

Mat.Compl.1. 2B enzymes recognition and cutting sites. All enzymes result in protuberant cutting pattern. The numbers in parenthesis before and after indicate the number of bases upstream and downstream of the recognition sites, respectively. The numbers above and below the diagonal indicate the number of bases where the cut is made in the sense and antisense strands, respectively. bp: (base pairs).

Sitios de reconocimiento y corte de las enzimas 2B. Todas las enzimas dan como resultado corte protuberante. Los números entre paréntesis antes y después indican el número de bases río arriba y río abajo del sitio de reconocimiento, respectivamente. Los números arriba y abajo de la diagonal indican el número de bases en donde se da el corte en las hebras sentido y antisentido, respectivamente. bp: pares de bases.

Enzyme (Manufacturer)	Recognition sequence and positions cut	Resulting fragment size (pb)
<i>BcgI</i> (NEB)	(10/12)CGA(N) ₆ TGC(12/10)	36
<i>BsaXI</i> (NEB)	(9/12)AC(N) ₅ CTCC(10/7)	33
<i>AlfI</i> (Thermofisher)	(10/12)GCA(N) ₆ TGC(12/10)	36
<i>CspCI</i> (NEB)	(11/13)CAA(N) ₅ GTGG(12/10)	36-38

Mat.Compl.2. Example of adaptors ligation (sequences in blue) with different numbers of selective bases (nucleotide bases in red) of fragments digested with the enzyme *BcgI* (sequences in yellow and orange).

Ejemplo de ligación de adaptadores (secuencias en azul) con diferentes números de bases selectivas (bases nucleotídicas marcadas en rojo) de fragmentos digeridos con la enzima *BcgI* (secuencias en amarillo y naranja).

***BcgI* (NEB)**

Adaptadores in bases selectivas

NNNNNNNNNNNN	NN	NNNNNNNNNNNN	CGANNNNNNNTGC	NNNNNNNNNNNN	NN	NNNNNNNNNNNN
NNNNNNNNNNNN	NN	NNNNNNNNNNNN	GCTNNNNNNNACG	NNNNNNNNNNNN	NN	NNNNNNNNNNNN

Adaptador con una base selectiva

NNNNNNNNNNNN	NN	NNNNNNNNNNNN	CGANNNNNNNTGC	NNNNNNNNNNNN	NG	NNNNNNNNNNNN
NNNNNNNNNNNN	NN	NNNNNNNNNNNN	GCTNNNNNNNACG	NNNNNNNNNNNN	NC	NNNNNNNNNNNN

Adaptador con dos bases selectivas

NNNNNNNNNNNN	NN	NNNNNNNNNNNN	CGANNNNNNNTGC	NNNNNNNNNNNN	GC	NNNNNNNNNNNN
NNNNNNNNNNNN	NN	NNNNNNNNNNNN	GCTNNNNNNNACG	NNNNNNNNNNNN	CG	NNNNNNNNNNNN

Adaptadores con tres bases selectivas

NNNNNNNNNNNN	NA	NNNNNNNNNNNN	CGANNNNNNNTGC	NNNNNNNNNNNN	GC	NNNNNNNNNNNN
NNNNNNNNNNNN	NT	NNNNNNNNNNNN	GCTNNNNNNNACG	NNNNNNNNNNNN	CG	NNNNNNNNNNNN

Adaptadores con cuatro bases selectivas

NNNNNNNNNNNN	CA	NNNNNNNNNNNN	CGANNNNNNNTGC	NNNNNNNNNNNN	GC	NNNNNNNNNNNN
NNNNNNNNNNNN	GT	NNNNNNNNNNNN	GCTNNNNNNNACG	NNNNNNNNNNNN	CG	NNNNNNNNNNNN

Mat.Compl.3. Commands for enzymes' recognition sites search in the *in silico* analyses.
The complements –A and –B in zgrep indicate the lines after and before of the searched line, respectively. The commands paste and sed are used to eliminate spaces, returns, and dashes for each recognition site to be kept in a single line. The cat command at the end joints all of them in a single file.

Comandos utilizados para búsqueda de sitios de reconocimiento de enzimas en los análisis *in silico*. Los complementos -A y -B del comando zgrep indican que se obtienen los renglones después y antes del renglón de interés, respectivamente. Los comandos paste y sed sirven para eliminar espacios, retornos de carro y guiones para que cada sitio reconocido quede en una sola línea. El comando cat al final une a cada uno de los archivos obtenidos en uno solo.

Código para la búsqueda y conteo de sitios de restricción de la enzima *Bcgl* con reconocimiento de la secuencia
CGA.....TGC en el genoma de *Seriola rivoliana*, donde los puntos indican cualquier base. Con el fin de contar los
sitios que quedan al final y al principio de los renglones se incluyen las diversas posibilidades usando
los símbolos \$ al final del renglón y ^ para el principio del renglón.

```
zgrep -A 1 -B 1 'CGA.....TGC' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--  
\n/g' > sitios_Bcgl_1.txt
```

```
zgrep -A 1 'CGA.....TG$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--  
\n/g' | grep 'CGA.....TGC' > sitios_Bcgl_2.txt
```

```
zgrep -A 1 'CGA.....T$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g'  
| grep 'CGA.....TGC' > sitios_Bcgl_3.txt
```

```
zgrep -A 1 'CGA.....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_4.txt
```

```
zgrep -A 1 'CGA.....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_5.txt
```

```
zgrep -A 1 'CGA....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_6.txt
```

```
zgrep -A 1 'CGA...$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_7.txt
```

```
zgrep -A 1 'CGA..$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_8.txt
```

```
zgrep -A 1 'CGA.$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_9.txt
```

```
zgrep -A 1 'CGA$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--\n/g' |  
grep 'CGA.....TGC' > sitios_Bcgl_10.txt
```

```
zgrep -B 1 '^A.....TGC' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'CGA.....TGC' > sitios_Bcgl_11.txt
```

```
zgrep -B 1 '^GA.....TGC' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'CGA.....TGC' > sitios_Bcgl_12.txt
```

```
cat sitios_Bcgl_1.txt sitios_Bcgl_2.txt sitios_Bcgl_3.txt sitios_Bcgl_4.txt sitios_Bcgl_5.txt sitios_Bcgl_6.txt  
sitios_Bcgl_7.txt sitios_Bcgl_8.txt sitios_Bcgl_9.txt sitios_Bcgl_10.txt sitios_Bcgl_11.txt sitios_Bcgl_12.txt >  
sitios_Bcgl_Fwdtotal.txt
```

Esto también debe ser calculado para la secuencia antisentido que es 'GCT.....ACG', pero dado que la secuencia solo la tenemos

en dirección sentido, se debe buscar en dirección inversa es decir 'GCA.....TCG'

```
zgrep -A 1 -B 1 'GCA.....TCG' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev1.txt
```

```
zgrep -A 1 'GCA.....TC$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev2.txt
```

```
zgrep -A 1 'GCA.....T$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev3.txt
```

```
zgrep -A 1 'GCA.....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev4.txt
```

```
zgrep -A 1 'GCA.....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev5.txt
```

```
zgrep -A 1 'GCA....$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev6.txt
```

```
zgrep -A 1 'GCA...$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev7.txt
```

```
zgrep -A 1 'GCA..$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev8.txt
```

```
zgrep -A 1 'GCA.$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev9.txt
```

```
zgrep -A 1 'GCA$' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev10.txt
```

```
zgrep -B 1 '^A.....TCG' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev11.txt
```

```
zgrep -B 1 '^CA.....TCG' GCA_002994505.1_ASM299450v1_genomic.fna.gz | paste -s | sed 's/\t//g' | sed 's/--/\n/g' | grep 'GCA.....TCG' > sitios_Bcgl_Rev12.txt
```

```
cat sitios_Bcgl_Rev1.txt sitios_Bcgl_Rev2.txt sitios_Bcgl_Rev3.txt sitios_Bcgl_Rev4.txt sitios_Bcgl_Rev5.txt  
sitios_Bcgl_Rev6.txt sitios_Bcgl_Rev7.txt sitios_Bcgl_Rev8.txt sitios_Bcgl_Rev9.txt sitios_Bcgl_Rev10.txt  
sitios_Bcgl_Rev11.txt sitios_Bcgl_Rev12.txt > sitios_Bcgl_Revtotal.txt
```

Mat.Compl.4. 2bRAD protocol from library preparation to sequencing.

Protocolo 2bRAD desde la preparación de genotecas hasta la secuenciación.

Mat.Compl.5. Samples location in the 96-well plates of each individual. Individuals in positions F6, G6, and H6 were used as replicates.

Ubicación de las muestras de cada uno de los ejemplares en una placa de 96 pocillos.

Muestras ubicadas en las posiciones F6, G6 y H6 se utilizaron como réplicas.

	1	2	3	4	5	6	7	8	9	10	11	12
A	1-TR1	10-TR2	18-TR2	8-J1	3-J4	11-J4	TH-42	PE-01	T27	P5	2-3	10-1
B	2-TR1	11-TR2	1-J1	9-J1	4-J4	12-J4	TH-43	PE-02	T28	P6	3-1	10-2
C	3-TR1	12-TR2	2-J1	10-J1	5-J4	13-J4	TH-44	PE-03	T29	P7	3-3	10-3
D	4-TR1	13-TR2	3-J1	11-J1	6-J4	14-J4	TH-45	PE-04	T30	P8	4-1	14-1
E	5-TR1	14-TR2	4-J1	12-J1	7-J4	15-J4	TH-46	PP-27	T31	P9	4-2	14-2
F	7-TR1	15-TR2	5-J1	13-J1	8-J4	P5-REP (ostión)	TH-47	PP-28	T32	P10	4-3	14-3
G	8-TR1	16-TR2	6-J1	1-J4	9-J4	18-TR2-REP (jurel)	TH-48	PP-29	T33	2-1	9-1	15-1
H	9-TR1	17-TR2	7-J1	2-J4	10-J4	TH42-REP (huachinango)	TH-49	PP-30	T34	2-2	9-3	15-3
JUREL							HUACHINANGO	LUNAREJO	TOTOABA	OSTION		

Mat.Compl.6. Adaptors and primers sequences used for library construction. The locations of the barcodes in the 96-well plate for the individuals' identification is also shown.

Secuencias de los adaptadores e iniciadores utilizados en la construcción de las genotecas así como la ubicación de los códigos de barra en la placa de 96 pozos para la identificación de cada uno de los ejemplares.

56. Listado de iniciadores y adaptadores utilizados para la construcción de genotecas 2bRAD con características de concentración (Scale) y método de purificación (PUR)					
Oligo ID	Secuencia	Scale	Pur	Observaciones	
TruSeq_Un1	AATGATACGGCGACCACCGAGATCTACACATC ACG ACACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD	Códigos de barra de placa	
TruSeq_Un2	AATGATACGGCGACCACCGAGATCTACACACT GA AACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD		
TruSeq_Un3	AATGATACGGCGACCACCGAGATCTACACTAG CTT ACACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD		
TruSeq_Un4	AATGATACGGCGACCACCGAGATCTACACGG CTA CACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD		
TruSeq_Un5	AATGATACGGCGACCACCGAGATCTACACTTAG GC AACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD		
TruSeq_Un6	AATGATACGGCGACCACCGAGATCTACACCGAT GT ACACTCTTTCCCTACACGACGCTCTTCCGATCT	20nmU	STD		
2bRAD-ILL-BC23	CAAGCAGAAGACGGCATACGAGAT CCACT CGTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD	Códigos de barra de renglón	
2bRAD-ILL-BC24	CAAGCAGAAGACGGCATACGAGAT GCTAC CTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC25	CAAGCAGAAGACGGCATACGAGATAT CAGT GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC26	CAAGCAGAAGACGGCATACGAGAT GCTCAT GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC27	CAAGCAGAAGACGGCATACGAGATAG GAAT GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC28	CAAGCAGAAGACGGCATACGAGAT CTTTT GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC29	CAAGCAGAAGACGGCATACGAGAT TAGTTG GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-ILL-BC30	CAAGCAGAAGACGGCATACGAGAT CCGGT GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT	20nmU	STD		
2bRAD-Adaptador_1fwd-TC-5ILL-NNRW	CTACACGACGCTCTTCCGATCTNNRW CTC	25nm	STD	Adaptador 1	
2bRAD-Adaptador_1rev-Anti5ill-NNRW	GGWYNNAGATCGG/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.1-TG-3illBC1	CAGACGTGTGCTCTTCCGATCT ACACTG	25nm	STD	Adaptadores 2 con Códigos de barra de columna FWD	
2bRAD-Adaptador_2.2-TG-3illBC2	CAGACGTGTGCTCTTCCGATCT GTCTTG	25nm	STD		
2bRAD-Adaptador_2.3-TG-3illBC3	CAGACGTGTGCTCTTCCGATCT TGGT TG	25nm	STD		
2bRAD-Adaptador_2.4-TG-3illBC4	CAGACGTGTGCTCTTCCGATCT CACTTG	25nm	STD		
2bRAD-Adaptador_2.5-TG-3illBC5	CAGACGTGTGCTCTTCCGATCT GATG TG	25nm	STD		
2bRAD-Adaptador_2.6-TG-3illBC6	CAGACGTGTGCTCTTCCGATCT TCAC TG	25nm	STD		
2bRAD-Adaptador_2.7-TG-3illBC7	CAGACGTGTGCTCTTCCGATCT CTGA TG	25nm	STD		
2bRAD-Adaptador_2.8-TG-3illBC8	CAGACGTGTGCTCTTCCGATCT AAGC TG	25nm	STD		
2bRAD-Adaptador_2.9-TG-3illBC9	CAGACGTGTGCTCTTCCGATCT GTAG TG	25nm	STD		
2bRAD-Adaptador_2.10-TG-3illBC10	CAGACGTGTGCTCTTCCGATCT GACA TG	25nm	STD		
2bRAD-Adaptador_2.11-TG-3illBC11	CAGACGTGTGCTCTTCCGATCT GTGA TG	25nm	STD	Adaptadores 2 con Códigos de barra de columna REV	
2bRAD-Adaptador_2.12-TG-3illBC12	CAGACGTGTGCTCTTCCGATCT AGTC TG	25nm	STD		
2bRAD-Adaptador_2.1-antiBC1	GTGT AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.2-antiBC2	AGAC AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.3-antiBC3	ACCA AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.4-antiBC4	AGTG AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.5-antiBC5	CATC AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.6-antiBC6	GTGA AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.7-antiBC7	TCAG AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.8-antiBC8	GCTT AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.9-antiBC9	CTAC AGATCGGA/3InvdT/	100nm	STD	Primers Illumina	
2bRAD-Adaptador_2.10-antiBC10	TGTC AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.11-antiBC11	TCAC AGATCGGA/3InvdT/	100nm	STD		
2bRAD-Adaptador_2.12-antiBC12	GACT AGATCGGA/3InvdT/	100nm	STD		
2bRAD-IC1-P5	AATGATACGGCGACCACCGA	25nm	STD	Primers Illumina	
2bRAD-IC2-P7	CAAGCAGAAGACGGCATACGA	25nm	STD		

			Adaptador 2											
			Adap-2.1	Adap-2.2	Adap-2.3	Adap-2.4	Adap-2.5	Adap-2.6	Adap-2.7	Adap-2.8	Adap-2.9	Adap-2.10	Adap-2.11	Adap-2.12
			TruSeq_Un1						TruSeq_Un2					
Oligo ILI-BC	ILI-BC23	A	1 Adap-2.1/ ILI-BC23	9 Adap-2.2/ ILI-BC23	17 Adap-2.3/ ILI-BC23	25 Adap-2.4/ ILI-BC23	33 Adap-2.5/ ILI-BC23	41 Adap-2.6/ ILI-BC23	49 Adap-2.7/ ILI-BC23	57 Adap-2.8/ ILI-BC23	65 Adap-2.9/ ILI-BC23	73 Adap-2.10/ ILI-BC23	81 Adap-2.11/ ILI-BC23	89 Adap-2.12/ ILI-BC23
	ILI-BC24	B	2 Adap-2.1/ ILI-BC24	10 Adap-2.2/ ILI-BC24	18 Adap-2.3/ ILI-BC24	26 Adap-2.4/ ILI-BC24	34 Adap-2.5/ ILI-BC24	42 Adap-2.6/ ILI-BC24	50 Adap-2.7/ ILI-BC24	58 Adap-2.8/ ILI-BC24	66 Adap-2.9/ ILI-BC24	74 Adap-2.10/ ILI-BC24	82 Adap-2.11/ ILI-BC24	90 Adap-2.12/ ILI-BC24
	ILI-BC25	C	3 Adap-2.1/ ILI-BC25	11 Adap-2.2/ ILI-BC25	19 Adap-2.3/ ILI-BC25	27 Adap-2.4/ ILI-BC25	35 Adap-2.5/ ILI-BC25	43 Adap-2.6/ ILI-BC25	51 Adap-2.7/ ILI-BC25	59 Adap-2.8/ ILI-BC25	67 Adap-2.9/ ILI-BC25	75 Adap-2.10/ ILI-BC25	83 Adap-2.11/ ILI-BC25	91 Adap-2.12/ ILI-BC25
	ILI-BC26	D	4 Adap-2.1/ ILI-BC26	12 Adap-2.2/ ILI-BC26	20 Adap-2.3/ ILI-BC26	28 Adap-2.4/ ILI-BC26	36 Adap-2.5/ ILI-BC26	44 Adap-2.6/ ILI-BC26	52 Adap-2.7/ ILI-BC26	60 Adap-2.8/ ILI-BC26	68 Adap-2.9/ ILI-BC26	76 Adap-2.10/ ILI-BC26	84 Adap-2.11/ ILI-BC26	92 Adap-2.12/ ILI-BC26
	ILI-BC27	E	5 Adap-2.1/ ILI-BC27	13 Adap-2.2/ ILI-BC27	21 Adap-2.3/ ILI-BC27	29 Adap-2.4/ ILI-BC27	37 Adap-2.5/ ILI-BC27	45 Adap-2.6/ ILI-BC27	53 Adap-2.7/ ILI-BC27	61 Adap-2.8/ ILI-BC27	69 Adap-2.9/ ILI-BC27	77 Adap-2.10/ ILI-BC27	85 Adap-2.11/ ILI-BC27	93 Adap-2.12/ ILI-BC27
	ILI-BC28	F	6 Adap-2.1/ ILI-BC28	14 Adap-2.2/ ILI-BC28	22 Adap-2.3/ ILI-BC28	30 Adap-2.4/ ILI-BC28	38 Adap-2.5/ ILI-BC28	46 Adap-2.6/ ILI-BC28	54 Adap-2.7/ ILI-BC28	62 Adap-2.8/ ILI-BC28	70 Adap-2.9/ ILI-BC28	78 Adap-2.10/ ILI-BC28	86 Adap-2.11/ ILI-BC28	94 Adap-2.12/ ILI-BC28
	ILI-BC29	G	7 Adap-2.1/ ILI-BC29	15 Adap-2.2/ ILI-BC29	23 Adap-2.3/ ILI-BC29	31 Adap-2.4/ ILI-BC29	39 Adap-2.5/ ILI-BC29	47 Adap-2.6/ ILI-BC29	55 Adap-2.7/ ILI-BC29	63 Adap-2.8/ ILI-BC29	71 Adap-2.9/ ILI-BC29	79 Adap-2.10/ ILI-BC29	87 Adap-2.11/ ILI-BC29	95 Adap-2.12/ ILI-BC29
	ILI-BC30	H	8 Adap-2.1/ ILI-BC30	16 Adap-2.2/ ILI-BC30	24 Adap-2.3/ ILI-BC30	32 Adap-2.4/ ILI-BC30	40 Adap-2.5/ ILI-BC30	48 Adap-2.6/ ILI-BC30	56 Adap-2.7/ ILI-BC30	64 Adap-2.8/ ILI-BC30	72 Adap-2.9/ ILI-BC30	80 Adap-2.10/ ILI-BC30	88 Adap-2.11/ ILI-BC30	96 Adap-2.12/ ILI-BC30

Mat.Compl.7 Listing of the 159 SNPs identified in almaco jack, according to their location in the *Seriola rivoliana* reference genome (GenBank accession: GCA_002994505.1 ASM299450v1; Seetharam et al. 2018). CHR: Chromosome or linkage group; POS: position; Bases: variants for each SNP.

Listado de los 159 SNPs identificados en jurel, con su ubicación respecto al genoma de referencia *Seriola rivoliana* (No. acceso GenBank: GCA_002994505.1 ASM299450v1; Seetharam et al. 2018). CHR: Cromosoma o grupo de ligamiento; POS: posición; Bases: variantes para cada SNP.

S7. Listado de los 159 SNPs identificados en jurel, con su ubicación respecto del genoma de referencia *Seriola rivoliana* (No. acceso GenBank: GCA_002994505.1 ASM299450v1; Seetharam et al. 2018). CHR: Cromosoma o grupo de ligamiento; POS: posición; Bases: variantes para cada SNP.

No.	CHR	POS	Bases	No.	CHR	POS	Bases	No.	CHR	POS	Bases
1	PVUN01001339.1	1586788	G, A	54	PVUN01001324.1	8218325	C, T	107	PVUN01001264.1	1532056	A, G
2	PVUN01001339.1	2027165	C, T	55	PVUN01001330.1	3271646	G, C	108	PVUN01001304.1	4005428	C, G
3	PVUN01001339.1	3874673	A, G	56	PVUN01001321.1	2090426	T, G	109	PVUN01001323.1	4730559	G, A
4	PVUN01001339.1	5170547	A, C	57	PVUN01001321.1	2253429	A, G	110	PVUN01001323.1	4972521	C, T
5	PVUN01001339.1	5893669	A, G	58	PVUN01001292.1	840391	C, T	111	PVUN01001323.1	6145626	C, G
6	PVUN01001339.1	15152641	C, T	59	PVUN01001215.1	237852	A, G	112	PVUN01001323.1	7169397	G, A
7	PVUN01001278.1	872150	A, G	60	PVUN01001242.1	668742	G, T	113	PVUN01001323.1	8790109	C, T
8	PVUN01001278.1	1766175	C, G	61	PVUN01001242.1	851576	C, T	114	PVUN01001323.1	9830097	A, T
9	PVUN01001329.1	6052527	T, C	62	PVUN01001342.1	8020704	C, A	115	PVUN01001275.1	1685186	C, A
10	PVUN01001329.1	7280702	G, A	63	PVUN01001342.1	11324852	A, G	116	PVUN01001327.1	1707765	G, A
11	PVUN01001217.1	75139	G, A	64	PVUN01001342.1	17283576	C, T	117	PVUN01001327.1	3006206	T, C
12	PVUN01001311.1	845763	A, T	65	PVUN01001307.1	2079846	G, A	118	PVUN01001327.1	8112332	C, A
13	PVUN01001311.1	5538737	G, A	66	PVUN01001332.1	627592	C, T	119	PVUN01001327.1	9547491	C, G
14	PVUN01001250.1	78062	T, C	67	PVUN01001332.1	684407	A, G	120	PVUN01001327.1	9900586	G, C
15	PVUN01001322.1	3643114	T, C	68	PVUN01001332.1	5596604	A, G	121	PVUN01001333.1	2683941	T, C
16	PVUN01001322.1	8153758	C, A	69	PVUN01001332.1	13334262	G, A	122	PVUN01001333.1	5561479	C, T
17	PVUN01001322.1	8933198	G, A	70	PVUN01001247.1	1265349	A, G	123	PVUN01001319.1	8782932	T, C
18	PVUN01001180.1	112784	C, G	71	PVUN01001338.1	180110	T, C	124	PVUN01001309.1	2880138	G, A
19	PVUN01001281.1	691673	C, A	72	PVUN01001338.1	1842729	G, A	125	PVUN01001309.1	5157959	C, T
20	PVUN01001331.1	7684615	A, T	73	PVUN01001338.1	4499572	G, A	126	PVUN01001294.1	1281258	C, T
21	PVUN01001331.1	12893116	G, A	74	PVUN01001338.1	18834241	C, T	127	PVUN01001301.1	522528	A, G
22	PVUN01001314.1	1676237	A, G	75	PVUN01001271.1	1113665	G, A	128	PVUN01001301.1	820088	A, G
23	PVUN01001314.1	3620958	G, C	76	PVUN01001255.1	1105301	A, C	129	PVUN01001301.1	3534021	T, G
24	PVUN01001314.1	4189160	C, T	77	PVUN01001255.1	1268528	C, T	130	PVUN01001301.1	4553114	T, C
25	PVUN01001314.1	4298964	A, G	78	PVUN01001306.1	3154547	C, A	131	PVUN01001287.1	2389821	C, T
26	PVUN01001314.1	4373910	G, A	79	PVUN01001306.1	3313041	A, C	132	PVUN01001287.1	3353021	A, G
27	PVUN01001257.1	1694357	C, T	80	PVUN01001252.1	198181	C, A	133	PVUN01001267.1	46801	G, A
28	PVUN01001273.1	1482717	G, A	81	PVUN01001252.1	253950	G, T	134	PVUN01001267.1	1448750	T, C
29	PVUN01001273.1	2192054	A, T	82	PVUN01001337.1	10840670	T, C	135	PVUN01001267.1	1926360	G, A
30	PVUN01001317.1	393690	C, T	83	PVUN01001293.1	400280	C, T	136	PVUN01001326.1	8303709	T, C
31	PVUN01001317.1	6625951	G, A	84	PVUN01001293.1	2878999	C, T	137	PVUN01001285.1	884630	A, G
32	PVUN01001284.1	1451849	C, T	85	PVUN01001293.1	3112516	T, C	138	PVUN01001246.1	34375	C, T
33	PVUN01001284.1	1703851	C, A	86	PVUN01001293.1	3350939	T, C	139	PVUN01001246.1	34381	C, T
34	PVUN01001284.1	1753138	T, G	87	PVUN01001239.1	254703	G, C	140	PVUN01001246.1	526653	A, G
35	PVUN01001236.1	731715	G, A	88	PVUN01001239.1	598456	T, C	141	PVUN01001246.1	1384871	T, A
36	PVUN01001318.1	7856996	A, G	89	PVUN01001291.1	2940620	A, G	142	PVUN01001216.1	542352	C, T
37	PVUN01001297.1	951943	G, A	90	PVUN01001222.1	147436	T, C	143	PVUN01001315.1	1847007	C, T
38	PVUN01001297.1	1891076	C, T	91	PVUN01001286.1	2577281	T, C	144	PVUN01001315.1	2499651	G, C
39	PVUN01001297.1	3962441	T, C	92	PVUN01001272.1	850788	G, T	145	PVUN01001315.1	4771815	G, A
40	PVUN01001316.1	4774822	T, C	93	PVUN01001303.1	2652271	G, A	146	PVUN01001315.1	4771836	C, T
41	PVUN01001316.1	4774823	A, G	94	PVUN01001303.1	4744078	C, A	147	PVUN01001315.1	5307686	A, C
42	PVUN01001316.1	5972187	A, G	95	PVUN01001340.1	7660772	A, G	148	PVUN01001334.1	2333857	C, T
43	PVUN01001316.1	7672458	G, A	96	PVUN01001325.1	5415973	T, A	149	PVUN01001334.1	7449836	G, A
44	PVUN01001279.1	492453	G, A	97	PVUN01001325.1	9624185	G, C	150	PVUN01001334.1	12481182	C, T
45	PVUN01001232.1	35369	G, A	98	PVUN01001280.1	2597078	C, A	151	PVUN01001260.1	879165	G, A
46	PVUN01001232.1	1027092	T, C	99	PVUN01001298.1	1610640	A, G	152	PVUN01001305.1	1344256	C, T
47	PVUN01001328.1	5226149	T, C	100	PVUN01001298.1	2617110	G, A	153	PVUN01001305.1	2407232	C, T
48	PVUN01001244.1	1121500	T, A	101	PVUN01001335.1	13696640	G, A	154	PVUN01001305.1	2679002	C, T
49	PVUN01001313.1	1811889	A, G	102	PVUN01001341.1	4328880	T, C	155	PVUN01001196.1	211346	C, T
50	PVUN01001245.1	124428	T, C	103	PVUN01001341.1	4328896	C, G	156	PVUN01001274.1	411988	C, T
51	PVUN01001245.1	312240	C, A	104	PVUN01001234.1	380380	C, T	157	PVUN01001274.1	1497655	G, T
52	PVUN01001245.1	848575	G, T	105	PVUN01001296.1	4107246	T, C	158	PVUN01001277.1	995350	T, A
53	PVUN01001324.1	907343	A, C	106	PVUN01001264.1	1532033	C, A	159	PVUN01001277.1	2696316	T, C

Mat.Compl.8. Listing of the 114 SNPs identified in oyster, according to their location in the *Crassostrea gigas* reference genome (GenBank accession: cgigas_uk_roslin_v1 NC_047559-NC_047568; Peñaloza et al. 2021). CHR: Chromosome or linkage group; POS: position; Bases: variants for each SNP.

Listado de los 114 SNPs identificados en ostión con su ubicación respecto al genoma de referencia *Crassostrea gigas* (No. acceso GenBank: cgigas_uk_roslin_v1 NC_047559-NC_047568; Peñaloza et al. 2021). CHR: Cromosoma o grupo de ligamiento; POS: posición; Bases: variantes para cada SNP.

S8. Listado de los 114 SNPs identificados en ostión con su ubicación respecto del genoma de referencia *Crassostrea gigas* (No. acceso GenBank: cgigas_uk_roslin_v1 NC_047559-NC_047568; Peñaloza et al. 2021). CHR: Cromosoma o grupo de ligamiento; POS: posición; Bases: variantes para cada SNP.

No.	CHR	POS	Bases	No.	CHR	POS	Bases	No.	CHR	POS	Bases
1	NC47559.1	4205289	C, A	39	NC47562.1	11696646	C, T	77	NC47565.1	59092294	A, G
2	NC47559.1	6126362	C, T	40	NC47562.1	23459031	A, G	78	NC47565.1	59857237	T, A
3	NC47559.1	8792864	G, A	41	NC47562.1	26685151	G, A	79	NC47565.1	61718014	G, C
4	NC47559.1	11810874	A, G	42	NC47562.1	27011633	T, C	80	NC47566.1	4457135	G, A
5	NC47559.1	17307821	T, C	43	NC47562.1	27366811	T, C	81	NC47566.1	10049850	G, T
6	NC47559.1	19156200	C, T	44	NC47562.1	34471465	C, A	82	NC47566.1	14427583	T, A
7	NC47559.1	20383773	G, A	45	NC47562.1	37511246	C, T	83	NC47566.1	16112404	T, G
8	NC47559.1	24423792	A, T	46	NC47562.1	41287841	G, A	84	NC47566.1	17912658	T, C
9	NC47559.1	27945080	C, T	47	NC47562.1	42451929	C, T	85	NC47566.1	24476648	T, G
10	NC47559.1	49060713	A, T	48	NC47562.1	47122232	G, A	86	NC47566.1	44056092	C, T
11	NC47559.1	55142231	G, T	49	NC47563.1	518994	C, T	87	NC47566.1	48018625	T, C
12	NC47560.1	6064189	C, T	50	NC47563.1	4000068	C, T	88	NC47566.1	49635166	A, G
13	NC47560.1	6344272	T, G	51	NC47563.1	6340923	C, T	89	NC47567.1	7816166	C, A
14	NC47560.1	21399250	G, A	52	NC47563.1	17546610	T, C	90	NC47567.1	8631012	G, T
15	NC47560.1	40103059	G, T	53	NC47563.1	57889163	T, C	91	NC47567.1	8957218	C, T
16	NC47560.1	40104415	G, A	54	NC47563.1	61170818	G, A	92	NC47567.1	10938865	C, T
17	NC47560.1	51590421	C, A	55	NC47564.1	4441221	G, A	93	NC47567.1	14817603	A, T
18	NC47560.1	54358847	T, A	56	NC47564.1	13998536	C, T	94	NC47567.1	19071900	T, A
19	NC47560.1	63917081	A, C	57	NC47564.1	19448288	A, G	95	NC47567.1	22768261	G, A
20	NC47560.1	69087293	C, T	58	NC47564.1	23308946	C, T	96	NC47567.1	24121638	T, A
21	NC47560.1	69995897	G, A	59	NC47564.1	29345320	T, A	97	NC47567.1	24183872	C, T
22	NC47561.1	12558422	G, A	60	NC47564.1	42710099	G, A	98	NC47567.1	27762074	C, T
23	NC47561.1	13255640	A, T	61	NC47564.1	43578484	C, G	99	NC47567.1	29593367	G, A
24	NC47561.1	13919358	C, A	62	NC47564.1	52394621	G, T	100	NC47567.1	32332479	G, A
25	NC47561.1	23992305	C, T	63	NC47564.1	57278856	A, G	101	NC47568.1	22213129	A, G
26	NC47561.1	26350028	C, T	64	NC47565.1	3716846	A, T	102	NC47568.1	53320817	A, G
27	NC47561.1	27893344	A, T	65	NC47565.1	6217681	G, C	103	NC47568.1	55469167	C, G
28	NC47561.1	27914101	G, A	66	NC47565.1	15679804	C, A	104	NW22994822.1	311195	G, A
29	NC47561.1	31921762	C, T	67	NC47565.1	18380662	C, T	105	NW22994823.1	50243	T, C
30	NC47561.1	33081701	G, A	68	NC47565.1	28499946	T, G	106	NW22994826.1	100311	A, T
31	NC47561.1	34126111	C, T	69	NC47565.1	29409438	T, C	107	NW22994833.1	245544	T, C
32	NC47561.1	46089137	A, G	70	NC47565.1	29485627	A, G	108	NW22994836.1	381260	G, C
33	NC47561.1	47054752	A, T	71	NC47565.1	32608963	A, T	109	NW22994852.1	91289	A, C
34	NC47561.1	49193823	G, A	72	NC47565.1	36033425	G, T	110	NW22994930.1	21568	G, T
35	NC47561.1	49546335	T, A	73	NC47565.1	41281896	A, T	111	NW22994952.1	155632	T, A
36	NC47561.1	51990417	C, T	74	NC47565.1	41680284	T, C	112	NW22994966.1	155	G, T
37	NC47561.1	53842101	T, A	75	NC47565.1	52425814	G, C	113	NW22994966.1	105588	A, G
38	NC47562.1	3127189	T, A	76	NC47565.1	56737860	A, C	114	NW22994993.1	156651	C, G