

**Table S1. Experimentally Verified *cis*-regulatory Elements in *Ciona intestinalis*. Data Derived from Comparison of the *C. intestinalis* Genome v.1 or v.2 As Noted [1] and Gene Models and *cis*-regulatory Information from the ANISEED Database [2] and Other References As Noted**

Ciona gene	Gene model	Genome	Trx. start site	GRE	Locus	Mean distance to TSS	Expression pattern	Reference
<i>Ci-achaete-scute-a-like2</i>	ci0100148570	v.1	scaffold_667: 25699	A	24704-25641	-0.53	anterior ant. sens. ves., mesenchyme, tail muscles	Y. Ohtsuka, ANISEED
<i>Ci-ADMP</i>	KH.C2.421.v1.A.nonSL4-1	v.2	scaffold_213: 107269	A	106593-107007	-0.47	CNS, epidermis, mesoderm	ANISEED
<i>Ci-AP2-like2</i>	KH.C7.43.v1.A.nonSL1-1	v.1	scaffold_107: 140192	A	141387-141664	-1.33	tail epidermis	ANISEED
<i>Ci-AP4</i>	KH.C14.448.v1.A.ND1-1	v.1	scaffold_73: 110517	A	109928-110292	+0.41	mesenchyme, muscle	Y. Ohtsuka, ANISEED
				B	110613-110767	-0.17	mesenchyme, muscle	
<i>Ci-Brachyury</i>	ci0100134430	v.2	scaffold_162: 25953	A	25588-25953	-0.21	notochord	[3]
<i>Ci-chordin</i>	KH.C6.145.v1.A.ND1-1	v.1	scaffold_8: 356794	A	356873-357169	-9.6	CNS, mesoderm	ANISEED
<i>Ci-COE</i>	ci0100133553	v.1	scaffold_229: 99269	A	108589-109151	-0.23	mesenchyme, muscle	[4]
<i>Ci-Delta2</i>	KH.L50.6.v1.A.SL1-1	v.1	scaffold_170: 33066	A	32545-33133	-0.23	epidermis, siphon primordia, TLCs, TVCs	Y. Ohtsuka, ANISEED
<i>Ci-derriere-like</i>	KH.C4.547.v1.A.nonSL2-1	v.1	scaffold_123: 191879	A	191627-191803	-0.16	epidermis	[4]
<i>Ci-DlIA</i>	KH.C7.346.v1.A.SL1-1	v.2	chr_07q: 1163893	A	1162089-1163705	-0.41	anterior neuroectoderm at tailbud stage	[5]
<i>Ci-DlIB</i>	KH.C7.243.v1.A.ND1-1	v.2	chr_07q: 1170654	A	1170826-1171284	-0.40	pan-animal hemisphere at gastrula stage	[6]
<i>Ci-DMRT1</i>	KH.S544.3.v1.A.nonSL2-1	v.2	chr_05q: 5020647 use v1 for gene map	A	5020616-5021001	-0.16	CNS, mesenchyme, tail muscles, palps	[4]
<i>Ci-ELKI</i>	KH.C8.247.v2.A.SL2-1	v.1	scaffold_3: 773886	A	773052-773898	-0.41	CNS, notochord, muscles, endoderm	[4]
				B	777331-777667	+3.61	mesenchyme, b-epidermis, nerve cord and b-muscle	
				C	781042-781175	+7.22	a6.5 & b6.5 at 110-cell stage	
<i>Ci-Emx</i>	ci0100151065	v.1	scaffold_402: 9128	A	9240-9653	-0.32	silencer	[4]
<i>Ci-EphrinA-c</i>	KH.C3.52.v1.A.SL2-1	v.1	scaffold_208: 134793	A	134817-135556	-0.39	head endoderm, notochord	[4]
<i>Ci-EphrinA-d</i>	KH.C3.716.v1.A.SL1-1	v.1	scaffold_208: 140900	A	140976-141642	-0.41	ectoderm and mesenchyme	[4]
<i>Ci-ERF-a</i>	KH.C4.366.v1.A.ND1-1	v.1	scaffold_6: 551867	A	562958-563160	-11.19	a6.5 & b6.5	[4]

Ciona gene	Gene model	Genome	Trx. start site	GRE	Locus	Mean distance to TSS	Expression pattern	Reference
<i>Ci-ets</i>	KH.C10.113.v1.A.SL1-1	v.1	scaffold_344: 72641	A	71681-72434	-0.58	tail muscles, mesenchyme, part of brain	[4]
<i>Ci-Ets97D</i>	ci0100130209	v.1	scaffold_28: 55481	A	53642-54159	-1.58	mesenchyme, notochord	[4]
<i>Ci-Eya</i>	ci0100137801	v.1	scaffold_368: 2214*	A	4544-5782	+2.95	epidermis, mesench., neurohyp., palps	[7]
<i>Ci-fog</i>	ci0100149797	v.1	scaffold 9: 331369	A	331487-331828	-0.29	pan-animal hemisphere at 32-cell stage	[8]
<i>Ci-FoxAa</i>	KYOTOGRAI L2005.63.50.1	v.1	scaffold_63: 269243	A	269751-269811	-0.54	lateral CNS	[9] & [2]
				B	270101-270571	-1.09	CNS	
				C	270572-270830	-1.49	autoregulation	
				D	270831-270971	-1.66	notochord & endoderm	
				E	270971-271801	-2.14	ectopic epidermis	
<i>Ci-FoxB</i>	ci0100145669	v.2 (v.1)	chr_04q: 4634207 (sc_129: 70240)	A	4630261-4630689 (73762-74192)	-3.73	notochord, epidermis	[4]
				B	4633083-4633346 (71106-71369)	-0.99	mesenchyme, neck, muscle, visc. ganglion	
<i>Ci-FoxC</i>	KH.L57.25.v1.A.SL1-1	v.1	scaffold_333: 73634	A	73706-74127	-0.28	palps, sensory vesicle	[4]
<i>Ci-FoxD</i>	ci0100146995	v.2	chr_08q: 2997576	A	2996334-2996492	-1.16	A5.1, A5.2, B5.1 lineages	[10]
<i>Ci-FoxF</i>	KH.C3.170.v1.A.SL1-1	v.1	scaffold_56: 139736	A	138750-138963	-0.88	trunk ventral cells at tailbud stage	[11]
<i>Ci-FoxN2/3</i>	KH.L13.24.v1.A.SL1-1	v.1	scaffold_160: 140569	A	138298-138668	-2.09	mesenchyme, tail muscles	[4]
				B	139364-140470	-0.65	CNS, mesenchyme, epidermis	
<i>Ci-orphanFoxl</i>	KH.C14.520.v1.A.ND1-1	v.1	scaffold_73: 311622	A	314878-315158	-3.4	mesenchyme	[4]
<i>Ci-GATAb</i>	KH.S696.1.v1.A.ND1-1	v.2	scaffold_95: 471757	A	469845-470050	-1.81	a-line ectoderm	[4]
				B	470580-470781	-1.08	mesenchyme	
<i>Ci-Hes-a</i>	KH.L34.9.v1.A.ND2-1	v.1	scaffold_275: 72799	A	74194-74407	-1.5	head endoderm, endodermal strand, epidermis	[4]
<i>Ci-Hndx</i>	ci0100140298	v.2	chr_01q: 4071779	A	4071838-4074717	-1.5	endoderm, trunk lateral & trunk ventral cells	[12]

Ciona gene	Gene model	Genome	Trx. start site	GRE	Locus	Mean distance to TSS	Expression pattern	Reference
<i>Ci-Hox1</i>	KHL171.16.v1.A.SL2-1	v.1	scaffold_148:187453	A	185772-183869*	+2.63	epidermis, neural tube	[13]
				B	187959-187795	-0.42	RA response element	
<i>Ci-Hox3</i>	KH.C1.38.v2.A.SL2-1	v.1	scaffold_87:133201	A	133815-133895	-1.91	brain	[14]
<i>Ci-Irx-B</i>	KH.C11.485.v1.A.SL1-1	v.1	scaffold_12:254812	A	256394-257214	-1.99	endoderm, palps, tail epidermis	[4]
<i>Ci-KLF1/2/4</i>	KH.C5.154.v1.A.ND1-1	v.2	scaffold_86:294192	A	294494-295143	-0.63	endodermal strand, mesenchyme, tail muscles	[4]
<i>Ci-Lhx3</i>	ci0100130659	v.2	chr_13q:2001122	A	2005216-2005510	-4.24	mesenchyme (B8.5 & B7.7 lines), muscle	[4]
<i>Ci-meis</i>	KH.C10.174.v1.A.SL2-1	v.1	scaffold_38:68952	A	62492-66776	-4.32	sensory vesicle, tail muscle	[15]
<i>Ci-mesp</i>	ci0100138454	v.2	chr_03q:2495630	A	2495593-2495781	-0.06	B7.5 cells at 112-cell stage	[16]
<i>Ci-Msxb</i>	KYOTOGRAIL2005.29.6.1	v.2	chr_02q:6152285	A	6152058-6152201	-0.16	CNS	[17]
				B	6151828-6152058	-0.34	pharynx	
				C	6149739-6151467	-1.68	ventral epidermis	
<i>Ci-neurogenin</i>	KH.C6.129.v1.A.nonSL6-1	v.1	scaffold_8:77488	A	77550-77932	-0.25	nerve cord, muscle, mesenchyme	[4]
<i>Ci-Nodal</i>	KHL106.16.v1.A.SL1-1	v.1	scaffold_490:16680	A	18759-18940	-2.17	notochord, tail epidermis, ventral head epidermis	[4]
				B	18415-18561	-1.81	b8.17, b8.18, b8.19, b8.20 at 112-cell stage	
<i>Ci-NPP</i>	KH.C2.514.v2.A.ND1-2	v.1	scaffold_240:82362	A	83459-82403	-0.57	head endoderm. TVCs	[12]
<i>Ci-Otx</i>	KH.C4.84.v2.A.SL4-1	v.2	chr_04a:4277070	A	4278481-4278604	-1.47	neuroectoderm from 32-cell stage ("a-element")	[18]
<i>Ci-paraxis</i>	KH.S781.11.v1.A.SL1-1	v.1	scaffold_781:19180	A	18941-19081	-0.17	primary muscle lineage	[19]
<i>Ci-Pax6</i>	KH.C9.68.v1.A.ND1-1	v.2	chr_09q:3323726	A	3321375-3321811	-2.13	nerve cord & sensory vesicle amplifier	[20]
				B	3321812-3322012	-1.81	sensory vesicle	
				C	3324100-3325800	+1.22	photoreceptors & nerve cord amplifier	
				D	3327800-3329900	+5.12	ectopic repression	
<i>Ci-Pitx</i>	KHL153.79.v2.A.SL2-1	v.1	scaffold_121:181422	A	170509-170703	-10.82	neurohypophysis	[21]

Ciona gene	Gene model	Genome	Trx. start site	GRE	Locus	Mean distance to TSS	Expression pattern	Reference
				B	183532-183691*	+2.19	epidermis	
<i>Ci-RAR</i>	KH.C9.580.v2.A.SL1-1	v.2	chr_09q:1244192	A	1244386-1244486	-0.24	muscle	[22]
				B	1244637-1244979	-0.62	CNS	
				C	1244980-1245493	-1.04	epidermis ("E element")	
<i>Ci-Rora</i>	KH.C8.101.v1.A.ND2-1	v.2	chr_08q:3106486	A	3107026-3107144	-0.60	a-line ectoderm at gastrula stage ("AS2")	[23]
<i>Ci-Rorb</i>	KH.C8.737.v1.A.SL1-1	v.2	chr_08q:3083185	A	3083629-3083788	-0.52	a-line ectoderm at gastrula stage ("BS1")	[23]
				B	3082245-3082494	+0.82	a-line neural ectoderm gastrula stage ("BS4")	
				C*	3084832-3078865	-1.34	neural gland of adult & early repressors ("BL")	
<i>Ci-Rx</i>	KH.C12.152.v1.A.SL1-1	v.1	scaffold_84:162648	A	163276-163080	-0.53	CNS	[24]
<i>Ci-sFRP1/5</i>	KYOTOGRAIL2005.148.4.1	v.1	scaffold_148:32589	A	33924-34041	-1.39	anterior gastrula ectoderm	[25]
<i>Ci-sna</i>	KH.C3.751.v1.C.SL1-1	v.2	chr_03q:4125486	A	4125656-4126157	-0.42	B4.1 lineage	[26]
<i>Ci-SoxB1</i>	KH.C1.99.v1.A.SL1-1	v.1	scaffold_92:251079	A	251295-251584	-0.36	ectoderm	[4]
				B	252621-252990	-1.73	mesenchyme	
<i>Ci-SoxC</i>	KH.C7.523.v1.A.SL1-1	v.2	chr_07q:3615183	A	3614302-3614949	-0.56	mesenchyme, muscle, epidermis (only midline), epidermal neurons, palps and a part of brain	[4]
<i>Ci-Tbx6b</i>	KH.S654.3.v1.A.nonSL1-1	v.1	scaffold_654:26946	A	27239-27383	-0.37	muscle??	[19]
<i>Ci-TTF1 (Nkx2-1)</i>	KH.C10.338.v1.A.nonSL1-1	v.1	scaffold_371:37135	A	36583-36807	-0.44	endoderm	[27]
<i>Ci-Trim2/3</i>	KH.C8.863.v1.A.SL1-1	v.1	scaffold_1:627630 need to update gene model on Vista	A	627756-627878	+0.19	anterior neural precursors (weak)	[4]
<i>Ci-Unc4A</i>	KH.C5.34.v1.A.SL1-1	v.1	scaffold_50:113746	A	108889-108759	-4.92	notochord	[4]
<i>Ci-Wnt5</i>	KH.L152.45.v1.A.SL1-1	v.1	scaffold_248:119170	A	118387-118506	-0.72	muscle precursors	[4]
<i>Ci-ZicL-B</i>	ci0100145774	v.1	scaffold_577:39659	A	39700-39997	-0.19	A6.2 & A6.4 lineages	[28]
				B	39998-	-0.57	B6.2 & B6.4	

Ciona gene	Gene model	Genome	Trx. start site	GRE	Locus	Mean distance to TSS	Expression pattern	Reference
					40451		lineages & later A-line notochord, nerve cord & muscle	
<i>Ci-Znf(C2H2)-24</i>	KH.C5.154.v1.A.ND1-1	v.1	scaffold_86:294192	A	294494-295143	-0.63	mesenchyme, endodermal strand, muscle	[4]
<i>Ci-Znf(C3H)</i>	KH.C4.182.v1.A.nonSL3-1	v.2	chr_14q:884369 use v1 for gene map	A	884346-884581	-0.09	CNS, mesenchyme, notochord, tail muscles, palps	[4]

\* This element not shown on alignment.

**Table S2. Experimentally Verified *cis*-regulatory Elements in Mouse. Data Were Derived from the References Noted**

Mouse gene	CRE name	5' end	3' end	Mean distance to TSS	Expression pattern	Notes	Reference
<i>Dll1</i>	msdII	-0.8	-0.08	-0.44	Somites		[29]
	H2	-1.16	-1.0	-1.08	Dors. sp. cord		
	msd	-12.76	-1.16	-6.96	Somites		
	H1	-3.04	-2.76	-2.9	Vent. sp. cord, sp. ganglia		
<i>Dlx1</i>	URE1	-17.6	-17	-17.3	not described	1	[30]
	URE2	-12.9	-12	-12.45	Forebrain		
	I12a	+6.4	+6.95	+6.68	Branchial arches		[31]
	I12b	+8.4	+8.8	+8.6	Forebrain		
<i>Fgf3</i>	n/a	-12.76	-7.1	-9.93	Brain, ectoderm, ganglia		[32]
<i>Foxa2</i>	NE	-14	-13.5	-13.75	Notochord		[33]
	FPE	+9.5	+10.0	+9.75	Floor plate		[34]
<i>Gli3</i>	CNE1	+26	+26.95	+26.48	Brain, sp. cord, face	2	[35]
<i>Gata1</i>	-25/6	-25.8	-24.2	-25.0	Erythrocytes		[36]
	-3.5	-3.8	-3.3	-3.55	Erythrocytes		
	+3.5	+3.2	+3.8	+3.5	Erythrocytes		
<i>Gata4</i>	G2	-38.7	-37.7	-38.2	Lateral mesoderm	5	[37]
	G9	-93.77	-93.36	-93.57	Endocardium		[38]
	G8	-80.95	-80.73	-80.84	Endoderm		[39]
	Prox	-0.18	-0.07	-0.13	Gonads		[40]
<i>Hb9</i>	A	-8.0	-7.87	-7.94	Motor neurons		[41]
<i>Hoxa1</i>	I	-6.7	-5.3	-6.0	Rhombomere 4		[42]
	II	-5.3	-3	-4.15	Rhombomere 2, somites		
	III	+4.39	+4.96	+4.68	Notochord, sp. cord		
<i>Hoxa2</i>	n.c.	-2.3	-1.85	-2.08	Neural crest		[43]
	r3/5	-2.65	-2.3	-2.48	Rhombomeres 3 & 5		
	exon	+1.69	+1.78	+1.74	Rhombomere 2		[44]
<i>Hoxa3</i>	r5/6	-4.64	-4.23	-4.44	Rhombomeres 5 & 6		[45]

Mouse gene	CRE name	5' end	3' end	Mean distance to TSS	Expression pattern	Notes	Reference
<i>Hoxa7</i>	AX470	-2.1	-1.6	-1.85	somites, sp. cord, sp. ganglia		[46]
<i>Hoxb1</i>	RAIDR5	+7.2	+6.5	+6.85	RA response		[47]
<i>Hoxb3</i>	Ia	-0.6	-0.1	-0.35	Rhombomere 5	4	[48][49]
	Ib	+1.0	+1.4	+1.2	Mesoderm		
	IIIa	+11.9	+12.4	+12.15	Hindbr. & neural crest		
	IVa	+17.4	+17.9	+17.65	Rhombomere 5		
	IVb	+18.4	+18.9	+18.65	Neural and mesoderm		
	Va	+19.4	+19.8	+19.6	Mesoderm		
<i>Hoxb4</i>	e	+0.95	+1.85	+1.4	sp. cord, somites		[50]
	Λ	+3.4	+6.4	+4.9	sp. cord		
	ENE	+6.2	+6.45	+6.33	Neural		[51]
	LNE	+5.0	+5.25	+5.13	Neural		
<i>Hoxb6</i>	early	-2.47	-2.22	-2.35	Lat. plt. mesoderm		[52]
<i>Hoxc8</i>	ENT	-3.85	-3.34	-3.6	Sp. cord, mesoderm		[53]
	Late	+11	+19	+15	Sp. cord, somites		
<i>Hoxc9</i>	CSE1	+2.16	+2.27	+2.22	Sp. cord		[54]
	intron	+0.81	+2.24	+1.53	Sp. cord		
<i>Hoxd4</i>	Autoreg	-2.0	-1.71	-1.85	Somites		[55]
	A	+3.6	+4.4	+4.0	CNS		[56]
<i>Msx1</i>	DE	-4.43	-4.18	-4.31	1st arch, nasal epithelium		[57]
	PE	-2.39	-2.31	-2.35	Myotome, limb mesench., other		
<i>Msx2</i>	n/a	-3.86	-3.30	-3.58	BMP response		[58]
	AER	-0.50	-0.44	-0.47	Apical ectodermal ridge		[59]
<i>Myf5</i>	EEE	-6.1	-5.6	-5.85	Epaxial somites	6	[60]
	PAE	-2.7	-1.7	-2.2	Branchial arches		
	CNSE	-1.7	-0.1	-0.9	CNS		
	n/a	+0.5	+3.3	+1.9	Hypaxial somites, branchial arches		
	Myf5-IV	-57.7	-55.9	-56.8	Myotome, limb muscles, brain		
		-16.8	-16.2	-16.5	Thoracic myotome		[61][62]
<i>Myf6</i>	n/a	-6.5	-5.6	-6.05	Epaxial myotome	6	[64]
	A17	-8.2	-7.6	-7.9	Thoracic myotome		[65]
<i>Nkx2-5</i>	n/a	-10.7	-8.5	-9.6	Rt. ventricle		[66]
	n/a	-5.0	-4.0	-4.5	Rt. ventricle		
	n/a	-3.5	-1.5	-2.5	Thyroid, spleen, stomach		[67]
<i>Nodal</i>	NDE	-9.5	-8.7	-9.1	Node		[68]
	ASE	+1.0	+1.34	+1.17	Assym. in lat. plt. meso.		
	LSE	-4.5	-4.0	-4.25	Left side lat. plt. meso.		
<i>Oct4</i>	PE	-1.13	-0.89	-1.01	ES cells	3	[69]
	DE	-2.1	-1.29	-1.70	ES cells		

Mouse gene	CRE name	5' end	3' end	Mean distance to TSS	Expression pattern	Notes	Reference
<i>Otx2</i>	CNE1	-3.1	-2.76	-2.93	Visc. endo., ceph. mesench.		[70][71]
	VE cis	-1.8	0	-0.9	Visc. endo.		
	2	-5.06	-4.91	-4.99	Retina		
	FM	-71.05	-70.7	-70.88	Forebrain & midbrain		
	FM2	+125.6	+126.6	+126.1	Forebrain & midbrain		
	AN	-91.2	-88.9	-90.05	Anterior neuroectoderm		
<i>Pax6</i>	A	-4.24	-4.0	-4.12	Pancreas		[72][73]
	B	-3.81	-3.64	-3.73	Lens		
	D/ $\alpha$	+13.27	+13.72	+13.50	Retina, spinal cord		
	P0	-2.35	-1.9	-2.13	Retina, pancreas		[74]
	P1	+3.45	+3.65	+3.55	Photoreceptors		
	7CE1	+17.7	+18.3	+18.0	Lens		[75]
	7CE2	+19.2	+19.77	+19.49	Brain, heart		
<i>Six1</i>	1-14	-1.91	-1.35	-1.63	Pre-placodal region		[76]
<i>Sox2</i>		-4.1	-3.3	-3.7	ES cells		[77]
		-2.4	-1.9	-2.15	ES cells		
		+3.6	+4.4	+4.0	ES cells		
<i>Sox10</i>	MCS2	-1.90	-1.21	-1.56	Neurons, craniofac., otic ves.		[78]
	MCS3	-10.29	-9.53	-9.91	Schwann cells		
	MCS4	-29.32	-28.51	-28.92	Neurons, craniofac., melanocytes		

## Notes:

- 1 - I12a & I12b enhancers located from Dlx1 TSS.
- 2 - Human elements tested in mouse (conserved in mouse sequence).
- 3 - a.k.a. *Oct3*, *Pou5f1*.
- 4 - Coordinates based on a 4-exon gene model.
- 5 - Coordinates based on NCBI37/mm9 assembly UCSC gene model.
- 6 - Some enhancers shared between *Myf5* and *Myf6* (a.k.a *MRF4*), e.g. *Myf5* -16.8 and *Myf6* -8.2 elements.

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