

Claims

1. A method for distinguishing between active and latent *Mycobacterium tuberculosis* (TB) infection in a patient suspected of being infected with TB, the method comprising: obtaining a gene expression dataset from a whole blood sample from the patient; determining the expression pattern of two or more genes selected from the genes listed in Table 6 that distinguish between active and latent infection; and distinguishing between active and latent TB infection based on the expression pattern of the two or more genes.
2. The method of claim 1, comprising determining the expression pattern of five or more, ten or more, or 15 or more genes selected from the genes listed in Table 6.
3. The method of claim 1, comprising determining the expression pattern of the genes: ST3GAL6, PAD14, TNFRSF12A, VAMP3, BR13, RGS19, PILRA, NCF1, LOC652616, PLAUR(CD87), SIGLEC5, B3GALT7, IBRDC3(NKLAM), ALOX5AP(FLAP), MMP9, ANPEP(APN), NALP12, CSF2RA, IL6R(CD126), BASGRP4, TNFSF14(CD258), NCF4, HK2, ARID3A and PGLYRP1(PGRP), which are underexpressed/underrepresented in the blood of latent TB patients but not in the blood of healthy individuals or active TB patients.
4. The method of claim 1, comprising determining the expression pattern of the genes: PSMB8(LMP7), APOL6, GBP2, GBP5, GBP4, ATF3, GCH1, VAMP5, WARS, LIMK1, NPC2, IL-15, LMTK2 and STX11(FHL4), which are overexpressed/overrepresented in the blood of active TB, and underexpressed/underrepresented in the blood of latent TB patients and healthy control individuals.
5. The method of claim 1, comprising determining the expression pattern of the genes: FLJ11259(DRAM), JAK2, GSDMDC1(DF5L)(FKSG10), SIPAIL1, [2680400](KIAA1632), ACTA2(ACTA) and KCNMB1(SLO-BETA), which are overexpressed/overrepresented in blood from active TB patients, and underexpressed/underrepresented in the blood from latent TB patients and healthy control individuals.

6. The method of claim 1, comprising determining the expression pattern of the genes: SPTAN1, KIAAD179(Nnp1)(RRP1), FAM84B(NSE2), SELM, IL27RA, MRP534, [6940246](IL23A), PRKCA(PKCA), CCDC41, CD52(CDW52), [3890241](ZN404), MCCC1(MCCA/B), SOX8, SYNJ2, FLJ21127 and FHIT, which are underexpressed/underrepresented in the blood of active TB patients but not in the blood of latent TB patients or healthy control individuals.

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1. A method for distinguishing between active and latent *Mycobacterium tuberculosis* (TB) infection in a patient suspected of being infected with TB, the method comprising: obtaining a gene expression dataset from a whole blood sample from the patient; determining the expression pattern of two or more genes selected from the genes listed in Table 6 that distinguish between active and latent infection; and distinguishing between active and latent TB infection based on the expression pattern of the two or more genes.
2. The method of claim 1, comprising determining the expression pattern of five or more, ten or more, or 15 or more genes selected from the genes listed in Table 6.
3. The method of claim 1, comprising determining the expression pattern of the genes: ST3GAL6, PAD14, TNFRSF12A, VAMP3, BRI3, RGS19, PILRA, NCF1, LOC652616, PLAUR(CD87), SIGLEC5, B3GALT7, IBRDC3(NKLAM), ALOX5AP(FLAP), MMP9, ANPEP(APN), NALP12, CSF2RA, IL6R(CD126), RASGRP4, TNFSF14(CD258), NCF4, HK2, ARID3A and PGLYRP1(PGRP), which are underexpressed/underrepresented in the blood of latent TB patients but not in the blood of healthy individuals or active TB patients.
4. The method of claim 1, comprising determining the expression pattern of the genes: PSMB8(LMP7), APOL6, GBP2, GBP5, GBP4, ATF3, GCH1, VAMP5, WARS, LIMK1, NPC2, IL-15, LMTK2 and STX11(FHL4), which are overexpressed/overrepresented in the blood of active TB, and underexpressed/underrepresented in the blood of latent TB patients and healthy control individuals.
5. The method of claim 1, comprising determining the expression pattern of the genes: FLJ11259(DRAM), JAK2, GSDMDC1(DF5L)(FKSG10), SIPA1L1, [2680400](KIAA1632), ACTA2(ACTSA) and KCNMB1(SLO-BETA), which are overexpressed/overrepresented in blood from active TB patients, and underexpressed/underrepresented in the blood from latent TB patients and healthy control individuals.

6. The method of claim 1, comprising determining the expression pattern of the genes: SPTAN1, KIAA0179(Nnp1)(RRP1), FAM84B(NSE2), SELM, IL27RA, MRPS34, PRKCA(PKCA), CCDC41, CD52(CDW52), MCCC1(MCCA/B), SOX8, SYNJ2, FLJ21127 and FHIT, which are underexpressed/underrepresented in the blood of active TB patients but not in the blood of latent TB patients or healthy control individuals,