The matching process was as follows:

1. Build a logistic regression model where the response variable is the binary indicator of treatment (0=non-TRT, 1=TRT) and the predictors are all pre-determined confounders;
2. From logistic regression model, obtain the predicted value of the probability of each sample that belongs to the TRT group, which is used as propensity score.
3. For each TRT sample, find its nearest k (k=5 in our study) non-TRT controls (nearest means that two samples’ propensity scores are closest);
4. During the matching process, some non-TRT controls may be matched to several TRT samples whereas others may not be matched to any TRT sample. We delete all non-TRT controls that are not matched to any TRT sample and give a weight to each remaining sample calculated by the following formula:

where means number of matched samples and means the number of remaining samples. Weight for each TRT sample is 1.

1. Use the matched TRT and non-TRT samples to build a weighted cross table and apply Fisher’s exact test to assess the effect of TRT on PCa.