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(54) Title: BIOMARKER SIGNATURE METHOD, AND APPARATUS AND KITS THEREFOR

(57) Abstract: The present invention discloses methods, kits, and apparatus as well as reagents and compositions associated therewith for deriving an indicator for use in diagnosing the presence, absence or degree of at least one condition in a biological subject or in prognosing at least one condition in a biological subject. Also disclosed is a biomarker signature for use in diagnosing the presence, absence or degree of at least one condition in a biological subject or in prognosing at least one condition in a biological subject. The present invention further discloses methods, kits and apparatus, as well as reagents and compositions associated therewith, for identifying biomarkers for use in a biomarker signature.

BIOMARKER SIGNATURE METHOD, AND APPARATUS AND KITS THEREFOR

[0001] This application claims priority to Australian Provisional Application No. 2014900363 entitled "Biomarker signature method, and apparatus and kits therefor" filed 6 February 2014, the entire contents of which are incorporated herein by reference.

Background of the Invention

[0002] The present invention relates to method, kit and apparatus and to reagents and compositions associated therewith for deriving an indicator for use in diagnosing the presence, absence or degree of at least one condition in a biological subject or in prognosing at least one condition in a biological subject, to a biomarker signature for use in diagnosing the presence, absence or degree of at least one condition in a biological subject or in prognosing at least one condition in a biological subject, and to a method, kit and apparatus, as well as reagents and compositions associated therewith, for identifying biomarkers for use in a biomarker signature.

Description of the Prior Art

[0003] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that the prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavor to which this specification relates.

[0004] The analysis of gene expression products for diagnostic purposes is known. Such analysis requires identification of one or more genes that can be used to generate a signature for use in distinguishing between different conditions. However, such identification can require the analysis of many gene expression products, which can be mathematically complex, computationally expensive and hence difficult. Much of the biomarker discovery process is devoted to identifying a subset of the data that may have relevant import, from which a signature is derived using a combination of these values to produce a model for diagnostic or prognostic use.

[0005] WO2004/044236 describes a method of determining the status of a subject. In particular, this is achieved by obtaining subject data including respective values for each of a number of parameters, the parameter values being indicative of the current biological status

of the subject. The subject data are compared to predetermined data that includes values for at least some of the parameters and an indication of the condition. The status of the subject, and in particular, the presence and/or absence of the one or more conditions, can then be determined in accordance with the results of the comparison.

[0006] US2010/0028876 describes methods for diagnosing biological states or conditions based on ratios of gene expression data from cell or tissue samples, such as cancer cell or tissue samples, by differentiating between cell types, including cancer cell types. The invention provides sets of genes that are expressed differentially in normal and cancer lung cells and tissues to be able to differentiate these cells and tissues. Such cellular differentiation is important in diagnosing cancer and cancer types. The sets of genes are identified by the degree (fold change) of up or down regulation. These sets of genes can be used to discriminate between normal and malignant cells or tissues, and between classes of malignant cells or tissues. Accordingly, diagnostic assays for classification of tumors, prediction of tumor outcome, selecting and monitoring treatment regimens and monitoring tumor progression/regression also are provided.

[0007] However, traditional methods for biomarker identification and traditional combinations of biomarkers use a relatively large number of biomarkers, which in turn makes tests expensive to perform, limiting their use in practice. In addition, the prior art does not describe the use of immune system biomarker ratios, or a method of identifying minimal sets of immune system biomarker ratios useful in determining the presence, absence, degree or prognosis of immune system-mediated medical conditions.

Summary of the Present Invention

[0008] In one broad form the present invention seeks to provide a method for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the method including:

a) determining a pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determining a derived biomarker value using the pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and,

c) determining the indicator using the derived biomarker value.

[0009] Typically the method includes:

a) determining a first derived biomarker value using a first pair of biomarker values, the first derived biomarker value being indicative of a ratio of concentrations of first and second immune system biomarkers;

b) determining a second derived biomarker value using a second pair of biomarker values, the second derived biomarker value being indicative of a ratio of concentrations of third and fourth immune system biomarkers; and,

c) determining the indicator by combining the first and second derived biomarker values.

[0010] Typically the method includes combining the derived biomarker values using a combining function, the combining function being at least one of:

a) an additive model;

b) a linear model;

c) a support vector machine;

d) a neural network model;

e) a random forest model;

f) a regression model;

g) a genetic algorithm;

h) an annealing algorithm;

i) a weighted sum;

j) a nearest neighbor model; and,

k) a probabilistic model.

[0011] Typically the method is performed at least in part using an electronic processing device.

[0012] Typically the method includes, in at least one electronic processing device:

a) obtaining at least two pairs of measured biomarker values, each measured biomarker value being a measured value of a corresponding immune system biomarker of the biological subject;
b) determining a first derived biomarker value indicative of a ratio of concentrations of first and second immune system biomarkers;
c) determining a second derived biomarker value indicative of a ratio of third and fourth immune system biomarkers; and,
d) determining the indicator by combining the first and second derived biomarker values.

[0013] Typically the method includes, in at least one processing device, generating a representation of the indicator.

[0014] Typically the representation includes:

a) an alphanumeric indication of the indicator;
b) a graphical indication of a comparison of the indicator to one or more indicator references;
c) an alphanumeric indication of a likelihood of the subject having at least one medical condition.

[0015] Typically the method includes:

a) comparing the indicator to an indicator reference; and,
b) determining a likelihood in accordance with results of the comparison.

[0016] Typically the indicator reference is based on at least one of:

a) an indicator threshold range;
b) an indicator threshold; and,
c) an indicator distribution.

[0017] Typically the indicator reference is derived from indicators determined for a number of individuals in a reference population.

[0018] Typically the indicator reference is based on a distribution of indicators determined for a group of a reference population, the group consisting of individuals diagnosed as having the medical condition or lacking the medical condition.

[0019] Typically the reference population includes:

a) a plurality of individuals of different sexes;
b) a plurality of individuals of different ethnicities;
c) a plurality of healthy individuals;
d) a plurality of individuals suffering from at least one diagnosed medical condition;
e) a plurality of individuals lacking the at least one diagnosed medical condition;
f) a plurality of individuals showing clinical signs of at least one medical condition;
g) first and second groups of individuals, each group of individuals suffering from a respective diagnosed medical condition; and,
h) first and second groups of individuals, the first group of individuals suffering from a diagnosed medical condition, and the second group lacking the diagnosed medical condition.

[0020] Typically the indicator is for use in determining the likelihood that a biological subject has at least one medical condition, and wherein the reference population includes:

a) individuals presenting with clinical signs of the at least one medical condition;
b) individuals diagnosed as having the at least one medical condition;
c) individuals diagnosed as lacking the at least one medical condition; and,
d) healthy individuals.

[0021] Typically the indicator reference is retrieved from a database.

[0022] Typically the likelihood is based on a probability generated using the results of the comparison.

[0023] Typically the indicator is for determining a likelihood of the subject having a first or second condition, and wherein the method includes:

a) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of first and second conditions; and,
b) determining the likelihood in accordance with the results of the comparison.

[0024] Typically the method includes:

a) determining first and second indicator probabilities using the results of the comparisons; and,
b) combining the first and second indicator probabilities to determine a condition probability indicative of the likelihood.

[0025] Typically the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with the first or second condition respectively.

[0026] Typically the method includes:

a) obtaining a sample taken from the biological subject, the sample including polynucleotide expression products; and,

b) quantifying at least some of the polynucleotide expression products within the sample to determine the pair of biomarker values.

[0027] Typically the method includes, determining the indicator at least in part using a ratio of concentrations of the polynucleotide expression products.

[0028] Typically the method includes:

a) quantifying polynucleotide expression products by:

b) amplifying at least some polynucleotide expression products in the sample; and,

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products; and,

d) determining the indicator by determining a difference between the amplification amounts.

[0029] Typically the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

[0030] Typically the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of a first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of a second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

[0031] Typically the immune system biomarker is a biomarker of an immune system of the biological subject that is altered, or whose level of expression is altered, as part of an inflammatory response to damage or pathogenic insult.

[0032] Typically:

a) the at least two immune system biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

b) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0033] Typically the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

[0034] Typically each immune system biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

[0035] Typically the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

[0036] Typically the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;

b) 0.5;

c) 0.6;

d) 0.7;

e) 0.8; and,

f) 0.9.

[0037] Typically the immune system biomarker value is indicative of a level or abundance of a molecule selected from one or more of a nucleic acid molecule and a proteinaceous molecule.

[0038] In some embodiments, the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein the method includes:

a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,

c) determining the indicator using the first and second pairs of biomarker values.

[0039] In some embodiments, the indicator is for determining a likelihood of the subject having inSIRS or a healthy condition, and wherein biomarker values are determined from at least one inflammatory response syndrome (IRS) immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *NUMB*, *RAB27A*, *USP3//LOC100130855*, *HIF1A*, *LBXCOR1//PIAS1//CALML4*, *SQRDL*, *C20orf74*, *IL10RB*, *PARP4*, *DNTTIP1*, *MTMR6//LOC646482*, *LAMP2*, *MAPK1*, *SERINC3//TTPAL*, *IGSF6//METTL9*, *RP2*, *C18orf32*, *LOC284757*, *MTMR10//MTMR15*, *SLC12A6*, *LCP1*, *CHP*, *PRR13*, *C20orf177*, *ZFP106*, *DICER1*, *PHF12*, *IFNAR1*, *BNIP2*, *UBE2A*, *NIN*, *MBD2//SNORA37*, *TM9SF2*, *RAB8B*, *CLIP1*, *WAS*, *DNAJC3*, *CDADC1*, *KIAA0317*, *MED13L*, *INTS6*, *PDK3*, *MYO5A*, *NUPL1*, *VEZF1*, *CUL4B*,

USP9X//USP9Y, *RPS6KA3*, *IL17RA//CECR7*, *ELF1*, *TMX4*, *TAOK1*, *ELMO2*, *STAT5B//STAT5A*, *PAN3//EEF1A1//CHCHD2*, *SIPA1L1//SNORD56B//LOC145474//LOC283567*, *OSBPL1A*, *SYNJ1*, *U2AF1*, *NPEPPS//TBC1D3F//LOC440434*, *AP1G1*, *SNTB2*, *ZNF230//ZNF222*, *LYRM1*, *ME2*, *GALNT1*, *DYRK1A*, *ZMYM2*, *ARID4A*, *TOB1*, *DOCK11*, *ACTR10*, *ZMYM5//ZMYM2*, *FNDC3A*, *NUFIP2*, *STRADA*, *SPG11//ISLR*, *SPATA13//C1QTNF9*, *BRWD3*, *BACH1*, *CLTC*, *LIG4*, *C21orf41//BACH1*, *KPNB1*, *DHRS7*, *USP8*, *LACTB*, *SYNE2*, *ZDHHC20//LOC728099*, *EAPP*, *MED13//LOC100129112*, *TAOK3*, *NLGN3*, *CIT*, *RIPK3*, *CP110*, *ABHD2*, *GNA13*, *GGNBP2*, *PXN* and *PTPN1* (hereafter referred to interchangeably herein as "group A IRS immune system biomarker genes" or "group A IRS biomarker genes"); and

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *AGFG1*, *BMX//HNRPDL*, *MCM5*, *TRIM28*, *GRWD1*, *ZNF574*, *ARRDC2*, *PELP1*, *SHPK*, *GPS1*, *FAM38A*, *FBXO31*, *C16orf58//LOC100128371*, *NLRC3*, *JMJD8*, *CDK10*, *TRAPPC2L*, *PRMT7*, *BRF1*, *MTA1//LOC647310//LOC100128343*, *PLD4*, *DDX54//CCDC42B*, *PLBD1*, *IRAK3*, *FGD4*, *ARG1*, *RANGAP1*, *UNC84B*, *SAMSN1//LOC388813*, *PFKL*, *S100A12*, *KIF22*, *LRRN1*, *CCDC134*, *LZTR1*, *GZMM*, *ICAM2*, *TMC8*, *LAT//SPNS1//NPIPL2//LOC728741//LOC730153//NPIPL3//SPIN1//LOC728888//LOC100289169//LOC728734//LOC729602//LOC100288442//LOC100288332*, *CLEC4D*, *CDK5RAP1*, *PPP1R16B*, *DAZAP1*, *LMF1*, *EDC4*, *IL21R//LOC283888*, *JMJD7-PLA2G4B//JMJD7//PLA2G4B*, *TMEM120B//RHOF*, *ENTPD1//C10orf131*, *ACSL1*, *ZC3H7B*, *CHERP//C19orf44//CALR3*, *U2AF2*, *PYGL*, *SOS2*, *ANKRD22*, *MEGF9*, *MGAM//LOC100124692*, *IL1R2*, *IL2RB*, *FCAR*, *IL27RA*, *DHX37*, *PATZ1*, *PRDM15*, *NOSIP*, *RPTOR*, *SPG7*, *DNAJA3*, *VNN1*, *SEPT9*, *THAP11*, *LPCAT2*, *MAN2C1*, *PITPNM2*, *NOC2L//SAMD11//LOC401010*, *ZMYM3*, *FTSJ1*, *KCNE1*, *ACTR5*, *FAM110A*, *FAM134C*, *LLGL2*, *INF2*, *KDM2B*, *ACSL4*, *B4GALT5*, *CD79B*, *BCL11B*, *ERLIN1*, *TLR4*, *EVL*, *SRGN*, *SLC37A3*, *GPR141*, *MSL3*, *MMP9//LOC100128028*, *MAP2K6*, *PHTF1*, *KLHL36*, *POLR3E*, *PCNX*, *PNKP*, *TMEM104*, *TRPV2*,

SEPT1, *APH1B*, *POLE*, *MED24*, *MPI*, *C12orf49*, *PES1*, *ERCC1//CD3EAP*, *CD177*, *CPD*, *MEF2A//LYSMD4*, *C14orf43*, *RPLP0*, *CDC25B*, *SYMPK*, *ARHGEF18//LOC100128573*, *PSTPIP2*, *HERC2//HERC2P2//HERC2P3//LOC440248*, *MAPK14*, *F5*, *PLCG1*, *ZNF416*, *AARS*, *KLHL2*, *APOBEC3A//APOBEC3B*, *CMTM1//CKLF*, *USP11*, *MAP3K14//LOC100133991*, *GOLGA3*, *TMEM204*, *S100A8*, *IL1R1*, *DHPS*, *PPP2R1A*, *UBTF*, *DRG2*, *DNMT1*, *USP36*, *ZBTB4*, *TSC2*, *KIAA0195*, *KIAA0182*, *ALOX5AP*, *TGIF2*, *ST20//C15orf37*, *FN3KRP*, *ABCD4*, *ZFP64*, *NEO1*, *PPIL2//YPEL1*, *RNPS1*, *NF2*, *SERPINB1*, *DDX51*, *PRPF6*, *TIMM22*, *SYS1//SYS1-DBNDD2//DBNDD2*, *RAB31*, *KRI1*, *SMARCA4*, *CLUAP1*, *C16orf67*, *C20orf4*, *CHTF8//HAS3*, *NPTN*, *CSRP2BP*, *AES*, *ODZ1*, *MTMR15//MTMR10*, *SIRPD*, *EEF2//SNORD37*, *DKC1//SNORA36A//SNORA56*, *CEACAM4*, *C12orf43*, *RANBP3*, *EEF2K*, *LOC338799*, *PLP2*, *AKAP8*, *ELAC2*, *AKAP1*, *TBC1D4*, *ALOX5*, *WSB1*, *BAZ1A*, *ETS2*, *GGA2*, *CSTF2//RAD21*, *METTL9*, *GYG1*, *CRAMP1L//HN1L*, *EVI2B*, *PPP1R13B*, *POP5*, *C20orf3*, *WDR59*, *KCNJ15*, *PGLYRP1*, *ELAVL1*, *SLC25A1*, *PSMD3*, *CDC42EP3*, *FTSJ3*, *C2CD2*, *RBM19*, *CDH26*, *TRMT2B*, *GTF2F1//LOC100130856*, *SNRPN//SNURF//IPW//SNORD116-16//SNORD116-18//SNORD116-21//SNORD116-22//SNORD116-17//SNORD116-19//PAR5//PAR-SN//SNORD116-2//SNORD116-25//SNORD116-26//SNORD107//SNORD115-12//SNORD115-5//SNORD115-6//SNORD115-9//SNORD116-11//SNORD116-12//SNORD116-13//SNORD116-28//SNORD116-4//SNORD64//PAR1//SNORD109A//SNORD109B//SNORD116-6//SNORD116-3//SNORD116-9//SNORD115-13//SNORD115-1//SNORD115-14//SNORD115-15//SNORD115-21//SNORD115-10//SNORD115-7//SNORD115-16//SNORD115-40//SNORD115-42//SNORD115-11//SNORD115-29//SNORD115-34//SNORD115-36//SNORD115-4//SNORD115-43//HBII-52-24//SNORD116-5//SNORD116-7//SNORD115-26//SNORD115-30//SNORD116-15//SNORD116-8//SNORD115-2//SNORD115-39//SNORD116-14//SNORD116-20//SNORD115-8//SNORD115-3//SNORD115-38//SNORD115-41//SNORD115-22//SNORD115-44//SNORD116-1//SNORD115-17//SNORD115-18//SNORD115-19//SNORD115-20//SNORD116@*, *SLC9A8*, *RPA1*, *ADARB1*, *AFG3L2*, *MCTP2*, *DACH1*, *SEH1L*,

RRP1B, *ZNF335*, *WDR73*, *TAF15*, *MOSPD2*, *WIPI1//ARSG*, *ARRB2*, *PLIN5//LRG1*, *SNRPD3//C22orf13*, *CTNNBL1*, *ZNF175*, *NCF4*, *DDX27*, *FBXO21*, *TDP1*, *ATXN2L*, *ILF3*, *VAPA*, *DDX19B//DDX19A*, *NCOR2*, *KL*, *MTHFS*, *TOM1L2//LOC246315*, *APOBEC3D*, *EXD2*, *CDR2//RRN3//LOC100131998//LOC653390*, *ADCY4*, *DHX33*, *CKLF*, *GTF3C1*, *PRKCSH*, *DHX35*, *HSPH1*, *CCDC92*, *BCOR*, *CCPG1//PIGB//DYX1C1*, *MCM3AP*, *FPR1*, *ZNF460*, *AKAP8L*, *DCAF7*, *RNF24*, *NSMCE1*, *PDHA1*, *SAFB2//SAFB*, *ITM2B*, *ZNF236*, *PI4KA//PI4KAP1//PI4KAP2//LOC100293141*, *CSTB*, *C14orf138*, *ITGAL*, *ARID3A*, *COG7*, *TYROBP*, *HP//HPR*, *SRCAP//SNORA30*, *COG1*, *GK//GK3P//FTL//LOC652904*, *C15orf63//SERF2*, *SERPINA6*, *SMG6//C17orf6*, *INO80*, *C16orf62*, *RAB35*, *PEF1*, *C14orf101*, *TMEM185A*, *LIMK2*, *CTCF*, *DIABLO//B3GNT4*, *VPS33A*, *UNQ1887*, *TBCB//POLR2I*, *ABHD13*, *SLC24A6*, *EDNRB*, *CA12*, *ANAPC5*, *TMC3*, *TRIAP1*, *ABHD12B*, *TDRD9*, *EIF2B1*, *CXorf59*, *LRRC37A3//LRRC37A2//LRRC37A//ARL17P1//LRRC37A4//LOC100294335//LOC644397*, *SDS*, *SYCP2*, *TBC1D8B*, *TMEM31*, *GUCY1B2*, *PFN1*, *SLC24A3*, *ABCC11//LONP2* and *ZNF257//ZNF492//ZNF99//ZNF98//LOC646864* (hereafter referred to interchangeably herein as "group B IRS immune system biomarker genes" or "group B IRS biomarker genes").

[0040] In some embodiments, the indicator is for determining a likelihood of the subject having ipSIRS or a healthy condition, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *LTBP3*, *LPHN1*, *NR1D1//THRA*, *METTL9*, *PLD4*, *MAPK14*, *FAM102A*, *MYBBP1A//SPNS2*, *FLJ10232*, *SEMA4C*, *LMF1*, *PLBD1*, *MAN1C1*, *B4GALT5*, *ENGASE*, *NDRG2*, *TLR5*, *WDR4*, *PATZ1*, *CD177*, *LILRA5*, *SIRPD*, *ADAMTS10*, *TCF7*, *GGT7*, *GYG1*, *CDAN1*, *BRF1*, *GPR84*, *TMC6//LOC100131096*, *PGAP3*, *GRAP//SNORD3B-1//SNORD3B-2//LOC400581*, *SHPK*, *NOG*, *PVRIG//PILRB//STAG3*, *TDRD9*, *TMC8*, *C14orf21*, *NLRC4*, *APBA2*, *TBL3*, *LDOC1L*, *C16orf58//LOC100128371*, *KLHL3*, *IRAK3*,

JMJD7-PLA2G4B//JMJD7//PLA2G4B, *RAB31*, *IL10RB*, *NFATC1//LOC100127994*, *S100A12*, *SLC2A3//SLC2A14*, *GPA33*, *PLXDC1*, *BCL6//LOC100131635*, *GTPBP3*, *SQRDL*, *CD7*, *TMEM177//LOC100125918*, *FBXO31*, *CACNA1E*, *LILRA4*, *FAM38A*, *UBE2J1*, *SBF1//SBF1P1*, *TMEM204*, *FCAR*, *CDK4/MARCH9/C3HC4*, *ZBTB4*, *PIWIL4*, *RNASE2//LOC643332*, *PRMT7*, *AGFG1*, *CMTM1//CKLF*, *MCTP1*, *ARL11*, *FMNL3//PRPF40B*, *FAM151B*, *BAHD1*, *OSBPL7*, *ZAP70*, *TUBGCP6*, *MAP2K6*, *NPTN*, *C3AR1*, *CD247*, *S100A8*, *TBCD*, *LMNB1//PCIF1*, *PFKL*, *GRWD1*, *PYGL*, *UPP1*, *OMG*, *SAMSN1//LOC388813*, *BLCAP*, *PTPRS*, *FAM20A*, *CARD6*, *SPPL2B*, *IL2RB*, *SORT1*, *BST1*, *TAF1C//ADAD2*, *SEMA4F*, *NCAPH2*, *MCTP2*, *ZAK*, *CCR7*, *MAN2C1*, *NEURL4//GPS2//D4S234E*, *BMX//HNRPDL*, *TRAPPC6A*, *LPCAT2*, *C19orf60*, *SLC4A10*, *C14orf101*, *TP53I3*, *IL1RN*, *AIM2*, *UBE2R2*, *PNKP*, *ZNF70*, *SEPT1*, *NEO1*, *MPRIP*, *DPH1//OVCA2*, *C16orf67*, *CD58*, *RAB27A*, *EEF2K*, *CLIC1*, *MBLAC2*, *IFNGR2*, *CRTC1//MAML2*, *CACNB1*, *GALNT3*, *C19orf6*, *C20orf74*, *RALB*, *GPRASP1*, *CA4*, *ETS2*, *RP2*, *MARS2*, *RAB32*, *FAIM3*, *C20orf24//SLA2*, *ZNF549*, *PIGL*, *PHTF1*, *IL18R1*, *IPO4*, *ZFP106*, *SLC12A4*, *DNTTIP1*, *S100A11*, *ZNF544*, *ATXN1*, *GNLY*, *MID2*, *BACH2*, *INF2*, *ARFGAP1*, *MSL3*, *SOS2*, *ARL8A*, *PTPRJ//OR4B1*, *NAT9*, *RHOT2//FBXL16*, *PNPLA1*, *DNAJC13*, *GNG5*, *FAM129C*, *PXK*, *C10orf119*, *BATF*, *LMO7*, *KLF2*, *NRD1*, *CLCN7*, *GLA*, *CFLAR*, *SYCP2*, *IMAGE5303689*, *LPGAT1*, *PTGDR*, *LAMP2*, *ZNF607*, *INSL3//JAK3*, *DUSP3*, *PCNX*, *CD79B*, *IRAK1*, *ZNF550//ZNF549*, *LOC100130950*, *SPTLC2*, *CTSA*, *RAP2C*, *ADCY9*, *MED12L*, *MTHFD2*, *CAP1*, *TOR1AIP2//TOR1AIP1//IFRG15*, *CHP*, *TSEN2*, *LYRM1*, *UBE2A*, *NUPL1*, *YIPF1*, *FRMD3*, *KAL1*, *CLTC*, *FLVCR2//RPS24*, *WSB2*, *KIAA0040*, *JAG1*, *GPR183*, *N6AMT1*, *ZNF563*, *AP3B2*, *SERPINB2//SERPINB10*, *CDH2*, *ITFG1*, *EDEM2*, *RNF135*, *HPSE*, *DSC1*, *FOXN2*, *RASSF2*, *ZNF420*, *ZFP28*, *UBE2G2//SUMO3*, *PTTG1IP*, *PRKCB*, *KIT*, *PLEK*, *MAP4K4*, *GBA//GBAP*, *CLIP1*, *EDEM3*, *SERINC3//TTPAL*, *TPST2*, *HNRPLL*, *TP53BP2*, *KCND1*, *GCLM*, *RIT1*, *OSCAR*, *DDX59*, *EDNRB*, *ELMO2*, *RRAGC*, *AFTPH*, *DCUN1D3//LYRM1*, *RSBN1*, *IFI30*, *SNX1*, *PTPN1*, *SEP15*, *ARMCX5*, *ALAS1*, *NFKBIA*, *STXBP2//LOC554363//LOC100131801*, *C15orf24*, *SRI*, *ASGR2*, *NSF//LOC728806*, *TRIM69*, *SEC23A*, *PLAUR*,

RAB3GAP2//AURKAPS1//AURKA//SNORA36B, *MAOB//NAT13*, *DEDD*, *SEC23B*, *COPA*, *EGF*, *STRADA*, *SIAE*, *C5*, *SLC30A1*, *ANXA4*, *NKG7*, *ABHD12B*, *TESK2*, *LONRF3*, *PIKFYVE*, *SH3BGRL3*, *ARMCX3*, *NEU1*, *SPAST*, *STX6//KIAA1614*, *TADA3L*, *LIN37//PSENEN*, *UBR3*, *WDR90*, *RTN2* and *TMUB2* (hereafter referred interchangeably herein as "group C IRS immune system biomarker genes" or "group C IRS biomarker genes"); and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *CNNM3*, *SLC25A45*, *UNC84B*, *ARHGEF18//LOC100128573*, *PIK3IP1*, *EPHX2*, *SEPT9*, *ITPKB*, *TSPYL2//GPR173*, *GALT*, *USP11*, *CBX7//LOC100128400*, *MAP3K14//LOC100133991*, *CDK5RAP1*, *KLHL36*, *SPG7*, *ZNF574*, *RASA3*, *KLHL22//KRT18*, *PYGO2*, *USP36*, *LCK*, *SKI*, *C5orf45//SQSTM1*, *PIK3C2B//LOC100130573*, *ANGEL1*, *ZCCHC14*, *CIRBP*, *ZMIZ2*, *TMEM120B//RHOF*, *NOC2L//SAMD11//LOC401010*, *PPP1R13B*, *ZNF416*, *PBXIP1*, *SMYD5//NOTO*, *ZNF529*, *EDC4*, *LENG8*, *TBC1D22A//LOC100289878*, *CORO7*, *COG8//PDF*, *CUL9*, *RASGRF2*, *CHERP//C19orf44//CALR3*, *POLR3E*, *CNNM4*, *TSC2*, *XYLT2//LOC100130580*, *TP53*, *LMBR1L*, *AKT1*, *SLC7A6//SLC7A6OS*, *LDLRAP1*, *SGSM2*, *ZNF764//ZNF747*, *AKAP1*, *RNPS1*, *ICAM2*, *KIF3A*, *TGIF2*, *VAC14//LOC100130894*, *CXXC5*, *DCAF15*, *TARBP1*, *RCAN3*, *IMP4*, *LUC7L*, *SIN3B*, *TRMT2B*, *POFUT2*, *AXIN1*, *PPIL2//YPEL1*, *NLRP1//LOC728392*, *TMEM63A*, *TMEM208*, *ZNF362*, *GNG7*, *CASS4*, *ZNF287*, *DGKE*, *CEP68*, *ASXL1*, *CLUAP1*, *WDR89*, *CD40LG*, *MGC57346//C17orf69*, *PPIE//CCDC25*, *FCHO1*, *TNPO2//SNORD41*, *CSNK1E//LOC400927*, *CLYBL*, *XAB2*, *METT10D//LOC284009*, *PRPF6*, *AKAP8*, *SH3BP1//PDXP*, *TOM1L2//LOC246315*, *ZNF329*, *ZNF274*, *FAM119A*, *SMYD3*, *UNC84A//C7orf20*, *ZNF256*, *PSD4*, *CCDC130*, *LIMD2//MAP3K3*, *ELP2*, *ZNF8*, *AFG3L2*, *TXK*, *DDX27*, *FBXL12*, *TNRC6C*, *TADA1L*, *KIAA0355//FLJ21369*, *ZNF211*, *ZNF808//ZNF578//ZNF611*, *SRCAP//SNORA30*, *BANP//RUNDC2C*, *ADARB1*, *CCDC71*, *KTI12*, *TCF25*, *XYLT1//LYRM2//ZC3H11A*, *DET1*, *ABCF3*, *PRKCZ*, *KIAA0141*, *CHI3L1*, *RPGRIP1*, *TTC31*, *MTMR15//MTMR10*, *MEF2D*, *TMEM50B*, *GLOD4*, *PRPF8*, *C14orf43*, *P2RX5*, *MSH2*, *PCCA*, *DENND4B*,

SLC43A2, *MAPK8IP3*, *TUBGCP5*, *C19orf2*, *SEH1L*, *CCDC104*, *TRIM62*, *TDRKH*, *COG1*, *POLR1B*, *AFG3L1*, *TYK2*, *RBM3*, *UBTF*, *RP11-94I2.2//NBPF16//NBPF11//NBPF15//NBPF8//NBPF20//NBPF10//NBPF14//NBPF1//LOC100288142//NBPF12//KIAA1245//LOC100290137*, *ZNF41*, *ZNF461*, *PI4KA//PI4KAP1//PI4KAP2//LOC100293141*, *THEM4*, *BCL11A*, *CC2D1B*, *WDR73*, *BBS2//OGFOD1*, *RRN3//LOC653390//LOC730092//LOC100131998*, *NOP58*, *NUCKS1*, *ZNHIT6*, *RXRB*, *AKT3*, *FANCM*, *ERN1*, *FAM117B*, *COX11//TOM1L1*, *ACVR2A*, *RP3-402G11.5*, *AHCTF1*, *CLN8*, *NVL*, *SAPS2*, *DPEP3*, *PDE3B*, *DPEP2*, *GGA1*, *CCDC50*, *SNRPN//SNURF//IPW//SNORD116-16//SNORD116-18//SNORD116-21//SNORD116-22//SNORD116-17//SNORD116-19//PAR5//PAR-SN//SNORD116-2//SNORD116-25//SNORD116-26//SNORD107//SNORD115-12//SNORD115-5//SNORD115-6//SNORD115-9//SNORD116-11//SNORD116-12//SNORD116-13//SNORD116-28//SNORD116-4//SNORD64//PAR1//SNORD109A//SNORD109B//SNORD116-6//SNORD116-3//SNORD116-9//SNORD115-13//SNORD115-1//SNORD115-14//SNORD115-15//SNORD115-21//SNORD115-10//SNORD115-7//SNORD115-16//SNORD115-40//SNORD115-42//SNORD115-11//SNORD115-29//SNORD115-34//SNORD115-36//SNORD115-4//SNORD115-43//HBII-52-24//SNORD116-5//SNORD116-7//SNORD115-26//SNORD115-30//SNORD116-15//SNORD116-8//SNORD115-2//SNORD115-39//SNORD116-14//SNORD116-20//SNORD115-8//SNORD115-3//SNORD115-38//SNORD115-41//SNORD115-22//SNORD115-44//SNORD116-1//SNORD115-17//SNORD115-18//SNORD115-19//SNORD115-20//SNORD116@*, *C17orf65//ASB16*, *ZNF317*, *SNRNP200*, *CXorf26*, *MTBP*, *NOL11//SNORA38B*, *CCNL2*, *ALDOC*, *PITPNC1*, *FASTKD2*, *ZZZ3*, *PIK3R5*, *WDR82*, *GLDN*, *CHML*, *C15orf40*, *DIDO1*, *CLCC1//GPSM2//C1orf62*, *SLC35D1*, *SCRN1*, *C15orf63//SERF2*, *ZNF460*, *SAFB2//SAFB*, *C16orf54*, *DDX18*, *CTPS2*, *ZNF382*, *ZNF101*, *LIPT1//MRPL30*, *ITGA6*, *KIF21B*, *INPP5B*, *SF3A1//CCDC157*, *ODF2L*, *NUAK2*, *CHCHD5*, *AHSA2//USP34*, *YLPM1*, *TERF2*, *ZNF830*, *MAN2B1//MORG1*, *GPATCH8*, *SHC1*, *SEPT4*, *SFRS2*, *TMC3*, *OTUD5*, *NARG1L*, *MKL1//KIAA1659*, *YTHDF1*, *SLC14A2*, *GGA3* and *EXOC7* (hereafter referred to interchangeably herein as “group D IRS immune system biomarker genes” or “group D IRS biomarker genes”).

[0041] In some embodiments, the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *ALKBH5 // FLJ13773*, *RPS19BP1*, *RFXANK // MEF2B // LOC729991*, *NA*, *CDC6*, *C19orf56*, *NA*, *ABCC2*, *THAP11*, *RTN2*, *MAZ*, *TAX1BP3*, *NUTF2*, *MPZL3*, *FBXW5*, *HIST1H2BM*, *CETP*, *PQLC1*, *H2AFX*, *KIAA0101 // CSNK1G1*, *STK17B*, *SMARCD3*, *LOC100134934 // CDK3*, *LPCAT4*, *LPP*, *MPZL2*, *ANKRD9*, *PRR13 // PCBP2*, *MDS2*, *RBM33*, *GATAD2B // PLIN2*, *PPTC7*, *MYBL2*, *OIP5*, *PLA2G7*, *CRIPT*, *RNF186*, *CCDC125*, *TLE3*, *C3orf35*, *SAP130*, *MXD1*, *ZHX2*, *CDK5RAP3*, *ENTPD1 // C10orf131*, *NDUFB7*, *POGZ*, *DOK3*, *MCM7*, *IL17F*, *CLPS* and *DUSP11* (hereafter referred to interchangeably herein as "group E IRS immune system biomarker genes" or "group E IRS biomarker genes"); and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *PIWIL4*, *C11orf82*, *ACRC*, *CLPTM1L*, *MAGED2*, *PLAC8*, *ZDHHC4*, *OTX1*, *INSIG1*, *BATF*, *MFSD11*, *DNASE1L1 // RPL10*, *C15orf24*, *CDS2*, *KEAP1*, *ARD1A*, *POLR2G*, *AHCY*, *SLC39A9*, *CUGBP1*, *FAM96B*, *TM7SF3*, *CTSZ*, *CD63*, *SPPL2A*, *ST3GAL2*, *SEC13*, *TM9SF1*, *IRAK2*, *GOSR2*, *ADIPOR2*, *TG*, *GABRR2*, *TPST2*, *DERL2*, *CCDC101 // LOC388242*, *VWA5A // OR10D1P*, *CD300A*, *MRPS34*, *PSMA7*, *MAPK6*, *JKAMP*, *TLR10*, *RAG1AP1*, *NEU1*, *SLC30A1*, *PDGFC*, *ATOX1*, *CYBASC3*, *TMEM205 // hCG_29977*, *FAM108B1*, *ACSS2*, *HIST1H4L*, *AGTRAP*, *RNF114*, *UBQLN2*, *EDF1*, *C20orf197*, *UBE2E1*, *RER1*, *ANKRD10*, *SEC22C*, *TM2D3*, *SLC15A2*, *TRIM28*, *COX15*, *CCDC109A*, *CSTF1*, *AIP*, *ACTR1A*, *HIST1H4I*, *YIF1B*, *TSPAN31*, *VPS26B*, *CNIH*, *TGFBR1*, *NIPA2 // CYFIP1*, *DDAH2*, *BID*, *CYB5R1*, *CEACAM4*, *KIT*, *GAB2*, *JAG1*, *RPGRIP1*, *VAT1*, *GNB5 // LOC100129973*, *SSR4 // IDH3G*, *LAMP1*, *MRPL41*, *RUNX2*, *ITFG1*, *DNASE1*, *ZNRD1 // NCRNA00171*, *NLRP1 // LOC728392*, *STT3A*, *MGAT4B // SQSTM1*, *KIAA1257 // ACAD9 //*

LOC100132731, *KLHL6*, *PTPN6*, *GALK2*, *DAD1 // OR6J1*, *PDLIM5*, *TMEM147*, *TRAM1 // LOC286190*, *LZTR1*, *TNPO1*, *ACSL5*, *C22orf37*, *PLK1*, *SYNE2*, *PSMD3*, *FLJ27255*, *PRKCD*, *RAB34*, *RPN2 // EEF1A2*, *SLC35B1*, *KCNIP3*, *PDE3B*, *PXMP2 // PGAM5*, *SDF2*, *HIST1H3I*, *LOC284757*, *TMEM33 // DCAF4L1*, *CSNK2A2*, *LSM10*, *PTTG1IP*, *ADRB3 // GOT1L1*, *PLXNA2*, *DIAPH2*, *BICD2*, *HAL*, *RPS6KC1*, *TMEM106C*, *CD1E*, *SLC35A5*, *C7orf26*, *IMP3*, *PICALM*, *ARF1*, *FHOD1 // SLC9A5*, *C19orf55*, *TOMM40L // NR1I3*, *INSIG2*, *NEK9*, *HCG27*, *SDHB*, *CUBN*, *PRDX3*, *CEPT1 // DRAM2*, *ERGIC1*, *KPNA3*, *VAV1*, *ELMO1*, *CUGBP2*, *LASP1*, *COL9A2*, *MEGF9*, *ELF4*, *SUZ12P*, *SULT1A2 // SULT1A1*, *FAM123C*, *FAR2*, *IER2*, *RGS2*, *MYBPH*, *MFAP3*, *RCHY1*, *MGAT1*, *MFSD4*, *CDH2*, *TMEM184C*, *CTRB2 // CTRB1*, *MPP4*, *PHF12*, *SLBP*, *ADAM19*, *HTR1B*, *TRIM55*, *CRNN*, *KLHDC7A*, *YIPF5*, *SLC11A1*, *GABBR1*, *CAMKV*, *SLC35F5*, *CHRNG*, *CXCL14*, *METTL6*, *PHC2*, *GPR153*, *TNFRSF10D*, *BAT2L*, *GALNT2*, *DENND3 // C8orf60*, *CLDN3*, *F11*, *CCDC93*, *FLJ46365*, *CYP21A2*, *ETV5*, *TRPM2*, *IL20*, *NBL1 // C1orf151*, *NGEF*, *POU6F2*, *PTEN // PTENP1*, *NPC1L1*, *CYP4B1*, *NFIC*, *PPARGC1A*, *PLIN3*, *THPO*, *TIMP4*, *CELSR2*, *DMBX1*, *CAMK2B*, *PPFIA1*, *HCLS1*, *SLC6A20*, *C17orf66 // RSL24D1*, *PIWIL2*, *DAZL // DAZ4 // DAZ3 // DAZ2*, *GAL3ST2*, *TPD52L1*, *C19orf34*, *RASGEF1C*, *BAALC // FLJ10489*, *NR4A2 // FLJ46875*, *HAPLN1*, *CLDN18*, *TAS1R1*, *TIMD4*, *SKI*, *CCDC48*, *MEGF10*, *OSBPL6*, *DNAH2*, *ARID1B*, *PGC*, *DCST1*, *SDK1*, *CHIA*, *REG4 // NBPF7*, *TMEM49 // CLTC // MIR21*, *TMEM44*, *NDUFB6 // DFFB*, *COL25A1*, *EPHX4*, *NCRNA00085*, *NTRK3*, *PKHD1*, *SLC2A7*, *NTRK1*, *ABHD1 // PREB*, *SLC4A9*, *GPNMB*, *SLC5A1*, *SLC7A8*, *RTCD1*, *PROC*, *C17orf64*, *FLJ14100 // C1orf86*, *NUP50*, *UNKL*, *C10orf18*, *TMEM61*, *C9orf68*, *CYTSA*, *MORN3*, *RAB17*, *CNNM3*, *CCDC28B*, *SH2D6*, *BARHL2*, *T*, *SNRK*, *TCP11*, *KDR*, *ENAM*, *UNKL*, *SPRR2C*, *GPR17 // LOC100291428 // LIMS2*, *C1orf175 // TTC4*, *CACNA1D*, *C2orf62*, *LOC100132686*, *UNQ6126*, *TRIM15*, *GPR113 // SELI*, *IL22*, *SCN10A*, *FAAH*, *MBOAT7*, *C7orf51*, *KIAA1530*, *TRPM8*, *C1orf95*, *DDC // LOC100129427*, *GABRA1*, *HCRTR1*, *DCST2*, *CHODL*, *PAN3 // EEF1A1 // CHCHD2*, *LYPD6B*, *UGT3A1* and *SERPINA6* (hereafter referred to interchangeably herein as “group F IRS immune system biomarker genes” or “group F IRS biomarker genes”).

[0042] In some embodiments, the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first, second, third and fourth IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *RPS19BP1*, *RFXANK//MEF2B//LOC729991*, *C19orf56*, *RTN2*, *HIST1H2BM*, *CETP*, *PQLC1*, *H2AFX*, *KIAA0101//CSNK1G1*, *LOC100134934//CDK3*, *LPCAT4*, *LPP*, *MPZL2*, *ANKRD9*, *RBM33*, *MYBL2*, *PLA2G7*, *OIP5*, *CRIPT*, *RNF186*, *C3orf35*, *ZHX2*, *NDUFB7* and *DUSP11* (hereafter referred to interchangeably herein as "group G IRS immune system biomarker genes" or "group G IRS biomarker genes");

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *PIWIL4*, *C11orf82*, *ACRC*, *PLAC8*, *ZDHHC4*, *OTX1*, *INSIG1*, *BATF*, *MFSD11*, *C15orf24*, *CDS2*, *POLR2G*, *SLC39A9*, *FAM96B*, *TM7SF3*, *SPPL2A*, *ADIPOR2*, *GOSR2*, *DERL2*, *TPST2*, *VWA5A//OR10D1P*, *CCDC101//LOC388242*, *MAPK6*, *PSMA7*, *JKAMP*, *TLR10*, *RAG1AP1*, *SLC30A1*, *PDGFC*, *ATOX1*, *TMEM205//hCG_29977*, *FAM108B1*, *UBQLN2*, *EDF1*, *C20orf197*, *RER1*, *UBE2E1*, *ANKRD10*, *SEC22C*, *TM2D3*, *SLC15A2*, *CCDC109A*, *HIST1H4I*, *TSPAN31*, *TGFBR1*, *CNIH*, *DDAH2*, *NIPA2//CYFIP1*, *BID*, *CYB5R1*, *KIT*, *RPGRIP1*, *MRPL41*, *RUNX2*, *ITFG1*, *ZNRD1//NCRNA00171*, *NLRP1//LOC728392*, *KIAA1257//ACAD9//LOC100132731*, *KLHL6*, *GALK2*, *DAD1//OR6J1*, *PDLIM5*, *TRAM1//LOC286190*, *TNPO1*, *ACSL5*, *SYNE2*, *RPN2//EEF1A2*, *SLC35B1*, *KCNIP3*, *TMEM33//DCAF4L1*, *CSNK2A2*, *LSM10*, *PLXNA2*, *DIAPH2*, *HAL*, *RPS6KC1*, *SLC35A5*, *PICALM*, *C19orf55*, *INSIG2*, *SDHB*, *PRDX3*, *CEPT1//DRAM2*, *KPNA3*, *SULT1A2//SULT1A1*, *FAR2*, *MYBPH*, *MFAP3*, *RCHY1*, *CDH2*, *TMEM184C*, *CTRB2//CTRB1*, *SLBP*, *CRNN*, *YIPF5*, *CHRNG*, *SLC35F5*, *METTL6*, *CLDN3*, *CCDC93*, *CYP21A2*, *NBL1//C1orf151*, *NGEF*, *POU6F2*, *NPC1L1*, *PPARGC1A*, *THPO*, *CELSR2*, *DMBX1*, *SLC6A20*,

C17orf66//RSL24D1, *GAL3ST2*, *C19orf34*, *BAALC//FLJ10489*, *CLDN18*, *TAS1R1*, *CCDC48*, *OSBPL6*, *SDK1*, *TMEM49//CLTC//MIR21*, *TMEM44*, *NDUFB6//DFFB*, *NCRNA00085*, *NTRK3*, *NTRK1*, *SLC4A9*, *SLC5A1*, *RTCD1*, *FLJ14100//C1orf86*, *PROC*, *C17orf64*, *UNKL*, *C9orf68*, *MORN3*, *RAB17*, *CNNM3*, *CCDC28B*, *BARHL2*, *UNKL*, *LOC100132686*, *UNQ6126*, *IL22*, *FAAH*, *C7orf51*, *DCST2*, *LYPD6B* and *SERPINA6* (hereafter referred to interchangeably herein as "group H IRS immune system biomarker genes" or "group H IRS biomarker genes");

c) the third IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *ALKBH5//FLJ13773*, *RNA243*, *ARD1A*, *CDC6*, *AHCY*, *MRPS34*, *CYBASC3*, *HIST1H4L*, *RNF114*, *TRIM28*, *CSTF1*, *CEACAM4*, *GAB2*, *GNB5//LOC100129973*, *THAP11*, *SSR4//IDH3G*, *STT3A*, *NUTF2*, *MPZL3*, *TMEM147*, *RAB34*, *PDE3B*, *PXMP2//PGAM5*, *HIST1H3I*, *LOC284757*, *TMEM106C*, *STK17B*, *IMP3*, *HCG27*, *CUBN*, *ERGIC1*, *ELMO1*, *CUGBP2*, *COL9A2*, *MEGF9*, *SUZ12P*, *FAM123C*, *RGS2*, *PRR13//PCBP2*, *PHF12*, *ADAM19*, *GATAD2B//PLIN2*, *SLC11A1*, *PPTC7*, *PHC2*, *BAT2L*, *DENND3//C8orf60*, *FLJ46365*, *ETV5*, *CCDC125*, *PTEN//PTENP1*, *TLE3*, *NFIC*, *TIMP4*, *PPFIA1*, *HCLS1*, *SAP130*, *MXD1*, *NR4A2//FLJ46875*, *SKI*, *ARID1B*, *ENTPD1//C10orf131*, *POGZ*, *DOK3*, *REG4//NBPF7*, *MCM7*, *SLC7A8*, *NUP50*, *C10orf18*, *TMEM61*, *SH2D6*, *SNRK*, *SPRR2C*, *CACNA1D*, *TRIM15*, *CLPS*, *MBOAT7*, *KIAA1530*, *C1orf95*, *GABRA1*, *HCRTR1*, *CHODL* and *PAN3//EEF1A1//CHCHD2* (hereafter referred to interchangeably herein as "group I IRS immune system biomarker genes" or "group I IRS biomarker genes"); and,

d) the fourth IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *CLPTM1L*, *MAGED2*, *DNASE1L1//RPL10*, *KEAP1*, *CUGBP1*, *CTSZ*, *CD63*, *ST3GAL2*, *SEC13*, *TM9SF1*, *IRAK2*, *GABRR2*, *TG*, *CD300A*, *NEU1*, *ACSS2*, *AGTRAP*, *UPF0627*, *COX15*, *ABCC2*, *ACTR1A*, *AIP*, *YIF1B*, *VPS26B*, *JAG1*, *VAT1*, *LAMP1*, *DNASE1*, *MAZ*, *TAX1BP3*, *MGAT4B//SQSTM1*, *FBXW5*, *PTPN6*, *LZTR1*, *PLK1*, *C22orf37*, *PSMD3*, *FLJ27255*, *PRKCD*, *SDF2*,

PTTG1IP, *ADRB3//GOT1L1*, *BICD2*, *CD1E*, *C7orf26*, *ARF1*, *FHOD1//SLC9A5*, *TOMM40L//NR1I3*, *NEK9*, *VAV1*, *SMARCD3*, *LASP1*, *ELF4*, *IER2*, *MGAT1*, *MFSD4*, *MDS2*, *MPP4*, *HTR1B*, *TRIM55*, *KLHDC7A*, *GABBR1*, *CAMKV*, *CXCL14*, *GPR153*, *TNFRSF10D*, *GALNT2*, *F11*, *IL20*, *TRPM2*, *CYP4B1*, *PLIN3*, *CAMK2B*, *PIWIL2*, *DAZL//DAZ4//DAZ3//DAZ2*, *TPD52L1*, *RASGEF1C*, *HAPLN1*, *TIMD4*, *CDK5RAP3*, *MEGF10*, *DNAH2*, *PGC*, *DCST1*, *CHIA*, *COL25A1*, *EPHX4*, *PKHD1*, *SLC2A7*, *ABHD1//PREB*, *GPNMB*, *CYTSA*, *T*, *TCP11*, *ENAM*, *KDR*, *GPR17//LOC100291428//LIMS2*, *C1orf175//TTC4*, *IL17F*, *C2orf62*, *GPR113//SELI*, *SCN10A*, *TRPM8*, *DDC//LOC100129427* and *UGT3A1* (hereafter referred to interchangeably herein as "group J IRS immune system biomarker genes" or "group J IRS biomarker genes").

[0043] In specific embodiments, the first IRS immune system biomarker is a *PLA2G7* expression product, the second IRS immune system biomarker is a *PLAC8* expression product, the third IRS immune system biomarker is a *CEACAM4* expression product and the fourth IRS immune system biomarker is a *LAMP1* expression product.

[0044] In some embodiments, the indicator is for determining a likelihood of the subject having mild sepsis or severe sepsis, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *N4BP2L2//CG030*, *FAM96A*, *MINPP1*, *MORC3//DOPEY2*, *LSM8*, *PLEKHA3*, *MITD1*, *ATF4*, *B2M*, *TMX3*, *ZNF273*, *PLEKHF2*, *UNQ2999*, *DPM1*, *OCLM*, *NADK*, *GPR65*, *SFRS3*, *ZNF28*, *PFDN4*, *COQ10B*, *SLC30A6//DDX50*, *KPNA5*, *ATP6V1G1*, *HAUS2*, *hCG_2039148*, *RAB33B*, *BET1*, *UBE2V2*, *ATP6AP2*, *SUB1//TMEM183A*, *TMEM188*, *ABHD3*, *LAPTM4A*, *RNF138*, *CCDC82*, *TMEM179B*, *PAPD4*, *VAMP2*, *CCDC126*, *ATG3*, *CHCHD5*, *RBM39//LOC643167*, *NAT8B*, *HAT1*, *CNOT6L*, *ZBED5*, *GOLT1B*, *TTC33*, *ACTN1*, *ACTR6*, *GNB4*, *TMEM208*, *CCNH*, *C4orf34*, *HAUS6//SCARNA8*, *TCTN1*, *SF3B14*, *TMEM138*, *TTC35*, *DLEU2//DLEU2L*, *MFSD8*, *COX7A2L*, *UGGT2*, *CEPT1//DRAM2*, *LEMD3*, *CREBZF*, *RPL21P44*, *ANGEL2*, *UFM1*,

XPO1, *CALM2//C2orf61*, *PLDN*, *CLK1//PPIL3*, *C1orf84*, *PPA2*, *FPGT//TNNI3K*, *ORC4L*, *SLC25A14*, *H3F3B//H3F3C*, *FAM188A*, *MCM9*, *KLHL9*, *NACA*, *PAFAH1B2*, *CRLS1*, *TSSK4*, *LOC152217*, *ZNF568*, *ATP6V0D1//LOC100132855*, *CDC37L1*, *FNTA*, *SHFM1*, *JKAMP*, *TMEM126B*, *MRPL47*, *DENND1B*, *ATP6V0E1//SNORA74B*, *LIN7C*, *HAUS3//POLN*, *SLC30A7*, *VAMP3*, *OBFC2A*, *MAGT1*, *STARD3NL*, *C5orf15*, *PSMD10*, *RERE*, *RNF139*, *SFT2D2*, *SKP1*, *RNPC3//AMY2B*, *MYOM1*, *TIPRL*, *HPRT1*, *TRIM21*, *VRK2*, *CDKN1B*, *ANKRA2*, *RAP2B*, *FAM127B//FAM127C//FAM127A*, *FAM126A*, *TMEM161B*, *UNQ1887*, *FANCF*, *SELT*, *CYP20A1*, *RWDD1*, *ARPP19*, *SC5DL*, *TICAM2//TMED7//TMED7-TICAM2*, *STAM*, *LEPROTL1*, *RNF44*, *DCP1B*, *TNNT3*, *UCHL5*, *UPRT*, *SON*, *PIK3C3*, *SFRS1//FLJ44342*, *FBXO22//FBXO22OS*, *SCFD1*, *C11orf31*, *TMTC3*, *CCDC132*, *TMBIM4//LOC100133322*, *ATAD1*, *APH1A*, *MYNN*, *HADHB*, *PIGN*, *RNA243*, *SLC38A9*, *C10orf84*, *CDKN1A*, *ATP7A*, *RPAP2*, *ZNF451*, *GSK3B//LOC100129275*, *TMSB10*, *KCTD5//PRO0461//PDPK1*, *VPS29*, *WIPF3//ZNRF2//LOC441208*, *SFRS5* and *C11orf73* (hereafter referred to interchangeably herein as “group K IRS immune system biomarker genes” or “group K IRS biomarker genes”); and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *C13orf1*, *PRKCB*, *APOBEC3A//APOBEC3B*, *SFRS9*, *NCAPD2//SCARNA10//FADS1*, *GATS*, *LOC284757*, *TSHZ2*, *JAK1*, *MAPK13*, *RPN1*, *GNAS*, *CYTSA*, *TRPM6*, *C22orf30*, *PCMTD1//PXDNL*, *CCDC69*, *ARSD*, *MLL3//BAGE2*, *NCOR1//C20orf191//LOC100131704*, *MRPS7*, *VEZF1*, *GSR*, *POU2F1*, *VPS4A*, *SMG7*, *PTP4A2*, *OSBP*, *GLCCI1//tcag7.903*, *DOCK2*, *PCNX*, *GLTP*, *FBXO18*, *YY2*, *TCF20*, *NR2C2//MRPS25*, *TEX2*, *BAMBI*, *WHSC1L1*, *UBTF*, *FAH*, *GEMIN4*, *DDEF1IT1*, *FAM50A*, *VPS13D*, *SATB1//TBC1D5*, *PARP6*, *SETD5*, *PHF21A*, *IRF4*, *ZNF217*, *UBE4A*, *HIVEP1*, *HDLBP*, *GNAI2*, *MED13L*, *FOXP1*, *NSD1*, *DDOST*, *TMBIM6*, *ABLIM1*, *SYNRG//LOC100131822*, *KDM3B*, *ASH1L*, *NCOA2*, *GPRIN3*, *NCOA1*, *KLF3*, *LOC100288114//MGC9913*, *VPS26B*, *AHCYL1*, *CDC6*, *PLCG2*, *IL16*, *GIT2*, *TACC3*, *MAP4K4*, *NEK9*, *FAM149B1//FAM149B2*, *VPS8*, *ATXN7*, *WDFY4*, *ZC3H11A//RP11-74E24.2*,

THRAP3, *ZNF346*, *AP3M2*, *CD14*, *CLASP1*, *ABCC2*, *ATXN7L1//RINT1//EFCAB10*, *INO80D*, *CTPS*, *LRRC37A3//LRRC37A2//LRRC37A//ARL17P1//LRRC37A4//LOC100294335//LOC644397*, *DNASE1*, *LRRN3*, *ZNF318*, *PRKAR2A*, *MRPS15*, *ANKHD1-EIF4EBP3//ANKHD1//EIF4EBP3*, *BTF3L4*, *DGKA*, *C10orf119*, *MBD5*, *C11orf30*, *CDC2L5*, *DPP4*, *DCTN4*, *TP53BP2*, *IMPDH2*, *GOT2*, *ELMO1* and *PARP1* (hereafter referred to interchangeably herein as "group L IRS immune system biomarker genes" or "group L IRS biomarker genes").

[0045] In some embodiments, the indicator is for determining a likelihood of the subject having mild sepsis or septic shock, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *EEF1DP3*, *GIMAP7*, *ZNF839*, *PYGL*, *TNFAIP8L2*, *SFRS9*, *VIM*, *GLTP*, *WDFY4*, *APPL2*, *C4orf3*, *PLD1*, *LIN7A*, *ELP2*, *ZDHHC3*, *UBAP1//KIF24*, *C20orf177*, *FAM149B1//FAM149B2*, *E2F3*, *SPATA1*, *DACH1*, *FAM47E//STBD1*, *SVIL//hCG_1783494*, *METTL9*, *LRRC42*, *NUPL1*, *UPP1*, *AFF2*, *SLC16A4*, *SET*, *CA4*, *HCK*, *C16orf72*, *EXT1*, *NOP58*, *FRZB*, *C9orf6//IKBKAP*, *VASP*, *ASB8//PHB*, *GTDC1*, *SLC39A9*, *FBXO34//KIAA0831*, *RABGEF1//tcag7.967//tcag7.951//KCTD7//LOC100293333*, *SLC28A3*, *WIPI1//ARSG*, *NFE2*, *GOLGA1//SCAI*, *C9orf84*, *RPS6KA2*, *PSMA7*, *C19orf59*, *ICA1*, *TOR1AIP2//TOR1AIP1//IFRG15*, *MSRA*, *FPR1*, *TP53I3*, *FOXL2*, *CD63*, *PIGC*, *CENPBD1*, *CYB5R1*, *GNB2*, *ZNF197*, *KLF7*, *NSFL1C*, *USF2*, *PARP6*, *MAP9*, *TSPO*, *CSTB*, *DDA1*, *SLC36A4*, *GFOD2*, *OCRL*, *ZNF232*, *APH1B*, *TALDO1//INTS8*, *DENND2C//BCAS2*, *RAB11FIP2*, *LARS*, *PLP2*, *EIF4E2*, *DNASE1L1//RPL10*, *AFTPH*, *TMCO3*, *RPA2*, *UQCRC1*, *ZDHHC3*, and *ACTR1A* (hereafter referred to interchangeably herein as "group M IRS immune system biomarker genes" or "group M IRS biomarker genes"); and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *CD6*, *ITPA*, *PVRIG//PILRB//STAG3*, *FLT3LG*, *IL12RB1*,

MAP3K14//LOC100133991, *FAM102A*, *TMC8*, *TMEM208*, *TMEM109*, *C1orf84*, *NADK*, *SEPT1*, *UBA7*, *CD5*, *C12orf62*, *C20orf112*, *FOXP4*, *EIF4A2//SNORA4*, *ZNF487//LOC439911*, *KCTD13*, *IL18BP//NUMA1*, *KPNA5*, *EDC4*, *ZNF587//ZNF417*, *NBR2*, *RPL28*, *ZNF738*, *SHFM1*, *CNO*, *C9orf82*, *RPL5//SNORA66//SNORD21//FAM69A*, *VAMP2*, *SIT1*, *SFRS3*, *LCK*, *IRF9*, *MRPS21*, *NEFM//LOC100129717*, *RCN2*, *BET1*, *C19orf6*, *SH2D1A*, *GLS*, *OR1C1*, *RBM14//RBM4*, *CCDC97*, *TUT1*, *MRPL14*, *ENOPH1*, *NAGK*, *DPM1*, *MPV17*, *SH2D3C*, *TMEM204*, *C3orf42*, *ARSD*, *FAM96A*, *LSM8*, *ATP5G1*, *KTI12*, *ARL4C*, *C11orf31*, *C16orf58//LOC100128371*, *CCDC109B//HIGD1A//CCDC13*, *NUDT21*, *ZFP106*, *ACTR6*, *LIX1L*, *MEF2D*, *ZNF407*, *TMEM18*, *NAT11*, *DNAJC24*, *PLEKHA3*, *GPN2*, *SMCR7*, *C7orf23//DMTF1*, *PPM1G*, *CNOT6L*, *NACA*, *FNTA*, *GRIA2*, *N4BP2L2//CG030*, *ENOSF1//TYMS*, *THBS4*, *LUC7L2*, *MOCS2*, *ZNF383*, *AKNA*, *UBE2Z*, *FLJ34077*, *SH3KBP1*, *POLR2F//LOC100131530*, *IL1A*, *UBE2V2*, *KIAA1919*, *PRKCB*, *SHOC2*, *RBM46*, *GRPEL2*, *KCNG3*, *PCDH10*, *XAB2*, *VPS52*, *MCCC2*, *NSMCE4A*, *PTP4A2*, *SNX2*, *COQ10A*, *C6orf182*, *RNF44*, *MOGS*, *DIRAS3*, *Mitochondrial*, *KIAA1826*, *SGK196*, *NSUN5//NSUN5B//NSUN5C*, *Mitochondrial*, *MORF4L2*, *MAK16//C8orf41*, *PILRB//PVRIG//STAG3*, *SAAL1*, *TMX3*, *PTPRG*, *MAPK1*, *DNAJA3*, *LEAP2*, *LMOD3*, *ASB6*, *MTMR10//MTMR15*, *HIBADH*, *MORC1*, *CORO1A//LOC606724*, *SFXN2*, *HSN2*, *AAAS*, *INHBA*, *MRPS7*, *LRRFIP1*, *KCTD7//RABGEF1*, *DCDC2//KAAG1*, *SLCO3A1*, *DENND4B*, *CFTR*, *MOG*, *QRFPR*, *BAT2//SNORA38*, *ITPR3*, *C3orf22*, *TNFRSF4*, *ZNF646//ZNF668*, *GCM2*, *CDK4//TSPAN31*, *FXC1*, *RNMT*, *CHST4*, *POLR3E*, *PDE8B*, *C6orf146*, *CHCHD5*, *TARBP1*, *TADA1L*, *PREX2*, *TRAP1//DNASE1*, *ZNHIT6*, *RGP1//GBA2*, *SMCP*, *ZC3H15*, *TRAPPC4*, *SARNP//DNAJC14*, *GNAS*, *C14orf104*, *IL20RA*, *WAC*, *SLIT3*, *C4orf39*, *TSEN54*, *PPP1R13B*, *TRIM35*, *HGC6.3*, *YIPF3*, *HQ0644/PRO0644*, *FAM13C//PHYHIPL*, *BCCIP//DHX32*, *ACADM*, *SUB1//TMEM183A*, *KPNA1*, *SPAG17//WDR3*, *KIAA1549*, *DIABLO//B3GNT4*, *ZBTB44*, *EIF1AD*, *RUNX1T1*, *TRIL*, *PTPLB*, *DHDDS*, *UPK1A*, *OTUB1*, *C1orf182*, *HAPLN2*, *SOBP*, *RYR3*, *LRRC17*, *TKTL2*, *TMBIM6*, and *GDNF* (hereafter referred to interchangeably herein as “group N IRS immune system biomarker genes” or “group N IRS biomarker genes”).

[0046] In some embodiments, the indicator is for determining a likelihood of the subject having severe sepsis or septic shock, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *SIRPG // SIRPA*, *GATA3*, *FAM102A*, *UPF3A*, *ATP13A5*, *CACNA1I* and *RANBP17 // USP12* (hereafter referred to interchangeably herein as "group O IRS immune system biomarker genes" or "group O IRS biomarker genes"); and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from the following IRS immune system biomarker genes: *GABRA6*, *HAPLN1*, *YSK4*, *FOXL2*, *TLL1*, *MECOM*, *COL3A1*, *HRG*, *SLC22A3*, *C8orf45*, *SCN7A* and *SNTG1* (hereafter referred to interchangeably herein as "group P IRS immune system biomarker genes" or "group P IRS biomarker genes").

[0047] In another broad form the present invention seeks to provide apparatus for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the apparatus including at least one electronic processing device that:

a) determines a pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determines a derived biomarker value using the pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and,

c) determines the indicator using the derived biomarker value.

[0048] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at

least one pair of reverse transcribed mRNAs comprising a first pair and a second pair of reverse transcribed mRNAs, wherein the first pair comprises a *PLAC8* reverse transcribed mRNA and a *PLA2G7* reverse transcribed mRNA and wherein the second pair comprises a *CEACAM4* reverse transcribed mRNA and a *LAMP1* reverse transcribed mRNA.

[0049] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group A IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group B IRS immune system biomarker genes.

[0050] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group C IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group D IRS immune system biomarker genes.

[0051] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group E IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group F IRS immune system biomarker genes .

[0052] In another broad form the present invention seeks to provide a composition comprising at least two pairs of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least two pairs of reverse transcribed mRNAs comprising a first pair and a second pair of reverse transcribed mRNAs, wherein the first pair comprises a reverse transcribed mRNA from a first IRS immune system biomarker gene and a reverse transcribed mRNA from a

second IRS immune system biomarker gene, and wherein the second pair comprises a reverse transcribed mRNA from a third IRS immune system biomarker gene and a reverse transcribed mRNA from a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes.

[0053] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group K IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group L IRS immune system biomarker genes.

[0054] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group M IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group N IRS immune system biomarker genes.

[0055] In another broad form the present invention seeks to provide a composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group O IRS immune system biomarker genes and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group P IRS immune system biomarker genes.

[0056] The at least one oligonucleotide primer or probe can be hybridized to an individual one of the reverse transcribed mRNAs.

[0057] The reverse transcribed mRNAs can be derived from components of the immune system.

[0058] The reverse transcribed mRNAs can be derived from leukocytes.

[0059] The reverse transcribed mRNAs can be derived from blood cells.

[0060] The reverse transcribed mRNAs can be derived from peripheral blood cells.

[0061] The composition can further comprise a labeled reagent for detecting the reverse transcribed mRNAs.

[0062] The labeled reagent can be a labeled said at least one oligonucleotide primer or probe.

[0063] The labeled reagent can be a labeled said reverse transcribed mRNA.

[0064] The labeled reagent can be a labeled oligonucleotide linker or tag for labeling a said reverse transcribed mRNA.

[0065] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least one pair of reagents comprising a first pair of reagents and a second pair of reagents, wherein the first pair of reagents comprises (i) a reagent that allows quantification of a polynucleotide expression product of the *PLA2G7* gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of the *PLAC8* gene, wherein the second pair of reagents comprises: (iii) a reagent that allows quantification of a polynucleotide expression product of the *CEACAM4* gene; and (iv) a reagent that allows quantification of a polynucleotide expression product of the *LAMP1* gene.

[0066] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and a healthy condition, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS

immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes.

[0067] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of ipSIRS and a healthy condition, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes.

[0068] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes.

[0069] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least two pairs of reagents comprising a first pair of reagents and a second pair of reagents, wherein the first pair of reagents comprises (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, and wherein the second pair of reagents comprises (i) a reagent that allows

quantification of a polynucleotide expression product of a third IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes.

[0070] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of mild sepsis and severe sepsis, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes.

[0071] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of mild sepsis and septic shock, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes.

[0072] In another broad form the present invention seeks to provide a kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of severe sepsis and septic shock, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a

polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes.

[0073] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the pair of biomarker values comprises at least one of:

a) a first pair of biomarker values comprising first and second biomarker values corresponding to first and second biomarkers, wherein the first immune system biomarker represents a polynucleotide expression product of the *PLA2G7* gene and wherein the second immune system biomarker representing a polynucleotide expression product of the *PLAC8* gene, and

b) a second pair of biomarker values comprises third and fourth biomarker values corresponding to third and fourth immune system biomarkers, respectively, wherein the third immune system biomarker represents a polynucleotide expression product of the *CEACAM4* gene and wherein the fourth immune system biomarker represents a polynucleotide expression product of the *LAMP1* gene.

[0074] Typically the indicator-determining method comprises: determining the first pair and second pair of biomarker values and determining a first derived biomarker value calculated using the first pair of biomarker values and a second derived biomarker value calculated using the second pair of biomarker values; and determining the indicator based on a combination of the first and second derived biomarker values.

[0075] In another broad form the present invention seeks to provide a method for inhibiting the development or progression of inSIRS in a subject, the method comprising: exposing the subject to a treatment regimen for treating inSIRS based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of inSIRS in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes.

[0076] In another broad form the present invention seeks to provide a method for inhibiting the development or progression of ipSIRS in a subject, the method comprising: exposing the subject to a treatment regimen for treating ipSIRS based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of ipSIRS in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one

corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes.

[0077] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to of first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system

biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes.

[0078] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least two pairs of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least two derived biomarker values using the at least two pairs of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of each pair of immune system biomarkers; and (c) determining the indicator based on the at least two derived biomarker values, wherein the at least one pair of biomarker values comprises a first pair of biomarker values comprising first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, and a second pair of biomarker values comprising third and fourth biomarker values corresponding to third and fourth immune system biomarkers, respectively, wherein the third immune system biomarker represents a polynucleotide expression product of a third IRS immune system biomarker gene and wherein the fourth immune system biomarker represents a polynucleotide expression product of a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes.

[0079] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of mild sepsis and severe sepsis, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes.

[0080] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of mild sepsis and septic shock, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value

being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes.

[0081] In another broad form the present invention seeks to provide a method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of severe sepsis and septic shock, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes.

[0082] In some embodiments, the method comprises taking the sample from the subject and obtaining the indicator according to the indicator-determining method.

[0083] In some embodiments, the method comprises: sending the sample taken from the subject to a laboratory at which the indicator is determined.

[0084] Typically, the sample comprises cells obtained from the subject or a nucleic acid sample thereof.

[0085] In another broad form the present invention seeks to provide a method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

[0086] In another broad form the present invention seeks to provide a method for differentiating between inSIRS and a healthy condition in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a

concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and healthy condition, respectively; and,

e) determining a likelihood of the subject having inSIRS or the healthy condition in accordance with the results of the comparison.

[0087] In another broad form the present invention seeks to provide a method for differentiating between ipSIRS and a healthy condition in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of ipSIRS and healthy condition, respectively; and,

e) determining a likelihood of the subject having ipSIRS or the healthy condition in accordance with the results of the comparison.

[0088] In another broad form the present invention seeks to provide a method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

[0089] In another broad form the present invention seeks to provide a method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of a third IRS immune system biomarker gene and a fourth IRS immune system biomarker gene, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

[0090] In another broad form the present invention seeks to provide a method for differentiating between mild sepsis and severe sepsis in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of mild sepsis and severe sepsis, respectively; and,

e) determining a likelihood of the subject having mild sepsis or severe sepsis in accordance with the results of the comparison.

[0091] In another broad form the present invention seeks to provide a method for differentiating between mild sepsis and septic shock in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of mild sepsis and septic shock, respectively; and,

e) determining a likelihood of the subject having mild sepsis or septic shock in accordance with the results of the comparison.

[0092] In another broad form the present invention seeks to provide a method for differentiating between severe sepsis and septic shock in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of severe sepsis and septic shock, respectively; and,

e) determining a likelihood of the subject having severe sepsis or septic shock in accordance with the results of the comparison.

[0093] Typically the method includes determining:

a) a first derived biomarker value indicative of a ratio of concentrations of the polynucleotide expression products using the first pair of biomarker values;

b) a second derived biomarker value indicative of a ratio of concentrations of the polynucleotide expression products using the first pair of biomarker values; and,

c) determining the indicator by combining the first and second derived biomarker values.

[0094] Typically the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with inSIRS and ipSIRS respectively.

[0095] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of:

i) a first pair of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0096] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0097] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression

product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0098] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0099] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of:

i) a first pair of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes;

ii) a second pair of polynucleotide expression products of a third IRS immune system biomarker gene and a fourth IRS immune system biomarker gene, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0100] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide

expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0101] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the second IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0102] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

[0103] Typically the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of the first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of the second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

[0104] Typically the method includes determining:

a) comparing the indicator to first and second indicator references, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, one of the first and second groups consisting of individuals diagnosed with the medical condition; and,

b) determining a likelihood of the subject having the medical condition in accordance with the results of the comparison.

[0105] Typically the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

[0106] In another broad form the present invention seeks to provide a method for use in assessing the likelihood of a biological subject having a medical condition, the method including, in one or more processing devices:

a) determining a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:
   i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
   ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;
b) determining an indicator indicative of a ratio of the concentrations of the polynucleotide expression products using the pair of biomarker values;
c) retrieving previously determined first and second indicator references from a database, the first and second indicator references being determined based on indicators determined from first and second groups of a reference population, one of the groups consisting of individuals diagnosed with the medical condition;
d) comparing the indicator to the first and second indicator references;
e) using the results of the comparison to determine a probability indicative of the subject having the medical condition; and,
f) generating a representation of the probability, the representation being displayed to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

[0107] Typically the method includes determining:

a) a first derived biomarker value indicative of a ratio of concentrations of the polynucleotide expression products using the first pair of biomarker values;
b) a second derived biomarker value indicative of a ratio of concentrations of the polynucleotide expression products using the first pair of biomarker values; and,
c) determining the indicator by combining the first and second derived biomarker values.

[0108] In another broad form the present invention seeks to provide apparatus for determining an indicator used in determining the likelihood of a biological subject having at least one medical condition, the apparatus including:

a) a sampling device that obtains a sample taken from a biological subject, the sample including polynucleotide expression products;

b) a measuring device that quantifies polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) at least one processing device that:

i) receives an indication of the pair of biomarker values from the measuring device;

ii) determines an indicator using a ratio of the concentration of the first and second polynucleotide expression products using the biomarker values; and,

iii) compares the indicator to at least one indicator reference; and,

iv) determines a likelihood of the subject having the at least one medical condition using the results of the comparison; and,

v) generates a representation of the indicator and the likelihood for display to a user.

[0109] In another broad form the present invention seeks to provide a method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) in a measuring device:

i) amplifying at least some polynucleotide expression products in the sample;

ii) determining an amplification amount representing a degree of amplification required to obtain a defined level of polynucleotide expression products including:

(1) amplification amounts for a first pair of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

(2) amplification amounts for a second pair of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) in a processing system:

i) retrieving the amplification amounts;

ii) determining an indicator by:

(1) determining a first derived biomarker value indicative of a ratio of concentrations of the first pair of polynucleotide expression products by determining a difference between the amplification amounts for the first pair;

(2) determining a second derived biomarker value indicative of a ratio of concentrations of the second pair of polynucleotide expression products by determining a difference between the amplification amounts for the second pair;

(3) determining the indicator by adding the first and second derived biomarker values;

iii) retrieving previously determined first and second indicator references from a database, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with inSIRS and ipSIRS respectively;

iv) comparing the indicator to the first and second indicator references;

v) using the results of the comparison to determine a probability of the subject being classified within the first or second group;

vi) generating a representation at least partially indicative of the indicator and the probability; and,

vii) providing the representation to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

[0110] In another broad form the present invention seeks to provide a method for determining an indicator used in assessing a likelihood of a biological subject having a

presence, absence, degree or prognosis of at least one medical condition, the method including:

a) determining a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determining the indicator using a combination of the plurality of biomarker values, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0111] Typically the method includes:

c) determining a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding biomarker of the biological subject; and,

d) determining the indicator by applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker.

[0112] Typically the function includes at least one of:

a) multiplying two biomarker values;

b) dividing two biomarker values;

c) adding two biomarker values;

d) subtracting two biomarker values;

e) a ratio of two biomarker values;

f) a weighted sum of at least two biomarker values;

g) a log sum of at least two biomarker values; and,

h) a sigmoidal function of at least two biomarker values.

[0113] Typically the method includes determining at least one derived biomarker value corresponding to a ratio of two measured biomarker values.

[0114] Typically the method includes combining at least two biomarker values to determine an indicator value representing the indicator.

[0115] Typically the method includes combining at least two biomarker values using a combining function, the combining function being at least one of:

a) an additive model;

b) a linear model;

c) a support vector machine;

d) a neural network model;

e) a random forest model;

f) a regression model;

g) a genetic algorithm;

h) an annealing algorithm;

i) a weighted sum;

j) a nearest neighbor model; and,

k) a probabilistic model.

[0116] Typically at least one of the at least two biomarkers is a derived biomarker.

[0117] Typically the method includes:

a) determining a first derived biomarker value, the first derived biomarker value being indicative of a ratio of concentrations of the first and second immune system biomarkers;

b) determining a second derived biomarker value, the second derived biomarker value being indicative of a ratio of concentrations of the third and fourth measured immune system biomarkers; and,

c) adding the first and second derived biomarker values to generate an indicator value.

[0118] Typically the method is performed at least in part using an electronic processing device.

[0119] Typically the method includes, in the electronic processing device:

a) receiving a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding immune system biomarker;

b) applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker; and,

c) combining at least one derived biomarker value and at least one other biomarker value to determine the indicator.

[0120] Typically the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

[0121] Typically each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

[0122] Typically the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

[0123] Typically the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;
b) 0.5;
c) 0.6;
d) 0.7;
e) 0.8; and,
f) 0.9.

[0124] Typically the biomarker value is indicative of a level or abundance of a molecule selected from one or more of a nucleic acid molecule and a proteinaceous molecule.

[0125] Typically the method includes generating a representation of the indicator.

[0126] Typically the representation includes:

a) an alphanumeric indication of the indicator;
b) a graphical indication of a comparison of the indicator to one or more indicator references;
c) an alphanumeric indication of a likelihood of the subject having at least one medical condition.

[0127] Typically the method includes:

a) comparing the indicator to an indicator reference; and,
b) determining a likelihood in accordance with results of the comparison.

[0128] Typically the indicator reference is based on at least one of:

a) an indicator threshold range;
b) an indicator threshold; and,
c) an indicator distribution.

[0129] Typically the indicator reference is derived from indicators determined for a number of individuals in a reference population.

[0130] Typically the indicator reference is based on a distribution of indicators determined for a group of a reference population, the group consisting of individuals diagnosed with the medical condition.

[0131] Typically the reference population includes:

a) a plurality of individuals of different sexes;
b) a plurality of individuals of different ethnicities;

c) a plurality of healthy individuals;

d) a plurality of individuals suffering from at least one diagnosed medical condition;

e) a plurality of individuals showing clinical signs of at least one medical condition; and,

f) first and second groups of individuals, each group of individuals suffering from a respective diagnosed medical condition.

[0132] Typically the indicator is for use in determining the likelihood that a biological subject has at least one medical condition, and wherein the reference population includes:

a) individuals presenting with clinical signs of the at least one medical condition;

b) individuals diagnosed with the at least one medical condition; and,

c) healthy individuals.

[0133] Typically the indicator reference is retrieved from a database.

[0134] Typically the likelihood is based on a probability generated using the results of the comparison.

[0135] Typically the indicator is for determining a likelihood of the subject having a first or second condition, and wherein the method includes:

a) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of first and second conditions; and,

b) determining the likelihood in accordance with the results of the comparison.

[0136] Typically the method includes:

a) determining first and second indicator probabilities using the results of the comparisons; and,

b) combining the first and second indicator probabilities to determine a condition probability indicative of the likelihood.

[0137] Typically the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with the first or second condition respectively.

[0138] Typically the method includes:

a) obtaining a sample taken from the biological subject, the sample including polynucleotide expression products;

b) quantifying at least some of the polynucleotide expression products within the sample to determine at least a pair of biomarker values;

c) determining the indicator at least in part using the pair of biomarker values;

[0139] Typically the method includes, determining the indicator at least in part using a ratio of concentrations of the polynucleotide expression products.

[0140] Typically the method includes:

a) quantifying polynucleotide expression products by:

b) amplifying at least some polynucleotide expression products in the sample; and,

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products; and,

d) determining the indicator by determining a difference between the amplification amounts.

[0141] Typically the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

[0142] Typically the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of a first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of a second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

[0143] Typically the immune system biomarker is an IRS biomarker of an immune system of the biological subject that is altered, or whose level of expression is altered, as part of an inflammatory response to damage or pathogenic insult.

[0144] Typically the indicator is for determining a likelihood of the subject having at least one of inSIRS and ipSIRS, and wherein the method includes:

a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,
c) determining the indicator using the first and second pairs of biomarker values.

[0145] Typically the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein the method includes:

a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,
c) determining the indicator using the first and second pairs of biomarker values.

[0146] Typically the indicator is for determining a likelihood of the subject having inSIRS or a healthy condition, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS immune system biomarker genes; and
b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group B IRS immune system biomarker genes.

[0147] Typically the indicator is for determining a likelihood of the subject having ipSIRS or a healthy condition, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS immune system biomarker genes; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS immune system biomarker genes.

[0148] Typically the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS immune system biomarker genes; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS immune system biomarker genes.

[0149] Typically the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first, second, third and fourth IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS immune system biomarker genes;

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS immune system biomarker genes;

c) the third IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS immune system biomarker genes; and,

d) the fourth IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS immune system biomarker genes.

[0150] Typically the first IRS immune system biomarker is a *PLA2G7* expression product, the second IRS immune system biomarker is a *PLAC8* expression product, the third IRS

immune system biomarker is a *CEACAM4* expression product and the fourth IRS immune system biomarker is a *LAMP1* expression product.

[0151] Typically the indicator is for determining a likelihood of the subject having mild sepsis or severe sepsis, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS immune system biomarker genes; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS immune system biomarker genes.

[0152] Typically the indicator is for determining a likelihood of the subject having mild sepsis or septic shock, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS immune system biomarker genes; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS immune system biomarker genes.

[0153] Typically the indicator is for determining a likelihood of the subject having severe sepsis or septic shock, and wherein biomarker values are determined from at least one IRS immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS immune system biomarker genes; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS immune system biomarker genes.

[0154] In another broad form the present invention seeks to provide apparatus for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the apparatus including a processing device that:

a) determines a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determines the indicator using a combination of the plurality of biomarker values, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0155] In one broad form the present invention seeks to provide a method for determining an indicator for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, the method including:

a) determining a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding biomarker of the biological subject;

b) determining the indicator using a combination of the plurality of biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition, wherein:

i) at least two markers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0156] Typically the method includes:

a) determining a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding biomarker of the biological subject; and,

b) applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker.

[0157] Typically the function includes at least one of:

a) multiplying two biomarker values;

b) dividing two biomarker values;

c) adding two biomarker values;

d) subtracting two biomarker values;

e) a weighted sum of at least two biomarker values;

f) a log sum of at least two biomarker values; and,

g) a sigmoidal function of at least two biomarker values.

[0158] Typically the method includes determining at least one derived biomarker value corresponding to a ratio of two measured biomarker values.

[0159] Typically the method includes combining at least two biomarker values to determine an indicator value representing the indicator.

[0160] Typically the method includes combining at least two biomarker values using a combining function, the combining function being at least one of:

a) an additive model;

b) a linear model;

c) a support vector machine;

d) a neural network model;
e) a random forest model;
f) a regression model;
g) a genetic algorithm;
h) an annealing algorithm;
i) a weighted sum;
j) a nearest neighbor model; and,
k) a probabilistic model.

[0161] Typically at least one of the at least two biomarkers is a derived biomarker.

[0162] Typically the method includes:

a) determining a first derived biomarker value, the first derived biomarker value being a ratio of first and second measured biomarker values;
b) determining a second derived biomarker value, the second derived biomarker value being a ratio of third and fourth measured biomarker values; and,
c) adding the first and second derived biomarker values to generate an indicator value.

[0163] Typically the method includes:

a) determining an indicator value;
b) comparing the indicator value to at least one indicator value range; and,
c) using a result of the comparison in diagnosing the presence, absence, degree or prognosis of at least one condition.

[0164] Typically the method is performed at least in part using an electronic processing device.

[0165] Typically the method includes, in the electronic processing device:

a) receiving a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding biomarker of the biological subject;
b) applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker; and,

c) combining at least one derived biomarker value and at least one other biomarker value to determine an indicator value.

[0166] Typically the method includes generating a representation in accordance with the at least one indicator value.

[0167] Typically the method includes:

a) comparing the indicator value to at least one indicator value range; and,

b) displaying a result of the comparison.

[0168] Typically the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

[0169] Typically each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

[0170] Typically the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

[0171] Typically the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;

b) 0.5;

c) 0.6;

d) 0.7;

e) 0.8; and,

f) 0.9.

[0172] Typically the biomarker value is indicative of a level or abundance of a molecule or entity selected from one or more of:

a) A nucleic acid molecule;

b) A proteinaceous molecule;

c) An amino acid

d) A carbohydrate;

e) A lipid;

f) A steroid;

g) An inorganic molecule;

h) An ion;

i) A drug;

j) A chemical;

k) A metabolite;

l) A toxin;

m) A nutrient;

n) A gas;

o) A cell;

p) A pathogenic organism; and,

q) A non-pathogenic organism.

[0173] In another broad form the present invention seeks to provide apparatus for determining an indicator for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, the apparatus including an electronic processing device that:

a) determines a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding biomarker of the biological subject;

b) determines the indicator using a combination of the plurality of biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0174] In another broad form the present invention seeks to provide a diagnostic signature for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, the diagnostic signature defining a combination of at least two biomarker values corresponding to values of biomarkers that can be measured for or derived from the biological subject, wherein:

a) at least two biomarkers have a mutual correlation for the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

b) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of the at least two biomarkers to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being a variance explained of at least 0.3.

[0175] Typically the diagnostic signature defines a function to be applied to at least one measured biomarker value to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker.

[0176] Typically the function includes at least one of:

a) multiplying two biomarker values;

b) dividing two biomarker values;

c) adding two biomarker values;

d) subtracting two biomarker values;

e) a weighted sum of at least two biomarker values;

f) a log sum of at least two biomarker values; and,

g) a sigmoidal function of at least two biomarker values.

[0177] Typically the at least one derived biomarker value corresponds to a ratio of two measured biomarker values.

[0178] Typically the diagnostic signature defines a combination of at least two biomarker values for determining an indicator value representing the indicator.

[0179] Typically the diagnostic signature defines a combining function for combining at least two biomarker values, the combining function being at least one of:

a) an additive model;

b) a linear model;

c) a support vector machine;

d) a neural network model;

e) a random forest model;

f) a regression model;

g) a genetic algorithm;

h) an annealing algorithm; and,

i) a weighted sum.

[0180] Typically at least one of the at least two biomarkers is a derived biomarker.

[0181] Typically the diagnostic signature defines:

a) a first derived biomarker value, the first derived biomarker value being a ratio of first and second measured biomarker values;

b) a second derived biomarker value, the second derived biomarker value being a ratio of third and fourth measured biomarker values; and,

c) a combination of the first and second derived biomarker values to generate an indicator value.

[0182] Typically the diagnostic signature defines at least one indicator value range and wherein comparison of at least one indicator value to the at least one indicator value range is used in diagnosing the presence, absence, degree or prognosis of at least one condition.

[0183] Typically the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

[0184] Typically each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

[0185] Typically the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

[0186] Typically the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;

b) 0.5;

c) 0.6;

d) 0.7;

e) 0.8; and,

f) 0.9.

[0187] Typically the biomarker value is indicative of a level or abundance of a molecule or entity selected from one or more of:

a) A nucleic acid molecule;

b) A proteinaceous molecule;

c) An amino acid

d) A carbohydrate;
e) A lipid;
f) A steroid;
g) An inorganic molecule;
h) An ion;
i) A drug;
j) A chemical;
k) A metabolite;
l) A toxin;
m) A nutrient;
n) A gas;
o) A cell;
p) A pathogenic organism; and,
q) A non-pathogenic organism.

[0188] In another broad form the present invention seeks to provide a method of identifying biomarkers for use in a diagnostic signature, the diagnostic signature being for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, the method including:

a) for a number of candidate biomarkers, ranking the candidate biomarkers in accordance with the ability of each biomarker to distinguish between the presence, absence, degree or prognosis of at least one condition in a biological subject;
b) selecting at least two candidate biomarkers in accordance with the ranking, the at least two biomarkers having a mutual correlation for the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9;
c) determining a performance value of a combination of the at least two candidate biomarkers; and,
d) defining a diagnostic signature in accordance with the combination of the at least two biomarkers if the performance value is greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0189] Typically the method includes determining a combination of at least two candidate biomarkers using a combining function, the combining function being at least one of:

a) an additive model;
b) a linear model;
c) a support vector machine;
d) a neural network model;
e) a random forest model;
f) a regression model;
g) a genetic algorithm;
h) an annealing algorithm; and,
i) a weighted sum.

[0190] Typically the method includes:

a) selecting a next combining function;
b) determining if a performance value of a combination of the at least two candidate biomarkers determined by the next combining function is greater than or equal to a performance threshold; and,
c) if the performance value is not greater than or equal to a performance threshold, repeating steps a) and b) for successive combining functions.

[0191] Typically the method includes:

a) selecting two candidate biomarkers;
b) determining if a performance value of a combination of the two candidate biomarkers is greater than or equal to a performance threshold; and,
c) if the performance value is not greater than or equal to a performance threshold:
    i) combining the selected candidate biomarkers with at least one additional candidate biomarker; and,
    ii) repeating steps a) and b) with at least one additional candidate biomarker.

[0192] Typically the method includes combining a number of candidate biomarkers up to a limit.

[0193] Typically the method includes:

a) selecting a highest ranked candidate biomarker;
b) selecting a next highest ranked candidate biomarker;

c) for the selected candidate markers, determining if the mutual correlation for the candidate biomarkers within the mutual correlation range; and,

d) if not, repeating steps b) and c) until two candidate biomarkers are selected having a mutual correlation within the mutual correlation range.

[0194] Typically the method includes:

a) defining at least two groups of candidate biomarkers, candidate biomarkers in different groups having a mutual correlation within the mutual correlation range;

b) ranking the candidate biomarkers in each group; and,

c) selecting candidate biomarkers from the different groups.

[0195] Typically the method includes:

a) using reference data for at least one individual to define a number of groups indicative of the presence, absence, degree or prognosis of the at least one condition; and,

b) using at least one analysis technique to identify a number of candidate biomarkers that are potentially useful for distinguishing the groups.

[0196] Typically the method includes using reference values measured for reference biomarkers for the at least one individual to identify the candidate biomarkers.

[0197] Typically the method includes using reference values to filter reference biomarkers to determine candidate biomarkers.

[0198] Typically at least one of the candidate biomarkers is a derived biomarker derived from at least one of the reference biomarkers using a function.

[0199] Typically the derived biomarkers are derived from filtered biomarkers.

[0200] Typically the method includes:

a) applying a function to at least one of the reference values to determine at least one derived reference biomarker value, the at least one derived reference biomarker value being indicative of a value of a corresponding derived reference biomarker; and,

b) determining at least one candidate biomarker using the at least one derived reference biomarker value.

[0201] Typically the method includes:

a) using reference data for at least one individual to define a number of groups indicative of the presence, absence, degree or prognosis of the at least one condition; and,

b) for each group, combining a range of at least two reference biomarker values to determine an indicator value range for the group.

[0202] Typically the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

[0203] Typically each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

[0204] Typically the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

[0205] Typically the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;

b) 0.5;

c) 0.6;

d) 0.7;

e) 0.8; and,

f) 0.9.

[0206] In another broad form the present invention seeks to provide apparatus for identifying markers for use in a diagnostic signature, the diagnostic signature being for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, the apparatus including an electronic process device that:

a) for a number of candidate biomarkers, ranks the candidate biomarkers in accordance with the ability of each biomarker to distinguish between the presence, absence, degree or prognosis of at least one condition in a biological subject;

b) selects at least two candidate biomarkers in accordance with the ranking, the at least two biomarkers having a mutual correlation for the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9;

c) determines a performance value of a combination of the at least two candidate biomarkers; and,

d) defines a diagnostic signature in accordance with the combination of the at least two biomarkers if the performance value is greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0207] In another broad form the present invention seeks to provide a method for diagnosing the presence or absence of inSIRS or a healthy condition in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and a healthy condition, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one

condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group B IRS biomarker genes.

[0208] In another broad form the present invention seeks to provide a method for diagnosing the presence or absence of ipSIRS or a healthy condition in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from ipSIRS and a healthy condition, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS biomarker genes.

[0209] In another broad form the present invention seeks to provide a method for diagnosing the presence or absence of inSIRS or ipSIRS in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker

values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and ipSIRS, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS biomarker genes.

[0210] In another broad form the present invention seeks to provide a method for diagnosing the presence or absence of inSIRS or ipSIRS in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and ipSIRS, wherein: (i) at least four IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least four IRS biomarkers is selected from a first IRS biomarker group, wherein at least one other of the at least four IRS biomarkers is selected from a second IRS biomarker group, wherein at least one other of the at least four IRS biomarkers is selected from a third IRS biomarker group, and wherein at least one other of the at least four IRS biomarkers is selected from a fourth IRS biomarker group, wherein the first IRS

biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS biomarker genes, wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS biomarker genes, wherein the third IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS biomarker genes and wherein the fourth IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS biomarker genes.

[0211] Suitably, the first IRS biomarker is a *PLA2G7* expression product, the second IRS biomarker is a *PLAC8* expression product, the third IRS biomarker is a *CEACAM4* expression product and the fourth IRS biomarker is a *LAMP1* expression product.

[0212] In another broad form the present invention seeks to provide a method for diagnosing the presence or absence of mild sepsis or severe sepsis in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from mild sepsis and severe sepsis, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS biomarker genes.

[0213] In another form the present invention seeks to provide a method for diagnosing the presence or absence of mild sepsis or septic shock in a biological subject, the method

comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from mild sepsis and septic shock, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS biomarker genes.

[0214] In another form the present invention seeks to provide a method for diagnosing the presence or absence of severe sepsis or septic shock in a biological subject, the method comprising: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from severe sepsis and septic shock, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a

second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS biomarker genes.

[0215] In another broad form the present invention seeks to provide a kit comprising: (i) a reagent that allows quantification of a first IRS biomarker; and (ii) a reagent that allows quantification of a second IRS biomarker, wherein the first and second IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a stage of ipSIRS selected from mild sepsis, severe sepsis and septic shock, which at least one condition lies within a mutual correlation range of between ±0.9, and wherein a combination of respective biomarker values for the first and second IRS biomarkers that are measured for or derived from a biological subject has a performance value greater than or equal to a performance threshold representing the ability of the combination of the first and second IRS biomarkers to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being a variance explained of at least 0.3.

[0216] Suitably, the kit further comprises: (iii) a reagent that allows quantification of a third IRS biomarker; and (iv) a reagent that allows quantification of a fourth IRS biomarker, wherein the third and fourth IRS biomarkers have a mutual correlation in respect of at the least one condition that lies within a mutual correlation range of between ±0.9, and wherein a combination of respective biomarker values for the third and fourth IRS biomarkers that are measured for or derived from a biological subject has a performance value greater than or equal to a performance threshold representing the ability of the combination of the third and fourth IRS biomarkers to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being a variance explained of at least 0.3.

[0217] Suitably, the kit is for diagnosing the presence or absence of inSIRS or a healthy condition, wherein the first IRS biomarker is selected from a first IRS biomarker group and wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS biomarker genes and wherein the second IRS biomarker group

consists of polynucleotide and/or polypeptide expression products from group B IRS biomarker genes.

[0218] Suitably, the kit is for diagnosing the presence or absence of ipSIRS or a healthy condition, wherein the first IRS biomarker is selected from a first IRS biomarker group and wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS biomarker genes.

[0219] Suitably, the kit is for diagnosing the presence or absence of inSIRS or ipSIRS, wherein the first IRS biomarker is selected from a first IRS biomarker group and wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS biomarker genes.

[0220] Suitably, the kit is for diagnosing the presence or absence of inSIRS or ipSIRS, wherein the first IRS biomarker is selected from a first IRS biomarker group, wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the third IRS biomarker is selected from a third IRS biomarker group and wherein the fourth IRS biomarker is selected from a fourth IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS biomarker genes, wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS biomarker genes, wherein the third IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS biomarker genes and wherein the fourth IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS biomarker genes.

[0221] Suitably, the first IRS biomarker is a *PLA2G7* expression product, the second IRS biomarker is a *PLAC8* expression product, the third IRS biomarker is a *CEACAM4* expression product and the fourth IRS biomarker is a *LAMP1* expression product.

[0222] Suitably, the kit is for diagnosing the presence or absence of mild sepsis or severe sepsis, wherein the first IRS biomarker is selected from a first IRS biomarker group and

wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS biomarker genes.

[0223] Suitably, the kit is for diagnosing the presence or absence of mild sepsis or septic shock, wherein the first IRS biomarker is selected from a first IRS biomarker group and wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS biomarker genes.

[0224] Suitably, the kit is for diagnosing the presence or absence of severe sepsis or septic shock, wherein the first IRS biomarker is selected from a first IRS biomarker group and wherein the second IRS biomarker is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS biomarker genes and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS biomarker genes.

[0225] In another broad form the present invention seeks to provide a method for treating, preventing or inhibiting the development of at least one condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis or septic shock) in a subject, the method comprising (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining an indicator using a combination of the plurality of IRS biomarker values, the indicator being at least partially indicative of the presence, absence or degree of the at least one condition, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at

least one condition, the performance threshold being indicative of an explained variance of at least 0.3; and (c) administering to the subject, on the basis that the indicator indicates the presence of inSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of inSIRS, or administering to the subject, on the basis that the indicator indicates the presence of ipSIRS or a particular stage of ipSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of ipSIRS or the particular stage of ipSIRS.

[0226] Suitably, the method further comprises: (1) determining a plurality of measured IRS biomarker values, each measured IRS biomarker value being a measured value of an IRS biomarker of the biological subject; and (2) applying a function to at least one of the measured IRS biomarker values to determine at least one derived IRS biomarker value, the at least one derived IRS biomarker value being indicative of a value of a corresponding derived IRS biomarker.

[0227] Suitably, the function includes at least one of: (a) multiplying two IRS biomarker values; (b) dividing two IRS biomarker values; (c) adding two IRS biomarker values; (d) subtracting two IRS biomarker values; (e) a weighted sum of at least two IRS biomarker values; (f) a log sum of at least two IRS biomarker values; and (g) a sigmoidal function of at least two IRS biomarker values.

[0228] In another broad form the present invention seeks to provide a method of monitoring the efficacy of a particular treatment regimen in a subject towards a desired health state, the method comprising: a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject after treatment with a treatment regimen; (b) determining an indicator using a combination of the plurality of IRS biomarker values, the indicator being at least partially indicative of the presence, absence or degree of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance

threshold being indicative of an explained variance of at least 0.3, and (c) determining that the treatment regimen is effective for changing the health status of the subject to the desired health state on the basis that the indicator indicates the presence of a healthy condition or the presence of a condition of a lower degree relative to the degree of the condition in the subject before treatment with the treatment regimen.

[0229] In another broad form the present invention seeks to provide a method of correlating a biomarker signature with an effective treatment regimen for a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), the method comprising: (a) determining a biomarker signature defining a combination of at least two IRS biomarker values corresponding to values of at least two IRS biomarkers that can be measured for or derived from a biological subject having the condition and for whom an effective treatment has been identified, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of the condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the condition, or to provide a prognosis for the condition, the performance threshold being indicative of an explained variance of at least 0.3; and (b) correlating the biomarker signature so determined with an effective treatment regimen for the condition.

[0230] In another broad form the present invention seeks to provide a method of determining whether a treatment regimen is effective for treating a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), the method comprising: (a) determining a plurality of post-treatment IRS biomarker values, each post-treatment IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject after treatment with the treatment regimen; (b) determining a post-treatment indicator using a combination of the plurality of post-treatment IRS biomarker values, the post-treatment indicator being at least partially indicative of the presence, absence or degree of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, wherein: (i) at the least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies

within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the post-treatment indicator has a performance value greater than or equal to a performance threshold representing the ability of the post-treatment indicator to diagnose the presence, absence or degree of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein the post-treatment indicator indicates whether the treatment regimen is effective for treating the condition in the subject on the basis that post-treatment indicator indicates the presence of a healthy condition or the presence of a condition of a lower degree relative to the degree of the condition in the subject before treatment with the treatment regimen.

[0231] In another broad form the present invention seeks to provide a method of correlating a biomarker signature with a positive or negative response or a side effect to a treatment regimen, the method comprising: (a) determining a biomarker signature defining a combination of at least two IRS biomarker values corresponding to values of at least two IRS biomarkers that can be measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; and (b) correlating the biomarker signature so determined with a positive or negative response to the treatment regimen.

[0232] In another broad form the present invention seeks to provide a method of determining a positive or negative response to a treatment regimen and/or a side effect of a treatment regimen by a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), the method: (a) correlating a reference biomarker signature with a positive or negative response or a side effect to the treatment regimen, wherein the biomarker signature defines a combination of at least two IRS

biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a control biological subject or control group, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; (b) determining a sample biomarker signature defining a combination of at least two IRS biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; wherein the sample biomarker signature indicates whether the subject is responding positively or negatively to the treatment regimen and/or is developing a side effect from the treatment regimen, based on the correlation of the reference biomarker signature with the positive or negative response or side effect to the treatment regimen.

[0233] In another broad form the present invention seeks to provide a method of determining a positive or negative response to a treatment regimen and/or a side effect to a treatment regimen by a biological subject, the method comprising: (a) determining a sample biomarker signature defining a combination of at least two IRS biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a

healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein the sample biomarker signature is correlated with a positive or negative response to the treatment regimen and/or to a side effect from the treatment regimen; and (b) determining whether the subject is responding positively or negatively to the treatment regimen and/or is developing a side effect from the treatment regimen based on the sample biomarker signature.

Brief Description of the Drawings

[0234] An example of the present invention will now be described with reference to the accompanying drawings, in which: -

[0235] Figure 1A is a flowchart of an example of a method for deriving an indicator for use in diagnosing the presence, absence or degree of at least one condition or in providing a prognosis of at least one condition in a biological subject;

[0236] Figure 1B is a flowchart of an example of a method for identifying biomarkers for use in a biomarker signature;

[0237] Figure 2 is a schematic diagram of an example of a distributed computer architecture;

[0238] Figure 3 is a schematic diagram of an example of a processing system of Figure 2;

[0239] Figure 4 is a schematic diagram of an example of a computer system of Figure 2;

[0240] Figure 5 is a flowchart of a specific example of a method for identifying biomarkers for use in a biomarker signature;

[0241] Figure 6A is a flowchart of a first example of a method for selecting candidate biomarkers;

[0242] Figure 6B is a flowchart of a second example of a method for selecting candidate biomarkers;

[0243] Figure 7 is a flowchart of a second example of a method for use in diagnosing the presence, absence or degree of at least one condition or in providing a prognosis of at least one condition in a biological subject;

[0244] Figure 8A is a plot of 941 mRNA biomarkers against the AUC for differentiating between healthy condition and post-surgical inflammation (PS) (also referred to herein as "infection-negative SIRS" (inSIRS)), for individual biomarkers having an AUC greater than 0.7;

[0245] Figure 8B is a box and whisker plot showing the best mRNA biomarker for separating healthy condition and PS;

[0246] Figure 8C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating healthy condition and PS with all derived biomarkers having an AUC of 1.0;

[0247] Figure 8D is a box and whisker plot of the best performing derived biomarker, based on AUC, for separating healthy condition and PS;

[0248] Figures 8E and 8F are two plots showing the correlation to each other of the biomarkers in each group;

[0249] Figures 8G and 8H are two plots demonstrating the AUC of the biomarkers in each group (groups 1 and 2);

[0250] Figure 8I is a box and whisker plot showing that when biomarkers are derived from group 1 and group 2 that a greater overall AUC is obtained;

[0251] Figure 9A is a plot of the 941 mRNA biomarkers against the AUC for differentiating between healthy condition and sepsis (also referred to herein as "infection-positive SIRS" (ipSIRS)) with all individual biomarkers having an AUC greater than 0.7;

[0252] Figure 9B is a box and whisker plot showing the best mRNA biomarker for separating healthy condition and sepsis;

[0253] Figure 9C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating healthy condition and sepsis with all derived biomarkers having an AUC of 1.0;

[0254] Figure 9D is a box and whisker plot of the best performing derived biomarker, based on AUC, for separating healthy condition and sepsis;

[0255] Figures 9E and 9F show the correlation to each other of the biomarkers groups correlated to each group;

[0256] Figures 9G and 9H are two plots demonstrating the AUC of the biomarkers in each group (bucketgroups 1 and 2);

[0257] Figure 9I is a box and whisker plot showing that when biomarkers are derived from bucketgroup 1 and bucketgroup 2 that a greater overall AUC is obtained;

[0258] Figure 10A is a plot of the 359 mRNA biomarkers against the AUC for differentiating between PS and sepsis with all individual biomarkers having had an AUC greater than 0.7;

[0259] Figure 10B is a box and whisker plot showing the best mRNA biomarker for separating PS and sepsis;

[0260] Figure 10C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating PS and sepsis with all derived biomarkers having an AUC of 0.9;

[0261] Figure 10D is a box and whisker plot of the best derived biomarker for separating PS and sepsis;

[0262] Figures 10E is a plot showing the correlation of the biomarkers in each bucketgroup to the condition;

[0263] Figures 10F is a box and whisker plot showing that when biomarkers are derived from bucketgroup 1 and bucketgroup 2 that a greater overall AUC is obtained;

[0264] Figures 10G is a plot demonstrating the AUC of the biomarkers in each of four bucketgroups;

[0265] Figure 10H is a box and whisker plot showing that when biomarkers are derived from each of the four bucketgroups a greater overall AUC is obtained;

[0266] Figure 11A is a plot of the 66 mRNA biomarkers against the AUC for differentiating between mild sepsis and severe sepsis with all individual biomarkers selected having an AUC greater than 0.7;

[0267] Figure 11B is a box and whisker plot showing the best mRNA biomarker for separating mild sepsis and severe sepsis;

[0268] Figure 11C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating mild sepsis and severe sepsis with all derived biomarkers have an AUC of at least 0.87;

[0269] Figure 11D is a box and whisker plot of the best performing derived biomarker, based on AUC, for separating mild sepsis and severe sepsis;

[0270] Figures 11E and 11F are plots showing the correlation to each other of the biomarkers in each group;

[0271] Figures 11G and 11H are plots demonstrating the AUC of the biomarkers in each group;

[0272] Figure 11I is a box and whisker plot showing that when biomarkers are derived from group 1 and group 2 that a greater overall AUC is obtained;

[0273] Figure 12A is a plot of the 48 mRNA biomarkers against the AUC for differentiating between mild sepsis and septic shock (also referred to herein as "infection-positive SIRS-shock" (ipSIRS-shock)) with all individual biomarkers having an AUC greater than 0.7;

[0274] Figure 12B is a box and whisker plot showing the best mRNA biomarker for separating mild sepsis and septic shock;

[0275] Figure 12C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating mild sepsis and septic shock with all derived biomarkers having an AUC of at least 0.793;

[0276] Figure 12D is a box and whisker plot of the best performing derived biomarker, based on AUC, for separating mild sepsis and septic shock;

[0277] Figures 12E and 12F are plots showing the correlation to each other of the biomarkers in each group;

[0278] Figures 12G and 12H are plots demonstrating the AUC of the biomarkers in each group;

[0279] Figure 12I is a box and whisker plot showing that when biomarkers are derived from group 1 and group 2 that a greater overall AUC is obtained;

[0280] Figure 13A is a plot of the 61 mRNA biomarkers against the AUC for differentiating between severe sepsis and septic shock with all individual biomarkers selected having an AUC greater than 0.7;

[0281] Figure 13B is a box and whisker plot showing the best mRNA biomarker for separating severe sepsis and septic shock;

[0282] Figure 13C is a plot of the AUC for the diagnostic ability of 1000 derived biomarkers in separating severe sepsis and septic shock with all derived biomarkers have an AUC of at least 0.821;

[0283] Figure 13D is a box and whisker plot of the best performing derived biomarker, based on AUC, for separating severe sepsis and septic shock;

[0284] Figures 13E and 13F are plots showing the correlation to each other of the biomarkers in each group;

[0285] Figures 13G and 13H are plots demonstrating the AUC of the biomarkers in each group;

[0286] Figure 13I is a box and whisker plot showing that when biomarkers are derived from group 1 and group 2 that a greater overall AUC is obtained;

[0287] Figure 14 is a user interface illustrating an example of a thermal cycler protocol;

[0288] Figure 15 is a diagram of an example of a report; and,

[0289] Figures 16A to 16L are box and whisker plots for the top twelve biomarker combinations for distinguishing between healthy condition and PS;

[0290] Figures 17A to 17L are box and whisker plots for the top twelve biomarker combinations for distinguishing between healthy condition and sepsis;

[0291] Figures 18A to 18L are box and whisker plots for the top twelve biomarker combinations for distinguishing between PS and sepsis;

[0292] Figures 19A to 19L are box and whisker plots for the top twelve biomarker combinations for distinguishing between sepsis and severe sepsis;

[0293] Figures 20A to 20L are box and whisker plots for the top twelve biomarker combinations for distinguishing between severe sepsis and septic shock;

[0294] Figures 21A to 21L are box and whisker plots for the top twelve biomarker combinations for distinguishing between sepsis and septic shock;

[0295] Figure 22 is a graph of the effect on AUC of adding biomarkers to a biomarker signature;

[0296] Figure 23 is a graph showing an example of the ability of the biomarker signature to distinguish between PS and sepsis for two patient populations;

[0297] Figure 24 is a flowchart of an example of a method for determining indicator references;

[0298] Figures 25A and 25B are a flowchart of an example of a method for validating an indicator derived from biomarker measurements;

[0299] Figures 26 is an example showing the comparison of an indicator value to an indicator reference; and,

[0300] Figures 27A and 27B are example representation of indicator values.

Detailed Description of the Preferred Embodiments

[0301] An example of a method for determining an indicator for use in diagnosing the presence, absence or degree of at least one condition in or of a biological subject, or in monitoring the progression of at least one condition in or of the subject, or in prognosing at least one condition in or of the subject, will now be described with reference to Figure 1A.

[0302] For the purpose of explanation, a number of different terms will be used. For example, the term "biomarker" refers to a measurable parameter, or combination of parameters, that can be used as an indicator of a biological state and includes, without limitation, proteins, nucleic acids, carbohydrates, lipids, metabolites, gases, steroids, ions, nutrients, toxins, cells, pathogenic organisms, non-pathogenic organisms, organic compounds and inorganic compounds. Biomarkers also encompass non-blood-borne factors, non-analyte physiological markers of health status, or other factors or biomarkers not measured from samples (*e.g.*, biological samples such as bodily fluids), such as "clinical" or "phenotypic" parameters, including, without limitation, age, ethnicity, gender, species, breed, genetic information, white blood cell count, diastolic blood pressure and systolic blood pressure, bone density, height, weight, waist and hip circumference, body-mass index, as well as others

such as Type I or Type II diabetes mellitus or gestational diabetes mellitus (collectively referred to here as diabetes), resting heart rate, homeostatic model assessment (HOMA), HOMA insulin resistance (HOMA-IR), intravenous glucose tolerance (SI(IVGT)), resting heart rate, β cell function, macrovascular function, microvascular function, atherogenic index, low-density lipoprotein/high-density lipoprotein ratio, intima-media thickness, body temperature, sequential organ failure assessment (SOFA) and the like. The "biomarkers" could also include "immune response biomarkers", which will be described in more detail below.

[0303] The term "biomarker value" refers to a value measured or derived for at least one corresponding biomarker of the biological subject and which is typically at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject. Thus, the biomarker values could be measured biomarker values, which are values of biomarkers measured for the subject, or alternatively could be derived biomarker values, which are values that have been derived from one or more measured biomarker values, for example by applying a function to the one or more measured biomarker values.

[0304] Biomarker values can be of any appropriate form depending on the manner in which the values are determined. For example, the biomarker values could be determined using high-throughput technologies such as mass spectrometry, sequencing platforms, array and hybridization platforms, immunoassays, flow cytometry, or any combination of such technologies and in one preferred example, the biomarker values relate to a level of activity or abundance of an expression product or other measurable molecule, quantified using a technique such as PCR, sequencing or the like. In this case, the biomarker values can be in the form of amplification amounts, or cycle times, which are a logarithmic representation of the concentration of the biomarker within a sample, as will be appreciated by persons skilled in the art and as will be described in more detail below.

[0305] The term "reference biomarkers" is used to refer to biomarkers whose activity has been quantified for a sample population of one or more individuals having one or more conditions, stages of one or more conditions, subtypes of one or more conditions or different prognoses. The term "reference data" refers to data measured for one or more individuals in a sample population, and may include quantification of the level or activity of the biomarkers

measured for each individual, information regarding any conditions of the individuals, and optionally any other information of interest.

[0306] The term "candidate biomarkers" refers to a subset of the reference biomarkers that have been identified as being potentially useful in distinguishing between different groups of individuals, such as individuals suffering from different conditions, or having different stages or prognoses. The number of candidate biomarkers will vary, but is typically about 200.

[0307] The term "signature biomarkers" is used to refer to a subset of the candidate biomarkers that have been identified for use in a biomarker signature that can be used in performing a clinical assessment, such as to rule in or rule out a specific condition, different stages or severity of conditions, subtypes of different conditions or different prognoses. The number of signature biomarkers will vary, but is typically of the order of 10 or less.

[0308] The term "biomarker signature" means a combination of at least two biomarker values corresponding to values of biomarkers that can be measured for or derived from one or more biological subjects, which combination is characteristic for a discrete condition, stage of condition, subtype of condition or a prognosis for a discrete condition, stage of condition, subtype of condition.

[0309] The terms "biological subject", "subject", "individual" and "patient" are used interchangeably herein to refer to an animal subject, particularly a vertebrate subject, and even more particularly a mammalian subject. Suitable vertebrate animals that fall within the scope of the invention include, but are not restricted to, any member of the phylum Chordata, subphylum vertebrata including primates, rodents (*e.g.*, mice rats, guinea pigs), lagomorphs (*e.g.*, rabbits, hares), bovines (*e.g.*, cattle), ovines (*e.g.*, sheep), caprines (*e.g.*, goats), porcines (*e.g.*, pigs), equines (*e.g.*, horses), canines (*e.g.*, dogs), felines (*e.g.*, cats), avians (*e.g.*, chickens, turkeys, ducks, geese, companion birds such as canaries, budgerigars etc.), marine mammals (*e.g.*, dolphins, whales), reptiles (snakes, frogs, lizards, etc.), and fish. A preferred subject is a primate (*e.g.*, a human, ape, monkey, chimpanzee).

[0310] As used herein, the term SIRS ("systemic inflammatory response syndrome") refers to a clinical response arising from a non-specific insult with two or more of the following measureable clinical characteristics; a body temperature greater than 38° C or less than 36° C, a heart rate greater than 90 beats per minute, a respiratory rate greater than 20 per minute, a white blood cell count (total leukocytes) greater than 12,000 per mm^3 or less than 4,000 per

mm^3, or a band neutrophil percentage greater than 10%. From an immunological perspective, it may be seen as representing a systemic response to insult (*e.g.*, major surgery) or systemic inflammation. As used herein, "inSIRS" (which includes within its scope "post-surgical" (PS) inflammation) includes the clinical response noted above but in the absence of a systemic infectious process. By contrast, "ipSIRS" (also referred to herein as "sepsis") includes the clinical response noted above but in the presence of a presumed or confirmed infection. Confirmation of infection can be determined using microbiological culture or isolation of the infectious agent. From an immunological perspective, ipSIRS may be seen as a systemic response to microorganisms, whether it is a local, peripheral or systemic infection.

[0311] As used herein, the term "degree" of a condition refers to the seriousness, severity, stage or state of a condition. For example, a condition may be characterized as mild, moderate or severe. A person of skill in the art would be able to determine or assess the degree of a particular condition. For example, the degree of a condition may be determined by comparing the likelihood or length of survival of a subject having a condition with the likelihood or length of survival in other subjects having the same condition. In other embodiments, the degree of a condition may be determined by comparing the clinical signs of a subject having a condition with the degree of the clinical signs in other subjects having the same condition.

[0312] It will be appreciated that the above described terms and associated definitions are used for the purpose of explanation only and are not intended to be limiting.

[0313] In this example, the method includes determining a plurality of biomarker values at step 100, each biomarker value being indicative of a value measured or derived for at least one biomarker of the biological subject.

[0314] The biomarker values and biomarkers corresponding to the biomarker values can be of any appropriate form and in particular can relate to any attribute of a subject for which a value can be quantified. This technique is particularly suited to high-throughput technologies such as mass spectrometry, sequencing platforms, array and hybridization platforms, or any combination of such technologies and in one preferred example, the biomarker values relate to a level of activity or abundance of an expression product or other measurable molecule.

[0315] The biomarker values could be measured biomarker values, which are values of biomarkers measured for the subject, or alternatively could be derived biomarker values,

which are values that have been derived from one or more measured biomarker values, for example by applying a function to the one or more measured biomarker values. As used herein, biomarkers to which a function has been applied are referred to as "derived markers".

[0316] The biomarker values may be determined in any one of a number of ways. In one example, the process of determining the biomarker values can include measuring the biomarker values, for example by performing tests on the biological subject. More typically however, the step of determining the biomarker values includes having an electronic processing device receive or otherwise obtain biomarker values that have been previously measured or derived. This could include for example, retrieving the biomarker values from a data store such as a remote database, obtaining biomarker values that have been manually input, using an input device, or the like.

[0317] At step 110, the indicator is determined using a combination of the plurality of biomarker values, the indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition.

[0318] The biomarker values can be combined in any one of a number of ways and this can include for example adding, multiplying, subtracting, or dividing biomarker values to determine an indicator value. This step is performed so that multiple biomarker values can be combined into a single indicator value, providing a more useful and straightforward mechanism for allowing the indicator to be interpreted and hence used in diagnosing the presence, absence or degree of the at least one condition in the subject, or prognosing the at least one condition in the subject.

[0319] Assuming the method is performed using an electronic processing device, at step 120 an indication of the indicator is optionally displayed or otherwise provided to the user. In this regard, the indication could be a graphical or alphanumeric representation of an indicator value. Alternatively however, the indication could be the result of a comparison of the indicator value to predefined thresholds or ranges, or alternatively could be an indication of the presence, absence, degree or prognosis for at least one condition, derived using the indicator.

[0320] In order to ensure an effective diagnosis or prognosis can be determined, at least two of the biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9. This

requirement means that the two biomarkers are not entirely correlated in respect of each other when considered in the context of the condition(s) being diagnosed or prognosed. In other words, at least two of the biomarkers in the combination respond differently as the condition changes, which adds significantly to their ability when combined to discriminate between at least two conditions, to diagnose the presence, absence or degree of at least one condition, and/or to provide a prognosis of at least condition in or of the biological subject. As used herein, "and/or" refers to and encompasses any and all possible combinations of one or more of the associated listed items, as well as the lack of combinations when interpreted in the alternative (or).

[0321] Typically, the requirement that biomarkers have a low mutual correlation means that the biomarkers may relate to different biological attributes or domains such as but not limited to different molecular functions, different biological processes and different cellular components. Illustrative examples of molecular function include addition of or removal of one of more of the following moieties to or from a protein, polypeptide, peptide, nucleic acid (*e.g.*, DNA, RNA): linear, branched, saturated or unsaturated alkyl (*e.g.*, C_1–C_{24} alkyl); phosphate; ubiquitin; acyl; fatty acid, lipid, phospholipid; nucleotide base; hydroxyl and the like. Molecular functions also include signaling pathways, including without limitation, receptor signaling pathways and nuclear signaling pathways. Non-limiting examples of molecular functions also include cleavage of a nucleic acid, peptide, polypeptide or protein at one or more sites; polymerization of a nucleic acid, peptide, polypeptide or protein; translocation through a cell membrane (*e.g.*, outer cell membrane; nuclear membrane); translocation into or out of a cell organelle (*e.g.*, Golgi apparatus, lysosome, endoplasmic reticulum, nucleus, mitochondria); receptor binding, receptor signaling, membrane channel binding, membrane channel influx or efflux; and the like.

[0322] Illustrative examples of biological processes include: stages of the cell cycle such as meiosis, mitosis, cell division, prophase, metaphase, anaphase, telophase and interphase, stages of cell differentiation; apoptosis; necrosis; chemotaxis; immune responses including adaptive and innate immune responses, pro-inflammatory immune responses, autoimmune responses, tolerogenic responses and the like. Other illustrative examples of biological processes include generating or breaking down adenosine triphosphate (ATP), saccharides, polysaccharides, fatty acids, lipids, phospholipids, sphingolipids, glycolipids, cholesterol,

nucleotides, nucleic acids, membranes (*e.g.*, cell plasma membrane, nuclear membrane), amino acids, peptides, polypeptides, proteins and the like.

[0323] Representative examples of cellular components include organelles, membranes, as for example noted above, and others.

[0324] It will be appreciated that the use of biomarkers that have different biological attributes or domains provides further information than if the biomarkers were related to the same or common biological attributes or domains.

[0325] In this regard, it will be appreciated if the at least two biomarkers are highly correlated to each other, the use of both biomarkers would add little diagnostic/prognostic improvement compared to the use of a single one of the biomarkers. Accordingly, the method uses biomarkers that are not well correlated with each other, thereby ensuring that the inclusion of each biomarker in the method adds significantly to the discriminative ability of the indicator.

[0326] Despite this, in order to ensure that the indicator can accurately be used in performing the discrimination between at least two conditions or the diagnosis of the presence, absence or degree of at least one condition or the prognosis of at least one condition, the indicator has a performance value that is greater than or equal to a performance threshold. The performance threshold may be of any suitable form but is to be typically indicative of an explained variance of at least 0.3, or an equivalent value of another performance measure.

[0327] It has been found that utilizing a combination of biomarkers that have a mutual correlation between ±0.9 and using these in a combination that provides an explained variance of at least 0.3, this allows an indicator to be defined that is suitable for ensuring that an accurate discrimination, diagnosis or prognosis can be obtained whilst minimizing the number of biomarkers that are required.

[0328] It will be appreciated that in this context, the biomarkers used within the above-described method can define a biomarker signature for the at least one condition, which includes a minimal number of biomarkers, whilst maintaining sufficient performance to allow the biomarker signature to be used in making a clinically relevant diagnosis, prognosis, or differentiation. Minimizing the number of biomarkers used minimizes the costs associated with performing diagnostic or prognostic tests and in the case of nucleic acid expression

products, allows the test to be performed utilizing relatively straightforward techniques such as nucleic acid array, and polymerase chain reaction (PCR) processes, or the like, allowing the test to be performed rapidly in a clinical environment.

[0329] Furthermore, producing a single indicator value allows the results of the test to be easily interpreted by a clinician or other medical practitioner, so that test can be used for reliable diagnosis in a clinical environment.

[0330] An example of the process for generating a suitable biomarker signature for use in the method of Figure 1A will now be described with reference to Figure 1B.

[0331] In particular, it is typical to generate a biomarker signature by analyzing a large number of biomarkers and then selecting a combination of biomarkers that meet the above described criteria.

[0332] In this example, at step 150 the process includes ranking a number of candidate biomarkers in accordance with the ability of each biomarker to distinguish between the presence, absence, degree or prognosis of at least one condition in a biological subject.

[0333] The candidate biomarkers can be obtained in any appropriate matter, but typically this would involve acquiring reference data including reference biomarker values relating to a number of reference biomarkers that have been measured or derived for one or more reference individuals having different presences, absences, degrees or prognoses of the one or more conditions of interest. Thus, it will be appreciated that the candidate biomarkers can include measured and/or derived biomarkers, as will be described in more detail below.

[0334] The reference data typically includes measurements of a plurality of reference biomarkers, the measurements including information regarding the activity, such as the level, abundance or functional activity, of any expression product or measurable molecule, as will be described in more detail below. The reference data may also include information such as clinical data regarding one or more conditions suffered by each individual. This can include information regarding a presence, absence, degree or progression of a condition, phenotypic information, such as details of phenotypic traits, genetic or genetically regulated information, amino acid or nucleotide related genomics information, results of other tests including imaging, biochemical and hematological assays, other physiological scores such as a SOFA

(Sequential Organ Failure Assessment) score, or the like and this is not intended to be limiting, as will be apparent from the description below.

[0335] The candidate biomarkers can include some or all of the reference biomarkers, depending on the preferred implementation. Thus, for example, reference biomarker values could be analyzed to determine correlations between the reference biomarkers and the at least one condition, with the reference biomarkers being coarsely filtered to remove those with a low correlation, for example with a correlation with the condition that is below 0.3.

[0336] At step 160 at least two candidate biomarkers are selected based on the ranking and a mutual correlation. In particular, at least two candidate biomarkers are selected which have a mutual correlation within a mutual correlation range of ±0.9. Thus, this process excludes any biomarkers which are highly mutually correlated, when considered in the context of the one or more conditions, and which would not therefore add significantly to the ability to discriminate between the presence, absence, degree or prognosis of at least one condition.

[0337] At step 170 a performance value of a combination of the selected candidate biomarkers is determined. As mentioned above the combination may be any combination of the candidate biomarker values, such as addition, subtraction, multiplication, or division of the candidate biomarker values, and this will not therefore be described in any further detail.

[0338] At step 180 it is determined if the performance value of the combination exceeds a performance threshold, the performance threshold being equivalent to an explained variance of at least 0.3. If so, the combination of the candidate biomarkers can be used to define a biomarker signature. Otherwise, the previous steps can be repeated, for example by determining alternative combinations of the candidate biomarkers, selecting different candidate biomarkers, or adding additional candidate biomarkers as will be described in more detail below. In this regard, it will be appreciated that other measures could be used, and reference to an explained variance of at least 0.3 is intended to be a particular example for illustrative purposes.

[0339] Accordingly, the above described method can be utilized to select a combination of candidate biomarkers that are suitable for use as signature biomarkers in a biomarker signature for diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject, for example using the method of Figure 1A above.

[0340] In one example, this is achieved by ensuring that at least two of the biomarkers used are not highly mutually correlated, thereby ensuring that each of these biomarkers contributes to the performance of the resulting signature.

[0341] A number of further features will now be described.

[0342] In one example, the method includes determining a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding biomarker of the biological subject and applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker.

[0343] The function used will therefore vary depending on the preferred implementation. In one example, the function includes at least one of multiplying two biomarker values; dividing two biomarker values; adding two biomarker values; subtracting two biomarker values; a weighted sum of at least two biomarker values; a log sum of at least two biomarker values; and, a sigmoidal function of at least two biomarker values.

[0344] More typically the function is division of two biomarker values, so that the derived biomarker value corresponds to a ratio of two measured biomarker values. There are a number of reasons why the ratio might be preferred. For example, use of a ratio is self-normalizing, meaning variations in measuring techniques will automatically be accommodated. For example, if the input concentration of a sample is doubled, the relative proportions of biomarkers will remain the same. As a result, the type of function therefore has a stable profile over a range of input concentrations, which is important because input concentration is a known variable for expression data. Additionally, many biomarkers are nodes on biochemical pathways, so the ratio of biomarkers gives information about the relative activation of one biological pathway to another, which is a natural representation of biological change within a system. Finally, ratios are typically easily interpreted.

[0345] The method typically includes combining at least two biomarker values to determine an indicator value representing the indicator. This is usually achieved by combining at least two biomarker values using a combining function, such as: an additive model; a linear model; a support vector machine; a neural network model; a random forest model; a regression model; a genetic algorithm; an annealing algorithm; and a weighted sum.

[0346] In one example, at least one of the at least two biomarkers is a derived biomarker and in a preferred example, the combining function is addition of derived biomarker values that are ratios, in which case the method includes determining first and second derived biomarker values from ratios of first and second and third and fourth measured biomarker values, and then adding the first and second derived biomarker values to generate an indicator value.

[0347] In one example, the method includes determining an indicator value, comparing the indicator value to at least one indicator value range, and using a result of the comparison in diagnosing the presence, absence, degree or prognosis of at least one condition.

[0348] The above-described process is typically performed using an electronic processing device, forming part of a processing system such as a computer system or the like. In this case, the method typically involves having the electronic processing device receive a plurality of measured biomarker values, apply a function to at least one of the measured biomarker values to determine the at least one derived biomarker value and combining at least one derived biomarker value and at least one other biomarker value to determine an indicator value.

[0349] The electronic processing device can then generate a representation in accordance with the at least one indicator value, for example by displaying a numerical indication of the indicator value. More typically however the electronic processing device compares the indicator value to at least one indicator value range and displays a result of the comparison. This can be used to compare the indicator to defined ranges representing specific stages, progressions or prognoses of one or more conditions, allowing an indication of the respective stage, progression or prognosis to be displayed.

[0350] The mutual correlation range is typically at least one of: ±0.8; ±0.7; ±0.6; ±0.5; ±0.4; ±0.3; ±0.2; and ±0.1. In this regard, it will be appreciated that the smaller the mutual correlation range used, the less correlated the biomarkers will be and hence the more useful these will be in discriminating between the specific stages, progressions or prognoses of one or more conditions.

[0351] It is also typical for the biomarkers used to have at least a minimum correlation with the condition. In one example, each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3. However, it will be

appreciated that the greater the range, the greater the correlation between the biomarker and condition, and hence the more use this will be in performing a diagnosis. Accordingly, the condition correlation is more typically one of: ±0.9; ±0.8; ±0.7; ±0.6; ±0.5; and ±0.4.

[0352] Furthermore, it will be appreciated that the greater the performance of the indicator, the greater use the indicator will be in performing the diagnosis. Accordingly, the performance threshold is typically indicative of an explained variance of at least one of: 0.4; 0.5; 0.6; 0.7; 0.8; and 0.9.

[0353] As described above, the biomarker value can be of any suitable form. However, the technique is particularly suited to biomarker values indicative of a level or abundance of a molecule selected from one or more of: a nucleic acid molecule; a proteinaceous molecule; an amino acid; a carbohydrate; a lipid; a steroid; an inorganic molecule; an ion; a drug; a chemical; a metabolite; a toxin; a nutrient; a gas; a cell; a pathogenic organism; and a non-pathogenic organism.

[0354] When determining biomarkers for use in a biomarker signature, the method typically includes selecting a combining function, determining if a performance value of a combination of the at least two candidate biomarkers determined by the combining function is greater than or equal to a performance threshold and if the performance value is not greater than or equal to a performance threshold, repeating these steps for successive different combining functions. Thus, this allows a number of different combining functions to be tried successively, allowing the best combining function to be identified.

[0355] The method typically further includes selecting two candidate biomarkers, determining if a performance value of a combination of the two candidate biomarkers is greater than or equal to a performance threshold and if not, combining the selected candidate biomarkers with at least one additional candidate biomarker before repeating the steps with at least one additional candidate biomarker. This allows a larger number of biomarkers to be used in the event two biomarkers are insufficient, and this can be repeated, with increasing numbers of candidate biomarkers used in combination and compared to the performance threshold until the required performance is reached, or up until a defined number limit of candidate biomarkers is reached.

[0356] To ensure the required mutual correlation is met when selecting the candidate biomarkers, the method typically includes selecting a highest and a next highest ranked

candidate biomarker, for the selected candidate biomarkers, determining if the mutual correlation for the candidate biomarkers within the mutual correlation range and if not repeating these steps until two candidate biomarkers are selected having a mutual correlation within the mutual correlation range. Alternatively however this can be achieved by defining at least two groups of candidate biomarkers, candidate biomarkers in different groups having a mutual correlation within the mutual correlation range, ranking the candidate biomarkers in each group and selecting candidate biomarkers from the different groups.

[0357] In general, the candidate biomarkers are determined by using reference data for at least one individual to define a number of groups indicative of the presence, absence, degree or prognosis of the at least one condition and then using at least one analysis technique to identify a number of candidate biomarkers that are potentially useful for distinguishing the groups. The groups can also be used to establish a range of at least two reference biomarker values to determine an indicator value range for the group.

[0358] In one example, reference values measured for reference biomarkers for the at least one individual can then be used to identify the candidate biomarkers, for example by filtering reference biomarkers to determine candidate biomarkers based on a correlation of each biomarker with the condition.

[0359] In one example, the process is performed by one or more processing systems operating as part of a distributed architecture, an example of which will now be described with reference to Figure 2.

[0360] In this example, the arrangement includes a number of processing systems 201 and computer systems 203 interconnected via one or more communications networks, such as the Internet 202, and/or a number of local area networks (LANs) 204. It will be appreciated that the configuration of the networks 202, 204 is for the purpose of example only, and in practice the processing and computer systems 201, 203 can communicate via any appropriate mechanism, such as via wired or wireless connections, including, but not limited to mobile networks, private networks, such as an 802.11 networks, the Internet, LANs, WANs, or the like, as well as via direct or point-to-point connections, such as Bluetooth, or the like.

[0361] The use of separate terms “processing system” and “computer system” is for illustrative purposes and to enable distinction between different devices, optionally having different functionality. For example, the processing and computer systems 201, 203 could

represent servers and clients respectively, as will become apparent from the following description. However, this is not intended to be limiting and in practice any suitable computer network architecture can be used.

[0362] An example of a suitable processing system 201 is shown in Figure 3. In this example, the processing system 201 includes an electronic processing device, such as at least one microprocessor 300, a memory 301, an optional input/output device 302, such as a keyboard and/or display, and an external interface 303, interconnected via a bus 304 as shown. In this example the external interface 303 can be utilized for connecting the processing system 201 to peripheral devices, such as the communications networks 202, 204, databases 211, other storage devices, or the like. Although a single external interface 303 is shown, this is for the purpose of example only, and in practice multiple interfaces using various methods (*e.g.*, Ethernet, serial, USB, wireless or the like) may be provided.

[0363] In use, the microprocessor 300 executes instructions in the form of applications software stored in the memory 301 to perform required processes, such as communicating with other processing or computer systems 201, 203. Thus, actions performed by a processing system 201 are performed by the processor 300 in accordance with instructions stored as applications software in the memory 301 and/or input commands received via the I/O device 302, or commands received from other processing or computer systems 201, 203. The applications software may include one or more software modules, and may be executed in a suitable execution environment, such as an operating system environment, or the like.

[0364] Accordingly, it will be appreciated that the processing systems 201 may be formed from any suitable processing system, such as a suitably programmed computer system, PC, web server, network server, or the like. In one particular example, the processing systems 201 are standard processing system such as a 32-bit or 64-bit Intel Architecture based processing system, which executes software applications stored on non-volatile (*e.g.*, hard disk) storage, although this is not essential. However, it will also be understood that the processing system could be or could include any electronic processing device such as a microprocessor, microchip processor, logic gate configuration, firmware optionally associated with implementing logic such as an FPGA (Field Programmable Gate Array), or any other electronic device, system or arrangement.

[0365] As shown in Figure 4, in one example, the computer systems 203 include an electronic processing device, such as at least one microprocessor 400, a memory 401, an input/output device 402, such as a keyboard and/or display, and an external interface 403, interconnected via a bus 404 as shown. In this example the external interface 403 can be utilized for connecting the computer system 203 to peripheral devices, such as the communications networks 202, 204, databases, other storage devices, or the like. Although a single external interface 403 is shown, this is for the purpose of example only, and in practice multiple interfaces using various methods (*e.g.*, Ethernet, serial, USB, wireless or the like) may be provided.

[0366] In use, the microprocessor 400 executes instructions in the form of applications software stored in the memory 401 to perform required processes, for example to allow communication with other processing or computer systems 201, 203. Thus, actions performed by a processing system 203 are performed by the processor 400 in accordance with instructions stored as applications software in the memory 401 and/or input commands received from a user via the I/O device 402. The applications software may include one or more software modules, and may be executed in a suitable execution environment, such as an operating system environment, or the like.

[0367] Accordingly, it will be appreciated that the computer systems 203 may be formed from any suitable processing system, such as a suitably programmed PC, Internet terminal, lap-top, hand-held PC, smart phone, PDA, tablet, or the like. Thus, in one example, the processing system 300 is a standard processing system such as a 32-bit or 64-bit Intel Architecture based processing system, which executes software applications stored on non-volatile (*e.g.*, hard disk) storage, although this is not essential. However, it will also be understood that the processing systems 203 can be any electronic processing device such as a microprocessor, microchip processor, logic gate configuration, firmware optionally associated with implementing logic such as an FPGA (Field Programmable Gate Array), or any other electronic device, system or arrangement.

[0368] It will also be noted that whilst the processing and computer systems 201, 203 are shown as single entities, it will be appreciated that this is not essential, and instead one or more of the processing and/or computer systems 201, 203 can be distributed over

geographically separate locations, for example by using processing systems provided as part of a cloud based environment.

[0369] Examples of the above-described method(s) will now be described in further detail. For the purpose of these examples, it is assumed that the process is performed by one or more of the processing systems 201, acting as diagnostic servers. Interaction by a user is via a user computer system 203, which is used to allow a user to submit raw data, for example obtained from measurements on a subject, with the processing system 201 generating the indicator, allowing this to be displayed on the computer system 203.

[0370] However, it will be appreciated that the above-described configuration assumed for the purpose of the following examples is not essential, and numerous other configurations may be used. It will also be appreciated that the partitioning of functionality between the processing and computer systems 201, 203 may vary, depending on the particular implementation.

[0371] An example of a specific method for identifying biomarkers for using a biomarker signature will now be described with reference to Figure 5.

[0372] In this example, at step 500 reference data is obtained from at least one individual. The reference data is typically in the form of measured biomarker values obtained for at least one individual for different stages of the at least one condition.

[0373] The reference data may be acquired in any appropriate manner but typically this involves obtaining gene expression product data from a plurality of individuals, selected to include individuals diagnosed with one or more conditions of interest, as well as healthy individuals. Detection of either types of gene expression in use of any of the methods described herein is encompassed by the present invention. The terms “expression” or “gene expression” refer to production of RNA only or production of RNA and translation of RNA into proteins or polypeptides. Thus, the term “expression products” encompass (i) polynucleotides including RNA transcripts and corresponding nucleic acids including complementary cDNA copies of RNA transcripts, and (ii) polypeptides encoded by RNA transcripts. The conditions are typically medical, veterinary or other health status conditions and may include any illness, disease, stages of disease, disease subtypes, severities of disease, diseases of varying prognoses or the like. The terms “healthy individual”, “healthy subject” and the like are used herein to refer to a subject, in particular a mammal, having no diagnosed

disease, disorder, infirmity, or ailment. The condition of such an individual or subject is referred to herein as a "healthy condition" such that in one example a condition can include healthy. In specific embodiments, a healthy subject lacks SIRS (*e.g.*, inSIRS or ipSIRS).

[0374] In order to achieve this, gene expression product data are collected, for example by obtaining a biological sample, such as a peripheral blood sample, and then performing a quantification process, such as a nucleic acid amplification process, including PCR (Polymerase Chain Reaction) or the like, in order to assess the activity, and in particular, level or abundance of a number of reference biomarkers. Quantified values indicative of the relative activity are then stored as part of the reference data.

[0375] Example reference biomarkers could include expression products such as nucleic acid or proteinaceous molecules, as well as other molecules relevant in making a clinical assessment. The number of biomarkers measured for use as reference biomarkers will vary depending upon the preferred implementation, but typically include a large number such as, 1000, 5000, 10000 or above, although this is not intended to be limiting.

[0376] The individuals also typically undergo a clinical assessment allowing any conditions to be clinically identified, and with an indication of any assessment or condition forming part of the reference data. Whilst any conditions can be assessed, in one example the process is utilized specifically to identify conditions such as SIRS (Systemic Inflammatory Response Syndrome) (M S Rangel-Frausto, D Pittet, M Costigan, T Hwang, C S Davis, and R P Wenzel, "The Natural History of the Systemic Inflammatory Response Syndrome (SIRS). a Prospective Study.", *JAMA : the Journal of the American Medical Association* 273, no. 2 (January 11, 1995): 117–123.). SIRS is an overwhelming whole body reaction that may have an infectious or non-infectious etiology, whereas sepsis is SIRS that occurs during infection. Both are defined by a number of non-specific host response parameters including changes in heart and respiratory rate, body temperature and white cell counts (Mitchell M Levy *et al.*, "2001 SCCM/ESICM/ACCP/ATS/SIS International Sepsis Definitions Conference", *Critical Care Medicine* 31, no. 4 (April 2003): 1250–1256.; K Reinhart, M Bauer, N C Riedemann, and C S Hartog, "New Approaches to Sepsis: Molecular Diagnostics and Biomarkers", *Clinical Microbiology Reviews* 25, no. 4 (October 3, 2012): 609–634) To differentiate these conditions they are referred herein to as SIRS (both conditions), infection-negative SIRS (SIRS without infection, hereafter referred to as "inSIRS") and infection-positive SIRS

(sepsis, SIRS with a known or suspected infection, hereafter referred to as "ipSIRS"). The causes of SIRS are multiple and varied and can include, but are not limited to, trauma, burns, pancreatitis, endotoxemia, surgery, adverse drug reactions, and infections (local and systemic). It will be appreciated from the following, however, that this can be applied to a range of different conditions, and reference to SIRS or sepsis is not intended to be limiting.

[0377] Additionally, the reference data may include additional biomarkers such as one or more phenotypic or clinical parameters of the individuals and/or their relatives. Phenotypic parameters can include information such as the gender, ethnicity, age, hair color, eye color, height, weight, waist and hip circumference, or the like. Also, in the case of the technology being applied to individuals other than humans, this can also include information such as designation of a species, breed or the like. Clinical traits may include genetic information, white blood cell count, diastolic blood pressure and systolic blood pressure, bone density, body-mass index, diabetes, resting heart rate, HOMA, HOMA-IR, IVGT, resting heart rate, β cell function, macrovascular function, microvascular function, atherogenic index, low-density lipoprotein/high-density lipoprotein ratio, intima-media thickness, body temperature, SOFA and the like.

[0378] Accordingly, in one example the reference data can include for each of the reference individuals information relating to at least one and desirably to a plurality of reference biomarkers and a presence, absence, degree or progression of a condition, .

[0379] The reference data may be collected from individuals presenting at a medical center with clinical signs relating to relevant any conditions of interest, and may involve follow-on consultations in order to confirm clinical assessments, as well as to identify changes in biomarkers, and/or clinical signs, and/or severity of clinical signs, over a period of time. In this latter case, the reference data can include time series data indicative of the progression of a condition, and/or the activity of the reference biomarkers, so that the reference data for an individual can be used to determine if the condition of the individual is improving, worsening or static. It will also be appreciated that the reference biomarkers are preferably substantially similar for the individuals within the sample population, so that comparisons of measured activities between individuals can be made.

[0380] This reference data could also be collected from a single individual over time, for example as a condition within the individual progresses, although more typically it would be

obtained from multiple individuals each of which has a different stage of the one or more conditions of interest.

[0381] It will be appreciated that once collected, the reference data can be stored in the database 211 allowing this to be subsequently retrieved by the processing system 201 for subsequent analysis. The processing system 201 also typically stores an indication of an identity of each of the reference biomarkers.

[0382] In one example, the measurements are received as raw data, which then undergoes preliminary processing. Such raw data corresponds to information that has come from a source without modification, such as outputs from instruments such as PCR machines, array (*e.g.*, microarray) scanners, sequencing machines, clinical notes or any other biochemical, biological, observational data, or the like. This step can be used to convert the raw data into a format that is better suited to analysis. In one example this is performed in order to normalize the raw data and thereby assist in ensuring the biomarker values demonstrate consistency even when measured using different techniques, different equipment, or the like. Thus, the goal of normalization is to remove the variation within the samples that is not directly attributable to the specific analysis under consideration. For example, to remove variances caused by differences in sample processing at different sites. Classic examples of normalization include z-score transformation for generic data, or popular domain specific normalizations, such as RMA normalization for microarrays.

[0383] However, it will also be appreciated that in some applications, such as a single sample experiment run on a single data acquisition machine, this step may not strictly be necessary, in which case the function can be a Null function producing an output identical to the input.

[0384] In one example, the preferred approach is a paired function approach over log normalized data. Log normalization is a standard data transformation on microarray data, because the data follow a log-normal distribution when coming off the machine. Applying a log transform turns the data into process-friendly normal data.

[0385] At step 505 different groups are defined using the reference data.

[0386] Prior to this occurring, the processing system 201 optionally removes a validation subgroup of individuals from the reference data to allow the processing system 201 to determine the candidate biomarkers using the reference data without the validation subgroup

so that the validation subgroup can be subsequently used to validate the candidate biomarkers or signatures including a number of the candidate biomarkers. Thus, data from the validation subgroup is used to validate the efficacy of the candidate or signature biomarkers in identifying the presence, absence, degree, stage, severity, prognosis or progression of any one or more of the conditions to ensure the potential or signature biomarkers are effective.

[0387] In one example, this is achieved by having the processing system 201 flag individuals within the validation subgroup or alternatively store these in either an alternative location within the database 211 or an alternative database to the reference data. The validation subgroup of individuals is typically selected randomly and may optionally be selected to include individuals having different phenotypic traits. When a validation subgroup of individuals is removed, the remaining individuals will simply be referred to as reference data for ease throughout the remaining description.

[0388] The reference data (*i.e.*, excluding the validation subgroup) are classified into groups. The groups may be defined in any appropriate manner and may be defined based on any one or more of an indication of a presence, absence, degree, stage, severity, prognosis or progression of a condition, other tests or assays, or measured biomarkers associated with the individuals.

[0389] For example, a first selection of groups may be to identify one or more groups of individuals suffering from SIRS, one or more groups of individuals suffering ipSIRS, one or more groups of individuals suffering inSIRS, and one or more groups of healthy individuals. Further groups may also be defined for individuals suffering from other conditions. The groups may include overlapping groups, so for example it may be desirable to define groups of healthy individuals and individuals having SIRS, with further being defined to distinguish inSIRS patients from ipSIRS patients, as well as different degree of inSIRS or ipSIRS, with these groups having SIRS in common, but each group of patients differing in whether a clinician has determined the presence of an infection or not. Additionally, further subdivision may be performed based on phenotypic traits, so groups could be defined based on gender, ethnicity or the like so that a plurality of groups of individuals suffering from a condition are defined, with each group relating to a different phenotypic trait.

[0390] It will also be appreciated, however, that identification of different groups can be performed in other manners, for example on the basis of particular activities of biomarkers

within the biological samples of the reference individuals, and accordingly, reference to conditions is not intended to be limiting and other information may be used as required.

[0391] The manner in which classification into groups is performed may vary depending on the preferred implementation. In one example, this can be performed automatically by the processing system 201, for example, using unsupervised methods such as Principal Components Analysis (PCA), or supervised methods such as k-means or Self Organizing Map (SOM). Alternatively, this may be performed manually by an operator by allowing the operator to review reference data presented on a Graphical User Interface (GUI), and define respective groups using appropriate input commands.

[0392] At step 510 biomarkers are filtered based on their ability to distinguish between the groups. This process typically examines the activity of the reference biomarkers for individuals within and across the groups, to identify reference biomarkers whose activities differ between and hence can distinguish groups. A range of different analysis techniques can be utilized including, for example, regression or correlation analysis techniques. Examples of the techniques used can include established methods for parametized model building such as Partial Least Squares, Random Forest or Support Vector Machines, usually coupled to a feature reduction technique for the selection of the specific subset of the biomarkers to be used in a signature.

[0393] Such techniques are known and described in a number of publications. For example, the use of Partial Least Squares is described in "Partial least squares: a versatile tool for the analysis of high-dimensional genomic data" by Boulesteix, Anne-Laure and Strimmer, Korbinian, from *Briefings in Bioinformatics* 2007 vol 8. no. 1, pg 32-44. Support Vector machines are described in "LIBSVM: a library for support vector machines" by Chang, C.C. and Lin, C.J. from ACM Transactions on Intelligent Systems and Technology (TIST), 2011 vol 2, no. 3,pg 27. Standard Random Forest in R language is described in "Classification and Regression by random Forest" by Liaw, A. and Wiener, M., in *R news* 2002, vol2, no. 3, pg 18-22.

[0394] The analysis techniques are implemented by the processing system 201, using applications software, which allows the processing system 201 to perform multiple ones of the analysis techniques in sequence. This is advantageous as the different analysis techniques typically have different biases and can therefore be used to identify different potential

biomarkers that can distinguish the groups, thereby reducing the risk of clinically relevant biomarkers being overlooked.

[0395] In one example, the process involves filtering out any biomarkers that demonstrate a correlation with the groups, and hence with the condition, that is below a certain correlation threshold, such as 0.3.

[0396] At step 515 derived biomarkers are generated from the filtered reference biomarkers using one or more functions. The nature of the derived biomarkers and the functions used will vary depending upon the preferred implementation. For example, functions can include division, subtraction, multiplication, addition of two markers, sigmoidal functions applied to the product of two biomarkers, negative logs of the division of two biomarkers, least-squares regression applied to two vectors of markers to produce a function (equation) output, concordance correlation coefficient of two vectors of categorical biomarkers, or the like.

[0397] In general, the function is selected based on a number of rules. These rules can include: utility, functions that provide the best results; interpretability, functions that can be understood in terms of biological function; output, functions that produce informative outputs; simplicity; performance assessment; least number of biomarkers for best performance; number of biomarkers at a statistical overfitting threshold or the like.

[0398] In one example, the preferred function is division, with the resulting biomarkers being different ratios. It will be appreciated that the division can be performed in multiple different ways, so that for three biomarkers, nine different derived biomarkers can be determined.

[0399] At step 520 a performance measure is determined for each of the candidate biomarkers, including the filtered reference biomarkers and any derived markers. The performance measure may be of any suitable form and typically includes a correlation or performance explained measure that is indicative of a correlation of the corresponding biomarker and its ability to distinguish between groups. In one example, the performance function used to determine the performance measure is a standard univariate statistical test over all candidate biomarkers. Other examples however include a t-test, a non-parametric equivalent or area under receiver operator curve, chi squared or regression analyses or their equivalents, extensions or derivatives may be used.

[0400] The outcome of the applying the performance function to each in the candidate selection step is a ranked list of biomarkers, with the top *N* ranked biomarkers proceeding to the next stage. The biomarkers falling below this threshold are no longer considered. The threshold applied may be an absolute number or proportion of all biomarkers, or determined by performance, such as a p value ≤ 0.05. The threshold should be chosen to contain a sufficiently large number of biomarkers to bias towards including sufficiently independent biomarkers (*i.e.*, low mutual correlation).

[0401] At step 525, the processing system 201 selects a next two candidate biomarkers based on the performance measure and on a mutual correlation. In this regard, two markers that are highly correlated with each other in terms of the context of the condition will not necessarily improve the ability to distinguish a particular presence, absence, degree or prognosis of the condition any more than a single one of the markers. Accordingly, it is typical to select biomarkers that have a high performance measure in respect of the condition, but which have a mutual correlation that falls below a mutual correlation threshold. The mutual correlation threshold used will vary depending upon the preferred implementation, and is typically selected to be as low as possible, as described above. Examples of the manner in which the biomarkers are selected will be described in more detail below with respect to Figures 6A and 6B.

[0402] At step 530, the processing system 201 determines a performance of a next candidate biomarker combination. In this regard, the processing system 201 will use a combining function such as addition, to combine the biomarker values of the selected candidate biomarkers and use this to determine and indicator value based on the combination of biomarker values. The performance can be determined in any suitable manner, such as using statistical measurements, correlation measurements, concordance measurements or aggregate performance measurements such as averages. In one particular example, the performance measure is a 'variance explained' (VE). A VE of "1" means that using the biomarkers, you can perfectly classify/predict the disease. A VE of "0.8" means that your markers account for 80% of the result in practice.

[0403] Accordingly, at step 535 the processing system 201 compares the performance of the indicator to a performance threshold and determines if this is exceeded at step 540. In the event that the threshold is exceeded, this indicates that the selected combination of markers

provides the required degree of discrimination allowing the presence, absence, degree or prognosis of the condition to be determined.

[0404] In the event that the threshold is not exceeded at step 540, it is determined if all combinations have been considered at step 545. In this regard, it is possible that multiple different combinations of the two selected biomarkers to be tried, so if each possible combination has not been considered, the processing system 201 returns to step 530 to determine the performance of a next candidate biomarker combination. In this regard, the combinations used will typically be ordered in terms of preference, so that preferred combinations are tried first, with less preferred combinations being tried only in the event that preferred combinations prove unsuccessful.

[0405] Once all candidate biomarker combinations have been considered for the two candidate biomarkers selected, and if the performance threshold has still not been exceeded, the process moves onto step 550 to compare the current number of candidate biomarkers being considered to a limit. In this regard, the limit is used to control the overall number of biomarkers in the biomarker signature, thereby minimizing signature size and hence the cost of performing the associated measurements and diagnosis.

[0406] If the limit has not been exceeded an additional biomarker is added based on the correlation and performance at step 560, with the process moving onto step 530 to determine a performance of the next candidate biomarker combination. Otherwise if a limit has been reached, then an alternative next two candidate biomarkers are selected at step 525. Thus, this process allows additional candidate biomarkers to be progressively included, with a combination of the multiple candidate biomarkers being compared to the performance threshold, to determine if the required performance is met. If this is not achieved before the number of candidate biomarkers reaches the limit, the process is recommenced using two different candidate biomarkers.

[0407] Once the performance threshold has been exceeded at step 540, the selected candidate biomarkers can be defined as signature biomarkers for inclusion in a biomarker signature for the one or more conditions at step 565.

[0408] It should be noted that before the biomarker signature is finalized at step 565, additional checks might be performed, to ensure that the candidate biomarkers included in the signature should not be excluded for any reason. For example, candidate biomarkers might

be excluded for cost considerations as some combinations of candidate biomarkers may cost more than others. For example, a larger number of biomarkers may cost more than a smaller number, and the additional cost may not be justified by a small improvement in performance. Alternatively, the cost might be increased if multiple different tests are required in order to measure required biomarker values.

[0409] Biomarkers might also be excluded from use for legal reasons, for example if their use is restricted for approval or intellectual property reasons. Some biomarkers may be difficult to measure from a technical perspective, for example very low expression *in vivo*, which increases variability and therefore reduces robustness.

[0410] The performance of each biomarker combination panel may also include some variability, typically expressed as confidence intervals around the reported performance. Although a point estimate for one panel may be higher than for another, if the difference given the variability is not significant, the combinations may be considered equivalent.

[0411] Once a particular combination of signature biomarkers has been defined, at step 570 the processing system 201 can determine an indicator value range associated with each group. In particular, the range of reference biomarker values for the signature biomarkers within each group are used to calculate indicator value ranges for each group. These can then be compared to an indicator value calculated for a biological subject having an unknown presence absence, degree or progression of the at least one condition and used to identify a group to which the subject would belong and hence the presence, absence, degree or progression of the condition.

[0412] Thus, the above-described process iteratively assesses the biomarkers, initially selecting two biomarkers, with various combinations of these being considered to determine if these have the required performance for use in diagnosing the presence, absence, degree or progression of a condition. In the event that the required performance is not provided, additional biomarkers can be added and further combinations tried. Thus the process can consider three biomarkers, four biomarkers, five biomarkers, six biomarkers, seven biomarkers, eight biomarkers, nine biomarkers or more. Typically this is performed to a limit which may be defined based for example on the number of biomarkers that can practically be measured within given cost or process parameters. In the event that the

required performance is not obtained the process moves onto to select alternative candidate biomarkers with this being repeated.

[0413] Thus it will be appreciated that the above process initially selects those biomarkers which have the suitable performance and which are not highly correlated on the basis that these provide the maximum performance. The ability of these biomarkers to distinguish is then tested and in the event that this is insufficient, further biomarkers can be added to a limit. If this still does not provide the required discriminatory performance alternative biomarkers can be selected.

[0414] The process of selecting two candidate biomarkers at step 525 can be achieved in any number of ways depending upon the preferred implementation and examples of this will now be described with reference to Figures 6A and 6B.

[0415] In the example of Figure 6A, at step 600 biomarkers are grouped according to their mutual similarity. Thus, highly correlated biomarkers are put together in common groups. Biomarkers within the group are ranked at step 610 based on their performance measure in terms of their correlation with the condition, with the highest ranked biomarkers from two of the groups being selected at step 620 to define the next two candidate biomarkers. It will be appreciated if additional candidate biomarkers are required, these can be selected from different groups to the first two candidate biomarkers.

[0416] An alternative process is shown in Figure 6B. In this example, at step 650 biomarkers are ranked based on their performance at discriminating the condition(s). At step 660 a next highest biomarker is selected, with the remaining biomarkers being re-ranked on the combination of their similarity with the selected biomarker, for example using mutual information, as well as their performance. The next highest biomarker is then selected at step 680 with this process being repeated as required.

[0417] Accordingly, it will be appreciated that the above-described processes provide mechanisms for selecting a combination of biomarkers, and more typically derived biomarkers, that can be used to form a biomarker signature, which in turn can be used in diagnosing the presence, absence or degree of at least one condition or in providing a prognosis of at least one condition. In this regard, the biomarker signature defines the biomarkers that should be measured (*i.e.*, the signature biomarkers), how derived biomarker values should be determined for measured biomarker values, and then how biomarker values

should be subsequently combined to generate an indicator value. The biomarker signature can also specify defined indicator value ranges that indicate a particular presence, absence, degree or prognosis of one or more conditions.

[0418] An example of the method of using a biomarker signature described above will now be described with reference to Figure 7.

[0419] In this example, at step 700 a plurality of measured biomarker values are measured for a biological subject whose condition is unknown, with these typically being provided to the processing system 201, for example by download from measuring equipment or the like.

[0420] After any required processing, such as normalization or the like, at step 710, the processing system 201 applies one or more functions to the measured biomarker values to determine any required derived biomarker values. A derived biomarker value and another biomarker value (*i.e.*, another derived biomarker value or a measured biomarker value) are combined to generate an indicator value, which can then be displayed or otherwise used in determining the presence, absence, degree or prognosis of one or more conditions. Thus, this can involve simply displaying the indicator value, allowing an assessment to be made by a medical practitioner or alternatively may involve further processing, such as comparing the indicator to defined indicator value ranges that indicate a particular presence, absence, degree or prognosis of one or more conditions, with the results of the comparison being displayed.

[0421] Accordingly, in the above-described method the biomarker signature defines the biomarker values that need to be measured and/or derived, allowing the processing system 201 to automatically generate an indicator value based on received measured biomarker values. Once this has been completed, the processing system 201 can compare the indicator value to the indicator value ranges, and either display results of the comparison, or alternative interpret the results of the comparison, allowing an indicator to be displayed that is indicative of the presence, absence, degree or prognosis of a condition. This can then be used by a medical practitioner as required in performing a medical diagnosis of the biological subject.

[0422] Using the above-described methods it has been identified that the use of ratios of "immune system biomarkers" is particularly beneficial when assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition.

[0423] As used herein, the term "immune system biomarker" refers to a biomarker of the host's immune system that is altered, or whose level of expression is altered, as part of an inflammatory response to damage or pathogenic insult, including metabolic, toxic, neurotoxic, iatrogenic, thermal or chemical insults, illustrative examples of which include trauma, surgery, drugs including chemotherapeutic drugs, radiation, disease including pathogenic infection, metabolic disease and ischemia, as well as foreign or implanted substances.

[0424] The term "immune system", as used herein, refers to cells, molecular components and mechanisms, including antigen-specific and non-specific categories of the adaptive and innate immune systems, respectively, that provide a defense against damage and insults and matter, the latter comprised of antigenic molecules, including but not limited to tumors, pathogens, and self-reactive cells.

[0425] The term "innate immune system" refers to a host's non-specific reaction to insult to include antigen-nonspecific defense cells, molecular components and mechanisms that come into action immediately or within several hours after exposure to almost any insult or antigen. Elements of the innate immunity include for example phagocytic cells (monocytes, macrophages, dendritic cells, polymorphonuclear leukocytes such as neutrophils, reticuloendothelial cells such as Küpffer cells, and microglia), cells that release inflammatory mediators (basophils, mast cells and eosinophils), natural killer cells (NK cells) and physical barriers and molecules such as keratin, mucous, secretions, complement proteins, immunoglobulin M (IgM), acute phase proteins, fibrinogen and molecules of the clotting cascade, and cytokines. Effector compounds of the innate immune system include chemicals such as lysozymes, IgM, mucous and chemoattractants (*e.g.*, cytokines or histamine), complement and clotting proteins.

[0426] The term "adaptive immune system" refers to antigen-specific cells, molecular components and mechanisms that emerge over several days, and react with and remove a specific antigen. The adaptive immune system develops throughout a host's lifetime. The adaptive immune system is based on leukocytes, and is divided into two major sections: the humoral immune system, which acts mainly *via* immunoglobulins produced by B cells, and the cell-mediated immune system, which functions mainly *via* T cells.

[0427] Accordingly, in one example, an indicator is determined that correlates to a ratio of immune system biomarkers, which can be used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition.

[0428] In this example, the method includes determining a pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject.

[0429] The biomarker values are used to determine a derived biomarker value using the pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers.

[0430] Thus, if the biomarker values are the concentrations of the biomarkers, then the derived biomarker value will be based on a ratio of the biomarker values. However, if the biomarker values are related to the concentrations of the biomarkers, for example if they are logarithmically related by virtue of the biomarker values being based on PCR cycle times, or the like, then the biomarker values may be combined in some other manner, such as by subtracting the cycle times to determine a derived biomarker value indicative of a ratio of the concentrations.

[0431] The derived biomarker is then used to determine the indicator, either by using the derived biomarker value as an indicator value, or by performing additional processing, such as comparing the derived biomarker value to a reference or the like, as will be described in more detail below.

[0432] In any event, combining biomarker values to determine a ratio of concentrations of immune system biomarkers, and then using this to determine an indicator allows indicators to be determined for use in determining a likelihood of a subject suffering from a range of different conditions, depending on the immune system biomarkers selected, which as it will be appreciated can be performed using the above described process.

[0433] A number of further features will now be described.

[0434] In one example, the process involves determining a first derived biomarker value using a first pair of biomarker values, the first derived biomarker value being indicative of a ratio of concentrations of first and second immune system biomarkers, determining a second

derived biomarker value using a second pair of biomarker values, the second derived biomarker value being indicative of a ratio of concentrations of third and fourth immune system biomarkers and determining the indicator by combining the first and second derived biomarker values. Thus, in this example, two pairs of derived biomarker values can be used, which can assist in increasing the ability of the indicator to reliably determine the likelihood of a subject having a condition.

[0435] The derived biomarker values could be combined using a combining function such as an additive model; a linear model; a support vector machine; a neural network model; a random forest model; a regression model; a genetic algorithm; an annealing algorithm; a weighted sum; a nearest neighbor model; and a probabilistic model.

[0436] In one example, the indicator is compared to an indicator reference, with a likelihood being determined in accordance with results of the comparison. The indicator reference is typically derived from indicators determined for a number of individuals in a reference population. The reference population typically includes individuals having different characteristics, such as a plurality of individuals of different sexes; and/or ethnicities, with different groups being defined based on different characteristics, with the subject's indicator being compared to indicator references derived from individuals with similar characteristics. The reference population can also include a plurality of healthy individuals, a plurality of individuals suffering from at least one diagnosed medical condition, a plurality of individuals showing clinical signs of at least one medical condition and/or first and second groups of individuals, each group of individuals suffering from a respective diagnosed medical condition.

[0437] It will be appreciated that the individuals selected will depend on the intended use of the indicator. In particular, when the indicator is for use in determining the likelihood that a biological subject has a specific medical condition, the sample population includes individuals presenting with clinical signs of the specific medical condition, individuals diagnosed with the specific medical condition and healthy individuals. This ensures that the assessment of indicator validity applies regardless of not or whether the individual has the specific condition or not.

[0438] It will also be appreciated that the sample population could also include a plurality of individuals of different sexes, ethnicities, ages, or the like, allowing the control value ranges

to be common across populations. However, this is not essential, and alternatively control value thresholds could be established that are specific to a particular sub-set of the population. In this case, it would be necessary to ensure that the control value threshold ranges used are appropriate for the subject under consideration.

[0439] The indicator can also be used for determining a likelihood of the subject having a first or second condition, in other words to distinguish between the conditions. In this case, this would typically be achieved by comparing the indicator to first and second indicator references, the first and second indicator references being indicative of first and second conditions and determining the likelihood in accordance with the results of the comparison. In particular, this can include determining first and second indicator probabilities using the results of the comparisons and combining the first and second indicator probabilities, for example using a Bayes method, to determine a condition probability corresponding to the likelihood of the subject having one of the conditions. In this situation the first and second conditions could include two medical conditions, or a single medical condition and a healthy condition.

[0440] In this case, the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with the first or second condition respectively. In this regard, this can be achieved by determining first and second groups of individuals, each group of individuals having a presence or absence of a diagnosed medical condition and determining first and second indicator references for the first and second groups respectively. This allows the indicator to be used to distinguish between first and second conditions, which could include different medical conditions, as well as healthy conditions. It will also be appreciated that whilst two groups are described, this is not essential and three or more groups could also be defined.

[0441] The process is usually performed using at least one electronic processing device, such as a suitably programmed computer system or the like.

[0442] In this case, the electronic processing device typically obtains at least two pairs of measured biomarker values, either by receiving these from a measuring or other quantifying device, or by retrieving these from a database or the like. The processing device then determines a first derived biomarker value indicative of a ratio of concentrations of first and

second immune system biomarkers and a second derived biomarker value indicative of a ratio of third and fourth immune system biomarkers. The processing device then determines the indicator by combining the first and second derived biomarker values.

[0443] The processing device can then generate a representation of the indicator, for example by generating an alphanumeric indication of the indicator, a graphical indication of a comparison of the indicator to one or more indicator references or an alphanumeric indication of a likelihood of the subject having at least one medical condition.

[0444] The method would also typically include obtaining a sample taken from the biological subject, the sample including polynucleotide expression products and quantifying at least some of the polynucleotide expression products within the sample to determine the pair of biomarker values. This can be achieved using any suitable technique, and will depend on the nature of the immune system biomarkers.

[0445] For example, if the indicator is based on a ratio of concentrations of the polynucleotide expression products, this process would typically include quantifying polynucleotide expression products by amplifying at least some polynucleotide expression products in the sample, determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products and determining the indicator by determining a difference between the amplification amounts. In this regard, the amplification amount is generally a cycle time, a number of cycles, a cycle threshold and an amplification time.

[0446] In this case, the method includes determining a first derived biomarker value by determining a difference between the amplification amounts of a first pair of polynucleotide expression products, determining a second derived biomarker value by determining a difference between the amplification amounts of a second pair of polynucleotide expression products and determining the indicator by adding the first and second derived biomarker values.

[0447] As previously discussed, the at least two immune system biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9 and the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to

diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0448] Typically the mutual correlation range is one of ±0.8; ±0.7; ±0.6; ±0.5; ±0.4; ±0.3; ±0.2; and, ±0.1.

[0449] Typically each immune system biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3 and more typically ±0.9; ±0.8; ±0.7; ±0.6; ±0.5; and, ±0.4. Typically the performance threshold is indicative of an explained variance of at least one of 0.4; 0.5; 0.6; 0.7; 0.8; and, 0.9.

[0450] The above-described method has been used to identify 1650 biomarkers of inflammatory response syndromes (also referred to interchangeably herein as "IRS biomarkers" or "IRS immune system biomarkers"), which are useful for assisting in distinguishing: (1) between SIRS affected subjects (*i.e.*, subjects having inSIRS or ipSIRS) and healthy subjects or subjects not affected by SIRS; (2) between subjects with inSIRS and subjects with ipSIRS; and/or (3) between subjects with different stages of ipSIRS (*e.g.*, sepsis, severe sepsis and septic shock). Based on this identification, the present inventors have developed various methods, compositions, apparatus and kits, which take advantage of these biomarkers to provide an indicator for use in diagnosing the presence, absence or degree of at least one condition, or for prognosing at least one condition, wherein the at least one condition is selected from a healthy condition (*e.g.*, a normal condition or one in which inSIRS and inSIRS are absent), inSIRS, ipSIRS, or a stage of ipSIRS (*e.g.*, a stage of ipSIRS with a particular severity, illustrative examples of which include mild sepsis, severe sepsis and septic shock). In advantageous embodiments, the methods and kits involve monitoring the expression of IRS biomarker genes in cells of the immune systems, including blood cells (*e.g.*, immune cells such as leukocytes), which may be reflected in changing patterns of RNA levels or protein production that correlate for example with the presence of active disease or response to disease.

[0451] The IRS biomarkers are expression products of genes (also referred to interchangeably herein as "IRS biomarker genes" or IRS immune system biomarker genes"), including polynucleotide and polypeptide expression products. As used herein, polynucleotide expression products of IRS biomarker genes are referred to herein as "IRS

biomarker polynucleotides." Polypeptide expression products of the IRS biomarker genes are referred to herein as "IRS biomarker polypeptides." The term "gene", as used herein, refers to a stretch of nucleic acid that codes for a polypeptide or for an RNA chain that has a function. While it is the exon region of a gene that is transcribed to form RNA (*e.g.*, mRNA), the term "gene" also includes regulatory regions such as promoters and enhancers that govern expression of the exon region.

[0452] Suitably, the IRS biomarker genes are selected from the group consisting of: *PRKCZ*, *SKI*, *RER1*, *TAS1R1*, *VAMP3*, *AGTRAP*, *VPS13D*, *KLHDC7A*, *NBL1//C1orf151*, *MDS2*, *RCAN3*, *LDLRAP1*, *MAN1C1*, *SH3BGRL3*, *DHDDS*, *HCRTR1*, *CCDC28B*, *LCK*, *ZNF362*, *THRAP3*, *PPIE//CCDC25*, *CAP1*, *CTPS*, *C1orf84*, *FAAH*, *DMBX1*, *CYP4B1*, *BTF3L4*, *LRRC42*, *C1orf175//TTC4*, *TMEM61*, *FPGT//TNNI3K*, *ACADM*, *SPATA1*, *EPHX4*, *RPAP2*, *RPL5//SNORA66//SNORD21//FAM69A*, *RTCD1*, *SLC30A7*, *RNPC3//AMY2B*, *CELSR2*, *AHCYL1*, *CEPT1//DRAM2*, *CHIA*, *LIX1L*, *UPF0627*, *MRPS21*, *TNFAIP8L2*, *SMCP*, *DCST1*, *RAG1AP1*, *C1orf182*, *HAPLN2*, *NTRK1*, *CD1E*, *TOMM40L//NR1I3*, *POU2F1*, *TIPRL*, *SFT2D2*, *CACNA1E*, *SMG7*, *OCLM*, *RGS2*, *ZC3H11A//RP11-74E24.2*, *MFSD4*, *IL20*, *RPS6KC1*, *C1orf95*, *ARF1*, *GALNT2*, *TNFRSF4*, *NADK*, *FLJ14100//C1orf86*, *GPR153*, *RERE*, *SLC2A7*, *SDHB*, *RNF186*, *DDOST*, *GPN2*, *RPA2*, *PEF1*, *PTP4A2*, *TRIM62*, *PHC2*, *LSM10*, *MRPS15*, *RRAGC*, *COL9A2*, *TESK2*, *NRD1*, *KTI12*, *CC2D1B*, *YIPF1*, *JAK1*, *SLC35D1*, *DIRAS3*, *ZZZ3*, *GNG5*, *ZNHIT6*, *ODF2L*, *SEP15*, *BARHL2*, *GCLM*, *CLCC1//GPSM2//C1orf62*, *SORT1*, *SLC16A4*, *PHTF1*, *RSBN1*, *DENND2C//BCAS2*, *CD58*, *SPAG17//WDR3*, *REG4//NBPF7*, *RP11-94I2.2//NBPF16//NBPF11//NBPF15//NBPF8//NBPF20//NBPF10//NBPF14//NBPF1//LOC100288142//NBPF12//KIAA1245//LOC100290137*, *APH1A*, *POGZ*, *TDRKH*, *THEM4*, *S100A11*, *CRNN*, *SPRR2C*, *S100A12*, *S100A8*, *GATAD2B//PLIN2*, *DENND4B*, *PBXIP1*, *PYGO2*, *SHC1*, *DCST2*, *GBA//GBAP*, *ASH1L*, *RIT1*, *MEF2D*, *AIM2*, *COPA*, *DEDD*, *TADA1L*, *GPA33*, *CD247*, *F5*, *PIGC*, *KIAA0040*, *TOR1AIP2//TOR1AIP1//IFRG15*, *STX6//KIAA1614*, *EDEM3*, *UCHL5*, *DENND1B*, *DDX59*, *KIF21B*, *ARL8A*, *CYB5R1*, *MYBPH*, *CHI3L1*, *PIK3C2B//LOC100130573*, *NUAK2*, *NUCKS1*, *FAIM3*, *PLXNA2*, *SLC30A1*, *LPGAT1*, *ANGEL2*, *RAB3GAP2//AURKAPS1//AURKA//SNORA36B*, *TP53BP2*, *NVL*, *TMEM63A*, *PARP1*, *ITPKB*, *TARBP1*, *CHML*, *AKT3*, *SMYD3*, *AHCTF1*, *OR1C1*, *NCOA1*, *HADHB*, *ABHD1//PREB*, *SPAST*, *SLC30A6//DDX50*, *CRIPT*, *MSH2*, *FOXN2*,

CCDC104, *VRK2*, *AHSA2//USP34*, *OTX1*, *AFTPH*, *CEP68*, *PLEK*, *ANXA4*, *MXD1*, *NAGK*, *SMYD5//NOTO*, *MTHFD2*, *TTC31*, *SEMA4F*, *TMSB10*, *SH2D6*, *GNLY*, *KCNIP3*, *CNNM4*, *CNNM3*, *ZAP70*, *LIPT1//MRPL30*, *MAP4K4*, *IL1R2*, *IL1R1*, *IL18R1*, *POLR1B*, *CHCHD5*, *IL1RN*, *PSD4*, *DDX18*, *INSIG2*, *TMEM177//LOC100125918*, *RALB*, *PROC*, *GPR17//LOC100291428//LIMS2*, *IMP4*, *FAM123C*, *ACVR2A*, *MBD5*, *LYPD6B*, *SLC4A10*, *UBR3*, *HAT1*, *ITGA6*, *ZAK*, *OSBPL6*, *PLEKHA3*, *ZC3H15*, *COL3A1*, *GLS*, *OBFC2A*, *COQ10B*, *MARS2*, *CFLAR*, *NOP58*, *FAM117B*, *CYP20A1*, *FASTKD2*, *PIKFYVE*, *C2orf62*, *SLC11A1*, *AGFG1*, *CHRNG*, *EIF4E2*, *TRPM8*, *LRRFIP1*, *GAL3ST2*, *TMEM18*, *LAPTM4A*, *SF3B14*, *TP53I3*, *UNQ2999*, *GPR113//SELI*, *MPV17*, *PPM1G*, *NLRC4*, *CDC42EP3*, *HNRPLL*, *COX7A2L*, *KCNG3*, *CALM2//C2orf61*, *BCL11A*, *XPO1*, *NAT8B*, *DUSP11*, *MOGS*, *SNRNP200*, *SEMA4C*, *MITD1*, *IL1A*, *SLC35F5*, *CCDC93*, *CLASP1*, *SAP130*, *YSK4*, *GTDC1*, *ORC4L*, *NR4A2//FLJ46875*, *DPP4*, *GALNT3*, *SCN7A*, *FRZB*, *STK17B*, *CLK1//PPIL3*, *MPP4*, *INO80D*, *KLF7*, *FAM119A*, *NGEF*, *ARL4C*, *RAB17*, *HDLBP*, *LRRN1*, *SETD5*, *IRAK2*, *C3orf42*, *TSEN2*, *NR2C2//MRPS25*, *UBE2E1*, *C3orf35*, *SNRK*, *ZNF197*, *GNAI2*, *ALAS1*, *PRKCD*, *CACNA1D*, *PXK*, *PTPRG*, *ATXN7*, *SLC35A5*, *SLC15A2*, *CCDC48*, *DNAJC13*, *CLDN18*, *GYG1*, *SELT*, *MED12L*, *RAP2B*, *MYNN*, *ABCF3*, *VPS8*, *HRG*, *EIF4A2//SNORA4*, *LPP*, *CCDC50*, *LOC152217*, *TADA3L*, *SEC13*, *TIMP4*, *METTL6*, *DAZL//DAZ4//DAZ3//DAZ2*, *SATB1//TBC1D5*, *SCN10A*, *SEC22C*, *ZDHHC3*, *ZDHHC3*, *SLC6A20*, *UQCRC1*, *PRKAR2A*, *IMPDH2*, *CCDC71*, *UBA7*, *CAMKV*, *WDR82*, *LMOD3*, *FOXP1*, *MORC1*, *ATG3*, *GSK3B//LOC100129275*, *HCLS1*, *KPNA1*, *PTPLB*, *C3orf22*, *RPN1*, *KIAA1257//ACAD9//LOC100132731*, *FOXL2*, *MECOM*, *PLD1*, *GNB4*, *MRPL47*, *KLHL6*, *THPO*, *ETV5*, *BCL6//LOC100131635*, *ATP13A5*, *TMEM44*, *KIAA1530*, *TACC3*, *CNO*, *BST1*, *KLF3*, *TMEM33//DCAF4L1*, *KIT*, *ENAM*, *FAM47E//STBD1*, *ENOPH1*, *PDLIM5*, *CCDC109B//HIGD1A//CCDC13*, *EGF*, *PCDH10*, *RAB33B*, *TMEM184C*, *RBM46*, *GRIA2*, *C4orf39*, *KLHL2*, *TLL1*, *F11*, *SLBP*, *HAUS3//POLN*, *PPARGC1A*, *TLR10*, *C4orf34*, *TXK*, *RPL21P44*, *KDR*, *RCHY1*, *CNOT6L*, *PLAC8*, *HPSE*, *GPRIN3*, *PPA2*, *COL25A1*, *C4orf3*, *QRFPR*, *MFSD8*, *MAP9*, *PDGFC*, *TKTL2*, *ACSL1*, *SUB1//TMEM183A*, *CARD6*, *MCCC2*, *TNPO1*, *PDE8B*, *PAPD4*, *THBS4*, *FAM151B*, *RASGRF2*, *SNX2*, *LMNB1//PCIF1*, *MEGF10*, *LEAP2*, *TCF7*, *KDM3B*, *CXXC5*, *SLC4A9*, *ANKHD1-EIF4EBP3//ANKHD1//EIF4EBP3*, *KIAA0141*, *GRPEL2*, *MFAP3*, *GABRA6*, *GABRA1*, *DOCK2*, *RANBP17//USP12*,

ERGIC1, *ATP6V0E1//SNORA74B*, *ZNF346*, *NSD1*, *CLPTM1L*, *UGT3A1*, *GDNF*, *TTC33*, *hCG_2039148*, *MOCS2*, *SLC38A9*, *CCDC125*, *ANKRA2*, *HAPLN1*, *CCNH*, *TMEM161B*, *MBLAC2*, *MCTP1*, *TICAM2//TMED7//TMED7-TICAM2*, *KIF3A*, *C5orf15*, *SKP1*, *CXCL14*, *KLHL3*, *CD14*, *YIPF5*, *LARS*, *DCTN4*, *CCDC69*, *ATOX1*, *TIMD4*, *ADAM19*, *SLIT3*, *RNF44*, *DOK3*, *MGAT4B//SQSTM1*, *C5orf45//SQSTM1*, *RASGEF1C*, *MGAT1*, *IRF4*, *HIVEP1*, *E2F3*, *HIST1H4I*, *HIST1H2BM*, *MOG*, *ZNRD1//NCRNA00171*, *TRIM15*, *HCG27*, *BAT2//SNORA38*, *CYP21A2*, *ITPR3*, *MAPK14*, *MAPK13*, *PNPLA1*, *SFRS3*, *CDKN1A*, *FOXP4*, *CUL9*, *RUNX2*, *ZNF451*, *SOBP*, *C6orf182*, *KIAA1919*, *RWDD1*, *KPNA5*, *TPD52L1*, *ARG1*, *RAB32*, *ARID1B*, *SLC22A3*, *SERPINB1*, *C6orf146*, *GCM2*, *ATXN1*, *DCDC2//KAAG1*, *HIST1H3I*, *HIST1H4L*, *GABBR1*, *RNA243*, *DDAH2*, *CLIC1*, *NEU1*, *RXRB*, *VPS52*, *TCP11*, *CLPS*, *PGC*, *ZNF318*, *YIPF3*, *MRPL14*, *PLA2G7*, *PKHD1*, *IL17F*, *HTR1B*, *GABRR2*, *UBE2J1*, *BACH2*, *MCM9*, *VNN1*, *IL20RA*, *FLJ27255*, *T*, *RPS6KA2*, *HGC6.3*, *UNC84A//C7orf20*, *SDK1*, *ZDHHC4*, *C7orf26*, *GLCCI1//tcag7.903*, *GPNMB*, *CCDC126*, *WIPF3//ZNRF2//LOC441208*, *GPR141*, *STARD3NL*, *POU6F2*, *CDC2L5*, *ZMIZ2*, *UPP1*, *ZNF273*, *KCTD7//RABGEF1*, *RABGEF1//tcag7.967//tcag7.951//KCTD7//LOC100293333*, *CCDC132*, *PVRIG//PILRB//STAG3*, *PILRB//PVRIG//STAG3*, *C7orf51*, *GNB2*, *LRRC17*, *LRRN3*, *CFTR*, *LSM8*, *LUC7L2*, *MGAM//LOC100124692*, *GIMAP7*, *INSIG1*, *RBM33*, *ICA1*, *FAM126A*, *HIBADH*, *TRIL*, *SCRN1*, *ELMO1*, *INHBA*, *CAMK2B*, *NPC1L1*, *DDC//LOC100129427*, *NSUN5//NSUN5B//NSUN5C*, *CLDN3*, *C7orf23//DMTF1*, *SRI*, *BET1*, *MCM7*, *GATS*, *ATXN7L1//RINT1//EFCAB10*, *KIAA1549*, *SLC37A3*, *SMARCD3*, *MLL3//BAGE2*, *CLN8*, *MSRA*, *PIWIL2*, *NEFM//LOC100129717*, *EPHX2*, *LEPROTL1*, *MAK16//C8orf41*, *AP3M2*, *FNTA*, *SGK196*, *UBE2V2*, *FLJ46365*, *SNTG1*, *TRIM55*, *C8orf45*, *PREX2*, *PLEKHF2*, *BAALC//FLJ10489*, *TTC35*, *MTBP*, *ZHX2*, *RNF139*, *TG*, *DENND3//C8orf60*, *TNFRSF10D*, *TRIM35*, *GSR*, *WHSC1L1*, *PCMTD1//PXDNL*, *NCOA2*, *TRAM1//LOC286190*, *RUNX1T1*, *EXT1*, *DDEF1IT1*, *CDC37L1*, *UBE2R2*, *UBAP1//KIF24*, *GALT*, *RGP1//GBA2*, *TGFBR1*, *C9orf6//IKBKAP*, *IMAGE5303689*, *ATP6V1G1*, *TLR4*, *SET*, *MRPL41*, *C9orf68*, *HAUS6//SCARNA8*, *KLHL9*, *C9orf82*, *NDUFB6//DFFB*, *SIT1*, *FAM108B1*, *TRPM6*, *FRMD3*, *SLC28A3*, *BICD2*, *C9orf84*, *AKNA*, *MEGF9*, *C5*, *GOLGA1//SCAI*, *SH2D3C*, *FAM102A*, *FLJ10232*, *ASB6*, *BAT2L*, *EDF1*, *FBXW5*, *C10orf18*, *FBXO18*, *GATA3*, *CUGBP2*, *VIM*, *STAM*, *WAC*, *BAMBI*, *ZNF487//LOC439911*, *ALOX5*, *WDFY4*, *SRGN*, *CCDC109A*, *FAM149B1//FAM149B2*,

MINPP1, *PTEN//PTENP1*, *ENTPD1//C10orf131*, *ABCC2*, *SFXN2*, *SHOC2*, *ACSL5*, *BCCIP//DHX32*, *FAM188A*, *CUBN*, *SVIL//hCG_1783494*, *FAM13C//PHYHIPL*, *ATAD1*, *ANKRD22*, *FLJ34077*, *COX15*, *ERLIN1*, *ACTR1A*, *ABLIM1*, *RAB11FIP2*, *C10orf84*, *PRDX3*, *C10orf119*, *NSMCE4A*, *TALDO1//INTS8*, *TNNT3*, *FXC1*, *PDE3B*, *DNAJC24*, *PTPRJ//OR4B1*, *C11orf31*, *TMEM109*, *CD6*, *CD5*, *TMEM138*, *POLR2G*, *TMEM179B*, *NAT11*, *OTUB1*, *RBM14//RBM4*, *AIP*, *PPFIA1*, *IL18BP//NUMA1*, *C11orf30*, *C11orf82*, *TMEM126B*, *C11orf73*, *PIWIL4*, *LOC100132686*, *PAFAH1B2*, *UBE4A*, *TRAPPC4*, *SC5DL*, *VWA5A//OR10D1P*, *STT3A*, *VPS26B*, *TRIM21*, *ZBED5*, *SAAL1*, *FANCF*, *LIN7C*, *PHF21A*, *CUGBP1*, *OSBP*, *CYBASC3*, *TUT1*, *SLC25A45*, *LTBP3*, *EIF1AD*, *GAB2*, *CREBZF*, *PICALM*, *SLC36A4*, *CCDC82*, *KIAA1826*, *MPZL3*, *MPZL2*, *H2AFX*, *SIAE*, *ZBTB44*, *HSN2*, *ADIPOR2*, *NCAPD2//SCARNA10//FADS1*, *PTPN6*, *CLEC4D*, *CDKN1B*, *GOLT1B*, *FAR2*, *FGD4*, *TMEM106C*, *TMBIM6*, *C12orf62*, *PRR13//PCBP2*, *DGKA*, *COQ10A*, *TSPAN31*, *CDK4/MARCH9/C3HC4*, *LEMD3*, *IRAK3*, *TMTC3*, *ACTR6*, *TCTN1*, *PXMP2//PGAM5*, *DCP1B*, *SLC2A3//SLC2A14*, *C3AR1*, *PLBD1*, *TM7SF3*, *ASB8//PHB*, *LMBR1L*, *FMNL3//PRPF40B*, *AAAS*, *NFE2*, *GPR84*, *CD63*, *SARNP//DNAJC14*, *NACA*, *CDK4//TSPAN31*, *TMBIM4//LOC100133322*, *IL22*, *LIN7A*, *HAL*, *APPL2*, *GLTP*, *GIT2*, *VPS29*, *PPTC7*, *DDX54//CCDC42B*, *SLC24A6*, *SDS*, *RBM19*, *MED13L*, *C12orf49*, *FBXO21*, *WSB2*, *TAOK3*, *CIT*, *RAB35*, *RPLP0*, *PXN*, *TRIAP1*, *SFRS9*, *POP5*, *UNQ1887*, *C12orf43*, *ANAPC5*, *KDM2B*, *MORN3*, *TMEM120B//RHOF*, *LOC338799*, *DIABLO//B3GNT4*, *VPS33A*, *CLIP1*, *PITPNM2*, *EIF2B1*, *CCDC92*, *NCOR2*, *DHX37*, *DDX51*, *POLE*, *GOLGA3*, *ZMYM2*, *SPATA13//C1QTNF9*, *NUPL1*, *PAN3//EEF1A1//CHCHD2*, *ALOX5AP*, *EEF1DP3*, *KL*, *UFM1*, *NARG1L*, *ITM2B*, *FNDC3A*, *CDADC1*, *ARL11*, *LMO7*, *DNAJC3*, *TM9SF2*, *CLYBL*, *PCCA*, *ABHD13*, *LAMP1*, *TMCO3*, *UPF3A*, *ZMYM5//ZMYM2*, *ZDHHC20//LOC728099*, *PARP4*, *MTMR6//LOC646482*, *HSPH1*, *N4BP2L2//CG030*, *ELF1*, *LCP1*, *KPNA3*, *C13orf1*, *DLEU2//DLEU2L*, *GUCY1B2*, *INTS6*, *DACH1*, *TBC1D4*, *EDNRB*, *UGGT2*, *GPR183*, *LIG4*, *ANKRD10*, *RASA3*, *RNASE2//LOC643332*, *RPGRIP1*, *IRF9*, *TSSK4*, *C14orf21*, *SCFD1*, *FANCM*, *ABHD12B*, *PTGDR*, *FBXO34//KIAA0831*, *C14orf101*, *ACTR10*, *ARID4A*, *JKAMP*, *HIF1A*, *SYNE2*, *EXD2*, *SLC39A9*, *SFRS5*, *PCNX*, *SIPA1L1//SNORD56B//LOC145474//LOC283567*, *YLPM1*, *BATF*, *FLVCR2//RPS24*, *GPR65*, *TDP1*, *EVL*, *ZNF839*, *TDRD9*, *INF2*, *PLD4*, *MTA1//LOC647310//LOC100128343*, *NDRG2*, *DAD1//OR6J1*, *SLC7A8*, *IPO4*, *TM9SF1*,

ADCY4, *RIPK3*, *EAPP*, *BAZ1A*, *NFKBIA*, *SEC23A*, *C14orf104*, *C14orf138*, *SOS2*, *NIN*, *PYGL*, *CNIH*, *DHRS7*, *WDR89*, *ACTN1*, *NUMB*, *C14orf43*, *ABCD4*, *KIAA0317*, *NEK9*, *ANGEL1*, *SPTLC2*, *SERPINA6*, *DICER1*, *BCL11B*, *ANKRD9*, *PPP1R13B*, *AKT1*, *BRF1*, *TUBGCP5*, *SNRPN//SNURF//IPW//SNORD116-16//SNORD116-18//SNORD116-21//SNORD116-22//SNORD116-17//SNORD116-19//PAR5//PAR-SN//SNORD116-2//SNORD116-25//SNORD116-26//SNORD107//SNORD115-12//SNORD115-5//SNORD115-6//SNORD115-9//SNORD116-11//SNORD116-12//SNORD116-13//SNORD116-28//SNORD116-4//SNORD64//PAR1//SNORD109A//SNORD109B//SNORD116-6//SNORD116-3//SNORD116-9//SNORD115-13//SNORD115-1//SNORD115-14//SNORD115-15//SNORD115-21//SNORD115-10//SNORD115-7//SNORD115-16//SNORD115-40//SNORD115-42//SNORD115-11//SNORD115-29//SNORD115-34//SNORD115-36//SNORD115-4//SNORD115-43//HBII-52-24//SNORD116-5//SNORD116-7//SNORD115-26//SNORD115-30//SNORD116-15//SNORD116-8//SNORD115-2//SNORD115-39//SNORD116-14//SNORD116-20//SNORD115-8//SNORD115-3//SNORD115-38//SNORD115-41//SNORD115-22//SNORD115-44//SNORD116-1//SNORD115-17//SNORD115-18//SNORD115-19//SNORD115-20//SNORD116@*, *APBA2*, *MTMR15//MTMR10*, *RYR3*, *BAHD1*, *CHP*, *JMJD7-PLA2G4B//JMJD7//PLA2G4B*, *HAUS2*, *C15orf63//SERF2*, *B2M*, *TRIM69*, *PLDN*, *SQRDL*, *GALK2*, *USP8*, *GLDN*, *MAPK6*, *LACTB*, *RAB8B*, *APH1B*, *USP3//LOC100130855*, *SNX1*, *LBXCOR1//PIAS1//CALML4*, *NEO1*, *MPI*, *FBXO22//FBXO22OS*, *RCN2*, *FAH*, *IL16*, *ABHD2*, *SLCO3A1*, *MCTP2*, *MEF2A//LYSMD4*, *NIPA2//CYFIP1*, *HERC2//HERC2P2//HERC2P3//LOC440248*, *MTMR10//MTMR15*, *C15orf24*, *SLC12A6*, *LPCAT4*, *INO80*, *OIP5*, *ZFP106*, *CDAN1*, *SPG11//ISLR*, *SPPL2A*, *GNB5//LOC100129973*, *MYO5A*, *ARPP19*, *RAB27A*, *CCPG1//PIGB//DYX1C1*, *BNIP2*, *CA12*, *FAM96A*, *KIAA0101//CSNK1G1*, *TLE3*, *PARP6*, *NPTN*, *MAN2C1*, *IMP3*, *MTHFS*, *ST20//C15orf37*, *TMC3*, *AP3B2*, *C15orf40*, *WDR73*, *NTRK3*, *DET1*, *TM2D3*, *WDR90*, *RHOT2//FBXL16*, *TMEM204*, *CRAMP1L//HN1L*, *MAPK8IP3*, *TBL3*, *TSC2*, *KCTD5//PRO0461//PDPK1*, *CLUAP1*, *DNASE1*, *DNAJA3*, *CP110*, *C16orf62*, *LYRM1*, *METTL9*, *EEF2K*, *POLR3E*, *PLK1*, *PRKCB*, *IL21R//LOC283888*, *SULT1A2//SULT1A1*, *ATXN2L*, *LAT//SPNS1//NPIPL2//LOC728741//LOC730153//NPIPL3//SPIN1//LOC728888//LOC100289169//LOC728734//LOC729602//LOC100288442//LOC100288332*, *KIF22*, *MAZ*,

CORO1A//LOC606724, *ITGAL*, *SRCAP//SNORA30*, *ZNF646//ZNF668*, *C16orf67*, *TMEM188*, *LPCAT2*, *CETP*, *CKLF*, *CMTM1//CKLF*, *TMEM208*, *CTCF*, *THAP11*, *NUTF2*, *EDC4*, *SLC7A6//SLC7A6OS*, *PRMT7*, *SNTB2*, *VPS4A*, *DDX19B//DDX19A*, *CHST4*, *HP//HPR*, *PLCG2*, *KLHL36*, *KIAA0182*, *BANP//RUNDC2C*, *TRAPPC2L*, *SPG7*, *CDK10*, *TCF25*, *AFG3L1*, *LUC7L*, *AXIN1*, *JMJD8*, *LMF1*, *UNKL*, *UNKL*, *CLCN7*, *MRPS34*, *RNPS1*, *NLRC3*, *TRAP1//DNASE1*, *ADCY9*, *CORO7*, *C16orf72*, *RRN3//LOC653390//LOC730092//LOC100131998*, *XYLT1//LYRM2//ZC3H11A*, *DCUN1D3//LYRM1*, *IGSF6//METTL9*, *CDR2//RRN3//LOC100131998//LOC653390*, *COG7*, *GGA2*, *NSMCE1*, *GTF3C1*, *CCDC101//LOC388242*, *C16orf54*, *KCTD13*, *SEPT1*, *ZNF764//ZNF747*, *C16orf58//LOC100128371*, *ITFG1*, *ABCC11//LONP2*, *NUDT21*, *BBS2//OGFOD1*, *CSNK2A2*, *GOT2*, *FAM96B*, *FHOD1//SLC9A5*, *ATP6V0D1//LOC100132855*, *GFOD2*, *SLC12A4*, *DPEP3*, *DPEP2*, *CHTF8//HAS3*, *COG8//PDF*, *TERF2*, *AARS*, *ST3GAL2*, *VAC14//LOC100130894*, *AP1G1*, *WDR59*, *CTRB2//CTRB1*, *TAF1C//ADAD2*, *FBXO31*, *ZCCHC14*, *FAM38A*, *CENPBD1*, *TIMM22*, *RPA1*, *DPH1//OVCA2*, *SGSM2*, *ARRB2*, *LOC100130950*, *DNAH2*, *PIGL*, *TRPV2*, *MPRIP*, *DRG2*, *ALKBH5//FLJ13773*, *SMCR7*, *WSB1*, *TAOK1*, *CPD*, *SUZ12P*, *RNF135*, *ZNF830*, *TAF15*, *GGNBP2*, *LASP1*, *PSMD3*, *CDC6*, *NBR2*, *TMUB2*, *MGC57346//C17orf69*, *NSF//LOC728806*, *GOSR2*, *NPEPPS//TBC1D3F//LOC440434*, *KPNB1*, *CDK5RAP3*, *ATP5G1*, *UBE2Z*, *XYLT2//LOC100130580*, *NOG*, *DGKE*, *AKAP1*, *TMEM49//CLTC//MIR21*, *CLTC*, *CA4*, *C17orf64*, *DCAF7*, *PITPNC1*, *NOL11//SNORA38B*, *MAP2K6*, *COG1*, *CD300A*, *TMEM104*, *MRPS7*, *KIAA0195*, *TSEN54*, *LLGL2*, *LOC100134934//CDK3*, *MFSD11*, *SEPT9*, *TNRC6C*, *TMC8*, *ENGASE*, *RPTOR*, *GPS1*, *FN3KRP*, *TBCD*, *GEMIN4*, *GLOD4*, *SLC43A2*, *PRPF8*, *SMG6//C17orf6*, *METT10D//LOC284009*, *SHPK*, *TAX1BP3*, *P2RX5*, *MYBBP1A//SPNS2*, *PELP1*, *PFN1*, *ZNF232*, *DHX33*, *DERL2*, *NLRP1//LOC728392*, *ASGR2*, *NEURL4//GPS2//D4S234E*, *ZBTB4*, *TP53*, *VAMP2*, *PIK3R5*, *ELAC2*, *NCOR1//C20orf191//LOC100131704*, *ZNF287*, *TOM1L2//LOC246315*, *GRAP//SNORD3B-1//SNORD3B-2//LOC400581*, *ALDOC*, *SDF2*, *RAB34*, *PHF12*, *NUFIP2*, *OMG*, *EVI2B*, *C17orf66//RSL24D1*, *SYNRG//LOC100131822*, *PLXDC1*, *CACNB1*, *PGAP3*, *MED24*, *NR1D1//THRA*, *CCR7*, *STAT5B//STAT5A*, *FAM134C*, *VAT1*, *DUSP3*, *C17orf65//ASB16*, *UBTF*, *GPATCH8*, *MAP3K14//LOC100133991*, *OSBPL7*, *SLC35B1*, *TOB1*, *COX11//TOM1L1*, *VEZF1*, *SFRS1//FLJ44342*, *SEPT4*,

MED13//LOC100129112, *LIMD2//MAP3K3*, *STRADA*, *FTSJ3*, *CD79B*, *ICAM2*, *ERN1*, *TEX2*, *LRRC37A3//LRRC37A2//LRRC37A//ARL17P1//LRRC37A4//LOC100294335//LOC644397*, *GNA13*, *WIPI1//ARSG*, *FAM20A*, *NAT9*, *GGA3*, *H3F3B//H3F3C*, *EXOC7*, *SFRS2*, *TMC6//LOC100131096*, *USP36*, *CD7*, *RAB31*, *VAPA*, *SEH1L*, *HQ0644/PRO0644*, *RNMT*, *RNF138*, *GALNT1*, *ELP2*, *PIK3C3*, *SLC14A2*, *ME2*, *SERPINB2//SERPINB10*, *ZNF407*, *ZNF236*, *NFATC1//LOC100127994*, *ENOSF1//TYMS*, *MYOM1*, *AFG3L2*, *ABHD3*, *OSBPL1A*, *CDH2*, *DSC1*, *PSTPIP2*, *C18orf32*, *MBD2//SNORA37*, *PIGN*, *TMX3*, *PQLC1*, *GZMM*, *ARID3A*, *CIRBP*, *DAZAP1*, *SPPL2B*, *NFIC*, *VAV1*, *ARHGEF18//LOC100128573*, *STXBP2//LOC554363//LOC100131801*, *C19orf59*, *ZNF317*, *ILF3*, *SMARCA4*, *PRKCSH*, *IER2*, *CCDC130*, *DCAF15*, *IL27RA*, *KLF2*, *SIN3B*, *DDA1*, *GTPBP3*, *FAM129C*, *FCHO1*, *ARRDC2*, *IFI30*, *C19orf60*, *CRTC1//MAML2*, *RFXANK//MEF2B//LOC729991*, *ZNF101*, *ZNF738*, *ZNF257//ZNF492//ZNF99//ZNF98//LOC646864*, *C19orf2*, *KIAA0355//FLJ21369*, *USF2*, *TMEM147*, *LIN37//PSENEN*, *C19orf55*, *TBCB//POLR2I*, *ZNF382*, *ZNF568*, *ZNF420*, *ZNF383*, *CCDC97*, *ZNF574*, *CD177*, *ZNF230//ZNF222*, *VASP*, *GRWD1*, *FLT3LG*, *ZNF175*, *NCRNA00085*, *PPP2R1A*, *ZNF808//ZNF578//ZNF611*, *LENG8*, *FCAR*, *RPL28*, *U2AF2*, *LOC100288114//MGC9913*, *ZFP28*, *ZNF460*, *ZNF549*, *ZNF211*, *ZNF587//ZNF417*, *ZNF274*, *ZNF544*, *ZNF8*, *TRIM28*, *C19orf6*, *C19orf34*, *GNG7*, *AES*, *EEF2//SNORD37*, *PLIN5//LRG1*, *PLIN3*, *PTPRS*, *SAFB2//SAFB*, *RANBP3*, *GTF2F1//LOC100130856*, *XAB2*, *ELAVL1*, *ADAMTS10*, *FBXL12*, *DNMT1*, *TYK2*, *KEAP1*, *KRI1*, *TMEM205//hCG_29977*, *ZNF563*, *MAN2B1//MORG1*, *C19orf56*, *DHPS*, *TNPO2//SNORD41*, *LPHN1*, *NDUFB7*, *AKAP8*, *AKAP8L*, *CHERP//C19orf44//CALR3*, *INSL3//JAK3*, *IL12RB1*, *UPK1A*, *TYROBP*, *ZNF529*, *ZNF461*, *ZNF607*, *YIF1B*, *PRR13*, *CEACAM4*, *PLAUR*, *TRAPPC6A*, *ERCC1//CD3EAP*, *RTN2*, *SYMPK*, *PGLYRP1*, *NOSIP*, *PNKP*, *NKG7*, *FPR1*, *ZNF28*, *OSCAR*, *MBOAT7*, *LILRA5*, *LILRA4*, *ZNF550//ZNF549*, *ZNF416*, *ZNF256*, *ZNF329*, *FAM110A*, *ITPA*, *CDC25B*, *CDS2*, *CRLS1*, *CSRP2BP*, *SEC23B*, *SLC24A3*, *HCK*, *ASXL1*, *ACSS2*, *C20orf4*, *TGIF2*, *C20orf24//SLA2*, *RPN2//EEF1A2*, *CTNNBL1*, *ACTR5*, *PPP1R16B*, *DHX35*, *PLCG1*, *MYBL2*, *SYS1//SYS1-DBNDD2//DBNDD2*, *DNTTIP1*, *CTSA*, *MMP9//LOC100128028*, *DDX27*, *SLC9A8*, *RNF114*, *PTPN1*, *TSHZ2*, *PFDN4*, *CSTF1*, *CASS4*, *GNAS*, *C20orf177*, *CDH26*, *C20orf197*, *LOC284757*, *ARFGAP1*, *PRPF6*, *NSFL1C*, *SIRPD*,

SIRPG//SIRPA, *RNF24*, *RASSF2*, *TMX4*, *JAG1*, *C20orf74*, *C20orf3*, *C20orf112*, *CDK5RAP1*, *AHCY*, *GGT7*, *EDEM2*, *RBM39//LOC643167*, *BLCAP*, *SERINC3//TTPAL*, *ZNF335*, *ELMO2*, *B4GALT5*, *DPM1*, *ZFP64*, *ZNF217*, *CTSZ*, *SYCP2*, *PSMA7*, *DIDO1*, *YTHDF1*, *CHODL*, *BACH1*, *C21orf41//BACH1*, *IL10RB*, *IFNAR1*, *IFNGR2*, *SON*, *MORC3//DOPEY2*, *DYRK1A*, *KCNJ15*, *ETS2*, *RRP1B*, *PFKL*, *TRPM2*, *ADARB1*, *SAMSN1//LOC388813*, *N6AMT1*, *SYNJ1*, *TMEM50B*, *KCNE1*, *PRDM15*, *C2CD2*, *WDR4*, *U2AF1*, *CSTB*, *UBE2G2//SUMO3*, *PTTG1IP*, *POFUT2*, *MCM3AP*, *IL17RA//CECR7*, *C22orf37*, *LZTR1*, *PPIL2//YPEL1*, *CYTSA*, *SNRPD3//C22orf13*, *NF2*, *LIMK2*, *SLC5A1*, *MCM5*, *NCF4*, *GGA1*, *SH3BP1//PDXP*, *POLR2F//LOC100131530*, *APOBEC3A//APOBEC3B*, *APOBEC3D*, *ATF4*, *CACNA1I*, *ZC3H7B*, *CCDC134*, *TSPO*, *NUP50*, *TBC1D22A//LOC100289878*, *RP3-402G11.5*, *SAPS2*, *NCAPH2*, *BID*, *SLC25A1*, *KLHL22//KRT18*, *PI4KA//PI4KAP1//PI4KAP2//LOC100293141*, *MAPK1*, *ZNF70*, *TPST2*, *SF3A1//CCDC157*, *PES1*, *PIK3IP1*, *PATZ1*, *C22orf30*, *IL2RB*, *CSNK1E//LOC400927*, *UNC84B*, *CBX7//LOC100128400*, *RPS19BP1*, *MKL1//KIAA1659*, *RANGAP1*, *TCF20*, *LDOC1L*, *UNQ6126*, *TUBGCP6*, *SBF1//SBF1P1*, *MSL3*, *MOSPD2*, *BMX//HNRPDL*, *PDHA1*, *YY2*, *PDK3*, *GK//GK3P//FTL//LOC652904*, *CXorf59*, *ATP6AP2*, *USP9X//USP9Y*, *RP2*, *USP11*, *RBM3*, *FTSJ1*, *WAS*, *PLP2*, *TSPYL2//GPR173*, *MAGED2*, *UBQLN2*, *NLGN3*, *ACRC*, *UPRT*, *CXorf26*, *ATP7A*, *DIAPH2*, *CSTF2//RAD21*, *ARMCX3*, *ARMCX5*, *GPRASP1*, *TMEM31*, *TBC1D8B*, *MID2*, *DOCK11*, *LONRF3*, *UBE2A*, *SH2D1A*, *OCRL*, *SLC25A14*, *HPRT1*, *CD40LG*, *AFF2*, *SSR4//IDH3G*, *FAM50A*, *DKC1//SNORA36A//SNORA56*, *ARSD*, *KAL1*, *CTPS2*, *RPS6KA3*, *BCOR*, *MAOB//NAT13*, *ZNF41*, *OTUD5*, *KCND1*, *ZMYM3*, *MAGT1*, *BRWD3*, *TRMT2B*, *GLA*, *MORF4L2*, *PSMD10*, *ACSL4*, *LAMP2*, *CUL4B*, *ODZ1*, *ELF4*, *RAP2C*, *FAM127B//FAM127C//FAM127A*, *TMEM185A*, *ARD1A*, *IRAK1*, *DNASE1L1//RPL10*, *SH3KBP1*, *Mitochondrial*, *Mitochondrial*, *CCNL2*, *INPP5B*, *TLR5*, *ADRB3//GOT1L1*, *NOC2L//SAMD11//LOC401010* and *SHFM1* (hereafter referred to interchangeably herein as "the full list of IRS immune system biomarker genes" or "full list IRS biomarker genes").

[0453] The methods, compositions, apparatus and kits of the present invention take advantage of the IRS biomarkers broadly described above and elsewhere herein to provide an indicator for use in diagnosing the presence, absence or degree of the at least one condition selected from a healthy condition (*e.g.*, a normal condition or one in which inSIRS and

inSIRS are absent), inSIRS, ipSIRS or a stage of ipSIRS (*e.g.*, a stage of ipSIRS with a particular severity such as mild sepsis, severe sepsis and septic shock), or in providing a prognosis of the at least one condition, which may involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values (also referred to herein as a "biomarker signature"), the indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition, wherein: (i) at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0454] In advantageous embodiments, the diagnostic or prognostic methods, compositions, apparatus and kits of the present invention involve: (1) determining a plurality of measured IRS biomarker values, each measured IRS biomarker value being a measured value of an IRS biomarker of the biological subject; and (2) applying a function to at least one of the measured IRS biomarker values to determine at least one derived IRS biomarker value, the at least one derived IRS biomarker value being indicative of a value of a corresponding derived IRS biomarker. The function suitably includes at least one of: (a) multiplying two IRS biomarker values; (b) dividing two IRS biomarker values; (c) adding two IRS biomarker values; (d) subtracting two IRS biomarker values; (e) a weighted sum of at least two IRS biomarker values; (f) a log sum of at least two IRS biomarker values; and (g) a sigmoidal function of at least two IRS biomarker values.

[0455] In some embodiments, the diagnostic or prognostic methods, compositions, apparatus and kits involve: determining at least one derived IRS biomarker value corresponding to a ratio of two measured IRS biomarker values. In these examples, the diagnostic or prognostic methods, apparatus and kits suitably include combining at least two IRS biomarker values to determine an indicator value representing the indicator and in illustrative examples of this

type, the at least two IRS biomarker values are combined using a combining function (*e.g.*, any one or more of: an additive model; a linear model; a support vector machine; a neural network model; a random forest model; a regression model; a genetic algorithm; an annealing algorithm; weighted sum; a nearest neighbor model; and a probabilistic model). Suitably, the diagnostic or prognostic methods, apparatus and kits include: (a) determining a first derived IRS biomarker value, the first derived IRS biomarker value being a ratio of first and second measured IRS biomarker values; (b) determining a second derived IRS biomarker value, the second derived IRS biomarker value being a ratio of third and fourth measured IRS biomarker values; and (c) adding the first and second derived IRS biomarker values to generate an indicator value.

[0456] In some embodiments, the methods, compositions, kits and apparatus of the present invention are useful for diagnosing that inSIRS or a healthy condition is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and a healthy condition, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS biomarker genes as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group B IRS biomarker genes as defined herein.

[0457] In other embodiments, the methods, apparatus and kits are useful for diagnosing that ipSIRS or a healthy condition is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from ipSIRS and a healthy condition, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS biomarker genes, as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS biomarker genes as defined herein.

[0458] In still other embodiments, the methods, apparatus and kits are useful for diagnosing that inSIRS or ipSIRS is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and ipSIRS, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3,

wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS biomarker genes as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS biomarker genes as defined herein.

[0459] In other embodiments, the methods, apparatus and kits are useful for diagnosing that inSIRS or ipSIRS is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from inSIRS and ipSIRS, wherein: (i) at least four IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least four IRS biomarkers is selected from a first IRS biomarker group, wherein at least one other of the at least four IRS biomarkers is selected from a second IRS biomarker group, wherein at least one other of the at least four IRS biomarkers is selected from a third IRS biomarker group, and wherein at least one other of the at least four IRS biomarkers is selected from a fourth IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS biomarker genes as defined herein, wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS biomarker genes as defined herein, wherein the third IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS biomarker genes as defined herein, and wherein the fourth IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS biomarker genes as defined herein.

[0460] In still other embodiments, the methods, apparatus and kits are useful for diagnosing that mild sepsis or severe sepsis is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from mild sepsis and severe sepsis, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS biomarker genes as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS biomarker genes as defined herein.

[0461] In still other embodiments, the methods, apparatus and kits are useful for diagnosing that mild sepsis or septic shock is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from mild sepsis and septic shock, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3,

wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS biomarker genes as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS biomarker genes as defined herein.

[0462] In still other embodiments, the methods, apparatus and kits are useful for diagnosing that severe sepsis or septic shock is present or absent in the biological subject, which suitably involve: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one IRS biomarker of a biological subject; (b) determining the indicator using a combination of the plurality of IRS biomarker values, the at least one indicator being at least partially indicative of the presence, absence, degree or prognosis of the at least one condition selected from severe sepsis and septic shock, wherein: (i) at least two IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein at least one of the at least two IRS biomarkers is selected from a first IRS biomarker group and wherein at least one other of the at least two IRS biomarkers is selected from a second IRS biomarker group, wherein the first IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS biomarker genes as defined herein, and wherein the second IRS biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS biomarker genes as defined herein.

[0463] As used herein, the terms “diagnosis”, “diagnosing” and the like are used interchangeable herein to encompass determining the likelihood that a subject will develop a condition, or the existence or nature of a condition in a subject. These terms also encompass determining the severity of disease or episode of disease, as well as in the context of rational therapy, in which the diagnosis guides therapy, including initial selection of therapy, modification of therapy (*e.g.*, adjustment of dose or dosage regimen), and the like. By

"likelihood" is meant a measure of whether a biological subject with particular measured or derived biomarker values actually has a condition (or not) based on a given mathematical model. An increased likelihood for example may be relative or absolute and may be expressed qualitatively or quantitatively. For instance, an increased likelihood may be determined simply by determining the subject's measured or derived biomarker values for at least two IRS biomarkers and placing the subject in an "increased likelihood" category, based upon previous population studies. The term "likelihood" is also used interchangeably herein with the term "probability".

[0464] In some embodiments, the biomarkers, including IRS biomarkers, are obtained from a biological sample. The term "biological sample" as used herein refers to a sample that may be extracted, untreated, treated, diluted or concentrated from an animal. The biological sample is suitably a biological fluid such as whole blood, serum, plasma, saliva, urine, sweat, ascitic fluid, peritoneal fluid, synovial fluid, amniotic fluid, cerebrospinal fluid, tissue biopsy, and the like. In certain embodiments, the biological sample contains blood, especially peripheral blood, or a fraction or extract thereof. Typically, the biological sample comprises blood cells such as mature, immature or developing leukocytes, including lymphocytes, polymorphonuclear leukocytes, neutrophils, monocytes, reticulocytes, basophils, coelomocytes, hemocytes, eosinophils, megakaryocytes, macrophages, dendritic cells natural killer cells, or fraction of such cells (*e.g.*, a nucleic acid or protein fraction). In specific embodiments, the biological sample comprises leukocytes including peripheral blood mononuclear cells (PBMC). By "obtained from" is meant to come into possession. Biological or reference samples so obtained include, for example, nucleic acid extracts or polypeptide extracts isolated or derived from a particular source. For instance, the extract may be isolated directly from a biological fluid or tissue of a subject.

[0465] The term "nucleic acid" or "polynucleotide" as used herein includes RNA, mRNA, miRNA, cRNA, cDNA mtDNA, or DNA. The term typically refers to a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms of DNA or RNA.

[0466] "Protein", "polypeptide" and "peptide" are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same.

[0467] In some embodiments, biomarker signatures are determined through analysis of measured or derived IRS biomarker values for IRS biomarkers of one or more control subjects that have or do not have a condition. These biomarkers are referred to herein as "reference IRS biomarkers". In specific examples, individual control subjects are selected from "healthy control subjects", "non-healthy control subjects", "SIRS control subjects", "inSIRS control subjects", "ipSIRS control subjects", "control subjects with a particular stage of ipSIRS", illustrative examples of which include "mild sepsis control subjects", "severe sepsis control subjects" and "septic shock control subjects", etc.), which are also referred to herein as control groups (*e.g.*, "healthy control group", "non-healthy control group", "SIRS control group", "inSIRS control group", "ipSIRS control group", "ipSIRS stage group", illustrative examples of which include "mild sepsis control group", "severe sepsis control group", and "septic shock control group", etc.).

[0468] Suitably, an individual measured or derived IRS biomarker value corresponds to the level or amount of a respective IRS biomarker or to a function that is applied to that level or amount. As used herein the terms "level" and "amount" are used interchangeably herein to refer to a quantitative amount (*e.g.*, weight or moles), a semi-quantitative amount, a relative amount (*e.g.*, weight % or mole % within class), a concentration, and the like. Thus, these terms encompass absolute or relative amounts or concentrations of IRS biomarkers in a sample.

[0469] In some embodiments, the presence, absence, degree or prognosis of at least one condition in a biological subject is established by determining a plurality of IRS biomarker values, wherein each IRS biomarker value is indicative of a value measured or derived for at least one IRS biomarker in a biological sample obtained from the biological subject. These biomarkers are referred to herein as "sample IRS biomarkers". In accordance with the present invention, a sample IRS biomarker corresponds to a reference IRS biomarker (also referred to herein as a "corresponding IRS biomarker"). By "corresponding IRS biomarker" is meant an IRS biomarker that is structurally and/or functionally similar to a reference IRS biomarker. Representative corresponding IRS biomarkers include expression products of allelic variants (same locus), homologues (different locus), and orthologues (different organism) of reference IRS biomarker genes. Nucleic acid variants of reference IRS biomarker genes and encoded IRS biomarker polynucleotide expression products can contain nucleotide substitutions,

deletions, inversions and/or insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product). For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of a reference IRS polypeptide.

[0470] Generally, variants of a particular IRS biomarker gene or polynucleotide will have at least about 40%, 45%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59% 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69% 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs known in the art using default parameters. In some embodiments, the IRS biomarker gene or polynucleotide displays at least about 40%, 45%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59% 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69% 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a nucleotide sequence selected from any one of SEQ ID NO: 1-1650, as summarized in Table 1.

[0471] Corresponding IRS biomarkers also include amino acid sequences that display substantial sequence similarity or identity to the amino acid sequence of a reference IRS biomarker polypeptide. In general, an amino acid sequence that corresponds to a reference amino acid sequence will display at least about 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 97, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or even up to 100% sequence similarity or identity to a reference amino acid sequence selected from any one of SEQ ID NO: 1651-3284, as summarized in Table 2.

[0472] In some embodiments, calculations of sequence similarity or sequence identity between sequences are performed as follows:

[0473] To determine the percentage identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison

purposes). In some embodiments, the length of a reference sequence aligned for comparison purposes is at least 30%, usually at least 40%, more usually at least 50%, 60%, and even more usually at least 70%, 80%, 90%, 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide at the corresponding position in the second sequence, then the molecules are identical at that position. For amino acid sequence comparison, when a position in the first sequence is occupied by the same or similar amino acid residue (*i.e.*, conservative substitution) at the corresponding position in the second sequence, then the molecules are similar at that position.

[0474] The percentage identity between the two sequences is a function of the number of identical amino acid residues shared by the sequences at individual positions, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. By contrast, the percentage similarity between the two sequences is a function of the number of identical and similar amino acid residues shared by the sequences at individual positions, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

[0475] The comparison of sequences and determination of percentage identity or percentage similarity between sequences can be accomplished using a mathematical algorithm. In certain embodiments, the percentage identity or similarity between amino acid sequences is determined using the Needleman and Wünsch, (1970, *J. Mol. Biol.* 48: 444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In specific embodiments, the percent identity between nucleotide sequences is determined using the GAP program in the GCG software package (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. An non-limiting set of parameters (and the one that should be used unless otherwise specified) includes a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0476] In some embodiments, the percentage identity or similarity between amino acid or nucleotide sequences can be determined using the algorithm of E. Meyers and W. Miller (1989, *Cabios*, 4: 11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

[0477] The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.*, (1990, *J Mol Biol.*, 215: 403-10). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 53010 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to YYYYY protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997, *Nucleic Acids Res*, 25: 3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used.

[0478] Corresponding IRS biomarker polynucleotides also include nucleic acid sequences that hybridize to reference IRS biomarker polynucleotides, or to their complements, under stringency conditions described below. As used herein, the term "hybridizes under low stringency, medium stringency, high stringency, or very high stringency conditions" describes conditions for hybridization and washing. "Hybridization" is used herein to denote the pairing of complementary nucleotide sequences to produce a DNA-DNA hybrid or a DNA-RNA hybrid. Complementary base sequences are those sequences that are related by the base-pairing rules. In DNA, A pairs with T and C pairs with G. In RNA, U pairs with A and C pairs with G. In this regard, the terms "match" and "mismatch" as used herein refer to the hybridization potential of paired nucleotides in complementary nucleic acid strands. Matched nucleotides hybridize efficiently, such as the classical A-T and G-C base pair mentioned above. Mismatches are other combinations of nucleotides that do not hybridize efficiently.

[0479] Guidance for performing hybridization reactions can be found in Ausubel *et al.*, (1998, *supra*), Sections 6.3.1-6.3.6. Aqueous and non-aqueous methods are described in that

reference and either can be used. Reference herein to low stringency conditions include and encompass from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization at 42° C, and at least about 1 M to at least about 2 M salt for washing at 42° C. Low stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at room temperature. One embodiment of low stringency conditions includes hybridization in 6 × sodium chloride/sodium citrate (SSC) at about 45° C, followed by two washes in 0.2 × SSC, 0.1% SDS at least at 50° C (the temperature of the washes can be increased to 55° C for low stringency conditions). Medium stringency conditions include and encompass from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization at 42° C, and at least about 0.1 M to at least about 0.2 M salt for washing at 55° C. Medium stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at 60-65° C. One embodiment of medium stringency conditions includes hybridizing in 6 × SSC at about 45° C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 60° C. High stringency conditions include and encompass from at least about 31% v/v to at least about 50% v/v formamide and from about 0.01 M to about 0.15 M salt for hybridization at 42° C, and about 0.01 M to about 0.02 M salt for washing at 55° C. High stringency conditions also may include 1% BSA, 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 0.2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 1% SDS for washing at a temperature in excess of 65° C. One embodiment of high stringency conditions includes hybridizing in 6 × SSC at about 45° C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 65° C.

[0480] In certain embodiments, a corresponding IRS biomarker polynucleotide is one that hybridizes to a disclosed nucleotide sequence under very high stringency conditions. One embodiment of very high stringency conditions includes hybridizing 0.5 M sodium phosphate, 7% SDS at 65° C, followed by one or more washes at 0.2 × SSC, 1% SDS at 65° C.

[0481] Other stringency conditions are well known in the art and a skilled addressee will recognize that various factors can be manipulated to optimize the specificity of the hybridization. Optimization of the stringency of the final washes can serve to ensure a high degree of hybridization. For detailed examples, see Ausubel *et al.*, *supra* at pages 2.10.1 to 2.10.16 and Sambrook *et al.* (1989, *supra*) at sections 1.101 to 1.104.

[0482] The IRS biomarkers disclosed herein each have significant sensitivity and specificity for diagnosing the presence, absence or degree of at least condition selected from a healthy condition (*e.g.*, a normal condition or one in which inSIRS and inSIRS are absent), inSIRS, ipSIRS or a stage of ipSIRS (*e.g.*, a stage of ipSIRS with a particular severity such as mild sepsis, severe sepsis and septic shock). Accordingly, it is feasible to use individual IRS biomarkers in methods, apparatus and kits that do not rely on the use of low mutual correlation between biomarkers to diagnose the presence, absence or degree of the at least condition. In illustrative examples of this type, the invention contemplates methods, kits and apparatus that are useful for diagnosing that inSIRS or a healthy condition is present or absent in a biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from inSIRS and a healthy condition, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group A and group B IRS biomarker genes as defined herein.

[0483] In other non-limiting examples, the methods, apparatus and kits are useful for diagnosing that ipSIRS or a healthy condition is present or absent in the biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from ipSIRS and a healthy condition, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based

on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group C and group D IRS biomarker genes as defined herein.

[0484] In still other non-limiting examples, the methods, apparatus and kits are useful for diagnosing that inSIRS or ipSIRS is present or absent in the biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from inSIRS and ipSIRS, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group E and group F IRS biomarker genes as defined herein.

[0485] In still other illustrative examples, the methods, apparatus and kits are useful for diagnosing that mild sepsis or severe sepsis is present or absent in the biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from mild sepsis and severe sepsis, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group K and group L IRS biomarker genes as defined herein.

[0486] In still other illustrative examples, the methods, apparatus and kits are useful for diagnosing that mild sepsis or septic shock is present or absent in the biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from mild sepsis and septic shock, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for

an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group M and group N IRS biomarker genes as defined herein.

[0487] In other non-limiting examples, the methods, apparatus and kits are useful for diagnosing that severe sepsis or septic shock is present or absent in the biological subject, which suitably involve: (1) correlating a reference biomarker signature with the presence or absence of a condition selected from severe sepsis and septic shock, wherein the reference biomarker signature evaluates at least one IRS biomarker; (2) obtaining a biomarker signature of a sample from a subject, wherein the sample biomarker signature evaluates for an individual IRS biomarker in the reference biomarker signature a corresponding IRS biomarker; and (3) diagnosing the presence or absence of the condition in the subject based on the sample biomarker signature and the reference biomarker signature, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group O and group P IRS biomarker genes as defined herein.

[0488] The biomarkers may be quantified or detected using any suitable technique. In specific embodiments, the biomarkers, including the IRS biomarkers, are quantified using reagents that determine the level or abundance of individual biomarkers. Non-limiting reagents of this type include reagents for use in nucleic acid- and protein-based assays.

[0489] In illustrative nucleic acid-based assays, nucleic acid is isolated from cells contained in the biological sample according to standard methodologies (Sambrook, *et al.*, 1989, *supra*; and Ausubel *et al.*, 1994, *supra*). The nucleic acid is typically fractionated (*e.g.*, poly A^+ RNA) or whole cell RNA. Where RNA is used as the subject of detection, it may be desired to convert the RNA to a complementary DNA. In some embodiments, the nucleic acid is amplified by a template-dependent nucleic acid amplification technique. A number of template dependent processes are available to amplify the IRS biomarker sequences present in a given template sample. An exemplary nucleic acid amplification technique is the polymerase chain reaction (referred to as PCR), which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, Ausubel *et al.* (*supra*), and in Innis *et al.*, ("PCR Protocols", Academic Press, Inc., San Diego Calif., 1990). Briefly, in PCR, two primer

sequences are prepared that are complementary to regions on opposite complementary strands of the biomarker sequence. An excess of deoxynucleotide triphosphates are added to a reaction mixture along with a DNA polymerase, *e.g.*, *Taq* polymerase. If a cognate IRS biomarker sequence is present in a sample, the primers will bind to the biomarker and the polymerase will cause the primers to be extended along the biomarker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the biomarker to form reaction products, excess primers will bind to the biomarker and to the reaction products and the process is repeated. A reverse transcriptase PCR amplification procedure may be performed in order to quantify the amount of mRNA amplified. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989, *supra*. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641. Polymerase chain reaction methodologies are well known in the art.

[0490] In certain advantageous embodiments, the template-dependent amplification involves quantification of transcripts in real-time. For example, RNA or DNA may be quantified using the Real-Time PCR technique (Higuchi, 1992, *et al.*, *Biotechnology* **10**: 413-417). By determining the concentration of the amplified products of the target DNA in PCR reactions that have completed the same number of cycles and are in their linear ranges, it is possible to determine the relative concentrations of the specific target sequence in the original DNA mixture. If the DNA mixtures are cDNAs synthesized from RNAs isolated from different tissues or cells, the relative abundance of the specific mRNA from which the target sequence was derived can be determined for the respective tissues or cells. This direct proportionality between the concentration of the PCR products and the relative mRNA abundance is only true in the linear range of the PCR reaction. The final concentration of the target DNA in the plateau portion of the curve is determined by the availability of reagents in the reaction mix and is independent of the original concentration of target DNA. In specific embodiments, multiplexed, tandem PCR (MT-PCR) is employed, which uses a two-step process for gene expression profiling from small quantities of RNA or DNA, as described for example in US Pat. Appl. Pub. No. 20070190540. In the first step, RNA is converted into cDNA and amplified using multiplexed gene specific primers. In the second step each individual gene is quantitated by real time PCR.

[0491] In certain embodiments, target nucleic acids are quantified using blotting techniques, which are well known to those of skill in the art. Southern blotting involves the use of DNA as a target, whereas Northern blotting involves the use of RNA as a target. Each provides different types of information, although cDNA blotting is analogous, in many aspects, to blotting or RNA species. Briefly, a probe is used to target a DNA or RNA species that has been immobilized on a suitable matrix, often a filter of nitrocellulose. The different species should be spatially separated to facilitate analysis. This often is accomplished by gel electrophoresis of nucleic acid species followed by "blotting" on to the filter. Subsequently, the blotted target is incubated with a probe (usually labeled) under conditions that promote denaturation and rehybridization. Because the probe is designed to base pair with the target, the probe will bind a portion of the target sequence under renaturing conditions. Unbound probe is then removed, and detection is accomplished as described above. Following detection/quantification, one may compare the results seen in a given subject with a control reaction or a statistically significant reference group or population of control subjects as defined herein. In this way, it is possible to correlate the amount of an IRS biomarker nucleic acid detected with the progression or severity of the disease. As used herein, the term "probe" refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term "probe" typically refers to a nucleic acid probe that binds to another nucleic acid, also referred to herein as a "target polynucleotide", through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the hybridization conditions. Probes can be labeled directly or indirectly and include primers within their scope. By "primer" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of a suitable polymerizing agent. The primer is preferably single-stranded for maximum efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerization agent. The length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example, depending on the complexity of the target sequence, the primer may be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, to one base shorter in

length than the template sequence at the 3' end of the primer to allow extension of a nucleic acid chain, though the 5' end of the primer may extend in length beyond the 3' end of the template sequence. In certain embodiments, primers can be large polynucleotides, such as from about 35 nucleotides to several kilobases or more. Primers can be selected to be "substantially complementary" to the sequence on the template to which it is designed to hybridize and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridize with a target polynucleotide. Desirably, the primer contains no mismatches with the template to which it is designed to hybridize but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize therewith and thereby form a template for synthesis of the extension product of the primer.

[0492] Also contemplated are biochip-based technologies such as those described by Hacia *et al.* (1996, *Nature Genetics* 14: 441-447) and Shoemaker *et al.* (1996, *Nature Genetics* 14: 450-456). Briefly, these techniques involve quantitative methods for analyzing large numbers of genes rapidly and accurately. By tagging genes with oligonucleotides or using fixed nucleic acid probe arrays, one can employ biochip technology to segregate target molecules as high-density arrays and screen these molecules on the basis of hybridization. See also Pease *et al.* (1994, *Proc. Natl. Acad. Sci. U.S.A.* 91: 5022-5026); Fodor *et al.* (1991, *Science* 251: 767-773). Briefly, nucleic acid probes to IRS biomarker polynucleotides are made and attached to biochips to be used in screening and diagnostic methods, as outlined herein. The nucleic acid probes attached to the biochip are designed to be substantially complementary to specific expressed IRS biomarker nucleic acids, *i.e.*, the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occur. This complementarity need not be perfect; there may be any number of base pair mismatches, which will interfere with hybridization between the target sequence and the nucleic acid probes of the present invention. However, if the number of mismatches is so great that no hybridization can occur under even the least stringent of hybridization conditions, the

sequence is not a complementary target sequence. In certain embodiments, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being desirable, are used to build in a redundancy for a particular target. The probes can be overlapping (*i.e.* have some sequence in common), or separate.

[0493] In an illustrative biochip analysis, oligonucleotide probes on the biochip are exposed to or contacted with a nucleic acid sample suspected of containing one or more IRS biomarker polynucleotides under conditions favoring specific hybridization. Sample extracts of DNA or RNA, either single or double-stranded, may be prepared from fluid suspensions of biological materials, or by grinding biological materials, or following a cell lysis step which includes, but is not limited to, lysis effected by treatment with SDS (or other detergents), osmotic shock, guanidinium isothiocyanate and lysozyme. Suitable DNA, which may be used in the method of the invention, includes cDNA. Such DNA may be prepared by any one of a number of commonly used protocols as for example described in Ausubel, *et al.*, 1994, *supra*, and Sambrook, *et al.*, 1989, *supra*.

[0494] Suitable RNA, which may be used in the method of the invention, includes messenger RNA, complementary RNA transcribed from DNA (cRNA) or genomic or subgenomic RNA. Such RNA may be prepared using standard protocols as for example described in the relevant sections of Ausubel, *et al*. 1994, *supra* and Sambrook, *et al*. 1989, *supra*).

[0495] cDNA may be fragmented, for example, by sonication or by treatment with restriction endonucleases. Suitably, cDNA is fragmented such that resultant DNA fragments are of a length greater than the length of the immobilized oligonucleotide probe(s) but small enough to allow rapid access thereto under suitable hybridization conditions. Alternatively, fragments of cDNA may be selected and amplified using a suitable nucleotide amplification technique, as described for example above, involving appropriate random or specific primers.

[0496] Usually the target IRS biomarker polynucleotides are detectably labeled so that their hybridization to individual probes can be determined. The target polynucleotides are typically detectably labeled with a reporter molecule illustrative examples of which include chromogens, catalysts, enzymes, fluorochromes, chemiluminescent molecules, bioluminescent molecules, lanthanide ions (*e.g.*, Eu^{34}), a radioisotope and a direct visual label. In the case of a direct visual label, use may be made of a colloidal metallic or non-

metallic particle, a dye particle, an enzyme or a substrate, an organic polymer, a latex particle, a liposome, or other vesicle containing a signal producing substance and the like. Illustrative labels of this type include large colloids, for example, metal colloids such as those from gold, selenium, silver, tin and titanium oxide. In some embodiments in which an enzyme is used as a direct visual label, biotinylated bases are incorporated into a target polynucleotide.

[0497] The hybrid-forming step can be performed under suitable conditions for hybridizing oligonucleotide probes to test nucleic acid including DNA or RNA. In this regard, reference may be made, for example, to NUCLEIC ACID HYBRIDIZATION, A PRACTICAL APPROACH (Homes and Higgins, eds.) (IRL press, Washington D.C., 1985). In general, whether hybridization takes place is influenced by the length of the oligonucleotide probe and the polynucleotide sequence under test, the pH, the temperature, the concentration of mono- and divalent cations, the proportion of G and C nucleotides in the hybrid-forming region, the viscosity of the medium and the possible presence of denaturants. Such variables also influence the time required for hybridization. The preferred conditions will therefore depend upon the particular application. Such empirical conditions, however, can be routinely determined without undue experimentation.

[0498] After the hybrid-forming step, the probes are washed to remove any unbound nucleic acid with a hybridization buffer. This washing step leaves only bound target polynucleotides. The probes are then examined to identify which probes have hybridized to a target polynucleotide.

[0499] The hybridization reactions are then detected to determine which of the probes has hybridized to a corresponding target sequence. Depending on the nature of the reporter molecule associated with a target polynucleotide, a signal may be instrumentally detected by irradiating a fluorescent label with light and detecting fluorescence in a fluorimeter; by providing for an enzyme system to produce a dye which could be detected using a spectrophotometer; or detection of a dye particle or a colored colloidal metallic or non-metallic particle using a reflectometer; in the case of using a radioactive label or chemiluminescent molecule employing a radiation counter or autoradiography. Accordingly, a detection means may be adapted to detect or scan light associated with the label which light may include fluorescent, luminescent, focused beam or laser light. In such a case, a charge

couple device (CCD) or a photocell can be used to scan for emission of light from a probe:target polynucleotide hybrid from each location in the micro-array and record the data directly in a digital computer. In some cases, electronic detection of the signal may not be necessary. For example, with enzymatically generated color spots associated with nucleic acid array format, visual examination of the array will allow interpretation of the pattern on the array. In the case of a nucleic acid array, the detection means is suitably interfaced with pattern recognition software to convert the pattern of signals from the array into a plain language genetic profile. In certain embodiments, oligonucleotide probes specific for different IRS biomarker polynucleotides are in the form of a nucleic acid array and detection of a signal generated from a reporter molecule on the array is performed using a 'chip reader'. A detection system that can be used by a 'chip reader' is described for example by Pirrung *et al.* (U.S. Patent No. 5,143,854). The chip reader will typically also incorporate some signal processing to determine whether the signal at a particular array position or feature is a true positive or maybe a spurious signal. Exemplary chip readers are described for example by Fodor *et al.* (U.S. Patent No., 5,925,525). Alternatively, when the array is made using a mixture of individually addressable kinds of labeled microbeads, the reaction may be detected using flow cytometry.

[0500] In certain embodiments, the IRS biomarker is a target RNA (*e.g.*, mRNA) or a DNA copy of the target RNA whose level is measured using at least one nucleic acid probe that hybridizes under at least low, medium, or high stringency conditions to the target RNA or to the DNA copy, wherein the nucleic acid probe comprises at least 15 (*e.g.*, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more) contiguous nucleotides of an IRS biomarker polynucleotide. In some embodiments, the measured level or abundance of the target RNA or its DNA copy is normalized to the level or abundance of a reference RNA or a DNA copy of the reference RNA. Suitably, the nucleic acid probe is immobilized on a solid or semi-solid support. In illustrative examples of this type, the nucleic acid probe forms part of a spatial array of nucleic acid probes. In some embodiments, the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by hybridization (*e.g.*, using a nucleic acid array). In other embodiments, the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by nucleic acid amplification (*e.g.*, using a polymerase chain reaction (PCR)). In still other embodiments, the level of nucleic

acid probe that is bound to the target RNA or to the DNA copy is measured by nuclease protection assay.

[0501] In other embodiments, IRS biomarker protein levels are assayed using protein-based assays known in the art. For example, when an IRS biomarker protein is an enzyme, the protein can be quantified based upon its catalytic activity or based upon the number of molecules of the protein contained in a sample. Antibody-based techniques may be employed including, for example, immunoassays, such as the enzyme-linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA).

[0502] In specific embodiments, protein-capture arrays that permit simultaneous detection and/or quantification of a large number of proteins are employed. For example, low-density protein arrays on filter membranes, such as the universal protein array system (Ge, 2000 *Nucleic Acids Res.* 28(2):e3) allow imaging of arrayed antigens using standard ELISA techniques and a scanning charge-coupled device (CCD) detector. Immuno-sensor arrays have also been developed that enable the simultaneous detection of clinical analytes. It is now possible using protein arrays, to profile protein expression in bodily fluids, such as in sera of healthy or diseased subjects, as well as in subjects pre- and post-drug treatment.

[0503] Exemplary protein capture arrays include arrays comprising spatially addressed antigen-binding molecules, commonly referred to as antibody arrays, which can facilitate extensive parallel analysis of numerous proteins defining a proteome or subproteome. Antibody arrays have been shown to have the required properties of specificity and acceptable background, and some are available commercially (*e.g.*, BD Biosciences, Clontech, Bio-Rad and Sigma). Various methods for the preparation of antibody arrays have been reported (see, *e.g.*, Lopez *et al.*, 2003 *J. Chromatogram.* B 787:19-27; Cahill, 2000 *Trends in Biotechnology* 7:47-51; U.S. Pat. App. Pub. 2002/0055186; U.S. Pat. App. Pub. 2003/0003599; PCT publication WO 03/062444; PCT publication WO 03/077851; PCT publication WO 02/59601; PCT publication WO 02/39120; PCT publication WO 01/79849; PCT publication WO 99/39210). The antigen-binding molecules of such arrays may recognize at least a subset of proteins expressed by a cell or population of cells, illustrative examples of which include growth factor receptors, hormone receptors, neurotransmitter receptors, catecholamine receptors, amino acid derivative receptors, cytokine receptors, extracellular matrix receptors, antibodies, lectins, cytokines, serpins, proteases, kinases,

phosphatases, ras-like GTPases, hydrolases, steroid hormone receptors, transcription factors, heat-shock transcription factors, DNA-binding proteins, zinc-finger proteins, leucine-zipper proteins, homeodomain proteins, intracellular signal transduction modulators and effectors, apoptosis-related factors, DNA synthesis factors, DNA repair factors, DNA recombination factors and cell-surface antigens.

[0504] Individual spatially distinct protein-capture agents are typically attached to a support surface, which is generally planar or contoured. Common physical supports include glass slides, silicon, microwells, nitrocellulose or PVDF membranes, and magnetic and other microbeads.

[0505] Particles in suspension can also be used as the basis of arrays, providing they are coded for identification; systems include color coding for microbeads (*e.g.*, available from Luminex, Bio-Rad and Nanomics Biosystems) and semiconductor nanocrystals (*e.g.*, QDots™, available from Quantum Dots), and barcoding for beads (UltraPlex™, available from Smartbeads) and multimetal microrods (Nanobarcodes™ particles, available from Surromed). Beads can also be assembled into planar arrays on semiconductor chips (*e.g.*, available from LEAPS technology and BioArray Solutions). Where particles are used, individual protein-capture agents are typically attached to an individual particle to provide the spatial definition or separation of the array. The particles may then be assayed separately, but in parallel, in a compartmentalized way, for example in the wells of a microtiter plate or in separate test tubes.

[0506] In operation, a protein sample, which is optionally fragmented to form peptide fragments (see, *e.g.*, U.S. Pat. App. Pub. 2002/0055186), is delivered to a protein-capture array under conditions suitable for protein or peptide binding, and the array is washed to remove unbound or non-specifically bound components of the sample from the array. Next, the presence or amount of protein or peptide bound to each feature of the array is detected using a suitable detection system. The amount of protein bound to a feature of the array may be determined relative to the amount of a second protein bound to a second feature of the array. In certain embodiments, the amount of the second protein in the sample is already known or known to be invariant.

[0507] In specific embodiments, the IRS biomarker is a target polypeptide whose level is measured using at least one antigen-binding molecule that is immuno-interactive with the

target polypeptide. In these embodiments, the measured level of the target polypeptide is normalized to the level of a reference polypeptide. Suitably, the antigen-binding molecule is immobilized on a solid or semi-solid support. In illustrative examples of this type, the antigen-binding molecule forms part of a spatial array of antigen-binding molecule. In some embodiments, the level of antigen-binding molecule that is bound to the target polypeptide is measured by immunoassay (*e.g.*, using an ELISA). Reference herein to "immuno-interactive" includes reference to any interaction, reaction, or other form of association between molecules and in particular where one of the molecules is, or mimics, a component of the immune system.

[0508] All the essential reagents required for detecting and quantifying the biomarkers of the invention, including IRS biomarkers, may be assembled together in a kit. In some embodiments, the kit comprises: (i) a reagent that allows quantification (*e.g.*, determining the level or abundance) of a first biomarker; and (ii) a reagent that allows quantification (*e.g.*, determining the level or abundance) of a second biomarker, wherein the first and second biomarkers have a mutual correlation in respect of at least one condition (*e.g.*, at least one of a healthy condition and one or more diseases such as but not limited to inSIRS, ipSIRS or a stage of ipSIRS (*e.g.*, a stage of ipSIRS with a particular severity such as mild sepsis, severe sepsis and septic shock)) that lies within a mutual correlation range of between ±0.9, and wherein a combination of respective biomarker values for the first and second biomarkers that are measured for or derived from a biological subject has a performance value greater than or equal to a performance threshold representing the ability of the combination of the first and second biomarkers to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being a variance explained of at least 0.3. In some embodiments, the kit further comprises (iii) a reagent that allows quantification (*e.g.*, determining the level or abundance) of a third biomarker; and (iv) a reagent that allows quantification (*e.g.*, determining the level or abundance) of a fourth biomarker, wherein the third and fourth biomarkers have a mutual correlation in respect of at the least one condition that lies within a mutual correlation range of between ±0.9, and wherein a combination of respective biomarker values for the third and fourth biomarkers that are measured for or derived from a biological subject has a performance value greater than or equal to a performance threshold representing the ability of the combination of the third and fourth biomarkers to diagnose the presence, absence or

degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being a variance explained of at least 0.3.

[0509] In advantageous embodiments, the kits of the present invention are useful for diagnosing the presence, absence or degree of at least one condition, or for providing a prognosis for at least one condition, wherein the at least one condition is selected from a healthy condition, inSIRS, ipSIRS or a stage of ipSIRS. In these embodiments, IRS biomarkers are suitably selected from a group as broadly described above and elsewhere herein.

[0510] In the context of the present invention, "kit" is understood to mean a product containing the different reagents necessary for carrying out the methods of the invention packed so as to allow their transport and storage. Materials suitable for packing the components of the kit include crystal, plastic (polyethylene, polypropylene, polycarbonate and the like), bottles, vials, paper, envelopes and the like. Additionally, the kits of the invention can contain instructions for the simultaneous, sequential or separate use of the different components contained in the kit. The instructions can be in the form of printed material or in the form of an electronic support capable of storing instructions such that they can be read by a subject, such as electronic storage media (magnetic disks, tapes and the like), optical media (CD-ROM, DVD) and the like. Alternatively or in addition, the media can contain Internet addresses that provide the instructions.

[0511] A "reagent that allows quantification of a biomarker" means a compound or material, or set of compounds or materials, which allow quantification of the biomarker. In specific embodiments, the compound, material or set of compounds or materials permit determining the expression level of a gene (*e.g.*, an IRS biomarker gene), including without limitation the extraction of RNA material, the determination of the level of a corresponding RNA, etc., primers for the synthesis of a corresponding cDNA, primers for amplification of DNA, and/or probes capable of specifically hybridizing with the RNAs (or the corresponding cDNAs) encoded by the genes, TaqMan probes, etc.

[0512] The kits may also optionally include appropriate reagents for detection of labels, positive and negative controls, washing solutions, blotting membranes, microtiter plates, dilution buffers and the like. For example, a nucleic acid-based detection kit may include (i) a biomarker polynucleotide (*e.g.*, an IRS biomarker polynucleotide) (which may be used as a

positive control), (ii) a primer or probe that specifically hybridizes to a biomarker polynucleotide (*e.g.*, an IRS biomarker polynucleotide). Also included may be enzymes suitable for amplifying nucleic acids including various polymerases (reverse transcriptase, *Taq*, Sequenase™, DNA ligase etc. depending on the nucleic acid amplification technique employed), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification. Such kits also generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each primer or probe. Alternatively, a protein-based detection kit may include (i) a biomarker polypeptide (*e.g.*, an IRS biomarker polypeptide) (which may be used as a positive control), (ii) an antibody that binds specifically to a biomarker polypeptide (*e.g.*, an IRS biomarker polypeptide). The kit can also feature various devices (*e.g.*, one or more) and reagents (*e.g.*, one or more) for performing one of the assays described herein; and/or printed instructions for using the kit to quantify the expression of a biomarker gene (*e.g.*, an IRS biomarker gene).

[0513] The reagents described herein, which may be optionally associated with detectable labels, can be presented in the format of a microfluidics card, a chip or chamber, a microarray or a kit adapted for use with the assays described in the examples or below, *e.g.*, RT-PCR or Q PCR techniques described herein. The term "microarray" refers to an arrangement of hybridizable array elements, *e.g.*, probes (including primers), ligands, biomarker nucleic acid sequence or protein sequences on a substrate.

[0514] The reagents also have utility in compositions for detecting and quantifying the biomarkers of the invention. For example, a reverse transcriptase may be used to reverse transcribe RNA transcripts, including mRNA, in a nucleic acid sample, to produce reverse transcribed transcripts, including reverse transcribed mRNA (also referred to as "cDNA"). The nucleic acid sample is suitably derived from components of the immune system, representative examples of which include components of the innate and adaptive immune systems as broadly discussed for example above. In specific embodiments, the reverse transcribed RNA is derived blood cells (*e.g.*, peripheral blood cells). Suitably, the reverse transcribed RNA is derived leukocytes.

[0515] The reagents are suitably used to quantify the reverse transcribed transcripts. For example, oligonucleotide primers that hybridize to the reverse transcribed transcript can be used to amplify at least a portion of the reverse transcribed transcript *via* a suitable nucleic

acid amplification technique, *e.g.*, RT-PCR or Q PCR techniques described herein. Alternatively, oligonucleotide probes may be used to hybridize to the reverse transcribed transcript for the quantification, using a nucleic acid hybridization analysis technique (*e.g.*, microarray analysis), as described for example above. Thus, in some embodiments, a respective oligonucleotide primer or probe is hybridized to a complementary nucleic acid sequence of a reverse transcribed transcript in the compositions of the invention. The compositions typically comprise labeled reagents for detecting and/or quantifying the reverse transcribed transcripts. Representative reagents of this type include labeled oligonucleotide primers or probes that hybridize to RNA transcripts or reverse transcribed RNA, labeled RNA, labeled reverse transcribed RNA as well as labeled oligonucleotide linkers or tags (*e.g.*, a labeled RNA or DNA linker or tag) for labeling (*e.g.*, end labeling such as 3' end labeling) RNA or reverse transcribed RNA. The primers, probes, RNA or reverse transcribed RNA (*i.e.*, cDNA) (whether labeled or non-labeled) may be immobilized or free in solution. Representative reagents of this type include labeled oligonucleotide primers or probes that hybridize to reverse transcribed and transcripts as well as labeled reverse transcribed transcripts. The label can be any reporter molecule as known in the art, illustrative examples of which are described above and elsewhere herein.

[0516] The present invention also encompasses non-reverse transcribed RNA embodiments in which cDNA is not made and the RNA transcripts are directly the subject of the analysis. Thus, in other embodiments, reagents are suitably used to quantify RNA transcripts directly. For example, oligonucleotide probes can be used to hybridize to transcripts for quantification of immune system biomarkers of the invention, using a nucleic acid hybridization analysis technique (*e.g.*, microarray analysis), as described for example above. Thus, in some embodiments, a respective oligonucleotide probe is hybridized to a complementary nucleic acid sequence of an immune system biomarker transcript in the compositions of the invention. In illustrative examples of this type, the compositions may comprise labeled reagents that hybridize to transcripts for detecting and/or quantifying the transcripts. Representative reagents of this type include labeled oligonucleotide probes that hybridize to transcripts as well as labeled transcripts. The primers or probes may be immobilized or free in solution.

[0517] The term "immobilized" means that a molecular species of interest is fixed to a solid support, suitably by covalent linkage. This covalent linkage can be achieved by different means depending on the molecular nature of the molecular species. Moreover, the molecular species may be also fixed on the solid support by electrostatic forces, hydrophobic or hydrophilic interactions or Van-der-Waals forces. The above described physico-chemical interactions typically occur in interactions between molecules. In particular embodiments, all that is required is that the molecules (*e.g.*, nucleic acids or polypeptides) remain immobilized or attached to a support under conditions in which it is intended to use the support, for example in applications requiring nucleic acid amplification and/or sequencing or in in antibody-binding assays. For example, oligonucleotides or primers are immobilized such that a 3' end is available for enzymatic extension and/or at least a portion of the sequence is capable of hybridizing to a complementary sequence. In some embodiments, immobilization can occur via hybridization to a surface attached primer, in which case the immobilized primer or oligonucleotide may be in the 3'-5' orientation. In other embodiments, immobilization can occur by means other than base-pairing hybridization, such as the covalent attachment.

[0518] The term "solid support" as used herein refers to a solid inert surface or body to which a molecular species, such as a nucleic acid and polypeptides can be immobilized. Non-limiting examples of solid supports include glass surfaces, plastic surfaces, latex, dextran, polystyrene surfaces, polypropylene surfaces, polyacrylamide gels, gold surfaces, and silicon wafers. In some embodiments, the solid supports are in the form of membranes, chips or particles. For example, the solid support may be a glass surface (*e.g.*, a planar surface of a flow cell channel). In some embodiments, the solid support may comprise an inert substrate or matrix which has been "functionalized", such as by applying a layer or coating of an intermediate material comprising reactive groups which permit covalent attachment to molecules such as polynucleotides. By way of non-limiting example, such supports can include polyacrylamide hydrogels supported on an inert substrate such as glass. The molecules (*e.g.*, polynucleotides) can be directly covalently attached to the intermediate material (*e.g.*, a hydrogel) but the intermediate material can itself be non-covalently attached to the substrate or matrix (*e.g.*, a glass substrate). The support can include a plurality of particles or beads each having a different attached molecular species.

[0519] The present invention also extends to the management of inSIRS, ipSIRS or particular stages of ipSIRS, or prevention of further progression of inSIRS, ipSIRS or particular stages of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), or assessment of the efficacy of therapies in subjects following positive diagnosis for the presence of inSIRS, ipSIRS or particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock) in a subject. The management of inSIRS or ipSIRS conditions is generally highly intensive and can include identification and amelioration of the underlying cause and aggressive use of therapeutic compounds such as, vasoactive compounds, antibiotics, steroids, antibodies to endotoxin, anti-tumor necrosis factor agents, recombinant protein C. In addition, palliative therapies as described for example in Cohen and Glauser (1991, Lancet 338: 736-739) aimed at restoring and protecting organ function can be used such as intravenous fluids and oxygen and tight glycemic control. Therapies for ipSIRS are reviewed in Healy (2002, *Ann Pharmacother.* 36(4): 648-54) and Brindley (2005, *CJEM.* 7(4): 227) and Jenkins (2006, *J Hosp Med.* 1(5): 285-295).

[0520] Typically, the therapeutic agents will be administered in pharmaceutical (or veterinary) compositions together with a pharmaceutically acceptable carrier and in an effective amount to achieve their intended purpose. The dose of active compounds administered to a subject should be sufficient to achieve a beneficial response in the subject over time such as a reduction in, or relief from, the symptoms of inSIRS, ipSIRS or particular stages of ipSIRS. The quantity of the pharmaceutically active compounds(s) to be administered may depend on the subject to be treated inclusive of the age, sex, weight and general health condition thereof. In this regard, precise amounts of the active compound(s) for administration will depend on the judgment of the practitioner. In determining the effective amount of the active compound(s) to be administered in the treatment or prevention of inSIRS, ipSIRS or particular stages of ipSIRS, the medical practitioner or veterinarian may evaluate severity of any symptom associated with the presence of inSIRS, ipSIRS or particular stages of ipSIRS including, inflammation, blood pressure anomaly, tachycardia, tachypnea fever, chills, vomiting, diarrhea, skin rash, headaches, confusion, muscle aches, seizures. In any event, those of skill in the art may readily determine suitable dosages of the therapeutic agents and suitable treatment regimens without undue experimentation.

[0521] The therapeutic agents may be administered in concert with adjunctive (palliative) therapies to increase oxygen supply to major organs, increase blood flow to major organs and/or to reduce the inflammatory response. Illustrative examples of such adjunctive therapies include non-steroidal-anti-inflammatory drugs (NSAIDs), intravenous saline and oxygen.

[0522] In specific embodiments of the present invention, the methods, apparatus and kits described above and elsewhere herein are contemplated for use in methods of treating, preventing or inhibiting the development of at least one condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis or septic shock) in a subject. These methods (also referred to herein as "treatment methods") generally comprise: (a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker of a biological subject; (b) determining an indicator using a combination of the plurality of IRS biomarker values, the indicator being at least partially indicative of the presence, absence or degree of the at least one condition, wherein: (i) at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; and (c) administering to the subject, on the basis that the indicator indicates the presence of inSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of inSIRS, or administering to the subject, on the basis that the indicator indicates the presence of ipSIRS or a particular stage of ipSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of ipSIRS or the particular stage of ipSIRS.

[0523] In advantageous embodiments, the treatment methods comprise: (1) determining a plurality of measured IRS biomarker values, each measured IRS biomarker value being a measured value of an IRS biomarker of the biological subject; and (2) applying a function to at least one of the measured IRS biomarker values to determine at least one derived IRS

biomarker value, the at least one derived IRS biomarker value being indicative of a value of a corresponding derived IRS biomarker. The function suitably includes at least one of: (a) multiplying two IRS biomarker values; (b) dividing two IRS biomarker values; (c) adding two IRS biomarker values; (d) subtracting two IRS biomarker values; (e) a weighted sum of at least two IRS biomarker values; (f) a log sum of at least two IRS biomarker values; and (g) a sigmoidal function of at least two IRS biomarker values.

[0524] In some embodiments the methods, apparatus and kits of the present invention are used for monitoring, treatment and management of conditions that can lead to inSIRS or ipSIRS, illustrative examples of which include retained placenta, meningitis, endometriosis, shock, toxic shock (*i.e.*, sequelae to tampon use), gastroenteritis, appendicitis, ulcerative colitis, Crohn's disease, inflammatory bowel disease, acid gut syndrome, liver failure and cirrhosis, failure of colostrum transfer in neonates, ischemia (in any organ), bacteremia, infections within body cavities such as the peritoneal, pericardial, thecal, and pleural cavities, burns, severe wounds, excessive exercise or stress, hemodialysis, conditions involving intolerable pain (*e.g.*, pancreatitis, kidney stones), surgical operations, and non-healing lesions. In these embodiments, the methods or kits of the present invention are typically used at a frequency that is effective to monitor the early development of inSIRS, ipSIRS or particular stages of ipSIRS, to thereby enable early therapeutic intervention and treatment of that condition. In illustrative examples, the diagnostic methods or kits are used at least at 1, 2, 3, 4,5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 hour intervals or at least 1, 2, 3, 4, 5 or 6 day intervals, or at least weekly, fortnightly or monthly.

[0525] The present invention can be practiced in the field of predictive medicine for the purpose of diagnosis or monitoring the presence or development of a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS in a subject, and/or monitoring response to therapy efficacy.

[0526] The biomarker signatures and corresponding indicators of the present invention further enable determination of endpoints in pharmacotranslational studies. For example, clinical trials can take many months or even years to establish the pharmacological parameters for a medicament to be used in treating or preventing inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock). However, these parameters may be associated with a biomarker signature and corresponding indicator of a

health state (*e.g.*, a healthy condition). Hence, the clinical trial can be expedited by selecting a treatment regimen (*e.g.*, medicament and pharmaceutical parameters), which results in a biomarker signature associated with a desired health state (*e.g.*, healthy condition). This may be determined for example by: a) determining a plurality of IRS biomarker values, each IRS biomarker value being indicative of a value measured or derived for at least one (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker of a biological subject after treatment with a treatment regimen; (b) determining an indicator using a combination of the plurality of IRS biomarker values, the indicator being at least partially indicative of the presence, absence or degree of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, wherein: (i) at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, and (c) determining that the treatment regimen is effective for changing the health status of the subject to the desired health state (*e.g.*, healthy condition) on the basis that the indicator indicates the presence of a healthy condition or the presence of a condition of a lower degree relative to the degree of the condition in the subject before treatment with the treatment regimen. As used herein, the term "degree" refers to the extent or stage of a condition. Thus, for example, mild sepsis is a stage or degree of sepsis that is lower than severe sepsis. Similarly, severe sepsis is a stage or degree of sepsis that is lower than septic shock. Accordingly, this aspect of the present invention advantageously provides methods of monitoring the efficacy of a particular treatment regimen in a subject (for example, in the context of a clinical trial) already diagnosed with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS. These methods take advantage of measured or derived IRS biomarker values that correlate with treatment efficacy to determine, for example, whether measured or derived IRS biomarker values of a subject undergoing treatment partially or completely normalize during the course of or following therapy or otherwise shows changes associated with responsiveness to the therapy.

[0527] As used herein, the term "treatment regimen" refers to prophylactic and/or therapeutic (*i.e.*, after onset of a specified condition) treatments, unless the context specifically indicates otherwise. The term "treatment regimen" encompasses natural substances and pharmaceutical agents (*i.e.*, "drugs") as well as any other treatment regimen including but not limited to dietary treatments, physical therapy or exercise regimens, surgical interventions, and combinations thereof.

[0528] Accordingly, the invention provides methods of correlating a biomarker signature with an effective treatment regimen for a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock), wherein the methods generally comprise: (a) determining a biomarker signature defining a combination of at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker values corresponding to values of at least two IRS biomarkers that can be measured for or derived from a biological subject having the condition and for whom an effective treatment has been identified, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of the condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the condition, or to provide a prognosis for the condition, the performance threshold being indicative of an explained variance of at least 0.3; and (b) correlating the biomarker signature so determined with an effective treatment regimen for the condition. The term "correlating" generally refers to determining a relationship between one type of data with another or with a state. In specific embodiments, an indicator or biomarker signature is correlated to a global probability or a particular outcome, using receiver operating characteristic (ROC) curves.

[0529] The invention further provides methods of determining whether a treatment regimen is effective for treating a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (*e.g.*, mild sepsis, severe sepsis and septic shock). These methods generally comprise: (a) determining a plurality of post-treatment IRS biomarker values, each post-treatment IRS biomarker value being indicative of a value measured or derived for at least one (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker of a biological subject after treatment with the treatment regimen; (b) determining a post-treatment indicator using a

combination of the plurality of post-treatment IRS biomarker values, the post-treatment indicator being at least partially indicative of the presence, absence or degree of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, wherein: (i) at the least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the post-treatment indicator has a performance value greater than or equal to a performance threshold representing the ability of the post-treatment indicator to diagnose the presence, absence or degree of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein the post-treatment indicator indicates whether the treatment regimen is effective for treating the condition in the subject on the basis that post-treatment indicator indicates the presence of a healthy condition or the presence of a condition of a lower degree relative to the degree of the condition in the subject before treatment with the treatment regimen.

[0530] The invention can also be practiced to evaluate whether a subject is responding (*i.e.*, a positive response) or not responding (*i.e.*, a negative response) to a treatment regimen or has a side effect to a treatment regimen. This aspect of the invention provides methods of correlating a biomarker signature with a positive or negative response or a side effect to a treatment regimen, which generally comprise: (a) determining a biomarker signature defining a combination of at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker values corresponding to values of at least two IRS biomarkers that can be measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; and (b) correlating the biomarker signature so determined with a positive or negative response to the treatment regimen. As used herein, the term “positive response” means that the result of the treatment regimen includes some

clinically significant benefit, such as the prevention, or reduction of severity, of symptoms, or a slowing of the progression of the condition. By contrast, the term "negative response" means that the treatment regimen provides no clinically significant benefit, such as the prevention, or reduction of severity, of symptoms, or increases the rate of progression of the condition.

[0531] The invention also encompasses methods of determining a positive or negative response to a treatment regimen and/or a side effect of a treatment regimen by a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS. These methods generally comprise: (a) correlating a reference biomarker signature with a positive or negative response or a side effect to the treatment regimen, wherein the biomarker signature defines a combination of at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a control biological subject or control group, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; (b) determining a sample biomarker signature defining a combination of at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3; wherein the sample biomarker signature

indicates whether the subject is responding positively or negatively to the treatment regimen and/or is developing a side effect from the treatment regimen, based on the correlation of the reference biomarker signature with the positive or negative response or side effect to the treatment regimen.

[0532] In related embodiments, the present invention further contemplates methods of determining a positive or negative response to a treatment regimen and/or a side effect to a treatment regimen by a biological subject. These methods generally comprise: (a) determining a sample biomarker signature defining a combination of at least two (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker values corresponding to values of at least two IRS biomarkers that are measured for or derived from a biological subject following commencement of the treatment regimen, wherein: (i) the at least two IRS biomarkers have a mutual correlation in respect of at least one condition selected from a healthy condition, inSIRS, ipSIRS or a particular stage of ipSIRS, which lies within a mutual correlation range, the mutual correlation range being between ±0.9; and (ii) the combination of at least two biomarker values has a performance value greater than or equal to a performance threshold representing the ability of the combination of at least two biomarker values to diagnose the presence, absence or degree of the at least one condition, or to provide a prognosis for the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3, wherein the sample biomarker signature is correlated with a positive or negative response to the treatment regimen and/or to a side effect from the treatment regimen; and (b) determining whether the subject is responding positively or negatively to the treatment regimen and/or is developing a side effect from the treatment regimen based on the sample biomarker signature.

[0533] This above methods can be practiced to identify responders or non-responders relatively early in the treatment process, *i.e.*, before clinical manifestations of efficacy. In this way, the treatment regimen can optionally be discontinued, a different treatment protocol can be implemented and/or supplemental therapy can be administered. Thus, in some embodiments, a sample IRS biomarker signature is obtained within about 2 hours, 4 hours, 6 hours, 12 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 6 weeks, 8 weeks, 10 weeks, 12 weeks, 4 months, six months or longer of commencing therapy.

[0534] A number of non-limiting example signatures for use in diagnosing respective conditions will now be described. For the purpose of illustration, the above-described process was used to select biomarkers that provided the theoretical best diagnostic biomarkers, selected from combinations including measured and/or derived biomarkers. Following this, other measured and/or derived biomarkers were grouped based on their correlation to the best diagnostic biomarkers, with the ability of biomarkers within these groups to act as a diagnostic signature then being assessed.

[0535] The results set out in detail below highlight that as long as the above-described criteria are met, the resulting signatures provide the required discriminatory ability for use in diagnosing the presence, absence, degree or prognosis of at least one condition in a biological subject.

Signature Derivation

[0536] An illustrative process for the identification of mRNA biomarkers for use in diagnostic algorithms will now be described.

Summary

[0537] Peripheral blood samples were obtained from healthy controls and patients retrospectively diagnosed by a panel of physicians with either inSIRS or ipSIRS (blood culture positive). ipSIRS patients were further classified retrospectively into "mild", "severe" or "shock" based on clinical parameters. Total RNA from patient samples was then used in gene expression analysis (GeneChip® and / or quantitative PCR (qPCR)). Gene expression data were analyzed using a variety of statistical approaches to identify individual and derived markers. Derived markers were divided into groups based on how they correlated to each of the markers in the top-performing (based on AUC) ratio. This ratio approach provides the best diagnostic power with respect to AUC for separating: healthy and post-surgical (PS) (also referred to herein as "inSIRS") conditions; healthy and sepsis (also referred to herein as "ipSIRS"); inSIRS and ipSIRS; mild ipSIRS and severe ipSIRS; mild ipSIRS and septic shock; and severe ipSIRS and septic shock.

Clinical Trials

[0538] Clinical trials were performed to determine whether certain mRNA transcripts could distinguish between healthy controls and various patient groups and within patient groups. Intensive care sepsis, post-surgical and inSIRS patients, as well as healthy controls were

prospectively enrolled and attended a single visit where blood was collected for gene expression and mRNA analyses using Affymetrix exon arrays and/or quantitative real-time PCR (qRT-PCR). A definitive diagnosis of infection-positive SIRS (mild, severe or shock) or inSIRS was unlikely to be known at the time patients were enrolled, and thus confirmation of a diagnosis and the assignment of patients to the cohorts were made retrospectively.

[0539] Patients who had clinical signs and/or symptoms of ipSIRS or inSIRS were consented and enrolled into the study as soon as possible after they had been identified, in most cases within 24 hours of admission. Final assessment of whether the participant had inSIRS, ipSIRS (mild, severe, or shock) was made retrospectively as clinical information and blood culture results became available.

[0540] Study participants were all over 18 years and either they or their surrogate decision maker signed and dated the clinical trial information sheet and consent form. All of the control participants were considered to be in good health based on a brief physical examination and their medical history at the time of enrolment.

[0541] Patients or their surrogate decision maker were offered the opportunity to participate in this study if the patient presented with signs and symptoms of either inSIRS or ipSIRS at the time of admission to ICU (using criteria based on the American College of Physicians and the Society of Critical Care Medicine standard definitions). That is, inSIRS and ipSIRS participants needed a variable combination of clinical conditions including two or more of the following within the last 24 hours: temperature >38°C or <36°C; heart rate >90 beats/min; respiratory rate >20 breathes/min or a $PaCO_2$ of <4.3kPa (<32 mm Hg); and evidence of a white blood cell count <4,000 cells/mm^3 (<4 x 10^9 cells/L) or >12,000 cells/mm^3 (>12 x 10^9 cells/L) or >10% immature neutrophils (band forms). Participants were excluded if they had any chronic systemic immune-inflammatory disorders including SLE, Crohn's disease, insulin-dependent diabetes mellitus (IDDM); were transplant recipients or were currently receiving chemotherapy treatment for cancer. Most patients had other underlying co-morbidities. All study participants were 18 years of age or older and had a body mass index of less than 40.

[0542] Demography, vital signs measurements (blood pressure, heart rate, respiratory rate, oxygen saturation, temperature), hematology (full blood count), clinical chemistry (urea, electrolytes, liver function enzymes, blood glucose) as well as microbial status was recorded.

[0543] Blood was collected for the purpose of extraction of high quality RNA into PAXgene™ tubes (PreAnalytix Inc., Valencia, CA, USA). Blood for bacterial culture was collected into BacTec Plus Aerobic (10ml) and BacTec Plus Anaerobic (10mL) tubes (Becton Dickinson) tubes for the detection of aerobic and anaerobic bacterial growth respectively.

[0544] A PAXgene blood RNA kit available from Qiagen Inc. (Valencia, CA, USA) was used to isolate total RNA from PAXgene tubes. Isolation begins with a centrifugation step to pellet nucleic acids in the PAXgene blood RNA tube. The pellet is washed and re-suspended and incubated in optimized buffers together with Proteinase K to bring about protein digestion. An additional centrifugation is carried out to remove residual cell debris and the supernatant is transferred to a fresh microcentrifuge tube. Ethanol is added to adjust binding conditions, and the lysate is applied to the PAXgene RNA spin column. During brief centrifugation, RNA is selectively bound to the silica-gel membrane as contaminants pass through. Remaining contaminants are removed in three efficient wash steps and RNA is then eluted in Buffer BR5. Determination of RNA quantity and quality was performed using an Agilent Bioanalyzer and Absorbance 260/280 ratio using a spectrophotometer.

Processing of Samples

[0545] Measurement of specific mRNA levels in a tissue sample can be achieved using a variety of technologies. A common and readily available technology that covers most of the known human mRNAs is GeneChip® analysis using Affymetrix technology. Details on the technology and methodology can be found at www.affymetrix.com. GeneChip® analysis has the advantage of being able to analyze thousands of RNA transcripts at a time. Another common and readily available technology is qPCR (quantitative polymerase chain reaction), which has the advantage of being able to analyze, in real-time and quantitatively, hundreds of RNA transcripts at a time. Details on one of these technologies (TaqMan®), chemistries and methodologies can be found on the Life Technologies website including published protocols entitled; "Protocol: Introduction to TaqMan SYBR Green Chemistries for Real-Time PCR" and "TaqMan Gene Expression Assays Protocol." Both GeneChip® and qPCR were used in the discovery and proof-of-concept stages for biomarker identification. qPCR was used exclusively for biomarker feasibility testing.

Analysis, Interpretation of Data and Selection of Biomarkers and Derived Biomarkers

Healthy Control versus inSIRS

[0546] A list of 941 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of Healthy and inSIRS was generated. Figure 8A plots these markers against the AUC and Figure 8B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (AGFG1 – ArfGAP with FG repeats 1). The conditions of Healthy and inSIRS are perfectly separated when using this mRNA biomarker alone.

[0547] From the 941 individual markers at least 1000 derived markers (ratios) were generated that had an AUC of 1.0. A plot of the AUC of these derived markers for separating the conditions of Healthy and inSIRS is shown in Figure 8C with the top performing ratio shown as a box and whisker plot in Figure 8D. The AUC for AGFG1 and PVRIG (poliovirus receptor related immunoglobulin domain containing) has a ratio is 1.0.

[0548] All 941 individual markers were then broken into two groups – those that correlate to AGFG1 and those that correlate to PVRIG. Figures 8E and 8F demonstrate the correlation between the two groups based on their similarity to either AGFG1 or PVRIG. In these plots the groups are referred to as either group 1 (AGFG1) or group 2 (PVRIG). It can be seen that each "group" contains those markers that are most highly correlated to each other.

[0549] The markers in each "group" also correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance Healthy versus inSIRS (PS)) as shown in Figures 8G and 8H.

[0550] By choosing mRNAs from these two groups to create derived markers a better AUC for separating Healthy and inSIRS is obtained than when markers are chosen from within groups ($p < 2.558e-13$) as demonstrated in Figure 8I, which shows a greater overall AUC is obtained compared to when using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.97, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.9.

Healthy Control Versus ipSIRS

[0551] A list of 941 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of Healthy and ipSIRS was generated. Figure 9A plots these markers against the AUC and Figure 9B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (LTBP3 – latent transforming growth factor beta binding protein 3). The

conditions of Healthy and ipSIRS are perfectly separated when using this mRNA biomarker alone.

[0552] From the 941 individual markers at least 1000 derived markers (ratios) were generated that had an AUC of 1.0. A plot of the AUC of these derived markers for separating the conditions of Healthy and inSIRS is shown in Figure 9C with the top performing ratio shown as a box and whisker plot in Figure 9D. The AUC for LTBP3 and LPHN1 (latrophilin 1) as a ratio is 1.0.

[0553] All 941 individual markers were then broken into two groups – those that correlate to LTBP3 and those that correlate to LPHN1. Both plots in Figures 9E and 9F demonstrate the correlation between the two groups based on their similarity to either LTBP3 or LPHN1. It can be seen that each "group" contains those markers that are most highly correlated to each other.

[0554] The markers in each "group" also correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance Healthy versus ipSIRS (sepsis)), as shown in Figures 9G and 9H.

[0555] By choosing mRNAs from these two groups to create derived markers a better AUC for separating Healthy and ipSIRS is obtained than when markers are chosen from within groups ($p < 2.2e-16$) as demonstrated in Figure 9I, which shows an improved AUC compared to using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.97, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.8.

inSIRS versus ipSIRS

[0556] A list of 359 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of inSIRS and ipSIRS was generated. Figure 10A plots these markers against the AUC and Figure 10B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (PIWIL4 – piwi-like RNA mediated gene silencing 4). The conditions of inSIRS (PS) and ipSIRS (sepsis) are well separated when using this mRNA biomarker alone.

[0557] From the 359 individual markers 1000 derived markers (ratios) were generated that had an AUC greater than 0.9. A plot of the AUC of these derived markers for separating the

conditions of inSIRS and ipSIRS is shown in Figure 10C with the top performing ratio of *PLA2G7* (phospholipase A2, Group VII, (platelet activating factor acetyl hydrolase, plasma)) and *PLAC8* (placenta-specific 8) shown as a box and whisker plot in Figure 10D.

[0558] All 359 individual markers were then broken into two groups – those that correlate to *PLA2G7* and those that correlate to *PLAC8*. The plot in Figure 10E demonstrates that the markers in each "group" correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance inSIRS (PS) versus ipSIRS (sepsis)).

[0559] By choosing mRNAs from these two groups to create derived markers a better AUC for separating inSIRS (PS) and ipSIRS (sepsis) is obtained than when markers are chosen from within groups ($p < 5.78e-5$) as demonstrated in Figure 10F compared to when using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.80, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.8.

[0560] In an alternative embodiment, the markers were broken into four groups – those that correlate to *CEACAM4* (bucket 3), those that correlate to *LAMP1* (bucket 4), those that correlate to *PLA2G7* (bucket 1) and those that correlate to *PLAC8* (bucket 2). The plots in Figure 10G demonstrate the markers in each group correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (*i.e.*, inSIRS (PS) versus ipSIRS (sepsis)). Like the two-bucket embodiment discussed above, choosing mRNAs from four groups to create derived markers results in an overall better AUC for separating inSIRS (PS) and ipSIRS (sepsis), as compared to when markers are chosen from within groups ($p < 0.2564$, as demonstrated in Figure 10H compared to when using markers from any one of groups 1 to 4. The mean AUC for markers derived from groups 1 to 4 is over 0.8 whereas the mean AUC for markers derived from any one of groups 1 to 4 is less than 0.8

Mild ipSIRS versus Severe ipSIRS

[0561] A list of 66 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of mild ipSIRS and severe ipSIRS was generated. Figure 11A plots these markers against the AUC and Figure 11B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (*N4BP2L2* – NEDD4 binding protein 2-like 2). The conditions of mild ipSIRS and severe ipSIRS are well separated when using this mRNA biomarker alone.

[0562] From the 66 individual markers at least 1000 derived markers (ratios) were generated that had an AUC of 0.87. A plot of the AUC of these derived markers for separating the conditions of mild ipSIRS and severe ipSIRS is shown in Figure 11C with the top performing ratio shown as a box and whisker plot in Figure 11D. The AUC for *N4BP2L2* and *ZC3H11A* (zinc finger CCCH-type containing 11A) as a ratio is 0.983.

[0563] All 66 individual markers were then broken into two groups – those that correlate to *N4BP2L2* and those that correlate to *ZC3H11A*. Both plots in Figures 11E and 11F demonstrate the correlation between the two groups based on their similarity to either *N4BP2L2* or *ZC3H11A*. In these plots the groups are referred to as either group 1 (*N4BP2L2*) or group 2 (*ZC3H11A*). It can be seen that each "group" contains those markers that are most highly correlated to each other. The markers in each "group" also correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance mild ipSIRS versus severe ipSIRS).

[0564] By choosing mRNAs from these two groups to create derived markers a better AUC for separating mild ipSIRS and severe ipSIRS is obtained than when markers are chosen from within groups ($p < 2.2e-16$) as demonstrated in Figure 11I, compared to when using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.89, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.6.

Mild ipSIRS versus ipSIRS – shock

[0565] A list of 48 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of mild ipSIRS and ipSIRS - shock was generated. Figure 12A plots these markers against the AUC and Figure 12B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (*CD6* – CD6 molecule). The conditions of mild ipSIRS and ipSIRS shock are well separated when using this mRNA biomarker alone.

[0566] From the 48 individual markers at least 1000 derived markers (ratios) were generated that had an AUC of at least 0.793. A plot of the AUC of these derived markers for separating the conditions of mild ipSIRS and ipSIRS shock is shown in Figure 12C with the top performing ratio shown as a box and whisker plot in Figure 12D. The AUC for *VAMP2* and *UBAP1* (ubiquitin associated protein 1) as a ratio is 0.978.

[0567] All 48 individual markers were then broken into two groups – those that correlate to *VAMP2* and those that correlate to *UBAP1*. Both plots in Figure 12E and 12F demonstrate the correlation between the two groups based on their similarity to either *VAMP2* or *UBAP1*. In these plots the groups are referred to as either group 1 (*VAMP2*) or group 2 (*UBAP1*). It can be seen that each "group" contains those markers that are most highly correlated to each other. The markers in each "group" also correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance mild ipSIRS versus ipSIRS - shock).

[0568] By choosing mRNAs from these two groups to create derived markers a better AUC for separating mild ipSIRS and ipSIRS - shock is obtained than when markers are chosen from within groups ($p< 2.2e-16$) as demonstrated in Figure 12I, compared to when using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.87, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.65.

Severe ipSIRS versus ipSIRS – shock

[0569] A list of 61 mRNA individual markers with an AUC of at least 0.7 for separating the two conditions of severe ipSIRS and ipSIRS - shock was generated. Figure 13A plots these markers against the AUC and Figure 13B is a box and whisker plot of the best mRNA biomarker for separating the two conditions (*SIRPG* – signal regulatory protein gamma). The conditions of severe ipSIRS and ipSIRS - shock are well separated when using this mRNA biomarker alone.

[0570] From the 61 individual markers at least 1000 derived markers (ratios) were generated that had an AUC of at least 0.821. A plot of the AUC of these derived markers for separating the conditions of severe ipSIRS and ipSIRS - shock is shown in Figure 13C with the top performing ratio shown as a box and whisker plot in Figure 13D. The AUC for *GATA3* (GATA binding protein 3) and *MECOM* (MDS1 and EVI1 complex locus) as a ratio is 0.936.

[0571] All 61 individual markers were then broken into two groups – those that correlate to *GATA3* and those that correlate to *MECOM*. Both plots in Figures 13E and 13F demonstrate the correlation between the two groups based on their similarity to either *GATA3* or *MECOM*. In these plots the groups are referred to as either group 1 (*GATA3*) or group 2 (*MECOM*). It can be seen that each "group" contains those markers that are most highly

correlated to each other. The markers in each "group" also correlate strongly (as demonstrated by AUC greater than 0.7 for all markers) to the condition being studied (in this instance severe ipSIRS versus ipSIRS - shock).

[0572] By choosing mRNAs from these two groups to create derived markers a better AUC for separating severe ipSIRS and ipSIRS - shock is obtained than when markers are chosen from within groups ($p < 2.2e-16$) as demonstrated in Figure 13I compared to when using markers from either group 1 or group 2 alone. The mean AUC for markers derived from groups 1 and 2 is over 0.82, whereas the mean AUC for markers derived from either group 1 or 2 alone is less than 0.7.

Signature Usage

[0573] Use of the above described markers and resulting signatures in patient populations and benefits in respect of differentiating inSIRS and ipSIRS, will now be described.

[0574] An assay capable of differentiating patients with inSIRS and ipSIRS can be used in multiple patient populations including:

1) Intensive Care Unit (medical and surgical ICU)
2) Post-surgical and medical wards
3) Emergency Department
4) Medical clinics.

[0575] Patients admitted to intensive care (ICU) often have ipSIRS, or develop ipSIRS during their ICU stay. The ultimate aim of intensive care is to ensure the patient survives and is discharged to a general ward in the minimum time. Patients in intensive care with diagnosed ipSIRS are usually administered a number of therapeutic compounds – many of which have opposing actions on the immune system and many of which could be counterproductive depending on the severity of ipSIRS (mild sepsis, severe sepsis, septic shock). Monitoring intensive care patients on a regular basis with biomarkers of the present invention will allow medical practitioners to differentiate inSIRS from ipSIRS and determine the stage of ipSIRS and hence choice of therapies, when to start and stop therapies, and patient management procedures, and ultimately response to therapy. Information provided by these biomarkers will therefore allow medical intensivists to tailor and modify therapies to ensure patients survive and spend less time in intensive care. Less time in intensive care leads

to considerable savings in medical expenses including through less occupancy time and appropriate use and timing of medications.

[0576] Surgical and general medical patients often develop inSIRS post-surgery or as a consequence of their condition or procedures and have a higher risk of developing ipSIRS. Post-operative and medical care in such patients therefore involves monitoring for signs of inSIRS and ipSIRS and differentiating between these two conditions. The treatment and management of inSIRS and ipSIRS patients post-surgically and in general wards is different, since inSIRS patients can be put on mild anti-inflammatory drugs or anti-pyretics and ipSIRS patients must be started on antibiotics as soon as possible for best outcomes. Monitoring post-surgical and medical patients on a regular basis with biomarkers of the present invention will allow nursing and medical practitioners to differentiate inSIRS and ipSIRS at an early stage and hence make informed decisions on choice of therapies and patient management procedures, and ultimately response to therapy. Information provided by these biomarkers will therefore allow medical practitioners to tailor and modify therapies to ensure patients recover quickly from surgery or other condition and do not develop ipSIRS. Less time in hospital and less complications leads to considerable savings in medical expenses including through less occupancy time and appropriate use and timing of medications.

[0577] Further, patients presenting to emergency departments often have a fever, which is one (of four) of the clinical signs of inSIRS. Such patients need to be assessed to determine if they have either inSIRS or ipSIRS. As mentioned above, the treatment and management of pyretic, inSIRS and septic patients are different. By way of example, a patient with a fever without other inSIRS clinical signs and no obvious source of infection may be sent home, or provided with other non-hospital services, without further hospital treatment. However, a patient with a fever may have early ipSIRS and not admitting such a patient may put their life at risk. Because these biomarkers can differentiate inSIRS and ipSIRS they will allow medical practitioners to triage emergency department patients quickly and effectively. Accurate triage decision-making insures that patients requiring hospital treatment are given it, and those that don't are provided with other appropriate services.

[0578] Further still, patients presenting to medical clinics often have any one of the four clinical signs of inSIRS (increased heart rate, increased respiratory rate, abnormal white blood cell count, fever or hypothermia). Many different clinical conditions can present with

one of the four clinical signs of inSIRS and such patients need to be assessed to determine if they have either inSIRS or ipSIRS and to exclude other differential diagnoses. By way of example, a patient with colic might also present with clinical signs of increased heart rate. Differential diagnoses could be (but not limited to) appendicitis, urolithiasis, cholecystitis, pancreatitis, enterocolitis. In each of these conditions it would be important to determine if there was a systemic inflammatory response (inSIRS) or whether an infection was contributing to the systemic response to the condition (ipSIRS). The treatment and management of patients with and without systemic inflammation and/or infection are different. Because these biomarkers can differentiate patients with a systemic inflammatory response to infection from those with a systemic inflammatory response without infection (inSIRS and ipSIRS), and determine the degree of systemic involvement, the use of them will allow medical practitioners to determine the next medical procedure(s) to perform to satisfactorily resolve the patient issue.

Determining the Extent of Systemic Inflammation in Sick Patients and Those With inSIRS and ipSIRS

[0579] As mentioned above, patients presenting to medical clinics often have any one of the four clinical signs of inSIRS. However, many different clinical conditions can present with one of the four clinical signs of inSIRS and such patients need to be assessed to determine if they have inSIRS, and if so the extent of inSIRS, or ipSIRS, and if so the extent of ipSIRS, and to exclude other differential diagnoses.

[0580] By way of example, a patient with respiratory distress is likely to present with clinical signs of increased respiratory rate. Differential diagnoses could be (but not limited to) asthma, pneumonia, congestive heart failure, physical blockage of airways, allergic reaction, collapsed lung, pneumothorax. In each of these conditions it would be important to determine if there was a systemic inflammatory response (inSIRS) or whether an infection was contributing to the condition. The treatment and management of patients with and without systemic inflammation and/or infection are different. Because these biomarkers can differentiate patients with a systemic inflammatory response to infection from those with a systemic inflammatory response without infection (inSIRS and ipSIRS), and determine the degree of systemic involvement, the use of them will allow medical practitioners to determine the next medical procedure(s) to perform to satisfactorily resolve the patient issue. Patients with a collapsed lung, pneumothorax or a physical blockage are unlikely to have a

large systemic inflammatory response and patients with congestive heart failure, allergic reaction or asthma are unlikely to have a large systemic inflammatory response due to infection. The extent of both inSIRS and ipSIRS, as indicated by biomarkers presented in this patent, also provides clinicians with information on next treatment and management steps. For example, a patient with respiratory distress and a strong biomarker response indicating ipSIRS is likely to be immediately hospitalized, placed on antibiotics and a chest X-ray performed. A patient with respiratory distress and a strong biomarker response indicating inSIRS but not ipSIRS is likely to be hospitalized and chest X-rayed along with other investigative diagnostic procedures, such as MRI, ECG, and angiogram. A patient with respiratory distress with a short history and no inSIRS or ipSIRS is likely to undergo further examination at a local clinic rather than requiring hospitalization.

[0581] Again, and as mentioned above, patients presenting to emergency departments often have a fever, which is one (of four) of the clinical signs of inSIRS. Such patients need to be assessed to determine if they have either inSIRS or ipSIRS. Further it is important to determine how sick they are to be able to make a Judgment call on whether to admit the patient or not. Accurate triage decision-making insures that patients requiring hospital treatment are given it, and those that don't are provided with other appropriate services.

[0582] Patients in ICU often have inSIRS and ipSIRS and it is important to differentiate these two conditions as treatment regimens differ. In patients with inSIRS it is important to determine the extent of the inflammatory response so that appropriate treatments and management regimens can be put in place. For example, a patient newly determined to have inSIRS that is not extensive may be able to be put on mild medication such a non-steroidal anti-inflammatory. A patient newly determined to have extensive inSIRS (*e.g.* trauma) may require stronger anti-inflammatory medication such as steroids to reduce the potential impact of the side effects of inflammation (swelling). In patients with ipSIRS it is also important to determine the extent of the inflammatory response to infection so that appropriate treatments and management regimens can be put in place or stopped. For example, for a patient with a persistent strong ipSIRS response the clinician may consider either changing, or adding to, the antibiotic treatment regimen in the absence of traditional bacterial culture and sensitivity results. Further, patients that are known to have had ipSIRS and have been on antimicrobial therapy for an extended period but have since demonstrated (by testing using biomarkers)

that they no longer have either an inSIRS or ipSIRS can therefore be safely taken off intravenous antibiotics.

Determining the Severity of ipSIRS

[0583] Patients admitted to intensive care (ICU) often have ipSIRS, or develop ipSIRS during their ICU stay. It is known that the severity of sepsis can be considered to be a continuum from less severe, or sepsis, to more severe, or severe sepsis, to the most severe, or septic shock. More severe sepsis (ipSIRS) requires more aggressive, immediate and tailored intervention compared to sepsis (although all are acute conditions). Patients in intensive care with diagnosed ipSIRS are usually administered a number of therapeutic compounds – many of which have opposing actions on the immune system and many of which could be counterproductive depending on the severity of ipSIRS (sepsis, severe sepsis, septic shock). Monitoring intensive care patients on a regular basis with biomarkers of the present invention will allow medical practitioners to determine the severity of ipSIRS (mild, severe or shock) and hence choice of therapies and patient management procedures, and ultimately response to therapy. Information provided by these biomarkers disclosed herein will therefore allow medical practitioners to tailor, modify or cease therapies and/or care to ensure patients survive and spend less time in intensive care. Less time in intensive care leads to considerable savings in medical expenses including through less occupancy time and appropriate use and timing of medications.

First Example Workflow

[0584] A first example workflow will now be described. The workflow involves up to seven steps depending upon availability of automated platforms. The assay uses quantitative, real-time determination of the amount of each transcript in the sample based on the detection of fluorescence on a qRT-PCR instrument (*e.g.* Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument, Applied Biosystems, Foster City, CA, catalogue number 440685; K082562). Transcripts are each amplified, detected, and quantified in a separate reaction well using a probe that is visualized in the FAM channel (by example). The reported score is calculated using interpretive software provided separately to the kit but designed to integrate with RT-PCR machines.

[0585] The workflow below describes the use of manual processing and a pre-prepared kit.

Pre-analytical

[0586] Blood collection

[0587] Total RNA isolation

Analytical

[0588] Reverse transcription (generation of cDNA)

[0589] qPCR preparation

[0590] qPCR

[0591] Software, Interpretation of Results and Quality Control

[0592] Output.

Kit Contents

[0593] Diluent

[0594] RT Buffer

[0595] RT Enzyme Mix

[0596] qPCR Buffer

[0597] Primer/Probe Mix

[0598] AmpliTaq Gold® (or similar)

[0599] High Positive Control

[0600] Low Positive Control

[0601] Negative Control

Blood Collection

[0602] The specimen used is a 2.5mL sample of blood collected by venipuncture using the PAXgene® collection tubes within the PAXgene® Blood RNA System (Qiagen, kit catalogue # 762164; Becton Dickinson, Collection Tubes catalogue number 762165; K042613). An alternate collection tube is Tempus® (Life Technologies).

Total RNA Isolation

[0603] Blood (2.5mL) collected into a PAXgene RNA tube is processed according to the manufacturer's instructions. Briefly, 2.5mL sample of blood collected by venipuncture using the PAXgene™ collection tubes within the PAXgene™ Blood RNA System (Qiagen, kit catalogue # 762164; Becton Dickinson, Collection Tubes catalogue number 762165; K042613). Total RNA isolation is performed using the procedures specified in the PAXgene™ Blood RNA kit (a component of the PAXgene™ Blood RNA System). The

extracted RNA is then tested for purity and yield (for example by running an $A_{260/280}$ ratio using a Nanodrop® (Thermo Scientific)) for which a minimum quality must be (ratio > 1.6). RNA should be adjusted in concentration to allow for a constant input volume to the reverse transcription reaction (below). RNA should be processed immediately or stored in single-use volumes at or below -70^{0}C for later processing.

Reverse Transcription

[0604] Determine the appropriate number of reaction equivalents to be prepared (master mix formulation) based on a plate map and the information provided directly below. Each clinical specimen is run in singleton.

a) **Each batch run must include the following specimens:**
b) High Control, Low Control, Negative Control, and No Template Control (Test Diluent instead of sample) in singleton each

Program the ABI 7500 Fast Dx Instrument as detailed below.

c) Launch the software.
d) Click Create New Document
e) In the New Document Wizard, select the following options:
    i) Assay: Standard Curve (Absolute Quantitation)
    ii) Container: 96-Well Clear
    iii) Template: Blank Document (or select a laboratory-defined template)
    iv) Run Mode: **Standard 7500**
    v) Operator: Enter operator's initials
    vi) Plate name: [default]
f) Click Finish
g) Select the Instrument tab in the upper left
h) In the Thermal Cycler Protocol area, Thermal Profile tab, enter the following times:
    i) 25 °C for 10 minutes
    ii) 45 °C for 45 minutes
    iii) 93 °C for 10 minutes
    iv) Hold at 25 °C for 60 minutes

[0605] In a template-free area, remove the test Diluent and RT-qPCR Test RT Buffer to room temperature to thaw. Leave the RT-qPCR Test RT Enzyme mix in the freezer and/or on a cold block.

[0606] In a template-free area, assemble the master mix in the order listed below.

RT Master Mix – Calculation:

	Per well	× N
RT-qPCR Test RT Buffer	3.5 µL	3.5 × N
RT-qPCR Test RT Enzyme mix	1.5 µL	1.5 × N
Total Volume	**5 µL**	**5** × N

[0607] Gently vortex the master mix then pulse spin. Add the appropriate volume (5 µL) of the RT Master Mix into each well at room temperature.

[0608] Remove clinical specimens and control RNAs to thaw. (If the specimens routinely take longer to thaw, this step may be moved upstream in the validated method.)

[0609] Vortex the clinical specimens and control RNAs, then pulse spin. Add 10 µL of control RNA or RT-qPCR Test Diluent to each respective control or negative well.

[0610] Add 10 µL of sample RNA to each respective sample well (150 ng total input for RT; OD_{260}/OD_{280} ratio greater than 1.6). Add 10 µL of RT-qPCR Test Diluent to the respective NTC well.

[0611] **Note:** The final reaction volume per well is 15 µL.

	Samples
RT Master Mix	5 µL
RNA sample	10 µL
Total Volume (per well)	**15 µL**

[0612] Mix by gentle pipetting. Avoid forming bubbles in the wells.

[0613] Cover wells with a seal.

[0614] Spin the plate to remove any bubbles (1 minute at 400 x *g*).

[0615] Rapidly transfer to ABI 7500 Fast Dx Instrument pre-programmed as detailed above.

[0616] Click Start. Click Save and Continue. Before leaving the instrument, it is recommended to verify that the run started successfully by displaying a time under Estimated Time Remaining.

[0617] qPCR master mix may be prepared to coincide roughly with the end of the RT reaction. For example, start about 15 minutes before this time. See below.

[0618] When RT is complete (*i.e.* resting at 25 °C; stop the hold at any time before 60 minutes is complete), spin the plate to collect condensation (1 minute at 400 x *g*).

qPCR Preparation

[0619] Determine the appropriate number of reaction equivalents to be prepared (master mix formulation) based on a plate map and the information provided in RT Preparation above.

[0620] Program the ABI 7500 Fast Dx with the settings below.

a) Launch the software.
b) Click Create New Document
c) In the New Document Wizard, select the following options:
    i) Assay: Standard Curve (Absolute Quantitation)
    ii) Container: 96-Well Clear
    iii) Template: Blank Document (or select a laboratory-defined template)
    iv) Run Mode: **Standard 7500**
    v) Operator: Enter operator's initials
    vi) Plate name: Enter desired file name
d) Click Next
e) In the Select Detectors dialog box:
    i) Select the detector for the first biomarker, and then click Add>>.
    ii) Select the detector second biomarker, and then click Add>>, etc.
    iii) Passive Reference: ROX
f) Click Next
g) Assign detectors to appropriate wells according to plate map.
    i) Highlight wells in which the first biomarker assay will be assigned
    ii) Click use for the first biomarker detector
    iii) Repeat the previous two steps for the other biomarkers
    iv) Click Finish

h) Ensure that the Setup and Plate tabs are selected
i) Select the Instrument tab in the upper left
j) In the Thermal Cycler Protocol area, Thermal Profile tab, perform the following actions, with the results shown in Figure 14:
    i) Delete Stage 1 (unless this was completed in a laboratory-defined template).
    ii) Enter sample volume of 25 µL.
    iii) 95 °C 10 minutes
    iv) 40 cycles of 95 °C for 15 seconds, 63 °C for 1 minute
    v) Run Mode: Standard 7500
    vi) Collect data using the "stage 2, step 2 (63.0@1:00)" setting
k) Label the wells as below using this process: Right click over the plate map, then select Well Inspector. With the Well Inspector open, select a well or wells. Click back into the Well Inspector and enter the Sample Name. Close the Well Inspector when completed.
    i) CONH for High Control
    ii) CONL for Low Control
    iii) CONN for Negative Control
    iv) NTC for No Template Control
    v) [Accession ID] for clinical specimens
l) Ensure that detectors and quenchers are selected as listed below.
    i) FAM for CEACAM biomarker 1; quencher=none
    ii) FAM for LAMP1 biomarker 2; quencher=none, etc.
    iii) FAM for PLA2G7; quencher=none
    iv) FAM for PLAC8; quencher=none
    v) Select "ROX" for passive reference

qPCR

[0621] In a template-free area, remove the assay qPCR Buffer and assay Primer/Probe Mixes for each target to room temperature to thaw. Leave the assay AmpliTaq Gold in the freezer and/or on a cold block.

[0622] Still in a template-free area, prepare qPCR Master Mixes for each target in the listed order at room temperature.

qPCR Master Mixes – Calculation Per Sample

	Per well	× N
qPCR Buffer	11 µL	11 × N
Primer/Probe Mix	3.4 µL	3.4 × N
AmpliTaq Gold®	0.6 µL	0.6 × N
Total Volume	**15 µL**	**15** × N

[0623] Gently mix the master mixes by flicking or by vortexing, and then pulse spin. Add 15 µL of qPCR Master Mix to each well at room temperature.

[0624] In a template area, add 130 µL of SeptiCyte Lab Test Diluent to each cDNA product from the RT Reaction. Reseal the plate tightly and vortex the plate to mix thoroughly.

[0625] Add 10 µL of diluted cDNA product to each well according to the plate layout.

[0626] Mix by gentle pipetting. Avoid forming bubbles in the wells.

[0627] Cover wells with an optical seal.

[0628] Spin the plate to remove any bubbles (1 minute at 400 x g).

[0629] Place on real-time thermal cycler pre-programmed with the settings above.

[0630] Click Start. Click Save and Continue. Before leaving the instrument, it is recommended to verify that the run started successfully by displaying a time under Estimated Time Remaining.

[0631] Note: Do not open the qPCR plate at any point after amplification has begun. When amplification has completed, discard the unopened plate.

Software, Interpretation of Results and Quality Control

[0632] Software is specifically designed to integrate with the output of PCR machines and to apply an algorithm based on the use of multiple biomarkers. The software takes into account appropriate controls and reports results in a desired format.

[0633] When the run has completed on the ABI 7500 Fast Dx Instrument, complete the steps below in the application 7500 Fast System with 21 CFR Part 11 Software, ABI software SDS v1.4.

[0634] Click on the Results tab in the upper left corner.

[0635] Click on the Amplification Plot tab in the upper left corner.

[0636] In the Analysis Settings area, select an auto baseline and manual threshold for all targets. Enter 0.01 as the threshold.

[0637] Click on the Analyze button on the right in the Analysis Settings area.

[0638] From the menu bar in the upper left, select File then Close.

[0639] Complete the form in the dialog box that requests a reason for the change. Click OK.

[0640] Transfer the data file (.sds) to a separate computer running the specific assay RT-qPCR Test Software.

[0641] Launch the assay RT-qPCR Test Software. Log in.

[0642] From the menu bar in the upper left, select File then Open.

[0643] Browse to the location of the transferred data file (.sds). Click OK.

[0644] The data file will then be analyzed using the assay's software application for interpretation of results.

Interpretation of Results and Quality Control

Results

[0645] Launch the interpretation software. Software application instructions are provided separately.

[0646] Following upload of the .sds file, the Software will automatically generate classifier scores for controls and clinical specimens.

[0647] Controls

[0648] The Software compares each CON (control) specimen (CONH, CONL, CONN) to its expected result. The controls are run in singleton.

Control specimen		
Designation	**Name**	**Expected result**
CONH	High Control	Score range
CONL	Low Control	Score range
CONN	Negative Control	Score range
NTC	No Template Control	Fail (no Ct for all targets)

[0649] If CONH, CONL, and/or CONN fail the batch run is invalid and no data will be reported for the clinical specimens. This determination is made automatically by the interpretive software. The batch run should be repeated starting with either a new RNA preparation or starting at the RT reaction step.

[0650] If NTC yields a result other than Fail (no Ct for all targets), the batch run is invalid and no data may be reported for the clinical specimens. This determination is made by visual inspection of the run data. The batch run should be repeated starting with either a new RNA preparation or starting at the RT reaction step.

[0651] If a second batch run fails, please contact technical services. If both the calibrations and all controls are valid, then the batch run is valid and specimen results will be reported.

[0652] Specimens

[0653] Note that a valid batch run may contain both valid and invalid specimen results.

[0654] Analytical criteria (*e.g.* Ct values) that qualify each specimen as passing or failing (using pre-determined data) are called automatically by the software.

[0655] Scores out of range – reported.

[0656] Quality Control

[0657] Singletons each of the Negative Control, Low Positive Control, and High Positive Control must be included in each batch run. The batch is valid if no flags appear for any of these controls.

[0658] A singleton of the No Template Control is included in each batch run and Fail (no Ct for all targets) is a valid result indicating no amplifiable material was detectable in the well.

[0659] The negative control must yield a Negative result. If the negative control is flagged as Invalid, then the entire batch run is invalid.

[0660] The low positive and high positive controls must fall within the assigned ranges. If one or both of the positive controls are flagged as Invalid, then the entire batch run is invalid.

Example Output

[0661] A possible example output from the software is presented below in Figure 15. The format of such a report depends on many factors including; quality control, regulatory authorities, cut-off values, the algorithm used, laboratory and clinician requirements, likelihood of misinterpretation.

[0662] In this instance the assay is called "SeptiCyte Lab Test". The result is reported as a number (5.8), a call ("Sepsis Positive"), a position on a 0-12 scale, and a probability of the patient having sepsis based on historical results and the use of a pre-determined cut-off (using results from clinical trials). Results of controls within the assay are also reported. Other information that could be reported might include: previous results and date and time of such results, probability of severe sepsis or septic shock, a scale that provides cut-off values for historical testing results that separate the conditions of healthy, inSIRS and ipSIRS (mild, severe and shock) such that those patients with higher scores are considered to have more severe inSIRS or ipSIRS.

Second Example Workflow

[0663] A second example workflow will now be described. Machines have been, and are being, developed that are capable of processing a patient sample at point-of-care, or near point-of-care. Such machines require few molecular biology skills to run and are aimed at non-technical users. The idea is that the sample would be pipetted directly into a disposable cartridge that is then inserted into the machine. The user presses "Start" and within 2-3 hours a result is generated. The cartridge contains all of the required reagents to perform Steps 2-5 in the example workflow above and the machine has appropriate software incorporated to allow Steps 6 and 7 to be performed.

[0664] Fresh, whole, anti-coagulated blood can be pipetted into an Idylla Cartridge (Biocartis NV) or similar (Unyvero, Curetis AG; Enigma ML, Enigma Diagnostics; DiagCore, STAT Diagnostica; Savannah, Quidel Corp; ePlex, GenMark Dx), and on-screen instructions on the Idylla machine followed to test for differentiating inSIRS and ipSIRS (by example). Inside the Idylla machine RNA is first extracted from the whole blood and is then converted into cDNA. The cDNA is then used in qRT-PCR reactions. The reactions are followed in real time and Ct values calculated. On-board software generates a result output (see Figure XX). Appropriate quality control measures for RNA quality, no template controls, high and low template controls and expected Ct ranges ensure that results are not reported erroneously.

Example Biomarker Ratios

[0665] Example biomarker ratios (the top 12 based on AUC) that are capable of separating different conditions are shown in the box and whisker plots as listed below, with each showing perfect separation.

- Figures 16A to 16L show Healthy Versus inSIRS (Post-Surgical)
- Figures 17A to 17L show Healthy Versus ipSIRS (Sepsis)
- Figures 18A to 18L show inSIRS (Post-Surgical) Versus ipSIRS (Sepsis)
- Figures 19A to 19L show Sepsis Versus Severe Sepsis
- Figures 20A to 20L show Severe Sepsis Versus Septic Shock
- Figures 21A to 21L show Sepsis Versus Septic Shock

Example Algorithm Combining Biomarker Ratios

[0666] Biomarker ratios (derived markers) can be used in combination to increase the diagnostic power for separating various conditions. Determining which markers to use, and how many, for separating various conditions can be achieved by calculating Area Under Curve (AUC).

[0667] Figure 22 shows the effect on AUC (in this instance for separating inSIRS and ipSIRS) of adding biomarkers to the diagnostic signature. Diagnostic power significantly increases (adjusted p-value = 0.0175) between a single mRNA biomarker (in this instance *PLA2G7*, AUC of 0.88, 95% CI 0.79 - 0.97) compared to the power of the two best performing markers in combination (in this instance *PLA2G7* and *PLAC8*, AUC of 0.96, 95% CI 0.91 - 1.0). Combinations of two, three, four and five biomarkers produced equally as

good differentiation of inSIRS and ipSIRS without significant differences. For commercial development of derived markers other factors come into play such as cost-effectiveness, assay complexity and capabilities of the qRT-PCR platform.

[0668] In this example, the addition of markers beyond 3 or 4 does not significantly improve performance and, conversely, a decline in AUC is observed in signatures of ≥5 genes probably because when a statistical model is forced to include biomarkers that add little additional information data over-fitting and addition of noise occurs.

[0669] As such, and by example, a 4-gene signature (0.986, 95% CI 0.964-1.00) offers the appropriate balance between simplicity, practicality and commercial risk for separating inSIRS and ipSIRS. Further, an equation using four markers weighs each biomarker equally which also provides additional robustness in cases of analytical or clinical variability.

[0670] One example equation that provides good diagnostic power for separating inSIRS and ipSIRS (amongst others) is:

$$\text{Diagnostic Score} = (PLA2G7 - PLAC8) + (CEACAM4 - LAMP1)$$

[0671] The value for each biomarker is a Ct value from a PCR. When clinical samples from patients with inSIRS and ipSIRS were tested using these four markers in a PCR the Ct values for each of the markers was found to fall between 26 and 34. In this patient population the first biomarker within each bracket pair has a higher value than the second biomarker within each bracket pair. Thus, the "Diagnostic Score" has been found to have values between 0 and 12. However, in theory the "Diagnostic Score could potentially be highest Ct value +/- highest Ct value.

[0672] In Figure 23 shows results of PCR and the use of the above algorithm have been calculated for two patient populations (N=63 for "Discovery" and N=70 for "Feasibility"). Each patient was clinically and retrospectively (note, not at the time the sample was taken) confirmed as having either inSIRS (black dots) or ipSIRS (red dots). Each patient sample has also had a SeptiCyte score calculated (Y axis on left hand side). On a scale of 0-12 it can be seen that patients with confirmed ipSIRS (red dots) obtain a higher Diagnostic Score compared to those with confirmed inSIRS. Further, it can be seen that an arbitrary cut-off line can be drawn that more or less separates the two conditions depending upon the desired false negative or false positive rate (compared to a retrospective diagnosis of inSIRS or

ipSIRS using clinical data). In this instance the line is drawn at a "SeptiCyte Score" of 4 such that the number of false negative ipSIRS calls in the Discovery Dataset is zero and the number of false negative ipSIRS calls in the Feasibility Dataset is 2. Conversely the number of false positive ipSIRS calls in the Discovery Dataset is four and the number of false positive ipSIRS calls in the Feasibility Dataset is 9. Clearly in this instance whether a patient sample is false positive or false negative depends on the artificial gold standard of a retrospective clinical call of inSIRS or ipSIRS.

[0673] Accordingly, in one example, when used for determining a likelihood of the subject having inSIRS or ipSIRS, the method can include determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene, determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene and then determining an indicator using the first and second pairs of biomarker values.

[0674] As previously discussed, the indicator could then be compared to indicator references specifically established to distinguish between inSIRS and ipSIRS.

[0675] An example process of a process for establishing indicator references will now be described in more details with reference to Figure 24.

[0676] In this example, at step 2400 the processing system 201 determines reference data in the form of measured biomarker values obtained for a reference population. The reference data may be acquired in any appropriate manner but typically this involves obtaining gene expression product data from a plurality of individuals.

[0677] In order to achieve this, gene expression product data are collected, for example by obtaining a biological sample, such as a peripheral blood sample, and then performing a quantification process, such as a nucleic acid amplification process, including PCR (Polymerase Chain Reaction) or the like, in order to assess the activity, and in particular, level or abundance of a number of reference biomarkers. Quantified values indicative of the relative activity are then stored as part of the reference data.

[0678] In one example, the measurements are received as raw data, which then undergoes preliminary processing. Such raw data corresponds to information that has come from a

source without modification, such as outputs from instruments such as PCR machines, array (*e.g.*, microarray) scanners, sequencing machines, clinical notes or any other biochemical, biological, observational data, or the like. This step can be used to convert the raw data into a format that is better suited to analysis. In one example this is performed in order to normalize the raw data and thereby assist in ensuring the biomarker values demonstrate consistency even when measured using different techniques, different equipment, or the like. Thus, the goal of normalization is to remove the variation within the samples that is not directly attributable to the specific analysis under consideration. For example, to remove variances caused by differences in sample processing at different sites. Classic examples of normalization include z-score transformation for generic data, or popular domain specific normalizations, such as RMA normalization for microarrays.

[0679] However, it will also be appreciated that in some applications, such as a single sample experiment run on a single data acquisition machine, this step may not strictly be necessary, in which case the function can be a Null function producing an output identical to the input.

[0680] In one example, the preferred approach is a paired function approach over log normalized data. Log normalization is a standard data transformation on microarray data, because the data follow a log-normal distribution when coming off the machine. Applying a log transform turns the data into process-friendly normal data.

[0681] The individuals are selected to include individuals diagnosed with one or more conditions of interest, as well as healthy individuals The conditions are typically medical, veterinary or other health status conditions and may include any illness, disease, stages of disease, disease subtypes, severities of disease, diseases of varying prognoses or the like, and in the current example would include at least some individuals with inSIRS and some individuals with ipSIRS. In this regard, the individuals also typically undergo a clinical assessment allowing the conditions to be clinically identified, and with an indication of any assessment or condition forming part of the reference data.

[0682] The biomarker values measured will depend on the predominant condition that is being assessed so, for example, in the case of determining the likelihood of a subject having inSIRS or ipSIRS, the biomarkers used will be *LAMP1*, *CEACAM4*, *PLAC8* and *PLA2G7*, as discussed above.

[0683] Once collected, the reference data can be stored in the database 211 allowing this to be subsequently retrieved by the processing system 201 for subsequent analysis, or could be provided directly to the processing system 201 for analysis.

[0684] As part of the above process, at step 2410 the measurements are validated using traditional prior art techniques, to ensure that the measurements have been performed successfully, and hence are valid.

[0685] At step 2420, each individual with the reference population is typically allocated to a group. The groups may be defined in any appropriate manner and may be defined based on any one or more of an indication of a presence, absence, degree, stage, severity, prognosis or progression of a condition, other tests or assays, or measured biomarkers associated with the individuals.

[0686] For example, a first selection of groups may be to identify one or more groups of individuals suffering from SIRS, one or more groups of individuals suffering ipSIRS, and one or more groups of individuals suffering inSIRS. Further groups may also be defined for individuals suffering from other conditions. The groups may include overlapping groups, so for example it may be desirable to define groups of healthy individuals and individuals having SIRS, with further being defined to distinguish inSIRS patients from ipSIRS patients, as well as different degree of inSIRS or ipSIRS, with these groups having SIRS in common, but each group of patients differing in whether a clinician has determined the presence of an infection or not. Additionally, further subdivision may be performed based on characteristics of the individuals, phenotypic traits, measurement protocols or the like, so groups could be defined based on these parameters so that a plurality of groups of individuals suffering from a condition are defined, with each group relating to a different phenotypic trait, measurement protocol or the like.

[0687] It will also be appreciated, however, that identification of different groups can be performed in other manners, for example on the basis of particular activities of biomarkers within the biological samples of the reference individuals, and accordingly, reference to conditions is not intended to be limiting and other information may be used as required.

[0688] The manner in which classification into groups is performed may vary depending on the preferred implementation. In one example, this can be performed automatically by the processing system 201, for example, using unsupervised methods such as Principal Components Analysis (PCA), or supervised methods such as k-means or Self Organizing Map (SOM). Alternatively, this may be performed manually by an operator by allowing the operator to review reference data presented on a Graphical User Interface (GUI), and define respective groups using appropriate input commands.

[0689] At step 2430, first and second derived biomarker values are determined representing respective indicator values. The first and second indicator values In_1, In_2 are determined on a basis of ratios of concentrations of first and second, and third and fourth biomarkers respectively:

$$In_1 = (PLA2G7/\ PLAC8)$$

$$In_2 = (CEACAM4/\ LAMP1)$$

[0690] The indicator values are then used to establish indicator references at step 2440, which are then used in analyzing measured indicator values for a subject to establish a likelihood of the subject having a condition.

[0691] In particular, indicator values for each reference group are statistically analyzed to establish a range or distribution of indicator values that is indicative of each group, and an example distribution is shown in Figure 26, as will be discussed in more detail below.

[0692] A further example will now be described with reference to Figures 25A and 25B.

[0693] In this example, at step 2500 a sample is acquired from the subject. The sample could be any suitable sample such as a peripheral blood sample, or the like, depending on the nature of the biomarker values being determined. At step 2505 the sample undergoes preparation allowing this to be provided to a measuring device and used in a quantification process at step 2510. For this purpose of this example, the quantification process involves PCR amplification, with the measuring device being a PCR machine, although other suitable techniques could be used. In this instance, amplifications times *At(PLA2G7)*, *At(PLAC8)*, *At(CEACAM4)*, *At(LAMP1)* are determined for each of the four biomarkers at step 2515, with the amplification times being transferred from the measuring device to the processing system

201 allowing the processing system 201 to perform analysis of the corresponding biomarker values.

[0694] Accordingly, at step 2520 the processing system 201 calculates ratios using the amplifications times. In this regard, as the amplification times represent a log value, the ratios are determined by subtracting amplifications times as will be appreciated by a person skilled in the art.

[0695] Accordingly, in this example the indicator values would be determined as follows:

$$In_1 = At(PLA2G7) - At(PLAC8)$$

$$In_2 = At(CEACAM4) - At(LAMP1)$$

[0696] At step 2525 the processing system 201 determines an indicator value by combining the ratios for the indicator values, as follows:

$$In = In_1 + In_2$$

[0697] The processing system 201 then compares the indicator value to one or more respective indicator references at step 2530.

[0698] As previously described, the indicator references are derived for a reference population and are used to indicate the likelihood of a subject suffering from inSIRS or ipSIRS. To achieve this, the reference population is grouped based on a clinical assessment into groups having / not having the conditions or a measure of severity, risk or progression stage of the condition, with this then being used to assess threshold indicator values that can distinguish between the groups or provide a measure of severity, risk or progression stage.

[0699] The comparison is performed by comparing the indicator to an indicator distribution determined for each group in the reference population. In the current example, there are two reference groups, with one corresponding to individuals diagnosed with inSIRS and the other for individuals diagnosed with ipSIRS. In this instance, the results of the comparison can be used to determine a likelihood of the individual having ipSIRS as opposed to inSIRS. This can be achieved using a number of different methods, depending on the preferred implementation.

[0700] An example of a reference distribution is shown in Figure 26, which shows the distribution of indicator values for a reference population containing both inSIRS and ipSIRS samples. The density (y axis) describes how common scores are in the reference population. In Figure 26, the most common values for the inSIRS population are in the range 1 to 8, and for the ipSIRS population are mostly in the range 5 to 13. By way of example, let us assume that the calculated indicator value for a new sample is 4. A value of 4 in the inSIRS population has a high density at this value (A), while the ipSIRS population has a low density at this value (B), meaning that this sample is more likely to be inSIRS. Conversely, if a sample has an indicator score of 10, this value in the ipSIRS reference population has a high density (C), while the inSIRS population has a low density (D), meaning this it is more probable that this sample with an indicator value of 10 belongs to the ipSIRS population.

[0701] In practice this process can be performed by determining a basic probability based on score bands. For a given score band (*i.e.* 4-6), the proportion of individuals with SIRS or SEPSIS is calculated. For example, if 40% of the scores between 4 and 6 were SEPSIS, then if an subject has an indicator value between 4 and 6, they have a 40% probability of sepsis. Thus, for a given range within the reference distribution, the probability of belonging to one group or another (SIRS/SEPSIS) can simply be the proportion of that group within the range.

[0702] An alternative technique is a standard Bayes method. In this case, the technique uses a distribution of inSIRS scores, a distribution of ipSIRS scores and an indicator value for the subject. In this example, a standard score or equivalent is used to generate a probability of the indicator value belonging to the inSIRS distribution: pr(inSIRS) and separately to the ipSIRS distribution: pr(ipSIRS). The Bayes method is used to generate the probability of ipSIRS given the individual distributions.

[0703] Thus, given derived biomarker distributions for two or more groups (*i.e.* inSIRS/ipSIRS), the probability of membership for a single unknown sample into each distribution can be calculated (p-value) using for example a standard score (z-score). Then the p-values for each distribution can be combined into an overall probability for each class (*i.e.* inSIRS/ipSIRS) using for example Bayes rule or any other probability calculation method (including frequentist or empirical or machine learned methods).

[0704] Thus, once the indicator value has been derived and compared to the indicator distributions, the results of this comparison are used by the processing system 201 to calculate a likelihood of the subject having ipSIRS at step 2535, with this being used to generate a representation of the results at step 2540, which is provided for display at step 2545, for example to a clinician or medical practitioner. This can be achieved by displaying the representation on a client device, such as part of an email, dashboard indication or the like.

[0705] An example of the representation is shown in Figures 27A and 27B.

[0706] In this example, the representation 2700 includes a pointer 2710 that moves relative to a linear scale 2720. The linear scale is divided into regions 2721, 2722, 2723, 2724 which indicate whether the subject is suffering from level 1, 2, 3 or 4. Corresponding indicator number values are displayed at step 2730 with an indication of whether the corresponding value represents a likelihood of SIRS (inSIRS) or SEPSIS (ipSIRS) being shown at step 2740. An alphanumeric indication of the score is shown at step 2751 together with an associated probability of the biological subject having SEPSIS at step 2752.

[0707] As shown in this example, regions of the linear scale where the pointer is situated are highlighted with the diagnosis that is most unlikely being greyed out to make it absolutely clear where the subject sits on the scale. This results in a representation which when displayed at step 2545 is easy for a clinician to readily understand and to make a rapid diagnosis.

[0708] It will be appreciated from the above that a method can be provided for use in assessing the likelihood of a biological subject having inSIRS or ipSIRS the method including, in one or more processing devices:

a) determining a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:
   i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
   ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

b) determining an indicator indicative of a ratio of the concentrations of the polynucleotide expression products using the pair of biomarker values;

c) retrieving previously determined first and second indicator references from a database, the first and second indicator references being determined based on indicators determined from first and second groups of a reference population, one of the groups consisting of individuals diagnosed with the medical condition;

d) comparing the indicator to the first and second indicator references;

e) using the results of the comparison to determine a probability indicative of the subject having the medical condition; and,

f) generating a representation of the probability, the representation being displayed to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

[0709] Similarly apparatus can be provided for determining the likelihood of a biological subject having inSIRS or ipSIRS, the apparatus including:

a) a sampling device that obtains a sample taken from a biological subject, the sample including polynucleotide expression products;

b) a measuring device that quantifies polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) at least one processing device that:

i) receives an indication of the pair of biomarker values from the measuring device;

ii) determines an indicator using a ratio of the concentration of the first and second polynucleotide expression products using the biomarker values; and,

iii) compares the indicator to at least one indicator reference; and,

iv) determines a likelihood of the subject having the at least one medical condition using the results of the comparison; and,

v) generates a representation of the indicator and the likelihood for display to a user.

[0710] A further method that can be provided includes differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) in a measuring device:

i) amplifying at least some polynucleotide expression products in the sample;

ii) determining an amplification amount representing a degree of amplification required to obtain a defined level of polynucleotide expression products including:

(1) amplification amounts for a first pair of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

(2) amplification amounts for a second pair of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) in a processing system:

i) retrieving the amplification amounts;

ii) determining an indicator by:

(1) determining a first derived biomarker value indicative of a ratio of concentrations of the first pair of polynucleotide expression products by determining a difference between the amplification amounts for the first pair;

(2) determining a second derived biomarker value indicative of a ratio of concentrations of the second pair of polynucleotide expression products by determining a difference between the amplification amounts for the second pair;

(3) determining the indicator by adding the first and second derived biomarker values;

iii) retrieving previously determined first and second indicator references from a database, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population,

the first and second group consisting of individuals diagnosed with inSIRS and ipSIRS respectively;

iv) comparing the indicator to the first and second indicator references;

v) using the results of the comparison to determine a probability of the subject being classified within the first or second group;

vi) generating a representation at least partially indicative of the indicator and the probability; and,

vii) providing the representation to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

[0711] Additionally, a method can be provided for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the method including:

a) determining a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determining the indicator using a combination of the plurality of biomarker values, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

[0712] Throughout this specification and claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers or steps but not the exclusion of any other integer or group of integers.

[0713] Persons skilled in the art will appreciate that numerous variations and modifications will become apparent. All such variations and modifications which become apparent to persons skilled in the art, should be considered to fall within the spirit and scope that the invention broadly appearing before described.

TABLE 1

HGNC § Gene Name	SEQ ID NO
PRKCZ	1
SKI	2
RER1	3
TAS1R1	4
VAMP3	5
AGTRAP	6
VPS13D	7
KLHDC7A	8
NBL1//C1orf151	9
MDS2	10
RCAN3	11
LDLRAP1	12
MAN1C1	13
SH3BGRL3	14
DHDDS	15
HCRTR1	16
CCDC28B	17
LCK	18
ZNF362	19
THRAP3	20
PPIE//CCDC25	21
CAP1	22
CTPS	23
C1orf84	24
FAAH	25
DMBX1	26
CYP4B1	27
BTF3L4	28
LRRC42	29
C1orf175//TTC4	30
TMEM61	31
FPGT//TNNI3K	32
ACADM	33
SPATA1	34
EPHX4	35
RPAP2	36
RPL5//SNORA66//SNORD21//FAM69A	37
RTCD1	38
SLC30A7	39
RNPC3//AMY2B	40
CELSR2	41
AHCYL1	42
CEPT1//DRAM2	43
CHIA	44
LIX1L	45
UPF0627	46
MRPS21	47
TNFAIP8L2	48
SMCP	49
DCST1	50
RAG1AP1	51
C1orf182	52
HAPLN2	53
NTRK1	54
CD1E	55
TOMM40L//NR1I3	56
POU2F1	57
TIPRL	58
SFT2D2	59
CACNA1E	60
SMG7	61
OCLM	62
RGS2	63
ZC3H11A//RP11-74E24.2	64
MFSD4	65
IL20	66
RPS6KC1	67
C1orf95	68
ARF1	69
GALNT2	70
TNFRSF4	71
NADK	72
FLJ14100//C1orf86	73
GPR153	74
RERE	75
SLC2A7	76
SDHB	77
RNF186	78
DDOST	79
GPN2	80
RPA2	81
PEF1	82
PTP4A2	83
TRIM62	84
PHC2	85
LSM10	86
MRPS15	87
RRAGC	88
COL9A2	89
TESK2	90
NRD1	91
KTI12	92
CC2D1B	93
YIPF1	94
JAK1	95
SLC35D1	96
DIRAS3	97
ZZZ3	98
GNG5	99
ZNHIT6	100
ODF2L	101
SEP15	102
BARHL2	103
GCLM	104
CLCC1//GPSM2//C1orf62	105
SORT1	106
SLC16A4	107
PHTF1	108
RSBN1	109
DENND2C//BCAS2	110
CD58	111
SPAG17//WDR3	112
REG4//NBPF7	113
RP11-94I2.2//NBPF16//NBPF11//NBPF15//N	114

BPF8//NBPF20//NBPF10//NBPF14//NBPF1//LOC100288142//NBPF12//KIAA1245//LOC100290137	
APH1A	115
POGZ	116
TDRKH	117
THEM4	118
S100A11	119
CRNN	120
SPRR2C	121
S100A12	122
S100A8	123
GATAD2B//PLIN2	124
DENND4B	125
PBXIP1	126
PYGO2	127
SHC1	128
DCST2	129
GBA//GBAP	130
ASH1L	131
RIT1	132
MEF2D	133
AIM2	134
COPA	135
DEDD	136
TADA1L	137
GPA33	138
CD247	139

F5	140
PIGC	141
KIAA0040	142
TOR1AIP2//TOR1AIP1//IFRG15	143
STX6//KIAA1614	144
EDEM3	145
UCHL5	146
DENND1B	147
DDX59	148
KIF21B	149
ARL8A	150
CYB5R1	151
MYBPH	152
CHI3L1	153
PIK3C2B//LOC100130573	154
NUAK2	155
NUCKS1	156
FAIM3	157
PLXNA2	158
SLC30A1	159
LPGAT1	160
ANGEL2	161
RAB3GAP2//AURKAPS1//AURKA//SNORA36B	162
TP53BP2	163
NVL	164
TMEM63A	165
PARP1	166
ITPKB	167

TARBP1	168
CHML	169
AKT3	170
SMYD3	171
AHCTF1	172
OR1C1	173
NCOA1	174
HADHB	175
ABHD1//PREB	176
SPAST	177
SLC30A6//DDX50	178
CRIPT	179
MSH2	180
FOXN2	181
CCDC104	182
VRK2	183
AHSA2//USP34	184
OTX1	185
AFTPH	186
CEP68	187
PLEK	188
ANXA4	189
MXD1	190
NAGK	191
SMYD5//NOTO	192
MTHFD2	193
TTC31	194
SEMA4F	195
TMSB10	196
SH2D6	197

GNLY	198
KCNIP3	199
CNNM4	200
CNNM3	201
ZAP70	202
LIPT1//MRPL30	203
MAP4K4	204
IL1R2	205
IL1R1	206
IL18R1	207
POLR1B	208
CHCHD5	209
IL1RN	210
PSD4	211
DDX18	212
INSIG2	213
TMEM177//LOC100125918	214
RALB	215
PROC	216
GPR17//LOC100291428//LIMS2	217
IMP4	218
FAM123C	219
ACVR2A	220
MBD5	221
LYPD6B	222
SLC4A10	223
UBR3	224
HAT1	225
ITGA6	226

ZAK	227
OSBPL6	228
PLEKHA3	229
ZC3H15	230
COL3A1	231
GLS	232
OBFC2A	233
COQ10B	234
MARS2	235
CFLAR	236
NOP58	237
FAM117B	238
CYP20A1	239
FASTKD2	240
PIKFYVE	241
C2orf62	242
SLC11A1	243
AGFG1	244
CHRNG	245
EIF4E2	246
TRPM8	247
LRRFIP1	248
GAL3ST2	249
TMEM18	250
LAPTM4A	251
SF3B14	252
TP53I3	253
UNQ2999	254
GPR113//SELI	255
MPV17	256

PPM1G	257
NLRC4	258
CDC42EP3	259
HNRPLL	260
COX7A2L	261
KCNG3	262
CALM2//C2orf61	263
BCL11A	264
XPO1	265
NAT8B	266
DUSP11	267
MOGS	268
SNRNP200	269
SEMA4C	270
MITD1	271
IL1A	272
SLC35F5	273
CCDC93	274
CLASP1	275
SAP130	276
YSK4	277
GTDC1	278
ORC4L	279
NR4A2//FLJ46875	280
DPP4	281
GALNT3	282
SCN7A	283
FRZB	284
STK17B	285
CLK1//PPIL3	286

MPP4	287
INO80D	288
KLF7	289
FAM119A	290
NGEF	291
ARL4C	292
RAB17	293
HDLBP	294
LRRN1	295
SETD5	296
IRAK2	297
C3orf42	298
TSEN2	299
NR2C2//MRPS25	300
UBE2E1	301
C3orf35	302
SNRK	303
ZNF197	304
GNAI2	305
ALAS1	306
PRKCD	307
CACNA1D	308
PXK	309
PTPRG	310
ATXN7	311
SLC35A5	312
SLC15A2	313
CCDC48	314
DNAJC13	315
CLDN18	316

GYG1	317
SELT	318
MED12L	319
RAP2B	320
MYNN	321
ABCF3	322
VPS8	323
HRG	324
EIF4A2//SNORA4	325
LPP	326
CCDC50	327
LOC152217	328
TADA3L	329
SEC13	330
TIMP4	331
METTL6	332
DAZL//DAZ4//DAZ3//DAZ2	333
SATB1//TBC1D5	334
SCN10A	335
SEC22C	336
ZDHHC3a	337
ZDHHC3b	338
SLC6A20	339
UQCRC1	340
PRKAR2A	341
IMPDH2	342
CCDC71	343
UBA7	344
CAMKV	345

WDR82	346
LMOD3	347
FOXP1	348
MORC1	349
ATG3	350
GSK3B//LOC100129275	351
HCLS1	352
KPNA1	353
PTPLB	354
C3orf22	355
RPN1	356
KIAA1257//ACAD9//LOC100132731	357
FOXL2	358
MECOM	359
PLD1	360
GNB4	361
MRPL47	362
KLHL6	363
THPO	364
ETV5	365
BCL6//LOC100131635	366
ATP13A5	367
TMEM44	368
KIAA1530	369
TACC3	370
CNO	371
BST1	372
KLF3	373

TMEM33//DCAF4L1	374
KIT	375
ENAM	376
FAM47E//STBD1	377
ENOPH1	378
PDLIM5	379
CCDC109B//HIGD1A//CCDC13	380
EGF	381
PCDH10	382
RAB33B	383
TMEM184C	384
RBM46	385
GRIA2	386
C4orf39	387
KLHL2	388
TLL1	389
F11	390
SLBP	391
HAUS3//POLN	392
PPARGC1A	393
TLR10	394
C4orf34	395
TXK	396
RPL21P44	397
KDR	398
RCHY1	399
CNOT6L	400
PLAC8	401
HPSE	402

GPRIN3	403
PPA2	404
COL25A1	405
C4orf3	406
QRFPR	407
MFSD8	408
MAP9	409
PDGFC	410
TKTL2	411
ACSL1	412
SUB1//TMEM183A	413
CARD6	414
MCCC2	415
TNPO1	416
PDE8B	417
PAPD4	418
THBS4	419
FAM151B	420
RASGRF2	421
SNX2	422
LMNB1//PCIF1	423
MEGF10	424
LEAP2	425
TCF7	426
KDM3B	427
CXXC5	428
SLC4A9	429
ANKHD1-EIF4EBP3//ANKHD1//EIF4EBP3	430
KIAA0141	431

GRPEL2	432
MFAP3	433
GABRA6	434
GABRA1	435
DOCK2	436
RANBP17//USP12	437
ERGIC1	438
ATP6V0E1//SNORA74B	439
ZNF346	440
NSD1	441
CLPTM1L	442
UGT3A1	443
GDNF	444
TTC33	445
hCG_2039148	446
MOCS2	447
SLC38A9	448
CCDC125	449
ANKRA2	450
HAPLN1	451
CCNH	452
TMEM161B	453
MBLAC2	454
MCTP1	455
TICAM2//TMED7//TMED7-TICAM2	456
KIF3A	457
C5orf15	458
SKP1	459
CXCL14	460

KLHL3	461
CD14	462
YIPF5	463
LARS	464
DCTN4	465
CCDC69	466
ATOX1	467
TIMD4	468
ADAM19	469
SLIT3	470
RNF44	471
DOK3	472
MGAT4B//SQSTM1	473
C5orf45//SQSTM1	474
RASGEF1C	475
MGAT1	476
IRF4	477
HIVEP1	478
E2F3	479
HIST1H4I	480
HIST1H2BM	481
MOG	482
ZNRD1//NCRNA00171	483
TRIM15	484
HCG27	485
BAT2//SNORA38	486
CYP21A2	487
ITPR3	488
MAPK14	489

MAPK13	490
PNPLA1	491
SFRS3	492
CDKN1A	493
FOXP4	494
CUL9	495
RUNX2	496
ZNF451	497
SOBP	498
C6orf182	499
KIAA1919	500
RWDD1	501
KPNA5	502
TPD52L1	503
ARG1	504
RAB32	505
ARID1B	506
SLC22A3	507
SERPINB1	508
C6orf146	509
GCM2	510
ATXN1	511
DCDC2//KAAG1	512
HIST1H3I	513
HIST1H4L	514
GABBR1	515
RNA243	516
DDAH2	517
CLIC1	518
NEU1	519

RXRB	520
VPS52	521
TCP11	522
CLPS	523
PGC	524
ZNF318	525
YIPF3	526
MRPL14	527
PLA2G7	528
PKHD1	529
IL17F	530
HTR1B	531
GABRR2	532
UBE2J1	533
BACH2	534
MCM9	535
VNN1	536
IL20RA	537
FLJ27255	538
T	539
RPS6KA2	540
HGC6.3	541
UNC84A//C7orf20	542
SDK1	543
ZDHHC4	544
C7orf26	545
GLCCI1//tcag7.903	546
GPNMB	547
CCDC126	548
WIPF3//ZNRF2//LO	549

C441208	
GPR141	550
STARD3NL	551
POU6F2	552
CDC2L5	553
ZMIZ2	554
UPP1	555
ZNF273	556
KCTD7//RABGEF1	557
RABGEF1//tcag7.967//tcag7.951//KCTD7//LOC100293333	558
CCDC132	559
PVRIG//PILRB//STAG3	560
PILRB//PVRIG//STAG3	561
C7orf51	562
GNB2	563
LRRC17	564
LRRN3	565
CFTR	566
LSM8	567
LUC7L2	568
MGAM//LOC100124692	569
GIMAP7	570
INSIG1	571
RBM33	572
ICA1	573
FAM126A	574
HIBADH	575

TRIL	576
SCRN1	577
ELMO1	578
INHBA	579
CAMK2B	580
NPC1L1	581
DDC//LOC100129427	582
NSUN5//NSUN5B//NSUN5C	583
CLDN3	584
C7orf23//DMTF1	585
SRI	586
BET1	587
MCM7	588
GATS	589
ATXN7L1//RINT1//EFCAB10	590
KIAA1549	591
SLC37A3	592
SMARCD3	593
MLL3//BAGE2	594
CLN8	595
MSRA	596
PIWIL2	597
NEFM//LOC100129717	598
EPHX2	599
LEPROTL1	600
MAK16//C8orf41	601
AP3M2	602
FNTA	603

SGK196	604
UBE2V2	605
FLJ46365	606
SNTG1	607
TRIM55	608
C8orf45	609
PREX2	610
PLEKHF2	611
BAALC//FLJ10489	612
TTC35	613
MTBP	614
ZHX2	615
RNF139	616
TG	617
DENND3//C8orf60	618
TNFRSF10D	619
TRIM35	620
GSR	621
WHSC1L1	622
PCMTD1//PXDNL	623
NCOA2	624
TRAM1//LOC286190	625
RUNX1T1	626
EXT1	627
DDEF1IT1	628
CDC37L1	629
UBE2R2	630
UBAP1//KIF24	631
GALT	632

RGP1//GBA2	633
TGFBR1	634
C9orf6//IKBKAP	635
IMAGE5303689	636
ATP6V1G1	637
TLR4	638
SET	639
MRPL41	640
C9orf68	641
HAUS6//SCARNA8	642
KLHL9	643
C9orf82	644
NDUFB6//DFFB	645
SIT1	646
FAM108B1	647
TRPM6	648
FRMD3	649
SLC28A3	650
BICD2	651
C9orf84	652
AKNA	653
MEGF9	654
C5	655
GOLGA1//SCAI	656
SH2D3C	657
FAM102A	658
FLJ10232	659
ASB6	660
BAT2L	661
EDF1	662

FBXW5	663
C10orf18	664
FBXO18	665
GATA3	666
CUGBP2	667
VIM	668
STAM	669
WAC	670
BAMBI	671
ZNF487//LOC439911	672
ALOX5	673
WDFY4	674
SRGN	675
CCDC109A	676
FAM149B1//FAM149B2	677
MINPP1	678
PTEN//PTENP1	679
ENTPD1//C10orf131	680
ABCC2	681
SFXN2	682
SHOC2	683
ACSL5	684
BCCIP//DHX32	685
FAM188A	686
CUBN	687
SVIL//hCG_1783494	688
FAM13C//PHYHIPL	689
ATAD1	690

ANKRD22	691
FLJ34077	692
COX15	693
ERLIN1	694
ACTR1A	695
ABLIM1	696
RAB11FIP2	697
C10orf84	698
PRDX3	699
C10orf119	700
NSMCE4A	701
TALDO1//INTS8	702
TNNT3	703
FXC1	704
PDE3B	705
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IMP3	1007

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UPRT	1592
CXorf26	1593
ATP7A	1594
DIAPH2	1595
CSTF2//RAD21	1596
ARMCX3	1597
ARMCX5	1598
GPRASP1	1599
TMEM31	1600

TBC1D8B	1601
MID2	1602
DOCK11	1603
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UBE2A	1605
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OCRL	1607
SLC25A14	1608
HPRT1	1609
CD40LG	1610
AFF2	1611
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FAM50A	1613
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/SNORA56	
ARSD	1615
KAL1	1616
CTPS2	1617
RPS6KA3	1618
BCOR	1619
MAOB//NAT13	1620
ZNF41	1621
OTUD5	1622
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ZMYM3	1624
MAGT1	1625
BRWD3	1626
TRMT2B	1627
GLA	1628
MORF4L2	1629
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ACSL4	1631
LAMP2	1632
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ODZ1	1634
ELF4	1635
RAP2C	1636
FAM127B//FAM127C//FAM127A	1637
TMEM185A	1638
ARD1A	1639
IRAK1	1640
DNASE1L1//RPL10	1641
SH3KBP1	1642
Mitochondrial1	1643
Mitochondrial2	1644
CCNL2	1645
INPP5B	1646
TLR5	1647
ADRB3//GOT1L1	1648
NOC2L//SAMD11//LOC401010	1649
SHFM1	1650

[§] HUGO Gene Nomenclature Committee

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TABLE 2

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MAN1C1	1663
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DHDDS	1665
HCRTR1	1666
CCDC28B	1667
LCK	1668
ZNF362	1669
THRAP3	1670
PPIE//CCDC25	1671
CAP1	1672
CTPS	1673
C1orf84	1674
FAAH	1675
DMBX1	1676
CYP4B1	1677
BTF3L4	1678
LRRC42	1679
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TMEM61	1681
FPGT//TNNI3K	1682
ACADM	1683
SPATA1	1684
EPHX4	1685
RPAP2	1686
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CELSR2	1691
AHCYL1	1692
CEPT1//DRAM2	1693
CHIA	1694
LIX1L	1695
UPF0627	1696
MRPS21	1697
TNFAIP8L2	1698
SMCP	1699
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CD1E	1705
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POU2F1	1707
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SMG7	1711
OCLM	1712
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ZC3H11A//RP11-74E24.2	1714
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ARF1	1719
GALNT2	1720
TNFRSF4	1721
NADK	1722
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SDHB	1727
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TRIM62	1734
PHC2	1735
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MRPS15	1737
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COL9A2	1739
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S100A8	1772
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RIT1	1781

MEF2D	1782
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MXD1	1839
NAGK	1840
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GTDC1	1927
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ARL4C	1941
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HDLBP	1943
LRRN1	1944
SETD5	1945
IRAK2	1946
C3orf42	1947
TSEN2	1948
NR2C2//MRPS25	1949
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C3orf35	1951
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ALAS1	1955
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GYG1	1966
SELT	1967
MED12L	1968
RAP2B	1969
MYNN	1970
ABCF3	1971
VPS8	1972
HRG	1973
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TIMP4	1980
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SCN10A	1984
SEC22C	1985
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UQCRC1	1989
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IMPDH2	1991
CCDC71	1992
UBA7	1993
CAMKV	1994
WDR82	1995
LMOD3	1996
FOXP1	1997
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KPNA1	2002
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ENAM	2025
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TMEM184C	2033

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GRIA2	2035
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F11	2039
SLBP	2040
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TLR10	2043
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KDR	2046
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PPA2	2052
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C4orf3	2054
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CARD6	2062
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SNX2	2070
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LEAP2	2073
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GABRA6	2082
GABRA1	2083
DOCK2	2084
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ERGIC1	2086
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ZNF346	2087

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GDNF	2091
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SLC38A9	2094
CCDC125	2095
ANKRA2	2096
HAPLN1	2097
CCNH	2098
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KIF3A	2103
C5orf15	2104
SKP1	2105
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CD14	2108
YIPF5	2109
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DCTN4	2111
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ATOX1	2113
TIMD4	2114

ADAM19	2115
SLIT3	2116
RNF44	2117
DOK3	2118
MGAT4B//SQSTM1	2119
C5orf45//SQSTM1	2120
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MGAT1	2122
IRF4	2123
HIVEP1	2124
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MAPK13	2136
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CUL9	2141
RUNX2	2142

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SOBP	2144
C6orf182	2145
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KPNA5	2148
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ARG1	2150
RAB32	2151
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SLC22A3	2153
SERPINB1	2154
C6orf146	2155
GCM2	2156
ATXN1	2157
DCDC2//KAAG1	2158
HIST1H3I	2159
HIST1H4L	2160
GABBR1	2161
RNA243	
DDAH2	2162
CLIC1	2163
NEU1	2164
RXRB	2165
VPS52	2166
TCP11	2167
CLPS	2168
PGC	2169
ZNF318	2170

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MRPL14	2172
PLA2G7	2173
PKHD1	2174
IL17F	2175
HTR1B	2176
GABRR2	2177
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BACH2	2179
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T	2184
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HGC6.3	2186
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SDK1	2188
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GPNMB	2192
CCDC126	2193
WIPF3//ZNRF2//LOC441208	2194
GPR141	2195
STARD3NL	2196
POU6F2	2197
CDC2L5	2198

ZMIZ2	2199
UPP1	2200
ZNF273	2201
KCTD7//RABGEF1	2202
RABGEF1//tcag7.967//tcag7.951//KCTD7//LOC100293333	2203
CCDC132	2204
PVRIG//PILRB//STAG3	2205
PILRB//PVRIG//STAG3	2206
C7orf51	2207
GNB2	2208
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LRRN3	2210
CFTR	2211
LSM8	2212
LUC7L2	2213
MGAM//LOC100124692	2214
GIMAP7	2215
INSIG1	2216
RBM33	2217
ICA1	2218
FAM126A	2219
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TRIL	2221
SCRN1	2222
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CAMK2B	2225
NPC1L1	2226
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NSUN5//NSUN5B//NSUN5C	2228
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MCM7	2233
GATS	2234
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KIAA1549	2236
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SMARCD3	2238
MLL3//BAGE2	2239
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PIWIL2	2242
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EPHX2	2244
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MAK16//C8orf41	2246
AP3M2	2247
FNTA	2248
SGK196	2249
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SNTG1	2251
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C8orf45	2253
PREX2	2254
PLEKHF2	2255
BAALC//FLJ10489	2256
TTC35	2257
MTBP	2258
ZHX2	2259
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TG	2261
DENND3//C8orf60	2262
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TRIM35	2264
GSR	2265
WHSC1L1	2266
PCMTD1//PXDNL	2267
NCOA2	2268
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EXT1	2271
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GALT	2276
RGP1//GBA2	2277

TGFBR1	2278
C9orf6//IKBKAP	2279
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C9orf68	2284
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KLHL9	2286
C9orf82	2287
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AKNA	2296
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BAT2L	2303
EDF1	2304

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FBXO18	2307
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BAMBI	2313
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ENTPD1//C10orf131	2322
ABCC2	2323
SFXN2	2324
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ACSL5	2326
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FAM188A	2328
CUBN	2329
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TNNT3	2344
FXC1	2345
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DNAJC24	2347
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CD6	2351
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TMEM138	2353
POLR2G	2354
TMEM179B	2355
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AIP	2359

PPFIA1	2360
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TRAPPC4	2370
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STT3A	2373
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TRIM21	2375
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SAAL1	2377
FANCF	2378
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EIF1AD	2387
GAB2	2388

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MPZL2	2395
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SIAE	2397
ZBTB44	2398
HSN2	2399
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Mitochondrial	N/A
Mitochondrial	N/A
CCNL2	3279
INPP5B	3280
TLR5	3281

ADRB3//GOT1L1	3282

NOC2L//SAMD11//	3283

LOC401010	

SHFM1	3284

§ HUGO Gene Nomenclature Committee

¶ Synonymous with SPNS1//NPIPL2//LOC728741//LOC730153//NPIPL3//SPIN1//LOC728888//LOC100289169//LOC728734//LOC729602//LOC100288442//LOC100288332

* Synonymous with SNURF//IPW//SNORD116-16//SNORD116-18//SNORD116-21//SNORD116-22//SNORD116-17//SNORD116-19//PAR5//PAR-SN//SNORD116-2//SNORD116-25//SNORD116-26//SNORD107//SNORD115-12//SNORD115-5//SNORD115-6//SNORD115-9//SNORD116-11//SNORD116-12//SNORD116-13//SNORD116-28//SNORD116-4//SNORD64//PAR1//SNORD109A//SNORD109B//SNORD116-6//SNORD116-3//SNORD116-9//SNORD115-13//SNORD115-1//SNORD115-14//SNORD115-15//SNORD115-21//SNORD115-10//SNORD115-7//SNORD115-16//SNORD115-40//SNORD115-42//SNORD115-11//SNORD115-29//SNORD115-34//SNORD115-36//SNORD115-4//SNORD115-43//HBII-52-24//SNORD116-5//SNORD116-7//SNORD115-26//SNORD115-30//SNORD116-15//SNORD116-8//SNORD115-2//SNORD115-39//SNORD116-14//SNORD116-20//SNORD115-8//SNORD115-3//SNORD115-38//SNORD115-41//SNORD115-22//SNORD115-44//SNORD116-1//SNORD115-17//SNORD115-18//SNORD115-19//SNORD115-20//SNORD116@

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the method including:
   a) determining a pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;
   b) determining a derived biomarker value using the pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and,
   c) determining the indicator using the derived biomarker value.
2. A method according to claim 1, wherein the method includes:
   a) determining a first derived biomarker value using a first pair of biomarker values, the first derived biomarker value being indicative of a ratio of concentrations of first and second immune system biomarkers;
   b) determining a second derived biomarker value using a second pair of biomarker values, the second derived biomarker value being indicative of a ratio of concentrations of third and fourth immune system biomarkers; and,
   c) determining the indicator by combining the first and second derived biomarker values.
3. A method according to claim 2, wherein the method includes combining the derived biomarker values using a combining function, the combining function being at least one of:
   a) an additive model;
   b) a linear model;
   c) a support vector machine;
   d) a neural network model;
   e) a random forest model;
   f) a regression model;
   g) a genetic algorithm;

h) an annealing algorithm;

i) a weighted sum;

j) a nearest neighbor model; and,

k) a probabilistic model.

4. A method according to any one of the claims 1 to 3, wherein the method is performed at least in part using an electronic processing device.

5. A method according to any one of the claims 1 to 4, wherein the method includes, in at least one electronic processing device:

a) obtaining the pairs of biomarker values;

b) determining the first derived biomarker value;

c) determining the second derived biomarker value; and,

d) determining the indicator by adding the first and second derived biomarker values.

6. A method according to any one of the claims 1 to 5, wherein the method includes, in at least one processing device, generating a representation of the indicator.

7. A method according to claim 6, wherein the representation includes:

a) an alphanumeric indication of the indicator;

b) a graphical indication of a comparison of the indicator to one or more indicator references;

c) an alphanumeric indication of a likelihood of the subject having at least one medical condition.

8. A method according to any one of the claims 1 to 7, wherein the method includes:

a) comparing the indicator to an indicator reference; and,

b) determining a likelihood in accordance with results of the comparison.

9. A method according to claim 8, wherein the indicator reference is based on at least one of:

a) an indicator threshold range;

b) an indicator threshold; and,

c) an indicator distribution.

10. A method according to claim 8 or claim 9, wherein the indicator reference is derived from indicators determined for a number of individuals in a reference population.

11. A method according to claim 10, wherein the indicator reference is based on a distribution of indicators determined for a group of a reference population, the group consisting of individuals diagnosed as having the medical condition or lacking the medical condition.

12. A method according to claim 10 or claim 11, wherein the reference population includes:
    a) a plurality of individuals of different sexes;
    b) a plurality of individuals of different ethnicities;
    c) a plurality of healthy individuals;
    d) a plurality of individuals suffering from at least one diagnosed medical condition;
    e) a plurality of individuals lacking the at least one diagnosed medical condition;
    f) a plurality of individuals showing clinical signs of at least one medical condition;
    g) first and second groups of individuals, each group of individuals suffering from a respective diagnosed medical condition; and,
    h) first and second groups of individuals, the first group of individuals suffering from a diagnosed medical condition, and the second group lacking the diagnosed medical condition.
13. A method according to any one of the claims 10 to 12, wherein the indicator is for use in determining the likelihood that a biological subject has at least one medical condition, and wherein the reference population includes:
    a) individuals presenting with clinical signs of the at least one medical condition;
    b) individuals diagnosed as having the at least one medical condition;
    c) individuals diagnosed as lacking the at least one medical condition; and,
    d) healthy individuals.
14. A method according to any one of the claims 8 to 13, wherein the indicator reference is retrieved from a database.
15. A method according to any one of the claims 8 to 14, wherein the likelihood is based on a probability generated using the results of the comparison.
16. A method according any one of the claims 8 to 15, wherein the indicator is for determining a likelihood of the subject having a first or second condition, and wherein the method includes:
    a) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of first and second conditions; and,
    b) determining the likelihood in accordance with the results of the comparison.
17. A method according to claim 16, wherein the method includes:
    a) determining first and second indicator probabilities using the results of the comparisons; and,

b) combining the first and second indicator probabilities to determine a condition probability indicative of the likelihood.

18. A method according to claim 16 or claim 17, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with the first or second condition respectively.

19. A method according to any one of the claims 1 to 18, wherein the method includes:

a) obtaining a sample taken from the biological subject, the sample including polynucleotide expression products; and,

b) quantifying at least some of the polynucleotide expression products within the sample to determine the pair of biomarker values.

20. A method according to claim 19, wherein the method includes, determining the indicator at least in part using a ratio of concentrations of the polynucleotide expression products.

21. A method according to claim 19 or claim 20, wherein the method includes:

a) quantifying polynucleotide expression products by:

i) amplifying at least some polynucleotide expression products in the sample; and,

ii) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products; and,

b) determining the indicator by determining a difference between the amplification amounts.

22. A method according to claim 21, wherein the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

23. A method according to claim 21 or claim 22, wherein the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of a first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of a second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

24. A method according to any one of the claims 1 to 23, wherein the immune system biomarker is a biomarker of an immune system of the biological subject that is altered, or whose level of expression is altered, as part of an inflammatory response to damage or pathogenic insult.

25. A method according to any one of the claims 1 to 24, wherein:

a) the at least two immune system biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

b) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

26. A method according to claim 25, wherein the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

27. A method according to claim 25 or claim 26, wherein each immune system biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

28. A method according to claim 27, wherein the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

29. A method according to any one of the claims 25 to 28, wherein the performance threshold is indicative of an explained variance of at least one of:
    a) 0.4;
    b) 0.5;
    c) 0.6;
    d) 0.7;
    e) 0.8; and,
    f) 0.9.
30. A method according to any one of the claims 1 to 29, wherein the immune system biomarker value is indicative of a level or abundance of a molecule selected from one or more of a nucleic acid molecule and a proteinaceous molecule.
31. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein the method includes:
    a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
    b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,
    c) determining the indicator using the first and second pairs of biomarker values.
32. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having inSIRS or a healthy condition, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:
    a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS immune system biomarker genes as herein defined; and
    b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group B IRS immune system biomarker genes as herein defined.
33. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having ipSIRS or a healthy condition, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS immune system biomarker genes as herein defined.

34. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS immune system biomarker genes as herein defined.

35. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one immune system biomarker in each of first, second, third and fourth IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS immune system biomarker genes as herein defined;

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS immune system biomarker genes as herein defined;

c) the third IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS immune system biomarker genes as herein defined; and,

d) the fourth IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS immune system biomarker genes as herein defined.

36. A method according to claim 35, wherein the first IRS immune system biomarker is a *PLA2G7* expression product, wherein the second IRS immune system biomarker is a *PLAC8* expression product, wherein the third IRS immune system biomarker is a *CEACAM4* expression product and wherein the fourth IRS immune system biomarker is a *LAMP1* expression product.

37. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having mild sepsis or severe sepsis, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:
    a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS immune system biomarker genes as herein defined; and,
    b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS immune system biomarker genes as herein defined.

38. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having mild sepsis or septic shock, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:
    a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS immune system biomarker genes as herein defined; and,
    b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS immune system biomarker genes as herein defined.

39. A method according to any one of the claims 1 to 30, wherein the indicator is for determining a likelihood of the subject having severe sepsis or septic shock, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:
    a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS immune system biomarker genes as herein defined.

40. Apparatus for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the apparatus including at least one electronic processing device that:

a) determines a pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determines a derived biomarker value using the pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and,

c) determines the indicator using the derived biomarker value.

41. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a first pair and a second pair of reverse transcribed mRNAs, wherein the first pair comprises a *PLAC8* reverse transcribed mRNA and a *PLA2G7* reverse transcribed mRNA and wherein the second pair comprises a *CEACAM4* reverse transcribed mRNA and a *LAMP1* reverse transcribed mRNA.

42. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group A IRS immune system biomarker genes as herein defined; and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group B IRS immune system biomarker genes as herein defined.

43. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group C IRS immune system biomarker genes as herein defined; and a reverse transcribed

mRNA from a second IRS immune system biomarker gene selected from group D IRS immune system biomarker genes as herein defined.

44. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group E IRS immune system biomarker genes as herein defined; and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group F IRS immune system biomarker genes as herein defined.

45. A composition comprising at least two pairs of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least two pairs of reverse transcribed mRNAs comprising a first pair and a second pair of reverse transcribed mRNAs, wherein the first pair comprises a reverse transcribed mRNA from a first IRS immune system biomarker gene and a reverse transcribed mRNA from a second IRS immune system biomarker gene, and wherein the second pair comprises a reverse transcribed mRNA from a third IRS immune system biomarker gene and a reverse transcribed mRNA from a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes as herein defined, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes as herein defined, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes as herein defined, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes as herein defined.

46. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group K IRS immune system biomarker genes as herein defined; and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group L IRS immune system biomarker genes as herein defined.

47. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse

transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group M IRS immune system biomarker genes as herein defined; and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group N IRS immune system biomarker genes as herein defined.

48. A composition comprising at least one pair of reverse transcribed mRNAs and at least one oligonucleotide primer or probe that hybridizes to an individual one of the reverse transcribed mRNAs, the at least one pair of reverse transcribed mRNAs comprising a reverse transcribed mRNA from a first IRS immune system biomarker gene selected from group O IRS immune system biomarker genes as herein defined; and a reverse transcribed mRNA from a second IRS immune system biomarker gene selected from group P IRS immune system biomarker genes as herein defined.
49. A composition according to any one of the claims 41 to 48, wherein the at least one oligonucleotide primer or probe is hybridized to an individual one of the reverse transcribed mRNAs.
50. A composition according to any one of the claims 41 to 48, wherein the reverse transcribed mRNAs are derived from components of the immune system.
51. A composition according to any one of the claims 41 to 48, wherein the reverse transcribed mRNAs are derived from leukocytes.
52. A composition according to any one of the claims 41 to 48, wherein the reverse transcribed mRNAs are derived from blood cells.
53. A composition according to any one of the claims 41 to 48, wherein the reverse transcribed mRNAs are derived from peripheral blood cells.
54. A composition according to any one of the claims 41 to 48, further comprising a labeled reagent for detecting the reverse transcribed mRNAs.
55. A composition according to claim 54, wherein the labeled reagent is a labeled said at least one oligonucleotide primer or probe.
56. A composition according to claim 54, wherein the labeled reagent is a labeled said reverse transcribed mRNA.
57. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least one pair of reagents comprising a first pair of reagents and a second pair of reagents, wherein the first pair of reagents comprises (i) a reagent that allows

quantification of a polynucleotide expression product of the *PLA2G7* gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of the *PLAC8* gene, wherein the second pair of reagents comprises: (iii) a reagent that allows quantification of a polynucleotide expression product of the *CEACAM4* gene; and (iv) a reagent that allows quantification of a polynucleotide expression product of the *LAMP1* gene.

58. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and a healthy condition, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes as herein defined.

59. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of ipSIRS and a healthy condition, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes as herein defined.

60. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes as herein defined.

61. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of inSIRS and ipSIRS, the kit comprising at least two pairs of reagents comprising a first pair of reagents and a second pair of reagents, wherein the first pair of reagents comprises (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, and wherein the second pair of reagents comprises (i) a reagent that allows quantification of a polynucleotide expression product of a third IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes as herein defined, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes as herein defined, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes as herein defined, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes as herein defined.
62. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of mild sepsis and severe sepsis, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes as herein defined.
63. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of mild sepsis and septic shock, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker

genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes as herein defined.

64. A kit for determining an indicator indicative of the likelihood of the presence or absence of at least one condition selected from the group consisting of severe sepsis and septic shock, the kit comprising at least one pair of reagents comprising (i) a reagent that allows quantification of a polynucleotide expression product of a first IRS immune system biomarker gene; and (ii) a reagent that allows quantification of a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes as herein defined.

65. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the pair of biomarker values comprises at least one of:

a) a first pair of biomarker values comprising first and second biomarker values corresponding to first and second biomarkers, wherein the first immune system biomarker represents a polynucleotide expression product of the *PLA2G7* gene and wherein the second immune system biomarker representing a polynucleotide expression product of the *PLAC8* gene, and

b) a second pair of biomarker values comprises third and fourth biomarker values corresponding to third and fourth immune system biomarkers, respectively, wherein the third immune system biomarker represents a polynucleotide expression product of

the *CEACAM4* gene and wherein the fourth immune system biomarker represents a polynucleotide expression product of the *LAMP1* gene.

66. A method according to claim 65, wherein the indicator-determining method comprises: determining the first pair and second pair of biomarker values and determining a first derived biomarker value calculated using the first pair of biomarker values and a second derived biomarker value calculated using the second pair of biomarker values; and determining the indicator based on a combination of the first and second derived biomarker values.

67. A method for inhibiting the development or progression of inSIRS in a subject, the method comprising: exposing the subject to a treatment regimen for treating inSIRS based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of inSIRS in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes as herein defined; and wherein the second IRS immune system biomarker is selected from group B IRS immune system biomarker genes as herein defined.

68. A method for inhibiting the development or progression of ipSIRS in a subject, the method comprising: exposing the subject to a treatment regimen for treating ipSIRS based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of ipSIRS in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value

being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes as herein defined; and wherein the second IRS immune system biomarker is selected from group D IRS immune system biomarker genes as herein defined.

69. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to of first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene,

wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes as herein defined; and wherein the second IRS immune system biomarker is selected from group F IRS immune system biomarker genes as herein defined.

70. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of inSIRS and ipSIRS, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least two pairs of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least two derived biomarker values using the at least two pairs of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of each pair of immune system biomarkers; and (c) determining the indicator based on the at least two derived biomarker values, wherein the at least one pair of biomarker values comprises a first pair of biomarker values comprising first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, and a second pair of biomarker values comprising third and fourth biomarker values corresponding to third and fourth immune system biomarkers, respectively, wherein the third immune system biomarker represents a polynucleotide expression product of a third IRS immune system biomarker gene and wherein the fourth immune system biomarker represents a polynucleotide expression product of a fourth IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes as herein defined, wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes as herein defined, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker

genes as herein defined, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes as herein defined.

71. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of mild sepsis and severe sepsis, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes as herein defined; and wherein the second IRS immune system biomarker is selected from group L IRS immune system biomarker genes as herein defined.

72. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of mild sepsis and septic shock, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken

from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes as herein defined; and wherein the second IRS immune system biomarker is selected from group N IRS immune system biomarker genes as herein defined.

73. A method for inhibiting the development or progression in a subject of at least one condition selected from the group consisting of severe sepsis and septic shock, the method comprising: exposing the subject to a treatment regimen for treating the at least one condition based on an indicator obtained from an indicator-determining method, wherein the indicator is indicative of the presence of the at least one condition in the subject, the indicator-determining method comprising: (a) determining at least one pair of biomarker values, each biomarker value being a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject, (b) determining at least one derived biomarker value using the at least one pair of biomarker values, the derived biomarker value being indicative of a ratio of concentrations of the at least one pair of immune system biomarkers; and (c) determining the indicator based on the at least one derived biomarker value, wherein the at least one pair of biomarker values comprises first and second biomarker values corresponding to first and second immune system biomarkers, respectively, wherein the first immune system biomarker represents a polynucleotide expression product of a first IRS immune system biomarker gene, and wherein the second immune system biomarker represents a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes as herein defined; and wherein the second IRS immune

system biomarker is selected from group P IRS immune system biomarker genes as herein defined.

74. A method according to any one of claims 65 to 73, comprising: taking the sample from the subject and obtaining the indicator according to the indicator-determining method.

75. A method according to any one of claims 65 to 73, comprising: sending the sample taken from the subject to a laboratory at which the indicator is determined.

76. A method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

77. A method for differentiating between inSIRS and a healthy condition in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker

genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and healthy condition, respectively; and,

e) determining a likelihood of the subject having inSIRS or the healthy condition in accordance with the results of the comparison.

78. A method for differentiating between ipSIRS and a healthy condition in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes as herein defined and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of ipSIRS and healthy condition, respectively; and,

e) determining a likelihood of the subject having ipSIRS or the healthy condition in accordance with the results of the comparison.

79. A method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration

of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

80. A method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes as herein defined;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of a third IRS immune system biomarker gene and a fourth IRS immune system biomarker gene, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes as herein defined, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of inSIRS and ipSIRS, respectively; and,

e) determining a likelihood of the subject having inSIRS or ipSIRS in accordance with the results of the comparison.

81. A method for differentiating between mild sepsis and severe sepsis in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of mild sepsis and severe sepsis, respectively; and,

e) determining a likelihood of the subject having mild sepsis or severe sepsis in accordance with the results of the comparison.

82. A method for differentiating between mild sepsis and septic shock in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of mild sepsis and septic shock, respectively; and,

e) determining a likelihood of the subject having mild sepsis or septic shock in accordance with the results of the comparison.

83. A method for differentiating between severe sepsis and septic shock in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) quantifying polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being indicative of a concentration of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes as herein defined;

c) determining an indicator indicative of a ratio of concentrations of the polynucleotide expression products using the pair of biomarker values; and,

d) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of severe sepsis and septic shock, respectively; and,

e) determining a likelihood of the subject having severe sepsis or septic shock in accordance with the results of the comparison.

84. A method according to claim 76 or claim 80, wherein the method includes:

a) determining a first derived biomarker using the first pair of biomarker values;

b) determining a second derived biomarker value using the second pair of biomarker values; and,

c) determining the indicator by combining the first and second derived biomarker values.

85. A method according to any one of claims 76 to 84, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a

reference population, the first and second group consisting of individuals diagnosed with inSIRS and ipSIRS respectively.

86. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:
    a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;
    b) amplifying at least some polynucleotide expression products in the sample;
    c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of:
        i) a first pair of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;
        ii) a second pair of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;
    d) determining the indicator by determining a difference between the amplification amounts; and,
    e) using the indicator to assess the likelihood of a biological subject having a medical condition.

87. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:
    a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;
    b) amplifying at least some polynucleotide expression products in the sample;
    c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group A IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group B IRS immune system biomarker genes as herein defined;
    d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

88. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group C IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group D IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

89. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group E IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group F IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

90. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of:

i) a first pair of polynucleotide expression products of a first IRS immune system biomarker gene and a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group G IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group H IRS immune system biomarker genes as herein defined;

ii) a second pair of polynucleotide expression products of a third IRS immune system biomarker gene and a fourth IRS immune system biomarker gene, wherein the third IRS immune system biomarker gene is selected from group I IRS immune system biomarker genes as herein defined, and wherein the fourth IRS immune system biomarker gene is selected from group J IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

91. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group K IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group L IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

92. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, , wherein the first IRS immune system biomarker gene is selected from group M IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group N IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

93. A method for determining an indicator used in assessing the likelihood of a biological subject having at least one medical condition, the method including:

a) obtaining a sample taken from a biological subject, the sample including polynucleotide expression products;

b) amplifying at least some polynucleotide expression products in the sample;

c) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products selected from the group consisting of: a polynucleotide expression product of a first IRS immune system biomarker gene and a polynucleotide expression product of a second IRS immune system biomarker gene, wherein the first IRS immune system biomarker gene is selected from group O IRS immune system biomarker genes as herein defined, and wherein the second IRS immune system biomarker gene is selected from group P IRS immune system biomarker genes as herein defined;

d) determining the indicator by determining a difference between the amplification amounts; and,

e) using the indicator to assess the likelihood of a biological subject having a medical condition.

94. A method according to any one of the claims 86 to 93, wherein the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of the first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of the second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

95. A method according to any one of the claims 86 to 94, wherein the method includes determining:

a) comparing the indicator to first and second indicator references, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, one of the first and second groups consisting of individuals diagnosed with the medical condition; and,

b) determining a likelihood of the subject having the medical condition in accordance with the results of the comparison.

96. A method according to any one of claims 76 to 95, wherein the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

97. A method for use in assessing the likelihood of a biological subject having a medical condition, the method including, in one or more processing devices:

a) determining a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

b) determining an indicator indicative of a ratio of the concentrations of the polynucleotide expression products using the pair of biomarker values;

c) retrieving previously determined first and second indicator references from a database, the first and second indicator references being determined based on indicators determined from first and second groups of a reference population, one of the groups consisting of individuals diagnosed with the medical condition;

d) comparing the indicator to the first and second indicator references;

e) using the results of the comparison to determine a probability indicative of the subject having the medical condition; and,

f) generating a representation of the probability, the representation being displayed to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

98. A method according to claim 97, wherein the method includes:

a) determining a first derived biomarker value using the first pair of biomarker values;

b) determining a second derived biomarker value using the second pair of biomarker values; and,

c) determining the indicator by combining the first and second derived biomarker values.

99. Apparatus for determining an indicator used in determining the likelihood of a biological subject having at least one medical condition, the apparatus including:

a) a sampling device that obtains a sample taken from a biological subject, the sample including polynucleotide expression products;

b) a measuring device that quantifies polynucleotide expression products within the sample to determine a pair of biomarker values, the pair of biomarker values being selected from the group consisting of:

i) a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

ii) a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) at least one processing device that:

i) receives an indication of the pair of biomarker values from the measuring device;

ii) determines an indicator using a ratio of the concentration of the first and second polynucleotide expression products using the biomarker values; and,

iii) compares the indicator to at least one indicator reference; and,

iv) determines a likelihood of the subject having the at least one medical condition using the results of the comparison; and,

v) generates a representation of the indicator and the likelihood for display to a user.

100. A method for differentiating between inSIRS and ipSIRS in a biological subject, the method including:

a) obtaining a sample taken from a biological subject showing a clinical sign of SIRS, the sample including polynucleotide expression products;

b) in a measuring device:

i) amplifying at least some polynucleotide expression products in the sample;

ii) determining an amplification amount representing a degree of amplification required to obtain a defined level of polynucleotide expression products including:

(1) amplification amounts for a first pair of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

(2) amplification amounts for a second pair of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene;

c) in a processing system:

i) retrieving the amplification amounts;

ii) determining an indicator by:

(1) determining a first derived biomarker value indicative of a ratio of concentrations of the first pair of polynucleotide expression products by determining a difference between the amplification amounts for the first pair;

(2) determining a second derived biomarker value indicative of a ratio of concentrations of the second pair of polynucleotide expression products by determining a difference between the amplification amounts for the second pair;

(3) determining the indicator by adding the first and second derived biomarker values;

iii) retrieving previously determined first and second indicator references from a database, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with inSIRS and ipSIRS respectively;

iv) comparing the indicator to the first and second indicator references;

v) using the results of the comparison to determine a probability of the subject being classified within the first or second group;

vi) generating a representation at least partially indicative of the indicator and the probability; and,

vii) providing the representation to a user to allow the user to assess the likelihood of a biological subject having at least one medical condition.

101. A method for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the method including:

a) determining a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determining the indicator using a combination of the plurality of biomarker values, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence,

absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

102. A method according to claim 101, wherein the method includes:

a) determining a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding biomarker of the biological subject; and,

b) determining the indicator by applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker.

103. A method according to claim 102, wherein the function includes at least one of:

a) multiplying two biomarker values;

b) dividing two biomarker values;

c) adding two biomarker values;

d) subtracting two biomarker values;

e) a ratio of two biomarker values;

f) a weighted sum of at least two biomarker values;

g) a log sum of at least two biomarker values; and,

h) a sigmoidal function of at least two biomarker values.

104. A method according to claim 102, wherein the method includes determining at least one derived biomarker value corresponding to a ratio of two measured biomarker values.

105. A method according to any one of the claims 101to 104, wherein the method includes combining at least two biomarker values to determine an indicator value representing the indicator.

106. A method according to claim 105, wherein the method includes combining at least two biomarker values using a combining function, the combining function being at least one of:

a) an additive model;

b) a linear model;

c) a support vector machine;

d) a neural network model;

e) a random forest model;

f) a regression model;

g) a genetic algorithm;

h) an annealing algorithm;

i) a weighted sum;

j) a nearest neighbor model; and,

k) a probabilistic model.

107. A method according to claim 105 or claim 106, wherein at least one of the at least two biomarkers is a derived biomarker.

108. A method according to any one of the claims 101 to 107, wherein the method includes:

a) determining a first derived biomarker value, the first derived biomarker value being indicative of a ratio of concentrations of the first and second immune system biomarkers;

b) determining a second derived biomarker value, the second derived biomarker value being indicative of a ratio of concentrations of the third and fourth measured immune system biomarkers; and,

c) adding the first and second derived biomarker values to generate an indicator value.

109. A method according to any one of the claims 101 to 108, wherein the method is performed at least in part using an electronic processing device.

110. A method according to any one of the claims 101 to 109, wherein the method includes, in the electronic processing device:

a) receiving a plurality of measured biomarker values, each measured biomarker value being a measured value of a corresponding immune system biomarker;

b) applying a function to at least one of the measured biomarker values to determine at least one derived biomarker value, the at least one derived biomarker value being indicative of a value of a corresponding derived biomarker; and,

c) combining at least one derived biomarker value and at least one other biomarker value to determine the indicator.

111. A method according to any one of the claims 101 to 110, wherein the mutual correlation range is at least one of:

a) ±0.8;

b) ±0.7;

c) ±0.6;

d) ±0.5;

e) ±0.4;

f) ±0.3;

g) ±0.2; and,

h) ±0.1.

112. A method according to any one of the claims 101 to 111, wherein each biomarker has a condition correlation with the presence, absence, degree or prognosis of the at least one condition that lies outside a condition correlation range, the condition correlation range being between ±0.3.

113. A method according to claim 112, wherein the condition correlation range is at least one of:

a) ±0.9;

b) ±0.8;

c) ±0.7;

d) ±0.6;

e) ±0.5; and,

f) ±0.4.

114. A method according to any one of the claims 101 to 113, wherein the performance threshold is indicative of an explained variance of at least one of:

a) 0.4;

b) 0.5;

c) 0.6;

d) 0.7;

e) 0.8; and,

f) 0.9.

115. A method according to any one of the claims 101 to 114, wherein the biomarker value is indicative of a level or abundance of a molecule selected from one or more of a nucleic acid molecule and a proteinaceous molecule.

116. A method according to any one of the claims 101 to 115, wherein the method includes generating a representation of the indicator.

117. A method according to claim 116, wherein the representation includes:

a) an alphanumeric indication of the indicator;

b) a graphical indication of a comparison of the indicator to one or more indicator references;

c) an alphanumeric indication of a likelihood of the subject having at least one medical condition.

118. A method according to any one of the claims 101 to 117, wherein the method includes:

a) comparing the indicator to an indicator reference; and,

b) determining a likelihood in accordance with results of the comparison.

119. A method according to claim 118, wherein the indicator reference is based on at least one of:

a) an indicator threshold range;

b) an indicator threshold; and,

c) an indicator distribution.

120. A method according to claim 118 or claim 119, wherein the indicator reference is derived from indicators determined for a number of individuals in a reference population.

121. A method according to claim 120, wherein the indicator reference is based on a distribution of indicators determined for a group of a reference population, the group consisting of individuals diagnosed as having the medical condition or lacking the medical condition.

122. A method according to claim 120 or claim 121, wherein the reference population includes:

a) a plurality of individuals of different sexes;

b) a plurality of individuals of different ethnicities;

c) a plurality of healthy individuals;

d) a plurality of individuals suffering from at least one diagnosed medical condition;

e) a plurality of individuals without the at least one diagnosed medical condition;

f) a plurality of individuals showing clinical signs of at least one medical condition;

g) first and second groups of individuals, each group of individuals suffering from a respective diagnosed medical condition; and,

h) first and second groups of individuals, the first group of individuals suffering from a diagnosed medical condition, and the second group not suffering the diagnosed medical condition.

123. A method according to any one of the claims 120 to 122, wherein the indicator is for use in determining the likelihood that a biological subject has at least one medical condition, and wherein the reference population includes:

a) individuals presenting with clinical signs of the at least one medical condition;

b) individuals diagnosed with the at least one medical condition;

c) individuals diagnosed without the at least one medical condition; and,

d) healthy individuals.

124. A method according to any one of the claims 118 to 123, wherein the indicator reference is retrieved from a database.

125. A method according to any one of the claims 118 to 124, wherein the likelihood is based on a probability generated using the results of the comparison.

126. A method according any one of the claims 118 to 125, wherein the indicator is for determining a likelihood of the subject having a first or second condition, and wherein the method includes:

a) comparing the indicator to first and second indicator references, the first and second indicator references being indicative of first and second conditions; and,

b) determining the likelihood in accordance with the results of the comparison.

127. A method according to claim 126, wherein the method includes:

a) determining first and second indicator probabilities using the results of the comparisons; and,

b) combining the first and second indicator probabilities to determine a condition probability indicative of the likelihood.

128. A method according to claim 126 or claim 127, wherein the first and second indicator references are distributions of indicators determined for first and second groups of a reference population, the first and second group consisting of individuals diagnosed with the first or second condition respectively.

129. A method according to any one of the claims 101 to 128, wherein the method includes:

a) obtaining a sample taken from the biological subject, the sample including polynucleotide expression products;

b) quantifying at least some of the polynucleotide expression products within the sample to determine at least a pair of biomarker values;

c) determining the indicator at least in part using the pair of biomarker values;

130. A method according to claim 129, wherein the method includes, determining the indicator at least in part using a ratio of concentrations of the polynucleotide expression products.

131. A method according to claim 129 or claim 130, wherein the method includes:

a) quantifying polynucleotide expression products by:

i) amplifying at least some polynucleotide expression products in the sample; and,

ii) determining an amplification amount representing a degree of amplification required to obtain a defined level of each of a pair of polynucleotide expression products; and,

b) determining the indicator by determining a difference between the amplification amounts.

132. A method according to claim 131, wherein the amplification amount is at least one of:

a) a cycle time;

b) a number of cycles;

c) a cycle threshold;

d) an amplification time; and,

e) relative to an amplification amount of another amplified product.

133. A method according to claim 131 or claim 132, wherein the method includes determining:

a) a first derived biomarker value by determining a difference between the amplification amounts of a first pair of polynucleotide expression products;

b) a second derived biomarker value by determining a difference between the amplification amounts of a second pair of polynucleotide expression products;

c) determining the indicator by adding the first and second derived biomarker values.

134. A method according to any one of the claims 101 to 133, wherein the immune system biomarker is a biomarker of an immune system of the biological subject that is altered, or whose level of expression is altered, as part of an inflammatory response to damage or pathogenic insult.

135. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having at least one of inSIRS and ipSIRS, and wherein the method includes:

a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,

c) determining the indicator using the first and second pairs of biomarker values.

136. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein the method includes:

a) determining a first pair of biomarker values indicative of a concentration of polynucleotide expression products of the *PLA2G7* gene and *PLAC8* gene;

b) determining a second pair of biomarker values indicative of a concentration of polynucleotide expression products of the *CEACAM4* gene and *LAMP1* gene; and,

c) determining the indicator using the first and second pairs of biomarker values.

137. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having inSIRS or a healthy condition, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group A IRS immune system biomarker genes as herein defined; and

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group B IRS immune system biomarker genes as herein defined as herein defined.

138. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having ipSIRS or a healthy condition, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group C IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group D IRS immune system biomarker genes as herein defined.

139. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group E IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group F IRS immune system biomarker genes as herein defined.

140. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having inSIRS or ipSIRS, and wherein biomarker values are determined from at least one immune system biomarker in each of first, second, third and fourth IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group G IRS immune system biomarker genes as herein defined;

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group H IRS immune system biomarker genes as herein defined;

c) the third IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group I IRS immune system biomarker genes as herein defined; and,

d) the fourth IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group J IRS immune system biomarker genes as herein defined.

141. A method according to claim 131, wherein the first IRS immune system biomarker is a *PLA2G7* expression product, wherein the second IRS immune system biomarker is a *PLAC8* expression product, wherein the third IRS immune system biomarker is a *CEACAM4* expression product and wherein the fourth IRS immune system biomarker is a *LAMP1* expression product.

142. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having mild sepsis or severe sepsis, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group K IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group L IRS immune system biomarker genes as herein defined.

143. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having mild sepsis or septic shock, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group M IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group N IRS immune system biomarker genes as herein defined.

144. A method according to any one of the claims 101 to 134, wherein the indicator is for determining a likelihood of the subject having severe sepsis or septic shock, and wherein biomarker values are determined from at least one immune system biomarker in each of first and second IRS immune system biomarker groups, wherein:

a) the first IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group O IRS immune system biomarker genes as herein defined; and,

b) the second IRS immune system biomarker group consists of polynucleotide and/or polypeptide expression products from group P IRS immune system biomarker genes as herein defined.

145. Apparatus for determining an indicator used in assessing a likelihood of a biological subject having a presence, absence, degree or prognosis of at least one medical condition, the apparatus including a processing device that:

a) determines a plurality of biomarker values, each biomarker value being indicative of a value measured or derived for at least one corresponding immune system biomarker of the biological subject and being at least partially indicative of a concentration of the immune system biomarker in a sample taken from the subject;

b) determines the indicator using a combination of the plurality of biomarker values, wherein:

i) at least two biomarkers have a mutual correlation in respect of the at least one condition that lies within a mutual correlation range, the mutual correlation range being between ±0.9; and,

ii) the indicator has a performance value greater than or equal to a performance threshold representing the ability of the indicator to diagnose the presence, absence, degree or prognosis of the at least one condition, the performance threshold being indicative of an explained variance of at least 0.3.

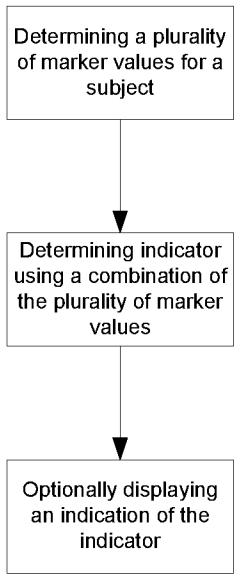

Determining a plurality of marker values for a subject
100
Determining indicator using a combination of the plurality of marker values
110
Optionally displaying an indication of the indicator
120

Fig. 1A

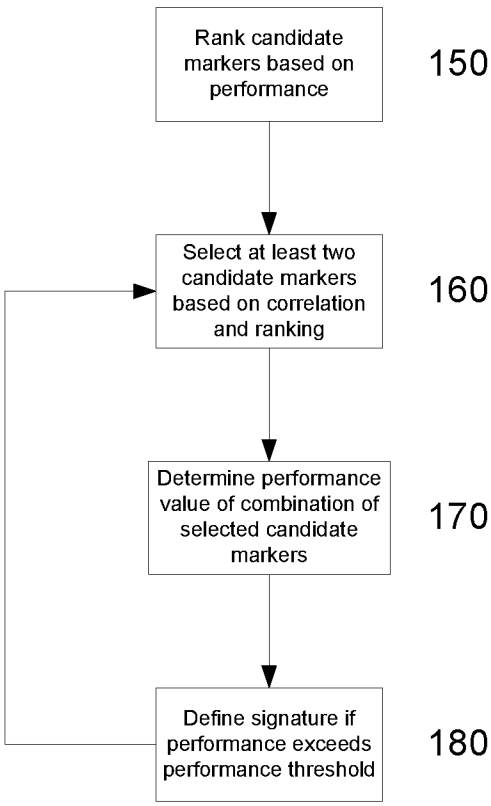

Rank candidate markers based on performance
150
Select at least two candidate markers based on correlation and ranking
160
Determine performance value of combination of selected candidate markers
170
Define signature if performance exceeds performance threshold
180

Fig. 1B

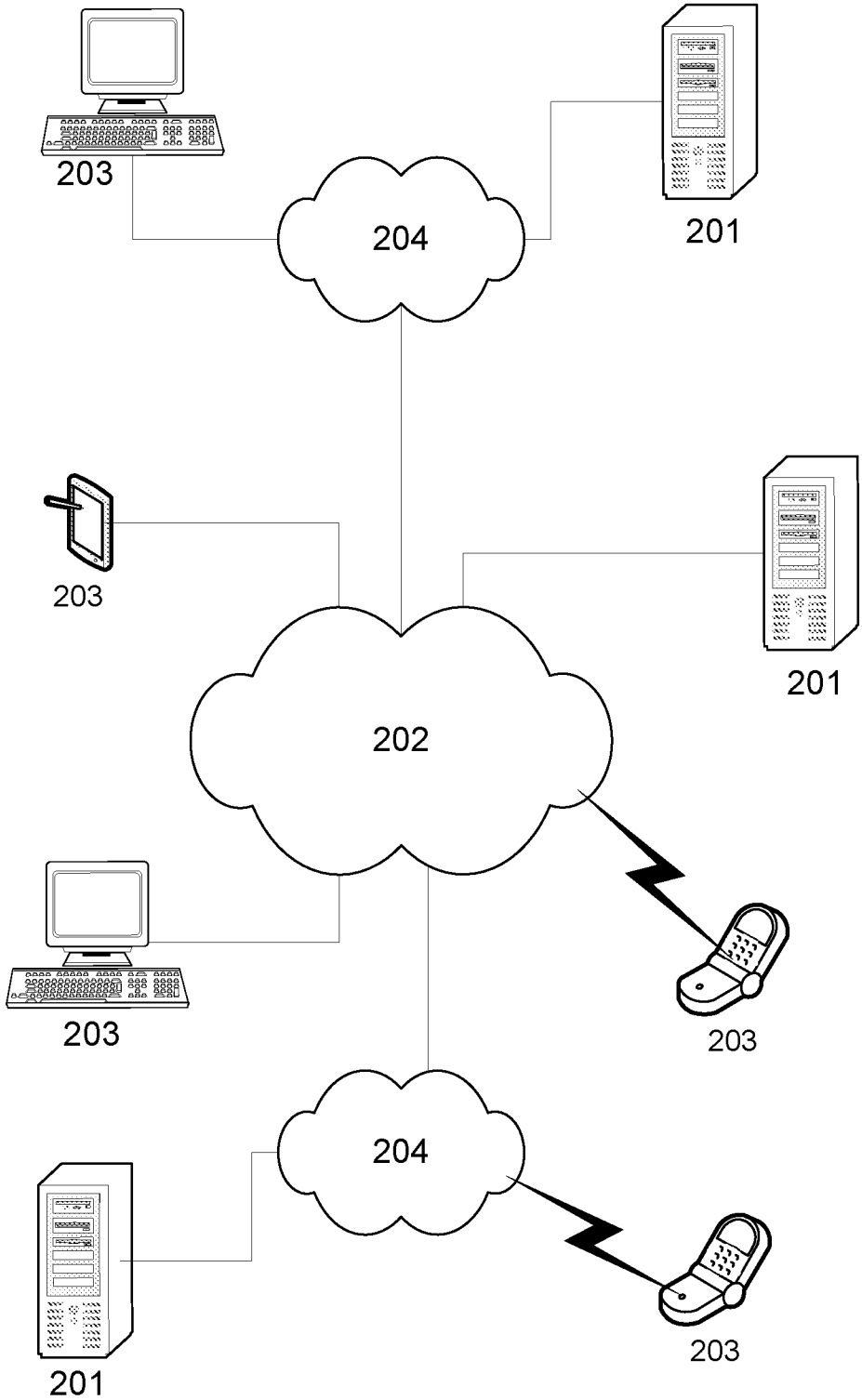


Fig. 2

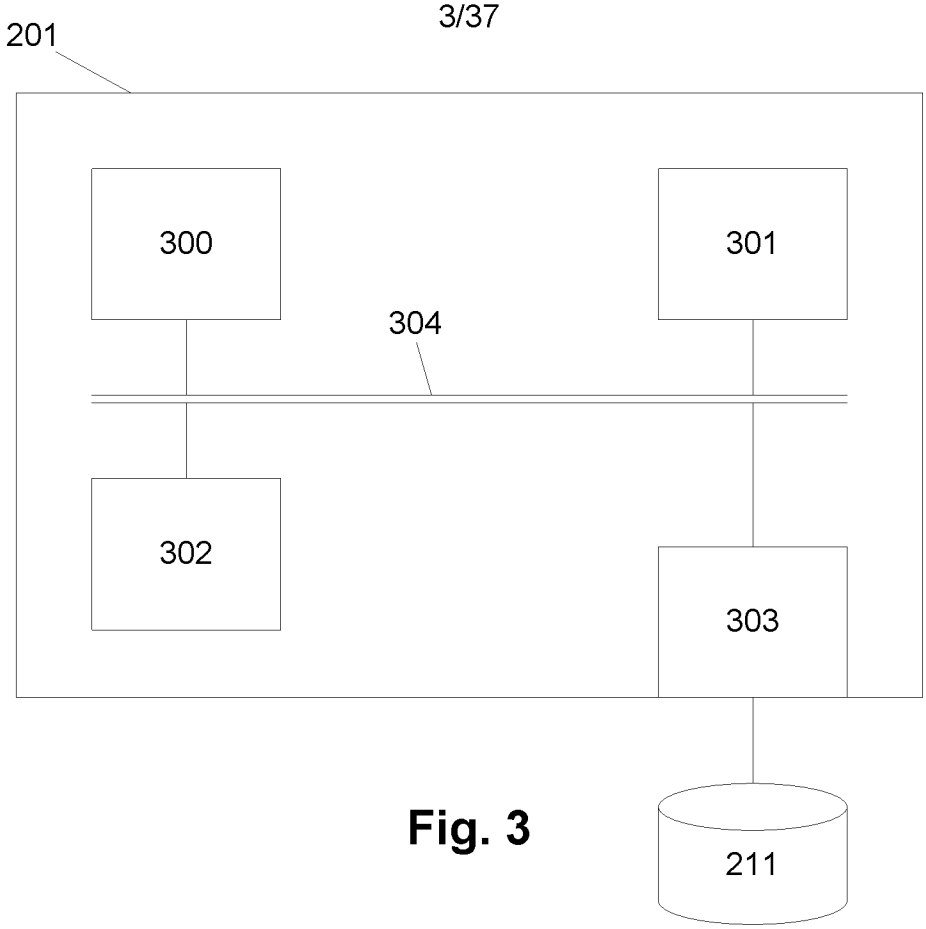


Fig. 3

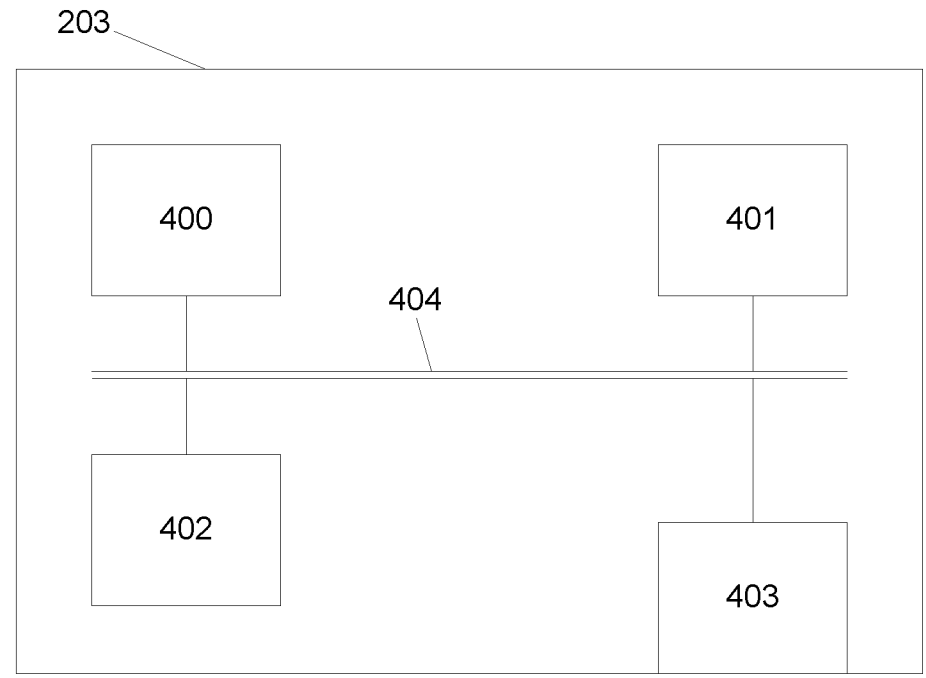


Fig. 4

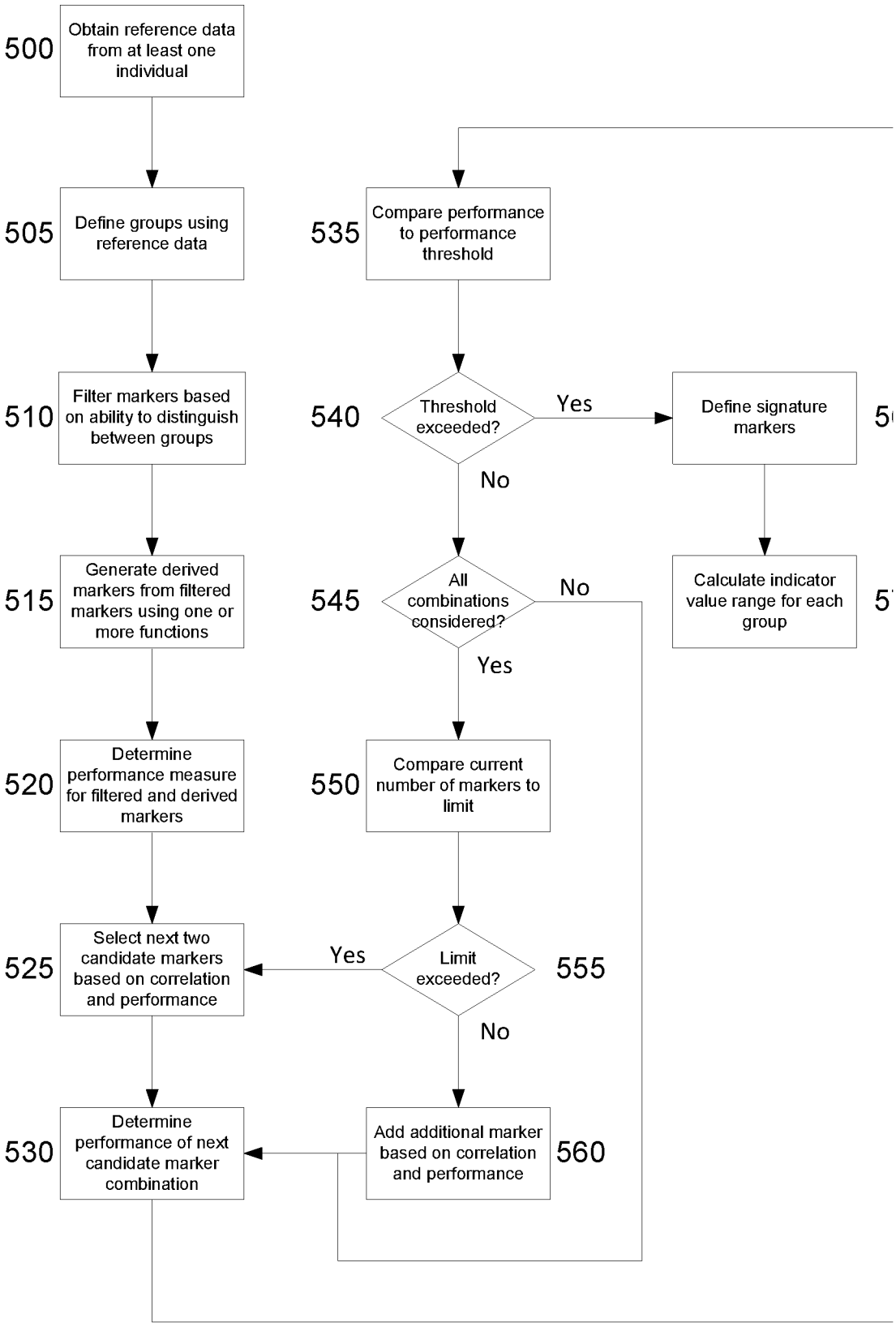

500
Obtain reference data from at least one individual
505
Define groups using reference data
510
Filter markers based on ability to distinguish between groups
515
Generate derived markers from filtered markers using one or more functions
520
Determine performance measure for filtered and derived markers
525
Select next two candidate markers based on correlation and performance
530
Determine performance of next candidate marker combination
535
Compare performance to performance threshold
540
Threshold exceeded?
Yes
No
Define signature markers
545
All combinations considered?
No
Yes
Calculate indicator value range for each group
550
Compare current number of markers to limit
555
Limit exceeded?
Yes
No
560
Add additional marker based on correlation and performance

Fig. 5

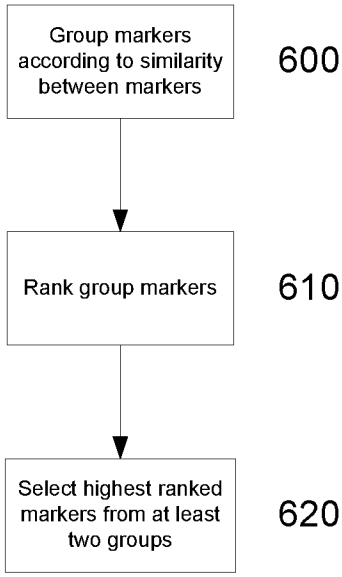

Group markers according to similarity between markers
600
Rank group markers
610
Select highest ranked markers from at least two groups
620

Fig. 6A

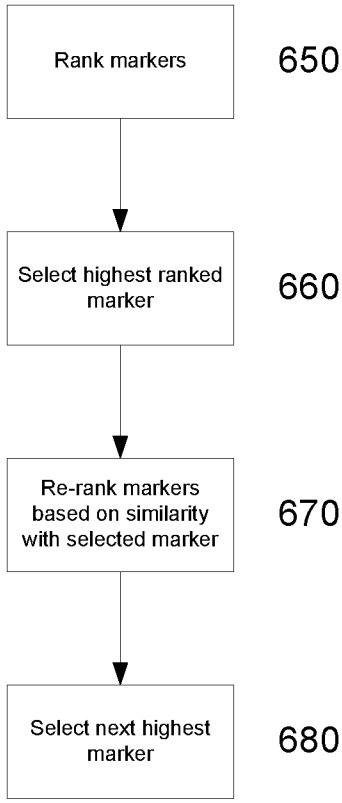

Rank markers
650
Select highest ranked marker
660
Re-rank markers based on similarity with selected marker
670
Select next highest marker
680

Fig. 6B

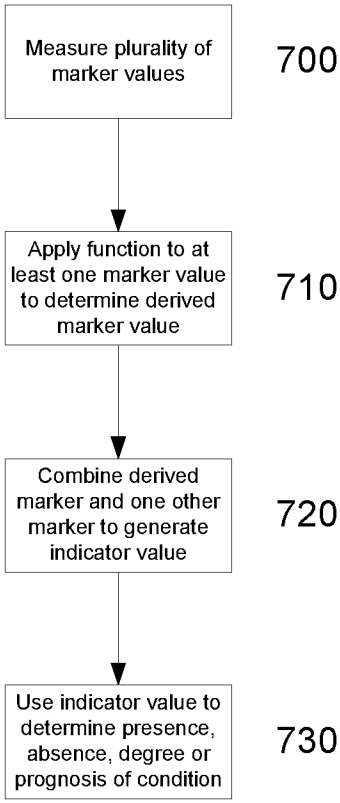

Measure plurality of marker values
700
Apply function to at least one marker value to determine derived marker value
710
Combine derived marker and one other marker to generate indicator value
720
Use indicator value to determine presence, absence, degree or prognosis of condition
730

Fig. 7

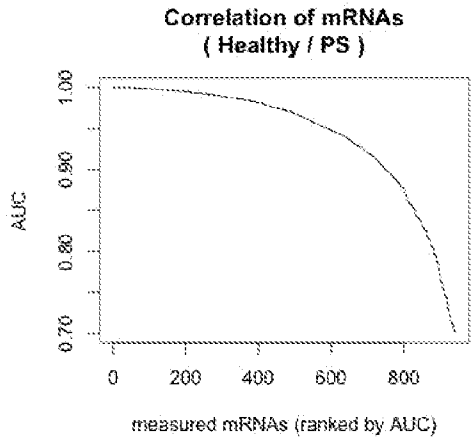


Fig. 8A

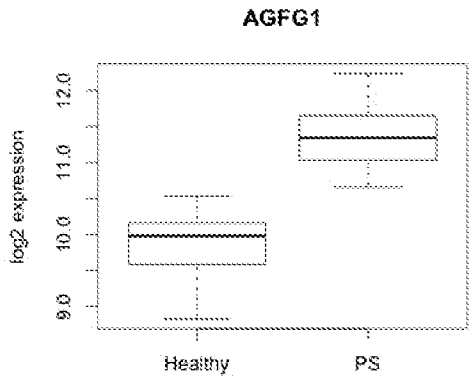


Fig. 8B

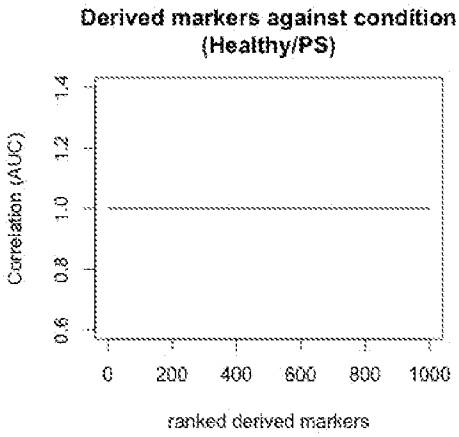


Fig. 8C

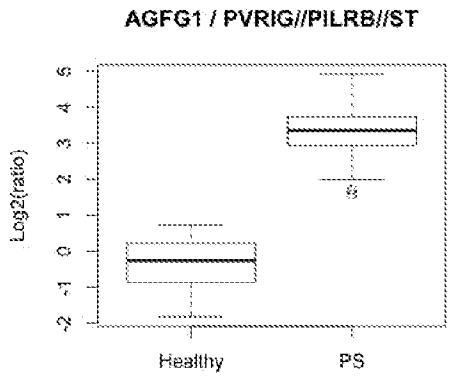


Fig. 8D

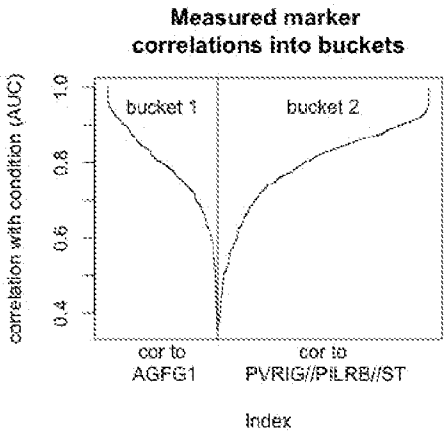


Fig. 8E

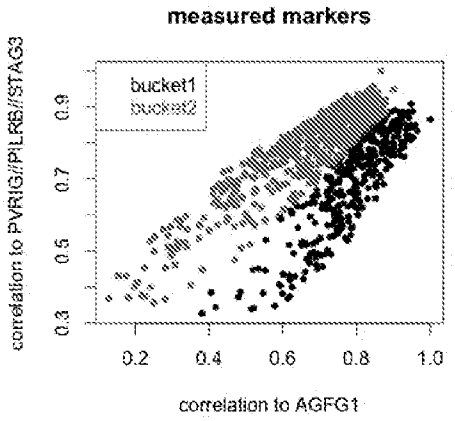


Fig. 8F

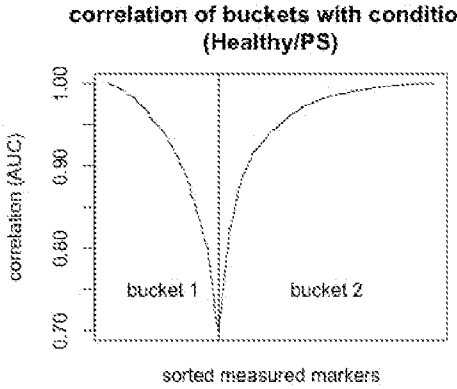


Fig. 8G

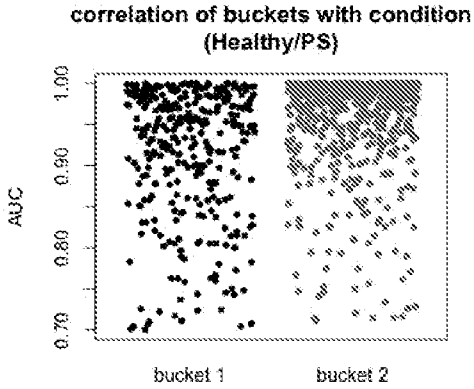


Fig. 8H

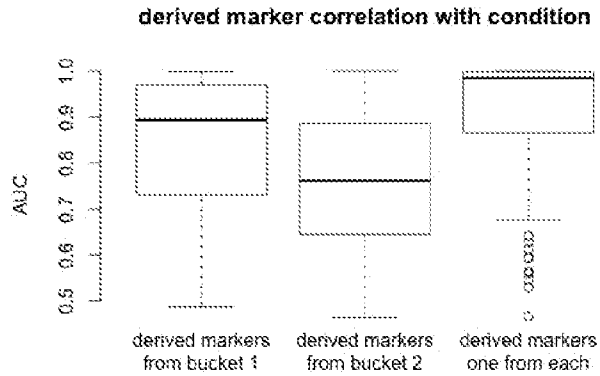


Fig. 8I

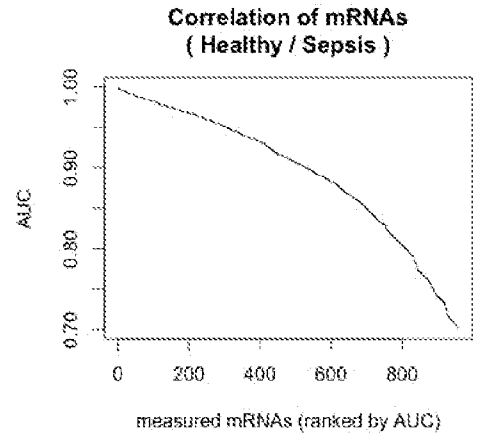


Fig. 9A

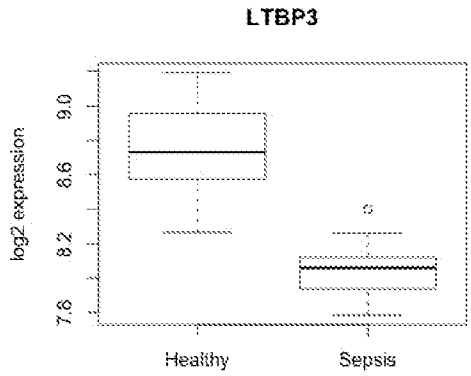


Fig. 9B

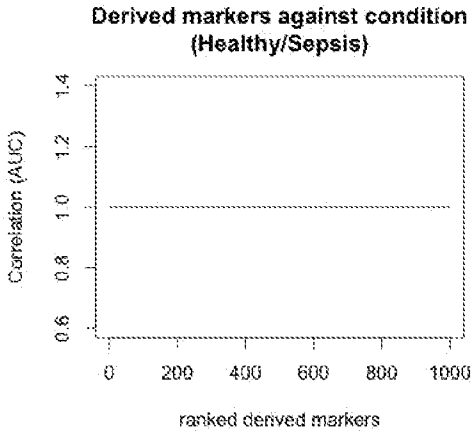


Fig. 9C

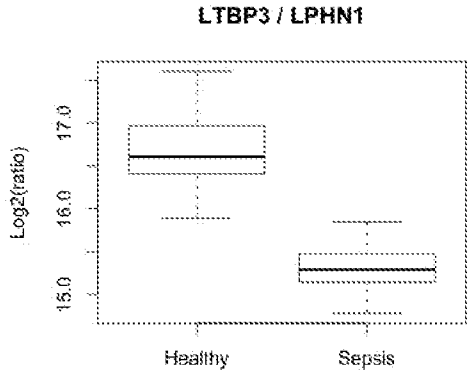


Fig. 9D

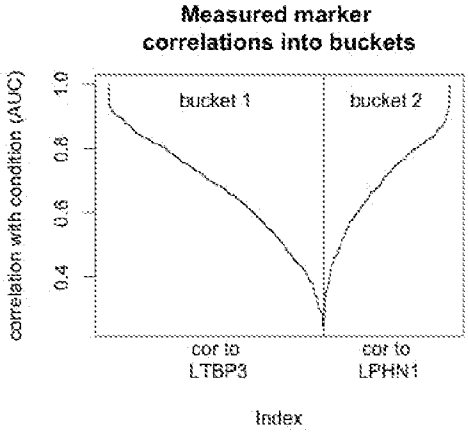


Fig. 9E

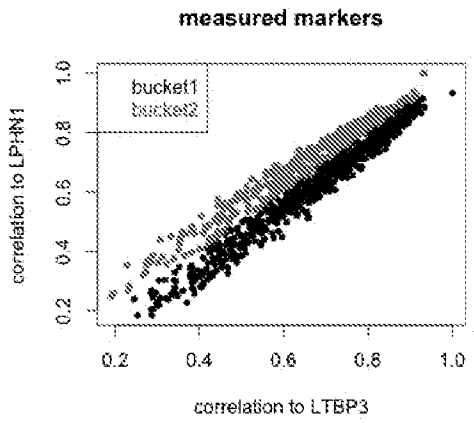


Fig. 9F

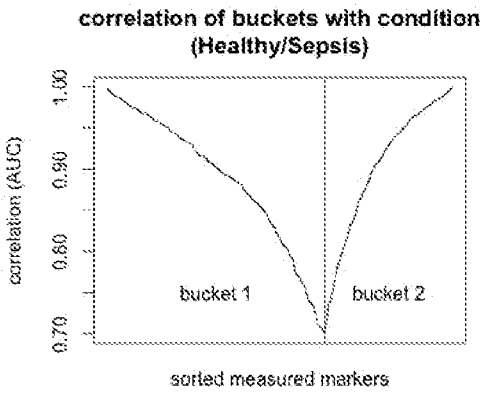


Fig. 9G

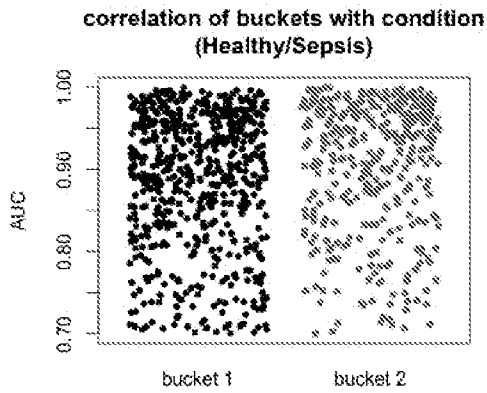


Fig. 9H

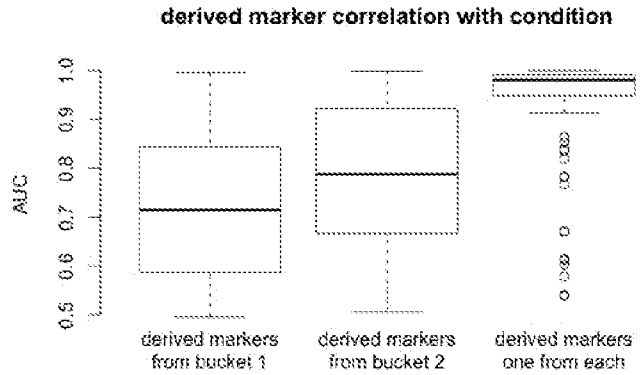


Fig. 9I

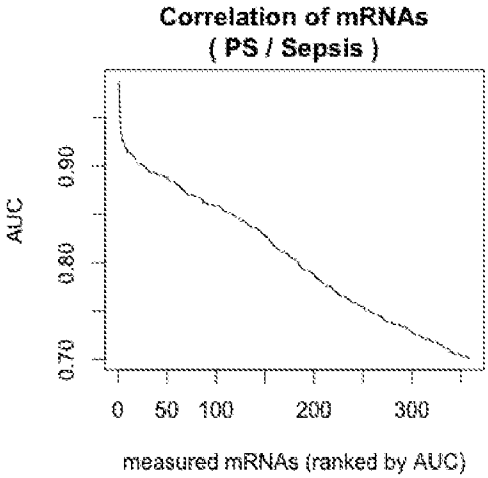


Fig. 10A

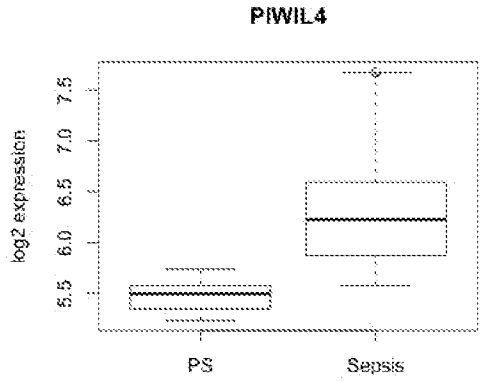


Fig. 10B

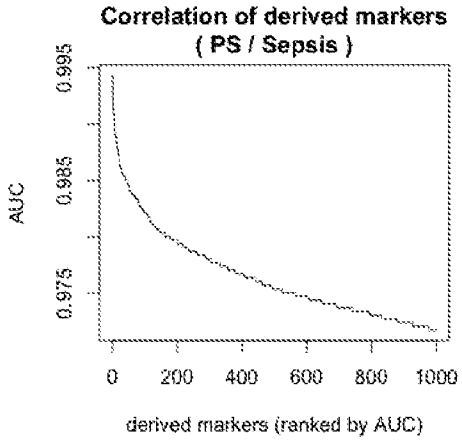


Fig. 10C

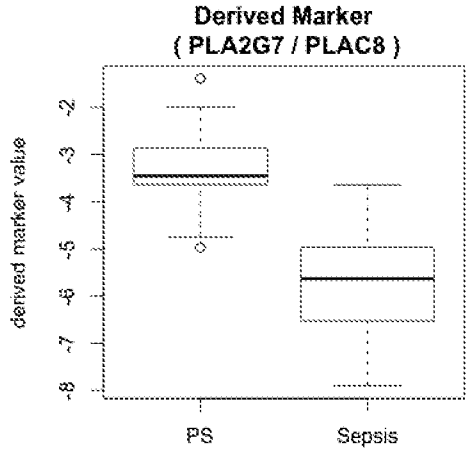


Fig. 10D

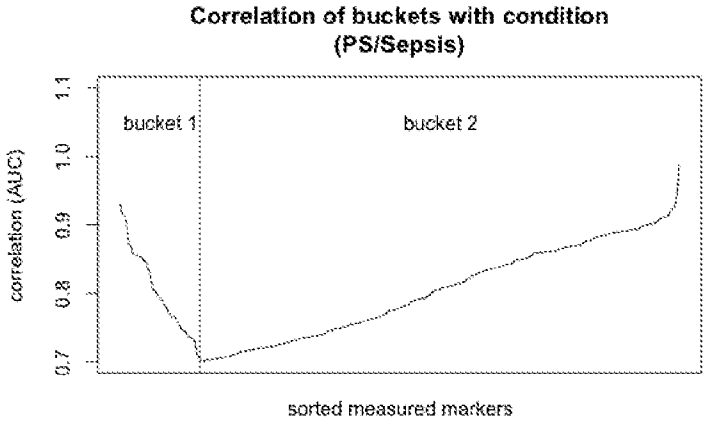


Fig. 10E

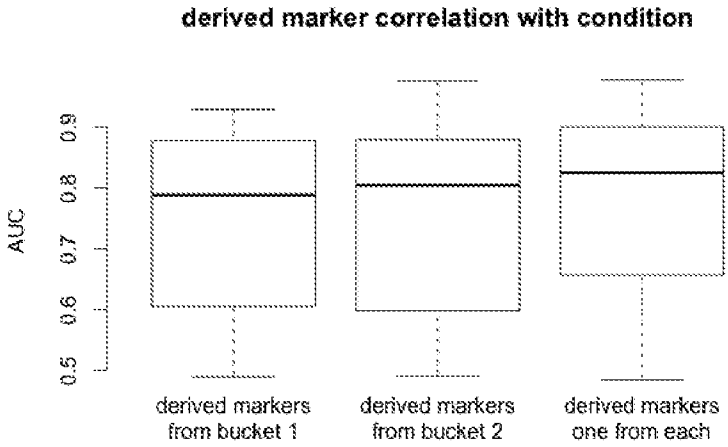


Fig. 10F

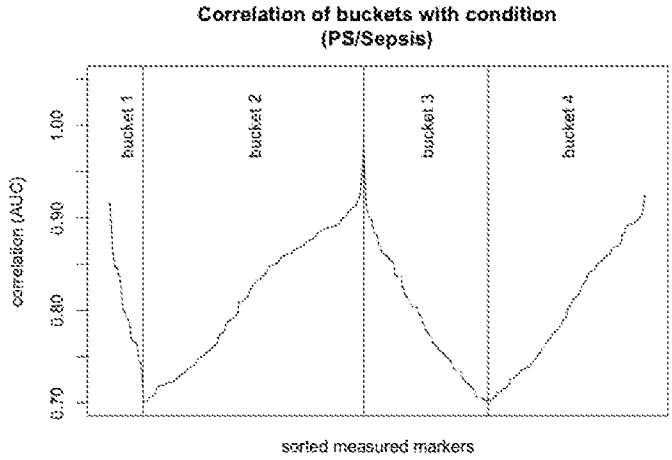


Fig. 10G

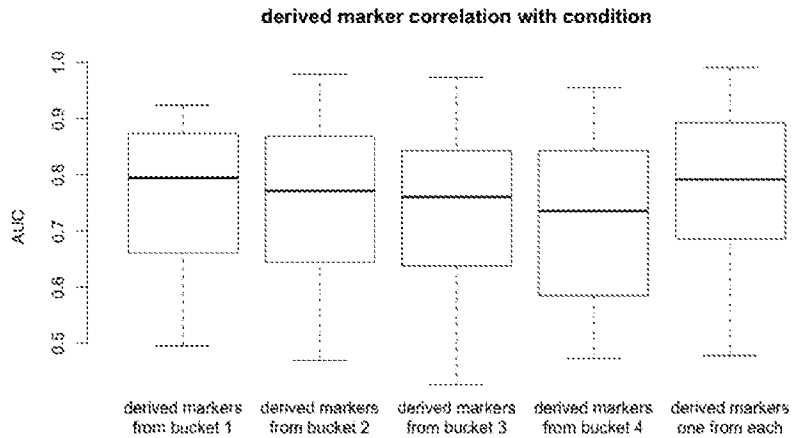


Fig. 10H

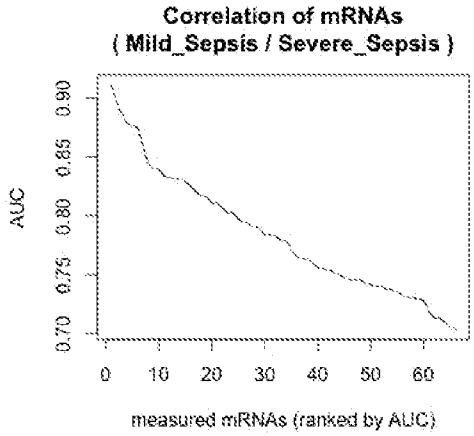


Fig. 11A

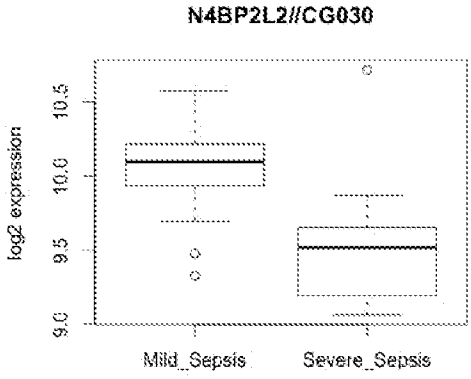


Fig. 11B

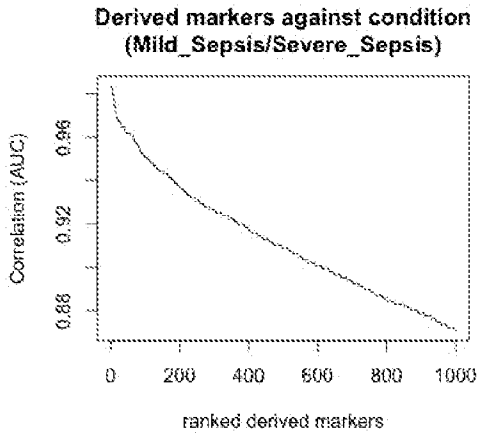


Fig. 11C

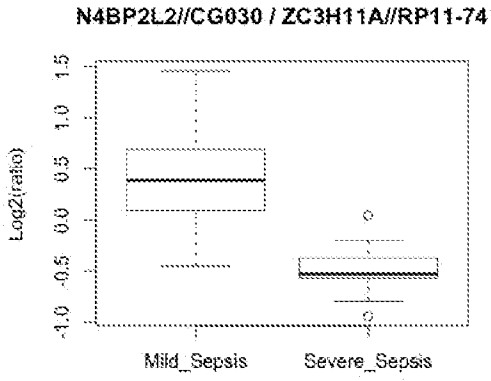


Fig. 11D

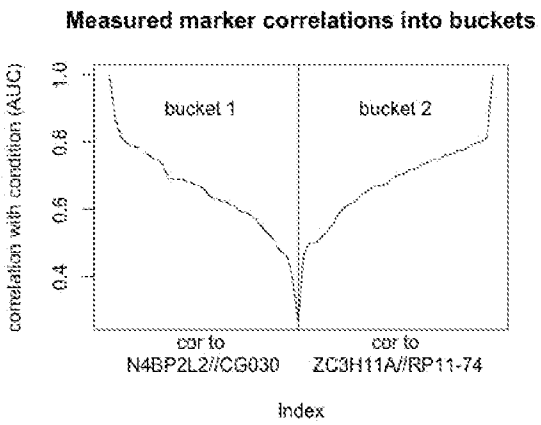


Fig. 11E

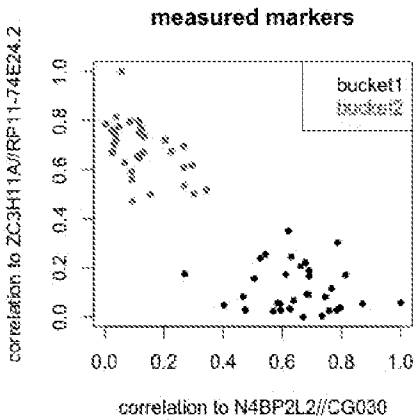


Fig. 11F

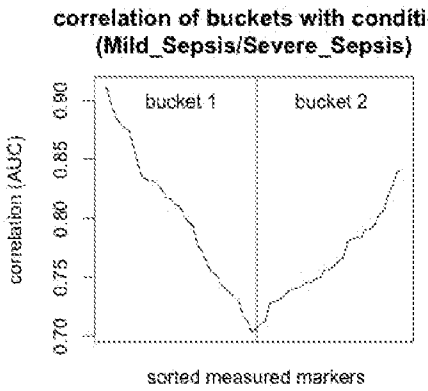


Fig. 11G

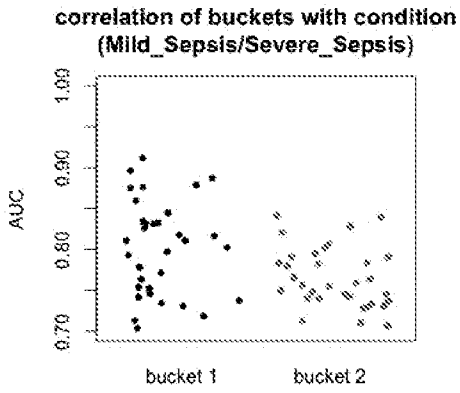


Fig. 11H

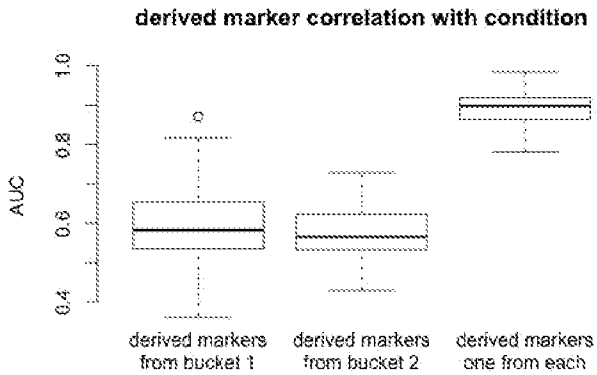


Fig. 11I

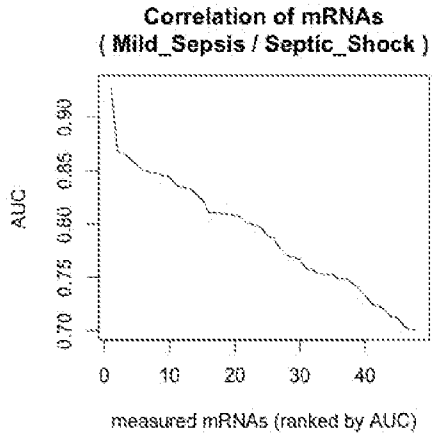


Fig. 12A

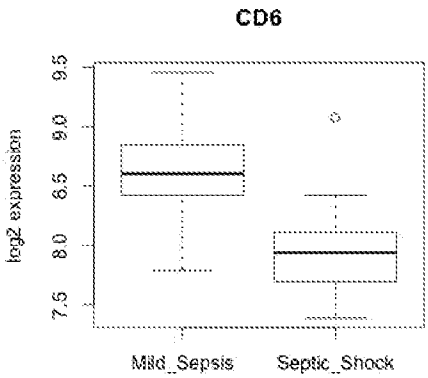


Fig. 12B

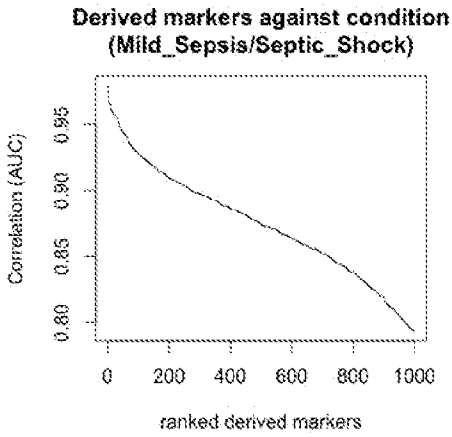


Fig. 12C

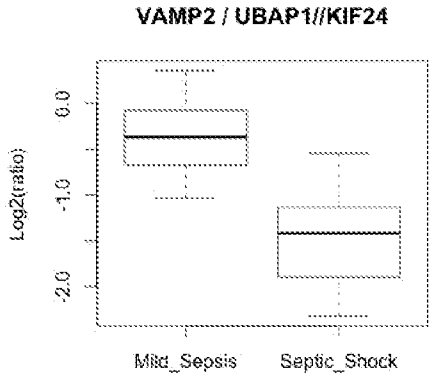


Fig. 12D

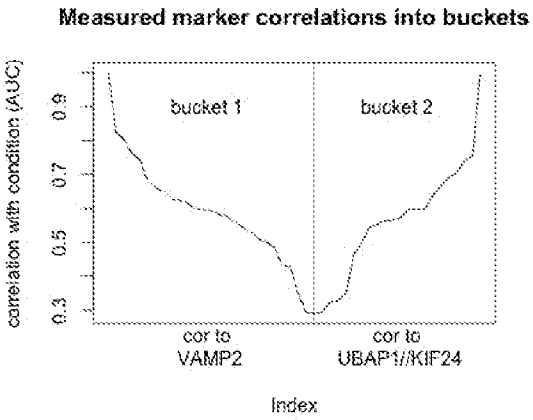


Fig. 12E

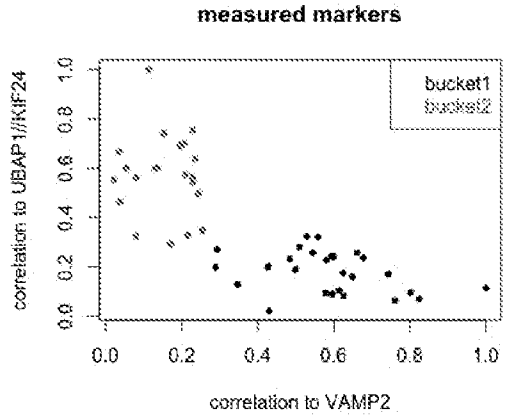


Fig. 12F

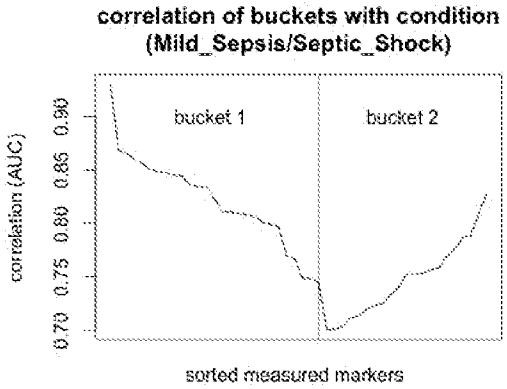


Fig. 12G

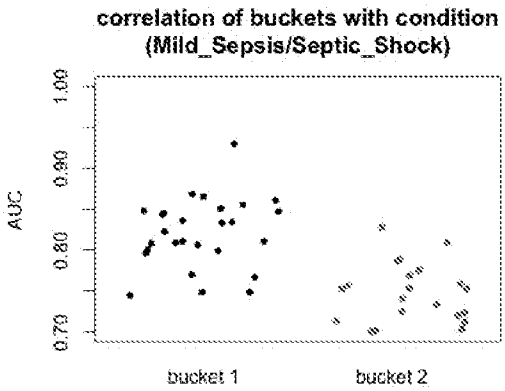


Fig. 12H

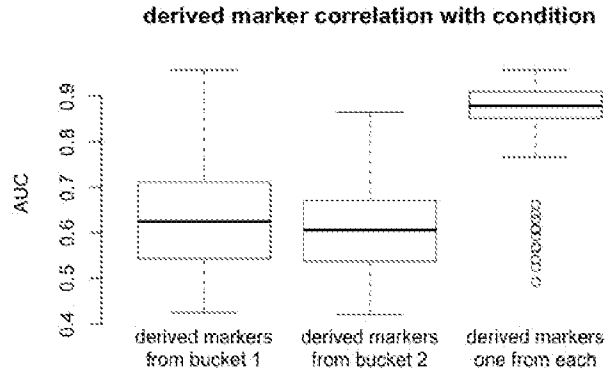


Fig. 12I

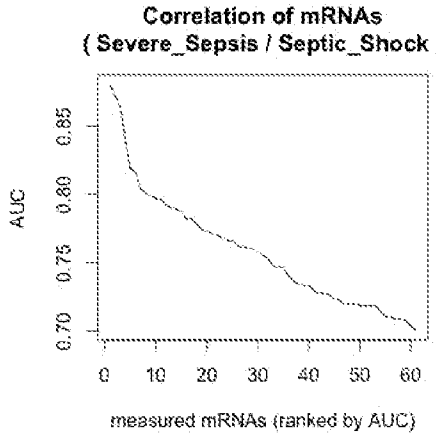


Fig. 13A

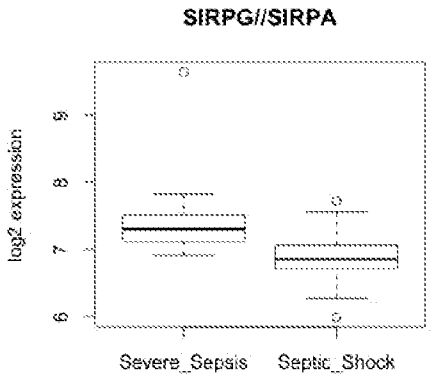


Fig. 13B

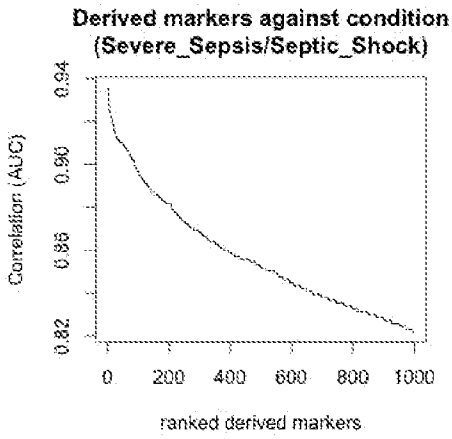


Fig. 13C

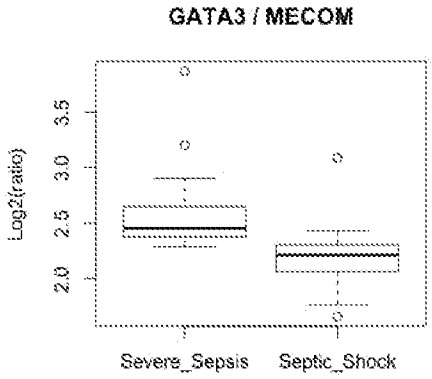


Fig. 13D

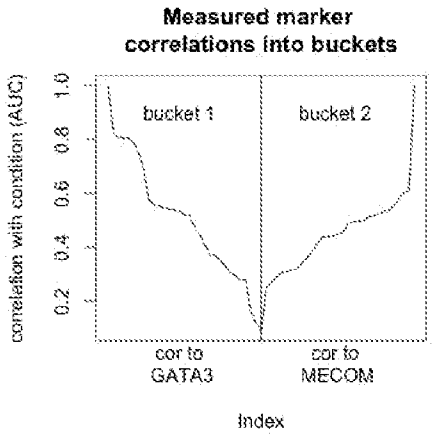


Fig. 13E

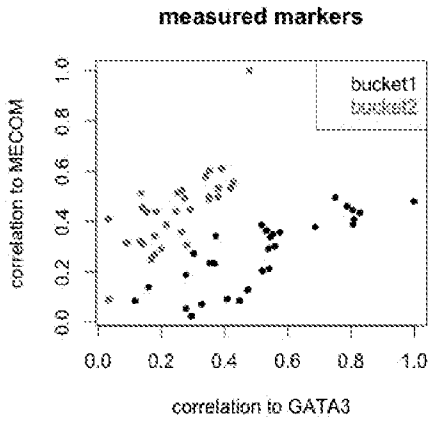


Fig. 13F

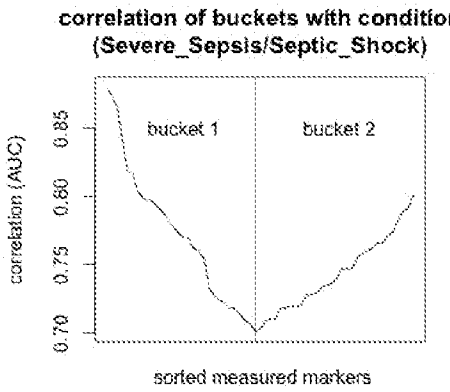


Fig. 13G

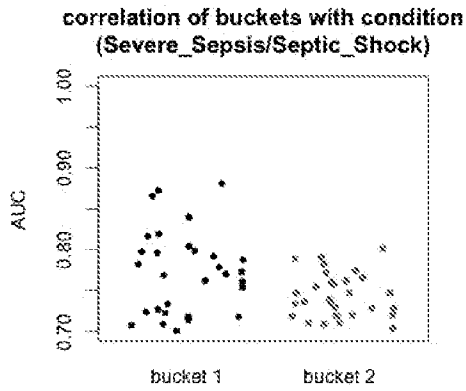


Fig. 13H

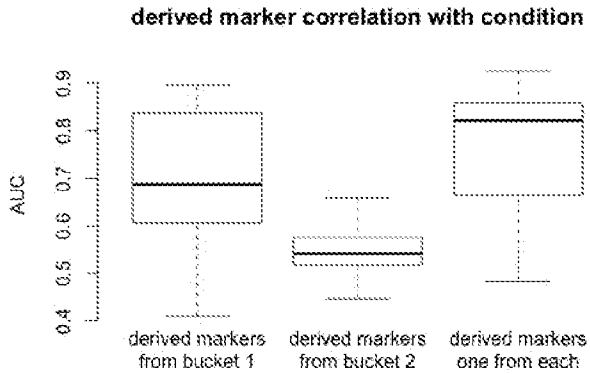
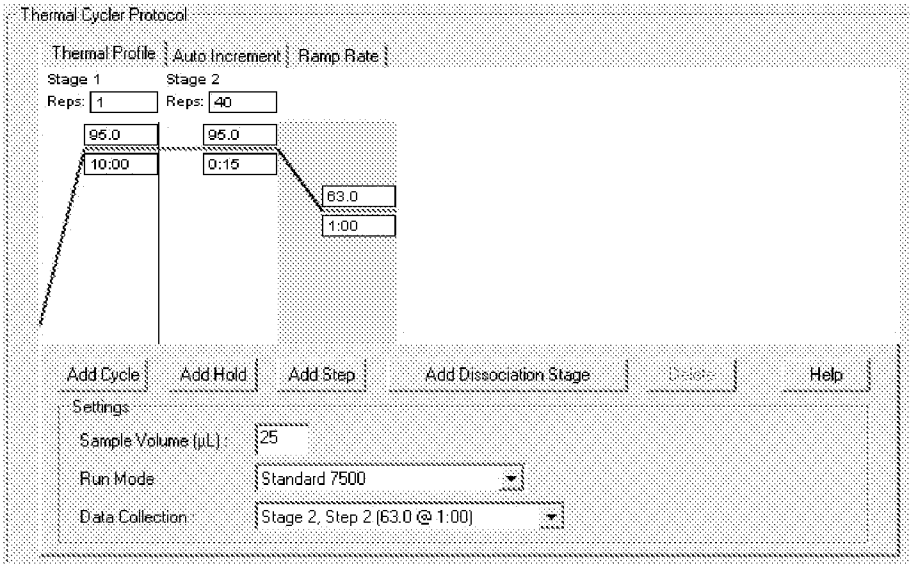


Fig. 13I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Auto Increment
Ramp Rate
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Reps: 1
Stage 2
Reps: 40
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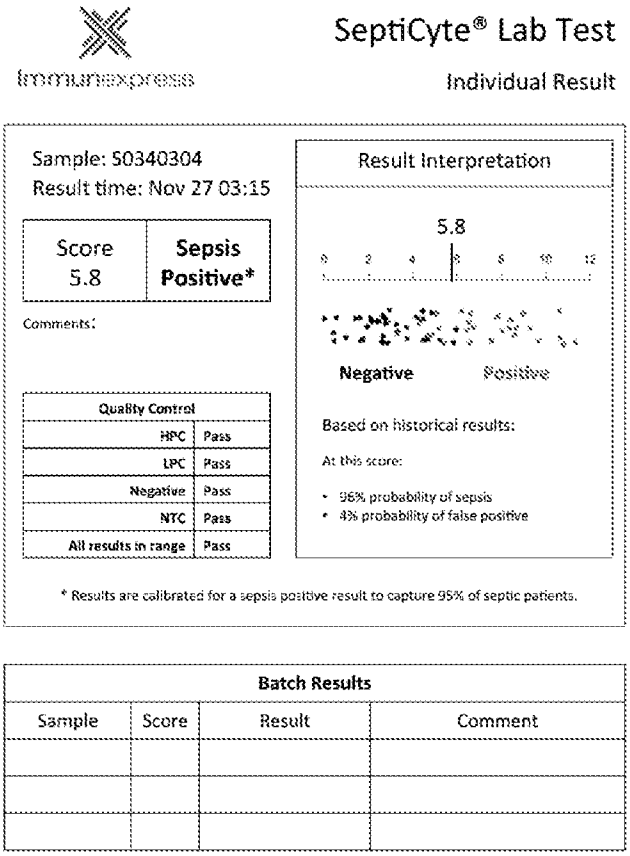
10:00
95.0
0:15
63.0
1:00
Add Cycle
Add Hold
Add Step
Add Dissociation Stage
Delete
Help
Settings
Sample Volume (µL): 25
Run Mode: Standard 7500
Data Collection: Stage 2, Step 2 (63.0 @ 1:00)

Fig. 14


immunexpress
SeptiCyte® Lab Test
Individual Result
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Result time: Nov 27 03:15
Score 5.8
Sepsis Positive*
Comments:
Quality Control
HPC Pass
LPC Pass
Negative Pass
NTC Pass
All results in range Pass
Result Interpretation
5.8
Negative
Positive
Based on historical results:
At this score:
• 96% probability of sepsis
• 4% probability of false positive
* Results are calibrated for a sepsis positive result to capture 95% of septic patients.
Batch Results
Sample
Score
Result
Comment

Fig. 15

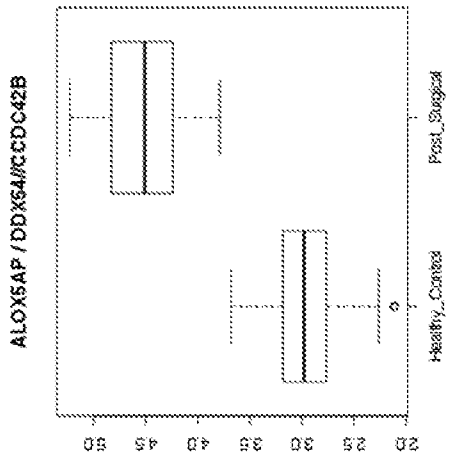

Fig. 16A

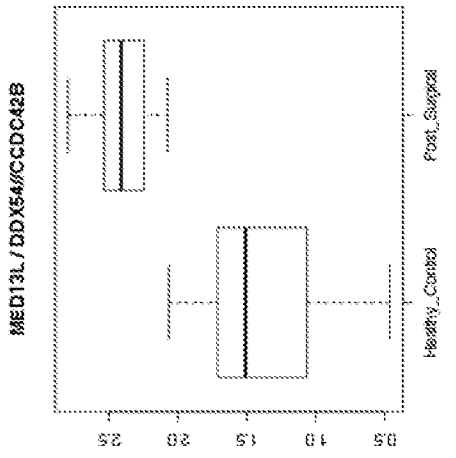

Fig. 16B

Fig. 16C

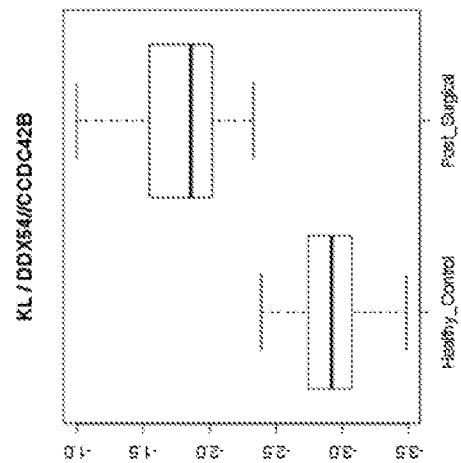

Fig. 16D

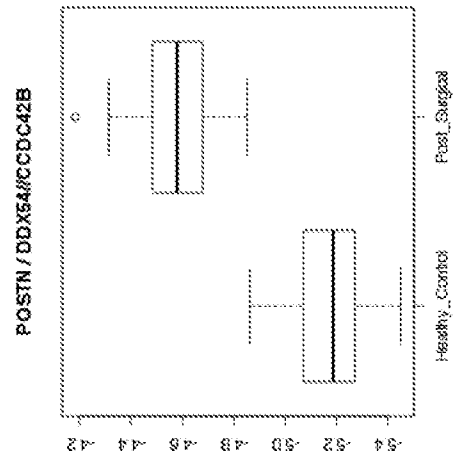

Fig. 16E

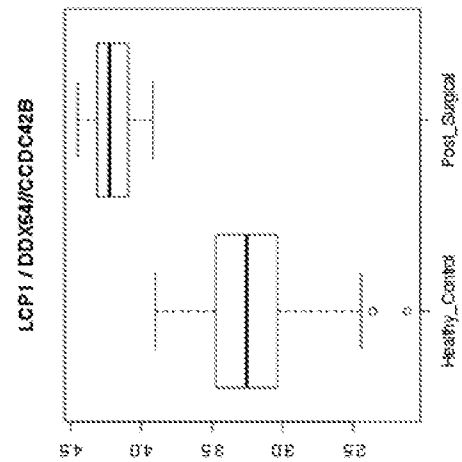

Fig. 16F

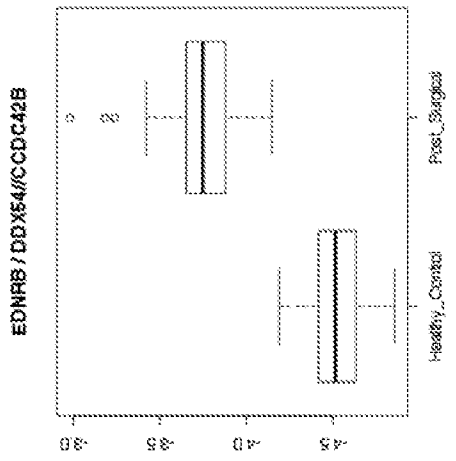

Fig. 16I

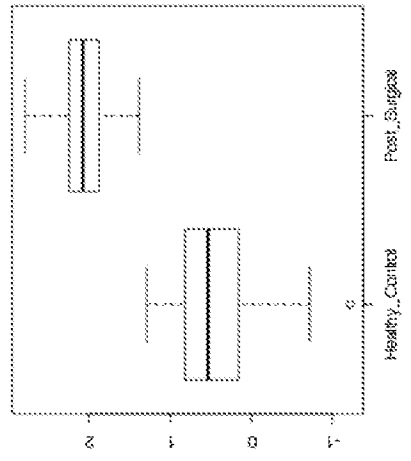

Fig 16I

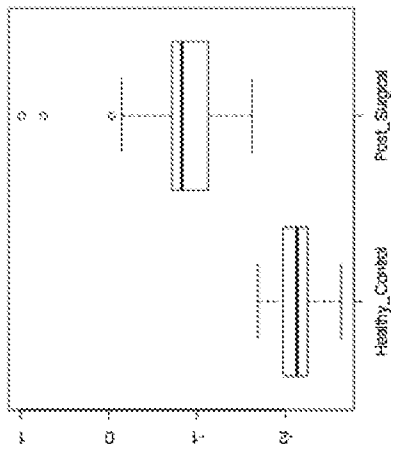

Fig. 16H

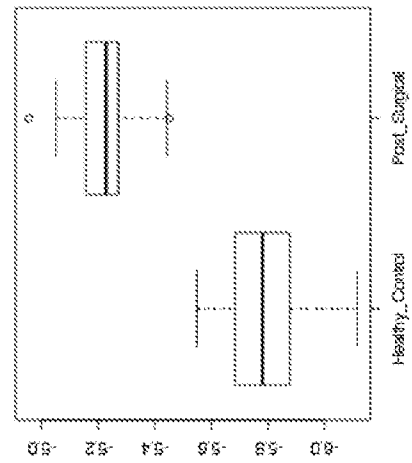

Fig 16K

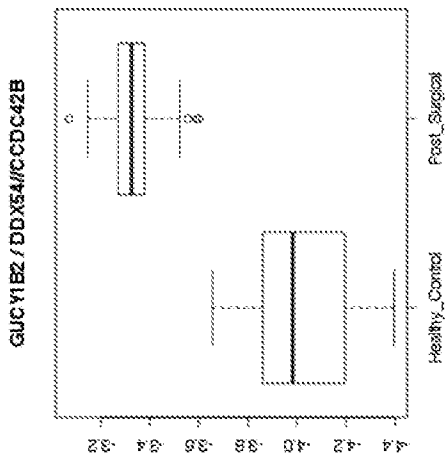

Fig. 16G

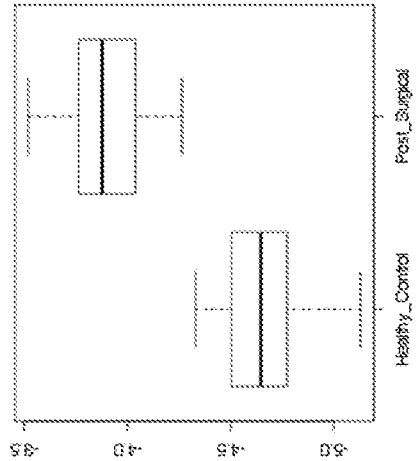

Fig 16J

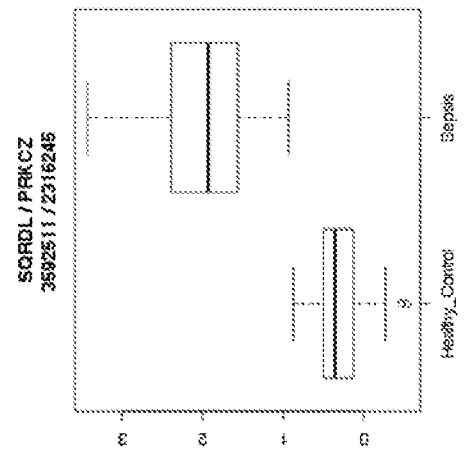

Fig. 17C

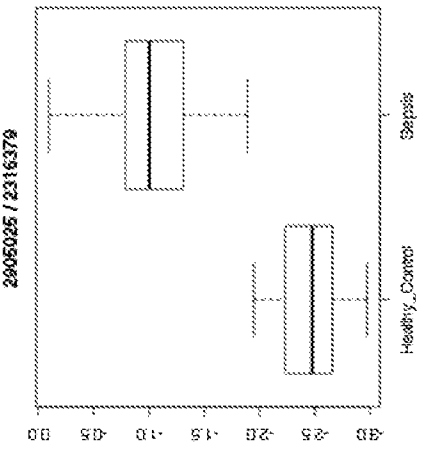

Fig. 17F

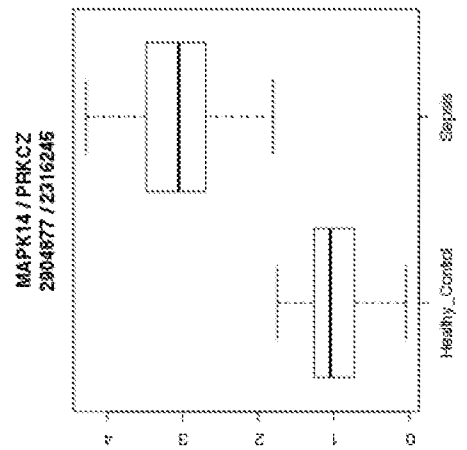

Fig. 17B

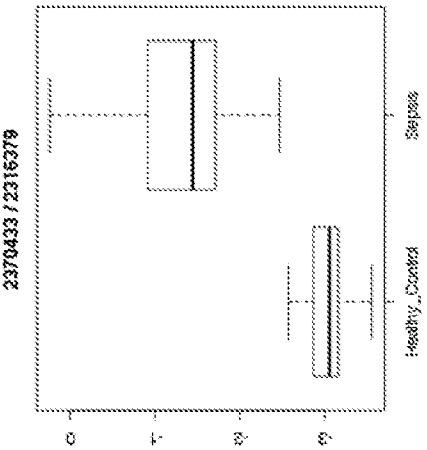

Fig. 17F

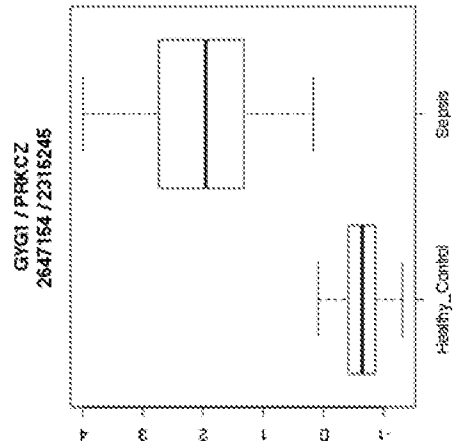

Fig. 17A

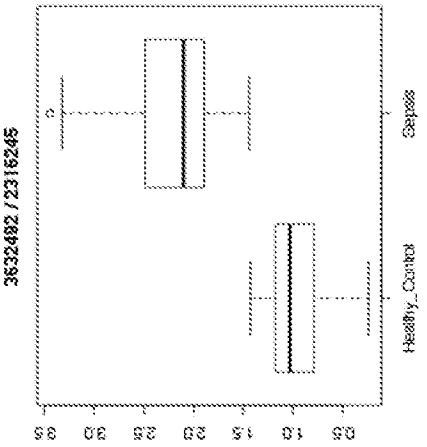

Fig. 17D

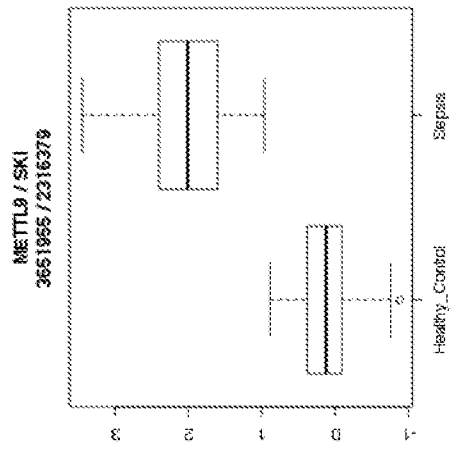

Fig. 17I

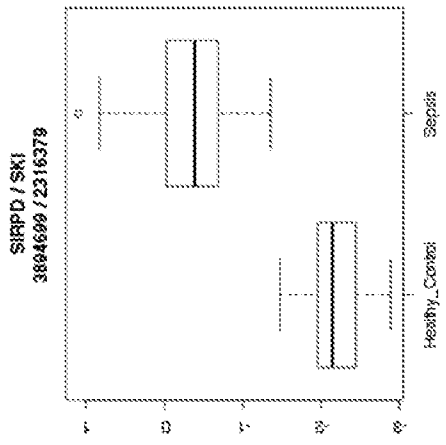

Fig 17I

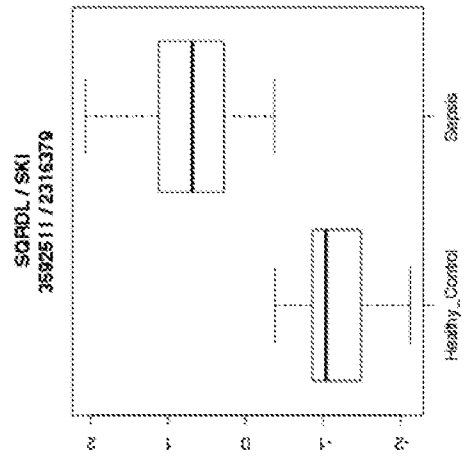

Fig. 17H

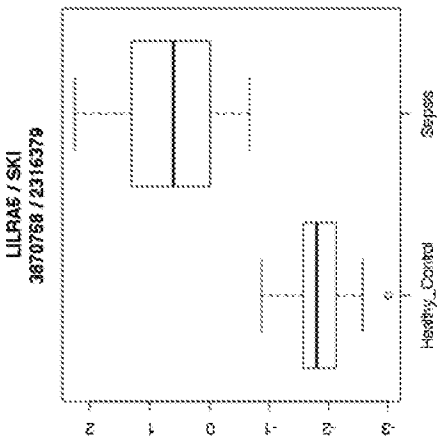

Fig 17K

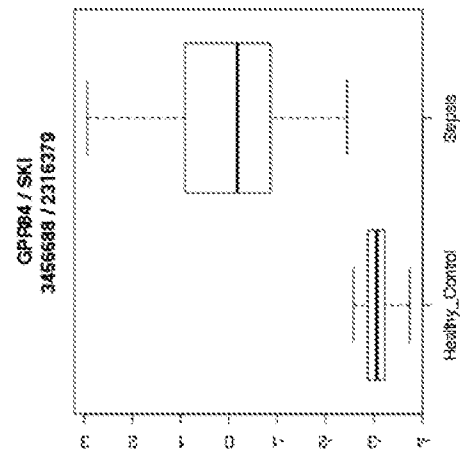

Fig. 17G

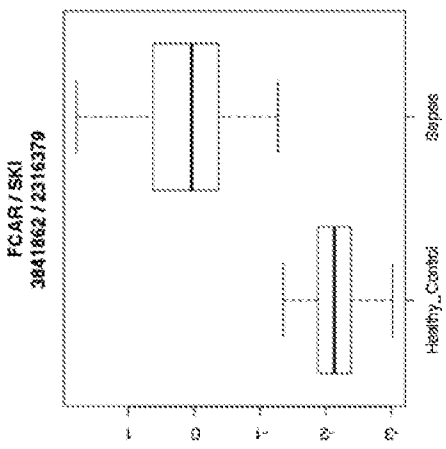

Fig 17.I

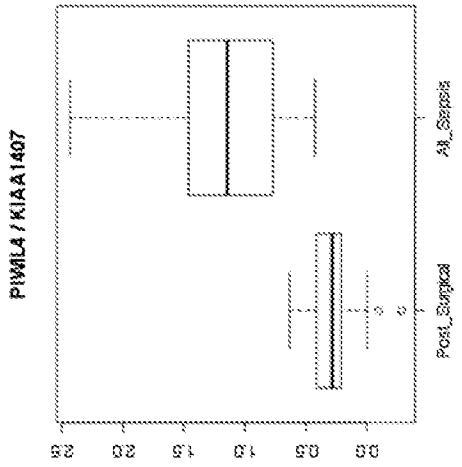

Fig. 18A

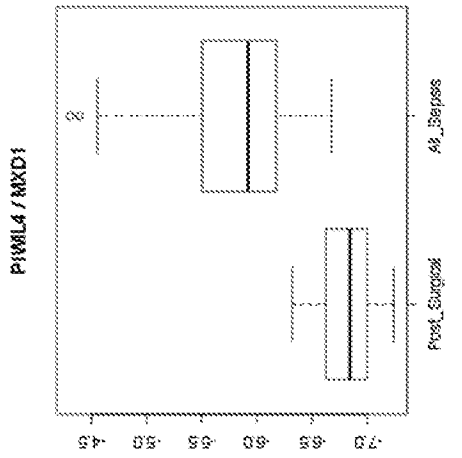

Fig. 18B

Fig. 18C

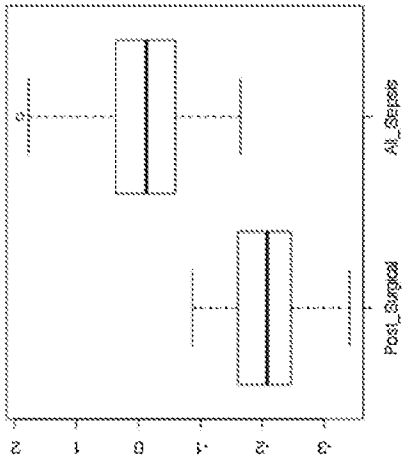

Fig. 18D

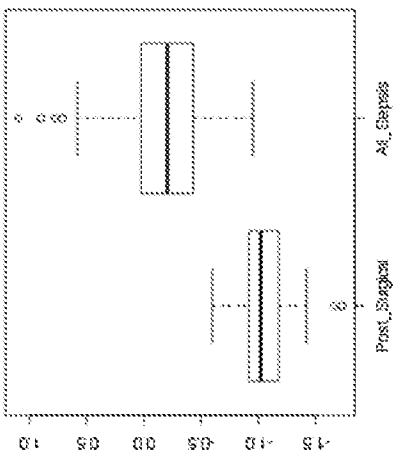

Fig. 18F

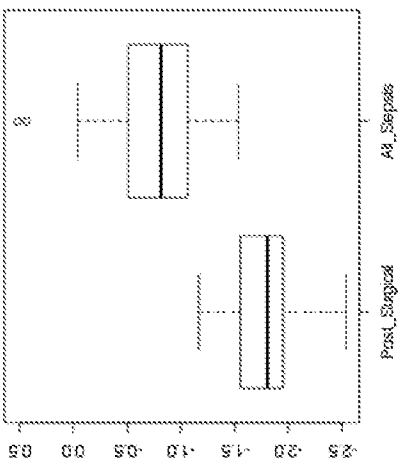

Fig. 18F

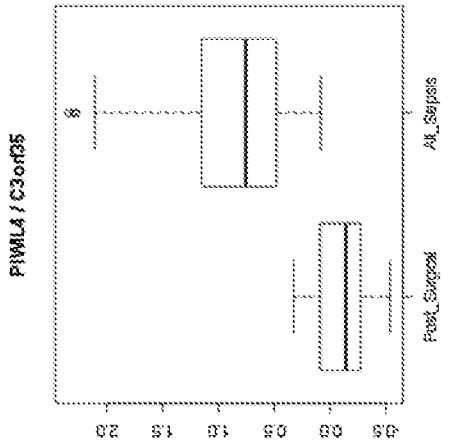

Fig. 18I

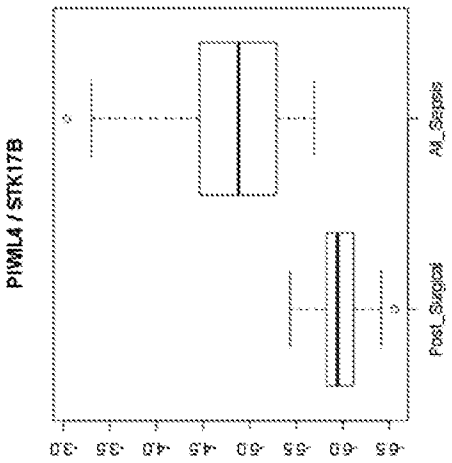

Fig. 18H

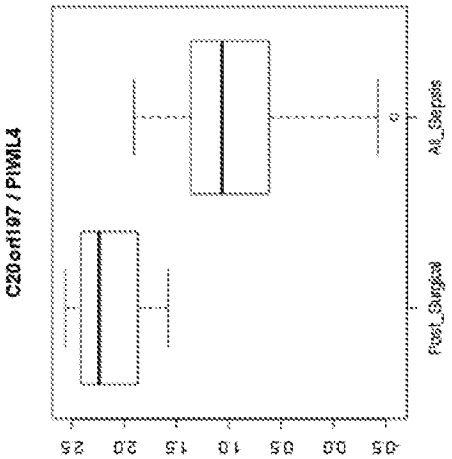

Fig. 18G

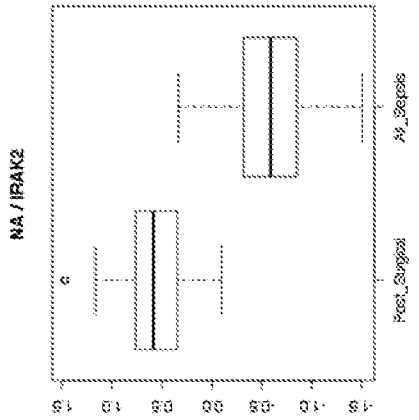

Fig. 18L

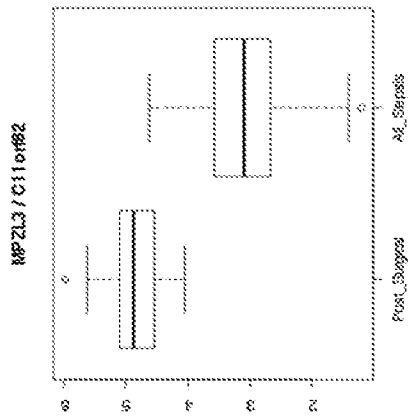

Fig. 18K

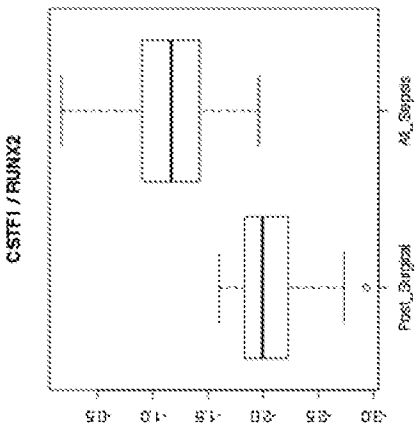

Fig. 18J

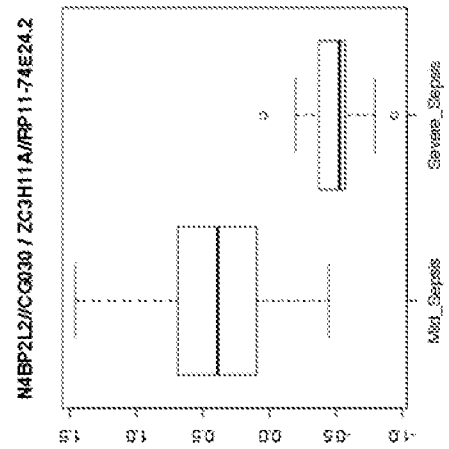

Fig. 19A

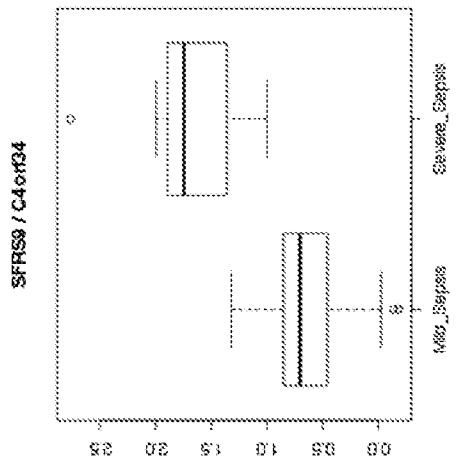

Fig. 19B

Fig. 19C

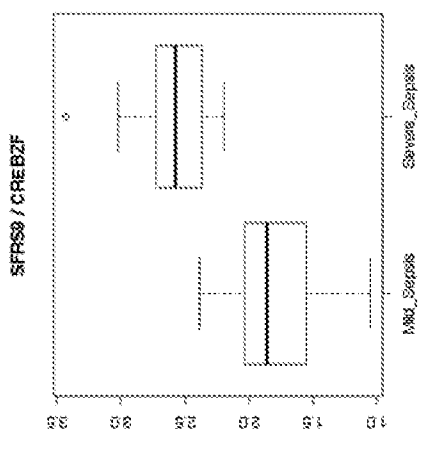

Fig. 19D

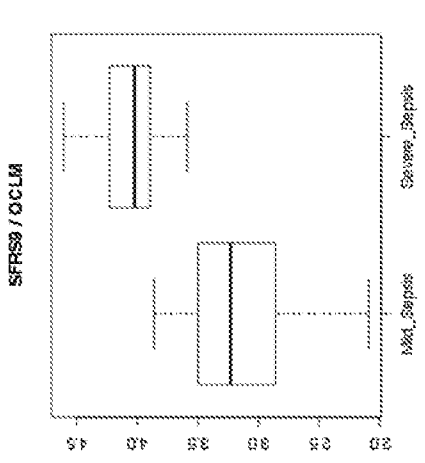

Fig. 19E

Fig. 19F

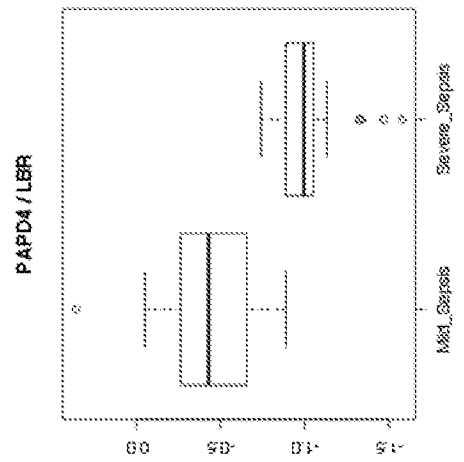

Fig. 19I

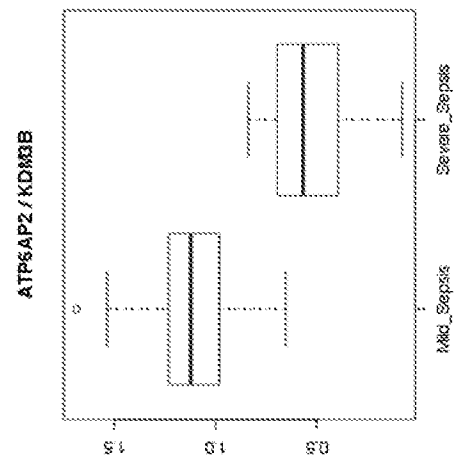

Fig. 19H

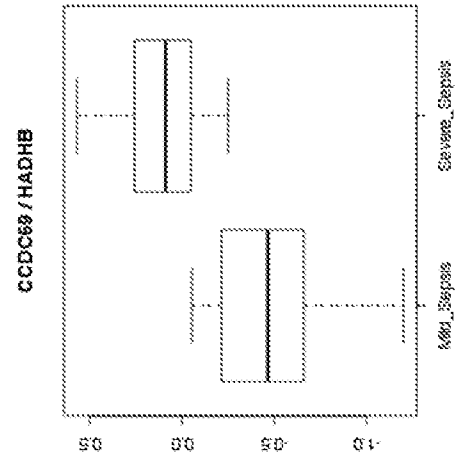

Fig. 19G

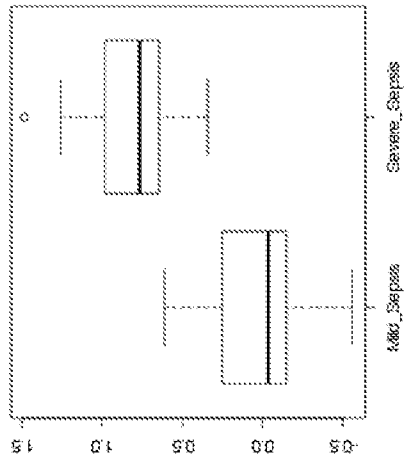

Fig. 19J

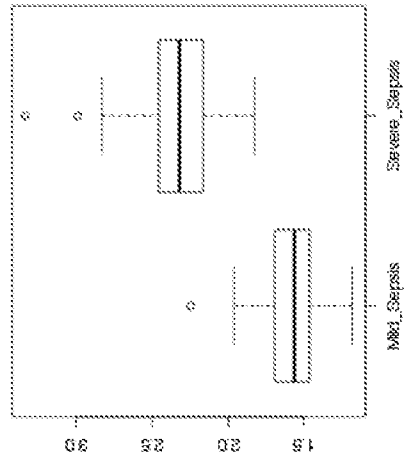

Fig. 19K

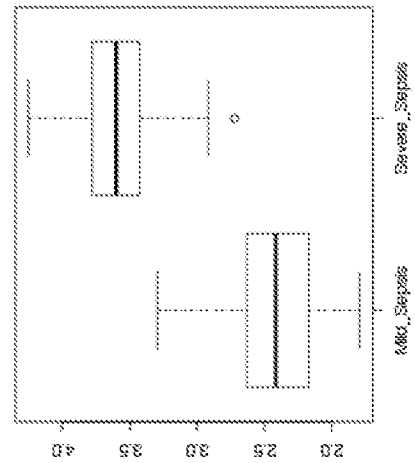

Fig. 19L

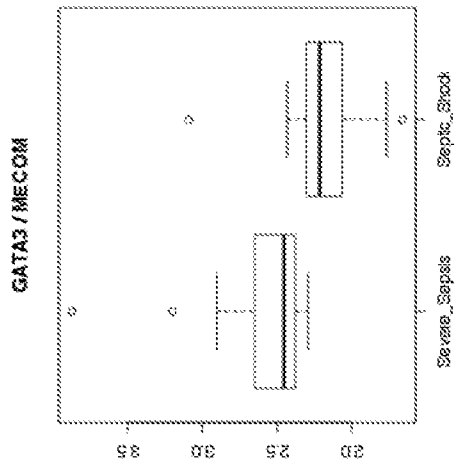

Fig. 20C

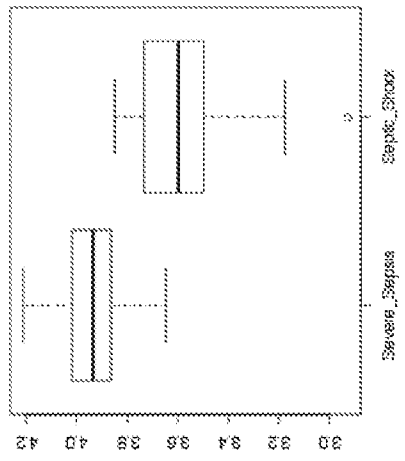

Fig. 20F

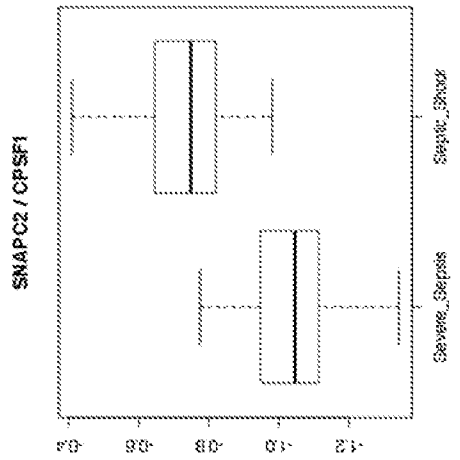

Fig. 20B

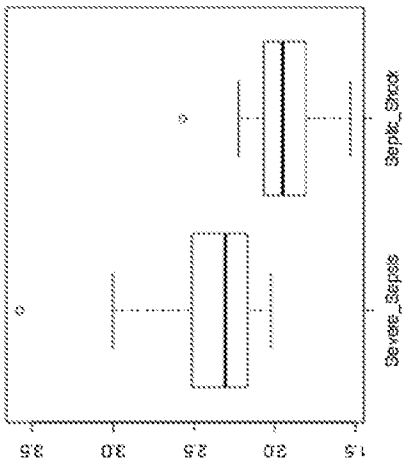

Fig. 20F

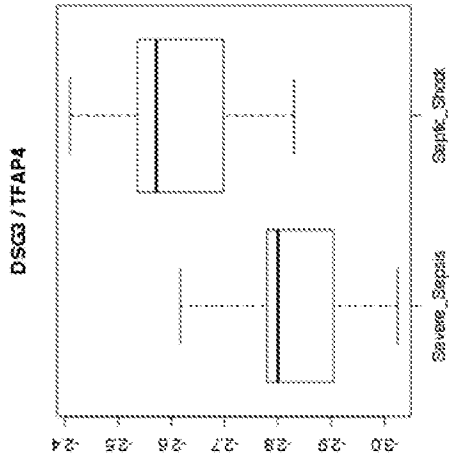

Fig. 20A

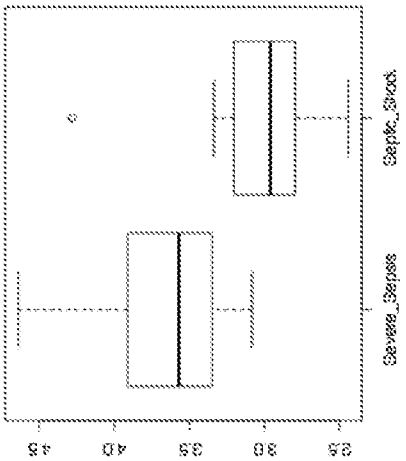

Fig. 20D

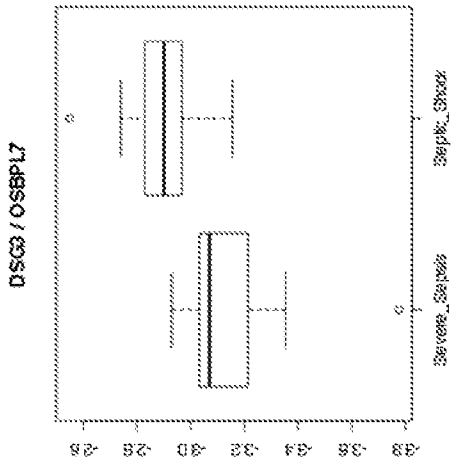

Fig. 20I

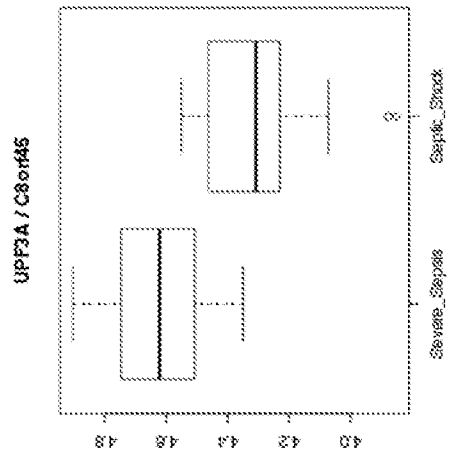

Fig. 20H

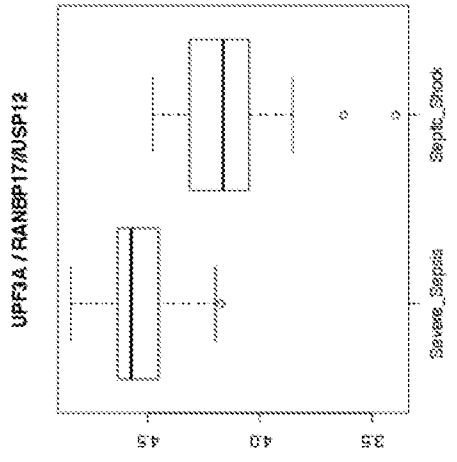

Fig. 20G

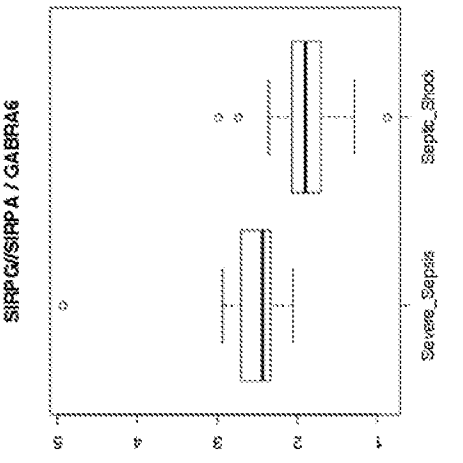

Fig. 20L

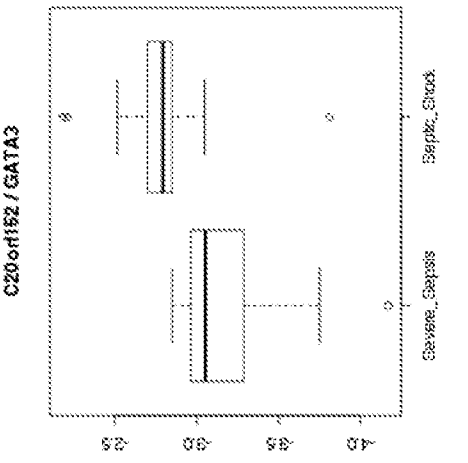

Fig. 20K

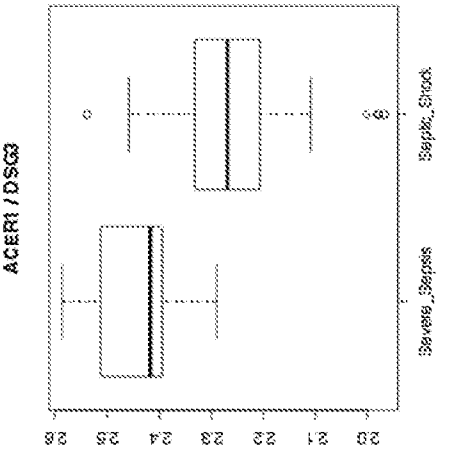

Fig. 20J

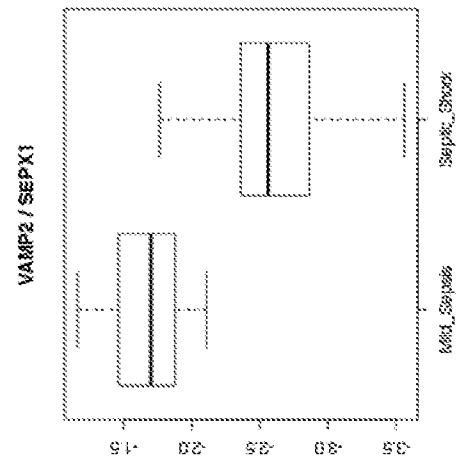

Fig. 21C

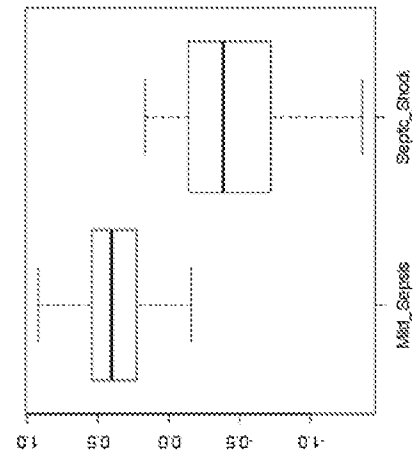

Fig. 21F

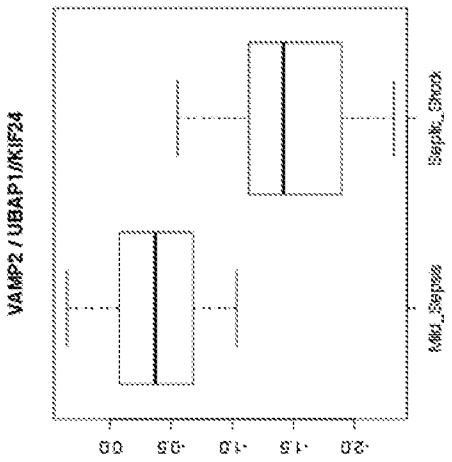

Fig. 21B

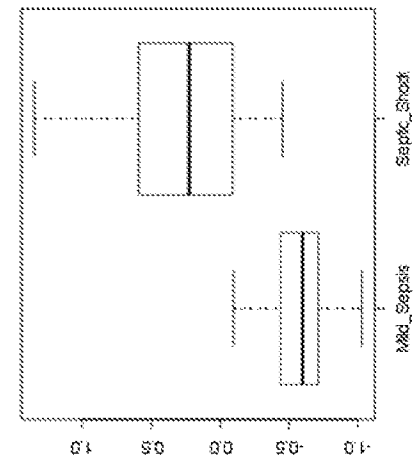

Fig. 21F

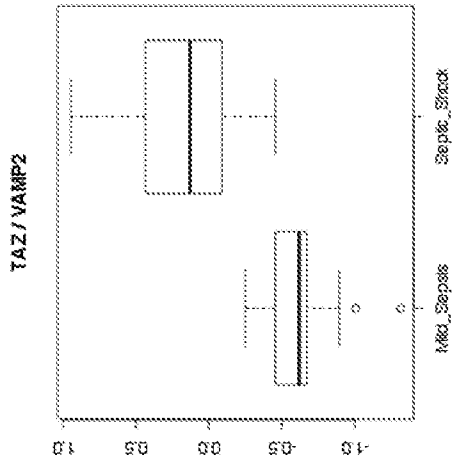

Fig. 21A

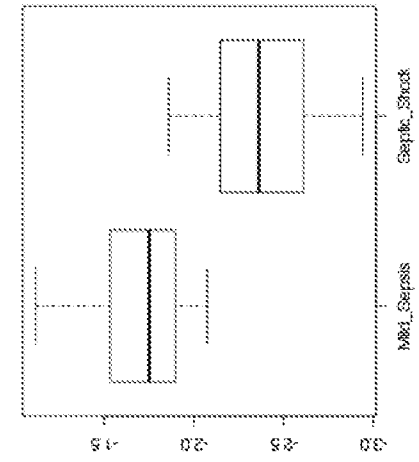

Fig. 21D

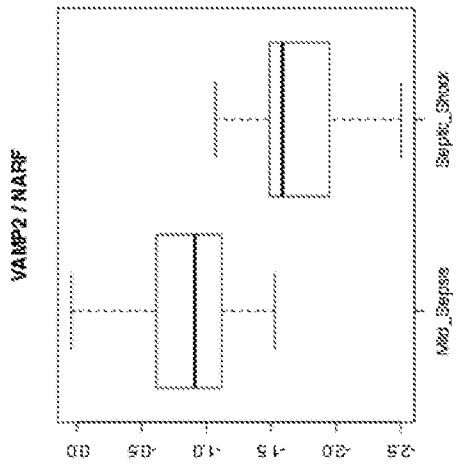

Fig. 21I

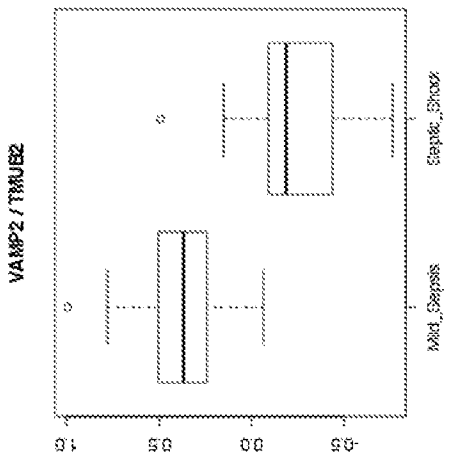

Fig. 21I

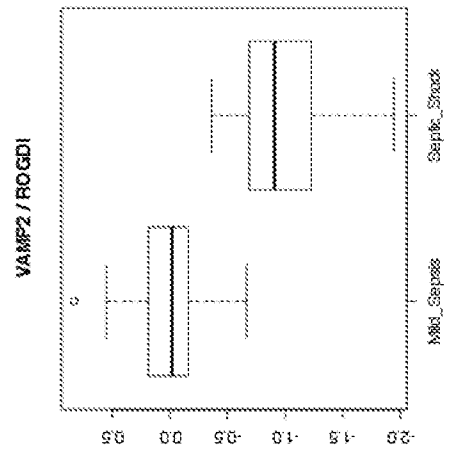

Fig. 21H

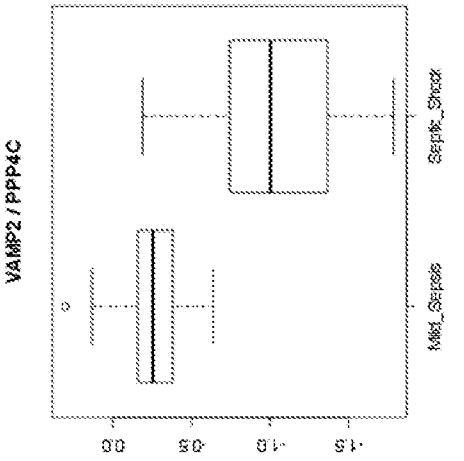

Fig. 21K

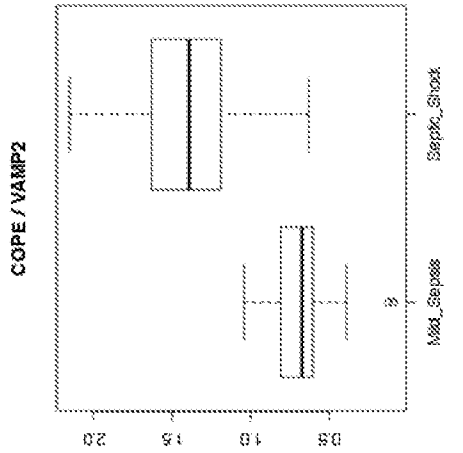

Fig. 21G

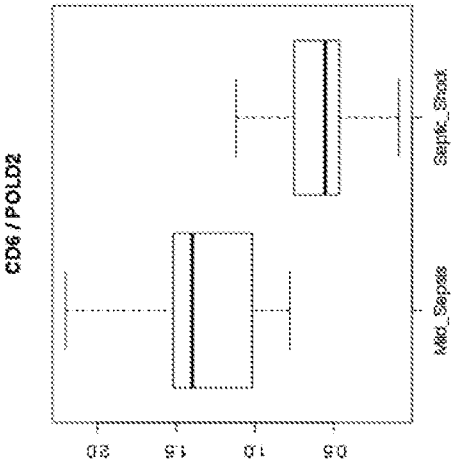

Fig. 21J

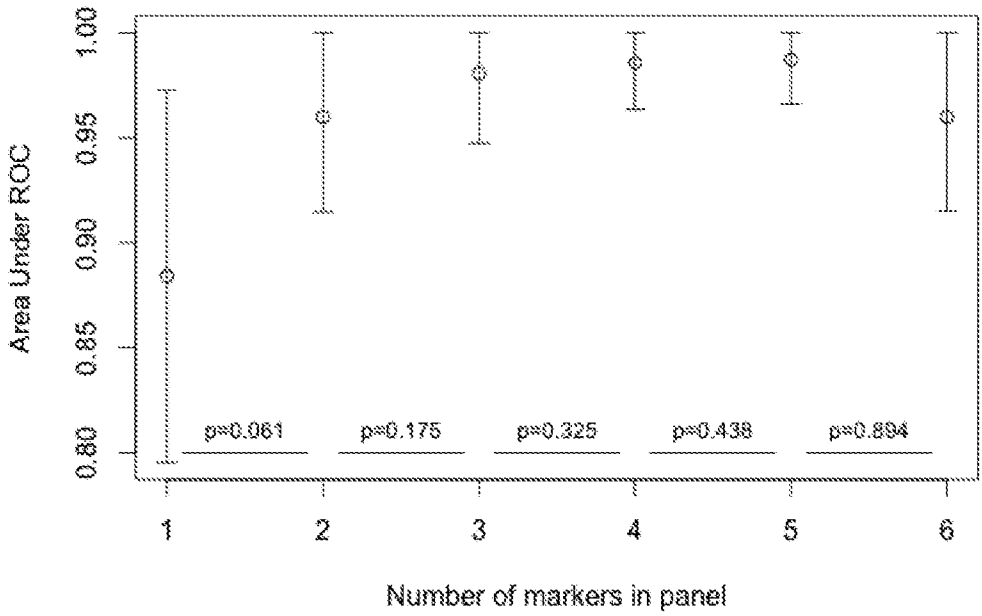
Area Under ROC
0.80
0.85
0.90
0.95
1.00
p=0.061
p=0.175
p=0.325
p=0.438
p=0.894
1
2
3
4
5
6
Number of markers in panel

Fig. 22

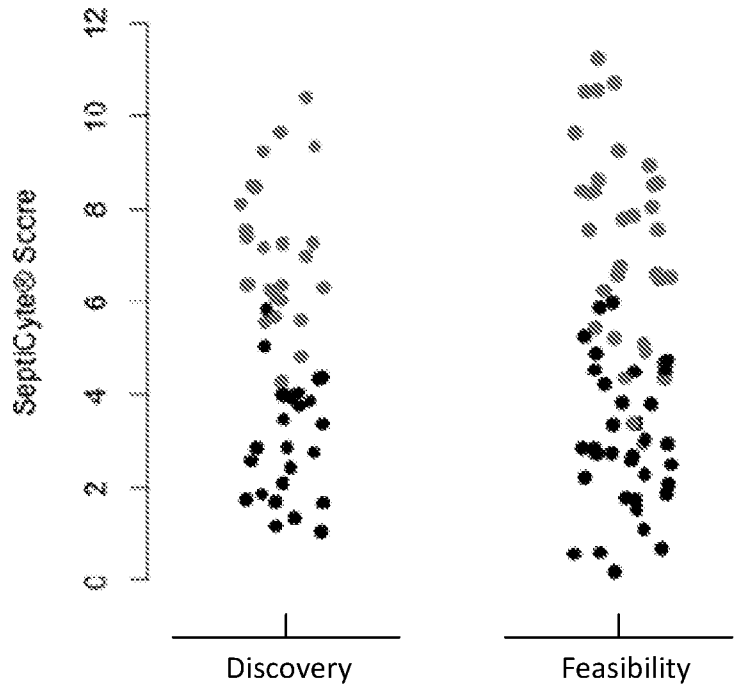
SeptiCyte® Score
0
2
4
6
8
10
12
Discovery
Feasibility

Fig. 23

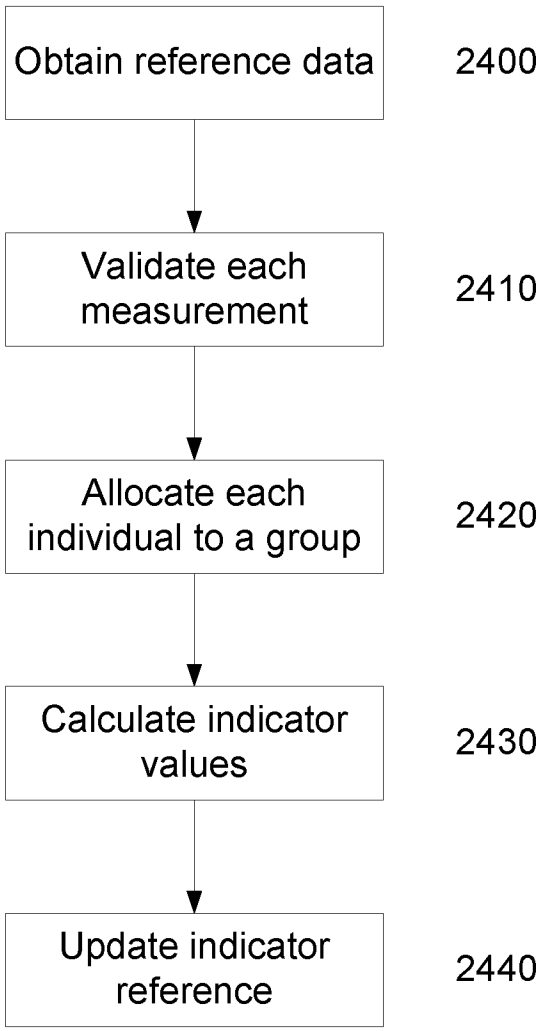
Obtain reference data
2400
Validate each measurement
2410
Allocate each individual to a group
2420
Calculate indicator values
2430
Update indicator reference
2440

Fig. 24

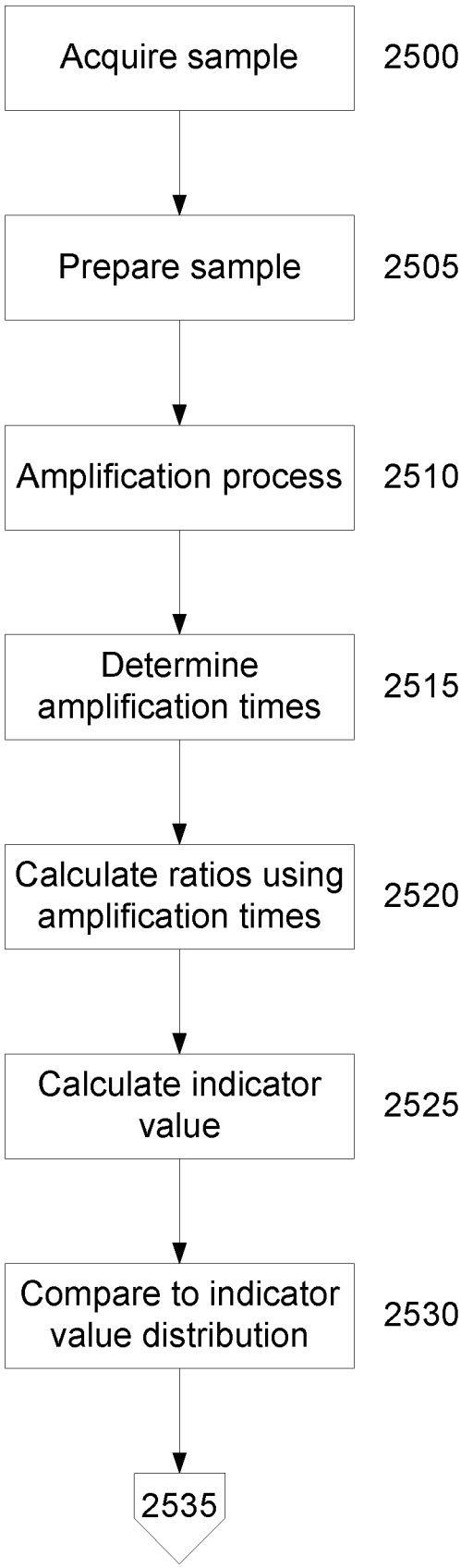
Acquire sample
2500
Prepare sample
2505
Amplification process
2510
Determine amplification times
2515
Calculate ratios using amplification times
2520
Calculate indicator value
2525
Compare to indicator value distribution
2530
2535

Fig. 25A

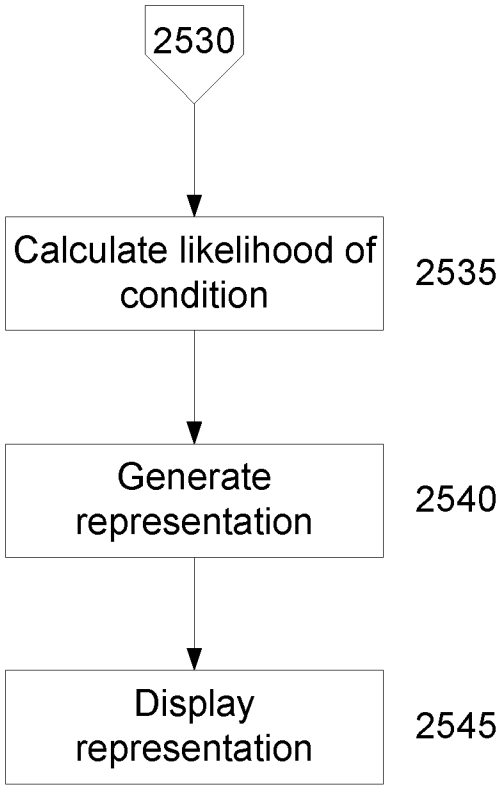
2530
Calculate likelihood of condition
2535
Generate representation
2540
Display representation
2545

Fig. 25B

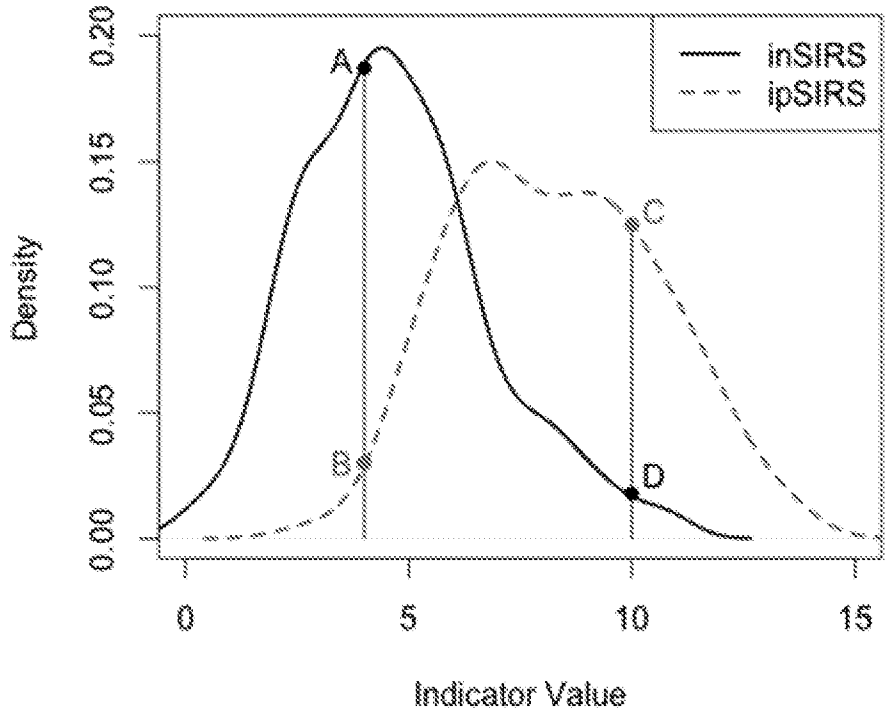
Density
0.00
0.05
0.10
0.15
0.20
0
5
10
15
Indicator Value
A
B
C
D
inSIRS
ipSIRS

Fig. 26

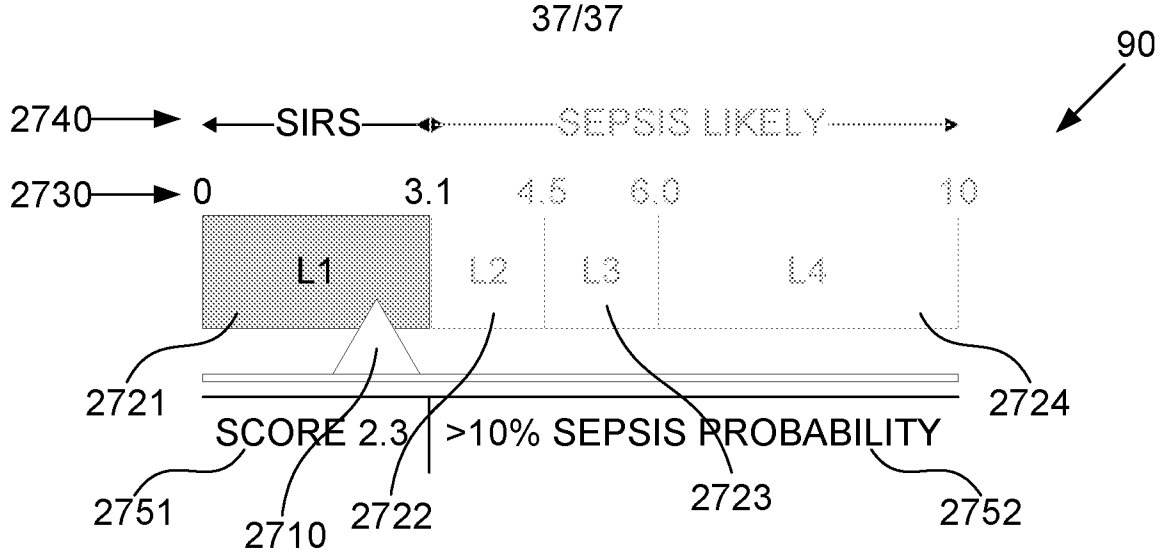

Fig. 27A

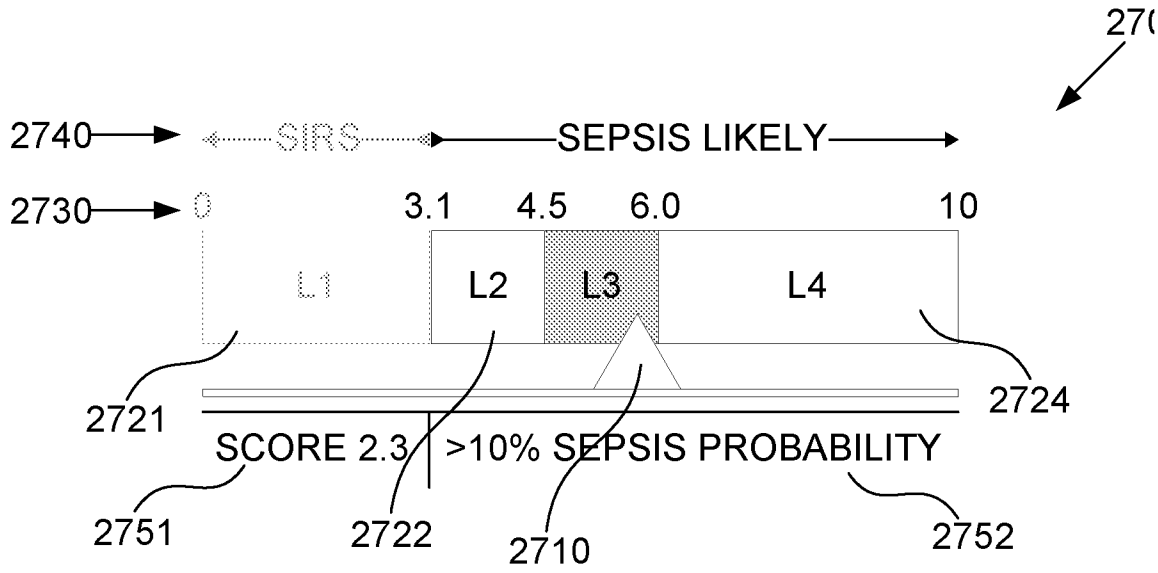

Fig. 27B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2015/050043

A. CLASSIFICATION OF SUBJECT MATTER

G06F 19/18 (2011.01) C12Q 1/68 (2006.01) G01N 33/50 (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPIAP, EPODOC, MEDLINE, HCAPLUS, BIOSIS & keywords: ratio, biomarker, mutual correlation, correlation coefficient, second pair, immune system, determine and like terms.

ESPACENET, AUSPAT & keywords: Immunexpress; Brandon, Richard Bruce; McHugh, Leo Charles

PUBMED & keywords: Brandon, Richard Bruce; McHugh, Leo Charles

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Documents are listed in the continuation of Box C	

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 April 2015	23 April 2015
Name and mailing address of the ISA/AU	**Authorised officer**
AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA Email address: pct@ipaustralia.gov.au	Richard Filmer AUSTRALIAN PATENT OFFICE (ISO 9001 Quality Certified Service) Telephone No. +61 2 6283 2735

INTERNATIONAL SEARCH REPORT		International application No.
C (Continuation).	DOCUMENTS CONSIDERED TO BE RELEVANT	**PCT/AU2015/050043**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2007/060647 A2 (THE PROVOST, FELLOWS AND SCHOLARS OF THE COLLEGE OF THE HOLY AND UNDIVIDED TRINITY OF QUEEN ELIZABETH, NEAR DUBLIN) 31 May 2007 Abstract; page 2 lines 11-18; page 6 lines 4-26; page 7 lines 25 – 29; page 18 lines 9-15; page 23 lines 20 – page 25 line 13; pages 48-54; claim 28	1-30, 40, 101-134, 145
X	WO 2010/083252 A2 (THE UNITED STATES OF AMERICA, as represented by the secretary, DEPARTMENT OF HEALTH AND HUMAN SERVICES) 22 July 2010 page 74 lines 12-15; pages 78-87	1-18, 24-30, 40, 101-117, 134, 145
X	WO 1999/045398 A1 (ARCTIC PARTNERS OY AB) 10 September 1999 page 5 line 24-page 6 line 10; page 16 lines 10-34; page 18 lines 18-31	1, 4-18, 24-30, 40, 101-107, 109-128, 134, 145
X	US 2003/0219760 A1 (GORDON et al.) 27 November 2003 [0066]-[0069], [0146], [0245], [0249], [0283], [0284], [0294]	1-24, 30, 40

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)

   ☐ on paper

   ☐ in electronic form

   b. (time)

   ☐ in the international application as filed

   ☐ together with the international application in electronic form

   ☐ subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

   An electronic sequence listing was filed with the application, but was not used for the purposes of the search and examination.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2015/050043

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:

because they relate to subject matter not required to be searched by this Authority, namely:

the subject matter listed in Rule 39 on which, under Article 17(2)(a)(i), an international search is not required to be carried out, including

2. ☐ Claims Nos.:

because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Supplemental Box for Details

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

1-30, 40, 101-134 and 145

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☒ No protest accompanied the payment of additional search fees.

Supplemental Box

Continuation of: **Box III**
This International Application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept.

PCT Rule 13.2, first sentence, states that unity of invention is only fulfilled when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding special technical features. PCT Rule 13.2, second sentence, defines a special technical feature as a feature which makes a contribution over the prior art.

This Authority has found that there are different inventions based on the following features that separate the claims into distinct groups.

Group 1 is defined by claims 1-30, 40, 101-134 and 145 and is directed to a method for determining an indicator of a medical condition comprising determining the ratio of concentrations a pair of immune system biomarkers, wherein the identities of the biomarkers are not specifically defined.

However this group does not comprise a special technical feature, as discussed below. Within this group the Authority has identified two individual features that, although not common to all claims of the group, may be special technical features that separate the claims into distinct inventions.

Invention 1 is defined by claims 2, 3 and 23 (completely) and claims 1, 4-22, 24, 30 and 40 (in part). The feature of a method for determining an indicator comprising combining the values of two ratios of biomarker concentrations, each value determined from a different pair of biomarkers, is specific to this group of claims.

Invention 2 is defined by claims 25-29, 101-134 and 145 (completely) and claims 1, 4-22, 24, 30 and 40 (in part). The feature of a method for determining an indicator wherein a pair of biomarkers has a mutual correlation range of between ±0.9 is specific to this group of claims.

It is not apparent that any other feature of these claims could serve as special technical feature.

Group 2 is defined by claims 31-39, 41-100 and 135-144 and is directed to kits, compositions and methods relating to specifically defined pairs of biomarkers.

Invention 3 is defined by claims 31, 36, 41, 57, 65, 66, 76, 86, 97-100, 135, 136 and 141 (completely) and claims 49-56, 74, 75, 84, 85 and 94-96 (in part). The feature of kits, compositions and methods relating to PLA2G7, PLAC8, CEACAM4 and LAMP1 is specific to this group of claims.

Further inventions are defined by claims 32-35, 37-39, 42-56, 58-64, 67-75, 77-85, 87-96, 137-140 and 142-144 (in part). The claims as they relate to each defined pair of biomarkers from Groups A to P each relates to a different invention. The number of inventions defined in this group of claims has not been determined.

When there is no special technical feature common to all the claimed inventions there is no unity of invention.

In the above groups of claims, the identified features may have the potential to make a contribution over the prior art but are not common to all the claimed inventions and therefore cannot provide the required technical relationship. The only feature common to all of the claimed inventions and which provides a technical relationship among them is a method of determining and indicator for diagnosing or prognosing a medical condition in a subject comprising determining the ratio of expression of two immune system biomarkers.

However this feature does not make a contribution over the prior art because it is disclosed in:

D1: WO 2007/060647 A2 (THE PROVOST, FELLOWS AND SCHOLARS OF THE COLLEGE OF THE HOLY AND UNDIVIDED TRINITY OF QUEEN ELIZABETH, NEAR DUBLIN) 31 May 2007

D2: WO 2010/083252 A2 (THE UNITED STATES OF AMERICA, as represented by the secretary, DEPARTMENT OF HEALTH AND HUMAN SERVICES) 22 July 2010

D3: WO 1999/045398 A1 (ARCTIC PARTNERS OY AB) 10 September 1999

Supplemental Box

D4: US 2003/0219760 A1 (GORDON et al.) 27 November 2003

Therefore in the light of these documents this common feature cannot be a special technical feature. Therefore there is no special technical feature common to all the claimed inventions and the requirements for unity of invention are consequently not satisfied *a posteriori*.

For the additional fee paid, the International Search Authority has searched and examined the claims to the extent that they pertain to Inventions 1 and 2.

INTERNATIONAL SEARCH REPORT Information on patent family members	International application No. **PCT/AU2015/050043**

This Annex lists known patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document/s Cited in Search Report		Patent Family Member/s	
Publication Number	**Publication Date**	**Publication Number**	**Publication Date**
WO 2007/060647 A2	31 May 2007	EP 1951899 A2	06 Aug 2008
		EP 1951899 B1	30 Jun 2010
		IE 20060853 A1	25 Jul 2007
		US 2009297474 A1	03 Dec 2009
		US 2013040299 A1	14 Feb 2013
WO 2010/083252 A2	22 July 2010	AU 2010204741 A1	07 Jul 2011
		CA 2749601 A1	22 Jul 2010
		EP 2380025 A2	26 Oct 2011
		EP 2380025 B1	11 Sep 2013
		EP 2667194 A2	27 Nov 2013
		EP 2667195 A2	27 Nov 2013
		JP 2012515334 A	05 Jul 2012
		JP 2014041162 A	06 Mar 2014
		NZ 593514 A	28 Mar 2013
		NZ 606687 A	29 Aug 2014
		US 2011306514 A1	15 Dec 2011
		US 2013210648 A1	15 Aug 2013
		WO 2014151079 A2	25 Sep 2014
WO 1999/045398 A1	10 September 1999	EP 1068534 A1	17 Jan 2001
		FI 980488 A	05 Sep 1999
		JP 2002506210 A	26 Feb 2002
US 2003/0219760 A1	27 November 2003	US 7622260 B2	24 Nov 2009
		AU 2002324881 A1	18 Mar 2003
		US 2011059854 A1	10 Mar 2011
		US 8551700 B2	08 Oct 2013
		US 2009104617 A1	23 Apr 2009
		WO 03021229 A2	13 Mar 2003

End of Annex

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.