**Supplemental Method 1. Detailed information of the method of propensity score matching**.

To adjust for the selection bias effect caused by group-by-group disparities in baseline covariates between groups A and B, we performed propensity score matching (PSM) which has been well-known to be useful in balancing the background covariates of interest. In PSM, the nearest-neighbor matching algorithm was performed for each group with a 1:1 ratio and a caliper width of 0.01 standard deviations of the logit of the propensity score was used. The propensity scores were constructed using a logistic regression model with a total of 16 baseline covariates. They included the age, sex, smoking history, body mass index, past medical history (hypertension, diabetes mellitus, dyslipidemia, cerebrovascular accident), presence of myocardial necrosis, left ventricular ejection fraction, and prescribed medications at discharge (antiplatelet agents, renin-angiotensin system inhibitors, statins, calcium channel blockers, beta-blockers, and long-acting nitrates). Since we performed PSM with one-to-one matching, then eliminates unmatched subjects, the reduction in the sample size in two different groups was induced in the PSM-adjusted analysis.

Patients with missing covariates or those lost to follow-up were excluded from the PSM-adjusted analysis.