

Name	Sequence of alignments	Length (AA)
TRAg_16_TR	----WNNWLKEMK---ISLTEKLEKES-QEYMEKLEQQWDEFM-KNSEDKWRHYNPQME-	126
TRAg_29_TR	----WDAWLKGTKKDYENLKCFAKGNL-YDWLCSVRDSFELYL-QSLESKWTSCSDNTT-	174
TRAg_32_TR	----WYTWLKGTKKDYETLKCFAKGNL-YDWLCNVRESFDLYL-QSLEKKWTTCSDSAT-	175
TRAg_30_TR	-----WLKDTKDEYENLKCQYRTCL-YDWRKINDEYNELL-NKLEEKWAKFPNDPK-	175
TRAg_31_TR	----WDDWLKSNKKDYANCKCEVRVNL-YDWFCKQSDLELNDSIYKNLEEKWSGFSKDE-	174
TRAg_14_TR	----FKNWLNLEKEYDAWKVSLVNDN-NEWILKKNEIFENIL-NRIKEKWESWNIYTL-	686
TRAg_1_TR	KEEAWDHWLTVLEPEWVTFNSFIEQKK-KRWIQKKEEDWSIWI-KDMEHKWVNYKKKKD-	153
TRAg_15_TR	----WLTFIQGLEGDWERLEVSLNKAR-ERWMEQRNKEWAGWL-RLIENKWSEYSQIST-	1246
TRAg_28_TR	KIKDWNQWMKQAKKDFSGYKGTMTQR-HEWTKEKEDELQKFC-KYLEKRWMNYTGND-	197
TRAg_13_TR	----FSNWLKKAEDWKEFHVVLEDER-TKWWANLGDLEKQWF-ETAEEKWNNYNPGLD-	173
TRAg_20_TR	----WKKWINNTEKQWGNFTQSFEQHK-QKWNKKESEWEEWL-TNIHYNWIGFTNKLE-	426
TRAg_27_TR	----WSEFLKSVGDGDFKEFLVLDNEK-NSWLEGGKDELWEQWK-ANMEKKWEHYDEYTF-	115
TRAg_34_TR	----WHEWMDEVQMDWKEFNSSLESEK-NKWFQKKEKEMMELI-KSIEDKWLDNFENMH-	113
TRAg_21_TR	----WHNWLKLEEDWDSFSTSLIRDK-KDFMKIKTDELNGWL-NLEENKWNNSFGYLS-	110
TRAg_7_TR	----WKYEMENVEEEWQLLNLEWIEEEK-QNWIESKDKELNWM-NKMENKCMHID-NIN-	230
TRAg_24_TR	----WGEWQLTFEEEFQNFLLSLENN-SDMLQEEKNEWDYWI-EKMQNKWSRPHGIMS-	121
TRAg_3_TR	-----WMVKLEGEWKDFASLENEK-IRWIQEKEKEWDEWL-EIMQEKWTHYDRNLN-	110
TRAg_18_TR	INPEWQNWMQDLKNEWSRYNAYIHKER-NKWFQKKEEFHKKFI-EDFQFKWMHYNKELL-	2490
TRAg_26_TR	----WDNWKTRLEEDFNEFYFSLDKEK-KEWIEEKEGEWEKLI-HEMGNKWTPEKGFND	147
TRAg_36_TR	----WNKWLKLEDNWKQFNLSLIKEK-NEWIQNVTKDWNWEM-QNMQHKWTHYIENMD-	110
TRAg_33_TR	----WDNFMKETERDWEKFNSTSMENLT-SSWFQKKELEWEGWI-KAMQNRWAYYNKNMDD	82
TRAg_12_TR	----WKEWIKKAESDLDFINALMDNEKEKKWYSEKEKEWKNWI-KGVEKKWMHYNKNIY-	233
TRAg_22_TR	----WNKWMRQLEEQWHFYFITLETKT-NDWMKQKEEFNTWL-TEMENKWMSYHNHLD-	537
TRAg_10_TR	----WENWMARLELDWKHFDNSIKSKK-EKWLEERVHSWEEWL-KQIEDKWEHYNAHMD-	146
TRAg_4_TR	-----WKSFDQMENER-KQWLEKKDAEWKWK-KYTEIKYMSYCVDIN-	145
TRAg_11_TR	----WSNWLKLEQDWKVFNEKLQNEK-KTFLEEKEEDWNTWI-KSVEKKWTHFNPMD-	144
TRAg_23_TR	----WNNWFMKLQSDWKYFNALSALENEK-QTWFDKEKEWQEWL-KSMENRWTHYENMD-	149
TRAg_17_TR	KKCAWNNWMMRLESEWENFNSTSMKSKK-NVWLQETEQEWEWI-KQMENKWMNCNENIN-	146
TRAg_5_TR	----WNNWMLRLESWKFHNDVVEEAK-TKWLHERDSAWSDWL-RSLQSKWSHYSEKML-	144
TRAg_9_TR	----WKAWMEQLDKDAEIFTTSLEHKK-DQWLVRLEWGDWV-KSMEEKWNHYNEKMG-	147
TRAg_2_TR	----WTDWMVQLDDDWKDFNAQIEEEK-KAWIEEKEGDWVILL-KHLQNKWLHFNPNLD-	147
TRAg_6_TR	----WNIWKKKNEEWWKIFNTSIENEK-DTWLQGIKEWQELL-EAMQNKWIHYNKMD-	279
TRAg_25_TR	----WNNWLIKTEEDWKLFNSTSVENKK-NRWLEKRDKELEVWL-MNMQNRWLHYRENEE-	521
TRAg_19_TR	----WYMWKKLNSSWEEFNSSVENGG-RKWLNVNKDKDWEDWL-KVMEKKWMHYNERME-	423
TRAg_35_TR	----WKNWKIGLEEDWEAFHDAIQNEK-NKWFEGIEKEWENWM-KTMEQKLNKFNSEHIN-	146
TRAg_8_TR	----WKNWGMKLEGEWVDFNNTIEKEK-GKWLNGKEKDWDEFI-QYMDNKWMHYHDGLD-	144
TRAg_16_TR	-----EEYQCSVYPLGLKWDD-EKWTAWF	149
TRAg_29_TR	-----TVFLCECLAESSGWGD-PQWESWV	197
TRAg_32_TR	-----TLFLCECFAESSGWND-SQWGNWM	198
TRAg_30_TR	-----NKDVFDNLKTSSLKND-EKKAQWM	198
TRAg_31_TR	-----LSAGLSGSSSWTN-EQWAEWM	194
TRAg_14_TR	-----KDINDDVIRLKDLDTE-EQWSKWL	709
TRAg_1_TR	-----RKYLSKYRDGTLNCSE-REWNVKM	176

TRAg_15_TR	-----KGKDPAGLRKR-EWSD-EKWKKWF	1268
TRAg_28_TR	-----RECRSDFLKSTQNWNE-SQWNKWV	220
TRAg_13_TR	-----LEYKSNILKKAKVWKE-GQWKWEI	196
TRAg_20_TR	-----GDYINDKVNAWTKWGE-KEWKGII	449
TRAg_27_TR	-----KELLADHAKDALTWND-KEWINWV	138
TRAg_34_TR	-----EVLNYAILKISLMWSF-SEWQKWI	136
TRAg_21_TR	-----DGYKNYLLKKSEKWND-ADWENWA	133
TRAg_7_TR	-----KEYQCMFIKSKLGDDQSQIKEQL	254
TRAg_24_TR	-----ESYKSYIYNKSATWTE-ADWKTWI	144
TRAg_3_TR	-----PTYKNYILKKSSEWDN-FDWEYWA	133
TRAg_18_TR	-----EDHSFDVYKSLKWQD-SKWIKWI	2513
TRAg_26_TR	-----RAHLSDSLEGSSTWND-SQWEDWI	170
TRAg_36_TR	-----ESHKSHILEKSLTWNN-ADWENWV	133
TRAg_33_TR	CVLNVIKNSLNWTFQWQKWI RLMKNKAMKHFESSGDEYILDVFRRNTSWTT-EQWKWEI	141
TRAg_12_TR	-----VEYRSLVFWVGLKWVE-SQWEKWI	256
TRAg_22_TR	-----TEYNTNLYKKYLTWDE-TDWKTWI	560
TRAg_10_TR	-----MSYKFYIFKISSAWNQ-SHWEQWA	169
TRAg_4_TR	-----NEFESNTLKDSSTWNR-NQWEDWI	168
TRAg_11_TR	-----KEFHTNMRRSINWTE-SQWREWI	167
TRAg_23_TR	-----AKFKSYILKNSQGWDD-NQWETWI	172
TRAg_17_TR	-----DEYKDYLIKSKSATWTD-EEWKWEI	169
TRAg_5_TR	-----KEHKSVMKESANWND-TQWGNWI	167
TRAg_9_TR	-----SEYYSVIYKNTSAWSD-EQWENWI	170
TRAg_2_TR	-----AEYQTDMLAKSETWDE-RQWKMWI	170
TRAg_6_TR	-----AEYQINILEKSSQWDD-TQWVEWI	302
TRAg_25_TR	-----NEYKAEAMKNSSTWDD-SQWEQWI	544
TRAg_19_TR	-----REYKSDLFERSADWDD-QQWEEWI	446
TRAg_35_TR	-----NTYPSITLTKKYDLDE-SHWEQLI	169
TRAg_8_TR	-----EEVKS DILKRSLTLDE-IEWKDWI	167

TRAg_16_TR	YEKGLWCLKKSFKTWLTDSSKKGYNTYMKNLLQEFGKQFYEDWCRRPEKRREDKICKRWGQ	209
TRAg_29_TR	KKELKEQLKTEAQAWISTKKKDFDGLTSKYFSLWKDHRRKELEEEAWK-----	245
TRAg_32_TR	NNQLKEQLKTEAEAWISTKKKDFDGLTSKYFSLWKDHRRKELEDAEWK-----	246
TRAg_30_TR	RKNLKDLMREQVDEWLEGGKKIYEGMSPTYWDAWEKKIAKGLMGAAW-----	245
TRAg_31_TR	RNNLKGKLEDEVKSWLAGKQKGYDAVRDTCFNQWKEGRKGALAPDVWS-----	242
TRAg_14_TR	DAQWKPYNKQTFWDLIDSYEKLYHQWKRTHWDKWKSRKMTIEWISQEWKVDEEEKWAQWES	769
TRAg_1_TR	KREVEAAMIADYKKWMRDAEENLQKWI SKDLDIWKKKKFDEWLKVEWKKEEDAHWSKDSN	236
TRAg_15_TR	KAEVKSQIDSHLKKWMDTHSNLKFILVKDMSQFENKKTKEWLMNHKKNERGYGSESFE	1328
TRAg_28_TR	KSEGKHHMNKQFQKWLVDYNYKYLQDWTNTEWKNKKTTVKEQLDDEEWK-----	268
TRAg_13_TR	DKSLKKYITDDFKKWMMDGHQENLNAALSVNWETWKRQKLECNVSGWRLKEDKHWRWTF	256
TRAg_20_TR	EMEWKRPMKVWTKLVEKNEKIWGDKLFNYWDNWKDKKWNWKNMNNWKKKEEKWNNSE-	508
TRAg_27_TR	SKKGRLAMKGDWKNWVNGHDVFFKDGINNDWKNWSDFKRKEFGSITWKYREDKFWTYWID	198
TRAg_34_TR	NKDGKRIENQWERWTISNKNLYYKIIMKEWFKWKNKKIKQWLKRNWLHHEGRILENWER	196
TRAg_21_TR	NTEMVAHLKDYHLWSLNTERSVNALVRGEWNQWQHDKMSSWLSDDWKKVGMAMYWDLQES	193
TRAg_7_TR	KHELKNFIYRDWKKWLRENESYLNLTWLVKQWIQWKNKIKFLMAEWKQEEDEYWNDEWK	314
TRAg_24_TR	HTDWKDYMEIDWHRWINDVEYDLDKLIDERWEQWKTHQIMTWLMSNWTDEEQQYIDKLEF	204
TRAg_3_TR	NTEWHELMEKDWKNWIYGNKLSLNKIIDNKWINWSNEKMAEWLIQELNDEEGSDTQTNI	193

TRAg_18_TR	EKDGESIMMMMEKWKIDKVKSEYDLWLLKDWEQWKTNKIMDWLLSEKKCDQYQYWLKWEY	2573
TRAg_26_TR	RTKGSQLEMEIEWENWIDEKDSLNFEMILKKWIQWKNSKIM-----	210
TRAg_36_TR	NTELKGLIDNEWQNWINQIESQRYTWIEDKQVHRSYQILTWLKSQDWHKHDENICWLRKEY	193
TRAg_33_TR	KTPIRESMEKDWEYWIAEDQYKLDNWMLENFQDKWTKRITWKEKKWKAEEDEYWANWEA	201
TRAg_12_TR	LSDGLEFLVMDWKKWIKENKSNFDEWLKSEWDTWTNSQMEEWKSSNWKLNEDEKRWEMWEN	316
TRAg_22_TR	KTVGKRLIEEDWVKWINDHECKLNEWFNGDWNQWKS LKNFNWEMNEWKSDEYERWAEWQN	620
TRAg_10_TR	KAELKYFIDREWHNVVYQNEQHLNNWITNEWSEWKNHIIAAWLTKNWKLSENAYWEKMAK	229
TRAg_4_TR	TTVGKEMIKSEYEKWIYENENYLDEWVKREWVEWKQKNISSWLSSEWKCKEDDSWSKWEQ	228
TRAg_11_TR	QTEGRLYLDIEWKKWFFENQSRLEDELIVKKWIQWKDKIINWLSMDWKRAEQEHWEFEE	227
TRAg_23_TR	KNDGKKFMETNYHKWIDENYSNYNAVWVKRWEQWKNEKILTWLLKDWRRNEFEYWKFKN	232
TRAg_17_TR	KTEGKNFMKTDLKWKIKAKETS LDDLLEWVQWKNEKIMAWLLSEWKTEEDTYWSQWEH	229
TRAg_5_TR	KTEGRKILEAQWEKWKIKGDDQLQKLILDKQVQWKNDKIRSWLSSEWKTEEDYWANVER	227
TRAg_9_TR	NTEAKQLMEIDWSDWISSESYVDVMMVKEWIVWKNKIMEWIMRDWKCKEDEQWDAWEK	230
TRAg_2_TR	STEGKQLLEMDLKKWFTNNEMIYCKWMTDEWNEWKNEKIKEWVTSEWKESEDQYWSKYD-	229
TRAg_6_TR	KTEGKQFMEQWQKMWLAQKEAHLNNVWVNEWIQWKNSQIMEWLT TDWRLQKEASWSNYEN	362
TRAg_25_TR	KTEGKKGMEADLKKWLNKETF LLDGWI SKEWVQWKNERMLQWLSVDWKHKEDETFEHYKS	604
TRAg_19_TR	RTEGEQFMELDWKKWMYENKFLDDWASKWAKWKKDKIMSWLLSDWKLTEQKYWDDWEN	506
TRAg_35_TR	KSEKQLMEIEWNNWIYHHESFLNVWCLKAWLKWKNDKIVQWLQKDWKLEKEDAYQNW-	228
TRAg_8_TR	KTEGKELMEKDWKNWITNNESYLDVWSVKEWLKWKQNRIVTWIMTDWKCEEDEYWSKWE-	226

TRAg_16_TR	KGLR-N--DNYYSLKWMQWR-NWKNRNHDQKHVVVTLMKDALKEYTGP-EFKLWTEFRKE	264
TRAg_29_TR	-----TKASSGGLSEWEELTDKMNTRYTNN-LDNMWSNYSGD	281
TRAg_32_TR	-----NKVSSGGLSEWEELTNKMNTRYRNN-LDNMWSHFSD	282
TRAg_30_TR	-----YKMNSSGRTEWDKLRNELETRYNKK-IKSLWGGFHRD	282
TRAg_31_TR	-----KSQSDGKSSWDKLVDDLRRHTNK-TDFLWKAYQKD	278
TRAg_14_TR	-QKW-E--KYFQRKEKKEWI----ERNEIEISIRDWLKEKESMPVQCDGWLEWDTWKQE	821
TRAg_1_TR	-TPYGD TMNPLFSVLKKS YD-MYTARKKREKEHWNKLTENIGKTLTNK-KYVDWENMKMT	293
TRAg_15_TR	VMTT-S--KLLNVAKSREWY-RANPNINRERRELMKWFLLEKENEYLGQ-EWKKWTHWKKV	1383
TRAg_28_TR	-----KKEAAGTKEWIKCTDKMEKCLKK-TKKHCKNWEKK	304
TRAg_13_TR	FSPNID--DIPVPKEFKALYENWKVRRKAETDQWKEWTDRIEKRVIFK-DTPAWTKWKND	313
TRAg_20_TR	-----KRKDLNKDENWK-EWKKRLLREKKEWENWVNEKEDFLMDS-EETHWEKWKKEY	558
TRAg_27_TR	HGKP-S--EPMFVIKMEMFK-KWQDRLKNEEEESNWLDEKQKKYIDV-EWDKVVQWKKE	253
TRAg_34_TR	-LPY-T--KILAMSEKKPWF-NSNAQVINERDYFLIWKKKEDFLVNE-ERDKWENWEYY	250
TRAg_21_TR	-RNWAS--YSHTDDMKEHWI-KWNDRNARENIEWSKWVQNKYFIMYA-RHSDIEQWKYD	248
TRAg_7_TR	TETW----KWLHFYKRRKQW-TWKNRVTSEKQEWENWVKIKEERVIYN-KYKKWTQWINA	368
TRAg_24_TR	-----G--KYSNKKEMEHFVKRWNKIIQWKTEKESWIQDKEGFITNI-KNEKWLQWKDD	256
TRAg_3_TR	-----G--KSSSSEENDEYLSLNDKIFSKNEEWEHWTDRKEKLIKKI-KNSNWSEWKNN	245
TRAg_18_TR	SN---E--KTSLRKERIDWY-KWKKIRQSEAKWQKWVREKDQALLEV-KNAIWLNWKED	2626
TRAg_26_TR	-----RENEMAKMERE	221
TRAg_36_TR	-IEW-N--KPSKVRNTGGWL-KWKERIYKQSLWLYVWVQNKKEIIQNI-KCSGWIRWKDD	247
TRAg_33_TR	KGSK-D--KSKVLIDRKNWN-LWKERTYREERQWEMYTERKKKEFFSK-DVVEWMKWKSE	256
TRAg_12_TR	DKKW-I--KWLYLKDWINCS-KWKKRIQKESKEWLRWTKLKEEMYKNK-YGDKWKEWRTD	371
TRAg_22_TR	-GNL-T--LWLNKKKKKKYL-TWKNRIEREKSEWDSWVRKDDLTLS-KTCKWIKWKNE	674
TRAg_10_TR	-KKW-V--KSLFRVVRKNWL-KWKERIDREFQQWDEWVVGKQHLTYTNNHEWDAVWKWTD	284
TRAg_4_TR	-TVW-G--KWLFTENREKWT-AWKERTLRERAEWLKWVQLKEYVYIND-EWIPWTKWKNE	282
TRAg_11_TR	-KSWSS--KFFQIFEKRNYE-DFKDRVSDWEDWFEWVKRKNDFITN-VLDQWIKWKEE	282
TRAg_23_TR	-MTL-P--EPLYERAKNNWN-KWNKRLSKEKEQWKKWVAAKYELYENS-ECKQWKKWKDD	286

TRAg_17_TR	-STW-L--KWLNLTKKKHWL-KWKERNHREGEQWSTWLHVKENVYIFS-EWNNWSIWKNE	283
TRAg_5_TR	-ATT-A--KWLQBAEKMHWL-KWKERINRESEQWVNWVQMKEVYINV-EWKKWPKWKND	281
TRAg_9_TR	-NKW-S--KWF SINERKKWT-QWKDRLSKETEETAWVENKEKQYLDN-EDRKLVEWKKN	284
TRAg_2_TR	-DAT-I--QTLTVAERNQWF-KWKERIYREGIEWKNWIAIKESKFVNA-NWNSWSEWKNE	283
TRAg_6_TR	-NKI-T--NMLQIKKRKQWN-KWKERINREREEDAWVRSKENIYINT-KWNKWSKWKKD	416
TRAg_25_TR	-SKF-T--NVLHIKKKKKWT-KWKERTNKEKEEWNWVKGKENLYVNN-KWDKWLKWKKD	658
TRAg_19_TR	-KAW-P--RFVYLDRDRENM-RWKERINREWEETSWVQDKDKVFNNA-KWVGWSKWRDD	560
TRAg_35_TR	-KMW-R--LVGNPTDRTNWL-KWRKRNDNQIIEWNLWVTTKEKLYINH-KWDKWINWKND	282
TRAg_8_TR	-ESW-A--KSPNMHDRTNWL-NWRERLNKEMVQWNSWVMMKEQQIREN-RSNNWSKWKSD	280

TRAg_16_TR	KIDFYKQWMQAFAEQWTQDKQWNTW-----	289
TRAg_29_TR	LLFRFDEWSPEVLEKWIENKQWNQW-----	306
TRAg_32_TR	LFFNFDEWAPQVLEKWIENKQWNRW-----	307
TRAg_30_TR	VYFRFKEWIEEVFNKWIENKQIDTW-----	307
TRAg_31_TR	TLFGTGEWAEELFNKWIENKQW-----	300
TRAg_14_TR	KFQHLDDYLNSLKNQWLAEKKW-----	843
TRAg_1_TR	KSGWYNEW-----	301
TRAg_15_TR	KFFVFNSMCTTFSGKRLTKEEW-----	1405
TRAg_28_TR	ANSSFKKWEQDFTKKWTSNKQWNSW-----	329
TRAg_13_TR	KTAAFEKWLAFTNKLVAQKQWNTW-----	338
TRAg_20_TR	KWNYLNEWMKQMEVDWLKSKPWEVW-----	583
TRAg_27_TR	NNKKFIDWMEYFVEKWTSNKQWNVW-----	278
TRAg_34_TR	KNDFQTMDSFLSHW-----	266
TRAg_21_TR	NYALYSTWRNDFINRWVSEKKW-----	270
TRAg_7_TR	KKPSINQWVESLADKCVNDSRWNTW-----	393
TRAg_24_TR	HYFLFNWRNDFIEDWISKKRWLLW-----	281
TRAg_3_TR	KYASFNQWRESFIKKWLRERQW-----	267
TRAg_18_TR	KKNIFFSMLHFFINNWIAKKQWNVW-----	2651
TRAg_26_TR	NQ-----	223
TRAg_36_TR	KNKIFNQWKECFLNWIREEKW-----	269
TRAg_33_TR	KTEMFENWKENTLSTWIKKQWNVW-----	281
TRAg_12_TR	KSIVYDDWKDDLAKRMIKKQWQVW-----	396
TRAg_22_TR	KRLLFNDWVENFINTWISRKQWNSW-----	699
TRAg_10_TR	KYALVKEVRKSFVTKWVTEKQWRW-----	309
TRAg_4_TR	NRLAFIDWIGSFMNEWINNQWNEW-----	307
TRAg_11_TR	KNLLYNNWADAFVTNWINKKQWVW-----	307
TRAg_23_TR	REVLFNWIESFINTWVAEKKQWNVW-----	311
TRAg_17_TR	KEEFFYKWMEDTINWINEKRW-----	305
TRAg_5_TR	KKILFNKWSTNLVYKWTLLKQWNVW-----	306
TRAg_9_TR	NYILFNKWMESFINKWIKEKQW-----	306
TRAg_2_TR	KRLEFNDWIEAFVEKWIRQKQWLIW-----	308
TRAg_6_TR	KRFIFSKWVEMFTNKLISERQWKEW-----	441
TRAg_25_TR	KRALYSQKFLTFINKWISDKQWTVW-----	683
TRAg_19_TR	RRALFDDWMKPFIEKWINQKQWQVW-----	585
TRAg_35_TR	KNILFHEWMECFINKWIGEKKW-----	304
TRAg_8_TR	KHVMFNLMWDTFINKWINEKQWVW-----	305

FIG S1 Sequence alignment of tryptophan-rich domain sequences of PvTRAg proteins. The sequence alignment of tryptophan-rich protein was analyzed by MUSCLE (MUltiple Sequence Comparison by Log-Expectation, <http://www.ebi.ac.uk/Tools/msa/muscle/>).

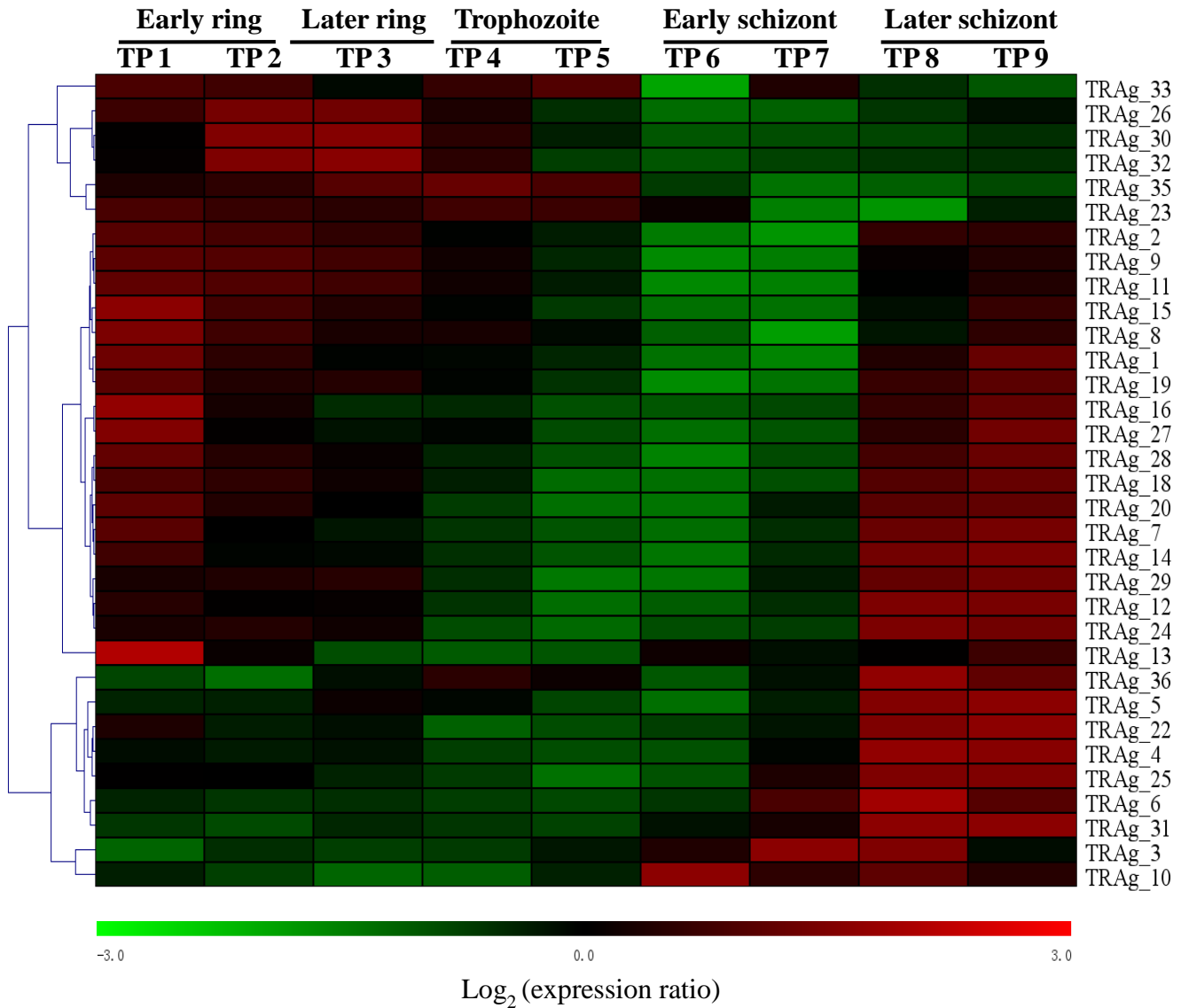


FIG S2 Transcriptome of the PvTRAg proteins of blood-stage vivax malaria. Thirty-three genes with transcriptome data out of 36 total PvTRAg genes were used in the analysis. The transcription data of *P. vivax* genes were collected from published microarray results (1). TP1–9 represent gene expression data in *P. vivax* that were correlated with the expression level of PvTRAGs after 9, 13, 17, 20, 23, 29, 35, 40, and 43 h of cultivation of *P. vivax* parasites, respectively.

TABLE S1 Summary of the expression region and geographic origin used for the construction of PvTRAg plasmids

Name	Gene ID	Chromosomal locations	Insert (bp)	Insert (aa) ^a	Geographic origin ^a	Polymorphisms (aa) ^b	References
PVX_096950	TRAg_1	Pv_Sal1_chr02: 50,597–52,235 (+)	894 (88–984)	298 (A30–L327)	Thai	N299D	(2)
PVX_096995	TRAg_2	Pv_Sal1_chr02: 110,463–112,049 (+)	1263 (181–1443)	421 (K61–A480)	Korean	Insertion of heptapeptide (GVAAAPG) at 332 aa	this study
PVX_002500	TRAg_3	Pv_Sal1_chr04: 41,747–42,706 (+)	762 (70–831)	254 (S23–N276)	Korean	/	this study
PVX_088810	TRAg_4	Pv_Sal1_chr05: 42,292–43,537 (+)	786 (292–1077)	263 (K98–E358)	Korean	/	(3)
PVX_088820	TRAg_5	Pv_Sal1_chr05: 49,904– 51,215 (+)	780 (172–951)	259 (A58–V316)	Korean	Q200P	this study
PVX_088825	TRAg_6	Pv_Sal1_chr05: 53,924–55,652 (+)	1161 (175–1335)	387 (F59–S444)	Korean	D155G, Q160K	this study
PVX_088850	TRAg_7	Pv_Sal1_chr05: 78,993–80,676 (+)	1191 (184–1374)	397 (F62–V457)	Korean	S102I, K153E, L160N, V186I, E316K	this study
PVX_090250	TRAg_8	Pv_Sal1_chr05: 1,263,606–1,264,574 (-)	969 (4–969)	323 (M2–K322)	Korean	K28N, N293S	(3)
PVX_090255	TRAg_9	Pv_Sal1_chr05: 1,269,456–1,270,922 (-)	978 (4–981)	326 (E2–N326)	Thai	S191P, F237L	(2)
PVX_090260	TRAg_10	Pv_Sal1_chr05: 1,273,169–1,274,463 (-)	861 (181–1041)	287 (S61–V346)	Korean	/	this study
PVX_090265	TRAg_11	Pv_Sal1_chr05: 1,277,770–1,279,489 (-)	978 (4–981)	326 (E2–K326)	Thai	T43I, I45T, N63E, S74G, I80L, K88R, V272A, A293T	(2)
PVX_090270	TRAg_12	Pv_Sal1_chr05: 1,283,152–1,284,624 (-)	1068 (202–1269)	357 (A68–E423)	Korean	A92S, deletion of octapeptide (TKVADKTG) at 121-128aa	(3)
PVX_090275	TRAg_13	Pv_Sal1_chr05: 1,288,045–1,289,739 (-)	951 (70–1020)	317 (A23–V339)	Korean	S71P	this study
PVX_094305	TRAg_14	Pv_Sal1_chr08: 126,035–128,911 (+)	939 (1672–610)	313 (T558–K870)	Korean	/	this study
PVX_092990	TRAg_15	Pv_Sal1_chr09: 1,912,378–1,917,122 (-)	870 (3376–4245)	290 (D1126–V1414)	Korean	Insertion of E at 1174aa, V1158I, H1380Q	this study
PVX_092995	TRAg_16	Pv_Sal1_chr09: 1,921,661–1,923,102 (-)	1005 (73–1077)	335 (S24–A358)	Thai	P36A, R45Q, S219A, W222L, Deletion of hexapeptide (KKKAAS) at 312-316aa	(2)
PVX_097577	TRAg_17	Pv_Sal1_chr10: 1,335,857–1,337,016 (-)	768 (181–948)	256 (S61–S315)	Korean	Q240E, V264A	(2)
PVX_097575	TRAg_18	Pv_Sal1_chr10: 1,339,589–1,348,572 (-)	840 (7150–7989)	280 (L2384–T2662)	Korean	K2466E, M2525I	this study
PVX_115465	TRAg_19	Pv_Sal1_chr11: 27,493–29,676 (+)	804 (994–1797)	268 (S332–S598)	Korean	S370G, K474E	this study
PVX_083550	TRAg_20	Pv_Sal1_chr12: 32,743–35,371 (+)	1650 (190–1839)	550 (I64–S612)	Korean	D82Y, K311E, T346A, M570V	this study

PVX_121897	TRAg_21	Pv_Sal1_chr14: 68,269–69,280 (+)	759 (70–828)	253 (S24–N275)	Korean	N60D	(2)
PVX_101510	TRAg_22	Pv_Sal1_chr14: 2,978,093–2,980,422 (-)	1935 (214–2148)	646 (K72–Y716)	Korean	K88R	(3)
PVX_101515	TRAg_23	Pv_Sal1_chr14: 2,983,295–2,984,636 (-)	963 (4–966)	321 (E2–S321)	Thai	K258E, D285G.	(2)
PVX_101525	TRAg_24	Pv_Sal1_chr14: 2,992,657–2,993,679 (-)	786 (79–864)	262 (H27–N287)	Thai		(2)
PVX_112655	TRAg_25	AAKM01000025: 23,247–25,581 (-)	1905 (175–2079)	635 (S59-L692)	Korean	S277N	this study
PVX_112660	TRAg_26	AAKM01000025: 28,035–29,062 (-)	450 (178–627)	165 (P60–TC210)	Korean	D197N	this study
PVX_112665	TRAg_27	AAKM01000025: 31,142–32,691 (-)	780 (88–867)	260 (D30–L288)	Korean	T194K	this study
PVX_112670	TRAg_28	AAKM01000025: 39,363–41,543 (-)	909 (100–1008)	303 (V34–K335)	Thai	E58G, Insertion of K at 59 aa, Insertion of tetrapeptide (EGAA) at 69aa	(2)
PVX_112675	TRAg_29	AAKM01000025: 45,585–47,015 (-)	843 (97–939)	281 (P33–K312)	Thai	V63L, D65E, Deletion of K at 68aa, D70G, N81S, G82T, L83I, K85N, I90V, K93N, V94L, K95N, E98A, L106P, L239F	(2)
PVX_112680	TRAg_30	AAKM01000025: 49,982–52,248 (-)	846 (97–942)	282 (P33–K313)	Thai	K115R, A244E	(2)
PVX_112685	TRAg_31	AAKM01000025: 56,111–57,670 (-)	861 (49–909)	287 (L17–K302)	Thai	G46A, K81E, Q150	(2)
PVX_112690	TRAg_32	AAKM01000025: 60,987–63,052 (-)	855 (88–942)	285 (E30–K313)	Thai	Q37R, D66G, E258D	(2)
PVX_112705	TRAg_33	AAKM01000025: 79,107–79,991 (-)	885 (4–885)	295 (K2–Y294)	Korean	/	(3)
PVX_125728	TRAg_34	AAKM01000032: 6,128–7,093 (+)	753 (88–840)	251 (K30–S279)	Korean	/	(2)
PVX_125730	TRAg_35	AAKM01000032: 9,260–10,694 (+)	816 (178–993)	272 (T60–K330)	Korean	K312E	this study
PVX_109280	TRAg_36	AAKM01000061: 5,896–6,877 (-)	774 (79–852)	258 (N27–Q283)	Thai	N59K, Deletion of K at 60aa	(2)

^a Genomic DNAs and complementary DNAs were obtained from *P. vivax* isolates from Korea and Thailand.

^b Positions of amino acid substitutions were compared with those of *P. vivax* Sal-I strain from PlasmoDB.

TABLE S2 Summary of In-fusion primers for cell-free expression of PvTRAgS

Name	Forward primer (5' → 3') ^a	Reverse primer (5' → 3') ^a
TRAg_2	gggcggatatctcgag AAAACCGAAACGGTGACCT	gcggtaccgggatcc CTAAGCGGAGGTGGAGGG
TRAg_3	gggcggatatctcgag TCTCTTCAATATGAACAAATTGAACC	gcggtaccgggatcc CTAATTTATCTGATTGTTAACCATTATTTTC
TRAg_5	gggcggatatctcgag GCGGCAGCTAATAGACCAAAA	gcggtaccgggatcc CTAAACTTGGGGTGCAGTATTTG
TRAg_6	gggcggatatctcgag TTTCTCCCCACACTTGGAAA	gcggtaccgggatcc TTATGATTTAACCATTCTTTCCATT
TRAg_7	gggcggatatctcgag TTCTTCAGTAAAAAGTCGAACAGACTC	gcggtaccgggatcc CTACACACTAAGAGCATTTTCTCCTTC
TRAg_10	gggcggatatctcgag TCCGTTAATAAGAAAAAGAAGGACAT	gcggtaccgggatcc TTAGACGGTTGACGGCCC
TRAg_13	gggcggatatctcgag GCTGCCCAAAGAAGGCA	gcggtaccgggatcc TTAGACCCAGTTGGTCCACTG
TRAg_14	gggcggatatctcgag ACTGTATTTCGCATGGAGGGA	gcggtaccgggatcc TTAATTGTCAGCTTTATCGTCAGC
TRAg_15	gggcggatatctcgag GATGTATTACAATTAGTAATACCATCGGA	gcggtaccgggatcc TCAAACTTTTATTTCATTAACAAATTGA
TRAg_18	gggcggatatctcgag CTTAACCTTGCAGATTACAAAGAATG	gcggtaccgggatcc TCAAGTTTCTGACAGTTCCCTGT
TRAg_19	gggcggatatctcgag TCGATAGAGAGGCAGCAAGAG	gcggtaccgggatcc TTAGGAATTATTTCTCCTAAGTGCAT
TRAg_20	gggcggatatctcgag ATCCTGCAGCCGCGAGAA	gcggtaccgggatcc TTAAGAGCTGACCGAATACTCCC
TRAg_25	gggcggatatctcgag TCTGTATTCAAAAAATTAAATAACACATT	gcggtaccgggatcc TTACAAAGTTGAACCACCTTGA
TRAg_26	gggcggatatctcgag CCTTCACTTATAGATAAGTACGATGCT	gcggtaccgggatcc TTA TATTTTTGAATTCTTCCACTGAA
TRAg_27	gggcggatatctcgag GATGCTCAGGGTGAGAACGT	gcggtaccgggatcc TTATAGTGTGATACAACACTGTTTCTCTCCTC
TRAg_35	gggcggatatctcgag ACCGTTTTAGAACCAGTGGAAG	gcggtaccgggatcc TCATTTGGATGCATCCATATGT

^a Lowercase letter of primer sequence indicates it is homologous to the vector sequence.

TABLE S3 Summary of primers used for *E. coli* expression of five PvTRAGs

Proteins	Forward primer (5' → 3') ^a	Vector (Tag)	Apparent molecular weights
TRAg_13	GCTGCCCAAAGAAGGCA TTAGACCCAGTTGGTCCACTG	pEXP5 NT TOPO (His)	36.5 kDa
TRAg_15	GATGTATTACAATTAGTAATACCATCGGA TCAAACCTTTTATTTTCATTAACAAATTGA	pEXP5 NT TOPO (His)	35.2 kDa
TRAg_16	gatccccaggaattccc TCACAAGGATGTTTCAGGATACC atgcggccgctcgag TTATGCTGCATTTGGTGCTG	pGEX-4T-2 (GST)	65.7 kDa
TRAg_26	CCTTCACTTATAGATAAGTACGATGCT TTA TAT TTT TGA ATT CTT CCA CTG AAT CC	pEXP5 NT TOPO (His)	18.3 kDa
TRAg_29	CCAAAACCTGCTCAGAACCT TTACTTTCTAACTTTTTTGACCCATTG	pEXP5 NT TOPO (His)	32.4 kDa

^a Lowercase letter of primer sequence indicates it is homologous to the vector sequence.

TABLE S4 Motifs identified in the PvTRAg family using MEME

Motif #	Length (aa) ^a	Amino acid sequence of motif
1	22	FNEWMESFI[NE]KWI[NS]EKQWNVWV
2	22	WKNKKIMEWL[SM]S[DE]WKL[EK]EDEYW
3	25	W[DN][DE]SQW[EK]EWIKTE[GL]KE[LF][MIL]Ex[DE]W[KE]KW
4	22	WL[EQ][EK]KEKEWEEW[LI]KSM[EQ]NKW[MT]H
5	25	WKENEW[NK]NW[ML]KKLEE[DE]W[KE]xFNxS[LI]E
6	25	W[KN][EK]RIN[RK]EKE[EQ]Wx[KN]WV[KQ]xKEKLYIN
7	16	VSx[LI]SI[AST]L[FL]ILSSAFL
8	16	[YF]NEN[MLI]DEEYKS[DN][IV][LY]KK
9	12	W[KD]KWSKWK[ND][DE]KR
10	24	PPKPVNDKDKD[DG]SNKTETK[DN]AKN[GT]

^aaa, amino acid.

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