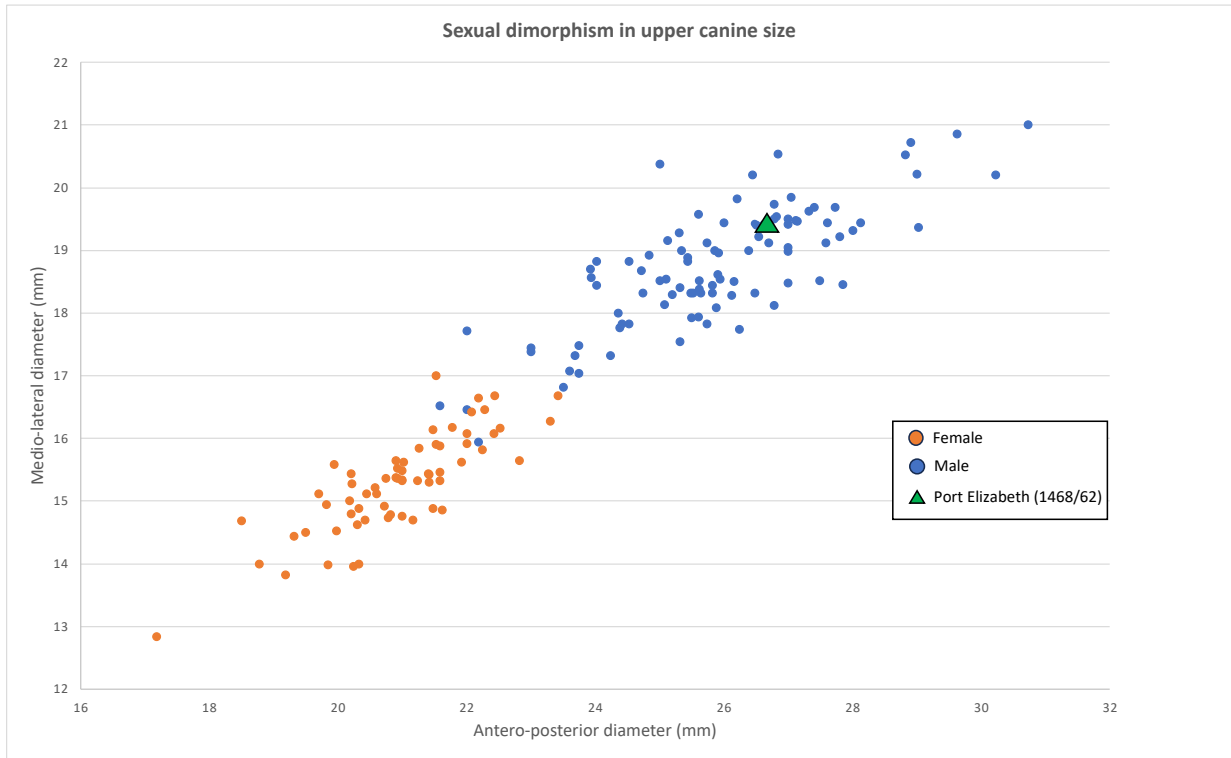


## Supplementary Information

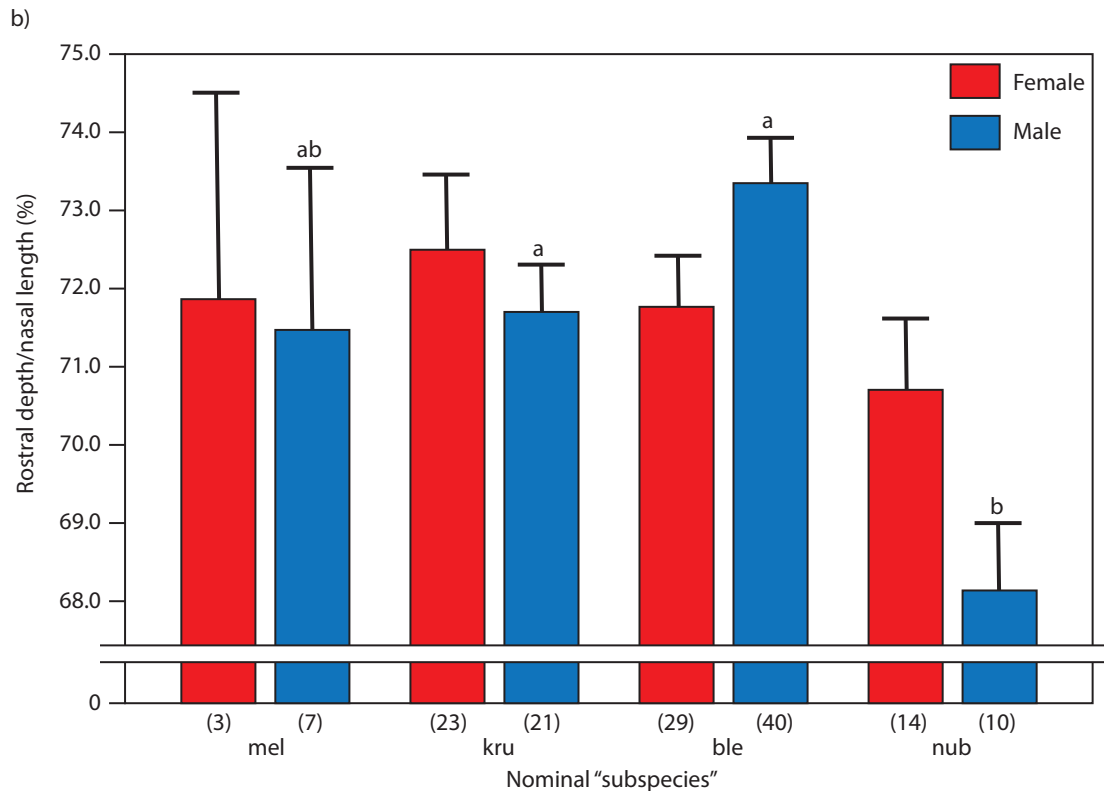
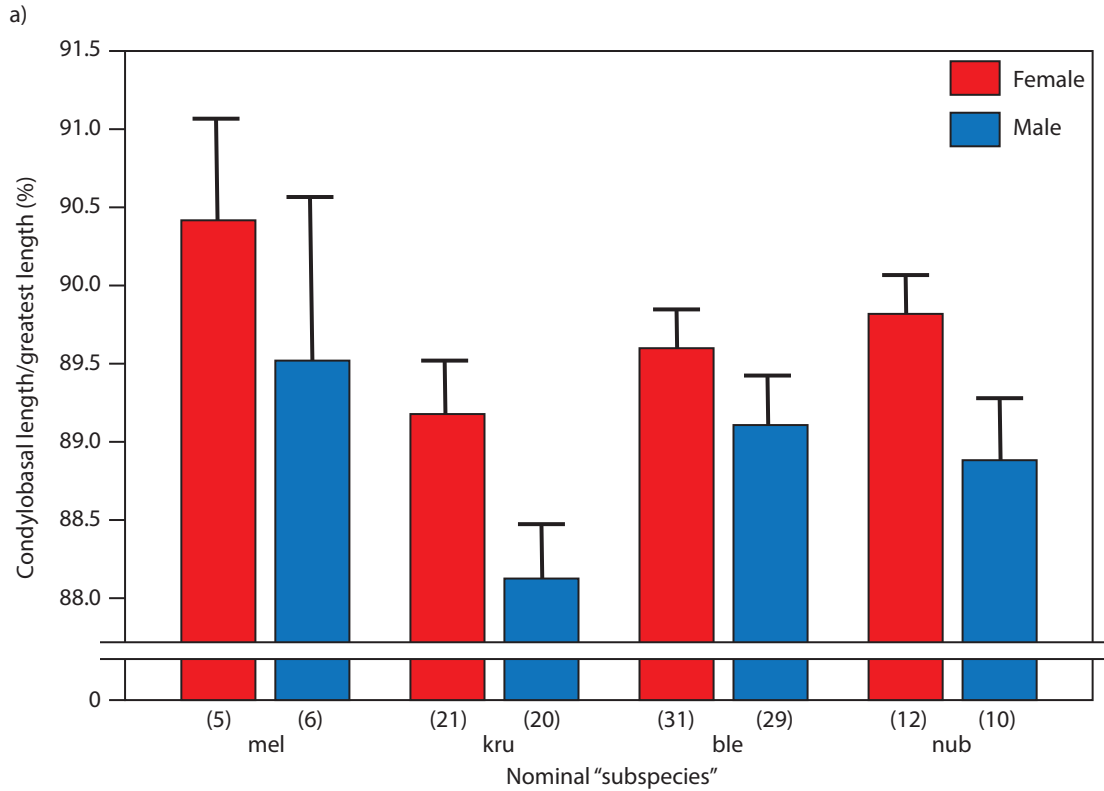
### Figure S1

Scatter plots showing the sexual size dimorphism of upper canine size in the wild lions of the southern African origins ( $n = 160$ ). The Port Elizabeth specimen of the “Cape” lion (1468/62) is very likely a male.



**Figure S2**

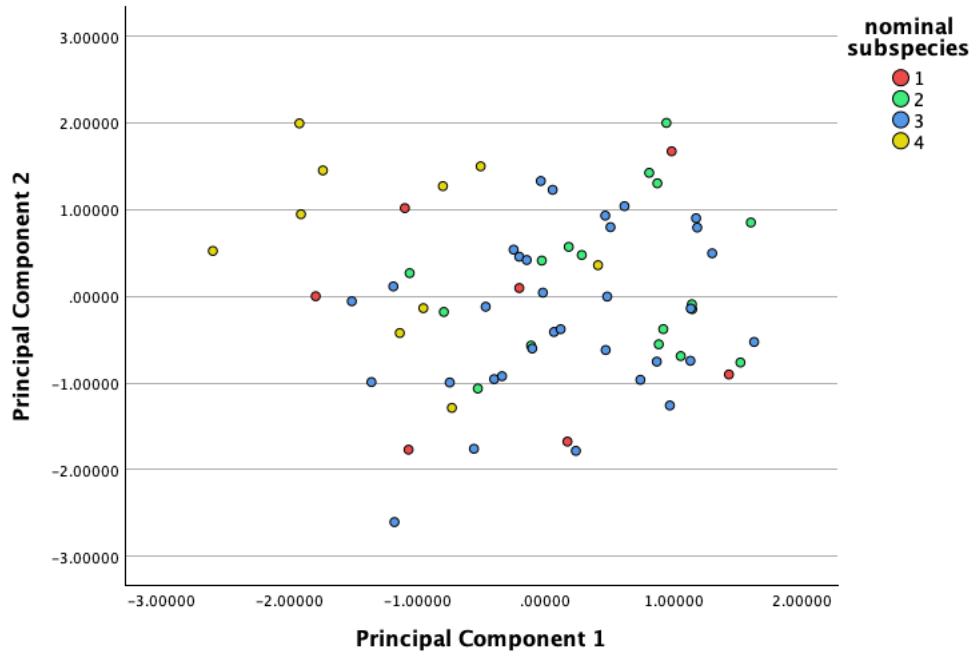
a) The ratio of the condylobasal length to the greatest length of the skull ( $Mean \pm Standard\ error$ ) of wild adult Southern African lions. b) The ratio of the rostral depth to the nasal length ( $Mean \pm Standard\ error$ ) of wild adult Southern African lion described in Mazak (1975)<sup>20</sup>. The different letters indicate statistically significant difference at the level of  $p < 0.05$ . The nominal “subspecies” are *Panthera leo melanochaita* (mel), *P.l. krugeri* (kru), *P.l. bleyenberghi* (ble), and *P.l. nubica* (nub).



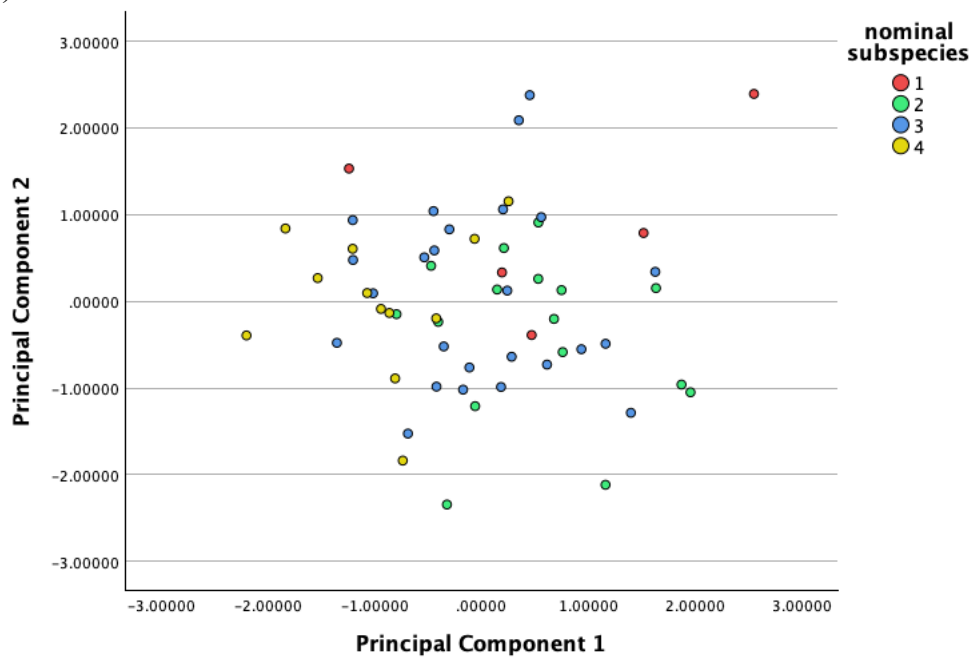
**Figure S3.**

Principal Component Analyses only for southern African lions: a) males based on 30 raw variables, and b) females based on 31 raw variables. Nominal “subspecies” were *Panthera leo melanochaita* (1), *P.l. krugeri* (2), *P.l. bleyenberghi* (3), and *P.l. nubica* (4).

a)



b)



**Table S1.** Comparison of key statistical values in Discriminant Function Analysis (DFA) amongst different sets of variables. The maximum sample size of the “Cape” lion is 12 (7 males and 5 females). The “Original” indicates the % that the DFA classified group members correctly whilst “Cross-validation” is the % correctness by the cross-validation test. All analyses were carried out using the SPSS29. Values are highlighted in darker shade, lighter shade, and no shade, where no shade is the most appropriate statistically whilst darker shade is the least appropriate. The model # in bold (models – 3b, 3c, 4c & 4d) indicate those that are used in the main text.

Model	# of variables	Smallest group size	Enter method	<i>P</i> for Box’s <i>M</i>	Original	Cross-validation	*Ratio
1a	19 (raw data)	12	together	<0.001	75.1	61.5	122.11
1b	19 (raw data)	12	stepwise	0.007	61.2	57.3	106.81
1c	19 (ln transformed)	12	together	<0.001	75.7	62.7	120.73
1d	19 (ln transformed)	12	stepwise	0.013	59.1	54.3	108.84
2a	2 (PCs)	12	together	0.048	53.3	52.7	101.14
2b	5 (PCs)	12	together	0.189	58.6	53.8	108.92
2c	5 (PCs)	12	together	0.152	50.0	42.0	119.05
2d	3 (PCs)	8	together	0.368	56.5	51.9	108.86
3a	30 (raw data)	7	together	Inappropriate to perform	93.0	60.5	153.72
<b>3b</b>	5 (PCs)	7	together	0.259	72.1	64.0	112.66
<b>3c</b>	6 (PCs)	7	together	0.596	67.2	58.2	115.46
4a	31 (raw data)	5	together	Inappropriate to perform	94.3	61.4	153.58
4b	6 (PCs)	5	together	<0.001	70.0	58.6	119.45
<b>4c</b>	4 (PCs)	5	together	0.120	61.4	48.6	126.34
<b>4d</b>	4 (PCs)	5	together	0.209	60.3	46.6	129.40

\*Ratio = (Original/Cross-validation) x 100

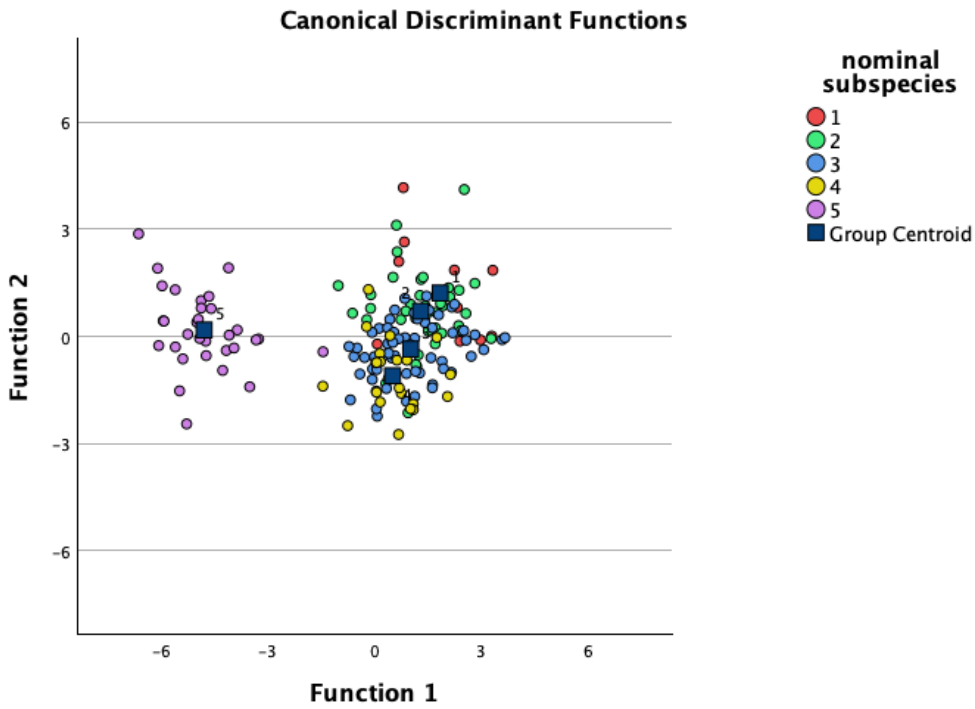
Note: Discriminant Function Analysis (DFA) is quite sensitive to the ratio of sample size to the number of predictor variables, and, at a minimum, the smallest group size must exceed the number of predictor variables<sup>49</sup>. The Box’s *M* tests if the variance/covariance matrices are equal across two or more groups, which is one of the assumptions – a statistically significant value suggests that the assumption is violated<sup>48</sup>. Also, the greater is the difference in the classification results between the original data set and cross-validation the lesser is the reliability of the model (e.g. over-fit to the original set of variables).

**Figures S4 – S18**

Discriminant Function Analyses corresponding to the models presented in Table S1. Each figure consists of scatter plots and classification results. Nominal “subspecies” were *Panthera leo melanochaita* (1), *P.l. krugeri* (2), *P.l. bleyenberghi* (3), *P.l. nubica* (4), and *P.l. persica* (5).

**Figure S4**

Scatter plots and classification results of Discriminant Function Analysis for the Model-1a in Table S1.



		Classification Results <sup>a,c</sup>						
nominal subspecies			Predicted Group Membership					Total
			1	2	3	4	5	
Original	Count	1	4	4	4	0	0	12
		2	0	24	12	3	0	39
		3	0	6	52	6	0	64
		4	0	1	5	17	0	23
		5	0	0	0	1	30	31
	%	1	33.3	33.3	33.3	0.0	0.0	100.0
		2	0.0	61.5	30.8	7.7	0.0	100.0
		3	0.0	9.4	81.3	9.4	0.0	100.0
		4	0.0	4.3	21.7	73.9	0.0	100.0
		5	0.0	0.0	0.0	3.2	96.8	100.0
Cross-validated <sup>b</sup>	Count	1	4	3	3	2	0	12
		2	1	20	15	3	0	39
		3	3	10	40	11	0	64
		4	0	2	10	11	0	23
		5	0	0	0	2	29	31
	%	1	33.3	25.0	25.0	16.7	0.0	100.0
		2	2.6	51.3	38.5	7.7	0.0	100.0
		3	4.7	15.6	62.5	17.2	0.0	100.0
		4	0.0	8.7	43.5	47.8	0.0	100.0
		5	0.0	0.0	0.0	6.5	93.5	100.0

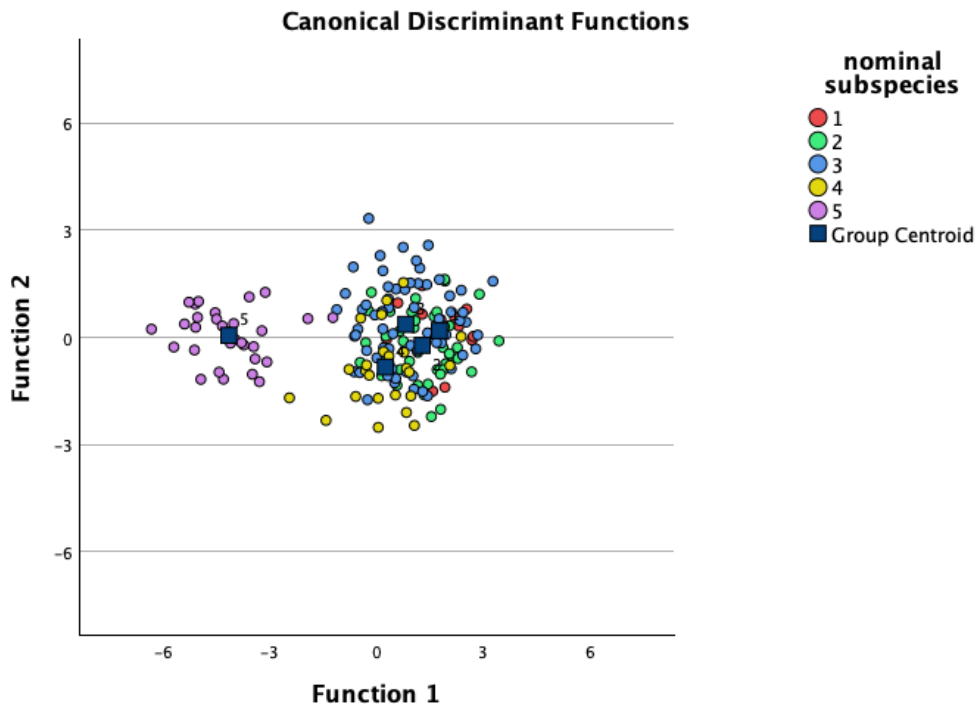
a. 75.1% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 61.5% of cross-validated grouped cases correctly classified.

**Figure S5**

Scatter plots and classification results of Discriminant Function Analysis for the Model-1b in Table S1.



nominal subspecies		Predicted Group Membership					Total	
		1	2	3	4	5		
Original	Count	1	0	6	6	0	0	12
		2	0	20	21	3	0	44
		3	1	9	50	7	0	67
		4	0	3	11	9	1	24
		5	0	0	1	0	30	31
	%	1	0.0	50.0	50.0	0.0	0.0	100.0
		2	0.0	45.5	47.7	6.8	0.0	100.0
		3	1.5	13.4	74.6	10.4	0.0	100.0
		4	0.0	12.5	45.8	37.5	4.2	100.0
		5	0.0	0.0	3.2	0.0	96.8	100.0
Cross-validated <sup>b</sup>	Count	1	0	6	6	0	0	12
		2	1	17	23	3	0	44
		3	1	11	47	8	0	67
		4	0	3	11	9	1	24
		5	0	0	2	0	29	31
	%	1	0.0	50.0	50.0	0.0	0.0	100.0
		2	2.3	38.6	52.3	6.8	0.0	100.0
		3	1.5	16.4	70.1	11.9	0.0	100.0
		4	0.0	12.5	45.8	37.5	4.2	100.0
		5	0.0	0.0	6.5	0.0	93.5	100.0

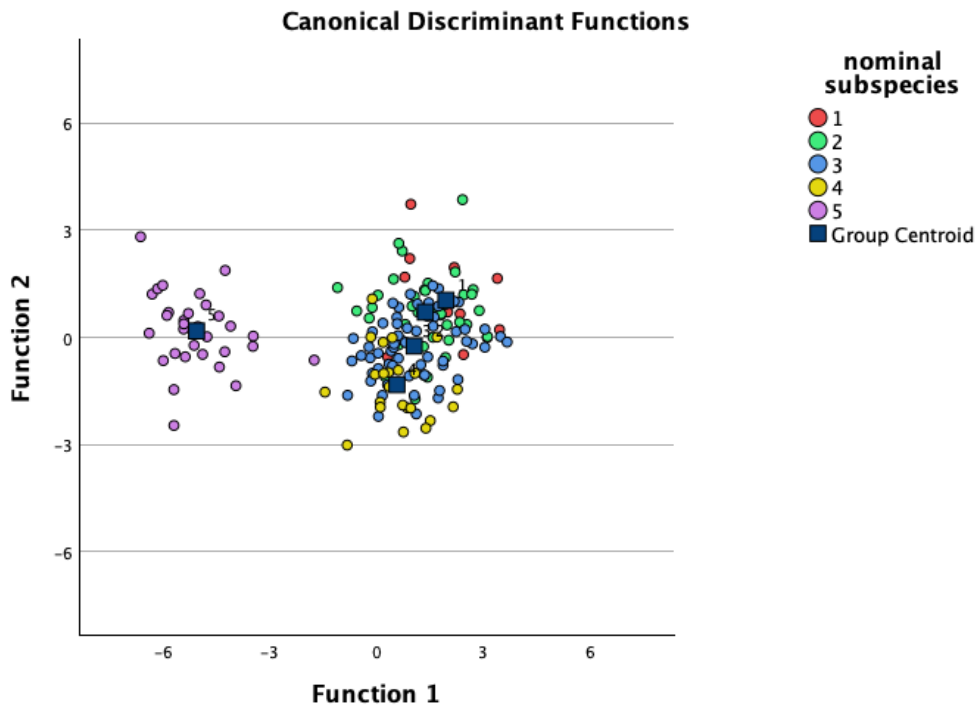
a. 61.2% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 57.3% of cross-validated grouped cases correctly classified.

**Figure S6**

Scatter plots and classification results of Discriminant Function Analysis for the Model-1c in Table S1.



		Predicted Group Membership					Total	
nominal subspecies		1	2	3	4	5		
Original	Count	1	5	4	3	0	0	12
		2	0	23	13	3	0	39
		3	0	6	51	7	0	64
		4	0	1	3	19	0	23
		5	0	0	0	1	30	31
	%	1	41.7	33.3	25.0	0.0	0.0	100.0
		2	0.0	59.0	33.3	7.7	0.0	100.0
		3	0.0	9.4	79.7	10.9	0.0	100.0
		4	0.0	4.3	13.0	82.6	0.0	100.0
		5	0.0	0.0	0.0	3.2	96.8	100.0
Cross-validated <sup>b</sup>	Count	1	3	4	3	2	0	12
		2	1	20	15	3	0	39
		3	2	11	41	10	0	64
		4	0	2	9	12	0	23
		5	0	0	0	1	30	31
	%	1	25.0	33.3	25.0	16.7	0.0	100.0
		2	2.6	51.3	38.5	7.7	0.0	100.0
		3	3.1	17.2	64.1	15.6	0.0	100.0
		4	0.0	8.7	39.1	52.2	0.0	100.0
		5	0.0	0.0	0.0	3.2	96.8	100.0

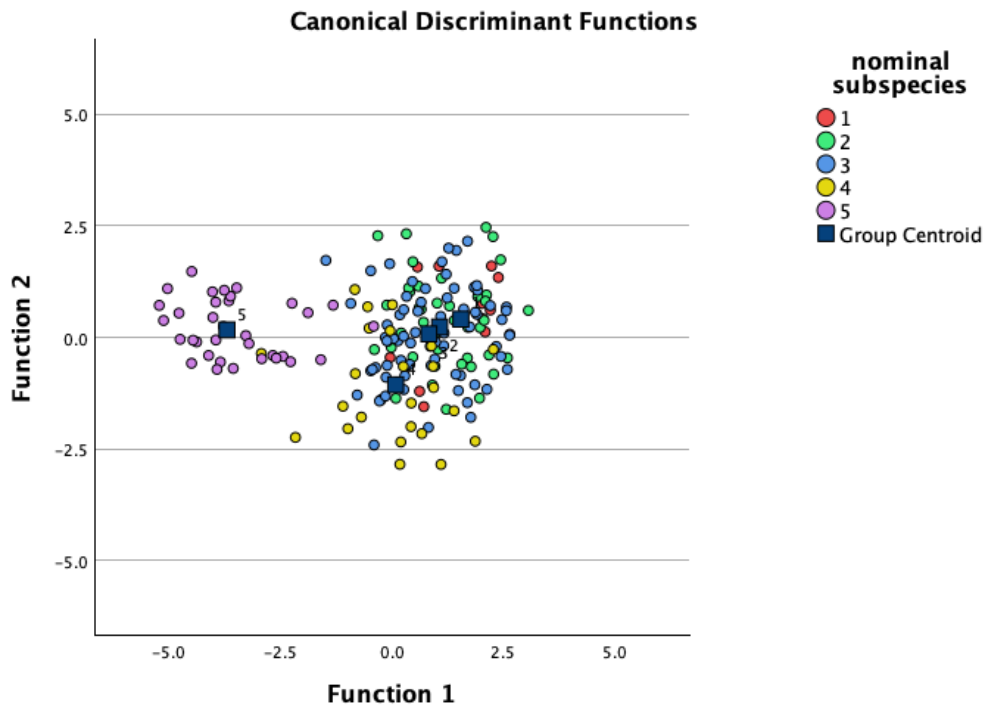
a. 75.7% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 62.7% of cross-validated grouped cases correctly classified.

**Figure S7**

Scatter plots and classification results of Discriminant Function Analysis for the Model-1d in Table S1.



		Predicted Group Membership					Total	
nominal subspecies		1	2	3	4	5		
Original	Count	1	0	3	9	0	0	12
		2	0	14	30	1	0	45
		3	0	9	54	8	0	71
		4	0	1	11	11	1	24
		5	0	0	2	1	31	34
	%	1	0.0	25.0	75.0	0.0	0.0	100.0
		2	0.0	31.1	66.7	2.2	0.0	100.0
		3	0.0	12.7	76.1	11.3	0.0	100.0
		4	0.0	4.2	45.8	45.8	4.2	100.0
		5	0.0	0.0	5.9	2.9	91.2	100.0
Cross-validated <sup>b</sup>	Count	1	0	3	9	0	0	12
		2	1	8	35	1	0	45
		3	0	10	52	8	1	71
		4	0	1	11	10	2	24
		5	0	0	2	1	31	34
	%	1	0.0	25.0	75.0	0.0	0.0	100.0
		2	2.2	17.8	77.8	2.2	0.0	100.0
		3	0.0	14.1	73.2	11.3	1.4	100.0
		4	0.0	4.2	45.8	41.7	8.3	100.0
		5	0.0	0.0	5.9	2.9	91.2	100.0

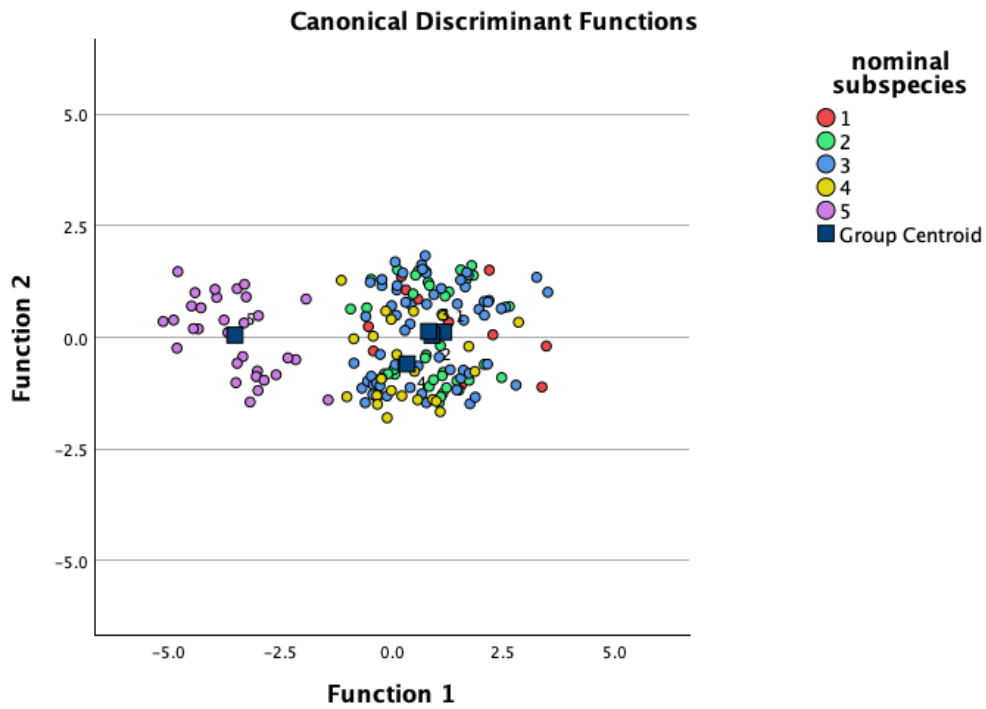
a. 59.1% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 54.3% of cross-validated grouped cases correctly classified.

**Figure S8**

Scatter plots and classification results of Discriminant Function Analysis for the Model-2a in Table S1.



		Predicted Group Membership					Total	
nominal subspecies		1	2	3	4	5		
Original	Count	1	0	0	11	1	0	12
		2	0	0	38	1	0	39
		3	0	0	56	8	0	64
		4	0	0	19	4	0	23
		5	0	0	0	1	30	31
	%	1	0.0	0.0	91.7	8.3	0.0	100.0
		2	0.0	0.0	97.4	2.6	0.0	100.0
		3	0.0	0.0	87.5	12.5	0.0	100.0
		4	0.0	0.0	82.6	17.4	0.0	100.0
		5	0.0	0.0	0.0	3.2	96.8	100.0
Cross-validated <sup>b</sup>	Count	1	0	0	11	1	0	12
		2	0	0	38	1	0	39
		3	0	0	55	9	0	64
		4	0	0	19	4	0	23
		5	0	0	0	1	30	31
	%	1	0.0	0.0	91.7	8.3	0.0	100.0
		2	0.0	0.0	97.4	2.6	0.0	100.0
		3	0.0	0.0	85.9	14.1	0.0	100.0
		4	0.0	0.0	82.6	17.4	0.0	100.0
		5	0.0	0.0	0.0	3.2	96.8	100.0

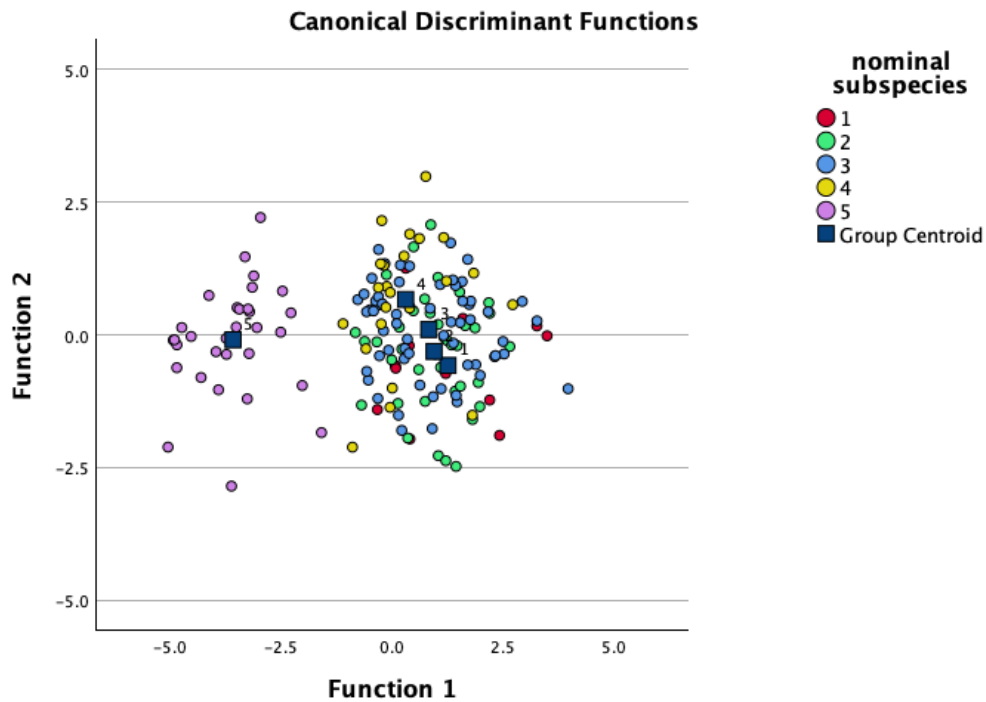
a. 53.3% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 52.7% of cross-validated grouped cases correctly classified.

**Figure S9**

Scatter plots and classification results of Discriminant Function Analysis for the Model-2b in Table S1.



nominal subspecies		Predicted Group Membership					Total	
		1	2	3	4	5		
Original	Count	1	0	5	7	0	0	12
		2	0	9	30	0	0	39
		3	0	5	54	5	0	64
		4	0	3	15	5	0	23
		5	0	0	0	0	31	31
	%	1	0.0	41.7	58.3	0.0	0.0	100.0
		2	0.0	23.1	76.9	0.0	0.0	100.0
		3	0.0	7.8	84.4	7.8	0.0	100.0
		4	0.0	13.0	65.2	21.7	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	0	5	7	0	0	12
		2	0	7	31	1	0	39
		3	1	8	49	6	0	64
		4	0	3	15	5	0	23
		5	0	1	0	0	30	31
	%	1	0.0	41.7	58.3	0.0	0.0	100.0
		2	0.0	17.9	79.5	2.6	0.0	100.0
		3	1.6	12.5	76.6	9.4	0.0	100.0
		4	0.0	13.0	65.2	21.7	0.0	100.0
		5	0.0	3.2	0.0	0.0	96.8	100.0

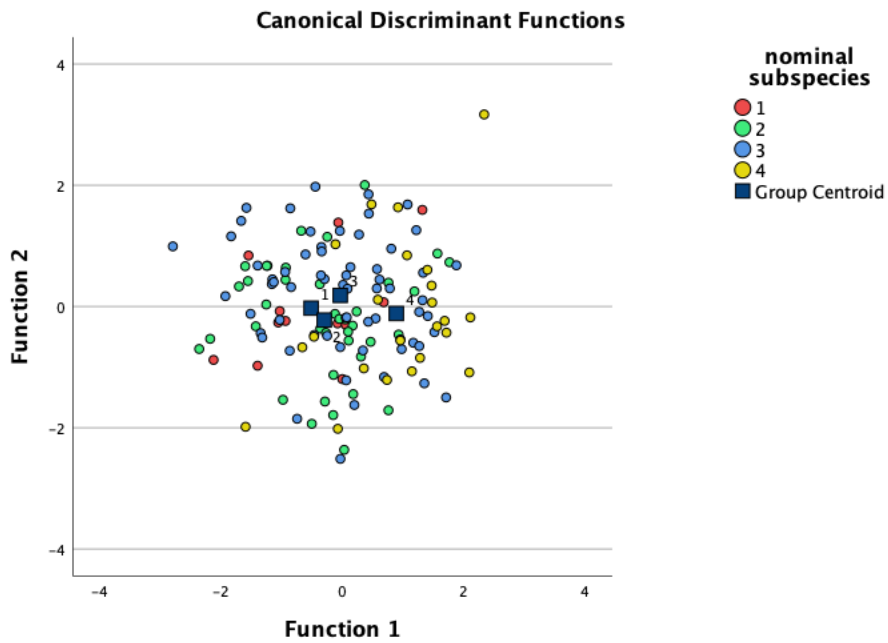
a. 58.6% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 53.8% of cross-validated grouped cases correctly classified.

**Figure S10**

Scatter plots and classification results of Discriminant Function Analysis for the Model-2c in Table S1.



		Classification Results <sup>a,c</sup>					
nominal subspecies			Predicted Group Membership				Total
	Count	1	2	3	4		
Original	Count	1	0	2	10	0	12
		2	0	8	30	1	39
		3	0	4	55	5	64
		4	0	2	15	6	23
	%	1	0.0	16.7	83.3	0.0	100.0
		2	0.0	20.5	76.9	2.6	100.0
		3	0.0	6.3	85.9	7.8	100.0
		4	0.0	8.7	65.2	26.1	100.0
Cross-validated <sup>b</sup>	Count	1	0	2	10	0	12
		2	1	5	32	1	39
		3	0	9	49	6	64
		4	0	2	17	4	23
	%	1	0.0	16.7	83.3	0.0	100.0
		2	2.6	12.8	82.1	2.6	100.0
		3	0.0	14.1	76.6	9.4	100.0
		4	0.0	8.7	73.9	17.4	100.0

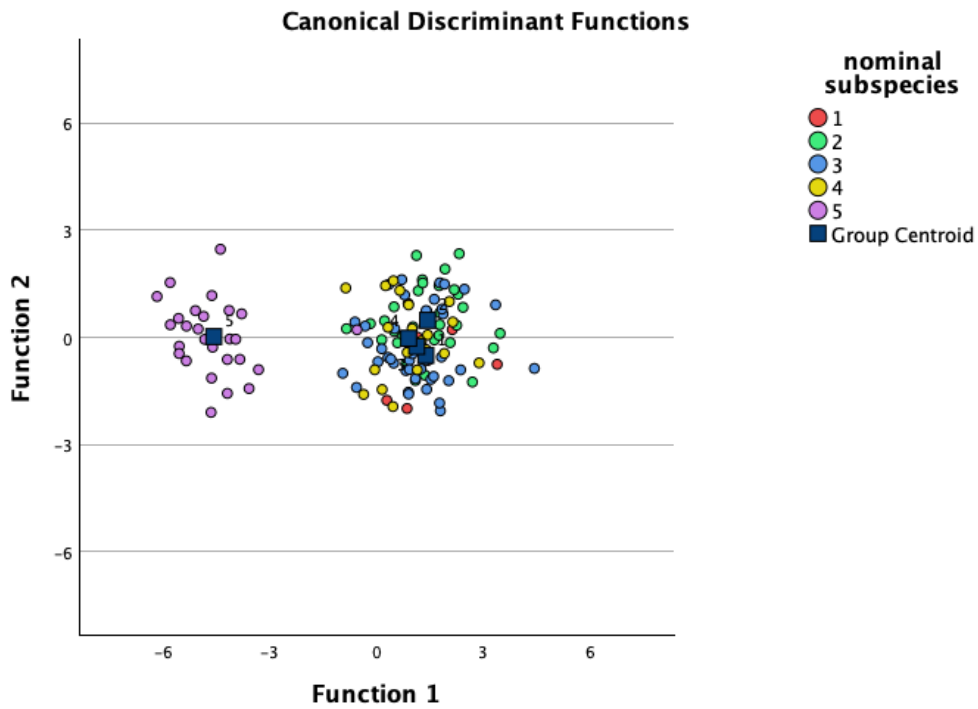
a. 50.0% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 42.0% of cross-validated grouped cases correctly classified.

**Figure S11**

Scatter plots and classification results of Discriminant Function Analysis for the Model-2d in Table S1.



		Predicted Group Membership					Total
nominal subspecies		1	2	3	4	5	
Original	Count	1	0	1	7	0	8
		2	0	13	17	1	31
		3	0	11	31	2	44
		4	0	5	12	4	21
		5	0	0	0	1	26
	%	1	0.0	12.5	87.5	0.0	100.0
		2	0.0	41.9	54.8	3.2	100.0
		3	0.0	25.0	70.5	4.5	100.0
		4	0.0	23.8	57.1	19.0	100.0
		5	0.0	0.0	0.0	3.7	96.3
Cross-validated <sup>b</sup>	Count	1	0	1	7	0	8
		2	0	13	17	1	31
		3	0	12	28	4	44
		4	0	6	14	1	21
		5	0	0	0	1	26
	%	1	0.0	12.5	87.5	0.0	100.0
		2	0.0	41.9	54.8	3.2	100.0
		3	0.0	27.3	63.6	9.1	100.0
		4	0.0	28.6	66.7	4.8	100.0
		5	0.0	0.0	0.0	3.7	96.3

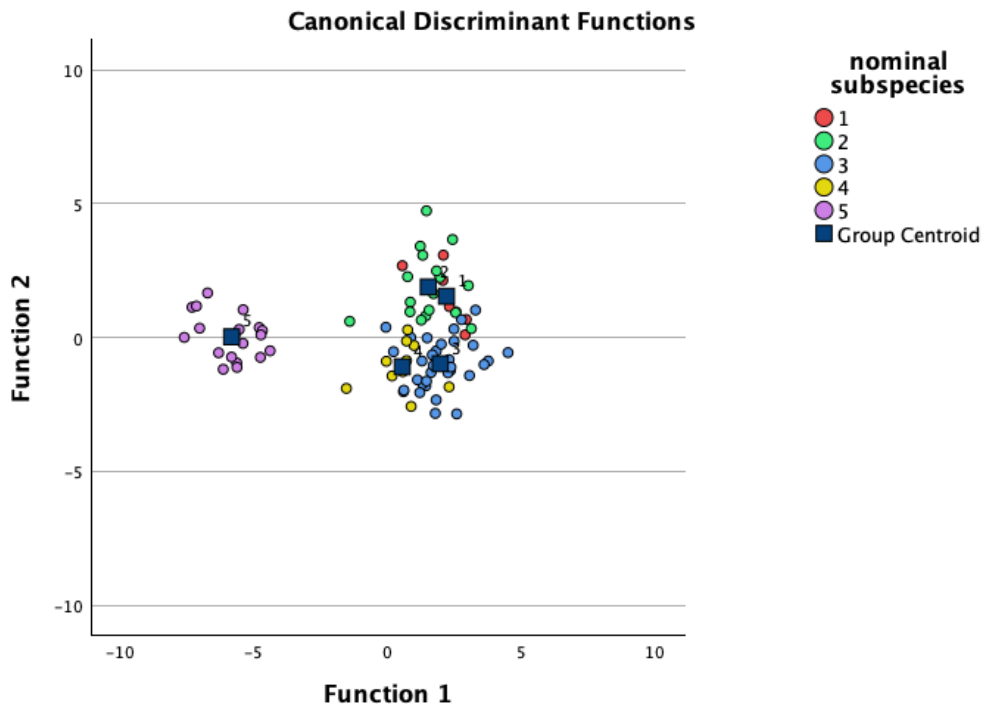
a. 56.5% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 51.9% of cross-validated grouped cases correctly classified.

**Figure S12**

Scatter plots and classification results of Discriminant Function Analysis for the Model-3a in Table S1.



Classification Results <sup>a,c</sup>								
nominal subspecies			Predicted Group Membership					Total
			1	2	3	4	5	
Original	Count	1	7	0	0	0	0	7
		2	0	15	2	0	0	17
		3	0	2	31	0	0	33
		4	0	0	2	8	0	10
		5	0	0	0	0	19	19
	%	1	100.0	0.0	0.0	0.0	0.0	100.0
		2	0.0	88.2	11.8	0.0	0.0	100.0
		3	0.0	6.1	93.9	0.0	0.0	100.0
		4	0.0	0.0	20.0	80.0	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	1	2	4	0	0	7
		2	1	8	4	3	1	17
		3	4	7	19	3	0	33
		4	0	2	2	6	0	10
		5	0	0	0	1	18	19
	%	1	14.3	28.6	57.1	0.0	0.0	100.0
		2	5.9	47.1	23.5	17.6	5.9	100.0
		3	12.1	21.2	57.6	9.1	0.0	100.0
		4	0.0	20.0	20.0	60.0	0.0	100.0
		5	0.0	0.0	0.0	5.3	94.7	100.0

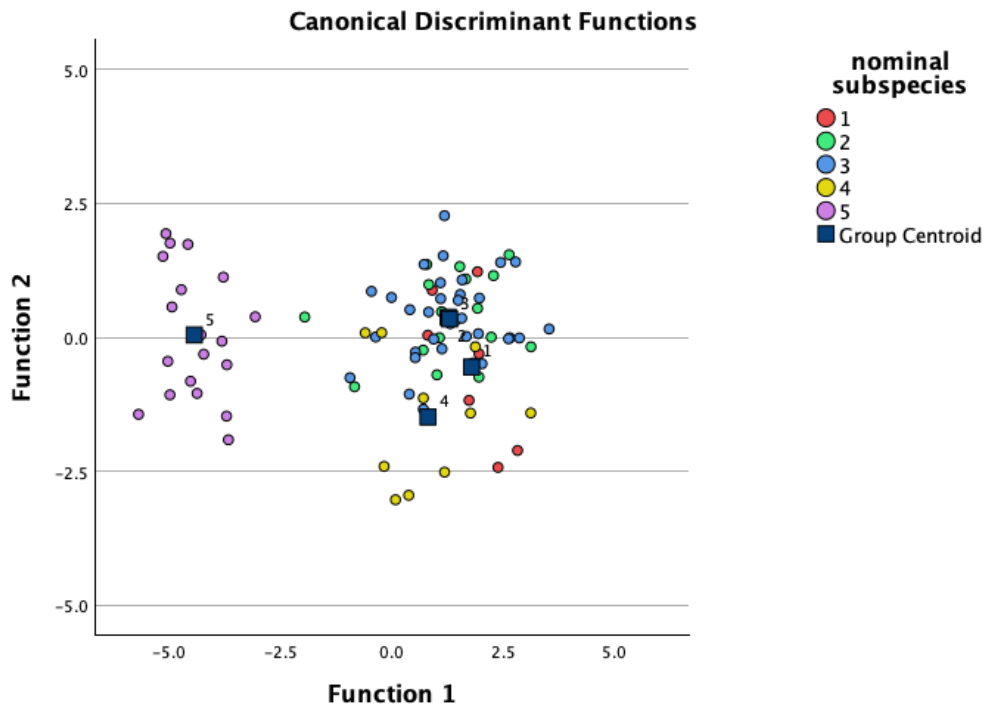
a. 93.0% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 60.5% of cross-validated grouped cases correctly classified.

**Figure S13**

Scatter plots and classification results of Discriminant Function Analysis for the Model-3b in Table S1.



		Predicted Group Membership					Total	
nominal subspecies		1	2	3	4	5		
Original	Count	1	2	1	3	1	0	7
		2	0	7	8	1	1	17
		3	0	4	29	0	0	33
		4	0	1	4	5	0	10
		5	0	0	0	0	19	19
	%	1	28.6	14.3	42.9	14.3	0.0	100.0
		2	0.0	41.2	47.1	5.9	5.9	100.0
		3	0.0	12.1	87.9	0.0	0.0	100.0
		4	0.0	10.0	40.0	50.0	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	1	2	2	2	0	7
		2	1	5	9	1	1	17
		3	0	6	25	2	0	33
		4	0	1	4	5	0	10
		5	0	0	0	0	19	19
	%	1	14.3	28.6	28.6	28.6	0.0	100.0
		2	5.9	29.4	52.9	5.9	5.9	100.0
		3	0.0	18.2	75.8	6.1	0.0	100.0
		4	0.0	10.0	40.0	50.0	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0

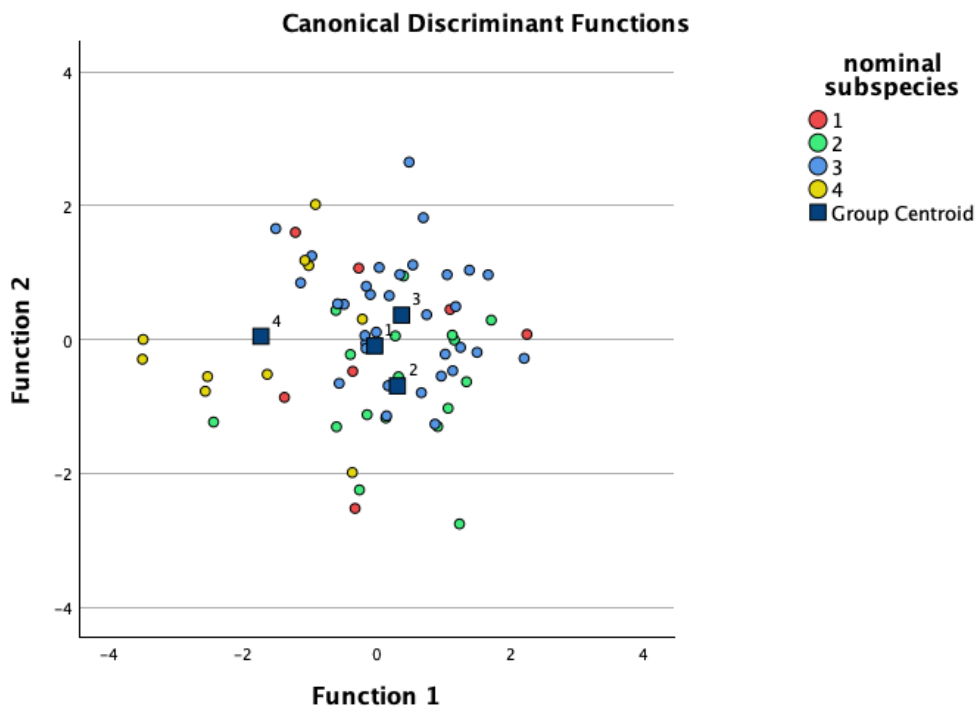
a. 72.1% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 64.0% of cross-validated grouped cases correctly classified.

**Figure S14**

Scatter plots and classification results of Discriminant Function Analysis for the Model-3c in Table S1.



		Classification Results <sup>a,c</sup>					
nominal subspecies			Predicted Group Membership				
			1	2	3	4	Total
Original	Count	1	3	1	3	0	7
		2	0	7	9	1	17
		3	0	2	30	1	33
		4	0	1	4	5	10
	%	1	42.9	14.3	42.9	0.0	100.0
		2	0.0	41.2	52.9	5.9	100.0
		3	0.0	6.1	90.9	3.0	100.0
		4	0.0	10.0	40.0	50.0	100.0
Cross-validated <sup>b</sup>	Count	1	1	1	5	0	7
		2	1	6	9	1	17
		3	0	5	27	1	33
		4	0	1	4	5	10
	%	1	14.3	14.3	71.4	0.0	100.0
		2	5.9	35.3	52.9	5.9	100.0
		3	0.0	15.2	81.8	3.0	100.0
		4	0.0	10.0	40.0	50.0	100.0

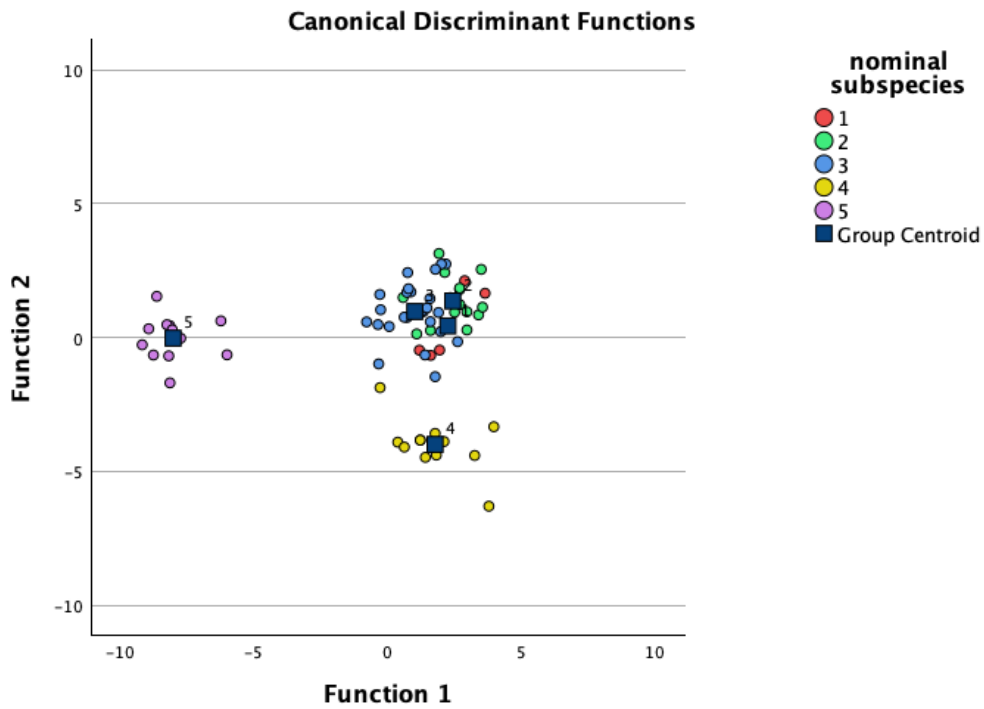
a. 67.2% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 58.2% of cross-validated grouped cases correctly classified.

**Figure S15**

Scatter plots and classification results of Discriminant Function Analysis for the Model-4a in Table S1.



		Predicted Group Membership					Total	
nominal subspecies		1	2	3	4	5		
Original	Count	1	4	1	0	0	0	5
		2	1	14	1	0	0	16
		3	0	1	24	0	0	25
		4	0	0	0	12	0	12
		5	0	0	0	0	12	12
	%	1	80.0	20.0	0.0	0.0	0.0	100.0
		2	6.3	87.5	6.3	0.0	0.0	100.0
		3	0.0	4.0	96.0	0.0	0.0	100.0
		4	0.0	0.0	0.0	100.0	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	0	2	1	2	0	5
		2	2	8	6	0	0	16
		3	0	8	14	3	0	25
		4	0	0	2	10	0	12
		5	1	0	0	0	11	12
	%	1	0.0	40.0	20.0	40.0	0.0	100.0
		2	12.5	50.0	37.5	0.0	0.0	100.0
		3	0.0	32.0	56.0	12.0	0.0	100.0
		4	0.0	0.0	16.7	83.3	0.0	100.0
		5	8.3	0.0	0.0	0.0	91.7	100.0

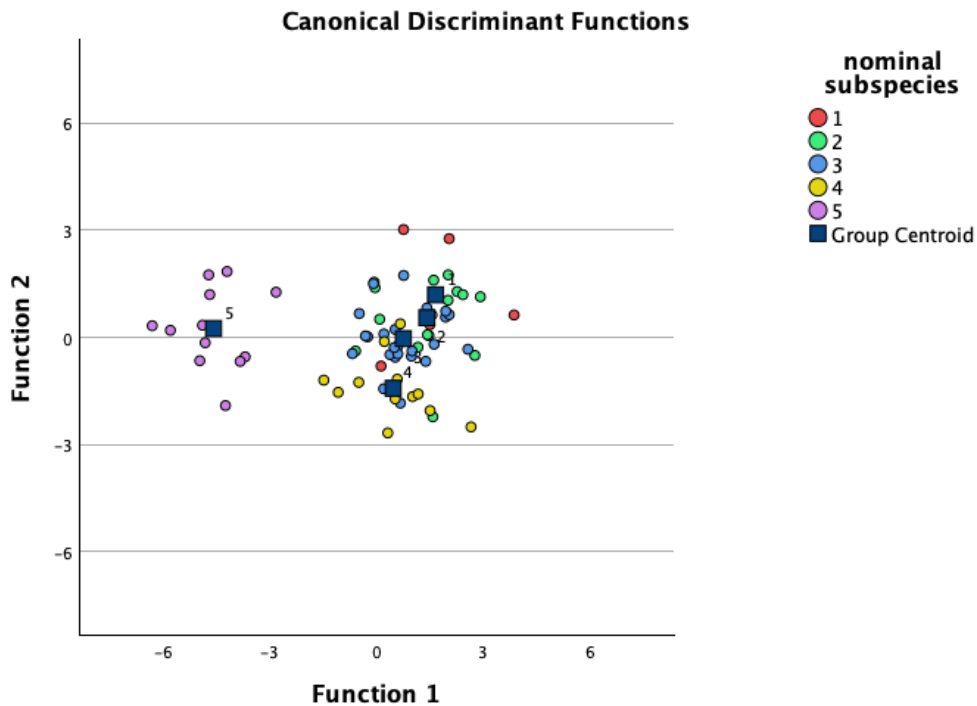
a. 94.3% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 61.4% of cross-validated grouped cases correctly classified.

**Figure S16**

Scatter plots and classification results of Discriminant Function Analysis for the Model-4b in Table S1.



nominal subspecies		Predicted Group Membership					Total	
		1	2	3	4	5		
Original	Count	1	2	2	0	1	0	5
		2	1	9	5	1	0	16
		3	2	3	18	2	0	25
		4	0	0	4	8	0	12
		5	0	0	0	0	12	12
	%	1	40.0	40.0	0.0	20.0	0.0	100.0
		2	6.3	56.3	31.3	6.3	0.0	100.0
		3	8.0	12.0	72.0	8.0	0.0	100.0
		4	0.0	0.0	33.3	66.7	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	1	2	1	1	0	5
		2	1	8	6	1	0	16
		3	2	5	16	2	0	25
		4	0	0	7	5	0	12
		5	0	1	0	0	11	12
	%	1	20.0	40.0	20.0	20.0	0.0	100.0
		2	6.3	50.0	37.5	6.3	0.0	100.0
		3	8.0	20.0	64.0	8.0	0.0	100.0
		4	0.0	0.0	58.3	41.7	0.0	100.0
		5	0.0	8.3	0.0	0.0	91.7	100.0

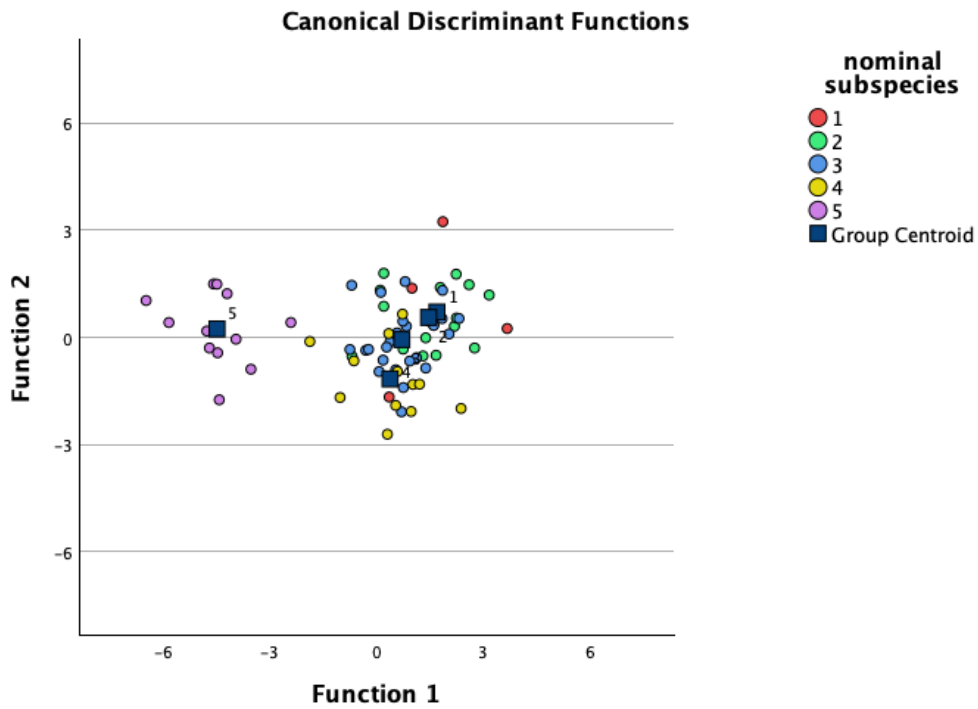
a. 70.0% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 58.6% of cross-validated grouped cases correctly classified.

**Figure S17**

Scatter plots and classification results of Discriminant Function Analysis for the Model-4c in Table S1.



		Classification Results <sup>a,c</sup>						
nominal subspecies		Predicted Group Membership						
		1	2	3	4	5	Total	
Original	Count	1	2	1	1	1	0	5
		2	1	7	8	0	0	16
		3	2	4	17	2	0	25
		4	0	0	7	5	0	12
		5	0	0	0	0	12	12
	%	1	40.0	20.0	20.0	20.0	0.0	100.0
		2	6.3	43.8	50.0	0.0	0.0	100.0
		3	8.0	16.0	68.0	8.0	0.0	100.0
		4	0.0	0.0	58.3	41.7	0.0	100.0
		5	0.0	0.0	0.0	0.0	100.0	100.0
Cross-validated <sup>b</sup>	Count	1	1	1	2	1	0	5
		2	1	6	9	0	0	16
		3	3	7	12	3	0	25
		4	0	0	8	4	0	12
		5	0	0	1	0	11	12
	%	1	20.0	20.0	40.0	20.0	0.0	100.0
		2	6.3	37.5	56.3	0.0	0.0	100.0
		3	12.0	28.0	48.0	12.0	0.0	100.0
		4	0.0	0.0	66.7	33.3	0.0	100.0
		5	8.3	0.0	8.3	0.0	91.7	100.0

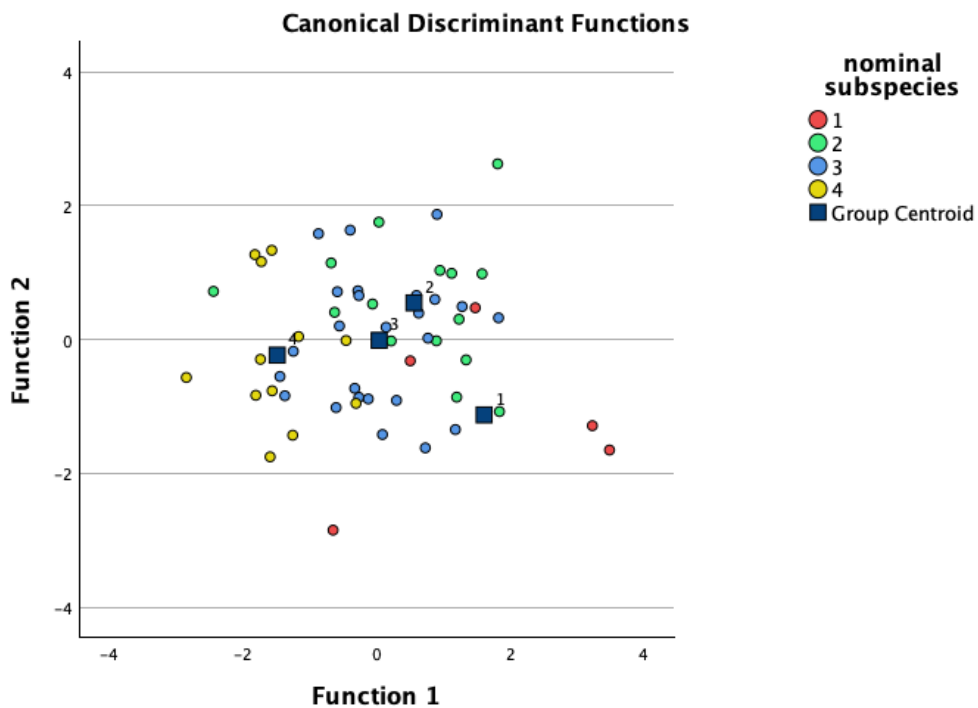
a. 61.4% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 48.6% of cross-validated grouped cases correctly classified.

**Figure S18**

Scatter plots and classification results of Discriminant Function Analysis for the Model-4d in Table S1.



		Classification Results <sup>a,c</sup>					
nominal subspecies			Predicted Group Membership				
			1	2	3	4	Total
Original	Count	1	2	1	2	0	5
		2	1	6	8	1	16
		3	0	5	18	2	25
		4	0	0	3	9	12
	%	1	40.0	20.0	40.0	0.0	100.0
		2	6.3	37.5	50.0	6.3	100.0
		3	0.0	20.0	72.0	8.0	100.0
		4	0.0	0.0	25.0	75.0	100.0
Cross-validated <sup>b</sup>	Count	1	2	1	1	1	5
		2	1	3	11	1	16
		3	0	7	15	3	25
		4	0	0	5	7	12
	%	1	40.0	20.0	20.0	20.0	100.0
		2	6.3	18.8	68.8	6.3	100.0
		3	0.0	28.0	60.0	12.0	100.0
		4	0.0	0.0	41.7	58.3	100.0

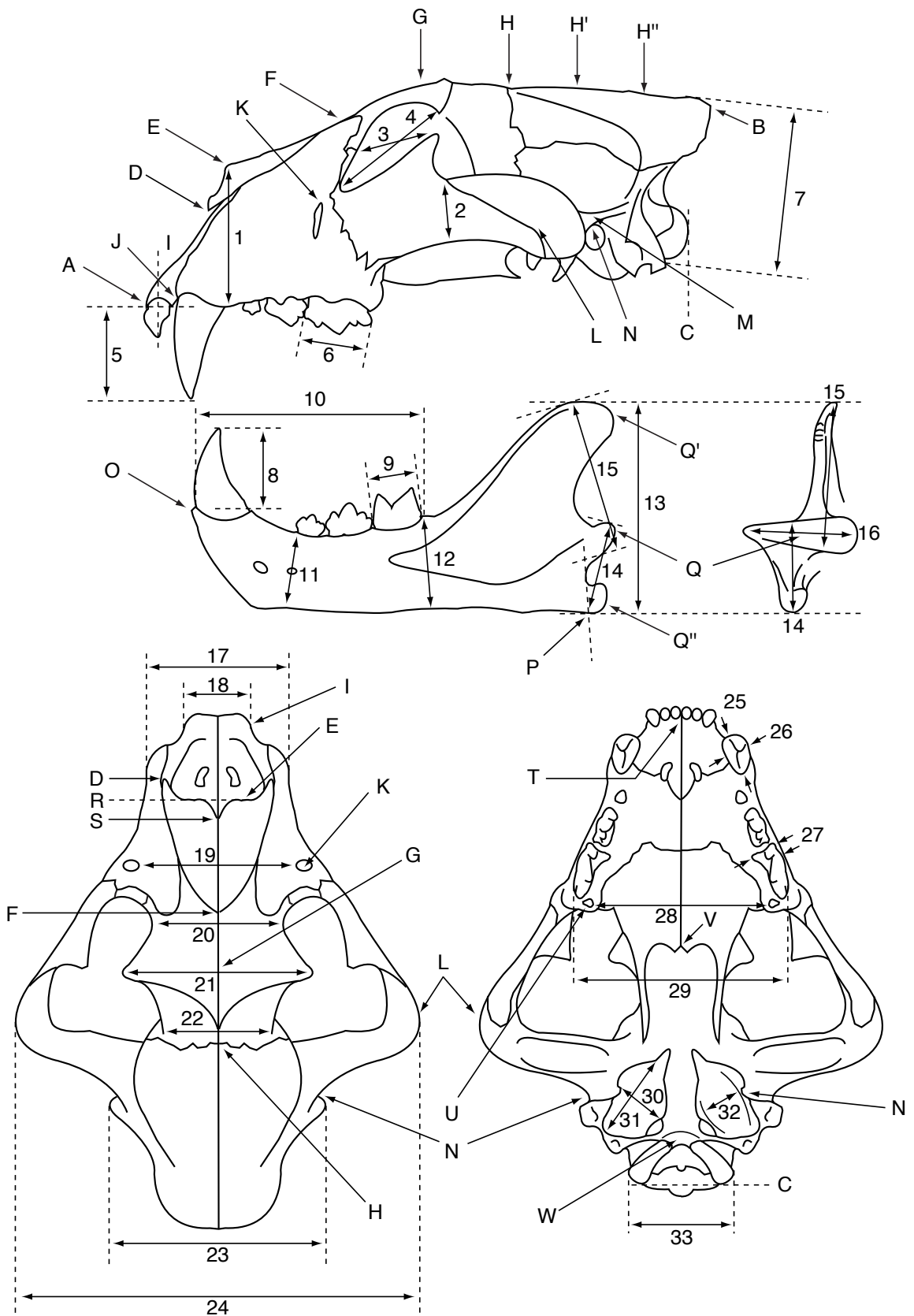
a. 60.3% of original grouped cases correctly classified.

b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

c. 46.6% of cross-validated grouped cases correctly classified.

**Figure S19**

Definitions of the measurements and the associated reference points on the skull. Numbers and letters are corresponding to those in Table S2.



**Table S2.** List of skull variables, definitions of the points, and measurement numbers, corresponding with those in Fig. S5.

List of variables.

01	Frontal breadth [21]
02	Greatest length [A-B]
03	Condylbasal length [A-C]
04	Palate-inion [V-B]
05	Nasal-inion [R-B]
06	Facial length [A-G]
07	Head length [G-B]
08	Bizygomatic breadth [24]
09	Zygomatic length [K-M]
10	Zygomatic length anterior [K-L] & posterior [L-M]
11	Orbit vertical [4] & horizontal [3]
12	Postorbital bar [2]
13	Facial length (anterior) [A-R] & (posterior) [R-G]
14	Sagittal crest [H-B]
15	Cranial height I [N-H], II [N-H']
16	Cranial height III [N-H''] & IV [N-B]
17	Interorbital breadth [20]
18	Postorbital breadth [22]
19	Nasal length-I [D-F], -II [S-F] & breadth [D-D]
20	Breadth between infra orbital foramina [19]
21	Rostral depth-I [1] & -II (E - most posterior end of canine alveolus)
22	Rostral breadth [17]
23	Nasal aperture [18]
24	Upper jaw [A-U]
25	Palate length [T-V]
26	Palate breadth-I [29] & -II [28]
27	Canine - Pm <sup>4</sup> & Pm <sup>2</sup> - Pm <sup>4</sup> : (alveolus - alveolus)
28	Upper canine height [5], breadth [25] & breadth-lateral [26]
29	Upper canine alveolus: greatest and smallest diameters
30	Pm <sup>4</sup> length [6] & breadth-I & -II [27]
31	Mastoid breadth [23]
32	Skull height-I [W-B] & -II [7]
33	Foramen magnum breadth & height [greatest distance: oblique]
34	Occipital condyles breadth [33]
35	Tympanic bulla length [31], breadth [30] & breadth' [32]
36	Mandible length [O-Q], -I (O-Q') & -II (O-Q'')
37	Mandible height [13]
38	Mandible height-I [14] & -II [15]
39	Maximum width of mandibular condyle [16]
40	Mandible depth-I [11] & -II [12]
41	Canine - M <sub>1</sub> & Pm <sub>3</sub> - M <sub>1</sub> : (alveolus - alveolus)
42	Lower canine height [8], breadth & breadth-lateral
43	Lower canine alveolus: greatest and smallest diameters
44	Pm <sub>4</sub> length & breadth (largest breadth towards the posterior end)
45	M <sub>1</sub> length [9] & breadth

## Definition of points

- A. Prosthion: the most anterior point of the skull
- B. Inion: the most posterior point of the skull
- C. The line connecting the most posterior points of occipital condyles
- D. The most anterior points of nasals
- E. The highest points on the vaults of the anterior ends of dorsal parts of nasals
- F. The most posterior point of the inter nasal suture
- G. The point where the line connecting the most outer points of postorbital process of frontal meets the mesion
- H. Bregma: where the coronal suture meets sagittal suture (if the sagittal crest is very well developed, use the place where the coronal suture reaches the top of the sagittal crest in the mesion - usually the point where sagittal suture closes)
- H' One third distance point between bregma and inion
- H'' Two third distance point between bregma and inion
- I. Vertical lines including the most outer points of the alveoli of I<sup>3</sup>s
- J. The most anterior point of alveolus of the upper canine
- K. The most dorsal point of infraorbital foramen (in case if there are more than one foramen, the most dorsal point of the foramina)
- L. The most outer point of the zygomatic arch (usually found along or just above the malar - temporal suture)
- M. A point where a vertical section including the most dorsal point of auditory meatus cuts the outer curve of the zygomatic process of temporal
- N. The most dorsal point of auditory meatus
- O. Pogonion: the most anterior point of mandible on the inter mandible suture
- P. The most ventral point around the angular process. If it is not obvious, use the point where the extended line of the middle line of inferior notch crosses the ventral edge of angular process as being shown in the figure (may sound difficult, but in practice there is little problem and a subtle difference of the position of "P" does not seem to affect the result either)
- Q. The point where the extended line of the ventral end of superior notch crosses the posterior edge of condyle (approximately the middle of condyle)
- Q'. The furthest point on the coronoid process from the pogonion
- Q''. The furthest point on the angular process from the pogonion
- R. The line connecting the highest points on the vaults of the anterior ends of dorsal parts of nasals
- S. The most anterior point of the inter nasal suture (be careful as the inter nasal suture of some skulls may be slightly opened towards the anterior end and it may be difficult to assess the real "S". In such case, ignore the part where the inner lines of the nasals forms a shallow angle (almost parallel) to the mesion, and find the point where the angle start to change)
- T. Orale: the point where the line connecting the most posterior points of I<sup>1</sup> alveoli meets the mesion
- U. The middle point along the posterior part of the alveolus of M<sup>1</sup>
- V. The most posterior point of the palate on the mesion
- W. The most ventral point in the mesion between occipital condyles

## Measurement numbers

1. The distance from R to the most posterior point of the upper canine alveolus
2. The shortest distance between the most dorsal point of the malar - temporal suture and the most ventral edge of the zygomatic arch
3. The distance between the tip of postorbital process of malar and the point where lacrimal - frontal suture crosses the edge of orbit
4. The longest distance between the tip of postorbital process of frontal and the edge of orbit (if the tip of postorbital process of frontal is not sharp, use the middle point of the rounded tip)
5. The distance along the buccal surface of an upper canine between the unworn tip and the point on the cemento - enamel junction where the mediolateral breadth of the canine becomes its maximum
6. The distance between the most anterior point of the buccal part of Pm<sup>4</sup> and the most posterior point of the tooth
7. The greatest distance between "W" and the sagittal crest around its posterior end. In most case, it is easy to measure this distance. However, if the sagittal crest of the skull is very well developed, careful assessment is necessary.
8. The distance along the buccal surface of a lower canine between the unworn tip and the point on the dentine - enamel junction where the mediolateral breadth of the canine becomes its maximum
9. The distance between the most anterior point of M<sub>1</sub> and the most posterior point of the tooth
10. The distance between the most anterior point of canine alveolus and the most posterior point of M<sub>1</sub> alveolus
11. The smallest of the greatest diameter of the section which cut the mandible in front of the most anterior point of Pm<sub>3</sub> alveolus: usually an oblique measurement like the one shown in the figure
12. The smallest of the greatest diameter of the section which cut the mandible just behind the most posterior point of M<sub>1</sub> alveolus: usually a vertical or slightly oblique measurement shown in the figure
13. The greatest distance between "P" and the dorsal part of coronoid process
14. The greatest distance between "P" and the dorsal part of condyle just outside the place where superior notch crosses the condyle: usually an oblique measurement shown in the figure
15. The greatest distance between the ventral part of condyle just inside the place where the condyle meets inferior notch and the dorsal part of coronoid process: usually an oblique measurement shown in the figure – in most cases use the point on the coronoid process that was used to measurement 13
16. Maximum width of mandibular condyle
17. The greatest breadth of the rostrum just above the canine alveoli (I always measure at the point above the alveoli by the mediolateral width of the mandibles of the calliper)
18. The breadth of nasal aperture above the most outer points of I<sup>3</sup> alveoli
19. The smallest distance between infraorbital foramina
20. Interorbital breadth: the smallest distance between the orbits excluding the distance between the constrictions between the postorbital processes of the frontal and the humps in front of the processes (in case such humps and constrictions exist)
21. The distance between the most outer points of postorbital process of frontal
22. Postorbital breadth: the smallest breadth of the postorbital constriction
23. Mastoid breadth: the distance between the most outer points of mastoidal processes
24. The distance between zygions: the most outer points of zygomatic arches
25. The greatest anteroposterior length of an upper canine at the cemento-enamel junction: the greater diameter of the canine
26. The greatest mediolateral length of an upper canine at the cemento-enamel junction: the smaller diameter of the canine

27. The greatest mediolateral length of an Pm<sup>4</sup>-I: between the inner process and the most anterior outer process, and -II: between the former and the second most anterior outer process of the tooth
28. The smallest distance between M<sup>1</sup> alveoli
29. The greatest distance between Pm<sup>4</sup> alveoli
30. The distance between the most anterior/inner meeting point between tympanic bulla and external auditory meatus and the most anterior meeting point between tympanic bulla and foramen lacerum posterius
31. The greatest length of tympanic bulla excluding styloid process and other processes attached to the tympanic bulla: fix one end of the calliper at the point where foramen lacerum medius meets the most prominent styloid process, and measure the greatest distance between that point and the posterior part of the tympanic bulla
32. The greatest mediolateral distance of the vault of the tympanic bulla: the smaller diameter of the vault of the tympanic bulla
33. The greatest breadth of occipital condyles

**Table S3.** List of the 19 variables included in the analyses for maximising the sample size of “Cape” lions of both sexes. See Table S17 and Fig. S5 for the details.

01	Frontal breadth
02	Facial length
03	Zygomatic length
04	Zygomatic length anterior
05	Zygomatic length posterior
06	Orbit vertical
07	Orbit horizontal
08	Postorbital bar
09	Cranial height I
10	Interorbital breadth
11	Postorbital breadth
12	Breadth between infra orbital foramina
13	Rostral breadth
14	Nasal aperture
15	Palate length
16	Canine - Pm <sup>4</sup>
17	Pm <sup>2</sup> - Pm <sup>4</sup>
18	Upper canine alveolus greatest diameter
19	Upper canine alveolus smallest diameter

**Table S4.** List of the 30 variables included in the analyses for maximising the sample size of male “Cape” lions. See Table S17 and Fig. S5 for the details.

01	Frontal breadth
02	Facial length
03	Bizygomatic breadth
04	Zygomatic length
05	Zygomatic length anterior
06	Zygomatic length posterior
07	Orbit vertical
08	Orbit horizontal
09	Postorbital bar
10	Facial length anterior
11	Facial length posterior
12	Cranial height I
13	Interorbital breadth
14	Postorbital breadth
15	Nasal length-I
16	Nasal length-II
17	Nasal breadth
18	Breadth between infra orbital foramina
19	Rostral depth-I
20	Rostral depth-II
21	Rostral breadth
22	Nasal aperture
23	Upper jaw
24	Palate length
25	Palate breadth-I
26	Palate breadth-II
27	Canine - Pm <sup>4</sup>
28	Pm <sup>2</sup> - Pm <sup>4</sup>
29	Upper canine alveolus greatest diameter
30	Upper canine alveolus smallest diameter

**Table S5.** List of the 31 variables included in the analyses for maximising the sample size of female “Cape” lions. See Table S17 and Fig. S5 for the details.

01	Frontal breadth
02	Greatest length
03	Condylbasal length
04	Palate-inion
05	Facial length
06	Head length
07	Zygomatic length
08	Zygomatic length anterior
09	Zygomatic length posterior
10	Orbit vertical
11	Orbit horizontal
12	Postorbital bar
13	Sagittal crest
14	Cranial height I
15	Cranial height II
16	Cranial height III
17	Cranial height IV
18	Interorbital breadth
19	Postorbital breadth
20	Breadth between infra orbital foramina
21	Rostral breadth
22	Nasal aperture
23	Palate length
24	Canine - Pm <sup>4</sup>
25	Pm <sup>2</sup> - Pm <sup>4</sup>
26	Upper canine alveolus greatest diameter
27	Upper canine alveolus smallest diameter
28	Skull height-I
29	Skull height-II
30	Foramen magnum height
31	Occipital condyles

**Table S6.** List of the 48 variables included in the analyses for maximising the number of variables whilst retaining as many “Cape” lions as possible. See Table S17 and Fig. S5 for the details.

01	Frontal breadth
02	Greatest length
03	Condylbasal length
04	Palate-inion
05	Facial length
06	Head length
07	Zygomatic length
08	Zygomatic length anterior
09	Zygomatic length posterior
10	Orbit vertical
11	Orbit horizontal
12	Postorbital bar
13	Sagittal crest
14	Cranial height I
15	Cranial height II
16	Cranial height III
17	Cranial height IV
18	Interorbital breadth
19	Postorbital breadth
20	Breadth between infra orbital foramina
21	Rostral breadth
22	Nasal aperture
23	Palate length
24	Upper canine - Pm <sup>4</sup>
25	Pm <sup>2</sup> - Pm <sup>4</sup>
26	Upper canine alveolus greatest diameter
27	Upper canine alveolus smallest diameter
28	Skull height-I
29	Skull height-II
30	Foramen magnum height
31	Occipital condyles
32	Mandible length
33	Mandible length-I (coronoid process)
34	Mandible length-II (angular process)
35	Mandible height
36	Mandible height-I (angular process)
37	Mandible height-II (coronoid process)
38	WMC
39	Mandible depth-I
40	Mandible depth-II
41	Lower canine – M <sub>1</sub>
42	Pm <sub>3</sub> – M <sub>1</sub>
43	Lower canine alveolus greatest diameter
44	Lower canine alveolus smallest diameter
45	Pm <sub>4</sub> length
46	Pm <sub>4</sub> breadth
47	M <sub>1</sub> length
48	M <sub>1</sub> breadth

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