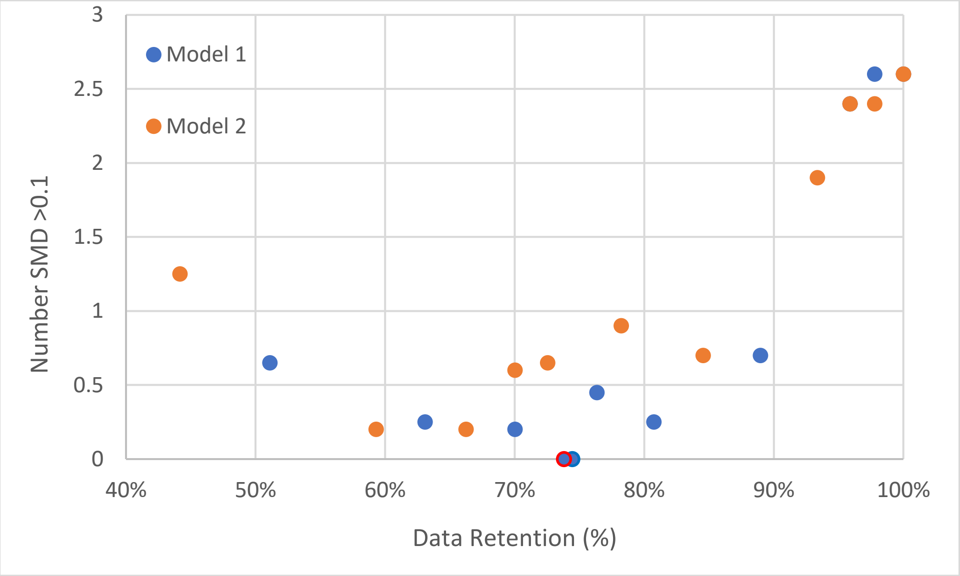
APPENDIX

Supplementary Table 1. Ranges of coarsened variables

Variable	**Ranges**
Prostate-specific antigen (ng/ml)	0, 20, 100, 300
	0, 20, 30, 50, 100, 300
	0, 6, 10, 20, 30, 50, 100, 300
Gleason score	6, 8, 10
	6, 7, 8, 9, 10
Clinical tumor stage	1, 2, 4,
	1a, 1b, 1c, 2a, 2b, 2c, 3a, 3b, 3c, 4a and 4b

Supplementary Fig. 1A. The average absolute standardized mean difference (SMD) is plotted per level of data retention for each matching caliper used in propensity score matching. The red dot indicates the matching strategy chosen.

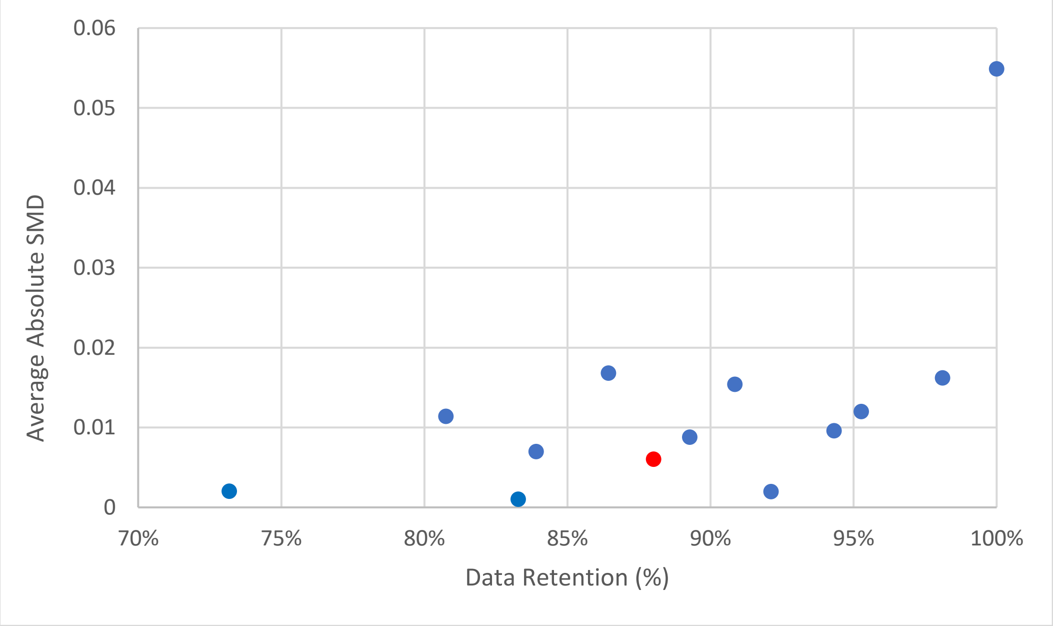
Supplementary Fig. 1B. The number of absolute standardized mean differences (SMD) that exceed the threshold of 0.1 is plotted per level of data retention for each matching caliper used in propensity score matching. The red dot indicates the matching strategy chosen.



Supplementary Fig. 1C. The average absolute standardized mean difference (SMD) for the proportion of patients in each treatment group occupying each ProCaRS risk-group (i.e., high-intermediate, high, and extremely high) is plotted per level of data retention for each matching caliper used in propensity score matching. The red dot indicates the matching strategy chosen.

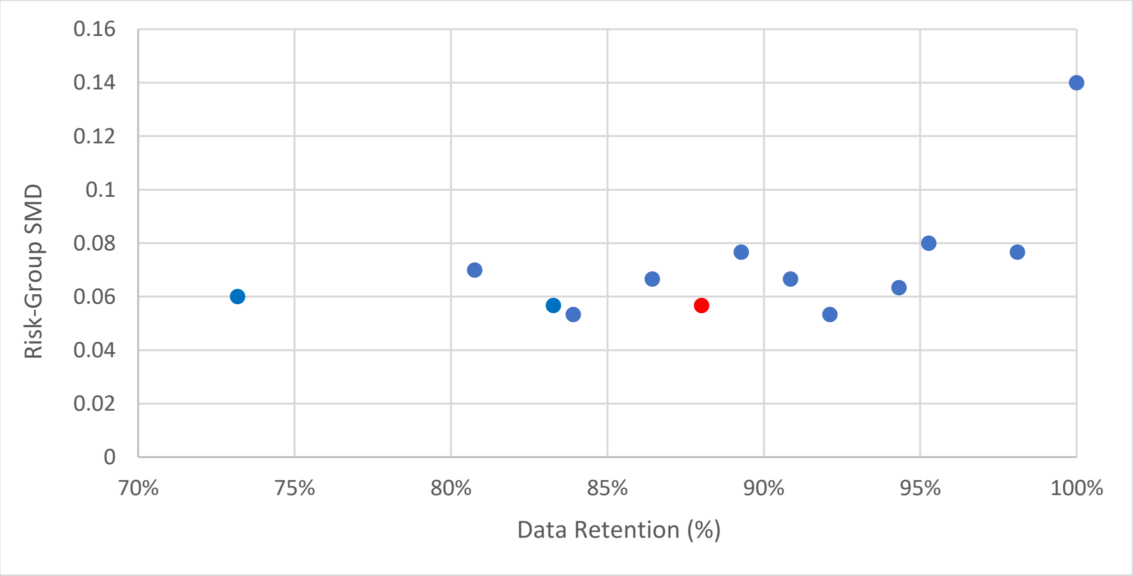
Supplementary Fig. 1D. The variance ratio for baseline prostate-specific antigen (PSA) between treatment groups is plotted per level of data retention for each matching caliper used in propensity score matching. The red dot indicates the matching strategy chosen.

Supplementary Fig. 2A. The average absolute standardized mean difference (SMD) is plotted per level of data retention for each combination of coarsened variables used in coarsened exact matching. The red dot indicates the matching strategy chosen.



Supplementary Fig. 2B. The number of absolute standardized mean differences (SMD) that exceed the threshold of 0.1 is plotted per level of data retention for each combination of coarsened variables used in coarsened exact matching. The red dot indicates the matching strategy chosen.

Supplementary Fig. 2C. The average absolute standardized mean difference (SMD) for the proportion of patients in each treatment group occupying each ProCaRS risk-group (i.e., high-intermediate, high, and extremely high) is plotted per level of data retention for each combination of coarsened variables used in coarsened exact matching. The red dot indicates the matching strategy chosen.



Supplementary Fig. 2D. The variance ratio for baseline prostate-specific antigen (PSA) between treatment groups is plotted per level of data retention for each combination of coarsened variables used in coarsened exact matching. The red dot indicates the matching strategy chosen.