**Supplemental Material**

## DETAILED METHODS

***LTL measurements, continued.*** To normalize the quantity of the input DNA, a single copy gene was amplified in parallel. The T/S ratio reflects the average length of the telomeres.

The telomere thermal cycling profile consists of: Cycling for T (telomic) PCR: 96°C for 1 minute; denature at 96°C for 1 second, anneal/extend at 54°C for 60 seconds, with fluorescence data collection, 30 cycles. Cycling for S (single copy gene) PCR: PCR: 96°C for 1 minute; denature at 95°C for 15 seconds, anneal at 58°C for 1 second, extend at 72°C for 20 seconds, 8 cycles; followed by denature at 96°C for 1 second, anneal at 58°C for 1 second, extend at 72°C for 20 seconds, hold at 83°C for 5 seconds with data collection, 35 cycles.

The primers for the telomere PCR are *tel1b* [5'-CGGTTT$(GTTTGG)_5$GTT-3'], used at a final concentration of 100 nM, and *tel2b* [5'-GGCTTG$(CCTTAC)_5$CCT-3'], used at a final concentration of 900 nM. The primers for the single-copy gene (human beta-globin) PCR are *hbg1* [5' GCTTCTGACACAACTGTGTTCACTAGC-3'], used at a final concentration of 300 nM, and *hbg2* [5'-CACCAACTTCATCCACGTTCACC-3'], used at a final concentration of 700 nM. The final reaction mix contains 20 mM Tris-HCl, pH 8.4; 50 mM KCl; 200 mM each dNTP; 1% DMSO; 0.4× Syber Green I; 22 ng *E. coli* DNA per reaction; 0.4 Units of Platinum Taq DNA polymerase (Invitrogen Inc.) per 11 microliter reaction; 6 ng of genomic DNA. Tubes containing 26, 8.75, 2.9, 0.97, 0.324 and 0.108 ng of a reference DNA (a pooled samples of leukocyte genomic DNA from

100 female donors) are included in each PCR run so that the quantity of targeted templates in each research sample can be determined relative to the reference DNA sample by the standard curve method. The same reference DNA was used for all PCR runs.

To control for inter-assay variability, 8 control DNA samples were included in each run. In each batch, the T/S ratio of each control DNA was divided by the average T/S for the same DNA from 10 runs to get a normalizing factor. This was done for all 8 samples and the average normalizing factor for all 8 samples was used to correct the participant DNA samples to get the final T/S ratio. The T/S ratio for each sample was measured twice. When the duplicate T/S value and the initial value vary by more than 7%, the sample was run the third time and the two closest values were reported. The average CV for this study is 2.1%. The DNA samples were de-identified and randomized. The lab personnel who performed the assays were blind to demographic and clinical data.

***PC Quantification by FACS.*** We incubated 300µl of peripheral blood of peripheral blood (anticoagulant: EDTA) with fluorochrome-labeled monoclonal anti-human mouse antibodies, namely, 15µl FITC-CD34 (BD Biosciences), 15µl PerCP-CD45 (BD Biosciences), 3µl PE-Cy7-conjugated anti-CXCR4 (EBioscience, clone 12G5) and 10ul APC-CD133 (Miltenyi) in the dark for 15 minutes. Thereafter 15ml of ammonium chloride lysing buffer was added to lyse red blood cells. 15ml of staining medium (PBS with 3% heat-inactivated serum and 0.1% sodium azide) was then added to stop the lysing reaction. After mixing gently, samples were centrifuged at 1500 rpm for 5 minutes and then washed with PBS. Thereafter cells were suspended in 500 µl of staining

medium, mixed and run on flow cytometer within 4 hours (BD FACS Canto II Flow Cytometer). Prior to flow cytometry, 100µl of AccuCheck Counting Beads (Invitrogen, Cat#: PCB100) were added to act as an internal standard for direct estimation of the concentration of target cell subsets. At least 2.5 million events were acquired from the Cytometer. Flow data were analyzed with Flowjo software (Treestar, Inc.). Absolute mononuclear cell count was estimated as the sum of lymphocytes and monocytes using a Coulter ACT/Diff cell counter (Beckman Coulter). $CD45^{med}$ cells are also referred to as $CD45^{dim}$ cells and their selection excludes $CD45^{bright}$ and CD45-(negative) cells. By excluding these CD45- cells we exclude nonhematopoioetic progenitors. By excluding the rare $CD45^{bright}$ cells we exclude lymphoblasts.

**Figure legends:**

**Online Figure I:** Incidence of cardiovascular events according to levels of various PCs subtypes. P values were derived from Kaplan Meier analysis.

**Online Figure II:** Incidence of cardiovascular events according to levels of LTL and various PC subtypes using binary cutoffs of Q1. A) Hazard ratio for short LTL and low $CD34^{+}/CD133^{+}$ of 3.2, 95% CI of 1.7-6.1, $p<0.001$. B) Hazard ratio for short LTL and low $CD34^{+}/CDXCR4^{+}$ of 3.3, 95% CI of 1.7-6.7, $p=0.001$. C) Hazard ratio for short LTL and low $CD34^{+}/CD133^{+}/CXCR4^{+}$ of 2.5 (1.2-5.2), 95% CI of $p=0.01$.

**Supplementary Tables**

**Online Table I: Bivariate and multivariable linear regression analyses predicting LTL as a continuous variable.**

| | Bivariate analysis | | Multivariable analysis | |
|---|---|---|---|---|
| | % LTL length difference (SE) | P value | % LTL length difference (SE) | P value |
| **Age, 10 years** | -5.9 (0.7) | <0.001 | -5.6 (0.7) | <0.001 |
| **Male sex** | -5.8 (1.6) | <0.001 | -5.2 (1.6) | 0.001 |
| **White race** | -7.8 (1.5) | <0.001 | -5.2 (1.5) | <0.001 |
| **BMI ≥30 kg/m$^2$** | 4.3 (1.4) | 0.003 | 2.1 (1.3) | 0.12 |
| **Hypertension** | -0.4 (1.6) | 0.78 | -2.2 (1.7) | 0.18 |
| **Diabetes** | 0.1 (1.5) | 0.94 | -1.4 (1.5) | 0.34 |
| **Dyslipidemia** | 0.8 (1.8) | 0.66 | 2.7 (1.8) | 0.13 |
| **Current/former smoking** | -2.7 (1.4) | 0.05 | -3 (1.3) | 0.02 |
| **Previous MI** | -0.2 (1.4) | 0.90 | -2.7 (1.4) | 0.04 |
| **Medication use** | | | | |
| **ACEI** | -1.4 (1.4) | 0.33 | 0.1 (1.5) | 0.95 |
| **ARBs** | 0.9 (1.8) | 0.62 | 1.7 (1.9) | 0.36 |
| **Aspirin** | -0.1 (2) | 0.97 | 0 (1.9) | 0.99 |
| **Statins** | 0.3 (2) | 0.89 | -0.6 (1.9) | 0.75 |
| **Beta blockers** | 2.8 (1.6) | 0.08 | 0.4 (1.6) | 0.82 |
| **CAD severity (log-transformed Gensini score)** | -0.5 (0.6) | 0.34 | -0.3 (0.5) | 0.53 |

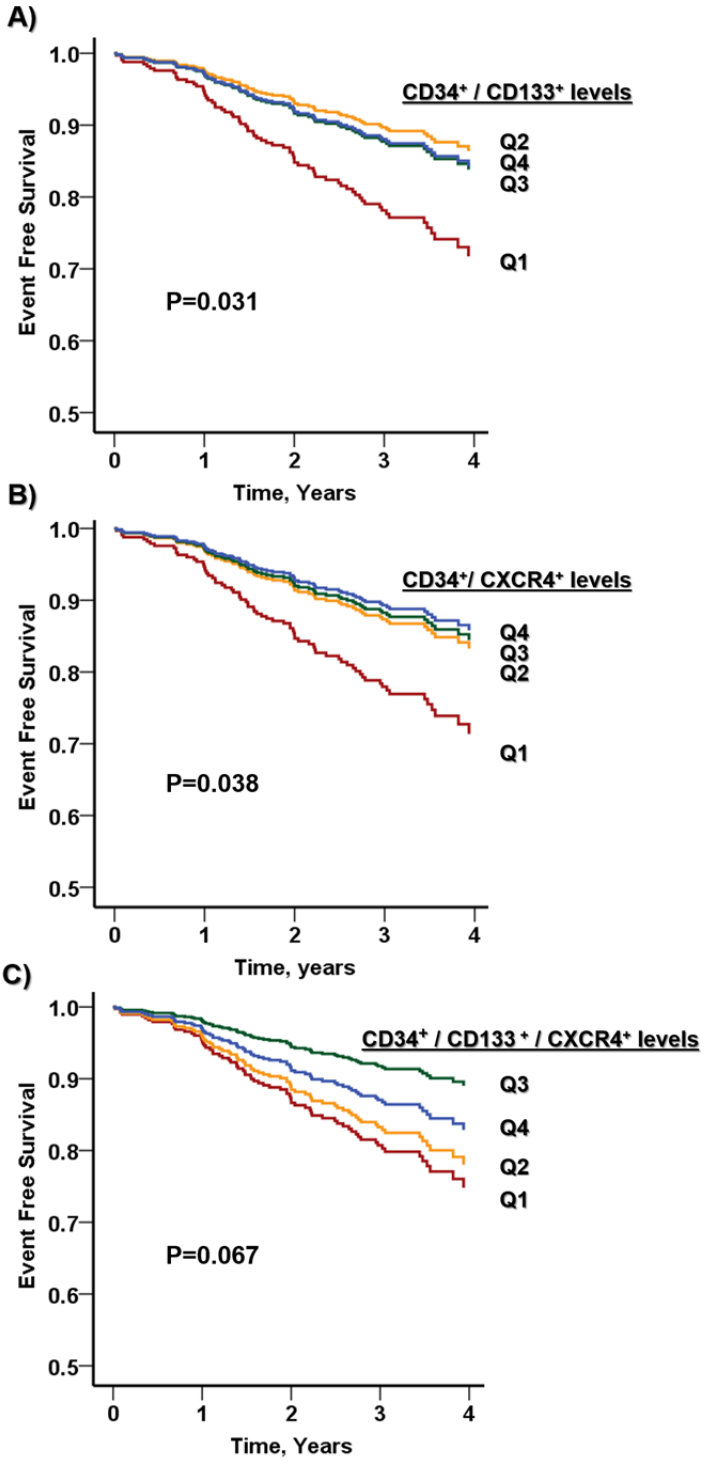
LTL: leucocyte telomere length. BMI: Body mass index. ARBs: Angiotensin receptor blockers. ACEI: angiotensin converting enzyme inhibitors; MI: myocardial infarction

**Online Table II: Multivariable linear regression analysis for factors associated with various PC classes.**

| | $CD34^+$ | | $CD34^+$/ $CD133^+$ | | $CD34^+$/$CXCR4^+$ | | $CD34^+$/$CXCR4^+$/$CD133^+$ | |
|---|---|---|---|---|---|---|---|---|
| | % Difference (SE) | P value | % Difference (SE) | P value | % Difference (SE) | P value | % Difference (SE) | P value |
| **Age, 10 years** | -14.7 (3.2) | <0.001 | -17.5 (3.4) | <0.001 | -14.3 (3.8) | <0.001 | -17.3 (4.1) | <0.001 |
| **Male sex** | 22.4 (6.7) | 0.002 | 15.3 (7.2) | 0.04 | 19 (8.2) | 0.03 | 14.2 (8.8) | 0.12 |
| **White race** | 34.2 (6.3) | <0.001 | 31.8 (6.8) | <0.001 | 29 (7.7) | <0.001 | 26.6 (8.3) | <0.001 |
| **BMI ≥30 kg/$m^2$** | 14.9 (5.8) | 0.014 | 17.7 (6.2) | 0.01 | 10.4 (7) | 0.14 | 16.6 (7.5) | 0.04 |
| **Hypertension** | 7.4 (7.3) | 0.31 | 7 (7.8) | 0.37 | -1.6 (8.9) | 0.85 | 0.8 (9.6) | 0.93 |
| **Diabetes** | 5.2 (6.3) | 0.41 | 8.6 (6.7) | 0.20 | 6.7 (7.6) | 0.38 | 10.5 (8.2) | 0.20 |
| **Dyslipidemia** | 5.7 (7.6) | 0.45 | 1.7 (8.2) | 0.83 | 10 (9.3) | 0.28 | 3.9 (10) | 0.69 |
| **Current/former smoking** | 5.6 (5.7) | 0.32 | 6.9 (6.1) | 0.26 | 10.6 (6.9) | 0.13 | 9.3 (7.4) | 0.21 |
| **Previous MI** | 5.4 (6) | 0.36 | 7.3 (6.4) | 0.26 | 5.4 (7.2) | 0.46 | 7.6 (7.8) | 0.33 |
| **ACEI** | -6.8 (6.4) | 0.25 | -4.7 (6.8) | 0.47 | -8 (7.7) | 0.26 | -6.5 (8.4) | 0.40 |
| **ARBs** | 3.5 (8.4) | 0.67 | 0.9 (8.9) | 0.92 | 6.9 (10.2) | 0.49 | 3.8 (11) | 0.72 |
| **Aspirin** | -9 (8.4) | 0.24 | -5.4 (9) | 0.52 | -12.1 (10.2) | 0.18 | -11.1 (11) | 0.26 |
| **Statins** | -3.4 (8.3) | 0.66 | -5.5 (8.9) | 0.51 | -6.4 (10.2) | 0.49 | -9.5 (11) | 0.34 |
| **Beta blocker** | 14.3 (7) | 0.05 | 11.4 (7.5) | 0.14 | 5.8 (8.6) | 0.49 | 4 (9.2) | 0.65 |
| **CAD severity (log-transformed Gensini score)** | 1.4 (2.3) | 0.54 | 1.1 (2.4) | 0.64 | -0.2 (2.7) | 0.93 | -0.6 (3) | 0.82 |

BMI: Body mass index. ARBs: Angiotensin receptor blockers. ACEI: angiotensin converting enzyme inhibitors. PC counts were log transformed

## Online Figure I



## Online Figure II