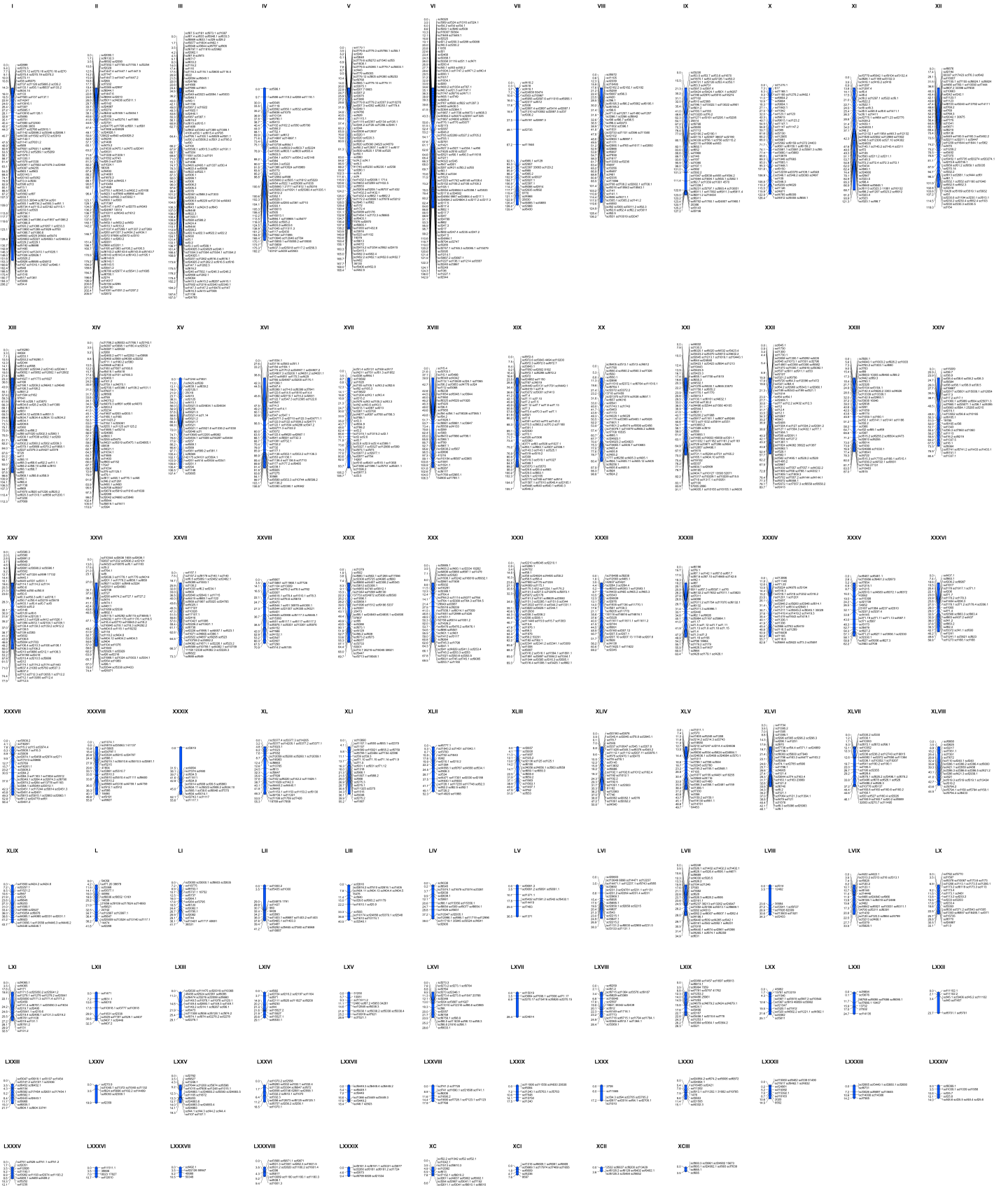


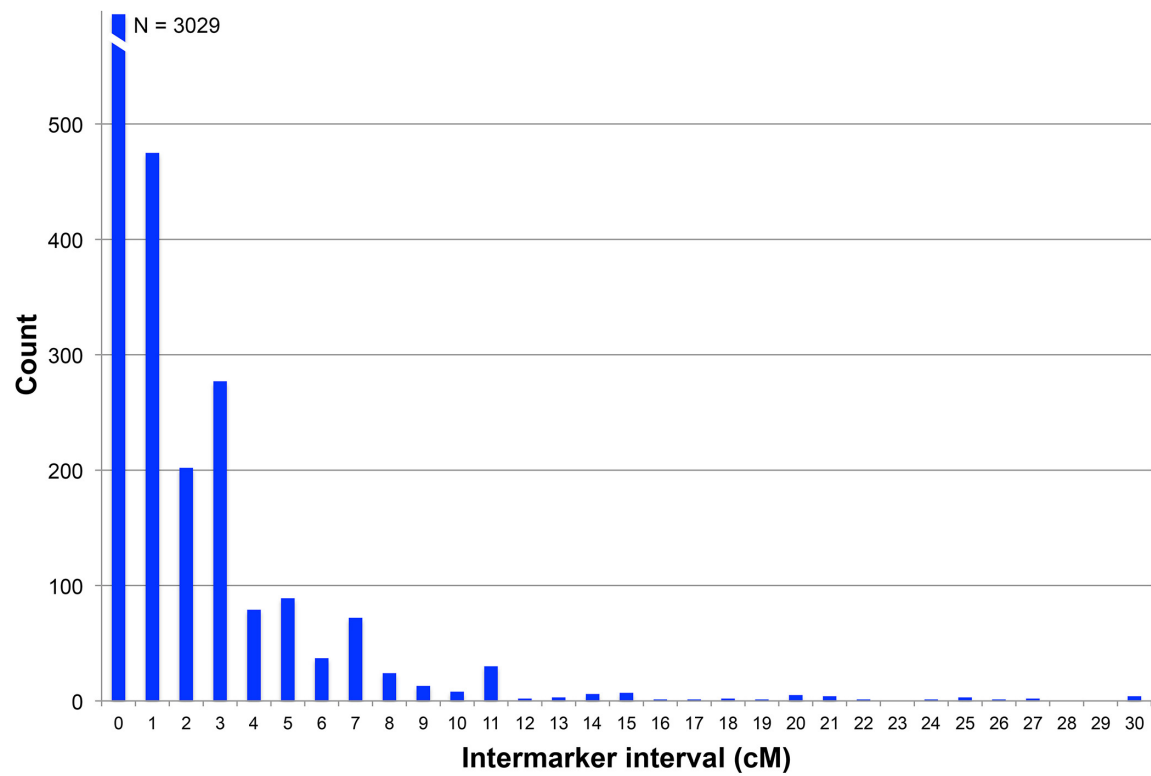
Smith and Keinath “*The Sea Lamprey Meiotic Map Improves Resolution of Ancient Vertebrate Genome Duplications*”

## **SUPPLEMENTARY FIGURES**

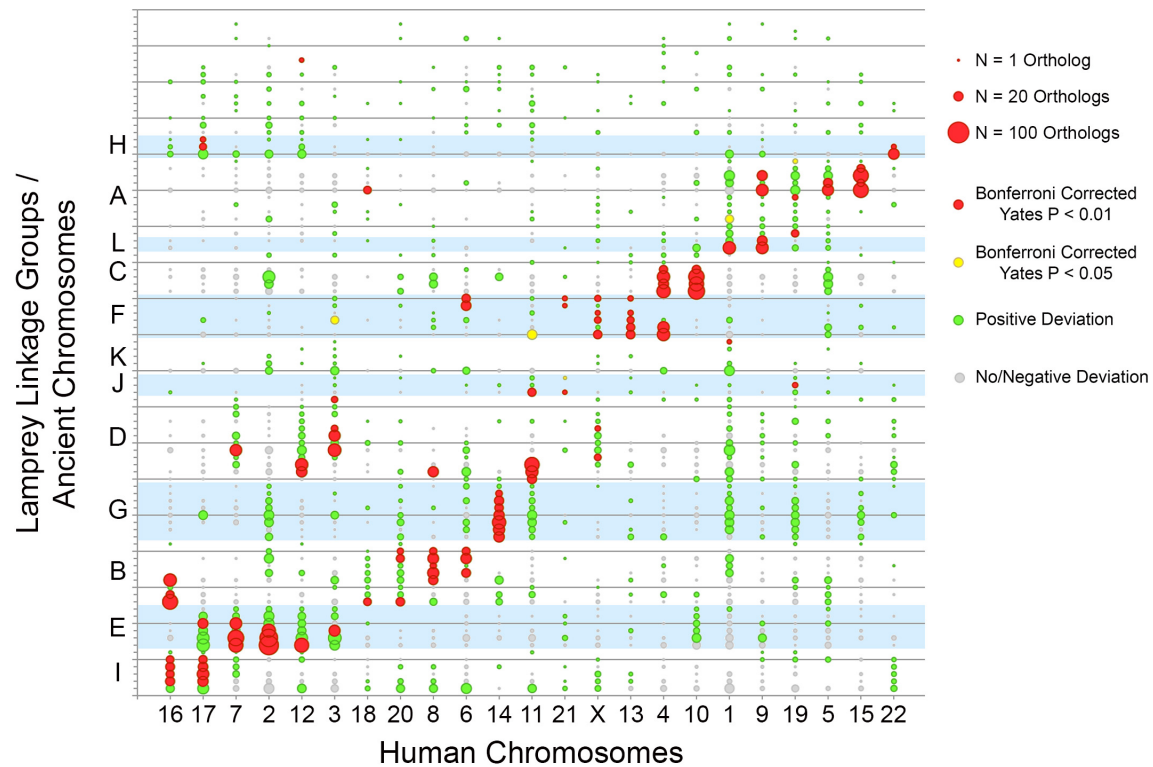




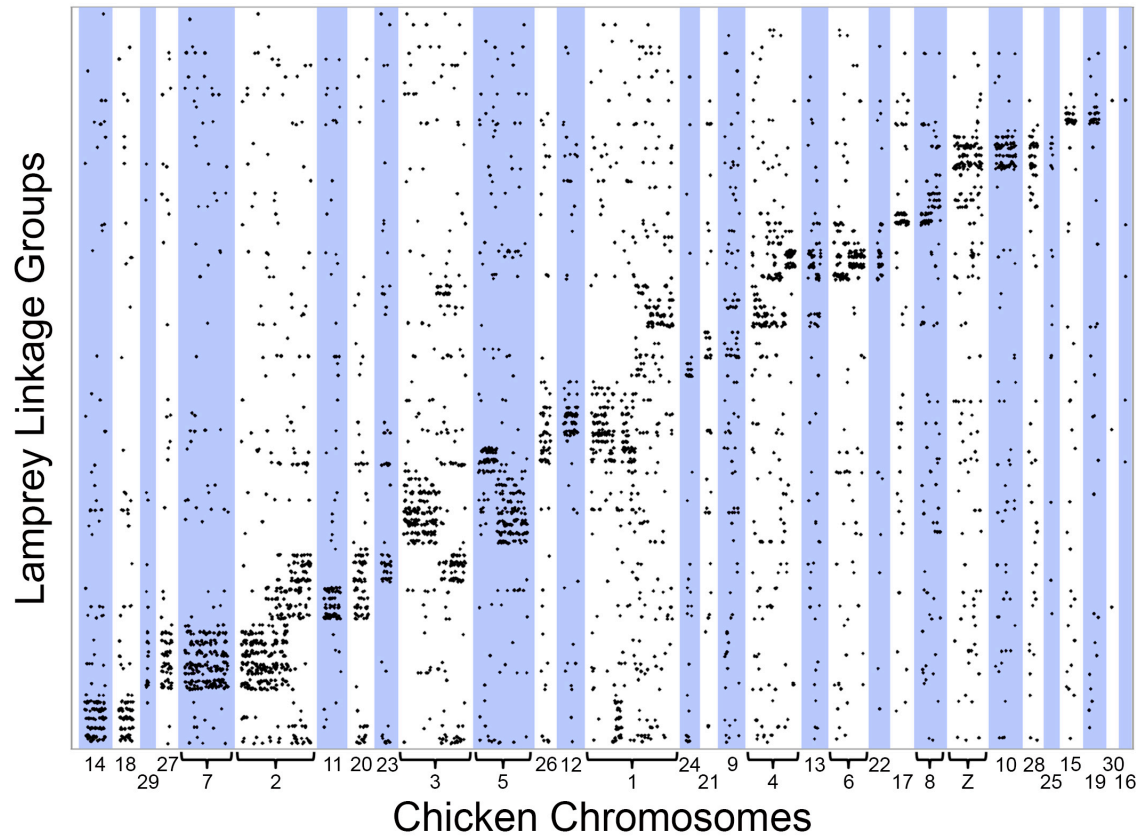
**Figure S1 (Previous Page)** – The lamprey genetic linkage map. Linkage distances are in centiMorgans. Marker names are separated by spaces and joined by vertical lines, in cases where more than one marker is assigned to a specific location.



**Figure S2** – The distribution of intermarker interval lengths across the 95 primary lamprey LGs. Note that only 1.9% of intermarker intervals are  $\geq 10\text{cM}$  and  $<0.5\%$  are  $\geq 20\text{cM}$ . Precise marker positions are provided in Table S1.



**Figure S3** – The distribution of conserved syntenic genes in lamprey and human genomes. The size of each circle is proportional to the number of orthologous genes located on the corresponding lamprey LG and human chromosome. The color of each circle represents the degree to which the number of observed orthologs deviates from null expectations under a uniform distribution across an identical number of LGs and chromosomes and genes per LG and chromosome. Shaded regions of the plot designate homology groups that correspond to presumptive ancestral chromosomes, marked A - M. The presumptive ancestral Hox-bearing chromosome is labeled “E”. The ordering of lamprey LGs along the y-axis is provided in Table S4.



**Figure S4** – The distribution of all presumptive orthologs in lamprey and chicken genomes. Each point corresponds to the relative location of an ortholog in the lamprey and chicken genome. The ordering of lamprey LGs along the y-axis is provided in Table S4.

## SUPPLEMENTARY TABLES

**Table S1** - The lamprey linkage map and anchored scaffolds from the lamprey genome assembly. (Uploaded Separately)

**Table S2** - The lamprey/chicken comparative map. (Uploaded Separately)

**Table S3** - The lamprey/human comparative map. (Uploaded Separately)

**Table S4** - Location of lamprey linkage groups on the y-axes of Figure 2, Fig. S2, Fig. S3 and Fig S4. (Uploaded Separately)

**Table S5: Correspondence between ancestral (pre-1R) chromosomes identified in this study and others.**

Current Study	Nakatani <i>et al</i> <sup>11</sup>	Putnam <i>et al</i> <sup>13</sup>
A	A	1,2
B	B	3,4
C	C	6,7
D	D	13
E	E	16
F	F	8,9,10
G	G	11,14
H	H	17
I	I	15
J	J	5
K	F	-
L	A	9
M	-	-

**Table S6: Comparison of observed and expected patterns of duplication under 2R (two whole genome duplications).**

# Dup.	Obs. s.	Exp. Exp.	Exp. (adj.)	G	P-value
1	8	0	0.5	35.20	2.98E <sup>-9</sup>
>1	5	13	12.5		

Dup – Duplications, Obs. – observed, Exp. – expected, adj. – expected values after continuity correction of expected values in order to permit calculation of conservative G-tests.

**Table S7: Observed numbers of duplicated or deleted segments under various models of chromosomal evolution.**

Ancestral chromosome	Conservative count of deletions	Liberal count of deletions	Conservative count of duplications	Liberal count of duplications
A	0	0	2 (1)	2 (1)
B	0	1	2 (1)	3 (2)
C	0	0	2 (1)	3 (2)
D	1	1	2 (1)	3 (2)
E	0	0	2 (1)	2 (1)
F	1	2	1	1
G	1	2	1	1
H	1	2	1	1
I	1	2	1	1
J	1	2	1	1
K	1	2	1	1
L	1	2	1	1
M	1	2	1	1
Total	9	18	18 (5)	21 (8)

See text for further details regarding the annotation of duplication events. Numbers in parentheses reflect counts in excess of those accounted for by one whole genome duplication.



**Table S8: Comparison of observed and expected patterns of duplication deriving from two rounds of whole genome duplication and large-scale segmental or chromosomal loss**

# Del	Conservative Model			Liberal Model			Optimal Permutation		
	Obs	Exp	G / P-value	Obs	Exp	G / P-value	Obs	Exp	G / P-value
0	4	6.51	7.82	3	3.26	10.33	4	5.16	2.35
1	9	4.50	2.01E-02	2	4.51	5.72E-03	6	4.77	0.31
2	0	1.56		8	3.12		3	2.20	
>2	0	0.43		0	2.12		0	0.87	

Counts of observed duplicates under conservative and liberal models are provided in Table 3. Dup - Duplications, Obs. - observed, Exp. - expected.

**Table S9: Comparison of observed and expected patterns of duplication deriving from segmental and chromosomal duplication.**

# Dup	Conservative Model			Liberal Model			Optimal Permutation		
	Obs	Exp	G / P-value	Obs	Exp	G / P-value	Obs	Exp	G / P-value
0	0	3.26	12.6	0	2.58	10.27	0	3.01	9.42
1	8	4.51	5.58E-03	8	4.18	1.64E-02	8	4.41	2.43E-02
2	5	3.12		2	3.37		4	3.22	
3	0	1.44		3	1.82		1	1.57	
>3	0	0.68		0	1.05		0	0.79	

Counts of observed duplicates under conservative and liberal models are provided in Table 3. Dup - Duplications, Obs. - observed, Exp. - expected.

**Table S10: Comparison of observed and expected patterns of duplication deriving from segmental and chromosomal duplication, in addition to one round of whole genome duplication.**

# Dup	Conservative Model			Liberal Model			Optimal Permutation		
	Obs	Exp	G / P-value	Obs	Exp	G / P-value	Obs	Exp	G / P-value
0	8	8.85	2.04	8	7.03	3.53	8	8.19	0.31
1	5	3.40	0.36	2	4.32	0.17	4	3.78	0.86
2	0	0.65		3	1.33		1	0.87	
>2	0	0.09		0	0.32		0	0.15	

Counts of observed duplicates under conservative and liberal models are provided in Table 3. Dup - Duplications, Obs. - observed, Exp. - expected.