Czernic et al., Figure S1



Supplemental Figure S1: Distribution of bacteroid morphotypes among papilionoid legumes. (*A*) Simplified phylogenetic tree with triangles representing the major legume clades. Notable species for which bacteroid morphotype has been characterized are indicated. In red, E-morphotype; green, S-morphotype and black, U-morphotype. Figure adapted from Oono et al. (2010). (*B*) Phylogeny of the genus *Aeschynomene* based on the ITS + *trnL*. Figure adapted from Chaintreuil et al. (2013). Species forming E-morphotype bacteroids are indicated in red, species forming S-morphotype bacteroids in green. The other species have not been analyzed.

Czernic et al., Figure S2



Supplemental Figure S2. Nodule specific expression of NCR genes in A. evenia. RNA was extracted from A. evenia spp. serrulata roots or mature nodules 14 days after inoculation with the Bradyrhizobium strain ORS285. Expression levels were calculated relative to $EF1\alpha$. Error bars indicate standard errors of the means of 3 biological replicates.



Supplemental Figure S3. NCR peptides colocalize with bacteroids in *A. afraspera* and *A. indica* nodules. Tricine-SDS-PAGE analysis and Coomassie blue staining of total protein extracts of nodules (nod), bacteroids (Boid), and cultured *Bradyrhizobium* strain ORS285 cells (B) reveal the specific presence of low molecular-weight peptides in nodules and bacteroids. The rectangle in the dashed line corresponds to the region of the gel analysed by LC-MS/MS.

Czernic et al., Figure S4



Supplemental Figure S4. Change in the bacterial cell shape during the symbiotic interaction between *Bradyrhizobium* strain ORS285 and *Aeschynomene indica*. *A. indica* nodules were elicited by a *Bradyrhizobium* ORS285 strain expressing GFP to easily visualize the bacteroids. Nodules were harvested at 4, 4.5 and 5 dpi, then sectioned and analysed by confocal microscopy. Red and yellow arrows show respectively early (U-morphotype) and final (S-morphotype) shape of bacteroids while white arrows point the transitory elongated shape of the bacteroids. Bars represent 10 µm.

Czernic et al., Figure S5

ТΤ $T \downarrow T$ Тт Τττ ТТТ 100 TTT Survival (% of control) 80 60 BTAi1 ■ BTAi1∆shc 40 ORS285 20 0 ASHCROZ NCR2AT NCR335 AINCROI AINCROZ Aancroit AINCROS Control NCR035 С В 1280 1C 100 2C Survival (% of control) 80 960 Counts 60 4C 640 40 320 20 0 10 0 7.5 30 1 100 AaNCR01 concentration in μM DNA content (PI fluorescence)

Supplemental Fig. S5. *In vitro* effect of synthetic *Aeschynomene* and *Medicago* NCR peptides. (*A*) Effect on the viability of BTAi1, hopanoid BTAi1 mutant (BTAi1 Δ shc) and ORS285 strains. The viability test was done according to Van de Velde *et al.* (2010) with 10 µM of each NCR. Control: cells treated with H₂O or NH₄OH 5% used to solubilize *Aeschynomene* anionic NCRs.

(*B*) and (*C*) Effect of AaNCR01 on *S. meliloti* bacteria. (*B*) Effect on the viability. The viability test was done according to Guefrachi et al. (2015) with 7.5 and 30 μ M of AaNCR01. (*C*) Flow cytometry analysis of DNA content in *S. meliloti*. Blue (no treated), pink (treated with 10 μ M of AaNCR01 during 4 h). Error bars in B and C are standard deviations.

Α



Supplemental Figure S6. Neighbor joining phylogeny of NCR protein sequences. The amino acid sequences of NCR genes were aligned using Muscle3.6. The evolutionary distances were computed using the Poisson correction method, and a tree was inferred from the distance matrix by Neighbor Joining using MEGA5. All ambiguous positions were removed for each sequence pair. There were a total of 210 positions in the final dataset. Percent of bootstrap replicates (1000 replicates) are indicated at each tree node (only if >50%). NCRs from *A. afraspera* and *A. indica* are in green and red respectively and those from different IRLC legumes are in blue (The accession numbers are indicated). A defensin from *Lotus*, a non-IRCL legume was used for tree rooting.

	A. afr	aspera	A. indica				
	Root	Nodule	Root	Nodule			
Number of cDNA sequenced	9492	9582	9621	9847			
EST summary:							
Number of high-quality ESTs	9017 (95%)	8688 (91%)	9117 (95%)	8768 (89%)			
Average EST lenght (bp) EST size range (bp)	551 102-819	513 102-817	528 101-803	510 101-782			
Non valid sequences Small size Low quality	475 (5%) 360 (76%) 115 (24%)	894 (9%) 729 (82%) 165 (18%)	504 (5%) 387 (77%) 117 (23%)	1079 (11%) 911 (84%) 168 (16%)			
<u>Cluster summary:</u> Number of clusters Number of singletons Number of contigs Average contig lenght (bp) Contig size range (bp)	923 4162 1161 750 220-1794	732 3493 903 723 122-2267	1006 4566 1268 729 146-1268	812 4164 1025 703 120-1025			

Supplemental Table S1: *Aeschynomene afraspera* and *Aeschynomene indica* root and nodule expressed sequenced tags (ESTs) and cluster collection statistics.

Supplemental Table S2. Nodule- specific Cys-rich putative peptides from *Aeschynomene indica, A. afraspera* and *A. evenia*. The NCR were named with the initials of the plant species and numbered according to the read count level in the EST nodule libraries (for *A. indica* and *A. afraspera*) or arbitarily for *A. evenia*. The NCR with a read count above 5 in the nodules are grey shaded. Signal peptides were determined using SignalP 4.0 (Petersen TN, Brunak S, von Heijne G, Nielsen H - 2011- SignalP 4.0: discriminating signal peptides from transmembrane regions. Nature Meth 8(10):785-786) and ajusted manually. Theoretical pl and MW were calculated for mature peptides from Expasy web site (Gasteiger E, et al. -2005-Protein Identification and Analysis Tools on the ExPASy Server; In John M. Walker (ed): The Proteomics Protocols Handbook, Humana Press). For the *A. evenia* NCRs, the pl and MW were calculated for the mature peptide even if the signal peptide was truncated or contained stop codon (indicated in the table). The presence of a signature corresponding to NCR motif 1 (1) or motif 2 (2), as defined in figure 3, is indicated in the last column. The 1* indicate a motif 1 where the spacing between Cyst 4 and 5 contains 5 amino acids instead of 4.

Sequence peptide (a) No Rev PI Nu Rod No Rodule No Rodule No Rodule No Rodule AndROB Classengt MALKUNANLAULUTVISMASHINGVOSILOPKOLDENSCHMURGLAMACHCVSSIC(DPDC) 46 6 6.87 5087.04 1 2.42 1 ANNCRO Classengt MALKUNANLAULUTVISMASHINGVOSICUMSCRIMICSNOPCICIPSCONCESCINGUNCSYNCPCOPEDIC CEG 54.4 67.72 487.44.33 0 4.5 1 ANNCRO Classenigt MALKUNANLAULUTVISMASHINGVOSIDPRICINGCONCESCINGUCGRIVENCEPTIC 46 6 4.87 7515.40 0 2.2 2 ANNCRO Classenigt MARTUNISULUTERMINISSULUTERMINISSULVICEDVIVADORCHVORUPORCECEPTERMUNESCANCENTRECONCEPTER 77 8 4.08 8373.2 0 2.22 2 ANNCRO Classenigt MARTUNESTINGUESCANCERSENVULDATECHTECHCLCSSENVULDATECHTECHCLCSENVUT 7 8 4.01 5478.0 0 10 1 ANNCRO Classenigt MARTUNESTINGUESCANCERSENVUTURESTINGUESCANCERSENVULDATECHTECHCLCSENVUTURESTINGUESCANCERSENVUTURESTINGUESCANCERSENVULDATECHTECHCLCSENVUTURESTINGUESCANCERSENVULDATECHTECHCLCSENVUTURESTINGUESCANCERSENVUTURESTINGUESCANCERSE				Mature	Nhr of Cur		Theoretical	Read	d count	NCD motif
A. operate A. NORGI CLSconlig MAKLINYAALEALLUTVINSMASHILQVQELINIDSWIDPRCPLEMSCKMSCERNINGGLIAMCH/VGSUCCPTDK 46 6 6.5 5087.04 1 242 1 ANNCRIZ CLISonlig MAKLINYALULAVISTSHILQVQELINIDSWIDPRCPLEMSCKMSCRIGHTAC/QUESCICPTDK 46 6 7.9 487.483 0 45 1 ANNCRIZ CLISonlig MAKLINYALULAVISTSHILQVGENKOSSCRIVEGALAVICAVISCEGAPTIC/COPECICE/CEFTERINGDDVN 66 8 4.57 7615.40 0 25 2 ANNCRIZ CLISonlig MAKTINILSULUT/GMUTSSDVTVAAGYNCVWRDPNCKAGDPNYCADD/CKNDPEKALD/CKTDVCCEFTEFTPNNGDDVN 66 8 4.57 7615.40 0 25 2 ANNCRIZ CLISONLIG MAKTINILSULUT/GMUTSSDVTVAAGYNCVWRDPNCGKGEDPNYCADD/CKNDPEKATCCDD/CFTPN 77 8 4.68 8773.32 0 14 2 ANNCRIZ CLISONLIG MAKTINUSUUT/GMUTSSDVTVAAGYNCVWCBNPCGEGSDVTVAAGYNCVCEPTPVCTPCDPN 47 8 4.68 8773.32 0 10 10 10 10 10 10 10 10 10 10 10 <td></td> <td></td> <td>Sequence</td> <td>peptide (aa)</td> <td>NOT OF CYS</td> <td>pl</td> <td>MW</td> <td>Root</td> <td>Nodule</td> <td>NCK MOUI</td>			Sequence	peptide (aa)	NOT OF CYS	pl	MW	Root	Nodule	NCK MOUI
ANNERIO CLEARING MARKIWAARIALUTYNEMMASHILQVVGERMICE/MDPC/FLEMXCMS/SCINNINGGLAMGE/CGSCICPTOR 46 6 6.77 967.04 1 242 1 ANNERGE CLEARINETULULVANDMASHINGUVGERMICE/MARCHEV/CVV/RDPC/ELEX/CMS/SCINPC/DPCEEDES/GF 70 10 5.44 676.8.2 0 7.1 2 ANNERGE CLEARINETULULVANDMASHINGUVGERMICE/MDPC/CLEARING/SCINPC/CPC/PDCEDES/GF 70 6 8 4.57 7615.40 0 2.5 2 ANNERGE CLEARING MARKIWAARIALULYTRAMINTSDYTVAG/MCV/VWBDP/CEAD/CG/CPC/PTFPNGDDVFCF 66 8 4.57 7615.40 0 2.3 no ANNERGE CLEARING MARTINUESULUTGAMINTSDYTVAAG/MCV/WWDP/CCG/CPC/FC/CPC/PDF 77 8 4.08 8573.32 0 2.2 2 ANNERGE CLEARING MARTINUESULUTGAMINTSDITVAAAG/MCC/FU/CLECESSYVLIDA/CCLU/CPC/FC/CPR/NP 77 8 4.08 8573.32 0 2.2 2 ANNERGE CLEARING MARTINUESULUTGAMINTSHILLUTGAMINTSHIPU/ASSCINVSM/MOTINCEFTCF/CLECESSYVLIDA/CEPR/PM 77 8 4.03 8770.6 0 0 0	A. afraspera	1								
ANNERGY CLI3contig1 MARLAMPTIVULWAYSITSHEQVAGESICENHEWEREINVESCREDCEGREGREGATINACCVG/CCCYDEDCEDECSIGE 59 10 5.44 676.85 0 71 2 ANNERGY CLIScontig1 MARLTUNELSVULTGENERSVERGENERSKESSKENHEGALAMERCVG/SIGCEPPINGDDIN 66 8 4.57 7615.40 0 25 2 ANNERGY CLIScontig1 MARTTUNELSVULTGENERSVERGESSKESSKENHEGALAMERCVG/SIGCEPPINGDDIN 66 8 4.57 7615.40 0 22 2 ANNERGY CLIScontig1 MARTTUNESVULTGENERSSKENGESSKENGERGESSKENGERGESSKENGERGENERGESSKENGERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGENERGESSKENGERGENERGESSKENGERGENERGESSKENGERGENERGENERGESSKENGERGENERGENERGESSKENGERGENERGENERGESSKENGERGENERGENERGESSKENGERGENERGENERGENERGENERGESSKENGERGENERGENERGENERGENERGENERGENERGENE	AaNCR01	CL3contig5	MAKLNWANLFALILLVTVMSMASHHLQVVGLRMIDSWIDPKCPLDEMSCMSSCRNKHGGLAMGHCVGSICICPFDK	46	6	6.87	5087.04	1	242	1
ANNCRIG CL3Contg3 MARKUWARAULULYUNSIASHHHQVQGERMUSWIPPRCLEMSCHSSCENNEGGLAME(CVSCIG)CPTPK 44 6 7.79 487483 0 45 1 ANNCRIG CL16contg1 MARTUNLSLUUTURSUNSVAGUEVUNDERCEKCEGDPVCADDCKNOPGERATARCRDUCTEPNUND 66 8 4.57 7615.40 0 25 2 ANNCRIG CL3contg1 MARTUNLSULUTESSUTVAGEVICUVUS ACTIVICVOUNDERCEKCEGDPVCADDCKNOPGERATARCRDUCFEPCAPUPS 77 8 4.08 8573.32 0 23 nno ANNCRIG CL3contg1 MARTUNLSULUTESSUTVAGEVICE/UNADTCERETCVQLCSDSVVUDACCKCRDPVCADCKNNHEEGAAQCRENERCFCIPCAPUPS 77 8 4.08 8573.32 0 23 nno ANNCRIG CL3contg1 MIRUTISTRIBULITSSUTVAGEGESDVFVDIDACCEGEDSVVUDACCKNNHEEGAEQCPDV 77 8 4.08 8570.65 0 10 </td <td>AaNCR02</td> <td>CL13contig1</td> <td>MAKLANFFTLVLLVAVISITSHHQVAESRLCNHRWFEIRCNVNESFCKNDCSGRHGDRTINAFCVIGYCSCYFDCPDGEDCSCIGF</td> <td>59</td> <td>10</td> <td>5.44</td> <td>6768.5</td> <td>0</td> <td>71</td> <td>2</td>	AaNCR02	CL13contig1	MAKLANFFTLVLLVAVISITSHHQVAESRLCNHRWFEIRCNVNESFCKNDCSGRHGDRTINAFCVIGYCSCYFDCPDGEDCSCIGF	59	10	5.44	6768.5	0	71	2
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AANCR04 CLEGONING GERNONNM GO 8 4.57 / / / / / / / / / / / / / / / / / / /			MARLTLINLLSLVLLITGILITSSDYTVAGYVCIVVWRDPNCGKGDPNYCAQDCKNDYGEKAIPVCRYDVCFCGYECTFPNNGDDYN							
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AARCR06 CL31contig1 MARILUMERPLUCTON/WARSHWXAGE/UDU/EDV/WADTNCE/REDS/FC/QECKNIKHIEEGAAQCRENR/CFCIFPCAPNIPS 77 8 4.08 8573.32 0 22 2 AaNCR06 CL31contig1 MTKLTSTINIALLUTAINSTEUDVANSCVHISHWOTTNCE/PETCVQLCSDSYK/UDARCEN/CYCEPON 47 8 4.01 5475.0 0 14 2 AaNCR08 CL64contig1 MTKLTSTINIALLUTAINSTEUDVANSCVHISHWOTTNCE/PETCVQLCSDSYK/UDARCEN/CYCEPON 47 8 4.00 8790.09 0 10 10 AaNCR08 CL64contig1 MTKLTSTINIALLUTAINSTEUDVANSCVHISHWOTTNCE/PETCVQLCSDSYKVEASRWPRMLIVKDEAPATVRDSLQESV/V 75 4 4.93 8570.6 0 10 no AaNCR10 CL32contig1 MARLTWARSKERAGREGESIN 77 5 4 4.94 8570.5 6 2 AaNCR12 CL746contig1 MARLTWARSKERAGREGESINDHOVGOVECLOSVECACROSVECAVICCONKCORTVECPCPESPRPHYPS 72 8 4.14 8446.1 0 6 2 AaNCR12 CL746contig1 MTKLTATSTINIALLUTAINSTINFALLUVAINSKERAGREGESINDHOVGOVECARCROSVECAVICE/CYNECCPUSCPCCD 50 8 7.67	AaNCR05	CL16contig2	MAKLTLINLLSLVLLVTGMLMTSSDYKVAAGYMCVVGWRDPNCGKGDPNYCAQDCKNDHGEKATAFCRDDVCFLWL	46	6	4.89	5202.85	0	23	no
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AANCRO? CLSBContig1 MTKLTSTHFALLEFTASMTSLHQVASNSCWHSWMDTNCEPETCVQLCSQSVVLPQIAPCEFCHL/CVCEYECPDN 47 8 4.01 5479.0 0 1.0 AANCRO8 CL64contig1 MTKLIGNEFAULUTATVILIKENEVAGEAGCEQSQSVLPQIAPCEGEFDHWVDRNCPTVOFFCKLECIKRERTGDGACNWIV CYCRYLPNSTSEDALRP 75 8 4.60 8790.69 0 1.0 1 AANCRO9 CL67contig1 MTKLTSTHFALLEFTASMTSLHQVASNSCWHSWMDTNCEPETCVQLCSQSVKVEASRWPRMLLVKDSLLQESVTV 75 4 4.94 8570.6 0 1.0 0 </td <td>AanCRUb</td> <td>CL31COntig1</td> <td>PISYDGGDDYNGEGINNNDGI</td> <td>//</td> <td>ð</td> <td>4.08</td> <td>8573.32</td> <td>0</td> <td>22</td> <td>Z</td>	AanCRUb	CL31COntig1	PISYDGGDDYNGEGINNNDGI	//	ð	4.08	8573.32	0	22	Z
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Aak CR03 CLOBUDINGL CVCRUPPRISTEEDARP 75 6 4.00 679.03 0 10 1 Aak CR03 CLOSTCONIGL MTKLTSTINSHALLTAINSTSHEQVASSCWHASTMODTCEPETCVQLCSDSYKVEASRWPRMLLVKDEAPATYRDSLLQSVTV APPLLUDFKIKRGPEGSIN 75 4 4.94 8570.6 0 10 no Aak CR11 CL32contig1 MAKLIWAKKVALILLTAINSTSHEQVASSCWHASTSHEQVEAKGTVDLCEPETCVQLCSDSYKVEASRCVGVLCECTYELC 47 7 4.46 5372.21 0 7 1 Aak CR11 CL132contig1 MAKLIWAKKVALILLTAINSTSHEQVASYCEDDCVEEDCVCEDCVCEDCVCEDCVCCCSCVCCSVCC 49 8 4.08 5565.15 0 6 2 Aak CR11 CL132contig1 MAKLIVATIKALUVTAISMENTEPVENDON KAKKODVEDDVCEDCVCEDCVCEDCVCEDCVCEDCVCEDCVCED		CI 6 Acontig1	MTKLILGNFFAIVLLMTVILIIKSHIEVAGEAGCEQSSDYLYPQIADYCEEGFDHWYDRNCPTVDFFCKLECIRKHGRTGDGACNWIY	75	0	4.60	9700.60	0	10	1
AshCR09 CL67contig1 MTKLTSTNIFALILIFTAISMTSLIQVASNSCWHSWMDTNCEPETCVQLCSDSYKVEASRWPRMLLIVKDEAPATVRDSLLQESVTV 75 4 4.94 8670.6 0 10 no AahCR10 CL3Contig1 MAKLINVAKFVALILLVTAMSMTSHHQVVGVEMKDTWIDLACTFDDLPCTSDCRNKYGVFAVGRCVGVLCECTYELC 47 7 4.46 5372.21 0 7 1 AahCR10 CL3Contig1 MAKLINVAKFVALILLVTAMSMTSHUQVGVEMKDTWIDEACTFDDLPCTSDCRNKYGVFAVGGCVGVLCECTYELC 47 7 4.46 5372.21 0 7 1 AahCR12 CL3Zoontig1 MAKLINVAKEVALILLVTAMSMTSHUQVGVEMKDTWDENKCVEDEVGEDCVGECKGQUPCCGVGCS 49 4.08 566.15 0 6 2 AahCR12 CL3Zoontig1 MARLINFAULUTAMSMTSEVGGNKMCRERWPDINCKCDEVFREGCMANCRERGYPKCGVCRGPD 50 8 7.67 599.977 0 6 2 AahCR16 CL21Contig1 MAKLINFAULUTAMWMTSEVGGNKMCREREWPDINCKCDEVFREGCMARCEGREGGD 50 7 5.19 7654.68 0 5 1 AahCR16 CL22Coontig1 MAKLINFAULUTAMSMESHGGNYMSEGNSDCJAGEGRWDCEVCDVCVGCGDVCCCDVCCGUPCCGUPCCGUPCCGUPCGLUV 53 8 4.75 <	AanCR08	CL64COntig1	CYCRYLPNSTSEDALRP	75	ð	4.60	8790.69	0	10	T
AANCHO CLOSODINGI AP.NUM OPEKKROPEGSIN AP.S4 BS7.00 O D0 IND AAANCED CLIZOCONTIGZ MAKLINARKAPULLIVTAINSMTSHHHQVVGVEMKOTWOLECTEDUCTSDCRNKYGVEAVGRCVGVLCECTVELC 47 7 4.46 537.22.1 0 7 1 AANCED CLIZOCONTIGZ MAKLINARKAVLULIVAINSMTSHHQVVGVEMKOTWOLECTEDUCTDCRNKRGVEAVGRCVPCEPEDSPMPNSP 72 8 4.14 844.81 0 6 2 AANCR12 CLIZZCONTIGI MTKLILATIFAULLINIASSIMITSEVDGNKKICKRFWVDLICKDPEYRGCMMCKCRNVGDTAVGFCQYPKCSCNVGCPD 50 8 7.67 5595.77 0 6 2 AANCR13 CLIZZCONTIGI MTKLILATIFAULLIVIAISSIMITSEVDGNKKICKRFWVDLICKDPEYRGCMMCKCKNVGDTAVGFCQYPKCSCNVGCPD 50 8 7.67 5595.77 0 6 2 AANCR13 CLIZZCONTIGI MTKLILATIFAULLIVIAISSIMITSEVDGNKKICKRFWVDLICKDVDFCNCKKRKVGDTAVGFCQYPKCSCNVGCPD 50 8 7.67 5.46 0 5 1 AANCR15 CLIZZCONTIGI MAKLINARTVULIVIAINSTEXCBAUCKDEWVDIRCINESCERVEDTORVCDEVHCGNCKCGGVCCHEVCEDIE 6 7 5.19 7654.68 0 <		CI 67contig1	MTKLTSTNIFALILLFTAISMTSLHQVASNSCWHSWMDTNCEPETCVQLCSDSYKVEASRWPRMLLVKDEAPATVRDSLLQESVTV	75	4	4.04	0570.0	0	10	20
AANCR10 CL3Contig12 MARLIWYAKYALLUZTAMSMTSHHIQVYGEMCDTWIDLRCTFDDLCTSDCNKYCYAUGGCYGVCECTYELC 47 7 4.46 5372.21 0 7 1 AANCR11 CL132contig1 MARLIFYLYELLUTANISTHAQVYGFLCDDWyDESCAERGDSDGCMODCKKHEMPTAGGFCGYGCSCYGCS 49 8 4.08 5656.15 0 6 2 AANCR13 CL122Contig1 MSRLTSAYFFSIVLUCAISKTSHHQVVANKCLDDWFDHNRYCVEDDCVQECKRQHNSTEGYCAYPCSCPYCECPEDSPMPPNPP 72 8 4.14 8448.1 0 6 2 AANCR13 CL122Contig1 MTKLLATFALLULMIAISMMTSEVGANKMCRRPWUDDNCKEDEYRGCMMECKSNYGDTAYGFCQYPKCSCNYGCPD 50 8 7.67 5959.77 0 6 2 AANCR15 CL21Lontig1 MARLIFYLYELAVUAGGYTCSEVVAGGYTCSEVVAGGMCCEYVEDGENGKGCFFECDLPFLS 85 8 4.22 9642.35 0 6 2 AANCR16 CL220Contig1 MARLISINFAULUTAISMPSHHQVESKCTDEWYDIRCNLNEGYCRVDCEVHGGLAKGYCGDYCCCNYCPGLIV 52 8 4.70 6009.86 4 2 AANCR16 CL220Contig1 MARLISINFAULUTAISMPSHHQVESKCTDEWYDIRCNLNEGYCRYCCLPHGGLAKGYCGDYCCCNYCPGLIV 53 8 4.75	AanCR09	CL67Contig1	APNLWDFKIKRGPEGSIN	75	4	4.94	8570.6	0	10	no
AakCR11 CL132contig1 MARLTFYVESLULVTAISTSHHQVVOFFLCLDDW/DDFXAFEGDSDACQCKRQHNSTEGYCQYSCFCSYQCS 49 8 4.08 5656.15 0 6 2 AakCR12 CL746contig1 MSRLTSAFFSHULVEALSKTSHHQVVANKCLDDWFDHNKYCVEDDCVQECKRQHNSTEGYCAPYNCFCPYCPEDSPMPPNSP 72 8 4.14 8448.1 0 6 2 AakCR13 CL127Contig1 MTKILLATFAULULIVTGMWMSTEKYCAGGKMCKCRFWQDLOXCKERGYCQDCYCCCYCQCD 50 8 7.67 5959.77 0 6 2 AakCR13 CL111Contig1 MARLIGNFAULULVTGMWMSTEKYCAGGKMCCSCWDDPNECKEDTYNCTONCKRKYGMKATSHCRGDKCFCIFECDLPFLPS PINYDGDYGMNEGDDVNSEGINNNNNDGT 8 4.22 9642.35 0 6 2 AakCR15 CL211contig1 MAKLINFAULULVTAISMFBHQVESKKCTDEWYDIRCNLNEGYCRYDCLEVHGGLAKGYCQGDYCCFDYYCPGILIV 52 8 4.70 6009.86 4 2 AaNCR16 CL230Contig1 MAKLISNFFAULULTAISMFBHQVESKKCTDEWYDIRCNLNEGYCRYDCLEVHGGLAKGYCQGDYCFCDYYCPGILIV 51 8 ND ND 0 4 2 AaNCR18 CL230Contig1 MAKLISNFFAULULTAISMFBHQVESKKCTDEWYDIRCNLSESOFRUPCLEVHGGLAKGYCQGDYCCCNVCCGYOCCNVC 66 12 4.02 7420.27 0 4 2	AaNCR10	CL3Contig2	MAKLNWAKFVALILLVTAMSMTSHHHQVVGVEMKDTWIDLRCTFDDLPCTSDCRNKYGVFAVGRCVGVLCECTYELC	47	7	4.46	5372.21	0	7	1
AaACR12 CL746contig1 MSRLTSAYFESIULUEAISKTSHHQVAANKCLDDWFDHNKYCVEDDCVQECKRQHNSTEGYCAYYNCFCPYECPEDSPMPPNSP 72 8 4.14 8448.1 0 6 2 AaNCR13 CL127Contig1 MTKULLATFALLLMIAISMMTSEVDGNKMCRRPW7DLNCKDPEYRGCMMECKSNYGDTAYGFCQYPKCSCNYGCPD 50 8 7.67 5959.77 0 6 2 AaNCR14 CL111Contig1 MARLKILMTFALLLUTGKMWMTSEVDGNKMCRRPW7DLNCKDPEYRGCMMECKSNYGDTAYGFCQYPKCSCNYGCPD 50 8 7.67 5959.77 0 6 2 AaNCR15 CL211contig1 MARLKIGNFAULLWTGIASMMSHQVGSKCTDEWDDPNCKKKOTGEVODPTVDFFCNSCKRKHPKGDGECSGIYCHCRYLESEI 66 7 5.19 7654.68 0 5 1 AaNCR15 CL211contig1 MAKLSNFAULLWTAINSMPSHQVESKCTDEWDIRCNLREGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIV 52 8 4.75 6219.02 0 4 1* AaNCR16 CL220contig1 MAKLSNFAULUTAINFMPSHQVESKCTDE*VDIRCNLREGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIV 51 8 ND ND 0 4 2 AaNCR16 CL220contig1 MAKLSNFAULUTAINFMPSHQVESKKCTDE*VDIRCNLREGYCRVDCLEVHGGLAKGYCQGDYCCCNYCGUYCCNYCGUYCCNYE	AaNCR11	CL132contig1	MARLTFVYLFSLLLLVTAISITSHHQVVGYFLCLDDWVDESCAERGDSDGCMQDCKNKHGYTAQGFCGYDSCFCSYQCS	49	8	4.08	5656.15	0	6	2
Particial CLPMODINGLA VSPDVDDSPNPPTWDLK 72 8 4.1.4 6446.1 0 6 2 AANCR13 CL127Contig1 MTKLILATIFALULLINIAISMMTSEVDGKIMCRRFWUDDPNCEKEDYTNCTQNCKRKYGDPACCED 50 8 7.67 5959.77 0 6 2 AANCR14 CL111Contig1 MARLINTFALULUTGMWMTSEYXAGGNTCSEVWDDPNCEKEDYTNCTQNCKRKYGMKATSHCRGDKCFCIFECDLPFLPS 85 8 4.22 9642.35 0 6 2 AANCR14 CL111Contig1 MAKLINFFAULUTAISMPSHIQVESKKCTDEVYDRCNLNEGYCRXPCCEKKRKHRKGDGECSGIVCCRYLESEI 66 7 5.19 7654.68 0 5 1 AANCR16 CL220Contig1 MAKLINFFAULUTAISMPSHIQVESKKCTDEVYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIUV 53 8 4.70 6009.86 0 4 2 AaNCR16 CL230Contig1 MAKLSNFFAULUTAISMPSHIQVESKKCTDE VYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIUV 53 8 4.70 6009.86 0 4 2 AaNCR19 CL266Contig1 MAKLSNFFAULUTAISMMSHQVESKKCTDE VYDIRCNLNEGYCRWDCLEVHGGLAKGYCQGDYCFCNYCPGLIUV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1	A-NCP12	CI 746 contig1	MSRLTSAYFFSIVLLVEAISKTSHHQVVANKCLDDWFDHNKYCVEDDCVQECKRQHNSTEGYCAYYNCFCPYECPEDSPMPPNSP	72	o	1 1 1	0440 4	0	6	2
AANCR13 CL127Contig1 MTKLILATIFALILUMIAISMMTESUDGNKMCCRRFWVDUNCKDPEYRGCMMECKSMVGCPD 50 8 7.67 5959.77 0 6 2 AaNCR14 CL111Contig1 MARLKTLINELAUVLUTGKWMTSSYKVAGGIYTCSEVWDDPNCEKEDYTNCTQNCKRKYGMKATSHCRGBKCFCIFECDLPFIPS PINVPGDYGNNEGDDYNSEGINNNNDGT 85 8 4.22 9642.35 0 6 2 AaNCR15 CL211contig1 MAKLIGNFFAVULUTGNESHEVAGEAGCKPSSDYQIAGFMFWIDMNCPTVDFFCNSECKRKHPKGDGECSGIYCHCRYLESEI REDEMMS 66 7 5.19 7654.68 0 4 2 AaNCR16 CL220Contig1 MAKLISNFFAVULUTAISMPSHHQVESKKCTDEWYDIRCNLEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIV 53 8 4.75 6219.02 0 4 1* AaNCR18 CL220Contig1 MAKLISNFFAVULUTAISMPSHHQVESKKCTDE*YDIRCNLEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1 MAKLANFFLIVULITAISMTSHQVARCKCDE*YDIRCNLEGYCRVDCLEVHGGLAKGYCQGDYCCCNVDCVQDYCSCNYE 66 12 4.02 7420.27 0 4 2 AaNCR20 CL266Contig1 MAKLANFFLIVULITAISMTSHQVARCKCDE*VDIRCNLEGYCRVDCVDVCVDVCVDVCSCN	Adivertz	CL/40COIItig1	VSPDYDDSPNPPTWDK	72	0	4.14	0440.1	0	0	2
AaNCR14 CL111Contig1 MARLKTUNFLAUVLUTGMWMTSEYKVAGG/VTCSEVWDDPNCEKEDYTNCTQNCKRKYGMKATSHCRGDKCFCIFECDLPFLPS 85 8 4.22 9642.35 0 6 2 AaNCR15 CL211contig1 MARLIGNFAVULUTVILIGGVCRVDCLEVHGGLAKGYCQGDVCFCCDYVCPGLUV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1 MAKLANFFLUVLUTVIAINMPSHHQVESKKCTDE *VDIRCNLESEDCRLDCIELYGGGPAKGYCVGDVCCCNVPCQUUCCNVPCQUVCCCNVPCQUUCCNVPCQUUCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCCNVPCQUVCCNVPCQUVPFN 55 8 5.99 6258.06 0 4 2 AaNCR20 CL30Contig1 MAKLANFFLIVULITAIMMTSHQVVEGCUVEDCSKLHGETAIGE/CEDIVCSCVPCDQ/CCSNVPFN 55 8 5.82 6841.71 0 4 2 AaNCR21 CL20FContig1 MAKLANFFLIVULITAIMISHAUVVARE	AaNCR13	CL127Contig1	MTKLILATIFALILLMIAISMMTSEVDGNKMCRRFWYDLNCKDPEYRGCMMECKSNYGDTAYGFCQYPKCSCNYGCPD	50	8	7.67	5959.77	0	6	2
Ranchit CLIFICONTIGI PINYDGDYGNNEGDDYNSEGIUNNNNDGT BJ B		CI 111Contig1	MARLKTLNFLALVLLVTGMWMTSEYKVAGGIYTCSEVWDDPNCEKEDYTNCTQNCKRKYGMKATSHCRGDKCFCIFECDLPFLPS	95	Q	1 22	0642.35	0	6	2
AANCR15 CL211contig1 MARLIGNFFAIVLINTVILIIKSHIEVAGEAGCKPSSDYQIAGFMFWIDMNCPTVDFFCNSECKRKHPKGDGECSGIYCHCRYLESEI 66 7 5.19 7654.68 0 5 1 AANCR16 CL220Contig1 MARLIGNFFAIVLIVTAISMPSHHQVESKKCTDE/WYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV 52 8 4.70 6609.86 0 4 2 AaNCR17 CL263Contig1 MAKLSNIFFAIVLIVTAISMPSHHQVESKKCTDE/WYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV 53 8 4.75 6219.02 0 4 1* AaNCR18 CL220Contig2 MAKLSNIFFAIVLIVTAISMTMNQQVEGKCTDE/WYDIRCNLESYCRVDCLEVHGGLAKGYCQGDYCCONYDCVGDYCSCNYE 66 12 4.02 7420.27 0 4 2 AaNCR19 CL266Contig1 MAKLANFFTIVLIUTAISMTMNQQVEGIKCNEMWYDIRCNLSESYCREDCIEKHGYLAKGYRMGNKCCCLTV 45 7 7.73 5279.24 0 4 0 4 2 AaNCR20 CL38Contig1 MAKLANFFTIVLIUTAISMISHAVWAREQUESYCREDCIEKHGYLAKGYRMGNKCCCLTV 57 7.73 5279.24 0 4 2 AaNCR21 CL297Contig1 MAKLANFFTIVLIUTAISMISHAVWAREQUESYCREDCISKLINGETSYRKEDCIENCKQUESYRKIK	Adiventit	CLITICONUSI	PINYDGDYGNNEGDDYNSEGINNNNNDGT	85	0	4.22	5042.55	0	0	2
AANCR10 CL211COM0g1 RRDEMMS OG 7 5.1.5 7.054.00 0 5 1 AANCR16 CL220Contig1 MAKLSNILFALVLLVTAISMPSHHQVESKKCTDEWYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV 52 8 4.70 6009.86 0 4 2 AANCR17 CL263Contig1 MAKLSNIFALVILVTAIMMPSHHQVESKCTDEWYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV 51 8 A.75 6219.02 0 4 1* AANCR18 CL220Contig1 MAKLSNIFALVILVTAIMMPSHHQVESKCTDE*YDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV 51 8 ND ND 0 4 2 AANCR19 CL266Contig1 MAKLANFFLVLLVTAISMTSHQVEGIKCNEMWYDIRCNLSESDCRLDCIELYGGGPAKGYCVGDYCCCNYCQGYCCCNYCQGYCCCNYC 66 12 4.02 7420.27 0 4 2 AANCR20 CL36Contig1 MAKLANFFLVLLVTAISMTSHQVEGQWCKNNKUDIRCGLSESYCREDCYCKYDCSCNYE 66 12 4.02 7420.27 0 4 2 AANCR20 CL36Contig1 MAKLANFFLVLLVTAIMITSHQUEGQWCKNNKUDIRCGLSESYCWEDCSCNYDCSCNYE 66 12 4.02 743.31 0	ADNCP15	CI 211 contig1	MAKLILGNFFAIVLLMTVILIIKSHIEVAGEAGCKPSSDYQIAGFMFWIDMNCPTVDFFCNSECKRKHPKGDGECSGIYCHCRYLESEI	66	7	5 10	7654.68	0	5	1
AANCR16 CL220Contig1 MAKLSNLFALVLLUTAISMPSHHQVESKKCTDEWYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIIV 52 8 4.70 6009.86 0 4 2 AaNCR17 CL263Contig1 MAKLSNLFALVLLUTAINMPSHHQVESKKCTDEWYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIIV 53 8 4.75 6219.02 0 4 1* AaNCR18 CL220Contig1 MAKLSNLFALVLLUTAINMPSHHQVESKKCTDE*YDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIIV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1 MAKLANFFTLVLLUTAISMTMNQQVEGIKCNEMWYDIRCNLSESDCRLDCIELYGGGPAKGYCQGDYCCCNYDCVGDYCCCNYDCVGDYCCSNYE 66 12 4.02 7420.27 0 4 2 AaNCR20 CL136Contig1 MAKLANFFTLVLLUTAINITSHQUVEGQWCKNKWLDIRGICSESYCREDCIEKHGVLAKGYMGNKCCCLTV 45 7 7.73 5279.24 0 4 2 AaNCR22 CL130Contig1 MAKLANFFTLVLLUTAINITSHQUVEGQWCKNKWLDIRGICSESYCREDCIEKHGVLAKGYMGNKCCCLTV 45 7 7.73 5279.24 0 4 2 AaNCR22 CL130Contig1 MTKLTSTNIFALULLTAINSTSHQVARECIDTWIDRCEYNVEICKLDCKDYQESSFAYCVDHNKKCHCPKCPQWPYFN 55 8 5.82 6841.71 0 4 <td< td=""><td>Addentis</td><td>CLZIICOIRIGI</td><td>RRDEMMS</td><td>00</td><td>'</td><td>5.19</td><td>7034.08</td><td>0</td><td>5</td><td>-</td></td<>	Addentis	CLZIICOIRIGI	RRDEMMS	00	'	5.19	7034.08	0	5	-
AANCR17 CL263Contig1 MAKLSNFFALVLLVTAIWMPSHHQVEGKECTDRWYDERCSLNESYCRVDCLEVHGGLAKGYCQGDYYCFCNYYCPGLLIV 53 8 4.75 6219.02 0 4 1* AANCR18 CL220Contig2 MAKLSNLFALVLLVTAIPMPSHHQVESKKCTDE*YDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLIIV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1 MAKLANFFTLVLLVTAISMTMNQQVEGIKCNEMWYDIRCNLSESDCRLDCIELYGGGPAKGYCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCCNYDCVGDYCCNYDCVGDYCCCNYDCVGDYCDYNVIEICCKLCCKCYCQCNDYCVDYCNDFYCVGCDYCCNYDCVGCNGYCCNYDCVGDYCCNYDCVGCNYDVYDDY 77 70 5.03 8817.89 0 4 1 AaNCR25 CL26Contig1 MXKLINFLAVILUVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV 77 10 5.03 8817.89 0 4 1 AaNCR25 CL226Contig1 MXKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDDYDNESFCNKDCSDLHGDAVAMFGFCVLDYC	AaNCR16	CL220Contig1	MAKLSNLFALVLLVTAISMPSHHQVESKKCTDEWYDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV	52	8	4.70	6009.86	0	4	2
AANCR18 CL220Contig2 MAKLANFFLVLLVTAIPMPSHHQVESKKCTDE*VDIRCNLNEGYCRVDCLE/HGGLAKGYCQGDYCFCDYYCPGLLIV 51 8 ND ND 0 4 2 AaNCR19 CL266Contig1 MAKLANFFLVLLVTAISMTMNQQVEGIKCNEMWYDIRCNLSESDCRLDCIE/GGGPAKGYCVGDYCCCNYDCVGDYCSCNYE 66 12 4.02 7420.27 0 4 2 AaNCR20 CL136Contig1 MAKLANFFLVLLVTAISMTMNQQVEGIKCNEMWYDIRCILSESYCREDCIEKHGVLAKGYRMGNKCCCLTV 45 7 7.73 5279.24 0 4 2 AaNCR20 CL136Contig1 MAKLANFFLVLLVTAIMITSHQLVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN 52 8 5.09 6258.06 0 4 2 AaNCR22 CL181Contig1 MTKLTSKNHFALUILVTAISMRSLHQVAARSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENHKCKCHYKCPQWPYFN 55 8 5.82 6841.71 0 4 1* AaNCR23 CL20Contig2 MTKLTSNIFALULITAISMRSLHQVAARSCWYSWDMDKYCEDETCVQSCNDTYKVLIDAFCENHKCKEQEVPKDK 49 8 4.28 5918.59 0 4 2 AaNCR24 CL217Contig1 MTKLTSNIFALULITAISMTSHQVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IYCYCRY 64 8 4.20 7493.43 0 4	AaNCR17	CL263Contig1	MAKLSNFFALVLLVTAIWMPSHHQVEGKECTDRWYDERCSLNESYCRVDCLEVHGGLAKGYCQGDYYCFCNYYCPGLLIV	53	8	4.75	6219.02	0	4	1*
AaNCR19CL266Contig1MAKLANFFTLVLLVTAISIMTMNQQVEGIKCNEMWYDIRCNLSESDCRLDCIELYGGGPAKGYCVGDYCCCNYDCVGDYCSCNYE QEQVCGGPQ66124.027420.27042AaNCR20CL136Contig1MAKLANFFTLVLLLTAISMTMNQQVEGIKCNEMWYDIRCILSESYCREDCIEKHGVLAKGYRMGNKCCCLTV4577.735279.2404noAaNCR20CL136Contig1MAKLANFFTLVLLVTAIMITSHQLVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN5285.096258.06041*AaNCR22CL131Contig1MTELTSKNHFALIILVTAISMRSLHQVVARECIDTWIDRNCENNYIEICKLDCKDYYGESSFAYCVDHHKCKCHYKCPQWPYFN5585.826841.71041*AaNCR23CL50Contig2MTKLTSTNIFALIILFTAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK4984.285918.59042AaNCR24CL217Contig1MTKLTLANIFAIVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL VCYCRY6484.207493.43041AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNFIALVILVTAISINGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT4585.065267.11032AaNCR27CL416Contig1MVKLTLTNFIALFLUTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHQVY	AaNCR18	CL220Contig2	MAKLSNLFALVLLVTAIPMPSHHQVESKKCTDE*YDIRCNLNEGYCRVDCLEVHGGLAKGYCQGDYCFCDYYCPGLLIV	51	8	ND	ND	0	4	2
ANTORIEDCELEBOORNIGEQEQVCGGPQOPPAaNCR20CL136Contig1MAKLANFLTLVLLLTAISMTMNQQVEGIKCNEMWYDIRCILSESYCREDCIEKHGVLAKGYRMGNKCCCLTV4577.735279.2404noAaNCR21CL297Contig1MAKLANFFTLVLLVTAIMITSHQLVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN5285.096258.06042AaNCR22CL181Contig1MTELTSKNHFALIILVTAISMTSLHQVARECIDTWIDRNCEYNYIEICKLDCKDYGESSFAYCVDHKKCKCHYKCPQWPYFN5585.826841.71041*AaNCR23CL50Contig2MTKLTSTNIFALILLFTAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK4984.285918.59042AaNCR24CL217Contig1MTKLTANIFAIVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IVCYCRY6484.207493.43041AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR25CL226Contig1MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNFIALFLLVLTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGERMIDSWIDPKCPLDIEGLIQSAYEMSCRNSCRNKHGGLAMGHCVGSICICFPK5566.876046.19021	AaNCR19	CI 266Contig1	MAKLANFFTLVLLVTAISMTMNQQVEGIKCNEMWYDIRCNLSESDCRLDCIELYGGGPAKGYCVGDYCCCNYDCVGDYCSCNYE	66	12	4 02	7420 27	0	4	2
AaNCR20 CL136Contig1 MAKLANFLTLVLILTAISMTMNQQVEGIKCNEMWYDIRCILSESYCREDCIEKHGVLAKGYRMGNKCCCLTV 45 7 7.73 5279.24 0 4 no AaNCR21 CL297Contig1 MAKLANFFTLVLLVTAIMITSHQVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN 52 8 5.09 6258.06 0 4 2 AaNCR22 CL181Contig1 MTELTSKNHFALIILVTAISMRSLHQVASRECIDTWIDRNCEYNYIEICKLDCKDYYGESSFAYCVDHHKCKCHYKCPQWPYFN 55 8 5.82 6841.71 0 4 1* AaNCR23 CL50Contig2 MTKLTSNIFALIILFTAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK 49 8 4.28 5918.59 0 4 2 AaNCR24 CL217Contig1 MTKLTSNIFALILVTAISITSHHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK 49 8 4.28 5918.59 0 4 1 AaNCR24 CL217Contig1 MTKLTSNIFALIUVIVMLIQSHDGVAGQDDYCEPNSDYLPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IYCYCRY 64 8 4.20 7493.43 0 4 1 AaNCR25 CL226Contig1 MAKLAKFLPIVULVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV 77 10 5.03 8817.89		crzoocontigi	QEQVCGGPQ	00		4.02	7420.27			-
AaNCR21 CL297Contig1 MAKLANFFTLVLLVTAIMITSHQLVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN 52 8 5.09 6258.06 0 4 2 AaNCR22 CL181Contig1 MTELTSKNHFALIILVTAISMRSLHQVVARECIDTWIDRNCEYNYIEICKLDCKDYYGESSFAYCVDHHKCKCHYKCPQWPYFN 55 8 5.82 6841.71 0 4 1* AaNCR23 CL50Contig2 MTKLTSTNIFALIILFTAISMRSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK 49 8 4.28 5918.59 0 4 2 AaNCR24 CL217Contig1 MTKLTLANIFALVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKKVGPTGDGVCIL IYCYCRY 64 8 4.20 7493.43 0 4 1 AaNCR25 CL226Contig1 MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV 77 10 5.03 8817.89 0 4 1 AaNCR26 CL779Contig1 MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC 48 7 4.28 5455.30 0 3 1 AaNCR26 CL3Contig1 MVKLTLTNFIALFLLVLAGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC 48 5.06 5267.11 0	AaNCR20	CL136Contig1	MAKLANFLTLVLLLTAISMTMNQQVEGIKCNEMWYDIRCILSESYCREDCIEKHGVLAKGYRMGNKCCCLTV	45	7	7.73	5279.24	0	4	no
AANCR22CL181Contig1MTELTSKNHFALIILVTAISMRSLHQVVARECIDTWIDRNCEYNVIEICKLDCKDYYGESSFAYCVDHHKCKCHYKCPQWPYFN5585.826841.71041*AANCR23CL50Contig2MTKLTSTNIFALILLFAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK4984.285918.59042AaNCR24CL217Contig1MTKLTLANIFAIVILVIVMIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IYCYCRY6484.207493.43041AaNCR25CL226Contig1MAKLAKLEPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNFIALFLLVLAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK5566.876046.19021	AaNCR21	CL297Contig1	MAKLANFFTLVLLVTAIMITSHQLVEGQWCKNKWLDIRCGLYESYCWEDCSKLHGETAIGFCEDIYCSCYYDCSRNIKN	52	8	5.09	6258.06	0	4	2
AANCR23CL50Contig2MTKLTSTNIFALILLFTAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK4984.285918.59042AaNCR24CL217Contig1MTKLTANIFAIVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IYCYCRY6484.207493.43041AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNIFALVILVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNIFALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK5566.876046.19021	AaNCR22	CL181Contig1	MTELTSKNHFALIILVTAISMRSLHQVVARECIDTWIDRNCEYNYIEICKLDCKDYYGESSFAYCVDHHKCKCHYKCPQWPYFN	55	8	5.82	6841.71	0	4	1*
AaNCR24CL217Contig1MTKLTANIFAIVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL IYCYCRY6484.207493.43041AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNIFALVILVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNIFALFLLVTAISIMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK5566.876046.19021	AaNCR23	CL50Contig2	MTKLTSTNIFALILLFTAISMTSLHQVASNSCWYSWMDKYCEDETCVQSCNDTYKVLIDAFCENIHCFCEYECPNKDK	49	8	4.28	5918.59	0	4	2
AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNFIALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK5566.876046.19021	AaNCR24	CL217Contig1	MTKLTLANIFAIVILVIVMLIQSHDGVAGQDDYCEPNSDYLYPQIANCWEDGLYSWFDLTCPMSNENCKLDCKRKVGPTGDGVCIL	64	8	4.20	7493.43	0	4	1
AaNCR25CL226Contig1MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV DEHCSCNYEQNNGLCVGV77105.038817.89041AaNCR26CL779Contig1MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC4874.285455.30031AaNCR27CL416Contig1MVKLTLTNFIALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIEAFCAGSYCFCKYECT4585.065267.11032AaNCR28CL3Contig1MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK5566.876046.19021			IYCYCRY					-	-	
ANCR26 CL779Contig1 MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC 48 7 4.28 5455.30 0 3 1 AaNCR27 CL416Contig1 MVKLTLTNFIALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT 45 8 5.06 5267.11 0 3 2 AaNCR28 CL3Contig1 MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK 55 6 6.87 6046.19 0 2 1	AaNCR25	CI 226Contig1	MAKLAKFLPIVLLVTAISITSHHQVAGKKLCNHRWFDIRCRNLVDYDNESFCNKDCSDLHGDAVAMFGFCVLDYCSCHYVSPTVPV	77	10	5.03	8817 89	0	4	1
AaNCR26 CL779Contig1 MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC 48 7 4.28 5455.30 0 3 1 AaNCR27 CL416Contig1 MVKLTLTNFIALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT 45 8 5.06 5267.11 0 3 2 AaNCR28 CL3Contig1 MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK 55 6 6.87 6046.19 0 2 1		0122000111.51	DEHCSCNYEQNNGLCVGV		10	5.05	001/105	•	·	-
AaNCR27 CL416Contig1 MVKLTLTNFIALFILVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT 45 8 5.06 5267.11 0 3 2 AaNCR28 CL3Contig1 MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK 55 6 6.87 6046.19 0 2 1	AaNCR26	CL779Contig1	MVKLTLTNLFALVLLVTGMLMRSDVDGVEVTDFWIDWNCRVDEINCMIDCQEKHGITAVGSCIAIICKCVFESNC	48	7	4.28	5455.30	0	3	1
AaNCR28 CL3Contig1 MSMASRHHQVVGLRMID5WIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK 55 6 6.87 6046.19 0 2 1	AaNCR27	CL416Contig1	MVKLTLTNFIALFLLVTAISMGSHQQVASDLCWNSWIIINCKKEDCKKQCSSEYPVIIEAFCAGSYCFCKYECT	45	8	5.06	5267.11	0	3	2
	AaNCR28	CL3Contig1	MSMASRHHQVVGLRMIDSWIDPKCPLDILGLIQSAYEMSCMSSCRNKHGGLAMGHCVGSICICPFDK	55	6	6.87	6046.19	0	2	1
AANCR29 CL491Contig1 MTKLTLANYFVLSLQITVIWMTSNGKKVAGEDCLCNWFDKNCRDGDSKECVKDCRDSHGNMAHGSCAYDLCVCSYSCPNSSPS 56 9 4.74 6286.88 0 2 2 2	AaNCR29	CL491Contig1	MTKLTLANYFVLSLQITVIWMTSNGKKVAGEDCLCNWFDKNCRDGDSKECVKDCRDSHGNMAHGSCAYDLCVCSYSCPNSSPS	56	9	4.74	6286.88	0	2	2
WDK WDK			WDK							
AaNCR30 CL820Contig1 MTNLDLTNFFAILLLVTAISMTSHHHQVVSEVCLDEFDMNCREIDSTICFEDCKYMHGKKTKGVCAFNHCTCMYEC 46 8 4.82 5395.21 0 2 2	AaNCR30	CL820Contig1	MTNLDLTNFFAILLLVTAISMTSHHHQVVSEVCLDEFDMNCREIDSTICFEDCKYMHGKKTKGVCAFNHCTCMYEC	46	8	4.82	5395.21	0	2	2
AaNCR31 CL414Contig1 MAKLNLKTFFAFVLUIAISMTSHHQVAGDVCYEYWADFLCLFGYSRSCSRYCEFAHQGVGATIGYCEDGKCTCSFQC 49 8 4.58 5587.25 0 2 2	AaNCR31	CL414Contig1	MAKLNLKTFFAFVLLIIAISMTSHHQVAGDVCYEYWADFLCLFGYSRSCSRYCEFAHQGVGATIGYCEDGKCTCSFQC	49	8	4.58	5587.25	0	2	2
AaNCR32 CL371Contig1 MAKLTLTNFFVVVLLVSVISMTSDHHQVVGSKCPDEGVDNKYICSSEWVDMNCTTGDSEDCSQECVNNYGIAEGSCAGTKCCCRY 62 10 4.05 6723.35 0 2 2	AaNCR32	CL371Contig1	MAKLTLTNFFVVVLLVSVISMTSDHHQVVGSKCPDEGVDNKYICSSEWVDMNCTTGDSEDCSQECVNNYGIAEGSCAGTKCCCRY YCPGSLE	62	10	4.05	6723.35	0	2	2
AaNCR33 CL310Contig1 MNTLTLANFFAVILSVTAISMTSYHHHQVVSEECLDMFDMNCIEEDSNKNCVEACKYMHAGDNNVDGKCVLDHCYCKYEC 49 8 4.27 5676.35 0 2 2	AaNCR33	CL310Contig1	MNTLTLANFFAVILSVTAISMTSYHHHQVVSEECLDMFDMNCIEEDSNKNCVEACKYMHAGDNNVDGKCVLDHCYCKYEC	49	8	4.27	5676.35	0	2	2

			Mature			Theoretical	Read	d count	
		Sequence	peptide (aa)	Nbr of Cys	pl	MW	Root	Nodule	NCR motif
AaNCR34	CL16Contig4	MARLTLINLLSLVLLITGILITSSDYTVAGYVCIVVWRDPNCGKGDPNYCAQDCKNGYGEKAIPVCRYDVCFCGYECTFPNNGDDYN	66	8	4.77	7557.36	0	2	2
	Cl 2Contig4		10	6	1 62	E 177 19	0	1	1
AaNCR35	CL3COntig4	WARLI WARVALLEV TAMENI STARQVAGIA TO SWIDTSCI TO SIMPONI DE CANAGENERA CONTRACTORISTICA DE CONTRACTORISTIC	48	7	4.03	5422.18	0	1	1
AdivCK30	CL304C0IIIIg1	IN ALL GATE MENTAL VEHICLE VAGEASCEPSDTLEPULARED DE D	58	/	4.05	0070.44	0	1	1
AaNCR37	CL278Contig1	DDVPVDEDCSCNYEQKCTVCWGSLGSCTNIVLPLVVGY	89	13	4.67	10038.41	0	1	2
		MARLTLINFLPLLLLVTGMWMTSQYKVAGSYICYVFWDDPNCKNEDYTNCTOECESKHGKEARPICREEKCFCRFDCDFPFLPTPN							
AaNCR38	CL77Contig1	DDGNYGNNDGI	68	8	4.37	7972.70	0	1	2
A. indica									
AiNCR01	CL27contig1	MTKLTLLNFFTEGLUTAMWMTSHHOVEGEOCIDMWEDEGCRNLDEHKCSEDCKGKHGAIGECADEYCECSYECDNNSPK	51	8	4.41	5875.44	0	21	2
AiNCR02	CL19contig1	MIKLTLTNLFALVLLITAMSMINHGEAAGTGEDSWVDKNCPOENFYCIHSCROKHGOSAMGECGGSECYCYYY	46	6	6.02	5242.79	0	19	1
AINCR03	CL25contig1	MTKETI TNVFALVI I VTVISITSHHOVTGI TAFDSW/DEVCATDNYNCIMSCRNKYGI TGRGNCNDVECVCFYKI I N	48	6	6.06	5563.34	0	17	1
AiNCR04	CL25contig2	MTKETLTNYFALALLYTVISITSHHOVTGITAEDSWYDFYCATDNYNCIMSCRNKYGITGRGNCNDVECVCEYKLLN	48	6	6.06	5563.34	0	8	1
AINCR05	CI 84contig1	MTKI TI KNEETI II SVTAII ITSHHOVASMGEDTWIDIDCPI NNHSCIMNCRTKYGI TASGKCNDVECCCEVYI I N	47	7	5 34	4250.84	0	8	1
AINCR06	CL45contig1		43	6	6.87	4840.44	0	7	1
AINCR07	CI 164contig1	MIKITI INIFALVI I VAVISSHHOVDSI ORYDYW/DINCI/NC/MDCINKHGDTA//GRC//GNI CYCTY	41	6	5.36	4799 50	0	7	- 1
AINCR08	CI 343 contig1	MINI LETKEFAL VI I MTAIISHHOVTGIFIYDYWYDMNCYYNCAIDCYKKHGYTAI GKCYCNI CYCRYNMS	44	7	6 70	5119.02	0	7	
/	0101000111.61	MVELTI VNEFALVU UTDISMTNHHOVAAEVECI NDWW/VDENCEKGVSINCMEDCINKYGDTSNGECCEFYNCYCOYKCPESPDSP			0.70	0110101			
AiNCR09	CL107contig1	NSKDSPIEPHN	67	8	4.13	7838.57	0	7	2
AiNCR10	CL19contig2	MTKLILTNLFTFVLLMTAISMINHGKAASTGFDSWIDKNCPMENFYCIHSCRQKHGQSAMGECGGSFCYCYYY	46	6	6.02	5289.90	0	6	1
AiNCR11	CL150contig1	MTKLILTNFFALALLMTVISIISHHQVTGITAFDSWVDFYCATDNYNCIMSCRNKHGITGMGNCKDVFCVCYYNLLN	48	6	5.36	5528.31	0	6	1
AiNCR12	CL46contig2	MTKLTLTKKFAIILLVTAMSMINHHQVAGATCIEIWTDLRCKLYDGGCWMDCLKKYGDASRGHCQDDYNCFCLYECRPKYLAK	54	8	6.74	6367.34	0	6	1*
AiNCR13	CL176contig1	MIRLILANFITLVLLVTIISITRKHQVVGSGFECWIDLDCPWENHTCIVSCRNKHGLTASGNCYDMFCYCYYTKY	45	7	5.35	5355.06	0	5	1
AiNCR14	CL698contig1	MVKLILTNFFAFILLMAVTSKTIHHQVIGYDCVEDWIDENCEKGDYSTCFFDCVDKHGDIAIGYCEGHNCFCQYGSCTHIKDHIDIGY	59	8	4.25	6795.41	0	5	2
AiNCR15	CL425contig1	MVKLILINFFALFVLLMPVTSKTIHRQVAAYDCVENWIDENCEKGDYSTCFFDCVDKHGDIAMGYCEGHKCFCQYGSCTHTKDHID	59	8	4.49	6814.48	0	5	2
AiNCR16	CL88contig1	MVKLILTNFFALVLLMSVISKTIHYQVTGYDCVENWIDENCEKGDYSTCFFDCVDKHGDIAMGYCEGHKCFCQYGSCTHTKDHIDI	59	8	4.49	6814.48	0	5	2
AiNCR17	CL172Contig1	MTKLVLTNLFALVFLITVISMRTHHQVAGYLGLDDWIDENCTRLFFSDSGCVKDCKHKHGDTGDGYCVDNRCFCSYEIPDSPNYGD	63	6	4.15	7192.72	0	5	1
AiNCR18	CI 286contig1	MSKI TI ANFESIVI I VTVII MITRHOVTSEEII DSWIDINCPMDNENCNWDCVHKHGATANGYCNGNICCCKYEI HS	48	7	4.83	5513 18	0	5	1
AiNCR19	CL615Contig1	MIRI II ANFETPVI I MSAISITGKHOVATI GEATWIDGHCPRENI NCIVNCRSEYGPSAKGMCNDVECECYYTIY	46	6	5.48	5276.03	0	4	1
AiNCR20	CI 848Contig1	MTRI TI INFEIDY I MSAISTISCHOVAGG/GEANWIDI FEPRANEYCMIDERSE/GPSA/GLENDV/FE/C/YTIN	47	6	4 44	5371.13	0	4	1
AiNCR21	CI 521Contig1	MIKITI ANERSI II VAAISMTSOHOVAESGEDKWIDEDCEVTSI NCIADCRERYGAI TRAYCNNVECHCEVTOYY	46	6	5.47	5487 19	0	4	1
AiNCR22	CI 907Contig1	MTRI TI ANFI III II VAAISMTSOHOVI AESGYDKWIDEDCPVTSI NCIADCRERYGAI TRAYCNNYEHCEVTOYY	48	6	5.47	5737.44	0	4	1
AINCR23	CL288Contig1	MTK11 ANEEL VI MTAISMTSOYOVADSGVDKWINI DCEVTTI NCIADCKKRYGPIARAYCSNIVCYCEYSYY	40	6	8.22	5583.40	0	4	1
AiNCR24	CL200Contig1	MTRI II ANEETI VI I MTAISMTSOHEVADSGVDKWIDI VEVTSI NCIAECKKRYGDIABAYCSSNIVCVEVSKY	47	6	8.22	5556 38	0	4	1*
AiNCR25	CI 255Contig1	NI HVI YHENSYI AAIWMASSOHOVYGDVCEDHWEDI GCYSIGEDRACI EDCTKOHGNI ATGECDEDYCICRYECDKCPYPI S	55	9	4.26	6391.05	0	4	2
AINCR26	CL255Contig1		53	8	4.20	6071.00	0	4	1*
AINCR27	CL205Contig1	MIKELETINI FALLYATAN MIKELETINI KAN MIKE	/3	6	6.87	/882.52	0	3	1
	CL43Contig2	MTNKLSLANFVAFMLLVTAISTSSHNPAMGILPCFDYWTDKNCPDNNDNCIQDCKDKYGNSVVGNCNGYYCYCRYACPRYTRME	75	0	5.50	9716.01	0	3	
AINCK28	CL92Contig2	GPHVLVDKVNGVINIDGMQYR	75	8	5.59	8716.81	0	3	2
AiNCR29	CL339Contig1	MASKLTLANFVVFMLLLTAIWTSCHNPAMGSIPCYDYWTDPNCPDDDDDYCIQVCKERYGNSAVGNCNGCYCYCRYSCPRYT	51	9	4.27	5957.55	0	3	2
AiNCR30	CL396Contig1	MSFKLTLANFFSIVLLVTAISMTTHHQVTSEEILDSWIDINCPLDNFNCNWDCVNKHGATANGYCNGNICCCKYFLHS	48	7	4.51	5472.10	0	3	1
AiNCR31	CL295Contig1	MTKLILTNVFALILLVTAISITSHHHVNSIQCFDNWVDIDCINNCMSDCIEKYGFTALGKCVGKTCYCCYESMS	45	8	4.23	5118.90	0	3	1
AiNCR32	CL468Contig1	MNKLNWACIFGFVFVVTAISMTNEVAGEDCLDFWNDPRCKYSNQYICKTNCKTKHGDLAIGSCLDRVCYCAYVC	47	8	6.77	5460.24	0	3	2
AiNCR33	CL45Contig3	MIKLSLTNFLALVLLLTAILMISHHEVACLGSDSWMDINCPGDDSFCNFHCKRKYGSSAWAMCSGSFCRCYH	43	6	6.87	4874.46	0	2	1
AiNCR34	CL831Contig1	MIKLILTNFFALFLLVTAILIISHREVASFGSDSWIDINCPRDNFFCNFNCRRKYGSSAWGICNGNFCHCYY	43	6	7.78	5082.65	0	2	1
AiNCR35	CL909Contig1	MASKLTLANFVVLMLLMTAISTSSHNPAMGSIPCYDYWTDPNCPDDDDVCVQVCQERYGNSAVGNCNGCYCYCRYSCPRYT	51	9	4.04	5943.48	0	2	2
AiNCR36	CL905Contig1	MTRIDFANFFTLILLITIIWMIIQHQVVGTGFECWIDLDCPWENHTCIVSCRNKHGLTASGNCYDMFCYCYYTKY	46	7	5.33	5456.16	0	2	1
AiNCR37	CL941Contig1	MSRLTLINFSAVILLVIVISVRNNHLVAGDLCYEEWVDENCINNGSYYCMRDCKKKYGNTGDGLCALLKCVCLYECPDSRDSPEPRI	58	8	4.50	6693.55	0	2	2

			Mature			Theoretical	Read	count	
		Sequence	peptide (aa)	Nbr of Cys	pl	MW	Root	Nodule	NCR motif
AiNCR38	CL906Contig1	MYISSQQILIFVKNSSHYTS*KNVTSKTIHHQVIGYDCVEDWIDENCKKGDYSTCFFDCVDKHGDIAIGYCEGHNCFCQYGSCTHIKD	59	8	4.46	6794.47	0	2	2
AINCR20	CI 10Contig2		12	6	6.01	1019 56	0	1	1
AINCR39	CL19COntig5	MIRELETING TO VIEW AND	45	7	1.01	4940.00	0	1	1
AINCR40	CL90COntig1	MPITHANPFSIVLEVIAISMITHINGVISEIMEDSWIDINGPNIDNIPUCIWDCVINAIGATANGTCNONICCENTERS	40	6	4.80	5552.22	0	1	1
AINCR41	CL073COntig1	WIGHTEVENTRAFTEVENTSMIRNDAGV VSGINTEDEWIGTSCHORENENDAGVEVELAN	40	6	6.06	5562 24	0	1	1
AINCIAZ	CL259COILig1	PLOADSTISTING VAALAA DSWEDT TOAT DD THOL MORE NOT ON ONE NO VEET RELEW	40	0	0.00	5505.54	0	1	1
AiNCR43	CL92Contig1	HVLEDKVK	63	7	5.42	7402.32	0	1	2
AiNCR44	CL127Contig1	MIPRLVKNYSHSLARNMTILMSSHNSVMVMGSLPCFDYWSNMNCPDDDDDCIQSCTDRYGDSAVGNCNDCYCCCRYVCPRNT	51	10	3.90	5820.35	0	1	2
A. evenia							Ren	narks	
AeNCR01	CL8618Contig1	MTKLNLTNLFAFILLMTAISMTNHGQVTAMECTDHWIDLNCLLDEINCMLDCRSRHGITALGNCMGNICVCYYELRLC	49	8	4.63	5671.64			1
AeNCR02	CL3731Contig1	MIKLTLTNLFTLILLMTVIWMINRVEMAGTGFDSWVDKNCPLENFYCIHSCRQKHGQSAMGECGGSFCYCYY	72	6	6.02	5064.64			1
AeNCR03	CL452Contig1	MTKLTLLNFFTFGLLMTAIWMASNDHQVSGDVCFDHWFDLGCKNGDFDRCLEDCTQQHGNLATGECDEDYCICRYECDKC	50	9	4.13	5833.36			2
AeNCR04	CL8618Contig3	NHGQVTAMECTDHWIDLNCLLDEINCMLDCRSRHGITALGNCMGNICVCYYELRLC	49	8	4.63	5671.64 si	gnal peptic	de truncated	1
AeNCR05	CL22258Contig1	MTKLTLANFSALVLLVAAISMISHHQVASIECIDHWIDINCPMDEINCTIDCKKRHGITAVGTCIGNICKCYYEL	46	7	4.96	5262.14			1
AeNCR06	CL10282Contig2	MSKITLINFLAFILLVTAMSMTSHRQVAAMKCVDHWFDILCPEDEINCMMDCRKKHGFTVVGNCIGIVCVCYCE	49	9	4.96	5202.18			1
AeNCR07	CL3940Contig1	MTKLTLINFFAFALLITAISMTNHHQVTGITAFDSWVDFYCATDNYNCIMSCRNKYGSTGRGNCNDVFCVCFYKL	46	6	6.06	5310.00			1
AeNCR08	CL10282Contig1	MSKITLINFLAFILLVTAMSMTSHRQVAAMKCVDHWFDILCPEDEINCMMDCRKKHGLRSLYDKLSS	38	4	6.00	4561.34			no
AeNCR09	CL295Contig1	MSKLTLANFFSIVLLVTAISMTTHHQVTSEEILDSWIDINCPMDNFNCNWDCVHKHGATANGYCNGNICCCKYFLH	47	7	4.83	5426.10			1
AeNCR10	CL7874Contig1	MVKLSLTNFFRLISLVAAISMTSHHQVSGMIGLDFWIDLECPMYNMSCVMDCKNQHGFTASGYCRDVFCYCYYQV	46	6	4.35	5465.33			1
AeNCR11	CL10838Contig1	MTKLTLSNFLALVLLITVISMTNYHQVATESYDLWIDIGCPLDNLNCKIDCRNKYGLKSSGECIHIFCYCYYDLS	46	6	4.59	5388.13			1
AeNCR12	CL9423Contig2	MTKLILINVFALILLVTVISMTSYHHVDSIQCFDNWVDIDCINNCMSDCIEKYGFTVLGKCVGKTCYCCYE	42	8	4.23	4841.60			1
AeNCR13	CL16157Contig1	MVELTLANFFALVLLVTGISKTNPYQVVGVKVFDFWVDMSCEFGDINCERACRNKYGYTAMGYCSGIFCYCRYE	45	6	5.00	5345.11			1
AeNCR14	CL15608Contig1	LVTAISMTSHHQVAAIFGFDSWIDGNCPSDNLNCNIDCINKHGLTGSGNCNGAICFCYYQL	46	6	4.13	5021.59 si	gnal peptic	de truncated	1
AeNCR15	CL2637Contig2	MTKLVLTNLFVLVFLITAISMTTHHQVAGYLCLDDWIDENCTRLFFSDSGCVKDCKHKHGDTGDGYCVDNRCFCSYE	48	7	4.51	5578.14			1
AeNCR16	CL5370Contig1	KLTLITFFVLFLLVTVISMKNHDKVVSGIMTFDYWIDISCIQSAFSCMTECRLRHGMTAVGSCSDIFCLCHYEL	47	6	4.80	5359.23 si	gnal peptic	de truncated	1
AeNCR17	CL17837Contig1	MTKSNLMNFFALGVLVTAISMTSDHQVAGIKVFNFWIDMNCEVTDIHCIMDCKIKYGKTSVGYCKGIYCCCRYD	45	7	7.72	5324.32			1
AeNCR18	CL10753Contig1	MTKLILTNFLALIVLLTAILMISHHEVASLDFDSWIDINCPMNSSNCKRDCKTKYGSSAWAVCSGSFCHCYY	43	6	6.70	4907.51			1
AeNCR19	CL4882Contig1	MAKLTLTNYFAIILLMTAISMISHHQVAGVTCIEIWTDLRCKLYDGGCWLDCLKKYGGASKGHCQDDYNCFCLYECR	48	8	5.57	5590.43			1*
AeNCR20	CL21671Contig1	MTRLTLANFLILILLLVAAISMTNEHQVLAFSGYDKWIDFDCPVTSLNCIADCRERYGALTRAYCNNVFCHCFY	44	6	5.47	5181.86			1
AeNCR21	CL11599Contig1	MAKIVLTNLFALILLVTVTSMTNHHQIAGIMCTKYWFDRRCKLYDGGCWQDCLTKHGVEARGHCEDDYNCSCQFE	46	7	5.46	5515.19			1*
AeNCR22	CL6083Contig1	MVKLILTNFFALVLLITVTSKTIHHQVAGYDCVENWIDENCEKGDYSTCFFDCVDKHGDIAIGYCEGHKCFCQY	45	7	4.23	5267.78			1
AeNCR23	CL21077Contig1	MTRLTLANFITLVLLVTIISMTSKHQVVGSGFECWIDLDCPWENHTCIVSCRNKHGLTASGNCYDMFCYCYY	43	7	4.80	5049.68			1
AeNCR24	CL5726Contig2	MTRLTLINFFAIIILVTAIWIKNHGQVAGDLCFEEWVDENCINNGSYDCMRDCKNKYGNTGDGLCAVLKCVCLYE	46	7	4.16	5247.90			1
AeNCR25	CL1Contig1190	KLILANFVAFMLLVTAISTSSHNPAMGILPCFDYWTDKNCPDNNDNCIQDCKDRYGNSAVGNCNGYYCYCRY	45	7	4.39	5301.81 si	gnal peptic	de truncated	1
AeNCR26	CL1531Contig1	MIKLTFTSTFIIVLLVTAISMKSHCEVATSEDLARWYDSNCLESDKTCQIECKFRYGITAQGGCCGDFLCCCYFLL	47	8	4.39	5373.11			1
AeNCR27	CL27026Contig1	MARLTLKNFFTLILSVTAILITSHHQVASMGFDTWIDIDCPQNNRGCIMNCRTKYGLTASGKCNDVFCCCFY	43	7	5.84	4908.66			1
AeNCR28	CL1Contig509	VSKLTLTNFVVLMLLMTAISTSSHNPAMGSIPCYDYWTDPNCPDDDDYCIQVCQERYGNSAVGNCNGCYCYCRYS	46	8	3.80	5336.78 si	gnal peptic	de truncated	1
AeNCR29	CL305Contig2	MTRLILANFFTLVLLMTAISMTSQHEVADSGYDKWIDLYCEVTNLNCIADCKKRYGPIARAYCSNIYCYCFYS	44	6	7.50	5190.95			1
AeNCR30	CL8283Contig1	MPKLILTSFFALILLVTAILMISHHVVGLGYDTWIDQNCPWESFYCRLSCRTKHGGKAMGECGGGPFCYCYY	44	6	6.71	5067.73			1
AeNCR31	CL4958Contig1	MIKLILTNFFALFLLVTAMLIISHHEVASFVSDSWMDINCPGDNFFCNFNCRRKYGSSAWGICNGNFCHCYY	43	6	6.70	5043.62			1
AeNCR32	CL1159Contig1	MIKLTLINFFALVLLITDISMTNHHQVTAFYFCLDDWFDENCEKGISIDCMEDCINKYGDTSNGFCEFYNCYCQYK	47	7	3.89	5684.27			1
AeNCR33	CL33734Contig1	MIRLTMVNFFTLVLLLTAISITSQHQVADLGFDQWIDFDCPETSLNCIADCRKRYGALARAYCTNVFCYCFY	43	6	4.78	5056.77			1
AeNCR34	CL10596Contig1	MGQLTLANFFALVLLGIVISMISHHHVAGDLCFEDWVDIYCIYDSNGCMQDCKNKYGKTGEGMCAYYRCLCMYE	45	7	4.24	5345.09			1
AeNCR35	CL7874Contig2	SISMTSHHQVSGMIGLDFWIDLECPMYNMSCVMDCKNQHGFTASGYCRDVFCYCYYQV	46	6	4.35	5465.33 si	gnal peptic	le truncated	1
AeNCR36	CL2051Contig1	MSKLTLAIFVPLVLLVTAILMSSHNSVMVMGSIPCFDYWSNMNCPDDDDNCIQTCKDRYGDSAVGNCNDCYCY	42	7	3.69	4828.20			no
AeNCR37	CL19550Contig1	INFGKLFAIILLVIVISTKNHHLVAGDVCFEEWVDLNCINNDPNYCMRDCKNKYGDTGDGLCAFLKCVCLYE	46	7	4.12	5334.03 si	gnal peptic	de truncated	1
AeNCR38	CL3827Contig2	MIKLSLTNFFALVMLLTAILMMISHHEVACLGSDSWMDINCPGDDSICNFHCKRRYGSSAWAMCSGSFCRCYH	43	6	6.87	4868.45			1
AeNCR39	CL5370Contig2	FAVISMKNHDKVVSGIMTFDYWIDISCIQSAFSCMTECRLRHGMTAVGSCSDIFCLCHYEL	47	6	4.80	5359.23 si	gnal peptic	de truncated	1
AeNCR40	CL305Contig5	MIRLTLEYFFILILLVAAISMTSQHQVLDSGYDKWIDLDCEVTILNCIADCKKRYGPIARAYCSNIYCYCFYS	44	6	5.91	5141.91			1
AeNCR41	CL5247Contig1	MIRLTLANFFTLVLLVSAISTRSQHQVVGHGVGFANWIDLECPRANFYCMIDCKSEYGPSAKGLCNDVFCFCYYTI	47	6	4.83	5366.15			1

			Mature	Nhr of Cur		Theoretical Read count	NCD motif
		Sequence	peptide (aa)	NOT OF CYS	pl	MW Root Nodule	NCR MOUI
AeNCR42	CL9423Contig1	KLNLYFN*YFAVISMTSYHHVDSIQCFDNWVDIDCINNCMSDCIEKYGFTVLGKCVGKTCYCCYE	42	8	4.23	4841.60 stop codon	1
AeNCR43	CL4722Contig2	MTKLTLINFFMFVLLVTAMLMTSYDQVSGEVCFRVWYDLSCYRGNSHRCSMACTNKYGDLAMGRCDRGHCNCRYESEEC	50	8	6.93	5879.59	1
AeNCR44	CL14243Contig1	MTKLTLAYIFVLVYLVTAISMTNEVAGEKCEEFWYEPQCKCPNYNGCMTDCKIKHGDSAKGACDYLDCYCTYD	46	8	4.56	5373.00	1
AeNCR45	CL26264Contig1	MTKLTLAYIFAFVLLVTAISLITEVAGEECLDYWYDRRCRRRNYKGCMRDCKDKYGDSANGFCDFLDCFCSFD	46	7	5.12	5670.31	1
AeNCR46	CL11729Contig1	MTKLTLINFFTFALLVAGILMTSYYHQVSGEVCFHLWSDLNCHKGDSLHCLVACTNKYGDLAKGRCDSDYCNCRYESEKC	50	8	5.80	5734.43	1
AeNCR47	CL6739Contig2	MIKLTLANIFLLTLLMTVISRTSSCEAAHIDGFVRWFDFSCAENDKSCHLECRLRFGATAQGFCEDVFCCCNY	46	7	4.96	5315.97	1
AeNCR48	CL3731Contig2	YFAVIWMINRVEMAGTGFDSWVDKNCPLENFYCIHSCRQKHGQSAMGECGGSFCYCYY	58	6	6.02	5064.64 signal peptide truncate	d 1
AeNCR49	CL13080Contig2	MAKLTSTNFFALTLLISVILMISHHEATEMGFESWIDIDCPVSDFHCKDICGKKYGPTTSAECNEIFCYCYY	45	6	4.28	5213.86	1
AeNCR50	CL682Contig4	MNKLNWACIFGLVFVVTAILMTNEVVGEDCLDFWSDPRCKYSNQYICKTNCKTKHGDLAIGSCLDRVCYCAY	45	7	6.78	5230.94	1
AeNCR51	CL12848Contig1	FTVILITSHHQVDSIQRYDYWVDINCIYNCMIDCINKHGDTALGRCVG	34	4	5.36	3966.55 signal peptide truncate	d no
AeNCR52	CL2051Contig2	MSKLTLAIFVPLVLLVTVMVMGSIPCFDYWSNMNCPDDDDDNCIQTCKDRYGDSAVGNCNDCYCY	42	7	3.69	4828.20	no
AeNCR53	CL4958Contig2	IFYFN*YFTAMLIISHHEVASFVSDSWMDINCPGDNFFCNFNCRRKYGSSAWGICNGNFCHCYY	43	6	6.70	5043.62 stop codon	1
AeNCR54	CL682Contig1	MNKLNWACIFGLVFVVTAISMTSEVAGEDCLDVWYEPHCEFQKSNVCKKNCKSKHGDLANGFCNASDLICY	44	6	5.44	5056.68	no
AeNCR55	CL1Contig16	LFIYT**KDAISTSSHNPAMGSIPCYDYWTDPNCPDDDDYCIQVCQERYGNSAVGNCNGCYCYCRYS	46	8	3.80	5336.78 stop codon	1
AeNCR56	CL10596Contig3	MGQLTLANFFALVLLGIVISMISHHHVAGDLCFEDWVDIYCIYDSNGCMQDCKNN	26	4	3.61	3107.42	no
AeNCR57	CL5726Contig1	LSFN*YFAAIWIKNHGQVAGDLCFEEWVDENCINNGSYDCMRDCKNKYGNTGDGLCAVLKCVCLYE	46	7	4.16	5247.90 stop codon	1
AeNCR58	CL4882Contig4	FAAISMISHHQVAGVTCIEIWTDLRCKLYDGGCWLDCLKKYGGASKGHCQDDYNCFCLYECR	48	8	5.57	5590.43 signal peptide truncate	d 1*
AeNCR59	CL2051Contig4	LINIFAAILMSSHNSVMVMGSIPCFDYWSNMNCPDDDDDNCIQTCKDRYGDSAVGNCNDCYCYCRY	45	8	3.90	5250.70 signal peptide truncate	J 1
AeNCR60	CL2051Contig3	TILMSSHNSVMVMGSIPCFDYWSNMNCPDDDDNCIQTCKDRYGDSAVGNCNDCYCY	42	7	3.69	4828.20 signal peptide truncate	d no
AeNCR61	CL27458Contig1	IFALVLLVTVILMTSNYRVTSTRSFKSWIDVQCPKEDLNCSKNCLENYGPIAWAMCNDIFC	61	5	4.86	4644.32 signal peptide truncate	d no
AeNCR62	CL682Contig3	FLALIFLLTAISMTSEVAGEDCLDVWYEPHCEFQKSNVCKKNCKSKHGDLANGFCNASDLICY	44	6	5.44	5056.68 signal peptide truncate	d no
AeNCR63	CL11599Contig2	NMHVIFHLN*YFAVTSMTNHHQIAGIMCTKYWFDRRCKLYDGGCWQDCLTKHGVEARG	33	4	8.49	3940.56 stop codon	no
AeNCR64	CL12457Contig1	MVKSTLATFFVFILLVTAILMTSHHPVMA GYCVELRPDENCLKEDPPTTCSQYCINKFGYYDTTVICDGDYCYCYYK	48	7	4.24	5657.32	1
AeNCR65	CL7951Contig1	IFALVFLVTAISMTSEATGEDCLHIWYEPQCEFRNHNVCNMNCKTKHGDIAVGVCGDFLCYCAYD	65	7	4.72	6237.01 signal peptide truncate	J 1
AeNCR66	CL24618Contig1	MTKLTLTNIFALVFLVSVISMISDVAGKKCGQSWYDLQCKDPNYNGCTKDCINKYG	29	4	8.45	3373.80	no
AeNCR67	CL19676Contig1	MIKLTLANVFSLIFLVSVISMTSEVVGDQMCQRFWYDLKCKHPNYDGCMMECINTYDYRAYGFCKYPHCVCTY	46	7	6.86	5708.56	1
AeNCR68	CL3827Contig1	ILHFY*YFTAILMMISHHEVACLGSDSWMDINCPGDDSICNFHCKRRYGSSAWAMCSGSFCRCYH	43	6	6.87	4868.45 stop codon	1
AeNCR69	CL10339Contig1	MTKLTLANNFALILLVAVISMTSDVAGDGKCIGKVWYDAQCQYPNYNGCVNDCRDKYGDLFEYGYCRNLYCFCF	47	7	4.86	5615.29	1
AeNCR70	CL4722Contig1	LTKIQTCNL*FEFIFVAMLMTSYDQVSGEVCFRVWYDLSCYRGNSHRCSMACTNKYGDLAMGRCDRGHCNCRYESEEC	50	8	6.93	5879.59 stop codon	1
AeNCR71	CL682Contig2	FVAILMTNEVVGEDCLDFWSDPRCKYSNQYICKTNCKTKHGDLAIGSCLDRVCYCAY	57	7	6.78	5230.94 signal peptide truncate	<u>1</u>
AeNCR72	CL8283Contig3	DTWIDQNCPWESFYCRLSCRTKHGGKAMGECGGGPFCYCYY	41	6	ND	ND signal peptide absent	1*
AeNCR73	CL24495Contig1	LSFN*YFVVISTKNHHLVAGDVCFEEWVDLNCINNDPNYCMRDCKNKYGDTGDGLC	36	5	3.98	4163.58 stop codon	no
AeNCR74	CL1101Contig4	MTKLIVANIFSVVLLVTAILMRSEVVDASSELVYDINCKDPGYNTECMQYCIDKHGYTARGSCLYNNYCYC	44	6	4.83	5073.64	1*
AeNCR75	CL1159Contig4	MIKLTLINFFALVLLITDDWFDENCEKGISIDCMEDCINKYGDTSNGFCEFYNCYCQYK	59	6	3.97	4895.36	1
AeNCR76	CL6739Contig3	FAVISRTSSCEAAHIDGFVRWFDFSCAENDKSCHLECRLRFGATAQGFCEDVFCCCNY	58	8	4.95	4822.45 signal peptide truncate	<u>1</u>
AeNCR77	CL6739Contig1	LKYHVISRTSSCEAAHIDGFVRWFDFSCAENDKSCHLECRLRFGATAQGFCEDVFCCCNY	60	8	4.96	4822.46 signal peptide truncate	<u>1</u>
AeNCR78	CL13080Contig1	YFAVILMISHHEATEMGFESWIDIDCPVSDFHCKDICGKKYGPTTSAECNEIFCYCYY	58	6	4.38	4795.39 signal peptide truncate	1 ل
AeNCR79	CL15279Contig1	IYKFYLNI*FVAISMTSKVDGKECLAVWYEPQCEYPNNNVCMMNCKTNHGYLAGGVCGDIFCYCNYD	67	7	4.50	5277.99 stop codon	1
AeNCR80	CL25922Contig1	FVAISLITEVAGEECLDYWYDRRCRRRNYKGCMRDCKDKYGDSANGFCDFLDCFCSFD	58	7	5.12	5670.31 signal peptide truncate	<u> </u>
AeNCR81	CL11729Contig2	KIQTHNLSF*FIFAGILMTSYYHQVSGEVCFHLWSDLNCHKGDSLHCLVACTNKYGDLAKG	34	4	6.27	3778.31 stop codon	no
AeNCR82	CL1101Contig2	TLLFLFLIEDAAILMRSEVVDASSELVYDINCKDPGYNTECMQYCIDKHGYTARGSCLYNNYCYC	65	6	4.83	5073.64 signal peptide truncate	d 1*

								ORS285 free-living state				Bacteroid A. indica - ORS285				Bacteroid A. afraspera - ORS285	
Gene name	Protein function	Protein mass (Da)	ORS285 free-living state	Bacteroid A. indica ORS285	Bacteroid A. afraspera ORS285	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications	Mascot Protein score	Proteir coverag (%)	Peptide sequences	Peptide modifications	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications
AaNCB15	NCR like	4928	/	/	74 / 32 5									74	32.5	GDGECSGIYCHCB	
AaNCR28	NCR like	8714		/	56/169									56	16.9		2 Oxidation (M)
AaNCR07	NCR like	7928	· /		53 / 31 3									53	31.3		2 Oxidation (in)
AaCI 26Contig2	Extensin-like protein	3497	1	1	56/46.9									56	46.9	NIPISI SI II NVCSB	
ADLOADA10YJ01CM1	putative monosaccharide-H+ symporter	20215	1	52 / 4.3	1					52	4	3 LASSILPR			- ,-		
AiNCR02	NCR like	8521	. /	78 / 25,7 52 / 24,3	/					78 52	25 24	7 HGQSAMGECGGSFCYCYYY 3 HGQSAMGECGGSFCYCYY	Oxidation (M) Oxidation (M)				
AiNCR18	NCR like	9165	/	64 / 21,8	/					64	21	8 HGATANGYCNGNICCCK	Deamidated (NQ)				
AINCR06	NCR like	8471	/	124 / 52,1	L /					124	52	YGSSAWAMCSGSFCR LGSDSWMDINCPGDDSICNFHCK	Oxidation (M) Acetyl (N-term)				
												PMDAHVIEOMIK				AAIPDAQVTIB	
BRAO285v1_1000198	conserved protein of unknown function, BolA-like protein	8661	/	233 / 55	195 / 53,8					233	5	5 VQQHQLVYQSLR GQMGDVLHALALQTGVPDQR	Oxidation (M)	195	53,8	VQQHQLVYQSLR GQMGDVLHALALQTGVPDQR	Oxidation (M)
BRAO285v1_1000199	conserved protein of unknown function	13240	/	56 / 10,7	/					56	10	7 VIADGVIIADTTR					
BRAO285v1_10004	rpsO 30S ribosomal subunit protein S15	10132	/	84 / 18,9	79 / 18,9					84	18	9 AGDTGSPEVQVAILSER		79	18,9	AGDTGSPEVQVAILSER	
BRAO285v1_1080022	conserved protein of unknown function	7973	/	115 / 35,5	5 134 / 35,5					115	35	5 TAAQLAPAPAGAPSPGIK	Oxidation (M)	134	35,5	GVQDFAMTR TAAQLAPAPAGAPSPGIK	Oxidation (M)
BRAO285v1_1080036	ppiB peptidyl prolyl cis-trans isomerase (rotamase B)	16915	53 / 5,2	/	60 / 5,2	53	5,2	AYMAADAA						60	5,2	AYMAADAA	
BRAO285v1_1090009	Cold shock protein, DNA binding	7136	109 / 29,9	396 / 76,1 68 / 29,9	L 52 / 29,9	109	29,9	AGLTTLNEGQTIEYEEIANR		396 68	76 29	DIFVHISAVQK WFNPTKGYGFIQPAAGGK AGLTTLNEGQTIEYEEIANR GLTTLNEGQTIEYEEIANR AGLTTLNEGQTIEYEEIANRGR AGLTTLNEGQTIEYEEIANRGR	Deamidated (NQ) Acetyl (N-term)	52	29,9	AGLTTLNEGQTIEYEEIANR	
BRAO285v1_1200057	nifH nitrogenase iron protein, nifH	32009	/	187 / 16,6	103 / 8,8 190 / 14,8					187	16	CVESGGPEPGVGCAGR 6 AVDESQIGKTAAELAATA VLEYAPESVQANHYR		103 190	8,8 14,8	TAAELAATA CVESGGFERGVGCAGR STAAELAATA AVDESQIGKTAAELAATA VUEVAPESVQANHYR	
BRAO285v1_1200058	nifD nitrogenase molybdenum-iron protein alpha chain, nifD	52328	/	61 / 2,8	54 123 / 2,8					61	2	8 SVIEKQSVAEIKAR		54 123	2,8	SVIEKQSVAEIKAR SVIEKQSVAEIK SVIEKQSVAEIKAR	
BRAO285v1_1200064	conserved protein of unknown function	7484	. /	328 / 77,6 164 / 34,3	5 172 / 34,3 3 363 / 77,6					328 164	77 34	SDLDTLKAEIK SDLDTLKAEIKK AHEAFAELEKKR MILHDLSEELPINWDQILPTAQK GAMDAKMNLHDLSEELPINWDQILPTAQK SDLDTLKAEIK AHEAFAELEKK SDLDTLKAEIKK	Oxidation (M)	172 363	34,3 77,6	SDLDTLKAEIK AHEAFAELEKK SDLDTLKAEIK AHEAFAELEKK SDLDTLKAEIKK AHEAFAELEKK AHEAFAELEKKR MILHDLSEELPINWDQILPTAQK	
BRAO285v1_1200086	conserved protein of unknown function	9454	/	65 / 13,8	/					65	13	8 CDASDVTEAPFR					

Supplemental Table 53. Protein identification by mass spectrometry in ORS285 free-living state and OR5285 bacteroids purified from A. indica or A. afraspera nodules. This table is a compilation of all the protein identification data sets of the different samples and processed by Mascot Distiller (v2.1.1.0) software (Matrix Science). The summary columns (4th to 6th) provide the Mascot protein score followed by the protein identification show the peptide sequences and the detected peptide modifications. NA: not applicable.

						I		ORS285 free-living state				Bacteroid A. indica - ORS285				Bacteroid A. afraspera - ORS285	
			ORS285	Bacteroid	Bacteroid	Mascot	Protein			Mascot	Protein			Mascot	Protein		
Gene name	Protein function	Protein	free-living	A. indica	A. afraspera	Protein	coverage	Peptide	Peptide	Protein	coverag	Peptide	Peptide	Protein	coverage	Peptide	Peptide
		mass (Da)	state	ORS285	ORS285	score	(%)	sequences	modifications	score	(%)	sequences	modifications	score	(%)	sequences	modifications
BRA0285v1_1200089	conserved protein of unknown function	7603	125 / 31	678 / 98,6 229 / 50,7	198 / 45,1 602 / 98,6	125	31	MDNITLHVR FAPDGTVAEISER	Oxidation (M)	678 229	98, 50,	AYQTFAGGR MDNITLHVR DQVEALKATAAA FAPDGTVAEISER AYQTFAGGRGVFK GISEAIGLAYDTFAGGR PATLTPQQWFNKLSEAIGLK FAPDGTVAEISERPATLTPQQWFNK GVFKTTR MDNITLHVR TTRDQVEALK FAPDGTVAEISER	Deamidated (NQ) Oxidation (M) Oxidation (M)	198 602	45, 1 98, 6	MDNITLHVR TTRQQVEALK FAPDGTVAEISER MDNITLHVR TTRDQVEALK FAPDGTVAEISER AYQTFAGGRGVFK PATLTPQQVFNK TTRQVEALKATAAA LSEAIGLKAYQTFAGGR PATLTPQQVFKUSEAIGLK FAPDGTVAEISERPATLTPQQWFNK	Oxidation (M) Deamidated (NQ) Oxidation (M)
BRAO285v1_1200091	conserved protein of unknown function	5597	55 / 17,9	76 / 17,9 108 / 64,3	105 / 64,3	55	17,9	LIEALASMPK	Oxidation (M)	76 108	17, 64,	LIEALASMPK 9 3 LIEALASMPK VDALELVAEOGPGADAEVILOPSI DE	Oxidation (M) Oxidation (M)	105	64,3	LIEALASMPK VDALELVAEQGPGAPAEVILQPSLDE	Oxidation (M)
BRAO285v1_1200098	conserved protein of unknown function	8237	/	262 / 67,9	64 / 11,5 342 / 83,3					262	67,	AMAATDIER GOMGGVUHALALETSLPK EAFPDAVVVIEDLAGDGDHYSAR LIKEAFPDAVVVIEDLAGDGDHYSAR	Oxidation (M)	64 342	11,5 83,3	AMAATDIER AMAATDIER GOMGGVLHALALETSLPK EAFPDAVVVIEDLAGDGDHYSAR VQQHGMVVSALKGQMGGVLHALALETSLPK	Oxidation (M)
BRAO285v1_1200103	nifH nitrogenase iron protein, nifH	31894	/	114 / 10,5	/					114	10,	CVESGGPEPGVGCAGR VLEYAPDSVQAGHYR					
BRAO285v1_1200113	mop putative Molybdenum-pterin binding protein (Mop)	6882	63 / 17,6	235 / 79,4 63 / 17,6	51 / 17,6 155 / 61,6	63		NVLPGKVISVAK		235 63	79, 17,	NVLPGKVISVAK VELAPGLTVFSAITNEAVEELGLAVGDQVSAVIK GATTAHVKVELAPGLTVFSAITNEAVEELGLAVGDQVSAVIK	ς.	51 155	17,6 61,6	NVLPGKVISVAK VELAPGLTVFSAITNEAVEELGLAVGDQVSAVIK GATTAHVKVELAPGLTVFSAITNEAVEELGLAVGDQVSAVIK	
BRAO285v1 1200160	conserved protein of unknown function	6926	72 / 20,6	78 / 20,6	79 / 20,6	72	20,6	GAPSSEAVESLR		78	20,	LGAPSSEAVESLR		79	20,6	LGAPSSEAVESLR	
	putative periplasmic mannitol-binding	40397	83 / 3,9	/	/	83	3,9	SLDTIYGGAEYMAK									
- BRA0285v1 1220119	protein conserved exported protein of unknown	9730	50 / 13 2	1		50	13.2	DEVYVVOGPSHR									
5101020301_1220113	function	5750	507 15,2	,	,		10,2	Service State									
BRAO285v1_130041	thiolase domain (Acetoacetyl-CoA thiolase)	40812	58 / 2,8	/	/	58	2,8	SDDVVIVSAAR									
BRAO285v1_1320032	conserved protein of unknown function	8776	76 / 11,1	/	/	76	11,1	VISPGSYVR									
BRAO285v1_1440053	conserved protein of unknown function	8501	/	99 / 22,5	99 / 22,5					99	22,	SAADPGGGYLCDIDTVAR		99	22,5	SAADPGGGYLCDIDTVAR	
BRA0285v1_1450020	putative glutaminase	68031	49 / 1,1	/	/	49	1,1	I NLAQLLA	Deamidated (NQ)								
BRAO285v1_1460012	function	10997	96 / 20	/	78 / 20	96	20	GAAIGAVIGAGTGAAIAADGER						78	20	GAAIGAVIGAGTGAAIAADGER	
BRAO285v1_1520084	gInA Glutamine synthetase I (Glutamate ammonia ligase I) (GSI)	52612	/	52 / 2,8	/					52	2,	8 AIKDNDVKYVDLR					
BRAO285v1_1580051	putative endoribonuclease L-PSP (protein synthesis inhibitor) (modular protein)	15831	104 / 12,2	/	/	104	12,2	AGTVEQTLAAQGINLPAPK									
BRAO285v1_1640009	putative 50S ribosomal protein L36	4987	/	68 / 21,4	/					68	21,	4 VYVINKVQR					
BRA0285v1_1740028	rpsP 30S ribosomal protein S16	12407	/	55/9	/					55		9 FLDTAGVKKR					
BRAO285v1_190026	conserved protein of unknown function	20668	52 / 4,2	54 / 4,2	63 / 4,2	52	4,2	IASLISPR		54	4,	2 IASLISPR		63	4,2	IASLISPR	
BRAO285v1_1910004	conserved protein of unknown function	7521	51 / 24,6	<u>58 / 4,2</u> 496 / 81,2	374 / 81,2	51	24,6	QITEQAASQSGAADEER		496	81,	LAQQSEELDALLK SLTDPTSLSAADLADR QITEQAASQSGAADEER LAQQSEELDALLKEQER SLTDPTSLSAADLADRIAILR VFDIELAGADKAQAEAALK	Deamidated (NQ)	374	81,2	JASLISFR SLTDPTSLSAADLADR QITEQAASQSCAADEER LAQQSEELDALLKEQER SLTDPTSLSAADLADRIAILR	
BRAO285v1_1910012	conserved protein of unknown function	6797	91/24,2	/	/	91	24,2	EAAFESAAAAATLALK									
BRAO285v1_1950033	50S ribosomal protein L29	7896	/	53 / 23,2	/					53	23,	2 AMSPDQMDDAIVNLKK	2 Oxidation (M)				
BRA0285v1_1950040	rplF 50S ribosomal subunit protein L6	19326	/	/	61 / 5,1									61	5,1	VGQVAAEIR	
BRAO285v1_1950043	rpmD 50S ribosomal subunit protein L30	7114	49 / 17,2	184 / 40,6	116 / 21,9	49	17,2	VTELPDTPAVR		184	40,	VTELPDTPAVR 5 TIKIEQIGSPIR IGRVTELPDTPAVR		116	21,9	VTELPDTPAVR IGRVTELPDTPAVR	

								ORS285 free-living state				Bacteroid A. indica - ORS285				Bacteroid A. afraspera - ORS285	
Gene name	Protein function	Protein mass (Da)	ORS285 free-living state	Bacteroid A. indica ORS285	Bacteroid A. afraspera ORS285	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications
BRAO285v1_2000062	conserved protein of unknown function	6768	336 / 69	69 / 22,4 72 / 22,4	73 / 22,4 67 / 22,4	336	69	TNDLKELVER MTNDLKELVER SFAYGNTNIENER QIEMTPDQLGEQR SFAYGNTNIENERITR	Deamidated (NQ) Oxidation (M)	69 72	22,4 22,4	SFAYGNTNIENER SFAYGNTNIENER		73 67	22,4 22,4	SFAYGNTNIENER SFAYGNTNIENER	
BRA0285v1_200016	putative transcriptional regulatory protein	14806	/	63/9,1	/					63	9,1	SAGKPDIELGKR			25.0		
BRA0285V1_200029	grol 60 kDa chaperonin (Protein Con60)	0115	/	/	55 / 25,9									22	25,9	AAFDEAANMPLKEE	
BRAO285v1_2010015	(groEL protein)	57790	/	/	54 / 2,2									54	2,2	NVVLDKSFGAPR	
BRA0285v1_2020033	cspA Cold shock protein, DNA binding	7526	/	274 / 78,9	397 / 78,9					274	78,5	SMGTVKWFNATK EGQKISYEIVADR AGLGTLREGOKISYEIVADR GYGFIQPDDGGNDVFVHISAVER	Oxidation (M)	397	78,9	SMGTVKWFNATK EGQKISYEIVADR AGIGTUREGQKISYEIVADR GYGFIQPDOGNDVFVHISAVER WFNATGGYGFIQPDOGNDVFVHISAVER SMGTVKWFNATK EGQKISYEIVADR EGQKISYEIVADR GGGIGPDDGGNDVFVHISAVER WFNATKGGFIQPDDGGNDVFVHISAVER	Oxidation (M)
BRAO285v1_2040006	conserved protein of unknown function	7257	/	334 / 80,6	121 / 16,1					334	80,6	LMVKDEIER LRQVTTETLH KLMVKDEIER AIQAHLVELER VLENELHEALVHPSTDDLR	Oxidation (M)	121	16,1	LMVKDEIER KLMVKDEIER	Oxidation (M)
BRAO285v1_2040025	putative transcriptional regulator/antitoxin,	8451	62 / 14,7	95 / 14,7	72 / 14,7	62	14,7	IGNSDGLLLPR		95	14,7	IGNSDGLLLPR		72	14,7	IGNSDGLLLPR	
BRA0285v1 2110001	conserved protein of unknown function	9052	60/11.6	/	/	60	11.6	DONSVSLLLR									
DDA 0205-1 2100017	putative Isomerase/Decarboxylase related		,	,	(7)(/-							<i>с</i> 7			
BRA0285V1_2190017	protein family		/	55 / 6	07/0					22		IAALDPASLPAVSGRPR		67	0	IAALDPASLPAVSGKPR	
BRA0285v1_2480007	cspA Cold shock protein, DNA binding		/	62 / 18,1	/					62	18,1	AMTGTVKFFNGER	Deamidated (NQ)				
BRAO285v1_2570023	putative ABC transporter (substrate-binding protein)	30727	51/3,1	54 / 3,1 60 / 3,1	64 / 3,1	51	3,1	VAVTSLVGP		54 60	3,1 3,1	VAVTSLVGP VAVTSLVGP		64	3,1	VAVTSLVGP	
BRAO285v1_2890040	aldehyde dehydrogenase	50682	52 / 2,7	/	/	52	2,7	AGNVNLQGVPNDR									
BRAO285v1_290022	conserved protein of unknown function		/	153 / 39,4	53 / 22,7 150 / 39,4					153	39,4	LLEILVCPMTK GPLEYDAAKQELVSR	Oxidation (M)	53 150	22,7 39,4	GPLEYDAAKQELVSR LLEILVCPMTK GPLEYDAAKQELVSR	
BRAO285v1_2940016	conserved protein of unknown function	6881	49 / 17,7	/	/	49	17,7	TAEFSEALDRK									
BRAO285v1_2940028	cspA Cold shock protein, DNA binding	7576	/	84 / 28,6	52 / 28,6					84	28,6	AGLTTLNENQAIEYDLVESR		52	28,6	AGLTTLNENQAIEYDLVESR	Deamidated (NQ)
BRAO285v1_2940061	conserved protein of unknown function	10103	125 / 22,2	/	/	125	22,2	VLVDDGTCPAGQVK VLVDDGTCPAGQVKEVLGSK									
BRAO285v1_2940101	conserved protein of unknown function	6698	147 / 55,7	/	/	147	55,7	QMLEMHGPAAIAQASQK AI SCESDGESEEAREWR	Oxidation (M)								
BRAO285v1_2960006	conserved exported protein of unknown function	10525	201 / 41,8	/	/	201	41,8	QFVESGDDTIK VVLDLSTMSCK FGTYCAEHPTVSIVTAAEK	Oxidation (M)								
BRA0285v1_2960016	protein of unknown function	9215	56 / 13,3	/	/	56	13,3	MFGYNDVATGR	Oxidation (M)								
BRA0285v1_2980014 BRA0285v1_210002	conserved protein of unknown function	15535	/5/9,9	/ 55/26	55/26	75	9,9	LGGYVIGVTEDQLR		55	24	MRPATRASR		50	26	MRPATRASR	
BRA0285v1_340006	conserved protein of unknown function	18871	/ 70 / 8,4	/ /	/ 2,0	70	8.4	LQMHLQETNQQLQR	Oxidation (M)		2,0				∠,0	init i contain	
	conserved exported protein of unknown	22000	,	,	104 / 9.2		.,.							104		AADDAQDKDVDPVAR	Deamidated (NQ)
BRA0285v1_340020	function conserved protein of unknown function	7016	/	/ 88 / 18,2 74 / 18,2	71 / 18,2					88 74	18,2	ALALGIGLGHQR		71	18,2	MKAADDAQDKDVDPVAR ALALGIGLGHQR	Oxidation (M)
BRA0285v1 520001	conserved protein of unknown function	16055	69/62	/	/	60	6.2	EETAOGLONR				ALALGIGLGHQR					
BRA0285v1_550007	putative phosphoribosylformylglycinamidine synthetase, PurS component	8255	51 / 13,6	/ 424 / 93,8	/ 298 / 64,2	51	13,6	SLGVDGVASVR		424	93,8	SLGVDGVASVR SLGVDGVASVRQGK AIEGALKSLGVDGVASVR VFDIELAGADKAQEAALK AAADKLLANTVIENYRVELLG		298	64,2	SLGVDGVASVR VTVTLKTGILDPQGK AIEGALKSLGVDGVASVR VFDIELAGADKAQAEAALK TGILPQGKAAEGALKSLGVDGVASVR	

		I			1	1		ORS285 free-living state					Bacteroid A. indica - ORS285				Bacteroid A. afraspera - ORS285	
Gene name	Protein function	Protein mass (Da)	ORS285 free-living state	Bacteroid A. indica ORS285	Bacteroid A. afraspera ORS285	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications	Mascot Protein score	Prote cover (%	ein rage 5)	Peptide sequences	Peptide modifications	Mascot Protein score	Protein coverage (%)	Peptide sequences	Peptide modifications
BRAO285v1_620078	HupA DNA-binding protein HU	10989	/	53 / 9,9	/					53		9,9 IA	ATTTELSKR					
BRAO285v1_620141	conserved protein of unknown function, putative SUF system FeS cluster assembly associated domain	13495	54 / 5,6	/	/	54	5,6	5 LSGEIIA	Acetyl (N-term)									
BRAO285v1_650005	conserved protein of unknown function, putative CsbD-like domain	7066	961 / 97,2	736 / 97,2 181 / 48,6	: 59 / 23,6 ; 341 / 79,2	961	97,2	QGIGEATGNDR DAVNTAAGAANKNL LQGEGAVQEVKGK MDKIKGATNEAVGK GKGQQALGDAKQATK QATKDAVNTAAGAANK STMDKIKGATNEAVGK GSTMDKIKGATNEAVGK QGIGEATGNDRLQGEGAVQEVK QGIGEATGNDRLQGEGAVQEVK AKQGIGEATGNDRLQGEGAVQEVK	Gin->pyro-Glu (N-term Q) Deamidated (NQ) Oxidation (M)	736 181		100 0, 0, 97,2 0, 48,6 6, 0, 48,6 6, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,	QEEGAVQEVK AVNTAAGAANKNL SEEGAVQEVKGK STMDKIKGATNEAVGK ATKDAVNTAAGAANKNL GIGEATGNDRLQEEGAVQEVK QQALGDAXQATKDAVNTAAGAANK GIGEATGNDRLQGEGAVQEVKGK KQGIGEATGNDRLQGEGAVQEVKK ATKDAVNTAAGAANKK STMDKIKGATNEAVGK	Gin->pyro-Glu (N-term Q) Oxidation (M) Gin->pyro-Glu (N-term Q) Oxidation (M)	59 341	23,I 79,2	GSTMDKIKGATNEAVGK QATKDAVNTAAGAANK GSTMDKIKGATNEAVGK QATKDAVNTAAGAANKNL QGIGEATGNDRLQGEGAVQEVK	Oxidation (M) Gln->pyro-Glu (N-term Q) Oxidation (M)
BRAO285v1_680003	Putative 4-oxalocrotonate tautomerase	7471	75 / 16,2	282 / 66,2 68 / 16,2	56 / 16,2 213 / 58,8	75	16,2	2 PEITINMAAGR	Oxidation (M)	282 68		PE 66,2 AL 16,2 DI PE	ETIINMAAGR ETIINMAAGRTEEQK LYTHLGVDPEAVVIQINEAPLTHK ISKALVTHLGVDPEAVVIQINEAPLTHK ETIINMAAGR	Oxidation (M) Oxidation (M)	56 213	16,: 58,i	PEITINMAAGR PEITINMAAGR AU/THLGVDPEAVVIQINEAPLTHK DISKALVTHLGVDPEAVVIQINEAPLTHK	Oxidation (M) Oxidation (M)
BRAO285v1_70003	conserved protein of unknown function	7015	/	67 / 19,7	/					67		19,7 Q	GTHGTSVPGVCR	GIn->pyro-Glu (N-term Q)				
BRAO285v1_710015	conserved protein of unknown function	8193	/	114 / 41,9	/					114		41,9 TI LS	TLLEQALQQVQR SADDQNAAAGALLDYVK					
BRAO285v1_720027	conserved protein of unknown function	7400	50 / 15,9	/	/	50	15,9	FAMATPDNVLR	Oxidation (M)									
BRAO285v1_80019 BRAO285v1_860016	rpmA 50S ribosomal subunit protein L27 conserved protein of unknown function	9587 6431	/ 72 / 21,7	55 / 10 121 / 53,3	/	72	21,7	AEPLDDYIDAVGR		55 121	!	10 VI 53,3 AE LV	IPGNIIAR EPLDDYIDAVGR VDEFSLADEAEPASVFTA		119	46,3	AEPLDDYIDAVGR ALSLPIEDSWRPAVR	
BRAO285v1_920004	thiS thiamine biosynthesis protein ThiS	7043	50 / 16,7	/	/	50	16,7	7 AGDEIEIITPR										
BRAO285v1_930001	putative ABC transporter, substrate-binding protein	44067	51/2,4	57 / 2,4	51 / 2,4	51	2,4	ASSPATASRR		57		2,4 AS	SSPATASRR		51	2,4	ASSPATASRR	Acetyl (N-term)
BRAO285v1_950060	pufB Light harvesting 1 beta subunit	8195	51/17,1	/	/	51	17,1	L GGSLSGLTESEAR										
BRAO285v1_950109	conserved protein of unknown function	7161	/	59 / 20 54 / 16,9	/					59 54		20 GI 16,9 PL	IVTYQTLTSPLR					
BRAO285v1_950136	bfr bacterioferritin (iron storage homoprotein)	18953	/	52 / 11,1	/					52	:	11,1 IG	GLELYTQKHVGGLESEH					
BRAO285v1_990037	Putative ABC-type RTX toxin transporter, ATPase and permease components	80711	52 / 1,2	52 / 1,2 58 / 1,2	52 / 1,2 52 / 1,2	52	1,2	2 ASSPAIRRA	Acetyl (N-term)	52 58		1,2 1,2 1,2 AS	SSPAIRRA	Acetyl (N-term) Acetyl (N-term)	52 52	1,1 1,1	ASSPAIRRA	Acetyl (N-term) Acetyl (N-term)
back to table 1																		

tills study.			
Species	Accession	Origin	Inoculated strain
A. indica	LSTM n°19	Senegal	ORS285
A. evenia ssp.serrulata	PI 572567	USA	ORS285
A. evenia ssp. evenia	PI 225551	Zambia	ORS285
A. virginica	LSTM n°63	USA	ORS285
A. scabra	PI 296044	Mexique	ORS285
A. sensitiva	LSTM n°28	Senegal	ORS285
A. afraspera	LSTM n° 1	Senegal	ORS285
A. aspera	IRRI 013020	Sri Lanka	ORS285
A. nilotica	IRRI 014040	Senegal	ORS285
A. americana	PI 544122	USA	ORS301
A. pfundii	LSTM n°54	Zimbabwe	ORS302
A. schimperi	IRRI 012156	Senegal	ORS305

Supplemental Table S4 : Accessions and origin of *Aeschynomene* species used in this study.

Gene	Forward primer	Reverse primer	Use
EFlα	AATGGTGATGCTGGTATGGTTAAG	TCTTCTTCTGTGCTGCCTTGG	RTqPCR
AeDNF1	TCTGCTCACCTTCGCCATAACC	ACCTCGTCATTGCCGTTGGG	RTqPCR
AeDNF1	CACCAGGTCAGATAGCGGTGTAAG	CAGAATGGTTATGGCGAAGG	RNAi
AaNCR	AAATTATTAGTTAAGATTCTCAC	ATCAAATGGGCATATACAAATG	ISH probe
AiNCR	TTGTCCACAGGAAAACTTCTATTG	GCTACCGCCACACTCTCC	ISH probe
Aa/AiLegHb	TGGTGAACTCATGGAATGTATTG	GAGATGGACAGAGCCTAAGTG	ISH probe
AaLegHb	CTCTTGTGGTGAACTCATGGAATG	AATGGTGGCATGTGTCTTGAG	RTqPCR
AaNCR1	CAATGGCAAGTCATCATCTTCAAG	${\it ATTTCATCTAACGGGCACTTTGG}$	RTqPCR
AaNCR2	ACAAGTCATCATCAAGTGGCAGAG	CAGGAACAGTCTTCACCATCAGG	RTqPCR
AaNCR4	ACTTATCTTGCTGGTGACAGTTATG	ATTTCATCTAACGGGCACTTTGG	RTqPCR
AaNCR6	GTATGGGCGGACACGAACTG	GGACTTGGGATATTGGGAGCAC	RTqPCR
AiLegHb	TAGGAGCCACCCATTTCAAATATG	CCCTTCATCTCTGCTGACCAC	RTqPCR
AiNCR1	CAGACAACATTTGCTACAAAGATG	AACCCTCGTCAAACCACATATC	RTqPCR
AiNCR2	TTGTCCACAGGAAAACTTCTATTG	GCTACCGCCACACTCTCC	RTqPCR
AiNCR3	CATCATCAAGTGACTGGCATAACG	AGCCTAACGCAAACTCCAAGC	RTqPCR
AiNCR5	GCCTCGGGAAAGTGTAACAA	TCTCTTGGACATTGCCATCA	RTqPCR

Supplemental Table S5: List of primer pairs used in this study and their utilization. The same primer pair designed for $EFI\alpha$ was used for the 3 *Aeschynomene* species.

Supplemental material and methods:

Proteins in the range of ~4-9 kDa (indicated with dashed line in Supplemental Figure S2) from freeliving bacteria and bacteroid extracts were cut out from Tricine SDS-PAGE gels gels and destained with 500 μ L of 25 mM NH₄HCO₃ then twice with 50 % acetonitrile in 25 mM NH₄HCO₃ before being dried in a vacuum centrifuge system. Fifteen microliters of a trypsin solution (Sequencing Grade Modified Trypsin, Promega, Madison, USA) at a concentration of 0.0125 μ g/ μ L in 25 mM NH₄HCO₃, was added to every gel slice which were kept for 15 min on ice. Ninety microliters of 25 mM NH₄HCO₃ were added, and the samples were kept another 15 min at room temperature. Digestion was performed overnight at 37°C then peptides were extracted twice by addition of 100 μ L of 80 % acetonitrile in water containing 2 % formic acid. Peptides were then dried in a vacuum centrifuge before being suspended in 10 μ l formic acid 2 % for LC-MS/MS analysis.

The protein digests were analyzed using a Q-TOF mass spectrometer (Maxis Impact; Bruker Daltonik GmbH, Bremen, Germany), interfaced with a nano-HPLC U3000 system (Thermo Scientific, Waltham, USA). Samples were concentrated with a pre-column (Thermo Scientific, C18 PepMap100, 300 μ m × 5 mm, 5 μ m, 100 A) at a flow rate of 20 μ L/min using 0.1% formic acid. After pre-concentration, peptides were separated with a reversed-phase capillary column (Thermo Scientific, C18 PepMap100, 75 μ m × 250 mm, 3 μ m, 100 A) at a flow rate of 0.3 μ L/min using a two steps gradient (8 % to 28 % acetonitrile in 40 min then 28 % to 42 % in 10 min), and eluted directly into the mass spectrometer. Proteins were identified by MS/MS by information-dependent acquisition of fragmentation spectra of multiple charged peptides. MS/MS raw data were analysed using Data Analysis software (Bruker Daltonik GmbH, Bremen, Germany) to generate the peak lists.

Protein identifications were obtained by searching locally with Mascot (v.2.4.0, Matrix Science) against a home-made nucleotide database (215376 sequences). This database was composed of A. afraspera and A. indica sequences from ESTtik databases (www.esttik.cirad.fr). All the NCRs were extracted from these libraries and their signal peptide sequences were manually removed. The following parameters were used: semi-trypsin as enzyme, two missed cleavage sites were allowed, carbamidomethylation of Cysteine as fixed modification and Acetyl (N-term), deamidated (NQ), Gln->pyro-Glu (N-term Q), Glu->pyro-Glu (N-term E), Oxidation (M), Phosphorylation (ST) and Phosphorylation (Y) were allowed as variable modifications. Mass tolerance was set to 30 ppm on full scans and 0.05 Da for fragment ions. Proteins were validated when at least one peptide with a p value <0.05 was identified. In addition, for all protein identified with only one peptide, MS/MS spectra were carefully checked manually for validation.

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