HIBINO et al. SUPPLEMENTARY MATERIALS

1. Table S1. Immune related gene models of the *S. purpuratus* genome.
2. Table S2. Toll-like receptor (TLR) gene models of the *S. purpuratus* genome.
3. Table S3. NACHT-LRR (NLR) gene models of the *S. purpuratus* genome.
4. Table S4. SRCR gene models of the *S. purpuratus* genome.
5. Table S5. Immune related transcription factor gene models of the *S. purpuratus* genome.
6. Figure legends for Supplementary Figures S1-S7.
7. Figure S1
8. Figure S2
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10. Figure S4
11. Figure S5
12. Figure S6
13. Figure S7

Supplementary Table S1. Complete categorized list of immunity-related genes found in *Strongylocentrotus purpuratus* genome sequence.

I. IMMUNITY

Gene Catergory	Gene model ID	Assigned name
I.A1 Immune receptors - Pattern Recognition Receptors (PRRs)		
Toll-Like Receptors (TLRs)	222 models	Please refer to Supplementary Table S2
NACTH and Leucine-rich Repeat receptors (NLRs)	203 models	Please refer to Supplementary Table S3
Scavenger Receptor Cysteine-Rich (SRCR) repeat proteins	218 models	Please refer to Supplementary Table S4
CD36-like	SPU_007495	*Sp-CD36 antigen-like*
	SPU_018904 **(E)**	*Sp-scavenger receptor B1-like*
	SPU_020799	*Sp-scavenger receptor B2-like1*
	SPU_025565	*Sp-scavenger receptor B2-like2*
	SPU_003486/26720 (1)	*Sp-scavenger receptor BIII-like*
PG-Recognition Proteins (PGRPs)	SPU_023247	*Sp-PGRP1*
	SPU_007946	*Sp-PGRP2*
	SPU_000222	*Sp-PGRP3*
	SPU_003882	*Sp-PGRP4*
	SPU_030064	*Sp-PGRP5*
Gram-Negative Binding Protein (GNBP)1/2/3	SPU_016163	*Sp-GNBP1/2/3A*
	SPU_006529/006530 (1)	*Sp-GNBP1/2/3B*
	SPU_024075	*Sp-GNBP1/2/3C*
RIG-I/LGP2/MDA-5	SPU_014310	*Sp-RIG-I like 1*
	SPU_025885	*Sp-RIG-I like 2*
	SPU_011866	*Sp-RIG-I like 3*
	SPU_014311	*Sp-RIG-I like 4*
	SPU_007126	*Sp-RIG-I like 5*
	SPU_014119	*Sp-RIG-I like 6*
	SPU_010536	*Sp-RIG-I like 7*
	SPU_005476	*Sp-RIG-I like 8*
	SPU_019617	*Sp-RIG-I like 9*
	SPU_016718 **(E)**	*Sp-RIG-I like 10*
	SPU_020020 **(E)**	*Sp-RIG-I like 11*
	SPU_000006 **(E)**	*Sp-RIG-I like 12*

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(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta *et al.* , 2006)

Table S1 (cont.) - Complete list of immunity-related genes

Gene Catergory	Gene model ID	Assigned name
IMCV (Ips-1/MAVS/Cardif/VISA)	SPU_017445	*Sp-IMCV-like*
I.A2 Immune receptors - C-type lectin domain proteins		
Echinoidin-like	SPU_000839	*Sp-echinoidin-like1*
	SPU_000906	*Sp-Echinoidin / Sp-echinoidin-like2*
	SPU_001821	*Sp-echinoidin-like3*
	SPU_005127	*Sp-echinoidin-like4*
	SPU_015211	*Sp-CLECT*
	SPU_022861	*Sp-CLECT*
	SPU_025892	*Sp-CLECT*
	SPU_008393	*Sp-CLECT*
	SPU_022396	*Sp-CLECT*
	SPU_007040	*Sp-CLECT*
	SPU_007882 **(E)**	*Sp-C-lectin*
Additional small C-type lectin domain proteins	SPU_028432	*Sp-CLECT*
	SPU_010101	*Sp-CLECT*
	SPU_003618	*Sp-CLECT*
	SPU_014221	*Sp-EL1-like3*
	SPU_003774	*Sp-CLECT*
I.A3 Immune receptors - Ig superfamily		
IG_V - $IG_{C1/C2}$ IGSF genes	SPU_013709	*Sp-VC1_1*
	SPU_030071 **(E)**	*Sp-VC1_2*
	SPU_030081	*Sp-VC1_3*
	SPU_000577	*Sp-IGv fragment*
	SPU_011076	*Sp-JAM-like1*
	SPU_002608 **(E)**	*Sp-VC2_1*
	SPU_012388	*Sp-IGv-c1*
	SPU_024439 **(E)**	*Sp-SIRPB/G-like1*
	SPU_024787	*Sp-IGv-fragment2*
B7-like IGSF genes	SPU_010746	*Sp-B7-like1*
	SPU_017228	*Sp-B7-like2*
	SPU_020457	*Sp-B7-like3*
	SPU_028300	*Sp-B7-like4*
	SPU_028510	*Sp-B7-like5*
ITAM-containing Ig	SPU_013624	*Sp-IG/ITAM-c1*

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(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta *et al.*, 2006)

Gene Catergory	Gene model ID	Assigned name
I.A3 Immune receptors - Ig superfamily (cont.)		
Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods* : CD14, CD244/NKCR2B4, KIR-like p91A, KIRs, KLRDs, LAIR, LIR, Ly49/NKR, NKp30, NKp44, NKp46, NKp80, NITR, CD66/CEACAM1, SIGLEC, Leukotriene B4 Receptor 1/2, Cysteinyl-leukotriene Receptor 1		
I.A4 Genes associated with VDJ recombination		
TdT/Pol-μ	SPU_009980	*Sp-TdTl / Pol- μ*
Rag1	SPU_027600 **(E)**	*Sp-Rag1L*
Rag2	SPU_030091 **(E)**	*Sp-Rag2L*
Ku70	SPU_009797 **(E)**	*Sp-Ku70-like*
Ku80	SPU_009224/006396 (1)	*Sp-Ku86-like*
DNA ligase IV	SPU_018243 **(E)**	*Sp-Dnl-4*
xrrc4	SPU_024517 **(E)**	*Sp-xrcc4*
Xlf / CERNUNNOS	SPU_012239 **(E)**	*Sp-Cernunnos*
DNA-PKcs	SPU_015484	*Sp-DNA-PKcs* - (N-terminus)
	SPU_015529 **(E)**	*Sp-DNA-PKcs* - (C-terminus)
DNA cross-link repair 1 /	SPU_003308	*Sp-Dclr-1*
Artemis	SPU_021517	*Sp-Dclr-2*
I.B1 Effector Genes - Complement		
C3/4/5	SPU_005182/012439/ 018503/017239 (1)	*Sp-064 / Sp-C3*
	SPU_000997 **(E)**	*Sp-C3-2*
Thioester-containing	SPU_022988 **(E)**	*Sp-TCP1*
	SPU_005193 **(E)**	*Sp-TCP2*
Mannose Binding Protein	SPU_004869	*SpSM30-F*
C2/Factor B	SPU_028188	*Sp-factor B*
	SPU_028187	*Sp-factor B-2 / SpBf-2*
	SPU_009091	*Sp-factor B-3 / SpBf-3*
C1q	SPU_005500	*Sp-C1q-like*
	SPU_006578 **(E)**	*Sp-C1q-like*
	SPU_009401	*Sp-C1q-like*
	SPU_009020	*Sp-C1q-like*
CD59	SPU_030142	*Sp-CD59 / Sca2-like1.*
	SPU_030143	*Sp-CD59 / Sca2-like2.*
Additional thioester	SPU_006406/026313 (1)	*Sp-thioester containing protein-1*
containing genes	SPU_019422 **(E)**	*Sp-thioester containing protein-2*
	SPU_013170/013169 (1)	*Sp-thioester containing protein-4/5*

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Gene Catergory	Gene model ID	Assigned name
I.B1 Effector Genes - Complement (cont.)		
Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: C1r, C1s, MASP1/2, C6-9 (terminal pathway), CR1, CR2, CR3/Mac-1/ITGAM, CR4/ITGAX, Curry, C3aR1, C5R1, MCP, DAF, H Factor, I Factor, D Factor/adipsin, Properdin.		
I.B2 Effector Genes - Cytolytic pathways		
Perforin-related (MACPF domain containing genes)	SPU_005223	*Sp-MACPF-A.1*
	SPU_022091	*Sp-MACPF-A.2*
	SPU_014984	*Sp-MACPF-A.3*
	SPU_017952	*Sp-MACPF-A.4*
	SPU_002548/002549[(1)] **(E)**	*Sp-MACPF-B.0*
	SPU_002550 **(E)**	*Sp-MACPF-B.1*
	SPU_015144 **(E)**	*Sp-MACPF-B.2*
	SPU_016546 **(E)**	*Sp-MACPF-B.3*
	SPU_001794 **(E)**	*Sp-MACPF-C.1*
	SPU_001797 **(E)**	*Sp-MACPF-C.2*
	SPU_014677	*Sp-MACPF-C.3*
	SPU_000751	*Sp-MACPF-D.1*
	SPU_022318	*Sp-MACPF-D.2*
	SPU_026119	*Sp-MACPF-D.3*
	SPU_027405	*Sp-MACPF-D.4*
	SPU_007159	*Sp-MACPF-E.1*
	SPU_028756	*Sp-MACPF-E.2*
	SPU_022230	*Sp-MACPF-E.3*
	SPU_008485	*Sp-MACPF-E.4*
	SPU_014229	*Sp-MACPF-F.1*
	SPU_006818	*Sp-MACPF-G.1*
Cathepsin A	SPU_012846 **(E)**	*Sp-Ppgb*
	SPU_013245	*Sp-Ppgb*
	SPU_015939 **(E)**	*Sp-Ppgb*
	SPU_026832 **(E)**	*Sp-Ppgb*
Cathepsin B	SPU_007151	*Sp-CTSB*
Cathepsin C	SPU_005834	*Sp-Cts1 / Sp-CtsC*
Cathepsin F	SPU_014914 **(E)**	*Sp-Cts10 / Sp-CtsF-like1*
Cathepsin L	SPU_009042 **(E)**	*Sp-Cts2 / CtsL-like1*
	SPU_014765	*Sp-Cts9 / CtsL-like5*
	SPU_014766	*Sp-Cts6 / CtsL-like2*
	SPU_014767	*Sp-Cts7 / Sp-CtsL-like3*
	SPU_014768	*Sp-Cts8 / Sp-CtsL-like4*
	SPU_015668	*Sp-Cts11 / Sp-CtsL-like6*

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Table S1 (cont.) - Complete list of immunity-related genes

Gene Catergory	Gene model ID	Assigned name
I.B2 Effector Genes - Cytolytic pathways (cont.)		
Cathepsin L (cont.)	SPU_020837	*Sp-Cts12 / Sp-CtsL-like7*
	SPU_020838	*Sp-Cts13 / Sp-CtsL-like8*
Cathepsin Z	SPU_009601 **(E)**	*Sp-Cts4 / Sp-CtsZ-like1*
	SPU_013893 **(E)**	*Sp-Cts5 / Sp-CtsZ-like2*
Novel Cathepsin	SPU_009368	*Sp-Cts3*
Granzymes	SPU_023706	*Sp-Gramar-like1 (Granzyme/Marapsin-like 1)*
	SPU_001588	*Sp-Gramar-like2 (Granzyme/Marapsin-like 2)*
	SPU_016107	*Sp-Gramar-like3 (Granzyme/Marapsin-like 3)*
I.B3 Effector genes - Additional cytotoxic effectors and regulators		
NOS	SPU_002328/025118 (1) **(E)**	*Sp-nNos.*
	SPU_016283/013373 (1)	*Sp-nNos*
	SPU_019970	*Sp-Nos1*
Peroxidase	SPU_008911	*Sp-Hdpx-1*
	SPU_019097	*Sp-Hdpx-2*
	SPU_002004 **(E)**	*Sp-Hdpx-3*

Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: Defensins/Cationic proteins, Antibacterial peptides, Lysozyme, Serglycin/PRG1, C-reactive protein, Cox1 /2*D. melanogaster* CLIP-domain serine proteases.

I.C Sea urchin immune response genes		
DD185/333	SPU_011836 **(E)**	*Sp-185/333-Ex*
	SPU_019327	*Sp-185/333-B3d (Possibly a pseudogene)*
	SPU_022178	*Sp-185/333-E2*
	SPU_022179	*Sp-185/333-D1*
	SPU_030144	*Sp-185/333-01*
	SPU_030145	*Sp-185/333-02*
	SPU_030146	*Sp-185/333-03*

II. REGULATORY PATHWAYS

Gene Catergory	Gene model ID	Assigned name
II.A1 Intracellular signal transduction - NFκB / IRF pathways		
NFκB	SPU_008177 **(E)**	*Sp-Nfkb*
	SPU_012203 **(E)**	*Sp-rel*
Iκ B	SPU_011197 **(E)**	*Sp-IkB*
IKK	SPU_008254/016839 (1)	*SpIKK1*
	SPU_008255/016839(1) **(E)**	*SpIKK2*

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Gene Catergory	Gene model ID	Assigned name
II.A1 Intracellular signal transduction - NFkB / IRF pathways (cont.)		
IKK (cont.)	SPU_027909/007638 (1)	*SpIKK epsilon*
TBK1/NAK	SPU_004671	*SpTBK1*
TRAF1-6	SPU_012840/010527(1) **(E)**	*Sp-Traf1*
	SPU_026479	*Sp-TRAF1*
	SPU_026495	*Sp-Traf3*
	SPU_008332	*Sp-Traf4*
	SPU_028898	*Sp-Traf6*
	SPU_023069 **(E)**	*Sp-Traf-B*
	SPU_003462 **(E)**	*Sp-Traf-A*
TRIAD	SPU_030065 **(E)**	*Sp-Triad*
TAK1/MAP3K7	SPU_002696 **(E)**	*Sp-TAK1*
MAP3K7IP1/TAB1	SPU_005254 **(E)**	*Sp-Tab1*
TAB2/3	SPU_012219/003955(1) **(E)**	*Sp-Tab2/3*
UBC13	SPU_018598 **(E)**	*Sp-Ubc13*
UEV1A	SPU_000742	*Sp-Ube2v1/2*
SINK	SPU_013349 **(E)**	*SpSINK*
IRF	SPU_010404	*Sp-Irf*
	SPU_026877	*Sp-Irf4*

Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: IKKgamma/NEMO, Sik/Brk/PTK6.

II.A2 Intracellular signal transduction - TLR adaptor molecules		
MYD88	SPU_007342/007343 (1)	*Sp-Myd88*
	SPU_001905	*Sp-Myd88-like1*
	SPU_022707 **(E)**	*Sp-Myd88-like2*
	SPU_022708	*Sp-Myd88-like3*
SARM	SPU_011042	*Sp-Sarm.*
Novel family of	SPU_006122	*Sp-Sarm-r1*
SARM-related genes	SPU_020008	*Sp-Sarm-r2*
	SPU_007020	*Sp-Sarm-r3*
	SPU_000764 **(E)**	*Sp-Sarm-r4*
	SPU_015127	*Sp-Sarm-r5*
	SPU_021841	*Sp-Sarm-r6*
	SPU_018859	*Sp-Sarm-r7*
	SPU_027639/027640 (1)	*Sp-Sarm-r8*

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Gene Catergory	Gene model ID	Assigned name
II.A2 Intracellular signal transduction - TLR adaptor molecules (cont.)		
Novel family of SARM-related genes (cont.)	SPU_018168	*Sp-Sarm-r9*
	SPU_003495	*Sp-Sarm-r10*
	SPU_004557 **(E)**	*Sp-Sarm-r11*
	SPU_004107	*Sp-Sarm-r12*
	SPU_008302	*Sp-Sarm-r13*
	SPU_007088	*Sp-Sarm-r14*
Novel family of TIR TIR domain containing genes	SPU_016014	*Sp-TIR-c1*
	SPU_007952/013299 (1)	*Sp-TIR-c2*
	SPU_014926	*Sp-TIR-c3*
	SPU_012671	*Sp-TIR-c4*
	SPU_003608	*Sp-TIR-c5*
	SPU_013352	*Sp-TIR-c6*
	SPU_020131 **(E)**	*Sp-TIR-c7*
ECSIT/SITPEC	SPU_012096 **(E)**	*Sp-Ecsit*
Tollip	SPU_026252/021673 (1)	*Sp-Tollip*

Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: TIRAP/MAL, TICAM-1 /TRIF, TICAM-2 /TRAM, SIGIRR, RIG-1, spatzle, tube.

II.A3 Intracellular signal transduction - NLR signaling		
PEPT1/slc15a1	SPU_012690	*Sp-Slc15a2*
GRIM19/Ndufa13	SPU_003408/024115 (1)	*Sp-Ndufa13*
RIPK1/RIP and	SPU_005215	*SpANKRD3*
RIPK2/RICK/CARDIAK	SPU_011816	*Sp-RIPK4*
CRADD- and ASC-like	SPU_019893	*Sp-PAN-1*
	SPU_006410 **(E)**	*Sp-PAN-2*
Caspase-1/4/5/11/12/13	SPU_002921	*Sp-ICE-like-1a*
	SPU_002923	*Sp-ICE-like-1b*
	SPU_011872	*Sp-ICE-like-3*
	SPU_012722	*Sp-ICE-like-4*
	SPU_021141	*Sp-ICE-like-2*
II.B1 Intercellular signaling (Cytokines and Growth Factors) - Interleukins, Cytokines and Hematopoietins		
MIF	SPU_011299	*Sp-Mif-1*
	SPU_030001	*Sp-Mif-2*
	SPU_017901	*Sp-Mif-3*
	SPU_020035 **(E)**	*Sp-Mif-4*
	SPU_020036 **(E)**	*Sp-Mif-5*

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Table S1 (cont.) - Complete list of immunity-related genes

Gene Catergory	Gene model ID	Assigned name
II.B1 Intercellular signaling (Cytokines and Growth Factors) - Interleukins, Cytokines and Hematopoietins (cont.)		
MIF (cont.)	SPU_016226 **(E)**	*Sp-Mif-6*
	SPU_001152 **(E)**	*Sp-Mif-7*
	SPU_012071	*Sp-Mif-like1*
	SPU_019323 **(E)**	*Sp-Mif-like2*
IL-1R/CD121a and associated genes	SPU_005871 **(E)**	*Sp-Il1r1*
	SPU_003911/003912 (1)	*Sp-IL1AP*
	SPU_013950/000409 (1)	*Sp-Ilr1-rs1*
Pellino	SPU_004517 **(E)**	*Sp-Pellino*
IL-17	SPU_005983	*Sp-Il17-1*
	SPU_012844	*Sp-Il17-2*
	SPU_012845	*Sp-Il17-3*
	SPU_019349	*Sp-Il17-4*
	SPU_019350	*Sp-Il17-5*
	SPU_019351	*Sp-Il17-6*
	SPU_022838	*Sp-Il17-7*
	SPU_027904	*Sp-Il17-8*
	SPU_030184	*Sp-Il17-9*
	SPU_030185	*Sp-Il17-10*
	SPU_030186	*Sp-Il17-11*
	SPU_030187	*Sp-Il17-12*
	SPU_030188	*Sp-Il17-13*
	SPU_030190	*Sp-Il17-14*
	SPU_030191	*Sp-Il17-15*
	SPU_030192	*Sp-Il17-16*
	SPU_030193	*Sp-Il17-17*
	SPU_030196	*Sp-Il17-18*
	SPU_030197	*Sp-Il17-19*
	SPU_030198	*Sp-Il17-20*
	SPU_030199	*Sp-Il17-21*
	SPU_030200	*Sp-Il17-22*
	SPU_030203	*Sp-Il17-23*
	SPU_030204	*Sp-Il17-24*
	SPU_030189	*Sp-Il17-p1*
	SPU_030194	*Sp-Il17-p2*
	SPU_030195	*Sp-Il17-p3*
	SPU_030201	*Sp-Il17-p4*
	SPU_030202	*Sp-Il17-p5*
IL-17RA/B	SPU_030141	*Sp-IL17receptor-like*

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Gene Catergory	Gene model ID	Assigned name
II.B1 Intercellular signaling (Cytokines and Growth Factors) - Interleukins, Cytokines and Hematopoietins (cont.)		
Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: IL-1a/b, IL-1R2/CD121b, IL-1R-like1, IL-2, IL-2RA/CD25, IL-2RB/CD122, IL-2Rgamma/CD132, IL-3, IL-3RA/CD123, IL-4, IL-4R/CD124, IL-5, IL-5R/CD125, IL-6, IL-6RA/CD126, IL-6ST/CD130/gp130, IL-7, IL-7RA/CD127, IL-8/CXCL8, IL-8RA/B, IL-9, IL-9R, IL-10RA, IL-10RB, IL-11, IL-11R/CD130, IL-12a/b, IL-12Rbeta1, IL-13, IL-13RA, IL-15, IL-16, IL-18, IL-18R, IL-19, IL-20, IL-20RA, IL-21, IL-21R, IL-22, IL-22RA, IL-23, IL-23R, IL-24, IL-26, IL-27, IL-27RA/WSX-1, IL-28, IL-28RA, IL-29, OSM, LIF, OSMR/LIFR, CSF1/M-CSF, CSF2/GM-CSF, CSF3/G-CSF, CSFR, INF-alpha/beta/gamma/kappa/omega/zeta, IFNR1/2, Epo, EpoR, CXCL1(ELR+) family [CXCL1,2,3,5,6,7,8,14,15], CXCR1/IL-8RA, CXCR2/IL-8RB, CXCL(ELR-) family [CXCL4,9,10,11,12,13,16], CXCR3-6, CCL family [CCL1-28], CCR1-10, XCL1/2, XCR1, CX3CL1, CX3CR1.		
II.B2 Intercellular signaling (Cytokines and Growth Factors) - TNF pathway		
TNF Superfamily	SPU_009527	*Sp-Tnfsf_like2*
	SPU_009528	*Sp-Tnfsf_like1*
	SPU_015654	*Sp-Tnfsf_like3*
	SPU_030072	*Sp-Tnfsf_like4*
TNFR Superfamily	SPU_012211	*Sp-Tnfrsf1a*
	SPU_010180	*Sp-Tnfrsf_cl1*
	SPU_010230	*Sp-Tnfrsf_like1*
	SPU_018915	*Sp-Tnfrsf_like1*
	SPU_020740	*Sp-Eda2r_like1 / Tnfrsf27-like1*
	SPU_020955	*Sp-Tnfrsf_like2*
	SPU_024584	*Sp-Eda2r_like2 / Tnfrsf27-like2*
	SPU_026216 **(E)**	*Sp-Tnfrsf_cl2*
FADD	SPU_010777	*Sp-FADD*
II.B3 Intercellular signaling (Cytokines and Growth Factors) - RTK signaling		
Tie1/2	SPU_024044 **(E)**	*Sp-Tie1/2*
Flk-1/Flt-1/Flt-4	SPU_000310 **(E)**	*Sp-PDGFR/VEGFR-like / Sp-VEGFR-10*
(VEGFR1-3)	SPU_021021 **(E)**	*Sp-PDGFR/VEGFR-like / Sp-VEGFR-7*
VEGF	SPU_014978	*Sp-VEGF-1*
	SPU_005737	*Sp-VEGF-2*
	SPU_030148	*Sp-VEGF-3*
Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: Angiopeitins 1-4, CSFR/MCSFR, CSF1-3, c-Kit, SCF/KITL, PDGF, CD34, FLT3/CD135/FLK2.		
II.B4 Intercellular signaling (Cytokines and Growth Factors) - Cytoplasmic adaptors and signal transducers		
IRAK	SPU_000073 **(E)**	*Sp-Pik1(Pelle/Irak1).*
	SPU_028724 **(E)**	*Sp-Pik2 (Pelle/Irak2).*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta *et al.*, 2006)

Table S1 (cont.) - Complete list of immunity-related genes

Gene Catergory	Gene model ID	Assigned name
II.B4 Intercellular signaling (Cytokines and Growth Factors) - Cytoplasmic adaptors and signal transducers (cont.)		
JAKs	SPU_030066	*Sp-Jak*
	SPU_022495 **(E)**	*SpJAK2*
SOCS	SPU_002792 **(E)**	*Sp-SOCS2/3*
	SPU_026496 **(E)**	*Sp-SOCS4/5*
	SPU_011298	*Sp-Socs6-like*
	SPU_010245	*Sp-Socs7*
PIAS	SPU_007964 **(E)**	*Sp-Pias1*
	SPU_011690 **(E)**	*Sp-Pias2/3*
Src Family Kinases	SPU_013522/023261 (1) **(E)**	*Sp-SFK1*
(SFKs)	SPU_024525 **(E)**	*Sp-SFK2*
	SPU_005419 **(E)**	*Sp-SFK3*
	SPU_012805	*Sp-SFK4*
	SPU_014473/026766 (1)	*SpYes-related kinase*
Abl	SPU_023952 **(E)**	*Sp-Abl*
Syk/ZAP-70	SPU_006988 **(E)**	*Sp-Syk/ZAP70*
WASP	SPU_003194 **(E)**	*Sp-similar to Wiskott-Aldrich syndrome putative homolog*
SH2-B	SPU_027685 **(E)**	*Sp-SH2-B-rs1*
SHP-1/2	SPU_013810 **(E)**	*Sp-Ptpn11*
FKBP-12	SPU_027840 **(E)**	*Sp-FKBP-12*
Nck	SPU_014752 **(E)**	*Sp-Nck*

Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods*: APS, NFAM1, Par-4, SLP-76, Sik/Brk/PTK6, Eif2ak2/Pkr.

III. COAGULATION and WOUND REPAIR

Gene Catergory	Gene model ID	Assigned name
III.a Coagulation cascade genes		
CF5/8	SPU_021228	*Sp-Cf5/8-like1*
	SPU_021229	*Sp-Cf5/8-like2*
CF13	SPU_005702 **(E)**	*Sp-transglutaminase-like*
TFPI	SPU_030138 **(E)**	*Sp-Tfpi-like*
Plasminogen	SPU_022934	*Sp-Plasminogen-like 1*
	SPU_014730/014731 (1)	*Sp-Plasminogen-like 2*
	SPU_005414	*Sp-Plasminogen-like 3*
	SPU_000633	*Sp-Plasminogen-related 1*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta *et al.*, 2006)

Table S1 (cont.) - Complete list of immunity-related genes

Gene Catergory	Gene model ID	Assigned name
III.a Coagulation cascade genes (cont.)		
Serpins (All Sp-serpin-like models Blast back to the B clade of mammalian serpins).	SPU_028469 **(E)**	*Sp-serpin-like 1*
	SPU_009346	*Sp-serpin-like 2*
	SPU_013377 **(E)**	*Sp-serpin-like 3*
	SPU_013378 **(E)**	*Sp-serpin-like 4*
	SPU_018632	*Sp-serpin-like 5*
	SPU_018631	*Sp-serpin-like 6*
	SPU_018630	*Sp-serpin-like 7*
	SPU_018196	*Sp-serpin-like 8*
	SPU_024263	*Sp-serpin-like 9*
	SPU_004543	*Sp-serpin-like 10*
	SPU_002711	*Sp-serpin-like 11*
	SPU_020278	*Sp-serpin-like 12*
Plasma Kallikrein B1	SPU_012390 **(E)**	*Sp-Klkb1*
	SPU_015878	*Sp-Klkb1-like1*
Alpha-2-Macroglobulin	SPU_011257 **(E)**	*Sp-A2M*

Genes for which no models with evident homology or similar domain structure could be found using the search criteria detailed in *Materials and Methods* : CF2/Thrombin, CF2R, CF3/Tissue factor, CF7, CF9, CF10, CF11, CF12, von Willebrand Factor, Bradykinin Receptor B1/2, Kininogen 1/2, Fibrinogen A alpha, Thrombomodulin, Protein C, Protein S, PLAT, PLAU, PLAUR/CD87, Plasma carboxypeptidase B2, Horseshoe crab clotting (Tt) factor G alpha/beta.

III.b Sea urchin clotting genes		
Amassin	SPU_003389	*Sp-OLF-like/Sp-amassin-like*
	SPU_006531	*Sp-OLF/Sp-amassin1*
	SPU_021526 **(E)**	*Sp-amassin*
Amassin (cont.)	SPU_023924	*Sp-OLF/Sp-amassin2*
	SPU_023926	*Sp-amassin2*
	SPU_026884	*Sp-OLF/Sp-amassin3*

IV. MISCELANEOUS

Gene	Gene model ID	Assigned name
CD109	SPU_024565 **(E)**	*Sp-CD109-like*
Serum amyloid protein	SPU_012667	*Sp-Saa-a*
	SPU_012668	*Sp-Saa-b*
CD45	SPU_021599 **(E)**	*Sp-PTPR1*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta *et al.*, 2006)

Supplementary Table S2. Full categorized list of TLR genes in the *Strongylocentrotus purpuratus* genome.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group IA	*Sp-Tlr003*	SPU_000199	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr008	SPU_000911	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr010	SPU_001877	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr019	SPU_004139	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr020	SPU_004150	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr030	SPU_005950	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr050	SPU_009037	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr058	SPU_010695	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr060	SPU_011454	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr062	SPU_011537	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr063	SPU_011539	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr064	SPU_011540	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr067	SPU_011949	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr079	SPU_015029	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr080	SPU_015066	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr082	SPU_015303	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr091	SPU_018100	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr103	SPU_019309	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr140	SPU_025719	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr061	SPU_011536	SP-NT-LRR(22)-CT-(XXX)-TIR	partial
	Sp-Tlr083	SPU_015533	SP-NT-LRR(22)-CT-TM-TIR(XXX)	partial
	Sp-Tlr098	SPU_018519	SP-NT-LRR(22)-CT-TM-TIR(XXX)	partial
	Sp-Tlr102	SPU_019042	SP-NT-LRR(22)-(XXX)-TIR	partial
	Sp-Tlr138	SPU_025263	(XXX)-LRR(9)-CT-TM-TIR	partial
	Sp-Tlr139	SPU_025312	SP-NT-LRR(21)-(XXX)-TIR	partial
	Sp-Tlr160	SPU_001650	(XXX)-TIR	partial
	Sp-Tlr175	SPU_009952	(XXX)-TIR	partial
	Sp-Tlr179	SPU_011277	(XXX)-TIR	partial
	Sp-Tlr181	SPU_011455	(XXX)-TM-TIR	partial
	Sp-Tlr187	SPU_030080	(XXX)-LRR(3)-CT-TM-TIR	partial
	Sp-Tlr210	SPU_030094	(XXX)-CT-TM-TIR(XXX)	partial
	Sp-Tlr212	SPU_021502	(XXX)-TIR	partial
	Sp-Tlr213	SPU_021907	(XXX)-CT-TM-TIR	partial
	Sp-Tlr214	SPU_021908	(XXX)-TIR	partial
	Sp-Tlr215	SPU_030137	(XXX)-LRR(5)-CT-TM-TIR(XXX)	partial
	Sp-Tlr224	SPU_030076	(XXX)-LRR(3)-CT-TM-TIR	partial
	Sp-Tlr227	SPU_030079	(XXX)-LRR(2)-CT-TM-TIR	partial
	Sp-Tlr024	SPU_004957		pseudo

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Table S2 (cont.) - Full list of TLR genes.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group IA	*Sp-Tlr040*	SPU_007850		pseudo
(cont.)	*Sp-Tlr057*	SPU_010619		pseudo
	Sp-Tlr059	SPU_010940		pseudo
	Sp-Tlr073	SPU_013751		pseudo
	Sp-Tlr114	SPU_021936		pseudo
	Sp-Tlr121	SPU_023544		pseudo
	Sp-Tlr141	SPU_009450		pseudo
	Sp-Tlr151	SPU_027798		pseudo
	Sp-Tlr206	SPU_020652		pseudo
	Sp-Tlr207	SPU_020654		pseudo
	Sp-Tlr220	SPU_027735		pseudo
Group IB	*Sp-Tlr015*	SPU_002538	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr031	SPU_006164	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr035	SPU_007105	SP-NT-LRR(25)-CT-TM-TIR	complete
	Sp-Tlr048	SPU_008962	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr049	SPU_008963	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr069	SPU_012464	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr075	SPU_014041	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr077	SPU_014191	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr134	SPU_024868	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr174	SPU_009933	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr203	SPU_020258	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr205	SPU_020644	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr001	SPU_030092	(XXX)-CT-TM-TIR	partial
	Sp-Tlr192	SPU_015553	(XXX)-TIR	partial
	Sp-Tlr201	SPU_019661	(XXX)-TIR	partial
	Sp-Tlr105	SPU_020259		pseudo
Group IC	*Sp-Tlr029*	SPU_005850	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr037	SPU_007429	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr065	SPU_011570	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr123	SPU_024204	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr124	SPU_024205	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr126	SPU_024208	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr002	SPU_030093	(XXX)-CT-TM-TIR	partial
	Sp-Tlr163	SPU_002803	(XXX)-TM-TIR	partial
	Sp-Tlr195	SPU_016554	(XXX)-TIR	partial
	Sp-Tlr218	SPU_024590	(XXX)-TIR	partial
	Sp-Tlr038	SPU_007430		pseudo

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Table S2 (cont.) - Full list of TLR genes.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group IC	*Sp-Tlr115*	SPU_022451		pseudo
(cont.)	*Sp-Tlr125*	SPU_024207		pseudo
Group ID	*Sp-Tlr087*	SPU_016536	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr156	SPU_028893	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr157	SPU_000375	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr200	SPU_018380	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr137	SPU_025136	(XXX) LRR(19)-CT-TM-TIR(XXX)	partial
	Sp-Tlr165	SPU_003846	(XXX)-TIR	partial
	Sp-Tlr173	SPU_009459	(XXX)-TIR(XXX)	partial
	Sp-Tlr193	SPU_016388	(XXX)-TIR	partial
	Sp-Tlr216	SPU_023491	(XXX)-LRR(4)-CT-TM-TIR	partial
	Sp-Tlr217	SPU_024501	(XXX)-LRR(1)-CT-TM-TIR	partial
	Sp-Tlr135	SPU_024960		pseudo
	Sp-Tlr208	SPU_020741		pseudo
Group IE	*Sp-Tlr021*	SPU_004311	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr078	SPU_014266	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr127	SPU_024385	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr130	SPU_024429	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr042	SPU_007986	SP-NT-LRR(11)-(XXX)-TIR	partial
	Sp-Tlr128	SPU_024386		pseudo
	Sp-Tlr152	SPU_027815		pseudo
Group I	*Sp-Tlr014*	SPU_002442	SP-NT-LRR(22)-CT-TM-TIR	complete
(Orphan)	*Sp-Tlr052*	SPU_009173	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr089	SPU_017529	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr120	SPU_023321	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr150	SPU_027721	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr154	SPU_028576	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr197	SPU_017530	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr054	SPU_009829	SP-NT-LRR(15)-(XXX)-CT-TM-TIR	partial
	Sp-Tlr178	SPU_010693	(XXX)-LRR(3)-CT-TM-TIR	partial
	Sp-Tlr018	SPU_003684		pseudo
	Sp-Tlr153	SPU_028404		pseudo
	Sp-Tlr166	SPU_004655		pseudo
Group IIA	*Sp-Tlr007*	SPU_000871	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr013	SPU_002224	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr025	SPU_005088	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr033	SPU_006458	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr047	SPU_008456	SP-NT-LRR(24)-CT-TM-TIR	complete

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Table S2 (cont.) - Full list of TLR genes.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group IIA	*Sp-Tlr074*	SPU_013824	SP-NT-LRR(24)-CT-TM-TIR	complete
(cont.)	*Sp-Tlr088*	SPU_017180	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr099	SPU_018534	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr110	SPU_021395	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr142	SPU_026200	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr145	SPU_027162	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr147	SPU_027164	SP-NT-(XXX)-LRR(21)-TM-TIR	partial
	Sp-Tlr086	SPU_016501		pseudo
	Sp-Tlr006	SPU_000870		pseudo
	Sp-Tlr032	SPU_006218		pseudo
	Sp-Tlr146	SPU_027163		pseudo
Group IIB	*Sp-Tlr004*	SPU_000428	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr022	SPU_004360	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr023	SPU_004791	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr026	SPU_005339	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr111	SPU_021415	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr132	SPU_024733	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr167	SPU_004792	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr169	SPU_005148	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr036	SPU_007418	(XXX)-LRR(5)-CT-TM-TIR	partial
	Sp-Tlr034	SPU_006939		pseudo
	Sp-Tlr204	SPU_020428		pseudo
	Sp-Tlr109	SPU_021225		pseudo
Group IIIA	*Sp-Tlr005*	SPU_000615	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr053	SPU_009435	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr068	SPU_012257	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr085	SPU_016468	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr108	SPU_021162	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr112	SPU_021420	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr119	SPU_023035	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr161	SPU_001862	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr168	SPU_004951	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr171	SPU_008229	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr182	SPU_011481	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr194	SPU_016438	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr211	SPU_021362	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr219	SPU_024847	SP-NT-LRR(23)-CT-TM-TIR	complete
	Sp-Tlr222	SPU_024479	SP-NT-LRR(23)-CT-TM-TIR	complete

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Table S2 (cont.) - Full list of TLR genes.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group IIIA	*Sp-Tlr051*	SPU_009129	(XXX)-TIR	partial
(cont.)	*Sp-Tlr136*	SPU_025076	(XXX)-LRR(1)-CT-TM-TIR	partial
	Sp-Tlr158	SPU_000986	(XXX)-LRR(4)-CT-TM-TIR(XXX)	partial
	Sp-Tlr162	SPU_001993	(XXX)-TM-TIR	partial
	Sp-Tlr164	SPU_003419	SP-NT-LRR(23)-CT-TM-TIR(XXX)	partial
	Sp-Tlr170	SPU_030136	SP-NT-LRR(23)-CT-TM-TIR(XXX)	partial
	Sp-Tlr172	SPU_009343	(XXX)-TIR(XXX)	partial
	Sp-Tlr221	SPU_015333	(XXX)-CT-TM-TIR	partial
	Sp-Tlr223	SPU_030075	(XXX)-CT-TM-TIR	partial
	Sp-Tlr225	SPU_030077	(XXX)-LRR(5)-CT-TM-TIR	partial
	Sp-Tlr226	SPU_030078	(XXX)-LRR(10)-CT-TM-TIR	partial
	Sp-Tlr009	SPU_000985		pseudo
	Sp-Tlr176	SPU_010320		pseudo
	Sp-Tlr188	SPU_014352		pseudo
	Sp-Tlr199	SPU_017794		pseudo
	Sp-Tlr202	SPU_019882		pseudo
Group IV	*Sp-Tlr039*	SPU_007790	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr045	SPU_008278	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr046	SPU_008396	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr096	SPU_018409	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr097	SPU_018410	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr122	SPU_024062	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr149	SPU_027698	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr191	SPU_015185	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr186	SPU_013162	(XXX)-TIR	partial
	Sp-Tlr209	SPU_021075	(XXX)-TM-TIR	partial
	Sp-Tlr055	SPU_009970		pseudo
	Sp-Tlr081	SPU_015132		pseudo
	Sp-Tlr177	SPU_010680		pseudo
	Sp-Tlr196	SPU_017104		pseudo
Group V	*Sp-Tlr056*	SPU_010575	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr084	SPU_016457	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr101	SPU_018928	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr183	SPU_030095	(XXX)-CT-TM-TIR	partial
	Sp-Tlr185	SPU_013111	(XXX)-TIR	partial
	Sp-Tlr198	SPU_017735	(XXX)-LRR(3)-CT-TM-TIR	partial
	Sp-Tlr104	SPU_019834		pseudo
	Sp-Tlr143	SPU_026274		pseudo

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Table S2 (cont.) - Full list of TLR genes.

Cluster	Gene name	Gene ID	Domain Structure *	Status
Group V (cont.)	*Sp-Tlr144*	SPU_026275		pseudo
Group VI	*Sp-Tlr044*	SPU_008267	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr071	SPU_013470	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr092	SPU_018211	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr093	SPU_018212	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr116	SPU_022909	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr117	SPU_022911	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr131	SPU_024731	SP-NT-LRR(24)-CT-TM-TIR	complete
	Sp-Tlr094	SPU_018213	(XXX)-NT-LRR(24)-CT-TM-TIR	partial
Group VII	*Sp-Tlr016*	SPU_003578	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr017	SPU_003579	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr090	SPU_018055	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr113	SPU_021787	(XXX)-LRR(20)-CT-TM-TIR	partial
	Sp-Tlr180	SPU_011328		pseudo
Orphan	*Sp-Tlr072*	SPU_013676	SP-NT-LRR(22)-CT-TM-TIR	complete
TLRs	*Sp-Tlr076*	SPU_014073	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr118	SPU_023033	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr129	SPU_024404	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr133	SPU_024815	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr148	SPU_027222	SP-NT-LRR(22)-CT-TM-TIR	complete
	Sp-Tlr155	SPU_028639	SP-NT-LRR(22)-CT-TM-TIR	complete
Fly-like	*Sp-Tlr041*	SPU_007859	SP-LRR(10)-CT-NT-LRR(4)-CT-TM-TIR	complete
TLRs	*Sp-Tlr043*	SPU_008228	SP-LRR(10)-CT-NT-LRR(4)-CT-TM-TIR	complete
	Sp-Tlr066	SPU_011823	SP-LRR(12)-CT-NT-LRR(4)-CT-TM-TIR	complete
Short TLRs	*Sp-Tlr011*	SPU_001970	SP-NT-LRR(8)-CT-TM-TIR	complete
	Sp-Tlr012	SPU_001971	SP-NT-LRR(8)-CT-TM-TIR	complete
	Sp-Tlr106	SPU_020996	SP-NT-LRR(8)-CT-TM-TIR	complete
	Sp-Tlr107	SPU_020997	SP-NT-LRR(8)-CT-TM-TIR	complete
	Sp-Tlr159	SPU_001458	SP-NT-LRR(8)-CT-TM-TIR	complete
Intron	*Sp-Tlr100*	SPU_018838	SP-NT-LRR(21)-CT-TM-TIR	complete
containing	*Sp-Tlr027*	SPU_005830	(XXX)-LRR(1)-CT-TM-TIR	partial
TLRs	*Sp-Tlr028*	SPU_005832	(XXX)-LRR(4)-CT-TM-TIR	partial

* Domain Structure: SP = Signal Peptide; LRR = Leucine-Rich Repeat; NT = N-terminal type LRR; CT = C-terminal type LRR; TM = Transmembrane domain; TIR = Toll/IL-1R domain; (XXX) Predicted missing sequence.

Supplementary Table S3. Full categorized list of NACTH-LRR (NLR) genes found in the *Strongylocentrotus purpuratus* genome.

Cluster	Gene model ID	Assigned name	Domain Structure *
Cluster 1	SPU_000863	*Sp-NLR-152*	D,N,(L)n
	SPU_001549	*Sp-NLR-169*	N,(L)n
	SPU_001884	*Sp-NLR-159*	N,(L)n
	SPU_002888	*Sp-NLR-172*	N,(L)n
	SPU_003247	*Sp-NLR-133*	D,N,(L)n
	SPU_003539	*Sp-NLR-3*	D,N,(L)n
	SPU_003553	*Sp-NLR-2*	N,C,(L)n
	SPU_003797	*Sp-NLR-136*	D,N,(L)n
	SPU_005026	*Sp-NLR-124*	D,D,N,(L)n
	SPU_005383	*Sp-NLR-140*	D,N,(L)n
	SPU_006610	*Sp-NLR-4*	D,N,(L)n
	SPU_007446	*Sp-NLR-150*	D,N,(L)n
	SPU_008498	*Sp-NLR-134*	N,(L)n
	SPU_008707	*Sp-NLR-149*	D,N,(L)n
	SPU_009659	*Sp-NLR-127*	D,N,(L)n
	SPU_010091	*Sp-NLR-176*	D,N,(L)n
	SPU_015033	*Sp-NLR-195*	N,(L)n
	SPU_011097	*Sp-NLR-196*	N,(L)n
	SPU_011776	*Sp-NLR-44*	D,N,(L)n,N,(L)n
	SPU_011855	*Sp-NLR-130*	D,N,(L)n
	SPU_013038	*Sp-NLR-193*	N,(L)n
	SPU_016060	*Sp-NLR-192*	N,(L)n
	SPU_016257	*Sp-NLR-142*	D,N,(L)n
	SPU_016810	*Sp-NLR-138*	D,N,(L)n
	SPU_016926	*Sp-NLR-143*	D,N,(L)n
	SPU_017196	*Sp-NLR-132*	D,N,(L)n
	SPU_017505	*Sp-NLR-131*	D,N,(L)n
	SPU_018384	*Sp-NLR-120*	D,N,(L)n
	SPU_022001	*Sp-NLR-137*	D,N,(L)n
	SPU_022564	*Sp-NLR-191*	D,N,(L)n
	SPU_023183	*Sp-NLR-141*	D,N,(L)n
	SPU_025166	*Sp-NLR-126*	D,N,(L)n
	SPU_025167	*Sp-NLR-156*	D,N,C,(L)n
	SPU_025179	*Sp-NLR-123*	D,N,(L)n
	SPU_026036	*Sp-NLR-151*	D,D,(L)n,N,(L)n
	SPU_026400	*Sp-NLR-155*	N,(L)n
	SPU_026622	*Sp-NLR-139*	N,(L)n
	SPU_027035	*Sp-NLR-194*	N,(L)n

* The domains are abbreviated as follows: D: DEATH, C: CARD, P: PYD, N: NACHT, L: LRR, E: EGF, T: TM, S: Signal peptide, F: FBG, SD: Sterol desaturase.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the S. purpuratus genome (Samanta et al., 2006)

Table S3 (cont.) - Full list of NLR genes.

Cluster	Gene model ID	Assigned name	Domain Structure *
Cluster 1	SPU_027207	*Sp-NLR-190*	N,(L)n
(cont.)	SPU_027511	*Sp-NLR-119*	D,N,(L)n
	SPU_027610	*Sp-NLR-135*	D,N,(L)n
	SPU_027808	*Sp-NLR-154*	D,N,(L)n
	SPU_028820	*Sp-NLR-138*	N,(L)n
Cluster 2	SPU_000672	*Sp-NLR-41*	D,N,(L)n,7T
	SPU_001054	*Sp-NLR-48*	D,N,C,(L)n
	SPU_001608	*Sp-NLR-181*	N,(L)n
	SPU_002423	*Sp-NLR-56*	D,N,(L)n
	SPU_002758	*SpNacht Death box containing protein*	D,N,(L)n
	SPU_003200	*Sp-NLR-9*	D,N,(L)n
	SPU_004053	*Sp-NLR-13*	D,N,(L)n
	SPU_006219	*Sp-NLR-198*	D,N,(L)n,T
	SPU_008547	*Sp-NLR-50*	D,N,C,(L)n
	SPU_009017	*Sp-NLR-10*	D,N,(L)n
	SPU_010053	*Sp-NLR-102*	D,N,(L)n
	SPU_013504	*Sp-NLR-51*	D,N,C(L)n
	SPU_015105	*Sp-NLR-63*	D,N,(L)n
	SPU_015768	*Sp-NLR-179*	N,(L)n
	SPU_015972	*Sp-NLR-33*	D,N,(L)n
	SPU_016794	*Sp-NLR-114*	N,(L)n
	SPU_016921	*Sp-NLR-49*	D,N,(L)n
	SPU_017129	*Sp-NLR-25*	N,(L)n
	SPU_017341	*Sp-NLR-52*	D,N,C,(L)n
	SPU_021447	*Sp-NLR-54*	D,N,(L)n
	SPU_025077	*Sp-NLR-46*	D,N,C,(L)n
	SPU_025680	*Sp-NLR-7*	D,D,N,(L)n
	SPU_026921	*Sp-NLR-14*	D,N,(L)n
	SPU_027513	*Sp-NLR-47*	D,N,C,(L)n
	SPU_028485	*Sp-NLR-182*	N,(L)n
	SPU_028681	*Sp-NLR-8*	D,N,(L)n
Cluster 3	SPU_000457	*Sp-NLR-91*	D,N,D,(L)n
	SPU_006203	*Sp-NLR-93*	D,N,(L)n
	SPU_008283	*Sp-NLR-88*	D,N,(L)n
	SPU_009111	*Sp-NLR-24*	D,N,(L)n
	SPU_023120	*Sp-NLR-79*	N,(L)n
	SPU_025204	*Sp-NLR-90*	D,N,(L)n
Cluster 4	SPU_001548	*Sp-NLR-53*	D,N,(L)n

* The domains are abbreviated as follows: D: DEATH, C: CARD, P: PYD, N: NACHT, L: LRR, E: EGF, T: TM, S: Signal peptide, F: FBG, SD: Sterol desaturase.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the S. purpuratus genome (Samanta et al., 2006)

Table S3 (cont.) - Full list of NLR genes.

Cluster	Gene model ID	Assigned name	Domain Structure *
Cluster 4	SPU_001781	*Sp-NLR-20*	D,N,(L)n
(cont.)	SPU_002641	*Sp-NLR-12*	D,N,(L)n
	SPU_005462	*Sp-NLR-65*	D,N,(L)n
	SPU_006733	*Sp-NLR-86*	N,(L)n
	SPU_008597	*Sp-NLR-76*	D,N,(L)n
	SPU_017054	*Sp-NLR-17*	D,N,(L)n
	SPU_019497	*Sp-NLR-185*	N,(L)n
	SPU_024649	*Sp-NLR-62*	D,N,(L)n
Cluster 5	SPU_002868	*Sp-NLR-27*	D,N,(L)n
	SPU_003186	*Sp-NLR-72*	D,N,(L)n
	SPU_005410	*Sp-NLR-184*	N,(L)n
	SPU_006019	*Sp-NLR-183*	N,(L)n
	SPU_008431	*Sp-NLR-61*	D,N,(L)n
	SPU_013465	*Sp-NLR-89*	D,N,(L)n
	SPU_015340	*Sp-NLR-16*	D,N,(L)n
	SPU_017993 **(E)**	*Sp-NLR-18*	D,N,(L)n
	SPU_020380	*Sp-NLR-29*	D,N,(L)n
	SPU_021478	*Sp-NLR-58*	C,D,N,(L)n
	SPU_022394	*Sp-NLR-60*	D,N,(L)n
	SPU_022780	*Sp-NLR-26*	D,N,(L)n
	SPU_023550	*Sp-NLR-67*	D,N,(L)n
	SPU_025138	*Sp-NLR-68*	D,N,(L)n
	SPU_026071	*Sp-NLR-57*	D,N,(L)n
	SPU_028294	*Sp-NLR-42*	D,N,(L)n
	SPU_028387	*Sp-NLR-69*	D,N,(L)n
Cluster 6	SPU_000015	*Sp-NLR-94*	S,D,N,(L)n
	SPU_000852	*Sp-NLR-71*	S,D,N,(L)n
	SPU_000896	*Sp-NLR-28*	S,D,N,(L)n
	SPU_001423	*Sp-NLR-200*	S,D,N,(L)n
	SPU_001444	*Sp-NLR-78*	S,D,N,(L)n
	SPU_001630	*Sp-NLR-166*	N,(L)n
	SPU_007620	*Sp-NLR-187*	N,(L)n
	SPU_008382	*Sp-NLR-21*	D,N,(L)n
	SPU_014503	*Sp-NLR-74*	S,D,N,(L)n
	SPU_015481 **(E)**	*Sp-NLR-85*	D,N,(L)n
	SPU_017245	*Sp-NLR-73*	S,D,N,(L)n
	SPU_019699	*Sp-NLR-82*	S,D,N,C,(L)n
	SPU_019700	*Sp-NLR-77*	D,N,(L)n

* The domains are abbreviated as follows: D: DEATH, C: CARD, P: PYD, N: NACHT, L: LRR, E: EGF, T: TM, S: Signal peptide, F: FBG, SD: Sterol desaturase.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the S. purpuratus genome (Samanta et al., 2006)

Table S3 (cont.) - Full list of NLR genes.

Cluster	Gene model ID	Assigned name	Domain Structure *
Cluster 6	SPU_020240	*Sp-NLR-110*	S,D,D,N,(L)n
(cont.)	SPU_021370	*Sp-NLR-186*	S,N,C,(L)n
	SPU_022130	*Sp-NLR-70*	S,D,N,(L)n
	SPU_023628	*Sp-NLR-23*	D,N,(L)n
	SPU_028805	*Sp-NLR-75*	S,D,N,(L)n
Cluster 7	SPU_000816	*Sp-NLR-81*	S,D,N,(L)n
	SPU_001016	*Sp-NLR-113*	S,D,N,(L)n
	SPU_002272	*Sp-NLR-105*	N,(L)n
	SPU_002372 **(E)**	*Sp-NLR-55*	S,D,N,(L)n
	SPU_003934	*Sp-NLR-64*	S,D,N,(L)n
	SPU_004043	*Sp-NLR-30*	D,N,(L)n
	SPU_004165	*Sp-NLR-84*	S,D,N,(L)n
	SPU_004872	*Sp-NLR-19*	S,D,N,(L)n
	SPU_005993	*Sp-NLR-92*	S,D,N,(L)n
	SPU_006456	*Sp-NLR-161*	N,(L)n
	SPU_008833	*Sp-NLR-112*	S,D,N,(L)n
	SPU_009488	*Sp-NLR-22*	S,D,N,(L)n
	SPU_014128	*Sp-NLR-11*	S,D,N,(L)n
	SPU_019696	*Sp-NLR-95*	S,D,N,(L)n
	SPU_024020	*Sp-FBG protein*	S,D,N,(L)n,E,F
	SPU_026020	*Sp-NLR-59*	D,N,(L)n
	SPU_026304	*Sp-NLR-180*	D,N,D,(L)n
	SPU_028060	*Sp-NLR-122*	S,D,N,(L)n
	SPU_028433	*Sp-NLR-129*	S,D,N,(L)n
	SPU_028483	*Sp-NLR-80*	S,D,N,(L)n
	SPU_028595	*Sp-NLR-115*	S,D,N,(L)n
	SPU_028630	*Sp-NLR-107*	S,D,N,(L)n
Cluster 8.1	SPU_005609	*Sp-NLR-128*	D,N,(L)n
	SPU_011439	*Sp-NLR-103*	N,D,(L)n
	SPU_011441	*Sp-NLR-101*	D,N,C,(L)n
	SPU_017708	*Sp-NLR-37*	D,N,(L)n
	SPU_025600	*Sp-NLR-147*	D,N,(L)n
Cluster 8.2	SPU_003715	*Sp-NLR-38*	D,N,(L)n
	SPU_006229	*Sp-NLR-104*	S,D,N,(L)n
	SPU_010667	*Sp-NLR-189*	N,(L)n
	SPU_013952	*Sp-NLR-83*	D,N,C,(L)n
	SPU_015052	*Sp-NLR-109*	D,N,(L)n
	SPU_017038	*Sp-NLR-35*	D,N,(L)n
	SPU_020916 **(E)**	*Sp-NLR-1*	D,N,(L)n

* The domains are abbreviated as follows: D: DEATH, C: CARD, P: PYD, N: NACHT, L: LRR, E: EGF, T: TM, S: Signal peptide, F: FBG, SD: Sterol desaturase.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the S. purpuratus genome (Samanta et al., 2006)

Table S3 (cont.) - Full list of NLR genes.

Cluster	Gene model ID	Assigned name	Domain Structure *
Cluster 8.3	SPU_002436	*Sp-NLR-34*	D,N,(L)n
	SPU_003366	*Sp-NLR-118*	D,N,(L)n
	SPU_003640 **(E)**	*Sp-NLR-116*	D,N,(L)n
	SPU_005301	*Sp-NLR-108*	D,N,(L)n
	SPU_005581 **(E)**	*Sp-NLR-87*	D,N,(L)n,N,(L)n
	SPU_010097	*Sp-NLR-106*	D,N,(L)n
	SPU_013206	*Sp-NLR-45*	D,N,P,(L)n
	SPU_014112	*Sp-NLR-32*	D,N,(L)n
	SPU_014761 **(E)**	*Sp-NLR-111*	D,D,N,(L)n
	SPU_021243	*Sp-NLR-40*	D,N,(L)n
	SPU_021844	*Sp-NLR-100*	N,(L)n
	SPU_022294	*Sp-NLR-39*	D,N,(L)n
	SPU_024975	*Sp-NLR-36*	D,N,(L)n
	SPU_026189	*Sp-NLR-121*	D,N,(L)n
	SPU_027858	*Sp-NLR-31*	D,N,(L)n
Cluster 9.1	SPU_003619	*Sp-NLR-201*	E,E,N,(L)n
	SPU_005732	*Sp-NLR-168*	D,N,(L)n
	SPU_011088	*Sp-NLR-157*	D,E,N,(L)n
	SPU_015206	*Sp-NLR-160*	D,E,N,(L)n
	SPU_021930	*Sp-NLR-197*	D,N,(L)n
	SPU_022070	*Sp-NLR-158*	N,(L)n
	SPU_022441	*Sp-NLR-163*	D,N,(L)n
	SPU_027300	*Sp-NLR-170*	D,E,N,(L)n
Cluster 9.2	SPU_001210	*Sp-NLR-144*	D,N,(L)n
	SPU_004343	*Sp-NLR-145*	D,N,(L)n
	SPU_011035	*Sp-NLR-162*	D,D,N,(L)n
	SPU_012713	*Sp-NLR-167*	D,N,(L)n
	SPU_014122	*Sp-NLR-146*	D,N,(L)n
	SPU_023642	*Sp-NLR-153*	D,N,(L)n
	SPU_024709	*Sp-NLR-173*	D,N,(L)n
Outliers	SPU_000523	*Sp-NLR-148*	D,N,(L)n
	SPU_002962	*Sp-NLR-66*	D,N,(L)n
	SPU_003762	*Sp-NLR-117*	D,N,(L)n
	SPU_006016	*Sp-NLR-203*	D,N,(L)n,SD
	SPU_013619	*Sp-NLR-5*	D,N,(L)n
	SPU_023532 **(E)**	*Sp-NLR-6*	D,N,(L)n
	SPU_025914 **(E)**	*Sp-NLR-15*	D,N,(L)n
	SPU_025948	*Sp-NLR-97*	D,D,N,(L)n

* The domains are abbreviated as follows: D: DEATH, C: CARD, P: PYD, N: NACHT, L: LRR, E: EGF, T: TM, S: Signal peptide, F: FBG, SD: Sterol desaturase.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the S. purpuratus genome (Samanta et al., 2006)

Supplementary Table S4. Full list of SRCR-containing genes in the *Strongylocentrotus purpuratus* genome.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR models	*Sp-SRCR-001*	SPU_000337	SP-SRCR(4)	pp
	Sp-SRCR-002	SPU_000492	SRCR(4) + SRCR(partial)	pp
	Sp-SRCR-003	SPU_000580	SRCR(2)	pp
	Sp-SRCR-004	SPU_000646	SP-SRCR(5)	pp
	Sp-SRCR-005	SPU_000654	SP-SRCR(2)	pp
	Sp-SRCR-006	SPU_000740	SP-SRCR(4)-TM	
	Sp-SRCR-007	SPU_000876	SRCR(2)	pp
	Sp-SRCR-008	SPU_000984	SRCR(5)	pp
	Sp-SRCR-011	SPU_001172	SRCR(3)-TM	pp
	Sp-SRCR-012	SPU_001177	SRCR(2)	pp
	Sp-SRCR-013	SPU_001229	SRCR(5)	pp
	Sp-SRCR-014	SPU_001266	SRCR(5)-TM	pp
	Sp-SRCR-018	SPU_001727	SRCR(9)	pp
	Sp-SRCR-019	SPU_001763	SP-SRCR(2)	pp
	Sp-SRCR-020	SPU_001863 **(E)**	SRCR(2)	pp
	Sp-SRCR-021	SPU_002028	SRCR(2)	pp
	Sp-SRCR-022	SPU_002041	SP-SRCR(3)-TM	
	Sp-SRCR-023	SPU_002350	SRCR(13)	pp
	Sp-SRCR-024	SPU_003127	SRCR(4)-TM	pp
	Sp-SRCR-025	SPU_003384	SRCR(4)	pp
	Sp-SRCR-026	SPU_003526	SRCR(6)	pp
	Sp-SRCR-027	SPU_003778	SP-SRCR(6)	pp
	Sp-SRCR-028	SPU_003930	SRCR(10)	pp
	Sp-SRCR-033	SPU_004011	SRCR(3)	pp
	Sp-SRCR-034	SPU_004086	SRCR(4)	pp
	Sp-SRCR-037	SPU_004160	SRCR(8)	pp
	Sp-SRCR-040	SPU_005000	SP-SRCR(5)	pp
	Sp-SRCR-041	SPU_005154	SRCR(7)	pp
	Sp-SRCR-043	SPU_005464	SRCR(6)-TM	pp
	Sp-SRCR-044	SPU_005556	SRCR(9)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR models	*Sp-SRCR-046*	SPU_006045	SRCR(2)	pp
(cont.)	*Sp-SRCR-047*	SPU_006055	SP-SRCR(4)-TM	
	Sp-SRCR-048	SPU_006254	SRCR(4)-TM	pp
	Sp-SRCR-049	SPU_006264	SRCR(4)	pp
	Sp-SRCR-050	SPU_006531	SRCR(4)	pp
	Sp-SRCR-053	SPU_006731	SP-SRCR(6)-TM	
	Sp-SRCR-054	SPU_007110	SRCR(7)	pp
	Sp-SRCR-055	SPU_007618 **(E)**	SP-SRCR(2)-TM	
	Sp-SRCR-056	SPU_007660	SRCR(3)-TM	pp
	Sp-SRCR-057	SPU_007718	SRCR(6)-TM	pp
	Sp-SRCR-060	SPU_007893	SRCR(6)	pp
	Sp-SRCR-067	SPU_008432	SRCR(4)	pp
	Sp-SRCR-068	SPU_008504	SRCR(16)	pp
	Sp-SRCR-069	SPU_008514	SRCR(2)-TM	pp
	Sp-SRCR-070	SPU_008598	SRCR(2)	pp
	Sp-SRCR-071	SPU_008642	SP-SRCR(8)	pp
	Sp-SRCR-072	SPU_008836 **(E)**	SP-SRCR(2)	pp
	Sp-SRCR-073	SPU_008885	SRCR(3)	pp
	Sp-SRCR-074	SPU_009145 **(E)**	SRCR(2)	pp
	Sp-SRCR-075	SPU_009354 **(E)**	SRCR(4)	pp
	Sp-SRCR-076	SPU_009496	SP-SRCR(6)	pp
	Sp-SRCR-077	SPU_009562	SRCR(2)	pp
	Sp-SRCR-080	SPU_009753	SRCR(3)	pp
	Sp-SRCR-082	SPU_010001	SRCR(2)	pp
	Sp-SRCR-083	SPU_010062	SRCR(6)	pp
	Sp-SRCR-086	SPU_010232	SP-SRCR(4)	pp
	Sp-SRCR-089	SPU_010409 **(E)**	SRCR(5)	
	Sp-SRCR-090	SPU_010501	SP-SRCR(4)	pp
	Sp-SRCR-091	SPU_010523	SRCR(2)	pp
	Sp-SRCR-092	SPU_010832	SRCR(3)-TM	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR models	*Sp-SRCR-093*	SPU_010909	SRCR(3)-TM	pp
(cont.)	*Sp-SRCR-094*	SPU_010953	SRCR(5)	pp
	Sp-SRCR-095	SPU_010991 **(E)**	SRCR(6)-TM	pp
	Sp-SRCR-099	SPU_011101	SP-SRCR(2)	pp
	Sp-SRCR-100	SPU_011146	SRCR(3)	pp
	Sp-SRCR-101	SPU_011222 **(E)**	SP-SRCR(13)-TM	
	Sp-SRCR-102	SPU_011752	SRCR(2)	pp
	Sp-SRCR-103	SPU_011977	SP-SRCR(4)	pp
	Sp-SRCR-104	SPU_012039	SP-SRCR(7)	pp
	Sp-SRCR-105	SPU_012159 **(E)**	SRCR(3)-TM	pp
	Sp-SRCR-107	SPU_012410	SP-SRCR(6)	pp
	Sp-SRCR-108	SPU_012888	SRCR(3)-TM	pp
	Sp-SRCR-109	SPU_013650 **(E)**	SP-SRCR(3)	pp
	Sp-SRCR-110	SPU_013831	SRCR(3)	pp
	Sp-SRCR-111	SPU_013958	SRCR(2)-TM	pp
	Sp-SRCR-112	SPU_014079	SRCR(4)-TM	pp
	Sp-SRCR-113	SPU_014080	SP-SRCR(2)	pp
	Sp-SRCR-114	SPU_014095	SP-SRCR(4)	pp
	Sp-SRCR-115	SPU_014602 **(E)**	SP-SRCR(6)	pp
	Sp-SRCR-116	SPU_014829	SRCR(7)	pp
	Sp-SRCR-117	SPU_014844 **(E)**	SP-SRCR(3)	pp
	Sp-SRCR-118	SPU_014859	SRCR(4)	pp
	Sp-SRCR-119	SPU_014860	SRCR(2)	pp
	Sp-SRCR-123	SPU_015123	SRCR(3)	pp
	Sp-SRCR-124	SPU_015325 **(E)**	SRCR(2)	pp
	Sp-SRCR-125	SPU_015387	SP-SRCR(4)	pp
	Sp-SRCR-127	SPU_015548	SRCR(4)-TM	pp
	Sp-SRCR-132	SPU_016195	SRCR(3)	pp
	Sp-SRCR-135	SPU_016531	SRCR(2)	pp
	Sp-SRCR-136	SPU_016880 **(E)**	SRCR(4)	pp
	Sp-SRCR-137	SPU_017127	SRCR(5)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR models	*Sp-SRCR-138*	SPU_017194	SRCR(2)	pp
(cont.)	*Sp-SRCR-139*	SPU_017453 **(E)**	SP-SRCR(2)-TM	
	Sp-SRCR-140	SPU_017933	SRCR(4)	pp
	Sp-SRCR-141	SPU_018252	SRCR(8)-TM	pp
	Sp-SRCR-144	SPU_018508 **(E)**	SP-SRCR(2)-TM	
	Sp-SRCR-145	SPU_018737	SP-SRCR(3)-TM	
	Sp-SRCR-146	SPU_018939	SRCR(5)-TM	pp
	Sp-SRCR-147	SPU_018985	SRCR(3)	pp
	Sp-SRCR-148	SPU_019241	SP-SRCR(4)	pp
	Sp-SRCR-151	SPU_019291	SRCR(2)	pp
	Sp-SRCR-154	SPU_019479	SRCR(7)	pp
	Sp-SRCR-155	SPU_019826	SRCR(5)-TM	pp
	Sp-SRCR-156	SPU_020081	SRCR(5)	pp
	Sp-SRCR-157	SPU_020161	SRCR(3)	pp
	Sp-SRCR-161	SPU_020822	SP-SRCR(4)-TM	
	Sp-SRCR-162	SPU_020868	SP-SRCR(2)	pp
	Sp-SRCR-163	SPU_021124	SP-SRCR(6)-TM	
	Sp-SRCR-164	SPU_021348	SP-SRCR(3)	pp
	Sp-SRCR-165	SPU_021457	SRCR(2)	pp
	Sp-SRCR-166	SPU_021509	SP-SRCR(6)	pp
	Sp-SRCR-169	SPU_021782	SRCR(3)	pp
	Sp-SRCR-170	SPU_021789	SRCR(7)-TM	pp
	Sp-SRCR-171	SPU_021890	SRCR(3)	pp
	Sp-SRCR-172	SPU_021987	SRCR(5)-TM	pp
	Sp-SRCR-173	SPU_021988	SP-SRCR(5)	pp
	Sp-SRCR-175	SPU_022085	SRCR(5)-TM	pp
	Sp-SRCR-190	SPU_022339	SP-SRCR(3)-TM	
	Sp-SRCR-197	SPU_022814	SRCR(4)	pp
	Sp-SRCR-198	SPU_023641 **(E)**	SP-SRCR(4)-TM	
	Sp-SRCR-199	SPU_023677	SRCR(5)-TM	pp
	Sp-SRCR-200	SPU_023840	SRCR(2)	pp
	Sp-SRCR-201	SPU_023991	SRCR(2)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR models	*Sp-SRCR-202*	SPU_024084	SRCR(4)	pp
(cont.)	*Sp-SRCR-204*	SPU_024408	SP-SRCR(7)-TM	
	Sp-SRCR-205	SPU_024440	SP-SRCR(4)-TM	
	Sp-SRCR-206	SPU_024487 **(E)**	SRCR(9)	pp
	Sp-SRCR-207	SPU_025862	SRCR(3)	pp
	Sp-SRCR-208	SPU_025865	SRCR(3)	pp
	Sp-SRCR-209	SPU_025968	SP-SRCR(3)	pp
	Sp-SRCR-210	SPU_025983	SRCR(27)	pp
	Sp-SRCR-211	SPU_026234	SRCR(3)	pp
	Sp-SRCR-212	SPU_026241 **(E)**	SRCR(2)	pp
	Sp-SRCR-213	SPU_026408	SP-SRCR(3)	pp
	Sp-SRCR-214	SPU_026709 **(E)**	SP-SRCR(4)	pp
	Sp-SRCR-217	SPU_027037	SP-SRCR(2)	pp
	Sp-SRCR-220	SPU_027379	SRCR(9)	pp
	Sp-SRCR-221	SPU_027503 **(E)**	SP-SRCR(3)	pp
	Sp-SRCR-222	SPU_027619	SRCR(5)	pp
	Sp-SRCR-223	SPU_028233	SP-SRCR(3)	pp
	Sp-SRCR-224	SPU_028382	SRCR(3)	pp
	Sp-SRCR-225	SPU_028612	SRCR(6)	pp
	Sp-SRCR-226	SPU_028669	SP-SRCR(3)	pp
	Sp-SRCR-228	SPU_028804	SRCR(3)	pp
Contiguous	*Sp-SRCR-009*	SPU_001004	TM/SP-SRCR(8)	pp
(fragmented?)	*Sp-SRCR-010*	SPU_001005	SRCR(4)	
models	*Sp-SRCR-029*	SPU_003963	SRCR(6)-TM	pp
	Sp-SRCR-030	SPU_003964	SRCR(3)-TM	pp
	Sp-SRCR-031	SPU_003965	SRCR(2)	pp
	Sp-SRCR-032	SPU_003966	SRCR(3)-TM	pp
	Sp-SRCR-035	SPU_004100 **(E)**	SP-SRCR(2)-TM	pp
	Sp-SRCR-036	SPU_004101	SP-SRCR(7)-TM	pp
	Sp-SRCR-051	SPU_006538	SRCR(2)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
Contiguous (fragmented?) models (cont.)	*Sp-SRCR-052*	SPU_006539	SP-SRCR(12)	pp
	Sp-SRCR-058	SPU_007781	SRCR(10)-TM	pp
	Sp-SRCR-059	SPU_007782	SRCR(5)	pp
	Sp-SRCR-061	SPU_007894	SRCR(4)	pp
	Sp-SRCR-062	SPU_007895	SRCR(2)	pp
	Sp-SRCR-063	SPU_007896	SRCR(7)-TM	pp
	Sp-SRCR-064	SPU_007897	SRCR(2)-TM	pp
	Sp-SRCR-065	SPU_007899	SP-SRCR(5)-TM	pp
	Sp-SRCR-066	SPU_007900	SRCR(4)-TM	pp
	Sp-SRCR-078	SPU_009676	SRCR(3)	pp
	Sp-SRCR-079	SPU_009677	SRCR(3)	pp
	Sp-SRCR-084	SPU_010226	SRCR(4)	pp
	Sp-SRCR-085	SPU_010227	F5_F8_type_C-SRCR(9)	pp
	Sp-SRCR-087	SPU_010240	SRCR(2)	pp
	Sp-SRCR-088	SPU_010241	SRCR(2)	pp
	Sp-SRCR-096	SPU_010992 **(E)**	SP-SRCR(2)-TM	pp
	Sp-SRCR-097	SPU_010993 **(E)**	SP-SRCR(5)	pp
	Sp-SRCR-098	SPU_010994 **(E)**	SRCR(2)-TM	pp
	Sp-SRCR-120	SPU_014992	SRCR(8)-TM	pp
	Sp-SRCR-121	SPU_014993	RNaseH-SRCR(4)-TM - possibly a wrong call	pp
	Sp-SRCR-122	SPU_014994	SRCR(9)	pp
	Sp-SRCR-128	SPU_015937 **(E)**	SRCR(2)-TM	pp
	Sp-SRCR-129	SPU_015938	SP-SRCR(3)	pp
	Sp-SRCR-130	SPU_015989	SRCR(2)	pp
	Sp-SRCR-131	SPU_015991	SP-SRCR(2)-TM	
	Sp-SRCR-133	SPU_016373 **(E)**	SRCR(2)-TM	pp
	Sp-SRCR-134	SPU_016374 **(E)**	SRCR(9)	pp
	Sp-SRCR-142	SPU_018429 **(E)**	SRCR(13)	pp
	Sp-SRCR-143	SPU_018430	SP-SRCR(5)	pp
	Sp-SRCR-149	SPU_019262	SRCR(2)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

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Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
Contiguous (fragmented?) models (cont.)	*Sp-SRCR-150*	SPU_019263	SRCR(3)	pp
	Sp-SRCR-167	SPU_021691	SP-SRCR(2)	pp
	Sp-SRCR-168	SPU_021692	SRCR(4)-TM	pp
	Sp-SRCR-176	SPU_022145	SP-SRCR(6)	pp
	Sp-SRCR-177	SPU_022146	SRCR(5)	pp
	Sp-SRCR-178	SPU_022147	SRCR(3)	pp
	Sp-SRCR-179	SPU_022148	SRCR(4)	pp
	Sp-SRCR-180	SPU_022149	SRCR(8)	pp
	Sp-SRCR-181	SPU_022150	SRCR(5)	pp
	Sp-SRCR-182	SPU_022151 **(E)**	SRCR(2)	pp
	Sp-SRCR-185	SPU_022285	SRCR(3)	pp
	Sp-SRCR-186	SPU_022286	SRCR(10)-TM	pp
	Sp-SRCR-187	SPU_022287	SRCR(4)-TM	pp
	Sp-SRCR-188	SPU_022288	SRCR(3)	pp
	Sp-SRCR-189	SPU_022289	SRCR(4)-TM	pp
	Sp-SRCR-191	SPU_022423	SRCR(4)	pp
	Sp-SRCR-192	SPU_022424	SRCR(8)-Sushi(2)	pp
	Sp-SRCR-194	SPU_022567	SRCR(5)-TM	pp
	Sp-SRCR-195	SPU_022568	SRCR(5)	pp
	Sp-SRCR-196	SPU_022569	SRCR(3)	pp
	Sp-SRCR-215	SPU_026848	SRCR(8)	pp
	Sp-SRCR-216	SPU_026849	SRCR(14)-TM	pp
	Sp-SRCR-218	SPU_027287	SRCR(4)	pp
	Sp-SRCR-219	SPU_027288	SP-SRCR(17)	pp
SRCR and additional domains	*Sp-SRCR-016*	SPU_001601	F5_F8_type_C(1)-SRCR(3)	pp
	Sp-SRCR-038	SPU_004642	SRCR(2)-Sushi(1)?	pp
	Sp-SRCR-042	SPU_005420 **(E)**	SRCR(5)-Sushi(1)-TM	pp
	Sp-SRCR-039	SPU_007349 **(E)**	WSC(2)-SRCR-WSC-SRCR-WSC-TM	pp
	Sp-SRCR-017	SPU_007370	SP-SRCR(2)-HYR	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

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Table S4 (cont.) - Full list of SRCR genes.

Group	Gene name	Gene ID	Domain Structure *	Status ‡
SRCR and additional domains (cont.)	*Sp-SRCR-015*	SPU_007372	SRCR(2)-HYR(2)-IgC2-GPS-SRCR(2)	pp
	Sp-SRCR-045	SPU_007840	CUB(4)-SRCR(2)	pp
	Sp-SRCR-184	SPU_009220	SP-SRCR-WSC-CUB	pp
	Sp-SRCR-183	SPU_010330	SP-SRCR(2)-HYR	
	Sp-SRCR-106	SPU_012230	SP-SRCR(4)-EGF	
	Sp-SRCR-126	SPU_015539	SP-SRCR(2)-WSC	
	Sp-SRCR-152	SPU_019370 **(E)**	SRCR(5)-Sushi-TM	pp
	Sp-SRCR-153	SPU_019374	SRCR(2)-HYR-SRCR(2)	pp
	Sp-SRCR-158	SPU_020273	EGF_CA(2)-SRCR(2)	pp
	Sp-SRCR-159	SPU_020597 **(E)**	SRCR(8)-Sushi(3)-HYR-Sushi-HYR(2)-Sushi(2)	pp
	Sp-SRCR-160	SPU_020650	TIL-SRCR(4)	pp
	Sp-SRCR-174	SPU_022000	Somat-SRCR-Somat-SRCR-CUB.	
	Sp-SRCR-193	SPU_022528	SRCR(9)-EGF-SRCR(5)	pp
	Sp-SRCR-203	SPU_024390	SP-SRCR(2)-WSC-TM	
	Sp-SRCR-227	SPU_028680	EGF_CA(6)-EGF-SRCR(2)-EGF(2).	
	Sp-SRCR/PTPc-1	SPU_005860	SRCR(3)-TM-PTPc	pp
	Sp-SRCR/LRR-1	SPU_006659	SRCR(6)-LRR(3)	pp
	Sp-Ig/SRCR-1	SPU_009988	Ig(2)-SRCR(6)	pp
	Sp-SRCR-081	SPU_009989	SRCR(6)	pp

* Domain Structure: SP, signal peptide; SRCR, Scavenger Receptor Cystein-Rich repeat; TM, transmembrane domain; WSC, WSC domain [carbohydrate binding domain present in Wall integrity and Stress response Component (WSC) proteins, polycystin and fungal exoglucanase]; HYR, Hyalin Repeat domain; GPS, G-protein-coupled receptor proteolytic site domain; TIL, domain found in proteinase inhibitors and many extracellular proteins; Somat, Somatomedin B-like domains; F5_F8_type_C, Factors V and VIII/discoidin (DS) domain; RNaseH, RNase H domain; PTPc, Protein tyrosine phosphatase, catalytic domain.

‡ Status: pp, probably partial gene model.

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Supplementary Table S5 - Full list of transcription factors with relevance to immune cell development and function in the *Strongylocentrotus purpuratus* genome sequence.

TF Family	Gene model ID	Assigned name
ETS		
Ets-1,2	SPU_002874 **(E)**	*Sp-Ets1/2*
Erg, Fli-1	SPU_018483 **(E)**	*Sp-Erg*
PU.1, Spi-B, Spi-C	SPU_030060	*Sp-PU1*
Elf-1	SPU_020124	*Sp-Elf-A*
	SPU_020123	*Sp-Elf-B*
Tel	SPU_008351/028479 (1) **(E)**	*Sp-Tel*
GABP	SPU_021557	*Sp-Gabp*
GATA		
GATA-1/2/3	SPU_027015 **(E)**	*SpGATAc*
Basic Helix-Loop-Helix (HLH) - Class I bHLH		
E2A, HEB, ITF-2	SPU_016343 **(E)**	*Sp-E12*
Basic Helix-Loop-Helix (HLH) - Class II bHLH		
SCL	SPU_028093 **(E)**	*Sp-SCL*
Basic Helix-Loop-Helix (HLH) - Class III bHLH		
MITF/TFE3	SPU_008175 **(E)**	*Sp-Mitf*
Basic Helix-Loop-Helix (HLH) - Class IV HLH/Id		
Id-2	SPU_015374 **(E)**	*Sp-Id*
Basic Helix-Loop-Helix (HLH) - Class VI Hairy/Hes		
Hes-1,Hes-4	SPU_006814 **(E)**	*SpHairy*
	SPU_006813 **(E)**	*SpHairy*
	SPU_015712 **(E)**	*SpHesL*
	SPU_021608 **(E)**	*Sp-Hes*
Hey/HERP	SPU_009465	*Sp-Hey*
RUNX		
Runx-1-3	SPU_025612/006917 (1) **(E)**	*Sp-Runt1*
	SPU_007852 **(E)**	*Sp-Runt2*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model..

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S5 (cont.) - Full list of immunity-related transcription factors

TF Family	Gene model ID	Assigned name
OLF/EBF		
EBF-1,2,3	SPU_004702	*Sp-EBF3*
PAX		
Pax-5	SPU_014539	*SpPax2-5-8*
C/EBP		
C/EBPalpha, beta, epsilon	SPU_001657	*Sp-C/EBPb/d*
C/EBPgamma	SPU_011002 **(E)**	*Sp-C/EBPg*
C2H2 Zinc Finger		
Ikaros	SPU_011260	*SpZ181*
Egr-1,2,3	SPU_015358 **(E)**	*Sp-z60, SpEgr-1*
LKLF, EKLF	SPU_020311 **(E)**	*Sp-LKLF*
Gfi-1	SPU_012645 **(E)**	*Sp-Gfi, Sp-z166*
Blimp-1	SPU_027235 **(E)**	*Sp-Blimp, Krox1a*
TCF/LEF Hmg Box		
TCF-1, LEF-1	SPU_003704/027853 (1) **(E)**	*Sp-Lef*
Interferon Response Factor		
IRF-1,2	SPU_010404	*Sp-IRF*
IRF-4/Pip, IRF-8/ICSBP	SPU_026877	*Sp-IRF4*
bZIP		
c-fos, Fos, Fra-1, Fra-2	SPU_021172 **(E)**	*Sp-Fos*
c-jun, JunB, JunD	SPU_003102 **(E)**	*Sp-Jun*
ATF-2, ATF-7, CREB	SPU_026905 **(E)**	*Sp-ATF2*
XBP-1	SPU_008703 **(E)**	*SpXBP-1*
NFE	SPU_011174 **(E)**	*Sp-Nfe2*
REL Homology Domain		
c-rel, RelA, RelB	SPU_012203 **(E)**	*Sp-rel*
NFkB1, NFkB p105	SPU_008177 **(E)**	*Sp-NFkB*
NFATc, NFAT-4	SPU_015908 **(E)**	*NFAT*
STATs		
STAT5	SPU_015108 **(E)**	*Sp-STAT*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model..

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

Table S5 (cont.) - Full list of immunity-related transcription factors

TF Family	Gene model ID	Assigned name
Nuclear Receptors		
RARalpha	SPU_018366	*Sp-RARa*
RARbeta	SPU_013178	*Sp-RARb*
SOX Hmg Box		
SOX4, SOX11, SOX22, SOX24	SPU_002603 **(E)**	*Sp-SOXC*
T-BOX		
T-bet	SPU_025584 **(E)**	*Sp-Tbr*
FORKHEAD		
FoxP1,2,3,4	SPU_009876 **(E)**	*Sp-FOXP*
SMAD		
SMAD4	SPU_004287 **(E)**	*Sp-SMAD4*
SMAD2,3	SPU_017642	*Sp-SMAD3*
SMAD1,5	SPU_020722 **(E)**	*Sp-SMAD1*
	SPU_023107 **(E)**	*Sp-SMAD5*
DEAD RINGER/BRIGHT		
Dead ringer	SPU_005718/025601 (1) **(E)**	*Sp-deadringer*
POU Domain		
Oct1, Oct 2	SPU_009262 **(E)**	*Sp-Oct1-2*
MYB		
c-myb	SPU_000861 **(E)**	*Sp-Myb*
Transcriptional Co-factors		
LMO1/2	SPU_013569	*Sp-Lmo2t*
FOG1/2	SPU_010168	*Sp-FOG.*

(1) Two or more model IDs have been assigned to the same gene due to any of the following reasons: a) They represent duplicated models of the same gene; b) They correspond to both alleles of the same locus; c) They contain partial fragments of a gene broken up into more than one model..

(E) indicates embryonic expression of the gene model as indicated by hybridization of pooled RNA samples from egg, early blastula, gastrula and prism stage embryos to a high-density tiling array of the *S. purpuratus* genome (Samanta et al., 2006)

LEGENDS TO SUPPLEMENTARY FIGURES

Figure S1. Structure of the sea urchin TLR types. **(A)** Representative typical sea urchin TLR of "vertebrate-type" structure (Sp-Tlr082, SPU_015303). **(B-C)** Two sea urchin TLRs with protostome-like structure: **(B)** Sp-Tlr066 (SPU_011823) and **(C)** Sp-Tlr041 (SPU_007859). **(D)** Structure of a "Short-type" TLR (Sp-Tlr159, SPU_001458). Box colors represent the following domains: Pink, signal peptide; red, LRRNT; blue, LRRCT; gray shading, transmembrane region; green, TIR domain. Amino acids highlighted in yellow denote consensus LRR hydrophobic residues. The consensus sequence is shown in (A).

Figure S2. Analysis of TIR domain sequences from sea urchin protostome-like TLR genes. **(A)** Phylogenetic tree of bilaterian Toll-like receptors. One Sp-Tlr is represented from each subgroup. Red genes denote protostome-like LRR pattern (see text), while blue genes denote vertebrate-like LRR pattern (single LRRNT and LRRCT flank all LRRs). All protostome-like TLR gene TIR sequences cluster together. This protostome TLR clade includes the TIR domains from the three sea urchin protostome-like TLR genes (shown in black ovals). *Caenorhabditis elegans* and *Nematostella vectensis* have only one TLR gene each and they are of the protostome type. A small divergent subclass of Sp-TLR genes with very short extracellular domains does not clearly cluster with either TLR class. **(B)** Alignment of C-terminal region of the TIR domain. TIR domains are composed of five β-sheets and five α-helices alternatively spaced (three of which are here denoted with green boxes). The region between the fifth β-sheet and α-helix is shorter in protostome-type Toll genes than in vertebrate genes (Rock et al, 1998). A

diagnostic gap after the fifth β-sheet is denoted by a shaded box. The three protostome-like Sp-TLR genes have shorter β-sheets than those in vertebrates and other Sp-TLR genes, and hence both the extracellular LRR motifs and cytoplasmic TIR domain structures exhibit affinities with the protostome-type TLRs.

Figure S3. Variation in LRR sequence among closely related TLR sequences. **(A)** Typical single amino acid substitutions and smaller insertion/deletions. These mutations are seen within LRR motifs. **(B)** An example of larger insertions flanking LRRs. TLR subfamily Group III has the largest insertion (16 amino acids) of the Sp-Tlr genes. Some gene models have a cysteine pair within the insertion. A smaller insertion is located at the end of LRR 5. **(C)** An unusual insertion of complete LRR motifs found in one sea urchin TLR subgroup (Group IB). The number of inserted LRRs (1-3) varies in closely related genes. The amino acid sequence is highly similar among inserted LRRs. LRR number designations are taken from the related Group IA which does not exhibit this type of insertion. Shaded amino acids denote insertions. Blue boxes delineate LRR motifs. Red residues denote conserved patterns of LRR hydrophobic amino acids.

Figure S4. Domain structure of representative Sp-NLRs. Sp-NLR protein sequences from Cluster 1 **(A)** and 2 **(B)** are shown with the different domains boxed in pink (DEATH), yellow (NACHT) and black (LRRs). The sequence in B is that of the GENSCAN prediction (Supertig112651_2: 4,654 -20,780), which has two DEATH domains; the Glean3 prediction has a single DEATH domain. LRRs that were found through a HMMER search using the Pfam LRR_1, LRR_2 and LRR_3 consensus sequences are designated. However, several other sequences related to the core LxxLxL

sequence can readily be identified. The LRRs in these genes are encoded in complex exon/intron structures that are poorly represented in the gene predictions. Nonetheless, clear evidence of their presence can be found in multiple gene models within each cluster of the phylogenetic tree (Fig. S5).

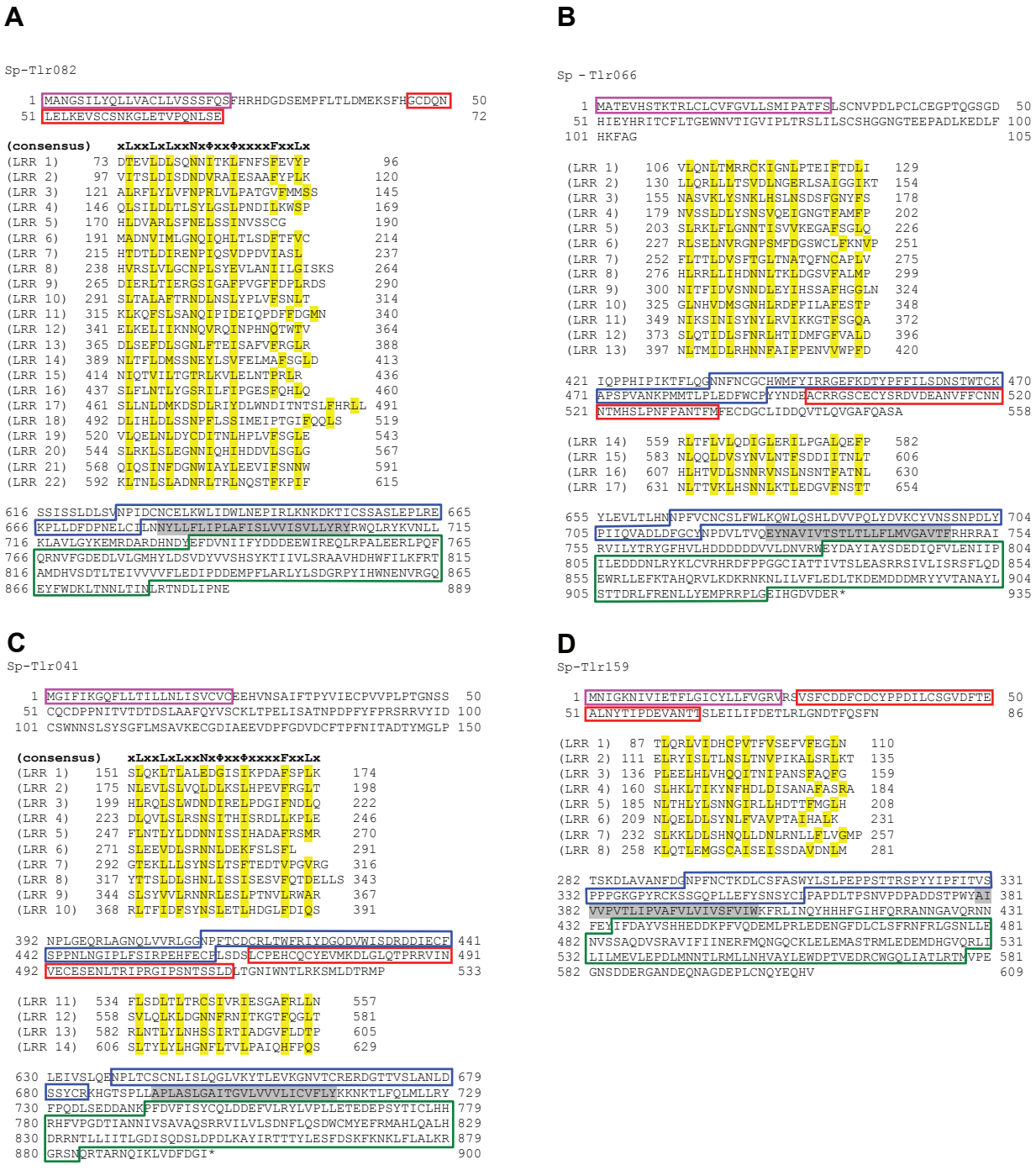
Figure S5. Neighbor joining tree of sea urchin NLR genes. This tree was constructed using 193 NLR NACHT domain amino acid sequences. Clusters referred to in the text and in Table S3 are indicated. Numbers indicate bootstrap values.

Figure S6. Expression analysis of NLRs from clusters 1 and 2. Quantitative PCR was performed as described elsewhere (Fugmann et al., 2006) on cDNA from adult tissues, including unseparated coelomocytes and coelomocyte fractions. Degenerate oligonucleotides that recognize a conserved region of the NACHT domain of gene models from clusters 1 and 2 were used as primers. TF: tube feet, OE: oesophagus, M: mesentary, GUT: gut, TE: testis, OV:ovary, C: coelomocytes, P: phagocytes, V: vibratile cells, CS: colorless spherule cells, RS: red spherule cells.

Figure S7. Phylogenetic tree of the thioester protein family. A pairwise alignment method was used to align the sequences in ClustalX (Thompson et al., 1997) and subsequent editing was done by hand using Bioedit sequence alignment editor (Hall, 1999). A consensus tree constructed in PAUP* (Swofford, 2002) using maximum parsimony method with 1000 bootstrap replicates is shown as a phylogram. The horseshoe crab $\alpha_2$macroglobulin sequence was chosen as the outgroup. Similar

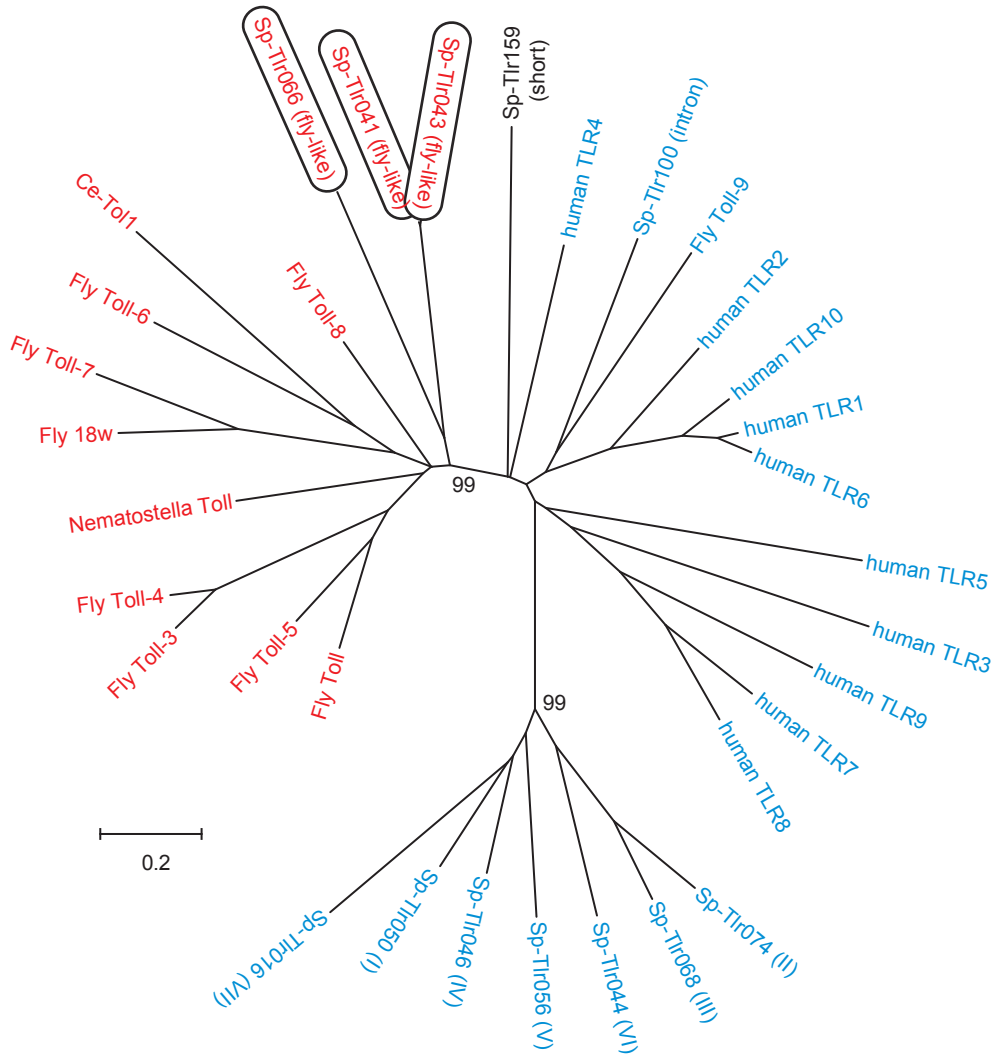
cladogram results were obtained using a maximum parsimony method in MEGA3 (Kumar et al., 2004), and a Bayesian method in Mr. Bayes (Ronquist and Huelsenbeck, 2003). The Bayesian method was used with default priors and a GTR gamma-distributed rate variation across sites and with a proportion of variable sites. The cladistic grouping of the sea urchin sequences, Sp-C3, Sp-C3-2, TCP-1, TCP-2 and Sp-a2m were the same using PAUP*, Bayesian and MEGA3 methods. Although the tree shows support for a separate clade that includes all invertebrate C3-like sequences with the exception of the protochordates, it is likely that this is an artifact caused by the limited number of invertebrate thioester proteins, and that these genes are orthologous to the vertebrate C3/4/5 genes. Furthermore, the placement within the tree of α2m from Ciona and sea urchin plus TCP-1 and -2 may be due to long branch attraction based on the elongated 3' end of these sequences. Whether these gene models are correct will require additional investigation. Amino acid sequences were collected from GenBank or the Sea Urchin Annotation website: C3 coral, *Swiftia exserta*, AY186744; C3 sea urchin, *Strongylocentrotus purpuratus*, AAC14396; C3-2 sea urchin, *Strongylocentrotus purpuratus*, SPU_000997; TCP-1 sea urchin, *Strongylocentrotus purpuratus*, SPU_022988; C3 amphioxus, *Brachiostoma belcheri*, AB050668; C3 halocynthia, *Halocynthia roretzi*, AB006964; C3 mouse, *Mus musculus*, P01027; C3 human, *Homo sapiens*, NM_000064; C3 hagfish, *Eptatretus burgeri*, Z11595; C3 lamprey, *Lethenteron japonica*, D10087; C3 cobra, *Naja naja*, Q01833; C3 chicken, *Gallus gallus*, I50711; C3 grass carp, *Ctenopharyngodon idella*, AAQ74974; C3-1 ciona, *Ciona intestinalis*, AJ320542; C3-2 ciona, *Ciona intestinalis*, AJ320543; C3 horseshoe crab, *Carcinoscorpius rotundicauda*, AAQ08323; C4 xenopus, *Xenopus laevis*, D78003; C4

mouse, *Mus musculus*, P01029; C4A human, *Homo sapiens*, K02403; TCP-2 sea urchin, *Strongylocentrotus purpuratus*, SPU_005198; C4 medaka, *Oryzias latipes*, BAA92287; C5 human, *Homo sapiens*, M57729; C5 mouse, *Mus musculus*, P06684; a2m mouse, *Mus musculus*, Q61838; a2m human, *Homo sapiens*, NM_000014; a2m horseshoe crab, Limulus sp., D83196; a2m lamprey, *Lethenteron japonica*, D13567; a2m sea urchin, *Strongylocentrotus purpuratus*, SPU_013170; a2m ciona, *Ciona intestinalis*, CAD24311.



Hibino et al. Figure S1

A



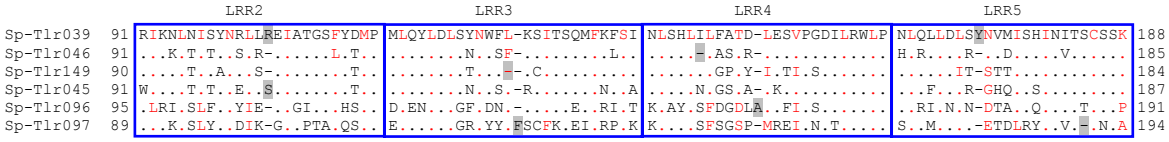
B

			α-helix 4		β-sheet 5		α-helix 5		
Sp-Tlr050(I)	843	...EMPF	LARLYLSDGR	PY	IHWTEN	V-RGQE	YFWDELTKDLTI	-NLRTNDLI	889
Sp-Tlr074(II)	889	...NLPY	LVRLFLSRNR	PY	MLWTED	-EDRQE	LFWAQFEKSTRA	-NRAINNAI	935
Sp-Tlr068(III)	867	...NLPY	LVRLLLSRNK	PY	LLWVFD	DEDGQE	LFWAKFEKNMRA	-NREMNNVI	914
Sp-Tlr046(IV)	823	...ELPF	LVRLYLSDRK	PY	LSWEEE	EERFQE	YFWQKLIKMLKM	-NLRCNNVI	870
Sp-Tlr056(V)	817	...ELPF	LIRLFLSDHR	PY	LVWPDD	-ERGQE	YFWEELIRDLTV	-NIRCNHLI	863
Sp-Tlr100(intron)	805	...TKYY	KLHKVMMKRT	-Y	LKWPME	PGVQRN	DFWMKLKTVLRE	PELRINNNV	852
human_TLR1	741	...SSYH	KLKSLMARRT	-Y	LEWPKE	-KSKRG	LFWANLRAAIN-	--IKLTEQA	784
human_TLR4	780	...RQQV	ELYRLLSRNT	-Y	LEWEDS	-VLGRH	IFWRRLRKALLD	-GKSWNPEG	825
Fly_Toll9	853	...KRPK	TLQYLMDVKT	—Y	IKWPTA	-KEDRK	LFWKRLKRSLEV	IGINSREIS	899
Sp-Tlr159(short)	542	...LMNN	TLRMLLNHVA	-Y	LEWDPT	---VED	RCWGQLIATLRT	-MVPEGNSD	585
Sp-Tlr041(fly-like)	847	...SLDP	DLKAYIRTTT	-Y	LESFDS	------	KFKNKLFLALKR	-GRSNQRTA	887
Sp-Tlr066(fly-like)	889	...EMDD	DMRYYVTANA	-Y	LSTTDR	------	LFRENLLYEMPR	--RPLGEIH	928
Fly_Toll	894	...KLDE	ELKAYLKMNT	-Y	LKWGDP	------	WFWDKLRFALPH	-RRPVGNIG	934
Fly_Toll3	749	...SLDS	ELRTYMAFNT	-Y	LERSHP	------	NFWNKLIYSMPH	-TKLR	785
Nematostella Toll	821	...TLDD	ETKLYLRTNT	-Y	LSVSNK	------	WFWQKLFYALPK	PLAPPQSYE	862

Hibino et al. Figure S2

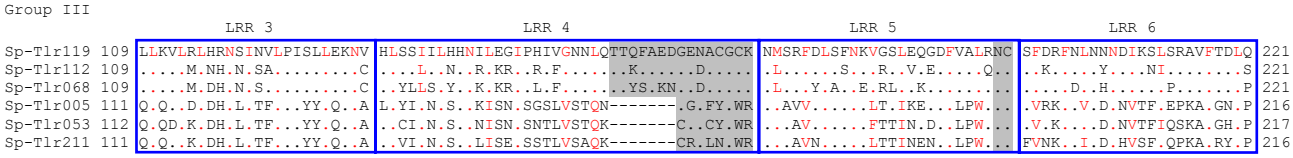
A

Group IV



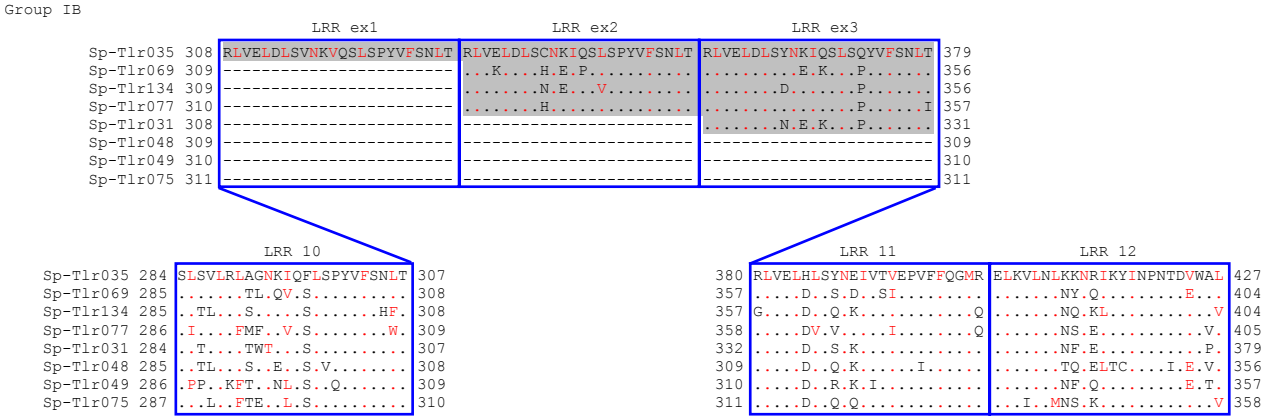
B

Group III

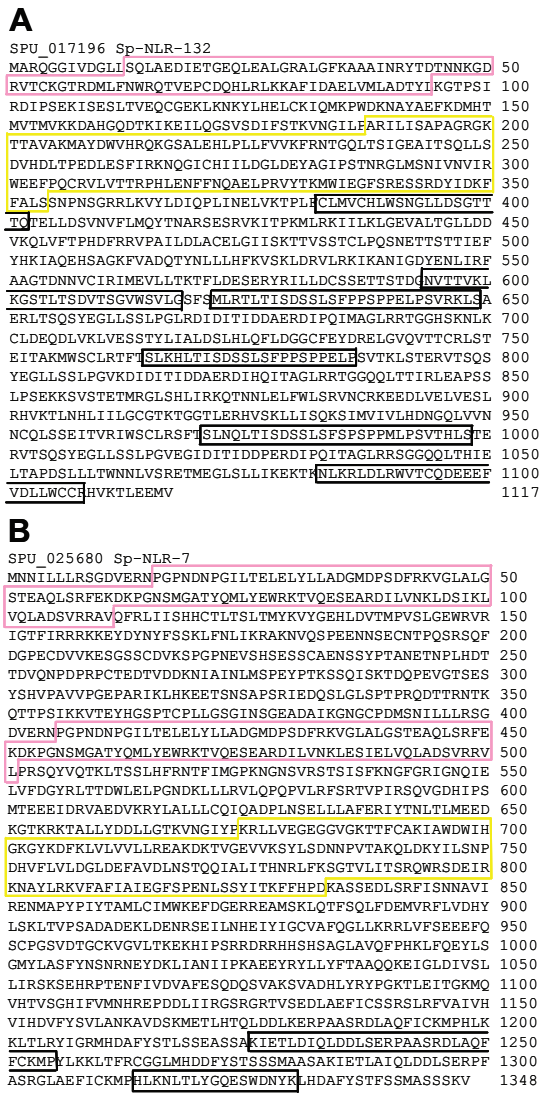


C

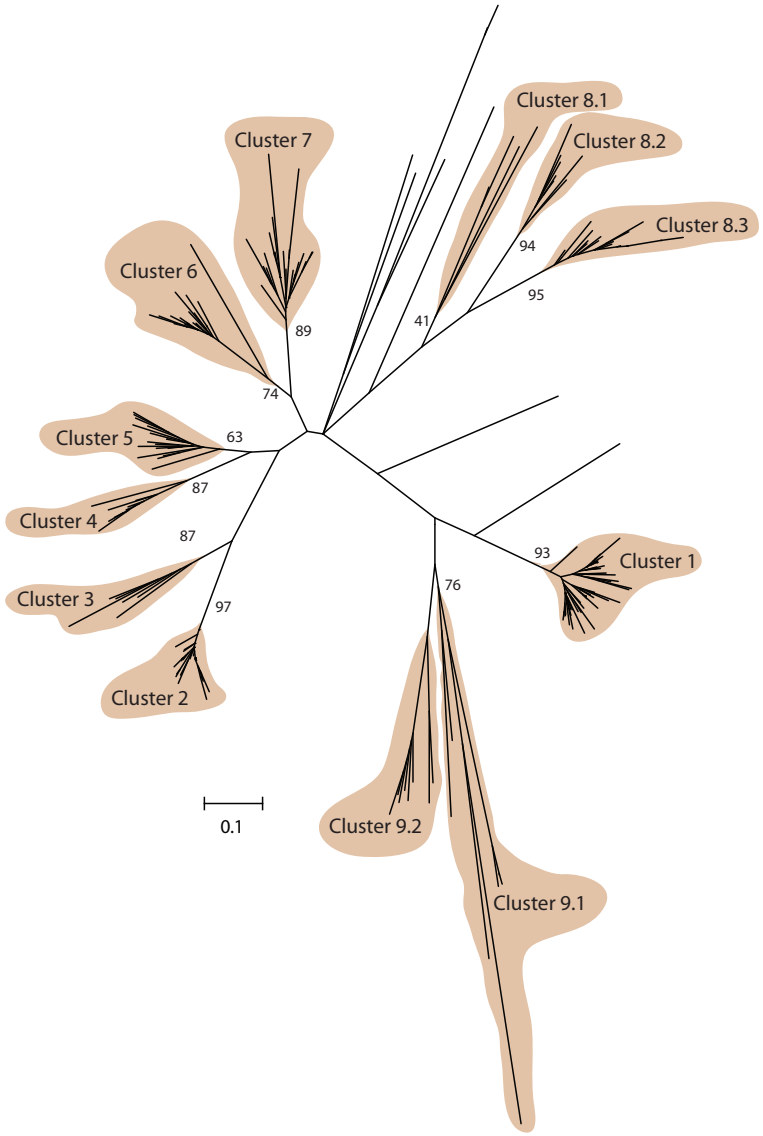
Group IB



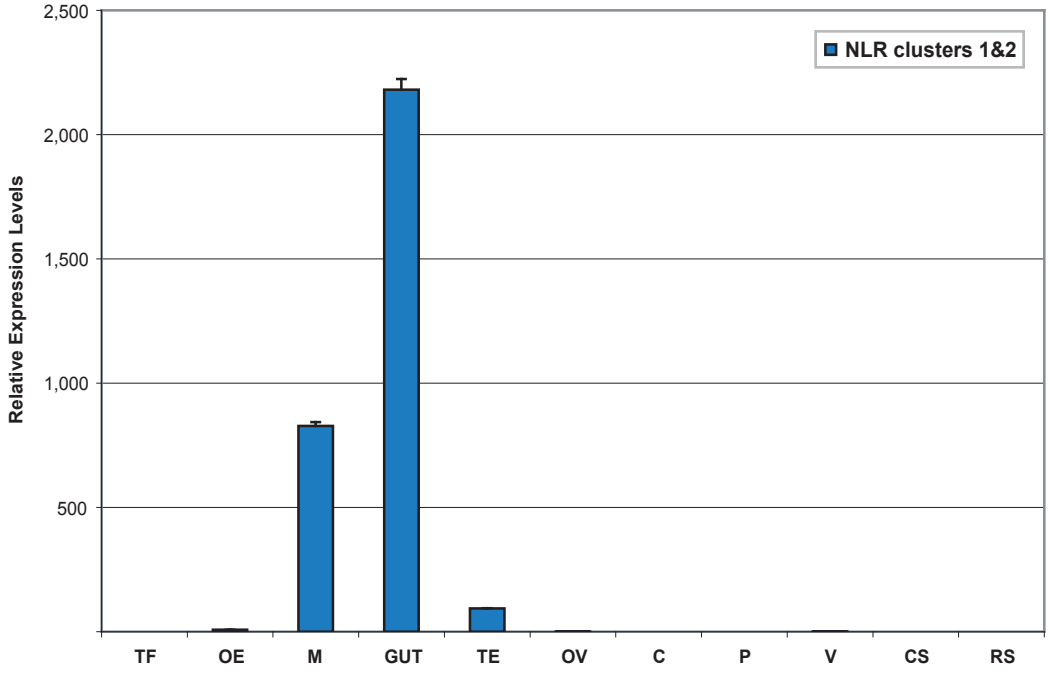
Hibino et al. Figure S3



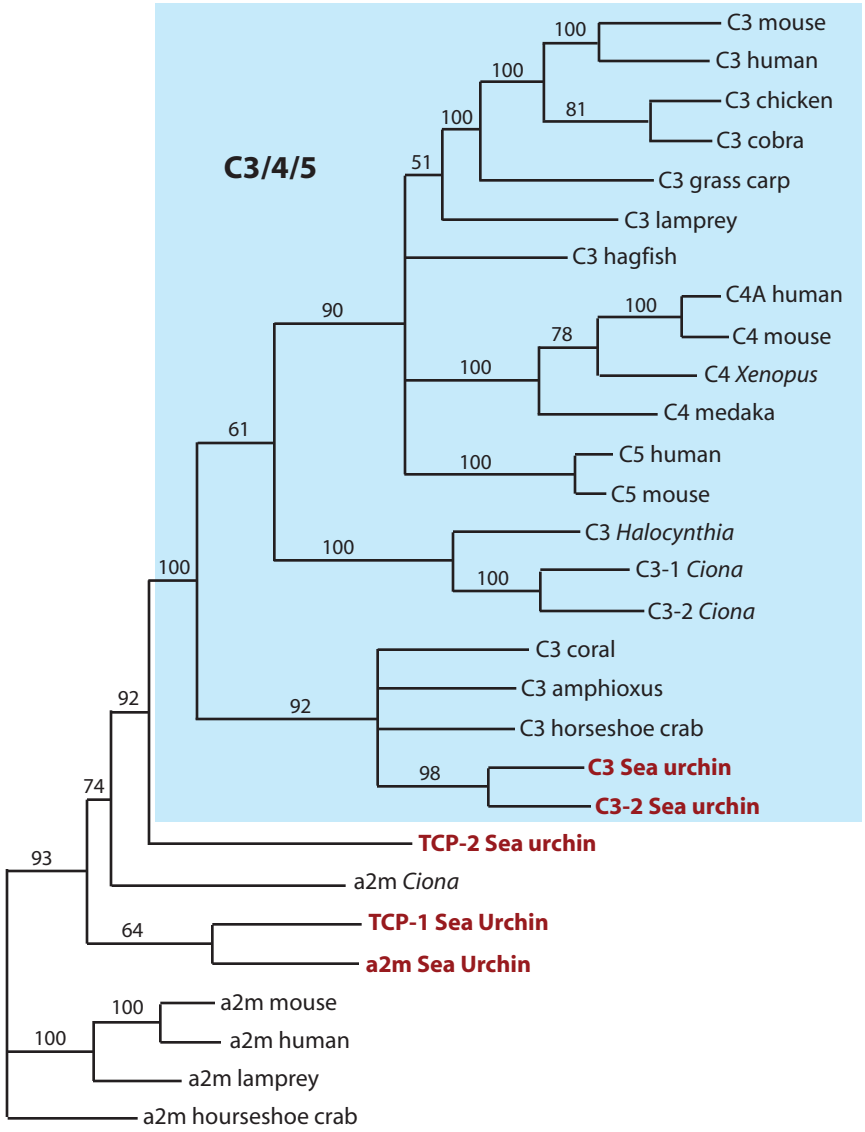
Hibino et al. Figure S4



Hibino et al. Figure S5



Hibino et al. Figure S6



Hibino et al. Figure S7