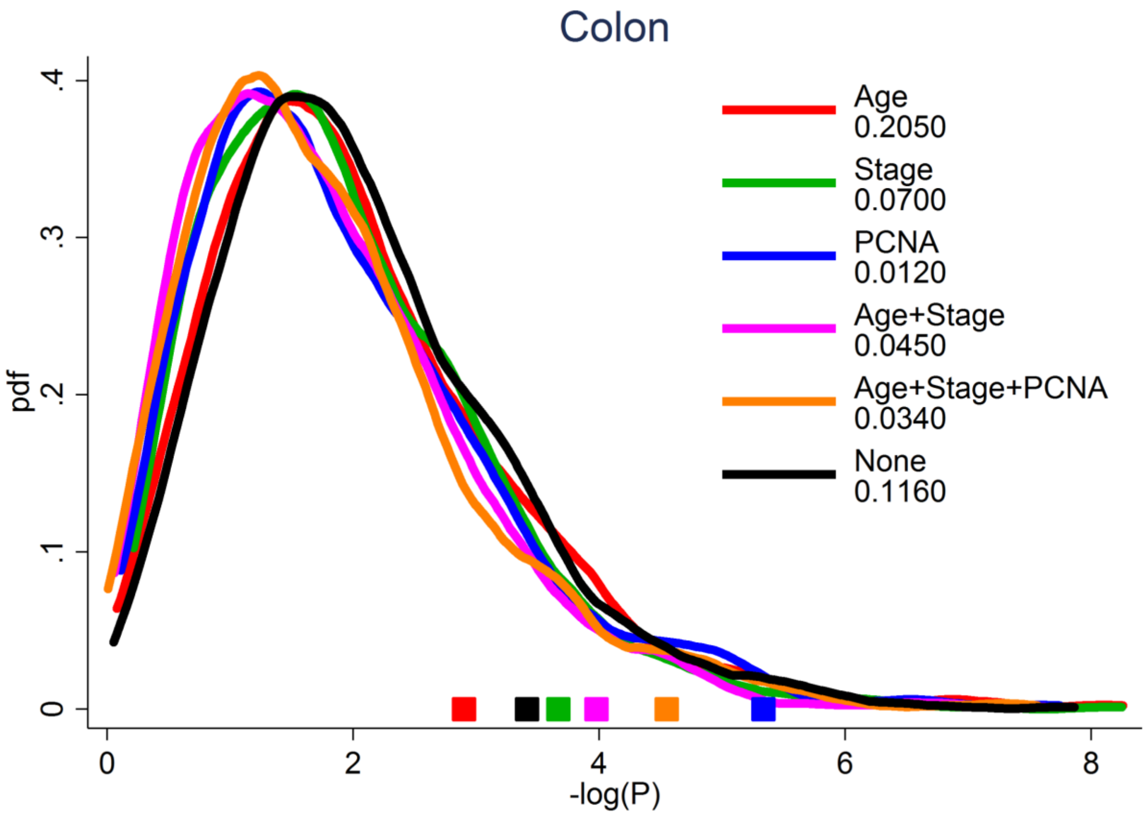


Figure S10. **Colorectal: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -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.**

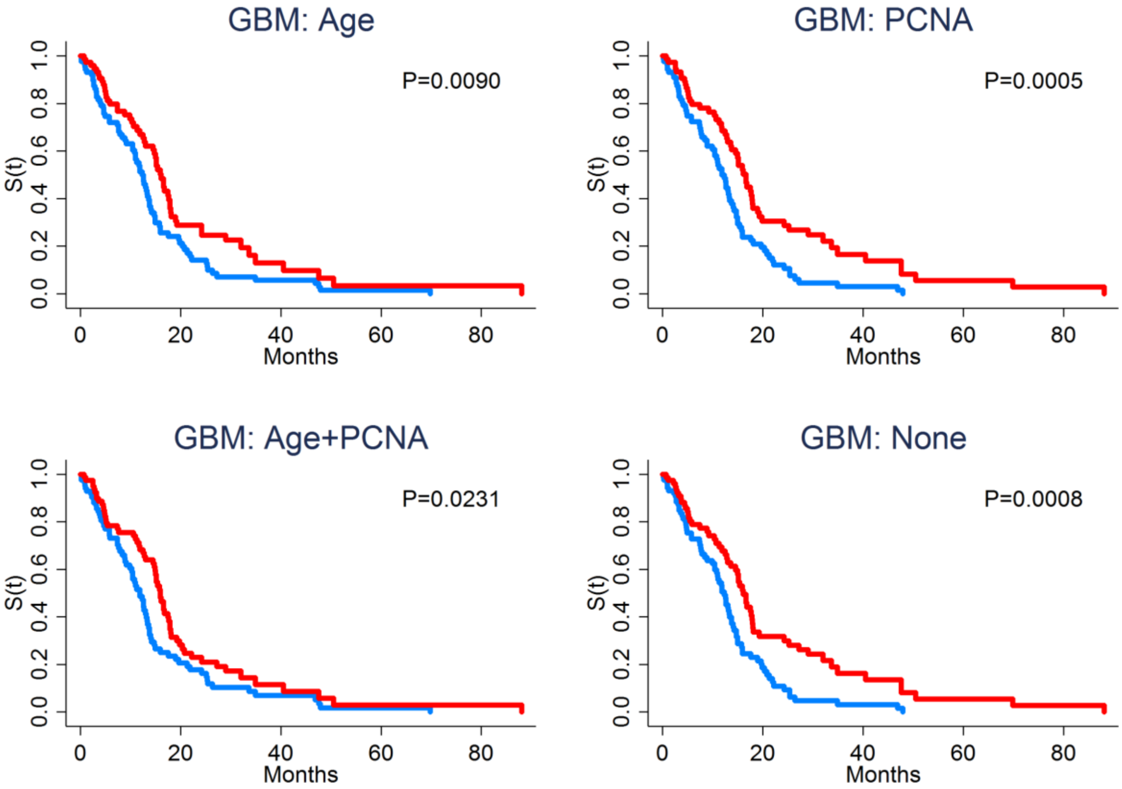


Figure S11. Glioblastoma Multiforme: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

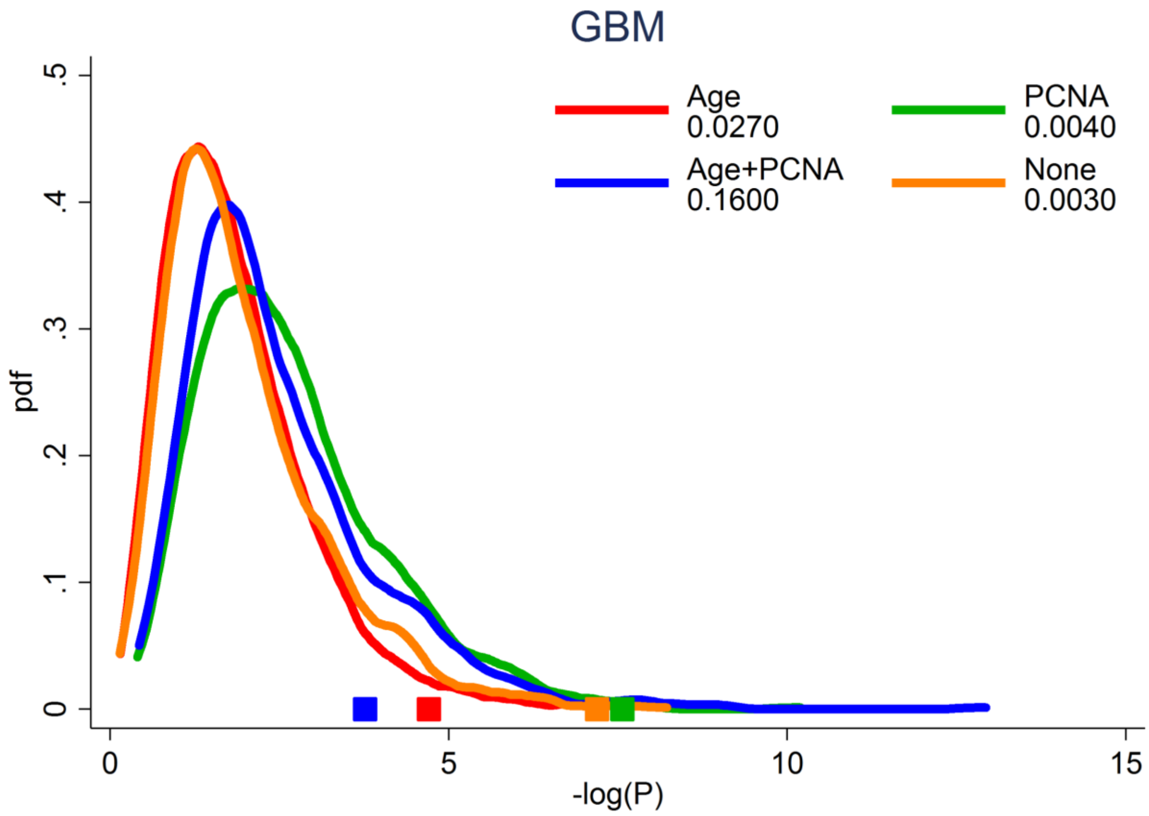


Figure S12. **Glioblastoma Multiforme: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the 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.**

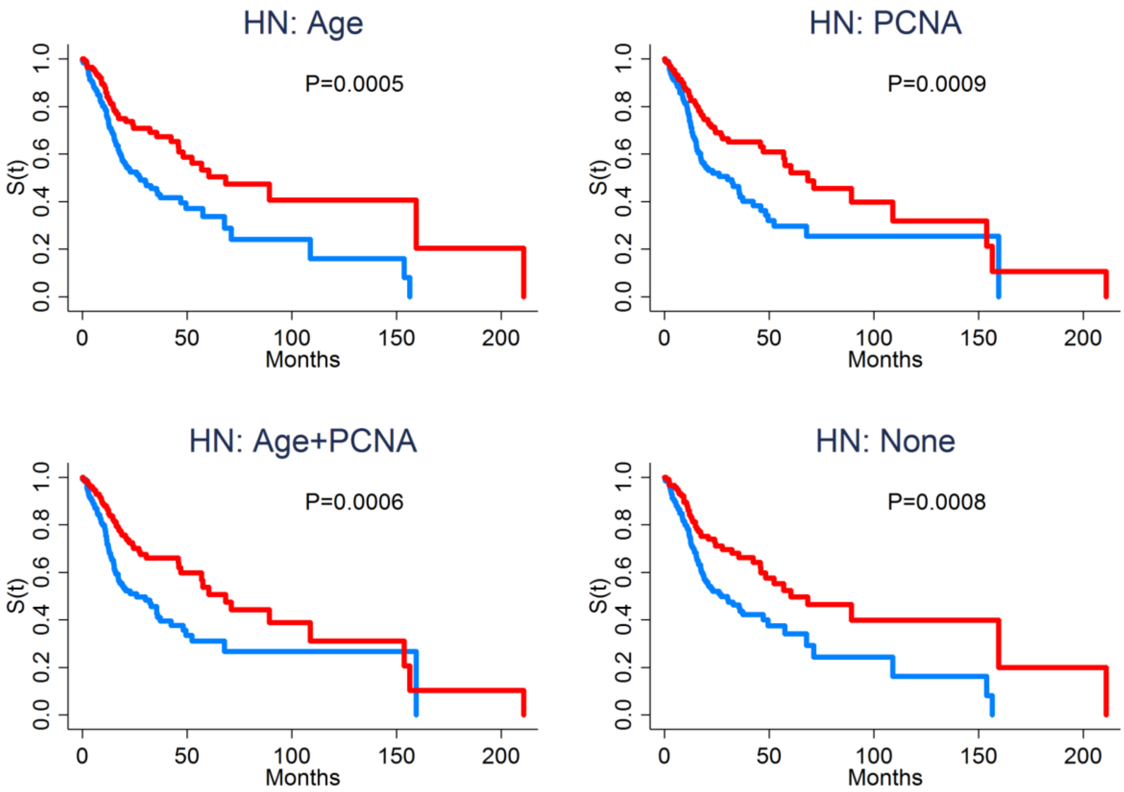


Figure S13. Head and Neck: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for *p* genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specificKM logrank tests.

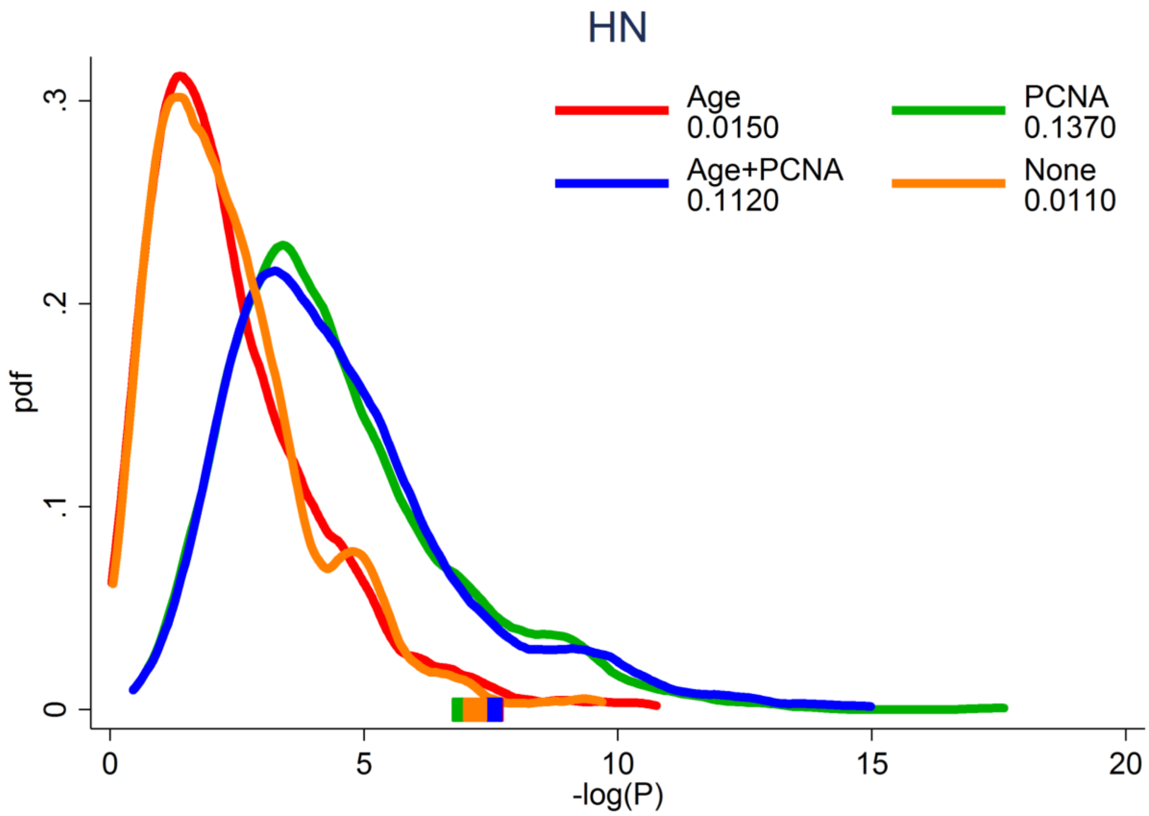


Figure S14. Head and Neck: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.

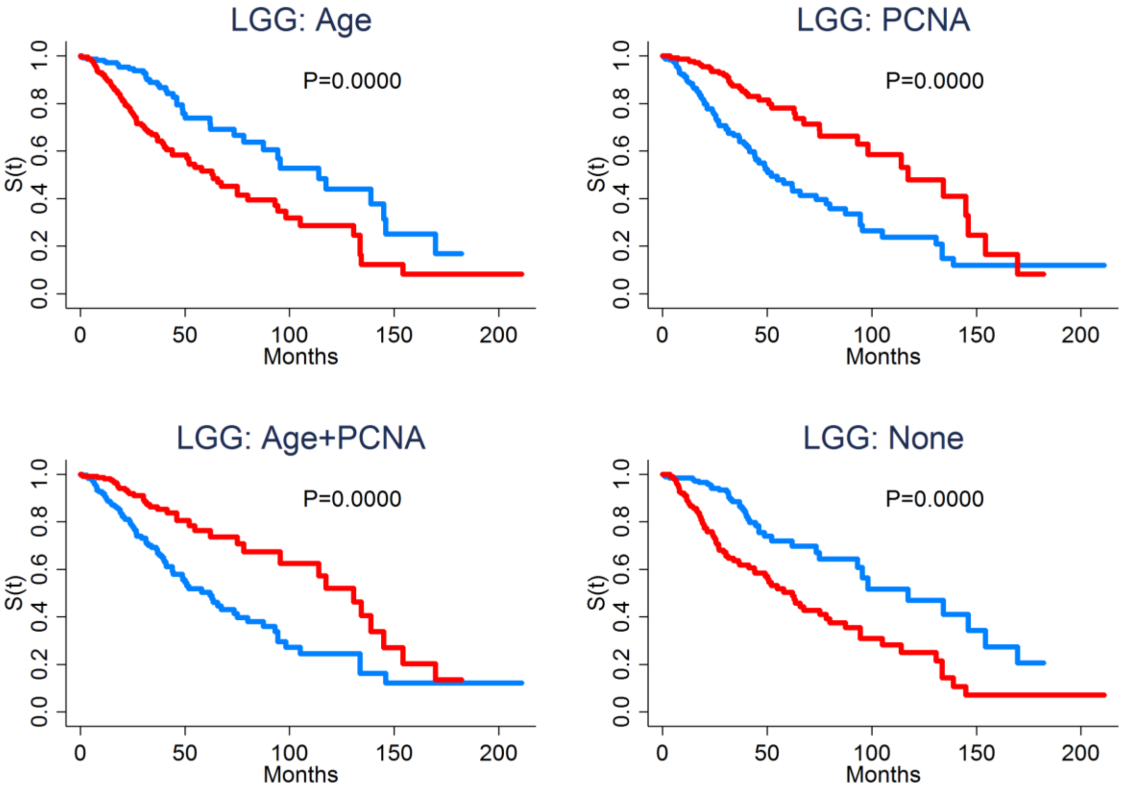


Figure S15. Low Grade Gliomas: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

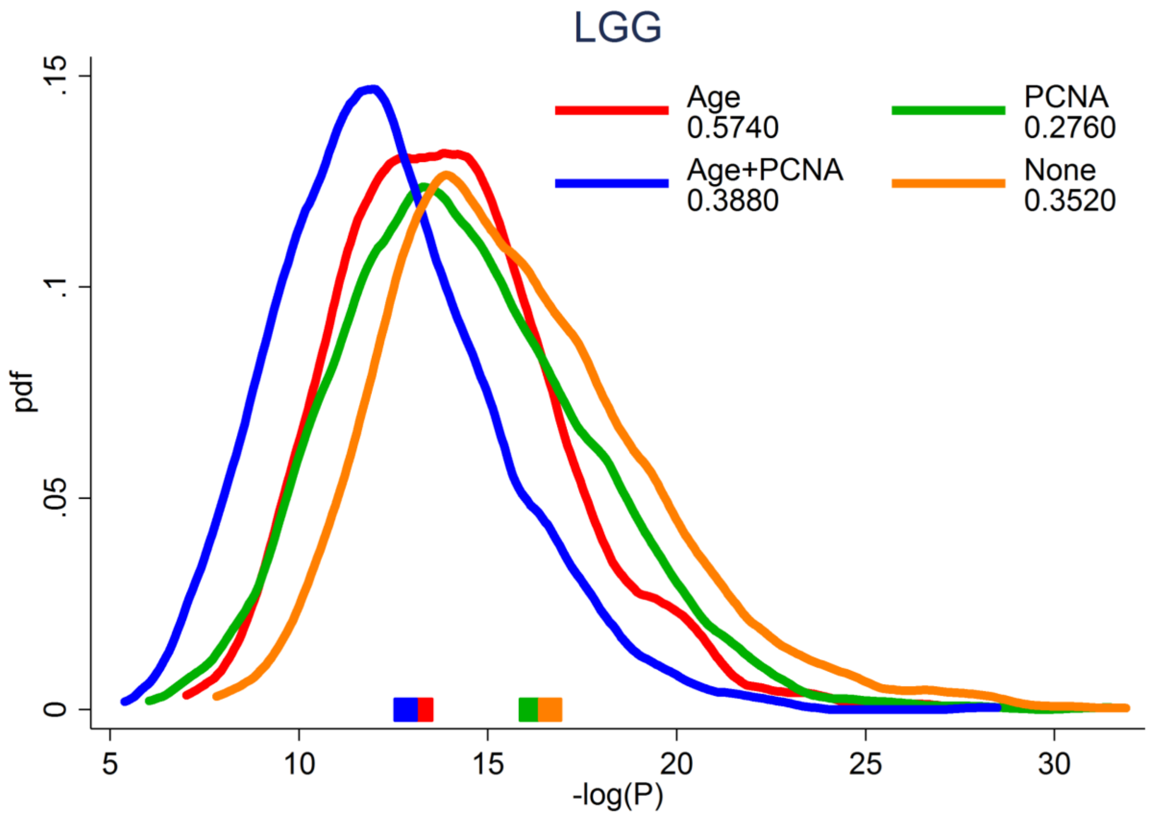


Figure S16. **Low Grade Gliomas: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specificKM logrank tests. Square symbols denote the observed -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.**

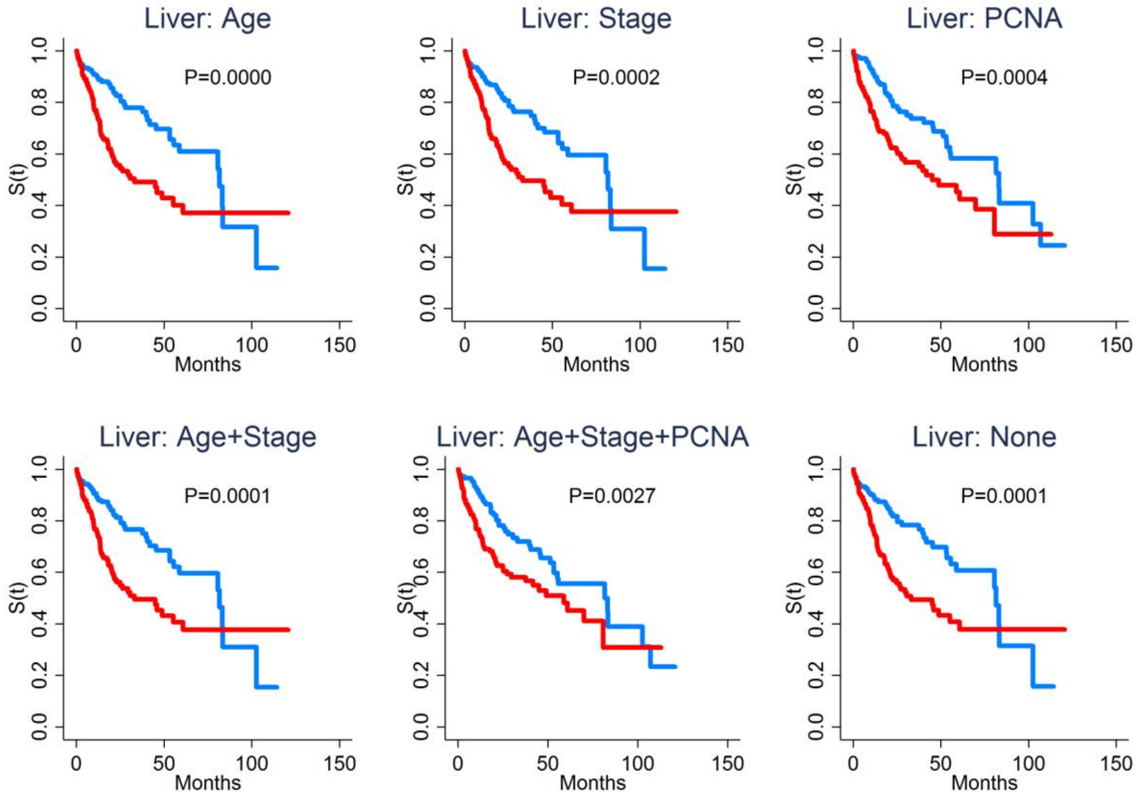


Figure S17. Liver: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

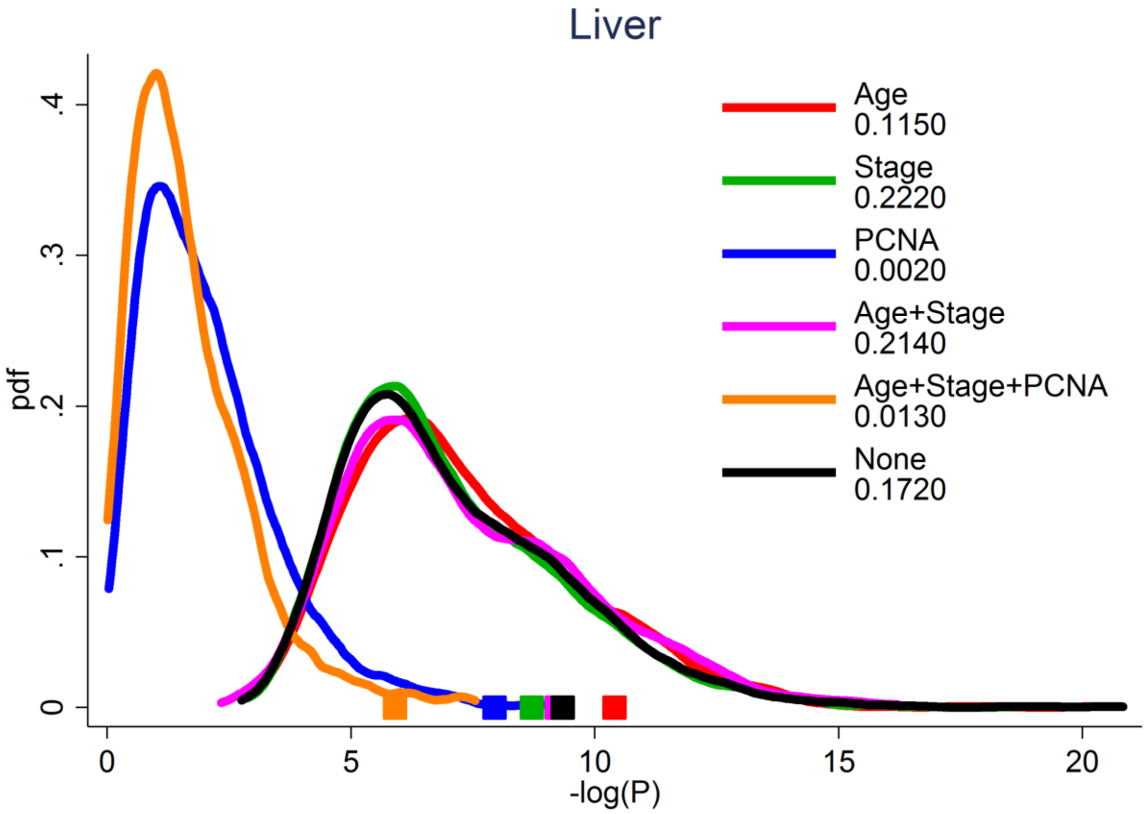


Figure S18. Liver: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.

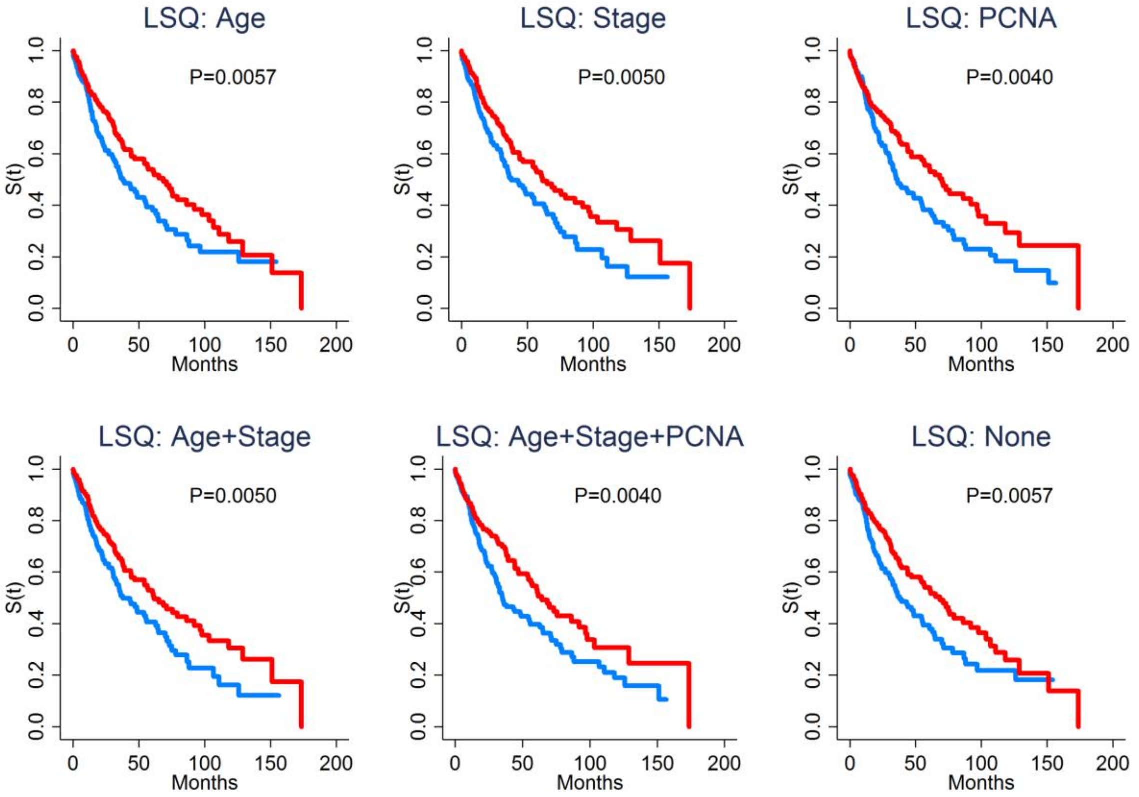


Figure S19. Lung Sq. Cell: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

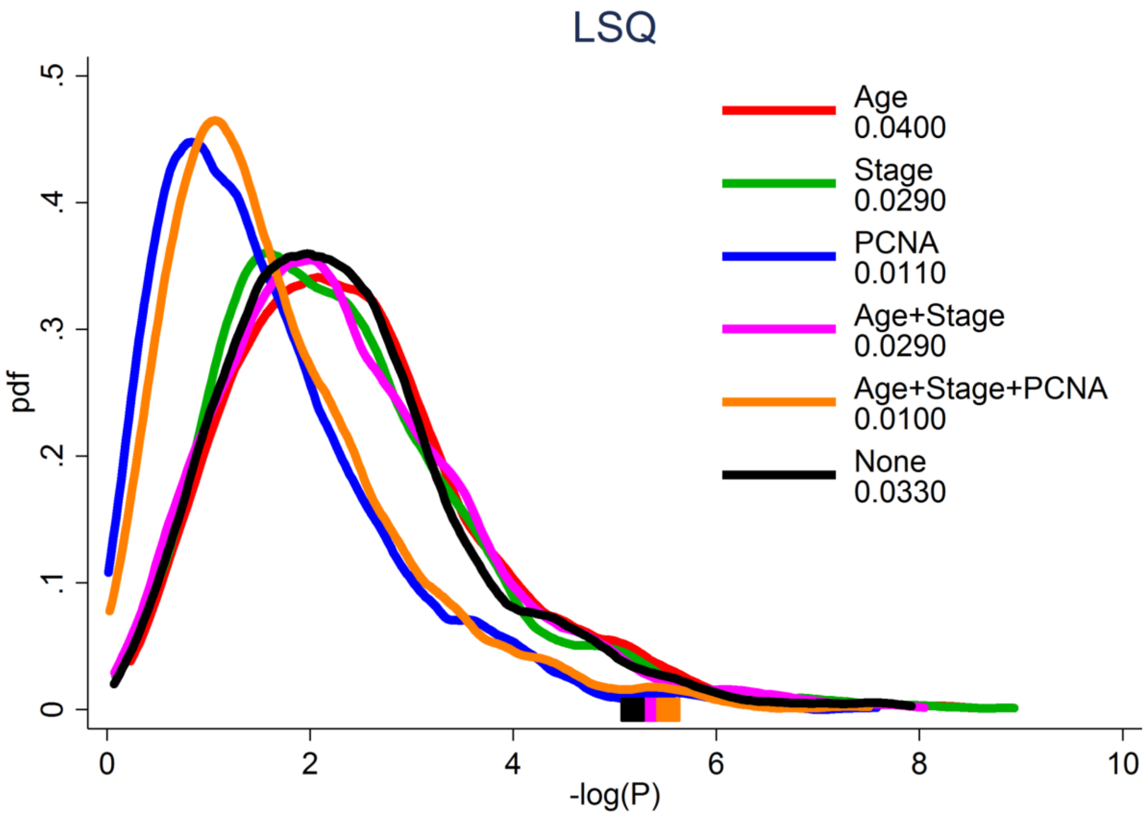
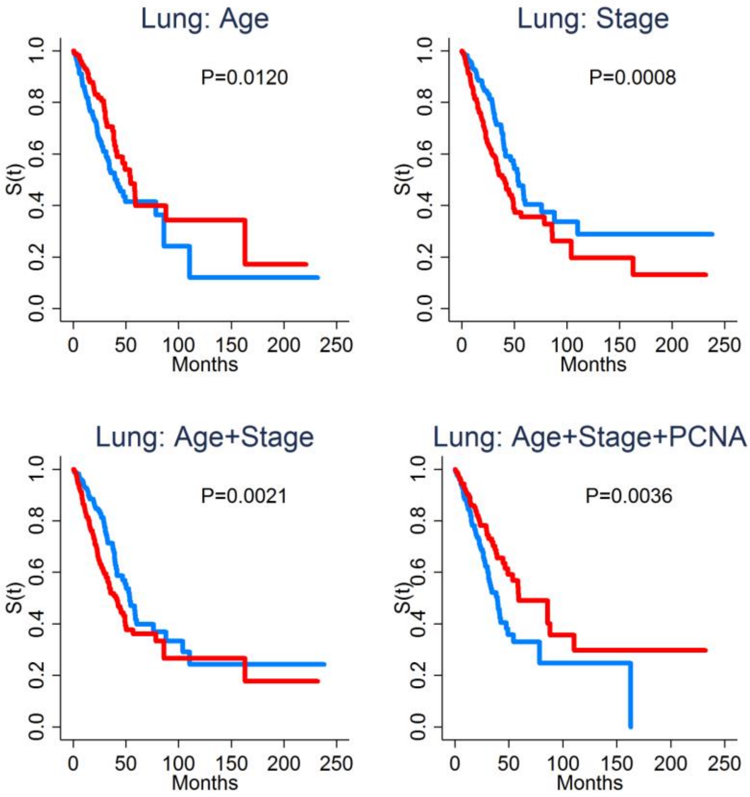


Figure S20. **Lung Sq. Cell: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -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.**



Lung: Age

Lung: Stage

Lung: PCNA

Lung: Age+Stage

Lung: Age+Stage+PCNA

Lung: None

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.

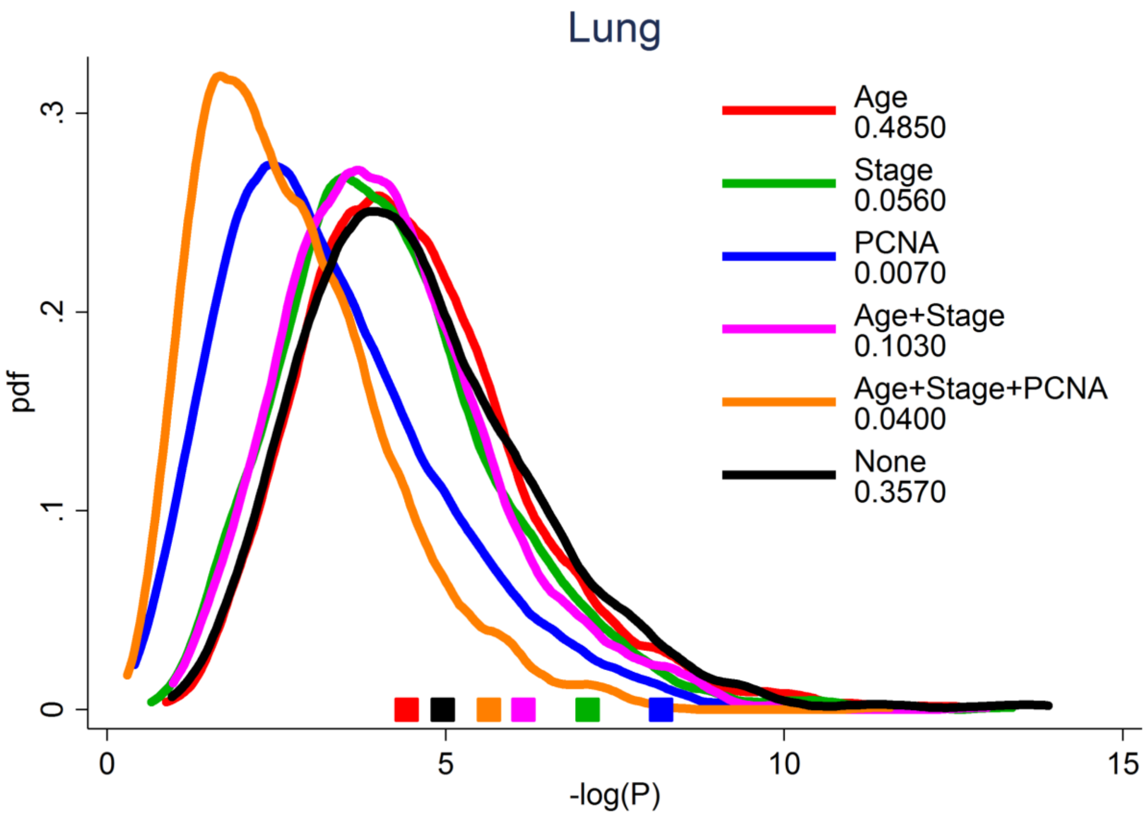


Figure S22. Lung: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.

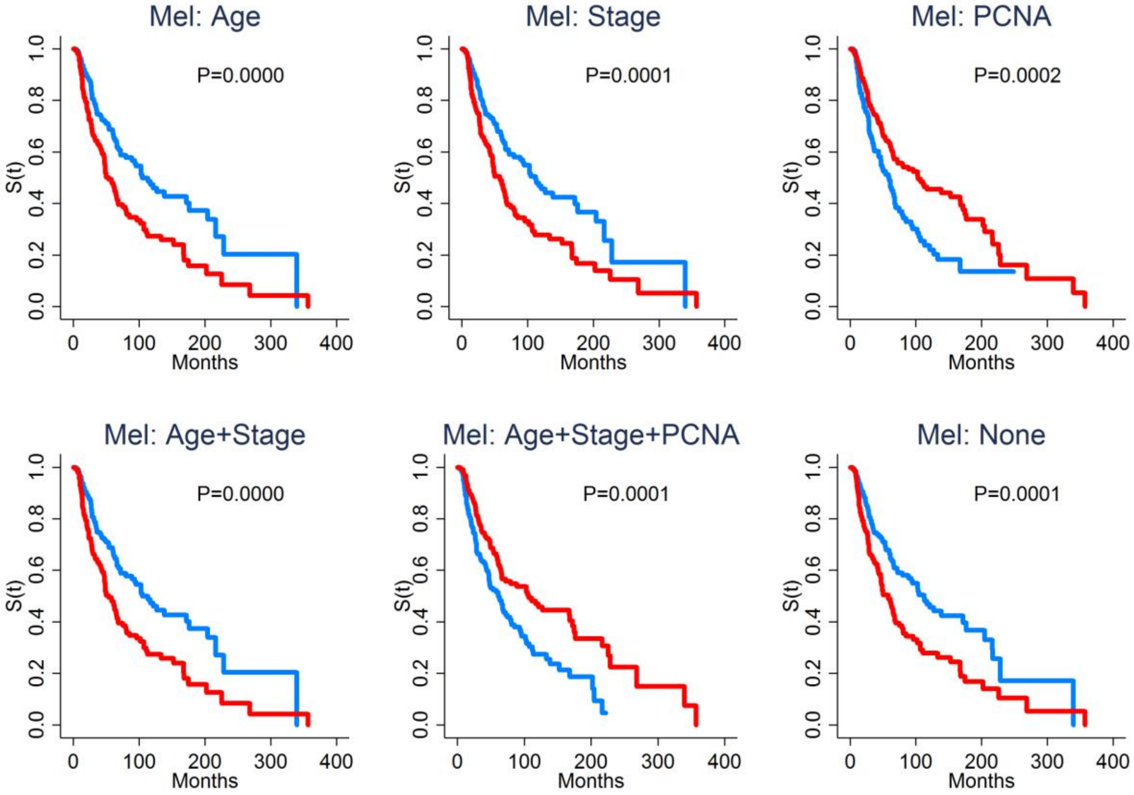


Figure S23. Melanoma: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

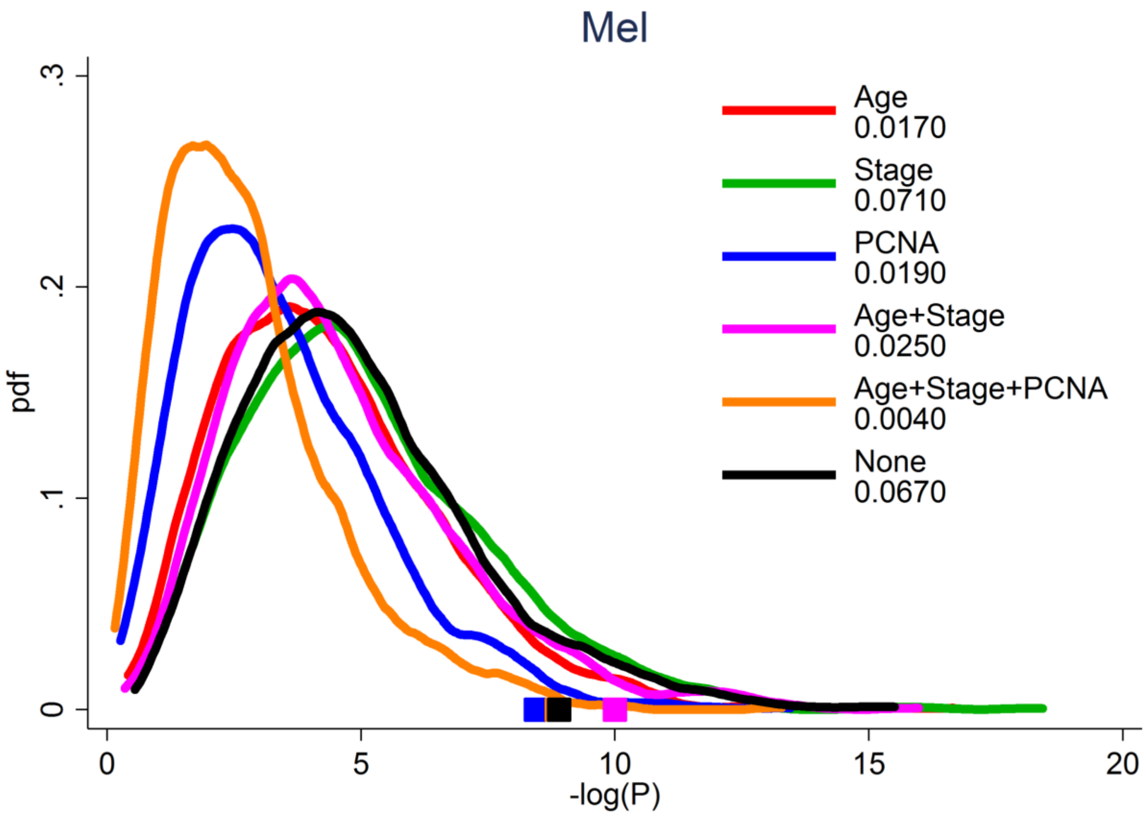


Figure S24. Melanoma: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -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.

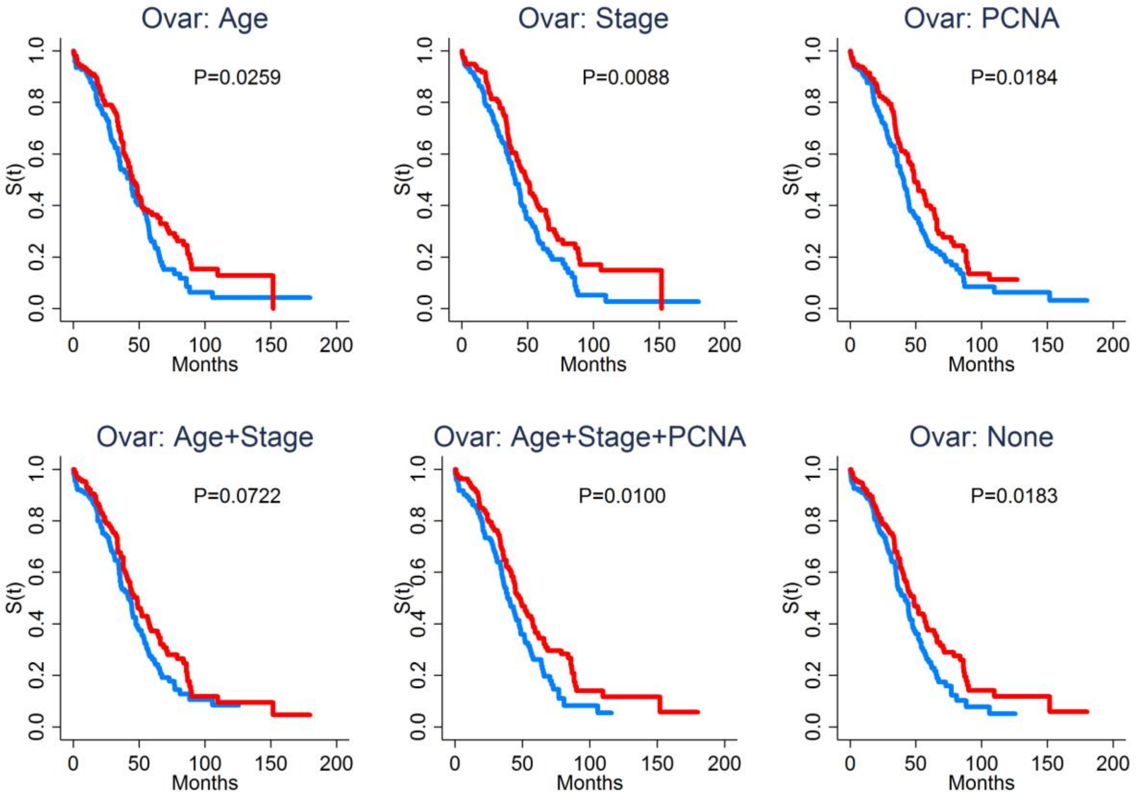


Figure S25. Ovarian: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

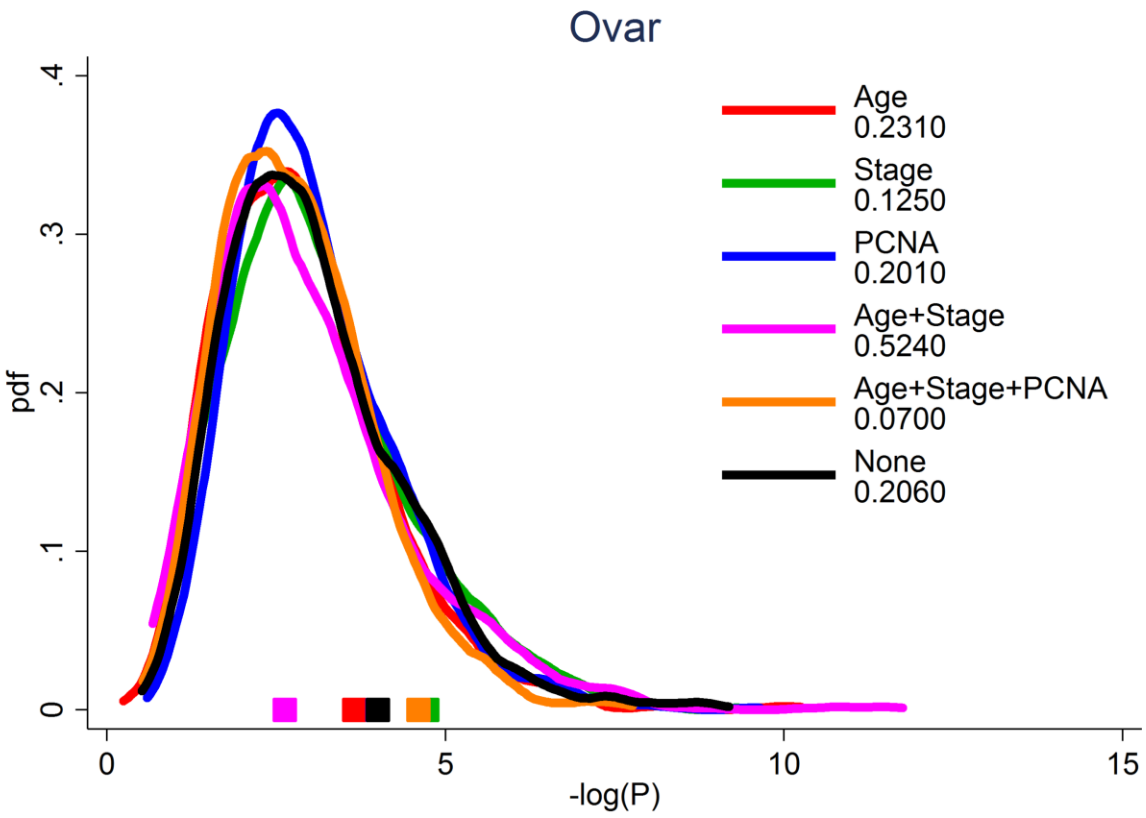


Figure S26. **Ovarian: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed -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.**

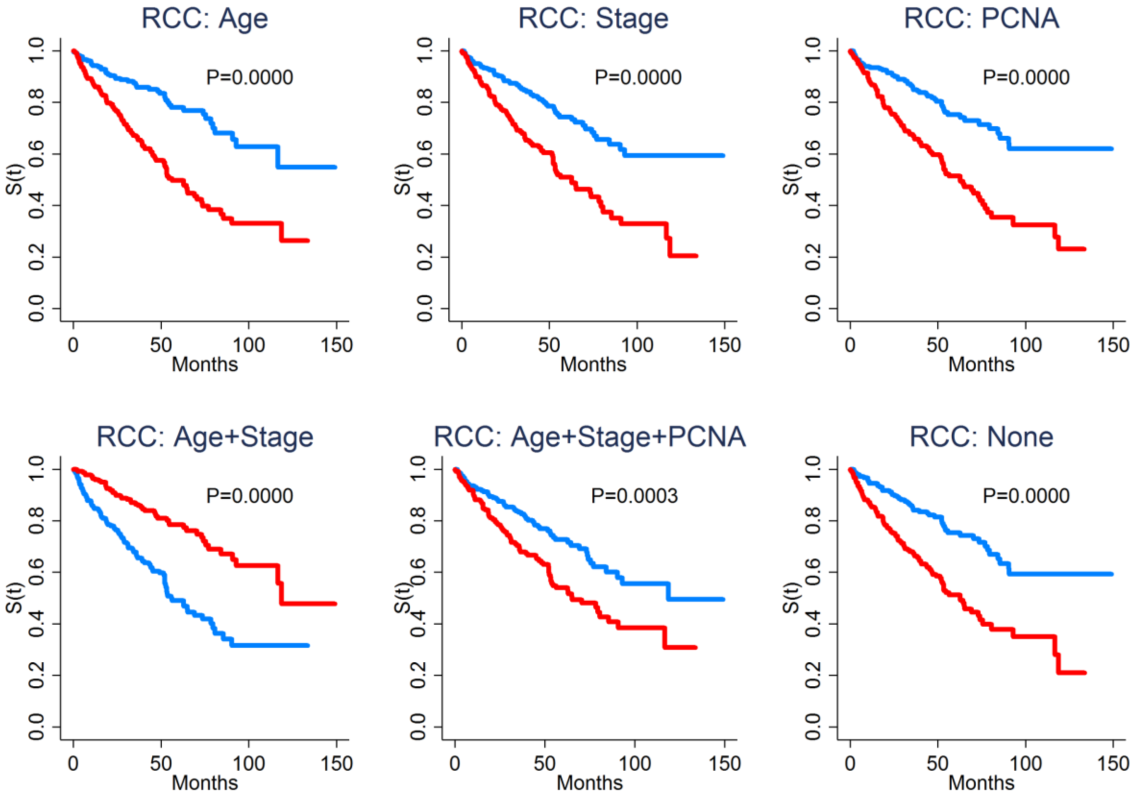


Figure S27. Renal Clear Cell: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for *p* genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

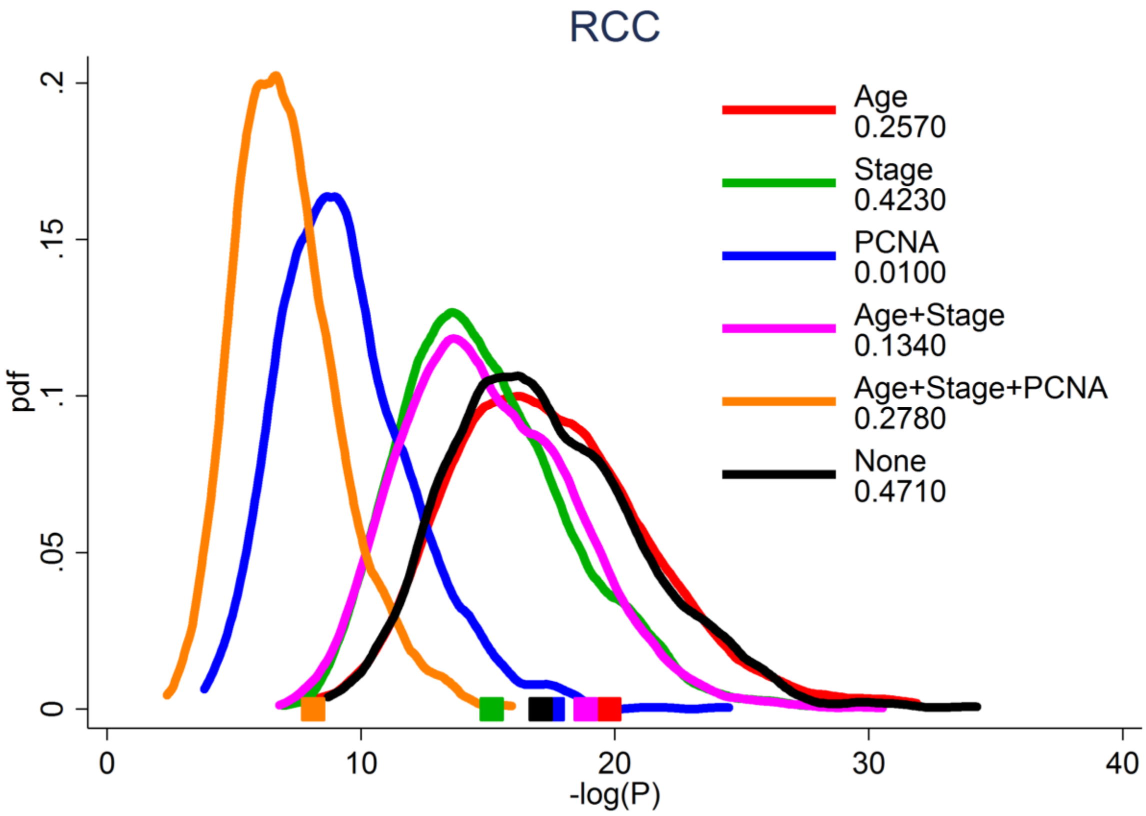


Figure S28. Renal Clear Cell: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the 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.

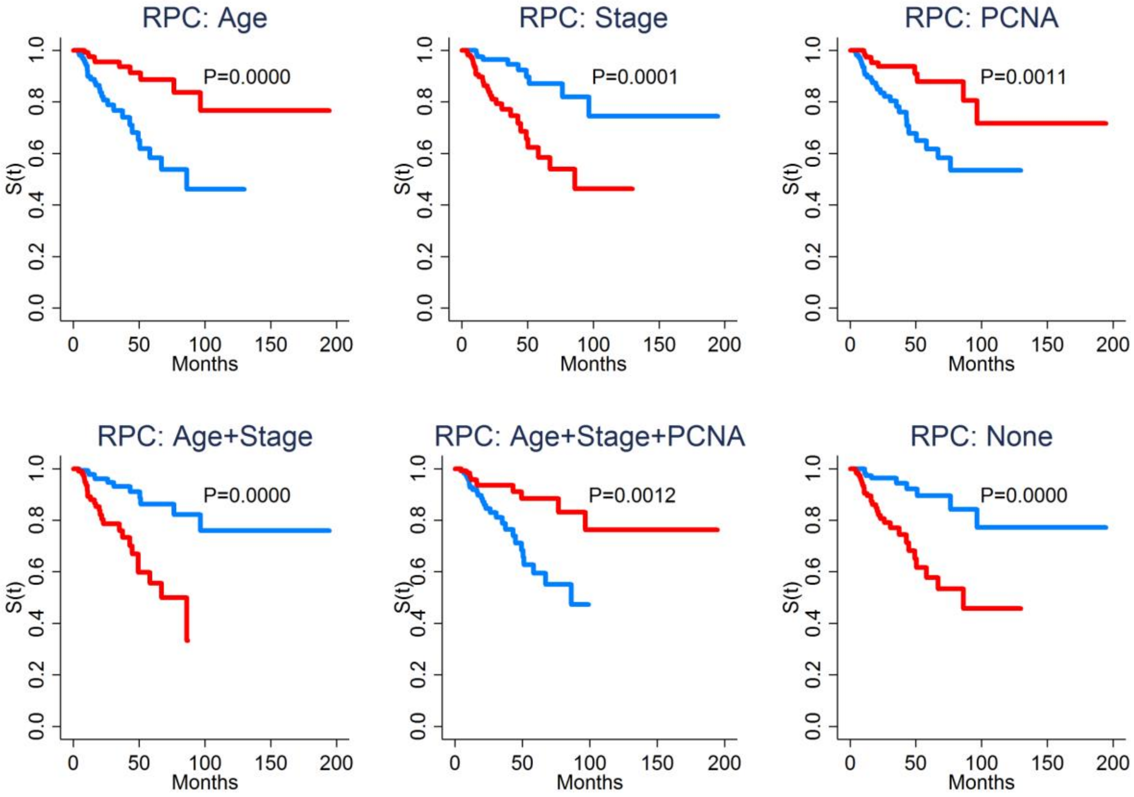


Figure S29. Renal Papillary: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

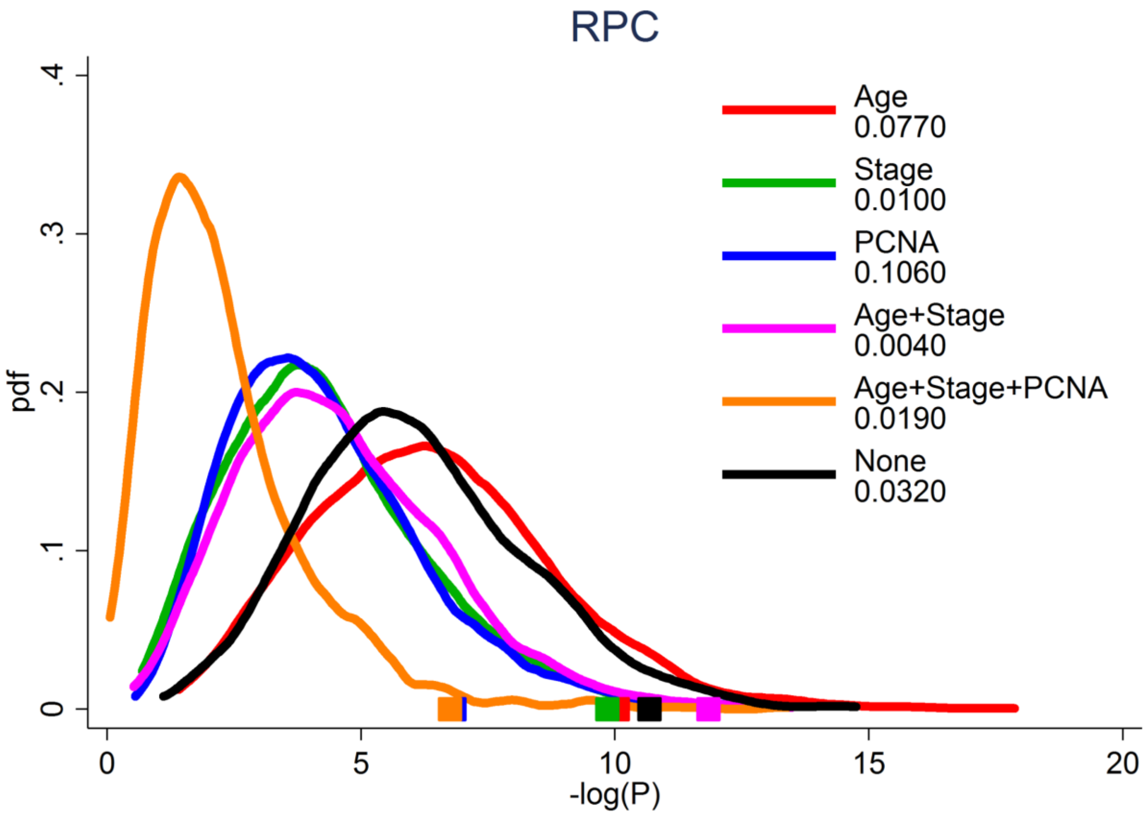


Figure S30. **Renal Papillary: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the 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.**

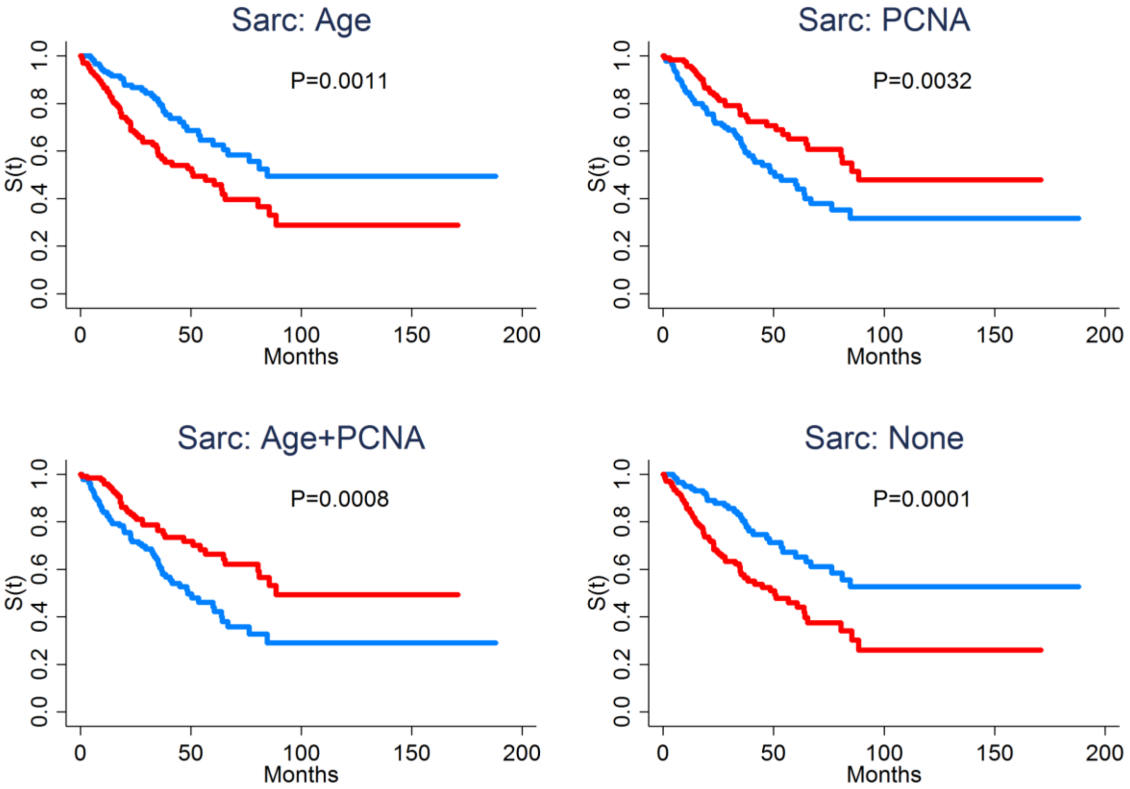


Figure S31. Sarcoma: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

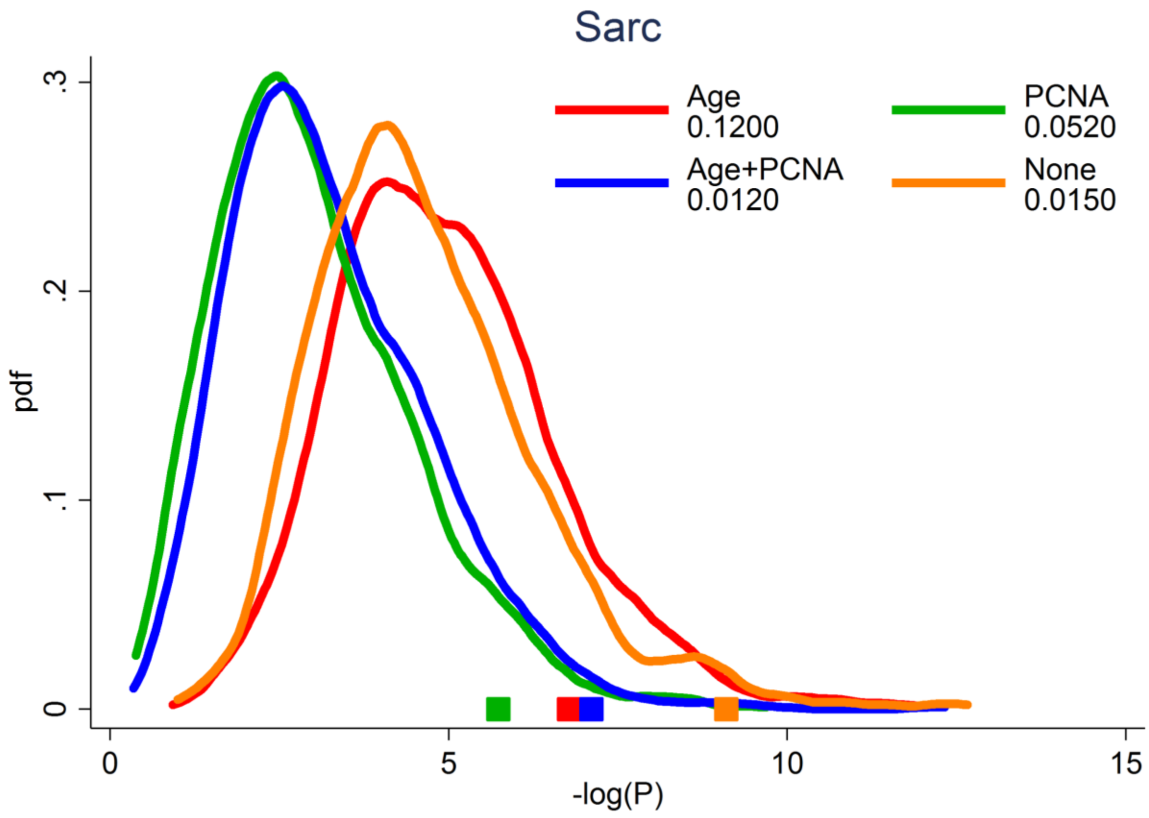


Figure S32. **Sarcoma: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, *PCNA* metagene) resulted in significant gene-specific KM logrank tests. Square symbols denote the observed -log(P) 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.**

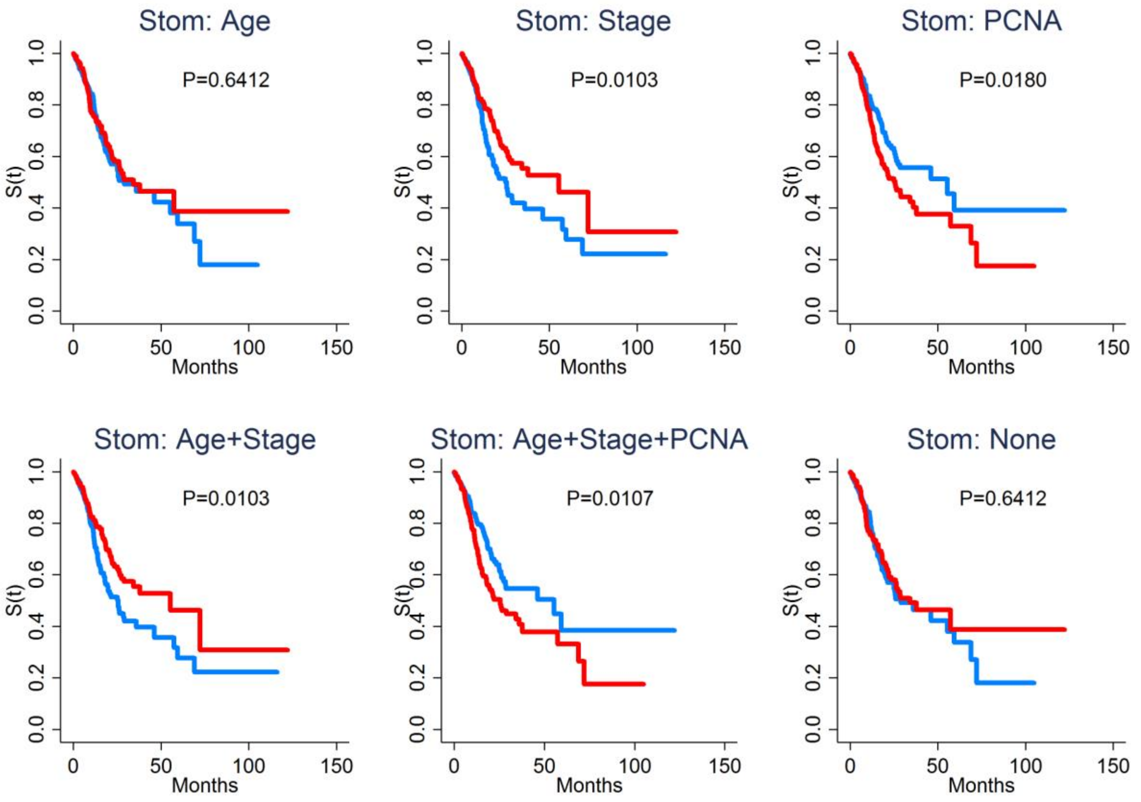


Figure S33. Stomach: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.

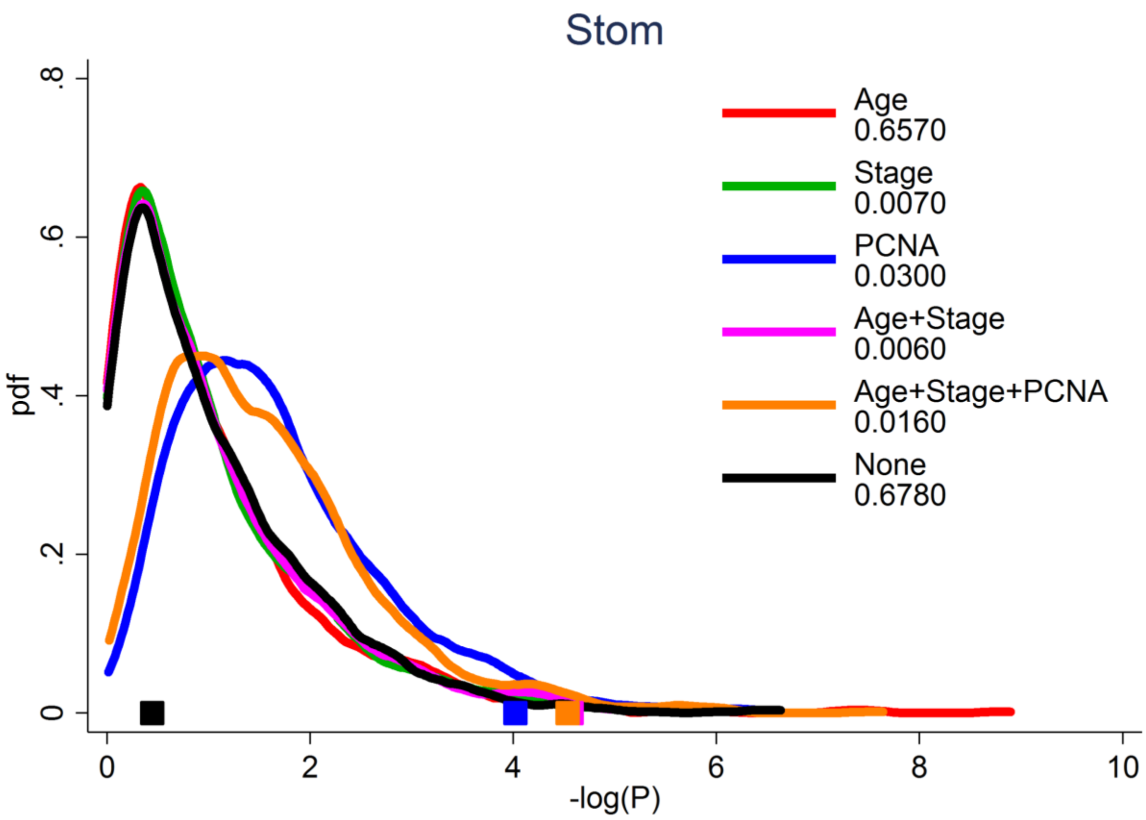


Figure S34. Stomach: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed -log(P) 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.

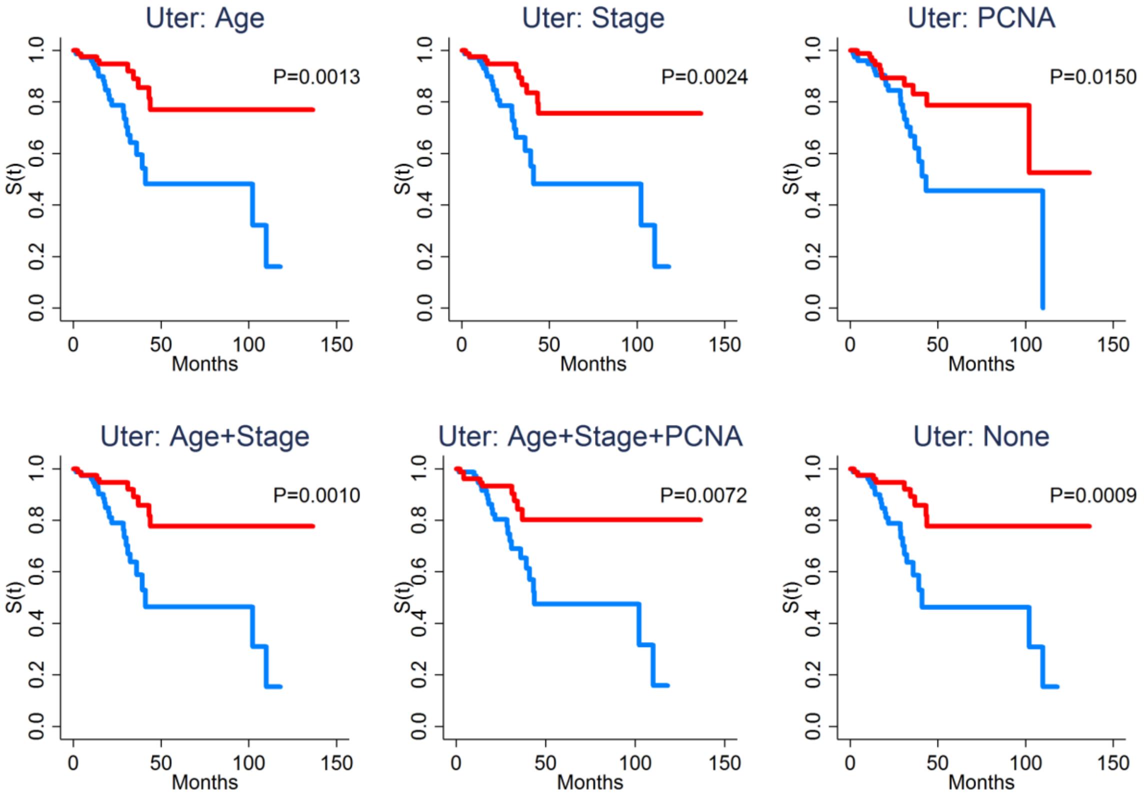


Figure S35. **Uterine: Kaplan-Meier logrank test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KM logrank tests.**

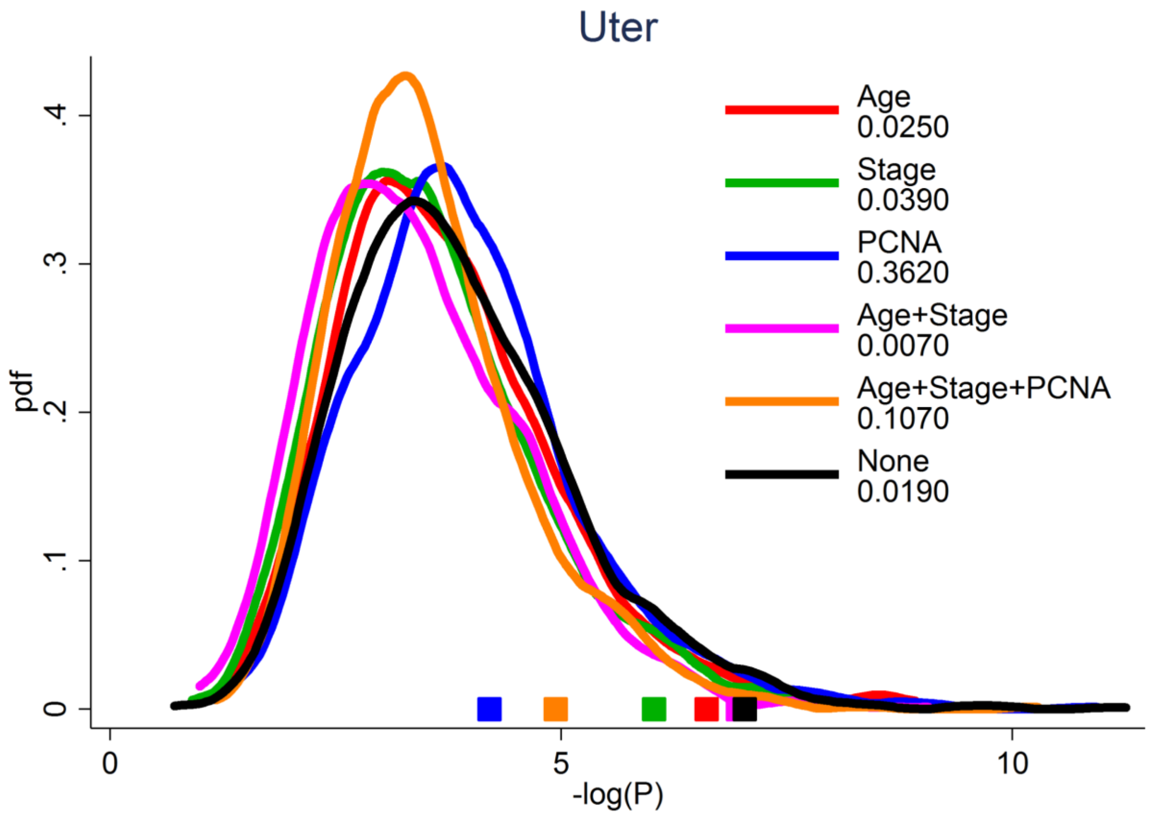


Figure S36. Uterine: Empirical p-value test results for single best binarized principal component (0,1) extracted from correlation matrix for p genes whose adjusted expression (via age, stage, *PCNA* metagene) resulted in significant gene-specific KMlogrank tests. Square symbols denote the observed -log(P) 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.