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Supplemental information

Genomes of endangered great hammerhead and shortfin mako sharks reveal historic population declines and high levels of inbreeding in great hammerhead

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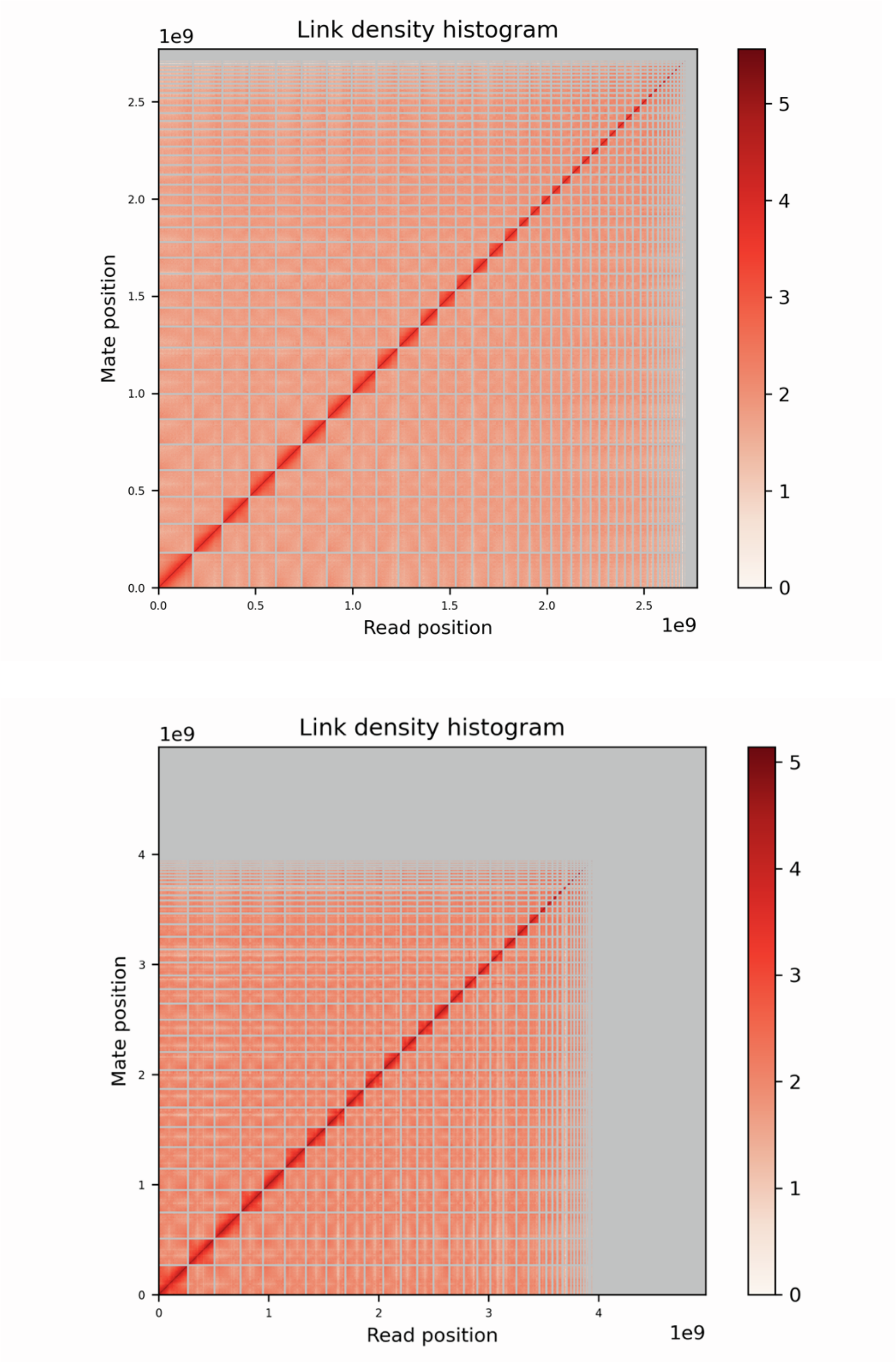

Figure S1. Link Density histogram plots from Dovetail HiRise assemblies for great hammerhead and shortfin mako. These plots depict the contiguity of the genome assemblies for **Top**: great hammerhead (Hi-C scaffolding); **Bottom**: shortfin mako (Omni-C scaffolding). The x and y axes give the mapping positions of the first and second read in the read pair respectively, grouped into bins. The axes are in gigabases of the genome assembly and the color scale is log scale of Hi-C/Omni-C density at each point; contact matrices were generated with Juicebox[1]. The horizontal and vertical lines indicate borders between scaffolds, which are organized along the diagonal from largest to smallest. Scaffolds less than 1Mbp are excluded.

Category	VGP Metric	Hammerhead	Mako
Continuity	Contig (NG50)	44.5Mbp	4.16Mbp
	Scaffolds (NG50)	89.8Mbp	145.5Mbp
	Gaps / Gbp	863	367
Structural accuracy	Reliable blocks	2.67 Gbp	3.40 Gbp
	False duplications	2.5%	3.8%
Base accuracy	Base pair QV	38.97	infinity
	k-mer completeness	96.4%	100%
Haplotype phasing	Phase block NG50	null	null
Functional completeness	Genes (BUSCO complete)	94.2%	90.6%
	Transcript mappability	92.84%	97.07%
Chromosome status	Assigned %	98%	81%
	sex chromosomes	null	null
	organelles (MT)	1 complete allele[2]	1 complete allele[3]

Table S1. Great hammerhead and shortfin mako genome assembly metrics. Metrics for great hammerhead and shortfin mako that meet or exceed the quality category “VGP-2016”, established by the Vertebrate Genome Project (VGP), as a minimum for chromosomal assembly[4], are indicated in red. These various metrics were calculated using the VGP working group’s genome assembly evaluation pipeline (https://github.com/VGP/vgp-assembly/tree/master/pipeline. The mitochondrial alleles come from earlier studies of ours; in the case of hammerhead[2] from a different individual than this genome sequence; in the case of mako[3] from this same individual.

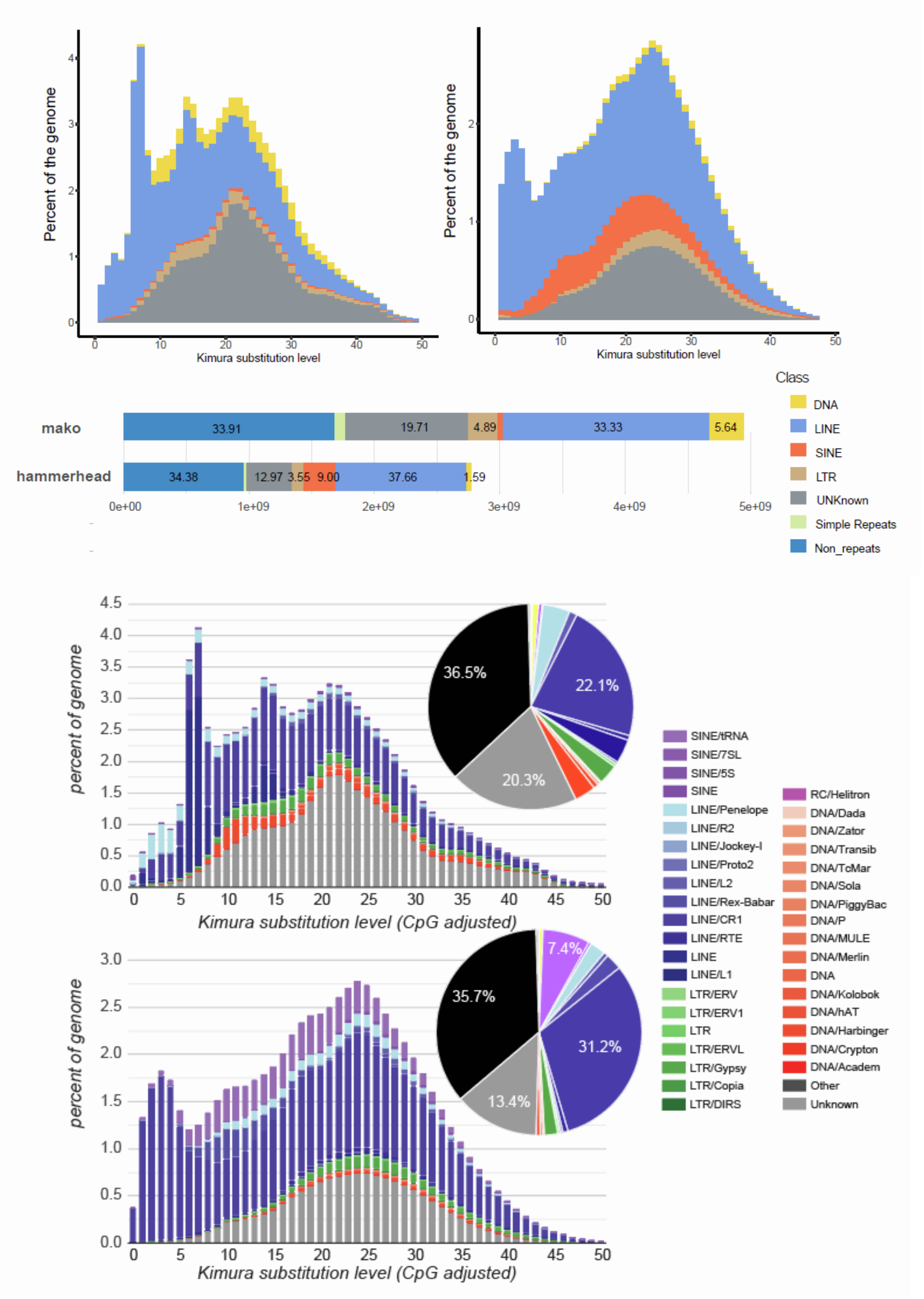

Figure S2. **Composition of repetitive elements in the shortfin mako and great hammerhead genomes. Top:** The overall landscape of major classes of transposable elements: shortfin mako on the left, great hammerhead on the right. **Middle**: The overall composition of repetitive elements for the entire genome for both species. The length of each box is proportional to their representation in the genome, and the number on the box indicates the percentage of each type of element in the genome. **Bottom**: More specific breakdown of repetitive elements from both genomes; shortfin mako on the top, great hammerhead on the bottom. The relative ages of different transposable elements can be inferred by the Kimura distance to their consensus sequences.

Species	Data type	Accession
Carcharodon carcharias	Genome assembly	GCA_003604245.1
	Genome sequence reads	SRR7693855, SRR7693869 SRR7693858
Chiloscyllium punctatum	Genome assembly	GCA_003427335.1
	Genome sequence reads	DRR111842, DRR111844
Scyliorhinus torazame	Genome assembly	GCA_003427355.1
	Genome sequence reads	DRR111851, DRR111854 DRR111848
Rhincodon typus (Ralph)	Genome assembly	GCA_001642345.3
	Genome sequence reads	SRR1521192, SRR1521195 SRR1521198
Rhincodon typus (KOGIC-WS-01)	Genome assembly	GCA_013626285.1
	Genome sequence reads	SRR7614630, SRR7614623 SRR7614624

Table S2. Genome data accession numbers for published sequences used for heterozygosity and PSMC analyses.

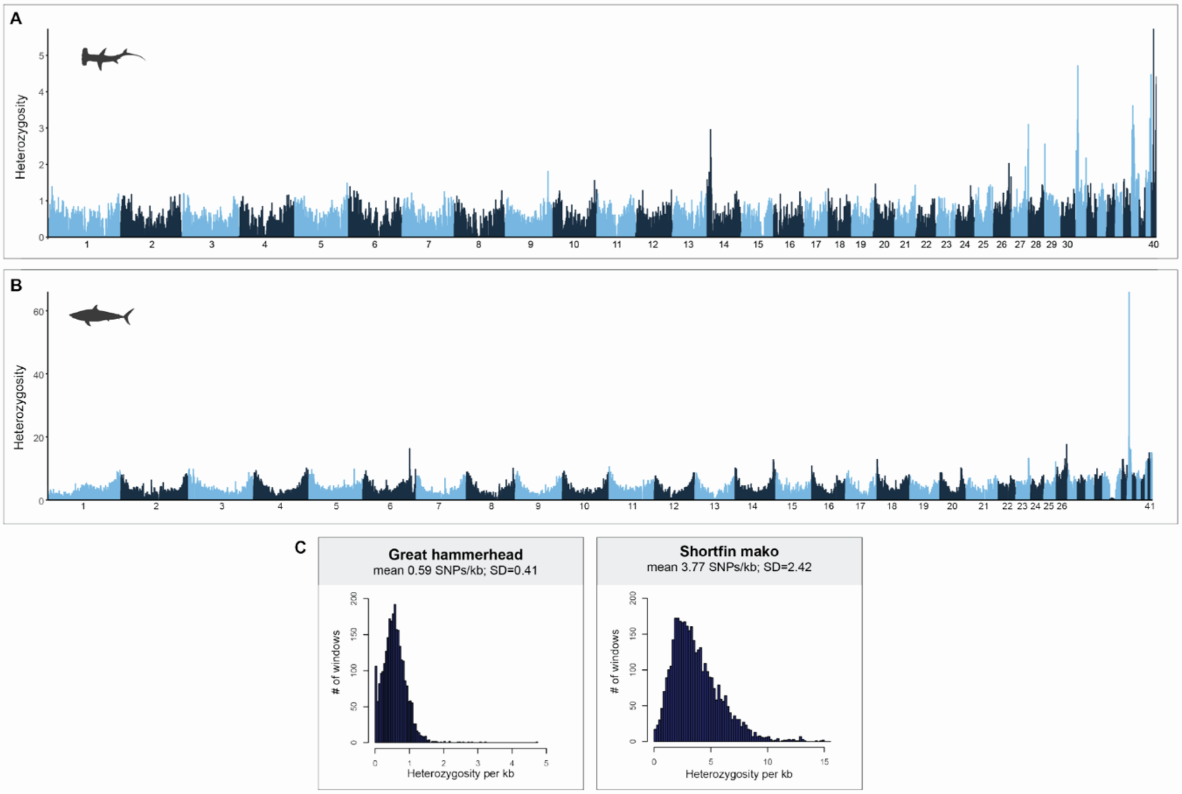

Figure S3. Genome wide heterozygosity calculated in nonoverlapping 1Mbp windows for great hammerhead and shortfin mako genomes. A. the 40 pseudo-chromosomes of the great hammerhead genome; B. the 41 pseudo-chromosomes of the shortfin mako genome; note differences in Y axis scale between the two sharks. C. Histograms for the per window heterozygosity for each of these species.

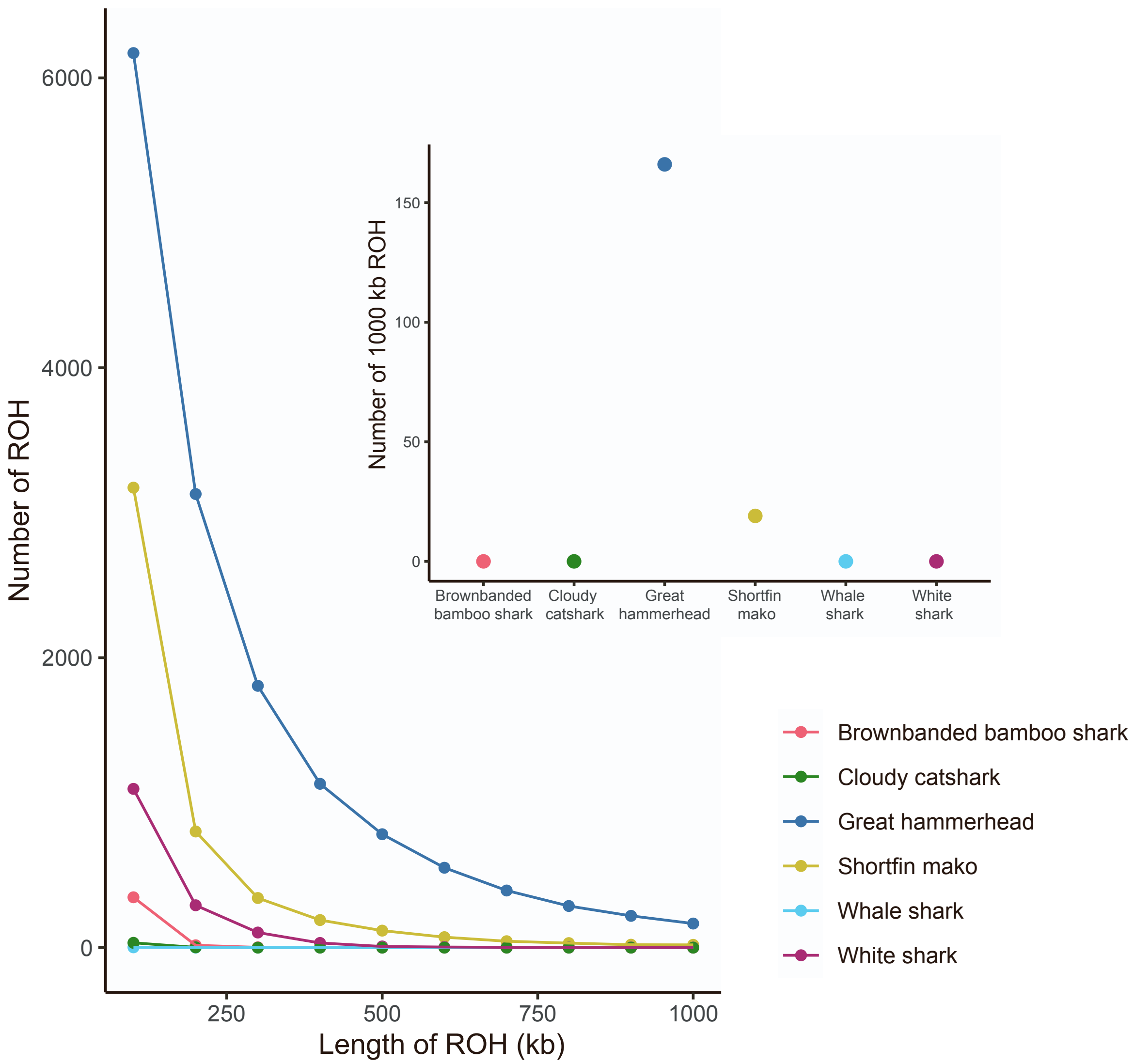

Figure S4. Comparative numbers of ROH of varying lengths between different species of sharks for the largest 24 scaffolds of each species. The whale shark here is KOGIC-WS-01[5], chosen because of its higher scaffold N50 statistic versus the other whale shark[6].

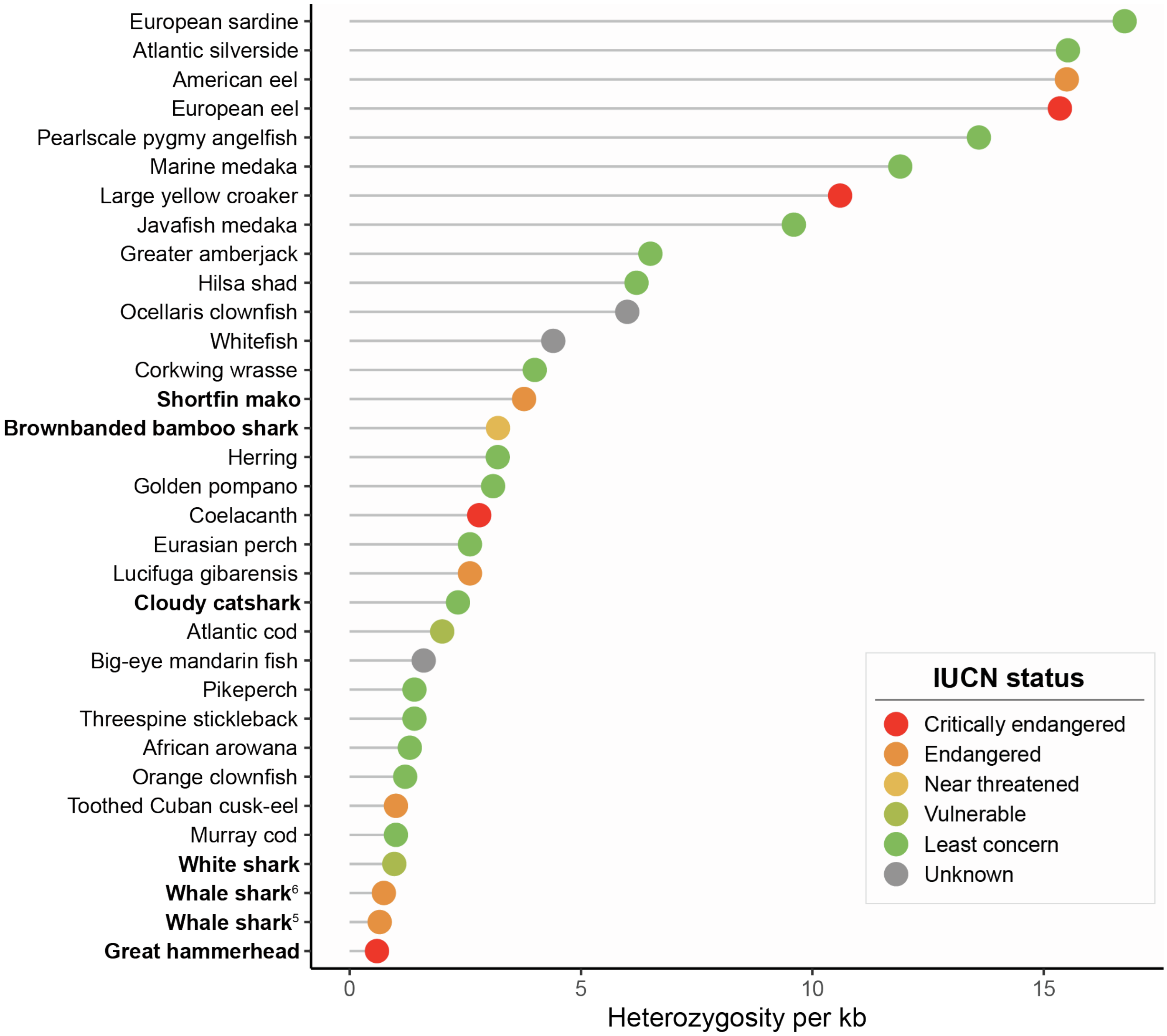

Figure S5. Genome wide heterozygosity of shark species compared to other species of fish. Estimates for white shark, brownbanded bamboo shark, whale shark, and cloudy catshark come from the largest 24 scaffolds of those published genomes (Table S2) and for great hammerhead and shortfin mako are derived from the 40 and 41 pseudo-chromosomes for each of those species. Data for the remaining fish species come from[7].

Supplementary References

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