## M\_tuberculosis\_H37Rv

M\_tuberculosis\_H37Rv M\_marinum\_M M\_kansasii\_ATCC\_12478 M\_ulcerans\_Agy99 M\_parascrofulaceum\_ATCC\_BAA-61 M\_intracellulare\_ATCC\_13950 M\_colombiense\_CECT\_3035 M\_avium\_subsp\_paratuberculosis M\_sp\_JDM601 M leprae TN M\_xenopi\_RIVM700367

## M\_tuberculosis\_H37Rv

M\_tuberculosis\_H37Rv

M\_tuberculosis\_H37Rv

M\_leprae\_TN M xenopi RIVM700367

M\_tuberculosis\_H37Rv

M\_tuberculosis\_H37Rv

M\_ulcerans\_Agy99

M\_xenopi\_RIVM700367

M\_tuberculosis\_H37Rv

M sp JDM601

M\_leprae\_TN

M\_sp\_JDM601

M\_tuberculosis\_H37Rv M marinum M M\_kansasii\_ATCC\_12478 M\_ulcerans\_Agy99 M parascrofulaceum ATCC BAA-61 M\_intracellulare\_ATCC\_13950 M\_colombiense\_CECT\_3035 M\_avium\_subsp\_paratuberculosis M\_sp\_JDM601 M\_leprae\_TN M xenopi RIVM700367



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M tuberculosis H37Rv	VQ
M_marinum_M	VQ
M kansasii ATCC 12478	VQ
M_ulcerans_Agy99	VQ
M_parascrofulaceum_ATCC_BAA-61	VQ
M_intracellulare_ATCC_13950	VQ
M_colombiense_CECT_3035	VQ
M_avium_subsp_paratuberculosis	VQ
M sp JDM601	VQ
M_leprae_TN	VQ
M_xenopi_RIVM700367	VQ

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	VÇ	V	G	V	K	т	v	L	D	т	L	P	Y	G	Е	W	K	т	H	s	R	v
	VÇ	v	G	v	K	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	V
	VÇ	v	G	v	ĸ	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	v
	VÇ	v	G	V	K	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	v
BAA-61	VÇ	v	G	v	ĸ	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	v
3950	vç	v	G	v	ĸ	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	v
;	vç	v	G	v	ĸ	т	v	L	D	т	L	P	Y	G	Е	W	ĸ	т	H	s	R	ν
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	vc	v	G	v	ĸ	т	v	L	D	т	L	P	Y	G	А	W	ĸ	т	н	R	R	ν
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Figure S1. Sequence alignment of the EspG<sub>5</sub> family members. Sequences with >98 % identity were excluded from the alignment. Identical residues are highlighted in red. Blue triangles at the top of the alignments indicate residues that are in contact with PPE41 in the *M. tuberculosis* PE25–PPE41–EspG<sub>5</sub> complex. The secondary structure elements of *M. tuberculosis* EspG<sub>5</sub> are shown at the top of the alignment. Black dashed lines indicate disordered residues.

	<i>Rv2430c</i>   <i>PPE41</i>	η1 000	α1 00000000	0 0000	000000000	α2 0000000000	000000000000.	0	00000	00000000	α3	000000
				20	30	40	50	<b>T</b> .	60	70	80	
	_Rv2430c   PPE41 Rv0388c   PPE9	MHFEAY	PPEVNSANI PPEINSARI	Y AGPGPDSML Y SGPGSRPLMO	AARAWRSL	DVEMTAVQRS ANELTATAAS	SFNRTLLSLMD. SYSSVISGLTGI	DWL	GPVVMQ GPSALS	LMEAAKPF MAAAAVPY	VRWLTDLCVQL VAWMRATAASA	SEVERQ
	Rv0915c PPE14	MDFGLL	PPEVN <mark>S</mark> SRM	YSGPGPESML	AAAAWDGV	AAEL <mark>T</mark> SAAVS	SYGSVVSTLIVE	P <mark>W</mark> M	<b>G</b> PAAAA	МААААТРҮ	<b>VGWLAATAALA</b>	KĒTATQ
	Rv1039c PPE15 Rv1168c PPE17	MDFGAL	PPEINSARM: PPEFNSLNI(	YAGAGAGPMM# DGSARPFLV	AGAAWNGL AANAWKNL	AAELGTTAAS SNELSYAASF	SYESVITRLTTE RFESEINGLIT.	SWM	GPASMA GPSSTI	MVAAAQPY MAAAVAPF	LAWLTYTAEAA RAWIVTTASLA	AHAGSQ
	Rv1196 PPE18	MVDFGAL	PPEIN <mark>S</mark> ARM	YAGPGSASLVA	AAQMWDSV	ASDLFSAASA	AFQSVVWGLTVG	S <mark>W</mark> I	GSSAGL	MVAAASPY	VAWMSVTAGQA	ELTAAQ
5	Rv1361c PPE19 Rv1705c PPE22	MVDFGAL	PPEINSARM PPEVNSGRM	Y AGPGSASLV# Y CGPGSAPMV#	AAKMWDSV	ASDLFSAAS# AAELSVAAVO	AFQSVVWGLTTC GYERVITTLOTE	SWI	GSSAGL GPASTL	MVAAASPY MVEAVAPY	VAWMSVTAGQA VAWMRATAIOA	EOAASO
ge	Rv1706c PPE23	MSNFGAL	PPEIN <mark>S</mark> GRM	Y S G P G S G P L M Z	<b>A</b> AAAWDGL	AAELSSAATO	GYGAAISELTNM	IRW <mark>W</mark> S	GPASDS	MVAAVLPF	VGWLSTTATLA	EQAAMQ
eag	Rv1787   PPE25 Rv1789   PPE26	MDFGAL	PPEINSGRM PPEVNSVRM	Y C G P G S G P M L F Y A G P G S A P M V F	AAAAWDGV	AVELGLAATC AAELSSAATC	GYASVIAELTGA GYETVITOLSSE	PWV	GAASLS GPASAA	МVАААТРҮ МАЕАVАРҮ	VAWLSQAAARA VAWMSAAAAAOA	EQAGMQ
olin	Rv1790 PPE27	MDFGAL	PPEIN <mark>S</mark> GRM	YCGPGSGPMLZ	AAAAWDGV	AVELGLAATO	GYASVIAÊLTG <i>A</i>	P <mark>W</mark> V	GAASLS	ΜVΑΑΑΤΡΥ	VAWLSQAAARA	EQAGMQ
sut	RV1801 PPE29 Rv1802 PPE30	MDFGLL	PPEINSGRM: PPEINSGRM	Y TGPGPGPGPML Y AGPGSGPML	AATAWDGL	AVELHATAAC ATELOSTAAL	GYASELSALT.C DYGSVISVLT.C		GOSSGT	MASAAAPY MAAAAAPY	VAWMSATAVHA VAWMSATAALA	REAAAO
ly (	Rv1807 PPE31	MDFATL	PPEIN <mark>S</mark> ARM	Y SGAGSAPML A	AASAWHGL	SAELRASALS	SYSSVLSTLTGE	E <mark>W</mark> H	GPASAS	МТАААРҮ	VAWMSVTAVRA	EQAGAQ
ami	RV1808 PPE32 Rv1809 PPE33	MDFGAL	PPEINSGRM: PPEITSGEM!	Y LGPGSGPLLF Y LGPGAGPMLF	AAAAWDAL	AAELYSAAAS AAELOSMAAS	SYGSTIEGLTVA SYASIVEGMASE		GPSSIT	MAAAVAPY MAAAAAPY	VAWISVTAGQA VTWMSGTSAQA	KAAADO
nbfa	Rv2352c PPE38	.MILDFSWL	PPEINSARI 1	YAGAGSGPLFN	AAAWEGL	AADLRASASS	SFDAVIAGLAA.	GPWS	GPASVA	MAGAAAPY	VGWLSAAAGQA	ELSAGQ
SL	Rv2768C PPE43 Rv2770c PPE44	MDFGAL	PPEINSTRM: PPEVNSARM:	YGGAGAADLLA	AAAAWNGI	AVELSTTASS AVEVSTAASS	SVGSVITRLSTE	UWL	GPASMS GPASLS	MAAAVOPY	LAWLTYTAESA LVWLTCTAESS	ALAAAQ
Ϋ́Ε	Rv2892c PPE45	MDFGVL	PPEINSGRM	YAGPGSGPMM	AAAAWDSL	AAELGLAAGO	GYRLAISELTGA		GPAAAS	MVAAVTPY	VAWLSATAGQA	EQAGMQ
0)	Rv3125C PPE49 Rv3136 PPE51	MDFALL	PPEVNSARM	Y TGPGAGSLL	AAGGWDSL	AAELATTAEA	AYGSVLSGLAAI		GPAAES GPAAES	MAVTAAPY	IGWLYTTAEKT	QUAAIQ
	Rv3478 PPE60	MVDFGAL	PPEINSARM	YAGPGSASLVA	AAKMWDSV	ASDLFSAASA	AFQSVVWGLTVG	S <mark>W</mark> I	GSSAGL	MAAAASPY	VAWMSVTAGQA	QLTAAQ
	_Rv3621c   PPE65	MLDFAQL	PPEVNSIKM	YAGPGSGPML	AAAAWEAL	AAELQTTAST	<b>TYDALITGLAD</b>	···P <mark>W</mark> Q	GSSAAS	MVAAATPQ	VAWLRSTAGQA	EQAGSQ
	Rv0305c PPE6	MDFVVS	APEVNSLRM	YLGAGSGPML	AAAAWDGL	ADELAVAASV	WFGSVTSGLAD.	AAWR	GPAAVA	MARAVAPY	L <mark>GWLISATAQA</mark>	EQAAAQ
S	Rv0442c PPE10	MTSPHFAWL	PPEINSARL PPEINSALMI	FAGPGSGPLIA	AATAWDGL	AEELLASIAS	SLGSVTSELTS.	GAWL	GPSAAA	MMAVATQY	LAWLSTAAAQA	EQAAAQ
le	Rv0755c PPE12	MVGFAWL	PPETNSLRM	Y L G A G S R P L L A	AAGAWDGL	AEELHAAASS	SFGSVTSELAG.	GAWQ	G P A S A A	MANAAGPY	ASWLTAAGAQA	ELAARQ
eac	Rv1135c PPE16	MSFLVL	PPEVNSAR1 PPEVNSALMI	FAGAGSGPTL	AAAAWDGL	AAELGQAANS	SFSSATAALAD.	TAWQ	GPAATA	MAAAAAPI	ASWLSTAATRA	LSAAAQ
lin	Rv1548c PPE21	MNFSVL	PPEINSALMI	FAGAGPGPML	AASAWTGL	AGDLGSAAAS	SFSAVTSQLAT.	GSWQ	GPASAA	MTGVAASY	ARWLTTAAAQA	EQAAGQ
sub	Rv1800   PPE28	.MLPNFAVL	PPEVNSARVI	FAGAGSAPML	AAAAWDDL	ASELHCAAMS	SFGSVTSGLVV.	GWWQ	GSASAA	MVDAAASY	IGWLSTSAAHA	EGAAGL
N (	Rv1917c PPE34	MNFSTL	PPEINSALII PPEINSALII	FGGAGSEPMSA	AAVAWDQL	AMELASAAAS	SFNSVTSGLVG.	ESWL	GPSSAA	MAAAVAPY	LGWLAAAAAQA	QRSATQ
m	Rv2356c PPE40	MVNFSVL	PPEINS GRMI	FFGAGSGPML	AAAAWDGL	AAELGLAAES	SFGLVTSGLAGO	SGQAWQ	GAAAAA	MVVAAAPY	AGWLAAAAARA	GGAAVQ
bfa	Rv2608 PPE42	MNFAVL	PPEVNSARII	FAGAGLGPML	AASAWDGL	AEELHAAAGS	SFASVTTGLAG.	DAWH	GPASLA	MTRAASPY MAAAADV	VGWLNTAAGQA	AQAAGQ
su	Rv3159c PPE53	MNYSVL	PPE INSLRMI	FTGAGSAPML	ASVAWDRL	AAELAVAASS	SFGSVTSGLAG.	QS <mark>W</mark> Q	GAAAAA	MAAAAAPY	AGWLAAAAAAA	AGASAQ
TR	Rv3343c PPE54	MSFVVM	PPEINSLLI PPEINSVLM	Y T G A G P G P L L F	AAAAWDE L	AAELGSAAA AEELGSAAVS	AFGSVTSGLVG.	GIWQ	GPSSVA	МАААААРҮ маааару	AGWLSAAAASA AGWLGSVAAOA	ESAAGQ
МΡ	Rv3350c PPE56	MEFPVL	PPEINSVLM	YSGAGSSPLL	AAAWDGL	AEELGSAAVS	SFGQVTSGLTA.	GV <mark>W</mark> Q	GAAAAA	MAAAAAPY	AGWLGSVAAAA	EAVAGQ
	Rv3533c   PPE62 Rv3558   PPE64	MNYAVL	PPELNSLRMI	FTGAGSAPMLA YIGAGSAPMI	AAVAWDGL	AAELGSAASS AAELGTAASS	SFGSVTSDLAS.	QAWQ	GPAAAA GPASAA	МАААААРҮ маааару	AGWLSAAAARA AGFLTTASAOA	AGAAAQ
				α4			α5					
	<i>Rv2430c PPE41</i>	<u>0000000000000000000000000000000000000</u>	20000 Q	α4 20000000000 110	120	<u>000000</u> 130	α5 200000000000 140	<u>000000</u>	000000	000 60	170	180
	<i>Rv2430c   PPE41</i> _Rv2430c   PPE41	000000000 90 IHEIVRAYE	QQQQQ Q 100 WAHHDMVPL	α4 2020202020 110 Α <mark>QIYNNR</mark> AER	120 IIIIDNNAL	<u>2020200</u> 130 G <mark>OFTAQIADI</mark>	α5 20000000000 140 LDQEYDDFWDEE	<u>000000</u> 150 GEVMRD	000000 1 VRLRVS	QQQ 69 DALSKLTP	<b>170</b> WKAPPPIAHST	180 VLV
	<i>Rv2430c</i>   <i>PPE41</i> Rv2430c   <i>PPE41</i> Rv0388c   <i>PPE9</i> Rv0915c   <i>PPE14</i>	000000000 90 IHEIVRAYE AVAAANAYE ABAAAAEAEG	00000 100 WAHHDMVPLJ SAYAATVPP TAFAMTVPP	α4 <u>0000000000</u> <b>110</b> AQIYNNRAERC VIAANRRTMI SLVAANRS BLN	120 120 SLVQTNVF	<u>0000000</u> <b>130</b> GOFTAQIADI GONSAAIATS	0.5 0.0000000000 1.40 1.00 5.5 THYGEWAAD 0.04 EVALEWAAD	000000 150 GEVMRD ILAMDG AAVMYS	Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	000 60 DALSKLTP .AASQLR. .AASALPP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA	<b>180</b> VLV GRVAE.
	Rv2430c   PPE41 Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15	000000000 90 iheivraye avaaanaye araaaeafg amasaaaye	OCOCO 100 WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP	04 00000000 110 AQIYNNAAERO TVIAANRTMI SLVAANRSRLN EVVAANRALLZ	120 120 ILIDNNAL SLVQTNVF SLVAANIL ALVATNVL	QQQQQQQ 130 GQFTAQIADI GQNTPAIATS GQNSAAIAAT GINTPAIMAT	025 00000000000 140 LDQEYDDFWDEI SETHYGEMWAHD FQAEVAEMWAQD FEALYAEMWAQD	GEVMRD ILAMDG AAVMYS ALAMYG	QQQQQQ I YRLRVS YAGASG YEGASA YAAASG	000 69 DALSKLTP AASQLR. AASALPP AAGMLQP	<b>170</b> WKAPPPIAHST RSPATGDHQR FTPPVQGTGPA L <mark>S</mark> PPSQTTNPG	<b>180</b> VLV GRVAE. GPA GLA
	Rv2430c/PPE41 Rv0388c PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c PPE15 Rv1168c PPE17 Rv1166 PPE18	000000000 90 IHEIVRAYE AVAAANAYE ARAAAEAFG AMASAAYE ISVVAGAYE VRVAAAYE	00000     01       100     01       XAHHDMVPLJ     01       XAYAATVPP     01       AYAATVPP     01       AAYAATVPLJ     01       TAFAATVPLJ     01	α4 <u>000000000000000000000000000000000000</u>	120 120 SLVQTNVF SLVAANIL ALVATNVL ALATTNIF TLIATNLIF	QQQQQQQ 130 GQFTAQIADI GQNTPAIATS GQNSAAIAAT GINTPAIMAT GINTPAIAAT GONTPAIATAT	CONTRACTOR	GEVMRD ILAMDG AAVMYS ALAMYG GEAMNIG	200000 TRLRVS YAGASG YEGASA YAAASG YAATMAA YAAATA	QQQ 69 DALSKLTP AASQLR. AASALPP AAARLTP AAARLTP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA LSPPSQTTNPG FSPPAPIANPG FEPAPEMTSAG	180 VLV GRVAE. GPA GLA ALARLY
S	Rv2430c/PPE41 Rv0388c PPE9 Rv0388c PPE9 Rv0915c PPE14 Rv1039c PPE15 Rv1168c PPE17 Rv11961 PPE18 Rv1361c PPE19 Rv1361c PPE19	000000000 90 HEIVRAYE AVAAANAYE ARAAAEAFG AMASAAAYE ISVVAGAYE VRVAAAAYE	QQQQQ 100 XAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP TAYGLTVPP TAYGLTVPP TAYGLTVPP	04 000000000 110 AQIYNNRAER VIAANRRTM SUVAANRALL VVAANRALL VVAANRALL PVIAERRAEL PVIAERRAEL	120 120 SLVQTNVF SLVAANIL ALATTNIF ILIATNLL	QQQQQQQ 130 GQFTAQIADI GQNTPAIATS GUNTPAIAAT GINTPAIMAT GINTPAIMAT GQNTPAIAVN GQNTPAIAVN	CONTRACTOR	GEVMRD ILAMDG AAVMYS ALAMYG GEAMNL AAAMFG AAAMFG	YRLRVS YRLRVS YAGASG YEGASA YAAASG YATMAA YAAATA YAATAA	000 60 DALSKLTP AASQLR. AASALPP AAAGMLQP AAARLTP TATATLLP TATATLLP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQEGPA LSPPSQTTNPG FSPPAPIANPG FEAPENTSAG FEDAPLITNPG	180 VLV GRVAE. GPA GLA ALARLY G
e IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1705c   PPE22	000000000 90 IHEIVRAYE AVAAANAYE ARAAAEAFG AMASAAAYE ISVVAGAYE VRVAAAAYE VRVAAAAYE ARAAAAAYE	QQQQQ 100 WAHHDMVPTJ SAYAATVPP TAFAMTVPP AAHAAHVPL TAYGLTVPP TAYGLTVPP TAYGLTVPP TAFAAIVPP	α4 200000000 110 AQIYNNRAERT VIAANRATHI SUVAANRATHI VIAENRAELI PVIAENRAELI PVIAENRAELI PVIAENRAELI PLIAANRATL	120 ILIDNNAL SLVQTNVF SLVANIL ALATTNVL ILIATNLL ILIATNLL SLVTHNVF	QQQQQQQ 130 GQFTAQIADI GQNTPAIATS GINTPAIATS GINTPAIMAT GINTPAIAV GQNTPAIAVN GQNTPAIAVN GQNTPAIAT	05 0000000000000 100EYDDFWDEI SETHYGEMWAHI TCALYAEMWAQI LDALYAQYWSQI NEAEYGEMWAQI NEAEYGEMWAQI TEAQYAEMWAQI TEAQYAEMWAQI	G Q Q Q Q Q Q G E VMR D I LAM DG AA VMY S ALAMY G G E AM NL AAAMF G AAAMF G AAAMF G AAAMY G AAAMY G	YRLRVS YAGASG YAGASG YAAASG YAAAASG YATMAA YAAATAA YAASSAA YASSAA	000 60 DALSKLTP AASQLR. AASALPP AAARLTP TATATLLP TATATLLP TATATLLP TATATLVTP .TATKVTP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA LSPPQTTNPG FEPAPENTSAG FEDAPLITNPG FAPPPTTSAG	180 VLV GRVAE. GLA ALARLY G AAA G
age IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1705c   PPE22 Rv1787   PPE25	COCOCOCO I HE IVRAYE AVAAANAYE ARAAAEAFG ISVVAGAYE ISVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAFE ARAAAAAFE	QQQQQ NAHHDMVPD SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP TAYGLTVPP TAYGLTVPP TAFAAIVPP AAFAMTVPP AAFAMTVPP	C/4 C C C C C C C C C C C C C C C C C C C	120 120 120 120 120 120 120 120 120 120	QQQQQQQ 130 GQFTAQIADI GQNTPAIATS GINTPAIATS GINTPAIATS GUNTPAIAVN GQNTPAIAVN GQNTPAIAVN GQNTPAIATS GQNTPAIATS	05 000000000000000 140 LDQEYDDFWDEI SETHYGEMWAHI TCALYAEMWAQI LDALYAQYWSQI NEAEYGEMWAQI NEAEYGEMWAQI NEAEYGEMWAQI TEAQYAEMWAQI TESQYAEMWAQI	GEVMRD ILAMDG AAVMYS ALAMYG GEAMNL AAAMFG AAAMFG AAAMYG AAAMYG AAAMYG	Q Q Q Q Q Q YRLRVS YAGASG YEGASA YAAASG YATMAA YAATAA YAATAA YAATAA YAASSAAA YAASAAA YASAAA	200 DALSKLTP AASQLRP AASALPP AAARLPP AAARLTP TATATLLP TATATLLP TATATLLP SASRLIP SASRLIP	170 WKAPPPIAHST .RSPATCDHQR FTPPVQGTGPA LSPPSQTTNPG FSPPAPIANPG FEAPENTSP FAPPPCTNAT FAPPPCTNAT FAPPCTNAT	180 VLV GRVAE. GLA ALARLY G AAA G GVV
lineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1706c   PPE22 Rv17787   PPE25 Rv1789   PPE26 Rv1789   PPE26 Rv1789   PPE26	COCOCOCO I HE I VRAYE AVAAANAYE AVAAANAYE ARAAAAAYE I SVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	QQQQQ NAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP AAHAAHVPL TAYGLTVPP TAFAAIVPP AAFAMTVPP AAFAMTVPP AAFVMTVPP	04 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	TLIDNNAL SLVQTNVF SLVQANIL ALVATNVL ALVATNVL SLVTHNVF TLVDTNVF TLVDTNVF TLIATNFF QLISTNVF	QQQQQQQ QQTTAQIAA QQNTPAIATS GQNTPAIATS GUNTPAIATS GINTPAIATAT GUNTPAIATAT GQNTPAIAVT GQNTPAIATT GQNTASIAAT GQNTSAIAAT GQNSAAIAVZ GQNSAIAAZ	00000000000000000000000000000000000000	GEVMRD ILAMDG AAVMYS GEAMNL AAAMFG AAAMFG AAAMYG AAAMYG SAAMYA SAAMYA AVAMYG	VRLRVS YAGASG YAGASG YAAASG YAATAA YAAATAA YAGSSA YASAAA YAGSSA YAAASA YAAASA	200 DALSKITP .AASQLRP .AASALP .AASMLQP .AAARLTP TATATLLP TATATLLP TATATLLP .SASRLIP .SASRLIP .SASRUIP	170 KAPPPIAHST .RSPATCDHQR FTPPVQGTGPA LSPPSQTTNPG FSPPAPIANPG FEDAPLIANPG FAPPPNTTSPS FAPPPQTTNAT FSTPPQTANPT FAPPFTTNSA FSTPPQTANPT	180 VLV GRVAE. GPA GLA GLA G G G GVV AQG GVV
sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1136   PPE19 Rv1705c   PPE22 Rv1706c   PPE23 Rv1787   PPE25 Rv1789   PPE26 Rv1789   PPE27 Rv17801   PPE29 Rv17801   PPE29 Rv1801   PVE30 Rv1801   P	COCOCOCO I HE I VRAYE AVAAANAYE ARAAAEAFG AMASAAAYE IS VVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAFE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	OCOOO WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP TAFAAIVPP AAFVMTVPP AAFVMTVPP AAFVATVPP AAFVATVPP	C/4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	TLIDNNAL SLVOTNVF SLVAANIL ALVAANIL ALVATNVL ALATTNIF TLVATNVF TLVDTNVF TLIATNFF OLISTNVF TLIATNFF VLIATNIF	QQQQQQQ QQTTAQIADI QQNTAIATS QQNTAIATS GUNTAIATS GUNTAIATS GUNTAIATA QQNTAIAVA GQNTAIAVA GQNTAIAVA GQNTAIAVA GQNSAIAVA GQNSAIAVA GQNSAIAVA GQNSAIAVA GQNSAIAVA	00 1 4 0 1 4 0	GEVMRD ILAMDG AAVMYS ALAMYG GEAMNL AAAMFG AAAMFG AAAMYG SAAMYA SAAMYG SAAMYA AVAMYG AVAMYG	YRLRVS YAGASG YEGASA YAAASG YATMAA YAAATA YAASAA YAGSSA YAGSSA YAASSA YAGSSA YAASSA	000 60 DALSKLTPP .AASQLR. .AASALPP .AAARLTP TATEALLP .TATEALLP .TATEALLP .SASRLIP .SASRLIP .SASRLIP .SASRLIP .SASRLIP	170 KAPPPIAHST RSPATCDHQR FTPPVQCTGPA ISPPSQTTNPG FSPPAPIANPG FEDAPLIANPG FAPPPNTTSPS FAPPPQTTNSA FSTPPQTTNSA FTEPPQTTNHG	180 VLV GRVAE. GLA ALARLY G G G G G.VV AQG OVV QVV QVV
y (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1361c   PPE19 Rv1705c   PPE22 Rv1705c   PPE23 Rv1787   PPE26 Rv1789   PPE26 Rv1780   PPE29 Rv1801   PPE30 Rv1801   PVE30 Rv1801	COCOCOCO C I HE I VRAYE AVAAANAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	00000 WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP TAYGLTVPP TAFAAIVPP AAFAMTVPP AAFAMTVPP AAFAATVPP AAFAATVPP AAFAATVPP	C/4 CONTRACTOR CONTRACTOR AQUINNEAERC TVIAANEAERC EVVAANEAERC EVVAANEAELL PVIETNELTE PVIENEAELL PVIEANEAELL PVIEANEAELL PVIEANEAELL PVIEANEAELL PVIEANEAELL PVIEANEAELL PVIEANEAELL	ILIDNNAL SLVOTNVF SLVAANIL ALVAANIL ALVATNVL ALATTNIF ILIATNLL SLVTHNVF TLVDTNWF TLVDTNWF VLIATNFF VLIATNFF VLIATNIF VLIATNIF	QQQQQQQQ QQTTAQIADI QQNTPAIATS QQNTPAIATS GQNTPAIATS GQNTPAIATA QQNTPAIATA GQNTPAIATA GQNTPAIATA GQNTASIAAT GQNTASIAAT GQNSAAIAVZ GQNSAAIAVZ GQNTSAIAAT GQNTAAIATA	00000000000000000000000000000000000000	GE VMR D I LAMDG A VMYS GE AMNL A A MFG A A AMFG A A AMFG A A AMYG A A AMYG A A AMYG A A AMYG A A AMYG A A AMYG A A AMYG	V PL IVS VAGASG VAGASG VAGASG VAGASG VAAATA VAAATA VAAATA VAAATA VAAASA VAASSA VAASSA VAGSSS VAGSSS	000 60 DALSKLTP AASQLR. AASALPP AAARLTP TATEALLP TATEALLP TATEALLP SASRLIP SASRLIP SASRLIP SASRLIP SASRUP ATAUQUTP	170 KAPPPIAHST RSPATCHQR FTPPVQCTGPA LSPPSQTTNPG FEPAPIANPG FAPPPTTNSA FSTPPQTTNSA FSTPPQTTNAS FTEPPQTTNAS FTEPPQTTNAS	180 VLV GRVAE. GPA GLA G G G G GVV QLGA GLAT
mily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1361c   PPE19 Rv1705c   PPE22 Rv1705c   PPE22 Rv1777   PPE25 Rv1787   PPE26 Rv1780   PPE29 Rv1801   PPE29 Rv1802   PPE30 Rv1808   PPE32 Rv1808   PPE32 Rv1808   PPE32 Rv1809   PPE30 Rv1809   PVE30 Rv1809	COCOCOCO C I HE I VRAYE AVAAANAYE AVAAANAYE ARAAAAYE VRVAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE	00000 WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP AAHAAHVPL TAYGLTVPP TAFAAIVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAATVPP AAFAATVPP TAFAATVPP TAFAATVPP	C/4 CONTRACTOR CONTRACTOR AQUININE AFEC TVIAANE AFEC EVVAANE ATLL EVVAANE ATLL EVVIETNE TET PVIETNE TET PVIEANE AFL PVIEANE AUL PVIEANE AQUA PVIEANE AQUA PVIEANE AQUA	ILIDNNAL SLVOTNVF SLVAANIL ALVAANIL ALVAANIL ILIATNLL SLVTHNVF TLVDTNWF TLIATNFF OLISTNVF TLIATNFF VLIATNIF VLIATNIF SLVATNIF SLVATNIF	QQQQQQQQ QQTTAQIADI QQNTPAIATS QQNTPAIATS GQNTPAIATS GQNTPAIATA QQNTPAIATA QQNTPAIATA GQNTPAIATA GQNTASIAAT GQNSAIAVZ GQNSAIAVZ GQNTSAIAAZ GQNTSAIAAZ GQNTAIANT GQNTAIAAT GQNTAIAAT	05 000000000000000 1 4 0 1 0 0 0 0 0 0 0 0 0 1 4 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0	COCCO GEVMRD ILAMDG CEAMNG GEAMNG GEAMNG GAAMFG AAAMFG AAAMFG AAAMFG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG	V PL RVS VAGASG VAGASG VAGASG VAGASG VATMAA VAAATA VAATAA VAASAA VAASSA VAGSSA VAGSSA VAGSSA VAGSSA VAGSSA	000 60 DALSKLTP AASQLR. AASALPP AAARLTP TATEALLP TATEALLP SASRLTP SASRLTP SASRLTP SASRLTP SASRLTP SASRLTP SASRLTP TATEALLP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA LSPPSQTTNPG FEPAPENTSAG FEPAPENTSAG FAPPPTTNSA FSTPPQTTNSA FTEPPQTTNHG FAAPPETTNAG FTEPPQTTNAS FTEPPQTTNAS FTEPPQTTNAS FTEPPQTTNAS FTEPPQTTNAS	180 VLV GRVAE. GRVAE. GLA ALARLY G AAA QCV QUGA QLGA GLA CLA
bfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1361c   PPE19 Rv1705c   PPE22 Rv1707c   PPE23 Rv1787   PPE26 Rv1789   PPE26 Rv1780   PPE29 Rv1801   PPE29 Rv1802   PPE30 Rv1808   PPE32 Rv1808   PPE32 Rv1809   PPE33 Rv2352c   PPE33	000000000         90         IHEIVRAYE         AVAAANAYE         ARAAAAAYE         ISVVAGAYE         VRVAAAAYE         ARAAAAAYE         ARAAAAAYE         ARAAAAAYE         ARAAAAAYE         ARAAAAAYE         ARAAAAAYE         ARAAAAAYE         AAAAAAYE         AAE         AAAAAAYE         AAAAAAYE         AAAAAAYE         AAAAAYE         AAAAAAYE         AAAAAAYE         AAAAAAYE         AAAAAAYE         AAAAAYE	00000         0           100         0           WAHHDMVPL/         0           SAYAATVPP         0           TAFAMTVPP         0           AAHAAHVPL/         0           TAYGLTVPP         0           AAHAAHVPL/         0           TAYGLTVPP         0           AAFAMTVPP         0           AAFVMTVPP         0           AAFVMTVPP         0           AAFVMTVPP         0           AAFAATVPP         0	C/4 CONTRACTOR CONTRACTOR AQUINING ACTOR CONTRACTON CONTRACTON CONTRACTON	TIDNNAL SLVDNAL SLVDNVF SLVDANVL ALVANVL ALVANVL ILIATNLL SLVTHNVF TLVDTNVF TLIATNFF OLISTNVF TLIATNFF VLAATNIF SLVATNIF SLVATNIF SLVATNIF	QQQQQQQ QQTTAQIAA QQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GUNTPAIAAT QQNTPAIAV QQNTASIAAT GQNTPAIAV GQNTASIAAT GQNTAIAAT GQNTSAIAAV GQNTGAIAAY GQNTGAIAAT GQNTGAIAAT GQNTPAIAMT GQNTPAIAAT	05 0000000000000000 140 LDQEYDDFWDEI SETHYGEMWAHD FQAEYAEMWAOI FCALYAEMWAOI ICALYACYWSOI NEAEYGEMWAOI ICEAQYAEMWAOI ICEAQYAEMWAOI AEAQYAEMWAOI AEAQYAEMWAOI AEAQYAEMWAOI AEAQYAEMWAOI ICEAQYAEWWAOI ICEA	000000           150           GEVMRD           11LAMDG           GEXMRD           GEXMRD           GEXMRD           GAAMFG           AAAMFG           AAAMFG           AAAMFG           AAAMFG           AAAMFG           AAAMYG           YGANVG           YGANVG	V Q Q Q Q Q I YRLRVS YEGASA YAGASG YEGASA YAAAAA YAATAA YAATAA YAASSA YAASSA YAASSA YAASSA YAASSSA YAGSSA YAGSSA YAGSSA	000 60. DALSKLTP AASQLR. AASALPP AAARLTP TATATLLP JAAARLTP TATEALLP SASRLTP SASRLIP SASRLIP SASRLIP TASRMTA VATQUTP TASRLTP TASRLTP TASRLTP AVAETLTP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA LSPPSQTTNPG FEDAPLTNPG FEDAPLTNPG FAPPPTTNSA FSTPPQTNHG FAAPPFTTNSA FTEPPQTTNHG FAPPTTNSA FTEPPQTTNAS FSEPPQTTNPS FSEPPQTTNPS FSEPPQTTNPS FSPPCLAGE	180 VLV GPVA GLA ALARLY G ALARLY G QCVV QCVV QLGA GLA GLA
subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1705c   PPE18 Rv1705c   PPE22 Rv1777   PPE22 Rv1787   PPE25 Rv1787   PPE26 Rv1780   PPE30 Rv1801   PPE30 Rv1802   PPE31 Rv1808   PPE32 Rv1809   PPE33 Rv2352c   PPE33 Rv2352c   PPE34 Rv2768c   PPE43 Rv2768c   PPE48 Rv2768c   PPE48 Rv2766c   PPE48 Rv2766c   PPE48 Rv2766c   PPE48 Rv2766c   PPE48	000000000 90 I HE I VRAYE AVAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAAYE AAAAAAYE AAAAAAYE AAAAAAYE AAAAAAYE AAAAAAYE	00000         0           100         0           XAH         VPP           XAATVPP         XATVPP           TAFAMTVPP         XAHAAHVPL           TAYGLTVPP         XAHAAHVPL           TAYGLTVPP         XAFAMTVPP           AAFAMTVPP         XAFAMTVPP           AAFVATVPP         XAFVATVPP           AAFAMTVPP         XAFAATVPP           AAFAATVPP         XAFAATVPP           XAFAATVPP	C/4 CONTRACTOR CONTRACTOR AQUININ RAFE (TVIAAN RAFTIN SLVAAN RALL/ PVIAEN RAFTIN PVIAEN RAFTIN PVIAEN RAFTIN PVIAEN RAFTIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIAEN RATIN PVIEN RATIN PVIEN RATIN PVIEN RATIN PVIEN RATIN PVIEN RATIN PVIEN RATIN	TIDNNAL SLVDTNVF SLVDTNVF SLVDTNVF SLVDTNVF SLVDTNVF TIDIATNLL SLVTHNVF TIJATNFF VIAATNIF SLVATNFF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF	QQQQQQQ QQTTAQIAA GQNTPAIAA GQNTPAIAA GUNSAAIAAA GUNSAAIAAA GUNSAAIAAA GQNTPAIAV GQNTPAIAV GQNTASIAAA GQNTAIAAA GQNTSAIAAA GQNTSAIAAA GQNTGAIAAA GQNTGAIAAA GQNTAAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA	05 0000000000000000 140 LDQEYDDFWDEI SETHYGEMWAHD ICQALYAEMWAOI ICALYAEMWAOI ICALYACYWSOI IEALYACYWSOI IEALYACYWSOI IEAQYAEMWAOI IEAQYAEMWAOI AEAQYAEMWAOI AEAQYAEMWAOI IEAQYAEWWAOI II	CCOCCC GEVMRD ILAMDG AAVMYS ALAMYG GEAMLY AAAMFG AAAMFG SAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG CAAMG	00000 1 YRLRVS YEGASA YAGASG YEGASA YAAAAA YAAAAA YAGSSA YAASSA YAASSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA	000 60. JALSKLTP AASQLR. AASALPP AAARLTP TATATLLP JAAARLTP TATEALLP SASRLIP SASRLIP SASRLIP SASRLIP SASRLIP TASRMTA VATQUTP TASRLTP AATQLTP AAGRLNP	170 WKAPPPIAHST .RSPATCHQR FTPPVQCTGPA LSPPSQTTNPA FSPPAPIANPG FEDAPLIANPG FAPPPTTNSA FSTPPQIANPT FAAPPTTNSA FSTPPQTTNHG FAAPPTTNSA FSEPPQTTNSS FSEP	180 VLV GPVA GLA ALARLY G ALARLY G G.VV QGVV QLGA GLA GLA GLA
VP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1705c   PPE17 Rv1705c   PPE22 Rv1770   PPE23 Rv1777   PPE25 Rv1787   PPE26 Rv1790   PPE37 Rv1802   PPE30 Rv1808   PPE32 Rv1809   PPE33 Rv2805   PPE33 Rv2768c   PPE43 Rv2768c   PPE44 Rv2892C   PPE45 Rv2892C   PPE45 Rv285 Rv2	00000000090IHEIVRAYEAVAAANAYEARAAAAAYEISVVAGAYEVRVAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAAAAYEARAAVVAYEARAAVVAYEARAAVVAYEARAAVAAFEAMASAAAFEARAAAAYEARAAAAYE	00000         0           100         0           XAHHDMVPL         2           XAYAATVPP         2           TAFAMTVPP         2           AAYAMTVPP         2           AAYAMTVPP         2           AAYAMTVPP         2           TAYGLTVPP         2           AAFAMTVPP         2           AAFAMTVPP         2           AAFAMTVPP         2           AAFAATVPP	C/4 CONTINUE ACTION AQUININE ACTION AQUININE ACTION CONTINUE ACTION C	TIIDNNÄL SLVOTNVF SLVANNIL ALVANNIL ALVANNIL SLVTNNF TIIATNIL SLVTNNFF OLISTNVF OLISTNVF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF ALVATNVIL ALVATNVIL	QQQQQQQQ QQTTAQIADI QQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIAVN GQNTPAIAVN GQNTPAIAT GQNTPAIAT GQNTPAIAT GQNTSAIAAN GQNTGAIAAT GQNTGAIAAT GQNTGAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT	05 0000000000000000 140 LDQEYDDFWDEI 5CTHYGEMWAHOI FQAEYAEMWAQI FEALYAEMWAQI FEALYAEMWAQI FEALYAEMWAQI FEAQYAEMWAQI AEAQYAEMWAQI AEAQYAEMWAQI AEAQYAEMWAQI TEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEAQYAEMWAQI FEFDYWWAQI FEFDYWWAQI FEFDYWWAQI	C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 YRLRVS YAGASG YEGASA YAGASA YAAAASA YAATAA YAGSSA YAASSA YAASSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA YAGSSA	000 60. JALSKLTP AASQLR. AASALPP AAARLTP TATATLLP TATATLLP SASRLIP SASRLIP SASRLIP SASRLIP SASRLIP AATQLTP TATSRLTP AAAQLAP AAAQLAP AAAGRLNP VAARLNP VAARLNP IATELTP	170 WKAPPPIAHST .RSPATCHQR FTPPVQCTGPA LSPPSQTTNPG FSPPAPIANPG FEDAPLTNPG FAPPPTTNSS FSPPQIANPTTNSA FSTPPQTNNG FAAPPTTNSA FSEPPQTTNSS FSEPPQTTNSS FSEPPQTTNSS FSEPPQTTNSS FSEPPQTTNSS FSVPPLAS	180 VLV GPVA GLA ALARLY G ALARLY G QUA QUCA GLA GLA GLA GLA ALA
SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1705c   PPE18 Rv1705c   PPE23 Rv1777   PPE25 Rv1778   PPE26 Rv1790   PPE37 Rv1801   PPE29 Rv1802   PPE30 Rv1808   PPE32 Rv1809   PPE33 Rv2352c   PPE33 Rv2768c   PPE43 Rv2768c   PPE44 Rv2892C   PPE44 Rv2892C   PPE49 Rv125c   PPE48 Rv125c   PPE49 Rv125c   PPE48 Rv125c   PPE48 Rv	000000000 90 I HE I VRAYE AVAAANAYE ARAAAEAFG I SVVAGAYE VRVAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAVAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVYAYE ARAAVAAFE AMASAAAFE AMASAAAFE ARAAAAYE	00000 NO WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP TAYGLTVPP TAYGLTVPP TAFAATVPP AAFAMTVPP AAFAATVPP AAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP AAFAMTVPP TAFAATVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAMTVPP	C/4 CONTRACTION OF CONTRACTOR A CITINNE A EFC TVIAANE REMI SLVAANE REMI SLVAANE REMI VVIAENE AELLA PVIAENE AELLA PVIAENE ACLA PVIAENE	TIIDNNÄL SLVQTNVF SLVQTNVF SLVANNIL ALVATNUL ILIATNLI SLVTNVF TLVATNVF OLISTNVF OLISTNVF VLAATNIF SLVATNIF SLVATNIF ALVATNIF SLVATNIF SLVATNIF SLVATNFF SLVATNFF SLVATNFF SLVATNFF	QQQQQQQ QQTTAQIADI QQNTPAIATS GQNTPAIATS GQNTPAIATS GUNSAAIAAT GUNSAAIAAT GQNTPAIAY GQNTPAIAY GQNTPAIAAT GQNTPAIAAT GQNTSAIAAA GQNTSAIAAA GQNTGAIAAAT GQNTGAIAAAT GQNTAAIAAT GQNTAAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT	05 0000000000000000 140 LDQEYDDFWDET 55THYGEMWAHU TQAEYAEMWAQU TEALYAEMWAQU TEALYAQWWAQU NEAEYGEMWAQU TEAQYAEMWAQU AEAQYAEMWAQU AEAQYAEMWAQU TEAQYAEMWAQU TEAQYAEMWAQU TEAQYAEMWAQU TEAQYAEMWAQU TEAQYAEMWAQU TEAQYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU TEAHYAEMWAQU	COCCO GEVMRD ILAMDG AAVMYS ALAMYG GEAMLY AAAMFG AAAMFG AAAMYG AAAMYG AAAMYG AAAMYG AAAMYG ALAMYG ALAMYG ALAMYG ASAMYG AAAMYG AAAMYG AAAMYG	V O O O O O I I YR L R V S Y A G A S G Y E G A S A Y A A S A Y A A S A Y A A S A Y A A S S A Y A A S S S Y A S S S S S S S S S S S S S S S S S S	000 60. JALSKLTP AASQLR. AASALPP AAARLPP TATATLLP TATEALLP TATEALLP SASRLIP SASRLIP SASRLIP SASRLIP AATQLTP TASRLTP AAAQLAP TASRLTP VAARLNP VAARLNP VAARLNP VAARLNP VAARLNP	170 WKAPPPIAHST RSPATCHQR FTPPVQCTGPA LSPPSQTTNPG FEDAPLTANPG FEDAPLTNPG FAPPPTTNSPS FAPPQTTNSP FTEPPQTNNA FSPPQTTNAS FSEPPQTTNPS FTAPPTTNAS FSEPPQTTNPS FTAPPTTNAS FSLPPQTTNPS FTAPPTTNAS FSLPPQTTNPS FTAPPTTSPA	180 VLV GRVAE. GRVAE. GLA ALARLY G G QLGA GLA GLA GLA GLA GLA CLA
SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1705c   PPE18 Rv1705c   PPE23 Rv1770   PPE25 Rv1770   PPE25 Rv1789   PPE26 Rv1790   PPE27 Rv1801   PPE29 Rv1802   PPE30 Rv1808   PPE32 Rv1808   PPE32 Rv1809   PPE33 Rv2768c   PPE33 Rv2768c   PPE44 Rv2769c   PPE45 Rv1270c   PPE44 Rv2892c   PPE51 Rv3478   PPE51 Rv3478   PPE51	00000000090IHEIVRAYEAVAAANAYEARAAAEAFGISVVAGAYEVRVAAAAYEARAAAAYEARA	00000         0           100         0           XAYAATVPP         1           XAYAATVPP         1           XAYAATVPP         1           XAYAATVPP         1           XAYAATVPP         1           AAYAMTVPP         1           XAYAATVPP         1           AAYAMTVPP         1           AAYAATVPP         1           AAFAATVPP	C/4 CONTINUE AFF( AQUININE AFF( TVIAANE AFT) EVVAANE ALLI EVVAANE ALLI PVIAENE AFT) PVIAENE AFT) PVIAENE AFT) PVIAENE ACLI PVIAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIVAENE ACLI PVIAENE ACLI P	TIIDNNÄL SLVQTNVF SLVQTNVF SLVANNIL ALVATNUL ILIATNLI SLVTHNVF TLVATNVL ILIATNFF QLISTNVF ILIATNFF VIAATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLIAANVL ALVATNFF TLAATNFF	QQQQQQQ QQTTAQIADI QQNTPAIATS GQNTPAIATS GQNTPAIATS GUNSAAIAAT GINTPAIFAI GQNTPAIAVA GQNTPAIAVA GQNTPAIAAT GQNTSAIAAA GQNTSAIAAA GQNTGAIAAA GQNTGAIAAA GQNTFAIAAA GQNTFAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA GQNTPAIAAA	05 0000000000000000 100000000000000000	C C C C C C C C C C C C C C C C C C C	V O O O O O O O O O O O O O O O O O O O	000 60. JALSKLTP AASQLR. AASALPP AAARLPP TATATLLP TATEALLP TATEALLP SASRLIP SASRLIP SASRLIP SASRLIP AATQUTP TASRLTP AAAQLLP VAARLNP SVAALLP SVAALLP SVAALLP	170 WKAPPPIAHST .RSPATGDHQR FTPPVQGTGPA LSPPSQTTNPG FEDAPLIANPG FEDAPLITNPG FAPPPTTNSA FSTPPQIANPT FAAPPKTTNSA FSEPPQTTNPS FTEPPQTTNPS FTEPPQTTNPS FTAPPTTNAS FSEPPQTTNPS FTAPPTTNAS FSEPPQTTNPS FTAPPTTSPA LTPSSHITNPA FSLPPVSLAGL FSLPPVSLAGL	180 VLV GRVAE. GRVAE. GLA ALARLY G G QUCA QLCA GLA GLA GLA GLA GLA GLA GLA GLA
SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE19 Rv1705c   PPE23 Rv1706c   PPE23 Rv1770   PPE25 Rv1787   PPE25 Rv1789   PPE26 Rv1790   PPE37 Rv1801   PPE29 Rv1802   PPE30 Rv1808   PPE32 Rv1809   PPE33 Rv2768c   PPE43 Rv2768c   PPE43 Rv2770c   PPE44 Rv2892c   PPE45 Rv3125c   PPE51 Rv3478   PPE61 Rv3478   PPE61 Rv3532   PPE61	000000000 90 I HE I VRAYE AVAAANAYE AVAAANAYE ARAAAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE	00000 100 WAHHDMVPL SAYAATVPP TAFAMTVPP AAYAMTVPP TAYGLTVPP TAYGLTVPP TAFAAIVPP AAFAMTVPP AAFAMTVPP AAFAATVPP AAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFAATVPP TAFALTVPP TAFALTVPP TAFALTVPP TAYRLTVPP TAYRLTVPP	CA CONTRACTOR CONTRACTON CONTRACTON CONTRACTON CONTRACTON CONTRACTON CONTRACTON CO	TIIDNNÄL SLVQTNVF SLVQTNVF SLVANNIL ALVATNUL ILIATNIL ILIATNIL SLVTHNVF TLVATNVF OLISTNVF OLISTNVF ILIATNFF VUAATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNFF SLIAANVL ALVATNFF SLIAANVL ALVATNFF SLIAANVL	QQQQQQQ QQTTAQIADI QQNTPAIATS GQNTPAIATS GQNTPAIATS GUNSAAIAAT GINTPAIATS GQNTPAIAVN GQNTPAIAVN GQNTPAIATS GQNTPAIATAT GQNTSAIAAT GQNTGAIAAT GQNTGAIAAT GQNTFAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT	05 000000000000000 100000000000000 50000000000	C C C C C C C C C C C C C C C C C C C	V O O O O O O I VRLRVS VAGASC VEGASA VAAASC VAAAASC VAATAA VAATAA VAASSA VASSSA VAASSSA VAASSSA VAASSSA VAASSSA VAASSSA VAASSA VAASSA VAASSA VAASSA VAASSSA VAASSSA VAASSSA VAASSSA VAASSSA VAASSSA VAASSA VAASSSA VAASSSA VAASSA VAASSSA VAASSA VAASSA VAASSA VAASSSA VAASSA VAASSSA VAASSA	000 DALSKLTP AASQLR. AASALPP AAAGMLQP TATATLLP TATEALLP TATEALLP SASRLIP SASRLIP SASRLIP SASRLIP AATQUTP TASQLAP TASRLTP VAARLNP VAARLNP VAARLNP SVAATLAP SVAATLAP AAARLIP SVAATLAP AAARLNP	170 WKAPPPIAHST RSPATCHQR FTPPVQGTGPA LSPPSQTTNPG FEDAPLITNPG FEDAPLITNPG FAPPPTTNSA FSTPPQIANPT FAAPPKTTNSA FSTPPQTTNAS FSEPPQTTNAS FSEPPQTTNPS FTAPPTTNAS FSEPPQTTNPS FTAPPTTNAS FSLPPVTTNAS FSLPPVTSPA FSLPPVSLAGL FSLPPVSLAGL FSLPPVSLAGL	180 VLV GRVAE. GRVAE. GLA ALARLY G G AQG AQG GVV QLGA GLA GLA GLA GLA GLA GLA CL G G C
SVP subfamily (sublineage IV)	Rv2430c/PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c PPE15 Rv1168c PPE17 Rv1166 PPE17 Rv1166 PPE23 Rv1705c PPE22 Rv1706 PPE23 Rv1770 PPE27 Rv1780 PPE26 Rv1789 PPE26 Rv1780 PPE27 Rv1801 PPE29 Rv1802 PPE31 Rv1809 PPE33 Rv2768c PPE33 Rv2762 PPE38 Rv2762 PPE38 Rv2762 PPE44 Rv2892c PPE44 Rv2892c PPE44 Rv2892c PPE45 Rv3136 PPE51 Rv3478 PPE66 Rv3532 PPE61 Rv3621c PPE55	OCOOOOOOO O I HE I VRAYE AVAAANAYE AVAAANAYE ARAAAAAYE I SVVAGAYE VRVAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAYE ARAAAAAAAYE ARAAAAAAYE ARAAAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	00000         0           100         0           XAYAATVPP         1           AAYAATVPP         1           AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	TIIDNNAL SIVQTNVF SIVQTNVF SIVQTNVF SIVATNIL ILIATNIL ILIATNIL ILIATNUF QUISTNVF QUISTNVF VUAATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIAANVI	QQQQQQQQ QQTPAQIADI QQNTPAIATS QQNTPAIATS GUNSAAIAAT GINTPAIATS GUNSAAIAAT GUNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTGAIAAT GQNTGAIAAT GQNTGAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT GQNTFAIAAT	000000000000000000000000000000000000	C C C C C C C C C C C C C C C C C C C	V O O O O O O I I VRLRVS VAGASC VEGASA VAAASC VAATAA VAATAA VAATAA VAASSA VAASSA VAGSS VAG	QQQ 60. JALSKLTP JAASQLIP. JAASALPP JAAARLTP TATEALLP TATEALLP TATEALLP SASAVTP SASAVTP SASAVTP SASAVTP JAATQLTP VAAQUTP TASQLAP TASRLTP VAARLNP VAARLNP VAARLNP VAARLNP VAARLNP VAARLNP JAAGRLNP VAARLNP JAAGRLNP JAAGRLNP JAAGRLNP JAAGRLNP JAAGRLNP JAAGRLNP JAAGNA JAAGNA J	170 WKAPPPIAHST .RSPATCDHQR FTPPVQGTGPA LSPPQTTANPG FEDAPLITNPG FEDAPLTNPG FAPPPTTNSA FSTPPQIANPT FAAPPKTTNSA FSTPPQTTNAS FSEPPQTTNAS FSEPPQTTNPS FTAPPTTNAA FTEPQTTNPS FSEPPQTTNPS FSPPQTTNPS FSVPPLDLAGL LTPSSHITNPA FSLPPVSLAGL FSPPRQTTNPA FSLPPVSLAGL FSPPRQTTNPA FDAPTTNPA FLAPVTSPA FSLPPVSLAGL FSPPRQTTNPA FDAPLTNPA	180 VLV GRVAE. GRVAE. GLA ALARLY G G QUCA GVV QLCA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA S GL S SE
<ul><li>SVP subfamily (sublineage IV)</li></ul>	Rv2430c/PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c PPE15 Rv1168c PPE17 Rv1166 PPE17 Rv1166 PPE23 Rv1705c PPE22 Rv1706 PPE23 Rv1787 PPE26 Rv1789 PPE26 Rv1789 PPE26 Rv1780 PPE27 Rv1801 PPE29 Rv1802 PPE31 Rv1808 PPE33 Rv2768c PPE33 Rv2762 PPE38 Rv2762 PPE38 Rv255c PPE44 Rv2892c PPE44 Rv2892c PPE45 Rv3136 PPE51 Rv3478 PPE66 Rv3552 PPE61 Rv3621c PPE85 Rv0355c PPE8 Rv0442c PPE8	00000000090IHEIVRAYEAVAAANAYEARAAAAAYEISVVAGAYEVRVAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAAAYEARAAYAYEARAAYAYEARAAYAYEARAYAYATETRLAAAAFEARAYAYATETRLAAAAFEARAYAYATETRLAAAAFE	U U U U U U U U U U U U U U U U U U U	CA CONTRACTION OF A CONTRACT A CITINE A CONTRACT CITINE A CONTRACT	TIIDNNÄL SLVQTNVF SLVANNIL ALVATNUL ILIATNIL ILIATNIL ILIATNUL SLVTHNVF GLISTNVF GLISTNVF GLISTNVF GLISTNVF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLIAANVL ALVATNIF SLIAANVL ALVATNIF SLIAANVL SLIATNFF SLIAANVL SLIATNFF SLIAANVL	QQQQQQQ QQTPAQIADI QQNTPAIATS QQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIAVN GQNTPAIAVN GQNTPAIATS GQNTPAIATS GQNTPAIAAT GQNTGAIAAT GQNTFAIAAT GQNTFAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTPAIAAT GQNTAAIAAT GQNTAAIAAT	00 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C C C C C C C C C C C C C C C C C C C	2 0 0 0 0 0 1 YR L R/V S Y A GA'S G Y E GA'S A Y A A A S G Y A A A A S Y A A A A A Y A A S A Y A A S A Y A A S S Y A A S S S Y A S S S S S Y A S S S S S S Y A S S S S S S S S S S S S S S S S S S	000 DALSKLTP AASQLR. AASQLP AAASALPP AAASALPP TATAATLLP TATEALLP TATEALLP SASAVTP SASAVTP SASAVTP SASAVTP SASAVTP TASQLAP TASQLAP TASQLAP VAAQUTP VAARLNP SVAATLP VAARLNP SVAATLAP AAGRLNP SVAATLAP AAGRLNP SVAATLAP AAARLNP SVAATLAP AAASALTP AAVSALTP	170 WKAPPPIAHST RSPATCDHQR FTPPVQGTGPA LSPPSQTTNPG FEDAPLITNPG FEDAPLITNPG FAPPPTTNSA FSTPPQIANPT FAAPPKTTNSA FSTPPQTTNAS FSEPPQTTNAS FSEPPQTTNAS FSEPPQTTNAS FSEPPQTTNPS FIAPPKTTNSA FSEPPQTTNAS FSUPPLLAGL LITPSUITNPA FSLPPVSLAGL FSPPQTTNPA FSLPPVSLAGL FSPPQTTNPA FSLPPVSLAGL FSPQQDTNSA FNPAQTINPA	180 VLV GRVAE. GRVAE. GLA ALARLY G G QVV QCGA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA C GL GLA C GL C C C C C
e V) SVP subfamily (sublineage IV)	Rv2430c / PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c PPE15 Rv1168c PPE17 Rv1166 PPE18 Rv1705c PPE22 Rv1706c PPE23 Rv1707 PPE26 Rv1709 PPE27 Rv1780 PPE26 Rv1789 PPE26 Rv1789 PPE26 Rv1789 PPE33 Rv1808 PPE33 Rv2766c PPE43 Rv276c PPE43 Rv2770c PPE44 Rv2892c PPE45 Rv3478 PPE51 Rv3478 PPE61 Rv3621c PPE51 Rv3621c PPE61 Rv3625c PPE8 Rv0442c PPE10 Rv045c PPE10 Rv	COCOCOCOC I HE IVRAYE AVAAANAYE AVAAANAYE AVAAAAYE I SUVAGAYE VRVAAAYE VRVAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	CCCCC NAME NUMPEL SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAMTVPP	C/4 C C C C C C C C C C C C C C C C C C C	TIIDNNAL SIVQTNVF SIVQTNVF SIVQTNVF SIVATNIL ILIATNIL ILIATNIL SIVTHVF QLISTNVF QLISTNVF QLISTNVF VIAATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIAANVI ALVATNIF SIVATNIF LAANVI ALVATNIF LAANVI SIVSNLL	QQQQQQQQ QQTPAQIADI QQNTPAIATS QQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIAVI GQNTPAIAVI GQNTPAIAT GQNTPAIAAT GQNTGAIAAT GQNTGAIAAT GQNTGAIAAT GQNTFAIAAT	000000000000000000000000000000000000	C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 YRLRVS YAGASC YEGASA YAAASC YAAAASC YAATAA YAATAA YAASSA YAASSA YAASSA YAASSA YAASSS YAGSSA YAGSSA YAASA YAASA YAASSA YAASSA YAASSA YAASSA YAASSA YAASSA YAASSA YAASSA YAASSA YAASSA YAASA YAASA YAASA YAASA YAASSA YAA	QQQ 60. JALSKLTP JAASQLIP. JAASALPP JAAARLTP TATAATLLP TATEALLP TATEALLP SASAVTP SASAVTP SASAVTP SASAVTP SASAVTP JAATQLTP TASQLAP TASQLAP TASQLAP VAAQUAP JAAAALTP SVAATLAP JAAAALTP JAATALP JAATALP JAACALLP JAACALP JAACALP JA	170 WKAPPPIAHST .RSPATCDHQR FTPPVQGTGPA LSPPQTTNPG FEDAPLINPG FEDAPLINPG FEDAPLTNPG FAPPPTTNAS FSTPPQIANPT FAAPPKTTNSA FSEPPQTTNPS FTEPPQTTNAS FSEPPQTTNPS FTAPPTTNAA FEQTANMA LTPPSHITNPA FSAPPCTTNPS FTAPPTTNAA FSPPQTTNPS FXVPPLDLAGL LTPSSHITNPA FSLPPVSLAGL FSPPQTTNPS FTAPVTSPA FSLPPVSLAGL FSPPQTTNPA FSLPPVLAGL FSPQQTTNPA FDAPLTNPG	180 VLV GRVAE. GRVAE. GLA ALARLY G G QVV QUCA GLA C C C C C C C
sage V) SVP subfamily (sublineage IV)	Rv2430c / PPE41 Rv0388c / PPE9 Rv0915c / PPE15 Rv1039c / PPE15 Rv1168c / PPE17 Rv11961 / PPE18 Rv1705c / PPE23 Rv1706c / PPE23 Rv1707 / PPE26 Rv1709 / PPE27 Rv1801 / PPE27 Rv1801 / PPE31 Rv1808 / PPE31 Rv1808 / PPE31 Rv1808 / PPE31 Rv270c / PPE33 Rv2770c / PPE44 Rv2892c / PPE45 Rv3126 / PPE51 Rv3478 / PPE61 Rv3621 / PPE51 Rv3621 / PPE61 Rv3621 / PPE61 Rv3621 / PPE12 Rv6878c / PPE13 Rv1135 / PPE13 Rv1135 / PPE13	COCOCOCOC I HE IVRAYE AVAAANAYE AVAAANAYE AVAAAAAYE ISVVAGAYE VRVAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAYE ARAAAAAAYE ARAAAAAAAAAAYE ARAAAAAAYE ARAAAAAYE ARAAAAAAYE ARAAAAAAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAAYE ARAAAAAAAAYE ARAAAAAYE ARAAAAAAAAAAAAAAYE ARAAAAAAAAAAAAAYE ARAAAAAYE ARAAAAAAAAAAAAAAYE ARAAAAAAAAAAAAAAYE ARAAAAAAAAAAAAAYE ARAAAAAAAAAAAAAAYE ARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CCCCC NAME DIA SAYAATVPP TAFAMTVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAFAMTVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAATVPP AAFAMTVPP	CA COMPANY AND A COMPANY AND A COMPANY A COMP	TIIDNNAL SIVQTNVF SIVQTNVF SIVQTNVF SIVATNUL SIVATNUL IIIATNLL SIVTHVF QUISTNVF QUISTNVF QUISTNVF VUAATNIF SIVATNIF	QQQQQQQQ QQTPAQIADI QQNTPAIATS QQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIATS GQNTPAIAVI GQNTPAIAVI GQNTPAIAVI GQNTPAIAAT GQNTPAIAAT GQNTGAIAAT GQNTFAIAAT	000000000000000000000000000000000000	C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 YRLRVS YAGASC YEGASA YAAASC YAAASC YAATAA YAATAA YAASSA YAASSA YAASSA YAASSA YAASSSA YAGSSS YAGSSS YAGSSA YAASA YAASA YAASA YAA	QQQ 60. JALSKLTP JAASQLIP. JAASALPP JAAARLTP TATATLLP TATEALLP TATEALLP TATEALLP SASAVTP SASAVTP SASAVTP SASAVTP SASAVTP JAATQLTP JAATQLAP TASSLLP VAAQLAP JAAAQLAS JAAAQLAS TVAAQLAP JAAAQLAS TVAAQLAP	170 WKAPPPIAHST RSPATCDHQR FTPPVQGTGPA LSPPQTTANPG FEPAPENTSAG FEDAPLITNPG FEDAPLTNPG FAPPPTTNAA FSTPPQIANPT FAAPPKTTNSA FSEPPQTTNPS FTEPPQTTNAS FSEPPQTTNPS FSEPPQTTNPS FSEPPQTTNPS FSPPQTTNPS FSPPQTTNPS FTAAPVTSPA FSLPPVSLAGL FSPPRQTTNPA FLAPVSLAGL FSPPQTTNPA FLAPVTSPA FLAPVTSPA FLAPVLAGL FSPPQTTNPA FLAPVLAGL FSPPQTTNPA FLAPVLAGL FSPPQTTNPA FLAPVLAGL FSPPQTTNPA FLAPVLAGL FSPPQTTNPA FLAPVLAGLAGL FQQLFTNPA FQQLFVLAGL FQQLFVLAGLAGLAGLAGLAGLAGLAGLAGLAGLAGLAGLAGLAGL	180 VLV GRVAE. GRVAE. GLA ALARLY G G QVV QUGA GLAT GLA CI
lineage V) SVP subfamily (sublineage IV)	Rv2430c / PPE41 Rv2430c / PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c / PPE15 Rv1168c / PPE17 Rv11961 / PPE18 Rv1705c / PPE22 Rv1706 / PPE23 Rv1707 / PPE26 Rv1709 / PPE27 Rv1801 / PPE26 Rv1790 / PPE27 Rv1802 / PPE31 Rv1808 / PPE31 Rv1808 / PPE31 Rv2706c / PPE33 Rv2770c / PPE44 Rv2892c / PPE45 Rv3126 / PPE45 Rv3126 / PPE51 Rv3478 / PPE61 Rv3478 / PPE61 Rv355c / PPE4 Rv0355c / PPE8 Rv0355c / PPE1 Rv035c / PPE13 Rv135c /	COOCOCOCO I HE I VRAYE AVAAANAYE ARAAAAAYE ISVVAGAYE VRVAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYA ARAAAAYE ARAAAAYE ARAAVAYAYE ARAAVAYAYE ARAAVAYAYE ARAAVAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE	CCCCC WAHHDMVPD SAYAATVPP TAFAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAYATVPP AAYATVPP AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	TI IDNNAL SIVQTNVF SIVQTNVF SIVQTNVF SIVATNUL ILIATNIF TI VATNUL SIVTHVF VIATNVF VIATNFF VIAATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNIF SIVATNUL SIVATNUF SIVATNUF SIVATNUF SIVATNFF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF SIVATNUF	GOUCOUC GOUCOUC GOUCOUC GOUCOUC GOUCOUC GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIATS GUNTPAIAAT	0.0         0.0 <td>C C C C C C C C C C C C C C C C C C C</td> <td>0 0 0 0 0 0 1 Y R L R V S Y E GASA Y E GASA Y A GASG Y A T MAA Y A A SAA Y A A SAA Y A A SAA Y A A SAA Y A A SSA Y A SSA Y</td> <td>QQQ 60. DALSKLTP AASQLIP AASALPP TATATLLP TATEALLP TATEALLP TATEALLP TATEALLP SASAUTP SASAUTP SASAUTP SASAUTP SASAUTP TASCLAP TASCLAP TASCLAP VAAQUAP NAARLNP VAARL</td> <td>170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA ISPPSCTTNPG FSPPAPIANPG FSPAPIANPG FE EAPENTSPC FAPPPCTNNSA FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FSPPPTNAA FTEPVQTTNSA FTEPVQTTNSA FSPPQTTNPS FSVPPLDLAGL ITPSCTANMA FTAPPCTNPS FSVPPLDLAGL FSPQQTTNSA FTSPQQDTNSA FNPAQCTINPA FTQQLKLAGL FGQALPTVAGG WQQLLSVLP.P FTQPSPSAAATP</td> <td>180 VLV GPA GRVAE. GLA ALARLY G GVV QLGA GLA</td>	C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 Y R L R V S Y E GASA Y E GASA Y A GASG Y A T MAA Y A A SAA Y A A SAA Y A A SAA Y A A SAA Y A A SSA Y	QQQ 60. DALSKLTP AASQLIP AASALPP TATATLLP TATEALLP TATEALLP TATEALLP TATEALLP SASAUTP SASAUTP SASAUTP SASAUTP SASAUTP TASCLAP TASCLAP TASCLAP VAAQUAP NAARLNP VAARL	170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA ISPPSCTTNPG FSPPAPIANPG FSPAPIANPG FE EAPENTSPC FAPPPCTNNSA FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FSPPPTNAA FTEPVQTTNSA FTEPVQTTNSA FSPPQTTNPS FSVPPLDLAGL ITPSCTANMA FTAPPCTNPS FSVPPLDLAGL FSPQQTTNSA FTSPQQDTNSA FNPAQCTINPA FTQQLKLAGL FGQALPTVAGG WQQLLSVLP.P FTQPSPSAAATP	180 VLV GPA GRVAE. GLA ALARLY G GVV QLGA GLA
sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1705c   PPE22 Rv1706   PPE23 Rv1707   PPE25 Rv1790   PPE27 Rv1801   PPE29 Rv1802   PPE30 Rv1802   PPE31 Rv1808   PPE31 Rv1808   PPE31 Rv2768c   PPE43 Rv2768c   PPE44 Rv2892c   PPE45 Rv3136   PPE51 Rv3126   PPE51 Rv3126   PPE51 Rv355c   PPE4 Rv0355c   PPE8 Rv0355c   PPE1 Rv0355c   PPE13 Rv1135c   PPE14 Rv1135c   PPE24 Rv1806   PPE24 Rv1806   PPE24	COOCOCOCO I HE I VRAYE AVAAANAYE ARAAAAAYE I SVVAGAYE VRVAAAYE VRVAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYA ARAAAAYE ARAAAAYA ARAAAAYE ARAAAAYA ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE	COCOC WAHHDMVPD SAYAATVPP TAFAMTVPP AAATATVPP AAYAMTVPP AAYAMTVPP AAYAMTVPP AAYATVPP AAYATVPP AAFAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP AALAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	TLIDNNAL SLVQTNVF SLVQANIL ALVANIL ALVANIL SLVTHNVF TLVDTNVF TLVDTNVF TLVDTNVF TLIATNLL SLVTHNVF VLAATNIF VLAATNIF SLVATNIF ALVATNIL SLVATNIF SLVATNIL SLVATNIF SLVATNIF SLVATNFF	GOUCOUC GOUTALIATS		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 Y R L R V S Y E GASA Y E GASA Y A GASSA Y A A A SA Y A A A SA Y A A SAA Y A SAAA Y A SSAA Y A A SSA Y A SSA	QQQ 60 DALSKLITP .AASQLR. .AASGUR. .AASGUR. .AASGUR. .AASGUR. .AASGUR. .AASGUR. .AASGUR. .AASGUR. .AATQUR .SASRLIP .SASRLIP .SASRLIP .SASRLIP .TASRLIP .AATQUTP .TASRLIP .AATQUTP .AATQUTP .AATQLIP .AATQLIP .AAAQLAP .AAAQLAP .AAAQLAP .AAAQLAP .AAAQLAP .AAAQLAP .AAAQLAP .AAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAQLAP .AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	170 KAPPPIAHST RSPATCDHQR FTPPVQCTGPA SPPAPIANPG FSPPAPIANPG FSPPAPIANPG FEAPEMTSAG FAPPPTTSPS FAPPPTTNSA FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FSPPQTTNPS FSVPPLDLAGL LTPPSTANPA FTAPPTTNSA FTAPPTTNSA FSPPQTTNPS FSVPPLDLAGL LTPSQTANPA FTAPPTTNSA FSPPQTTNPS FSVPPLDLAGL FSPPQTTNPA FTAPPTTSPA FTSPQUTNSA FTSPQUTNSA FDSPQTTNPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPQUTNSA FNPAQTINPA FTSPSAAT	180 VLV GPA GRVAE. GLA ALARLY G G QLGA QLGA QLGA GLA GLA GLA GLA GLA GLA GLA GLA TA G C C C C C C
y (sublineage V) SVP subfamily (sublineage IV)	Rv2430c / PPE41 Rv0388c PPE9 Rv0915c PPE14 Rv1039c / PPE15 Rv1168c PPE17 Rv1196   PPE18 Rv1361c PPE19 Rv1705c PPE22 Rv1706 (PPE23 Rv1707 PPE26 Rv1709 PPE27 Rv1801 PPE29 Rv1802 PPE30 Rv1807 PPE31 Rv1808 PPE31 Rv1808 PPE31 Rv2768c PPE43 Rv2768c PPE43 Rv2768c PPE43 Rv2768c PPE43 Rv2768c PPE43 Rv3125c PPE45 Rv3125c PPE45 Rv3126 PPE51 Rv3478 PPE60 Rv3532 PPE61 Rv3621c PPE51 Rv352 PPE51 Rv355c PPE8 Rv0355c PPE8 Rv0355c PPE8 Rv0442c PPE10 Rv055c PPE1 Rv0575c PPE12 Rv0755c PPE12 Rv0755c PPE12 Rv0755c PPE13 Rv1135c PPE16 Rv1548c PPE21 Rv153c PPE24 Rv1800 PPE24 Rv1800 PPE34 Rv1917c PPE44	COOCOCOCO I HE I VRAYE AVAAANAYE AVAAAAYE I SVVAGAYE I SVVAGAYE VRVAAAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAVAYAYE ARAAVAYAYE ARAAVAYAYE ARAAYAYAYE ARAAYATAFE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAYAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYAYE ARAAYYE ARAAYAYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYE ARAAYYYE	COCOC NAHHDMVPJ SAYAATVPP TAFAMTVPP AAATATVPP AAHAAHVPPI AAYAMTVPP AAFAMTVPP AAFAATVPP	C/4 Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	TI IDNNAL SLVOTNVF SLVAANIL ALVATNVF ALATTNF TLVATNVF TLVATNVF TLVATNVF VIAATNIF VIAATNIF SLVATNVF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNFF SLAANVFF SLVATNFF SLV	GOUCOUCOU GOUCOUCOUCOUCOUCOUCOUCOUCOUCOUCOUCOUCOUCO		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 Y R L R V S Y R L R V S Y E G A S A Y A G A S G Y A T MA A Y A G A S A Y A G A S A Y A G S S A Y A G	QQQ 60 DALSKLITP .AASQLIP. .AASQLIP. .AASALPP .AAARLTP TATATLLP .TATKUTP .TATKUTP .SASRLIP .SASRLIP .SASRLIP .SASRLIP .SASRLIP .TASQLAP .TASQLIP .AATQUTP .TASQLIP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLTP .AATQLIP .AAT	170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA ISPPSQTTNPG FSPPAPIANPG FSPPAPIANPG FECAPENTSAS FFEDAPENTTSPS FAPPKTTNSA FTEPVQTTNAS FTEPVQTTNAS FTEPVQTTNAS FSEPPQTTNPS FSVPPLDLAGL LTPPSTANPUTSPA FTAPPCTNPS FSVPPLDLAGL LTPSQTANMA FTAPQTTNPA FSLPPVSLAGL FSPQQTINPA FTQQLKKLAGL FSPQQTINPA FQQLEVVAGG WQQLLSVLP.P WAQAVRALPP.	180 VLV GPA GRVAE. GLA ALARLY G GLA G QLGA GLA CLA GLA GLA GLA CLA C C C C C C.
mily (sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1706   PPE23 Rv1707   PPE25 Rv1709   PPE27 Rv1801   PPE29 Rv1802   PPE31 Rv1802   PPE31 Rv1808   PPE31 Rv2352c   PPE43 Rv2352c   PPE43 Rv2370c   PPE44 Rv2892c   PPE45 Rv3136   PPE51 Rv3136   PPE51 Rv33621c   PPE65 Rv0355c   PPE48 Rv0355c   PPE48	COOCOCOC I HE I VRAYE AVAAAAYE AVAAAAYE AVAAAAYE I SVVAGAYE I SVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAYE ARAAY	COCOC WAHHDMVPL SAYAATVPP TAFAMTVPP AAATVPP AAHAAHVPL TAYGLTVPP AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	ILIDNNAL SLVOTNVF SLVAANIL ALVATNVL ALATTNIF ILIATNLL SLVTHNVF TLVDTNVF TLVDTNVF VLAATNIF VLAATNIF VLAATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNVF	GOODE CONTRACTOR CONTR		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 Y R L R V S Y R L R V S Y E G AS A Y A G AS G Y A G AS G Y A T MA A Y A A S Y	000 60 DALSKLITP AASOLR. AASALPP AAASALPP TATATLLP TATATLLP TATATLLP SASSAUTP SASSAUTP SASSUIP SASSUIP TASSUIP TASSUIP AATQUIP TASSUIP AATQUIP TASSUIP AAAQLIP NAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIP SAASLIP AAATQLIS AAATQLIS AAAQLAS TVASQLIP AAAAQLAS TVASQLIP AAAAQLAS TVASQLIP AAAAQLAS TVASQLIP AAAAQLAS TVASQLIP AAAAALIP	170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA FSPPAPIANPG FSPPAPIANPG FECAPTTSPG FAPPPTTSPS FAPPPTTNSA FTEPVQTTNSA FTEPVQTTNSA FTEPVQTTNSA FTEPVQTTNSS FSVPPLDLAGL LTPPSTANPUTSPA FTAPPCTTNPA FTAPPCTTNPA FTAPQTTNPS FSVPPLDLAGL LTPSCTANMA FTAPQTTNPA FTAPQUTSPA FTQQLKKLAGL FSPPQTTNPA FTQQLKKLAGL FSPPQTTNPA FTQQLKKLAGL FSPQAUTNPA FTQQLKKLAGL FSPLQUKALAGL FSPLQUKALAGL FSPLQUKALAGL FSPLQUKALAGL FTPSQCAUTNPA FTQQLKSLAGA SOPPLOTSA FTPSPQCTNPA FTQQLKLAGL FSPLQUKALAGL FSPLQUKALAGL FAPPQNLTDL FAPPQNLTDL FAPPQNLTDL FAPPQNLTDL FAPPQNLTDL	180 VLV GPA GRVAE. GLA ALARLY G G G QLGA GLA QLGA GLA
bfamily (sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1706c   PPE23 Rv1707   PPE25 Rv1709   PPE27 Rv1801   PPE29 Rv1802   PPE31 Rv1802   PPE31 Rv1808   PPE31 Rv2352c   PPE43 Rv2352c   PPE43 Rv2776c   PPE43 Rv2776c   PPE43 Rv2352c   PPE43 Rv3136   PPE51 Rv3136   PPE51 Rv3136   PPE51 Rv33621c   PPE65 Rv0355c   PPE46 Rv0355c   PPE48 Rv0442c   PPE10 Rv0355c   PPE48 Rv0442c   PPE10 Rv0355c   PPE48 Rv0442c   PPE10 Rv0355c   PPE48 Rv0355c   PPE48 Rv0442c   PPE10 Rv0355c   PPE48 Rv0442c   PPE11 Rv1375c   PPE48 Rv0442c   PPE11 Rv1753c   PPE48 Rv1135c   PPE48 Rv1135c   PPE48 Rv1917c   PPE34 Rv1918c   PPE34	COOCOCOC HEIVRAYE AVAAAAYE AVAAAAYE AVAAAAYE AVAAAAYE ISVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAVAYE ARAAAAYE ARAAYAYA ARAAAAYE ARAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAYE ARAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAYAAAYE ARAAYAAYE ARAAYAAYE ARAAYE ARAAYAAYE ARAAYAAYE ARAAYE ARAAYAAYE ARAAYAAYE ARAAYE ARAAYE ARAAAAYE ARAAYAAAYE ARAAYE ARAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAYE ARAAYE ARAAAAYE	OCCOO WAHHDMVPL SAYAATVPP TAFAMTVPP AAATVPP AAHAAHVPL TAYGLTVPP AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	ILIDNNAL SLVOTNVF SLVAANIL ALVATNVL ALATTNIF ILIATNLL SLVTHNVF TLVDTNVF TLVDTNVF TLVDTNVF VLIATNIF VLIATNIF SLVATNIF	GONTPAIAAA GONTPAIAAA GONTPAIAAA GINTPAIFAI GINTPAIFAI GINTPAIFAI GONTPAIAAA GONTPAIAAA GONTPAIAAA GONTAAIAAA GONTAAIAAA GONTPAIAAA GONAPAIAAA GONAPAIAAA GONAPAIAAA GONAPAIAAA GONAPAIAAA		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 Y R L R V S Y R L R V S Y A G A S Y E G A S Y A G A S Y A G A S Y A A A S Y A A A S Y A A	000 60 DALSKLITP .AASQLIP .AASALPP .AASALPP .AAARLTP TATATLLP .TATKUTP .TATKUTP .SASRLIP .SASRLIP .SASRLIP .SASRLIP .TASRMTA .VATQUTP .TASRLIP .TASRLIP .AATQUTP .TASRLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLIP .AATQLISP .AATQLISP .AAAQLAS TVASQLIP .AATQLISP .AAAQLAS 	170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA FSPPAPIANPG FSPPAPIANPG FEDAPLITNPG FAPPKTTNSA FTEPVQTTNSA FSPPQTTNHG FAPPKTTNSA FTEPVQTTNAS FSPPQTTNAS FSPPQTTNAS FSVPPLDLAGL LTPPSTANAVTSPA FTAPPCTTNPA FTAPQUTKLAGL FSPPQTTNPA FTAPQUKKLAGL FSPPQTTNPA FTQQLKKLAGL FSPPQTINPA FTQQLKKLAGL FSPPQTINPA FTQQLKKLAGL SPPRQTNPA FTQQLKKLAGL SPPRQTNPA FTQQLKLAGL SPPRQTNPA FTQQLKLAGL SPPRQTNPA FTQQLKLAGL SPPRQTNPA TQQLKSAATP FSKPLQNLAGL WQQAVRALPNP SAPPCNLTDL FAPPCNLTDL FAPPCNLTDL	180 VLV GPVA GRVAE GLA ALARLY G QLGA QLGA QLGA QLGA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA CLA
subfamily (sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PPE9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1706c   PPE23 Rv1707   PPE25 Rv1709   PPE27 Rv1801   PPE29 Rv1802   PPE31 Rv1808   PPE31 Rv1808   PPE31 Rv2352c   PPE48 Rv2770c   PPE43 Rv2770c   PPE43 Rv2352c   PPE45 Rv3125c   PPE45 Rv3125c   PPE45 Rv3125c   PPE45 Rv3125c   PPE45 Rv0355c   PPE46 Rv0355c   PPE66 Rv0355c   PPE66 Rv0355c   PPE66 Rv0355c   PPE66 Rv0355c   PPE67 Rv0378c   PPE11 Rv1753c   PPE24 Rv1800   PPE34 Rv1918c   PPE34 Rv1918c   PPE34 Rv2166   PPE42 Rv3144c   PPE35 Rv3144c   PPE52 Rv3144c   PPE52 Rv3156	COOCOCOC I HE I VRAYE AVAAAAYE AVAAAAYE AVAAAAYE I SVVAGAYE I SVVAGAYE I SVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE	COCOC WAHHDMVPL SAYAATVPP TAFAMTVPP AAFAMTVPP AAFAMTVPP AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	ILIDNNAL SLVQANIL ALVANNYL ALVANNYL ALVANNYL ALVATNYL ALVATNYL SIVANNYF TLVDTNWF TLVDTNWF VLIATNIF VLIATNIF SIVATNIF	GONTPAIAAA GONTPAIAAA GONTPAIAAA GINTPAIFAI GUNTPAIFAI GUNTPAIFAI GUNTPAIFAI GUNTPAIAAA GUNTPAIAAA GUNTASIAAA GUNTASIAAA GUNTPAIAAA GUNAPAIAAA GUNAPAIAAA GUNAPAIAAA		C C C C C C C C C C C C C C C C C C C	Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	000 60 DALSKLIP AASQULP AASALPP AASALPP AAASALPP TATATLLP TATATLLP SASSAUTP SASSUIP SASSUIP SASSUIP TASSRUIP TASSRUIP TASSLIP TASSLIP TASSLIP AATQUIP TASSLIP AAAQULP AAAQLIS AAAQUAS TVASQUP AAAQLAS TVASQUP AAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAQLAS AVAALIP AAAAAQLAS AVAALIP AAAAAQLAS	170 WKAPPPIAHST .RSPATCDHQR FTPPVQCTGPA FSPPAPIANPG FSPPAPIANPG FECAPENTSAS FAPPFTTNSA FTEPPQTTNHG FAAPPKTTNSA FTEPPQTTNHG FAAPPKTTNSA FTEPVQTTNHS FSVPPLDLAGL LITPSGTANMA FTAPPGTTNPS FSVPPLDLAGL LITPSGTANMA FTAPQUTKLAGL FSPPRQTTNPA FTSPQQLKLAGL FSPPRQTNNPA FTSPQQLKLAGL FSPPRQTNNPA FTSPQQLKLAGL FSPRQTNNPA FTSPQQLKLAGL SEVPLDNSA FNPAQTINPA FTSPQQLKLAGL SEVPLONSA FNPAQTINPA FTSPQQLKLAGL SEVPLONSA FNPAQTINPA FTSPQQLKLAGL SEVPLONSA FNPAQTINPA FTSPQCLKLAGL SUPCONSA FNPAQULS FISPPQCLKLAGL SUPCONSA FTSPQCLS SUPCONSA FTAPPCNLTDL FALPPCNLTDL FALPCONSA SUPCONSA	180 VLV GPVA GRVAE GLA ALARLY G AAA G QLGA QLGA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA C GLA GLA C CLA GLA C CLA C CLA C CLA C C
TR subfamily (sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41 Rv0388c   PP9 Rv0915c   PPE14 Rv1039c   PPE15 Rv1168c   PPE17 Rv1196   PPE18 Rv1361c   PPE19 Rv1705c   PPE22 Rv1706c   PPE23 Rv1787   PPE25 Rv1780   PPE27 Rv1801   PPE29 Rv1802   PPE31 Rv1808   PPE31 Rv1808   PPE31 Rv1808   PPE31 Rv2352c   PPE48 Rv27766c   PPE43 Rv27762c   PPE45 Rv3125c   PPE45 Rv3125c   PPE45 Rv3125c   PPE45 Rv3055c   PPE6 Rv0355c   PPE16 Rv1548c   PPE21 Rv1753c   PPE3 Rv114c   PPE35 Rv2366c   PPE42 Rv3144c   PPE54 Rv343c   PPE54 Rv345c   PP5	COOCOCOC I HE I VRAYE AVAAAAYE AVAAAAYE AVAAAAYE I SVVAGAYE I SVVAGAYE I SVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE	OCCOO WAHHDMVPC SAYAATVPP TAFAMTVPP TAFAMTVPP AAFAMTVPP TAYGLTVPP TAYGLTVPP TAYGLTVPP TAFAATVPP AAFAMTVPP AAFAATVPP	C/4 C C C C C C C C C C C C C C C C C C C	ILIDNNAL SLVQANY SLVQANY ALVANYL ALVANYL ALVANYL ALVANYL SLVTHNVF TLVDTNVF TLVDTNVF TLVDTNVF VLIATNIF VLIATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNIF SLVATNFF SLVATNIF SLVATNFF SLVSNLF SLVSNLF SLVSNLF SLVSNLF SLVSNLF SLVSNLF SLVSNFF SLVSNFF SLVSNFF SLVSNLF SLVS	GOODE CONTRACTOR GONTPALATS		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 1 Y R L R V S Y L R V S Y L G AS G Y E GAS A Y A A A AS G Y A A A AS Y A A T A Y A A S S A Y A S S S S S S S S S S S S S S S S S S	000 60 DALSKLIP AASQUP AASQUP AAASUPP AAASUPP AAASUPP TATATLLP TATATLLP TATEALLP SASSUP SASSUP SASSUP TASSUTP AATQUTP TASSULP AATQUTP TASSULP AAAQULP AAAQULP AAAQULSS AAAAQUAS TVASQLP AVAALLPP AAAQULSS AAAAQUAS AVAAQUAP AVAALLPA AVAALLPP AAAQULSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAQUSS AAAAAQUSS	170 WKAPPPIAHST RSPATCHPVQCTGPA FSPPAPIANPG FFPPVQCTGPA FSPPAPIANPG FEPPAPITSPS FAPPFTTNSA FFEPPQTTNHG FAPPFTTNSA FTEPPQTTNHG FAPPFTTNSA FTEPPQTTNSA FTEPPQTTNSS FSVPPLDLAGL LITPSGTANMA FTAPPTTNSA FSVPPLDLAGL LITPSGTANMA FTAPPVTSPA FSVPPLDLAGL LITPSGTANMA FTAPPVTSPA FSVPPLDLAGL KRSPUTSPA FSVPLDLAGL FSVPQTNPS FSVPQTNPS FSVPQTNPS FSVPQTNPS FSVPQTNPS FSVPQTNPA FTSPQQLKLAGL WQQLSVLP.P WAQAVRALPNP FSVPQLSSAATP FLPVQLSSAATP FLPVCLSSAATP FAPPCNLTDL FAPPCNLTDL FAPPCNLTDL FALPCNLSSAATP FSPPQCLSSAATP FSPQALSSAATP FSPQALSSAATP FSPQALSSAATP FSPLASSAATP FSSPQCLQLSSAATP FSPLASSAATP FSSPQCLQLSSAATP FSSPQCLQLS SSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP FSSPLASSAATP	180 VLV GPVA GLA GLA ALARLY G G QLGA QLGA QLGA QLGA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA GLA C GLA GLA C CLA C CLA C CLA C C
MPTR subfamily (sublineage V) SVP subfamily (sublineage IV)	Rv2430c   PPE41           Rv0388c   PPE9           Rv0388c   PPE9           Rv0915c   PPE14           Rv1039c   PPE15           Rv1168c   PPE17           Rv1168c   PPE17           Rv1168c   PPE17           Rv1168c   PPE18           Rv1705c   PPE22           Rv1707c   PPE25           Rv1708   PPE26           Rv1709   PPE27           Rv1801   PPE29           Rv1802   PPE31           Rv1808   PPE31           Rv2352c   PPE38           Rv2770c   PPE44           Rv2892c   PPE45           Rv31326   PPE51           Rv3325   PPE61           Rv3325   PPE61           Rv30355c   PPE6           Rv0355c   PPE6           Rv0355c   PPE16           Rv0575c   PPE13           Rv1548c   PPE21           Rv1548c   PPE21           Rv1548c   PPE21           Rv1800   PPE28           Rv1917c   PPE34           Rv1918c   PPE35           Rv2608   PPE42           Rv3434c   PPE52           Rv3343c   PPE54           Rv3343c   PPE54           Rv3343c   PPE54           Rv3343c   PPE54           Rv3343c   PPE54           Rv3343c	COOCOCOC I HE I VRAYE AVAAAAYE AVAAAAYE AVAAAAYE AVAAAAYE I SVVAGAYE I SVVAGAYE VRVAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE ARAAAAYE	COCOC WAHHDMVPL SAYAATVPP TAFAMTVPP AAATVPP AAHAAHVPL TAYGLTVPP TAFAATVPP AAFAMTVPP AAFAMTVPP AAFAATVPP	C/4 Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	ILIDNNAL SLVQANVE SLVQANVE SLVQANVE ALVATNVE ALVATNVE SLVATNVE SLVATNVE SLVATNVE TLVDTNWF TLVDTNWF VLIATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVATNIE SLVSNLF	GOORDALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTASLAAA GONTASLAAA GONTASLAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONTPALAAA GONAPALAAA		C C C C C C C C C C C C C C C C C C C	Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	000 60 DALSKLIP AASQUP AASQUP AAASUPP AAASUPP AAASUPP AAASUPP TATATLLP TATATLLP SASSUP SASSUP SASSUP TASSNUP AATQUP TASSULP AATQUP TASSULP AAAQULP AAAQULP AAAQULS AAAQUAS AVAALLP AAAQULS AVAALPA	170 WKAPPPIAHST RSPATCHPVQCTGPA FSPPAPIANPG FSPPAPIANPG FSPPAPIANPG FEAPEMTSAG FEAPEMTSAG FAPPFTTNSA FTEPPQTTNHG FAAPPTTNSA FTEPPQTTNHG FAAPPTTNSA FTEPVQTTNPS FSVPPIDLAGL LITPSGTANMA FTAAPVTTSPA FSPPQTTNPS FSVPIDLAGL LITPSGTANMA FTAPPCTNPS FSVPQTNPSA FSPPRQTNPA FSPPRQTNPA FTSPQQLKLAGL FSPPRQTNPA FTSPQQLKLAGL WQQLSVLP.P WAQAVRALPNP FSKPLQNLAGL WQQLSS.I IQEGLQQLQN WSIGLQQALPA FSPPAQALGGG	180 VLV GRVALS. GRVALS. GLA GLA ALARLY G GLA QLGA QLGA GL

**Figure S2. Sequence alignment of the ESX-5-specific PPE proteins from** *M. tuberculosis* H37Rv. Only the core PPE domain sequences (~180 residues) are aligned. Identical residues are highlighted in red. The PPE and WxG motifs are highlighted in blue. Residues that are in contact with  $EspG_5$  and PE25 in the *M. tuberculosis* PE25–PPE41– $EspG_5$  complex are labeled by purple and cyan triangles, respectively. Purple stars indicate two hydrophobic residues in the  $\alpha$ 4– $\alpha$ 5 loop of PPE proteins that comprise the hh motif. The secondary structure elements of PPE41 are shown at the top of the alignment.



**Figure S3. Circular dichroism analysis of the wild-type and mutant PE25-PPE41 complexes.** Spectra between wavelengths 200 nm and 260 nm are plotted against mean residue ellipticity. The mutant complexes exhibit a similar secondary structure content as the wild-type PE25-PPE41.









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M_tuberculosis MMAR_5448 MKAN_14525 MKAN_07595 M_hassiacum_DSM_44199 M_smegmatis_str_MC2_155 M_phlei Mycobacterium_sp_MCS M_fortuitum M_tusciae MMAR_5417 M_thermoresistibile Mycobacterium_sp_160MFTsu5.1 M_neoaurum_VKM_Ac-1815D Mycobacterium_sp_155 Mycobacterium_sp_155 M_gilvum_PYR-GCK M_vacaae M_vanbaalenii_PYR-1	.         .	MPPELNTARLMAG MPPELNTARLMAG MPPELNTARLMAG MPPEVNTGRLMAG LPPEVNTGRLMAG LPPEVNTGRLMAG LPPEVNTGRLMAG LPPEVNTARLMAG MPPEVNTARLMAG MPPEVNTARLMAG MPPEVNTGRLMAG FPPENTGRLMAG MPPEVNTGRLMAG MPPEVNTGRLMAG FPPENTGRLMAG MPPEVNTGRLMAG MPPEVNTGRLMAG	AG PAPMLAAAA GWOTLSAA AG PAPMLAAAA GWEALAAA AG PAPMLAAAT GWAAFAAA AG SAPMLAAAT GWAAFAAA AG SAPMLAAAT GWEALAAT AG SAPMLQAAA GWEALAAT AG PAPMLQAAA GWEALATS AG AAPMLQAAA GWEALATS AG PAPMLQAAA GWEALATS AG PUPMLQAAA GWEALATS AG PUPMLQAAA GWEALATS AG PUPMLQAAA GWEALATS AG AU PMLQAAA GWEALATS	DAQAVELTARLINSLGE DAQAVELTARLINSLGE DAQAVELTARLINSLGE DAQAVELTARLINSLGE DAQAAEVSARINSLRE ETQADELAASIVSLTS ETQADELAASIVSLTS ETQADELAASIVSLTS ETQADELAASIVSLGS ETQADELAASLANLSS ETQADELAASLAALS ETQADELAASLAALS ETQADELAASLAALS ETQADELAASLAALS ETQADELAASLAALAG ETQADELAASLAALAG ETQADELAASLAALAG ETQADELAASLAALAG ETQADELAASLAALAG ETQADELAASLAALSS ETQADELAASLAALSS ETQADELAASLAALSS ETQADELAASLAALSS ETQADELAASLAALSS ETQADELAASLASLAS ETQADELAASLASLSQ ETQADELSSSLASLSQ ETQADELSSSLASLSQ ETQADELAASLASLSQ
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**Figure S6. Sequence alignment of PPE68 homologs from** *Mycobacteria.* Only the core PPE domain sequences (~180 residues) are aligned. The PPE and WxG motifs are highlighted in blue. The predicted secondary structure elements are shown at the top of the alignments. Purple stars indicate the hh motif. The majority of mycobacterial genomes contain a single PPE68 homolog, whereas *M. marinum* and *M. kansasii* have several PPE68 homologs.

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Rv0256c PPE2	.MTAPIWN	MASPPEVH	SALLSSGPG	PGPLLVS	A E G W H S <mark>L </mark> S I A Y	AETADELAALI	A A V Q A G T W D G
Rv0280 PPE3	.MTLWN	MASPPEVH	SALLSSGPG	P G S V L S A Z	AGVWSS <mark>LSA</mark> EY	AAVADELIGLI	GAVQTGAWQG
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Rv0453 PPE11	MTSALIWN	M <mark>asppev</mark> h	SALLSSGPG	PGPVLAA	ATGWSSLGREY	AAVAEELGALI	A A V Q A G V W Q G
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<b>Rv3021c PPE47</b>	.MTAP <mark>VW</mark> I	LASPPEVH	SALLSAGPG	PGSLQAA	AGWSALSAEY	AAVAQELSVVV	AAVGAGVWQG
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RV0280 PPE3	PSAAAYVA	AAHAPYLA	WLMRASETS.	AEAAARHI	STVAAAY TTAV	AAMPTLVELAA	NHTLHGVLVA
RV0286 PPE4	PSAEWYVI	AAHLPYVA	WLTQASADA.	AGAAAQHI	SAAAAAYTTAL	AAMPTLAELAA	NHVIHTVLVA
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RV1387 PPE20	QAAEAFVI	AAYMPFLA	WLIQASADC	VEMAAQQI	IVVIEAYTAAV	ELMPTQVELAA	NOIKLAVLVA
RV2123   PPE3/	PSADREV	VAHQPFRY	WLTHAATVA		TAAAGYTSAL	GGMPTLAELAA	NHAMHGALVT
RV3018C PPE46	PSAELFVI	AAYVPYVA	WLVQASADS.	AAAAGEHI		AEMPTLPELAA	NHLTHAVLVA
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1:	20	130	140	150	160	170	180
PTOOS PPET	TNEECIN	TVDTALNE	A D V V P MWL O		מעזיד ממ ה מ זו מ ס	VPSTOPAPTE	APCCDAAD
RV0056c PPF2	TNEEGIN	TTTTALNE	S D V A P MW T O				K D
Rv0280 PPE3	TNEEGIN	TTPTALNE	A DVARMWTO	AASTMAD	VOAVAFAAVAS		ΔΔΕΔ
Rv0286 PPE4	TNFFGIN	TTPTTNE	ADVVRMWLO	AAAVMGT	TOAASGAAT.AS	APRTVPAPTVM	NP.
Rv0453 PPE11	TNFFGIN	TPTAVNE	ADVVRMWLO	AATTMAT	OAVADSAVRS	TPDSVPPPRTT	К
Rv1387 PPE20	TNFFGIN	TPTATNE	AEVVEMWVR	AATTMAT	STUSBSALSA	MPHTSPPPLTT	KSD
Rv2123 PPE37	TNFFGVN	TPTALNE	ADVIRMWIO	AATVMSH	OAVAHESVAA	TPSTPPAPOTV	TS
Rv3018c PPE46	TNFFGIN	TPTALNE	ADYVRMWVO	AATVMSA	EAVVGAALVA	TPHTGPAPVTV	КР
Rv3021c PPE47	TNFFGIN	TPTALNE	ADYVRMWVO	AATVMSA	EAVVGAALVA	TPHTGPAPVTV	КР

**Figure S7. Sequence alignment of the ESX-3-specific PPE proteins from** *M. tuberculosis* H37Rv. Only the core PPE domain sequences (~180 residues) are aligned. The PPE and WxG motifs are highlighted in blue. The predicted secondary structure elements are shown at the top. The hh motif is indicated by purple stars.



**Figure S8. Co-purification of EspG**<sub>5</sub> **and PE25-PPE41 mutant variant dimers.** PE25-PPE41 dimers were co-expressed in *E. coli* with either *M. tuberculosis* EspG<sub>5</sub> (EspG<sub>5mtu</sub>) or *M. marinum* EspG<sub>5</sub> (EspG<sub>5mma</sub>). Proteins were purified using immobilized Ni<sup>2+</sup> affinity chromatography. Notably, the excess of EspG<sub>5mma</sub> chaperone leads to complete solubility of PE25-PPE41 with no dimer present in the insoluble fraction.



**Figure S9. Effect of increased hydrophobicity in the hh motif of PPE41 on protein solubility.** PE25–PPE41 dimers were expressed in *E. coli* in the absence of chaperone or co-expressed with *M. marinum* EspG<sub>5</sub> (EspG<sub>5mma</sub>). Proteins were purified using immobilized Ni<sup>2+</sup> affinity chromatography. Total cell lysate (T), soluble fraction (S), insoluble fraction (I), flow-through fraction (FT), wash fraction (W) and eluted proteins (E) were analyzed by SDS-PAGE. Notably, the excess of EspG<sub>5mma</sub> chaperone leads to complete solubility of PE25–PPE41 with no dimer present in the insoluble fraction.



**Figure S10. Effect of disruptive mutations in the PPE41 interface on the binding of PE25– PPE41 heterodimer to** *M. marinum* **EspG**<sub>5</sub>**.** PE25–PPE41 variants were co-expressed with EspG<sub>5mma</sub> and purified via immobilized Ni<sup>2+</sup> affinity chromatography. The results are comparable with *M. tuberculosis* EspG<sub>5</sub> binding (Figure 3D).



**Figure S11. Effect of disruptive mutations in the PPE18 on the binding of PE31–PPE18 heterodimer to** *M. marinum* **EspG**<sub>5</sub>**.** PE31–PPE18 variants were co-expressed with EspG<sub>5mma</sub> and purified via immobilized Ni<sup>2+</sup> affinity chromatography.

 Table S1
 Summary of isothermal calorimetry data

Complex	K <sub>d</sub> (nM)	$\Delta H$ (kcal mol <sup>-1</sup> )	T∆S (kcal mol⁻¹)	$\Delta G$ (kcal mol <sup>-1</sup> )	n
EspG <sub>5</sub> -PE25-PPE41	48.1±31	-3.4±02	6.8±07	-10.3±0.05	1.08±0.05
EspG <sub>5</sub> -PE25-PPE41 <sup>L125E</sup>	No binding detectable				
EspG <sub>5</sub> -PE25-PPE41 <sup>L125R</sup>	No binding detectable				
EspG <sub>5</sub> -PE25-PPE41 <sup>T129D/A130R</sup>	No binding detectable				