

Supplementary Information

Table S1. Primer sequences used in the research.

Gene	Sequence (5' → 3')		purpose
	Forward	Reverse	
sNPF	ACCTCAGCTCCCTCGTAT	ACTCCTTGCGGAAGTTGTCG	cDNA
	ACAACGCAATGAAAGTATTCTCTCT	AATCGGTTATCACACAGTTTCAAG	3'RACE
	TCGCCAGAATACGAGGGAGC	TAATTGTGGTGACCGTCCAG	5' RACE
	AACAACGCAATGAAAGTATTCTCTC	GGGATACGTTTAGTTGTCGTTAGTG	Full-length
	TTCAACTCTTAACACCCAGTCTTCG	TGAATAAGCATGTCAATCAGTTCTC	qPCR
	TAATACGACTCACTATAGGGTCAGCCCCCTCTTA	TAATACGACTCACTATAGGGGTGATGT	RNAi
	TTCTGG	CATTCAAGCCGGT	
sNPFR	ACGAATCGCATGCTGATCG	TCCTTGCGGAAGTTGTCG	cDNA
	GGCGGTGTTTCTCATCTCCT	TGGCTTAACGACAACCTCCG	3'RACE
	GTGAAGGGCACAGCCAATAC	CATCAAGGTAAGCGTGGA	5' RACE
	GCTGACCGAAGCAATCAACGTGACC	GAACTAGGGGTAGTCTTGTGGATGT	Full-length
	AGCAGTGGTATCAACGCAGAG	GCATTCATTGGCATCATCAG	qPCR
	TAATACGACTCACTATAGGGACATTTCCACGCTT	TAATACGACTCACTATAGGGTCCCTAT	RNAi
	ACCTTG	CCGCTTCCTCTTT	
GFP	TAATACGACTCACTATAGGGATGGTGTTCATGC	TAATACGACTCACTATAGGGCTCTCTT	RNAi
	TTTTCA	TTCGTTGGGGTCT	

At_sNPFR	MDVNGTNTLTANRELYQGKSLIIINNELVQIIFFMIYTAIFILGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGS	99
Ag_sNPFR	MNNTTPVKMASAVSNDDTNENIINDNTVQVVFHMVYTIIFVLGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGR	99
Ld_sNPFRMNSFSNNTTVENIINENI.VQVAFHMVYTIIFVLGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGR	91
Dv_sNPFRMAGAVSNNTTSEIINDNTVQVAFHMVYTIIFVLGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGR	91
So_sNPFRMPVVDGI NVTTVHKLIIDKKG.VQVLFLLIAYTIIFVVGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGS	94
Rf_sNPFRMPVVDGI NVTTVHKLIIDKKG.VQVLFLLIAYTIIFVVGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGN	94
Dp_sNPFRNSLTDGI NVTTAAQQLIINDKKG.VQVLFHVIYTIIFVVGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGG	94
Da_sNPFRNSLTDGI NVTTTPQQLIINDKGGVQVLFHVIYTIIFVVGIGGNVLVCYVVFERNKACTVTNLFITNLALSDI	LLCVLAVPFTPLYTLGKVI	FGG	95
At_sNPFR	IIICHVVPAAQGSVYI STLTLSIAIDRFVII YPFHPRMKLSTCVIIIIIIIVLFSLLVTPYGIYMRQAKGI ANSSTYQEENLFCBEDVPSDRVRKLF			199
Ag_sNPFR	IIICHVVSAAQGISVYI STLTLSIAIDRFVII YPFHPRMKLSTCIIIIIIIVLFSMLVTPYGVYMRHTT.ENTSEI AI EKYFCLENVPSEBVRRTFG			197
Ld_sNPFR	IIICHVVSAAQGISVYI STLTLSIAIDRFVII YPFHPRMKLSTCIIIIIIIVLFSMLVTPYGVYMRK.TESYTDKFCBETVPSEBVRRTFG			185
Dv_sNPFR	IIICHVVSAAQGISVYI STLTLSIAIDRFVII YPFHPRMKLSTCIIIIIIIVLFSMLVTPYGVYMRKLT.PAEKNAEYFCBENVPSEBVRRTFG			186
So_sNPFR	IIICHVVPAAQGSVYI STLTLSIAIDRFVII YPFHPRMKLSTCVIIIIIIIVLFSLLVTPYGIYMRK.DPNNI TRYCEBDEVPVEQVRAAFG			189
Rf_sNPFR	IIICHVVPAAQGSVYI STLTLSIAIDRFVII YPFHPRMKLSTCVIIIIIIIVLFSLLVTPYGIYMRK.DPNHETRYCEBDEVPVEQVRAAFG			189
Dp_sNPFR	IIICHVVPAAQGSVYI STLTLSIAIDRFVII YPFHPRMKLSTCVIIIIIIIVLFSLLVTPYGIYMRHME.DPSNI SRFFCEBDEVPVEQVRAAFG			189
Da_sNPFR	IIICHVVPAAQGSVYI STLTLSIAIDRFVII YPFHPRMKLSTCVIIIIIIIVLFSLLVTPYGIYMRHME.DPGNI TRFFCEBDEVPVEQVRAAFG			190
At_sNPFR	GIITTLQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFN. DLIIVKVIYLSFSLV	TAIA	298
Ag_sNPFR	GIITTLQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFYQQNEHVVDNYLTFFFT	TAIA	297
Ld_sNPFR	GIITTLQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFYQLQDQVAFYLTFFFT	TAIA	285
Dv_sNPFR	GIITTLQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFCQQNEKVNFYLTFFFT	TAIA	286
So_sNPFR	VITAAALQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFNKENI AVVEYFSLFSLV	QMA	289
Rf_sNPFR	VITAAALQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFNKDNI SVVEYFSLFSLV	QMA	289
Dp_sNPFR	VITAAALQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFNTDNI KVEYFSLFSLV	QMA	289
Da_sNPFR	VITAAALQFIIIPFLIYAGCYII CVSI KLNDRARPKGSKNSRKEEADREKRTNRMLI	SVAVFLMSVLP LNIIINDFNTDNI KVEYFSLFSLV	QMA	290
At_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFG. ANR.VVNNAGRLGNVSERTCNGN.ITQESLLP. SQIHRASIVKRNKTI PPPPKTDSVE			386
Ag_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFG. PTG.RVPSACRFENVSERTCNGN.ETQESLLPSSQIHRASIRERKLI PPPPKTDSVE			386
Ld_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFGSAG.RLPSACRFENVSERTCNGN.ETQESLLPSSQIHRASIRERKLI PPPPKTDSVE			376
Dv_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFG. ASR.RVF. ACRFENVSERTCNGN.ETQESLLPSSQIHRASIRERKLI PPPPKTDSVE			375
So_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFGASITKYSNRKVPSNSRFTNVSERTCN.GNETQETLLS. SQIHRASIRERKLI PPPPKTDSVE			383
Rf_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFGASIVR.VPSNSRFTNVSERTCNGNEAYGNETQETLLS. SQIHRASIRERKLI PPPPKTDSVE			383
Dp_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFGASGRR.APSTCRFTNVSERTCNGNETLAI NETQESLLP. SQIHRGSSFRERKLI PPPPKTDSVE			383
Da_sNPFR	MSSTCYNPFYAWLNENFRKEFKQVLPCEFGASGRR.APSTCRFTNVSERTCNGNETFAI NETQESLLP. SQIHRGSSFRERKLI PPPPKTDSVE			384
At_sNPFR	MENVLPVNI G.VVYDSLETSVRLRYI SEBEPPIYDTQQ.			424
Ag_sNPFR	MENVLPVSI G.VVYDSASDI VRLKLI TEBEPPIYEAAPRKDEE.			428
Ld_sNPFR	MENVLPVAVG.VVYDSASDI VRLKLI TEBEPPIYEAAPRKDEE.			418
Dv_sNPFR	MENVLPVSNA.VVYDSASDI VRLKLI TEBEPPIYEAAPKAVSE.			418
So_sNPFR	MENVLPNMGV.BYDSALEVVKLNLI TEBEPPIYNEGRMSE.			425
Rf_sNPFR	MENVLPNMGVBYDSALEVVKLNLI TEBEPPIYNDTKSSSE.			427
Dp_sNPFR	IENVLPNSTV.BYDSNLEVVKLNLI TEBEPPIYSEI HKTTTPSSD			427
Da_sNPFR	MENVLPNSTV.BYDSNLEVVKLNLI TEBEPPIYSDI HKTTTPSSD			428

Figure S1. Comparison of the amino acid sequence of *D. arandi* sNPFR with those of other species. They include *Dendroctonus ponderosae* (Dp sNPFR, XP_019761868.1), *Rhynchophorus ferrugineus* (Rf sNPFR, QGA72517.1), *Sitophilus oryzae* (So sNPFR, XP_030746843.1), *Diabrotica virgifera virgifera* (Dv sNPFR, XP_028151444.1), *Leptinotarsa decemlineata* (Ld sNPFR, XP_023019356.1), *Anoplophora glabripennis* (Ag sNPFR, XP_018571523.1), *Aethina tumida* (At sNPFR, XP_019867538.1). The predicted seven transmembrane domains are underlined by a solid line. Identical amino acid residues in all proteins are shown in black, grey parts indicate similar amino acids.

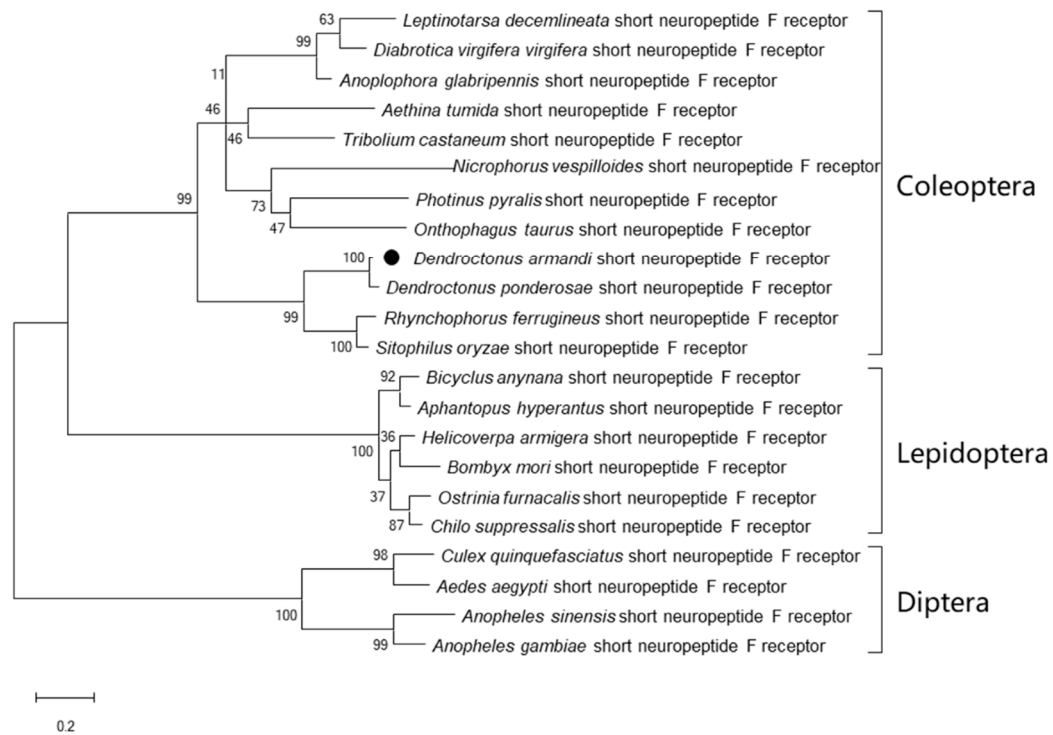


Figure S2. Phylogenetic trees based on amino acid sequences of sNPFR from other insect species. They include *Leptinotarsa decemlineata* (XP_023019356.1), *Diabrotica virgifera virgifera* (XP_028151444.1), *Anoplophora glabripennis* (XP_018571523.1), *Aethina tumida* (XP_019867538.1), *Tribolium castaneum* (XP_015833194.1), *Nicrophorus vespilloides* (XP_017779804.1), *Photinus pyralis* (XP_031348170.1), *Onthophagus taurus* (XP_022909330.1), *Dendroctonus ponderosae* (XP_019761868.1), *Rhynchophorus ferrugineus* (QGA72517.1), *Sitophilus oryzae* (XP_030746843.1), *Bicyclus anynana* (XP_023934255.1), *Aphantopus hyperantus* (XP_034831358.1), *Helicoverpa armigera* (XP_021184191.1), *Bombyx mori* (ALP48446.1), *Ostrinia furnacalis* (XP_028173698.1), *Chilo suppressalis* (ALM88307.1), *Culex quinquefasciatus* (AVR59280.1), *Aedes aegypti* (XP_021705044.1), *Anopheles sinensis* (KFB49968.1), *Anopheles gambiae* (ABD96049.1). The phylogenetic tree constructed by the Maximum Likelihood method using the amino acid substitution model WAG++G+I+F122 in MEGA 6.0. Bootstrap values after 500 pseudo-replicates are shown at nodes. The bootstrap values (in %) are given at each branch point. The black dot indicates *D. armandi* sNPFR.