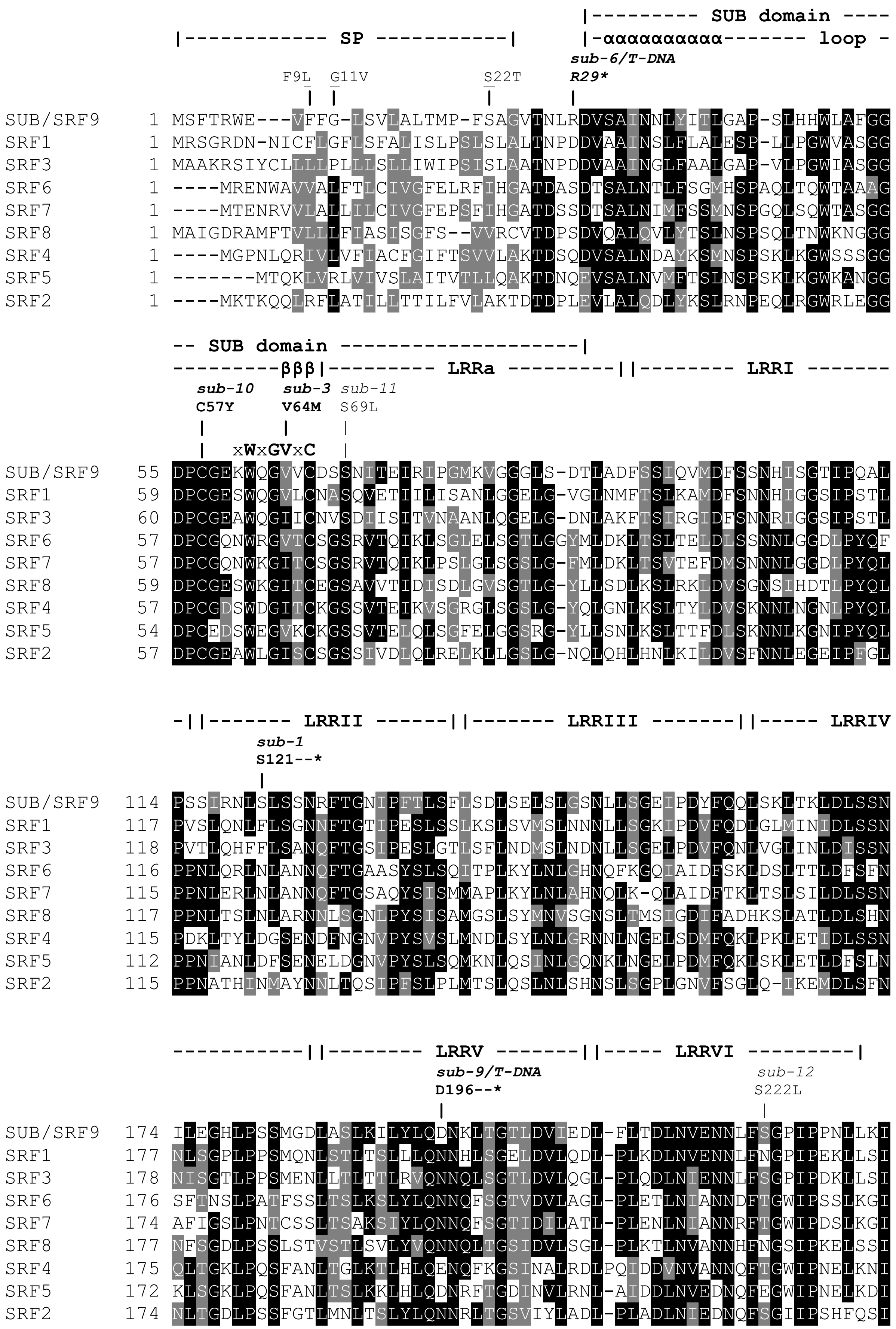
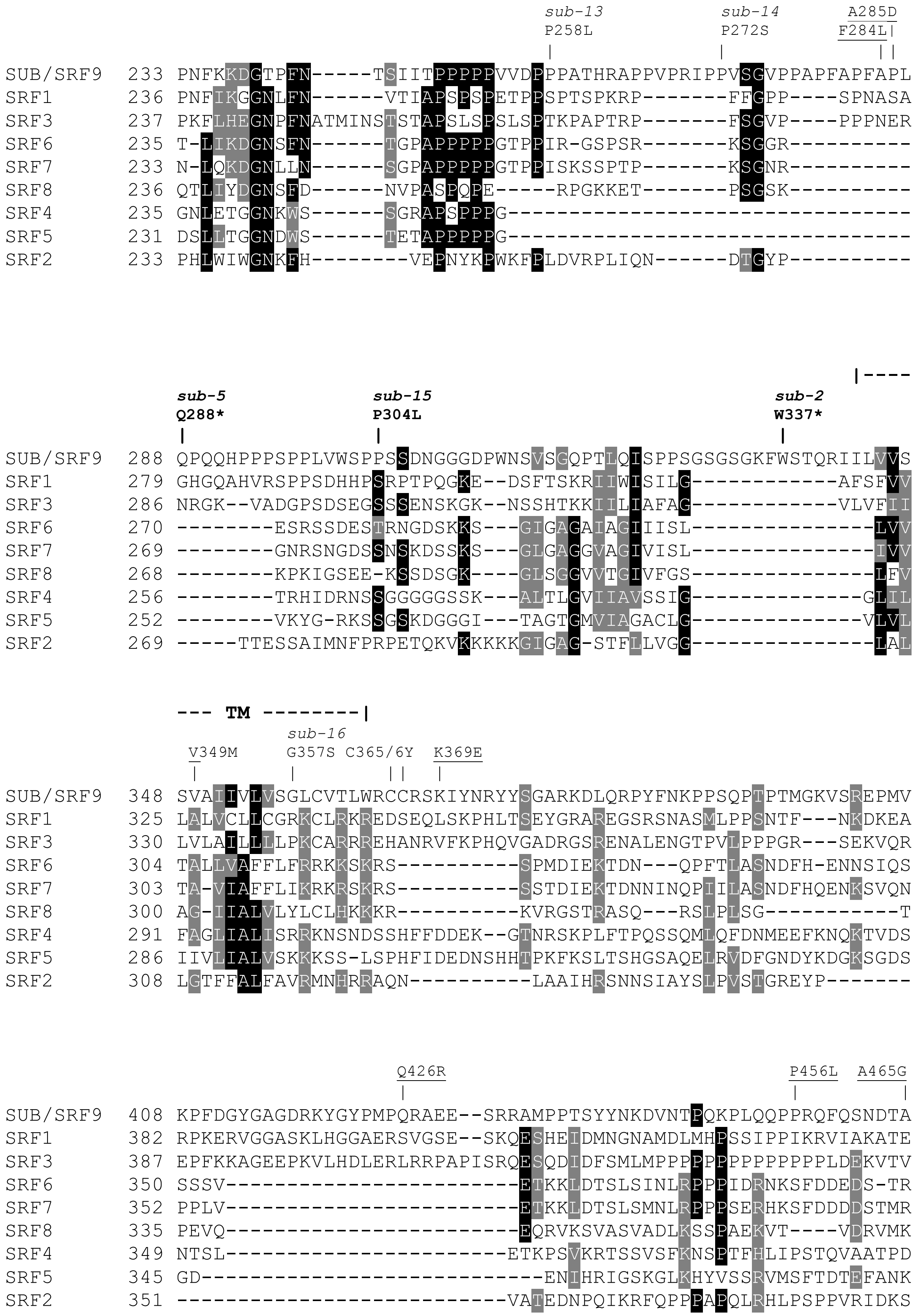


```
                                                  |--------- SUB domain ----
                |------------ SP -----------|     |-αααααααααα------- loop -
                                                 sub-6/T-DNA
                         F9L G11V         S22T   R29*
                           | |            |      |
SUB/SRF9      1 MSFTRWE---VFFG-LSVLALTMP-FSAGVTNLRDVSAINNLYITLGAP-SLHHWLAFGG
SRF1          1 MRSGRDN-NICFLGFLSFALISLPSLSLALTNPDDVAAINSLFLALESP-LLPGWVASGG
SRF3          1 MAAKRSIYCLLLLPLLLSLLIWIPSISLAATNPDDVAAINGLFAALGAP-VLPGWIASGG
SRF6          1 ----MRENWAVVALFTLCIVGFELRFIHGATDASDTSALNTLFSGMHSPAQLTQWTAAAG
SRF7          1 ----MTENRVVLALLILCIVGFEPSFIHGATDSSDTSALNIMFSSMNSPGQLSQWTASGG
SRF8          1 MAIGDRAMFTVLLLFIASISGFS--VVRCVTDPSDVQALQVLYTSLNSPSQLTNWKNGGG
SRF4          1 ----MGPNLQRIVLVFIACFGIFTSVVLAKTDSQDVSALNDAYKSMNSPSKLKGWSSSGG
SRF5          1 -------MTQKLVRLVIVSLAITVTLLQAKTDNQEVSALNVMFTSLNSPSKLKGWKANGG
SRF2          1 ----MKTKQQLRFLATILLTTILFVLAKTDTDPLEVLALQDLYKSLRNPEQLRGWRLEGG

                -- SUB domain --------------------|
                ---------βββ|--------- LRRa ---------||-------- LRRI -------
                  sub-10 sub-3 sub-11
                  C57Y   V64M S69L
                  |      |    |
                  |  xWxGVxC  |
SUB/SRF9     55 DPCGEKWQGVVCDSSNITEIRIPGMKVGGGLS-DTLADFSSIQVMDFSSNHISGTIPQAL
SRF1         59 DPCGESWQGVLCNASQVETIILISANLGGELG-VGLNMFTSLKAMDFSNNHIGGSIPSTL
SRF3         60 DPCGEAWQGIICNVSDIISITVNAANLQGELG-DNLAKFTSIRGIDFSNNRIGGSIPSTL
SRF6         57 DPCGQNWRGVTCSGSRVTQIKLSGLELSGTLGGYMLDKLTSLTELDLSSNNLGGDLPYQF
SRF7         57 DPCGQNWKGITCSGSRVTQIKLPSLGLSGSLG-FMLDKLTSVTEFDMSNNNLGGDLPYQL
SRF8         59 DPCGESWKGITCEGSAVVTIDISDLGVSGTLG-YLLSDLKSLRKLDVSGNSIHDTLPYQL
SRF4         57 DPCGDSWDGITCKGSSVTEIKVSGRGLSGSLG-YQLGNLKSLTYLDVSKNNLNGNLPYQL
SRF5         54 DPCEDSWEGVKCKGSSVTELQLSGFELGGSRG-YLLSNLKSLTTFDLSKNNLKGNIPYQL
SRF2         57 DPCGEAWLGISCSGSSIVDLQLRELKLLGSLG-NQLQHLHNLKILDVSFNNLEGEIPFGL

                -||------- LRRII ------||------- LRRIII -------||----- LRRIV
                       sub-1
                       S121--*
                       |
SUB/SRF9    114 PSSIRNLSLSSNRFTGNIPFTLSFLSDLSELSLGSNLLSGEIPDYFQQLSKLTKLDLSSN
SRF1        117 PVSLQNLFLSGNNFTGTIPESLSSLKSLSVMSLNNNLLSGKIPDVFQDLGLMINIDLSSN
SRF3        118 PVTLQHFFLSANQFTGSIPESLGTLSFLNDMSLNDNLLSGELPDVFQNLVGLINLDISSN
SRF6        116 PPNLQRLNLANNQFTGAASYSLSQITPLKYLNLGHNQFKGQIAIDFSKLDSLTTLDFSFN
SRF7        115 PPNLERLNLANNQFTGSAQYSISMMAPLKYLNLAHNQLK-QLAIDFTKLTSLSILDLSSN
SRF8        117 PPNLTSLNLARNNLSGNLPYSISAMGSLSYMNVSGNSLTMSIGDIFADHKSLATLDLSHN
SRF4        115 PDKLTYLDGSENDFNGNVPYSVSLMNDLSYLNLGRNNLNGELSDMFQKLPKLETIDLSSN
SRF5        112 PPNIANLDFSENELDGNVPYSLSQMKNLQSINLGQNKLNGELPDMFQKLSKLETLDFSLN
SRF2        115 PPNATHINMAYNNLTQSIPFSLPLMTSLQSLNLSHNSLSGPLGNVFSGLQ-IKEMDLSFN

                -----------||-------- LRRV -------||----- LRRVI ---------|
                                      sub-9/T-DNA                sub-12
                                      D196--*                   S222L
                                      |                          |
SUB/SRF9    174 ILEGHLPSSMGDLASLKILYLQDNKLTGTLDVIEDL-FLTDLNVENNLFSGPIPPNLLKI
SRF1        177 NLSGPLPPSMQNLSTLTSLLLQNNHLSGELDVLQDL-PLKDLNVENNLFNGPIPEKLLSI
SRF3        178 NISGTLPPSMENLLTLTTLRVQNNQLSGTLDVLQGL-PLQDLNIENNLFSGPIPDKLLSI
SRF6        176 SFTNSLPATFSSLTSLKSLYLQNNQFSGTVDVLAGL-PLETLNIANNDFTGWIPSSLKGI
SRF7        174 AFIGSLPNTCSSLTSAKSIYLQNNQFSGTIDILATL-PLENLNIANNRFTGWIPDSLKGI
SRF8        177 NFSGDLPSSLSTVSTLSVLYVQNNQLTGSIDVLSGL-PLKTLNVANNHFNGSIPKELSSI
SRF4        175 QLTGKLPQSFANLTGLKTLHLQENQFKGSINALRDLPQIDDVNVANNQFTGWIPNELKNI
SRF5        172 KLSGKLPQSFANLTSLKKLHLQDNRFTGDINVLRNL-AIDDLNVEDNQFEGWIPNELKDI
SRF2        174 NLTGDLPSSFGTLMNLTSLYLQNNRLTGSVIYLADL-PLADLNIEDNQFSGIIPSHFQSI
```

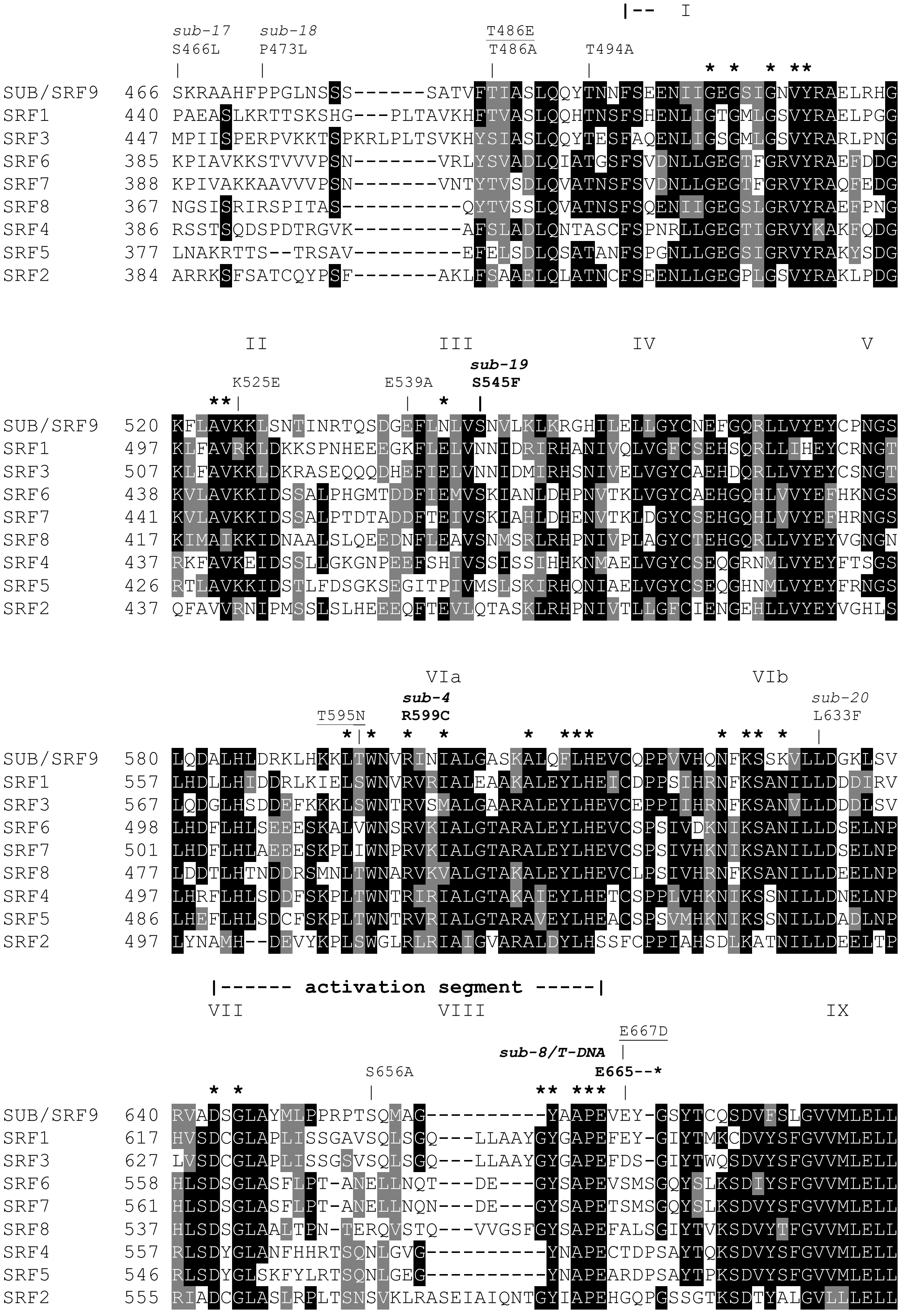


```
                                               sub-13        sub-14     A285D
                                               P258L         P272S     F284L|
                                               |             |            ||
SUB/SRF9     233 PNFKKDGTPFN-----TSIITPPPPPVVDPPPATHRAPPVPRIPPVSGVPPAPFAPFAPL
SRF1         236 PNFIKGGNLFN------VTIAPSPSPETPPSPTSPKRP-------FFGPP----SPNASA
SRF3         237 PKFLHEGNPFNATMINSTSTAPSLSPSLSPTKPAPTRP-------FSGVP----PPPNER
SRF6         235 T-LIKDGNSFN------TGPAPPPPPGTPPIR-GSPSR-------KSGGR----------
SRF7         233 N-LQKDGNLLN------SGPAPPPPPGTPPISKSSPTP-------KSGNR----------
SRF8         236 QTLIYDGNSFD------NVPASPQPE-----RPGKKET-------PSGSK----------
SRF4         235 GNLETGGNKWS------SGRAPSPPPG---------------------------------
SRF5         231 DSLLTGGNDWS------TETAPPPPPG---------------------------------
SRF2         233 PHLWIWGNKFH--------VEPNYKPWKFPLDVRPLIQN------DTGYP----------

                                                                        |----
                 sub-5           sub-15                           sub-2
                 Q288*           P304L                            W337*
                 |               |                                |
SUB/SRF9     288 QPQQHPPPSPPLVWSPPSSDNGGGDPWNSVSGQPTLQISPPSGSGSGKFWSTQRIILVVS
SRF1         279 GHGQAHVRSPPSDHHPSRPTPQGKE--DSFTSKRIIWISILG------------AFSFVV
SRF3         286 NRGK--VADGPSDSEGSSSENSKGK--NSSHTKKIILIAFAG------------VLVFII
SRF6         270 --------ESRSSDESTRNGDSKKS---GIGAGAIAGIIISL---------------LVV
SRF7         269 --------GNRSNGDSSNSKDSSKS---GLGAGGVAGIVISL---------------IVV
SRF8         268 --------KPKIGSEE-KSSDSGK----GLSGGVVTGIVFGS---------------LFV
SRF4         256 --------TRHIDRNSSGGGGGSSK---ALTLGVIIAVSSIG--------------GLIL
SRF5         252 --------VKYG-RKSSGSKDGGGI---TAGTGMVIAGACLG--------------VLVL
SRF2         269 -----TTESSAIMNFPRPETQKVKKKKKGIGAG-STFLLVGG---------------LAL

                 --- TM --------|
                         sub-16
                  V349M  G357S C365/6Y  K369E
                  |       |       ||  |
SUB/SRF9     348 SVAIIVLVSGLCVTLWRCCRSKIYNRYYSGARKDLQRPYFNKPPSQPTPTMGKVSREPMV
SRF1         325 LALVCLLCGRKCLRKREDSEQLSKPHLTSEYGRAREGSRSNASMLPPSNTF---NKDKEA
SRF3         330 LVLAILLLLPKCARRREHANRVFKPHQVGADRGSRENALENGTPVLPPPGR---SEKVQR
SRF6         304 TALLVAFFLFRRKKSKRS----------SPMDIEKTDN---QPFTLASNDFH-ENNSIQS
SRF7         303 TA-VIAFFLIKRKRSKRS----------SSTDIEKTDNNINQPIILASNDFHQENKSVQN
SRF8         300 AG-IIALVLYLCLHKKKR----------KVRGSTRASQ---RSLPLSG-----------T
SRF4         291 FAGLIALISRRKNSNDSSHFFDDEK--GTNRSKPLFTPQSSQMLQFDNMEEFKNQKTVDS
SRF5         286 IIVLIALVSKKKSS-LSPHFIDEDNSHHTPKFKSLTSHGSAQELRVDFGNDYKDGKSGDS
SRF2         308 LGTFFALFAVRMNHRRAQN----------LAAIHRSNNSIAYSLPVSTGREYP-------

                                   Q426R                           P456L  A465G
                                   |                               |        |
SUB/SRF9     408 KPFDGYGAGDRKYGYPMPQRAEE--SRRAMPPTSYYNKDVNTPQKPLQQPPRQFQSNDTA
SRF1         382 RPKERVGGASKLHGGAERSVGSE--SKQESHEIDMNGNAMDLMHPSSIPPIKRVIAKATE
SRF3         387 EPFKKAGEEPKVLHDLERLRRPAPISRQESQDIDFSMLMPPPPPPPPPPPPPPLDEKVTV
SRF6         350 SSSV------------------------ETKKLDTSLSINLRPPPIDRNKSFDDEDS-TR
SRF7         352 PPLV------------------------ETKKLDTSLSMNLRPPPSERHKSFDDDDSTMR
SRF8         335 PEVQ------------------------EQRVKSVASVADLKSSPAEKVT----VDRVMK
SRF4         349 NTSL-----------------------ETKPSVKRTSSVSFKNSPTFHLIPSTQVAATPD
SRF5         345 GD----------------------------ENIHRIGSKGLKHYVSSRVMSFTDTEFANK
SRF2         351 ---------------------------VATEDNPQIKRFQPPPAPQLRHLPSPPVRIDKS
```

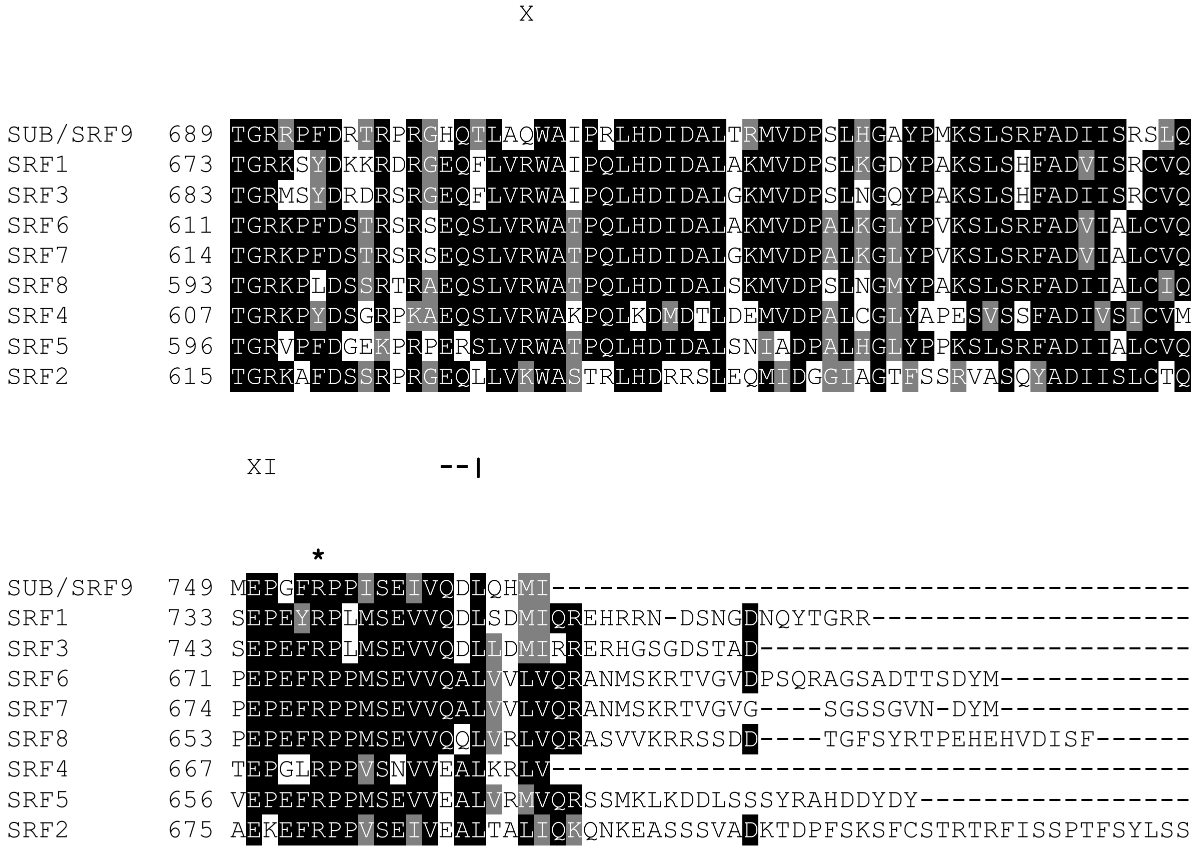


```
                                                   |--  I
              sub-17 sub-18             T486E
              S466L  P473L              T486A   T494A
              |      |                  |       |
                                                          * *  * **
SUB/SRF9  466 SKRAAHFPPGLNSSS------SATVFTIASLQQYTNNFSEENIIGEGSIGNVYRAELRHG
SRF1      440 PAEASLKRTTSKSHG---PLTAVKHFTVASLQQHTNSFSHENLIGTGMLGSVYRAELPGG
SRF3      447 MPIISPERPVKKTSPKRLPLTSVKHYSIASLQQYTESFAQENLIGSGMLGSVYRARLPNG
SRF6      385 KPIAVKKSTVVVPSN-------VRLYSVADLQIATGSFSVDNLLGEGTFGRVYRAEFDDG
SRF7      388 KPIVAKKAAVVVPSN-------VNTYTVSDLQVATNSFSVDNLLGEGTFGRVYRAQFEDG
SRF8      367 NGSISRIRSPITAS----------QYTVSSLQVATNSFSQENIIGEGSLGRVYRAEFPNG
SRF4      386 RSSTSQDSPDTRGVK---------AFSLADLQNTASCFSPNRLLGEGTIGRVYKAKFQDG
SRF5      377 LNAKRTTS--TRSAV---------EFELSDLQSATANFSPGNLLGEGSIGRVYRAKYSDG
SRF2      384 ARRKSFSATCQYPSF-------AKLFSAAELQLATNCFSEENLLGEGPLGSVYRAKLPDG

                     II              III             IV                V
                                      sub-19
                  K525E        E539A  S545F
                 **|             |  *  |
SUB/SRF9  520 KFLAVKKLSNTINRTQSDGEFLNLVSNVLKLKRGHILELLGYCNEFGQRLLVYEYCPNGS
SRF1      497 KLFAVRKLDKKSPNHEEEGKFLELVNNIDRIRHANIVQLVGFCSEHSQRLLIHEYCRNGT
SRF3      507 KLFAVKKLDKRASEQQQDHEFIELVNNIDMIRHSNIVELVGYCAEHDQRLLVYEYCSNGT
SRF6      438 KVLAVKKIDSSALPHGMTDDFIEMVSKIANLDHPNVTKLVGYCAEHGQHLVVYEFHKNGS
SRF7      441 KVLAVKKIDSSALPTDTADDFTEIVSKIAHLDHENVTKLDGYCSEHGQHLVVYEFHRNGS
SRF8      417 KIMAIKKIDNAALSLQEEDNFLEAVSNMSRLRHPNIVPLAGYCTEHGQRLLVYEYVGNGN
SRF4      437 RKFAVKEIDSSLLGKGNPEEFSHIVSSISSIHHKNMAELVGYCSEQGRNMLVYEYFTSGS
SRF5      426 RTLAVKKIDSTLFDSGKSEGITPIVMSLSKIRHQNIAELVGYCSEQGHNMLVYEYFRNGS
SRF2      437 QFAVVRNIPMSSLSLHEEEQFTEVLQTASKLRHPNIVTLLGFCIENGEHLLVYEYVGHLS

                                   VIa                        VIb
                                 sub-4                             sub-20
                          T595N  R599C                             L633F
                            *|*  *  *      *  ***          * ** *  |
SUB/SRF9  580 LQDALHLDRKLHKKLTWNVRINIALGASKALQFLHEVCQPPVVHQNFKSSKVLLDGKLSV
SRF1      557 LHDLLHIDDRLKIELSWNVRVRIALEAAKALEYLHEICDPPSIHRNFKSANILLDDDIRV
SRF3      567 LQDGLHSDDEFKKKLSWNTRVSMALGAARALEYLHEVCEPPIIHRNFKSANVLLDDDLSV
SRF6      498 LHDFLHLSEEESKALVWNSRVKIALGTARALEYLHEVCSPSIVDKNIKSANILLDSELNP
SRF7      501 LHDFLHLAEEESKPLIWNPRVKIALGTARALEYLHEVCSPSIVHKNIKSANILLDSELNP
SRF8      477 LDDTLHTNDDRSMNLTWNARVKVALGTAKALEYLHEVCLPSIVHRNFKSANILLDEELNP
SRF4      497 LHRFLHLSDDFSKPLTWNTRIRIALGTAKAIEYLHETCSPPLVHKNIKSSNILLDNELNP
SRF5      486 LHEFLHLSDCFSKPLTWNTRVRIALGTARAVEYLHEACSPSVMHKNIKSSNILLDADLNP
SRF2      497 LYNAMH--DEVYKPLSWGLRLRIAIGVARALDYLHSSFCPPIAHSDLKATNILLDEELTP

                 |------ activation segment -----|
                 VII                VIII                            IX
                                                   E667D
                                       sub-8/T-DNA |
                              S656A              E665--*
                 * *          |             ** *** |
SUB/SRF9  640 RVADSGLAYMLPPRPTSQMAG----------YAAPEVEY-GSYTCQSDVFSLGVVMLELL
SRF1      617 HVSDCGLAPLISSGAVSQLSGQ---LLAAYGYGAPEFEY-GIYTMKCDVYSFGVVMLELL
SRF3      627 LVSDCGLAPLISSGSVSQLSGQ---LLAAYGYGAPEFDS-GIYTWQSDVYSFGVVMLELL
SRF6      558 HLSDSGLASFLPT-ANELLNQT---DE---GYSAPEVSMSGQYSLKSDIYSFGVVMLELL
SRF7      561 HLSDSGLASFLPT-ANELLNQN---DE---GYSAPETSMSGQYSLKSDVYSFGVVMLELL
SRF8      537 HLSDSGLAALTPN-TERQVSTQ---VVGSFGYSAPEFALSGIYTVKSDVYTFGVVMLELL
SRF4      557 RLSDYGLANFHHRTSQNLGVG----------YNAPECTDPSAYTQKSDVYSFGVVMLELL
SRF5      546 RLSDYGLSKFYLRTSQNLGEG----------YNAPEARDPSAYTPKSDVYSFGVVMLELL
SRF2      555 RIADCGLASLRPLTSNSVKLRASEIAIQNTGYIAPEHGQPGSSGTKSDTYALGVLLLELL
```



```
                                   X

SUB/SRF9  689 TGRRPFDRTRPRGHQTLAQWAIPRLHDIDALTRMVDPSLHGAYPMKSLSRFADIISRSLQ
SRF1      673 TGRKSYDKKRDRGEQFLVRWAIPQLHDIDALAKMVDPSLKGDYPAKSLSHFADVISRCVQ
SRF3      683 TGRMSYDRDRSRGEQFLVRWAIPQLHDIDALGKMVDPSLNGQYPAKSLSHFADIISRCVQ
SRF6      611 TGRKPFDSTRSRSEQSLVRWATPQLHDIDALAKMVDPALKGLYPVKSLSRFADVIALCVQ
SRF7      614 TGRKPFDSTRSRSEQSLVRWATPQLHDIDALGKMVDPALKGLYPVKSLSRFADVIALCVQ
SRF8      593 TGRKPLDSSRTRAEQSLVRWATPQLHDIDALSKMVDPSLNGMYPAKSLSRFADIIALCIQ
SRF4      607 TGRKPYDSGRPKAEQSLVRWAKPQLKDMDTLDEMVDPALCGLYAPESVSSFADIVSICVM
SRF5      596 TGRVPFDGEKPRPERSLVRWATPQLHDIDALSNIADPALHGLYPPKSLSRFADIIALCVQ
SRF2      615 TGRKAFDSSRPRGEQLLVKWASTRLHDRRSLEQMIDGGIAGTFSSRVASQYADIISLCTQ

                XI          --|

                   *
SUB/SRF9  749 MEPGFRPPISEIVQDLQHMI----------------------------------------
SRF1      733 SEPEYRPLMSEVVQDLSDMIQREHRRN-DSNGDNQYTGRR--------------------
SRF3      743 SEPEFRPLMSEVVQDLLDMIRRERHGSGDSTAD---------------------------
SRF6      671 PEPEFRPPMSEVVQALVVLVQRANMSKRTVGVDPSQRAGSADTTSDYM------------
SRF7      674 PEPEFRPPMSEVVQALVVLVQRANMSKRTVGVG----SGSSGVN-DYM------------
SRF8      653 PEPEFRPPMSEVVQQLVRLVQRASVVKRRSSDD----TGFSYRTPEHEHVDISF------
SRF4      667 TEPGLRPPVSNVVEALKRLV----------------------------------------
SRF5      656 VEPEFRPPMSEVVEALVRMVQRSSMKLKDDLSSSYRAHDDYDY-----------------
SRF2      675 AEKEFRPPVSEIVEALTALIQKQNKEASSSVADKTDPFSKSFCSTRTRFISSPTFSYLSS
```