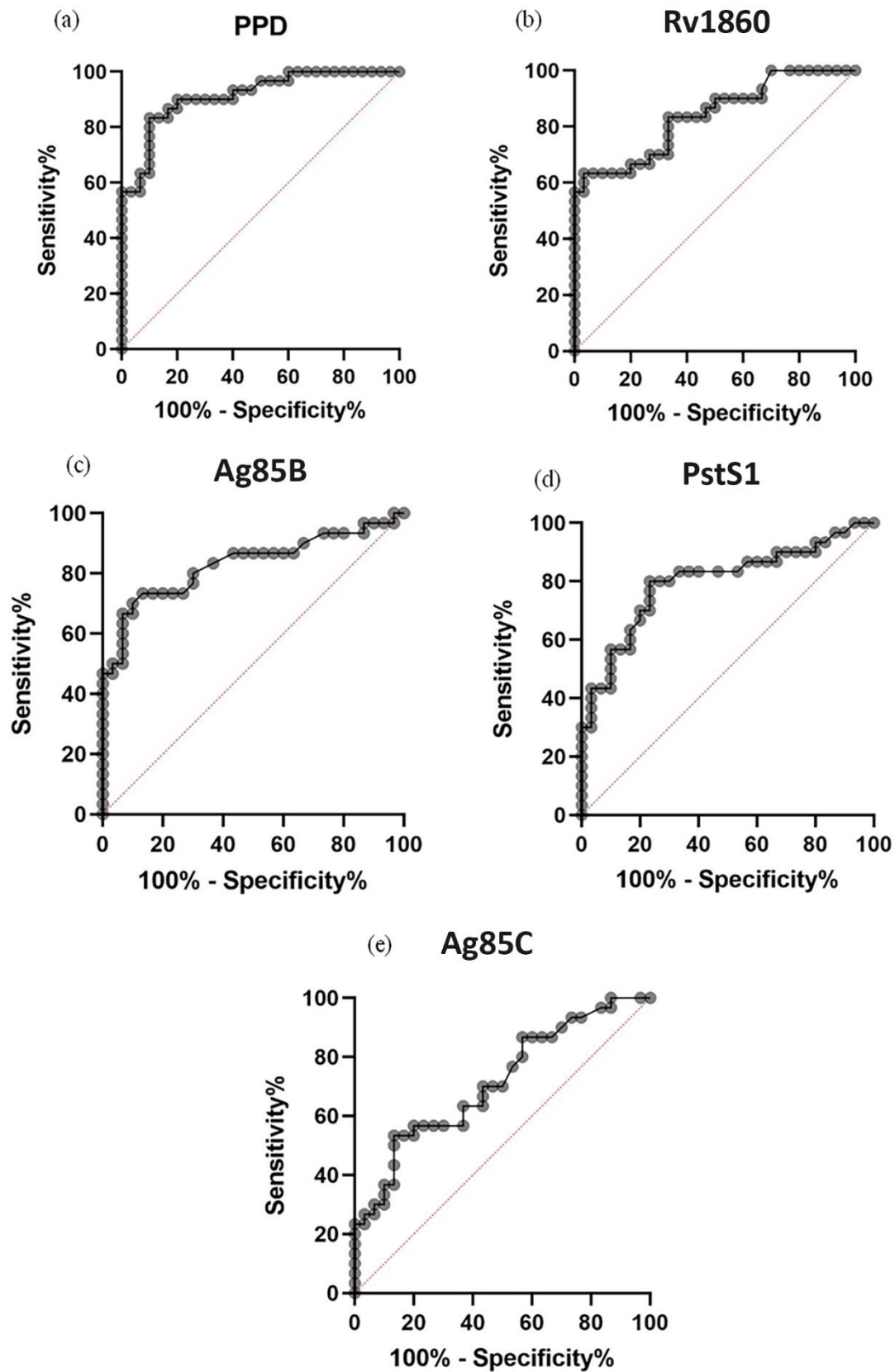
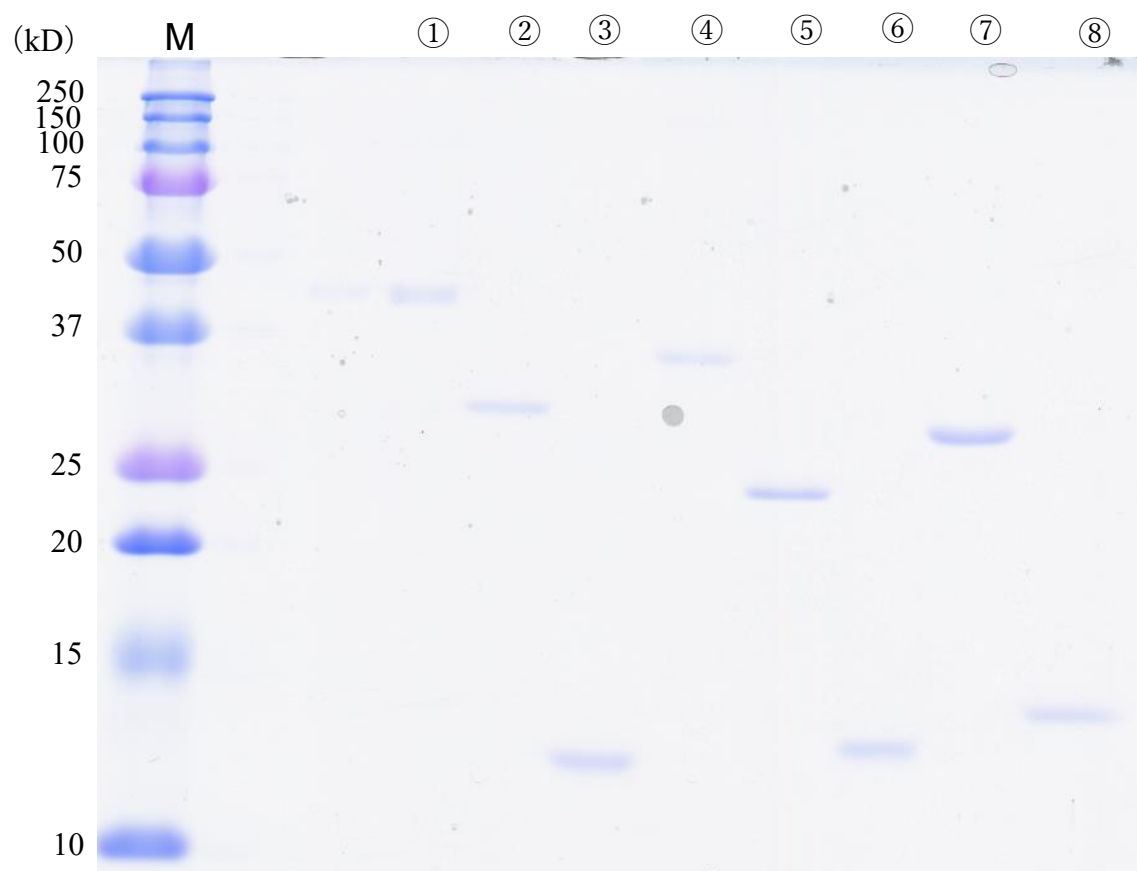


Supplementary Fig. S1



Receiver-operator characteristic (ROC) curve of the IgG concentration of the (a) PPD, (b) Rv1860, (c) Ag85B, (d) PstS1, and (e) Ag85C antigen between 30 TB patients and healthy controls.

**Supplementary Fig. S2**



### ① Rv1860

Protein sequence coverage: 52%

Matched peptides shown in **bold red**.

```

1 MHQVDFNLTR RKGRLLALAI AAMASASLVT VAVPATANAD PEPAPFVFTT
51 AASPPSTAAA PPAPATPVAP PPPAAANTPN AQPQDFNAAP PPADFNAPPP
101 PVIAPNAPQP VRIDNFGVGF SFALPAGWVE SDAAHFDYGS ALLSKTTGDP
151 FFPQQFFFA NDTRIVLGR L DQKLYASAEA TDSKAAARLG SDMGFTMPY
201 PGTRINQETV SLDANGVSGS ASYIEVKFSD PSKPNQIWT GVIGSPAANA
251 PDAGFPQRWF VVNLGTANNP VDKGAALKALA ESIRPLVAPP PAPAPAPAEF
301 APAPAPAGEV APTFTTPTTQ RTLPA

```

### ② Ag85C

Protein sequence coverage: 32%

Matched peptides shown in **bold red**.

```

1 MTFEQVRLR RSAATTLERR LAIAAMGAVL VYGLVGTGG PATAGAFSRP
51 GLPVEYLQVP SASMRDIDV QFQGGGPHAV YLLDGLRAQD DYNWDINTP
101 AFEYYQSG L SVIMFVGGQS SFYTDWYQPS QSNQNYTYK WETFLTREMP
151 AWLQANKGVS PTGNAAVGLS MSGGSALILA AYYFQQFFYA ASLSGFLNPS
201 EGWNP TLIGL AMNDSGGYNR NSMWGSSDP ANKRNDFMVQ IPRLVANTR
251 IWVCGNGTF SDLGNDIPA KFLEGLTLRT NQTFRDYAA DGGRRGVNF
301 PFNGTHSWPY WNEQLVAMKA DIQHVLNGAT PPAAPAAPAA

```

### ③ Thioredoxin

Protein sequence coverage: 36%

Matched peptides shown in **bold red**.

```

1 MTDSEKATI KVIDASFATD VLSSNKFVLV DFNATWCGFC KGVAPVLEEI
51 ATERATDLTV AKLDVDNPE TARNFQVSI PTLILFKDQGV FVKRIVGAKG
101 KAALLRELS VVPNLN

```

### ④ PstS1

Protein sequence coverage: 53%

Matched peptides shown in **bold red**.

```

1 MKIRLHTLLA VLTAAPLLLA AAGCGSKFSS GSPETGAGAG TVATTTPASSP
51 VTIAETGSTL LYPLFNWGP AFHERYPNVT ITAQGTGSGA GIAQAAAGTV
101 NIGASDAYLS EGDMAAHKGL HNIALAISAQ QVNNLPGVS EHLKLNKVL
151 AAMYQGTIXT WDDPQIAALN PGVNLPGTAV VFLNRSDDSG DTFLFTQYLS
201 KQDFEGWGS PGFGTTVDFF AVPGALGENG NGGMVTGCAE TPGCVAYIGI
251 SFLDQASQRG LGEAQLGNSS GNFLFPDAQS IQAAAAGFAS KTFANQAISM
301 IDGPAPDGYF IINYEYAIYN NRQKDAATAQ TLQAFILHAI TDGNAASFID
351 QVHFQFLPFA VVKLSDALIA TISS

```

### ⑤ Rv3803c

Protein sequence coverage: 46%

Matched peptides shown in **bold red**.

```

1 MKGRSALLRA LWIAALSFLG GGVAVAAEPT AKAAPYENLM VPSFSMGRDI
51 EVAFLAGGPH AVYLLDAFNA GPDVSNWVTA GNAMNTLAGK GISVVAPAGG
101 AYSMTNWEQ DGSKQWDTFL SAELPDWLAA NRGLAPGGHA AVGAAQGGYG
151 AMALAAFHPD RFGFAGSMG FLYPSNTTIN GAIAAGMQQF GGVDTNGMWG
201 APQLGRNKH DPWVHASLLA QNTRVWVHS PTNPGASDPA AMIGQAAEAM
251 GNSRMFTNYQ RSVGGHNGHF DFPASGDNGW GSWAPQLGAM SGDIVGAIR

```

### ⑥ Rv2878c

Protein sequence coverage: 38%

Matched peptides shown in **bold red**.

```

1 MSLRLVSPIK AFADGIVAVA IAVVLMFGLA NTPRAVADE RLQFTATTLS
51 GAPFDGASLQ GKPAVLNFWT PWCPCNAEA PSLSQVAAAN PAVTFVGIAT
101 RADVGAQSF VSKYNLNFN LNDADGVIWA RYNVFWQPAF VFYRADGTST
151 FVNNTAAMS QDELSGRVAA LTS

```

### ⑦ Ag85B

Protein sequence coverage: 26%

Matched peptides shown in **bold red**.

```

1 MTDVSRKIRA WRRRLMIGTA AAVVLPGLVG LAGGAATAGA FSRPGLPEY
51 LQVSPSPMGR DIKVQFQSGG NNSPAVYLLD GLRAQDDYNG WDINTPAFEW
101 YYQSGLSIVM FVGGQSSFS DWYSPACGKA GCQTYKNETF LTSELPQWLS
151 ANRAVKPTGS AAIGLSMAGS SAMILAAYHP QQFIYAGSL ALLDPSQGMG
201 PSLIGLAMGD AGGYKAADMW GPSSDPAPER NDPTQQIFKL VANNTRLWVY
251 CGNGTPNELG GANIPAEFL NEVRSSNLKF QDAYNAAGGH NAVENFPNG
301 THSWEYGAQ LNAMKGDLQS SLGAG

```

### ⑧ Rv1926c

Protein sequence coverage: 57%

Matched peptides shown in **bold red**.

```

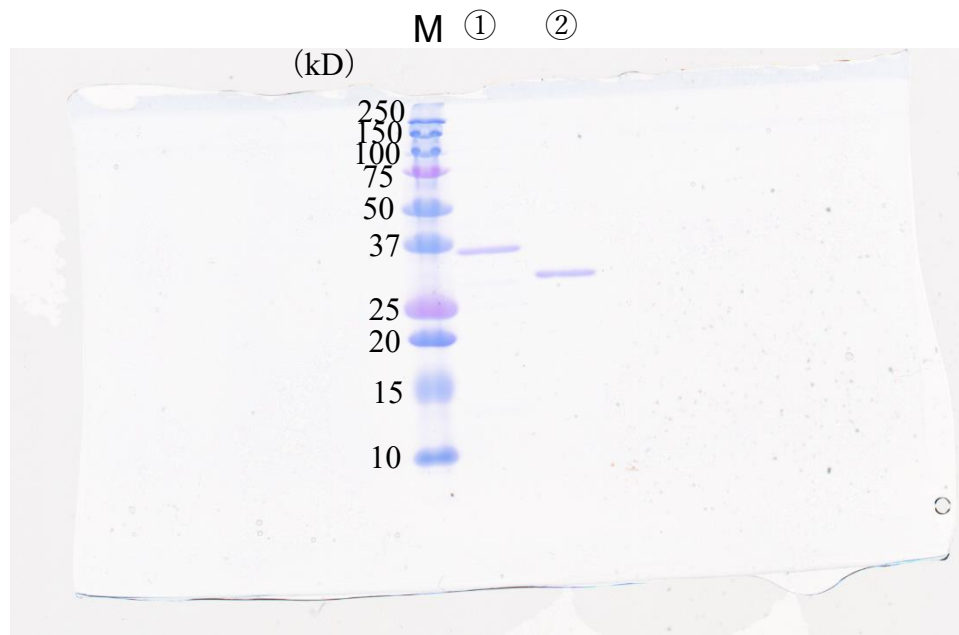
1 MKLTTMIKTA VAVVMAAIA TFAAPVALAA YPITKLGSE LTMTDTVGQV
51 VLGKVVSDLK SSTAVIFGYF VAGQVWEATA TVNAIRGSVT PAVSQFNART
101 ADGINYRVLW QAAGPDTISG ATIPQGEQST GKIYFDVTGP SPTIVAMNNG
151 MEDLLINEP

```

SDS-PAGE analysis of native purified *M. tuberculosis* proteins and their mass spectrometry analyses are shown.

M, protein molecular standards, ① Rv1860; ② Ag85C; ③ Thioredoxin; ④ PstS1; ⑤ Rv3803c; ⑥ Rv2878c; ⑦ Ag85B; ⑧ Rv1926c. Identified amino acid sequence are marked in red

Supplementary Fig. S3



### ① ePstS1

Protein sequence coverage: 66%

Matched peptides shown in **bold red**.

1	MKIRLHTLLA	VLTAAPLLLA	AAGCGSKPPS	GSPETGAGAG	TVATTPASSP
51	VTLAETGSTL	LYPLFNLWGP	AFHERYPNVT	<b>ITAQGTGSGA</b>	<b>GIAQAAAGTV</b>
101	<b>NIGASDAYLS</b>	<b>EGDMAAHKGL</b>	<b>MNIALAISAQ</b>	<b>QVNYNLPGVS</b>	<b>EHLKLNKVL</b>
151	<b>AAMYQGTIKT</b>	<b>WDDPQIAALN</b>	<b>PGVNLPGTAV</b>	<b>VPLHRSDGSG</b>	<b>DTFLFTQYLS</b>
201	<b>KQDPEGWGKS</b>	PGFGTTVDFF	AVPGALGENG	NGGMVTGCAE	TPGCVAYIGI
251	SFLDQASQRG	<b>LGEAQLGNSS</b>	<b>GNFLLPDAQS</b>	<b>IQAAAAGFAS</b>	<b>KTPANQAISM</b>
301	<b>IDGPAPDGYP</b>	<b>IINYEYAIYN</b>	<b>NRQKDAATAQ</b>	<b>TLQAFLHWAI</b>	<b>TDGNKASFLD</b>
351	<b>QVHFQPLPPA</b>	<b>VVKLSDALIA</b>	<b>TISS</b>		

### ② eAg85B

Protein sequence coverage: 46%

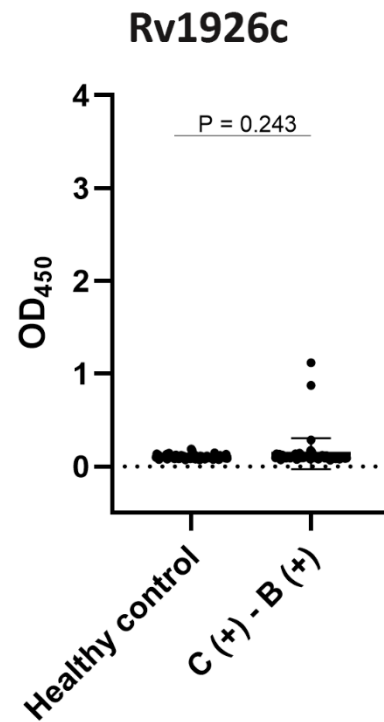
Matched peptides shown in **bold red**.

1	MTDVSRKIRA	WGRRLMIGTA	AAVVLPGIVG	LAGGAATAGA	FSRPGLEVEY
51	LQVPSPSMGR	<b>DIKVFQSGG</b>	<b>NNSPAVYLLD</b>	<b>GLRAQDDYNG</b>	<b>WDINTPAFEW</b>
101	YYQSGLSIVM	FVGGQSSFYS	DWYSPACGKA	<b>GCQTYKWETF</b>	<b>LTSELPQWLS</b>
151	<b>ANRAVKFTGS</b>	<b>AAIGLSMAGS</b>	<b>SAMILAAYHP</b>	<b>QQFIYAGSLS</b>	<b>ALLDPSQGMG</b>
201	<b>PSLIGLAMGD</b>	<b>AGGYKAADMW</b>	<b>GPSSDPAWER</b>	<b>NDPTQQIPKL</b>	<b>VANNTRLWVY</b>
251	<b>CGNGTPNELG</b>	<b>GANIPAEFLE</b>	<b>NFVRSSNLKF</b>	<b>QDAYNAAGGH</b>	<b>NAVENFPFNG</b>
301	<b>THSWEYWGAQ</b>	<b>LNAMKGDLS</b>	<b>SLGAG</b>		

SDS-PAGE analysis of recombinant *M. tuberculosis* proteins from *E. coli* and the mass spectrometry analyses of ePstS1 and eAg85B are shown.

M, protein molecular standards, ① ePstS1; ② eAg85B. Identified amino acid sequence are marked in red.

# Supplementary Fig. S4



Graphic of the IgGs amount. ELISA optical density of antigen Rv1926c indicating the serum antibody concentration in the clinically positive – bacteriology test positive [C (+) - B (+)] and HC groups. The results were analyzed as individually and the data presented as mean  $\pm$  SD