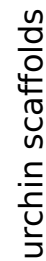
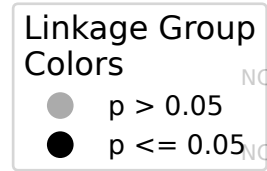


diamond: 1070 orthologs on 29 BCnS LGs scaffolds and 19 urchin scaffolds.



	BCnS_LGs scaf	urchin scaf	p (FET)	Count	Group	Color
0	A1a	NC_054746.1	3.86e-24	42	A1a	#C23D51
1	A2	NC_054747.1	1.53e-04	6	A2	#8b4d68
2	B1	NC_054752.1	5.08e-12	15	B1	#ffff58
3	B2	NC_054742.1	1.13e-04	11	B2	#1a7798
4	B3	NC_054740.1	2.39e-06	16	B3	#fd9827
5	C1	NC_054744.1	2.76e-14	21	C1	#de6768
6	D	NC_054741.1	1.82e-14	38	D	#469581
7	Ea	NC_054742.1	7.87e-07	17	Ea	#aa7e27
8	F	NC_054740.1	5.75e-17	40	F	#9b6870
9	G	NC_054741.1	5.15e-21	45	G	#EB7A47
10	H	NC_054749.1	6.08e-23	33	H	#47B8EB
11	I	NC_054751.1	3.55e-33	34	I	#0b24fb
12	J1	NC_054740.1	1.89e-04	18	J1	#54ab53
13	J2	NC_054756.1	3.78e-07	10	J2	#e54656
14	K	NC_054743.1	1.80e-26	35	K	#8e7ec1
15	L	NC_054750.1	7.57e-24	28	L	#7CC19E
16	M	NC_054754.1	1.44e-27	33	M	#a55530
17	N	NC_054755.1	7.34e-18	21	N	#dabd3b
18	O1	NC_054748.1	3.68e-09	11	O1	#fed86f
19	O2	NC_054758.1	4.59e-10	10	O2	#ab5ba9
20	P	NC_054753.1	3.11e-13	15	P	#C23D51

d BCnS_LGs vs urchin FET, whole chroms.

	BCnS_LGs scaf	urchin scaf	p (FET)	Count
0	G	NC_054741.1	5.15e-21	45
1	A1a	NC_054746.1	3.86e-24	42
2	F	NC_054740.1	5.75e-17	40
3	D	NC_054741.1	1.82e-14	38
4	K	NC_054743.1	1.80e-26	35
5	I	NC_054751.1	3.55e-33	34
6	M	NC_054754.1	1.44e-27	33
7	H	NC_054749.1	6.08e-23	33
8	L	NC_054750.1	7.57e-24	28
9	N	NC_054755.1	7.34e-18	21
10	C1	NC_054744.1	2.76e-14	21
11	J1	NC_054740.1	1.89e-04	18
12	Ea	NC_054742.1	7.87e-07	17
13	B3	NC_054740.1	2.39e-06	16
14	P	NC_054753.1	3.11e-13	15
15	B1	NC_054752.1	5.08e-12	15
16	O1	NC_054748.1	3.68e-09	11
17	B2	NC_054742.1	1.13e-04	11
18	O2	NC_054758.1	4.59e-10	10
19	J2	NC_054756.1	3.78e-07	10
20	A2	NC_054747.1	1.53e-04	6
21	R	NC_054745.1	5.19e-02	4
22	Qa	NC_054757.1	1.73e-02	4

	BCnS_LGs scaf	urchin scaf	p (FET)	Count
0	G : 0-end	NC_05474741.1 : 0-end	5.15e-21	45
1	A1a : 0-end	NC_05474746.1 : 0-end	3.86e-24	42
2	F : 0-end	NC_05474740.1 : 0-end	5.75e-17	40
3	D : 0-end	NC_05474741.1 : 0-end	1.82e-14	38
4	K : 0-end	NC_05474743.1 : 0-end	1.80e-26	35
5	I : 0-end	NC_05475751.1 : 0-end	3.55e-33	34
6	M : 0-end	NC_05475754.1 : 0-end	1.44e-27	33
7	H : 0-end	NC_05474749.1 : 0-end	6.08e-23	33
8	L : 0-end	NC_05475750.1 : 0-end	7.57e-24	28
9	N : 0-end	NC_05475755.1 : 0-end	7.34e-18	21
10	C1 : 0-end	NC_05474744.1 : 0-end	2.76e-14	21
11	J1 : 0-end	NC_05474740.1 : 0-end	1.89e-04	18
12	Ea : 0-end	NC_05474742.1 : 0-end	7.87e-07	17
13	B3 : 0-end	NC_05474740.1 : 0-end	2.39e-06	16
14	P : 0-end	NC_05475753.1 : 0-end	3.11e-13	15
15	B1 : 0-end	NC_05475752.1 : 0-end	5.08e-12	15
16	O1 : 0-end	NC_05474748.1 : 0-end	3.68e-09	11
17	B2 : 0-end	NC_05474742.1 : 0-end	1.13e-04	11
18	O2 : 0-end	NC_05475758.1 : 0-end	4.59e-10	10
19	J2 : 0-end	NC_05475756.1 : 0-end	3.78e-07	10
20	A2 : 0-end	NC_05474747.1 : 0-end	1.53e-04	6
21	R : 0-end	NC_05474751.1 : 0-end	5.19e-02	4
22	Qa : 0-end	NC_05475757.1 : 0-end	1.73e-02	4

(a) depicts the chromosomes/scaffolds of BCnS_LGs (x-axis) plotted against the chromosomes/scaffolds of urchin (y_axis). Each dot in the plot represents an ortholog, specifically a reciprocal best diamond blastp match between two species. The unit of the x- and y-axes are the number of orthologous proteins between these two species: 1070 orthologs found between 29 BCnS_LGs scaffolds and 19 urchin scaffolds. If there are chromosome breaks, Fisher's exact test is used to calculate the significance of the interactions between the sub-chromosomal pieces. Otherwise Fisher's exact test is calculated on whole chromosomes. The opacity of the dots depict the significance from Fisher's exact test. Dots that are a solid color are in cells with a FET p-value less than or equal to 0.05. Dots that are translucent are in cells with a FET p-value greater than 0.05. The Dx and Dy values depict places where there may be sudden breaks in synteny. See the supplementary information the following paper for more information on Dx and Dy: Simakov, Oleg, et al. Deeply conserved synteny resolves early events in vertebrate evolution. *Nature Ecology & Evolution* 4.6 (2020): 820-830. (b) depicts the same information as panel a, but it is plotted in the organisms chromosome basepair coordinates rather than gene index. This is useful for visualizing gene-poor regions of the chromosomes (c) shows which gene groups are most prevalent in each chromosome pair. The FET p-value in this table corresponds to the whole-chromosome FET p-value, and is not a FET value of the correlation between the chromosome pair and the gene group. (d) shows chromosome-scale significance values. This table shows the same information as c, but does not factor in gene group information. (e) shows the FET p-values of the sub-chromosomal compartments. Useful for showing if single arms of chromosomes are correlated with other regions.