

Table S20. Transcripts encoding ionotropic acetylcholine receptors in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_FX_18766	XP_013080421.1 PREDICTED: uncharacterized protein LOC106066011 [Biomphalaria glabrata] *	742	631	56.4
evgLocus_FX_17627	ABA60389.1 nicotinic acetylcholine receptor subunit type K [Lymnaea stagnalis]	501	501	100
evgLocus_FX_18804	ABA60390.1 nicotinic acetylcholine receptor subunit type J [Lymnaea stagnalis]	582	550	100
evgLocus_FX_18879	ABA60381.1 nicotinic acetylcholine receptor subunit type B [Lymnaea stagnalis]	527	527	100
evgLocus_FX_20189	ABA60386.1 nicotinic acetylcholine receptor subunit type G [Lymnaea stagnalis]	618	618	100
evgLocus_FX_22234	ABA60387.1 nicotinic acetylcholine receptor subunit type H [Lymnaea stagnalis]	467	450	100
evgLocus_FX_23187	ABA60384.1 nicotinic acetylcholine receptor subunit type E [Lymnaea stagnalis]	538	538	100
evgLocus_FX_27048	ABA60388.1 nicotinic acetylcholine receptor subunit type I [Lymnaea stagnalis]	527	527	100
evgLocus_scallop_AH_33824	ABA60383.1 nicotinic acetylcholine receptor subunit type D [Lymnaea stagnalis]	103	554	100
evgLocus_FX_20255	ABA60382.1 nicotinic acetylcholine receptor subunit type C [Lymnaea stagnalis]	506	506	99.8
evgLocus_FX_21433	ABA60380.1 nicotinic acetylcholine receptor subunit type A [Lymnaea stagnalis]	485	485	99.8
evgLocus_Scallop_AE_39077	ABA60387.1 nicotinic acetylcholine receptor subunit type H [Lymnaea stagnalis]	346	450	99.6
evgLocus_FX_17911	XP_013094583.1 PREDICTED: neuronal acetylcholine receptor subunit beta-4-like [Biomphalaria glabrata]	625	311	88.6
evgLocus_stringtie_AF_41679	ABA60385.1 nicotinic acetylcholine receptor subunit type F [Lymnaea stagnalis]	571	488	86.6
evgLocus_Scallop_AE_34677	XP_013067706.1 PREDICTED: neuronal acetylcholine receptor subunit beta-3-like [Biomphalaria glabrata]	469	499	82.9
evgLocus_strawberry_AF_33628	XP_005093258.1 PREDICTED: neuronal acetylcholine receptor subunit alpha-7-like [Aplysia californica]	567	468	78.6
evgLocus_FX_21891	XP_013088338.1 PREDICTED: neuronal acetylcholine receptor subunit alpha-2-like [Biomphalaria glabrata]	509	509	75.1
evgLocus_FX_19484	NP_001297423.1 neuronal acetylcholine receptor subunit alpha-10-like precursor [Aplysia californica]	538	541	72.9
evgLocus_FX_19956	XP_005094753.2 PREDICTED: neuronal acetylcholine receptor subunit beta-3-like [Aplysia californica]	499	509	69.2
evgLocus_FX_16787	NP_001297424.1 acetylcholine receptor subunit alpha-type acr-16-like precursor [Aplysia californica]	604	635	68
evgLocus_FX_18755	ABA60390.1 nicotinic acetylcholine receptor subunit type J [Lymnaea stagnalis]	544	550	67.4
evgLocus_FX_21106	NP_001267733.1 acetylcholine receptor subunit beta-like 1-like [Aplysia californica]	587	593	65.3
evgLocus_FX_20080	XP_013090302.1 PREDICTED: neuronal acetylcholine receptor subunit beta-3-like [Biomphalaria glabrata]	581	567	63.9
evgLocus_strawberry_AG_62696	XP_021342101.1 neuronal acetylcholine receptor subunit alpha-10-like [Mizuhopecten yessoensis]	317	482	63.6
evgLocus_FX_19442	XP_021342101.1 neuronal acetylcholine receptor subunit alpha-10-like [Mizuhopecten yessoensis]	487	482	61.1
evgLocus_Scallop_AE_39871	XP_013094335.1 PREDICTED: neuronal acetylcholine receptor subunit beta-3-like [Biomphalaria glabrata]	279	418	60.7
evgLocus_stringtie_AH_15026	XP_013060683.1 PREDICTED: acetylcholine receptor subunit alpha-like [Biomphalaria glabrata]	320	437	55.3
evgLocus_strawberry_AG_33123	XP_021351690.1 neuronal acetylcholine receptor subunit alpha-10-like, partial [Mizuhopecten yessoensis]	620	637	52.8
evgLocus_stringtie_AH_58757	XP_013094335.1 PREDICTED: neuronal acetylcholine receptor subunit beta-3-like [Biomphalaria glabrata]	333	418	51.2
evgLocus_Trinity_AG_42558	XP_013066091.1 PREDICTED: acetylcholine receptor subunit alpha-like [Biomphalaria glabrata]	311	447	50.8
evgLocus_FX_25160	XP_013071749.1 PREDICTED: neuronal acetylcholine receptor subunit alpha-7-like [Biomphalaria glabrata]	449	423	50.4
evgLocus_Trinity_AF_41395	XP_013066091.1 PREDICTED: acetylcholine receptor subunit alpha-like [Biomphalaria glabrata]	460	447	50.4
evgLocus_FX_24558	XP_013066091.1 PREDICTED: acetylcholine receptor subunit alpha-like [Biomphalaria glabrata]	432	447	49.4
evgLocus_FX_22924	XP_013071749.1 PREDICTED: neuronal acetylcholine receptor subunit alpha-7-like [Biomphalaria glabrata]	407	423	46.8
evgLocus_stringtie_AE_5950	XP_012940025.1 PREDICTED: acetylcholine receptor subunit alpha-like [Aplysia californica]	269	397	42
evgLocus_Trinity_AG_60798	NP_001267746.1 ligand-gated ion channel 4-like precursor [Aplysia californica] *	521	518	83.1

* Contains InterPro signature of ionotropic acetylcholine receptor.

Table S21. Transcripts encoding ionotropic GABA or glycine receptors in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_FX_19329	CAA50492.1 gamma-aminobutyric acid-gated chloride-ion channel/receptor, zeta subunit [<i>Lymnaea stagnalis</i>]	437	437	100
evgLocus_FX_21251	P26714.1 RecName: Full=Gamma-aminobutyric acid receptor subunit beta	529	499	99.4
evgLocus_FX_20044	XP_013091826.1 PREDICTED: gamma-aminobutyric acid receptor alpha-like isoform X1 [<i>Biomphalaria glabrata</i>]	443	488	90.2
evgLocus_Trinity_AE_79821	XP_013063333.1 PREDICTED: gamma-aminobutyric acid receptor subunit alpha-6-like [<i>Biomphalaria glabrata</i>]	711	706	84.2
evgLocus_FX_26671	XP_013094258.1 PREDICTED: gamma-aminobutyric acid receptor subunit alpha-2-like [<i>Biomphalaria glabrata</i>]	459	447	72.4
evgLocus_FX_25484	NP_001191520.1 GluClAc2 [<i>Aplysia californica</i>]	425	429	79.4
evgLocus_FX_23008	XP_013092685.1 PREDICTED: glycine receptor subunit alpha-3-like isoform X1 [<i>Biomphalaria glabrata</i>]	425	420	74.6
evgLocus_FX_28954	XP_021342615.1 glycine receptor subunit alphaZ1-like [<i>Mizuhopecten yessoensis</i>]	412	387	47.6

Table S22. Transcripts encoding ionotropic glutamate receptors in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_FX_16972	XP_012938956.1 PREDICTED: uncharacterized protein LOC101860416 [Aplysia californica] *	1549	1692	55.3
evgLocus_FX_19909	P26591.1 RecName: Full=Glutamate receptor	917	917	99.8
evgLocus_scallop_AF_4621	CAA60854.1 glutamate receptor InvGluR-K1 polypeptide [Lymnaea stagnalis]	953	953	99.7
evgLocus_FX_19001	AAT40576.1 NMDA-type glutamate receptor [Lymnaea stagnalis]	963	963	99.5
evgLocus_Strawberry_DRR_22588	XP_013081818.1 PREDICTED: glutamate receptor ionotropic, NMDA 2B-like [Biomphalaria glabrata]	1336	1569	61.5
evgLocus_Stringtie_DRR_39190	OWF44765.1 Glutamate receptor ionotropic, NMDA 3A [Mizuhopecten yessoensis]	805	1203	61.5
evgLocus_FX_17076	NP_001191485.1 NR2 [Aplysia californica]	1504	1164	58.7
evgLocus_Trinity_GG_DRR_75560	XP_013072954.1 PREDICTED: glutamate receptor 1-like, partial [Biomphalaria glabrata]	979	935	76.9
evgLocus_strawberry_AE_34164	XP_013081052.1 PREDICTED: glutamate receptor ionotropic, kainate 2-like isoform X1 [Biomphalaria glabrata]	852	549	75.3
evgLocus_FX_19753	NP_001191539.1 glutamate receptor subunit protein GluR1 precursor [Aplysia californica]	945	925	75.1
evgLocus_FX_18618	AAP41206.1 glutamate receptor subunit protein GluR4 [Aplysia californica]	899	906	75
evgLocus_strawberry_AF_7153	NP_001191543.1 glutamate receptor subunit protein GluR7 precursor [Aplysia californica]	899	890	74.9
evgLocus_Trinity_RF_Nov18_27402	XP_013092521.1 PREDICTED: glutamate receptor ionotropic, kainate 2-like [Biomphalaria glabrata]	858	780	74.9
evgLocus_Trinity_AE_24441	XP_012945575.1 PREDICTED: glutamate receptor 3-like [Aplysia californica]	517	407	74.8
evgLocus_strawberry_AF_15779	NP_001191540.1 glutamate receptor subunit protein GluR2 precursor [Aplysia californica]	953	911	72.2
evgLocus_Trinity_AF_81772	NP_001191542.1 glutamate receptor subunit protein GluR6 [Aplysia californica]	768	875	66.9
evgLocus_FX_17854	NP_001191542.1 glutamate receptor subunit protein GluR6 [Aplysia californica]	851	875	63.8
evgLocus_Trinity_AG_83842	NP_001191542.1 glutamate receptor subunit protein GluR6 [Aplysia californica]	804	875	63.6
evgLocus_FX_18725	XP_005102071.2 PREDICTED: glutamate receptor ionotropic, kainate 3 [Aplysia californica]	521	506	62.8
evgLocus_FX_18690	XP_013077978.1 PREDICTED: glutamate receptor 2-like [Biomphalaria glabrata]	569	449	59.9
evgLocus_stringtie_AE_28436	XP_012940304.1 PREDICTED: glutamate receptor ionotropic, kainate 3-like [Aplysia californica]	1033	985	57.1
evgLocus_FX_20287	XP_005107294.2 PREDICTED: glutamate receptor ionotropic, kainate 4-like [Aplysia californica]	494	501	53.4
evgLocus_Trinity_AG_4349	NP_001191541.1 glutamate receptor subunit protein GluR5 precursor [Aplysia californica]	618	903	49.8
evgLocus_scallop_AG_32790	NP_001191541.1 glutamate receptor subunit protein GluR5 precursor [Aplysia californica]	913	903	47.5
evgLocus_Trinity_RF_Nov18_20632	OWF49654.1 Glutamate receptor ionotropic, delta-1 [Mizuhopecten yessoensis]	671	852	46.6
evgLocus_FX_18551	XP_021345787.1 glutamate receptor 4-like [Mizuhopecten yessoensis]	876	909	45.5
evgLocus_Trinity_GG_DRR_28841	XP_009064312.1 hypothetical protein LOTGIDRAFT_131225 [Lottia gigantea] *	1516	865	50.2

* Contains InterPro signature of ionotropic glutamate receptor.

Table S23. Transcripts encoding K⁺ channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_stringtie_AG_14914	XP_005093895.1 PREDICTED: uncharacterized protein LOC101849827 [Aplysia californica] #	1463	1558	69.3
evgLocus_scallop_AF_13162	XP_005108858.1 PREDICTED: uncharacterized protein LOC101862142 [Aplysia californica] #	221	401	35.9
evgLocus_scallop_AF_8899	XP_013095351.1 PREDICTED: uncharacterized protein LOC106078854 [Biomphalaria glabrata] §	1474	1360	68
evgLocus_strawberry_AE_56499	XP_013068853.1 PREDICTED: calcium-activated potassium channel slowpoke-like isoform X9 [Biomphalaria glabrata]	1070	1099	91.9
evgLocus_Strawberry_DRR_58351	XP_013068787.1 PREDICTED: calcium-activated potassium channel slowpoke-like isoform X1 [Biomphalaria glabrata]	1122	1122	91
evgLocus_Trinity_AF_124854	XP_013090634.1 PREDICTED: small conductance calcium-activated potassium channel protein-like [Biomphalaria glabrata]	825	793	80.8
evgLocus_scallop_AF_38033	XP_013090634.1 PREDICTED: small conductance calcium-activated potassium channel protein-like [Biomphalaria glabrata]	801	793	79.8
evgLocus_strawberry_AG_22928	XP_005107423.2 PREDICTED: small conductance calcium-activated potassium channel protein 3-like [Aplysia californica]	204	571	79.2
evgLocus_strawberry_AE_762	XP_005090058.2 PREDICTED: small conductance calcium-activated potassium channel protein-like [Aplysia californica]	475	519	75.5
evgLocus_strawberry_AE_39140	XP_013083299.1 PREDICTED: TWiK family of potassium channels protein 18-like [Biomphalaria glabrata]	563	546	68.5
evgLocus_scallop_AG_37588	ABR37307.1 TASK two-pore domain potassium channel [Lymnaea stagnalis]	364	361	100
evgLocus_FX_24354	XP_009057266.1 hypothetical protein LOTGIDRAFT_121567 [Lottia gigantea] *	465	274	48.7
evgLocus_Trinity_AE_27410	XP_009057266.1 hypothetical protein LOTGIDRAFT_121567 [Lottia gigantea] *	488	274	45.2
evgLocus_Trinity_GG_DRR_75469	NP_001191546.1 Shaw potassium channel Kv3.1a [Aplysia californica]	614	514	93.3
evgLocus_strawberry_AH_31305	XP_013080373.1 PREDICTED: potassium voltage-gated channel protein Shaw-like [Biomphalaria glabrata]	188	697	91
evgLocus_scallop_AG_2744	XP_013063673.1 PREDICTED: G protein-activated inward rectifier potassium channel 4-like isoform X2 [Biomphalaria glabrata]	486	493	89.7
evgLocus_FX_17791	XP_012942106.1 PREDICTED: potassium voltage-gated channel subfamily KQT member 1-like [Aplysia californica]	665	560	88.6
evgLocus_Scallop_AE_33310	XP_013076045.1 PREDICTED: potassium voltage-gated channel protein Shaw-like [Biomphalaria glabrata]	419	571	86.9
evgLocus_FX_17983	XP_013086501.1 PREDICTED: potassium channel subfamily T member 2-like [Biomphalaria glabrata]	1128	1030	86.1
evgLocus_Stringtie_DRR_22702	XP_012934690.1 PREDICTED: potassium voltage-gated channel subfamily KQT member 1-like [Aplysia californica]	533	623	85.1
evgLocus_scallop_AH_32316	XP_005094519.1 PREDICTED: potassium channel subfamily K member 2-like [Aplysia californica]	420	423	83.7
evgLocus_FX_17005	XP_012939351.1 PREDICTED: potassium channel subfamily K member 1-like [Aplysia californica]	348	339	76.3
evgLocus_Trinity_AG_130536	XP_013067170.1 PREDICTED: potassium channel subfamily K member 4-like [Biomphalaria glabrata]	381	352	69
evgLocus_FX_17605	XP_013094150.1 PREDICTED: potassium voltage-gated channel subfamily H member 2-like [Biomphalaria glabrata]	1111	663	83.5
evgLocus_FX_21655	XP_005091742.1 PREDICTED: potassium voltage-gated channel protein Shal-like [Aplysia californica]	689	717	80.3
evgLocus_FX_19780	XP_012944327.1 PREDICTED: potassium channel subfamily T member 2 [Aplysia californica]	1028	1234	79.3
evgLocus_strawberry_AH_21570	XP_013072553.1 PREDICTED: potassium channel subfamily T member 2-like [Biomphalaria glabrata]	1277	1267	72.3
evgLocus_FX_28708	XP_013064952.1 PREDICTED: ATP-sensitive inward rectifier potassium channel 1-like [Biomphalaria glabrata]	453	430	77.9
evgLocus_FX_21494	XP_013080109.1 PREDICTED: potassium voltage-gated channel protein Shaw-like [Biomphalaria glabrata]	667	674	73.9
evgLocus_strawberry_AG_44481	XP_012944008.1 PREDICTED: ATP-sensitive inward rectifier potassium channel 12-like [Aplysia californica]	436	418	71.5
evgLocus_Stringtie_DRR_27728	XP_013085598.1 PREDICTED: potassium voltage-gated channel protein egl-36-like [Biomphalaria glabrata]	310	817	70.5
evgLocus_stringtie_AF_28143	XP_013085598.1 PREDICTED: potassium voltage-gated channel protein egl-36-like [Biomphalaria glabrata]	356	817	68.5
evgLocus_stringtie_AG_29537	XP_005107164.1 PREDICTED: potassium voltage-gated channel subfamily H member 6-like [Aplysia californica]	1239	1365	67.3
evgLocus_FX_17230	XP_013083954.1 PREDICTED: potassium voltage-gated channel protein Shaw-like isoform X1 [Biomphalaria glabrata]	549	540	66.6
evgLocus_Scallop_DRR_4779	XP_005098785.1 PREDICTED: inward rectifier potassium channel 2-like [Aplysia californica]	576	512	59.3
evgLocus_FX_21050	XP_013091822.1 PREDICTED: potassium channel subfamily K member 9-like [Biomphalaria glabrata]	683	389	51.3

* Contains InterPro signature of TASK channel.

Contains InterPro signature of voltage-gated K⁺ channel.

§ Contains InterPro signature of ELK channel.

Table S24. Transcripts encoding Ca²⁺ channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_Scallop_AE_23909	XP_013069789.1 PREDICTED: two pore calcium channel protein 1-like [Biomphalaria glabrata]	817	793	72.5
evgLocus_FX_19019	XP_012943292.1 PREDICTED: two pore calcium channel protein 2-like [Aplysia californica]	818	898	62.2
evgLocus_FX_21501	XP_005089220.2 PREDICTED: two pore calcium channel protein 1-like [Aplysia californica]	827	779	75.6
evgLocus_scallop_AG_24453	XP_013069789.1 PREDICTED: two pore calcium channel protein 1-like [Biomphalaria glabrata]	282	793	67.7
evgLocus_FX_42627	AAO83838.2 voltage-dependent L-type calcium channel alpha-1 subunit isoform a [Lymnaea stagnalis]	207	2078	100
evgLocus_scallop_AG_4605	AAO83838.2 voltage-dependent L-type calcium channel alpha-1 subunit isoform a [Lymnaea stagnalis]	1441	2078	99.7
evgLocus_strawberry_AE_27300	AAO83843.2 voltage-dependent T-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	2878	2886	98.9
evgLocus_Scallop_AE_17458	AAO83843.2 voltage-dependent T-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	2891	2886	98.2
evgLocus_Trinity_AH_85872	AAO83843.2 voltage-dependent T-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	1427	2886	93
evgLocus_strawberry_AG_27619	AAO83843.2 voltage-dependent T-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	2673	2886	92.6
evgLocus_FX_17353	AAO83841.1 voltage-dependent non-L-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	1340	2141	96.6
evgLocus_Strawberry_DRR_59689	AAO83841.1 voltage-dependent non-L-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	1705	2141	99.3
evgLocus_Trinity_GG_DRR_50598	AAO83841.1 voltage-dependent non-L-type calcium channel alpha-1 subunit isoform A [Lymnaea stagnalis]	2196	2141	95
evgLocus_FX_35751	XP_005090384.1 PREDICTED: protein orai-2-like [Aplysia californica]	222	226	85.7
evgLocus_Trinity_GG_DRR_35036	XP_013068048.1 PREDICTED: inositol 1,4,5-trisphosphate receptor type 1-like isoform X7 [Biomphalaria glabrata]	2750	2658	94.5
evgLocus_Stringtie_DRR_40665	XP_013068047.1 PREDICTED: inositol 1,4,5-trisphosphate receptor type 1-like isoform X6 [Biomphalaria glabrata]	2739	2663	93.8
evgLocus_Trinity_AE_111397	XP_012935906.1 PREDICTED: inositol 1,4,5-trisphosphate receptor type 1-like [Aplysia californica]	2956	2978	85
evgLocus_Trinity_AE_111398	XP_012935906.1 PREDICTED: inositol 1,4,5-trisphosphate receptor type 1-like [Aplysia californica]	2980	2978	84.8
evgLocus_strawberry_AG_55149	XP_005096332.1 PREDICTED: inositol 1,4,5-trisphosphate receptor type 3-like [Aplysia californica]	1882	2879	78.1
evgLocus_Trinity_AH_95415	XP_009059256.1 hypothetical protein LOTGIDRAFT_123762 [Lottia gigantea] *	5044	5045	67.3
evgLocus_Trinity_GG_DRR_44867	XP_013065477.1 PREDICTED: ryanodine receptor 44F-like [Biomphalaria glabrata]	5238	4926	79
evgLocus_Trinity_AG_97056	XP_013065477.1 PREDICTED: ryanodine receptor 44F-like [Biomphalaria glabrata]	5217	4926	78.9
evgLocus_FX_16361	XP_013065477.1 PREDICTED: ryanodine receptor 44F-like [Biomphalaria glabrata]	5293	4926	77.9
evgLocus_Trinity_GG_DRR_44870	XP_013065477.1 PREDICTED: ryanodine receptor 44F-like [Biomphalaria glabrata]	2015	4926	77.5

* Contains InterPro signature of ryanodine receptor.

Table S25. Transcripts encoding Na⁺ channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_Trinity_AG_31670	AAK20896.1 FMRFamide-gated and pH-modulated sodium channel [Lymnaea stagnalis]	632	632	100
evgLocus_Trinity_GG_DRR_56848	AAK20896.1 FMRFamide-gated and pH-modulated sodium channel [Lymnaea stagnalis]	615	632	90
evgLocus_strawberry_AF_2915	AAF80601.1 FMRFamide-gated Na ⁺ channel [Planorbella trivolvis]	616	622	72.2
evgLocus_Trinity_GG_DRR_14950	AKH03688.1 voltage-gated sodium channel alpha subunit LNav14b21+ [Lymnaea stagnalis]	2011	2006	99.8
evgLocus_strawberry_AE_20077	AKH03687.1 voltage-gated sodium channel alpha subunit LNav14a21+ [Lymnaea stagnalis]	1653	2007	88.6
evgLocus_Scallop_DRR_41110	XP_013076160.1 PREDICTED: amiloride-sensitive sodium channel subunit alpha-like [Biomphalaria glabrata]	550	453	48.4
evgLocus_FX_21168	XP_005095704.2 PREDICTED: amiloride-sensitive sodium channel subunit beta-2-like [Aplysia californica]	487	489	37.3
evgLocus_strawberry_AH_4559	XP_005095704.2 PREDICTED: amiloride-sensitive sodium channel subunit beta-2-like [Aplysia californica]	480	489	35.7
evgLocus_Trinity_AH_110125	XP_009044219.1 hypothetical protein LOTGIDRAFT_228153 [Lottia gigantea] *	621	536	38.1
evgLocus_Trinity_AE_42211	XP_013083408.1 PREDICTED: degenerin del-1-like [Biomphalaria glabrata]	152	313	39.5
evgLocus_Stringtie_DRR_20189	XP_011430312.1 PREDICTED: uncharacterized protein LOC105330372 [Crassostrea gigas] *	347	930	39.4
evgLocus_FX_56442	No match *	134	-1	-1

* Contains InterPro signature of epithelial sodium channel

Table S26. Transcripts encoding Cl⁻ channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_Trinity_AG_17389	XP_013082752.1 PREDICTED: anoctamin-7-like, partial [Biomphalaria glabrata]	1067	862	85.3
evgLocus_FX_17795	XP_013082752.1 PREDICTED: anoctamin-7-like, partial [Biomphalaria glabrata]	871	862	82.9
evgLocus_Trinity_AF_68258	XP_013082999.1 PREDICTED: anoctamin-1-like isoform X5 [Biomphalaria glabrata]	948	950	81.3
evgLocus_Trinity_GG_DRR_87780	XP_013070323.1 PREDICTED: anoctamin-4-like isoform X6 [Biomphalaria glabrata]	921	1022	78.9
evgLocus_Scallop_AE_2473	XP_005096667.1 PREDICTED: anoctamin-10-like isoform X3 [Aplysia californica]	738	703	72.7
evgLocus_stringtie_AH_5459	XP_013070321.1 PREDICTED: anoctamin-4-like isoform X4 [Biomphalaria glabrata]	1038	1037	70.6
evgLocus_Trinity_AH_48109	XP_013070321.1 PREDICTED: anoctamin-4-like isoform X4 [Biomphalaria glabrata]	532	1037	69.4
evgLocus_FX_16654	XP_013086831.1 PREDICTED: anoctamin-8-like [Biomphalaria glabrata]	1157	1155	67.2
evgLocus_scallop_AH_23138	XP_012939123.1 PREDICTED: bestrophin-3-like, partial [Aplysia californica]	565	365	81.5
evgLocus_strawberry_AF_34562	XP_013073025.1 PREDICTED: bestrophin-2-like [Biomphalaria glabrata]	653	340	78.7
evgLocus_stringtie_AG_1836	XP_013070043.1 PREDICTED: chloride channel protein 2-like [Biomphalaria glabrata]	955	949	75.7
evgLocus_Stringtie_DRR_46452	XP_012944768.1 PREDICTED: chloride channel protein A-like [Aplysia californica]	1421	1425	67.3
evgLocus_scallop_AH_14301	XP_013083884.1 PREDICTED: chloride channel CLIC-like protein 1 [Biomphalaria glabrata]	691	585	41.8
evgLocus_Trinity_RF_Nov18_45322	XP_013083884.1 PREDICTED: chloride channel CLIC-like protein 1 [Biomphalaria glabrata]	603	585	40.8
evgLocus_Trinity_AG_27801	XP_013083884.1 PREDICTED: chloride channel CLIC-like protein 1 [Biomphalaria glabrata]	297	585	38.9
evgLocus_FX_21811	XP_013083884.1 PREDICTED: chloride channel CLIC-like protein 1 [Biomphalaria glabrata]	567	585	38.8
evgLocus_Trinity_AE_85637	XP_013073248.1 PREDICTED: H(+)/Cl(-) exchange transporter 3-like [Biomphalaria glabrata]	843	836	84.6
evgLocus_FX_21027	XP_005096600.1 PREDICTED: H(+)/Cl(-) exchange transporter 7-like [Aplysia californica]	808	816	71.4

Table S27. Transcripts encoding cation channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_Trinity_AG_6913	XP_005093850.1 PREDICTED: cyclic nucleotide-gated cation channel alpha-3-like isoform X1 [Aplysia californica]	664	669	89.5
evgLocus_Trinity_AG_2741	XP_013063129.1 PREDICTED: cyclic nucleotide-gated cation channel beta-1-like [Biomphalaria glabrata]	1478	541	89.3
evgLocus_scallop_AG_4831	XP_013068727.1 PREDICTED: cyclic nucleotide-gated cation channel beta-1-like [Biomphalaria glabrata]	882	1135	89
evgLocus_strawberry_AE_52253	XP_013063129.1 PREDICTED: cyclic nucleotide-gated cation channel beta-1-like [Biomphalaria glabrata]	1239	541	86.5
evgLocus_FX_40927	XP_013081417.1 PREDICTED: cyclic nucleotide-gated channel rod photoreceptor subunit alpha-like, partial [Biomphalaria glabrata]	225	784	94.2
evgLocus_Trinity_AG_111551	XP_013061334.1 PREDICTED: potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4-like [Biomphalaria glabrata]	1229	1251	75.4
evgLocus_FX_26159	XP_013074477.1 PREDICTED: trimeric intracellular cation channel type B-A-like [Biomphalaria glabrata]	291	291	92.8
evgLocus_Trinity_AH_10150	XP_005102510.1 PREDICTED: trimeric intracellular cation channel type A-like [Aplysia californica]	121	269	67
evgLocus_FX_32684	XP_005102510.1 PREDICTED: trimeric intracellular cation channel type A-like [Aplysia californica]	277	269	64.9
evgLocus_Trinity_AH_67380	AGC13755.1 LNALCN [Lymnaea stagnalis]	1742	1742	99.9
evgLocus_FX_16447	XP_013084437.1 PREDICTED: piezo-type mechanosensitive ion channel component 2-like [Biomphalaria glabrata]	1947	2397	70.9
evgLocus_Trinity_AG_136890	CDJ97773.1 Protein FAM38A [Haemonchus contortus]	213	1730	42.1
evgLocus_Trinity_RF_Nov18_88607	XP_013079313.1 PREDICTED: acid-sensing ion channel 5-like isoform X1 [Biomphalaria glabrata]	552	556	69.8
evgLocus_scallop_AF_10390	XP_013067221.1 PREDICTED: CSC1-like protein 2 isoform X3 [Biomphalaria glabrata]	805	804	89.3
evgLocus_FX_26464	XP_005093106.1 PREDICTED: uncharacterized protein LOC101850633 [Aplysia californica] *	360	339	65.2
evgLocus_FX_33387	XP_005100666.1 PREDICTED: voltage-gated hydrogen channel 1-like [Aplysia californica]	218	281	48.1
evgLocus_Scallop_DRR_19272	XP_013062540.1 PREDICTED: uncharacterized protein LOC106051876 isoform X2 [Biomphalaria glabrata] *	517	485	42.1

* Contains InterPro signature of voltage-gated hydrogen channel.

Table S28. Transcripts encoding TRP channels in the *L. stagnalis* CNS.

Sequence ID	Nr hit	Query length	Subject length	Percent identity
evgLocus_Stringtie_DRR_44113	XP_013074930.1 PREDICTED: uncharacterized protein LOC106061369 [Biomphalaria glabrata] *	460	1247	62.6
evgLocus_strawberry_AH_26500	XP_013074930.1 PREDICTED: uncharacterized protein LOC106061369 [Biomphalaria glabrata] *	610	1247	72.5
evgLocus_Trinity_AF_71664	XP_013083118.1 PREDICTED: transient receptor potential cation channel subfamily V member 5-like [Biomphalaria glabrata]	299	811	70.2
evgLocus_Scallop_AE_1234	XP_011431159.1 PREDICTED: uncharacterized protein LOC105330915 isoform X3 [Crassostrea gigas] *	1037	1120	53.1
evgLocus_stringtie_AH_8895	XP_005101687.1 PREDICTED: uncharacterized protein LOC101851051 [Aplysia californica] *	977	979	52.3
evgLocus_Stringtie_DRR_23400	XP_013094766.1 PREDICTED: transient receptor potential cation channel subfamily A member 1 homolog [Biomphalaria glabrata]	1260	1273	74.5
evgLocus_scallop_AF_8457	XP_012939582.1 PREDICTED: transient receptor potential cation channel subfamily A member 1-like [Aplysia californica]	1271	1264	68.8
evgLocus_Trinity_GG_DRR_1427	XP_012934963.1 PREDICTED: short transient receptor potential channel 4-like [Aplysia californica]	1110	1145	74.5
evgLocus_Trinity_AE_79874	XP_012936952.1 PREDICTED: short transient receptor potential channel 3-like [Aplysia californica]	1033	1047	74.2
evgLocus_Trinity_AH_82800	XP_012936952.1 PREDICTED: short transient receptor potential channel 3-like [Aplysia californica]	559	1047	72.9
evgLocus_FX_18071	XP_012939119.1 PREDICTED: short transient receptor potential channel 7-like [Aplysia californica]	997	779	70
evgLocus_Trinity_AG_2187	XP_012939119.1 PREDICTED: short transient receptor potential channel 7-like [Aplysia californica]	971	779	67.9
evgLocus_FX_18462	XP_012936952.1 PREDICTED: short transient receptor potential channel 3-like [Aplysia californica]	958	1047	64.4
evgLocus_scallop_AH_33484	XP_013076601.1 PREDICTED: short transient receptor potential channel 3-like [Biomphalaria glabrata]	1660	921	83.1
evgLocus_FX_21483	XP_012936952.1 PREDICTED: short transient receptor potential channel 3-like [Aplysia californica]	806	1047	79.4
evgLocus_FX_19171	XP_013080473.1 PREDICTED: short transient receptor potential channel 3-like [Biomphalaria glabrata]	984	1021	48.4
evgLocus_Trinity_AH_49952	XP_021376838.1 transient-receptor-potential-like protein [Mizuhopecten yessoensis]	977	935	63
evgLocus_Trinity_AE_48360	XP_021376838.1 transient-receptor-potential-like protein [Mizuhopecten yessoensis]	952	935	62.1
evgLocus_Scallop_AE_2814	XP_013083410.1 PREDICTED: transient receptor potential cation channel subfamily M member 1-like [Biomphalaria glabrata]	1735	1714	69.3
evgLocus_Trinity_GG_DRR_79297	XP_013083410.1 PREDICTED: transient receptor potential cation channel subfamily M member 1-like [Biomphalaria glabrata]	1840	1714	66
evgLocus_Scallop_DRR_21600	XP_013061400.1 PREDICTED: transient receptor potential cation channel subfamily M member 5-like [Biomphalaria glabrata]	1613	1515	65.4
evgLocus_stringtie_AF_16138	XP_013061400.1 PREDICTED: transient receptor potential cation channel subfamily M member 5-like [Biomphalaria glabrata]	351	1515	61.8
evgLocus_FX_30259	XP_013061400.1 PREDICTED: transient receptor potential cation channel subfamily M member 5-like [Biomphalaria glabrata]	403	1515	59.1
evgLocus_stringtie_AH_11414	XP_013090385.1 PREDICTED: transient receptor potential cation channel subfamily M member 3-like [Biomphalaria glabrata]	509	1426	58.2
evgLocus_Scallop_DRR_73768	XP_013071668.1 PREDICTED: transient receptor potential cation channel subfamily M member 1-like isoform X1 [Biomphalaria glabrata]	672	332	52.8
evgLocus_Trinity_AE_125438	XP_013071668.1 PREDICTED: transient receptor potential cation channel subfamily M member 1-like isoform X1 [Biomphalaria glabrata]	685	332	52.2
evgLocus_Scallop_DRR_44684	XP_013065691.1 PREDICTED: transient receptor potential cation channel subfamily M member 5-like [Biomphalaria glabrata]	1065	877	32.6
evgLocus_Stringtie_DRR_24326	XP_005105591.2 PREDICTED: polycystic kidney disease protein 1-like 2 [Aplysia californica]	583	1857	71.2
evgLocus_Trinity_GG_DRR_24759	XP_005098719.2 PREDICTED: polycystic kidney disease 2-like 1 protein [Aplysia californica]	856	883	85.7
evgLocus_Scallop_DRR_54844	XP_012934947.1 PREDICTED: polycystic kidney disease protein 1-like 2 [Aplysia californica]	1157	1089	60.9
evgLocus_Stringtie_DRR_46096	XP_005088946.2 PREDICTED: polycystic kidney disease protein 1-like 1 [Aplysia californica]	4350	2480	56.9
evgLocus_Trinity_AE_49453	XP_013078401.1 PREDICTED: polycystic kidney disease protein 1-like 2 [Biomphalaria glabrata]	614	1838	50.5
evgLocus_FX_22051	XP_013071763.1 PREDICTED: mucolipin-3-like [Biomphalaria glabrata]	727	592	75.6

* Contains InterPro signature of TRPV channel.