**Supplemental Figure 2 - Empirical Type I error and power with 4 sub-populations**

500 individuals in each sub-populations of 500 individuals, $F_{st} = 0.01$. The odds ratio for power was simulated to be 1.2 (log additive model). $p_i$ is the risk allele frequency in sub-population $i$, $i=1,2,3,4$. The x-axis is the various methods of selecting PCs for inclusion in the model of association and the symbols in the plot represent the phenotypic structure. When the number of cases is the same in each of the sub-populations (125/125/125/125 = 125 cases from each sub-population), there is no phenotypic structure. When the number of cases is different in each of the sub-populations, there is phenotypic structure. The y-axis is the proportion of logistic regression models adjusting for the selected PCs for which the SNP p-values are significant at 0.05.