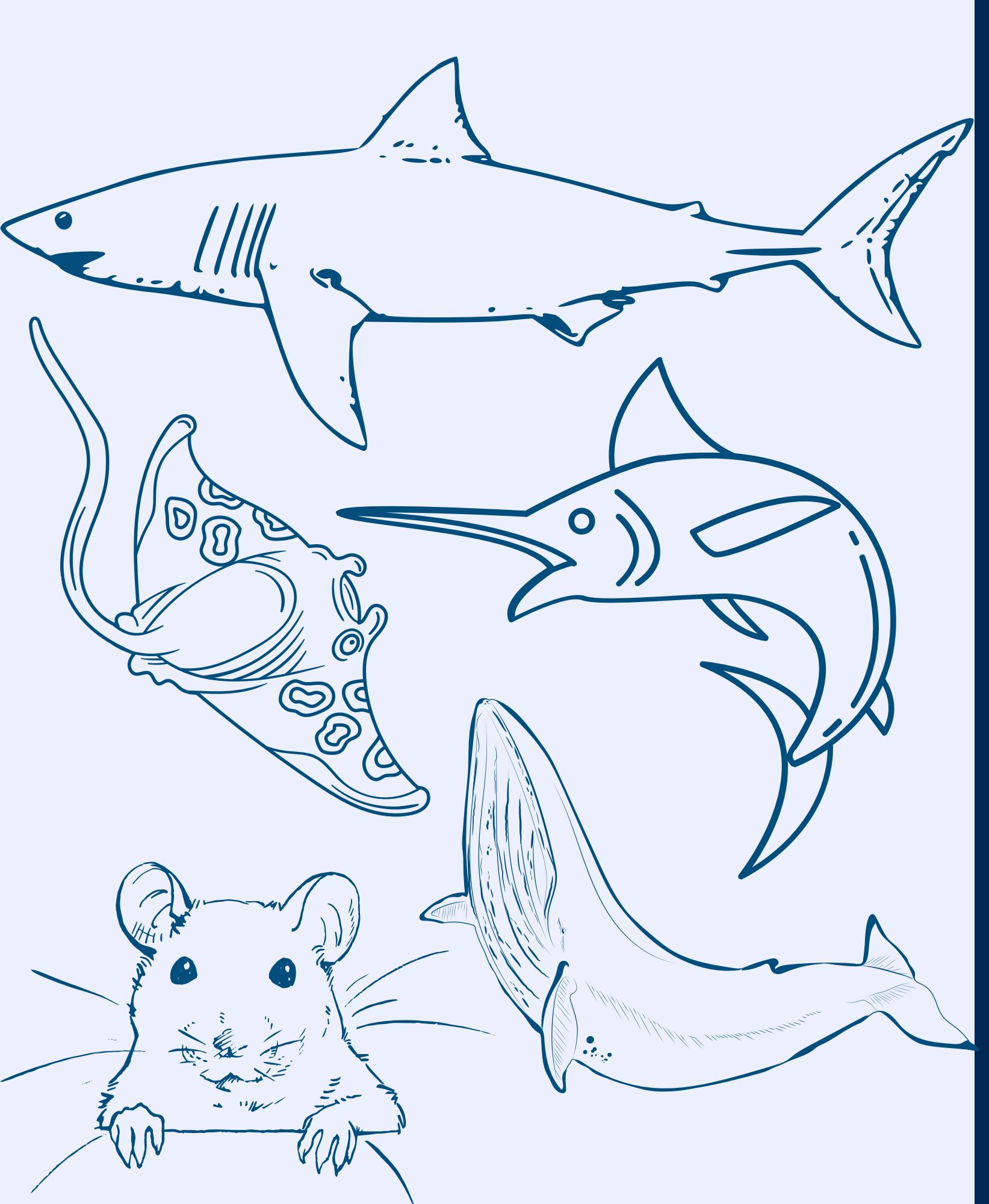




PROYECTO FINAL

ANÁLISIS DEL GEN HoxD

Por: Ana Paloma Orozco Carstensen



GENES Hox

HoxD

Polyodon spathula
Acipenser Ruthenus
Danio rerio
Scyliorhinus canicula
S. torazame
Amblyraja radiata
Carcharodon carcharias
Chiloscyllium plagiosum
Rhinocodon typos
Callorhincus milli
Mus musculus

Pez espátula
Esturión
Pez zebra
Tiburón gato
Tiburón gato nublado
Raya radiante
Tiburón blanco
Tiburón pintaroja
Tiburón ballena
Tiburón fantasma
Ratón

ANÁLISIS

1

TRANSCRIPCIÓN Y TRADUCCIÓN

ADN -> ARN -> Proteína

2

PORCENTAJE DE GC

Funcionalidad, estabilidad y evolución

3

FRECUENCIA DE AMINOÁCIDOS

Funcionalidad, modificaciones post-traduccionales

4

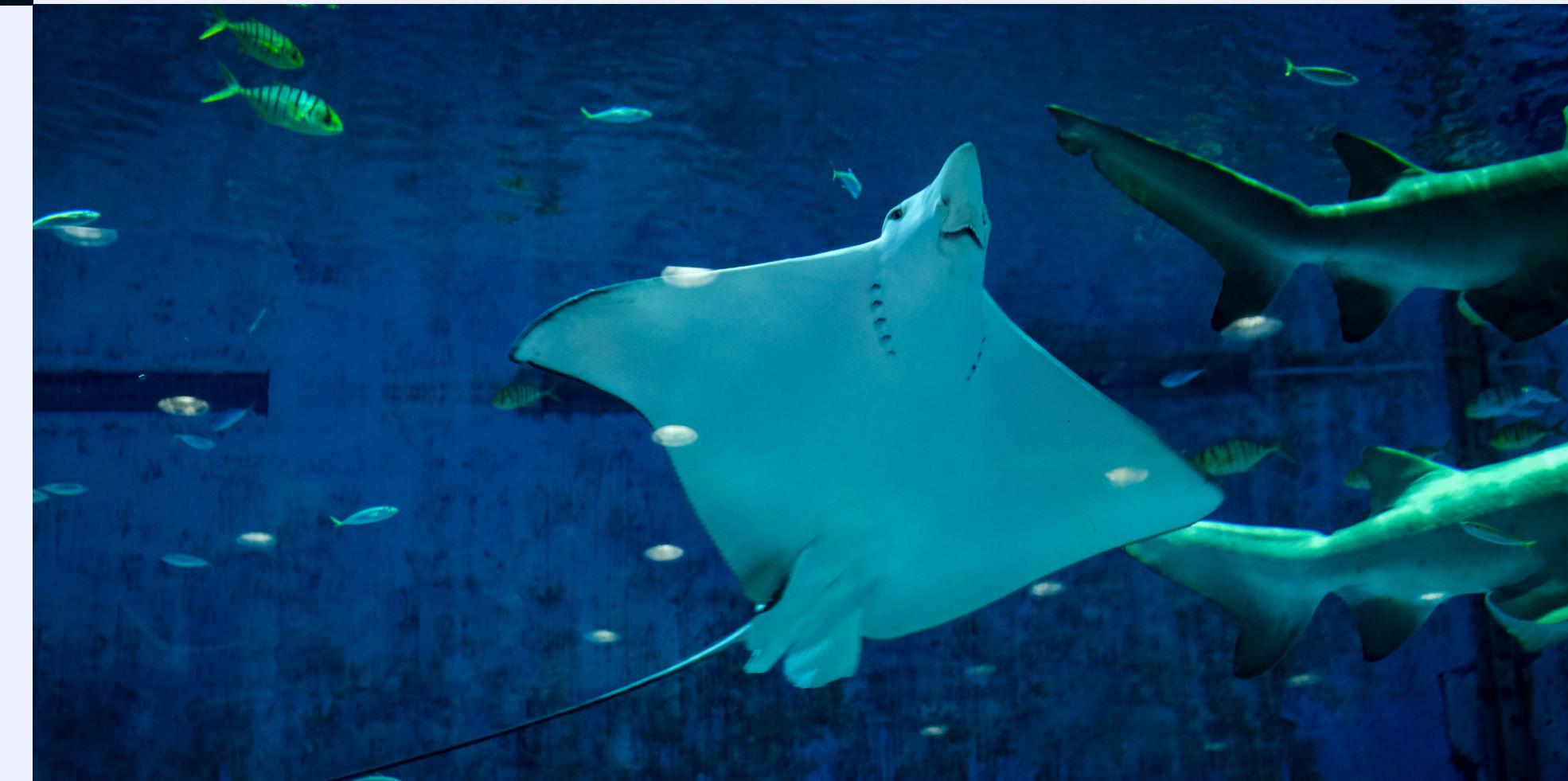
ALINEAMIENTO Y ÁRBOLES FILOGENÉTICOS

Evolución del gen



TRADUCCIÓN

```
Proteins <- Biostrings::translate  
[Seq_HoxD]
```



TRANSCRIPCIÓN

```
Seq_RNA <- gsub ("T", "U", Seq_DNA)
```

FRECUENCIAS

AMINOÁCIDOS

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	U	O	B	J	Z	X	*
[1,]	61	79	78	25	36	64	43	52	38	73	137	76	22	76	44	115	68	26	55	74	0	0	0	0	0	0	63
[2,]	23	30	25	15	19	36	16	23	16	26	41	33	10	25	25	43	29	9	19	31	0	0	0	0	0	0	10
[3,]	29	40	28	14	22	30	24	37	22	28	63	44	12	46	35	67	32	10	20	32	0	0	0	0	0	0	34
[4,]	37	29	28	20	29	33	28	42	26	31	64	52	11	52	33	66	34	10	28	38	0	0	0	0	0	0	32
[5,]	4	7	4	2	6	3	2	3	4	9	15	4	3	13	2	3	7	1	4	14	0	0	0	0	0	0	4
[6,]	46	66	52	25	38	45	32	56	29	54	112	51	13	59	47	96	49	13	30	55	0	0	0	0	0	0	42
[7,]	12	23	27	14	14	25	24	16	11	22	41	28	12	21	19	35	28	3	24	17	0	0	0	0	0	0	15
[8,]	24	27	33	14	40	31	38	21	20	21	51	35	9	35	26	55	30	6	30	33	0	0	0	0	0	0	24
[9,]	3	16	8	8	2	8	8	11	5	12	22	13	3	6	9	16	17	3	5	9	0	0	0	0	0	0	4
[10,]	24	23	26	12	13	19	25	15	10	24	43	23	9	21	23	59	15	6	19	16	0	0	0	0	0	0	11
[11,]	46	70	19	16	23	34	31	76	33	44	106	35	10	41	44	82	32	14	12	53	0	0	0	0	0	0	36

NOMBRES

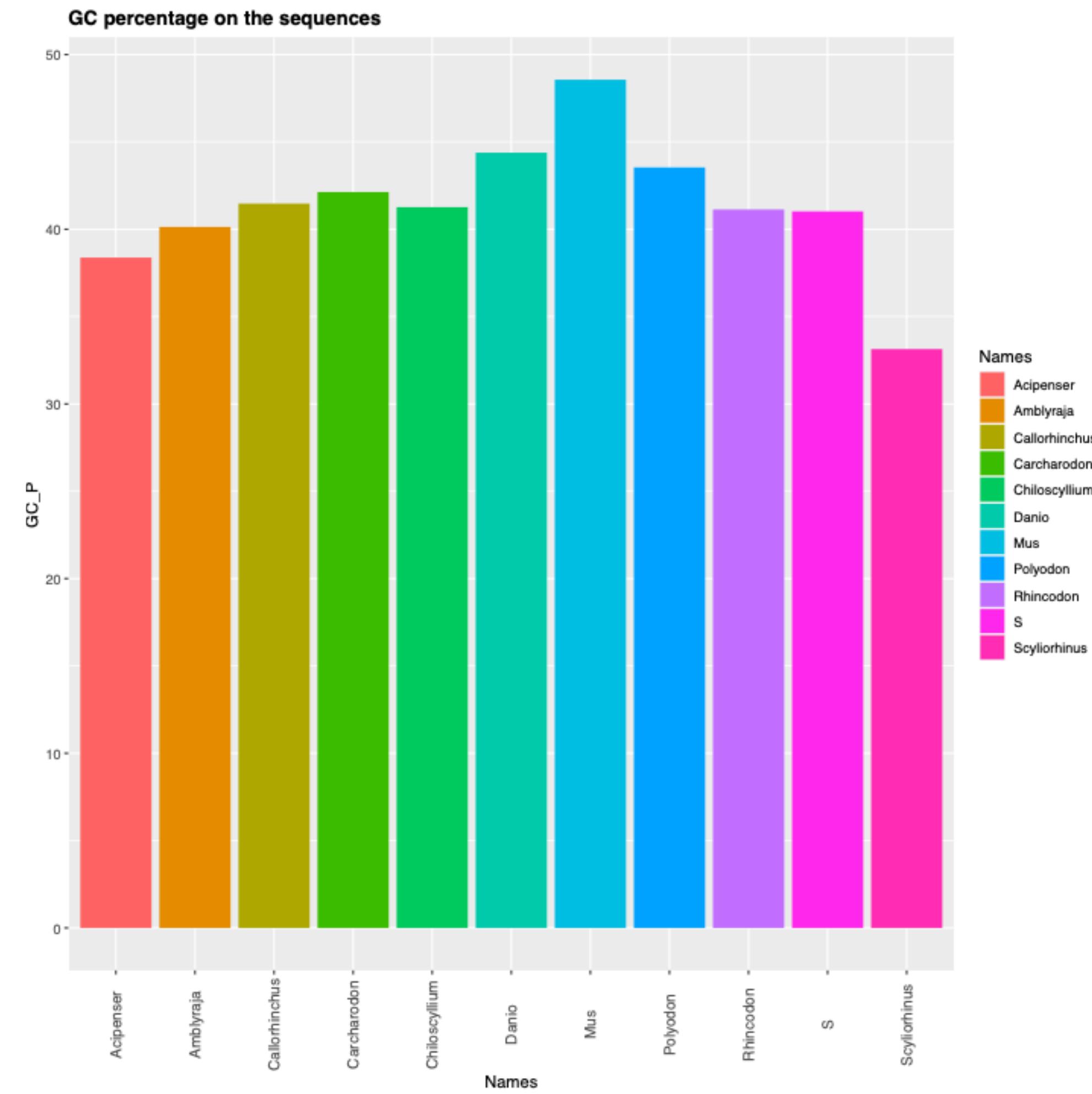
- [1] "Amblyraja"
- [2] "Carcharodon"
- [3] "Chiloscyllium"
- [4] "Rhincodon"
- [5] "Scyliorhinus"
- [6] "S"
- [7] "Acipenser"
- [8] "Callorhinchus"
- [9] "Polyodon"
- [10] "Danio"
- [11] "Mus"

NUCLEÓTIDOS

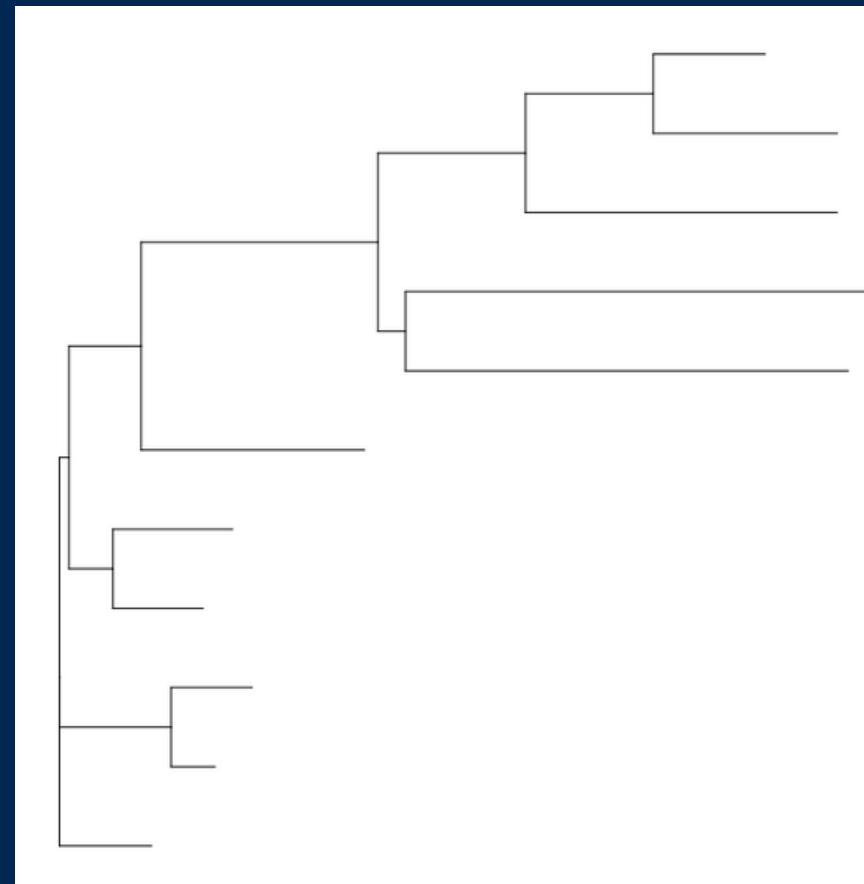
	A	C	G	T
[1,]	1188	766	806	1157
[2,]	458	322	315	417
[3,]	611	410	419	569
[4,]	661	438	455	617
[5,]	94	45	69	136
[6,]	895	615	628	892
[7,]	444	251	246	354
[8,]	534	365	386	526
[9,]	194	127	119	125
[10,]	382	303	278	346
[11,]	625	630	619	698

PORCENTAJE DE GC

```
GC_P <- [Seq_Width - Frequency_nt [,1]  
- Frequency_nt [,4]] * 100 / Seq_Width
```

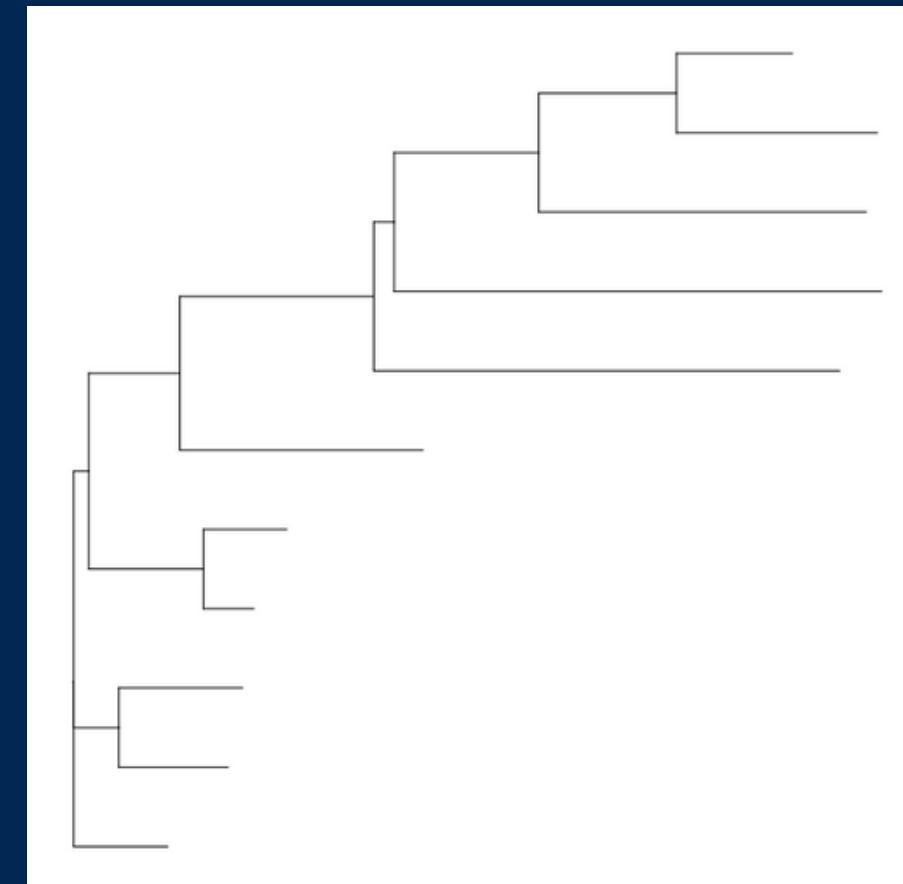


ALINEAMIENTO



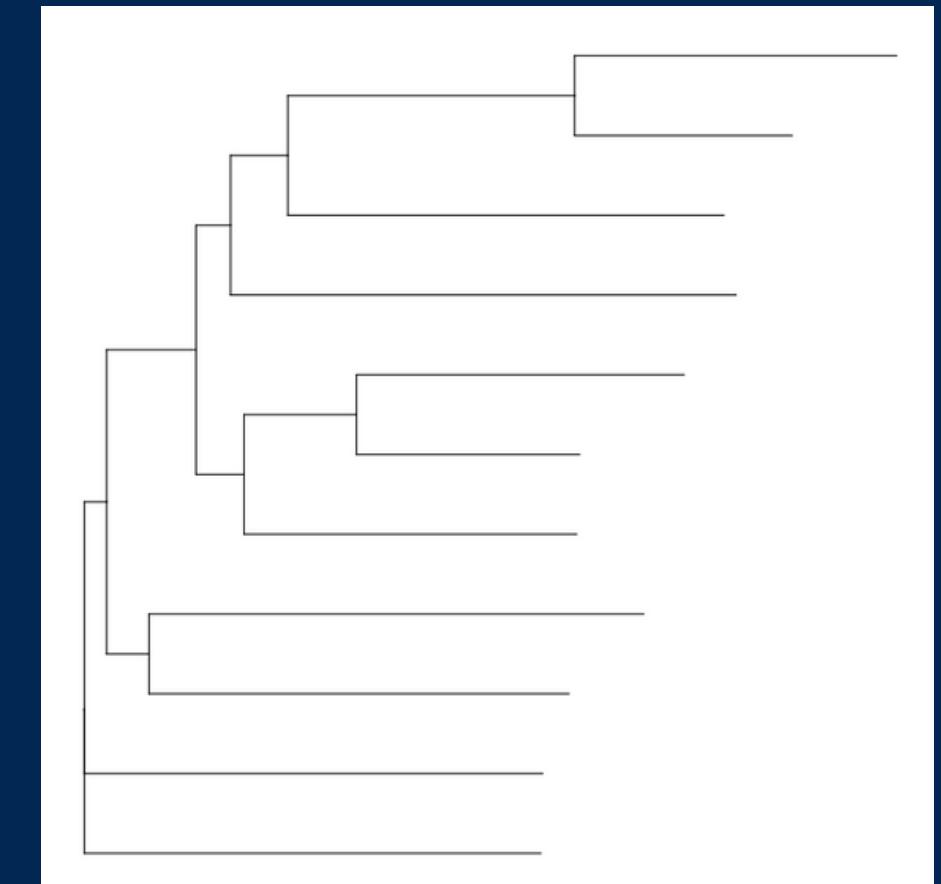
CLUSTAL W

```
Alig_HoxD_Clustal_W <- msa  
[Seq_HoxD, method =  
"ClustalW"]
```



CLUSTAL O

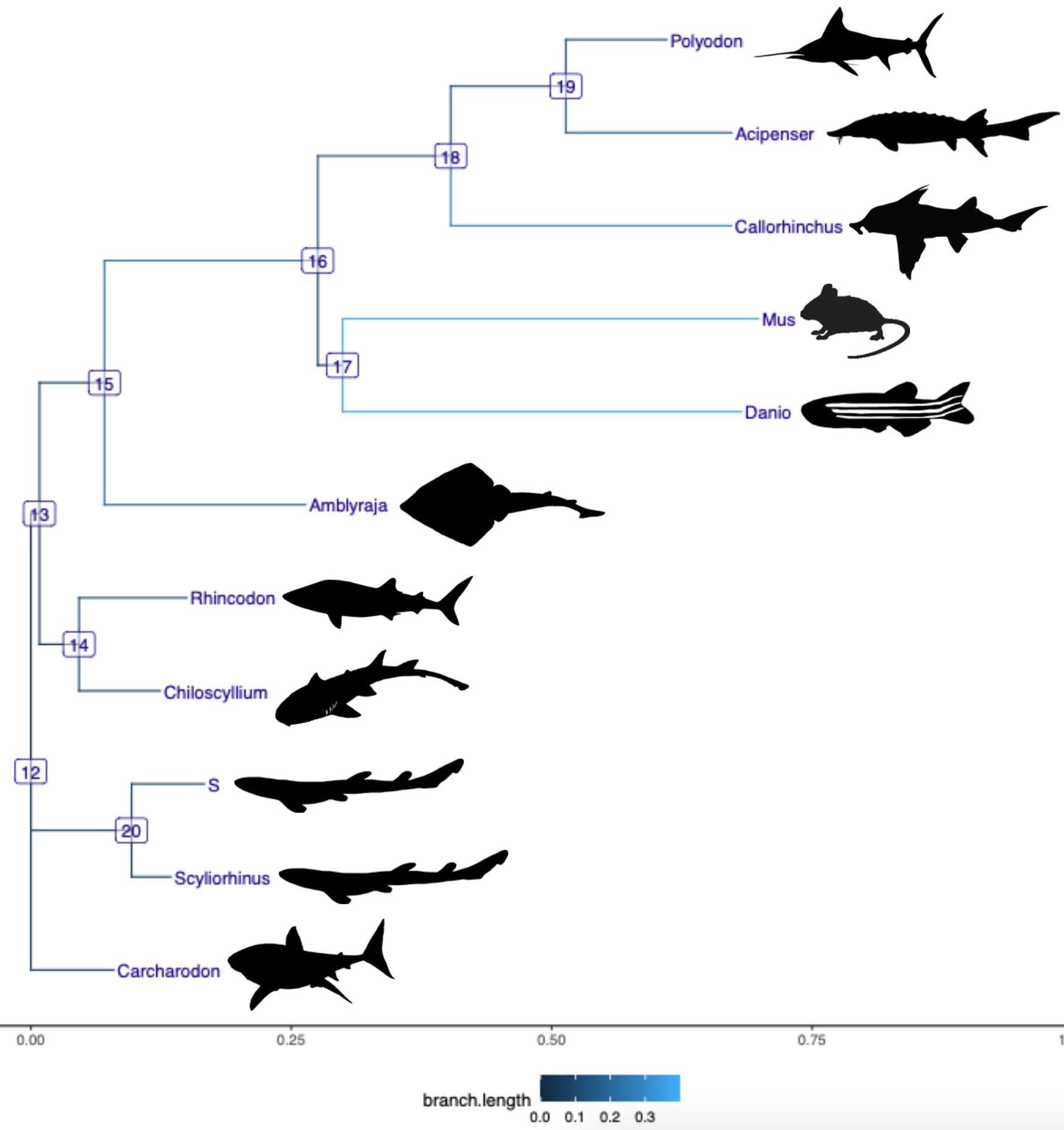
```
Alig_HoxD_Clustal_O <- msa  
[Seq_HoxD, method =  
"ClustalOmega"]
```



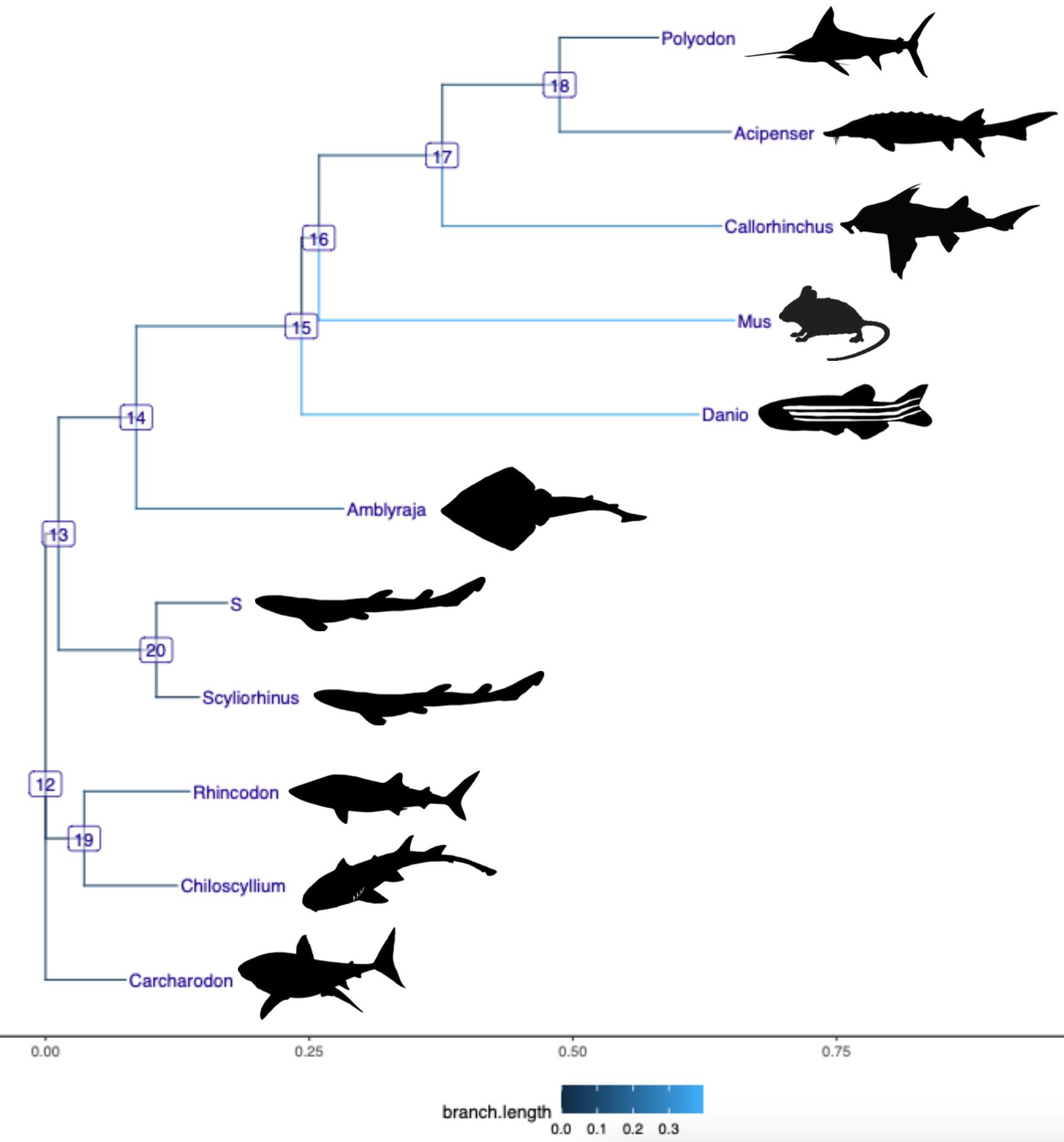
MUSCLE

```
Alig_HoxD_Muscle <- msa  
[Seq_HoxD, method =  
"Muscle"]
```

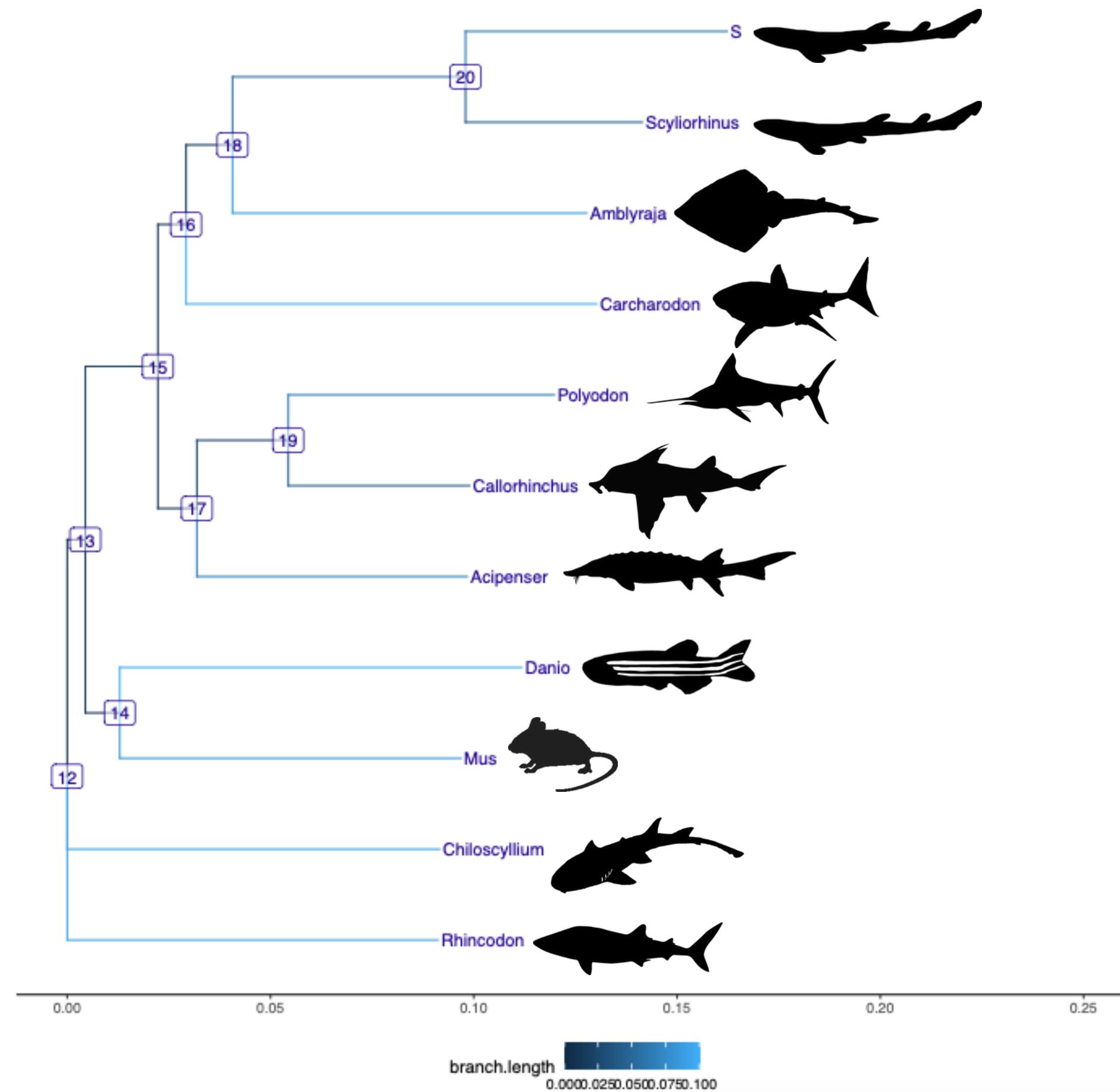
CLUSTAL W



CLUSTAL O



MUSCLE





PROYECTO FINAL

ANÁLISIS DEL GEN HOXD

Por: Ana Paloma Orozco Carstensen