

Embodiment 61. The method of embodiment 59, wherein the abnormal stress test is a treadmill or nuclear medicine based test.

Embodiment 62. The method of embodiment 59, wherein the imaging suggesting coronary heart disease is an angiogram showing coronary artery stenosis of 50% or greater.

Embodiment 63. The method of any one of embodiments 27-62, comprising determining the risk of the subject having a secondary cardiovascular event within four years from the date the sample was taken from the subject.

Embodiment 64. The method of embodiment 63, wherein the risk of the subject having a secondary cardiovascular event is within one, two, three, or four years from the date that the sample was taken from the subject.

Embodiment 65. The method of embodiment 63 or 64, wherein the secondary cardiovascular event is myocardial infarction, stroke, trans-ischemic attack, hospitalization for heart failure, or death.

Embodiment 66. The method of any one of embodiments 63-65, wherein the risk is determined as a quantitative probability.

Embodiment 67. The method of any one of embodiments 63-65, wherein the risk is determined as a qualitative level of risk.

Embodiment 68. The method of embodiment 67, wherein the qualitative level of risk is low, moderate, or high.

[0019] In some embodiments, methods for screening a subject for the risk of a cardiovascular event (CV) event are provided. In some such embodiments, a method comprises

- (a) forming a biomarker panel comprising N protein biomarkers selected from N-terminal pro-BNP, sTREM-1, MMP-12, Antithrombin III, GPR56, Gelsolin, ST4S6, CHSTC, FSH, IL-1 sRII, PLXB2, SAP, and TFPI, wherein N is an integer from 3 to 13; and
- (b) detecting the level of each of the N biomarkers of the panel in a sample from the subject.

[0020] In some embodiments, a method for screening a subject for the risk of a cardiovascular event (CV) event comprises

- (a) forming a biomarker panel comprising N protein biomarkers selected from BNP, sTREM-1, MMP-12, SVEP1, ARL11, ANTR2, CA125, GOLM1, PPR1A, ERBB3, suPAR, GDF-11/8, JAM-B, ATS13, Spondin-1, NCAM-120,

TFF3, SIRT2, ANP, NELL1, LRP11, NDST1, PTPRJ, CILP2, CA2D3, ITI heavy chain H2, and IGDC4, wherein N is an integer from 8 to 27; and

- (b) detecting the level of each of the N biomarkers of the panel in a sample from the subject.

[0021] In some embodiments, methods for predicting the likelihood that a subject will have a CV event are provided. In some such embodiments, a method comprises

- (a) forming a biomarker panel comprising N protein biomarkers selected from BNP, sTREM-1, MMP-12, Antithrombin III, GPR56, Gelsolin, ST4S6, CHSTC, FSH, IL-1 sRII, PLXB2, SAP, and TFPI, wherein N is an integer from 3 to 13; and
- (b) detecting the level of each of the N biomarkers of the panel in a sample from the subject.

[0022] In some embodiments, a method for predicting the likelihood that a subject will have a CV event comprises

- (a) forming a biomarker panel comprising N protein biomarkers selected from BNP, sTREM-1, MMP-12, SVEP1, ARL11, ANTR2, CA125, GOLM1, PPR1A, ERBB3, suPAR, GDF-11/8, JAM-B, ATS13, Spondin-1, NCAM-120, TFF3, SIRT2, ANP, NELL1, LRP11, NDST1, PTPRJ, CILP2, CA2D3, ITI heavy chain H2, and IGDC4, wherein N is an integer from 8 to 27; and
- (b) detecting the level of each of the N biomarkers of the panel in a sample from the subject.

[0023] In some embodiments, methods for screening a subject for the risk or likelihood of a cardiovascular event (CV) event are provided, comprising detecting the level of at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, or 27 of the biomarkers in the panel comprising N biomarkers.

[0024] In some embodiments, the risk or likelihood of the subject having a CV event within 4 years is high if the levels of at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, or at least 13 biomarkers of the set of biomarkers are each abnormal relative to a control level of the respective biomarker.