a eleventh gene expression level for the IL-5 gene taken from the wound effluent on the thirtieth measurement day; and

a twelfth gene expression level for the RANTES gene taken from the wound effluent on the third measurement day.

3. The method according to claim **2**, wherein the biomarker levels include:

a lower first gene expression level, a middle first gene expression level, and an upper first gene expression level, the middle first gene expression level having a lower limit of 2427 mean fluorescent intensity (MFI) and an upper limit of 4040 MFI;

a lower second gene expression level, a middle second gene expression level, and an upper second gene expression level, the middle second gene expression level having a lower limit of 1371 MFI and an upper limit of 4108 MFI;

a lower third gene expression level, a middle third gene expression level, and an upper third gene expression level, the middle third gene expression level having a lower limit of 2164 MFI and an upper limit of 3509 MFI;

a lower fourth gene expression level, a middle fourth gene expression level, and an upper fourth gene expression level, the middle fourth gene expression level having a lower limit of 174 MFI and an upper limit of 955 MFI;

a lower fifth gene expression level, a middle fifth gene expression level, and an upper fifth gene expression level;

a lower sixth gene expression level, a middle sixth gene expression level, and an upper sixth gene expression level, the middle sixth gene expression level having a lower limit of 352 MFI and an upper limit of 709 MFI;

a lower seventh gene expression level, a middle seventh gene expression level, and an upper seventh gene expression level, the middle seventh gene expression level having a lower limit of 40.5 MFI and an upper limit of 199 MFI;

a lower eighth gene expression level, a middle eighth gene expression level, and an upper eighth gene expression level, the middle eighth gene expression level having a lower limit of 50.3 MFI and an upper limit of 352 MFI;

a lower ninth gene expression level, a middle ninth gene expression level, and an upper ninth gene expression level, the middle ninth gene expression level having a lower limit of 35.9 MFI and an upper limit of 88 MFI;

a lower tenth gene expression level, a middle tenth gene expression level, and an upper tenth gene expression level, the middle tenth gene expression level having a lower limit of 2.2 MFI and an upper limit of 8.7 MFI;

a lower eleventh gene expression level, a middle eleventh gene expression level, and an upper eleventh gene expression level, the middle eleventh gene expression level having a lower limit of 10.5 MFI and an upper limit of 50 MFI; and

a lower twelfth gene expression level, a middle twelfth gene expression level, and an upper twelfth gene expression level, the middle twelfth gene expression level having a lower limit of 122 MFI and an upper limit of 7538 MFI.

4. The method according to claim **2**, wherein:

the twelfth gene expression level is usable to estimate the fourth gene expression level;

the fourth gene expression level is usable to estimate the seventh gene expression level;

the seventh gene expression level is usable to estimate the fifth gene expression level;

the first gene expression level is usable to estimate the eighth gene expression level;

the eighth gene expression level is usable to estimate the second gene expression level;

the second gene expression level is usable to estimate the third gene expression level;

the tenth gene expression level is usable to estimate the sixth gene expression level;

the sixth gene expression level is usable to estimate the second gene expression level;

the ninth gene expression level is usable to estimate the eighth gene expression level; and

the eleventh gene expression level is usable to estimate the first gene expression level.

5. The method according to claim **1**, wherein the biomarker levels further include gene expression levels for an IL-1a gene, IL-10 gene, IL-2 gene, IL-3 gene, IL-4 gene, IL-7 gene, IL-8 gene, IL-10 gene, IL-12(p40) gene, IL-12(p70) gene, IL-13 gene, IL-15 gene, Eotaxin gene, IFN-γ gene, GM-CSF gene, MIP-1a gene, and TNFα gene.

6. The method according to claim **1**, wherein the clinical parameters further include RNA transcripts and translation products of genes selected from the group consisting: ACTA2, ACVR1, ADM, ALCAM, ANGPT 1, ANGPT 2, ANGPT 4, BAX, BCL2, BCL2L, 18S, 18S, CAV2, CCL1, CCL11, CCL17, CCL19, CCL 2, CCL 20, CCL22, CCL25, CCL27, CCL28, CCL3, COL3A1, COL4A1, COL4A3, CSSF1, CSF2, CSF3, CTGF, CX3CL1, CXCL1, CXCL10, CXCL11, CXCL12, FGF10, FGF11, FGF12, FGF13, FGF17, FGF2, FGF3, FGF5, FGF7, FGF8, FGF9, FIGF, IFNG, IGF1, IGF2, IGFBP1, IGFBP2, IGFBP3, IGFBP3, IGFBP4, IGFBP5, IGFBP6, IGFBP7, IL10, IL11, IL6, IL7, IL8, IL9, ITGA5, ITGAL, ITGAM, ITGB2, KDR, KITLG, LBP, LTA, MMP7, MMP8, MMP9, MPO, NCAM2, NFKB1, NFKB2, NOS2A, OSMR, PDGFA, PDGFB, PECAM1, SMAD6, SMAD7, SOCS1, SOCS3, SOCS5, STAT3, TEK, TGFA, TGFB1, TGFB2, TGFB3, TGFBR1, DCL2L2, BMP1, BMP15, BMP5, BMP3, BMP4, BMP5, BMP6, BMP7, BMP8A, BMP8B, CALCA, CALCB, CAV1, CCL4, CCL4L1, CCL4L2, CCL5, CCL7, CD14, CD4, CD40, CD40LG, CD83, CD8A, CD8B, COL18A1, COL1A1, CXCL13, CXCL2, CXCL5, CXCL9, ECGF1, EDN1, EGF, EGR1, EPO, FADD, FAS, FGF1, FLT1, FN1, GAPDH, GDF3, GDF5, MSTN, GDF9, HGF, HMGB1, IAPP, ICAM2, IFNB1, IL12A, IL13, ILLS, IL16, IL17A, IL18, IL1A, 1L1B, 1L2, IL3, IL4, IL5, MAPK14, MET, MMP1, MMP10, MMP11, MMP12, MMP13, MMP14, MMP15, MMP2, MMP24. MMP3, PF4, PLA2G4A, PTGS1, PTGS2, SELE, SELP, SERPINE1, SLPI, SMAD1, SMAD2, SMAD3, SMAD4, TIE1, TIMP1, TIMP2, TIMP3, TNC, TNF, TNFSF10, VCAM1, VEGFB, VEGFC, XCL1, XCL2.

7. The method according to claim **1**, wherein the clinical parameters further include Injury Severity Score (ISS), Acute Physiology and Chronic Health Evaluation II (APACHE-II) scores, wound size, and associated vascular injury.

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