

## *Supplementary Material*

>TMAsat

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```

**Supplementary Figure 1.** TMAsat consensus sequence, in fasta format, generated by TAREAN.

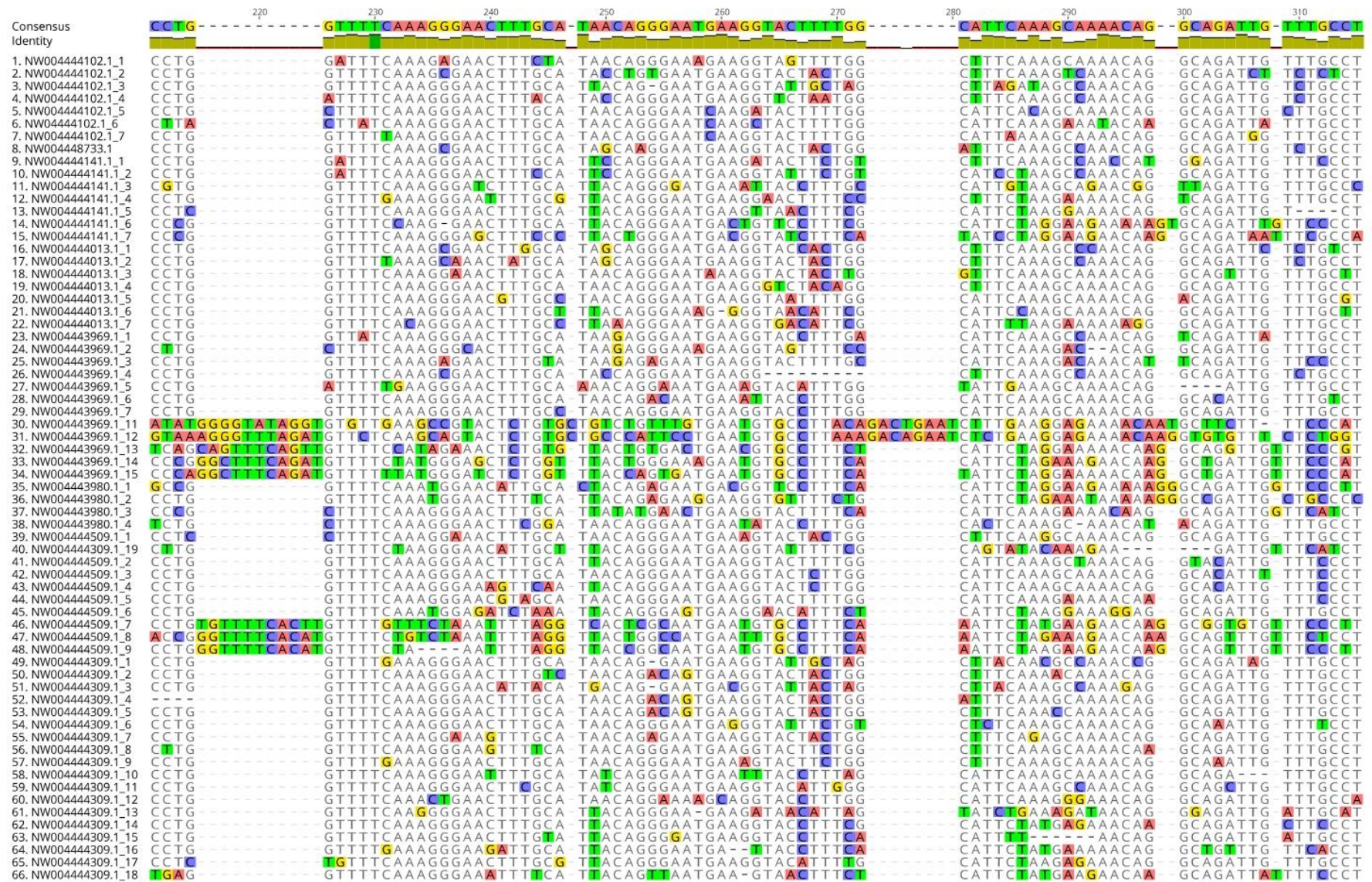
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part one of eight.





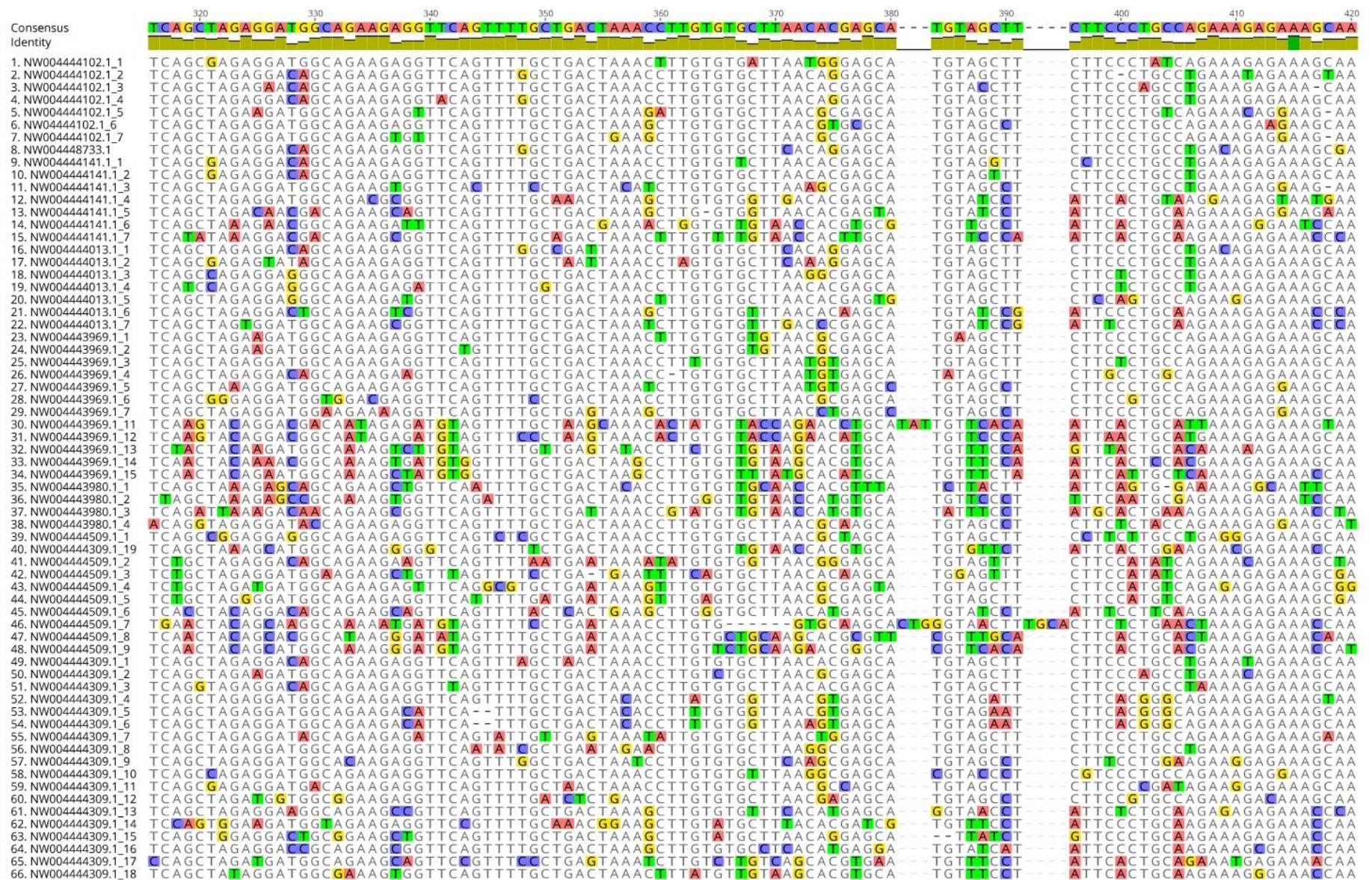
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part two of eight.





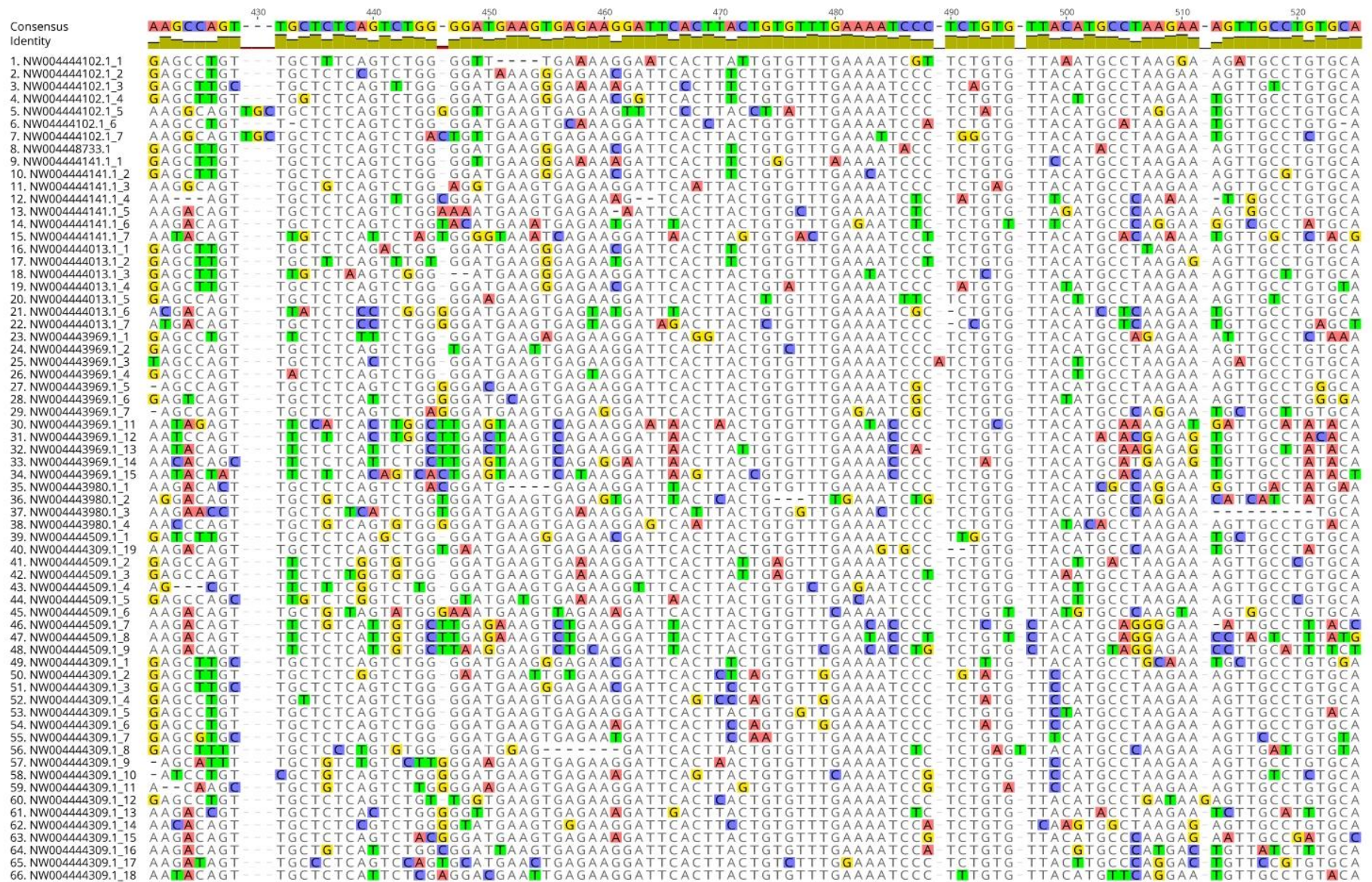
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part three of eight.





**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part four of eight.





**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part five of eight.





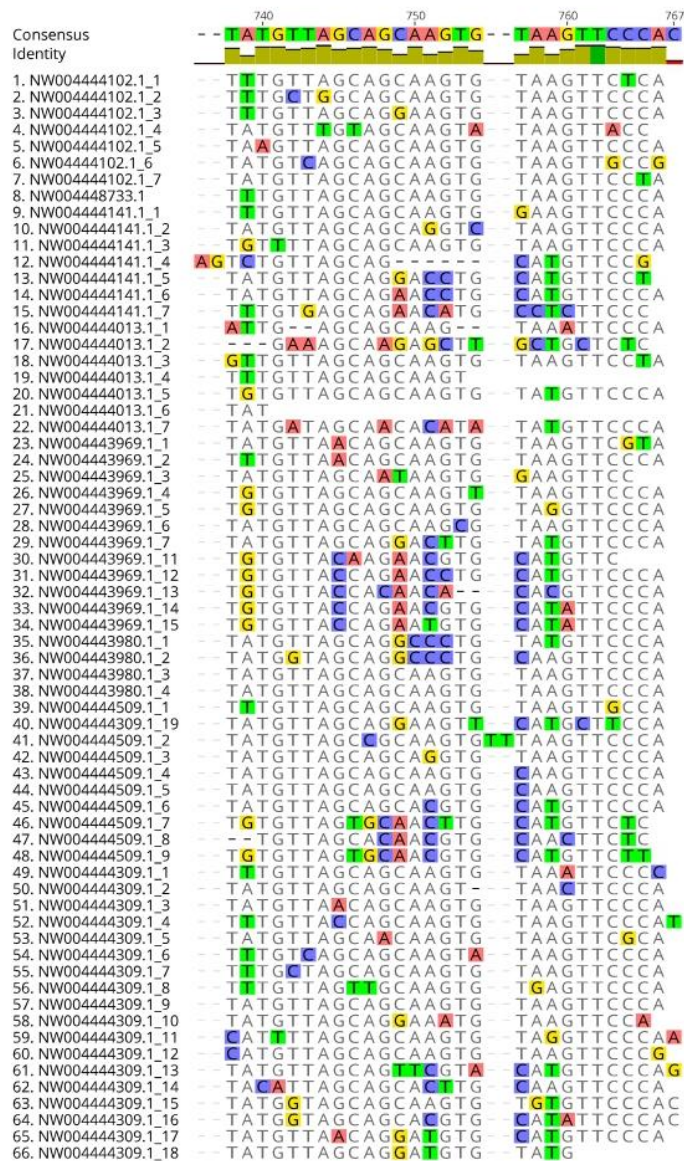
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part six of eight.





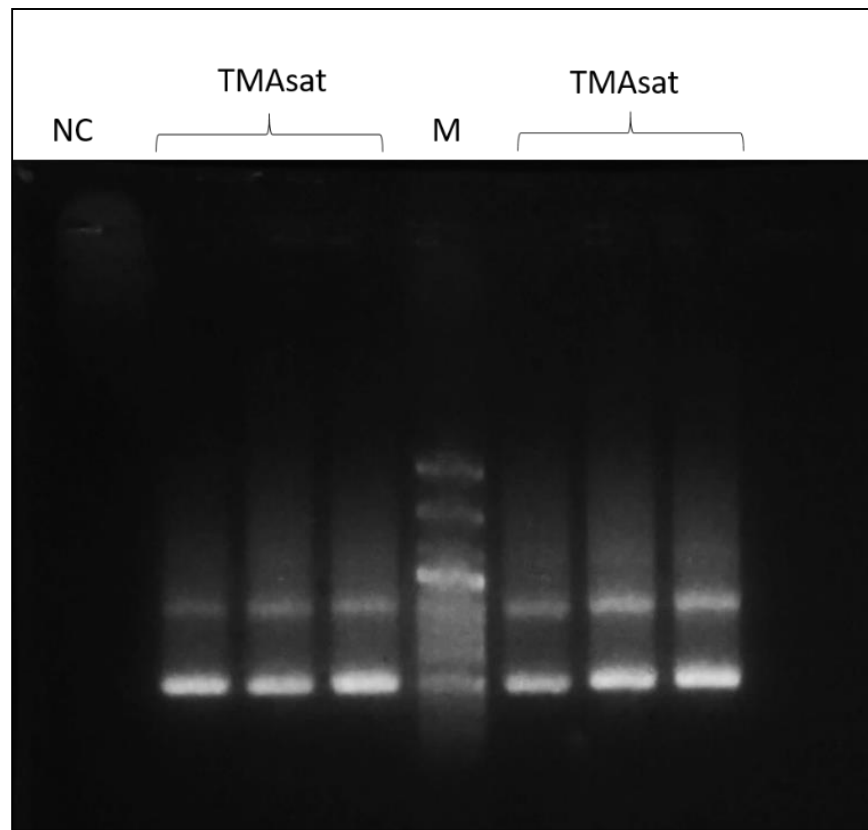
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part seven of eight.





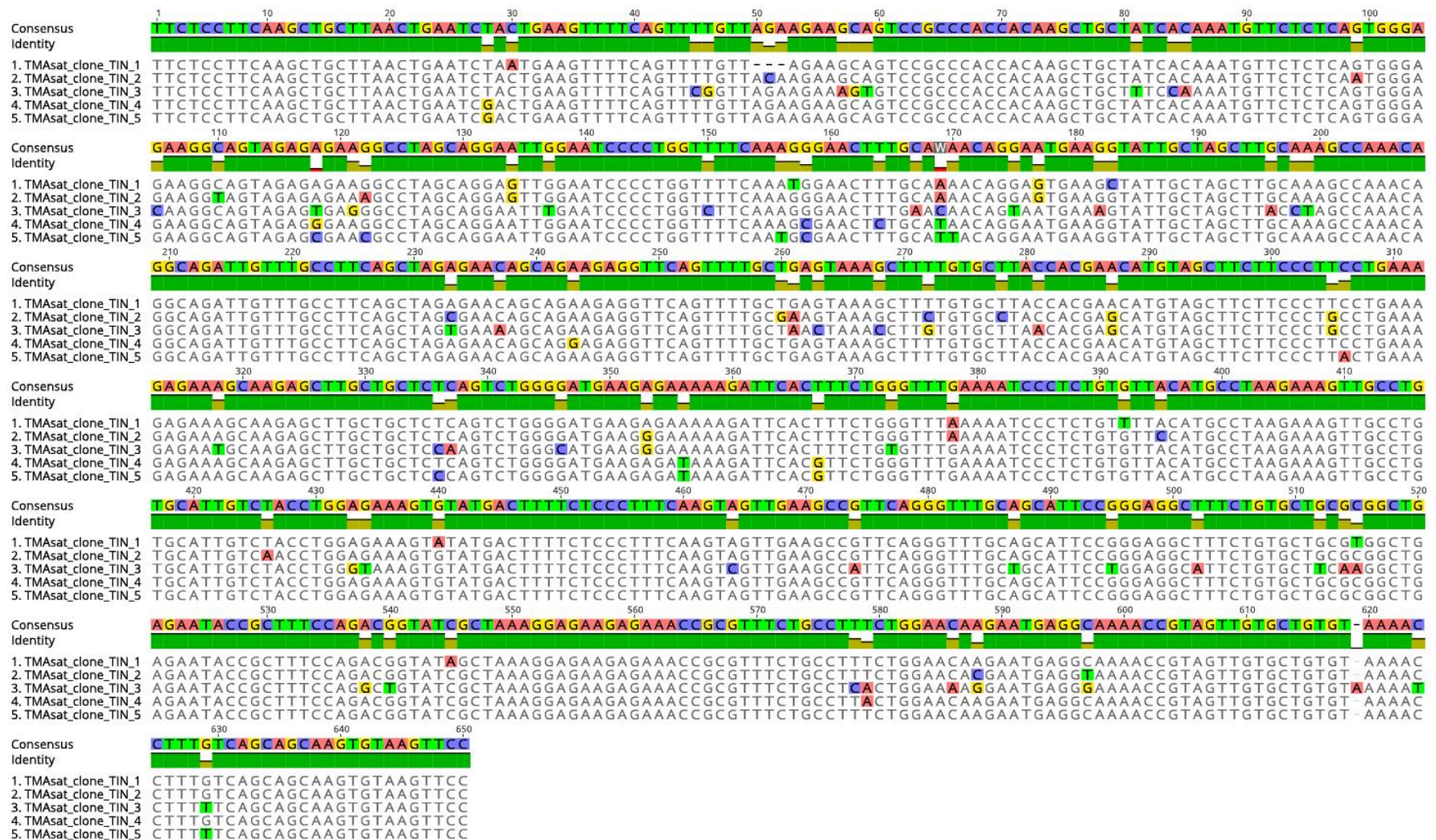
**Supplementary Figure 2.** Alignment of 66 monomers manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1). Part eight of eight.





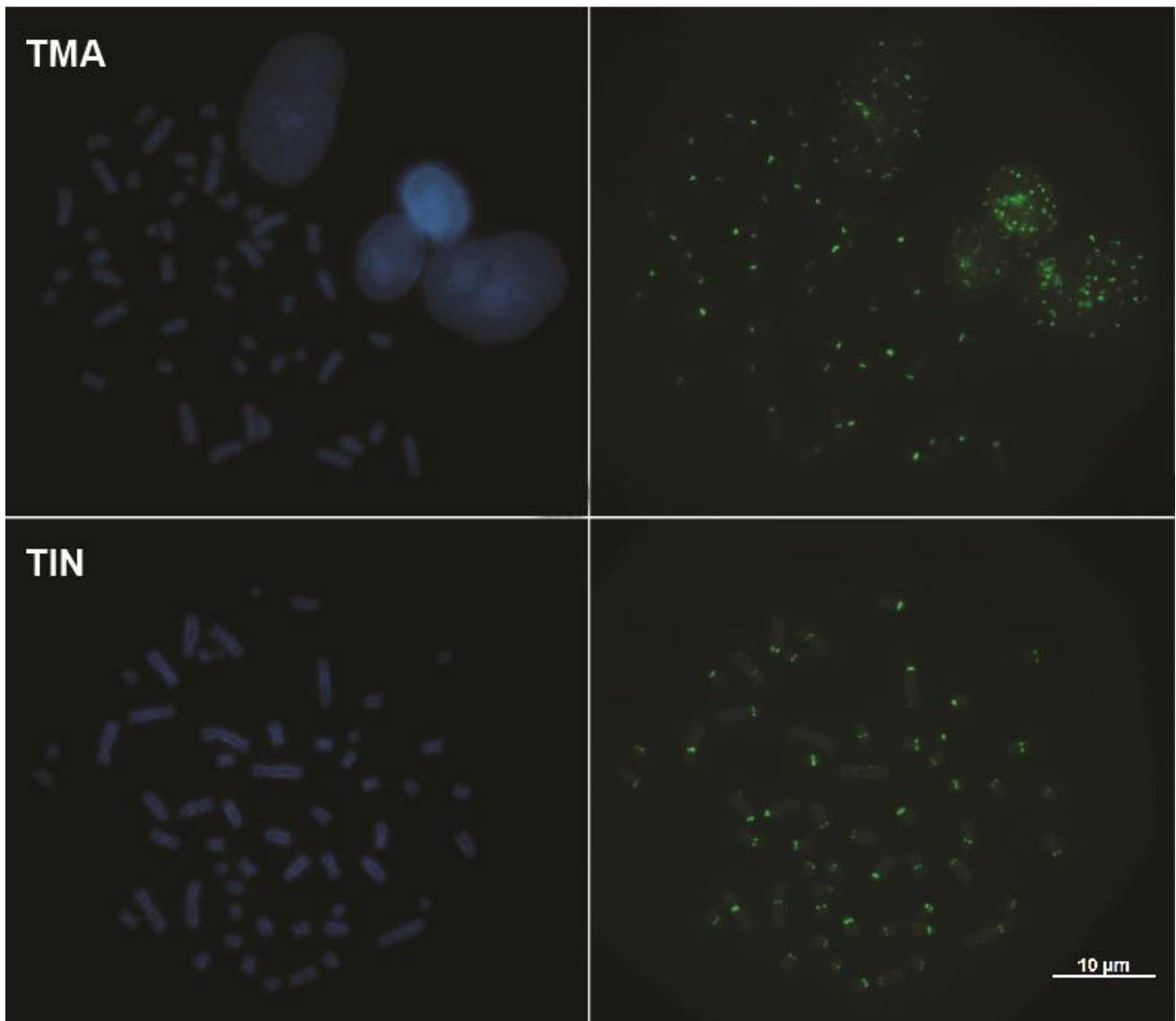
**Supplementary Figure 3.** Agarose gel (1%) showing the PCR products of *Trichechus inunguis* using the TMA sat primers. M - DNA size marker of 100 bp ladder; NC – Negative control (no DNA).





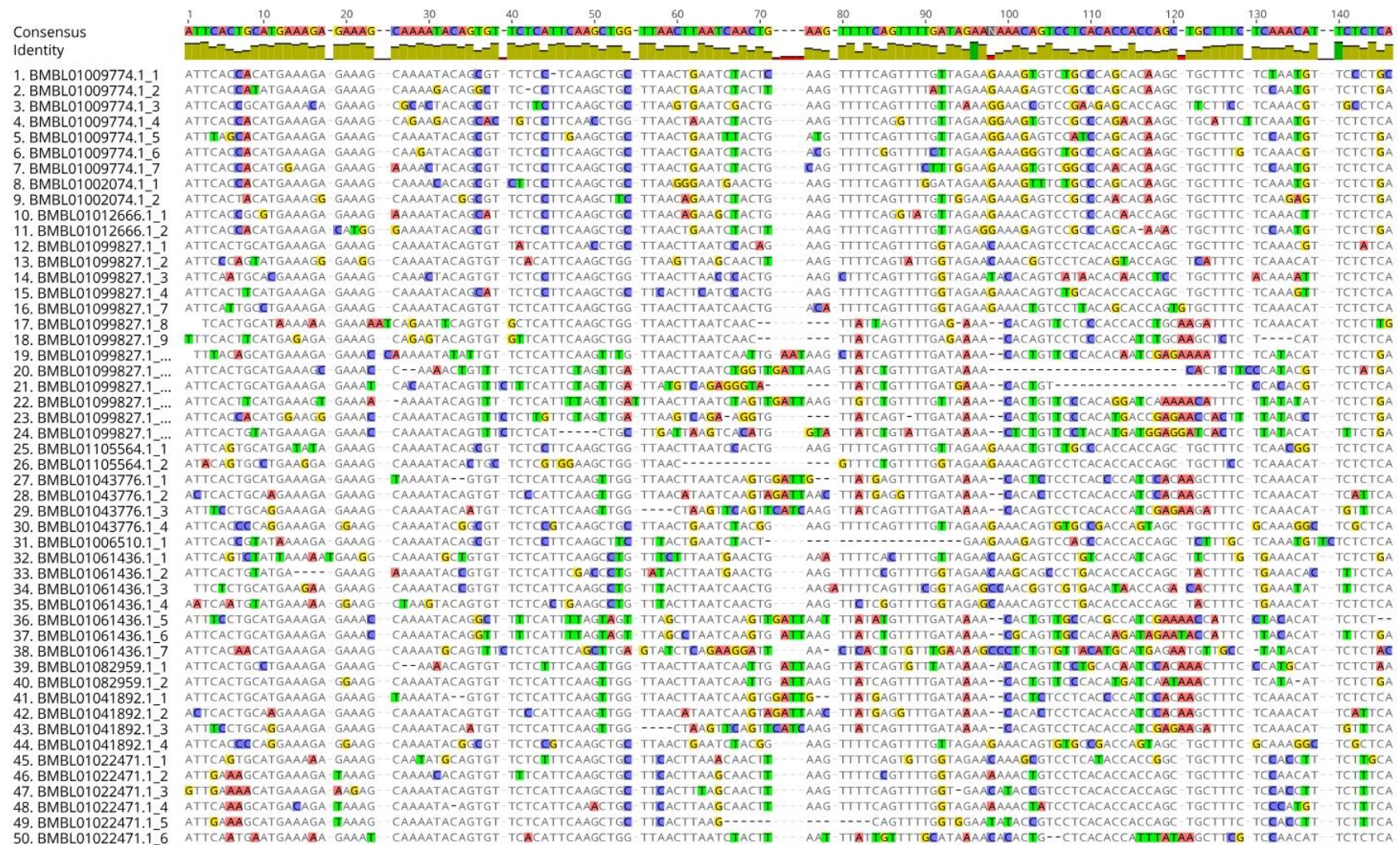
**Supplementary Figure 4.** Alignment of five TMAsat monomers cloned and sequenced from the *Trichechus inunguis* genome (accession MW272776- MW272780).





**Supplementary Figure 5.** Metaphases of *T. manatus* (TMA) and *T. inunguis* (TIN) after FISH with the TMA sat probe. Channels are presented separately, DAPI on left in blue and TMA sat probe on right in green.



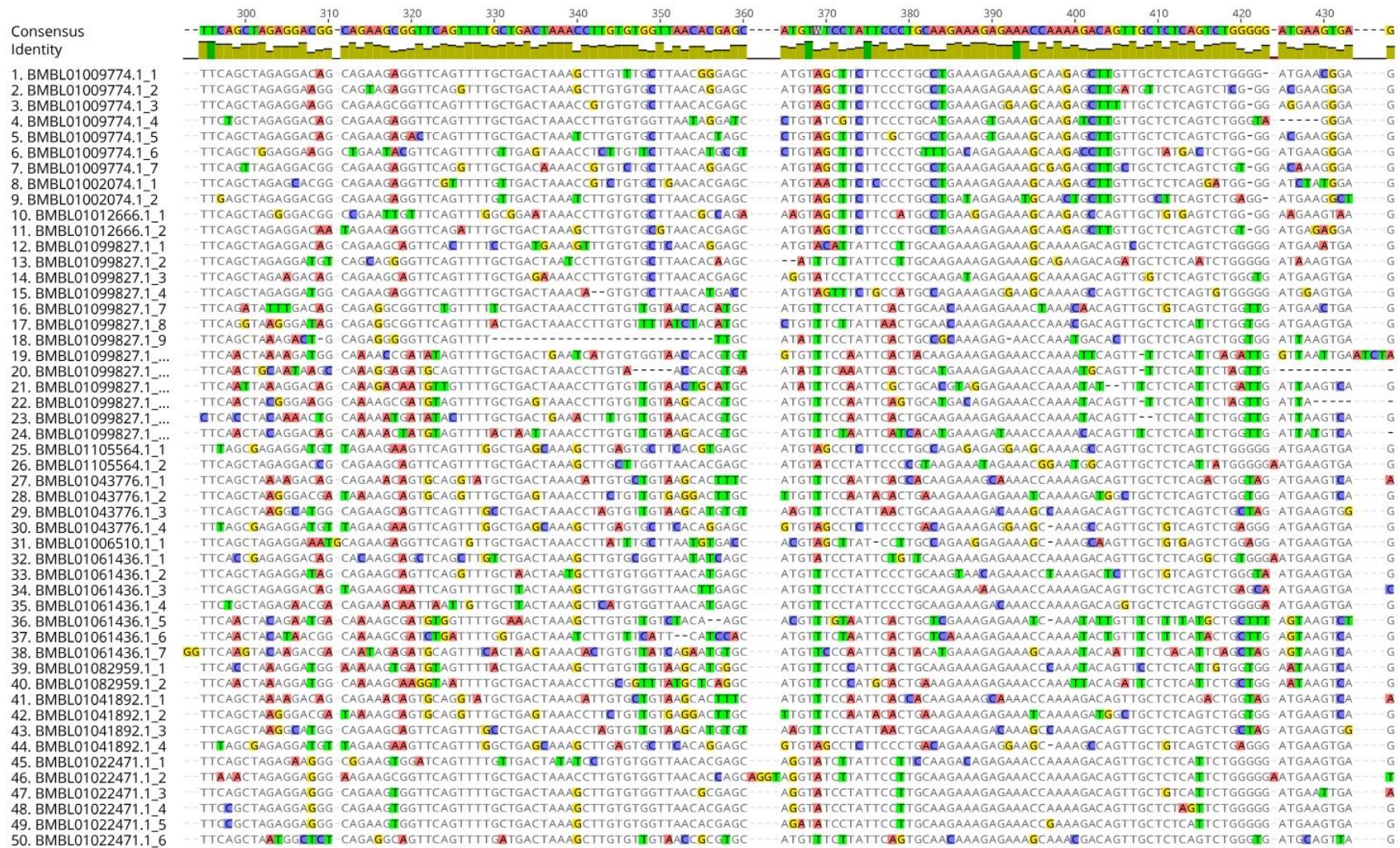


**Supplementary Figure 6.** Alignment of 50 monomers manually isolated from the *Dugong dugon* assembled reference genome (accession GCA\_015147995.1). Part one of six.



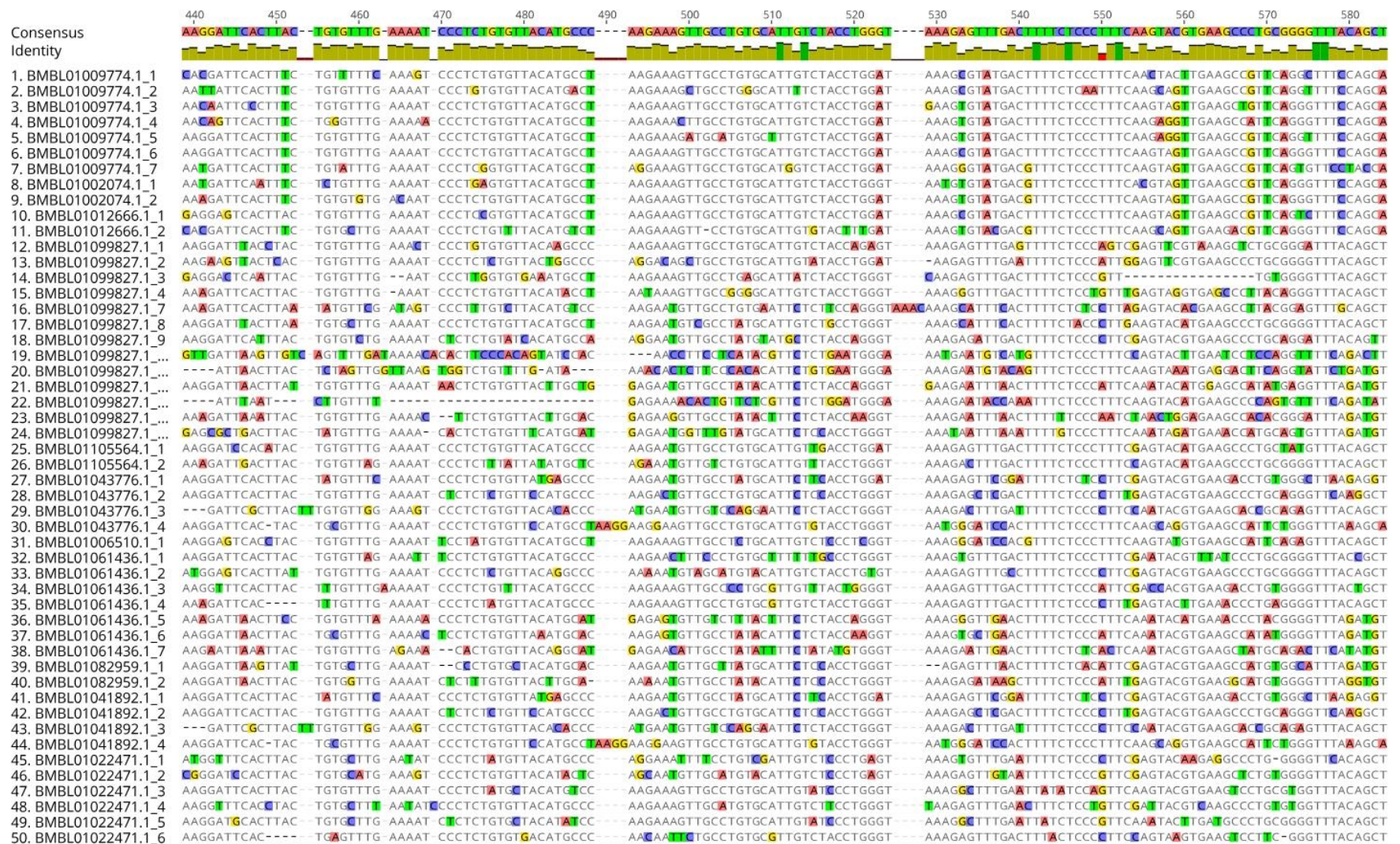






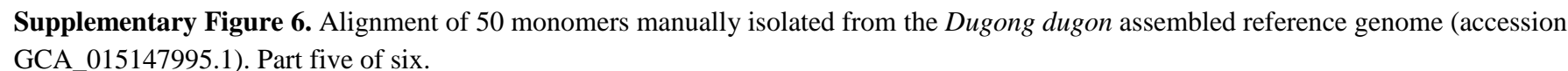
**Supplementary Figure 6.** Alignment of 50 monomers isolated from the *Dugan dugan* assembled reference genome (accession GCA\_015147995.1). Part three of six.



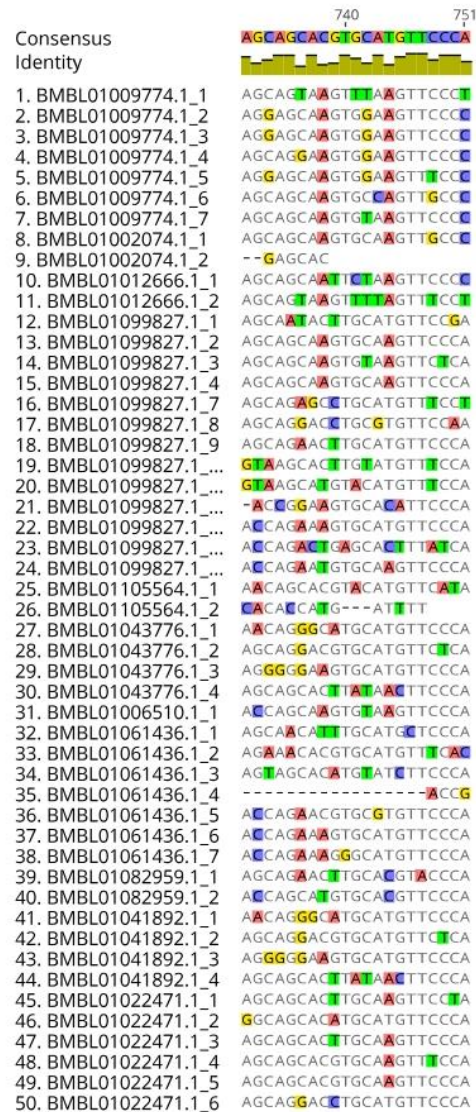


**Supplementary Figure 6.** Alignment of 50 monomers manually isolated from the *Dugong dugon* assembled reference genome (accession GCA\_015147995.1). Part four of six.



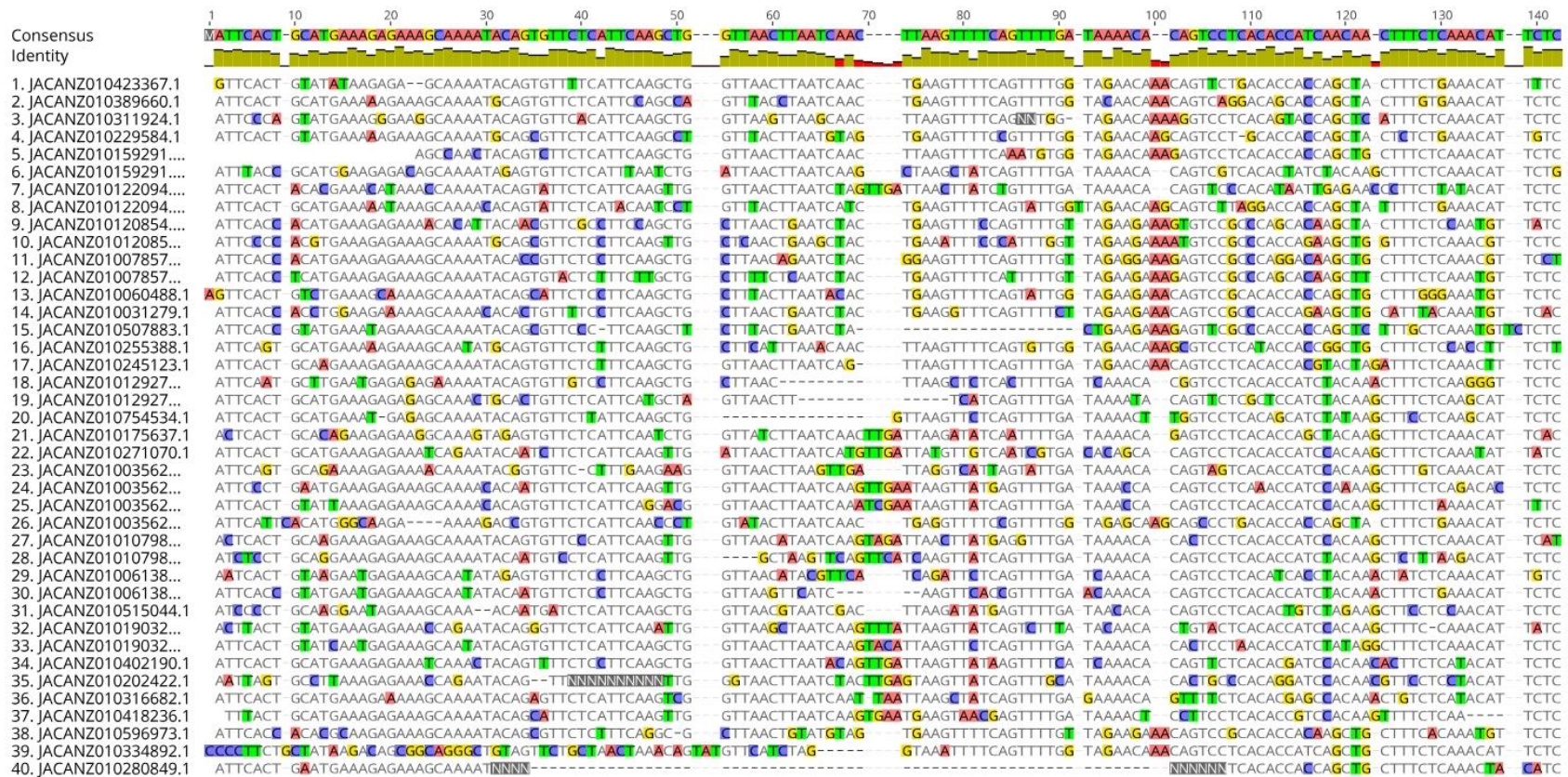






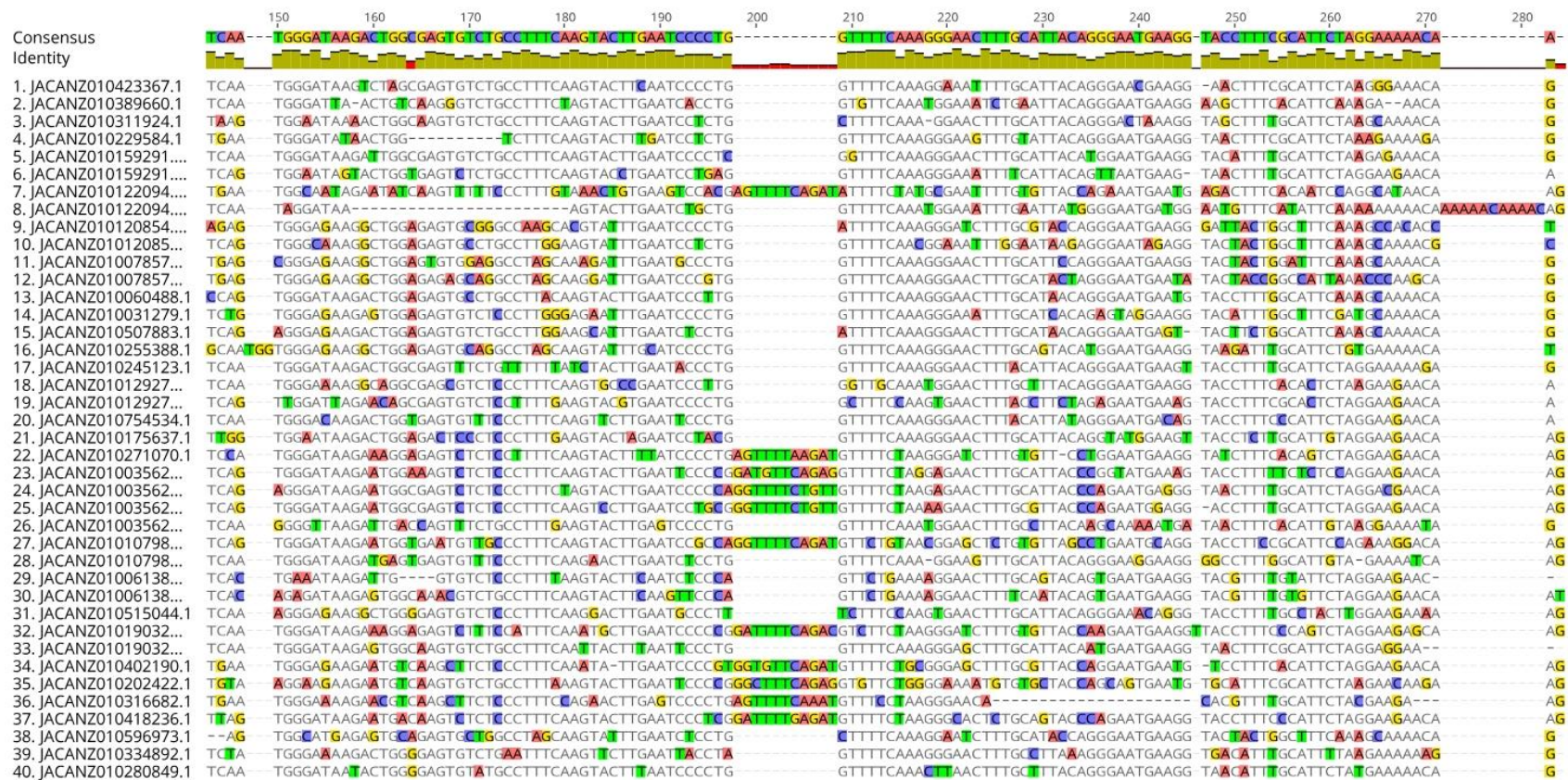
**Supplementary Figure 6.** Alignment of 50 monomers manually isolated from the *Dugong dugon* assembled reference genome (accession GCA\_015147995.1). Part six of six.





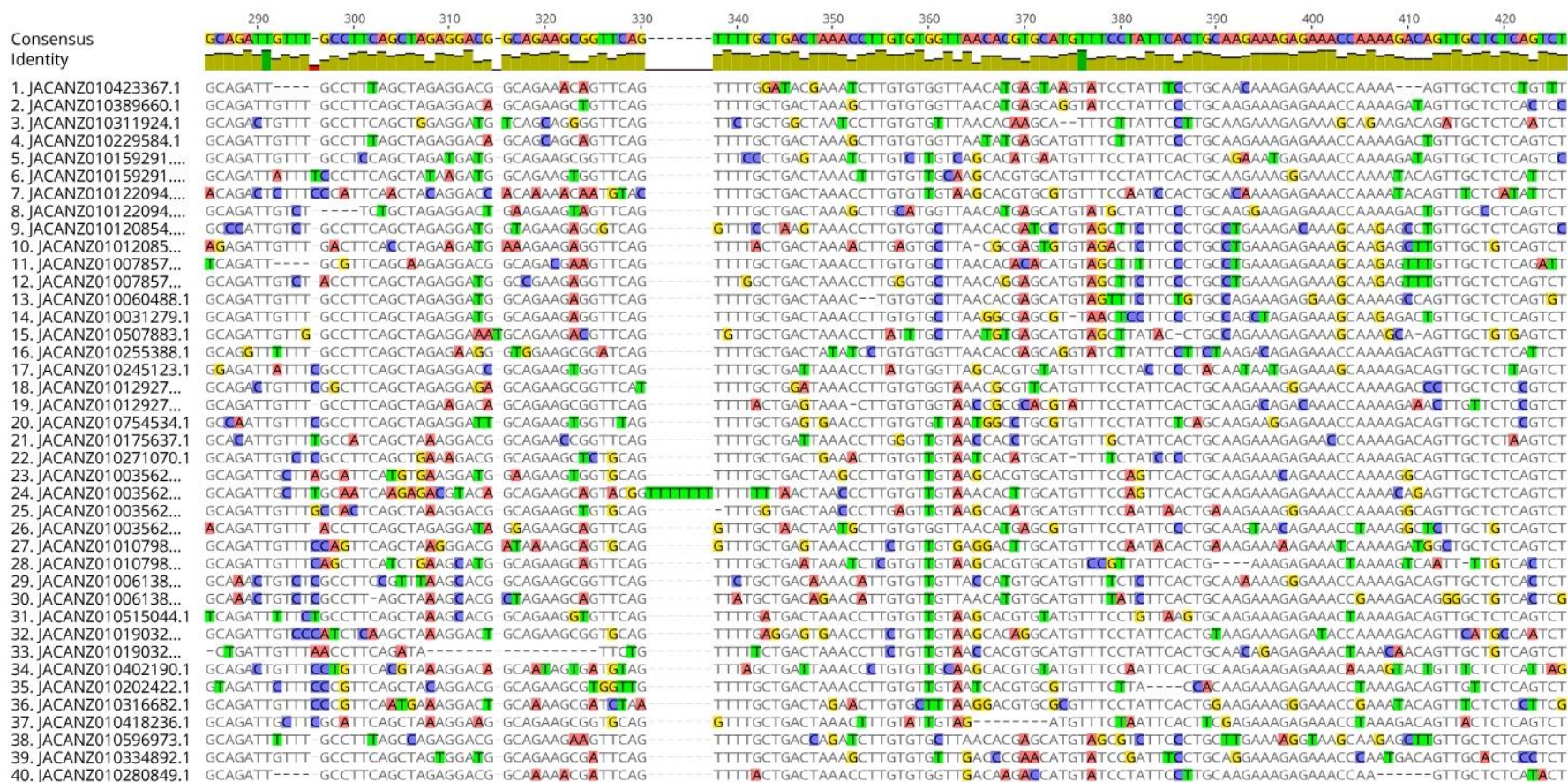
**Supplementary Figure 7.** Alignment of 40 monomers manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1). Part one of six.





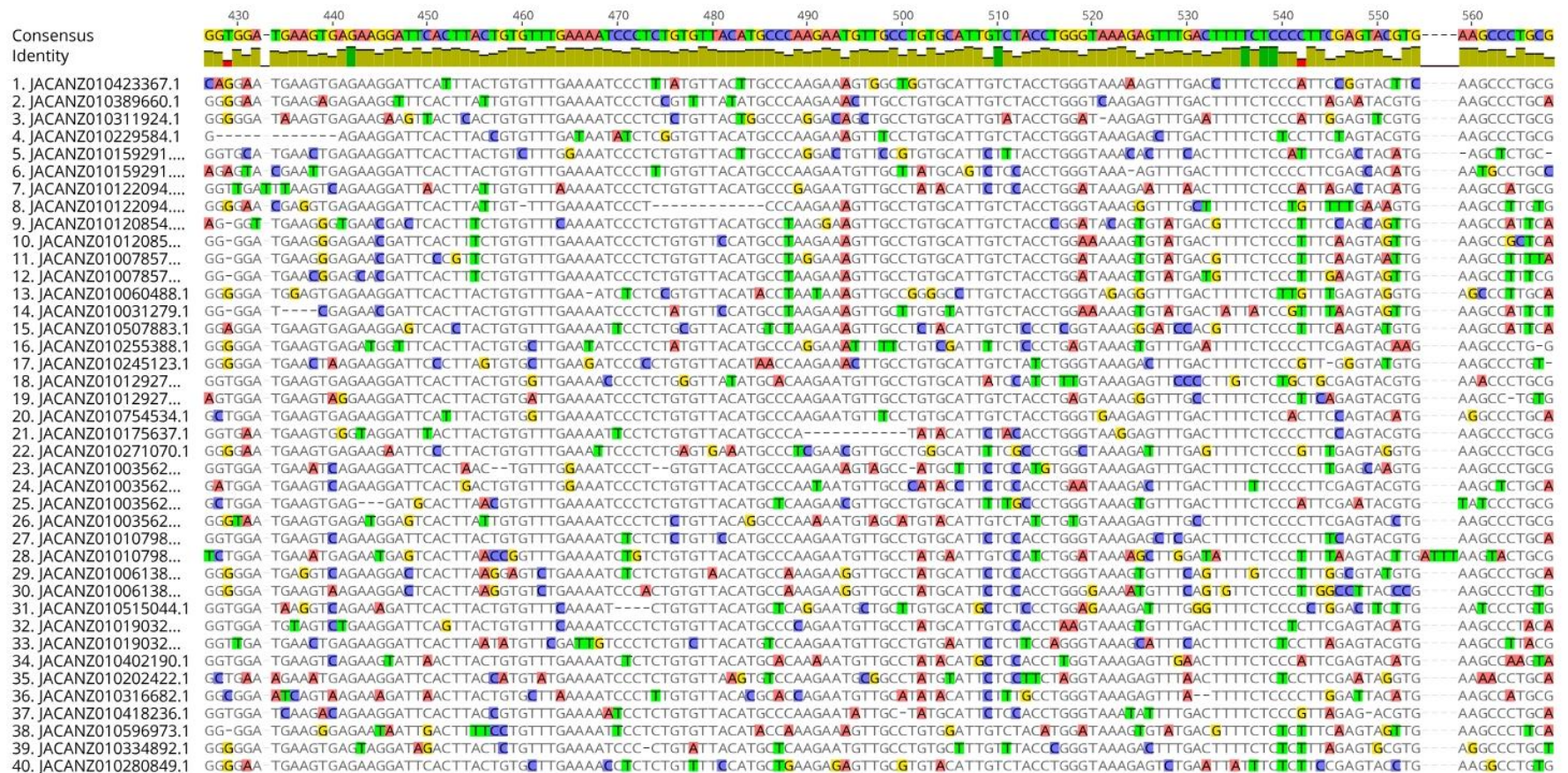
**Supplementary Figure 7.** Alignment of 40 monomers manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1). Part two of six.





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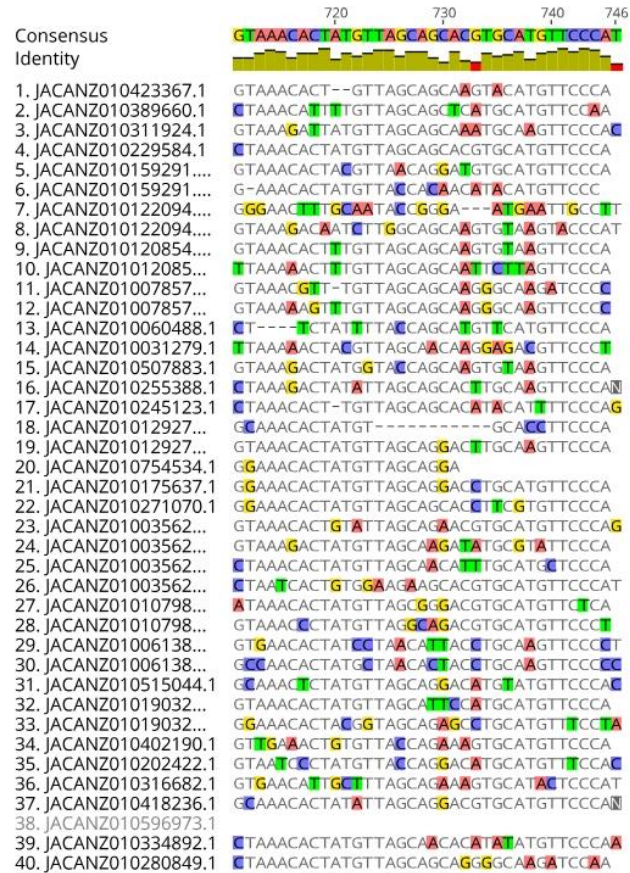
**Supplementary Figure 7.** Alignment of 40 monomers manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1). Part four of six.





**Supplementary Figure 7.** Alignment of 40 monomers manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1). Part five of six.





**Supplementary Figure 7.** Alignment of 40 monomers manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1). Part six of six.



**Supplementary Table 1.** Estimates of average nucleotide divergence (number of base substitutions per site) over all sequence pairs within and between species.

	TMA	TIN	DDU	HGI
TMA	0.32			
TIN	0.285	0.06		
DDU	0.354	0.357	0.37	
HGI	0.342	0.356	0.355	0.33

TMA: *T. manatus*, TIN: *T. inunguis*, DDU: *D. dugon*, HGI: *H. gigas*



**Supplementary Table 2.** Blast searches using the TMAst Most Common Sequence (MCS) from *Trichechus manatus* as query against the GenBank Mammalia (NCBI:txid40674) wgs database excluding Sirenia (NCBI:txid9774).

Species	Description	Coverage (%)	Identity [%]	E-value	Accession number
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.14052, whole genome shotgun sequence	60	68.94	7,00E-10	AAGU03014053.1
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.64816, whole genome shotgun sequence	62	68.29	8,00E-09	AAGU03064817.1
<i>Elephas maximus</i>	isolate Icky scaffold_1324, whole genome shotgun sequence	60	68.51	3,00E-08	JABTCH010005241.1
<i>Elephas maximus</i>	isolate Icky scaffold_65, whole genome shotgun sequence	35	70.22	1,00E-07	JABTCH010002495.1
<i>Elephas maximus</i>	isolate Icky scaffold_751, whole genome shotgun sequence	58	65.02	1,00E-07	JABTCH010005233.1
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.85517, whole genome shotgun sequence	58	65.02	1,00E-07	AAGU03085518.1
<i>Elephas maximus</i>	isolate Icky scaffold_1495, whole genome shotgun sequence	47	68.00	1,00E-06	JABTCH010003728.1
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.56850, whole genome shotgun sequence	47	68.00	1,00E-06	AAGU03056851.1
<i>Procavia capensis</i>	isolate Dallas Zoo Isis #01D731 contig_177334, whole genome shotgun sequence	13	75.53	4,00E-06	ABRQ02177336.1
<i>Heterohyrax brucei</i>	isolate US064 HetBruBak_scaffold_45440, whole genome shotgun sequence	6	89.36	1,00E-05	PVJQ01022728.1
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.91379, whole genome shotgun sequence	26	70.17	5,00E-05	AAGU03091380.1
<i>Elephas maximus</i>	isolate Icky scaffold_624, whole genome shotgun sequence	13	74.19	5,00E-05	JABTCH010004173.1
<i>Loxodonta africana</i>	isolate ISIS603380 cont3.14053, whole genome shotgun sequence	7	84.91	5,00E-05	AAGU03014054.1



**Supplementary Sequence File 1.** TMAst monomeric sequences (in fasta) manually isolated from the *Trichechus manatus* assembled reference genome (accession GCA\_000243295.1).

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>NW004444141.1\_3

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**Supplementary Sequence File 2.** TMAst monomeric sequences (in fasta) manually isolated from the *Dugong dugon* assembled reference genome (accession GCA\_015147995.1).

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**Supplementary Sequence File 3.** TMAst monomeric sequences (in fasta) manually isolated from the *Hydrodamalis gigas* assembled reference genome (accession GCA\_013391785.1).

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