Supplemental References

1. Rowley JW, Oler A, Tolley ND, et al. Genome wide RNA-seq analysis of human and mouse platelet transcriptomes. Blood 2011.
2. Raghavachari N, Xu X, Harris A, et al. Amplified expression profiling of platelet transcriptome reveals changes in arginine metabolic pathways in patients with sickle cell disease. Circulation 2007;115:1551-62.
3. Watkins NA, Gusnanto A, de Bono B, et al. A HaemAtlas: characterizing gene expression in differentiated human blood cells. Blood 2009;113:e1-e9.
4. Lood C, Amisten S, Gullstrand B, et al. Platelet transcriptional profile and protein expression in patients with systemic lupus erythematosus: up-regulation of the type I interferon system is strongly associated with vascular disease. Blood 2010.
5. Krishnan S, Gaspari M, Corte AD, et al. OFFgel-based multidimensional LC-MS/MS approach to the cataloguing of the human platelet proteome for an interactomic profile. Electrophoresis 2011;32:686-95.
6. Gnatenko DV, Dunn JJ, McCorkle SR, Weissmann D, Perrotta PL, Bahou WF. Transcript profiling of human platelets using microarray and serial analysis of gene expression. Blood 2003;101:2285-93.

Figure 1 An overview of the discovery and validation cohorts for platelet function outcomes and samples analyzed by microarray analysis (dashed outline). Healthy volunteers cohorts (HV1 and HV2) were challenged with 325mg/day aspirin at Duke University Medical Center as previously described(1). Outpatient cardiology (OPC) patients were treated with 81mg/day aspirin at The George Washington University. Three subgroups within the OPC cohort were selected for microarray analysis based on VerifyNow Aspirin Response Units (ARU): aspirin resistant (AR, ARU > 550), High normal (HN, 500 < ARU < 550); and Aspirin sensitive (AS, ARU < 550). **HV2 subjects were screened with a test dose of 325mg aspirin and those in the 1st and 4th quartile of the 3 hour platelet function score (PFS) were selected to continue through the study protocol. *Three HV2 subjects had participated in HV1 and were dropped from the HV2 cohort.

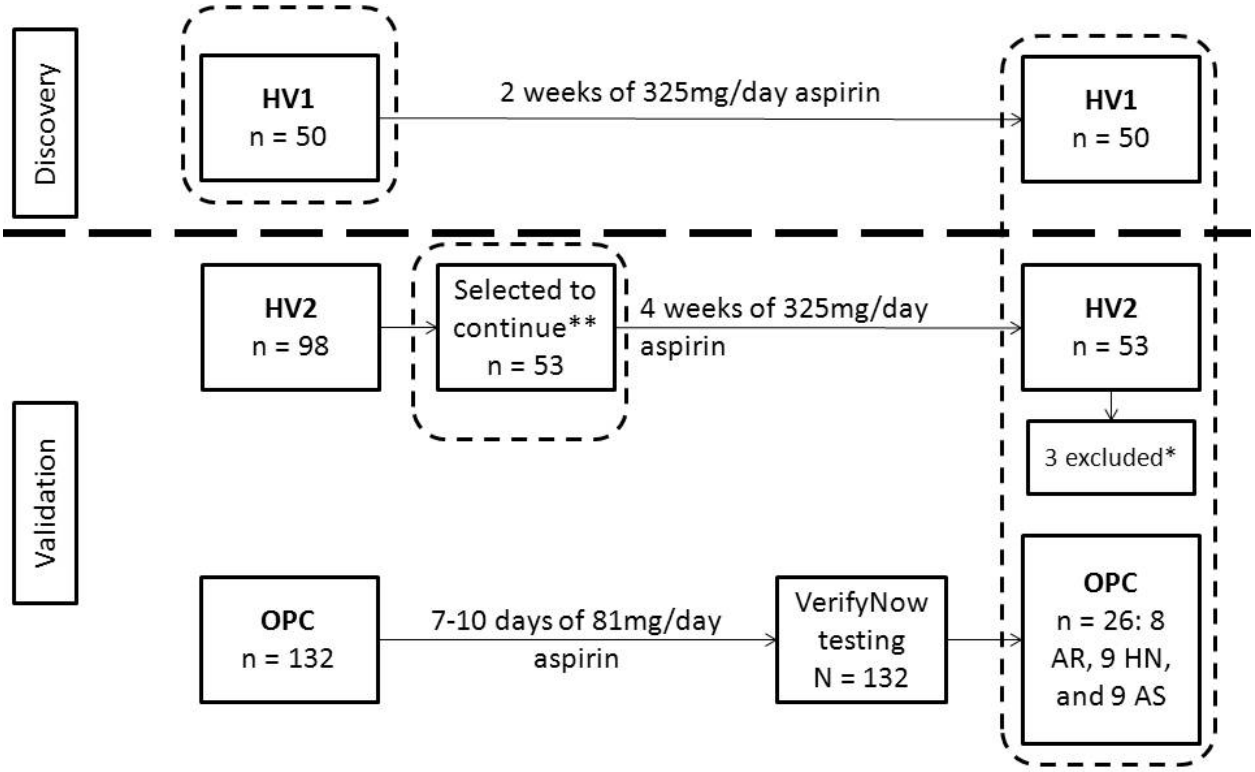
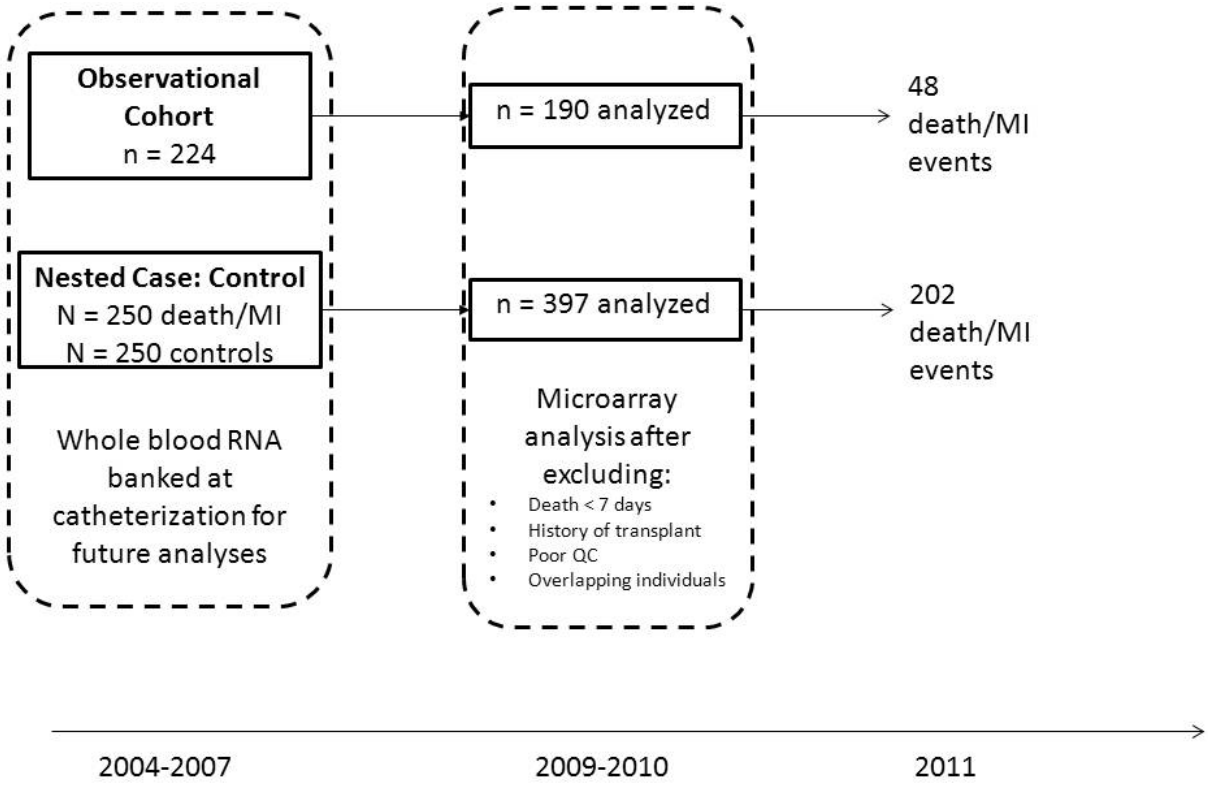


Figure 2

Two patient cohorts from within the CATHGEN (http://cathgen.duhs.duke.edu) biorepository were available for microarray analysis. In 2009, an observational cohort of 224 banked, sequential samples were selected, of which 190 were available for analysis. In 2010, a nested case:control cohort of 250 cases of death/myocardial infarction and 250 age-, sex-, and race-matched controls who were free of death/MI > 2 years after cardiac catheterization was identified as part of the MURDOCK Horizon 1 Cardiovascular Disease Study(2), of which 397 were available for analysis. In 2011, dates for death, myocardial infarction, and last follow-up were ascertained from the Duke Databank for Cardiovascular Disease as previously described(3).