

INVERTEBRATE ORTHOLOGS OF THE HUMAN SDR FAMILY VARIANTS

SDR7C1	H. sapiens	-----MV-EL--MFPLL--L		
SDR7C2	H. sapiens	-----MLVTLGLL		
SDR7C3	H. sapiens	-----MSRYLLP		
SDR7C4	H. sapiens	-----MAVATA-----AAVL-A---ALGGALW		
SDR7C5	H. sapiens	-----ME-----ALLLGAGLL		
SDR40C1	H. sapiens	-----MSLYRSVVW		
SDR7-1C1	C. intestinalis	MSTFVANPPSSHIFESLVPYYAEALLGAQNN---NTAGE---EISHPNG--HSVTNGVW		
SDR7-1C2	C. intestinalis	-----		
SDR7-3C2	C. intestinalis	-----MSIYQKTAF		
SDR7-3C3	C. intestinalis	-----MSRFRVIVW		
SDR7-3C4	C. intestinalis	-----MQARYRL		
SDR7-1C1	S. purpuratus	-----		
SDR7-1C3	S. purpuratus	-----MDIVNRI--FHPRYTLP		
SDR7-2C2	S. purpuratus	-----MISLSTLS-----LERVPDFGQRGPGDLEW		
SDR7-1C3	M. domestica	-----MEGLFSF--LRSRPVFW		
SDR7-1C1	B. malayi	-----MIEFSESSMTSDE-----GY--FG-----SLS		
SDR7-1C2	A. californica	-----MRPEQHAKM--AA-EMKQRLKVEELENIDELEDV--VEDVFPI--LIL--TVF		
SDR7-1C3	A. californica	-----MTLQEYSLPVSVVGTVALAVFFnf--LDF---V	1p.1	
x x x				
SDR7C1	H. sapiens	LLLPFL-LY-MAAPQIr ^k MLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKELAQrgARV	1p.1	2p.2
SDR7C2	H. sapiens	TSFFSF-LY-MVAPSIr ^k FFAGGVCRTNVQLPGKVVVITGANTGIGKETARELASrgARV	1p.1	2p.2
SDR7C3	H. sapiens	LSALGT-VA-GAVALLkdYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARrgGNI	1p.1	2p.2
SDR7C4	H. sapiens	LAARRF-----VGPRVQRLRRG---GDPGLMHGKTVLITGANSGLGRATAAELLRLGARV		
SDR7C5	H. sapiens	LG-----AYVLVYYNLVKAPPCGGMGNLGRGTAVVtgANSGIGKMTALELARRGARV		1p.2
SDR40C1	H. sapiens	FAKGLR--EYTksGYESACKDFVPHDLEVQIPGRVFLVTGGNSGIGKATALEIAKrgGTV	1p.1	2p.2
SDR7-1C1	C. intestinalis	VLLVGTLLW--SYILLVILAKKPKCDCTARLDGKTVVItgatDGVGKATAFELASRGAEI		1p.2
SDR7-1C2	C. intestinalis	-----MKSVRNGWVRSDISMVGKNIITGANAGIGFITTRDLVKRGGRV		
SDR7-3C2	C. intestinalis	FIKGR--QFTngGYAKAAKSFHPEDTKKDVSDQVFMVTGANSGLGKAAAIAIAKNGGEV	1p.1	
SDR7-3C3	C. intestinalis	SSLICA---VAYLWIVFIKRGPICVSNKRLDGKTVLItggNTGVGEATVFEVAKLGARI		1p.2
SDR7-3C4	C. intestinalis	SGFVGS-LS-----KMVKSARGSWVRSDVKMTGKTVVITGANTGIGLETAIDLVKREARV		
SDR7-1C1	S. purpuratus	-----MDGKTVIITGCNTGIGKETAKDLAKrgARV		1p.2
SDR7-1C3	S. purpuratus	FTTFGA-LV-GGTLLLkdYGGDKCPCSTARVDGKTVIITGANSGIGKETALELAKrgGKI	1p.1	2p.2
SDR7-2C2	S. purpuratus	TTIALMMVVLVGLYYYYVVKVADRCSCKPRLDGKTVIVtgANTGIGKETARDLARRGARV		1p.2
SDR7-1C3	M. domestica	TSVAGT-TVGVAC-FVkdMMQGGKFTKPTRADGKVIIVTGSNTGIGKETVRELAKRGATV	1p.1	
SDR7-1C1	B. malayi	VPLFGV-LTCAGIYf ^l rRYLKGAQFNEYVEAGGKIALVTGASAGIGKQTALENLRGATV	1p.2	
SDR7-1C2	A. californica	VAVLLL-IIIFLIRLYLR---WFAPNPSKNRMDGKTVLItgGTSGIGKCTAIELAKRNARV		1p.2
SDR7-1C3	A. californica	IGLLLI-LVPVSCILLKEYMSGGRYYGKERIDGKTVVITGANCGIGKETARDLAGrgGRI		2p.2
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SDR7C1	H. sapiens	YLACRDVEKGELVAKEIQTT-----TGNQQVLVRKLDLSDTKSIRAFAGFL		
SDR7C2	H. sapiens	YIACRDVLKGESAASEIRVD-----TKNSQVLVRKLDLSDTKSIRAFAGFL		
SDR7C3	H. sapiens	ILACRDMEKCEAAAKDIRGE-----TLNHHVNARHLDLASLKSIREFAAKI I		
SDR7C4	H. sapiens	IMGCRDRARAEAAAGQLRRELRLQAACGPEPGVSGVGELIVRELDLASLRSVRAFCQEML		
SDR7C5	H. sapiens	VLAQRSQERGEAAAFDLr ^q e-----SGNNEVIFMALDLASLASVRAFAFAL	2p.0	
SDR40C1	H. sapiens	HLVCRDQAPAEARGEIIRE-----SGNqnIFLHIVDLSDPKQIWKFVENFK		3p.0
SDR7-1C1	C. intestinalis	VIPCRNAEkgrrVAREIADI-----TGNHKKIQVVYVDFTNLESVKVCTQILK	2p.2	
SDR7-1C2	C. intestinalis	ILACRNMEALAAKDt ⁱ IKETG-----KEEKYVVVKKLDLSSLQSIRDFAHNIN	1p.0	
SDR7-3C2	C. intestinalis	HMVCRNLERANQAKEDIVKE-----SGSnITVHVLDISNTKEVVEFAKNFS		2p.0
SDR7-3C3	C. intestinalis	VIASRNKTKSEVDKIRVKA-----TGNQniRVMELDLGDSDSVRKFKVKNFN	2p.0	
SDR7-3C4	C. intestinalis	ILGCRNMEKAEAAKQr ⁱ FKEAG-----GKDDTVVIKQLDLSSLASVRAFAKDIN	1p.0	
SDR7-1C1	S. purpuratus	IMACRNVEKAKEAQLDVIKE-----SGSSNVVVKKLDLASMKSIREFVEELK		
SDR7-1C3	S. purpuratus	ILACRDIKAEKAREEIVAA-----SGNTDVKVLQLDLASLSSIRQFADKIS		
SDR7-2C2	S. purpuratus	ILACRDVVRGREAEDIRMS-----TGNDVVI FMKLNLSAFDSIRHFAQEFN		
SDR7-1C3	M. domestica	YMACRDMKKCEeaREEIVLE-----TKNKVYVCRECDLASLESIRQFAEafK	2p.0	3p.1

SDR7-1C1	B. malayi	YMLCRDRAKSENARIELT kl -G-----CNPTRLILKDVLDLASFATIRKFADEIR	2p.0	
SDR7-1C2	A. californica	LIAGREKAKVEAVARNI rk K-----TGNQHVNALVLDLGNLRSIQEFAEDFR	2p.1	
SDR7-1C3	A. californica	IMACRDLEKCEQAKKEIVEE-----TGKNNIECQKLDLASFASIRAFKLIN		
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SDR7C1	H. sapiens	aeEKHLHVLINNAGVMMCPYS-KTAD-GFEMHIGVNHlgHFLLT HLLEKLKE ---SAPS	3p.2	4p.2
SDR7C2	H. sapiens	aeEKQLHILINNAGVMMCPYS-KTAD-GFETHLGVNHlgHFLLT YLLERLKV ---SAPA	3p.2	4p.2
SDR7C3	H. sapiens	eeEERV VD LINNAGVMRC PHW -TTED-GFEMQFGVNHlgHFLLT NLLDKLKA ---SAPS	3p.2	4p.2
SDR7C4	H. sapiens	qeEPRLDVLINNAGIFQCPYM-KTED-GFEMQFGVNHlgHFLLT NLLGLLKS ---SAPS	1p.0	
SDR7C5	H. sapiens	SSEPRLDILIH Na gISSCGR---TRE-AFNLLLRVNHIGPFLT THLLPCLKA ---CAPS		3p.2
SDR40C1	H. sapiens	QEH-KLHV li nNAGCMVNKRE-LTED-GLEKNFAANTlgVYILT TGLIPVLEK ---EHDP	4p.0	5p.2
SDR7-1C1	C. intestinalis	KSLKKVDILIN Na gIGNVG--TTLD-GFPLVFGVNHAPFLFTTELP LLrk ---APTA		3p.2 4p.1
SDR7-1C2	C. intestinalis	QTERRIDVLIN Na gVM LC PET-KTKD-GFESHFGVNHlgHFLLT NLLDLkh ---SAPS	2p.2	3p.0
SDR7-3C2	C. intestinalis	SNHEKLNVLVNNAGCMVNDRK-TTEVGNLELN FATNTVGT YVLTQELV PLLLK ---STKP		
SDR7-3C3	C. intestinalis	ETEEHLD FLIN agLLGYG--QTKQ-GINKLYAVNHFGPFLT NLLLPKMKEQSKSRPV	3p.2	
SDR7-3C4	C. intestinalis	DNESKIDVLLN Na gIMLV PKG -KTED-GFELHYGVNHlgHFLLT NLLDLkr ---SAPS	2p.2	3p.0
SDR7-1C1	S. purpuratus	KEEKSLDVLVNNagVMMCPRW-ETED-GFEMQFGTNHlgHFLLT LLLDLIKA ---SAPS		
SDR7-1C3	S. purpuratus	sdEEGVDVLVNNAGLMRC PKW -KTED-GFEMQFGVNHlgHFYLT NLLDKLKA ---SAPS	3p.2	4p.2
SDR7-2C2	S. purpuratus	NTEERLDILVNNagVIN DGSL -RTEE-GHELVEFGVNHlgHFLLT NILLDKLQK ---CAPS	2p.2	
SDR7-1C3	M. domestica	AEQKRLDILINNAGVMRCPRS-LTKE-GFELQIGVNHMGHFLLT NLLDDELkk ---SAPS		4p.0
SDR7-1C1	B. malayi	yeVDKIDILVNNAGIMFY PKFELT ED-GHEMTWQ TNY lgHFLLT TELLPLIKK ---SSNG	3p.2	4p.2
SDR7-1C2	A. californica	KDEKYLHVLINNAym-GPLS-KTDD-GLERSFGVNYLGHFYLT YLLSDkl KK--NAPS	3p.2	4p.2
SDR7-1C3	A. californica	stESHVDILINNAGVMMCPKM-LTED-GLEMQIGVNHfgHFLLT QLLMDKLKA ---SAPS	3p.2	4p.2
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SDR7C1	H. sapiens	RIVNVSSLAHHLGR--IHFNHLQGE--KFY-NAGLAYCHSKLANILFTQELARRLkgSGV	5p.2	
SDR7C2	H. sapiens	RVNVNSSVAHHIGK--IPFHD LQSE --KRY-SRGFAYCHSKLANVLF TRELAKRL qgTGV	5p.2	
SDR7C3	H. sapiens	RIINLSSLAHVAGH--IDFDDLNWQT-RKY-NTKAA Y CQSKLAIVLFT KELSRRL qgSGV	5p.2	
SDR7C4	H. sapiens	RIVVVSSKLYKYGD--INFDDLNSE--QSY-NKSF CYS RSKLANILFT TRELARR LEG TNV		
SDR7C5	H. sapiens	RVVVVASAAHCRGR--LDFKRLDRPV-VGWRQELRAYADTKLANVLFARELANQLEATGV		
SDR40C1	H. sapiens	RviTVSSGGMLVQK--LNTNDLQSE--RTPFDGTMVYAQN kr QQVVLTERWAQGH P --AI	6p.0	7p.0
SDR7-1C1	C. intestinalis	RIVCVSSVTHLWGN--INFDELQDLGGSLPSQF RAYSR SKLANVLF FAQLHRN ESQHGI		
SDR7-1C2	C. intestinalis	RVVIVASEAHRIGKTYTQWSDMNSG--EGM-D---TYCRSKLMN ILFA RELSDRLkgSGV		4p.2
SDR7-3C2	C. intestinalis	RviTVSSGGMYTQK--LNVKDLQSE--KGTFGSDMAYAQK RQ qviL TEE WAKMHP--DI	3p.0	
SDR7-3C3	C. intestinalis	RIINLSSSAH ra SP--LD FSKI YEPA-EGVLENFRVYSNTKLAT IYFTTE LLKRIEGFDI	4p.0	
SDR7-3C4	C. intestinalis	RIVTVSSEAHRLGTPKIDFKDMNFD--NNY-DES VAYGR SKLMN ILFT KELSKR Leg TNV		4p.2
SDR7-1C1	S. purpuratus	RIVNVSSLAHQFGK--INFDDIMSK--EKY-SDMDAYGQSKLANVLF TRELATRL kgSGV		3p.2
SDR7-1C3	S. purpuratus	RIINVSSVAHQVGK--INFEDINSD--QRY-NSAEAYANSKLAKVLF TRELSKR LegTGV		5p.2
SDR7-2C2	S. purpuratus	RVINVSSDAYMFGK--LDLERLSVN----D-GRVKS YAR SKLANVLF TROLAD KMAGTGV		
SDR7-1C3	M. domestica	RIVVLSSMAHTRGE--INVGD LNSE --KSY-DEGKAYNQSKLANIL TRELARR LegTGV		5p.2
SDR7-1C1	B. malayi	RIINVSSSLHKTADS-V DS IVNN--KKYFSK SM PYSRSKLAqvMHVREL TRRLR TKDP	5p.0	
SDR7-1C2	A. californica	RIINVVSDSYKQGE--LDLDDLAMN--KGY-SVYSAY TRSKLAQ VMFNLECHKRYIGNCV		
SDR7-1C3	A. californica	RIIFVSSLGHTLGK--MNFEDLNSE--KSY-SKL NAYQ SKLANILCSREMA RR LegTGV	5p.2	
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SDR7C1	H. sapiens	----TYSVHPGTVQSELV-RHSSF-----MRMMWWLFSFFIKTPQQGAQTSLHC		
SDR7C2	H. sapiens	----TTYAVHPGVVRSELV-RHSSL-----LCLLWLRFSPFVK TAREGA QTSLHC		
SDR7C3	H. sapiens	----TVNALHPGVARTELG-RHTGIHGSTF----SSTTlgPIFWLLVKSP ELAAQ PSTYL		6p.2
SDR7C4	H. sapiens	----TVNVLHPGIVRTNLG-RHIH---PLL----VKPLFNLVSWAFFKTPVEGAQTSIYL		
SDR7C5	H. sapiens	----TCYAAHpgPVNSELFLRHVP GW LRPL-----LRPLAWLVLRAPRGG AQ TPLYC	4p.2	
SDR40C1	H. sapiens	----HFSMHPGWADTpgVRQAMP GFHAR -----FGDRLRSEAQ GAD TMLWL		8p.2
SDR7-1C1	C. intestinalis	----STYIAHpgWTFTAIF-RDSPVLAKL-----LLFP LLY FLYTPAQGAQTQIHL	5p.2	
SDR7-1C2	C. intestinalis	----TVNSLHPGVIRSGLW-QHLHDELSIWRVWLHKTMNPFMKMF WKS PEYGAQT TIYC		
SDR7-3C2	C. intestinalis	----HFSAMHPGWADTPAVRTSM PGF YFY-----MKDNLRTAE gg ADTIVWL		5p.2
SDR7-3C3	C. intestinalis	----STYAVHpgYISSELF-ENFPVPFN YI -----GRIPLILF ks TYYG Q TTMYC	5p.2	6p.1
SDR7-3C4	C. intestinalis	----TANCLHPGVIKSELW-RHMDGSRK PVR DFF----VGTFVRWF GK TIHGAQT NIYC		

SDR7-1C1	S. purpuratus	----TSYAVHPGGVDTDLA-RHRDS--YPF----YLRVLLPLMVPFIKTSEEGAQTNIYC		
SDR7-1C3	S. purpuratus	----TANVLHPGVVKTNIIG-RHTGMHQSGF----SMAILGPIFWLFRSPQQAQTSVYC		
SDR7-2C2	S. purpuratus	----VSFSLHpgSVNTEIK-RNWAGWLRAL-----APLISFFFLKSVKAGAQTSIHC	3p.2	
SDR7-1C3	M. domestica	----TVNALHPGVVDTELF-RHMGFFNSFF----ASLIFKPLSWPFLKSPKNGAQTTLYA		
SDR7-1C1	B. malayi	GTTVTINAVHPGVCFTELM-RYTVFSRKY----ILKIIISPLLWFFMKTDkdGAQTTLVY		6p.0
SDR7-1C2	A. californica	----WSFAAHpgPTATDLRLNYPGMWGNA-----LRLVSRIMFKPPEDGCQTLVYL	5p.2	
SDR7-1C3	A. californica	----TVNSLHPGTVSTELT-RHLSFWNSSI----FKVFAGPFQYILLKTPMQGAQTSITL		

SDR7C1	H. sapiens	ALTEG-LEILSGNHFsdcHVAWVSAQ-----A-RNETIARRLWDVSCDLLGLPID---	6p.1	
SDR7C2	H. sapiens	ALAEG-LEPLSGKYFsdcCKRTWVSPR-----A-RNNKTAERLWNVSCCELLGIRWE---	6p.1	
SDR7C3	H. sapiens	AVAEELADVSGKYFDGLKQKAPAPE-----A-EDEEVARRLWAESARLVGLEAPSVR		
SDR7C4	H. sapiens	ASSPE-VEGVSGRYFGDCKEEELLPK-----A-MDESVARKLWDISEVMVGLLK----		
SDR7C5	H. sapiens	ALQEG-IEPLSGRYFANCHVEEVPPA-----A-RDDRAAHLWEASKRLAGLPGGEDA		
SDR40C1	H. sapiens	ALSSAAAQPSGRFFqdkRPVSTHLPLATASSSPAEEKLEILEQLAQTFK-----	9p.2	
SDR7-1C1	C. intestinalis	ALAPG-IESSSGNFYVSCPKPARTGKS-----A-KDIELASNLWSYSEKAVASALNQSV		
SDR7-1C2	C. intestinalis	SVAPE-LLNVTGKYFsdcCAIAYESGE-----A-KSKRNAVKLWNISCELTGINEFITF	5p.1	
SDR7-3C2	C. intestinalis	SVSDAALAQPSGLFFldRKAVPTHLALAWTRESAEDRNTFLTIAEIANQFKP-----	6p.2	
SDR7-3C3	C. intestinalis	MLDDM-VTEFSGHYFASCRKTEPQSF-----A-HNQTAQKLWQLSLEITEFSEQ---		
SDR7-3C4	C. intestinalis	CMAPE-IEDVTGKYFsdcCAVASENSQ-----A-KKDKNAEQLWQVSLQATGLSEA---	5p.1	
SDR7-1C1	S. purpuratus	SVDEK-AGQETGLYYsdcCAVKQAAKQ-----G-RDDEAARKLWDLSLKLVLGLEE----	4p.1	
SDR7-1C3	S. purpuratus	AVDPE-LEKVSQYFrdCKKSECDAS-----G-KDDEVAAKLWDVSCQLTGLSSEETK	6p.1	
SDR7-2C2	S. purpuratus	AVSDD-ILDQSGEFFKGCQVQKLSRT-----A-QDQDLAQRLWDVSLMTGLQSS---		
SDR7-1C3	M. domestica	ALDED-LATVSGKYFSDCNIKDVAPQ-----A-KDDALAKWLWAVSEKWTRLTK---		
SDR7-1C1	B. malayi	ALSKN-VEAISGRYFgeCKEHTPSPN-----S-LDDTKCNILYNQSLEAVKLSE----	7p.1	
SDR7-1C2	A. californica	AVADG-LREFsgKLFTDCKAVKTNEK-----VKANKELSSRLWNVSAHLCGFEGDALM	6p.2	
SDR7-1C3	A. californica	AVDPR-LEKVTGKYFsdcCWEKRTARQ-----A-EDDGAACKLWEISEWTRLKQD---	6p.1	
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SDR7C1	H. sapiens	-----		
SDR7C2	H. sapiens	-----		
SDR7C3	H. sapiens	EQPLPR-----		
SDR7C4	H. sapiens	-----		
SDR7C5	H. sapiens	EPDEDPQSEDSEAPSSSLSTPHPEEPTVSQPYSPSQSSPDLSKMTTHRIQAKVEPEIQLS		
SDR40C1	H. sapiens	-----		
SDR7-1C1	C. intestinalis	GYCTSI-----		
SDR7-1C2	C. intestinalis	----PTHRL-----		
SDR7-3C2	C. intestinalis	-----		
SDR7-3C3	C. intestinalis	-----		
SDR7-3C4	C. intestinalis	-----		
SDR7-1C1	S. purpuratus	-----		
SDR7-1C3	S. purpuratus	EKSAKTHDVVKEAER-----		
SDR7-2C2	S. purpuratus	-----		
SDR7-1C3	M. domestica	-----		
SDR7-1C1	B. malayi	-----		
SDR7-1C2	A. californica	PEDEPEATPNAAEEAGEATA---EEEEKSQ-----		
SDR7-1C3	A. californica	-----		

Figure S25. Alignment of the invertebrate orthologs of the human SDR7C family and of the human SDR40C1 variants. × and + symbols mark the structure consensus and the catalysis consensus respectively; the couples of amino acid symbols in red lowercase mark the splicing-site positions; * symbol marks the position of identical amino acid residues of the aligned SDR protein sequences. The splicing sites are progressively numbered and the phase (p.) type is indicated after the splicing-site number; the phase symbols, highlighted in a same color, belong to orthologous splicing sites.

SDR9C1	H. sapiens	-----MSTFF--SDTAWICLAVPTVLCGTVFCKYKKSSGQLWSWMVCLAG
SDR9C2	H. sapiens	-----ME---RWPWP--SGGAWLLVAARALLQL--LRSDLRLGRPLLAALALLAA
SDR9C3	H. sapiens	-----
SDR9C4	H. sapiens	-----
SDR9C5	H. sapiens	-----
SDR9C6	H. sapiens	-----
SDR9C7	H. sapiens	-----
SDR9C8	H. sapiens	-----
SDR9-1C2	C. intestinalis	-----MH
SDR9-1C2	S. purpuratus	-----
SDR9-1C2	C. elegans	-----
SDR9-1C4	C. elegans	-----
SDR9-1C2	A. californica	MEIDIQNELNRDGIVFYSVLYSSVTVIFAFVLS---KFLTNEFRFGFRSFLSLVTLFL
SDR9-1C5	A. californica	-----

SDR9C1	H. sapiens	GKTLACDRENGA ^x r ^x P-LLGST---SFIPIGRRTYASAAE ^x p ^x VGSKAVLV ^x TGCDS--GF	1p.1 2p.0
SDR9C2	H. sapiens	LCAVCLLILSPFWGLILFSVSCFLMY-----TYLSGQELLPVDQKAVLV ^x tg ^x GDC--GL	1p.2
SDR9C3	H. sapiens	LDWLCQRLPPPAALAVLAAAGWIAL-----SRLARPQRLPVATRAVL ^x tg ^x CDS--GF	1p.2
SDR9C4	H. sapiens	-----MLFWVL---GLLILC-GFLW--TRKGLKIEDITDKYIFITGCD ^x S--GF	
SDR9C5	H. sapiens	-----MWLPLLGA-LLW-AVLW--LLRDR-QSLPASNAFVFITGCD ^x S--GF	
SDR9C6	H. sapiens	-----MWLYLAAFVGLYY-LLHW--YRERQ-VVSHLQDKYVFITGCD ^x S--GF	
SDR9C7	H. sapiens	-----MAALTDLSF-MYRW--FKNCN-LVGNLSEKYVFITGCD ^x S--GF	
SDR9C8	H. sapiens	-----MWLYLAVFVGLYY-LLHW--YRERQ-VLSHLRDKYVFITGCD ^x S--GF	
SDR9-1C2	C. intestinalis	-----MAKSHQKNVVI ^x tg ^x CDIPN ^x S ^x	1p.2
SDR9-1C2	S. purpuratus	EAP ^x la ^x KCIMSFLTLVGLTVGVIVAR-MIEY--LIRRP ^x HIDNITK ^x D ^x ky ^x VFITGCDT--GF	1p.2 2p.1
SDR9-1C2	C. elegans	---MVVCC ^x CLCTLT ^x FWLYFVAVVVVW ^x NIV ^x ry ^x --ILELIPEGGS ^x LQDRAILITGCDT--GF	1p.1
SDR9-1C4	C. elegans	----MLSASTIFAWVAIFGSYV-AY ^x kv ^x YNF--LI--KQRVDNYGKK ^x TVAISGCD ^x S--GF	1p.2
SDR9-1C2	A. californica	GEPLCQFLVEGPGSLVVFSLGCLIIY-----Y-ILPASHLPIKNRSVL ^x I ^x tg ^x CDS--GF	1p.2
SDR9-1C5	A. californica	-----MWLMIAAIVTGIV-GYLFINRFLRSLDVGDYGNKYVFITGCDT--GF	

SDR9C1	H. sapiens	GFSLAKHLHSGKGLVFAGCLM ^x kd ^x KGHDGVKELDSL-NSDRLRTV-QLNVCSS ^x EEVEK ^x VVE	3p.0
SDR9C2	H. sapiens	GHALCKYLDELGFTVFAGVLNENGP--AEELRRTC-SPRLSVL-QMDITKPVQIKDAYS	
SDR9C3	H. sapiens	GKETAKKLDSMGFTVLATVLELNSPG--AIELRTCC-SPRLRL-QLMDITKPGDISRVLE	
SDR9C4	H. sapiens	GNLAARTFDKKG ^x FHVIAACLTESGST-A---LKAET-SERLRTV-LLDVTDPENVKRTAQ	
SDR9C5	H. sapiens	GRLLALQLDQGRFVLASCLTPSGAE-D---LQ ^x RVA-SSRLHTT-LLDITDPQSVQQA ^x AK	
SDR9C6	H. sapiens	GNLLARQLDARGLRVLAACLT ^x EKGAE-Q---LRGQT-SDRLETV-TLDVTKMESIAAATQ	
SDR9C7	H. sapiens	GNLLAKQLVDRGMQVLAACFTEEGSQ-K---LQ ^x RD ^x T-SYRLQTT-LLDVTKSES ^x IKAAAQ	
SDR9C8	H. sapiens	GKLLARQLDARGLRVLAACLT ^x EKGAE-Q---LRGQT-SDRLETV-TLDVTKTESVAAAAQ	
SDR9-1C2	C. intestinalis	GYELALCLDHQGYVVFAGCTDCNSVG--ARSLASRG-STRLAVM-QIDVTKQDEIDDATE	
SDR9-1C2	S. purpuratus	GNKLAKQLDIMGVHVIAGCLTEKGR ^x T-D---LDDVT-SDRVKTL-ILDVTDHESVLRAYE	
SDR9-1C2	C. elegans	GRELAKKCAKNGLVFAGCLT ^x Tea ^x AK-T---LESESANPRLRTV-PLDVSKDESVEKTVE	2p.0
SDR9-1C4	C. elegans	GRLLAVRLVKQGVPIAGVLK ^x enge ^x -S---LKKEVNTPSLLTFGILNVANDES ^x VKEFVK	2p.0
SDR9-1C2	A. californica	GHALTIKLD ^x SLGIQVFAGCLEDRGPG-AL-ELKNRC-SD ^x r ^x l ^x HIL-KLDVTNSKDIAEASN	2p.1
SDR9-1C5	A. californica	GHRLS ^x ir ^x LNMKG ^x FHVISGCLTQKGAD-T---LTQLC-PDRLSAL-LLNVADSDSIQKAYK	1p.1

SDR9C1	H. sapiens	IVRSSLKDPE ^x kg ^x MWGLVNNAGISTF-GEVEFTSLETYKQVAEVLN ^x WGTVRMTKSFLPLIR	4p.2
SDR9C2	H. sapiens	KVAAML--QD ^x rg ^x LWAVINNAGVLGFP ^x TGELLMTDYKQCMANVFFGTVEVTKTFLPLL ^x R	2p.2
SDR9C3	H. sapiens	F ^x TKAHT--TS ^x tg ^x LWGLVNNAGHNEVVADAELSPVATFRSCMEVNFFGALELT ^x KGLPLLR	2p.2
SDR9C4	H. sapiens	WVK ^x NQV--GE ^x kg ^x LWGLINNAGVPGVLAPT ^x DWLTLEDYREPIEVNLFGLISVTLNMLPLV ^x K	1p.2
SDR9C5	H. sapiens	WVEMHV--KE ^x ag ^x LFGLVN ^x NAGVAGII ^x GTPWLT ^x RDDFQ ^x RVLN ^x VNTMGPIGVTLALLPLLQ	1p.2
SDR9C6	H. sapiens	WVKEHV--GD ^x rg ^x LWGLVNNAGILTPITLCEWLNTEDSMNMLKVNLI ^x GIQVTL ^x SMLPLVR	1p.2
SDR9C7	H. sapiens	WVRDKV--GE ^x qg ^x LWALVNNAGVGLPSGPN ^x EWLT ^x KDDFVKVINVN ^x LVGLIEVTLHMLPMVK	1p.2
SDR9C8	H. sapiens	WVKECV--RD ^x kg ^x LWGLVNNAGISLPTAPNELLTKQDFVTILDVNLLGVIDVTL ^x SLLPLVR	1p.2
SDR9-1C2	C. intestinalis	MIQDMI--G ^x deg ^x LWAVVNCAE ^x FYTV- ^x AEADWCSVEDYEQSMQVNYLGTVRVTKSLLHLIR	2p.2

Accession	Species	Sequence	Score
SDR9-1C2	S. purpuratus	EVKKIIP-HKaaLWGVVNNAGISGLAGYLEWTRREDYDEYKVLAVNLFGVVDVTLTFLPLLK	3p.2
SDR9-1C2	C. elegans	FVKKSL--GNHKLWGVVNNAGIFSCYGPDDWCRMNDYKALADVNCGLGIVRVTQAFKKLVK	
SDR9-1C4	C. elegans	LVEKTV--ENRGLWGVVANAGILGNSGPDWLSAQDYIntMQVNTFGVMRFIQGLKKFVK	3p.0
SDR9-1C2	A. californica	YIKSRV--GegLWGLVNNAGVWCF-AELGMTSETIVQKVMVDNLFGLAVRMTRAVLPLIK	2p.2
SDR9-1C5	A. californica	HVQDLLP-AGkgLWAVVNNAGISGNTSRIEMCTKQDFVDAIDINLFGPIEVSRFTFLPLLK	2p.2
		* * * *	
		+ +	
SDR9C1	H. sapiens	RAkgRVVNISMLGRMANPARSPYCITKFGVEAFSDCLRYEMYPLGV--KVSVVEPGNFI	5p.2
SDR9C2	H. sapiens	KSKGRLVNVSSMggGAPMERLASYGSSKAAVTMFSSVMRLELSKWGI--KVASIQPGGFL	3p.2
SDR9C3	H. sapiens	SSRGRIVTVGSPagDMPYPCLGAYGTSKAAVALLMDTFSCCELLPWGV--KVSIIQPGCFK	3p.2
SDR9C4	H. sapiens	KAQGRVINVSSVGGRLAI-VGGGYTPSKYAVEGFNDSLrrDMKAFGV--HVSCIEPGLFK	2p.1
SDR9C5	H. sapiens	QARGRVINITSVLGRLLAA-NGGGYCVSKFGLEAFSDSLrrDVAHFGI--RVSIVEPGFFR	2p.1
SDR9C6	H. sapiens	RARGRIVNVSSILGRVAF-FVGGYCVSKYGVFAFSDILrrEIQHFGV--KISIVEPGYFR	2p.1
SDR9C7	H. sapiens	RARGRVNVMSSSGRVAV-IGGGYCVSKFGVEAFSDSIrrELYFGV--KVCIEPGNYR	2p.1
SDR9C8	H. sapiens	RARGRVNVSSVMGRVSL-FGGGYCISKYGVFAFSDSLrrELSYFGV--KVAMIEPGYFK	2p.1
SDR9-1C2	C. intestinalis	RGRGRIVNLSSMagCLARAGQSAYSASKFALEAFTDSLRLQEMLKWGV--YVTLVEPAYFP	3p.2 4p.2
SDR9-1C2	S. purpuratus	ESSGRLVNVSSAGRVSA-LPGGYCESKFAVEAFSDAVrrERKHFGYLFKVSIIIEPGGFA	4p.1
SDR9-1C2	C. elegans	AAKGRIVTVTSVNGRLSTPAAGPYVVSFKGAAAYMDCIrrELYNFGV--KVSILEPGIFR	3p.1
SDR9-1C4	C. elegans	KQEGrvVIISSISGRTPRPTVGPYCVSKHAVEAYADVrrhelIDFNV--SVHLLPEPGFFT	4p.1 5p.1
SDR9-1C2	A. californica	QAQGRIVNVSSLIgRISVEGCGAYSMSKHALVAFTNTLRMEMKKWGV--CVSLVEPTGYF	4p.2
SDR9-1C5	A. californica	QTRGRVVCITSILGRYPS-GPAPYCTSKCGLEAFCDVrrEVYLQGI--KVSILEPGVFR	3p.1
		** * * * *	
SDR9C2	H. sapiens	--tnIAGTSDKWEKLEKDILDHLPAEVQEDYQGDYILAQRNFLLL-INSL-----	4p.2
SDR9C3	H. sapiens	--teSVRNVGQWEKRRKQLLLANLPQELLQAYGKDYIEHLHGQFLH-SRLR-----	4p.2
SDR9C1	H. sapiens	AATSLYS-PESIQAIAKKMWEELPEVVRKDYGKKYFDEKIAKMET-YCSS-----	
SDR9C4	H. sapiens	--TNLAD-PVKVIEKKLAIWEQLSPDIKQQYGEgyIEksLDKLKG-NKSY-----	3p.2
SDR9C5	H. sapiens	--TPVTN-LESLEKTLQACWARLPATQAHYGGAFLTkyLKMQRIMNLI-----	3p.2
SDR9C6	H. sapiens	--TGMTN-MTQSLERMKQSWKEAPKHiketYQGOYFDalYNIMKE-GLLN-----	3p.2
SDR9C7	H. sapiens	--TAILG-KENLESRMKRLWRLPQETRDSYGEDYFRiyTDKLKN-IMQV-----	3p.2
SDR9C8	H. sapiens	--TAVTS-KERFLKSFLEIWRSSPEVKEAYGEKFVAdyKKSAEQ-MEQK-----	3p.2
SDR9-1C2	C. intestinalis	eGSLVLS-----EPQTSVRLKRPVDPHVKEVYGEDYFVDFINSVSRNDPTTQEEGKSKSTE	
SDR9-1C2	S. purpuratus	--TPLAS-KDNLRSVTAAWERLSDVQKKEFPESMLHefVDEKSSLISSM-----	5p.2
SDR9-1C2	C. elegans	--TPLLD-EQAMLKRVVDHVTQIDDETRETEYGETFKNyfAKMWNKTYISM-----	4p.2
SDR9-1C4	C. elegans	--TNITQ---TATNDLDAVWERLDDETKKEYGKEFYDdyKNSRF-SRLSH-----	6p.2
SDR9-1C2	A. californica	--tgVMQ-EHSLQRKKEELWSALDEETRqiYKGKEYFDSAYAHILT-HAQS-----	5p.2 6p.2
SDR9-1C5	A. californica	--TNIMD-FESLKSCESSFDQASDEVKTAYGPDYVKnYVTLVSE-TMKG-----	4p.2
SDR9C1	H. sapiens	-----GSTDSPVIDAVTHALTATTPYTRYHPMDY--YWWLRMQIMTHLPGAISDMI	
SDR9C2	H. sapiens	-----ASKDFSPLVRDIQHAILAKSPFAYYTPGKGAYLWIC---LAHYLPIGIYDYF	

SDR9C3	H. sapiens	-----AMSDLTPVVDAITDALLAARPRRRYPGQGLGLMYF---IHYYLPEGLRRRF
SDR9C4	H. sapiens	-----VNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWI---PLSHMPAALQDFL
SDR9C5	H. sapiens	-----CDPDLTKVSRCLEHALTARHPRTRYSPGWDAKLLWL---PASYLPAASLVDAV
SDR9C6	H. sapiens	-----CSTNLNLVTDCEMEHALTSVHPRTRYAGWDAKFFFI---PLSYLPTSLADYI
SDR9C7	H. sapiens	-----AEPRVRDVINSMEHAIVSRSPRIRYNPGLDAKLLYI---PLAKLPTPVTDFI
SDR9C8	H. sapiens	-----CTQDLSLVTNCMEHALIACHPRTRYAGWDAKLLYL---PMSYMPFTFLVDAI
SDR9-1C2	C. intestinalis	SSTLKSSPDFGNTNRVLHALSEAVTAYSPKVRYFVGSEFQDRMVK--SASAFLLPTVVMDDY
SDR9-1C2	S. purpuratus	-----ATTDLISKVTDVIEHALFSKWPKTRYAVGWDKVMVW---PMSYMPSWIQDRL
SDR9-1C2	C. elegans	-----STTKIHYVVDNYYHALTAKYPRHRYCGWDAIFVYV---PLSLLPTWWADYV
SDR9-1C4	C. elegans	-----CADDLNPVIDAYDHALLGKYPKTRYWVGWDTILFYI---PLATLPTFAQDWF
SDR9-1C2	A. californica	-----YPRDLSPVIRCLRSALLSKRPREFPCGGGAEILMC---VYPLLPMVMADCV
SDR9-1C5	A. californica	-----ASTDIDQVVDAYVHAITSKFPRTRYVVGNDAKFIYI---PLSLVPDWCWDWI
		* * *
SDR9C1	H. sapiens	YIR-----
SDR9C2	H. sapiens	AKRHFGQDK-PMPRALRMP-----NYKKKAT-----
SDR9C3	H. sapiens	LQAFFIS-H-CLPRALQPGQPGTTPQDAAQDPNLSPGPSPAVAR
SDR9C4	H. sapiens	LLKQKAEL--ANPKAV-----
SDR9C5	H. sapiens	LTWVLPKP--AQAVY-----
SDR9C6	H. sapiens	LTRSWPKP--AQAV-----
SDR9C7	H. sapiens	LSRYLPRP--ADSV-----
SDR9C8	H. sapiens	MYWVSPSP--AKAL-----
SDR9-1C2	C. intestinalis	LTSGSLSK--CVPKVIKEKQE-----
SDR9-1C2	S. purpuratus	CP-----
SDR9-1C2	C. elegans	IRSLGKQE--VVPACLEDSESMK-----KKN-----
SDR9-1C4	C. elegans	ISFQRCSR--PVPASMKNNH-----
SDR9-1C2	A. californica	SSSINLVKQLRPQALSGMTT-----R-----
SDR9-1C5	A. californica	VRSLINYT--ISKKR-----

Figure S26. Alignment of the invertebrate orthologs of the human SDR9C family variants. For further details see Fig. S25 and Table S28.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR10E1 H. sapiens	-----
SDR10E2 H. sapiens	-----
SDR10-1E1 C. intestinalis	-----
SDR10-2E1 C. intestinalis	-----
SDR10-1E1 S. purpuratus	-----
SDR10-1E1 D. melanogaster	MSHAVANKTETEAAPNSSLKQSAAPQPANSH-----DAKLLNGTLAR
SDR10-1E1 A. gambiae	-----
SDR10-1E1 A. mellifera	-----
SDR10-1E1 C. elegans	-----
SDR10-1E1 A. californica	MSEDCEQG-----GGEMTVSSPQQPSKTNQSSSIVKDLIMKTTMVPEKEVVVNGFHNT

SDR10E1 H. sapiens	-----
SDR10E2 H. sapiens	-----
SDR10-1E1 C. intestinalis	-----
SDR10-2E1 C. intestinalis	-----
SDR10-1E1 S. purpuratus	-----MPCF--DDNGPICAPLDG-----
SDR10-1E1 D. melanogaster	TNGL-----THAASVATSSSGSYGS
SDR10-1E1 A. gambiae	-----
SDR10-1E1 A. mellifera	-----
SDR10-1E1 C. elegans	-----
SDR10-1E1 A. californica	LNGAGEDQETLRKPGDSNTFTNSNGSNKIPTSMDPVTSPLSPLTQVASTLAPSLKQYED

SDR10E1 H. sapiens	-----M
SDR10E2 H. sapiens	-----M
SDR10-1E1 C. intestinalis	-----MA--DSQEIPVNV
SDR10-2E1 C. intestinalis	-----MDYSDVLPkky
SDR10-1E1 S. purpuratus	----EHSMSGGV-----VDVTDEAFA--mkLNNLPASMAY
SDR10-1E1 D. melanogaster	SSAAGSNAGSGGPTSSASLSIAAGVASSTALPLPPSSNGLQMPYE-----RFRADDTSY
SDR10-1E1 A. gambiae	-----MDDEQQRSMATTVVQREMMATTTTTTAAAA
SDR10-1E1 A. mellifera	-----MSTISDNQC
SDR10-1E1 C. elegans	-----MA
SDR10-1E1 A. californica	FLPKTTQDGVGSPSRTP-----EMSILHEHYEHRHATSPKLAVSAGE

1p.0
1p.0

	x x x
SDR10E1 H. sapiens	VSIPYYEGKNVLLTGATGFLGKVLLEKLLRSCPKVNSVYVLVRQKAGQTPQERVEEVLS
SDR10E2 H. sapiens	STIAAFYGGKSILITGATGFLGKVLMEKLFRTSPDLKVIYILVRPKAGQTLQQRVFAQILD
SDR10-1E1 C. intestinalis	PSIAEFFSGKSVAITGATGFIGTCLVEKILRCCPGVLKIFVFIREKKDKSATERLAHLTQ
SDR10-2E1 C. intestinalis	PTIADFYAGKTVAMTGGTGFLGQGITEKLLRCCPDINKIILFIRHKRNCDPKERLQQLAQ
SDR10-1E1 S. purpuratus	CSIGEFYAGKTLMITGATGFIGKVMLEKLMRCCPDIKKVFLLRPKSGQRAAAARIQEITA
SDR10-1E1 D. melanogaster	VP1AQFYAGRSVFITGGTGFMGkvLVEKLLRSCPEIRNIYLLIRPKRGQEV SARLTLLN
SDR10-1E1 A. gambiae	ASIAESYAGRSIFITGATGFMGKIMVEKLLRDCGELRCIYLLIRAKKGVDPAQRKEEYVK
SDR10-1E1 A. mellifera	TSVRDFYKDRSIFITGGTGFMGKVLVEKLLRSCPGIKNIYILMRPKKSQDIQORLQKLLD
SDR10-1E1 C. elegans	FSVRDVFYAGSSVLLTGGTGFLGKVIVEKLLWTIDDIQNIYLMIRTRKGNPQERLSGLLh
SDR10-1E1 A. californica	LTVPLYYAGKSVLLTGGTGFMGKVLVEKLLRSCPELDSLYCLIRPKNKQSIEARLNEITS
	** *** * ** * *

1p.0

1p 0

SDR10E1 H. sapiens	Gk1FDRLRDENPDFREKIIAINSELTPQKLALSEEDKEVIIDST-----
SDR10E2 H. sapiens	Sk1FEKVEVCNPNVHEKIRAIYADLNQNDFAISKEDMQELLSC-----
SDR10-1E1 C. intestinalis	LqvFDTVRTQQPDFQLKLVAVPCDLEKEGFDLSEESQTQIQNEV-----
SDR10-2E1 C. intestinalis	KpaFDILRKTPQNFQAEKLAFAVSCDLEADDGLSKEDRKTQLQNEV-----
SDR10-1E1 S. purpuratus	G11FDKVREAQPNFQSKLIAIDCDLTPDLALKEEDIKTLQEETELAFHVAATVRFDEKL
SDR10-1E1 D. melanogaster	Ap1FESLRQEKPKELSKVIPISGDITSEELGISEKDqnLLCRNV-----
SDR10-1E1 A. gambiae	NIVFDHVRERYSERLGKIRLIRGDILSPGLGLSDDDRRELTENV-----
SDR10-1E1 A. mellifera	Vp1FDKLRRDTPDELLKIIPIAGDVTHELGISEADQNVIIRDV-----
SDR10-1E1 C. elegans	dPLFNRIHQEKPEAFDKLKAIGGDMMVENLGMPDPEDVMLIRDnv-----

1p.0
1p.0
1p.0
2p.0
2p.0
2p.0 3p.0

1p.0
2p.0

SDR10-1E1 A. californica	Tk1FDRLRKERPDPFASKLRPIHGDMLLPDLGLSPEDRAELEQKI-----	1p.0
	* *	
SDR10E1 H. sapiens	-----	
SDR10E2 H. sapiens	-----	
SDR10-1E1 S. purpuratus	s1SLHLNVYATKKILQLAQGMKKL11FDKVEAQPNFQSKLIAIDCDLTEPDLALKEEDI	3p.1 4p.0
SDR10-1E1 C. intestinalis	-----	
SDR10-2E1 C. intestinalis	-----	
SDR10-1E1 D. melanogaster	-----	
SDR10-1E1 A. gambiae	-----	
SDR10-1E1 A. mellifera	-----	
SDR10-1E1 C. elegans	-----	
SDR10-1E1 A. californica	-----	
SDR10E1 H. sapiens	-----NIIFHCAATVRFNENLrdAVQLNVIATRQLILLAQQMKNLEVFMHVSTAYAYC	2p.1
SDR10E2 H. sapiens	-----NIIFHCAATVRFDDTLrhAVQLNVTATRQLLLMASQMPKLEAFIHISTAYSNC	2p.1
SDR10-1E1 C. intestinalis	-----NIFIHSAATLRFNEHIrlSYQINTLGVRTMLKLCRTIKNLVSIVHISTaYSFC	2p.1 3p.2
SDR10-2E1 C. intestinalis	-----NVFYHSAATLKFNEHLriSFDINVQCVRKLLKLR--WDNLQAFVHISTaYAHT	3p.1 4p.2
SDR10-1E1 S. purpuratus	KTLQEETELAFHVAATVRFDEKLSLSLHLNVYATKKILQLAQGMKKLlvFQHVSTAYANC	5p.0
SDR10-1E1 D. melanogaster	-----SVVFHSAATVKFDEKLKLSVTINMLGTRKRLVELCHRMLSLdaliHVSTAYCNC	4p.0
SDR10-1E1 A. gambiae	-----ELVFHCAANVRFDQHIRQAVDINLNGTIRVLGLAEQMRRLVSFVHVSTAYCQC	
SDR10-1E1 A. mellifera	-----SIVFHSAATVKFDEPLKRSVHINMIGTKQLNLCHRMHNLlealiHVSTAYCNC	2p.0
SDR10-1E1 C. elegans	-----NVVIHSAATVKFDEHLRAAVTMNVIGTKRIIDLCHQIKDLkvLVHVSTAYANC	3p.0
SDR10-1E1 A. californica	-----NIVFHSAATIRFDEPLRVAVMNVVAVRKMLALARKLEHLleaFVHVSTAYANC	2p.0
	* ** * *	
	+ +	
SDR10E1 H. sapiens	NRKHIDEVVYPPVPDPKKLIDSLewMDDGLVNDITPKLIGDRPNTYIYTKALAEYVVQQE	3p.1
SDR10E2 H. sapiens	NLKHIDEVIYPCPVEPKKIIDSLeWDDAIIDEITPKLIRDWPNIIYTYTKALGEMVVQQE	3p.1
SDR10-1E1 C. intestinalis	DRKDIGEEVYKTGWNFNKLHDTMQWMNDMLTKLTPDILDRpNTYTLTKAFGEEVIVKE	4p.1
SDR10-2E1 C. intestinalis	DRKFVGEFFYDCGVLDLEAMFKWMDDDTVEQLTPSLLSKsrpNTYTLTKALAEADAVCRE	5p.1
SDR10-1E1 S. purpuratus	DRSRIEEVVYPPVPDPYKMLDAVewMSEDMIQTLPKLLGKRPNNTYFTTKALAEYVVMEE	6p.1
SDR10-1E1 D. melanogaster	DRTDVSEVIYAPPYNPDDIISLINWLPEDILDqlTPRLIGKRPNNTYFTTKALAEHMLLKE	5p.0
SDR10-1E1 A. gambiae	NEAVLEEKHYPAFQNPBGISKMVGLDDDDLDIITPr1LNNLPNTYAYTKALTEDMVYQY	1p.1
SDR10-1E1 A. mellifera	DRYDVAAEIIYPVSAPEEIEIMALTKLMDSQMDNITPTLIGNRPNTYFTTKALTERMLQSE	
SDR10-1E1 C. elegans	DRFETTEkiYKSPMAPQKLVDALSWMDDETLTkitPKILGLRPNTYTLTKALAESTIETE	4p.0 5p.0
SDR10-1E1 A. californica	DRPYIEETVYPPVPVEPQKIIDVLeWMDDEMLELFTPKLMGEKPNTYTYTKQLAEHLITE	3p.1
	* * ** * * *	
SDR10E1 H. sapiens	GAKLNVAIVRPSIVGASWKEPFpgWIDNFNGPSGLFiaaGKGILRTIRASNNALADLVPV	4p.0 5p.0
SDR10E2 H. sapiens	SRNLNIAIIRPSIVGATWQEPFpgWVDNNGNGNGIIiatGKGFLRAIKATPMAVADVIVP	4p.0 5p.0
SDR10-1E1 C. intestinalis	GEGLPVCIVRPSIVGATYSDPVagWCSNFNGATGLFIAYGKGLMRSLYVKRDICMDIIPA	5p.0
SDR10-2E1 C. intestinalis	SGNLPICIVRPSMIIPAWREPMpgWCTNVYGTAFIIAYGKGVLRCCADRKINADNIP	6p.0
SDR10-1E1 S. purpuratus	GKGMPICITRPSIVGASWKEPFpgWIDNFNGPSGVFIavGKGLLRMTIGDADAVVDISP	7p.0 8p.0
SDR10-1E1 D. melanogaster	AGNLPAIVRPSivTASLNEPFAGWVDNFNGPTGLVSALAKGMFRMTMCEKNYVADMVPV	6p.0
SDR10-1E1 A. gambiae	RGKLPiAIARPSIVTAAMKEPLPGWEGGTNGPTGLLIGAGRGVIRSMHCNGEYLADFMPV	
SDR10-1E1 A. mellifera	CGHLPIAIVRPSIVLSSFREPVSGWVDNLNGPTGIVAAAGKGFfrsMLCQKNMVADLVPV	3p.1
SDR10-1E1 C. elegans	AKDIPVIIIRPSIVGAMWQGPLPGWTDNNGPTGIFAAVGRGVLTNMGCSSESKADIIPV	
SDR10-1E1 A. californica	GAGLPLAIVRPSIVGAAWKEPFpgWIDNNGPSGIYIAAGRGIILRSMKGESKAIADIVPV	4p.2
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SDR10E1 H. sapiens	DVVVNMSLAAAWYS-GVN-----	
SDR10E2 H. sapiens	DTVVNMLAVGWYT-AVH-----	
SDR10-1E1 C. intestinalis	DLVVNGTIAAAWRNAVCHNPVSANSVLSTSPliDRRSNSTFSSASDLSEL-----RTL	6p.2
SDR10-2E1 C. intestinalis	DFIVNGAVSAGMKT-ACD-----FVHRRRSSGYNSSDGEESLDDGVEELSSG	
SDR10-1E1 S. purpuratus	DFVVNAMIGATWHT-GVH-----	

SDR10-1E1	D. melanogaster	DIVINLMIAAAWRT-ATR-----		
SDR10-1E1	A. gambiae	DVTMNAIIAIGTERMANA-----		
SDR10-1E1	A. mellifera	DIVINLMICTAWRT-ATN-----		
SDR10-1E1	C. elegans	DIVANMIIASASYR-TSI-----		
SDR10-1E1	A. californica	DIPVNMIVVAWYT-AVA-----		
		* *		
SDR10E1	H. sapiens	-----rPNIMVYNCTTGSTNPFHWGEveYHVISTFKR	6p.1	7p.2
SDR10E2	H. sapiens	-----rPKSTLVYHITSGNMNPCNWHKmgVQVLATFEK	6p.1	7p.2
SDR10-1E1	C. intestinalis	R-----EREESPEIELRRKTLPIYNLVASSSNPVLMRewndIMTSSYTn		7p.2
SDR10-2E1	C. intestinalis	TERSDSPGSsvFAESAVVEIPSSAARKSTKIPIYNINSSTTNPLLLHDleIYTKETIDV	7p.2	8p.2
SDR10-1E1	S. purpuratus	-----kPANIPIYNLVTSFPVNPNRWGDveII-PDLYNR	9p.1	10p.2
SDR10-1E1	D. melanogaster	-----KSNLLIYNCCGTGQRNPIIWSEFVKHAMTSVRK		
SDR10-1E1	A. gambiae	-----RKEDVMYYNLTSSADNPISWGEVLEMGRGILNQ		
SDR10-1E1	A. mellifera	-----RTKTIPIYHCCTGQQNPITWQQFVELILKYNRm		
SDR10-1E1	C. elegans	-----ntTEIPVIHCSSGELNPLYWGHIVLFLEQFYKk	6p.1	7p.0
SDR10-1E1	A. californica	-----KPGQVLTyHATTGGCNPYTWGDIsGIVNKSyKQ		5p.2

SDR10E1	H. sapiens	NPLEQA-FRRPNVNLTNSHLLYHYWIAVSHKAPAFlyDIYLRMTGRSPrmMKTITRLHKA		8p.1
SDR10E2	H. sapiens	IPFERP-FRRPNANFTSnsFTSQYWNNAVSHRAPAIYDCYLRLTGRKPrmTKLMNRLLRt		8p.1
SDR10-1E1	C. intestinalis	YPLDA--LMSpDLKVASnkIMFRVLFffKQYIPAYIFDAGLILIGKKPqllRWTQRVSGT	8p.1	9p.1
SDR10-2E1	C. intestinalis	YPMKSASFFPPSCILTTnqkVMDYATFALQTVPAHIIDTILALTKQKRqmVKWDGKIRSG	9p.1	10p.1
SDR10-1E1	S. purpuratus	IPLEKV-FRRPRAALTKYpIAfEYVNLVSAKIPAYIMDCALRLQGKKPqmMKVNSKITKM	11p.1	12p.1
SDR10-1E1	D. melanogaster	HPleGC-LWYPTGDLRMNRPMTNLNCIAKHFLPAYILDGVARIMGKKPfvVNVQNKIAKA	7p.2	8p.1
SDR10-1E1	A. gambiae	NPFCFA-LWYPDGSIKSNLYLHLLCVLFLHYLPAYLIDFLMVLLRRKPlVKVQKRISAG		2p.1
SDR10-1E1	A. mellifera	HPPNDT-IWWPDGKCHTFAIVNNVCKLFQHLPAHILDfIFRLRGKPAIMVGLHEKIDKA		
SDR10-1E1	C. elegans	yPMEQC-FAVPSTYFHKSRSFLINYYIKHHIPAAISDISARLIGKRknVKLYSKVWKM		8p.1
SDR10-1E1	A. californica	IPLEGC-FRRPNVAIVSNnflLHEYWTCVSHLIPAYMIDLAYRMMGKKPrMVRLYNKLHRS	6p.1	7p.1
		* * ** *		
SDR10E1	H. sapiens	MVFLEYFTSNsWVWNTENVNMLMNQLNPEDKktFNIDVRQLHWAeyIENYCLGTkKYVLN	9p.0	
SDR10E2	H. sapiens	VSMLEYFINRSWEWSTYnTEMLMSELSPEDQrvFNFDVRQLNWLEYIENYVLGVkKYLLK	9p.0	
SDR10-1E1	C. intestinalis	IGVLQFFLTsqQWNWNNStQKLQREMEQDRkqFNMDAAVVDWEQYMNNYAKGtKKFILK	10p.0	
SDR10-2E1	C. intestinalis	MEVMGFFFTNGFVWNRDETDRLHNCLHPKDQktFTLDARAFVWREYfNDYILGAKKFILK	11p.0	
SDR10-1E1	S. purpuratus	VHTLKYFTNNTWEWTNQNTIALSAAmSEEDRkvYFTDVRPLHWPTyLEAYCLGTkKYVLK	13p.0	
SDR10-1E1	D. melanogaster	VECLEYFATRQWRfKDDNVHALLHTLSPKDRIEIFVFDVRHINWDKYVERYVLGFREFLFK		
SDR10-1E1	A. gambiae	LTILQYYTTKEWVFRCdNTKSlyQLSPDDRKRfYFDVNEINyKTYLYDFILGARQYILK		
SDR10-1E1	A. mellifera	VKCLEYFTMQQWNFRDDNVrQLSGELSPEDRQIFMFDVKQIDWPSyLEQYILGIRQFIK		
SDR10-1E1	C. elegans	IETLHFFTTRGWSfNARGLPEffEKMTpADQKEYNFdVRQVDWNSyLFDyVMGIKKFLLK		
SDR10-1E1	A. californica	IDVLKFFTCNEWQWSSTNHdMLKHQLTPlDQkmFYFDPKPLHWPTyIENyCMGAKKYVLN	8p.0	
		* * * *		
SDR10E1	H. sapiens	EEMSGLPAARKHLNklRNIRYGFNTILV---IL-----IWRIFIARSQm--	10p.1	
SDR10E2	H. sapiens	EDMAGIPKAKQLKklRNIHYLFNTALF---LI-----AWRLLIARSQm--	10p.1	
SDR10-1E1	C. intestinalis	EDPMNYPAAARRHVqr1RILGYCSQLLVF---MV-----VWRLLVPRSGI--	11p.1	
SDR10-2E1	C. intestinalis	ENIEDFSKEQKAMqrmkTlSKVGLQTIAGVSALGLASAVGLTSSlWELSSyVLG-----	12p.1	
SDR10-1E1	S. purpuratus	EDMDIPAAARSHLkmLRNIrWTFNTVLL---VV-----FWRVLIARSQl--	14p.1	
SDR10-1E1	D. melanogaster	QRPESLPASRKRMLr1YYLHQLTKLVAV---LL-----TWRFLMSRSKR--	9p.1	
SDR10-1E1	A. gambiae	EAPETLPKARKLLRklYIMDKIVQIGLY---LF-----GLWLAWTYLEVVT---	3p.1	
SDR10-1E1	A. mellifera	DSPETLPAAARSHIKklYWIQKVVEFGML---LV-----VLRFLLLRIPM--	4p.1	
SDR10-1E1	C. elegans	ENLENLNRsRAHLLkmRIRRQVIAAIVY---AG-----FISTI-GRKWKKT	9p.1	
SDR10-1E1	A. californica	EDLSGLPAARAHVRklRIIRYLFNMSVA---VV-----LWRVLIAKSQF--	9p.1	

SDR10E1	H. sapiens	-ARNIWYFVVS [*] LCYK--FLSYFRASSTMRY-----
SDR10E2	H. sapiens	-ARNVWFFIVSFCYK--FLSYFRASSTLKV-----
SDR10-1E1	C. intestinalis	-AKNLWHLFMSLWFK--FLGFFQISSTLHRSNFFSR----ILSSS
SDR10-2E1	C. intestinalis	-DGLSWFV-----
SDR10-1E1	S. purpuratus	-ARNLWAFVINIFFR--FLRYCRVTSTIAR---TH-----
SDR10-1E1	D. melanogaster	-LNDLWSSFLENALR--M---ARLIPFL-----
SDR10-1E1	A. gambiae	--G-----SIQFVFD-----TAIESLRG--TTVRQGL-----
SDR10-1E1	A. mellifera	-AQSACFTLLSAILR--M---CRMIV-----
SDR10-1E1	C. elegans	TQYLTWFGAMLATYTYTEVSFRRHIPLKSLKDYTQTS [*] DYSRYLQKS
SDR10-1E1	A. californica	-ARNLWFFIVGLVSK--FVQYFRITSTMHK-----

Figure S27. Alignment of the invertebrate orthologs of the human SDR10E1 family variants. For further details see Fig. S25 and Table S29.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

		x x x		
SDR11E1	H. sapiens	----MAMTGWSCSLVTGAGGFLGQRIIRLLV---KEKELKEIRVLDKAFGPPELREEFskLQ		1p.2
SDR11E2	H. sapiens	-----MGWSCSLVTGAGGLLGQRIVRLLV---EKEKELKEIRALDKAFRPPELREEFskLQ		1p.2
SDR11E3	H. sapiens	MADSAQAQKLVLVLTGGCGFLGEHVVRMLLQ--REPRLGELRVFDQHLGPWLEELktg--		1p.2
SDR11-1E1	S. purpuratus	---MPGTEGEVVMVTGASGFLGQHILKQLLEQ-GEFLIKEVRTFDLQPFPTWCPEL-evHN		1p.2
SDR11-1E1	M. domestica	-----MASGEVVLVTGGSGFIGQHIIRLLKDKSELGIKEVRVVDLNAFKNTI---dd--		1p.2
SDR11-1E1	C. briggsae	-----MYTVAIVTGGAGLVGRVYVQRLL-NEQIAEVRVIDRQSTS-----re--		1p.2
		*** * *		
SDR11E1	H. sapiens	NKTKLTVLEGDILDEPFLKRACQDVSVIHTACII----DVFGVTHRESIMNVNVkgTQL		2p.2
SDR11E2	H. sapiens	NRTKLTVLEGDILDEPFLKRACQDVSVIHTACII----DVFGVTHRESIMNVNVkgTQL		2p.2
SDR11E3	H. sapiens	-PVRVTAIQGDVTAHEVAAVAGAHVVIHTAGLV---DVFGRASPKTIHEVNVqgTRN		2p.2
SDR11-1E1	S. purpuratus	PTTQLSHIKGDLLECMEEVRAFAKGVTVVIHTAGVI---DVSPVPDAELLRSVNIqgSEN		2p.2
SDR11-1E1	M. domestica	EKLDIKTFVGDLCPEPDSVEDAFKGVDTVFHCAGKM---SLQYPPKYDELNRNNIeatQS		2p.2
SDR11-1E1	C. briggsae	ESRKLLKLYLMDLNRKPLENALLGCDGVICHAPHFPILYSKNKAEIDQMWRDNLdaces		2p.2
		* * *		
SDR11E1	H. sapiens	LLEACVQASVPVFIYTSSIEVAGPNSYKEI---IQNGHEEEP-----LENTW		
SDR11E2	H. sapiens	LLEACVQASVPVFIYTSSIEVAGPNSYKEI---IQNGHEEP-----LENTW		
SDR11E3	H. sapiens	VIEACVQTGTRFLVYTSSMEVVGPNTKGHP---FYrgNEDTP-----YEAVH	3p.1	
SDR11-1E1	S. purpuratus	VLQACIHHNIQYLVYTSTVDVIGQ---EP---ITAGTETIL-----GIPQHHH		
SDR11-1E1	M. domestica	VVDLCLKHNVQRILIYTSVCGSVCMPFKGSSSTVVINQTESKAATPMFDAKKPEEFDKQFI		
SDR11-1E1	C. briggsae	VVDTMISMNIRNLVNIGCAYSPIPNEDNYG-----LAQDV-----FIdYPRNYM	3p.1	
		+ +		
SDR11E1	H. sapiens	PAPYPHKKLAEKAVLAANGWNLKNGG-TLYTCALRPMYIYGEGSRFLSA-SINEALNNN		
SDR11E2	H. sapiens	PTPYPSKKLAEKAVLAANGWNLKNGD-TLYTCALRPTYIYGEGGPFLSA-SINEALNNN		
SDR11E3	H. sapiens	RHPYPCSKALAEWLVLLEANGRkvRGGL-PLVTCALRPTGIYGEHGQIMRD-FYRQGLRLG	4p.0	
SDR11-1E1	S. purpuratus	FGLYATTKYEAKEIVLKASNLILKNGK-RLQTCALRPTPVYGEEDTYNRD-VLRQACHYK		
SDR11-1E1	M. domestica	IRGYSSSKLKAQIVLSAHGKTLKNGTGQLTTAAIRPPLTYGEGDTFFMPDMLRYLSRHS		
SDR11-1E1	C. briggsae	LDKYGESRTRGEMYARKAA-----KRGSLNALFLRPTFVYGQKSKRIE-AIKELVQNA		
		* * *		
SDR11E1	H. sapiens	GILS-SVGKFSTVNPVYVGNVAWAHILALRALQDPKKAPSIRGQFYIISDDTPHQSYDNL		
SDR11E2	H. sapiens	GILS-SVGKFSTVNPVYVGNVAWAHILALRALRDPKKAPSVRGQFYIISDDTPHQSYDNL		
SDR11E3	H. sapiens	GWLFRAIPASVEHGRVYvgNVAWMHVLAAARELEQ--RATLMGGQVYFCYDGSPYRSYEDF	5p.2	
SDR11-1E1	S. purpuratus	MMV-RMGSESSRYQCTYAGNIAWGHVLAVKELLKPTTNESPAQGAFFLTDETTPVSKVSDF		
SDR11-1E1	M. domestica	YVYPKIAGAGGKQQLCYagNVAWGHMCAYKSLKA--APKSVGGLPVFITDDTPLYDTSRF	3p.2	
SDR11-1E1	C. briggsae	ALPFVVTGERGMHQfiYAGNLAAIAEKSFCLLQ--DQKKFNGEIVFCMDENCAHSIRdf	4p.0	5p.0
		* * *		
SDR11E1	H. sapiens	NYTLSKEFG-LRLDSRW-SFPLSLMYWIGFLLEIVSFLLRPIYTYRPPFN---RHIVTSL		
SDR11E2	H. sapiens	NYILSKEFG-LRLDSRW-SLPLTLMYWIGFLLEVVSFLLSPIYSYQPPFN---RHTVTLS		
SDR11E3	H. sapiens	NMEFLGPCG-LRLVGARPLLPHYWLLVFLAALNALLQWLLRPLVLYAPLLN---PYTLAVA		
SDR11-1E1	S. purpuratus	FTPFGVIGVD-AK--MSSFSLPFWLLYSIAVVIEICAWLLQPIYKVKFFLT---TATVTYA		
SDR11-1E1	M. domestica	IQKIGLVSGKYKARHSSWSIPHFIFFAMLTFLFDLLEPVKKITLKYSI--RSLSSYA		
SDR11-1E1	C. briggsae	FENRFLNPN-Y-----SNDVAVNYWPSFVSSYTTYWKNQLGLpvPDKSLNHVSFRLFF	6p.0	
		* * *		
SDR11E1	H. sapiens	NSVFTFSYKKAQRDLAYKPLYSWEEAKQKTVEWVGSVLDVRHKE----TL--KSKTQ		
SDR11E2	H. sapiens	NSVFTFSYKKAQRDLAYKPLYSWEEAKQKTVEWVGSVLDVRHKE----TL--KSKTQ		
SDR11E3	H. sapiens	NTTFTVSTDKAQRHFGYEPFLFSWEDSRTRTILWVQAATGSAQ-----		
SDR11-1E1	S. purpuratus	YGVYFQCCEGAERCLGYEPLYTYDDAVERSLVYRRECGLS-----		
SDR11-1E1	M. domestica	SSIIFFNRLRASIHMDYVPLIDEETS VGNSAKWYGKWWENIGKGQRNGVAKSKNN		
SDR11-1E1	C. briggsae	EKTVGFPNKKLRLLLDKSKPEISQEEALANYANPKSFTTDS TKRSVAVKG-----		
		*		

Figure S28. Alignment of the invertebrate orthologs of the human SDR11E family variants. For further details see Fig. S25 and Table S30.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

Accession	Species	Sequence	Position
SDR12C1	H. sapiens	-----ME-----SALPAAGFLYVWGAGTVA--YLA	
SDR12C2	H. sapiens	-----MGDVLEQFFILTGLLVCLACLA	
SDR12C3	H. sapiens	-----MAAVDSFYLLYREIA--RSCN--CYMEALALVGAWYT-----	
SDR12C-1C1	C. intestinalis	-----MAAVDSVKLLVNQMTSDLQNYSSF-AWNLLSVIGAWYTLKYSVK	
SDR12C-2C1	C. intestinalis	-----ME-----CWLFTYIGIAT-C-SIVA	
SDR12C-1C1	S. purpuratus	-----MAAVDVGFDLLFRQVS--NGFH--IYSEVLSLIGAYYV-----	
SDR12C-2C1	S. purpuratus	-----	
SDR12C-1C1	D. arizonae	-----MQPALELSIYTLRMAF-----IWQLISVAIYLVGTLAIAAYLYD	
SDR12C-1C1	D. ananassae	-----MD-----SEL--LNILSVISISV-----	
SDR12C-1C1	A. gambiae	-----M-----VTT--SSVLGSTAVL-----	
SDR12C-2C1	A. gambiae	-----MLI-----ASQALWGLALIGVWALAWWMYD	
SDR12C-3C1	A. gambiae	-----MFCSLAACLGYYAAVWLYE	
SDR12C-1C1	A. mellifera	MMFHLRFFIGVHDDLPSLPVPTFQPFSSATKFKDRDYIQFI W kMILEIV--FWLF----F-	1p.1
SDR12C-1C1	C. elegans	-----MESSDNLHDIDNL----- E ngNMACQCFLVGAGYVALAAV-	1p.2
SDR12C-1C1	C. remanei	-----MDLQWFAAGAGAVALLFI-	
SDR12C-1C1	A. californica	-----MIRQ-----YLGDSVDLFSVIGAGVTV--FVA	
SDR12C-2C1	A. californica	-MLSNRWFGS-----FRTFSLQLT-PSRILHFSDFIDVFAFLGAYYFVKKCLK	

[illegible]

SDR12C1	H. sapiens	elAKHGMKVVLISRSKDKLDQVSSEike-KF-KVETRTIAVDFAS---EDIY---DKIKT	2p.0	3p.2
SDR12C2	H. sapiens	elAKRGLNVVLSRTLEKLEAIETieR-TT-GRSVKIIQADFTK---DDIY---EHIKE	2p.0	3p.2
SDR12C3	H. sapiens	ELASRGGLNIILISRNEEKLQVAKDAID-TY-KVETDIIVADFSSG--REIY---LPPIRE		
SDR12C-1C1	C. intestinalis	KLAHEGLNIILVSRNKCDEEEAKfIET-AY-GVQTLVLRVQDLENL-TPFIT---KQIKQD	2p.1	
SDR12C-2C1	C. intestinalis	alAARGQNIALISRNPEKLKTVATEleT-KY-NVQTKYLVIDFTQD---ESIY---EKIEE	2p.0	3p.2
SDR12C-1C1	S. purpuratus	ELAHHGVMNIIILISRNEKLRKVASEies-FY-GVKTHVIAQDFSLG--SEIY---EDIST		2p.2
SDR12C-2C1	S. purpuratus	LLVKHDMKVVGVCARNLDKlaIDGELKK-EE-GGSFPPIQCDLTQR--DQIYAMFEKIKT	1p.0	
SDR12C-1C1	D. arizonae	ELARQGLNLVLSIRSKEKLIIVATNEies-EH-KVKTKWIAVDFGKG--REAY---EQIEK		2p.2
SDR12C-1C1	D. ananassae	elARRGLKLVLISRSLEKLNVAKEigD-KY-GVEVRVIDVDFTGG--AEIY---DKIQE	2p.0	3p.2
SDR12C-1C1	A. gambiae	alARKGLNIILVSRSLKLEDVAKEiet-EF-KVRTMVIADAFDTKG--AEIY---EQIQE	2p.0	3p.2
SDR12C-2C1	A. gambiae	QLASRGGLNVVLSRSTDKLVAVAEIES-KY-SVKTWIAVDFSSG--REIY---DHLRR		
SDR12C-3C1	A. gambiae	YLAAGMAIVLVARNAAKLNKVADEIRA-KH-GVETKVLVADFSKG--AEIY---PQLEK		
SDR12C-1C1	A. mellifera	ELATRKINLVLSRSLEKLEKTRNEIMQENP-TVEIKIIVADFSKG--KEIF---EKLAE		
SDR12C-1C1	C. elegans	ELARRGFNVLLVSRTQSKLEDTKKEILE-KYSSIEVTRTAADFDTNA-APSA---KDLLA		
SDR12C-1C1	C. remanei	ELARRGFNTYLVSRSTQSKLEQTKKEILQ-QYSNVVEVFATYDFDTNP-SPADY---QKLLD		
SDR12C-1C1	A. californica	qlAAKGLNVVLSRTLSKLEDMAKeskS-KY-KVETKVIADFSR---EDIY---DGIKL	2p.0	3p.2
SDR12C-2C1	A. californica	ELARRGLNVVLSISERNRLRSTQVLleG-RF-AVKVEYIVVDFASADQTEVY---NRIWE		2p.2

SDR12C1	H. sapiens	GLAGLEIGILvNNVGMSYE-YPEYFLDVPDL-DnvIKKMININILSVCKmT----QLVLP	4p.2	5p.0	6p.0
SDR12C2	H. sapiens	KLAGLEIGILvNNVGMLPNLLPSHFLNA-PDEIQsL---IHCNITSVVkmT----QLILK	4p.2	5p.0	6p.0
SDR12C3	H. sapiens	ALKDKDVGILVNNVGVFYP-YPQYFTQLSE---DKLWDIINVNIAAASLMV---HVVLP			
SDR12C-1C1	C. intestinalis	RINELDIGILNNAGLH-E-SPKSFTeveI---SLHAMVQVNMNAVAVMT----AAVLP	3p.1		
SDR12C-2C1	C. intestinalis	FLQGM DIGTLVNNVGMASP--LAFYLDTKNL-SQILPAIMKVNVMSVFkmT----QIVLP			4p.0
SDR12C-1C1	S. purpuratus	KLQGMQIGILvNNVGAM-D-YPQLFLEMDA---DRIRQLININIGAATmmT----KLVLV	4p.2		4p.0
SDR12C-2C1	S. purpuratus	HHGGV--DVCINNAGMAYP--SSLLDGTP---EEWQKSldlNVIALCLCT---KLSVQ	2p.0		
SDR12C-1C1	D. arizonae	ELAGIPVGILvNNVGRMYD-YPETFLDVPE---DTIWDILTINIGAVTMLT---RKIVP	2p.2		
SDR12C-1C1	D. ananassae	KTAGLDIGVLVNNVGISYS-HPEYFLDCYKADPQFLRNIVAANIHSVTHMS---ALFLP			
SDR12C-1C1	A. gambiae	QIENMEIGVLVNNVGMSYS-NPEYLLGLPDY-EKLINLLSCNILLSVTRMC---QLVMP			
SDR12C-2C1	A. gambiae	ELESVPVGILvNNVGANVD-YPDDLHIPE---DKLWQLININVGAVTMLT---RTVLP	2p.2		
SDR12C-1C1	A. gambiae	ALVPLDVGILvNNVGVSHD-TPMYVDEVPO---QTLWDLIHVNVAATLLC---NILAP	2p.2		
SDR12C-1C1	A. mellifera	QLKDIPIGILvNNVGMQYS-HPMYLEEVEPE---DDLWDIININIGATTMLT---RIVIG	2p.2		
SDR12C-1C1	C. elegans	TLNQVEIGVLINNVGMSYE-YPDVLHKVDGG-IERLANITINTLPPT1fLTQLSAGILP			3p.0
SDR12C-1C1	C. remanei	KLNEVNIGILINNVGMFFE-YPDVLHEIQGG-IEFLANVAVVNILPPT11S---AGILP			3p.0
SDR12C-1C1	A. californica	KMNGLDIGVLVNNVGCSYE-YPEYFGEVEEA--dfSQKMIHMNCTSVAmT----EIVLP		4p.0	5p.0
SDR12C-2C1	A. californica	VLEDKDIGLlvNNVGVSYSR-CPDVLLSISR---EDLWRLIYVNI GAATmmT----HMLLP	3p.2		4p.0

		+ +			
SDR12C1	H. sapiens	GMVERsK--GAILNISSGS---GMLPVPLLTIIYSATktFVDFFSQCLHEEYRSKGV----	7p.1	8p.0	
SDR12C2	H. sapiens	HMESrqK--GLILNISSGI---ALFPWPLYSMYSASkaFVCAFSKALQEEYKAKEV----	7p.1	8p.0	
SDR12C3	H. sapiens	GMVERKK--GAIVTISSGS---CKKPTQLAAFSASkaYLDHFSRALQY EYASKGI----		2p.0	
SDR12C-1C1	C. intestinalis	GMLSRQR--GLIVNMSSGG---GMFPVPLISLYSSTkaFVDHFSQALHYEVASKNI----		4p.0	
SDR12C-2C1	C. intestinalis	GMMERKR--GLILNISSAS---SLVPVNGFSVYGATKALVNYFSKCISRECEGHGI----			
SDR12C-1C1	S. purpuratus	QMVERKC--GVVNVVSSGT---SIHSPQLALYSACktYVDVFSQALEY EYKDYGI----		5p.0	
SDR12C-2C1	S. purpuratus	QMKEGVDGDGHILLNsmGGHRLIQGSNYLHFYAGTKHMKV KALTEGYRDEL RQKNS---K	3p.1		
SDR12C-1C1	D. arizonae	QMKAARR--GAIVNIGSGS---ELQPMPNMVYAASKKYVS YFTQALEQE LAEHNV----			
SDR12C-1C1	D. ananassae	GMIARKR--GVIINLSSTA---GVIPNPLLSVYSSTkaFVNKFSDDLQTEYKEHGI----		4p.0	
SDR12C-1C1	A. gambiae	GMVKRHA--GVVINISSLT---AVIPAPLLTVYAASKAFMDKFSEDLASEYAKHNI----			
SDR12C-2C1	A. gambiae	GMKKRGQ--GAIVNISSGS---ELQPLPYMTVYAATKVTVGRHPAHHGASkCHKRLVKIL	3p.2		
SDR12C-3C1	A. gambiae	SMKRRQR--GLIINVSSIA---SVGPSPCMATYAASKAYMTSFSIALRDEL RPFGV----			
SDR12C-1C1	A. mellifera	QMQRKGK--GAIVNVSSAS---GFIPPLPLMTVYSATKVYIISFTEALRAEY SKFGL----			
SDR12C-1C1	C. elegans	QMVARKA--GVIVNVGSSA---GANQMALWAVYSATkkyVSWLTA ILRKEYEHQGI----		4p.0	
SDR12C-1C1	C. remanei	QMVSRAK--GIIVNIGSAA---GAVPMAKWSVYSASkkyVSWLTATLRKEYGHQGI----		3p.0	
SDR12C-1C1	A. californica	AMVAKKR--GYVINIGSSA---GFKPAPLLALYSGTkgYVEMFTRSLYHEY IGRGV----		6p.0	
SDR12C-2C1	A. californica	GMVKQGR--GGLVVVSAGS---STQITPQMTVYSATkrYLDYFIQGVAYEYRHSGL----		5p.0	
		* *			
		*			
SDR12C1	H. sapiens	-FVqsVLPYFVATKLAKIRK-----PTLDKPSPETFVKSAIKTVGLQSR TNGYLIHALm	9p.0	10p.0	
SDR12C2	H. sapiens	-IIqvLTPYAVSTAMTKYLN-----TNVITKTADEFVKESLNYVTIGGETCGCLAHEI1	9p.0	10p.0	
SDR12C3	H. sapiens	-FVQSLIPFYVATSM TAPSNFLHR--CSWLVPSPKVYAHHAVSTLGISKR TTGYWSHSIQ		3p.0	
SDR12C-1C1	C. intestinalis	-HVQSLTPMYISTRMTDYSTINS--NKFTPSVETVYVKHALPTLGRFRSNTGYFPHTIQ		5p.0	
SDR12C-2C1	C. intestinalis	-TVqsVKPFFVSTNMVNNVK-----PNMLVMDADYYVNSLLGTIGKERESDGCWQHGLq	5p.0	6p.0	
SDR12C-1C1	S. purpuratus	-IVQTL LPSYVATKMADFGETMPR--SRFLIPSAAVYAKHAVASIGIANRTAGYWPHAVq		6p.0	
SDR12C-2C1	S. purpuratus	IRVsaLSPGLVESEFVV-----RLFGDDDPDKGR-----KVLQTTp cLKREDV	4p.0	5p.0	
SDR12C-1C1	D. arizonae	-TVQLVMPMFVITKMNEYSDSVMR--GGFLIPNARSFARS AVFTLGKTSMTTGFWTHGLQ			
SDR12C-1C1	D. ananassae	-LIQSVQPGFVATNM SKIRK-----ASVFAPSPETYVRSALSTLG IATQTAGYLP HALL			
SDR12C-1C1	A. gambiae	-VVQSVLP GPVATNM SKIRK-----SSWMACSPKVFANSAISTLGHTRKTTGYFP HALL			
SDR12C-2C1	A. gambiae	VVQGSNQTMPRFAvmN NFSTTIME--GGLFIPNAEMYAKFATFTLGKTKQTTGYWSHGIQ	4p.0		
SDR12C-3C1	A. gambiae	-EVQTVRPSFVHTNM TDFLVTGKEKWSKNMVRVDNFMAYAGCTIGKVDMTSGHWSHGLQ			
SDR12C-1C1	A. mellifera	-TIQHLSPFFVNTKMNAFSNLqv--SNILVPSATTYAKNAVN TLGKIDSSTGYWSHGIQ	4p.0		
SDR12C-1C1	C. elegans	-TVQTIAPMMVATKMSKVKR-----TSFFTPDGAVFAKSALNTVGNTSDTTGYITHQLQ			
SDR12C-1C1	C. remanei	-IFQTITPLMVATKMAGSPD-----TSFFCPTS DAFKSA LNTIGNSSDTTGYITHQLE			
SDR12C-1C1	A. californica	-TFqyVAPYFVVS KLSKFRR-----TSLMVSPN A FVRNALKTVGVQAYTTGYWAHDVq	7p.0	8p.0	
SDR12C-2C1	A. californica	-TFQCLMPFVYVNT RMTGFSDTLTR--SRGFPSAKQYASNAI LTLGRASLT TGYFYHTLq		6p.0	

SDR12C1	H. sapiens	----gSIISNLPSWI----YLKIVNMNKNSTRAHYLKKTCK--N-----	
SDR12C2	H. sapiens	----aGFLSLIPAWAFYS---GAFQRLLLTHYVAYLKLNTK--VR-----	
SDR12C3	H. sapiens	----fLFAQYMPPEWLWVW---GANILNRSRKEALSCTA-----	
SDR12C-1C1	C. intestinalis	----cYFAMLCPRFLVVK----FSHRMLNLQKEAASIQKKAK-----	
SDR12C-2C1	C. intestinalis	----gFFVRHMTGTFNALMKR-RMKTMQRNL--SLAGKAA--KKD---N-----	
SDR12C-1C1	S. purpuratus	----sWIARQIPRNTWMW---GANILNSALRRQAEVRRKLKIVKSSSKGKLASKSPTAESASKSV	
SDR12C-2C1	S. purpuratus	AELVVMVMQQPPNVqiHD---ILVRDQVQK-----	6p.0
SDR12C-1C1	D. arizonae	----yFFMKMAPQHLMRL---IGHQLTRRLRLEGLSQKKLT-----	
SDR12C-1C1	D. ananassae	----QLIIHFTEAVFGDQFARNLVLNILGTRKRALRRLAK--EQ-----	
SDR12C-1C1	A. gambiae	----ELSINALSFV-SPRLAEKITINTMQNIRARAMKKSTA--RSSAPADSTAVLTA--SS-----	
SDR12C-2C1	A. gambiae	----YGVMKLVPEWIRTM---IGGMMNKQFRKEYYDQQQKPAQAS-----	
SDR12C-3C1	A. gambiae	----LAGLSLVPEVVRVY----IFGLINKKLREQFHVQNNNKKR-----	
SDR12C-1C1	A. mellifera	----KIIVLLVPIEIRTK---LAMILNMIFRKEYFKQKRNI-----	
SDR12C-1C1	C. elegans	----LELMDLIPTFIRDK---ILTNMSVGTRAAALRKKER--EAKSQ-----	
SDR12C-1C1	C. remanei	----YEMMNLMPFIIDK---AVIRSSAKLREAAALAKKEE--KLLS-----	
SDR12C-1C1	A. californica	----rFVHSFMPAS-----MSMSMMQGARKKALKKKAA--AKSQ-----	
SDR12C-2C1	A. californica	----lWLAWMLPSGLWMW---GSEKLNNALRREAQNRALRRVHKSASDETMVSVAMTPA-----	

Figure S29. Alignment of the invertebrate orthologs of the human SDR12C family variants. For further details see Fig. S25 and Table S31.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR16C1	H. sapiens	-----MVWKRILGALVMF
SDR16C2	H. sapiens	-----MKFLLDILL
SDR16C3	H. sapiens	-----MNIILEILL
SDR16C4	H. sapiens	-----MNIVVEFFVV
SDR16C5	H. sapiens	-----MSFNLQSSKKLFIF
SDR16C-1C1	C. intestinalis	-----MDFQDVGNLLWA
SDR16C-1C1	S. purpuratus	-----MIFIDFLDLVWM
SDR16C-1C2	S. purpuratus	-----MENPIVIFLWL
SDR16C-1C3	S. purpuratus	-----MSDA-----SDREHSSTAMSI LEFVGELMIL
SDR16C-1C1	D. melanogaster	MEKNNNELSAEDAQILANGHAHPNANGVVHQKTEPVAPAADGWRQVLWNTWDAFADVAWF
SDR16C-1C1	A. gambiae	-----MDVIVF
SDR16C-1C1	A. mellifera	-----MQLAEWIIILY-----DFLLF
SDR16C-1C1	C. elegans	-----MFDIILEIVIL
SDR16C-1C2	C. elegans	-----MQDI-----LESVVV
SDR16C-1C3	C. elegans	-----MDRA-----LDFVKM
SDR16C-1C1	A. californica	-----MSLF-----LEFLVV
SDR16C-1C2	A. californica	-----MDMQIIFDGITA

SDR16C1	H. sapiens	PLQMIYLVVKAAGVGLVP---AKLRDLSRENVLITGGGRGIGRQLAREFAERGARKiVLW	1p.0
SDR16C5	H. sapiens	LGKSLFSLLEAMIFALLP---KPRKNVAGEIVLITGAGSGLGRLLALQFARLGSV-LVLW	
SDR16C2	H. sapiens	LPLLIIVCSLESFVKLFIP---KRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK-LVLW	
SDR16C3	H. sapiens	LITIIYSYLESIVKFFIP---QRRKSVAGEIVLITGAGHGIGRQTTEYFAKRQSI-LVLW	
SDR16C4	H. sapiens	TFKVLWAFVLAARWLVR---PKEKSVAGQVCLITGAGSGLGRLEFAEFARRAL-LVLW	
SDR16-1C1	C. intestinalis	LLVSLYYCLEAIVMFFVP---TGRKVVRGQTVLITGAGSGigQRLSVEFAKLGCT-IVGV	1p.0
SDR16-1C1	S. purpuratus	LLSVLYYIGELVLCVPTSF-RKNSIEGELVLTGAGSGIGRLQAIFAAAGCD-VVLW	
SDR16-1C2	S. purpuratus	IAKICFYNFVGFDINIPGSWKPKQDVSKIEVLVTGGGMGIGRLMSLTFAKLGAT-VIIW	
SDR16-1C3	S. purpuratus	HLQVLLVSMEAFLEKWLIPSSL-RSKSLEGETMLITGAGSGIGRLFAKFAALgVVR-VVLW	1p.2
SDR16-1C1	D. melanogaster	IICCIGYILqd--LYYIAFGY-PEKELNTDIALITGGGNGLGRLLAERLGKMGTK-VVIW	1p.1
SDR16-1C1	A. gambiae	LLTSLGYILqa--FYYQIFGV-PKKNLNGEIALVTGGGGGLGRLLALRLIKLGAK-VVLW	1p.0
SDR16-1C1	A. mellifera	MGMALIYISEAIIILTFIPKRY-RIKSVKGEIALVTGGAGGIGRLIAIKLAKLGAH-VVIW	
SDR16-1C1	C. elegans	LFNLLIQNLISLIKALPYSLLPKKDLYRKVLTITGAGNGLGKLLAQKFAARGAT-LILW	
SDR16-1C2	C. elegans	TLHAICLLIISTIRNCFPMGWLLRKDVrgQTVLITGSGSGLGRLLMAFEFGKLGAR-LVLW	1p.2
SDR16-1C3	C. elegans	VVGTLFFIVLNFFKNFLPNGVLPKRSVEGKKVLTITGSGSGLGRLLMALEFAKLGAE-VVIW	
SDR16-1C1	A. californica	LVNAIWLWLVAIYKALVPVSMQWTKDMSKDTVLVTGAGSGIGRLMSLKFAEMGCR-LVIW	
SDR16-1C2	A. californica	VRNIFAAFFLSWIRFFFS-G-YKKKSVTEEIVLITGAGSGMGQGMAMEFAKLGAV-VVLW	

SDR16C1	H. sapiens	GRTEKCLKETTEEIRQ-----MGTECHYFICDVGNREEVY	
SDR16C2	H. sapiens	DINKhGLEETAACKG-----LGAKVHTFVVDCSNREDIY	1p.0
SDR16C3	H. sapiens	DINkrGVEETAACERK-----LGVTAHAYVVDCSNREEIY	1p.0
SDR16C4	H. sapiens	DINTQSNEETAGMVRHIYRDLEAADAALqaGNGEELPHCNLQVFTYTCDVGKRENVY	1p.2
SDR16C5	H. sapiens	DINKEGNEETCKMA-REA-----GATRVHAYTCDSCSQKEGVY	
SDR16-1C1	C. intestinalis	DISIVGLGETKKKLEDLN-----MKVKYHCYKCDLSDREQIY	
SDR16-1C1	S. purpuratus	DINTkgIEETAQLVRK-----TGRKAWYCICDVSKREKVY	1p.2
SDR16-1C2	S. purpuratus	DINKETAQGVVKEIre-----AGGKAYSIVVDCCDNEAVY	1p.1
SDR16-1C3	S. purpuratus	DINASDVEETAKLVRV-----NGGKAWWYCDVTEMAKVN	
SDR16-1C1	D. melanogaster	DINKkgIAETVQIVVE-----AGGYCKGYVVDISKKEEVY	2p.2
SDR16-1C1	A. gambiae	DINQegLDDSVKLIQS-----LGGLCKGYKVDISNKEEVY	2p.2
SDR16-1C1	A. mellifera	DINRIgLESTVQEIRH-----NGGKCWGYCDITNKKEIY	1p.2
SDR16-1C1	C. elegans	DINLQSVDELKNEIRG-----NQGeaHSYEVNLCDPGKIA	1p.0
SDR16-1C2	C. elegans	DINEQGNKETLKELEA-----MGVeaKAYTVDLSEYKEIN	2p.0
SDR16-1C3	C. elegans	DVNKDGAEETKNQVVK-----AGGKASTFVVDLSQYKDIH	
SDR16-1C1	A. californica	DINEEGNLETARQIEA-----KGSKVKAYTVDLNKSESIY	
SDR16-1C2	A. californica	DVNNKGLEETVKMVKA-----VEGVCHTYICDVsdRAAVR	1p.1

SDR16C1	H. sapiens	QTAKAVRE ^{kv} GDITILVNNAAVVHGKSLMDSDDDALLKSHINTLGQF ^{wt} TKAFLPRMLE	2p.0	3p.0
SDR16C2	H. sapiens	SSAK ^{kv} KAEIGDVSILVNNAAGVVYTSDLFATQDPQIEKTFEVNVLAHF ^{wt} TKAFLPAMTK	2p.0	3p.0
SDR16C3	H. sapiens	RSLN ^{qv} KKEVGDTVILVNNAAGTVYSDLLSTKDEITKTTFEVNLAHF ^{wt} TKALLPSMME	2p.0	3p.0
SDR16C4	H. sapiens	LTAERV ^{kv} KEVGESVSVLNNAAGVVSGHLLLECPDELIERTMMVNCHAHF ^{wt} TKAFLPTMLE		2p.0
SDR16C5	H. sapiens	RVAD ^{qv} KKEVGDVSLINNAGIVTGKKFLDCPDELMEKSFVDNFKAHL ^{wt} YKAFLPAMIA	1p.0	2p.0
SDR16-1C1	C. intestinalis	DVAD ^{kv} KSDVGDDVILINNAGIVTGKRLMDCPDKLMIKTMDVNAVAHF ^{wt} IKAFLPSMLE	2p.0	3p.0
SDR16-1C1	S. purpuratus	EAAAKVKREAGEVTTILVNNAAGIAGHKFINLTDDAIQKTMEVNALAHAF ^{wt} LKAFLPDMMK		2p.0
SDR16-1C3	S. purpuratus	ETAQVR ^{kv} EEVGDTVMLVNNAAGIVTGKYFQDLNEEDFHKTNLVNSLAHF ^{wt} LKAFLPNMLE		2p.0
SDR16-1C2	S. purpuratus	RTADKVREDIGHVTILINNAGIVSGKKLLQCPDSLKKTMDLNINAHF ^{wt} LKAFLPHMLE		2p.0
SDR16-1C1	D. melanogaster	KAADVIRDEVG ^{di} TLLINNAGVVSGHLLLDTPDHLIERSFNVNVAHF ^{wt} TKAFLPKMIE	3p.0	4p.0
SDR16-1C1	A. gambiae	KYAKIIQEEIG ^{dv} TLLFNNAAGVVSGRALLDTPDHLIERSFSVNVLAHF ^{wt} TKAFLPAMLK	3p.0	4p.0
SDR16-1C1	A. mellifera	RMAKIVQIEVG ^{sv} TLLINNAGVVSGKIFWELSDVEIDRTYKVNILSHY ^{wt} NKTFLKDMMK	2p.0	3p.0
SDR16-1C1	C. elegans	QVGQQVINDIGKVDILVNNAAGI ^{ata} KMILDSSENEINRSFDVNVKAHF ^{yt} VQQFLPAMLK	2p.2	3p.0
SDR16-1C2	C. elegans	RTADLVKSEVGKVDILVNNAAGIV ^{tg} KKLLQCPDELMVKT ^{sv} VNTNALF ^{ft} TKNFLPGMLE	3p.2	4p.0
SDR16-1C3	C. elegans	KVAKETKEAVGDIDILINNAGIV ^{tg} KKLFCPDELMEKTMAVNTNALF ^{yt} AKNFLPSMLE	1p.2	2p.0
SDR16-1C1	A. californica	ETAA ^{kv} KADVGNVDVLVNNAAGIVTGRKFLDCPDGLVEKTMENVNTNAHF ^{wt} TKSFLPEMME	1p.0	2p.0
SDR16-1C2	A. californica	ETADKVRSEVGDTVMLVNSAGVVAGRRLLDLTDQIEHTFGVNLMPGI ^{wt} TKEFLPSMLE		2p.0

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SDR16C1	H. sapiens	LQNGHIVCLNSVLALSIPAIDYCTSKASAFAMESLTGLGL--DCPGVSATTVLPFHT		
SDR16C2	H. sapiens	NNHGHIVTVASAAGHVSVPFLLAY ^{cs} SKFAAVGFHKTLTDELAALQITGVKTTCLCPNFV	4p.1	
SDR16C3	H. sapiens	RNHGHIVTVASVCGHEGIPYLIPI ^{cs} SKFAAVGFHRLTSELQALGKTGIKTSCLCPVFV	4p.1	
SDR16C4	H. sapiens	INHGHIVTVASSLGLFSTAGV ^{edy} CASKFGVVGFFHESLSHELKAAEKDGIKTTLVCPYLV	3p.0	
SDR16C5	H. sapiens	NDHGHILVCISSAGLSGVNGL ^{ady} CASKFAAFGFAESVFVET ^{fv} QKQKGIKTTIVCPFFI	3p.2	
SDR16-1C1	C. intestinalis	KNCGHIVTIIASGAGVFGLPALLDYCA ^{sk} FAAVGLSEALDLELWQQRKDGIVTVVCPYYI	4p.1	
SDR16-1C1	S. purpuratus	RDHGHIVTIIASIMGEISAAGMSEYCMSKFASVGLHEAVLRETRAAGKLGINFTLVNPMYI		
SDR16-1C2	S. purpuratus	KNHGHIVTIIASLAGHLGVSLVDYCA ^{sk} FAAVGLDDALYHELQYSGKTGVKCTVVCIFYI		
SDR16-1C3	S. purpuratus	RNHGHIVTVASIMGEIVVPLSDYCMSKFAAVALHESLLREARAQKGDGVHFTLINPYKI		
SDR16-1C1	D. melanogaster	NDRGHITIIASLAGHVGISKLV ^{dy} CASK ^{fa} AVGFDEALRLELEVLGHTNIRTTTICPFFI	5p.0	
SDR16-1C1	A. gambiae	NDHGHITIIASLAGHVGISKLV ^{dy} CSSKFA ^{av} GFDEALRLELEHLRAQGVFTTVICPYFI	5p.0	
SDR16-1C1	A. mellifera	NNHGHIVTVASVAGLLGTGYKCTDYSATKFAAIGYHESLFT ^{kt} EL ^{kt} HGYDGIHATLICPYFI	4p.0	
SDR16-1C1	C. elegans	DNNGHIVTIIASAAGKMSSG ^{la} DYSSSTKHAAGVGFHDSLVAEIMESEKNGVKTTLVCPYYV	4p.0	
SDR16-1C2	C. elegans	SNKGHIVTIIASMAGKCGVAGL ^{lv} DYCA ^{sk} HGAVGFNDLSAELYALK-KDVKT ^{sv} TVCPYYI	5p.0	
SDR16-1C3	C. elegans	KDNGLHVTIIASMAGTGCVLVDYCA ^{sk} HGAIGCHDSIAMEILAQKKYGVNTTLVCPFFI		
SDR16-1C1	A. californica	RNHGHIVTIIASSAGLFGVATLADYCA ^{sk} FGAVGFDESI ^{rs} EMLKYRKTGVHTTVCPFFI	3p.1	
SDR16-1C2	A. californica	NNQGHIVNMASSCGLIGLSHLTDY ^{sa} SKFGVVGFTQTLN ^{ye} IEIHFSGH ^{dg} VHTTLVCPSEFV	3p.1	

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SDR16C1	H. sapiens	S-TEMFQGM ^{rv} Rf--PNLFPPLPKETVARRTVEAVQLNQALLLLPWTMHALVILK ^{sil} LPQ	4p.1	5p.1
SDR16C2	H. sapiens	N-TGFIKNPST ^{sl} -----GPTLEPEE ^{vv} NRLMHGILTEQKMI ^f IPSSIAFLTTLE ^{ril} LP	5p.1	6p.1
SDR16C3	H. sapiens	N-TGFTKNPST ^{rl} -----WPVLETDEVVRS ^{ld} GILTNKKMIFVPSYINIFLRLQ ^{kfl} LP	5p.1	6p.1
SDR16C4	H. sapiens	D-TGMFRGCR ^{ir} keTEPFLPPLKPDYCVQKAMKAILTDQPMICTPRLMYIVTFMK ^{sil} LPF	4p.1	5p.1
SDR16C5	H. sapiens	K-TGMFEGCT ^{tg} --PSLLPILEPKYAVEKIVEAILQEKMYLYMPKLLYFMMFLK ^{sfl} LPL	4p.1	5p.1
SDR16-1C1	C. intestinalis	D-TGMFKGVST ^{pi} -----LPTLKP ^{ey} AVNRMVDAILKNKRM ^{ll} LLPGFSYVYALK ^{gfl} LPS	5p.1	6p.1
SDR16-1C1	S. purpuratus	N-TGMFAGTKI ^{ry} --EMIVPTLEPEYVAGKVVEAVQTRTALV ^{rt} PVLLHLMVLLK ^{dil} LPQ	3p.1	4p.1
SDR16-1C2	S. purpuratus	K-TGMFDGVKA ^{kr} --SIMIDLMEPEYAVEQIILAIRT ⁿ Q ^{rv} VLILPKSLYFFPGLKNLWHP	3p.1	
SDR16-1C3	S. purpuratus	D-TGMFNGATIKK ^{sa} QLLFP ^{tl} LKPEFVADKVVEAVQTN rd V ^{rt} PFIFNMV ^{vv} LT ^{km} LPL	3p.1	4p.1
SDR16-1C1	D. melanogaster	QATGMFDDVNA ^{rw} -----VPTL ^{ds} NDVADKII ^{eg} VQKNEKYV ⁱⁱ IPGYLR ^{lm} LAIK ^{wm} FPW	6p.1	7p.1
SDR16-1C1	A. gambiae	QSTGMFDDVNS ^{rw} -----VPTL ^{ds} NDVADKII ^{eg} VQKNEKYV ⁱⁱ IPGYLR ^{lm} LAIK ^{wm} FPW	6p.1	7p.1
SDR16-1C1	A. mellifera	N-TGMFHGVEP ^{rl} -----MPMLEPEYVAQEVVSGILLN ^{qv} VVVLPGSV ^{rv} FLPLK ^{cl} LPA	5p.1	6p.1
SDR16-1C1	C. elegans	H-TSMF ^{dat} GAAT ^{rf} PWIFPILDTDYV ^{vv} QKIFEAIETEQEFLVTP ^{raf} YLVFAGI ^{qil} LPY	5p.1	6p.1
SDR16-1C2	C. elegans	N-TGMFDGIATK--WPTLLPILSP ^{ey} VVD ^{ci} MEAVLTDRAFLAIPKFSYIFIAL ^{agl} LPT		6p.1
SDR16-1C3	C. elegans	D-TGMFHGVTT ^{kc} --PALFPILEANYAVECIVEAILTNR ^{pl} LLCMPKASYLILALIGLLPI	3p.1	
SDR16-1C1	A. californica	K-TGMFEGAKS ^{rf} --PWLLP ^{le} PEYAADKIMDAVRTN ^q PMLCAPRVLYLLYFLR ^{gv} FPS	4p.1	5p.1
SDR16-1C2	A. californica	T-TGMFQGCRMA ^{af} --PLLIPELEQNATVQIRIMHAILTNQSEVYIPRLVYFMNSLK ^{ti} IPV	4p.1	5p.1

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SDR16C1	H. sapiens	AALEEIHKFSGT---YTCMNTFKGRT-----		
SDR16C2	H. sapiens	RFLAVLKRKISV---K--FDAVIGYKMKAQ-----		
SDR16C3	H. sapiens	RASAILNRMQNI---Q--FEAVVGHKIKMK-----		
SDR16C4	H. sapiens	EAVVCMYRFLGA---DKCMYPFIAQRKQATNNNEA----KNGI-----		
SDR16C5	H. sapiens	KTGLLIADYLG I---LHAMDGFVDQKKKL-----		
SDR16-1C1	C. intestinalis	KAMYVMGEACGI---NTSMDTFIGRKKE-----		
SDR16-1C1	S. purpuratus	KAIFSMEDFFET---AKAMDNFVGRRHVKSS-----		
SDR16-1C2	S. purpuratus	KAVQAAYDMNGI---QDMNNTFTGRTKED-----		
SDR16-1C3	S. purpuratus	KANLLEDDFLEN---EKVMKNFVGRRGQKAVEQTG----AKIE-----		
SDR16-1C1	D. melanogaster	GCVGGLLKRLVPDASPHGLPSSIAVPTVPL---NSNSKLTAADIAALDAELSSVTLPAKP		
SDR16-1C1	A. gambiae	GCNSGFLRRLVPDAAPQHTITPLNNS-----		
SDR16-1C1	A. mellifera	KLCWALMYNIIR--GPQGMMMFKGREEVQVLKNNNNITMSKGTIH-----		
SDR16-1C1	C. elegans	KAQAMVAQFFGL---VQNLERFHK-----		
SDR16-1C2	C. elegans	EVLNLYGDHFGI---THSMDFKGRQSRQA-----		
SDR16-1C3	C. elegans	ESQVMMADFFGT---NESMNDFKGRQKND-----		
SDR16-1C1	A. californica	TVADVLAEFI G I---SASMDDFVGR TKPKTA-----		
SDR16-1C2	A. californica	SAMLEVIRFFRA---DKFMHSFVGRKDELSLPAK----EE-----		
SDR16C1	H. sapiens	-----		
SDR16C2	H. sapiens	-----		
SDR16C3	H. sapiens	-----		
SDR16C4	H. sapiens	-----		
SDR16C5	H. sapiens	-----		
SDR16-1C1	C. intestinalis	-----		
SDR16-1C1	S. purpuratus	-----		
SDR16-1C2	S. purpuratus	-----		
SDR16-1C3	S. purpuratus	-----		
SDR16-1C1	D. melanogaster	PSMLIQRTPSLGERVL		
SDR16-1C1	A. gambiae	-----		
SDR16-1C1	A. mellifera	-----		
SDR16-1C1	C. elegans	-----		
SDR16-1C2	C. elegans	-----		
SDR16-1C3	C. elegans	-----		
SDR16-1C1	A. californica	-----		
SDR16-1C2	A. californica	-----		

Figure S30. Alignment of the invertebrate orthologs of the human SDR16C family variants. For further details see Fig. S25 and Table S32.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

		x x x		
SDR21C1	H. sapiens	MSSGIIHVALVTGGNKGIGLAIVRDLCLRF--SGDVVLTARDVTRGQAAVQQQLQAEGLSPR		
SDR21C2	H. sapiens	MSSCSRVALVTGANRGIGLAIARELCRQF--SGDVVLTARDVARGQAAVQQQLQAEGLSPR		
SDR21-1C1	C. intestinalis	-MSTTRVAIVSGSNRGLGLAIVRGLCKDF--KGDVYLCRSRSEASGKEAVKSLETEGLCPK		
SDR21-1C1	S. purpuratus	MSSRKTIAlvTGANKGIGFGIVRALCKELGERGVVYLASRDEGRGEKAVQELKGEGLNPR	1p.0	
SDR21-1C1	M. rotundata	---MTRVAvvTGGNKGIGFAIVKALCKQF--DGVVYLTARDVNRGQNAVQLEDDQLTPK	1p.2	
SDR21-1C2	A. californica	-MSLKRVAvvTGSNKGIGLAIVRGLCKDF--QGDVVLtaRDEGRGRAAVQVLEKEGFSPK	1p.0	2p.2
		* * * * *		
SDR21C1	H. sapiens	FHQLDIDDLQSI RALRDFLRKEYGGDLVLVNNAGIAFkvADPTPFHIQAEVTMKTNFFGT	1p.2	
SDR21C2	H. sapiens	FHQLDIDDLQSI RALRDFLRKEYGGDLVLVNNAAVAFksDDPMFEDIKAEMTLKTNFFAT	1p.2	
SDR21-1C1	C. intestinalis	YHQLDICDENSVL SLKEFLVKNYGGDLVLVNNAGFAYKSASTEPFGKQARDTVDVNYGT		
SDR21-1C1	S. purpuratus	CIQLDICNNDHISKVADYFRDITYGGDLILVNNAGIAFkaAATEPDSIQAPVTVETNVFAT	2p.0	
SDR21-1C1	M. rotundata	FHQLDVTDENSISTFRDYLQKTYGGDLILVNNAAIAFkmaATEPFSVQAEETVRVNYFAL	2p.0	
SDR21-1C2	A. californica	FHLLDISDHQSI VIKLRDFLKETYQGLDVLVNNAAILYnedSTLPFPDQARETIKVNYNN	3p.0	
		** * * * *		
SDR21C1	H. sapiens	RDVCTELLPLIKPqgRVVNVSSIMSVRALKSCSPELQQKFRSETITEEELVGLMNKFVED	2p.2	
SDR21C2	H. sapiens	RNMCNELLPI MKPhgRVVNISSLQCLRAFENCSEDLQERFHSETLTGEDLVLMKKFVED	2p.2	
SDR21-1C1	C. intestinalis	LKISNILLPI MKKGRVVNVSSFVSLMSIKKCSEELQSIFRSQTITEEELSSKMEEFVAH		
SDR21-1C1	S. purpuratus	LRLCRALIPLIRSHGrvVTVASQAGSSIYGRGPDQLQKRFKTVT-SEQGVIDL MNEFI sa	3p.1	4p.1
SDR21-1C1	M. rotundata	RKVCTLLYPLLKPHARVVHVSSSSGRLSL-IPSES LRKRFSDPNLTEEELDNIMHEFVnt		3p.1
SDR21-1C2	A. californica	LDVCEVLFPLLRPHArvCNMSSLANAIAFKVLSPELRTKFLNPQITMPEVSSSLMTQFVda	4p.1	5p.1
		* * * * *		
		+ +		
SDR21C1	H. sapiens	TKKGVHQKEGWP---SSAYGVTKIGVTVLSRIHARKLSEQRKGDKILLNACCPGWVRTDM		
SDR21C2	H. sapiens	TKNEVHEREGWP---NSPYGVSKLGVTVLSRILARRLDEKRRKADRILVNACCPGPVKTDM		
SDR21-1C1	C. intestinalis	ARAGDHVTHGWP---DTAYGVSKVGVSVMTWIQARQMR-MRGLDDVLINACCPGWVRTDM		
SDR21-1C1	S. purpuratus	AKEEKKKELGWG---SSNYGVSKLGVIALTRIQQGDI IKDSSREDILINscCPGYVDTDM	5p.0	
SDR21-1C1	M. rotundata	AKTNTHLENGWS---NSAYVASKVGVSAALARVHQMFN-SDSREDLAVNAVHPGYVDTDM		
SDR21-1C2	A. californica	AQENKHEEQGF LSRVSSYGISKIGLTLM SAIQQRDFD-AQGAVDIVVNscSPGYVNTDM	6p.0	
		* * * *		
SDR21C1	H. sapiens	AGPKATKSPEEGAETPVYLALLP PDAEGPHGQFVSEKRVEQW----		
SDR21C2	H. sapiens	DGKDSIRTVEEGAETPVYLALLP PDATEPQGQLVHDKVVQNW----		
SDR21-1C1	C. intestinalis	AGPKATKSPDEGAITPLYCALLPEGAKEPHGKFLSDKTIKEW----		
SDR21-1C1	S. purpuratus	SSHKGPLTIDQGAVTPVYLALLP GGC SHQGLFFYQKAVKDFW----		
SDR21-1C1	M. rotundata	TSHKGTLTDPQGAVAPVFAALLP ENTDIKGYIWFDKSLVEWTKDA		
SDR21-1C2	A. californica	TQKGKPLTVEegAVTPLYLCLLP PDVSGPRGLFIREKAIYDWT TT-	7p.2	
		* * * *		

Figure S31. Alignment of the invertebrate orthologs of the human SDR21C family variants. For further details see Fig. S25 and Table S33.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR25C1	H. sapiens		-----MLSAVARGY-----QGFHPCA--RLSVRMS		
SDR25C2	H. sapiens		-----MHKAGLLGLCARAWNSVRMA		
SDR25C1C1	S. purpuratus		-----MFSLTRLLSVGRSINHFRMA		
SDR25-1C1	D. melanogaster	MLHLSKQLVVRAPKIRLNASAVSGSQSSSFQNSNNYSRKLVGPNLQCHKRLLSSSS-Q			
SDR25-1C1	A. mellifera		-----MLRS-----SINRSMQQIN-R		
SDR25-1C1	C. elegans		-----		
SDR25-1C1	A. californica		-----		
		x x x			
SDR25C1	H. sapiens	STGIDRKGVLANRVAVVTGSTsgigFAIARRLRADGAHVVISRRKQONVDRAAKLQGEG	1p.1		
SDR25C2	H. sapiens	SSGMTTRDPLANKVALVTASTdgiGFAIARRLAQDGAHVVSRRKQONVDQAVATLQGEG	1p.1		
SDR25-1C1	S. purpuratus	SAAATGSRRLLEGKVAVVTASTEGIGYAI AKRLGEEGAHVVISRRKQAHVDHALKTLEKAN			
SDR25-1C1	D. melanogaster	SSTATGMKRLAGKVAVVTASTdgiGFAIAKRLAEDGAAVVISRRKQNVD SALAE LRKL N	1p.1		
SDR25-1C1	A. mellifera	NLSEIKYKRLEGKVAIVTASTqgiGFAIAKRLAEEGAKVMISRRKEENVQNALKELKS KN	1p.1		
SDR25-1C1	C. elegans	--MPSNCRRFEGKVAIVTAATKgiGLAIAERLLDEGASVVI GSRNQKNVDEAIEYLKNKG	1p.1		
SDR25-1C1	A. californica	----MAGLAGKVAIVTASTdgiGFAIARRLAQDGAKVMVSSRKQNNVDNAVKALKQEN	1p.1		
		* * *			
SDR25C1	H. sapiens	LS-VAGIVCHVGKAEDREQLVkaLEHCGGVDFLVCSAGVNPLVGSTLTGTSEQIWDkiLS	2p.0		3p.0
SDR25C2	H. sapiens	LS-VGTGTVCHVGKAEDRERLVtaVKLHGGDILVSNAAVNPFPGSIMDVTEEVWdk tLD	2p.0		3p.0
SDR25-1C1	S. purpuratus	LS-VSGLVCHVGKQADRakLietaVKENGGLDILVSNAAANPHFGNlLdcDEQAwdkiFD	1p.0	2p.0	3p.0
SDR25-1C1	D. melanogaster	LN-VHGLKCHVSEPEDRKQLFEETISKFKGLNILVSNAA TNPAVGGVLECDEK VWDKI FD			
SDR25-1C1	A. mellifera	LN-VCGMTCHVGKNEDRKS LLektIQEFHGLDILVLNAGINPSASTFFFTSES VWDKIFE	2p.0		
SDR25-1C1	C. elegans	LTKVAGIAGHIAS TDDQKKLVdf tLQKF GKINILVNNHGINPAGHILEVSDQVWDKLF E	2p.0		
SDR25-1C1	A. californica	LN-VEGLVCHVAKKEDRSKLFnetVKKFGGIDVLVSNAA SStyFGPTLnt PEDSydkmFD	2p.0	3p.0	4p.0
		* * *			
		+ +			
SDR25C1	H. sapiens	VNVKSPALLS QLLPYMENrr-GAVILVSSIAAYNPvvaLGVINVSKTALLGLTRTLAE	4p.1	5p.0	
SDR25C2	H. sapiens	INVKAPALMTKAVVPMEKRGgggsVVIVSSIAAFSPspgFSPYNVSKTALLGLTKTLAE	4p.1	5p.0	
SDR25-1C1	S. purpuratus	INVKSTFLLVKESVPHMVSRgggsIVVSS IAGYMPFELLGPYSVSKTALLGLTKALT PQ	4p.1		
SDR25-1C1	D. melanogaster	VNVKSSYLLAKEALPLL RQKNSSIVFVSSIAGYDAfel LGAYS VKTALI GLTKAAAKD		2p.0	
SDR25-1C1	A. mellifera	INVKSTFLLRDSLPLFLRKS KSA SVILLSSIVGS PFDmLGVSISKTTILGINQVAANI		3p.0	
SDR25-1C1	C. elegans	VNVKAGFQM TKLVHPHIAKBEgggaiIFNASYSAYKSPPGAAYGVTKTTLVGLTRALAMG			
SDR25-1C1	A. californica	LNVKSSFMLCKEVPMEKRGsgsmILVSSIAAYTPmsmIGIYSLTKTALLGLNKVLAPE	5p.1	6p.0	
		** *			
SDR25C1	H. sapiens	LAPKD IRVNCVPGIIKTFDSkvfHGNE SLWKNF---KEHHQLQRiGESED CAGIVSFLC	6p.0	7p.1	
SDR25C2	H. sapiens	LAPRNIRVNCLAPGLIKTSF SRmlWMDKEKEESM---KETLRIRrlGEPEDCAGIVSFLC	6p.0	7p.1	
SDR25-1C1	S. purpuratus	LSDMNIRVNCVAPGLVKTFKSSalLSSEESTKLA---LSGIPMKRAGTPDEISGIVSFLA	5p.0		
SDR25-1C1	D. melanogaster	LAPEGIRVNCLAPGVRTIKFSKALYENESANEAA---LSKIPMGRLGTSEEMAGVVSFLV			
SDR25-1C1	A. mellifera	LAPEGIRVNCIAPGI IKTFsqiliYENET-GEMM---LSKIPMNKFGKSDNIGSVAFLA	4p.0		
SDR25-1C1	C. elegans	LAKDNIRVNGIAPGVIKTKMSQvlWDGGEDA EKELTDIQEI ALGRLGVPDDCAGTVAYLA	3p.0		
SDR25-1C1	A. californica	LAAHNIRINCIAPGI IKTFSnalTQNE DALNVA---LSTIPLGr lGTPEEC SGASFLA	7p.0	8p.1	
		* ** *			
SDR25C1	H. sapiens	SPDASYVNGENIAVAGYSTRL-			
SDR25C2	H. sapiens	SEDASYITGETVVVGGGTPSRL			
SDR25-1C1	S. purpuratus	SDDASYITGENILVAGGAPSRL			
SDR25-1C1	D. melanogaster	SEDAGYITGESIVAGGGM TARL			
SDR25C1C1	C. elegans	SDDSSYITGEMII IAGGVQARL			
SDR25C1C1	A. mellifera	SDDASYITGETIVVAGGM RSRL			
SDR25-1C1	A. californica	SDDSAYMTGETIVVSGG MTRL			
		* * *			

Figure S32. Alignment of the invertebrate orthologs of the human SDR25C family variants. For further details see Fig. S25 and Table S34.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR26C1	H. sapiens	-----MAFMKKYLLPILGLFMAYYYYSANE-----EF		
SDR26C2	H. sapiens	-----MKVLLLTGLGAL--FFAYYWD-----NF		
SDR26-1C2	C.intestinalis	-----MSYCFKALFVIIVA-IVTYSFIQPD-----DY		
SDR26-1C4	C.intestinalis	-----MGWLRVTAVVVIA--CILYSAVRES-----GY		
SDR26-1C1	S. purpuratus	MALGTIYLIALCIAAVFILLSIRVLYFIALFLLVTFLICFFLSMVSDGDLTLMLYELIGN		
<div> <div></div> <div> <div>x</div> <div>x</div> <div>x</div> </div> </div>				
SDR26C1	H. sapiens	RpeMLQGKKVIVTGASKGIGREMAYHLAKMGAHVVTARSKETLQkvVSHCLELGAASAH	1p.2	2p.0
SDR26C2	H. sapiens	DpaSLQGARVLLTGANAGVGEELAYHYARLGSHLVLTATHEALQkvVGNCRLGAPKVF	1p.2	2p.0
SDR26-1C2	C.intestinalis	DtgILKNKRVLITGASQNIIGEELATQYAQSGAKIVITARREDKLKevAAKCRKAGATSVD	1p.2	2p.0
SDR26-1C4	C.intestinalis	NpdEVKGLRVVITGASSGIGEQIAYKFASMGAKLHITARRESILQkvAARAKELGAIESH	1p.2	2p.0
SDR26-1C1	S. purpuratus	KgdNMMGRVVWITGASSGIGEEELAYQLARKgAKVVLsARRVNElERVGNcVRFpEVREE	1p.2	2p.0
<div> <div></div> <div> <div>*</div> <div>***</div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> </div> </div>				
SDR26C1	H. sapiens	---YIAGTMEDMTFAEQFVAQAGKlmgGLDMLILNHITNTSLNLFHDD---IHHVRKSM	3p.2	
SDR26C2	H. sapiens	---YIAADMASPEAPESVVQFALDKlgGLDYLVNLHIGGAPAGTRARS---PQATRWM	3p.2	
SDR26-1C2	C.intestinalis	---YIVADMADIEQVKNVVKDAVALlgGLDQLVLNHVTGLNHPGMWNNSQFNLDYAQnsA	3p.2	4p.1
SDR26-1C4	C.intestinalis	---YLTISLSSYENSTLAVKDALEKlgGIDVLIILNHFTNNYLGsYRHE---AKDIEKLF	3p.2	
SDR26-1C1	S. purpuratus	NILVLPMDATKYETHGQVAETIVDRYgkiDILINNSGRsQRAL--VQ--DCKIEVDKAIM	3p.0	
<div> <div></div> <div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> </div> </div>				
<div> <div></div> <div> <div>+</div> <div>+</div> </div> </div>				
SDR26C1	H. sapiens	EVNFLSYVVLTVAAALPMLKQ-SNGSIVVSSlAgKVAYPMVAAYSASKFALDGFSSIRK		4p.2
SDR26C2	H. sapiens	qvNFVSYVQLTSRALPSLTD-SKGSILVVSSlAgRVPTSFSSTPYSAAKFALDGFGLRR	4p.0	5p.2
SDR26-1C2	C.intestinalis	IVNYVSYIHLSTHAIPHLE-SNGNLIVVSSlAgHVPTINTAIYGATKASLNHFYASLRL		5p.2
SDR26-1C4	C.intestinalis	MPNMLTHAHLASVAMESLIE-NKGRIATSSAvaLLGGAFTVPYTTTKFALGGFFRSLEH		4p.2
SDR26-1C1	S. purpuratus	DLNLMGPISLFEKVALPYMLENNYGQIINISSATGIMPAPLSSAYCASKHGMhgFFNSVRS	4p.0	
<div> <div></div> <div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> <div>**</div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> </div> </div>				
SDR26C1	H. sapiens	EYSVS-RVNVsITLCVLGLIDteTAMKAVSGIVHMQAAPKEECA-LEI-----	5p.2	
SDR26C2	H. sapiens	ELDVQ-DVNVAITMCVLGLRDRASAAEAavrSSTSRPRQPEHRGVPLQSQTAMFLPP----	6p.2	
SDR26-1C2	C.intestinalis	EMMASERDPYSITICMMGPIETDRSRWS-----KfpDKVNMKGNPIDDTAAQI-----	6p.1	
SDR26-1C4	C.intestinalis	ELTIN-KTGVSVSLIQLGYvatNSSKAIAD-KIKATGASKIECASE-----I-----	5p.2	
SDR26-1C1	S. purpuratus	ELSYR---NIAVTMVCPGPPVSNIVENALREDFTrpAAKPYDGTADRSYKVLMSTERCAA	5p.0	
<div> <div></div> <div> <div>*</div> <div>*</div> </div> </div>				
SDR26C1	H. sapiens	--IKGGALR-----QEEVYYDSSLWTTL--IRNPCRKILE		
SDR26C2	H. sapiens	-TVPGARTLTETPLRGWPQPKMKSSRQKSKTEKNDGHLEPVTAWEVQVPRVRRLCRGLAR		
SDR26-1C2	C.intestinalis	--IkaGTTRR-----SYLFIPWWTKYASAVKAIPSQLVD	7p.2	
SDR26-1C4	C.intestinalis	--VRGIMTR-----EKLIYFPGYVSWIPLMRALFPNYVD		
SDR26-1C1	S. purpuratus	LTVVAIANK---LNEVWVARQP-----I--LLFYMAQYMPGFtKwmTPLIG--RGRV-	6p.1	
SDR26C1	H. sapiens	FLYSTSYNMDRFINK		
SDR26C2	H. sapiens	P---HLFGHD----		
SDR26-1C2	C.intestinalis	RMFLKIFYNK----		
SDR26-1C4	C.intestinalis	KMTREAYYEGAFD--		
SDR26-1C1	S. purpuratus	----KQYNQSQAQ--		

Figure S33. Alignment of the invertebrate orthologs of the human SDR26C family variants. For further details see Fig. S25 and Table S35.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR28C1	H. sapiens	-----	
SDR28C2	H. sapiens	-----	
SDR28-1C2	C.intestinalis	MVYVVHLTDEVTKSFLSQKRATYRNMFTGELGRSVFGATVFTFVFALGVPWIGSTIFYIL	
SDR28-1C1	S. purpuratus	-----	
SDR28-1C2	S. purpuratus	-----	
SDR28-1C3	S. purpuratus	-----	
SDR28-1C1	A. californica	-----MMW--	
x x x			
SDR28C1	H. sapiens	-----MARTVVLITGCSSGIGLHL	
SDR28C2	H. sapiens	-----MNGQSQVLPGGGHESREGINMAAAPRTVLISGCSSGIGLEL	
SDR28-1C2	C. intestinalis	GLNYgcCTSTIAFFA-----TC-FLALLIFAVFPRGRLNPKDKAVLITGCDSGFGPLL	1p.2
SDR28-1C1	S. purpuratus	-----MAPLVVLISGCSTGIGLAL	
SDR28-1C2	S. purpuratus	-----MAPLVVLISGCSTGIGLAL	
SDR28-1C3	S. purpuratus	-----MAPLITLITGCSTGIGLTT	
SDR28-1C1	A. californica	LLLLPCGLALAVLLAVLFAFADTDFLLAL--YEKFGKDCGSLSGKVWITGASSGIGEHI	
* * * *			
SDR28C1	H. sapiens	AVRLASDPSQSFkvYATLRDLKTQGRLEWAAARA----LACPPGSLETQLQDVRDSKSVAA	1p.2
SDR28C2	H. sapiens	AVQLAHPKKRYqvVATMRDLGKKETLEAAAGE----AL--GQTLTVAQLDVCSDSVAQ	1p.2
SDR28-1C2	C. intestinalis	AKQLHALGMHVFagC-LLKDKGGEGAKHL-----MKIQSSRFHVLQLDVTNDSEIKM	2p.2
SDR28-1C1	S. purpuratus	AVRLAQDPDKKYLVIYATMRNLAKKEGLEKAASD----AL--DKTLFVRQLDVTVDQVKS	
SDR28-1C2	S. purpuratus	AVRLAQDPDKKYLVIYATMRNLAKKEAIEKAAGD----AL--DKTLFVRQLDVTVDQVKT	
SDR28-1C3	S. purpuratus	AVKMAKD-AKKYIVYATMRNLAKKGDLEQAAGS----AL--NDTLFVRQLDITEESIVA	
SDR28-1C1	A. californica	AYCLAKSGCRLVL---TARRVEELERVQACISQGPNSAALEKNILVLPDVLVHFHKhRE	
* **			
SDR28C1	H. sapiens	ARERV--T---EGRVDVlv-CNAGLGLLGPLEALGEDAVASVLDVNVVGTVRMLQAFLPD	2p.2
SDR28C2	H. sapiens	CLSCI-----QGEVDVlv-NNAGMGLVGPLEGLSLAAMQNVFDTNFVGAVRLVKAVLPG	2p.2
SDR28-1C2	C. intestinalis	AVQYIGMHIPPNDqgLWGI VNNAGASAFGEIEWSSIDLYKKVAEVLN LGVIRCTQACLPL	3p.2
SDR28-1C1	S. purpuratus	IFEFIMEK---HGRVDVli-NNAGFGFGPLEAMSMEKAKNMFDTNYFGTVRLIRAALPI	1p.2
SDR28-1C2	S. purpuratus	IFEFIMGHGRVDV---lvKNNAGFGFGFALEAMSMEKAKNMFDTNYFGTVRLIRAALPI	1p.2
SDR28-1C3	S. purpuratus	IVKQIKEK---HGKIDILVNNAAFGWMGPLEEMTMTHMRNMSETNIVGTFRMTQEVLP	
SDR28-1C1	A. californica	AVQTVLEH----FGqiDILVNNAARGQFAEWIKVELDVDELFTETNLVGPVSLSQEVVPH	1p.0
** * *			
+ +			
SDR28C1	H. sapiens	MKRRGSGRVLVTGVSvgLmgLPFNDVYCASKFALEGLCESLAVLLL PFGVhLSLIECGPV	3p.2 4p.1
SDR28C2	H. sapiens	MKRRRQGHIVVISSVMGLggVIFNDVYAASKFALEGFFESLAIQLLQFNIfiSLVEPGPV	3p.2 4p.1
SDR28-1C2	C. intestinalis	I-RrakGRVVNMASGFGRMIA GRSVYGITKWAVEGFS DCLRYEMRRWGvkvSIIIEPGNY	4p.1 5p.0
SDR28-1C1	S. purpuratus	MKKQKSGRIVNISSMVGHlaLPYMDMYNASKFAMEGLSESLLPQLKNFGIsiSTVQPGPV	2p.2 3p.1
SDR28-1C2	S. purpuratus	MKKQKSGRIVNISSVvGHlaLPYMDMYNASKFAMEGLSESLLPQLKNFGIsiSTVQPGPV	2p.2 3p.1
SDR28-1C3	S. purpuratus	MKKQKSGRIVNISSLAGIngFPFSAVYSASKFALEGFTESLHPELKCfNIkiSTVC PGPV	1p.2 2p.1
SDR28-1C1	A. californica	MIKRGGGQIVVTSSMAGKmgLPGARSYTGSKHaihgyFESLRTEMAGKNIEVTLICPGPT	2p.2 3p.0
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SDR28C1	H. sapiens	HTAFM-----EKVLGSPE--EVLDRDTIH TFRFYQ-YLAHSKQVFREAAQN-PEEVAe	5p.0
SDR28C2	H. sapiens	VTEFE-----GKLLAQVSMAEFFPG-TDPETLHYFRDLYLPASRKLFC SVGQN-PQDVVq	5p.0
SDR28-1C2	C. intestinalis	IAGTSIFTEDGVKKLGDSMWEKMPDNVKEDYGKKLFDLrvAE-MQTYCSKGMDDL RPVLN	6p.0
SDR28-1C1	S. purpuratus	ATNFG-----EALANAGTEEDNKDVSEETVKQMTAFRLLL-HKPDLFAAQQ-TEPVID	
SDR28-1C2	S. purpuratus	ATNFG-----EALVANAGTEEDNKDVSEETVkgMTAFRLLL-SKPDLF TAE-TGPVID	4p.0
SDR28-1C3	S. purpuratus	ITSFK-----DNMSANQDPEAKSSDAENPTKklFTGAIAAM-MPHMKSA AQT-SDEIAD	3p.0
SDR28-1C1	A. californica	FSQLY-----LTAATER-LGetLGLRMEKTQKRMSTS-----RCAYLSCVAM-ANQVSE	4p.0
SDR28C1	H. sapiens	vFL-----TALRAPKPTLRYFTTTERFLPLLRLDDPSGGSNYVTAMHREVFGDVPAK	
SDR28C2	H. sapiens	aIV-----NVISSRTPPLRQTNI RYSPLTTLKTVDSGSLYVRTTHRLLFRCPRLL	
SDR28-1C2	C. intestinalis	AYE--DALLSRIPLIRYQPM EAYWTIRSFVTHFPFSFIADyly-----IYRKAKK-	7p.1

SDR28-1C1	S. purpuratus	VIV-----ECVEAEKPKLRYPTSESVRHLI-----
SDR28-1C2	S. purpuratus	VIV-----ECVQAEKPKLRYPTSENVRSWVAKRYREEGVT-GLESIFE-----
SDR28-1C3	S. purpuratus	VII-----DCIKAEDPALRYGTNEGTSKRVTDRFGGGIGDAAAQNWKMLEPASKI-
SDR28-1C1	A. californica	AWIMQQPVLLTAYIIQYAPVLGRWLLKKFGPKQVQKIREGK-----
		*
SDR28C1	H. sapiens	AEAGAE-AGGGAGPGAEDAGRGAVGDPELGDPAPQ
SDR28C2	H. sapiens	-NLGLQCLSCGCLPTRVRPR-----
SDR28-1C2	C. intestinalis	-----
SDR28-1C1	S. purpuratus	-----
SDR28-1C2	S. purpuratus	-----
SDR28-1C3	S. purpuratus	-----
SDR28-1C1	A. californica	-----

Figure S34. Alignment of the invertebrate orthologs of the human SDR28C family variants. For further details see Fig. S25 and Table S36.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR32C1	H. sapiens	MVSPATrkSLPKVKAMDFITS----TAILPLLFGCLG----VFGLFRLLQWVRGKAYLRN	1p.1		
SDR32C2	H. sapiens	-----MGVMAMLMPLLLLLGISGLLFI-YQEVSRSLWSKSAVQN			
SDR32-1C2	C. intestinalis	-----MEEMKN			
SDR32-1C1	S. purpuratus	-----MSSASSMNSLTVATAAIFGSLG----LLWLYKKLRSQRRRAGLKD			
SDR32-1C1	D. busckii	-----MKLHEMEKCAPSSDWNVLYWVIGTILMPIALPLALINIWRFRQNYRNQLPG			
SDR32-1C1	A. gambiae	-----MKNLAERSAGSLYWLLATLFLPIAIPGLVLKLLTMMKEQRNARHLNG			
SDR32-1C1	A. dorsata	-----MTEESLKSWHLIWWLFKLFGPITIPWLIYHFLDIMQQKRRKKTNG			
SDR32-1C1	H. robusta	-----MSVLLF--SVGVGLLSVAGTV--YYFFCYKKCSSSLKG			
SDR32-1C1	A. californica	-----MGIRANAVWAVLGLPFSLLS----VFYYIYVY-CCKEKLMLKD			
		x x x			
SDR32C1	H. sapiens	AVVVITGATSGLGkeCAKVFYAAGAKLVLCGRNGGALEELIRELTASHATkv----QTH		2p.2	3p.0
SDR32C2	H. sapiens	KVVVITbAISGLGkeCARVFHTGGARVLVLCGNWERLENLYDALISVADPSkq----TF		1p.2	2p.0
SDR32-1C2	C. intestinalis	KVVLITtgASSGIGEGGLACAFARQGASLSLCGRNVENLKKVAEKCVCSEGAakt-----	1p.2	2p.0	
SDR32-1C1	S. purpuratus	KVVLITGASSGVGeaCAIAFYRLGCKVILCARRAPELERVKKELMGPEigSRD---TSTH		1p.2	2p.2
SDR32-1C1	D. busckii	kvVLITGASSGLGESLAHVFFYRAGCKVILAARRVQELERVKKDLALD--vq-PA----Y	1p.0	2p.0	
SDR32-1C1	A. gambiae	kvVLITGASSGLGEALAHSSFFLAGCKVLAARRKDELERVRKDLLELHAtVPT-----H	1p.0	2p.0	
SDR32-1C1	A. dorsata	kvVIITGASSGLGEALAHVFIACGCKIILISRKEELDRVKNTLMNTHvtVPT-----Y	1p.0	2p.0	
SDR32-1C1	H. robusta	KVVLIVGASSGIGeCAHIFYKENCKLILCAKDLPDLERVKKEVEESYRKT DENCESTSE		1p.2	
SDR32-1C1	A. californica	KVVFITGASSGLGaCAEAIFYTAGCRLVLSGRNVEKLNLLKVRMEKSKegTGF-----H		1p.2	2p.0
		** * * * * * *			
SDR32C1	H. sapiens	KPYLVTFDLTDSGAIVAAAAEILQCFGYVDILVNNAGISYRGTIMDTVDVDRVMETNY			
SDR32C2	H. sapiens	TPKLVLLDLSDISCPVDVAKEVLDICYGCVDILINNASVKVKGAHKISLELDKKIMDANY			
SDR32-1C2	C. intestinalis	--IQVVADVKNVKDMERMVDETVAKLQIDVLINNAGYGCKGGIengTLEQFDEVFSVNL	3p.0		
SDR32-1C1	S. purpuratus	TPC-HTLRPRKTRRVTDKAKEALALHGHVDILINNGMSGRGSVAETVLSVHQKIMNVNH			
SDR32-1C1	D. busckii	PPTVLALDLSELNSIPQFAKRVLEVYNQVDILINNGGISVRADVSTAVDVLKVMIVNY			
SDR32-1C1	A. gambiae	PPILPLDLSDLNSIGGKVQSVLEIHGAIDILVNNGGISVRGDALSTAIDVDIRIMLVNY			
SDR32-1C1	A. dorsata	PPVILPVDITNINNLTQETITKIIDIHGRIDILINNAGISYRGEIINTNMVDIKVMLTNY			
SDR32-1C1	H. robusta	EVTIFQLDISNLNETTKISECIQHGHIDILGIGAGISFRGKI IETELSDQLIMSVNY			
SDR32-1C1	A. californica	SPAIVTMDLEDLPSIKEKVKEVLAAFGHVDILINNAGKSYRGVALHTKLEVDKMLMDVNY			
		* *			
		+ +			
SDR32C1	H. sapiens	FGPVALTkaLLPSMIKRRQGHIVAIAISSIQGKMSIPFRSayaASKHATQAFFDCLRAEMEQ	4p.2	5p.2	
SDR32C2	H. sapiens	FGPITLTkaLLPNMISRRTGQIVLVNNIQGKGFI PFRTtyAASKHAALGFFDCLRAEVEE	3p.2	4p.2	
SDR32-1C2	C. intestinalis	KAPYYLMQLCLPHLK-KTkgCVINLSSCYTNMFVPDAVHYSMTKVGLDHLTKCAAieLGK	4p.2	5p.2	
SDR32-1C1	S. purpuratus	FGSLVLTsaILPNMISRSGHILSVSSQIGRAIPFRSaysASKHAMQAFDLSLRAEVAE	3p.2	4p.2	
SDR32-1C1	D. busckii	FGTVALTkaLLPSMIKRNKGHCIFISSVQGKFAIPQRAAYSASKHAMQAFADSLRAEMAN	3p.2		
SDR32-1C1	A. gambiae	FGSVALTKACLPMMARKEGRIVS ISSVQGKFAIPHRSAAYSASKHAMQAFCDLSLRAEVAK			
SDR32-1C1	A. dorsata	FAQIALAkvILPYMIKQQSGHIVCISSIQGKISIPYrsAYAASKYALQAWCDCCRAELHD	3p.2	4p.1	
SDR32-1C1	H. robusta	FGHVAATkaVLKSMVERRSGHIVYSSSQGKLSIPFRSAYSASKHAIQAFADCLRAEVAq	2p.2	3p.1	4p.2
SDR32-1C1	A. californica	FAHVEVTraILQMVERKTGQIVAIGSVQSRIAIPHRTsyaASKHAMQAYFDVLRSEVAQ	3p.2	4p.2	
		* * *			
SDR32C1	H. sapiens	YEIEVTVISPGYIHTNLSVNAI-TADGSRygvM-DTT---TAQGRSPVEVAQDVL-----	6p.2		
SDR32C2	H. sapiens	YDVVISTVSPTFIRSYHYPEQGNWEASIWkfF-FRK---LTYGVHPVEVAEEVM-----	5p.2		
SDR32-1C2	C. intestinalis	YGIRVNNVnpGLVVTEMVKANWKPDELEAFCKDFLSNTPLENESLSIQEVADVVI FLTSS	6p.0		
SDR32-1C1	S. purpuratus	HNIQVTVLSPSYIKTNISLSAL-DGDGSVhakM-DST---TAGGMSTVYVADKVV-----	5p.2		
SDR32-1C1	D. busckii	KNIYVSCVSPSYIRTQLSMNAL-TGAGSSYgkM-DET---TAKGMSPDKLAERIL-----	4p.2		
SDR32-1C1	A. gambiae	DNIKVTLISPGYINTALSLNAL-TGTGASYgkM-DAA---TAGGASPDQTASSIL-----	3p.2		
SDR32-1C1	A. dorsata	QNIKITIVSPGYIKTSLSLNAL-TGNGQIYgvM-DKT---IQEGYYPKYVAERIL-----	5p.2		
SDR32-1C1	H. robusta	fNVRVSVVSPAYVRTNLSLNALTSSGSLHGkm--DEN---QKSGMSAEVGVQAVV-----	5p.2		

SDR32-1C1 A. californica YNIGVSVNPPYYIATNLSTNAV-SADGSAYgkL-DAN---TKAGLQPEYVASKVV----- Sp.2

*

SDR32C1 H. sapiens -----AAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS--

SDR32C2 H. sapiens -----RTVRRKKQEVFMANPIPKAAVYVRTFFPEFFFAVVACGVKEKLVPEEG-

SDR32-1C2 C. intestinalis AAKSITGTCLPVEKGRI LMGN-----

SDR32-1C1 S. purpuratus -----DAVAKQQRDVVLGPFTHGAIIYIRALVPNLYFWIMAGRARKGTKMED---

SDR32-1C1 D. busckii -----QCILRKEPDVIVSDLQAKIAYYLRHILPSAYFWIMAKRALKLERAEKKKD

SDR32-1C1 A. gambiae -----KAIARDEKDVMLAPIAPRAAYWLRHLAPSVYFWIMKKRAEKLNST-----

SDR32-1C1 A. dorsata -----KAVLKEEKDILITPFIPKAAMYLRTLCPSLYFWIMQKRAKNTKEKE----

SDR32-1C1 H. robusta -----QAVLLDKKEVLLANCSYKMIVYFRNFLSDIYFMAMARRARSS-----

SDR32-1C1 A. californica -----SCVVNRTSELTVPAPHIDLAIALRAMSPWLFFKIMERRAKKEQREMKNDR

Figure S35. Alignment of the invertebrate orthologs of the human SDR32C family variants. For further details see Fig. S25 and Table S37.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

SDR42E1	H. sapiens	-----
SDR42E2	H. sapiens	MKSNPPRSSLEACKAAGQGEKSCPVCQACGEVSGPRSGSGSESERPAPKPGAI PGPGLGPK
SDR42-1E1	C. intestinalis	-----
SDR42-1E1	S. purpuratus	-----
SDR42-1E2	C. elegans	-----
SDR42-2E2	C. elegans	-----
SDR42-1E2	C. remanei	-----
SDR42-1E1	A. californica	-----

SDR42E1	H. sapiens	-----
SDR42E2	H. sapiens	AIPGPQAGSGTVPRPGAISGTGPGLGPGAGSVPGPGAGSV PGLGARSVPGPAGAGSVPG
SDR42-1E1	C. intestinalis	-----
SDR42-1E1	S. purpuratus	-----
SDR42-1E2	C. elegans	-----
SDR42-2E2	C. elegans	-----
SDR42-1E2	C. remanei	-----
SDR42-1E1	A. californica	-----

SDR42E1	H. sapiens	-----
SDR42E2	H. sapiens	PGAGSVPGPGAGSVPGPGAGSGPGLGGGLGPGVGVAGPGAGSVPGPGAGSVPGPGAGSVPG
SDR42-1E1	C. intestinalis	-----
SDR42-1E1	S. purpuratus	-----
SDR42-1E2	C. elegans	-----
SDR42-2E2	C. elegans	-----
SDR42-1E2	C. remanei	-----
SDR42-1E1	A. californica	-----

SDR42E1	H. sapiens	-----MDPKRSQKESV	
SDR42E2	H. sapiens	PGAGSVPGAGAGSTPEPELGPGLRQSGGTGPRPSESTTTPTPAPQKQTQAKPTKAARQKV	
SDR42-1E1	C. intestinalis	-----MDSVSDLTDTLGLPENFKLKTGTNGHsrRLKF	1p.1
SDR42-1E1	S. purpuratus	-----	
SDR42-1E2	C. elegans	-----MSIKRLSMRLKKGIIHRSWNRMTSLEAGLEEEKEIKIVEEpePRPWKV	1p.2
SDR42-2E2	C. elegans	-----MGHY	
SDR42-1E2	C. remanei	-----MKHY	
SDR42-1E1	A. californica	-----MVQTRSSAQSRDKEIH	

		x x x	
SDR42E1	H. sapiens	LITGGSGYFGFr1GCALNQNGVHVILFDISSPA-----Q---T	1p.1
SDR42E2	H. sapiens	LVTGGGGYLGFSLGSHLAKSGTSVILLDRRRPQ-----W---E	
SDR42-1E1	C. intestinalis	LVTGGCGYFGYKLGKVLHTLGADVTLLDIQLPQ-----KIQES	
SDR42-1E1	S. purpuratus	-----	
SDR42-1E2	C. elegans	LITGGAGHLAENLVAKLEEMTRDSIRPKIREMLEKEMPAVISTKVDKEVEKRLPMYIQIV	
SDR42-2E2	C. elegans	VIVGGGGFLGAHVISALQKIGCKERIIVVDPCPQ-E---FKTIKID---KSNISY---	
SDR42-1E2	C. remanei	VITGGAGLLGSQLISSIQKNGDFTKCVVIDPTPYRP---FDTIKLD---TSFVEYIQVS	
SDR42-1E1	A. californica	VVTGGGGFPGFSLAKYLARKGHHVKLIDVKEPV-----W---D	

SDR42E1	H. sapiens	-----IPEGIKFIQGDIRHLSDVEKAFQDADVTCVFHIASYGMSGREQLN--R	
SDR42E2	H. sapiens	-----LSPETKFIqaDVRDEEALYRA--FEGVDCVFHVASYGMSGAEk1Q--K	1p.0 2p.0
SDR42-1E1	C. intestinalis	-----LDDHLKFIrgDIRDYDVLKS--SAGMDCVYHIASFGMSGKDq1Y--K	2p.0 3p.0
SDR42-1E1	S. purpuratus	-----MTKVQRGDIRDRELLDKL--CEGVDCVFHIASYGMSGREmmKA-S	1p.0
SDR42-1E2	C. elegans	LVDVLEPRGRVL-KHHVAFVkcSFDDECTMKTA--LEQVDTVYHLAAVGMTQYarDR--	2p.0 3p.0

SDR42-2E2	C. elegans	-----IkaSFLDDKVLNI--LNGASAVVHLAAVGHTGLIagDR--	1p.0	2p.0
SDR42-1E2	C. remanei	-----SKIDSVSYSYISIQGSFLDETVLNRV--LSNCVTVFHLCAIGHTGRFgaQKYK		1p.0
SDR42-1E1	A. californica	-----LEANMEFIKGSICDDNQLQSV--VEGASAVYHMASYGMGREQLN--K		
		* * * *		
SDR42E1	H. sapiens	NLIKEVNVRGTDNQLQVCQRRRVPRLVYTSTFNVIFGGQVIRNGDE-SLPYLPHLHPDH		
SDR42E2	H. sapiens	EQIESINVGGTKLVIdivCVRRRVPRLIYTSTVNVAFGGKPIEQGDEDSVPYFPLDehVDH	3p.2	4p.0
SDR42-1E1	C. intestinalis	DLTEAINVDGTRNVIkaCQMNNVQRLIYTSSYNVLEGNPIIGGDE-TLPYADPNkiVDY	4p.2	5p.0
SDR42-1E1	S. purpuratus	DFIESINVGGTENIVeaCIKQNVPRLVYTSTHNVVFAQQDIENGDE-TLPPLPLSahKDD	2p.2	3p.0
SDR42-1E2	C. elegans	KACMDINAVGTMNLLIWARNSGVQRFIYTSSVGVVFSGEPMYNATE-EVGYPD--dfYNY		4p.0
SDR42-2E2	C. elegans	KSVHNFNVNGTKQLIKQCKALGVKRFYASSVAVSFIGEPLDNVTE-DDPLPDPKkyLDF		3p.0
SDR42-1E2	C. remanei	SRAHQFNVLGTIQLIKKCKENGQVRFIYSSSIADVFTGKPLYSCNE-AEPYPKQSeYLDI		2p.0
SDR42-1E1	A. californica	KLIEKVNIGGTEAVLkaCLSQDVTRLVYTSTYNVVFGGQEILDGDE-RLPYLTDDkfTDH	1p.2	2p.0
		* ** * * * *		
		+ +		
SDR42E1	H. sapiens	YSRTKSIAEQVLEANATPLDRGDGVLRTCALRPAGIYGPGEQRHLPRIVSYIEKGLFKF		
SDR42E2	H. sapiens	YSRTKAIADQLTLMANGMP-LpgGGTLRTCVLRPPGIYGPEEQRHLPRVagHIKKRLFMF	5p.2	6p.0
SDR42-1E1	C. intestinalis	YSKSKLKADKLILEANNT-LndGRQLKTCLRPAGIYGPGERRHMQRIakFIDWGIIL	6p.2	7p.0
SDR42-1E1	S. purpuratus	YSRTKSMAEQLAMKSNGRETKkd-SILNVCVIRPVAIYGAGEQRHFPRIVkNMEQGLLCM	4p.2	5p.0
SDR42-1E2	C. elegans	YCESKAHAERIVQKASGHR-----MRTTVLRFNNGIYGPGEKRVTERVvkFMLTGMWIA		5p.0
SDR42-2E2	C. elegans	YSASKAEAETVYLSQSTPD-----FKTVCLRFRIYGPEDPNVTLKVanLIKNGLFIG		4p.0
SDR42-1E2	C. remanei	YSSTKAEAESFILSQSCLD-----FKTTCILRFRAIYGPQDVSAEKVvnMVRKNLFMV		3p.0
SDR42-1E1	A. californica	YSKTKMLAEKKVLASNGAK-TSGGATLRCCVLRLAGVYGPGLRHLPRIVsYLEQGLVKV		3p.0
		* * * * *		
SDR42E1	H. sapiens	VYG--DPRSLVEFVHVDNLVQAHILASEALRADKGHIASGQPYFISDGRPVNNFEFFRPL		
SDR42E2	H. sapiens	RFG--DHKARMNWVHVNHLVQAHVLAEEALTTAKGYVasGQAYYINDGESVNLFEWMAPl	7p.0	8p.0
SDR42-1E1	C. intestinalis	RIG--D--AVVDWTHVNNLIQAHLAIPLGLSKTSGYVaaGKAYFISDNRLPRVFEFLRPL	8p.0	9p.0
SDR42-1E1	S. purpuratus	KIG--SSHIKVPWVHVDNLVNGHILAAEGLSSHKEHiaaGQVYFIADKAPVNQFEFLRPL	6p.0	
SDR42-1E2	C. elegans	TCKPNGVEAQTQLSSVANCISQLVKAEALALRWSDT--PHGQIYNIMDKTPVGTFSFWTPL		
SDR42-2E2	C. elegans	MVSAHGRESVSCASSGVNCAKAFALADQMLQNPDG--LHGraYYILDGENVGQFQFWTPL	5p.0	
SDR42-1E2	C. remanei	KISRHDHESISNMSSAENCGQAFHLANQVLAEQNG--PHGqaYFITDGETVGQYEVWSPL	4p.0	
SDR42-1E1	A. californica	TYG--PRESLVDFLHVDNLVQAHALAAEGLTEGRSYVaaGRAYFISDDKPVNNFEFFRPl	4p.0	5p.0
		* * * * *		
SDR42E1	H. sapiens	VEGLGYTFPSTRPLPLTLVYCFALFTEMVHFILGRLYNFQPFLLTRTEVYKTGVTHYFSLEK		
SDR42E2	H. sapiens	fEKLGYSPWIVQVPTSWVYLtaAVMERLHLALRPICSLPPLLTRSevRSVAVTHTFQIAK	9p.2	10p.0
SDR42-1E1	C. intestinalis	fNGLGQEVFPQYKCPYTIYIilaILMEMLHYILKPVLVIEPLLTRNeiMKMGIDHHHKMDQ	10p.2	11p.0
SDR42-1E1	S. purpuratus	ITGLGYRPSLIVPVWFMYIvaLLSEWLHTILKPVINFQPLMVRTelFQVAVTHHFSIEK	7p.2	8p.0
SDR42-1E2	C. elegans	NIALGFSSSMITVPATPIRLFAY-L---SQIIADMRIDPIVSVLEVDDLNVNNTFNIEK		
SDR42-2E2	C. elegans	VIALGKQPPSFYTPYDFIKAVVPYF---QNVCGYGVFKLPPLLTKFELSILAVDNTYSIER		
SDR42-1E2	C. remanei	IRALGKTPPVHVSVPYPIVSAFVSIS---SFFCYEIFHSSPPMTRFELETTLVDNTYSIEK		
SDR42-1E1	A. californica	fEGLGYGYPVNLPLPFLPVFYfaWLTEIVHYIVSTVYNFQPILTRTEvYKTGVTHYFSVQR	6p.2	7p.0
		** * * *		
SDR42E1	H. sapiens	AKKELGYKAQ-PFDLQEAWEWFKAHGHGRSSGSRDSE--CFVWDGLLVFLLI IAVL----		
SDR42E2	H. sapiens	ARAQLGYAPD-KFRFADAVELYVQSTTRRPRGSTARTLLRLLRLLLFLGLLALAL----		
SDR42-1E1	C. intestinalis	AINDLGYKPM-FYDFADTVALYLKERGsVSEKSKI--AFHPLWTSVLFTIVTVIIT----	12p.2	
SDR42-1E1	S. purpuratus	AKKQLGYEPV-ERDLTDMVQYFLERGHRKKSSSIGA---FLFTVILAVLFVLLM----		
SDR42-1E2	C. elegans	AERDLGYEPS-VSAIPEiIEHYLHRLPPDVVRPKGRSD-FYVKVAVLVGLTILIFVAVFS	6p.0	
SDR42-2E2	C. elegans	ARRELGYEPE-PCVMTdvAKYYQDLENEVATA--TTE-WKSAISILIVFIS-----	6p.0	
SDR42-1E2	C. remanei	AEKELGYVPG-KNHFKktVDYRIQPIQSTTHN--FGS-WFNFDTLFLMILI-----	5p.0	
SDR42-1E1	A. californica	ARTDLGYSPTVQNDLSQVVITYYKKLGRVKGHSMPLL--FYFVNAIIFIISIFM----		
		* ***		
SDR42E1	H. sapiens	----MWLPSSVILSL----		

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SDR42E2  H. sapiens      ----HFLGLQPLHAAVERL
SDR42-1E1 C. intestinalis ----ISLCL-----
SDR42-1E1 S. purpuratus ----SLLPLAE-----
SDR42-1E2 C. elegans     FTFWMYLIFQRLSRWNP-F
SDR42-2E2 C. elegans     IAFLLFLFNLN-----
SDR42-1E2 C. remanei     -IFWTIISF-----
SDR42-1E1 A. californica ----HVLPRVTTD-----

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Figure S36. Alignment of the invertebrate orthologs of the human SDR42E family variants. For further details see Fig. S25 and Table S38.

* symbol marks the position of identical amino acid residues of the aligned SDR protein sequences.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa	Structure consensus	Catalytic consensus
<i>Homo sapiens</i>	RDH11	51109	14	SDR7C1	7	122221	318	GANTGIG	YCHSK
	RDH12	145226		SDR7C2			316		
	RDH13	112724	19	SDR7C3	7	122222	331		
	RDH14	57665	12	SDR7C4	2	0	336	GANSGLG	YSRSK
	DHRS13	147015	17	SDR7C5	5	2022	377	GANSIG	YADTK
	DHRS12	79758	13	SDR40C1	10	120020022	317	GGNSIG	YAQNK
<i>Ciona intestinalis</i>	LOC100177351	100177351	4	SDR7-1C1	6	22212	372	GATDGVG	YSRSK
	LOC100179350	100179350	3	SDR7-1C2	6	02021	313	GANAGIG	YCRSK
	LOC100176936	100176936	6	SDR7-3C2	7	100022	320	GANSGLG	YAQQK
	LOC100182258	100182258	7	SDR7-3C3	7	202021	321	GGNTGVG	YSNTK
	LOC100178007	100178007	6	SDR7-3C4	6	02021	322	GANTGIG	YGRSK
<i>Strongylocentrotus purpuratus</i>	LOC764557	764557	-	SDR7-1C1	5	2221	283	GCNTGIG	YGQSK
	LOC589120	589120	-	SDR7-1C3	4	222	355	GANTGIG	YARSK
	LOC585181	585181	-	SDR7-2C2	5	2221	357	GANAGIG	YNRSK
<i>Musca domestica</i>	LOC101892171	101892171	-	SDR7-1C3	6	10102	328	GSNTGIG	YNQSK
<i>Brugia malayi</i>	Bm1_24195	6099738	-	SDR7-1C1	8	2022001	340	GASAGIG	YSRSK
<i>Aplysia californica</i>	LOC101848777	101848777	-	SDR7-1C1	7	212222	382	GGTSGIG	YTRSK
	LOC101852273	101852273	-	SDR7-1C3	7	122221	344	GANCGIG	YGQSK

Table S27. Genetic and molecular data of the invertebrate orthologs of the human SDR7C family and of the SDR40C1 variants. Chr, chromosome; phase formula contains phase type symbols aligned according to the sequence of their relative splicing sites; aa n., number of the variant amino acids.

Species	Gene symbol	Gene ID:	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	BDH1	5622	3	SDR9C1	6	10022	343	GCDSGFG	YCITK
	HSD17B2	3294	16	SDR9C2	5	2222	387	GGDCGLG	YGSSK
	HSD11B2	3291		SDR9C3			405	GCDSGFG	YGTSK
	DHRS9	10170	2	SDR9C4	4	212	319	GCDSGFG	YTPSK
	RDH5	5959	12	SDR9C5			317		YCVSK
	HSD17B6	8630		SDR9C6			313		
	SDR9C7	121214		SDR9C7			317		
	RDH16	8608		SDR9C8			317		YCISK
<i>Ciona intestinalis</i>	LOC100175276	100175276	-	SDR9-1C2	5	2222	383	GCDIPNSYG	YSASK
<i>Strongylocentrotus purpuratus</i>	LOC581727	581727	-	SDR9-1C2	6	21212	327	GCDTGFG	YCESK
<i>Caenorhabditis elegans</i>	dhs-20	17959	v	SDR9-1C2	5	1012	342	GCDTGFG	YVVSK
	drd-5	186315	X	SDR9-1C4	7	200112	331	GCDSGFG	YCVSK
<i>Aplysia californica</i>	LOC101862944	101862944	-	SDR9-1C2	7	212222	394	GCDSGFG	YSMSK
	LOC101861767	101861767	-	SDR9-1C5	5	1212	322	GCDTGFG	YCTSK

Table S28. Genetic and molecular data of the invertebrate orthologs of the human SDR9C family variants. The atypical structure consensus of *Ciona intestinalis* is highlighted in turquoise. For further details see Table S27.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	FAR1	84188	11	SDR10E1	11	0110012101	515	GATGFLG	YIYTK
	FAR2	55711	12	SDR10E2					YTYTK
<i>Ciona intestinalis</i>	LOC100177355	100177355	12	SDR10-1E1	12	0121022110	584	GATGFIG	YTLTK
	LOC100179698	100179698	12	SDR10-2E1	12	00121022110	573	GGTGFLG	YTLTK
<i>Strongylocentrotus purpuratus</i>	LOC584999	584999	-	SDR10-1E1	11	0010010012	644	GATGFIG	YTFTK
<i>Drosophila melanogaster</i>	CG5065	36860	2R	SDR10-1E1	9	00000021	625	GGTGFMG	YTFTK
<i>Anopheles gambiae</i>	AgaP_AGAP002279	1269279	2R	SDR10-1E1	4	111	543	GATGFMG	YAYTK
<i>Apis mellifera</i>	FAR1	551233	-	SDR10-1E1	5	0011	516	GGTGFMG	YTFTK
<i>Caenorhabditis elegans</i>	fard-1	180582	X	SDR10-1E1	11	0000010111	536	GGTGFLG	YTLTK
<i>Aplysia californica</i>	LOC101853321	101853321	-	SDR10-1E1	10	001221101	671	GGTGFBG	YTYTK

Table S29. Genetic and molecular data of the invertebrate orthologs of the human SDR10E family variants. For further details see Table S27.

Species	Gene Symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	HSD3B1	3283	1	SDR11E1	3	22	375	GAGGFLG	YPHSK
	HSD3B2	3284		SDR11E2			372	GAGGLLG	YPYSK
	HSD3B7	80270	16	SDR11E3	6	22102	369	GGCGFLG	YPCSK
<i>Strongylocentrotus purpuratus</i>	LOC592634	592634	-	SDR11-1E1	3	22	366	GASGFLG	YATTK
<i>Drosophila arizonae</i>	LOC108612818	108612818	4	SDR11-1E1	3	22	380	GGSGFLG	YSSSK
<i>Caenorhabditis briggsae</i>	CBG02636	8572428	II	SDR11-1E1	7	221000	357	GGAGLVG	YPRNY

Table S30. Genetic and molecular data of the invertebrate orthologs of the human SDR11E family variants. For further details see Table S27. The atypical tyrosine (Y) of the *Caenorhabditis briggsae* is highlighted in turquoise.

Species	Gene Symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	HSD17B12	51144	11	SDR12C1	11	2022001000	312	GSTDGIG	YSATK
	HSD17B3	3293	9	SDR12C2			310	GAGDGIG	YSASK
	HSDL1	83693	16	SDR12C3	4	100	330	GATDGIG	FSASK
<i>Ciona intestinalis</i>	LOC100179389	100179389	14	SDR12-1C1	6	21100	335	GCSSGIG	YSSTK
	LOC100176329	100176329	3	SDR12-2C1	7	202000	310	GCTSGIG	YGATK
<i>Strongylocentrotus purpuratus</i>	LOC583990	583990	-	SDR12-1C1	7	222000	356	GSTDGIG	YSACK
	LOC574750	574750	-	SDR12-2C1	7	001000	242	GASEGIG	YAGTK
<i>Drosophila arizonae</i>	LOC108610536	108610536	3	SDR12-1C1	5	2220	335	GATDGIG	YAASK
<i>Drosophila ananassae</i>	Dana\GF21190	6503875	-	SDR12-1C1	5	2020	318	GSTDGIG	YSSTK
<i>Anopheles gambiae</i>	AgaP_AGAP004532	1274678	2R	SDR12-1C1	4	202	329	GATDGIG	YAASK
	AgaP_AGAP008570	1275433	3R	SDR12-2C1	4	220	330	GSTDGIG	YAATK

	AgaP_AGAP007879	4578212	3R	SDR12-3C1	3	22	316	GASD GIG	YAASK
<i>Apis mellifera</i>	LOC410227	410227	-	SDR12-1C1	5	1220	359	GSTD GIG	YSATK
<i>Caenorhabditis elegans</i>	let-767	175895	III	SDR12-1C1	5	2200	337	GATD GIG	YSATK
<i>Caenorhabditis remanei</i>	CRE_05435	9824494	-	SDR12-1C1	4	200	215	GATD GIG	YSASK
<i>Aplysia californica</i>	LOC101847547	101847547	-	SDR12-1C1	9	20200000	315	GCTD GIG	YSGTK
	LOC101853549	101853549	-	SDR12-2C1	6	22200	361	GSSE GIG	YSATK

Table S31. Genetic and molecular data of the invertebrate orthologs of the human SDR12C family variants. The atypical phenylalanine (F) of the human catalysis consensus is highlighted in turquoise. For further details see Tables S27 and Consensuses in Online Resources 1.

Species	Gene Symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	SDR16C1	9249	1	SDR16C1	6	00011	302	GGGR GIG	YCTSK
	SDR16C2	51170	4	SDR16C2	7	000111	300	GAGH GIG	YCSSK
	SDR16C3	345275		SDR16C3					
	SDR16C4	157506	8	SDR16C4	6	20011	341	GAGSG LIG	YCASK
	SDR16C5	195814		SDR16C5		00211	309		
<i>Ciona intestinalis</i>	LOC100185899	100185899	-	SDR16-1C1	7	000111	304	GAGSG GIG	YCASK
<i>Strongylocentrotus purpuratus</i>	LOC755823	755823	-	SDR16-1C1	5	2011	311	GAGSG GIG	YCMSK
	LOC581999	581999	-	SDR16-1C2	4	101	311	GGGM GIG	YCASK
	LOC589689	589689	-	SDR16-1C3	5	2011	334	GAGSG GIG	YCMSK
<i>Drosophila melanogaster</i>	CG9265	35369	2L	SDR16-1C1	8	1200011	399	GGGN LIG	YCASK
<i>Anopheles gambiae</i>	AgaP_AGAP010232	1279655	3R	SDR16-1C1	8	0200011	298	GGGG LIG	YCSSK
<i>Apis mellifera</i>	LOC552689	552689	-	SDR16-1C1	7	220011	326	GGAG GIG	YSATK
<i>Caenorhabditis elegans</i>	dhs-4	172810	I	SDR16-1C1	7	020011	305	GAGN LIG	YSSTK
	dhs-3	172603	I	SDR16-1C2	7	202001	307	GGSG LIG	YCASK
	dhs-19	179578	V	SDR16-1C3	4	201	307	GGSG GIG	YCASK
<i>Aplysia californica</i>	LOC101846838	101846838	-	SDR16-1C1	6	00111	309	GAGSG GIG	YCASK
	LOC101853580	101853580	-	SDR16-1C2	6	10111	315	GAGSG MG	YSASK

Table S32. Genetic and molecular data of the invertebrate orthologs of the human SDR16C family variants. For further details see Table S27.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis Consensus
<i>Homo sapiens</i>	CBR1	873	21	SDR21C1	3	22	277	GGNK GIG	YGVTK
	CBR3	874		SDR21C2				GANK GIG	YGVSK
<i>Ciona intestinalis</i>	LOC100182286	100182286	-	SDR21-1C1	1	-	275	GSNR LIG	YGVSK
<i>Strongylocentrotus purpuratus</i>	LOC755162	755162	-	SDR21-1C1	6	00110	278	GANK GIG	YGVSK
<i>Megachile rotundata</i>	LOC100877141	100877141	-	SDR21-1C1	4	201	276	GGNK GIG	YVASK
<i>Aplysia californica</i>	LOC101846277	101846277	-	SDR21-1C2	8	0201102	281	GSNK GIG	YGISK

Table S33. Genetic and molecular data of the invertebrate orthologs of the human SDR21C family variants. For further details see Table S27.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	DHRS2	10202	14	SDR25C1	8	1001001	280	GSTSGIG	YNVSK
	DHRS4	10901		SDR25C2			278	ASTDGIG	
<i>Strongylocentrotus purpuratus</i>	LOC764565	764565	-	SDR25-1C1	6	00010	278	ASTEGIG	YSVSK
<i>Drosophila melanogaster</i>	CG10672	38598	3L	SDR25-1C1	3	10	317	ASTDGIG	YSVSK
<i>Apis mellifera</i>	DHRS4	412304	-	SDR25-1C1	5	1000	272	ASTQGIG	YSISK
<i>Caenorhabditis elegans</i>	dhrs-4	179772	V	SDR25-1C1	3	100	260	AATKGIG	YGVTK
<i>Aplysia californica</i>	LOC101862311	101862311	-	SDR25-1C1	8	2000100	253	ASTDGIG	YSLTK

Table S34. Genetic and molecular data of the invertebrate orthologs of the human SDR25C family variants. For further details see Table S27 and Consensuses in Online Resources 1.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis Consensus
<i>Homo sapiens</i>	SDR26C1	3290	1	SDR26C1	6	20222	292	GASKGIG	YSASK
	SDR26C2	374875	19	SDR26C2	7	202022	315	GANAGVG	YSAAK
<i>Ciona intestinalis</i>	LOC100176102	100176102	7	SDR26-1C2	8	2021212	292	GASQNGIG	YGATK
	LOC100179203	100179203	9	SDR26-1C4	6	20222	287	GASSGIG	YTTTK
<i>Strongylocentrotus purpuratus</i>	LOC580541	580541	-	SDR26-1C1	7	200001	348	GASSGIG	YCASK

Table S35. Genetic and molecular data of the invertebrate orthologs of the human SDR26C family variants. The atypical asparagine (N) of *Ciona intestinalis* structure consensus is highlighted in turquoise. For further details see Table S27.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis Consensus
<i>Homo sapiens</i>	HSD17B1	3292	17	SDR28C1	6	22210	328	GCSSGIG	YCASK
	RDH8	50700	19	SDR28C2			331		YAASK
<i>Ciona intestinalis</i>	LOC100176396	100176396	1	SDR28-1C2	8	2221001	389	GCDSGFG	YGITK
<i>Strongylocentrotus purpuratus</i>	LOC762727	762727	-	SDR28-1C1	4	221	266	GCSTGIG	YNASK
	LOC592953	592953	-	SDR28-1C2	5	2210	283	GCSTGIG	YNASK
	LOC577205	577205	-	SDR28-1C3	4	210	291	GCSTGIG	YSASK
<i>Aplysia californica</i>	LOC101854946	101854946	-	SDR28-1C1	5	0200	322	GASSGIG	YTGSK

Table S36. Genetic and molecular data of the invertebrate orthologs of the human SDR28C family variants. For further details see Table S27.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons n.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo sapiens</i>	DHRS7B	25979	17	SDR32C1	6	120222	325	GATSGLG	YAASK
	DHRS7C	201140		SDR32C2	11	20222	312	DAISGLG	
<i>Ciona intestinalis</i>	LOC104266214	104266214	11	SDR32C-1C2	7	200220	256	GASSGIG	YSMTK
<i>Strongylocentrotus purpuratus</i>	LOC588555	588555	-	SDR32C-1C1	6	22222	314	GASSGVG	YSASK
<i>Drosophila busckii</i>	LOC108603035	108603035	3R	SDR32C-1C1	5	0022	326	GASSGLG	YSASK
<i>Anopheles gambiae</i>	DHRS7 ANOGA	1276215	2L	SDR32C-1C1	4	002	317	GASSGLG	YSASK
<i>Apis dorsata</i>	LOC102677319	102677319	-	SDR32C-1C1	6	00212	317	GASSGLG	YAASK
<i>Helobdella robusta</i>	HELRODRAFT_194864	20213175	-	SDR32C-1C1	6	22122	306	GASSGIG	YSASK
<i>Aplysia californica</i>	LOC101858248	101858248	-	SDR32C-1C1	6	20222	312	GASSGLG	YAASK

Table S37. Genetic and molecular data of the invertebrate orthologs of the human SDR32C family variants. The atypical aspartate (N) of *Ciona intestinalis* structure consensus is highlighted in turquoise. For further details see Table S27 and Consensuses in Online Resources 1.

Species	Gene symbol	Gene ID	Chr	Variant symbol	Exons N.	Phase formula	aa n.	Structure consensus	Catalysis consensus
<i>Homo Sapiens</i>	SDR42E1	93517	16	SDR42E1	2	1	393	GGSGYFG	YSRTK
	SDR42E2	100288072		SDR42E2	12	0020200020	626	GGGGYLG	
<i>Ciona intestinalis</i>	LOC100186801	100186801	-	SDR42E-1E1	13	100202000202	406	GGCGYFG	YSKSK
<i>Strongylocentrotus purpuratus</i>	LOC575739	575739	-	SDR42E-1E1	9	02020020	334	-	YSRTK
<i>Caenorhabditis elegans</i>	hsd-1	189371	I	SDR42E-1E1	6	20000	462	GGAGHLA	YCESK
	hsd-2	191049	X	SDR42E-1E2	7	000000	374	GGGGFLG	YSASK
<i>Caenorhabditis remanei</i>	Cre-hsd-3	9824419	-	SDR42E-1E1	6	00000	390	GGAGLLG	YSSTK
<i>Aplysia californica</i>	LOC101864466	101864466	-	SDR42E-1E1	8	2000020	394	GGGGFPG	YSKTK

Table S38. Genetic and molecular data of the invertebrate orthologs of the human SDR42E family variants. The atypical (A) alanine of *Caenorhabditis elegans* structure consensus is highlighted in turquoise. For further details see Table S27.

Species	Variants	Phase formula	Splicing-site phases																																
<i>Homo sapiens</i>	SDR7C1	122221			1		2								2					2														1	
	SDR7C2				1		2								2					2														1	
	SDR7C3		122222			1		2							2					2										2					
	SDR7C4	0																																	
	SDR7C5	2022					2			0																									
	SDR40C1	120020022		1												0																		2	
<i>Ciona intestinalis</i>	SDR7C-1C1	22212					2																												
	SDR7C-1C2	02021																																	
	SDR7C-3C2	100022		1																															
	SDR7C-3C3	202021																																2	
	SDR7C-3C4	02021																																	
<i>Strongylocentrotus purpuratus</i>	SDR7C-1C1	2221																																	
	SDR7C-1C3	122221				1										2																			
	SDR7C-2C2	222					2																												
<i>Musca domestica</i>	SDR7C-1C3	10102				1																													
<i>Brugia malayi</i>	SDR7C-1C1	2022001															0																		
<i>Aplysia californica</i>	SDR7C-1C2	212222					2																												
	SDR7C-1C3	122221	1																																

Table S39a. Splicing site organization of the human SDR7C family, of the SDR40C1 variants, and of their respective invertebrate orthologs. The phase type symbols are aligned according to the sequence of their relative splicing sites. Phase symbols, in a same column and highlighted in green or pink, mark the orthologous splicing sites. Note, this figure is identical to Table S2a in the main text.

Species	Variants	% identity					
		SDR7C1	SDR7C2	SDR7C3	SDR7C4	SDR7C5H	SDR40C1
<i>Homo sapiens</i>	SDR7C2	71.66					
	SDR7C3	49.20	48.89				
	SDR7C4	45.31	46.75	48.72			
	SDR7C5H	45.87	47.21	42.01	45.39		
	SDR40C1	30.20	31.00	28.05	28.72	26.33	
<i>Ciona</i>	SDR7C-1C1	37.26	38.78	34.46	36.31	35.62	26.40
	SDR7C-1C2	46.05	48.11	47.68	46.08	36.79	24.64
	SDR7C-3C2	26.00	27.48	25.25	26.51	25.83	54.57
	SDR7C-3C3	36.69	35.48	33.02	32.57	34.50	25.33
	SDR7C-3C4	46.25	46.93	44.73	46.91	39.54	23.67
<i>Strongylocentrotus</i>	SDR7C-1C1	54.12	53.76	53.36	50.53	44.04	30.71
	SDR7C-1C3	47.17	47.78	59.09	48.90	40.30	29.61
	SDR7C-2C2	42.49	42.77	42.86	42.44	45.02	27.63
<i>Musca domestica</i>	SDR7C-1C3	49.37	51.91	53.92	47.78	44.52	31.25
<i>Brugia malayi</i>	SDR7C-1C1	36.77	39.48	38.54	41.40	33.66	27.67
<i>Aplysia californica</i>	SDR7C-1C2	39.81	41.04	41.38	36.86	33.13	29.24
	SDR7C-1C3	49.05	46.47	52.05	47.34	40.26	28.57

Table S39b. Percent identity values of the human SDR7C family, of the SDR40C1 variants and of their invertebrate orthologs. Note, this figure is identical to Table S2b in the main text.

Species	Variants	Phase formula	Splicing-site phases															
<i>Homo sapiens</i>	SDR9C1	10022		1			0				0			2		2		
	SDR9C2	2222							2				2			2		
	SDR9C3								2				2			2		
	SDR9C4	212											2			1		2
	SDR9C5												2			1		2
	SDR9C6												2			1		2
	SDR9C7												2			1		2
	SDR9C8												2			1		2
<i>Ciona intestinalis</i>	SDR9-1C2	2222							2				2			2	2	
<i>Strongylocentrotus purpuratus</i>	SDR9-1C2	21212	2				1					2				1		2
<i>Caenorhabditis elegans</i>	SDR9-1C2	1012				1					0					1		2
	SDR9-1C4	200112			2						0		0	1		1		2
<i>Aplysia californica</i>	SDR9-1C2	212222							2			1	2			2	2	
	SDR9-1C5	1212								1			2				1	2

Table S40a. Splicing site organization of the human SDR9C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity							
<i>Homo sapiens</i>		SDR9C1	SDR9C2	SDR9C3	SDR9C4	SDR9C5	SDR9C6	SDR9C7	SDR9C8
	SDR9C2	31.50							
	SDR9C3	31.29	38.54						
	SDR9C4	36.33	30.57	30.03					
	SDR9C5	35.12	29.17	30.87	43.63				
	SDR9C6	38.67	31.09	31.83	44.90	49.37			
	SDR9C7	36.36	32.47	30.29	44.19	47.76	50.80		
	SDR9C8	37.67	32.05	32.48	46.18	51.58	66.25	51.76	
<i>Ciona intestinalis</i>	SDR9-1C2	34.63	32.66	31.21	28.28	29.31	35.07	31.94	32.99
<i>Strongylocentrotus purpuratus</i>	SDR9-1C2	35.76	31.76	28.62	43.65	41.37	43.32	40.92	46.25
<i>Caenorhabditis elegans</i>	SDR9-1C2	35.14	26.67	29.13	34.17	34.91	37.54	34.82	37.54
	SDR9-1C4	32.03	27.73	26.17	34.82	33.33	35.37	35.50	36.01
<i>Aplysia californica</i>	SDR9-1C2	35.89	31.72	32.89	34.50	34.41	34.08	33.88	33.12
	SDR9-1C5	34.54	30.89	27.16	34.49	36.59	39.12	38.98	39.43

Table S40b. Percent identity values of the human SDR9C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phase																												
<i>H. sapiens</i>	SDR10E1	0110012101				0				1				1				0	0			1	2				1	0	1		
	SDR10E2					0				1				1				0	0			1	2				1	0	1		
<i>Ciona intestinalis</i>	SDR10-1E1	0121022110				0				1	2				1			0			2				1		1	0	1		
	SDR10-2E1	00121022110		0		0				1	2				1			0			2		2			1		1	0	1	
<i>Strongylocentrotus purpuratus</i>	SDR10-1E1	0010010012	0			0			1	0		0			1				0	0			1	2			1		1	0	1
<i>Drosophila melanogaster</i>	SDR10-1E1	00000021			0		0				0				0											2			1	0	1
<i>Anopheles gambiae</i>	SDR10-1E1	111				0										1												1		1	
<i>Apis mellifera</i>	SDR10-1E1	0011				0					0										1									1	
<i>Caenorhabditis elegans</i>	SDR10-1E1	0000010111				0			0			0		0									1		0			1		1	
<i>Aplysia californica</i>	SDR10-1E1	001221101				0						0			1				0				2			1	1			0	1

Table S41a. Splicing site organization of the human SDR10E family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity	
		SDR10E1	SDR10E2
<i>Homo sapiens</i>	SDR10E2	59.03	
<i>Ciona intestinalis</i>	SDR10-1E1	37.74	34.63
	SDR10-2E1	35.58	34.36
<i>Strongylocentrotus purpuratus</i>	SDR10-1E1	52.72	47.47
<i>Drosophila melanogaster</i>	SDR10-1E1	38.82	38.43
<i>Anopheles gambiae</i>	SDR10-1E1	36.65	36.06
<i>Caenorhabditis elegans</i>	SDR10-1E1	38.13	34.05
<i>Apis mellifera</i>	SDR10-1E1	38.58	39.17
<i>Aplysia californica</i>	SDR10-1E1	53.79	48.54

Table S41b. Percent identity values of the human SDR10E family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing site phases											
<i>Homo sapiens</i>	SDR11E1	22	2		2									
	SDR11E2		2		2									
	SDR11E3	22102	2		2	1	0			2				
<i>Strongylocentrotus purpuratus</i>	SDR11-1E1	22	2		2									
<i>Musca domestica</i>	SDR11-1E1	222	2		2					2				
<i>Caenorhabditis briggsae</i>	SDR11-1E1	221000	2		2		1			0		0	0	0

Table S42a. Splicing site organization of the human SDR11E family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity		
		SDR11E1	SDR11E2	SDR11E3
<i>Homo sapiens</i>	SDR11E2	93.55		
	SDR11E3	38.40	39.00	
<i>Strongylocentrotus purpuratus</i>	SDR11-1E1	32.03	32.87	33.98
<i>Musca domestica</i>	SDR11-1E1	26.98	26.85	26.04
<i>Caenorhabditis briggsae</i>	SDR11-1E1	18.21	19.10	19.52

Table S42b. Percent identity values of the human SDR11E family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases																	
<i>Homo sapiens</i>	SDR12C1	2022001000			2		0			2	2		0		0	1		0		0
	SDR12C2				2		0			2	2		0		0	1		0		0
	SDR12C3	100				1											0			0
<i>Ciona intestinalis</i>	SDR12C-1C1	21100				2			1			1					0			0
	SDR12C-2C1	202000			2		0			2	2				0			0		0
<i>Strongylocentrotus purpuratus</i>	SDR12C-1C1	222000			2					2	2				0		0			0
	SDR12C-2C1	001000						0					0			2		0		0
<i>Drosophila arizonae</i>	SDR12C-1C1	2220			2					2	2									
<i>Drosophila ananassae</i>	SDR12C-1C1	2020			2		0			2							0			
<i>Anopheles gambiae</i>	SDR12C-1C1	202			2		0			2										
	SDR12C-2C1	220			2					2	2						0		0	
	SDR12C-3C1	22			2					2	2									
<i>Apis mellifera</i>	SDR12C-1C1	1220		1	2					2									0	
<i>Caenorhabditis elegans</i>	SDR12C-1C1	2200	2		2									0			0			
<i>Caenorhabditis remanei</i>	SDR12C-1C1	200			2									0			0			
<i>Aplysia californica</i>	SDR12C-1C1	20200000			2		0			2			0		0		0		0	0
	SDR12C-2C1	22200			2					2	2				0		0			0

Table S43a. Splicing site organization of the human SDR12C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity		
		SDR12C1	SDR12C2	SDR12C3
<i>Homo sapiens</i>	SDR12C2	40.47		
	SDR12C3	41.02	34.25	
<i>Ciona intestinalis</i>	SDR12C-1C1	35.84	32.42	41.19
	SDR12C-2C1	37.67	33.33	34.14
<i>Strongylocentrotus purpuratus</i>	SDR12C-1C1	41.89	35.71	49.54
	SDR12C-2C1	27.23	27.43	19.67
<i>Drosophila arizonae</i>	SDR12C-1C1	37.79	32.55	39.56
<i>Drosophila ananassae</i>	SDR12C-1C1	46.86	38.93	38.74
<i>Anopheles gambiae</i>	SDR12C-1C1	44.33	34.68	39.00
	SDR12C-2C1	37.25	29.67	39.03
	SDR12C-3C1	31.97	30.54	37.00
<i>Apis mellifera</i>	SDR12C-1C1	37.75	33.78	42.86
<i>Caenorhabditis elegans</i>	SDR12C-1C1	39.46	31.44	32.48
<i>Caenorhabditis remanei</i>	SDR12C-1C1	35.40	34.01	34.01
<i>Aplysia californica</i>	SDR12C-1C1	45.54	36.33	38.13
	SDR12C-2C1	33.00	27.27	41.51

Table S43b. Percent identity values of the human SDR12C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases																										
<i>Homo sapiens</i>	SDR16C1	00011					0										0										1		1
	SDR16C2	000111					0									0											1		1
	SDR16C3						0									0											1		1
	SDR16C4	20011										2															0		1
	SDR16C5	00211														0											2		1
<i>Ciona intestinalis</i>	SDR16-1C1	000111			0											0											1		1
<i>Strongylocentrotus purpuratus</i>	SDR16-1C1	2011									2																1		1
	SDR16-1C2	101																									1		
	SDR16-1C3	2011					2																					1	1
<i>Drosophila melanogaster</i>	SDR16-1C1	1200011	1													0											0		1
<i>Anopheles gambiae</i>	SDR16-1C1	0200011	0													0											0		1
<i>Apis mellifera</i>	SDR16-1C1	220011									2						2										0		1
<i>Caenorhabditis elegans</i>	SDR16-1C1	020011												0				2	0	0								1	1
	SDR16-1C2	202001		2										0					2	0	0								1
	SDR16-1C3	201																	2	0								1	
<i>Aplysia californica</i>	SDR16-1C1	00111														0										1		1	1
	SDR16-1C2	10111													1												1		1

Table S44a. Splicing site organization of the human SDR16C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% Identity				
		SDR16C1	SDR16C2	SDR16C3	SDR16C4	SDR16C5
<i>Homo sapiens</i>						
	SDR16C2	33.67				
	SDR16C3	32.31	63.67			
	SDR16C4	36.45	40.67	39.67		
	SDR16C5	34.67	41.95	40.27	45.25	
<i>Ciona intestinalis</i>	SDR16-1C1	37.92	42.42	41.08	42.05	48.84
<i>Strongylocentrotus purpuratus</i>	SDR16-1C1	37.67	40.13	38.13	42.95	40.98
	SDR16-1C2	33.22	37.46	37.79	38.16	43.97
	SDR16-1C3	38.67	38.80	38.46	42.54	41.18
<i>Drosophila melanogaster</i>	SDR16-1C1	32.20	38.72	36.36	35.41	38.54
<i>Apis mellifera</i>	SDR16-1C1	34.14	40.48	39.46	37.05	38.85
<i>Anophele gambiae</i>	SDR16-1C1	33.22	41.52	37.02	35.40	42.07
<i>Caenorhabditis elegans</i>	SDR16-1C1	30.20	35.71	35.71	36.54	38.46
	SDR16-1C2	37.16	40.68	40.34	43.67	47.68
	SDR16-1C3	35.35	39.32	35.93	40.33	48.18

Table S44b. Percent identity values of the human SDR16C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases							
					2	2				
<i>Homo sapiens</i>	SDR21C1	22			2	2				
	SDR21C2				2	2				
<i>Ciona intestinalis</i>	SDR21C-1C1	-	No splicing sites							
<i>Strongylocentrotus purpuratus</i>	SDR21C-1C1	00110	0		0		1	1	0	
<i>Megachile rotundata</i>	SDR21C-1C1	201	2		0			1		
<i>Aplysia californica</i>	SDR21C-1C2	0201102	0	2	0		1	1	0	2

Table S45a. Splicing site organization of the human SDR21C family variants and of their invertebrate orthologs. For further details see Table S39a.

Specie	Variants	% identity	
<i>Homo sapiens</i>		SDR21C1	SDR21C2
	SDR21C2	71.84	
<i>Ciona intestinalis</i>	SDR21C-1C1	55.64	49.45
<i>Strongylocentrotus purpuratus</i>	SDR21C-1C1	46.01	44.20
<i>Megachile rotundata</i>	SDR21C-1C1	48.16	45.96
<i>Aplysia californica</i>	SDR21C-1C2	50.91	48.73

Table S45b. Percent identity values of the human SDR21C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases											
<i>Homo sapiens</i>	SDR25C1	1001001		1	0		0	1		0	0	1		
	SDR25C2			1	0		0		1	0	0	1		
<i>Strongylocentrotus purpuratus</i>	SDR25-1C1	00010			0	0	0		1		0			
<i>Drosophila melanogaster</i>	SDR25-1C1	10		1						0				
<i>Apis mellifera</i>	SDR25-1C1	1000		1	0					0	0			
<i>Caenorhabditis elegans</i>	SDR25-1C1	100		1	0						0			
<i>Aplysia californica</i>	SDR25-1C1	2000100	2		0	0	0		1	0	0	1		

Table S46a. Splicing site organization of the human SDR25C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% Identity	
		SDR25C1	SDR25C2
<i>Homo sapiens</i>	SDR25C2	59.78	
<i>Strongylocentrotus purpuratus</i>	SDR25-1C1	47.97	56.12
<i>Drosophila melanogaster</i>	SDR25-1C1	46.59	49.46
<i>Apis mellifera</i>	SDR25-1C1	44.15	43.38
<i>Caenorhabditis elegans</i>	SDR25-1C1	40.55	46.09
<i>Aplysia californica</i>	SDR25-1C1	49.80	56.92

Table S46b. Percent identity values of the human SDR25C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases											
<i>Homo sapiens</i>	SDR26C1	20222	2		0	2			2			2		
	SDR26C2	202022	2		0	2		0	2			2		
<i>Ciona intestinalis</i>	SDR26-1C2	2021212	2		0	2		1	2				1	2
	SDR26-1C4	20222	2		0	2			2		2			
<i>Strongylocentrotus purpuratus</i>	SDR26-1C1	200001	2	0			0			0			0	1

Table S47a. Splicing site organization of the human SDR26C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity	
<i>Homo sapiens</i>		SDR26C1	SDR26C2
	SDR26C2	41.22	
<i>Ciona intestinalis</i>	SDR26-1C2	32.37	34.41
	SDR26-1C4	28.62	28.26
<i>Strongylocentrotus purpuratus</i>	SDR26-1C1	24.10	25.08

Table S47b. Percent identity values of the human SDR26C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases											
<i>Homo sapiens</i>	SDR28C1	22210		2			2		2		1			0
	SDR28C2			2			2		2		1			0
<i>Ciona intestinalis</i>	SDR28-1C2	2221001	2	2	2			1			0		0	1
<i>Strongylocentrotus purpuratus</i>	SDR28-1C1	221					2		2		1			
	SDR28-1C2	2210					2		2		1		0	
	SDR28-1C3	210							2		1		0	
<i>Aplysia californica</i>	SDR28-1C1	0200				0			2	0		0		

Table S48a. Splicing site organization of the human SDR28C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity	
<i>Homo sapiens</i>		SDR28C1	SDR28C2
	SDR28C2	44.59	
<i>Ciona intestinalis</i>	SDR28-1C2	25.91	23.71
<i>Strongylocentrotus purpuratus</i>	SDR28-1C1	42.53	47.71
	SDR28-1C2	39.21	44.80
	SDR28-1C3	35.31	40.42
<i>Aplysia californica</i>	SDR28-1C1	27.76	26.95

Table S48b. Percent identity values of the human SDR28C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases															
<i>Homo sapiens</i>	SDR32C1	120222	1			2		0			2			2				2
	SDR32C2	20222				2			0		2			2				2
<i>Ciona intestinalis</i>	SDR32-1C2	200220		2			0		0		2					2		0
<i>Strongylocentrotus purpuratus</i>	SDR32-1C1	22222			2	2				2			2					2
<i>Drosophila busckii</i>	SDR32-1C1	0022		0			0			2								2
<i>Anopheles gambiae</i>	SDR32-1C1	002		0			0											2
<i>Apis dorsata</i>	SDR32-1C1	00212		0			0			2		1						2
<i>Helobdella robusta</i>	SDR32-1C1	22122				2					2			1		2		2
<i>Aplysia californica</i>	SDR32-1C1	20222				2	0				2			2				2

Table S49a. Splicing site organization of the human SDR32C family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% Identity	
<i>Homo sapiens</i>		SDR32C1	SDR32C2
	SDR32C2	43.19	
<i>Ciona intestinalis</i>	SDR32-1C2	26.36	24.58
<i>Strongylocentrotus purpuratus</i>	SDR32-1C1	46.43	33.66
<i>Drosophila busckii</i>	SDR32-1C1	43.49	32.35
<i>Anopheles gambiae</i>	SDR32-1C1	47.08	30.69
<i>Apis dorsata</i>	SDR32-1C1	44.81	30.26
<i>Helobdella robusta</i>	SDR32-1C1	43.34	31.67
<i>Aplysia californica</i>	SDR32-1C1	45.90	37.09

Table S49b. Percent identity values of the human SDR32C family variants and of their invertebrate orthologs.

Species	Variants	Phase formula	Splicing-site phases															
<i>Homo sapiens</i>	SDR42E1	1			1													
	SDR42E2	0020200020				0	0	2	0	2	0	0		0	2	0		
<i>Ciona intestinalis</i>	SDR42-1E1	100202000202		1		0	0	2	0	2	0	0		0	2	0		2
<i>Strongylocentrotus purpuratus</i>	SDR42-1E1	02020020					0	2	0	2	0	0			2	0		
<i>Caenorhabditis elegans</i>	SDR42-1E1	20000	2			0	0		0		0							0
	SDR42-2E1	000000				0	0		0		0		0					0
<i>Caenorhabditis remanei</i>	SDR42-1E2	00000					0		0		0		0					0
<i>Aplysia californica</i>	SDR42-1E1	2000020						2	0			0	0		0	2	0	

Table S50a. Splicing site organization of the human SDR42E family variants and of their invertebrate orthologs. For further details see Table S39a.

Species	Variants	% identity	
		SDR42E1	SDR42E2
<i>Homo sapiens</i>		47.18	
<i>Ciona intestinalis</i>	SDR42-1E1	41.58	40.69
<i>Strongylocentrotus purpuratus</i>	SDR42-1E1	49.55	43.88
<i>Caenorhabditis elegans</i>	SDR42-1E1	27.01	27.54
	SDR42-2E1	24.72	29.46
<i>Caenorhabditis remanei</i>	SDR42-1E2	28.33	31.58
<i>Aplysia californica</i>	SDR42-1E1	48.97	39.69

Table S50b. Percent identity values of the human SDR42E family variants and of their invertebrate orthologs. Note, this figure is identical to Table S4b in the main text.