

the gene expression levels for the CD-40 gene, the CD4 gene and the CD3E gene are usable to estimate the gene expression level for the CCR-5 gene,

the gene expression levels for the CTLA-4 gene, the TNF gene and the CX3CR1 gene are usable to estimate the gene expression level for the CD-40 gene,

the gene expression level for the CXCL9 gene is usable to estimate the gene expression level for the TNF gene,

the gene expression levels for the FOXP-3 gene and the EDN-1 gene are usable to estimate the gene expression level for the CX3CR1 gene,

the gene expression levels for the TBX-21 gene and the C-3 gene are usable to estimate the gene expression level for the CD-4 gene,

the gene expression level for the FASLG gene is usable to estimate the gene expression level for the TBX-21 gene,

the gene expression level for the CXCR-3 gene is usable to estimate the gene expression level for the CD3E gene, and

the gene expression level for the CCL-5 gene is usable to estimate the gene expression level for the CXCR-3 gene.

38. The method according to claim **30**, wherein the biomarker levels include gene expression levels for the VCAM1 gene, MMP9 gene, Banff C4d gene, MMP7 gene, LAMC2 gene, TNC gene, S100A4 gene, NPHS1 gene, NPHS2 gene, AFAP gene, PDGF8 gene, SERPINH1 gene, TIMP4 gene, TIMP3 gene, VIM gene, SERPINE1 gene, TIMP1 gene, FN1 gene, ANGPT2 gene, TGFB1 gene, ACTA2 gene, TIMP2 gene, COL4A2 gene, MMP2 gene, COL1A1 gene, COL3A1 gene, GREM1_2 gene, SPARC gene, IGF1 gene, SMAD3 gene, HSPG2 gene, FN1 gene, ANGPT2 gene, TGFB1 gene, ACTA2 gene, THBS1 gene, CTNNA1 gene, FGF2 gene, TJP1 gene, FAT gene, CDH1 gene, SMAD7 gene, CD2AP gene, CDH3 gene, CTGF gene, ACTN4 gene, SPP1 gene, AGRN gene, VEGF gene, and BMP7 gene.

39. The method according to claim **38**, wherein:

the gene expression levels for the TNC gene, the THBS-1 gene and the AFAP gene are usable to estimate the gene expression level for the LAMC-2 gene,

the gene expression levels for the NPHS-1 gene and the S100A4 gene are usable to estimate the gene expression level for the TNC gene,

the gene expression level for the NPHS-2 gene is usable to estimate the gene expression level for the NPHS-1 gene,

the gene expression level for the CTNNA-1 gene is usable to estimate the gene expression level for the THBS-1 gene,

the gene expression levels for the FGF-2 gene and the TJP-1 gene are usable to estimate the gene expression level for the CTNNA-1 gene,

the gene expression level for the CD-80 gene is usable to estimate the gene expression level for the CXCL-11 gene,

the gene expression levels for the FAT gene, the CDH-1 gene, the CD2AP gene, the CTGF gene and the ACTN-4 gene are usable to estimate the gene expression level for the TJP-1 gene,

the gene expression level for the SMAD-7 gene is usable to estimate the gene expression level for the CDH-1 gene,

the gene expression level for the CDH-3 gene is usable to estimate the gene expression level for the CD2AP gene,

the gene expression levels for the SPP-1 gene, the AGRN gene, the VEGF gene are usable to estimate the gene expression level for the ACTN-4 gene,

the gene expression level for the BMP-7 gene is usable to estimate the gene expression level for the VEGF gene,

the gene expression levels for the PDGFB gene, the TIMP-3 gene and the VIM gene are usable to estimate the gene expression level for the AFAP gene,

the gene expression level for the SERPINH-1 gene is usable to estimate the gene expression level for the PDGFB gene,

the gene expression level for the TIMP-4 gene is usable to estimate the gene expression level for the SERPINH-1 gene,

the gene expression levels for the SERPINE-1 gene, the TIMP-2 gene, the FN-1 gene, the TGFB-1 gene and the TIMP-1 gene are usable to estimate the gene expression level for the VIM gene,

the gene expression levels for the COL4A2 gene, the MMP-2 gene, the SMAD-3 gene and the HSPG-2 gene are usable to estimate the gene expression level for the TIMP-2 gene,

the gene expression level for the COL1A1 gene is usable to estimate the gene expression level for the MMP-2 gene,

the gene expression levels for the COL3A1 gene, the GREM-1-2 gene and the SPARC gene are usable to estimate the gene expression level for the COL1A1 gene,

the gene expression level for the IGF-1 gene is usable to estimate the gene expression level for the SPARC gene,

the gene expression level for the ANGPT-2 gene is usable to estimate the gene expression level for the FN-1 gene, and

the gene expression level for the ACTA-2 gene is usable to estimate the gene expression level for the TGFB-1 gene.

40. The method according to claim **30**, wherein said collecting of the clinical parameters includes collecting polymerase chain reaction data.

41. The method according to claim **30**, wherein the biopsy tissue includes tissue from a renal allograft biopsy.

42. The method according to claim **30**, further including outputting the patient-specific probability of disease to at least one of a web browser, a desktop user interface, and an electronic medical record.

43. The method according to claim **30**, wherein said receiving of the clinical parameters for the individual patient further includes receiving the clinical parameters the individual patient from at least one of a database interface and a web interface.

44. The method according to claim **30**, wherein said collecting of the clinical parameters for the individual patient includes collecting an incomplete record wherein at least one of the clinical parameters is unknown, and wherein said outputting of the patient-specific probability of disease from the fully unsupervised Bayesian Belief Network model includes calculating the patient-specific probability of disease based on the incomplete record.

45. The method according to claim **30**, wherein said receiving of the clinical parameters for the individual patient into the fully unsupervised Bayesian Belief Network model includes receiving the clinical parameters for the individual patient into nodes of the fully unsupervised Bayesian Belief Network model, wherein each of the nodes include at least two bins, and wherein the bins in at least one of the nodes are sized such that data from the training database is evenly distributed between the bins.