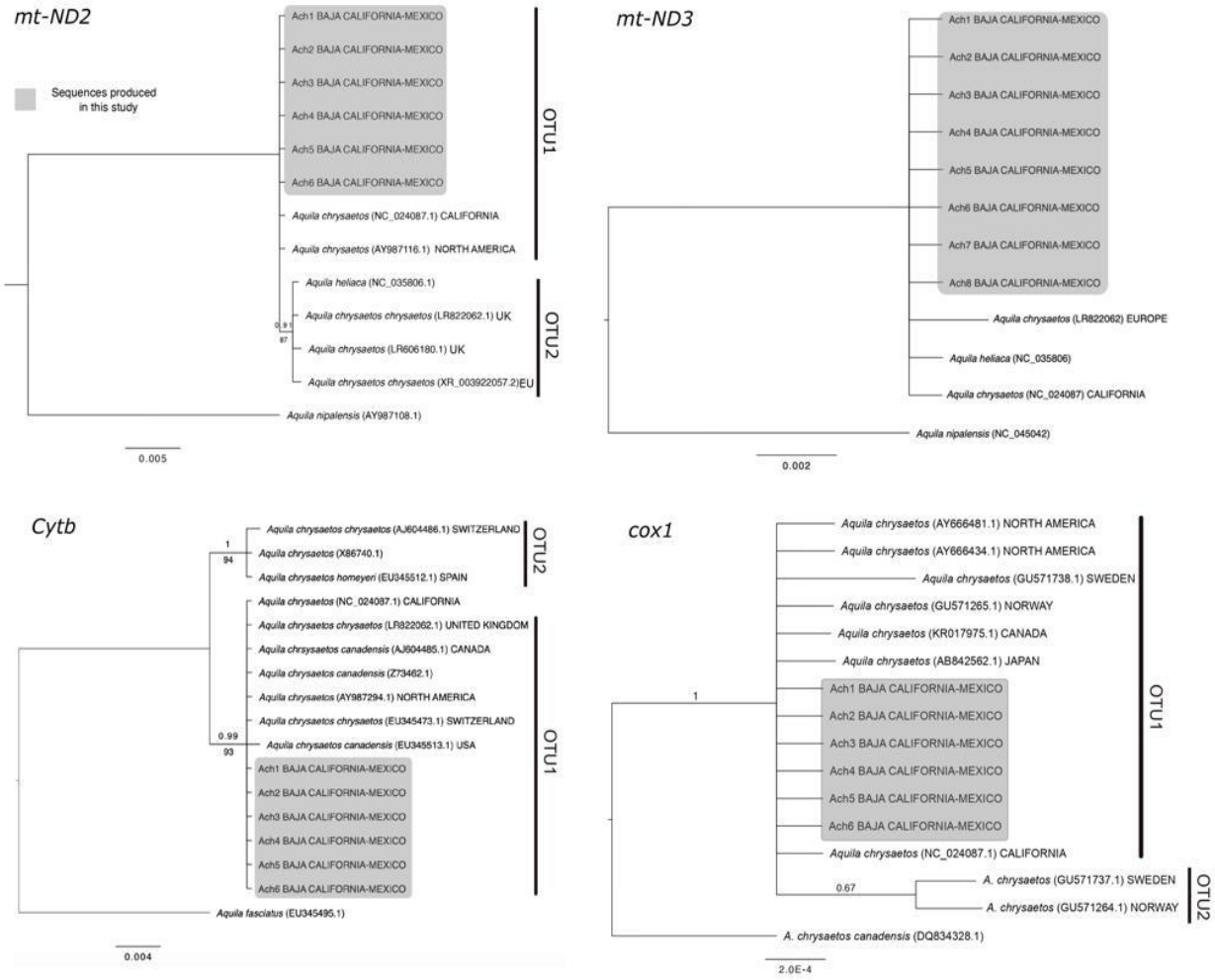
Supplementary material

Supplementary F1. Bayesian phylogenetic trees from individual gene fragments. Maximum likelihood bootstraps are shown above internal nodes, while the posterior probabilities from the Bayesian analysis are shown below internal nodes. Sequences from the northwestern Baja California individuals are highlighted under the grey boxes. Sequences used as reference are found in supplementary table 5.



Supplementary T1. Collection data of Golden Eagle voucher specimens from northwestern Baja California, México used in this study. The identification code, catalog number, and type of tissue used for DNA extraction is provided. N-a = Not available.

Specimen ID	UABC catalog number	Locality	Date of collection	Type or tissue used	Geographical coordinates
Ach 1	UABC-820	Rosarito	15/Oct/1995	Foot pad	32°22'14.2" N 117°02'52.8" W
Ach 2	UABC-092	Rosarito	01/Mar/1996	Foot pad	32°20'32" N 117°03'22" W
Ach 3	UABC-1989	Ojos Negros	18/Sep/2013	Foot pad	31°51'37.7" N 116°16'16.3" W
Ach 4	UABC-1783	San Quintín	29/Apr/2007	Foot pad	30°28'54.8" N 115°58'53.4" W
GOEA 5	UABC-2101	Ojos Negros	20/Jan/2014	Foot pad	31°51'40.4" N 116°16'17.0" W
Ach 6	Not catalogued	La Bellota	N-a	Blood/ feathers	32°09'27.46" N 116°27'42.68" W

Supplementary T2. A. Number of raw and processed sequences by means of quality control and reads aligned with the reference genome (*A. chrysaetos*, GenBank accession number of KF905228). B. Basic statistics of the *de novo* assembly of the *A. chrysaetos* mitogenome, nd = not available.

A)

Specimen ID	Total readings	Raw reads	Reads after filter	Discarded sequences	Alignment rate	Aligned readings	Average coverage
Ach 1	5,952,996	3,324,579	3,251,746	72,833 (2.19%)	0.04 %	2,661	30.5
Ach 2	1,240,200	738,931	718,629	20,302 (2.75%)	0.08 %	938	11.6
Ach 3	2,325,548	1,364,493	1,335,053	29,440 (2.16%)	0.04 %	873	11.9
Ach 4	924,052	539,825	526,875	12,950 (2.40%)	0.15 %	1,350	18.0
Ach 5	1,169,902	695,574	681,055	14,519 (2.09%)	0.09 %	1,083	14.6
Ach 6	4,557,654	2,714,901	2,656,332	58,569 (2.16%)	0.52 %	23,931	168.3

B)

Specimen ID	Average coverage	Scaffolds	Length of the largest scaffold	N50	% GC
Ach 1	2.0	2,600,450	10,270	198	nd
Ach 2	2.0	4,645	9,927	711	41.4
Ach 3	5.0	2,948	12,235	756	51.5
Ach 4	2.0	1,805	16,761	713	42.8
Ach 5	3.0	1,938	19,231	729	46.6
Ach 6	8.0	2,532	17,472	572	47.1

Supplementary T3. Reference sequences used for phylogenetic analyses. NR: Geographic locality of sample is not reported.

Gene	Species	GenBank accesion code	Geographic origin
	A. chrysaetos	NC_024087.1	California (North America)
	A. chrysaetos	AY987116.1	North America
	A. heliaca	NC_035806.1	NR
	A. chrysaetos chrysaetos	LR822062.1	United Kingdom (Europe)

ND2	*A. chrysaetos*	LR606180.1	United Kingdom (Europe)
	A. chrysaetos chrysaetos	XR_003922057.2	Europe
	A. nipalensis	AY987108.1	NR
ND3	*A. chrysaetos*	LR822062.1	United Kingdom (Europe)
	A. heliaca	NC_035806.1	NR
	A. chrysaetos	NC_024087.1	California (North America)
	A. nipalensis	NC_045042.1	China (Asia)
Cytb	*A. chrysaetos chrysaetos*	AJ604486.1	Switzerland (Europe)
	A. chrysaetos	X86740.1	Switzerland (Europe)
	A. chrysaetos homeyeri	EU345512.1	Spain (Europe)
	A. chrysaetos	NC_024087.1	California (North America)
	A. chrysaetos chrysaetos	LR822062.1	United Kingdom (Europe)
	A. chrysaetos candensis	AJ604485.1	Canada (North America)
	A. chrysaetos canadensis	Z73462.1	NR
	A. chrysaetos	AY987294.1	North America
	A. chrysaetos chrysaetos	EU345473.1	Switzerland (Europe)
	A. chrysaetos canadensis	EU345513.1	USA (North America)
coxI	*A. chrysaetos*	AY666481.1	Ontario, Canada (North America)
	A. chrysaetos	AY666434.1	British Columbia, Canada (North America)
	A. chrysaetos	GU571738.1	Sweden (Europe)
	A. chrysaetos	GU571265.1	Norway (Europe)
	A. chrysaetos	KR017975.1	Quebec, Canada (North America)
	A. chrysaetos	AB842562.1	Japan (Asia)
	A. chrysaetos	NC_024087.1	California (North America)
	A. chrysaetos	GU571737.1	Sweden (Europe)
	A. chrysaetos	GU571264.1	Norway (Europe)

Supplementary T4. Mitogenome annotation made by MITOS webserver. (+) DNA heavy chain. (-). Length is described in number of base pairs. The DNA substitution model that was used for every mitochondrial annotated region is shown in the "Model" column.

Gen	Start	Finish	Chain	Length	ARNt codon	Model
tRNA-Phe	1	69	+	69	ttc	TPM3+I
12S rRNA	70	1,041	+	972		TrN
tRNA-Val	1,042	1,113	+	72	gta	JC
16S rRNA	1,114	2,709	+	1,596		TIM1
tRNA-Leu	2,701	2,775	+	75	tta	K80
mt-ND1	2,784	3,761	+	978		TIM3
tRNA-Ile	3,760	3,831	+	72	atc	K80
tRNA-Gln	3,844	3,915	-	72	caa	HKY
tRNA-Met	3,915	3,983	+	69	atg	JC
mt-ND2	3,984	5,024	+	1,041		HKY
tRNA-Trp	5,023	5,094	+	72	tga	F81
tRNA-Ala	5,096	5,164	-	69	gca	K80
tRNA-Asn	5,168	5,239	-	72	aac	K80
tRNA-Cys	5,243	5,308	-	66	tgc	TrNef
tRNA-Tyr	5,309	5,380	-	72	tac	HKY
cox1	5,380	6,930	+	1,551		TPM3uf
tRNA-Ser	6,922	6,996	-	75	tca	TrN
tRNA-Asp	7,001	7,069	+	69	gac	HKY
cox2	7,072	7,755	+	684		HKY
tRNA-Lys	7,756	7,827	+	72	aaa	K80+I
ATP 8	7,829	7,996	+	168		HKY
ATP 6	7,987	8,670	+	684		TIM3+I
mt-CO3	8,670	9,452	+	783		TrN
tRNA-Gly	9,454	9,522	+	69	gga	TrN
mt-ND3a	9,523	9,729	+	207		TrN
mt-ND3b	9,731	9,874	+	144		F81
t-RNA-Arg	9,882	9,950	+	69	cga	HKY
mt-NDL4	9,952	10,248	+	297		TrN
mt-ND4	10,242	11,648	+	1,407		HKY
tRNA-His	11,620	11,689	+	70	cac	HKY
tRNA-Ser	11,690	11,755	+	66	agc	TrN
tRNA-Leu	11,756	11,826	+	71	cta	K80
mt-ND5	11,827	13,644	+	1,818		GTR
Cytb	13,656	14,798	+	1,143		TrN+G
tRNA-Thr	14,803	14,872	+	70	aca	HKY
tRNA-Pro	16,031	16,101	-	71	cca	F81
mt-ND6	16,114	16,632	-	519		TPM2uf
tRNA-Glu	16,636	16,707	-	72	gaa	HKY
D-loop	14,873	16,030	+	1,158		TrN+I
Pseudo-Control Region	16,708	17,472	+	765		TrN

Supplementary T5. Synteny of genes with respect to reference mitogenome. The *Aquila chrysaetos* mitogenome from an individual captured in Southern Sierra Nevada, California, USA (GenBank accession KF905228.1). (+) Indicates sense strand is located on heavy chain, while (-) indicates sense strand is located on light chain.

Genome	**Order of genes**
KF905228	*+Cytb +tRNA-Thr -tRNA-Pro -ND6 -tRNA-Glu +tRNA-Phe +12S rRNA +tRNA-Val +LSU rRNA 16S +tRNA-Leu +ND1 +tRNA-Ile -tRNA-Gln +tRNA-Met +ND2 +tRNA-Trp -tRNA-Ala – tRNA-Asn -tRNA-Cys -tRNA-Tyr +coxI -tRNA-Ser +tRNA-Asp +coxII +tRNA-Lys +ATP8 +ATP6 +coxIII +tRNA-Gly +ND3 +tRNA-Arg +ND4L +ND4 +tRNA-His +tRNA-Ser +tRNA-Leu +ND5*
Ach 6	*+tRNA-Phe +12S rRNA +tRNA-Val +LSU rRNA 16S +tRNA-Leu +ND1 +tRNA-Ile -tRNA-Gln +tRNA-Met +ND2 +tRNA-Trp -tRNA-Ala -tRNA-Asn -tRNA-Cys -tRNA-Tyr +coxI -tRNA- Ser +tRNA-Asp +coxII +tRNA-Lys +ATP8 +ATP6 +coxIII +tRNA-Gly +ND3a +ND3b +tRNA-Arg +ND4L +ND4 +tRNA-His +tRNA-Ser +tRNA-Leu +ND5 +Cytb +tRNA-Thr -tRNA-Pro -ND6 -tRNA-Glu*

Supplementary T6. Uncorrected p-distances between the distinct phylogenetic groups found within *A. chrysaetos* species complex. "- "genetic distance could not be estimated since clade in tree was composed of a single individual. Sequences included in each taxonomic group are specified in figure 3 and supplementary figure 1.

	Cyt B	***COXI***	***ND2***	**Mitogenome**
OTU1	0.00015	0.00052	0	0.0005
OTU2	0.00069	0	0	-
OTU1 vs OTU2	0.00864	0.00259	0.00137	0.00244