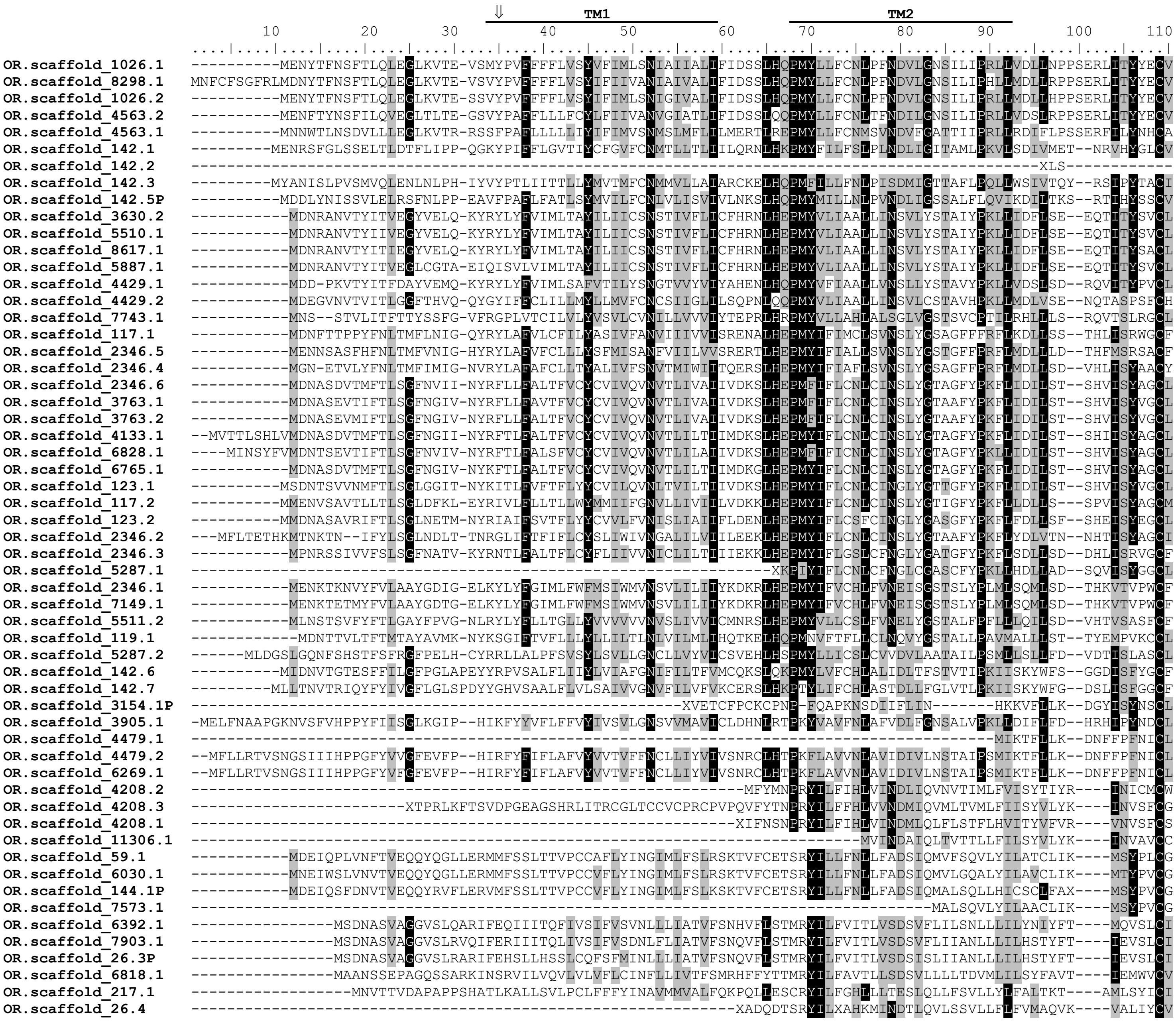
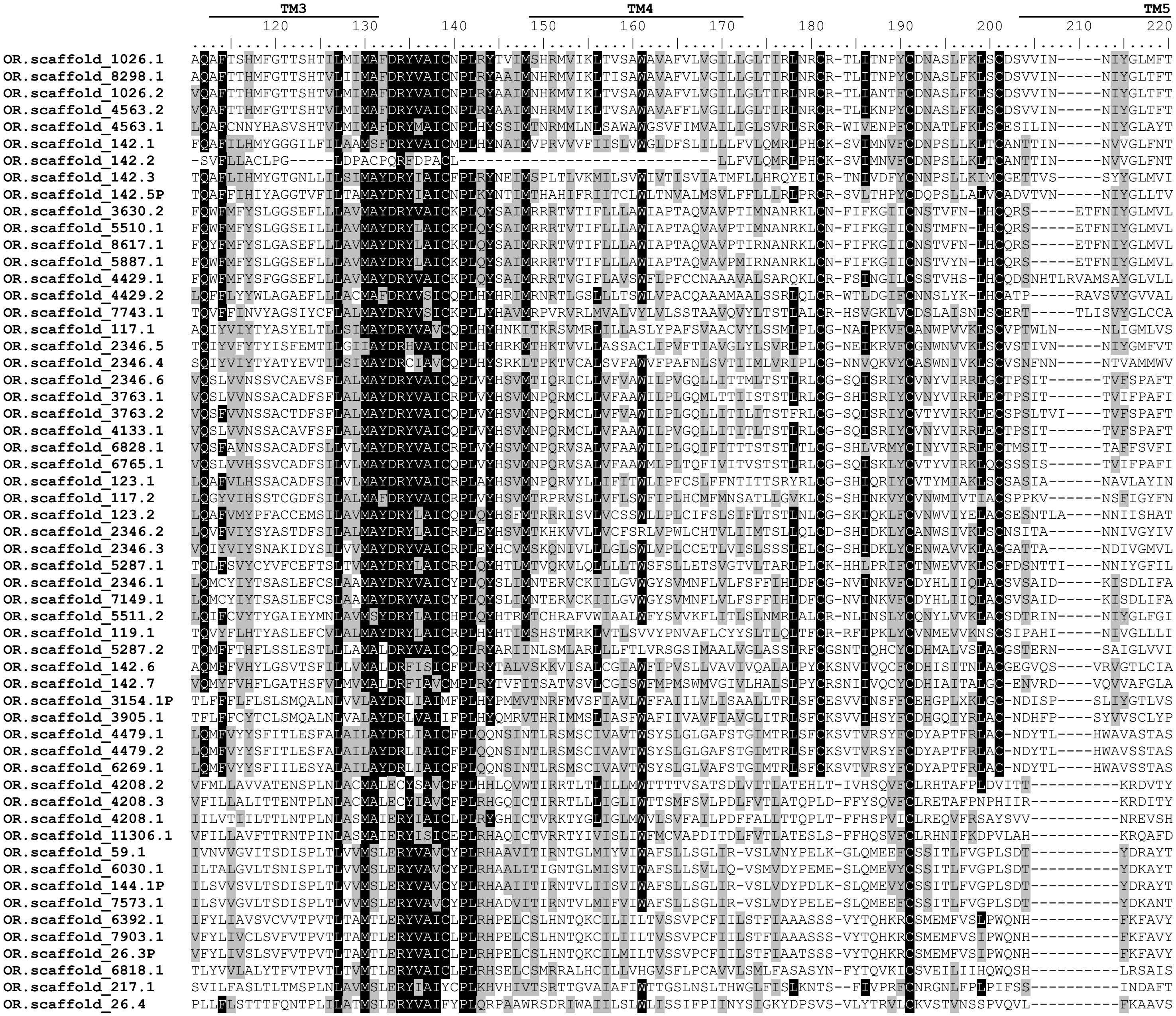


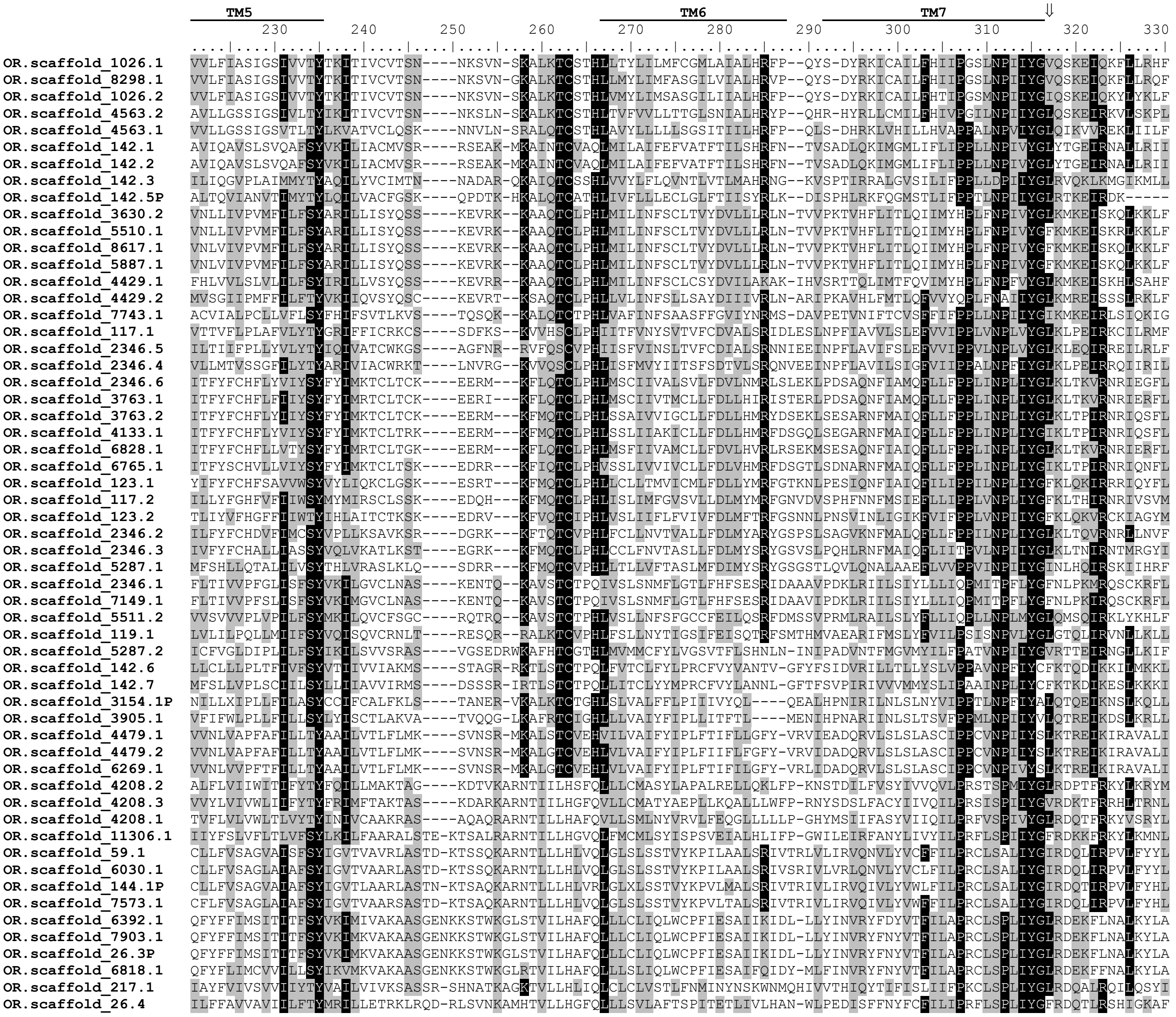
```
                                                             ⇓      TM1                          TM2
                        10        20        30        40        50        60        70        80        90       100       110
               ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
OR.scaffold_1026.1    ----------MENYTFNSFTLQLEGLKVTE-VSMYPVFFFFLVSYVFIMLSNIAIIALIFIDSSLHQPMYLLFCNLPFNDVLGNSILIPRLLVDLLNPPSERLITYYECV
OR.scaffold_8298.1    MNFCFSGFRLMDNYTFNSFTLQLEGLKVTE-VSVYPVFFFFLVSYIFIIVANIAIVALIFIDSSLHQPMYLLFCNLPFNDVLGNSILIPHLLMDLLRPPSERLITYYECV
OR.scaffold_1026.2    ----------MENYTFNSFTLQLEGLKVTE-SSVYPVFFFFLVSYIFIMLSNIGIVALIFIDSSLHQPMYLLFCNLPFNDVLGNSILIPRLLMDLLHPPSERLITYYECV
OR.scaffold_4563.2    ----------MENFTYNSFILQVEGLTLTE-GSVYPAFFLLLFCYLFIIVANVGIATLIFIDSSLQQPMYLLFCNLTFNDILGNSILIPRLLVDSLRPPSERLITYYECV
OR.scaffold_4563.1    ----------MNNWTLNSDVLLLEGLKVTR-RSSFPAFLLLLLIYIFIMVSNMSLMFLILMERTLREPMYLLFCNMSVNDVFGATTIIPRLLRDIFLPSSERFILYNHCA
OR.scaffold_142.1     ---------MENRSFGLSSELTLDTFLIPP-QGKYPIFFLGVTIYCFGVFCNMTLLTLIILQRNLHKPMYFILFSLPLNDLIGITAMLPKVLSDIVMET--NRVHYGLCV
OR.scaffold_142.2     -----------------------------------------------------------------------------------------------XLS------------
OR.scaffold_142.3     ---------MYANISLPVSMVQLENLNLPH-IYVYPTLIITTLLYMVTMFCNMMVLLAIARCKELHQPMFILLFNLPISDMIGTTAFLPQLLWSIVTQY--RSIPYTACI
OR.scaffold_142.5P    ----------MDDLYNISSVLELRSFNLPP-EAVFPAFLFATLSYMVILFCNLVLISVIVLNKSLHQPMYMILLNLPVNDLIGSSALFLQVIKDILTKS--RTIHYSSCV
OR.scaffold_3630.2    -----------MDNRANVTYITVEGYVELQ-KYRYLYFVIMLTAYILIICSNSTIVFLICFHRNLHEPMYVLIAALLINSVLYSTAIYPKLLIDFLSE--EQTITYSVCL
OR.scaffold_5510.1    -----------MDNRANVTYIIVEGYVELQ-KYRYLYFVIMLTAYILIICSNSTIVFLICFHRNLHEPMYVLIAALLINSVLYSTAIYPKLLIDFLSE--EQTITYSVCL
OR.scaffold_8617.1    -----------MDNRANVTYITIEGYVELQ-KYRYLYFVIMLTAYILIICSNSTIVFLICFHRNLHEPMYVLIAALLINSVLYSTAIYPKLLIDFLSE--EQTITYSACL
OR.scaffold_5887.1    -----------MDNRANVTYITVEGLCGTA-EIQISVLVIMLTAYILIICSNSTIVFLICFHRNLHEPMYVLIAALLINSVLYSTAIYPKLLIDFLSE--EQTITYSVCL
OR.scaffold_4429.1    -----------MDD-PKVTYITFDAYVEMQ-KYRYLYFVIMLSAFVTILYSNGTVVYVIYAHENLHQPMYVFIAALLVNSLLYSTAVYPKLLVDSLSD--RQVITYPVCL
OR.scaffold_4429.2    -----------MDEGVNVTVITLGGFTHVQ-QYGYIFFCLILLMYLLMVFCNCSIIGLILSQPNLQQPMYVLIAALLINSVLCSTAVHPKLLMDLVSE--NQTASPSFCH
OR.scaffold_7743.1    -----------MNS--STVLITFTTYSSFG-VFRGPLVTCILVLYVSVLCVNILLVVVIYTEPRLHRPMYVLLAHLALSGLVGSTSVCPTILRHLLLS--RQVTSLRGCL
OR.scaffold_117.1     -----------MDNFTTPPYFNLTMFLNIG-QYRYLAFVLCFILYASIVFANVIIIVVISRENALHEPMYIFIMCLSVNSLYGSAGFFFRFLKDLLSS--THLISRWGCF
OR.scaffold_2346.5    -----------MENNSASFHFNLTMFVNIG-HYRYLAFVFCLLLYSFMISANFVIILVVSRERTLHEPMYIFIALLSVNSLYGSTGFFPRFLMDLLLD--THFMSRSACF
OR.scaffold_2346.4    -----------MGN-ETVLYFNLTMFIMIG-NVRYLAFAFCLLTYALIVFSNVTMIWIITQERSLHEPMYIFIAFLSVNSLYGSAGFFPRFLMDLLSD--VHLISYAACY
OR.scaffold_2346.6    -----------MDNASDVTMFTLSGFNVII-NYRFLLFALTFVCYCVIVQVNVTLIVAIIVDKSLHEPMFIFLCNLCINSLYGTAGFYPKFLIDILST--SHVISYAGCL
OR.scaffold_3763.1    -----------MDNASEVTIFTLSGFNGIV-NYRFLLFAVTFVCYCVIVQVNVTLIVAIIVDKSLHEPMFIFLCNLCINSLYGTAAFYPKFLIDILST--SHVISYVGCL
OR.scaffold_3763.2    -----------MDNASEVMIFTLSGFNGIV-NYRFLLFALTFVCYCVIVQVNVTLIVAIIVDKSLHEPMFIFLCNLCINSLYGTAAFYPKFLIDILST--SHVISYVGCL
OR.scaffold_4133.1    --MVTTLSHLVMDNASDVTMFTLSGFNGII-NYRFTLFALTFVCYCVIVQVNVTLILTIIMDKSLHEPMYIFLCNLCINSLYGTAGFYPKFLIDILST--SHIISYAGCL
OR.scaffold_6828.1    ----MINSYFVMDNTSEVTIFTLSGFNVIV-NYRFTLFALSFVCYCVIVQVNVTLILAIIVDKSLHEPMFIFICNLCINSLYGTAGFYPKLLIDILST--SHVISYAGCL
OR.scaffold_6765.1    -----------MDNASDVTMFTLSGFNGIV-NYKFTLFALTFVCYCVIVQVNVTLILTIIMDKGLHEPMYIFLCNLCINSLYGTAGFYPKFLIDILST--SHVISYAGCL
OR.scaffold_123.1     ----------MSDNTSVVNMFTLSGLGGIT-NYKITLFVFTFLYYCVILQVNLTVILTIIVDKSLHEPMYIFLCNLCINGLYGTTGFYPKFLIDILST--SHVISYVGCL
OR.scaffold_117.2     ----------MMENVSAVTLLTLSGLDFKL-EYRIVLFLLTLLWYMMIIFGNVLLIVIILVDKKLHEPMYIFLCNLCINSLYGTIGFYPKFLLDLLS---SPVISYAGCM
OR.scaffold_123.2     ----------MMDNASAVRIFTLSGLNETM-NYRIAIFSVTFLYYCVVLFVNISLIAIIFLDENLHEPMYIFLCSFCINGLYGASGFYPKFLFDLLSF--SHEISYEGCL
OR.scaffold_2346.2    ---MFLTETHKMTNKTN--IFYLSGLNDLT-TNRGLIFTFIFLCYSLIWIVNGALILVIILEEKLHEPMYIFLCNLCINSLYGTAAFYPKFLYDLVTN--NHTISYAGCI
OR.scaffold_2346.3    -----------MPNRSSIVVFSLSGFNATV-KYRNTLFALTFLCYFLIIVVNICLILTIIIEKKLHEPMYIFLGSLCFNGLYGATGFYPKFLSDLLSD--DHLISRVGCF
OR.scaffold_5287.1    -----------------------------------------------------------------XKPIYIFLCNLCFNGLCGASCFYPKLLHDLLAD--SQVISYGGCL
OR.scaffold_2346.1    -----------MENKTKNVYFVLAAYGDIG-ELKYLYFGIMLFWFMSIWMVNSVLILIIYKDKRLHEPMYIFVCHLFVNEISGSTSLYPLMLSQMLSD--THKVTVPWCF
OR.scaffold_7149.1    -----------MENKTETMYFVLAAYGDTG-ELKYLYFGIMLFWFMSIWMVNSVLILIIYKDKRLHEPMYIFVCHLFVNEISGSTSLYPLMLSQMLSD--THKVTVPWCF
OR.scaffold_5511.2    -----------MLNSTSVFYFTLGAYFPVG-NLRYLYFLLTGLLYVVVVVVNVSLIVVICMNRSLHEPMYVLLCSLFVNELYGSTALFPFLLLQILSD--VHTVSASFCF
OR.scaffold_119.1     ------------MDNTTVLTFTMTAYAVMK-NYKSGIFTVFLLLYLLILTLNLVILMLIHQTKELHQPMNVFTFLLCLNQVYGSTALLPAVMALLLST--TYEMPVKCCL
OR.scaffold_5287.2    ------MLDGSLGQNFSHSTFSFRGFPELH-CYRRLLALPFSVSYLSVLLGNCLLVYVICSVEHLHSPMYLLICSLCVVDVLAATAILPSMLLSLLFD--VDTISLASCL
OR.scaffold_142.6     ----------MIDNVTGTESFFILGFPGLAPEYYRPVSALFLIIYLVIAFGNIFILTFVMCQKSLQKPMYLVFCHLALIDLTFSTVTIPKIISKYWFS--GGDISFYGCF
OR.scaffold_142.7     ---------MLLTNVTRIQYFYIVGFLGLSPDYYGHVSAALFLVLSAIVVGNVFILVFVKCERSLHKPTYLIFCHLASTDLLFGLVTLPKIISKYWFG--DSLISFGGCF
OR.scaffold_3154.1P   -------------------------------------------------------XVETCFPCKCPNP-FQAPKNSDIIFLIN-------HKKVFLLK--DGYISYNSCL
OR.scaffold_3905.1    -MELFNAAPGKNVSFVHPPYFIISGLKGIP--HIKFYYVFLFFVYIVSVLGNSVVMAVICLDHNLRTPKYVAVFNLAFVDLFGNSALVPKLLDIFLFD--HRHIPYNDCL
OR.scaffold_4479.1    ------------------------------------------------------------------------------------------MIKTFLLK--DNFFPFNICL
OR.scaffold_4479.2    --MFLLRTVSNGSIIIHPPGFYVVGFEVFP--HIRFYFIFLAFVYVVTVFFNCLLIYVIVSNRCLHTPKFLAVVNLAVIDIVLNSTAIPSMIKTFLLK--DNFFPFNICL
OR.scaffold_6269.1    --MFLLRTVSNGSIIIHPPGFYVFGFEVFP--HIRFYFIFLAFVYVVTVFFNCLLIYVIVSNRCLHTPKFLAVVNLAVIDIVLNSTAIPSMIKTFLLK--DNFFPFNICL
OR.scaffold_4208.2    --------------------------------------------------------------MFYMNPRYILFIHLVINDLIQVNVTIMLFVISYTIYR----INICMCW
OR.scaffold_4208.3    ------------------------XTPRLKFTSVDPGEAGSHRLITRCGLTCCVCPRCPVPQVFYTNPRYILFFHLVVNDMIQVMLTVMLFIISYVLYK----INVSFCG
OR.scaffold_4208.1    -------------------------------------------------------------XIFNSNPRYILFIHLVINDMLQLFLSTFLHVITYVFVR----VNVSFCS
OR.scaffold_11306.1   ---------------------------------------------------------------------------MVINDAIQLTVTTLLFILSYVLYK----INVAVCC
OR.scaffold_59.1      -----------MDEIQPLVNFTVEQQYQGLLERMMFSSLTTVPCCAFLYINGIMLFSLRSKTVFCETSRYILLFNLLFADSIQMVFSQVLYILATCLIK----MSYPLCG
OR.scaffold_6030.1    -----------MNEIWSLVNVTVEQQYQGLLERMMFSSLTTVPCCVFLYINGIMLFSLRSKTVFCETSRYILLFNLLFADSIQMVLGQALYILAVCLIK----MTYPVCG
OR.scaffold_144.1P    -----------MDEIQSFDNVTVEQQYRVFLERVMFSSLTTVPCCVFLYINGIMLFSLKSKTVFCETSRYILLFNLLFADSIQMALSQLLHICSCLFAX----MSYPVCG
OR.scaffold_7573.1    -----------------------------------------------------------------------------------MALSQVLYILAACLIK----MSYPVCG
OR.scaffold_6392.1    ----------------MSDNASVAGGVSLQARIFEQIIITQFIVSIFVSVNLLLIATVFSNHVFLSTMRYILFVITLVSDSVFLILSNLLLILYNIYFT----MQVSLCI
OR.scaffold_7903.1    ----------------MSDNASVAGGVSLRVQIFERIIITQLIVSIFVSDNLFLIATVFSNQVFLSTMRYILFVITLVSDSVFLIIANLLLILHSTYFT----IEVSLCI
OR.scaffold_26.3P     ----------------MSDNASVAGGVSLRARIFEHSLLHSSLCQFSFMINLLLIATVFSNQVFLSTMRYILFVITLVSDSISLIIANLLLILHSTYFT----IEVSLCI
OR.scaffold_6818.1    ----------------MAANSSEPAGQSSARKINSRVILVQVLVLVFLCINFLLIVTFSMRHFFYTTMRYILFAVTLLSDSVLLLLTDVMLILSYFAVT----IEMWVCV
OR.scaffold_217.1     ------------------MNVTTVDAPAPPSHATLKALLSVLPCLFFFYINAVMMVALFQKPQLLESCRYILFGHLLLTESLQLLFSVLLYLFALTKT----AMLSYICI
OR.scaffold_26.4      -------------------------------------------------------------XADQDTSRYILXAHKMINDTLQVLSSVLLFLFVMAQVK----VALIYCV
```

Figure S2



```
                                 TM3                                TM4                                  TM5
                                  120       130       140       150       160       170       180       190       200       210       220
                              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
OR.scaffold_1026.1            AQAFTSHMFGTTSHTILMIMAFDRYVAICNPLRYTVIMSHRMVIKLTVSAWAVAFVLVGILLGLTIRLNRCR-TLITNPYCDNASLFKLSCDSVVIN-----NIYGLMFT
OR.scaffold_8298.1            AQAFTTHMFGTTSHTVLIIMAFDRYVAICNPLRYAAIMNHRMVIKLTISAWAVAFVLVGILLGLTIRLNRCR-TLITNPYCDNASLFKLSCDSVVIN-----NIYGLTFT
OR.scaffold_1026.2            VQAFTTHMFGTTSHTVLMIMAFDRYVAICNPLRYAAIMNHKMVIKLTVSAWAVAFVLVGILLGLTIRLNRCR-TLIANTFCDNASLFKLSCDSVVIN-----NIYGLTFT
OR.scaffold_4563.2            VQAFTTHMFGTTSHTVLMIMAFDRYVAICNPLRYAAIMNHRMVIKLTVSAWAVAFFLVGILLGLTIRLNRCR-TLIKNPYCDNASLFKLSCDSVVIN-----NIYGLTFT
OR.scaffold_4563.1            LQAFCNNYHASVSHTVLMIMAFDRYMAICNPLHYSSIMTNRMMLNLSAWAWGSVFIMVAILIGLSVRLSRCR-WIVENPFCDNATLFKLSCESILIN-----NIYGLAYT
OR.scaffold_142.1             FQAFILHMYGGGILFILAAMSFDRYVAICMPLHYNAIMVPRVVVFIISLVWGLDFSLILLLFVLQMRLPHCK-SVIMNVFCDNPSLLKLTCANTTIN-----NVVGLFNT
OR.scaffold_142.2             -SVFLLACLPG-----LDPACPQRFDPACL----------------------------LLFVLQMRLPHCK-SVIMNVFCDNPSLLKLTCANTTIN-----NVVGLFNT
OR.scaffold_142.3             TQAFLIHMYGTGNLLILSIMAYDRYIAICFPLRYNEIMSPLTLVKMILSVWIVTISVIATMFLLHRQYEICR-TNIVDFYCNNPSLLKIMCGETTVS-----SYYGLMVI
OR.scaffold_142.5P            TQAFFIHIYAGGTVFILTAMAYDRYIAICNPLKYNTIMTHAHIFRIITCLWLTNVALMSVLFFLLLRLPRCR-SVLTHPYCDQPSLLALVCADVTVN-----NIYGLLTV
OR.scaffold_3630.2            FQWFMFYSLGGSEFLLLAVMAYDRYVAICKPLQYSAIMRRRTVTIFLLLAWIAPTAQVAVPTIMNANRKLCN-FIFKGIICNSTVFN-LHCQRS-----ETFNIYGLMVL
OR.scaffold_5510.1            FQWFMFYSLGGSEILLLAVMAYDRYLAICKPLQYSAIMRRRTVTIFLLLAWIAPTAQVAVPTIMNANRKLCN-FIFKGIICNSTMFN-LHCQRS-----ETFNIYGLMVL
OR.scaffold_8617.1            FQYFMFYSLGASEFLLLAVMAYDRYLAICKPLQYSAIMRRRTVTIFLLLAWIAPTAQVAVPTIRNANRKLCN-FIFKGIICNSTVFN-LHCQRS-----ETFNIYGLMVL
OR.scaffold_5887.1            FQWFMFYSLGGSEFLLLAVMAYDRYLAICKPLQYSAIMRRRTVTIFLLLAWIAPTAQVAVPMIRNANRKLCN-FIFKGIICNSTVYN-LHCQRS-----ETFNIYGLMVL
OR.scaffold_4429.1            FQWFMFYSFGGSEFLLLAVMAYDRYVAICKPLQYSAIMRRRTVGIFLAVSWFLPFCCNAAAVALSARQKLCR-FSINGILCSSTVHS-LHCQDSNHTLRVAMSAYGLVLL
OR.scaffold_4429.2            LQFFLYYWLAGAEFLLLACMAFDRYVSICQPLHYHRIMRNRTLGSLLLTSWLVPACQAAAMAALSSRLQLCR-WTLDGIFCNNSLYK-LHCATP-----RAVSVYGVVAL
OR.scaffold_7743.1            TQVFFINVYAGSIYCFLALMAYDRYVSICKPLLYHAVMRPVRVRLMVALVYLVLSSTAAVQVYLTSTLALCR-HSVGKLVCDSLAISNLSCERT-----TLISVYGLCCA
OR.scaffold_117.1             AQIYVIYTYASYELTLLSIMAYDRYVAVCQPLHYHNKITKRSVMRLILLASLYPAFSVAACVYLSSMLPLCG-NAIPKVFCANWPVVKLSCVPTWLN-----NLIGMLVS
OR.scaffold_2346.5            TQIYVFYTYISFEMTILGIIAYDRHVAICNPLHYHRKMTHKTVVLLASSACLIPVFTIAVGLYLSVRLPLCG-NEIKRVFCGNWNVVKLSCVSTIVN-----NIYGMFVT
OR.scaffold_2346.4            SQIYVIYTYATYEVTILSIMAYDRCIAVCQPLHYSRKLTPKTVCALSVFAWVFPAFNLSVTIIMLVRIPLCG-NNVQKVYCASWNIVKLSCVSNFNN-----NTVAMMWV
OR.scaffold_2346.6            VQSLVVNSSVCAEVSFLALMAYDRYVAICQPLVYHSVMTIQRICLLVFVAWILPVGQLLITTMLTSTLRLCG-SQISRIYCVNYVIRRLGCTPSIT------TVFSPAFT
OR.scaffold_3763.1            VQSLVVNSSACADFSFLALMAYDRYVAICRPLVYHSVMNPQRMCLLVFAAWILPLGQMLTTIISTSTLRLCG-SHISRIYCVNYVIRRLECTPSIT------TVIFPAFI
OR.scaffold_3763.2            VQSFVVNSSACTDFSFLALMAYDRYVAICQPLVYHSVMNPQRMCLLVFVAWILPLGQLLITILITSTFRLCG-SQISRIYCVTYVIRKLECSPSLTVI----TVFSPAFT
OR.scaffold_4133.1            VQSLVVNSSACAVFSFLALMAYDRYVAICQPLVYHSVMNPQRMCLLVFAAWILPVGQLLITITLTSTLRLCG-SQISRIYCVNYVIRRLECTPSIT------TVFSPAFT
OR.scaffold_6828.1            VQSFAVNSSACADFSLLVLMAYDRYVAICRPLVYHSVMNPQRVSALVFAAWILPLGQIFITTTSTSTLTLCG-SHLVRMYCINYVIRRLECTMSIT------TAFFSVFI
OR.scaffold_6765.1            VQSLVVHSSVCADFSILVLMAYDRYVAICQPLVYHSVMNPQRVSALVFAAWMLPLTQFIVITVSTSTLRLCG-SQISKLYCVTYVIRKLQCSSSIS------TVIFPAFI
OR.scaffold_123.1             LQAFVLHSSACADFSILVLMAYDRYVAICRPLAYHSVMNPQRVYLLIFITWLIPFCSLFFNTITTSRYRLCG-SHIQRIYCVTYMIAKLSCSASIA------NAVLAYIN
OR.scaffold_117.2             LQGYVIHSSTCGDFSILALMAFDRYVAICRPLVYHSVMTRPRVSLLVFLSWFIPLHCMFMNSATLLGVKLCS-SHINKVYCVNWMIVTIACSPPKV------NSFIGYFN
OR.scaffold_123.2             LQAFVMYPFACCEMSILAVMAYDRYLAICQPLQYHSFMTRRRISVLVCSSWLLPLCIFSLSIFLTSTLNLCG-SKIQKLFCVNWVIYELACSESNTLA----NNIISHAT
OR.scaffold_2346.2            LQVFVIYSYASTDFSILALMAYDRYLAICRPLEYHSVMTKHKVVLLVCFSRLVPWLCHTVLIIMTSLLQLCD-SHIDKLYCANWSIVKLSCNSITA------NNIVGYIV
OR.scaffold_2346.3            VQIYVIYSNAKIDYSILVVMAYDRYVAICRPLEYHCVMSKQNIVLLLGLSWLVPLCCETLVISLSSSLELCG-SHIDKLYCENWAVVKLACGATTA------NDIVGMVL
OR.scaffold_5287.1            TQLFSVYCYVFCEFTSLTVMAYDRYLAICRPLQYHTLMTVQKVLQLLLLTWSFSLLETSVGTVLTARLPLCK-HHLPRIFCTNWEVVKLSCFDSNTTI----NNIYGFIL
OR.scaffold_2346.1            LQMCYIYTSASLEFCSLAAMAYDRYVAICYPLQYSLIMNTERVCKIILGVWGYSVMNFLVLFSFFIHLDFCG-NVINKVFCDYHLIIQLACSVSAID-----KISDLIFA
OR.scaffold_7149.1            LQMCYIYTSASLEFCSLAAMAYDRYVAICYPLQYSLIMNTERVCKIILGVWGYSVMNFLVLFSFFIHLDFCG-NVINKVFCDYHLIIQLACSVSAID-----KISDLIFA
OR.scaffold_5511.2            LQIFCVYTYGAIEYMNLAVMSYDRYLAICHPLQYHTRMTCHRAFVWIAALWFYSVVKFLITLSLNMRLALCR-NLINSLYCQNYLVVKLACSDTRIN-----NIYGLFGI
OR.scaffold_119.1             TQVYFLHTYASLEFCVLALMAYDRYLAICRPLHYHTIMSHSTMRKLVTLSVVYPNVAFLCYYSLTLQLTFCR-RFIPKLYCVNMEVVKNSCSIPAHI-----NIVGLLLI
OR.scaffold_5287.2            TQMFFTHFLSSLESTLLLAMALDRYVAICQPLRYARIINLSMLARLLLFTLVRSGSIMAALVGLASSLRFCGSNTIQHCYCDHMALVSLACGSTERN-----SAIGLVVI
OR.scaffold_142.6             AQMFFVHYLGSVTSFILLVMALDRFISICFPLRYTALVSKKVISALCGIAWFIPVSLLVAVIVQALALPYCKSNVIVQCFCDHISITNLACGEGVQS----VRVGTLCIA
OR.scaffold_142.7             VQMYFVHFLGATHSFVLMVMALDRFIAVCMPLRYTVFITSATVSVLCGISWFMPMSWMVGIVLHALSLPYCRSNIIVQCYCDHIAITALGC-ENVRD----VQVVAFGLA
OR.scaffold_3154.1P           TLFFFLFLSLSMQALNLVVLAYDRLIAIMFPLHYPMMVTNRFMVSFIAVLWFFAIILVLISAALLTRLSFCESVVINSFFCEHGPLXKLGC-NDISP----SLIYGTLVS
OR.scaffold_3905.1            TFLFFCYTCLSMQALNLVALAYDRLVAIIFPLHYQMRVTHRIMMSLIASFWAFIIVAVFIAVGLITRLSFCKSVVIHSYFCDHGQIYRLAC-NDHFP----SYVVSCLYP
OR.scaffold_4479.1            LQMFVYYSFITLESFALAILAYDRLIAICFPLQQNSINTLRSMSCIVAVTWSYSLGLGAFSTGIMTRLSFCKSVTVRSYFCDYAPTFRLAC-NDYTL----HWAVASTAS
OR.scaffold_4479.2            LQMFVYYSFITLESFALAILAYDRLIAICFPLQQNSINTLRSMSCIVAVTWSYSLGLGAFSTGIMTRLSFCKSVTVRSYFCDYAPTFRLAC-NDYTL----HWAVSSTAS
OR.scaffold_6269.1            LQMFVYYSFIILESYALAILAYDRLIAICFPLQQNSINTLRSMSCIVAVTWSYSLGLVAFSTGIMTRLSFCKSVTVRSYFCDYAPTFRLAC-NDYTL----HWAVSSTAS
OR.scaffold_4208.2            VFMLLAVVATENSPLNLACMALECYSAVCFPLHHLQVWTIRRTLTLILLMWTTTTVSATSDLVITLATEHLT-IVHSQVFCLRHTAFPLDVITT----------KRDVTY
OR.scaffold_4208.3            VFILLALITTENTPLNLACMALECYIAVCFPLRHGQICTIRRTLLLIGLIWTTSMFSVLPDLFVTLATQPLD-FFYSQVFCLRETAFPNPHIIR----------KRDITY
OR.scaffold_4208.1            IILVTIILTTLNTPLNLASMAIERYIAICLPLRYGHICTVRKTYGLIGLMWVLSVFAILPDFFALLTTQPLT-FFHSPVICLREQVFRSAYSVV----------NREVSH
OR.scaffold_11306.1           VFILLAVFTTRNTPINLASMAIERYISICEPLRHAQICTVRRTYIVISLIWFMCVAPDITDLFVTLATESLS-FFHQSVFCLRHNIFKDPVLAH----------KRQAFD
OR.scaffold_59.1              IVNVVGVITSDISPLTLVVMSLERYVAVCYPLRHAAVITIRNTGLMIYVIWAFSLLSGLIR-VSLVNYPELK-GLQMEEFCSSITLFVGPLSDT----------YDRAYT
OR.scaffold_6030.1            ILTALGVLTSNISPLTLVVMSLERYVAVCYPLRHAALITIGNTGLMISVIWAFSLLSVLIQ-VSMVDYPEME-SLQMEVYCSSITLFVGPLSDT----------YDKAYT
OR.scaffold_144.1P            ILSVVSVLTSDISPLTLVVMSLERYVAVCYPLRHAAIITIRNTVLIISVIWAFSLLSGLIR-VSLVDYPDLK-SLQMEVYCSSITLFVGPLSDT----------YDRAYT
OR.scaffold_7573.1            ILSVVGVLTSDISPLTLVVMSLERYVAVCYPLRHADVITIRNTVLMIFVIWAFSLLSGLIR-VSLVDYPELE-SLQMEEFCSSITLFVGPLSDT----------YDKANT
OR.scaffold_6392.1            IFYLIAVSVCVVTPVTLTAMTLERYVAICLPLRHPELCSLHNTQKCILIILTVSSVPCFIILSTFIAAASSS-VYTQHKRCSMEMFVSLPWQNH----------FKFAVY
OR.scaffold_7903.1            VFYLIVCLSVFVTPVTLTAMTLERYVAICLPLRHPELCSLHNTQKCILIILTVSSVPCFIILSTFIAAASSS-VYTQHKRCSMEMFVSIPWQNH----------FKFAVY
OR.scaffold_26.3P             VFYLIVSLSVFVTPVTLTAMTLERYVAICLPLRHPELCSLHNTQKCILMILTVSSVPCFIILSTFIAATSSS-VYTQHKRCSMEMFVSIPWQNH----------FKFAVY
OR.scaffold_6818.1            TLYVVLALYTFVTPVTLTVMTLERYVAICLPLRHSELCSMRRALHCILLVHGVSFLPCAVVLSMLFASASYN-FYTQVKICSVEILIIHQWQSH----------LRSAIS
OR.scaffold_217.1             SVILFASLTLTMSPLNLAVMSLERYIAIYCPLKHVHIVTSRTTGVAIAFIWTTGSLNSLTHWGLFISLKNTS--FIVPRFCNRGNLFPLPIFSS----------INDAFT
OR.scaffold_26.4              PLLFLSTTTFQNTPLILATMSLERYVAIFYPLQRPAAWRSDRIWAIILSLWLISSIFPIINYSIGKYDPSVS-VLYTRVLCKVSTVNSSPVQVL----------FKAAVS
```

Figure S2



```
                        TM5                                                TM6                      TM7           ⇓
                                230       240       250       260       270       280       290       300       310       320       330
                        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
OR.scaffold_1026.1      VVLFIASIGSIVVTYTKITIVCVTSN----NKSVN-SKALKTCSTHLLTYLILMFCGMLAIALHRFP--QYS-DYRKICAILFHIIPGSLNPIIYGVQSKEIQKFLLRHF
OR.scaffold_8298.1      VVLFIASIGSIVVTYTKITIVCVTSN----NKSVN-GKALKTCSTHLLMYLIMFASGILVIALHRVP--QYS-DYRKICAILFHIIPGSLNPIIYGVQSKEIQKFLLRQF
OR.scaffold_1026.2      VVLFIASIGSIVVTYTKITIVCVTSN----NKSVN-SKALKTCSTHLVMYLIMSASGILIIALHRFP--QYS-DYRKICAILFHTIPGSMNPIIYGIQSKEIQKYLYKLF
OR.scaffold_4563.2      AVLLGSSIGSIVLTYIKITIVCVTSN----NKSLN-SKALKTCSTHLTVFVVLLTTGLSNIALHRYP--QHR-HYRLLCMILFHIVPGILNPIIYGLQSKEIRKVLSKPL
OR.scaffold_4563.1      VVLLGSSIGSVTLTYLKVATVCLQSK----NNVLN-SRALQTCSTHLAVYLLLLLSGSITIILHRFP--QLS-DHRKLVHILLHVAPPALNPVIYGLQIKVVREKLIILF
OR.scaffold_142.1       AVIQAVSLSVQAFSYVKILIACMVSR----RSEAK-MKAINTCVAQLMILAIFEFVATFTILSHRFN--TVSADLQKIMGMLIFLIPPLLNPIVYGLYTGEIRNALLRII
OR.scaffold_142.2       AVIQAVSLSVQAFSYVKILIACMVSR----RSEAK-MKAINTCVAQLMILAIFEFVATFTILSHRFN--TVSADLQKIMGMLIFLIPPLLNPIVYGLYTGEIRNALLRII
OR.scaffold_142.3       ILIQGVPLAIMMYTYAQILYVCIMTN----NADAR-QKAIQTCSSHLVVYLFLQVNTLVTLMAHRNG--KVSPTIRRALGVSILIFPPLLDPIIYGLRVQKLKMGIKMLL
OR.scaffold_142.5P      ALTQVIANVTIMYTYLQILVACFGSK----QPDTK-HKALQTCATHLIVFLLLECLGLFTIISYRLK--DISPHLRKFQGMSTLIFPPTLNPIIYGLRTKEIRDK-----
OR.scaffold_3630.2      VNLLIVPVMFILFSYARILLISYQSS----KEVRK--KAAQTCLPHLMILINFSCLTVYDVLLLRLN-TVVPKTVHFLITLQIIMYHPLFNPIVYGLKMKEISKQLKKLF
OR.scaffold_5510.1      VNLLIVPVMFILFSYARILLISYQSS----KEVRK--KAAQTCLPHLMILINFSCLTVYDVLLLRLN-TVVPKTVHFLITLQIIMYHPLFNPIVYGFKMKEISKRLKKLF
OR.scaffold_8617.1      VNLVIVPVMFILFSYARILLISYQSS----KEVRK--KAAQTCLPHLMILINFSCLTVYDVLLLRLN-TVVPKTVHFLITLQIIMYHPLFNPIVYGFKMKEISKQLKKLF
OR.scaffold_5887.1      VNLVIVPVMFILFSYARILLISYQSS----KEVRK--KAAQTCLPHLMILINFSCLTVYDVLLLRLN-TVVPKTVHFLITLQIIMYHPLFNPIVYGFKMKEISKQLKKLF
OR.scaffold_4429.1      FHLVVLSLVLILFSYIRILLVSYQSS----KEVRR--KAAQTCLPHLMILINFSCLCSYDVILAKAK-IHVSRTTQLIMTFQVIMYHPLFNPFVYGLKMKEISKHLSAHF
OR.scaffold_4429.2      MVSGIIPMFFILFTYVKIIQVSYQSC----KEVRT--KSAQTCLPHLLVLINFSLLSAYDIIIVRLN-ARIPKAVHLFMTLQFVVYQPLFNAIIYGLKMREISSSLRKLF
OR.scaffold_7743.1      ACVIALPCLLVFLSYFHIFSVTLKVS----TQSQK--KALQTCTPHLVAFINFSAASFFGVIYNRMS-DAVPETVNIFTCVSFFIFPPLLNPIIYGIKMKEIRLSIQKIG
OR.scaffold_117.1       VTTVFLPLAFVLYTYGRIFFICRKCS----SDFKS--KVVHSCLPHIITFVNYSVTVFCDVALSRIDLESLNPFIAVVLSLEFVVIPPLVNPLVYGLKLPEIRKCILRMF
OR.scaffold_2346.5      ILTIIFPLLYVLYTYIQIVATCWKGS----AGFNR--RVFQSCVPHIISFVINSLTVFCDIALSRNNIEEINPFLAVIFSLEFVVIPPVLNPLVYGLKLEQIRREILRLF
OR.scaffold_2346.4      VLLMTVSSGFILYTYARIVIACWRKT----LNVRG--KVVQSCLPHLISFMVYIITSFSDTVLSRQNVEEINPFLAVILSIGFVIIPPALNPFIYGLKLPEIRRQIIRIL
OR.scaffold_2346.6      ITFYFCHFLYVIYSYFYIMKTCLTCK----EERM---KFLQTCLPHLMSCIIVALSVLFDVLNMRLSLEKLPDSAQNFIAMQFLLFPPLINPLIYGLKLTKVRNRIEGFL
OR.scaffold_3763.1      ITFYFCHFLFIIYSYFYIMRTCLTCK----EERI---KFLQTCLPHLMSCIIVTMCLLFDLLHIRISTERLPDSAQNFIAMQFLLFPPLINPLIYGLKLTKVRNRIERFL
OR.scaffold_3763.2      ITFYFCHFLYIIYSYFYIMKTCLTCK----EERM---KFMQTCLPHLSSAIVVIGCLLFDLLHMRYDSEKLSESARNFMAIQFLLFPPLINPLIYGLKLTPIRNRIQSFL
OR.scaffold_4133.1      ITFYFCHFLYVIYSYFYIMKTCLTRK----EERM---KFMQTCLPHLSSLIIAKICLLFDLLHMRFDSGQLSEGARNFMAIQFLLFPPLINPLIYGIKLTPIRNRIQSFL
OR.scaffold_6828.1      ITFYFCHFLLVTYSYFYIMRTCLTGK----EERM---KFLQTCLPHLMSFIIVAMCLLFDVLHVRLRSEKMSESAQNFIAIQFLLFPPLINPLIYGLKLTKVRNRIERFL
OR.scaffold_6765.1      ITFYSCHVLLVIYSYFYIMKTCLTSK----EDRR---KFIQTCLPHVSSLIVVIVCLLFDLVHMRFDSGTLSDNARNFMAIQFLLFPPLINPLIYGIKLTPIRNRIQNFL
OR.scaffold_123.1       YIFYFCHFSAVVWSYVYLIQKCLGSK----ESRT---KFMQTCLPHLLCLLTMVICMLFDLLYMRFGTKNLPESIQNFIAIQFILIPPILNPLIYGFKLQKIRRRIQYFL
OR.scaffold_117.2       ILLYFGHFVFIIWSYMYMIRSCLSSK----EDQH---KFMQTCLPHLISLIMFGVSVLLDLMYMRFGNVDVSPHFNNFMSIEFLLIPPLVNPLIYGFKLTHIRNRIVSVM
OR.scaffold_123.2       TLIYVFHGFFIIWTYIHLAITCTKSK----EDRV---KFVQTCIPHLVSLIIFLFVIVFDLMFTRFGSNNLPNSVINLIGIKFVIFPPLVNPIIYGFKLQKVRCKIAGYM
OR.scaffold_2346.2      ILFYFCHDVFIMCSYVPLLKSAVKSR----DGRK---KFTQTCVPHLFCLLNVTVALLFDLMYARYGSPSLSAGVKNFMALQFLLFPPILNPLIYGLKLTQVRNRLLNVF
OR.scaffold_2346.3      IVFYFCHALLIASSYVQLVKATLKST----EGRK---KFMQTCLPHLCCLFNVTASLLFDLMYSRYGSVSLPQHLRNFMAIQFLIITPVLNPIIYGLKLTNIRNTMRGYI
OR.scaffold_5287.1      MFSHLLQTALILVSYTHLVRASLKLQ----SDRR---KFMQTCVPHLLTLLVFTASLMFDIMYSRYGSGSTLQVLQNALAAEFLVVPPVINPIIYGINLHQIRSKIIHRF
OR.scaffold_2346.1      FLTIVVPFGLISFSYVKILGVCLNAS----KENTQ--KAVSTCTPQIVSLSNMFLGTLFHFSESRIDAAAVPDKLRIILSIYLLLIQPMITPFLYGFNLPKMRQSCKRFL
OR.scaffold_7149.1      FLTIVVPFSLISFSYVKIMGVCLNAS----KENTQ--KAVSTCTPQIVSLSNMFLGTLFHFSESRIDAAVIPDKLRIILSIYLLLIQPMITPFLYGFNLPKIRQSCKRFL
OR.scaffold_5511.2      VVSVVVPLVPILFSYMKILQVCFSGC----RQTRQ--KAVSTCTPHLVSLLNFSFGCCFEILQSRFDMSSVPRMLRAILSLYFLLIQPLLNPLMYGLQMSQIRKLYKHLF
OR.scaffold_119.1       LVLILPQLLMIIFSYVQISQVCRNLT----RESQR--RALKTCVPHLFSLLNYTIGSIFEISQTRFSMTHMVAEARIFMSLYFVILPSISNPVLYGLGTQLIRVNLLKLL
OR.scaffold_5287.2      ICFVGLDIPLILFSYIKILSVVSRAS----VGSEDRWKAFHTCGTHLMVMMCFYLVGSVTFLSHNLN-INIPADVNTFMGVMYILFPATVNPIIYGVRTTEIRNGLLKIF
OR.scaffold_142.6       LLCLLLPLTFIVFSYVTIIVVIAKMS----STAGR-RKTLSTCTPQLFVTCLFYLPRCFVYVANTV-GFYFSIDVRILLTLLYSLVPPAVNPFIYCFKTQDIKKILMKKL
OR.scaffold_142.7       MFSLLVPLSCIILSYLLIIAVVIRMS----DSSSR-IRTLSTCTPQLLITCLYYMPRCFVYLANNL-GFTFSVPIRIVVVMMYSLIPAAINPLIYCFKTKDIKESLKKKI
OR.scaffold_3154.1P     NILLXIPLLFILASYCCIFCALFKLS----TANER-VKALKTCTGHLSLVALFFLPIIIVYQL----QEALHPNIRILNLSLNYVIPPTLNPFIYALQTQEIKNSLKQLL
OR.scaffold_3905.1      VFIFWLPLLFILLSYLYISCTLAKVA----TVQQG-LKAFRTCIGHLLLVAIYFIPLLITFTL----MENIHPNARIINLSLTSVFPPMLNPIIYVLQTREIKDSLKRLL
OR.scaffold_4479.1      VVNLVAPFAFILLTYAAILVTLFLMK----SVNSR-MKALSTCVEHVILVAIFYIPLFTIFLLGFY-VRVIEADQRVLSLSLASCIPPCVNPIIYSLKTREIKIRAVALI
OR.scaffold_4479.2      VVNLVAPFAFILLTYAAILVTLFLMK----SVNSR-MKALGTCVEHLVLVAIFYIPLFIIFLFGFY-VRVIDADQRVLSLSLASCIPPCVNPIIYSLKTREIKIRAVALI
OR.scaffold_6269.1      VVNLVVPFTFILLTYAAILVTLFLMK----SVNSR-MKALGTCVEHLVLVAIFYIPLFTIFILGFY-VRLIDADQRVLSLSLASCIPPCVNPIVYSLKTREIKIRAVALI
OR.scaffold_4208.2      ALFLVIIWITIFYTYFQILLMAKTAG----KDTVKARNTIILHSFQLLLCMASYLAPALRELLQKLFP-KNSTDILFVSYIVVQVLPRSTSPMIYGLRDPTFRKYLKRYM
OR.scaffold_4208.3      VVYLVIVWLIIFYTYFRIMFTAKTAS----KDARKARNTIILHGFQVLLCMATYAEPLLKQALLLWFP-RNYSDSLFACYIIVQILPRSISPIIYGVRDKTFRRHLTRNL
OR.scaffold_4208.1      TVFLVLVWLTLVYTYINIVCAAKRAS----AQAQRARNTILLHAFQVLLSMLNYVRVLFEQGLLLLLP-GHYMSIIFASYVIIQILPRFVSPIVYGLRDQTFRKYVSRYL
OR.scaffold_11306.1     IIYFSLVFLTLVFSYLKILFAARALSTE-KTSALRARNTILLHGVQLFMCMLSYISPSVEIALHLIFP-GWILEIRFANYLIVYILPRFLSPIIYGFRDKKFRKYLKMNL
OR.scaffold_59.1        CLLFVSAGVAISFSYIGVTVAVRLASTD-KTSSQKARNTLLLHLVQLGLSLSSTVYKPILAALSRIVTRLVLIRVQNVLYVCFFILPRCLSALIYGIRDQLIRPVLFYYL
OR.scaffold_6030.1      CLLFVSAGLAIAFSYIGVTVAARLASTD-KTSSQKARNTLLLHLVQLGLSLSSTVYKPILAALSRIVSRIVLVRLQNVLYVCLFILPRCLSALIYGIRDQLIRPVLFYYL
OR.scaffold_144.1P      CLLFVSAGVAIAFSYIGVTLAARLASTN-KTSAQKARNTLLLHLVRLGLXLSSTVYKPVLMALSRIVTRIVLIRVQIVLYVWLFILPRCLSALIYGIRDQTIRPVLFYHL
OR.scaffold_7573.1      CFLFVSAGLAIAFSYIGVTVAARSASTD-KTSAQKARNTLLLHLVQLGLSLSSTVYKPVLTALSRIVTRIVLIRVQIVLYVWFFILPRCLSALIYGIRDQLIRPVLFYHL
OR.scaffold_6392.1      QFYFFIMSITITFSYVKIMIVAKAASGENKKSTWKGLSTVILHAFQLLLCLIQLWCPFIESAIIKIDL-LLYINVRYFDYVTFILAPRCLSPLIYGLRDEKFLNALKYLA
OR.scaffold_7903.1      QFYFFIMSITITFSYVKIMKVAKAASGENKKSTWKGLSTVILHAFQLLLCLIQLWCPFIESAIIKIDL-LLYINVRYFNYVTFILAPRCLSPLIYGLRDEKFLNALKYLA
OR.scaffold_26.3P       QFYFFIMSITITFSYVKIMKVAKAASGENKKSTWKGLSTVILHAFQLLLCLIQLWCPFIESAIIKIDL-LLYINVRYFNYVTFILAPRCLSPLIYGLRDEKFLNALKYLA
OR.scaffold_6818.1      QFYFLIMCVVILLSYIKVMKVAKAASGENKKSTWKGLRTVILHAFQLLLSLIQLWCPFIESAIFQIDY-MLFINVRYFNYVTFILAPRCLSPLIYGLRDEKFFNALKYLA
OR.scaffold_217.1       IAYFVIVSVVIIYTYVAILVIVKSASSR-SHNATKAGKTVLLHLIQLCLCLVSTLFNMINYNSKWNMQHIVVTHIQYTIFISLIIFPKCLSPLIYGLRDQALRQILQSYI
OR.scaffold_26.4        ILFFAVVAVIILFTYMRILLETRKLRQD-RLSVNKAMHTVLLHGFQLLLSVLAFTSPITETLIVLHAN-WLPEDISFFNYFCFILIPRFLSPLIYGFRDQTLRSHIGKAF
```

Figure S2

```
                             340       350       360       370       380       390       400       410
                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
OR.scaffold_1026.1   FHQKVLQSK----------------------------------------------------------------------------
OR.scaffold_8298.1   FHQKVFAVKINYLVAPLVH------------------------------------------------------------------
OR.scaffold_1026.2   QARKIMSSY----------------------------------------------------------------------------
OR.scaffold_4563.2   MHMKSLSFS----------------------------------------------------------------------------
OR.scaffold_4563.1   TRNSKTASIIQH-------------------------------------------------------------------------
OR.scaffold_142.1    KKRSISV------------------------------------------------------------------------------
OR.scaffold_142.2    KKRSISV------------------------------------------------------------------------------
OR.scaffold_142.3    KRNVFLK------------------------------------------------------------------------------
OR.scaffold_142.5P   -------------------------------------------------------------------------------------
OR.scaffold_3630.2   GKKGLF-------------------------------------------------------------------------------
OR.scaffold_5510.1   GKKRFVLTCVYTLHHK---------------------------------------------------------------------
OR.scaffold_8617.1   GKKGLF-------------------------------------------------------------------------------
OR.scaffold_5887.1   GKKRFVLTCVYILHHK---------------------------------------------------------------------
OR.scaffold_4429.1   HLEPQLNASV---------------------------------------------------------------------------
OR.scaffold_4429.2   C------------------------------------------------------------------------------------
OR.scaffold_7743.1   QRILQQP------------------------------------------------------------------------------
OR.scaffold_117.1    HNPK---------------------------------------------------------------------------------
OR.scaffold_2346.5   TRHNIII------------------------------------------------------------------------------
OR.scaffold_2346.4   RLKH---------------------------------------------------------------------------------
OR.scaffold_2346.6   CRKS---------------------------------------------------------------------------------
OR.scaffold_3763.1   CRKR---------------------------------------------------------------------------------
OR.scaffold_3763.2   CRKSM--------------------------------------------------------------------------------
OR.scaffold_4133.1   CMKSL--------------------------------------------------------------------------------
OR.scaffold_6828.1   CRKS---------------------------------------------------------------------------------
OR.scaffold_6765.1   GKEI---------------------------------------------------------------------------------
OR.scaffold_123.1    WTKHVCI------------------------------------------------------------------------------
OR.scaffold_117.2    HMKRKVALQSKK-------------------------------------------------------------------------
OR.scaffold_123.2    SRK----------------------------------------------------------------------------------
OR.scaffold_2346.2   KGKG---------------------------------------------------------------------------------
OR.scaffold_2346.3   CR-----------------------------------------------------------------------------------
OR.scaffold_5287.1   SHKAEH-------------------------------------------------------------------------------
OR.scaffold_2346.1   LGHKINIFM----------------------------------------------------------------------------
OR.scaffold_7149.1   LGHKINIFM----------------------------------------------------------------------------
OR.scaffold_5511.2   S------------------------------------------------------------------------------------
OR.scaffold_119.1    MRHKIPLTKLSKTVRQS--------------------------------------------------------------------
OR.scaffold_5287.2   KLQVKKLIKVSPV------------------------------------------------------------------------
OR.scaffold_142.6    RNTGFGMKVNIYS------------------------------------------------------------------------
OR.scaffold_142.7    FSRISTNLKPG--------------------------------------------------------------------------
OR.scaffold_3154.1P  KFRVQTKIV-RKL------------------------------------------------------------------------
OR.scaffold_3905.1   KLGRKSKTTPRKLPNLPQTAACKC-------------------------------------------------------------
OR.scaffold_4479.1   RKNKIKVIKF---------------------------------------------------------------------------
OR.scaffold_4479.2   RKNKIKVMKF---------------------------------------------------------------------------
OR.scaffold_6269.1   RKSKIKGTKF---------------------------------------------------------------------------
OR.scaffold_4208.2   LARSS--------------------------------------------------------------------------------
OR.scaffold_4208.3   LCRPPRAPEEPAQT-----------------------------------------------------------------------
OR.scaffold_4208.1   LCKMGLGGH----------------------------------------------------------------------------
OR.scaffold_11306.1  QIRRCGVPRPEVAPVNTL-------------------------------------------------------------------
OR.scaffold_59.1     CCRLTLSVFPAKGYK----------------------------------------------------------------------
OR.scaffold_6030.1   CCRLTLSVFPSKGYK----------------------------------------------------------------------
OR.scaffold_144.1P   CCQLKLQSFCLKATNRPFLQTLICMYFYICLLQCFCGDINPLINENKWSTIDPIMRPTEFSHHNEIVFGFYFV------------
OR.scaffold_7573.1   CCRLNYQSFRVKATNRPFLQTLIYMYYHTCFLRCLCGVRELRVAAVAYFCLSYPEISFVTRGNIFPFSEIKQTVMLCLSQGQGQ-
OR.scaffold_6392.1   LCGLYKKKIGFT-------------------------------------------------------------------------
OR.scaffold_7903.1   LCGLYKKKIDYX-------------------------------------------------------------------------
OR.scaffold_26.3P    LXXXXXXXXXXXXXXXXXDFLPLSLICVRATFX----------------------------------------------------
OR.scaffold_6818.1   LCGLYKKRLDLFDE-----------------------------------------------------------------------
OR.scaffold_217.1    PFRFTAAARTFASS-----------------------------------------------------------------------
OR.scaffold_26.4     LCCSNRGRPCVRRKQCDRVFAF---------------------------------------------------------------
```

Figure S2