

Table S1. The number and proportion of deleterious and neutral mutations accumulated in mitochondrial protein genes in various deer lineages.

Species	Number		Proportion	
	deleterious	neutral	deleterious	neutral
<i>C. albirostris</i>	6	40	0.13	0.87
<i>C. canadensis</i>	5	37	0.12	0.88
<i>C. elaphus</i>	12	65	0.16	0.84
<i>C. hanglu</i>	7	14	0.33	0.67
<i>C. nippon</i>	48	82	0.37	0.63
<i>R. unicolor</i> and <i>timorensis</i>	10	34	0.23	0.77

Table S2. Results of Tajima's and Fu's neutrality tests calculated for nucleotide sequences of protein-coding genes from various deer groups.

Group	m	S	π	D	Fs
Ce+Ch	16	773	0.014	-1.30	-0.04
Ce	15	457	0.011	-0.59	-0.26
Cc+Cn+Ca	22	1202	0.027	-0.23	-0.07
Cc+Cn	20	984	0.025	0.07	0.07
Cc	8	241	0.008	-0.34	1.00
Cn	12	707	0.020	-0.11	1.11
mainland Cn	9	318	0.012	0.97	1.24

m - number of sequences, S - Number of segregating sites, π - nucleotide diversity, D - the Tajima's test statistic, Fs - the Fu's test statistic; Ca - *C. albirostris*; Cc - *C. canadensis*; Ce - *C. elaphus*; Ch - *C. hanglu*; Cn - *C. nippon*.

Table S3. List of the 13 mitochondrial genomes of *Cervus* obtained in this study, with their sampling locality, geographic coordinates and accession numbers.

Sample ID	Species/subspecies	Locality	Coordinates	Length [bp]	GenBank acc. num.
WEST1	<i>C. elaphus</i>	Alfredówka, Poland	50°27' N 21°45' E	16351	OL679912
WEST2	<i>C. elaphus</i>	Maków Podhalański, Poland	49°43' N 19°40' E	16351	OL679913
WEST3	<i>C. elaphus</i>	Trzebielino, Poland	54°11' N 17°05' E	16352	OL679914
WEST4	<i>C. elaphus</i>	Bytnica, Poland	52°09' N 15°10' E	16352	OL679915
EAST1	<i>C. elaphus</i>	Łazy, Poland	50°25' N 19°23' E	16355	OL679916
EAST2	<i>C. elaphus</i>	Ocieka, Poland	50°08' N 21°35' E	16355	OL679917
EAST3	<i>C. elaphus</i>	Łądek Zdrój, Poland	50°20' N 16°52' E	16354	OL679918
MAR1	<i>C. elaphus maral</i>	Mazandaran, Iran	36°27' N 52°06' E	16350	OL679919
MES1	<i>C. elaphus</i>	Rymanów, Poland	49°33' N 21°51' E	16351	OL679920
MES2	<i>C. elaphus italicus</i>	Riserva Naturale Bosco della Mesola, Italy	44°51' N 12°14' E	16351	OL679921
TUN1	<i>C. elaphus barbarus</i>	Zoological Park Belvédère in Tunis, from El Feidja National Park, Tunisia	36°29' N 8°19' E	16353	OL679922
SIB1	<i>C. canadensis sibiricus</i>	Kyzyl, Tuva, Russia	52°10' N 95°45' E	16428	OL679923
XAN1	<i>C. canadensis xanthopygus</i>	Terneysky District, Primorsky Krai, Russia	45°18' N 136°78' E	16353	OL679924

Table S4. List of primer pairs used for PCRs and DNA sequencing of *Cervus elaphus* (haplogroups A-E), *C. canadensis sibiricus* (SIB) and *C. c. xanthopygus* (XAN) mitogenomes.

Primer	Primer sequence	mtDNA position	Tm [°C]	Product length [bp]	Amplified genes	Primer source	<i>C. elaphus</i>					<i>C. canadensis</i>	
							A	B	C	D	E	SIB	XAN
12S-FW 12S-REV	GGTAAATCTCGTGCCAGCCA TCCAGTATGCTTACCTTGTTACGAC	00295 01006	57.3 56.2	711	<12s_rRNA>	Fajardo et al. (2007)	•	•	•	•	•	•	•
00868cee_F 01461cee_R	AGTGCTTAGTTGAACTAGGCCAT TTCTGGACAACCAGCTATCACCA	00869 01461	55.8 57.6	592	<12s_rRNA...tRNA-Val...16s_rRNA>	This study		•		•			
00871c_F 02052c_R	TGCTTAGTTGAATTAGGCAATG AGAGAACAAGTGATTATGCTACC	00871 02049	51.3 52.2	1178	<12s_rRNA...tRNA-Val...16s_rRNA>	Matosiuk et al. (2014)	•		•		•	•	•
01438cee_F 02033cee_R	TGGTGATAGCTGGTTGTCCAGAA TACCTTTGCACGGTCAGGATA	01439 02030	57.6 55.3	591	<16s_rRNA>	This study		•		•			
01950c_F 03402c_R	ACCTCCAGCATAACTAGTATTGG AATGGTCTGCTGCATACTCTA	01947 03401	53.7 55.2	1454	<16s_rRNA...tRNA-Leu...ND1>	Matosiuk et al. (2014)	•	•	•	•	•	•	•
02233cee_F 02667cee_R	TGGGCTAACAGCTTTGGTTG AAGCCCTTTTCTAGGGCAAG	02231 02664	55.8 55.1	433	<16s_rRNA...tRNA-Leu>	This study		•					
02683cee_F 03412cee_R	CCCGGTAATTGCGTAAACT ATAGGGCAAATGGTCCTGCT	02681 03409	53.2 56.2	728	<tRNA-Leu...ND1>	This study		•					•
03140c_F 04165c_R	CTACGAGCAGTAGCTCAAACA ACAGTTCATTGGCCTGAAAATA	03139 04165	54.1 52.5	1026	<ND1...tRNA-Ile...tRNA-Gln...trNA-Met...ND2>	Matosiuk et al. (2014)	•	•	•	•	•	•	•
3910cee_F 4300cee_F2 5430cee_R	CCTTCCCGTACTAATAAACCC TCATCAGGCCTAATTCTACT TATGCCTGCTCARGCACCAA	03896 04281 05417	50.0 - 56.0	1521	<tRNA-Met...ND2...tRNA-Trp...tRNA-Ala...tRNA-Asn...tRNA-Cys...tRNA-Tyr...COX1>	This study	•		•		•	•	
03986cee_F 04812cee_R	TGACTACTTGTCTGAATCGG CAGTGGAATATGTGAGTCGT	03984 04809	51.3 51.6	825	<ND2>	This study		•		•		•	•
04637cee_F 05475cee_R	CTAGTCTCATTACCCTCCT AGTACCAGTTGGCCAGTTC	04635 05471	52.1 59.1	836	<ND2...tRNA-Trp...tRNA-Ala...tRNA-Asn...tRNA-Cys...tRNA-Tyr...COX1>	This study		•		•			•
COX1_F COX1_R	TCAGCCATTTTACCTATGTTCA ATRTAGCCAAARGTTCTTTTT	05319 06145	51.7 48.5	826	<tRNA-Tyr...COX1>	GQ336878.1	•	•	•	•	•	•	•
05986c_F 06999c_R	TTCTTTGACCCAGCAGGAGGC ACCTGTAACCTTAACCTTGACAAAG	05988 07000	59.6 53.0	1012	<COX1...tRNA-Ser...tRNA-Asp>	Matosiuk et al. (2014)	•	•	•		•	•	•
06011cee_F 06815cee_R	TCTTTGACCCAGCAGGAGG GTTCTACGGTTGAGACTTCTCG	05989 06792	56.6 54.8	803	<COX1>	This study				•			
06381cee_F 07029cee_R	ACAGTTGGAGGCTTGACTGGAAT GCCATATGAGATGTACGGGG	06378 07025	58.2 54.9	647	<COX1...tRNA-Ser...tRNA-Asp...COX2>	This study				•			
06680cee_F 07760cee_R	GCATACACAACATGAAAYACCA CTAGCTTAAAAGGCTAGCGCTATT	06669 07745	52.2 54.8	1076	<COX1...tRNA-Ser...tRNA-Asp...COX2...tRNA-Lys>	This study	•		•		•	•	•
06822cee_F 07740cee_R	AATGGATGTCCCCACCATATCA AAGGCTAGCGCTATTCTAGC	06819 07736	57.6 54.1	917	<COX1...tRNA-Ser...tRNA-Asp...COX2...tRNA-Lys>	This study		•		•			

07723cee_F 08650cee_R	GAATAGCGCTAGCCTTTTAAGC GTGATAAGCGTGGGTTTGGT	07721 08644	54.2 55.4	923	<tRNA-Lys...ATP8...ATP6...COX3>	This study		•		•			•
07540cee_F 08940cee_R	GCAATTCAGGTCGCCTCAAC AGGCTTGAGTGGTAAATGCTC	07546 08934	59.0 55.4	1388	<COX2...ATP8...ATP6...COX3>	This study	•	•	•	•	•	•	•
08750cee_F 09560cee_R	CAATAGTCCTATTAACACTTGGC TAATTGAGGGAGTCAGAATGC	08733 09551	51.4 52.1	818	<COX3...tRNA-Gly...ND3>	This study	•		•		•	•	•
08820cee_F 09610cee_R	GACACCATACTCCAGCCGTC GATCCTATGGGGTCAATCCAC	08823 09607	57.3 56.9	784	<COX3... tRNA-Gly...ND3>	This study		•		•			
09302c_F 10872c_R	AAGCCACCATTTTGGTTTGAAGC GCTGCAAGGACTATAGAGCCTG	09304 10874	57.5 57.2	1570	<COX3... tRNA-Gly...ND3...tRNA-Arg...ND4L...ND4>	Matosiuk et al. (2014)	•	•	•	•	•	•	•
09930cee_F 10304cee_R	AGTGGCCCTAGCAGGACTA TAAGGAGAAGGCTTGAGGCT	09925 10300	56.7 57.5	375	<ND4L...ND4>	This study		•		•	•	•	
10349cee_F 11010cee_R	TTCCGACTCCCTATCAGCAC GGAGGCAGATTGAGCTGGT	10347 11008	55.9 57.2	661	<ND4>	This study		•		•			
10740cee_F 12060cee_R	AGTACAACCCCTACCTAATCC TCATGTAACAAATAGTCTACTG	10722 12048	55.1 50.4	1326	< ND4...tRNA-His...tRNA-Ser...tRNA-Leu...ND5>	This study	•		•		•	•	
10730cee_F 11480cee_R	CCTACCTAATCCTGATCAAACG TCCCGTGTAAGGAGGGTGT	10731 11474	54.7 57.5	743	<ND4>	This study		•		•			•
11265cee_F 12058cee_R	CAAGCCTAACTAATCTAGCTCTC GATGGATCATGTAACAAATAGTGC	11261 12054	52.7 52.1	793	<...tRNA-His...tRNA-Ser...tRNA-Leu...ND5>	This study		•		•			•
11710cee_F 13150cee_R	TTAGAGGATGACAGAAATCCGTT TCCTGCGAAAAGGCTTCCAAT	11689 13149	53.3 57.1	1460	< tRNA-Leu...ND5>	This study	•		•		•	•	•
11920cee_F 12700cee_R	ATCCATACTGGCCAAGAAATA ATTATGAGGCTAGTTGGCT	11917 12695	51.0 53.0	778	<ND5>	This study		•		•			
12570cee_F 13363cee_R	AGTTTGACAAATCCATCCTACTA CGGTGTATAATTGTGGGGAAATA	12566 13358	53.6 52.6	792	<ND5>	This study		•		•			
13020cee_F 14240cee_R	ACCTCCTTCACAGCCATCTACA TGGGAGGTCAATAAATGCGTTG	13000 14225	57.2 55.6	1225	<ND5...ND6...tRNA-Glu..cytb>	This study	•		•		•	•	•
13268cee_F 14232cee_R	ATCAGCAACATAACCCAAAACCT GCTGGGAGGTCAATAAATGCG	13264 14227	54.9 56.5	963	<ND5...ND6...tRNA-Glu..cytb>	This study		•		•			
14096cee_F 15235cee_R	CTCACATGGAATCTAACCATGAC TAAGACAGATGCTAGTTGTCCAA	14091 15230	53.3 53.2	1139	< tRNA-Glu...cytb>	This study		•					
ML103 ML104	GACTAATGATATGAAAAACCATCGTTG TTGTTCTTCATCTCTGGTTACAAGAC	14111 15354	52.8 55.0	1243	<tRNA-Glu...cytb...tRNA-Thr>	Chikuni et al. (1995)	•		•	•	•	•	•
15180cee_F 15530cee_R	ACATGAATCGGAGGACAACCA TGTTGAGTGGAAGCTGTATTG	15165 15531	55.8 53.2	366	<cytb...tRNA-Thr...tRNA-Pro...d-loop>	This study	•	•	•	•	•	•	•
tRNA-PRO tRNA-PHE	CACCATCAACCCCAAAGCTGAAG CAGTGCCTTGCTTTGGGTTAAGC	15393 00034	60.7 59.5	1003	<tRNA-Pro...d-loop...tRNA-Phe>	Wood and Phua (1996)	•	•	•	•	•	•	•
16104c_F 00487c_R	CTGGACTTAAGTGCATCTTGAGC CAGTTTGGGTCTTAGCTATCGTG	16093 00487	55.9 55.4	756	<d-loop...tRNA-Phe...12s_RNA>	Matosiuk et al. (2014)	•	•	•	•	•	•	•

• primers pairs used in a given phylogenetic lineage/haplogroup analysi

Table S5. List of *Cervinae* representatives and GenBank accession numbers of their mitogenomic sequences used in phylogenetic analyses. The names are given as found in GenBank, not necessarily according to the presently accepted taxonomy.

Acc. num.	Taxon
NC_020680.1	<i>Axis axis</i>
MF435989.1	<i>Axis porcinus</i>
MH443787.1	<i>Axis porcinus</i>
MH443790.1	<i>Axis porcinus</i>
NC_020681.1	<i>Axis porcinus</i>
NC_050863.1	<i>Cervus canadensis</i>
NC_039923.1	<i>Cervus canadensis kansuensis</i>
KJ025072.1	<i>Cervus canadensis songaricus</i>
NC_014703.1	<i>Cervus canadensis songaricus</i>
KP172593.1	<i>Cervus elaphus</i>
MF872247.1	<i>Cervus elaphus</i>
MF872248.1	<i>Cervus elaphus</i>
NC_007704.2	<i>Cervus elaphus</i>
KU942399.1	<i>Cervus elaphus alxaicus</i>
KT290948.1	<i>Cervus elaphus hippelaphus</i>
KX449334.1	<i>Cervus elaphus macneilli</i>
NC_013840.1	<i>Cervus hanglu yarkandensis</i>
NC_006993.1	<i>Cervus nippon centralis</i>
HQ191428.1	<i>Cervus nippon hortulorum</i>
KR868807.1	<i>Cervus nippon hortulorum</i>
KX689229.1	<i>Cervus nippon hortulorum</i>
NC_013834.1	<i>Cervus nippon hortulorum</i>
JN389444.1	<i>Cervus nippon kopschi</i>
NC_016178.1	<i>Cervus nippon kopschi</i>
NC_018595.1	<i>Cervus nippon sichuanicus</i>
EF058308.1	<i>Cervus nippon taiouanus</i>
NC_008462.1	<i>Cervus nippon taiouanus</i>
NC_007179.1	<i>Cervus nippon yakushimae</i>
NC_006973.1	<i>Cervus nippon yesoensis</i>
NC_020700.1	<i>Dama dama</i>
NC_024819.1	<i>Dama mesopotamica</i>
NC_008749.1	<i>Elaphodus cephalophus</i>
NC_050383.1	<i>Elaphodus cephalophus cephalophus</i>
JN632632.1	<i>Elaphurus davidianus</i>
NC_018358.1	<i>Elaphurus davidianus</i>
NC_004577.1	<i>Muntiacus crinifrons</i>
NC_041100.1	<i>Muntiacus feae</i>
NC_048506.1	<i>Muntiacus gongshanensis</i>
NC_004563.1	<i>Muntiacus muntjak</i>
NC_036430.1	<i>Muntiacus putaoensis</i>
NC_004069.1	<i>Muntiacus reevesi</i>
NC_008491.1	<i>Muntiacus reevesi micrurus</i>
MK050505.1	<i>Muntiacus vaginalis</i>
NC_016920.1	<i>Muntiacus vuquangensis</i>
JN632697.1	<i>Panolia eldii</i>
NC_014701.1	<i>Panolia eldii</i>
KU133959.1	<i>Panolia eldii eldii</i>
JN632690.1	<i>Przewalskium albirostris</i>
MF966595.1	<i>Przewalskium albirostris</i>
NC_016707.1	<i>Przewalskium albirostris</i>
NC_020743.1	<i>Rucervus duvaucelii</i>
MG788693.1	<i>Rucervus duvaucelii branderi</i>
NC_045060.1	<i>Rucervus duvaucelii branderi</i>
NC_020744.1	<i>Rusa alfredi</i>
NC_020745.1	<i>Rusa timorensis</i>
NC_031835.1	<i>Rusa unicolor</i>
KY946815.1	<i>Rusa unicolor hainana</i>
EF035448.1	<i>Rusa unicolor swinhoei</i>






Table S6. Substitution models and partitions applied in phylogenetic analyses of data set including representatives of Muntiacini and Cervini. A digit 1, 2 or 3 after the dot indicates the codon position in protein-coding genes.

Software	Substitution model	Partitions
IQ-TREE	TIM2+F+R3	atp6.1, atp8.1, cyt.1, nd2.1, nd4.1, nd5.1, rRNA, 12s, rRNA, 16s, tRNA-Arg, tRNA-Asp, tRNA-Gly, tRNA-His, tRNA-Ile, tRNA-Leu2, tRNA-Lys, tRNA-Phe, tRNA-Thr, tRNA-Trp, tRNA-Tyr, tRNA-Val
	HKY+F+R2	atp6.2, cox1.2, cox2.2, cox3.2, cyt.2, nd1.2, nd2.2, nd3.2, nd4L.2, nd4.2, nd5.2, nd6.2, tRNA-Met
	TN+F+I+Γ4	atp6.3, atp8.3, cox1.3, cox2.3, nd4L.3
	K3Pu+F+R3	atp8.2, tRNA-Ser2, control region
	TNe+I+Γ4	cox1.1, cox2.1, cox3.1, nd1.1, nd3.1, nd4L.1
	TIM2+F+I+Γ4	cox3.3, cyt.3, nd1.3, nd2.3, nd3.3, nd4.3, nd5.3
	HKY+F+I+Γ4	nd6.1, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Gln, tRNA-Glu, tRNA-Leu1, tRNA-Pro, tRNA-Ser1
	HKY+F+Γ4	nd6.3
MrBayes	mixed+I+Γ5	nd4.1, atp6.1, cyt.1
	mixed+I+Γ5	nd5.2, nd2.2, atp6.2
	mixed+I+Γ5	atp6.3, cox1.3, cox2.3
	mixed+Γ5	tRNA-Ser2, atp8.1, tRNA-Asp, tRNA-Lys
	mixed+I+Γ5	atp8.2, tRNA-Arg
	mixed+Γ5	atp8.3
	mixed+I+Γ5	tRNA-Cys, cox1.1
	mixed+I	cox2.2, cox3.2, cox1.2
	mixed+Γ5	nd3.1, cox2.1
	mixed+I+Γ5	cox3.1, tRNA-Met, tRNA-Ile
	mixed+I+Γ5	cox3.3, nd1.3, nd4L.3, nd4.3, cyt.3, nd5.3
	mixed+I+Γ5	cyt.2
	mixed+I+Γ5	nd1.1, tRNA-Trp, nd4L.1
	mixed+I+Γ5	nd1.2, nd3.2, nd4L.2, nd4.2
	mixed+I+Γ5	nd2.1, tRNA-Val, tRNA-Thr, nd5.1
	mixed+Γ5	nd2.3, nd3.3
	mixed+I+Γ5	nd6.1
	mixed+I	nd6.2
	mixed+Γ5	nd6.3
	mixed+I+Γ5	rRNA 12s, tRNA-Gly, tRNA-Tyr, rRNA 16s, tRNA-Leu2
Beast	mixed+I+Γ5	tRNA-Gln, tRNA-Glu, tRNA-Ala
	mixed+I	tRNA-Leu1, tRNA-Asn, tRNA-Pro, tRNA-Ser1
	mixed+I+Γ5	tRNA-His, tRNA-Phe
	mixed+I+Γ5	control region
	TRN+I+Γ5	nd4.1, atp6.1, cyt.1
	TRN+I+Γ5	nd5.2, nd2.2, atp6.2
	TRN+I+Γ5	atp6.3, cox1.3, cox2.3
	HKY+Γ5	tRNA-Ser2, atp8.1, tRNA-Asp, tRNA-Lys
	HKY+I+Γ5	atp8.2, tRNA-Arg
	HKY+Γ5	atp8.3
	TIMEF+I+Γ5	tRNA-Cys, cox1.1
	HKY+I	cox2.2, cox3.2, cox1.2
	TRNEF+Γ5	nd3.1, cox2.1
	TRNEF+I+Γ5	cox3.1, tRNA-Met, tRNA-Ile
	GTR+I+Γ5	cox3.3, nd1.3, nd4L.3, nd4.3, cyt.3, nd5.3
	TRN+I+Γ5	cyt.2
	SYM+I+Γ5	nd1.1, tRNA-Trp, nd4L.1
	GTR+I+Γ5	nd1.2, nd3.2, nd4L.2, nd4.2
	TRN+I+Γ5	nd2.1, tRNA-Val, tRNA-Thr, nd5.1
	TRN+Γ5	nd2.3, nd3.3
	GTR+I+Γ5	nd6.1
	HKY+I	nd6.2
	HKY+Γ5	nd6.3
	GTR+I+Γ5	rRNA 12s, tRNA-Gly, tRNA-Tyr, rRNA 16s, tRNA-Leu2
	TRN+I+Γ5	tRNA-Gln, tRNA-Glu, tRNA-Ala
	HKY+I	tRNA-Leu1, tRNA-Asn, tRNA-Pro, tRNA-Ser1
	HKY+I+Γ5	tRNA-His, tRNA-Phe
	TIM+I+Γ5	control region

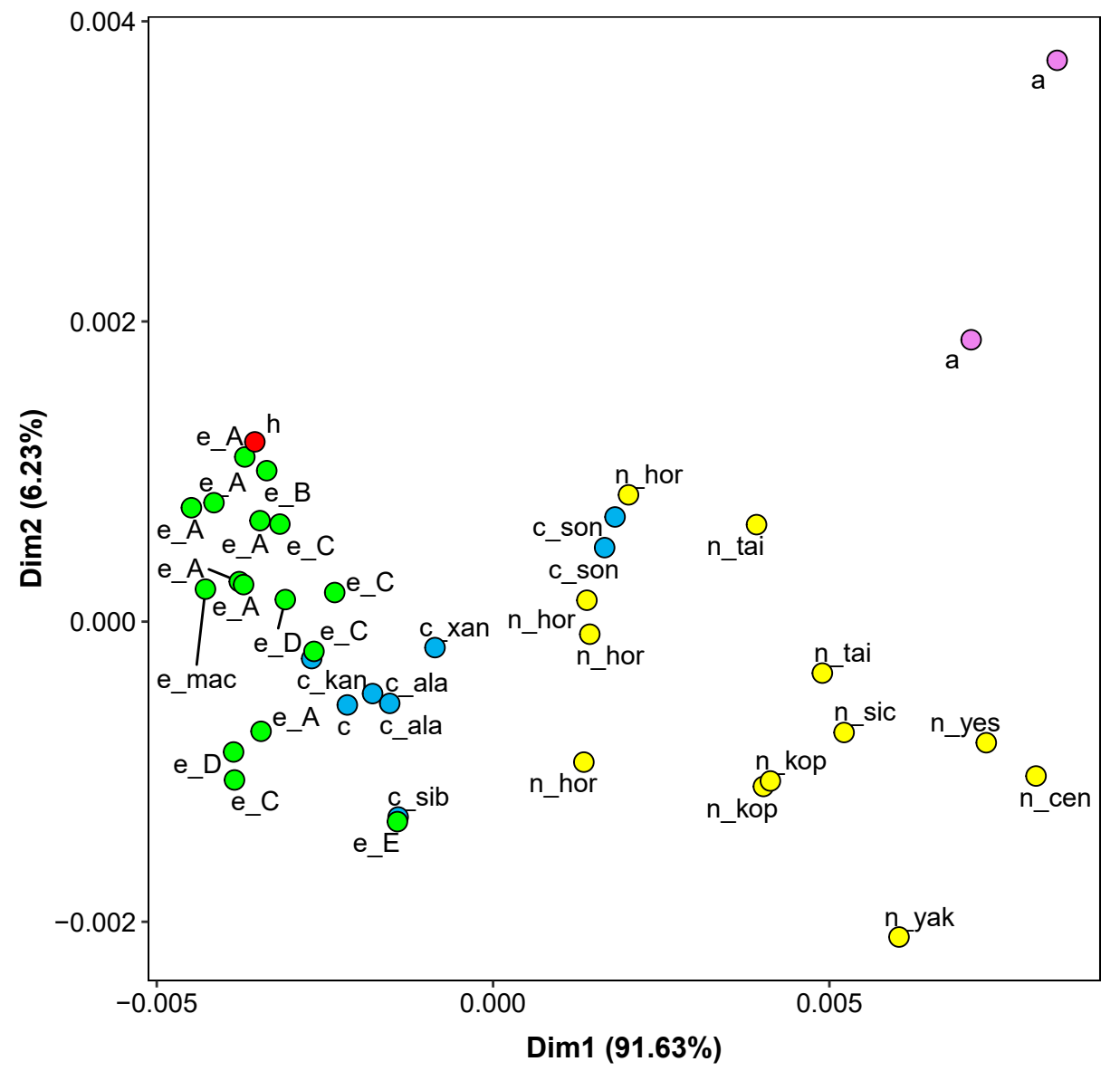
Table S7. Substitution models and partitions applied in Beast analyses of data set including only representatives of *Cervus*. A digit 1, 2 or 3 after the dot indicates the codon position in protein-coding genes.

Substitution model	Partitions
HKY+I	atp6.1, tRNA-Ser2
TIM+I	atp6.2, nd2.2, nd4L.2, nd3.2, nd4.2
TRN+Γ5	atp6.3
HKY+Γ5	atp8.1, atp8.2
K81UF+I	atp8.3, cox2.3
TRN+I	cox1.1
HKY+I	nd6.2, cox1.2, cytb.2, cox3.2
GTR+Γ5	cox1.3
K80+I	nd4L.1, cox2.1
F81	cox2.2
TRNEF+I+Γ5	nd1.1, tRNA-Met, nd3.1, cox3.1
TRN+Γ5	cox3.3, nd5.3
TRN+I	cytb.1, nd5.1
TRN+Γ5	cytb.3
K81UF+I	nd1.2, nd5.2
TRN+Γ5	nd2.3, nd3.3, nd4.3, nd1.3, nd4L.3
TRN+I+Γ5	nd2.1, tRNA-Val, rRNA 12s, tRNA-Trp, nd4.1, tRNA-Thr
GTR	nd6.1
TVM	nd6.3
HKY+I+Γ5	tRNA-Leu1, tRNA-Leu2, tRNA-Gly, tRNA-Arg, rRNA 16s
TRN+I	tRNA-Ala, tRNA-Glu
HKY	tRNA-Cys, tRNA-Gln, tRNA-Asn, tRNA-Ser1, tRNA-Pro
HKY+Γ5	tRNA-Lys, tRNA-Phe, tRNA-Asp, tRNA-Tyr
HKY	tRNA-Ile, tRNA-His
TIM+I+Γ5	control region

Figure S1. Correspondence analysis plots obtained for the nucleotide composition of 13 protein-coding genes (PCG), RNA genes and control region (CR) from various *Cervus* taxa: a - *C. albirostris*; c - *C. canadensis*; c_ala - *C. canadensis alashanicus*; c_kan - *C. canadensis kansuensis*; c_sib - *C. canadensis sibiricus*; c_son - *C. canadensis songaricus*; c_xan - *C. canadensis xanthopygus*; e_A - *C. elaphus* haplogroup A; e_B - *C. elaphus* haplogroup B; e_C - *C. elaphus* haplogroup C; e_D - *C. elaphus* haplogroup D; e_E - *C. elaphus* haplogroup E; e_mac - *C. elaphus macneilli*; h - *C. hanglu yarkandensis*; n_cen - *C. nippon centralis*; n_hor - *C. nippon hortulorum*; n_kop - *C. nippon kopschi*; n_sic - *C. nippon sichuanicus*; n_tai - *C. nippon taiouanus*; n_yak - *C. nippon yakushimae*; n_yes - *C. nippon yesoensis*.

-  *C. albirostris*
-  *C. canadensis*
-  *C. elaphus*
-  *C. hanglu*
-  *C. nippon*

PCG+RNA+CR



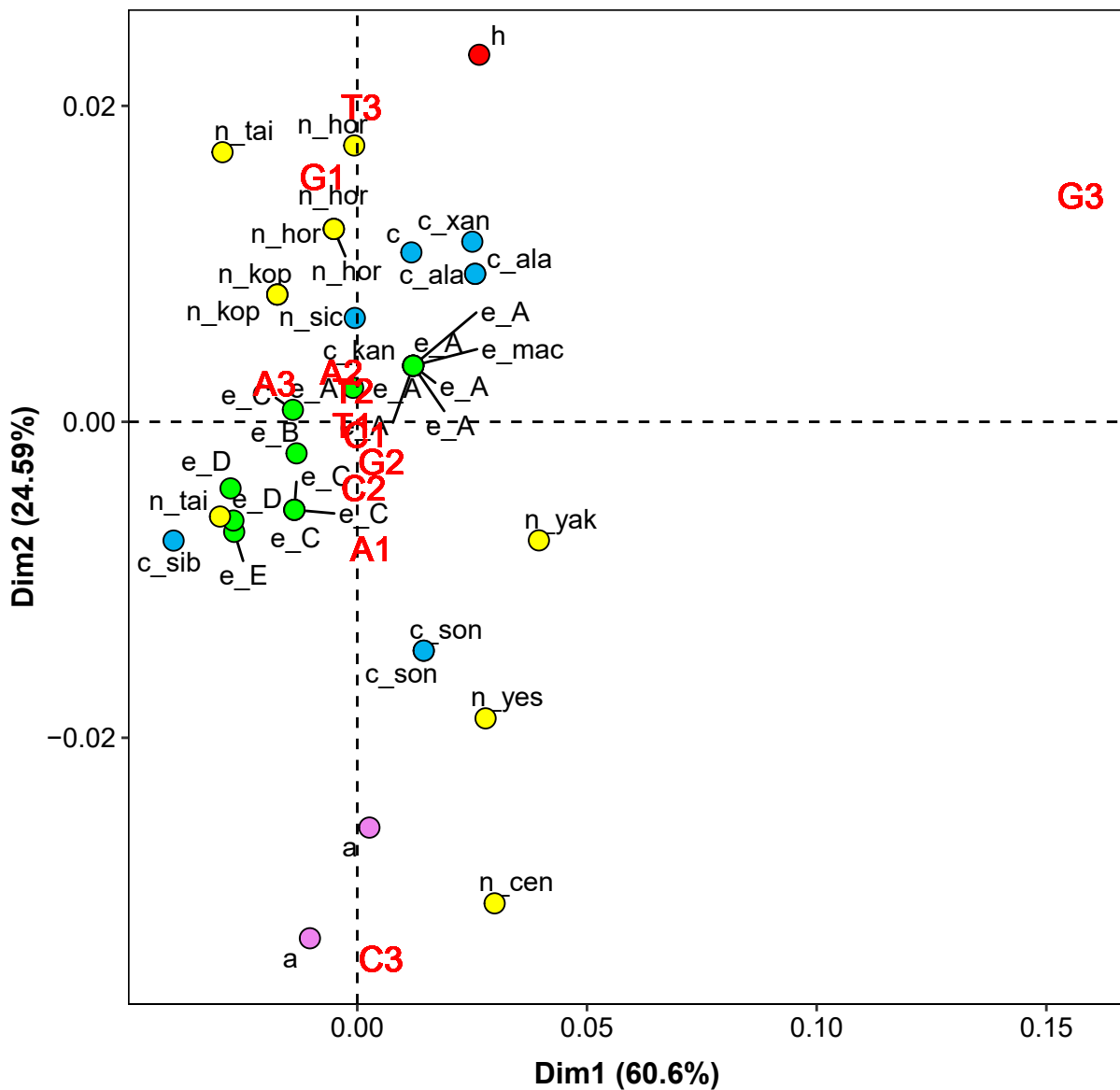
Dim2 (6.23%)

Dim1 (91.63%)

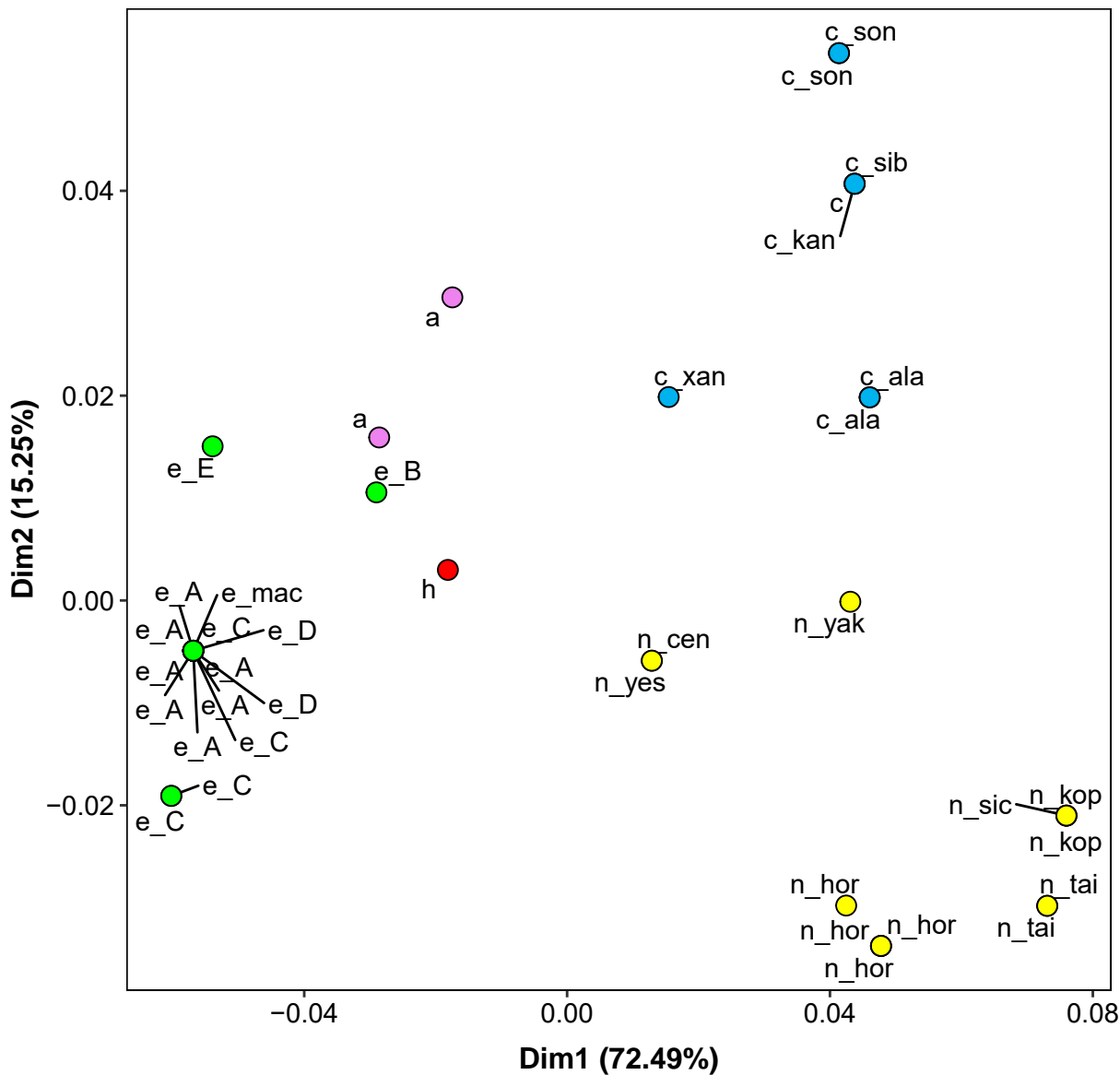
Scatter plot showing the first two principal components (Dim1 and Dim2) for 20 variables. The x-axis is Dim1 (60.6%) and the y-axis is Dim2 (24.2%). Variables are colored by group: blue (c_sib, c, c_kan, c_ala, c_xan, c_son), yellow (n_tai, n_hor, n_sic, n_kop, n_yak, n_cen), green (e_D, e_E, e_C, e_B, e_A, e_mac), pink (a), and red (h). Lines connect related variables: n_kop to n_sic, e_D to e_E, e_C to e_B, e_A to e_mac, e_A to e_A, e_A to e_A, e_A to e_A, c_ala to c_xan, c_son to c_son, and a to a.

Dim2 (24.59%)

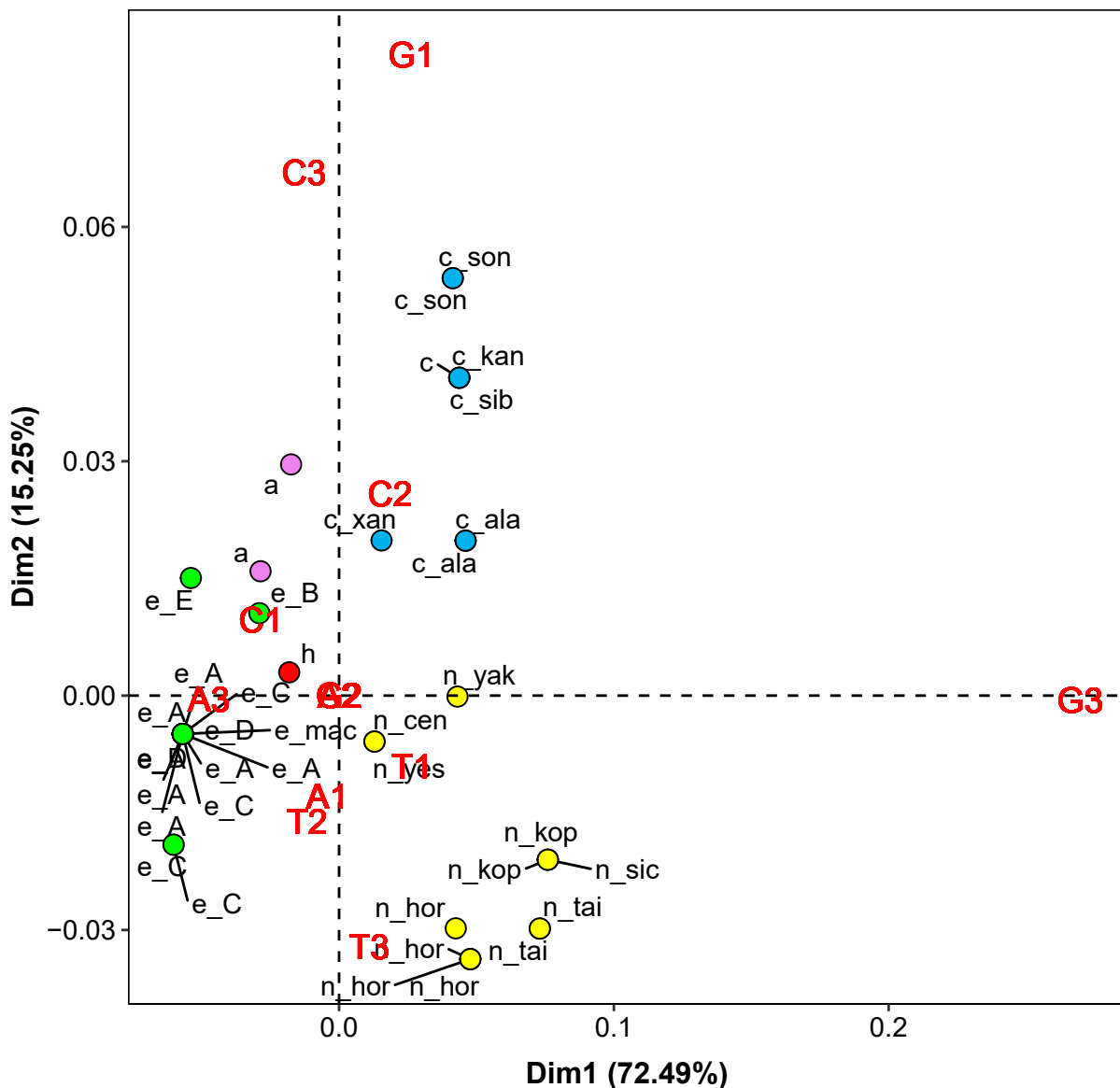
ATP6



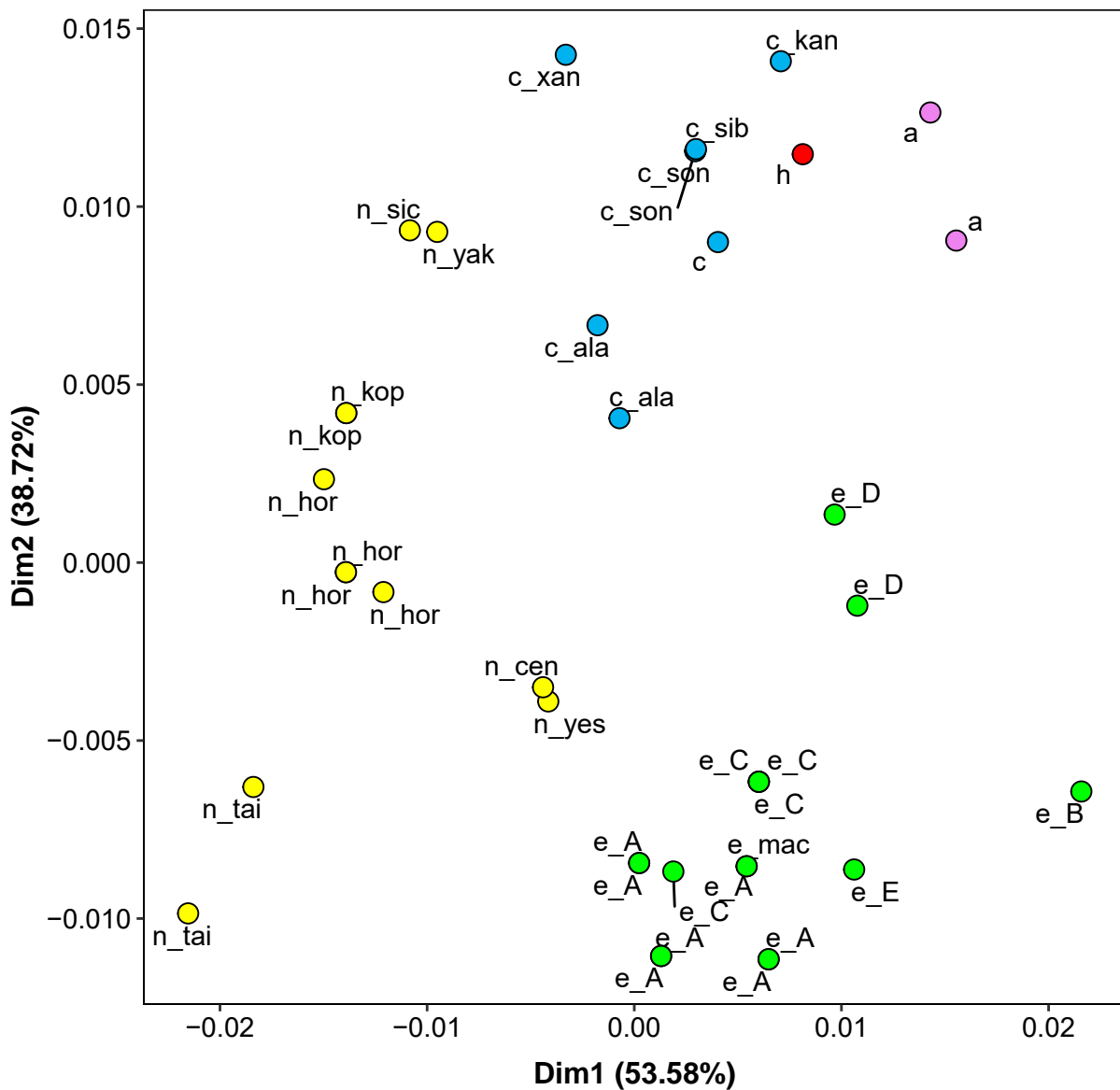
ATP8



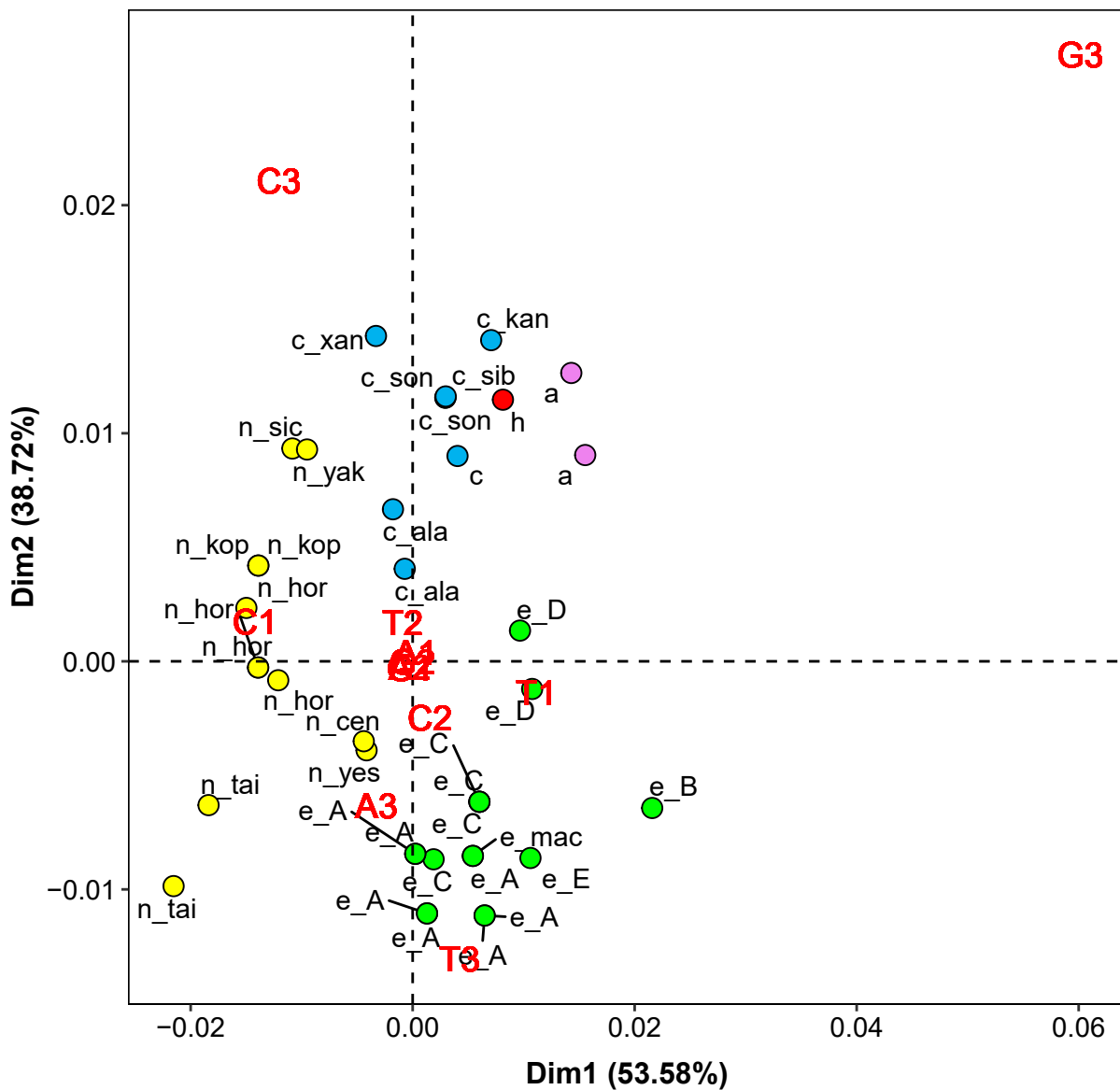
ATP8



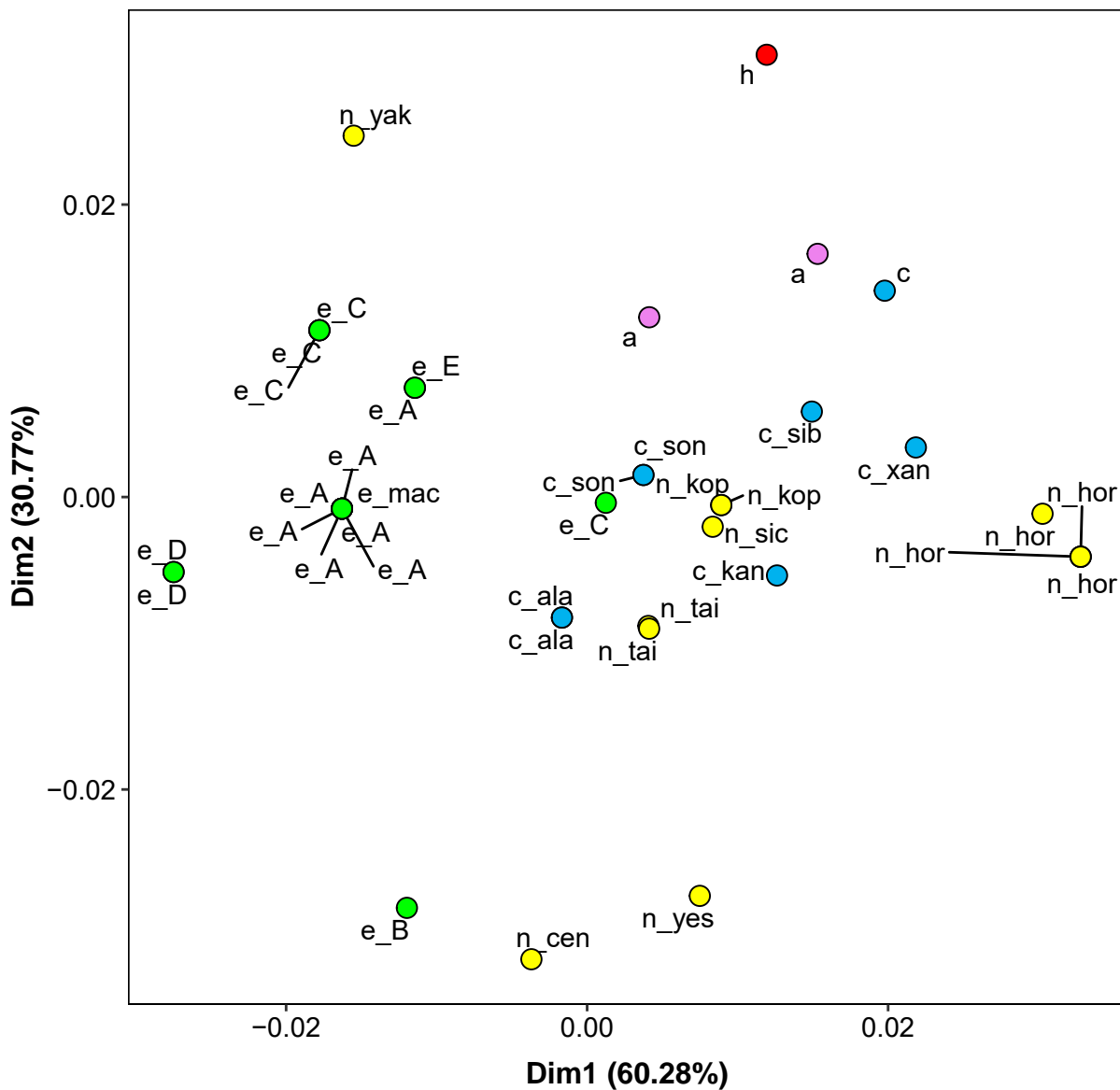
COX1



COX1



COX2



Dim2 (30.77%)

Dim1 (60.28%)

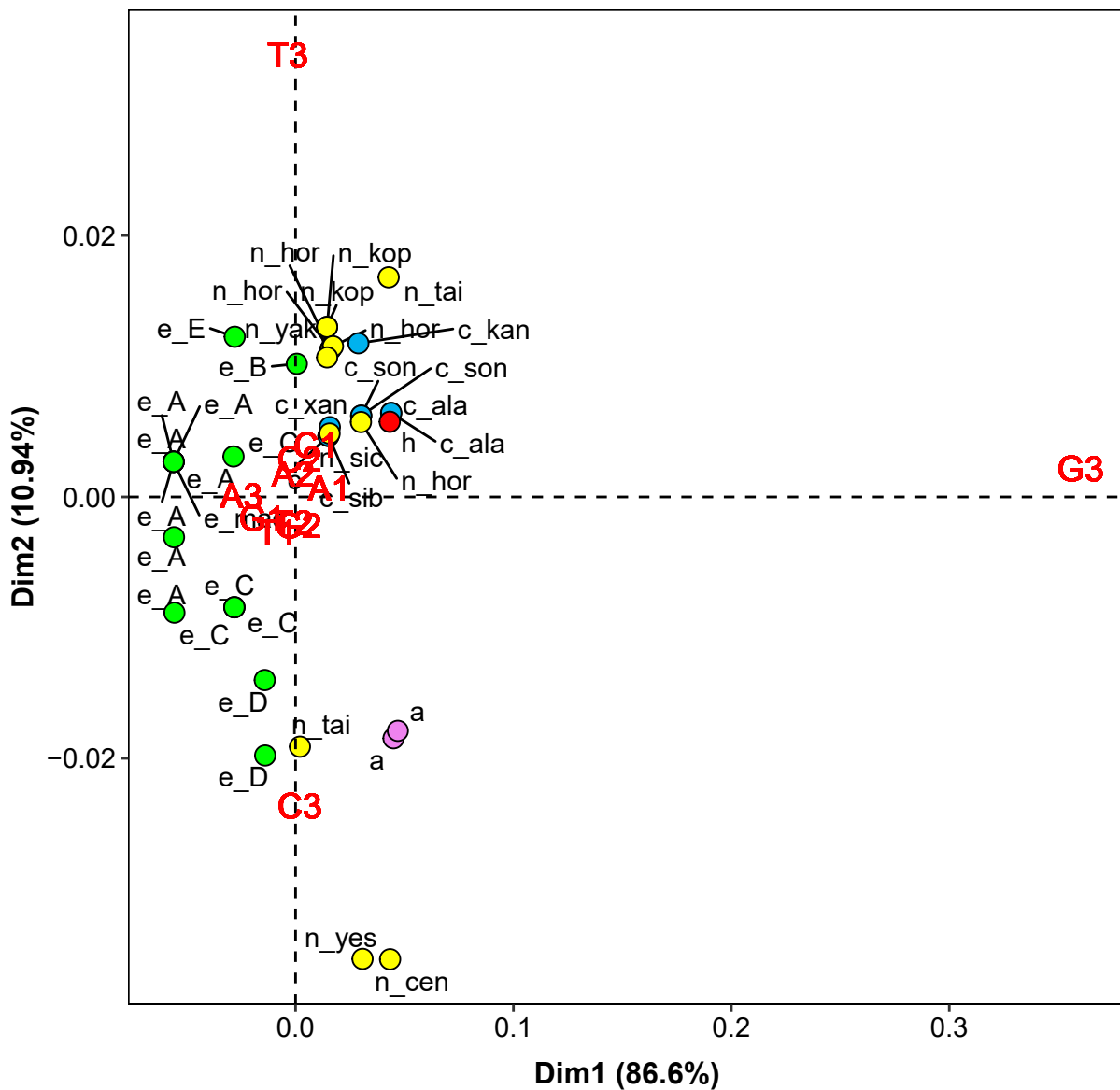
[illegible]

-0.06

0.00

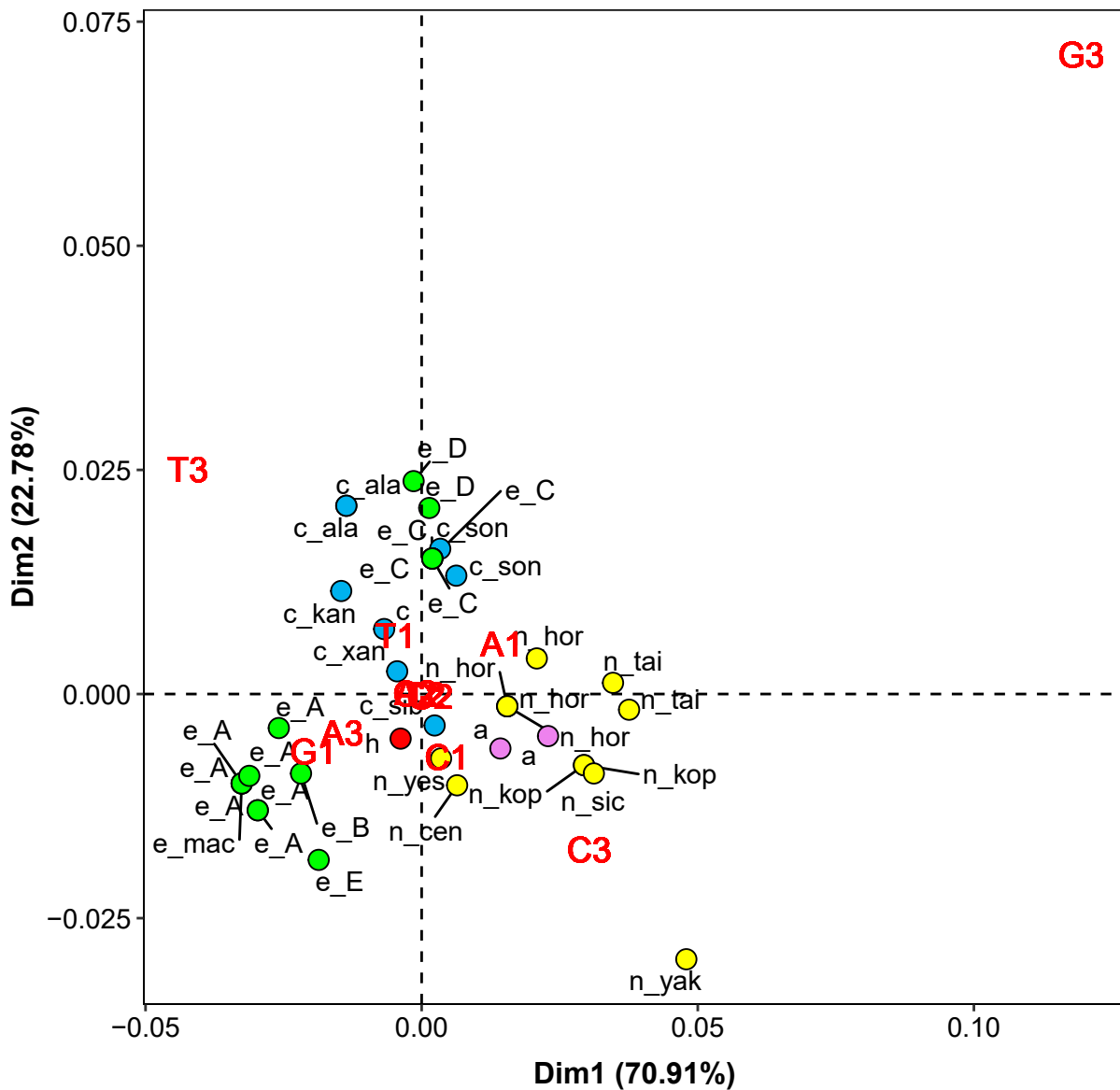
0.03

COX3

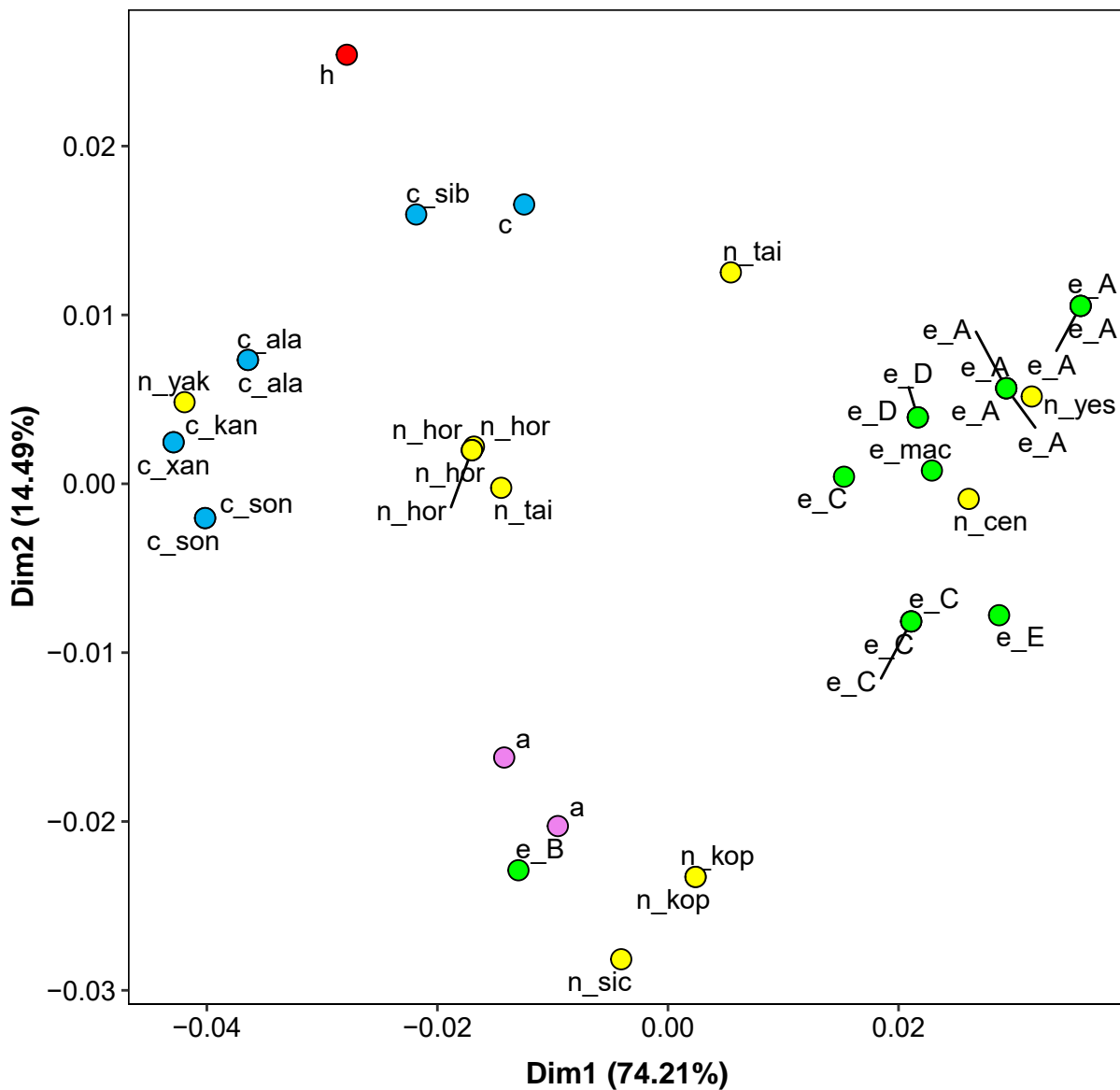


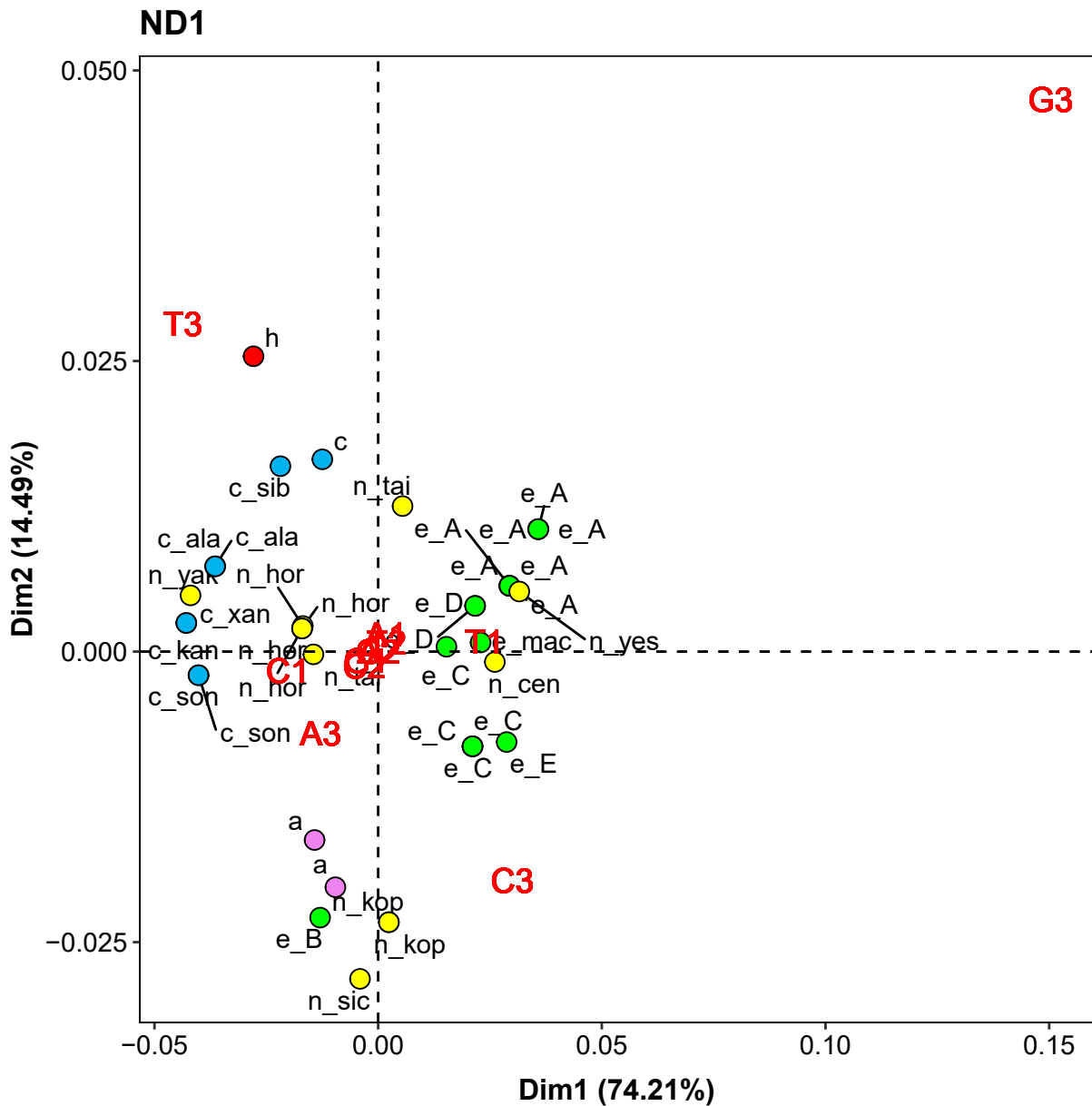
Dim2 (22.78%)

CYTB



ND1

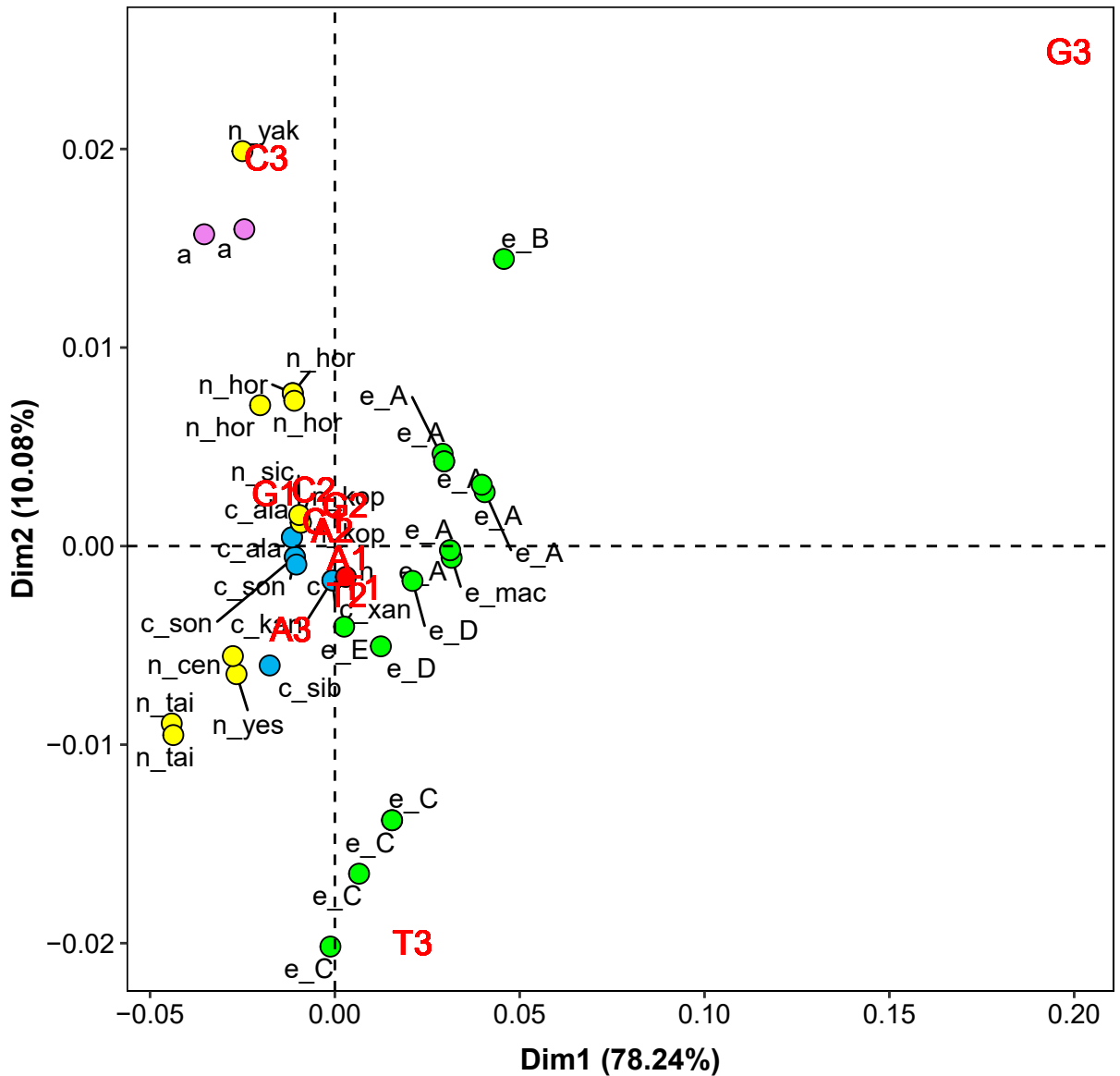




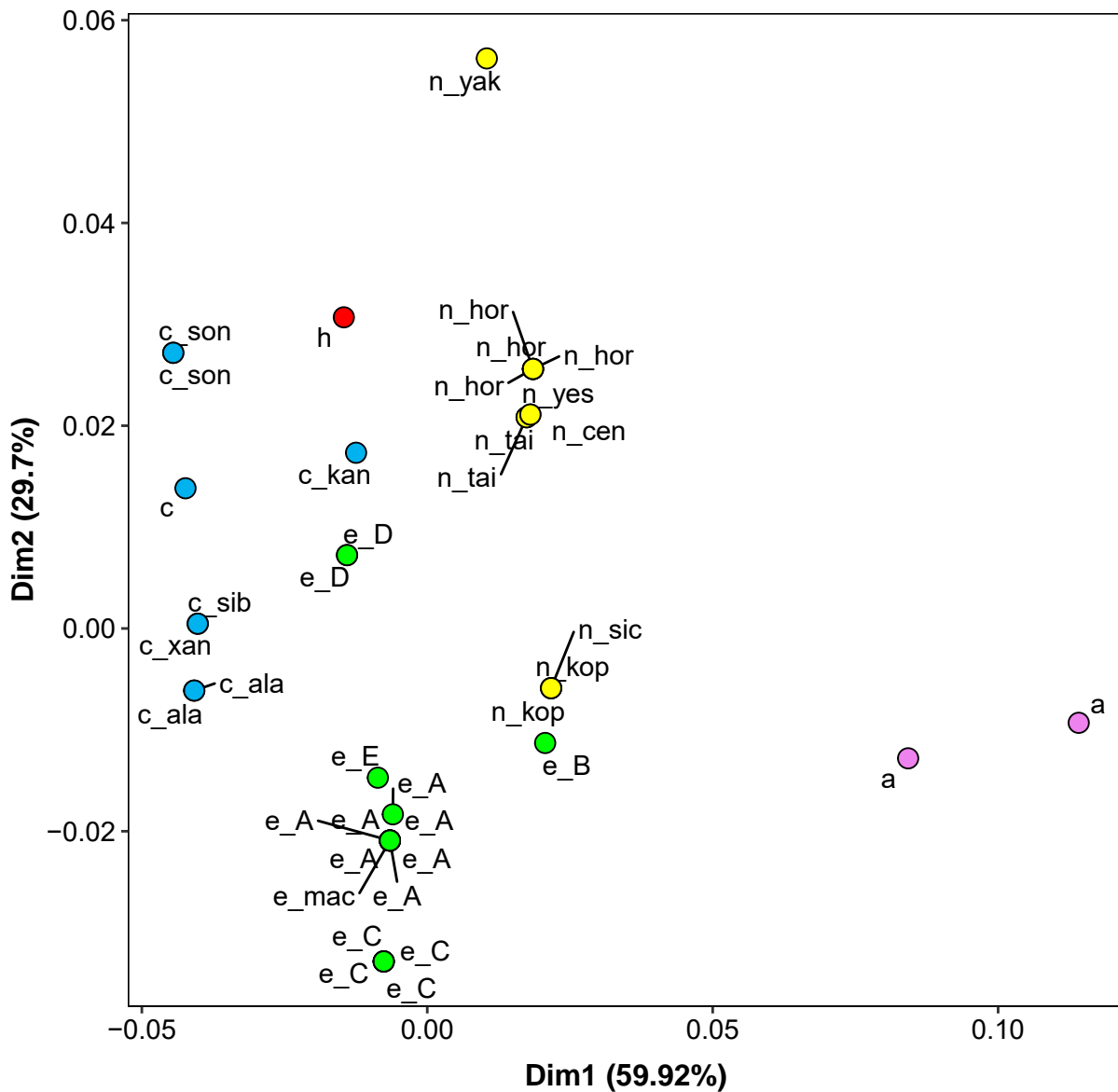
Dim2 (10.08%)

Dim1 (78.24%)

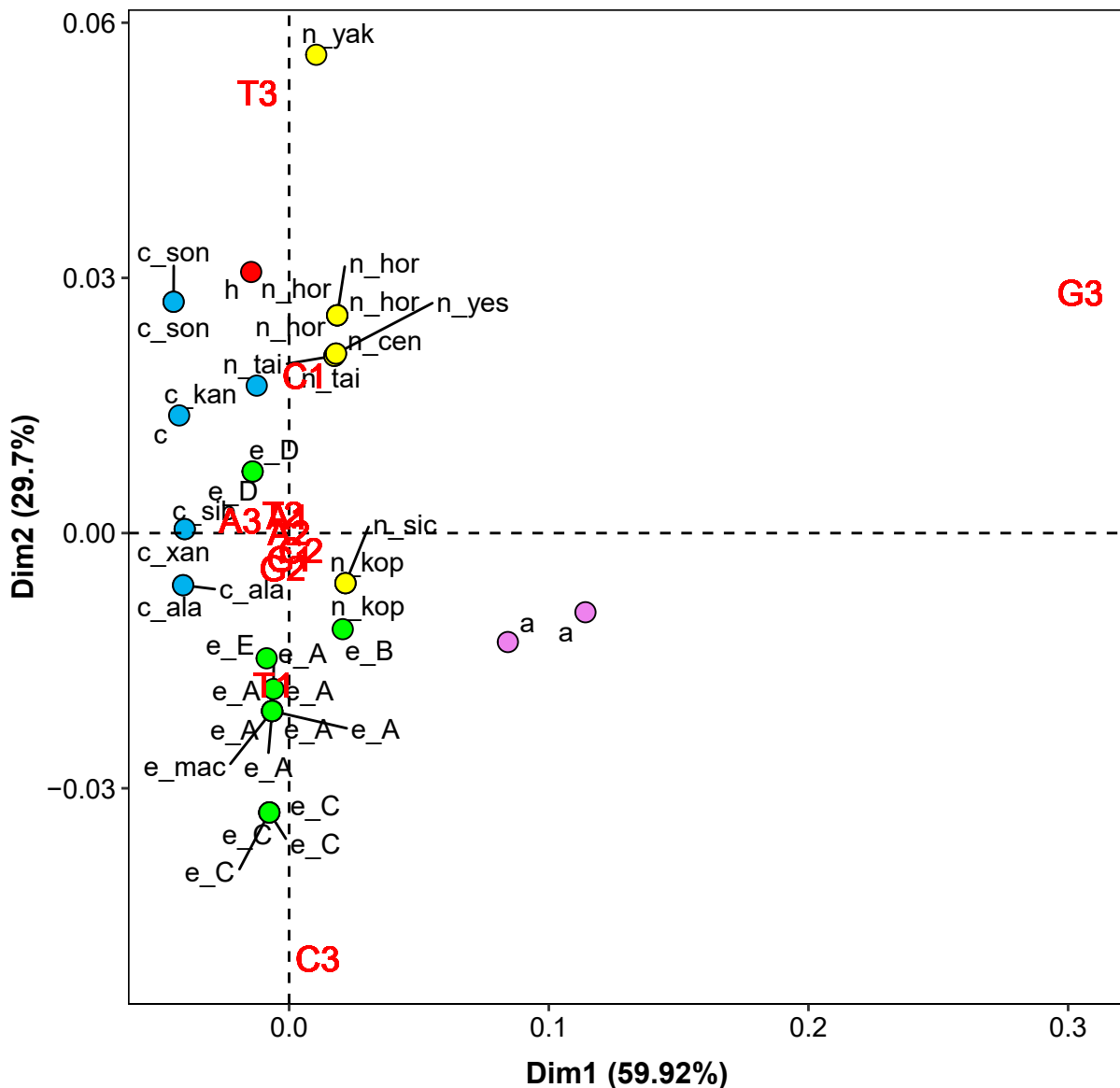
ND2



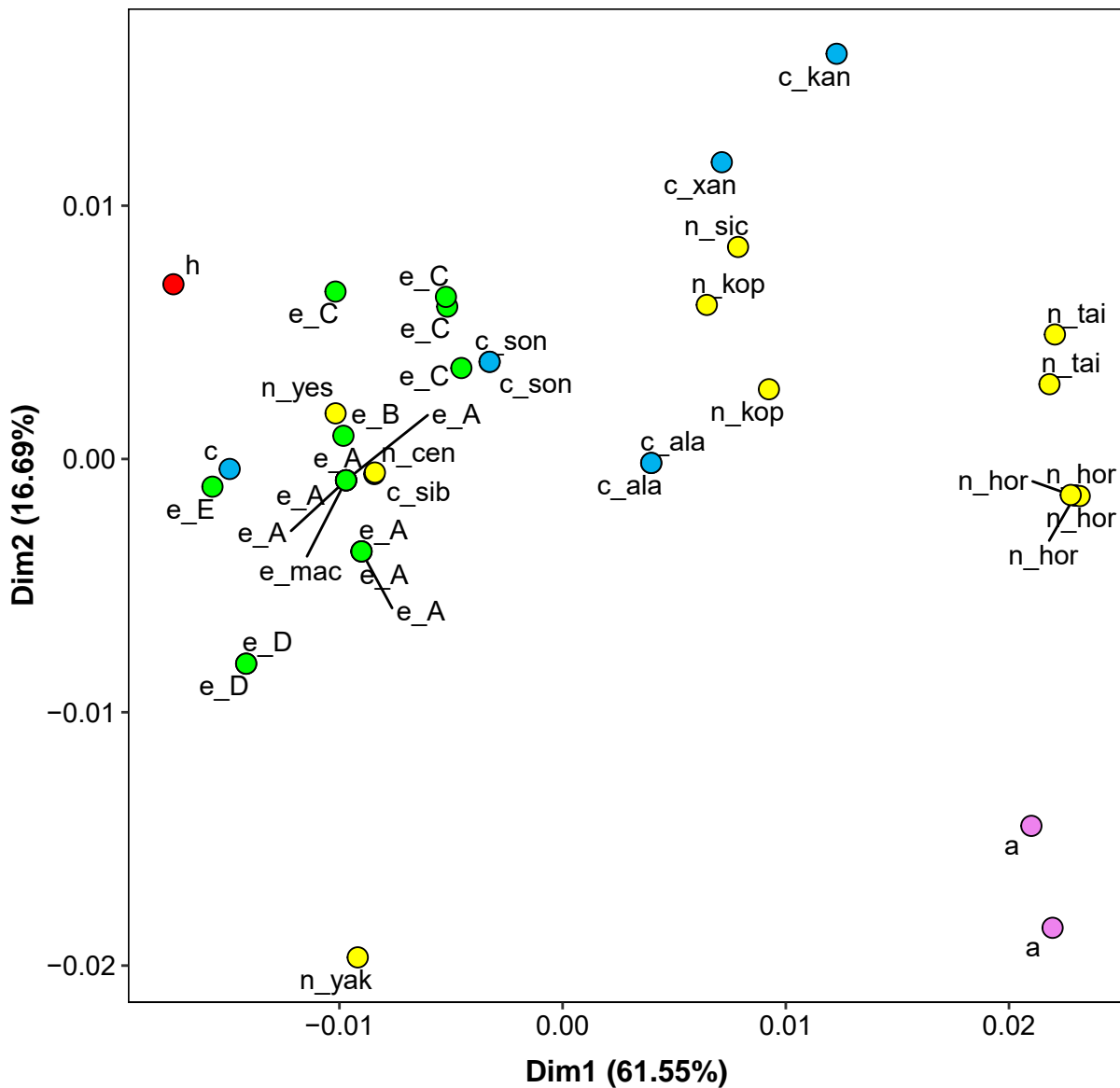
ND3



ND3



ND4



Dim2 (16.69%)

Dim1 (61.55%)

A PCA plot showing the first two principal components of genetic data. The x-axis is labeled 'Dim1 (48.08%)' and ranges from -0.06 to 0.02. The y-axis is unlabeled. Data points are colored by population: blue (c_ala, c_sib, c_son, c_xan, c_kan), yellow (n_yak, n_sic, n_kop, n_cen, n_tai, n_hor, n_yes), red (h), and green (e_C, e_A, e_E, e_D, e_mac). Lines connect points representing the same population. The plot shows a clear separation of populations along the x-axis, with c_ala and c_sib on the left, c_son and c_xan on the right, and n_yak at the bottom left. The e_C, e_A, e_E, e_D, and e_mac points are clustered on the far right.

Dim2 (42.19%)

Dim1 (48.08%)

G3

T3

T1

Th

551

A2

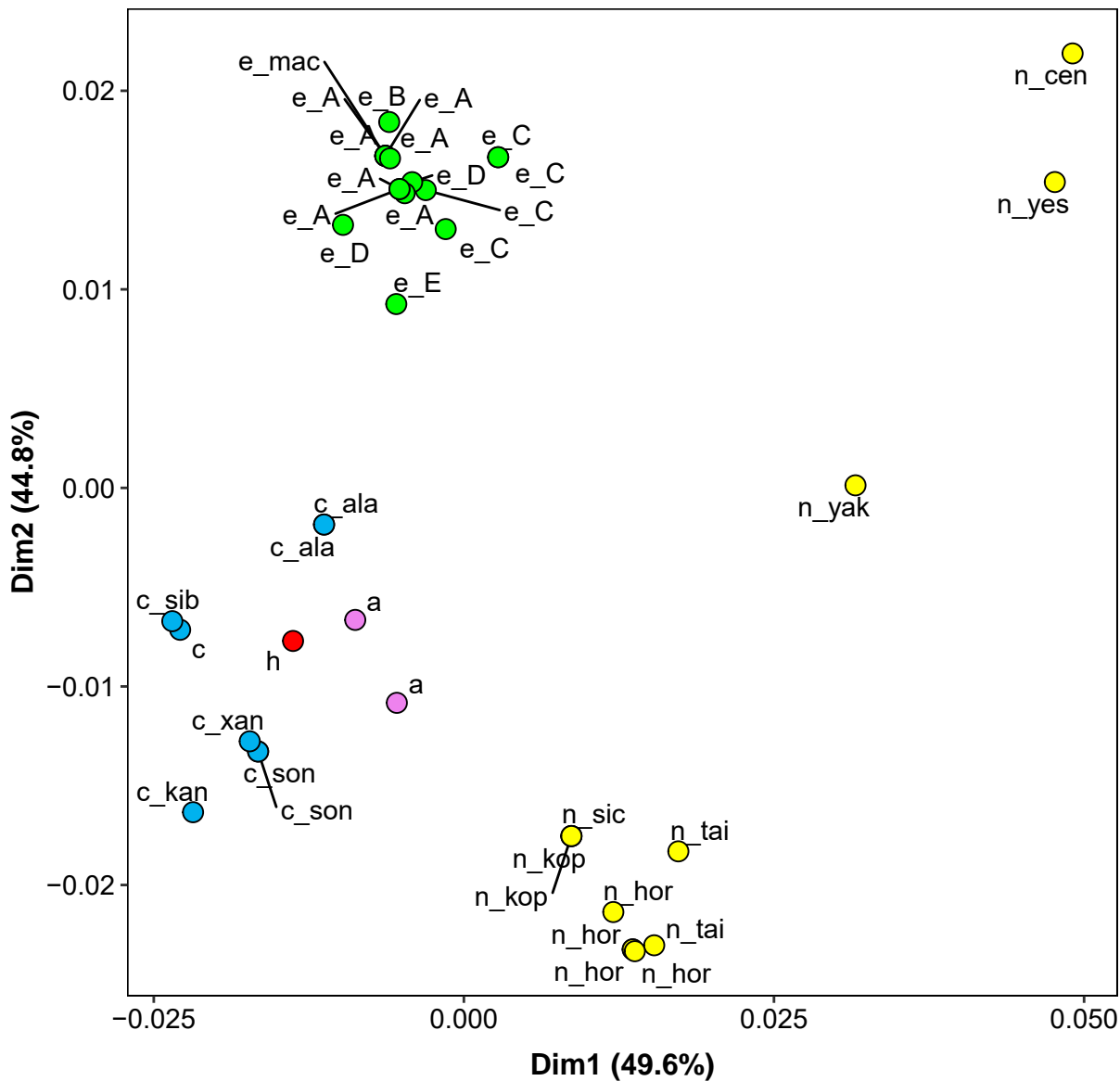
11e

A3

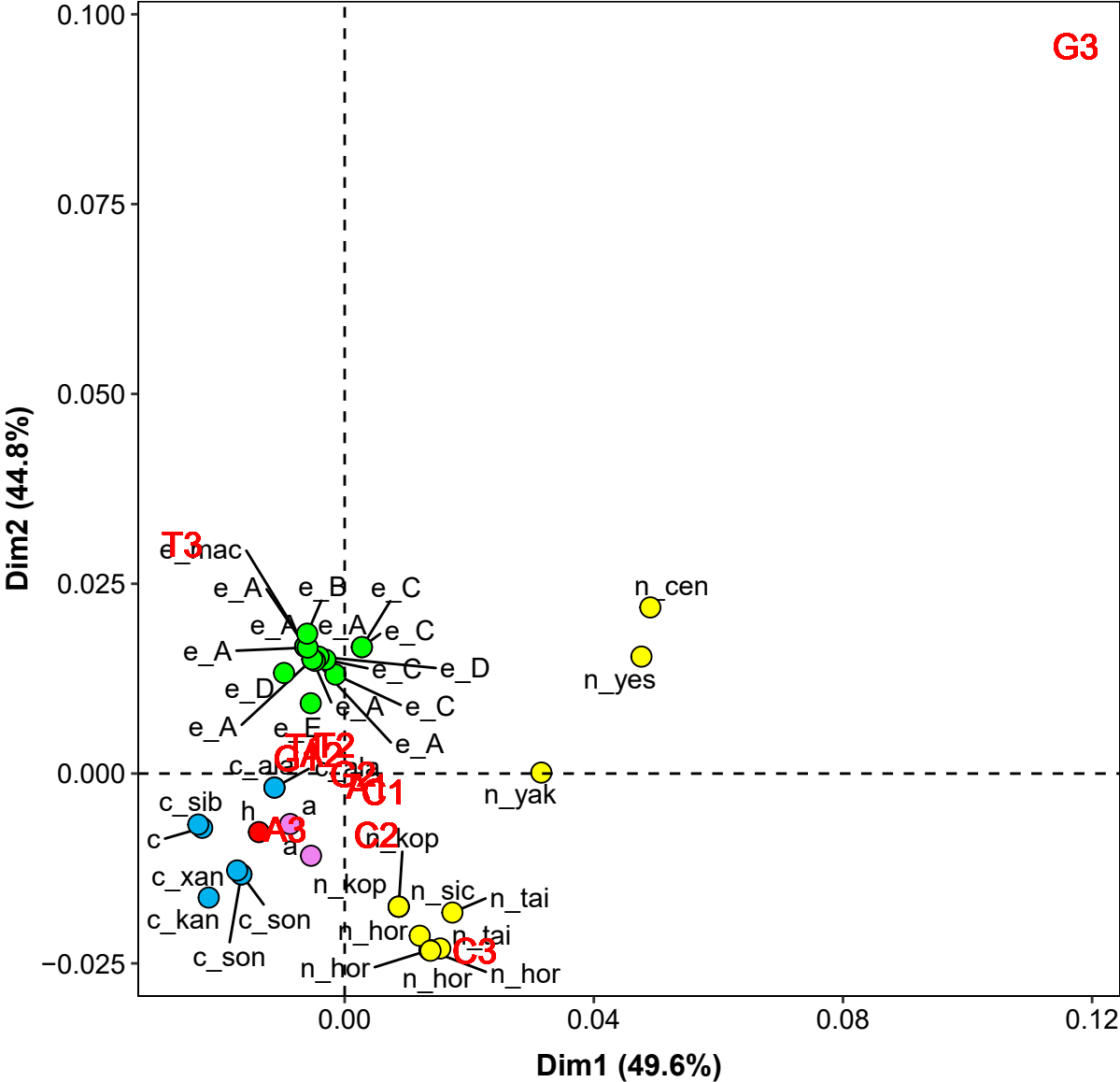
C3

C1

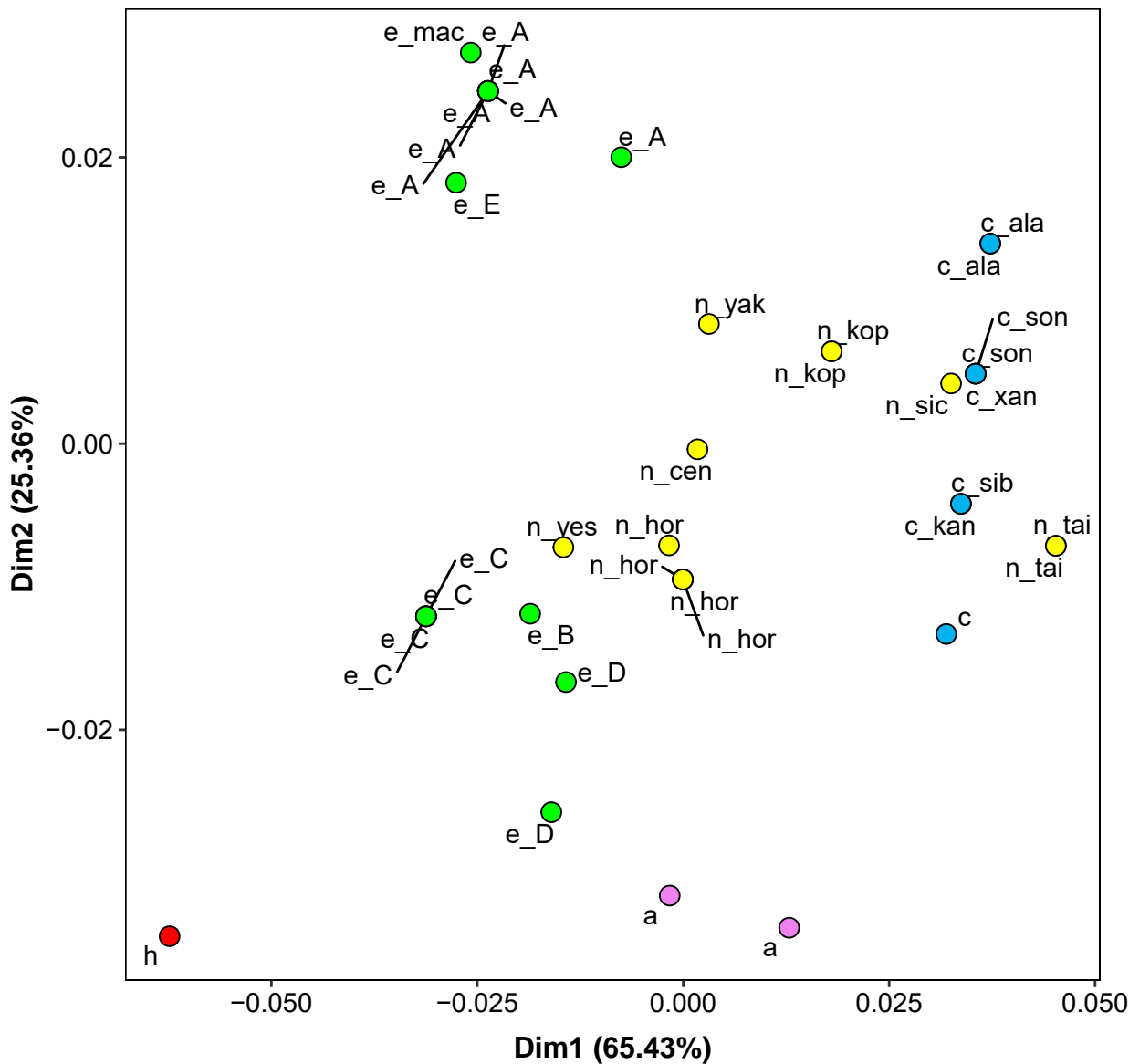
ND5



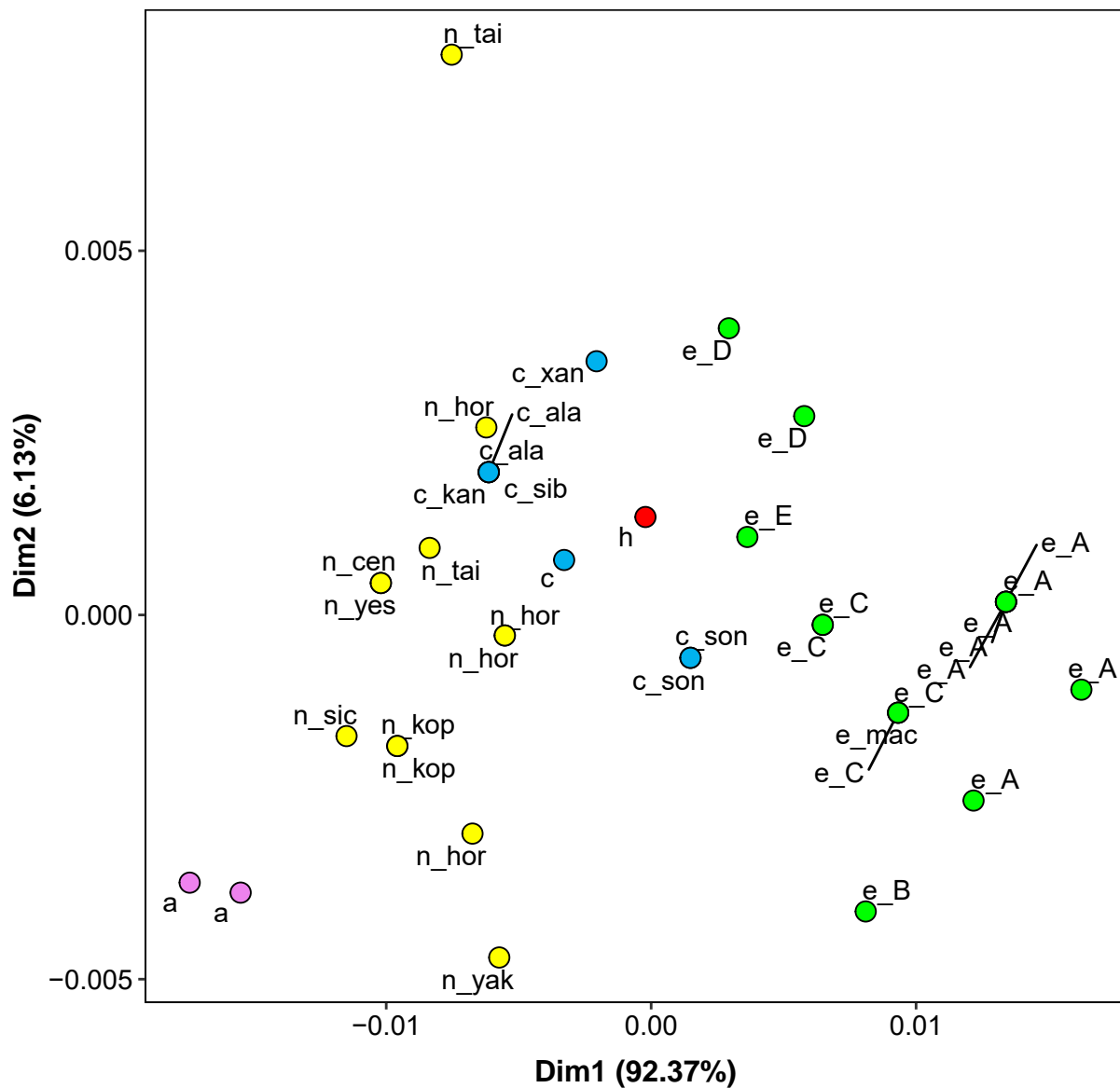
ND5



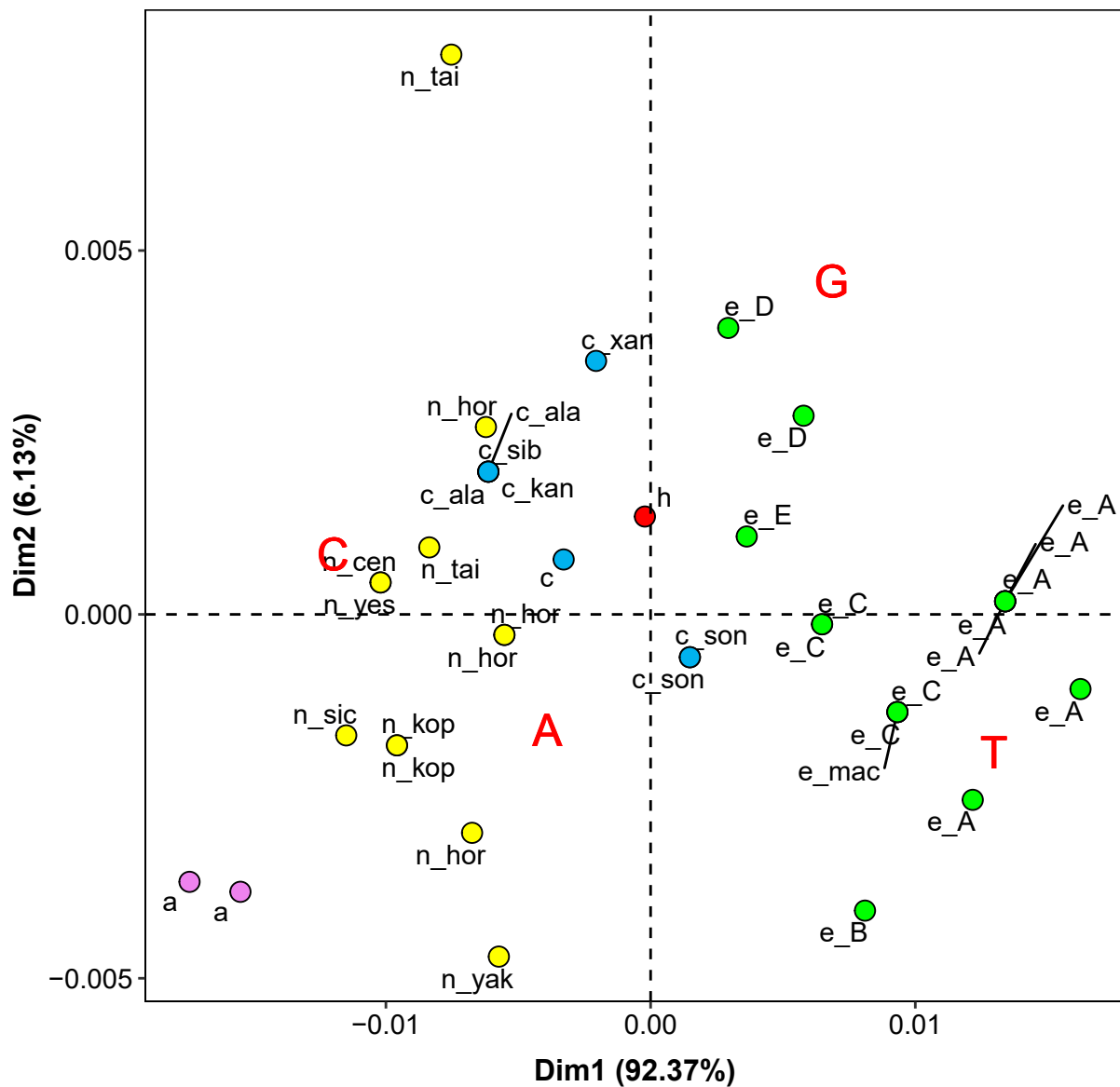
ND6



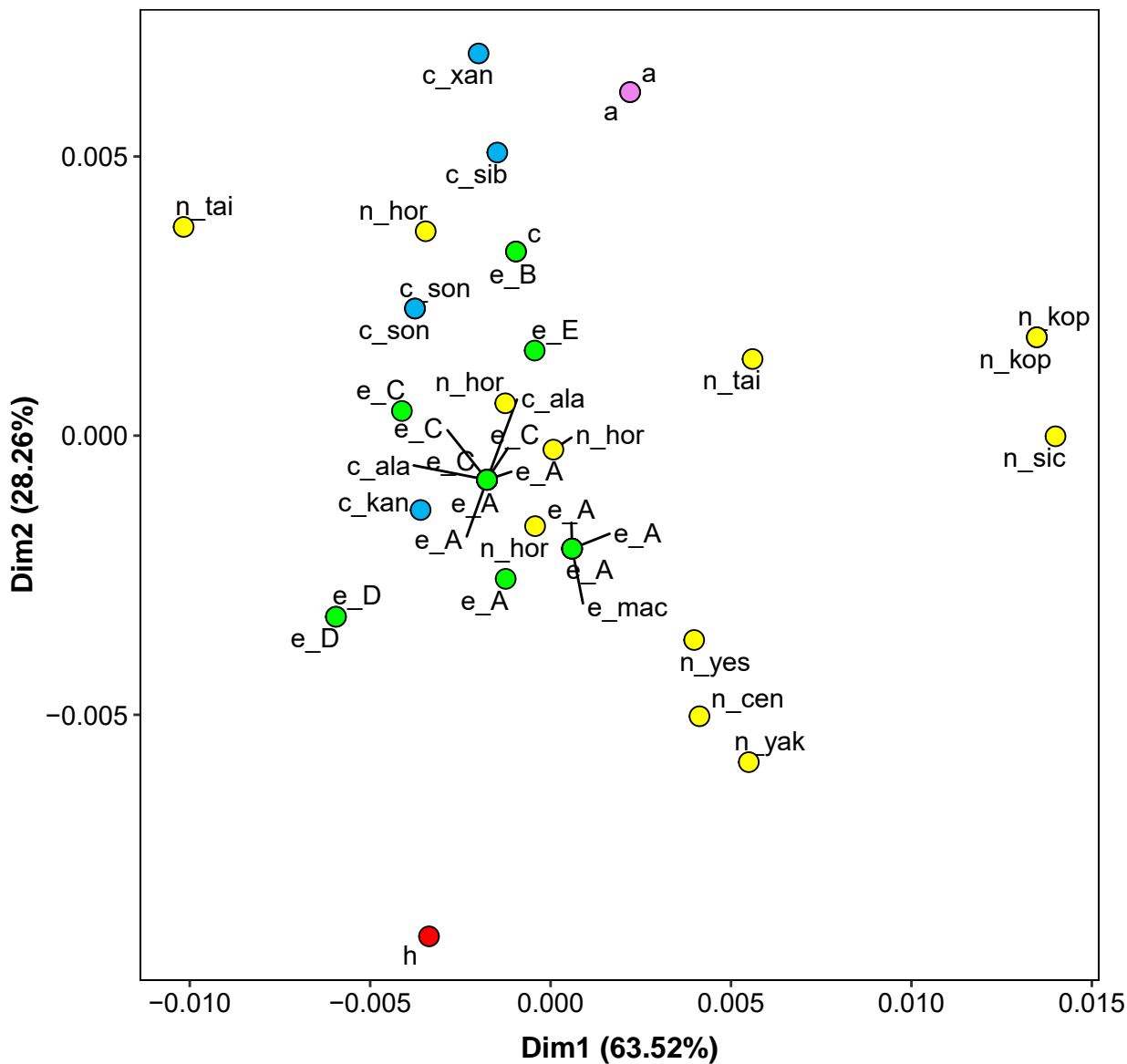
12S_RNA



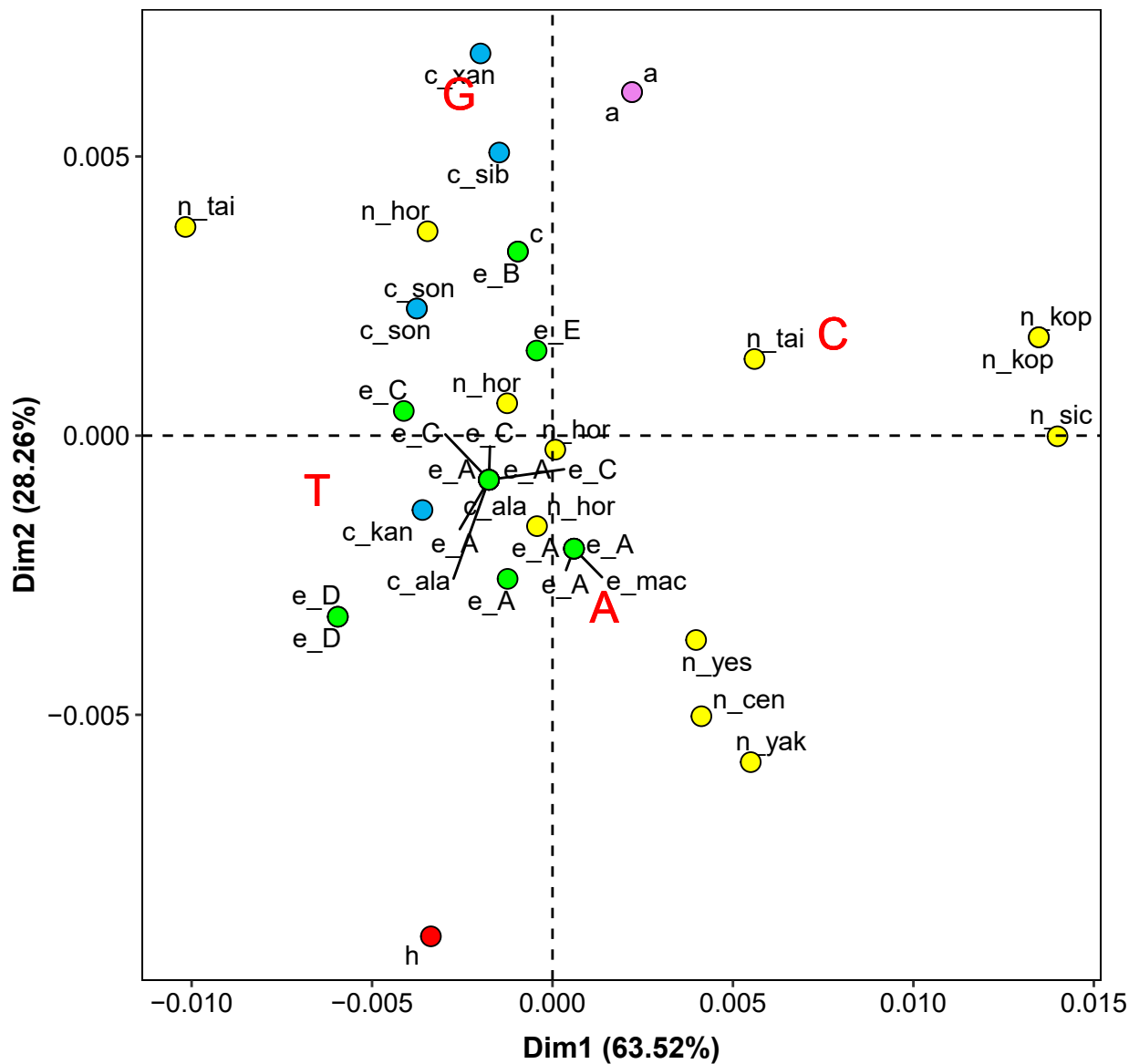
12S_RNA



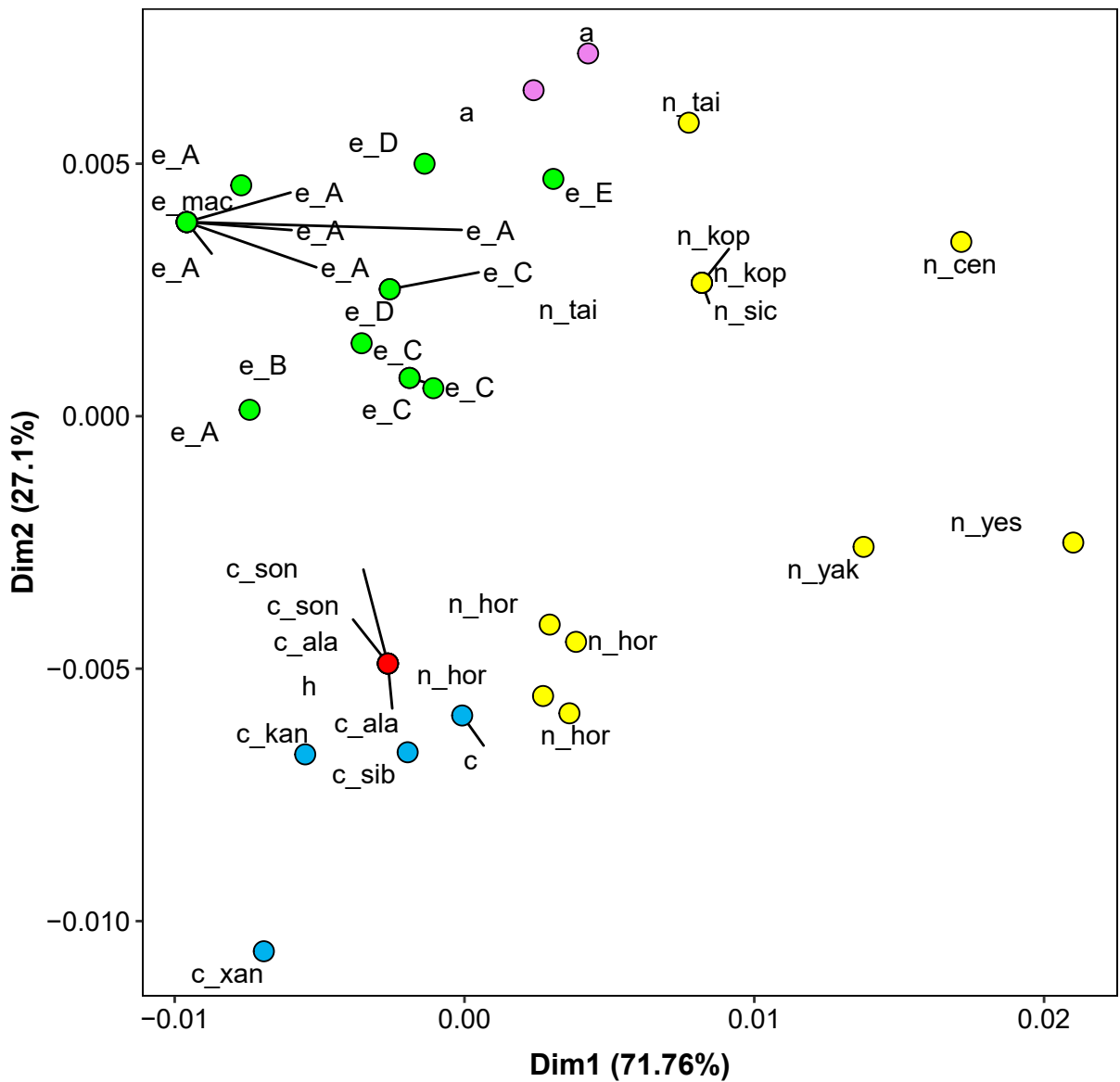
16S_RNA



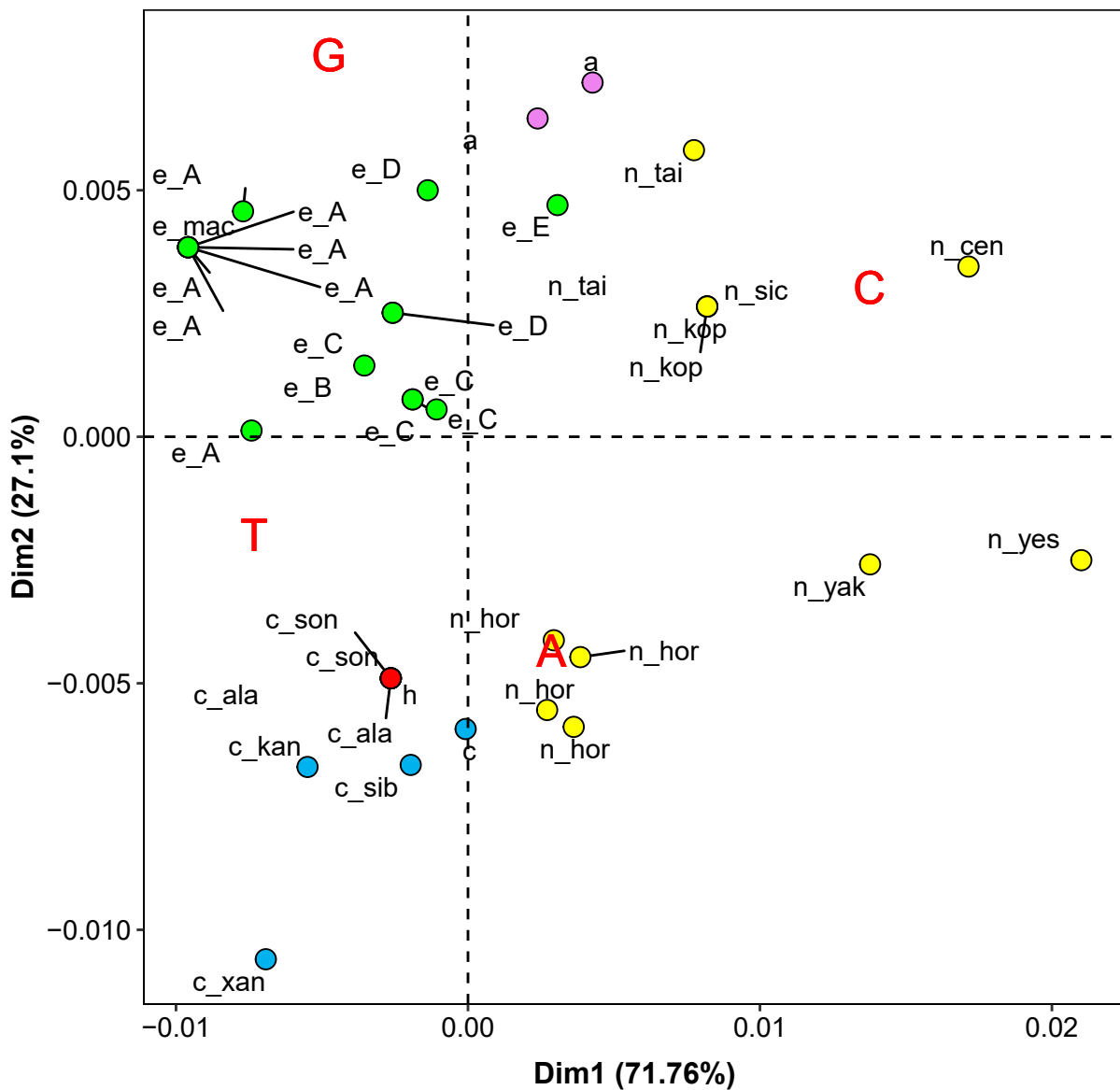
16S_RNA



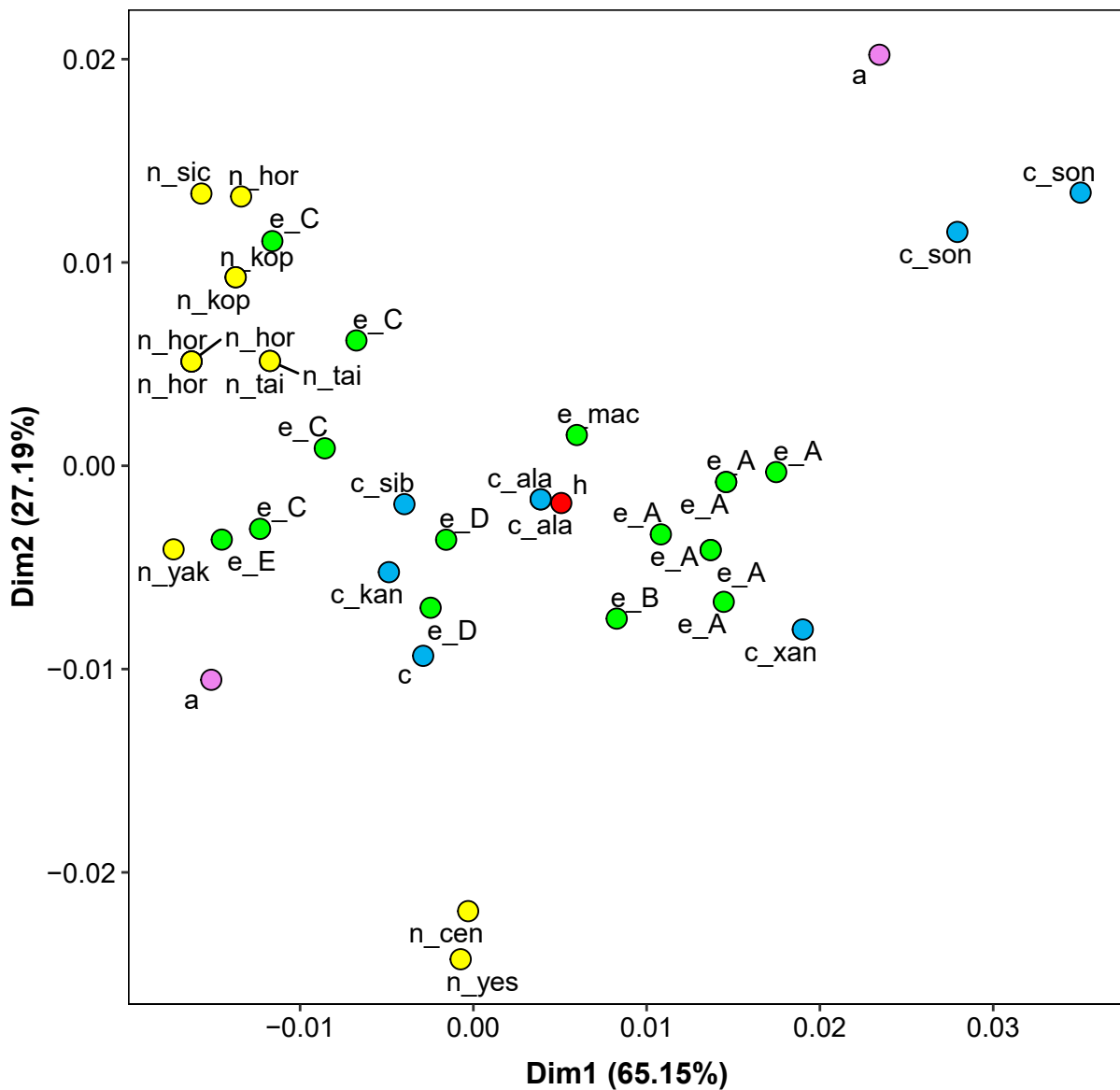
tRNA



tRNA



CR



CR

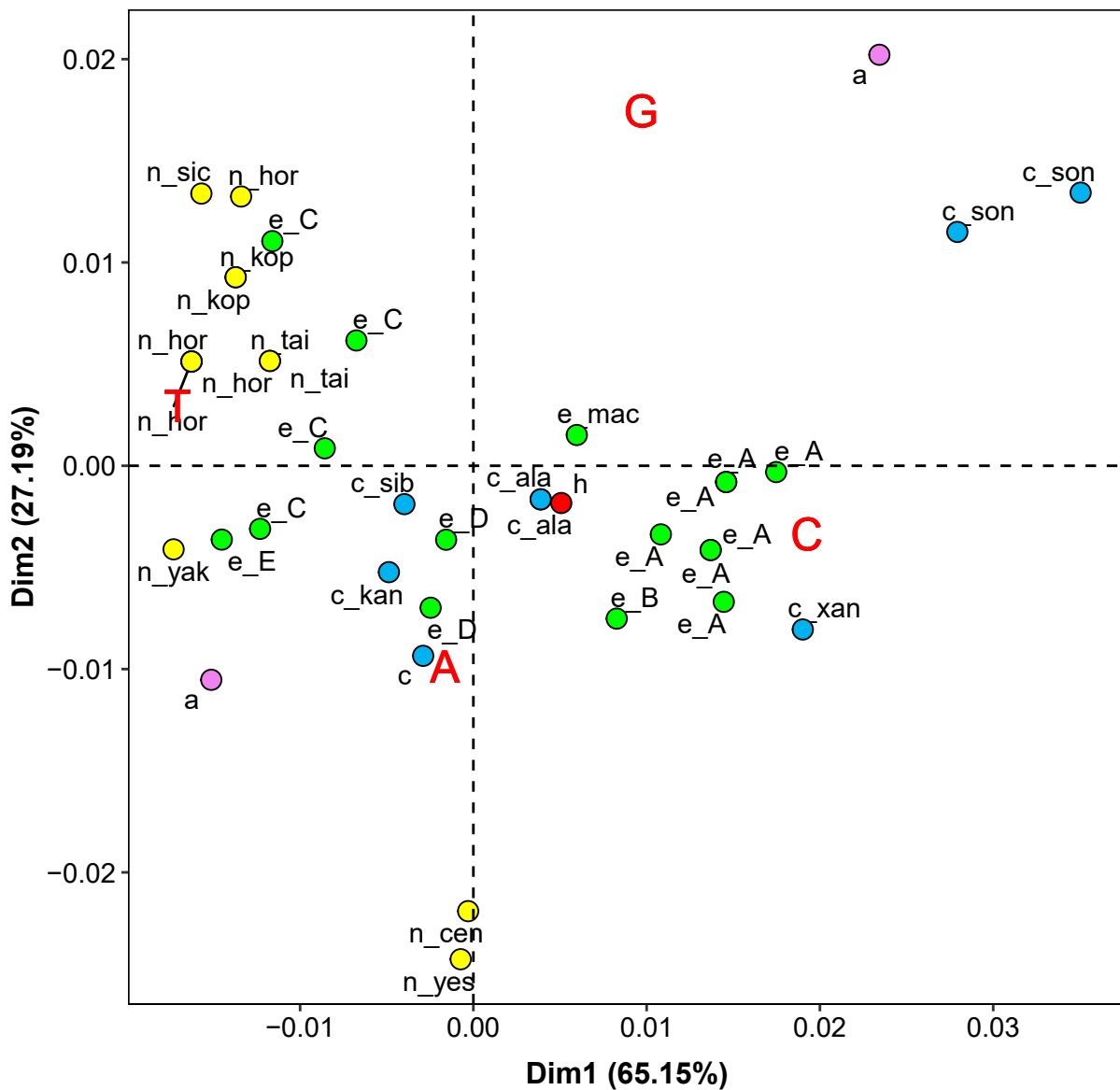
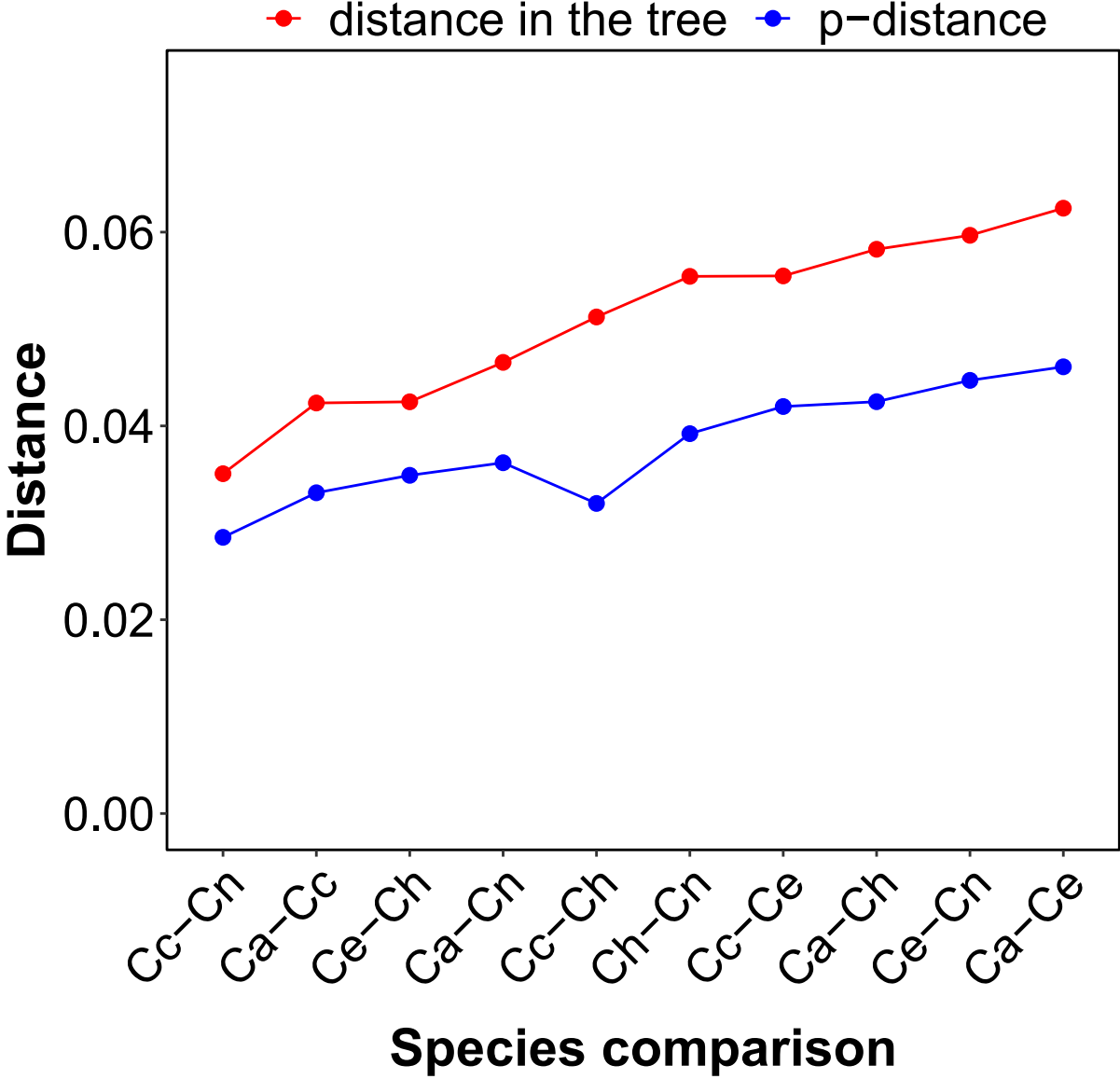
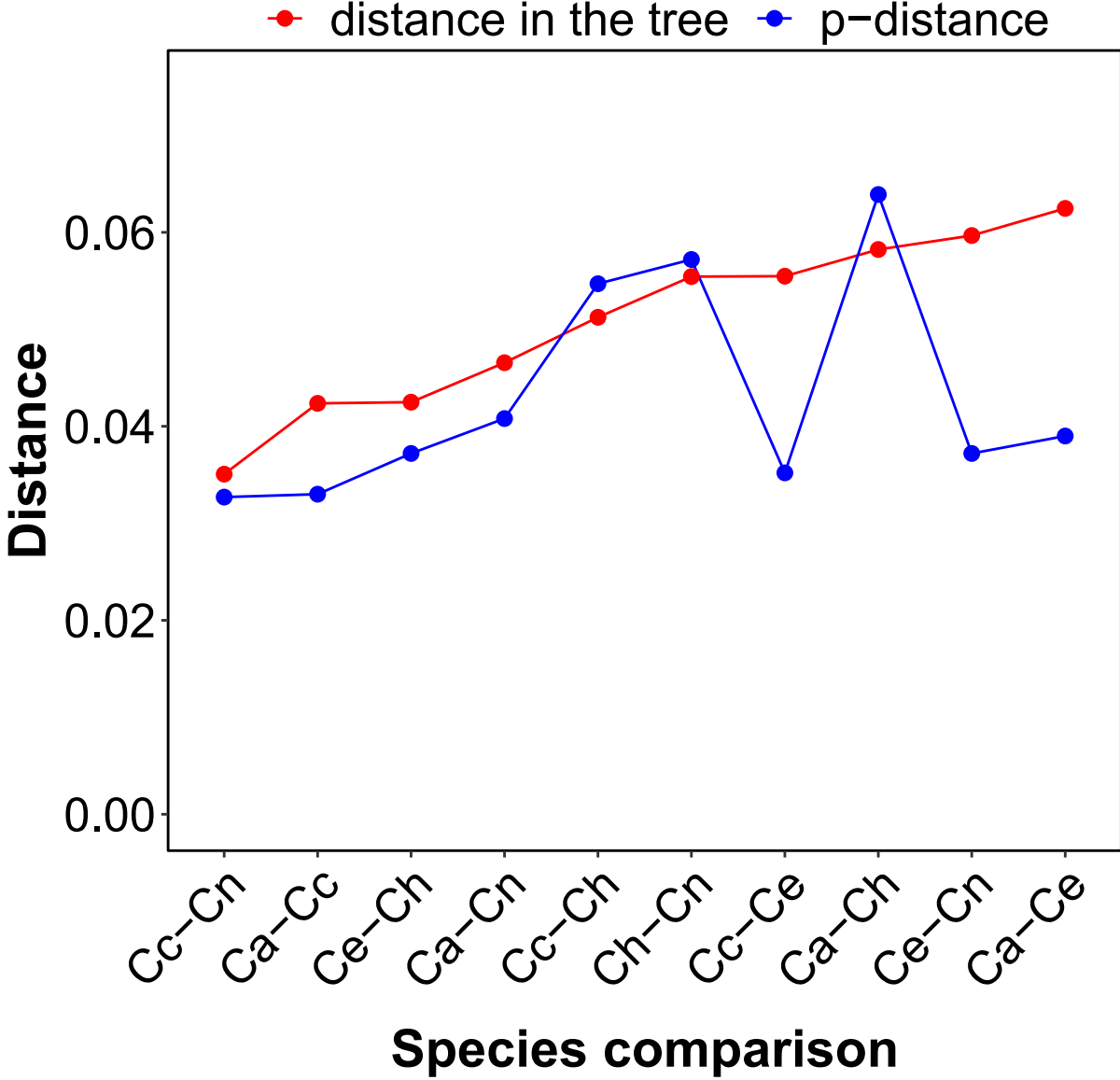


Figure S2. Comparison of p-distances for all pairs of *Cervus* species with the distances obtained from the MrBayes phylogenetic tree for 13 protein-coding genes (PCG), RNA genes and control region (CR). The species pairs were arranged according to the tree distance. Ca - *C. albirostris*; Cc - *C. canadensis*; Ce - *C. elaphus*; Ch - *C. hanglu*; Cn - *C. nippon*.

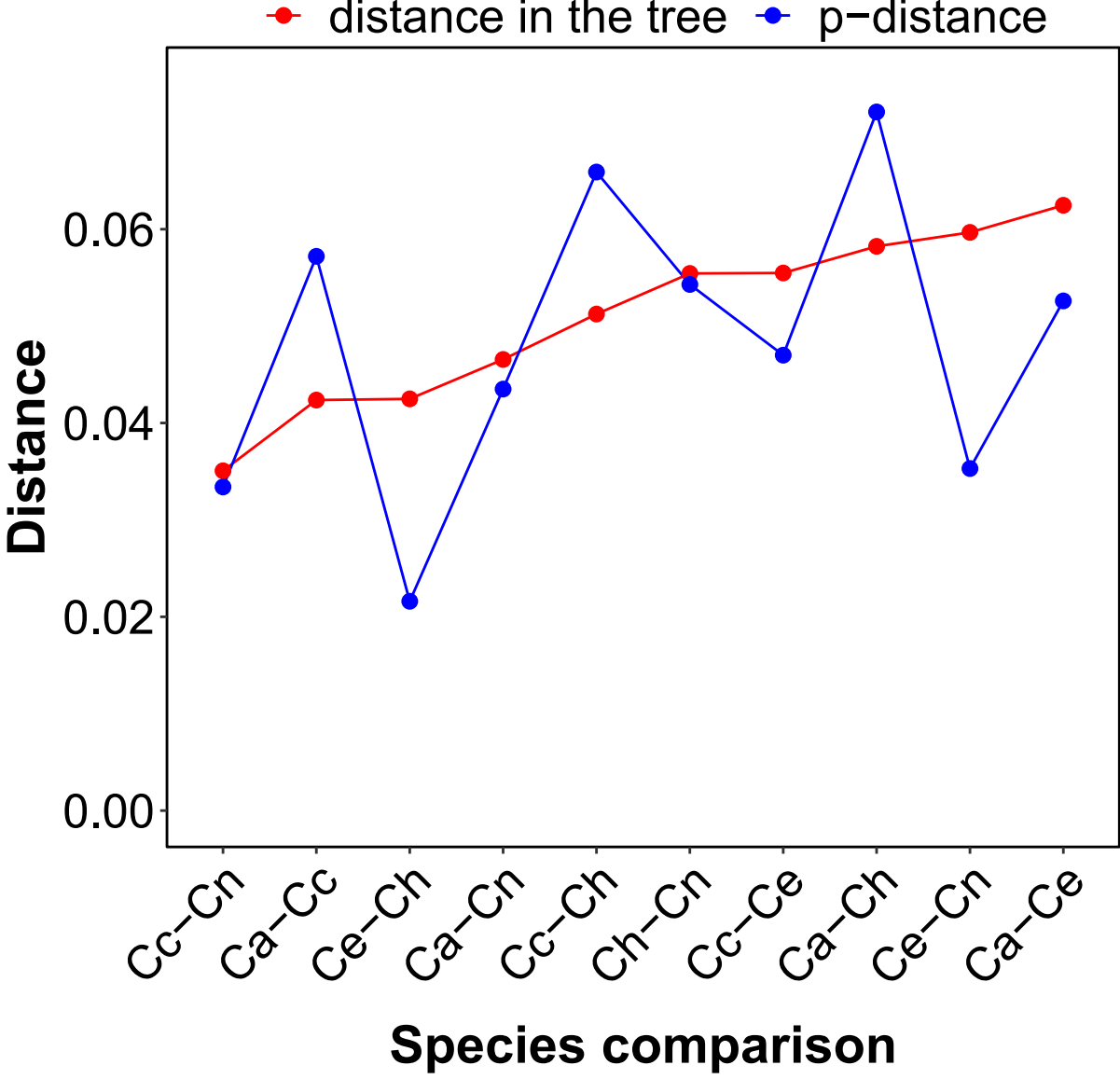
PCG+RNA+CR



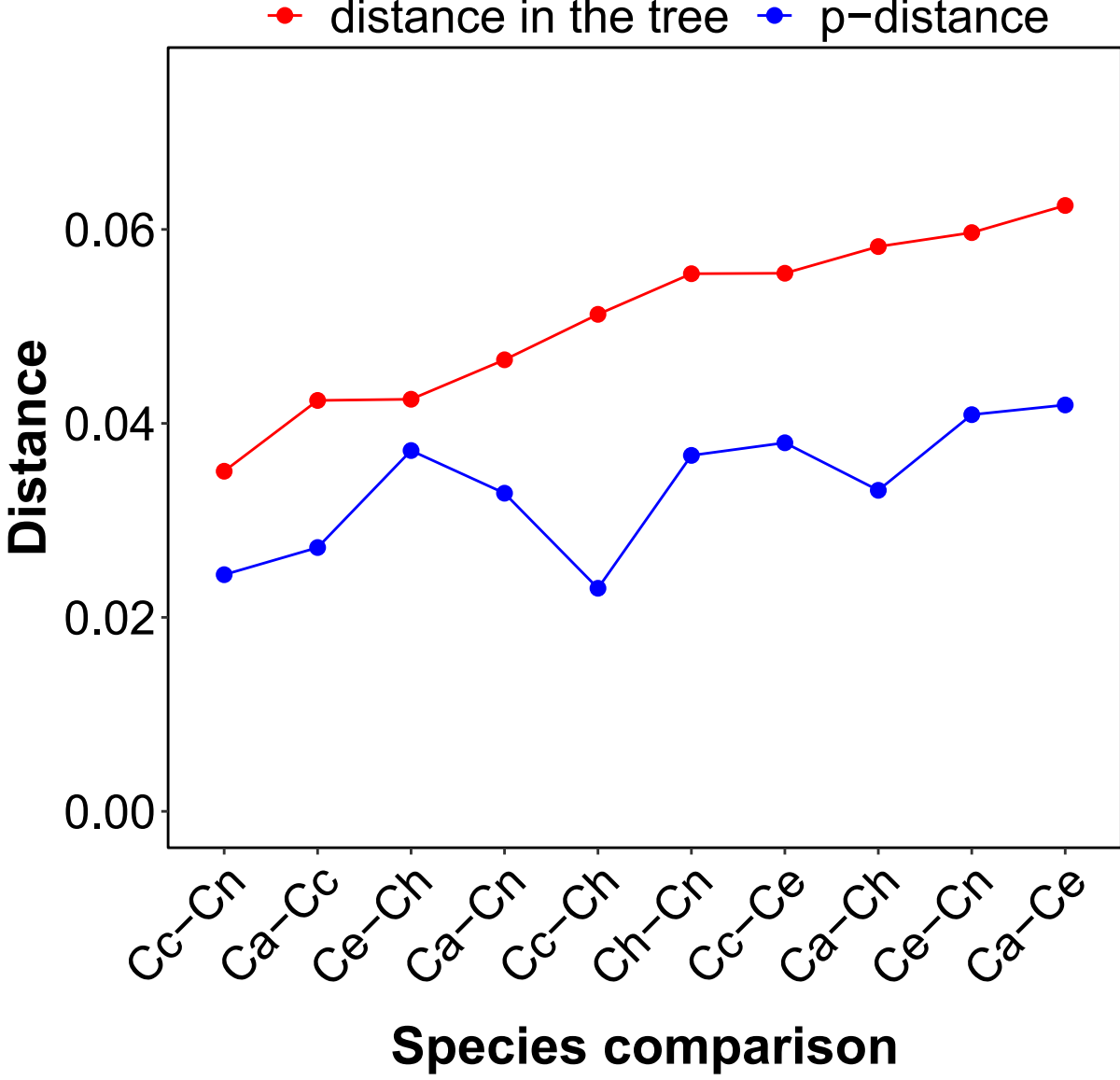
ATP6



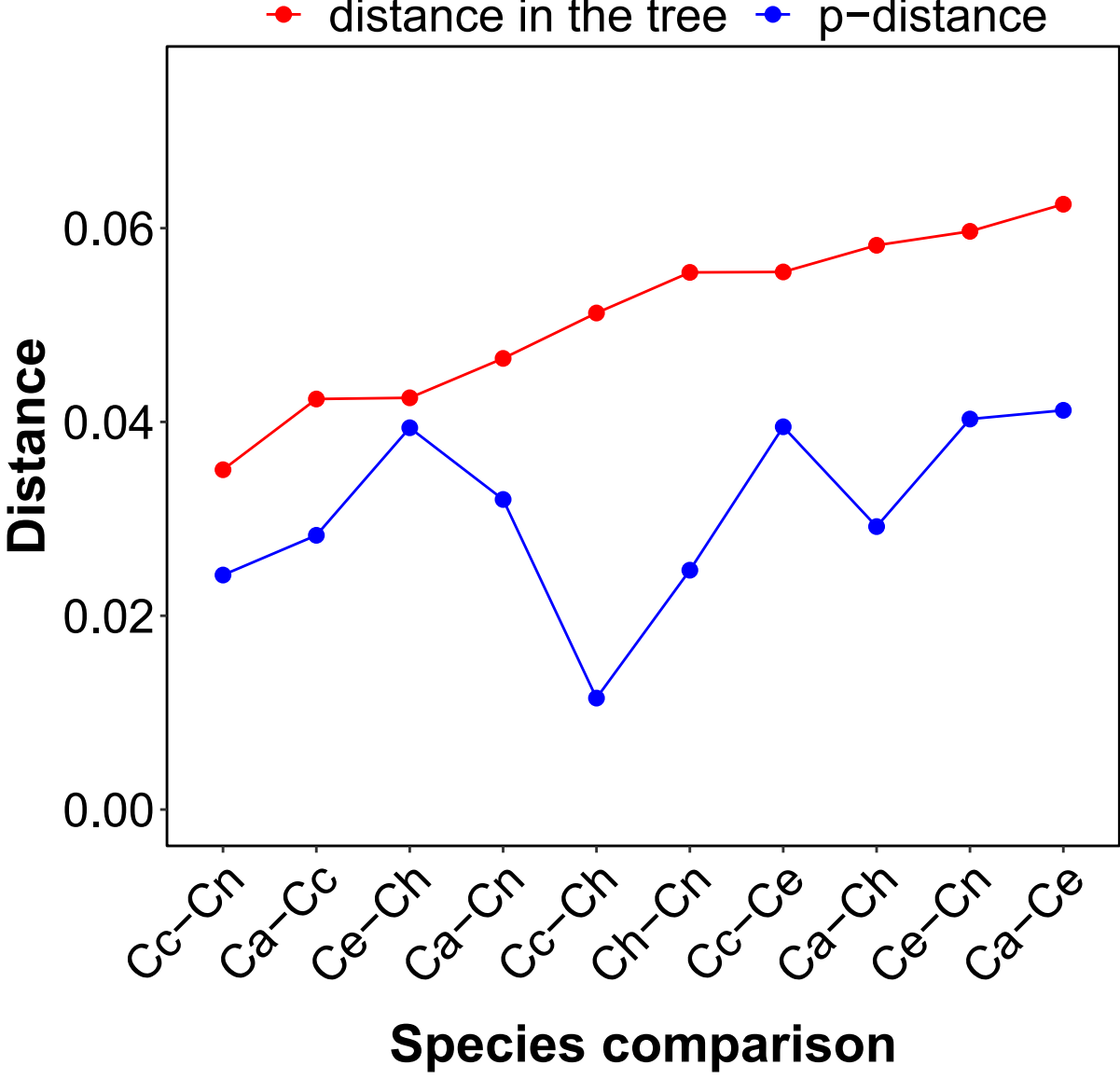
ATP8



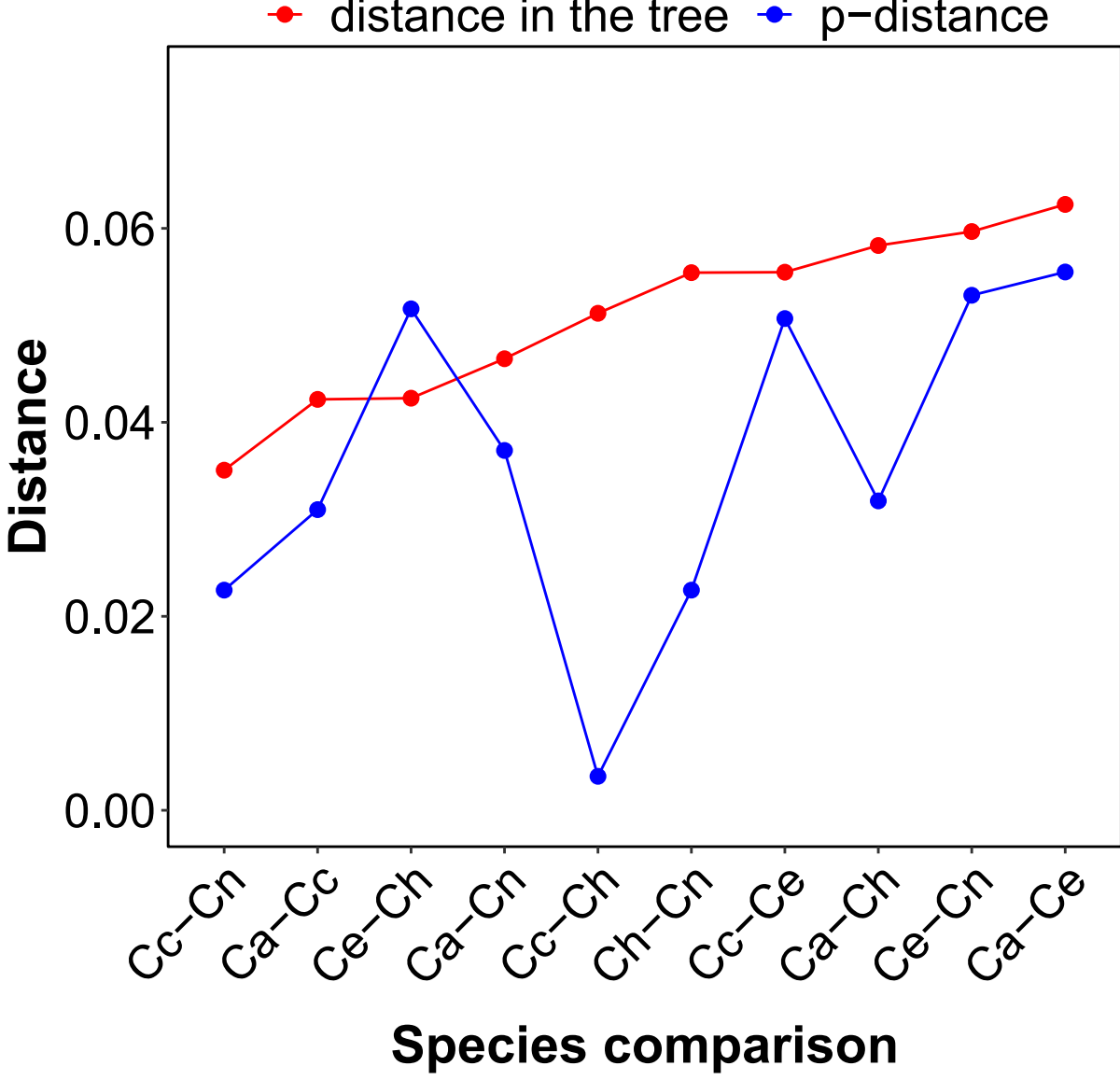
COX1



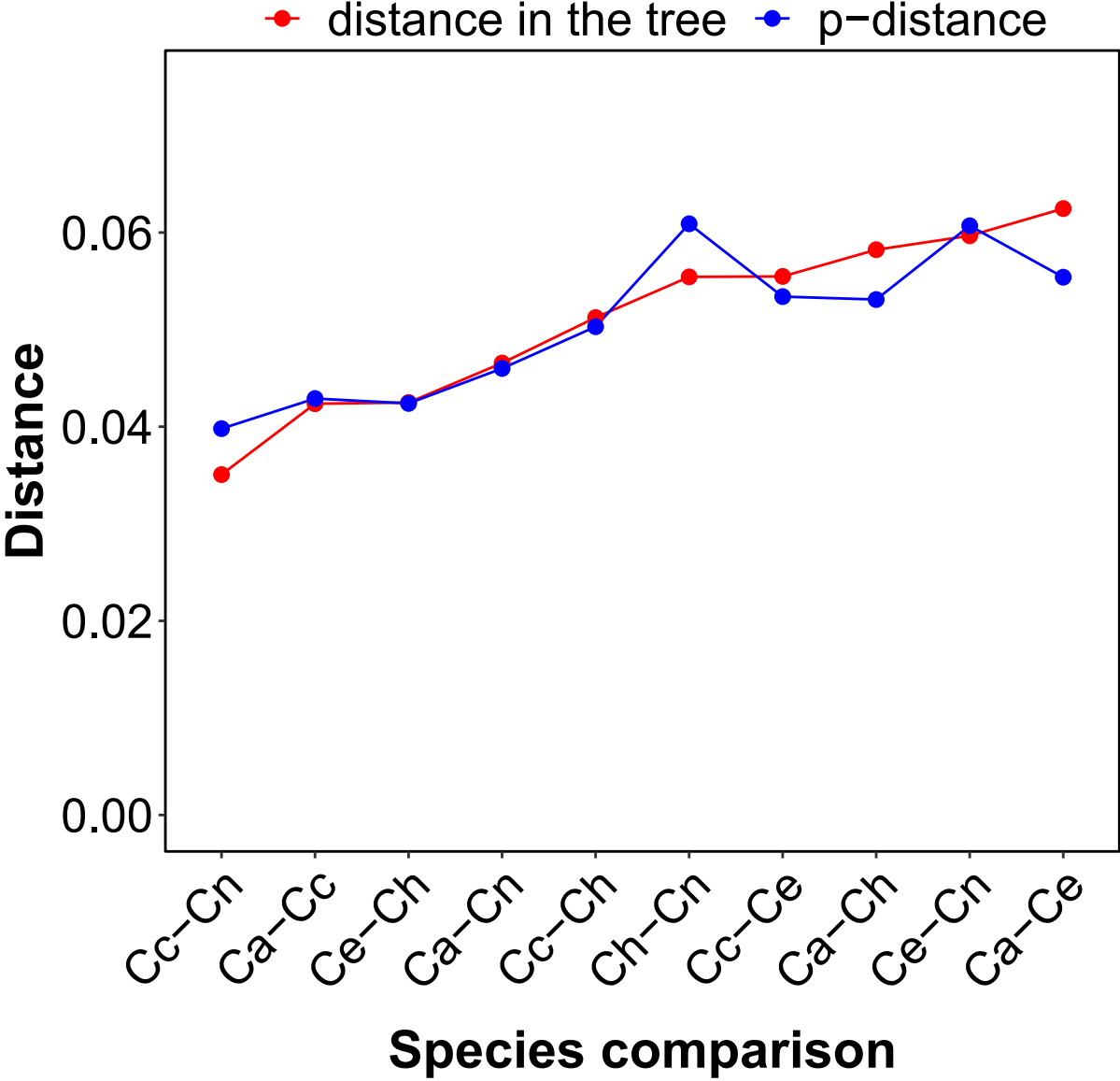
COX2



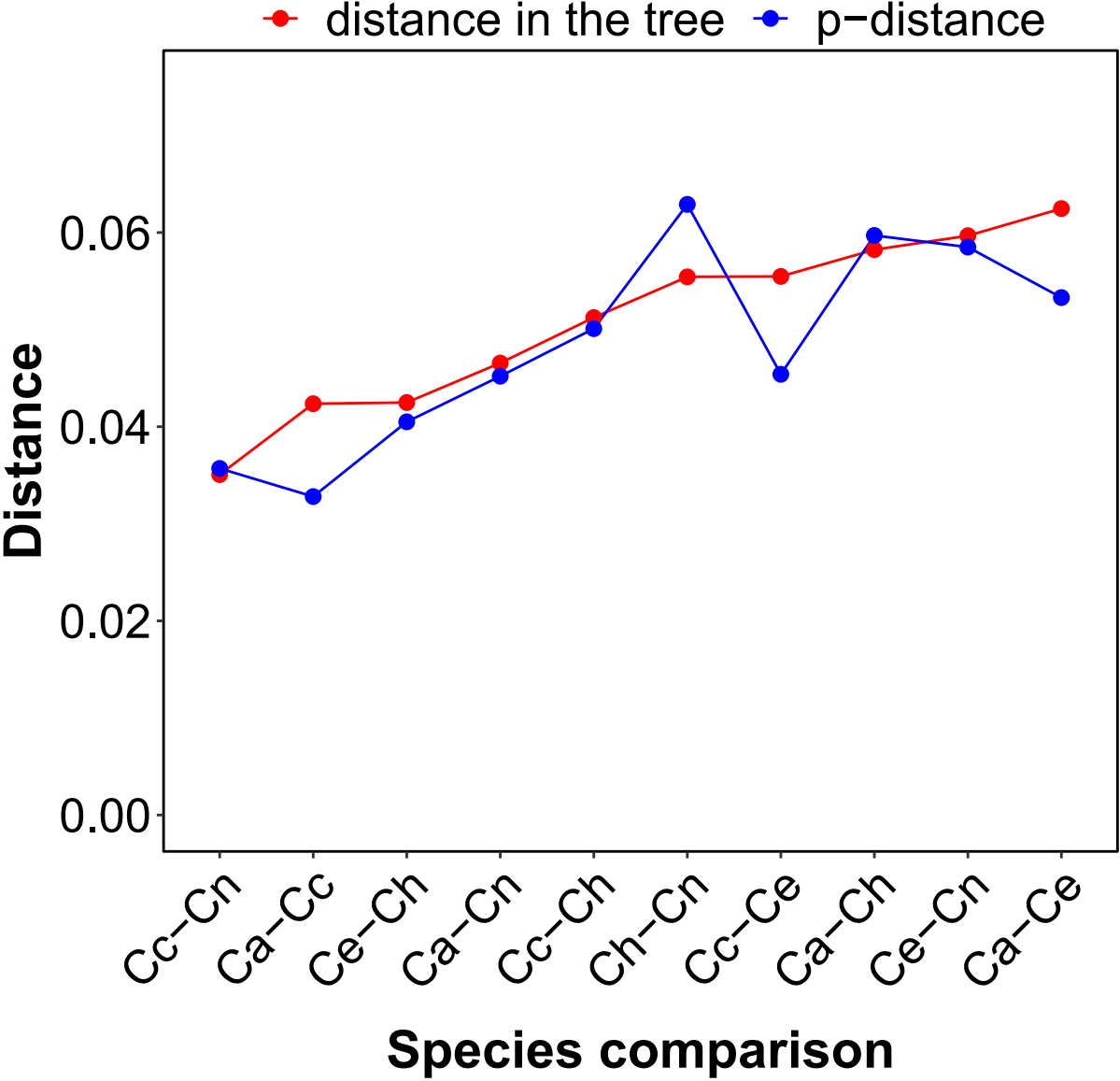
COX3



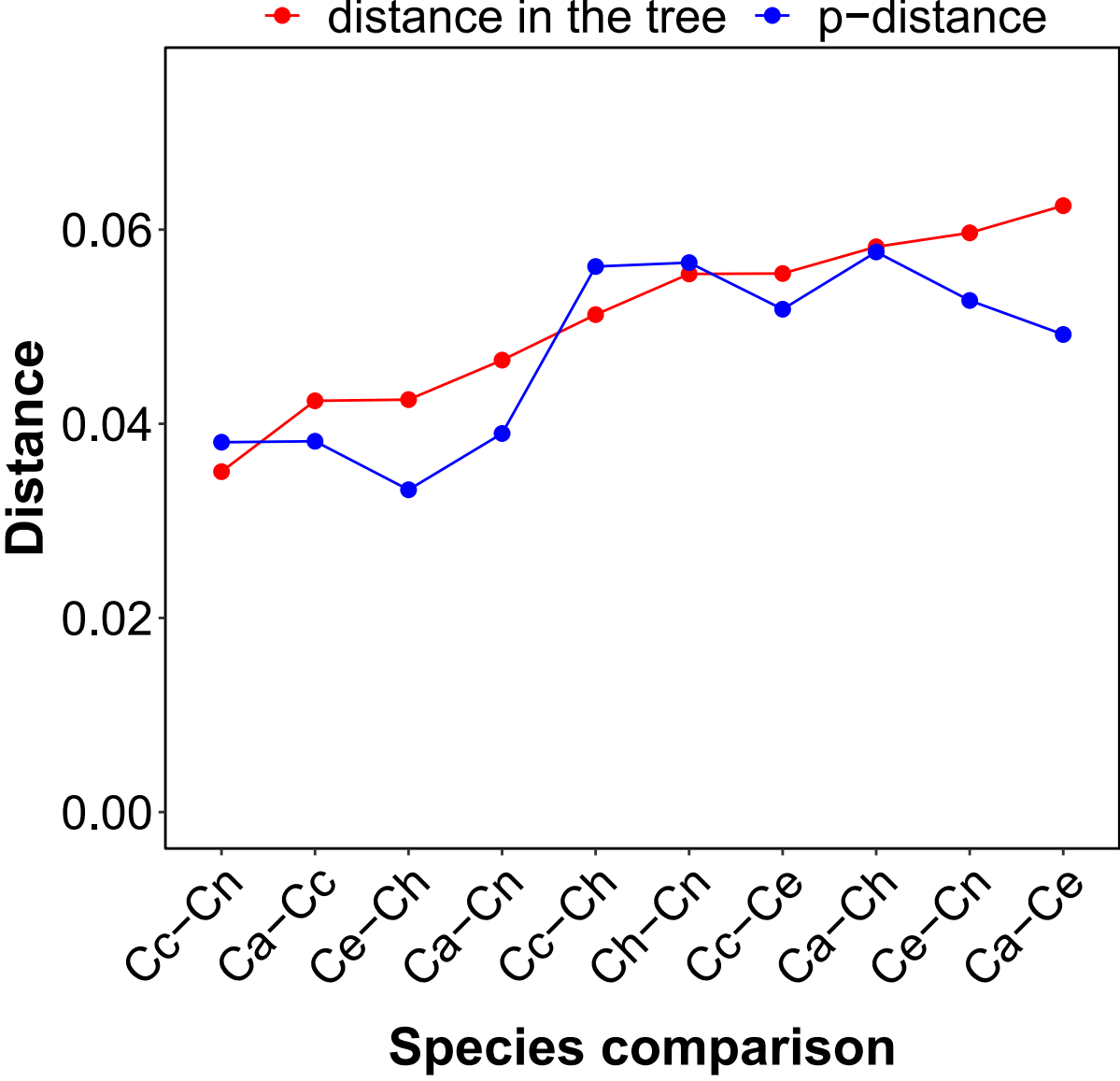
CYTB



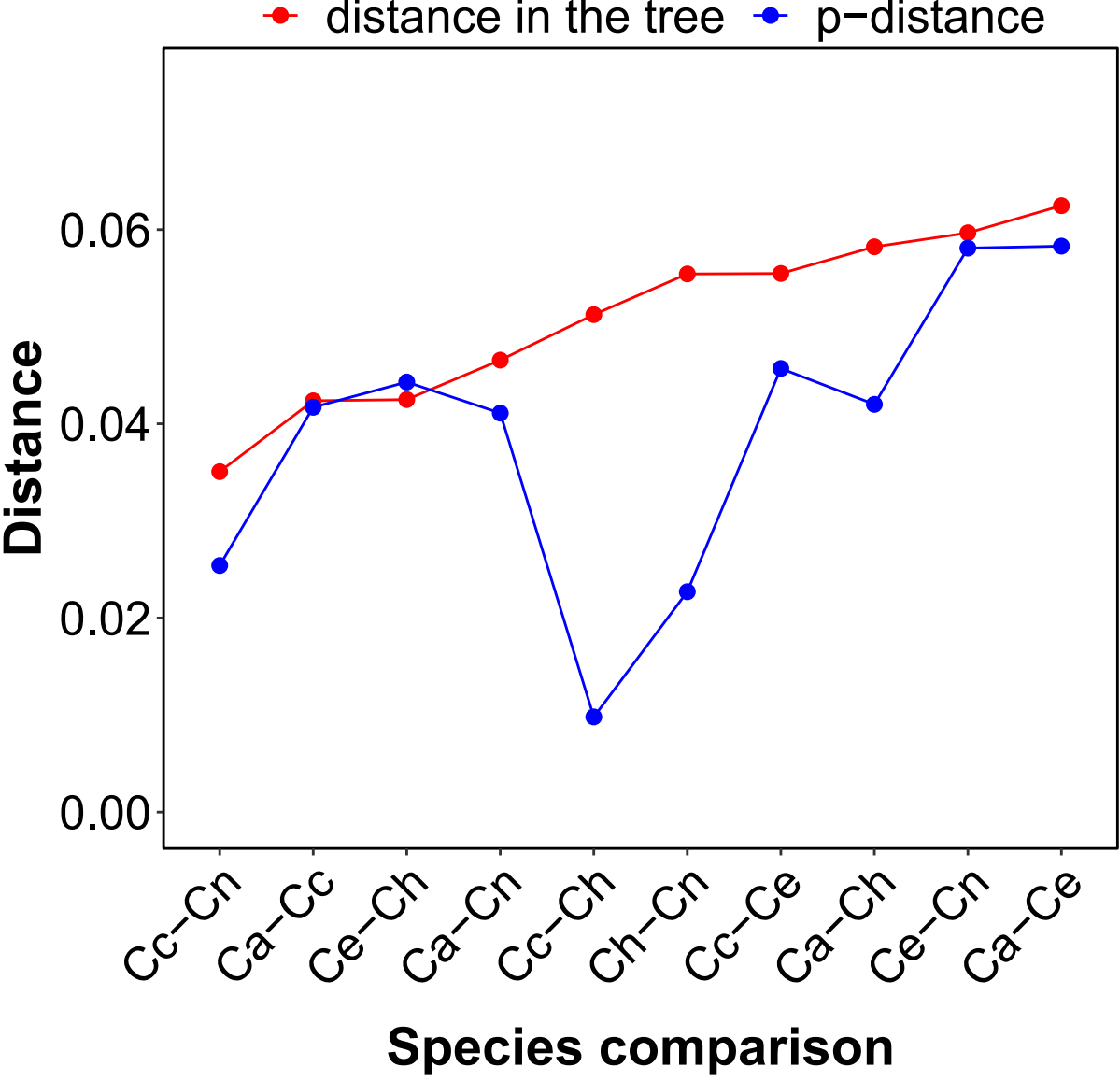
ND1



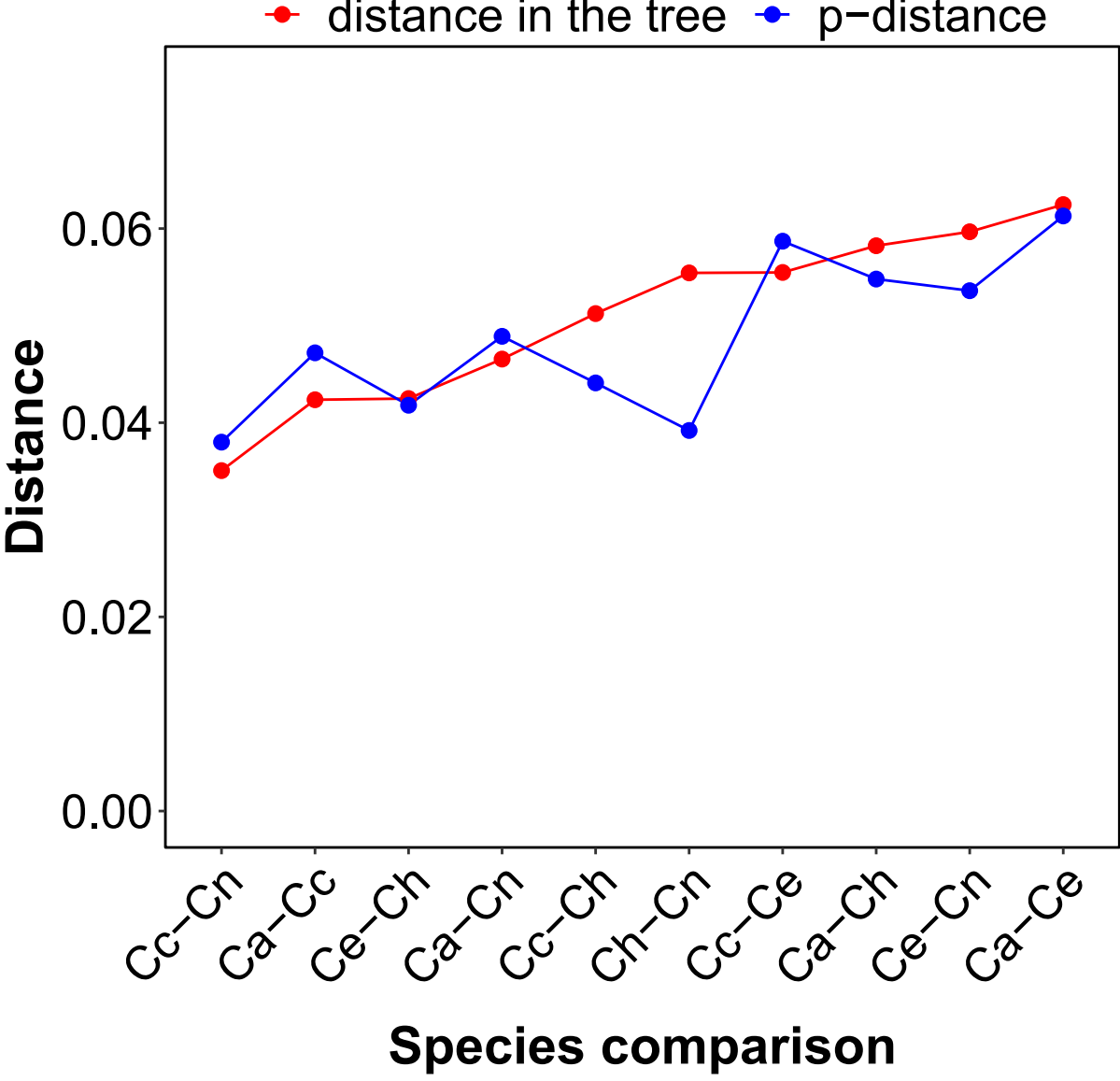
ND2



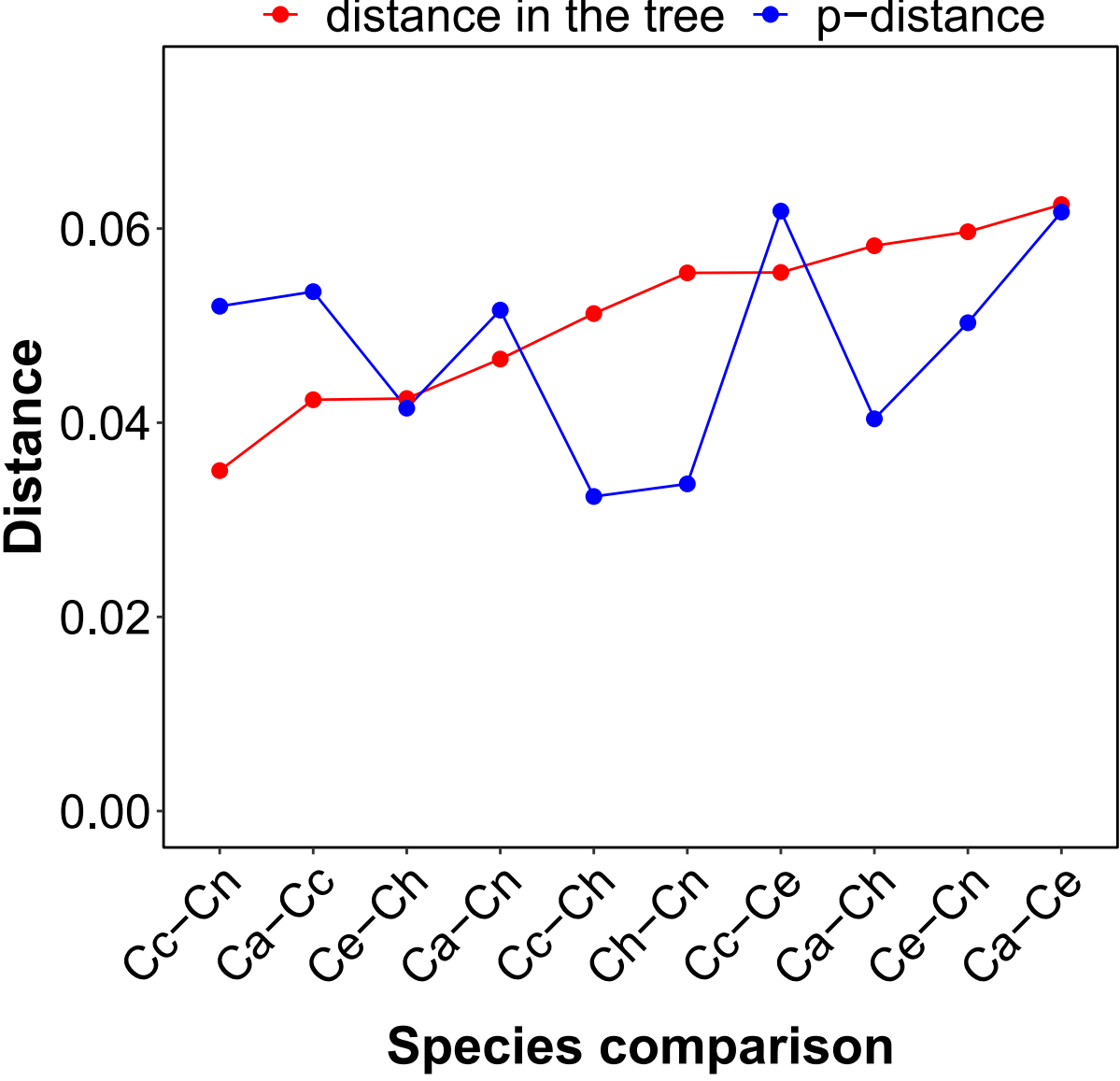
ND3



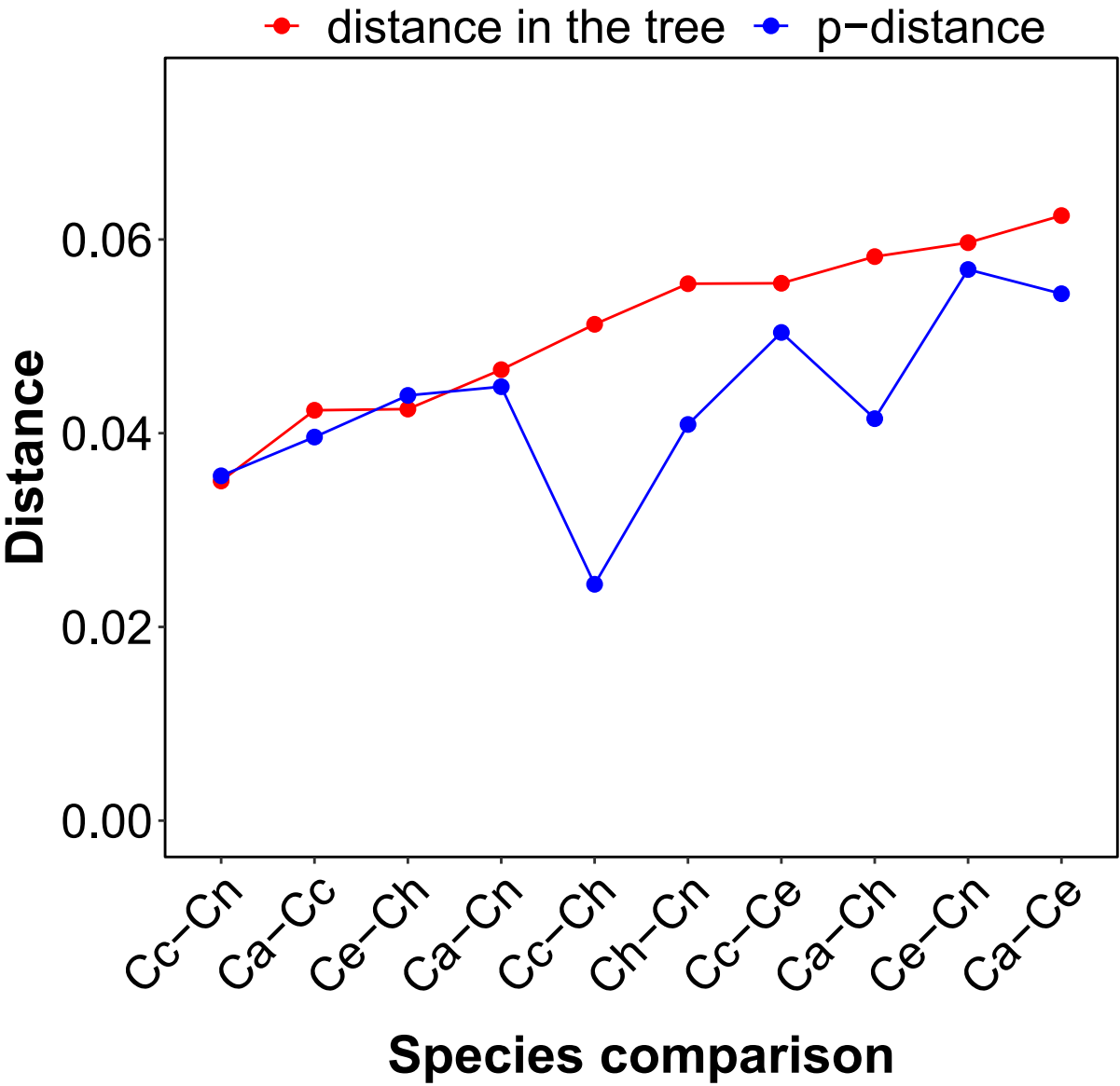
ND4



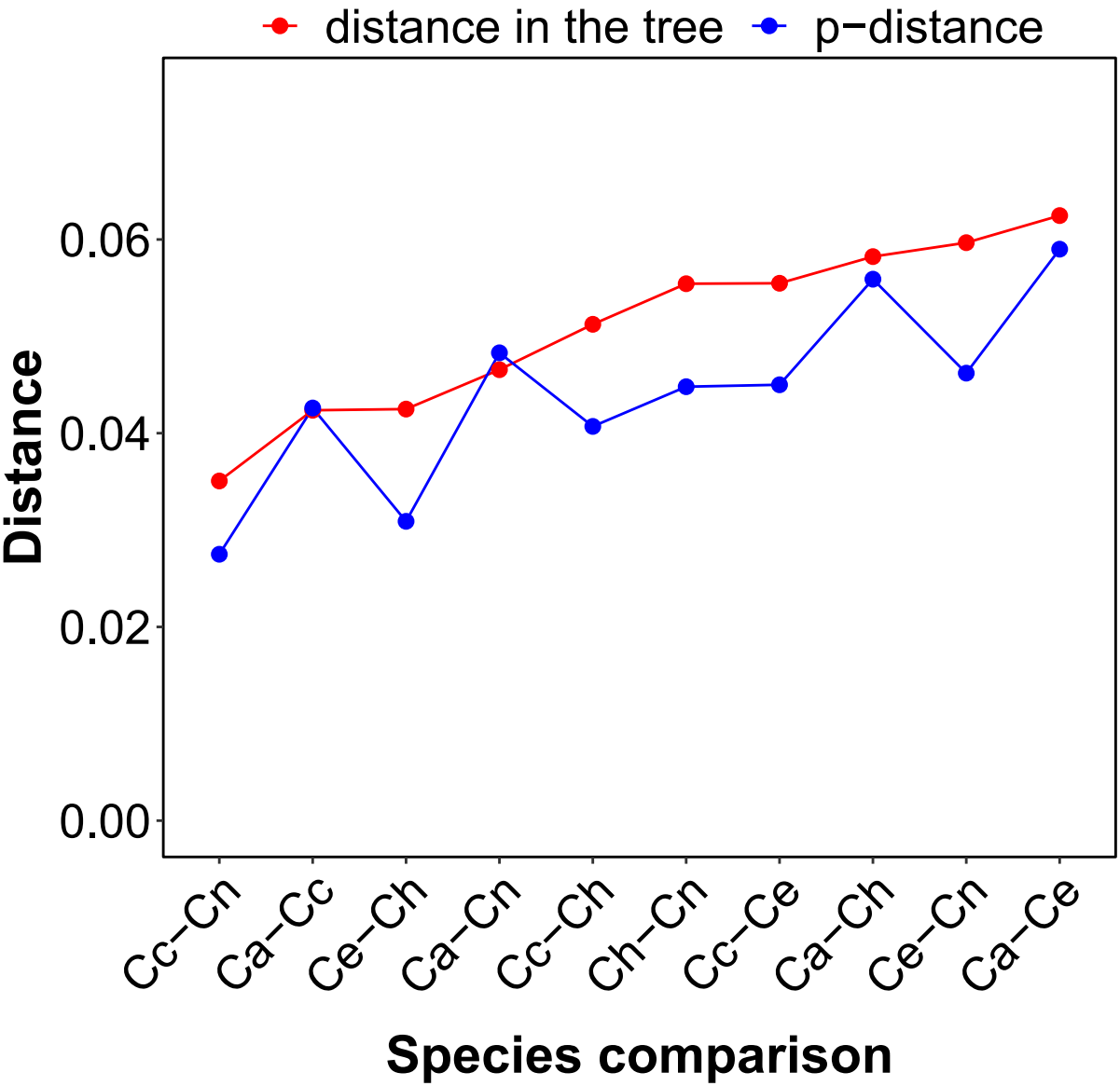
ND4L



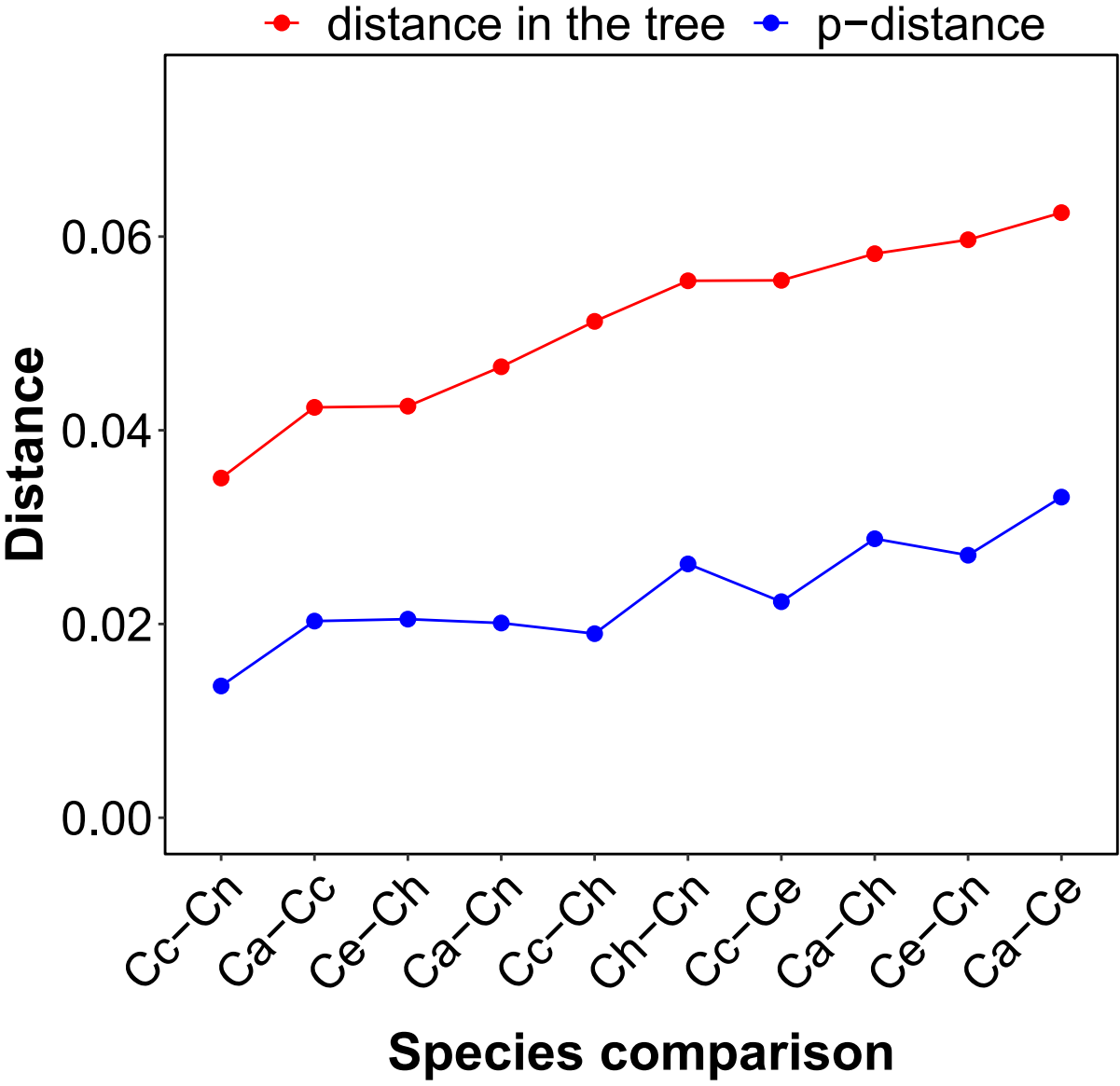
ND5



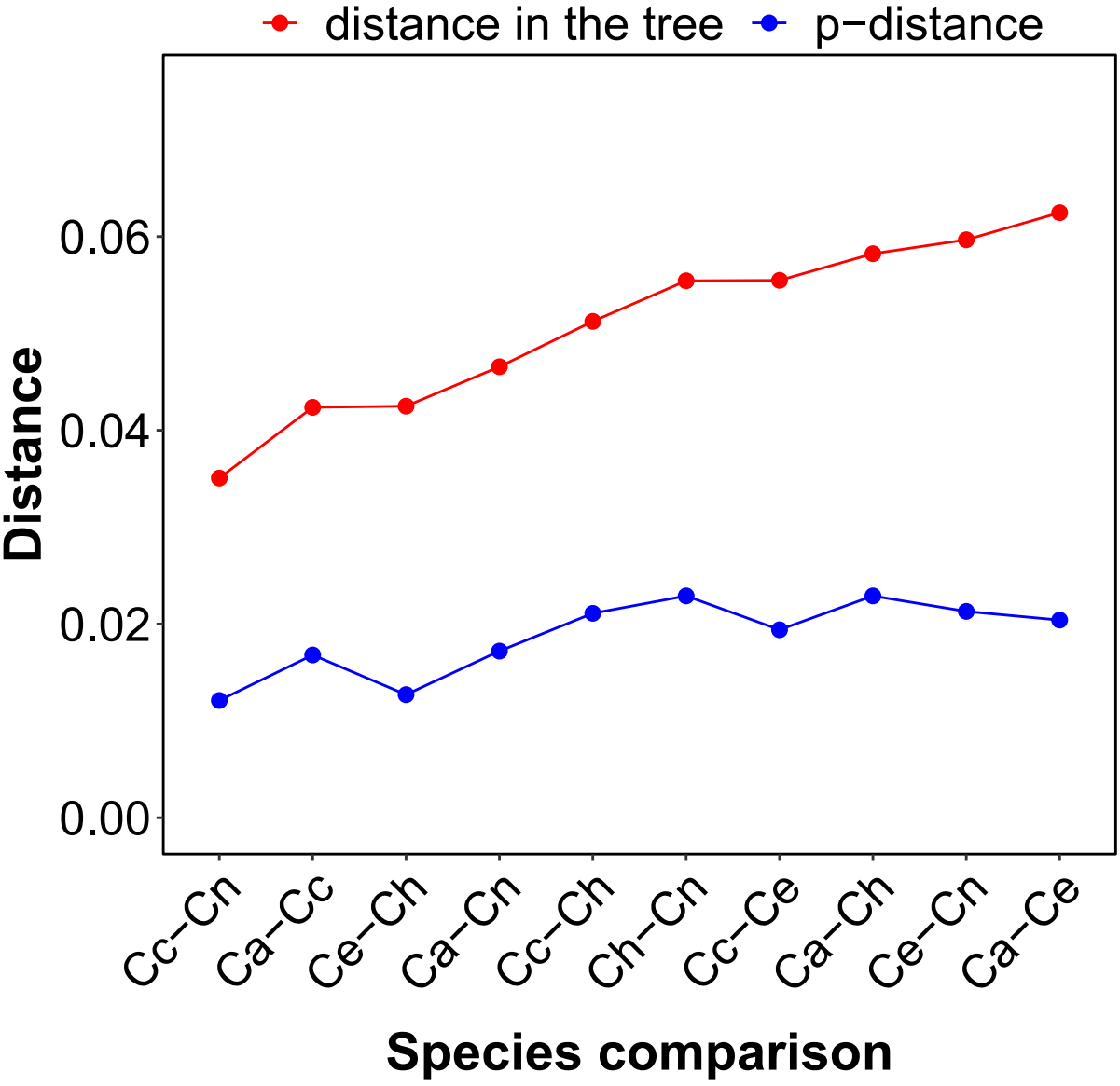
ND6



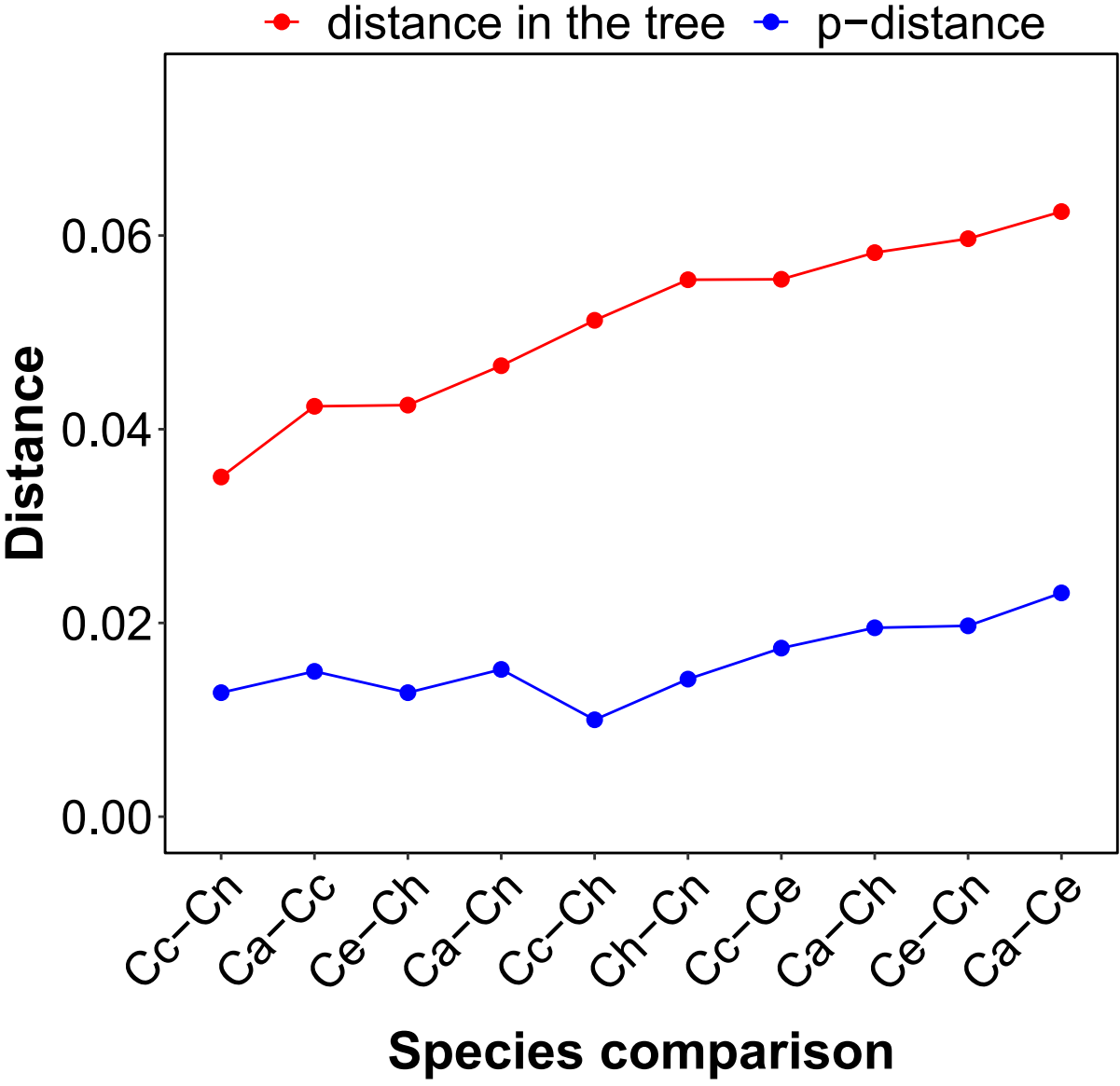
12S rRNA



16S rRNA



tRNA



CR

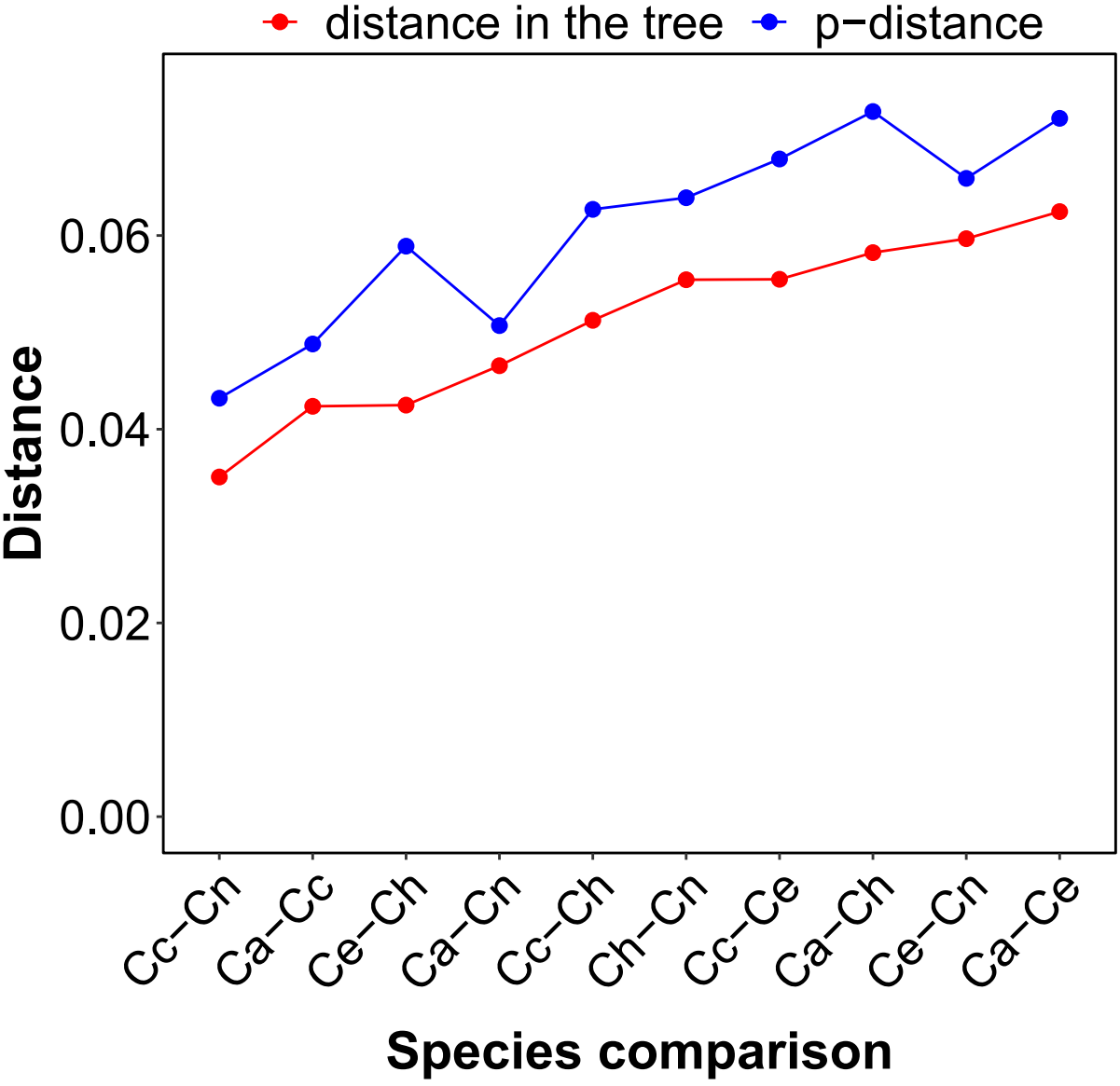
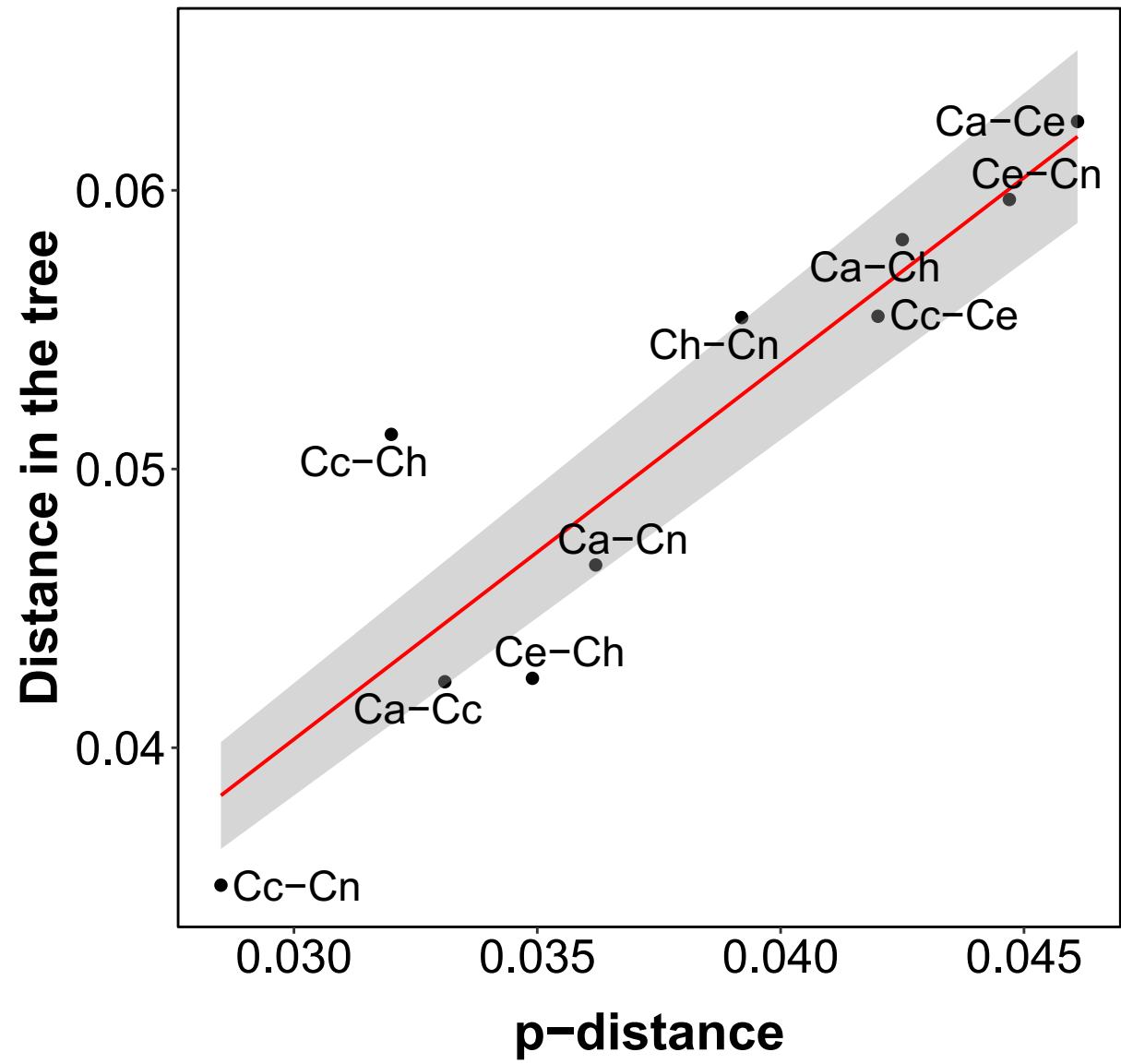
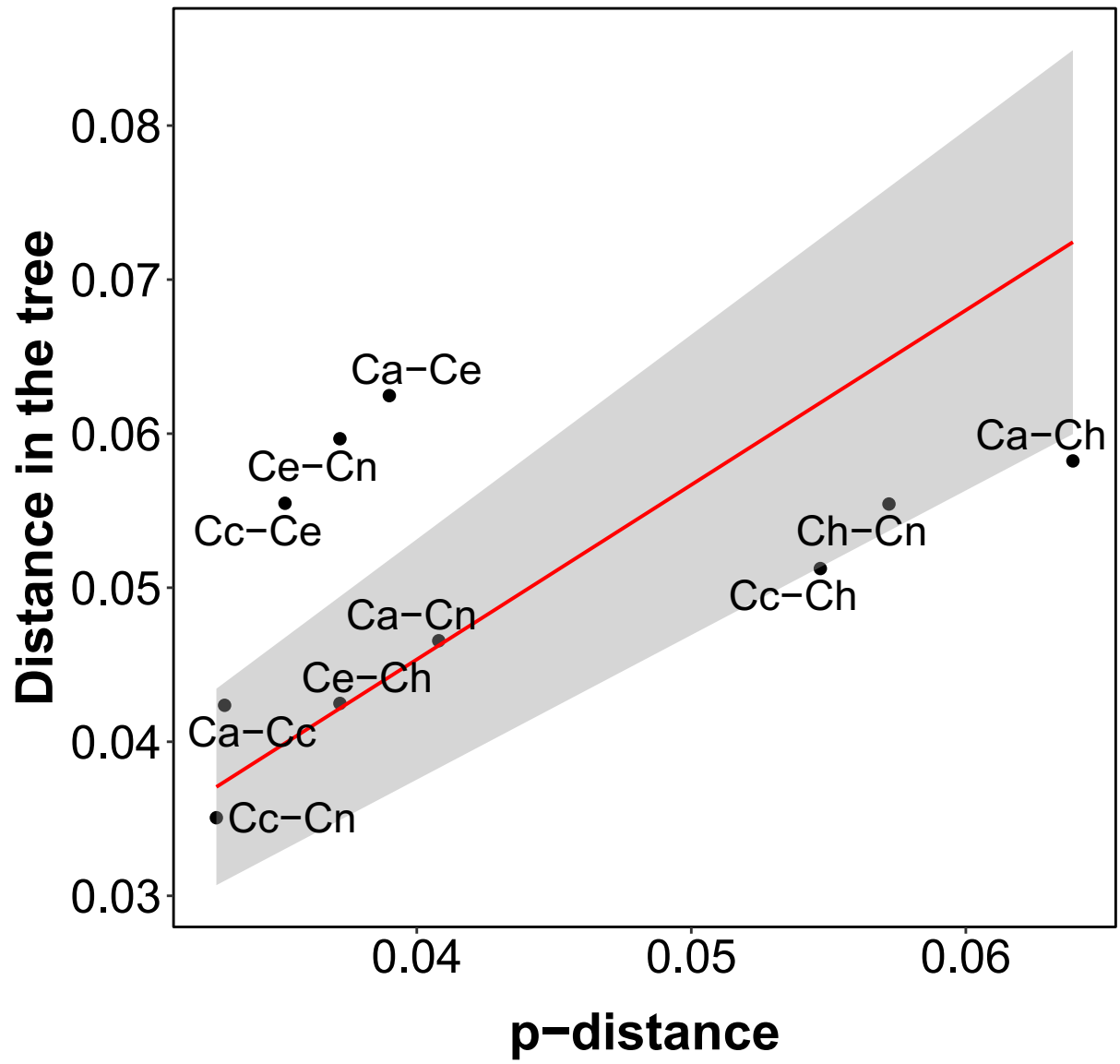


Figure S3. Relationships between the distances in the MrBayes phylogenetic tree and p-distances for all pairs of *Cervus* species and 13 protein-coding genes (PCG), RNA genes and control region (CR). A regression line (red line) with 95% confidence interval (grey area) was also presented. Ca - *C. albirostris*; Cc - *C. canadensis*; Ce - *C. elaphus*; Ch - *C. hanglu*; Cn - *C. nippon*.

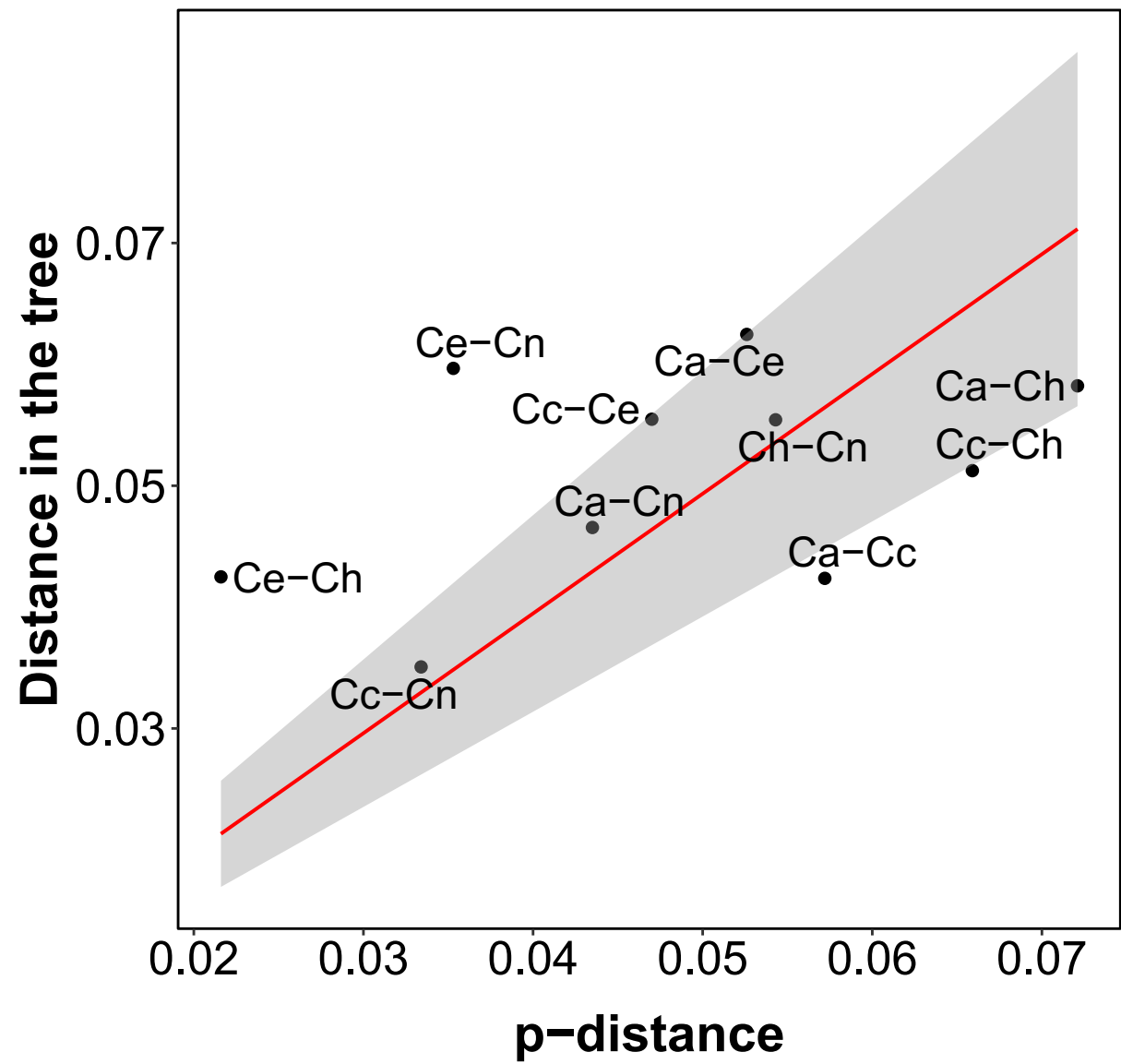
PCG+RNA+CR



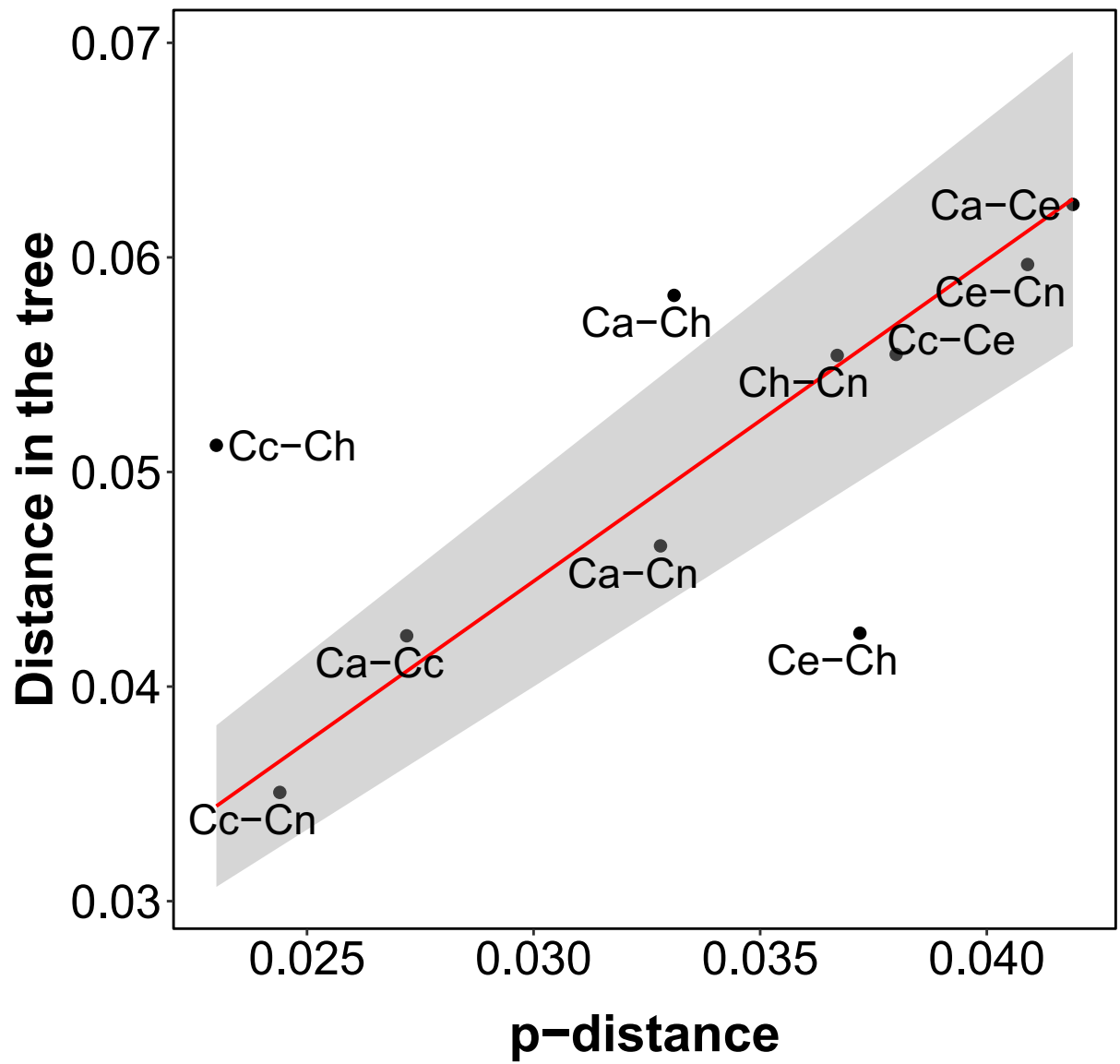
ATP6



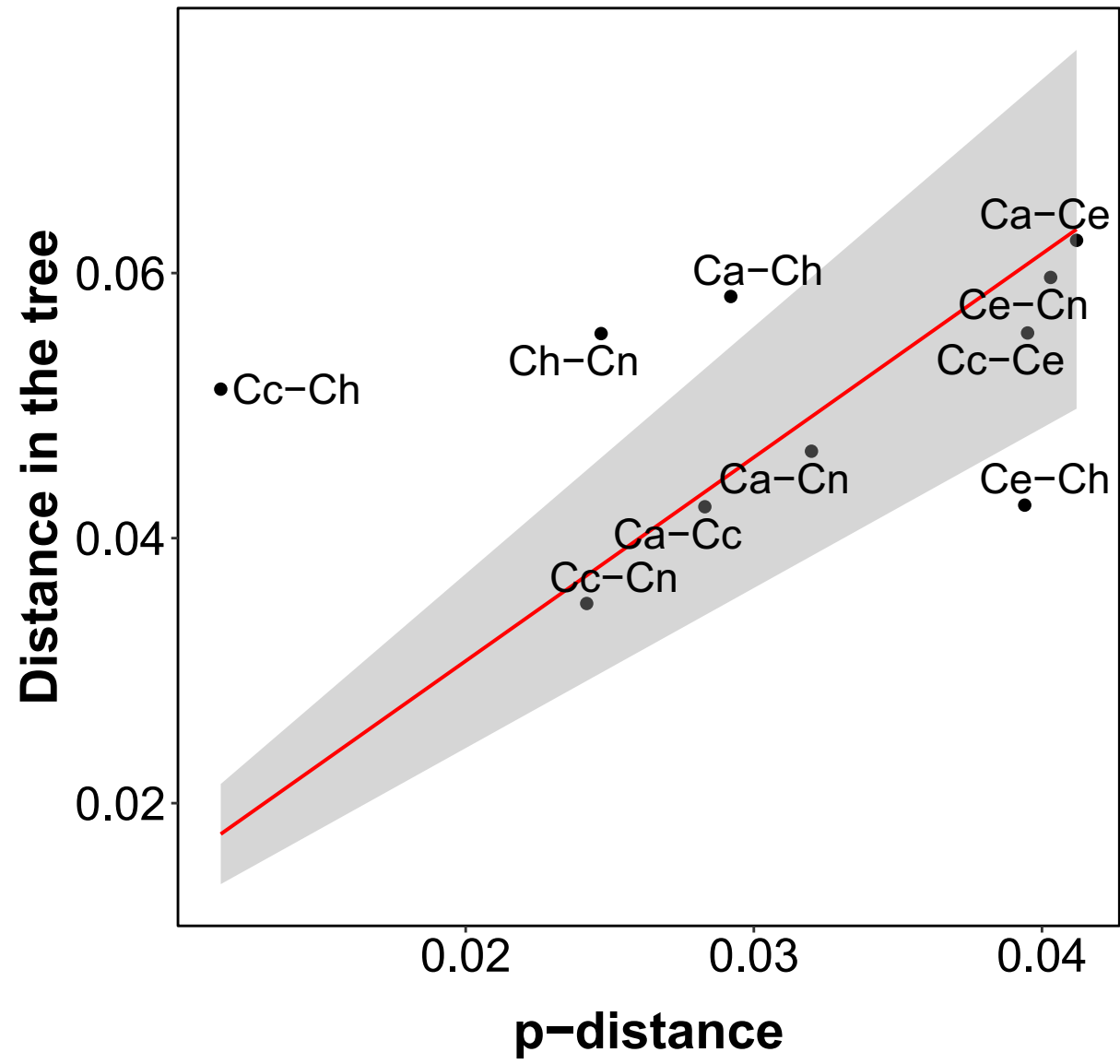
ATP8



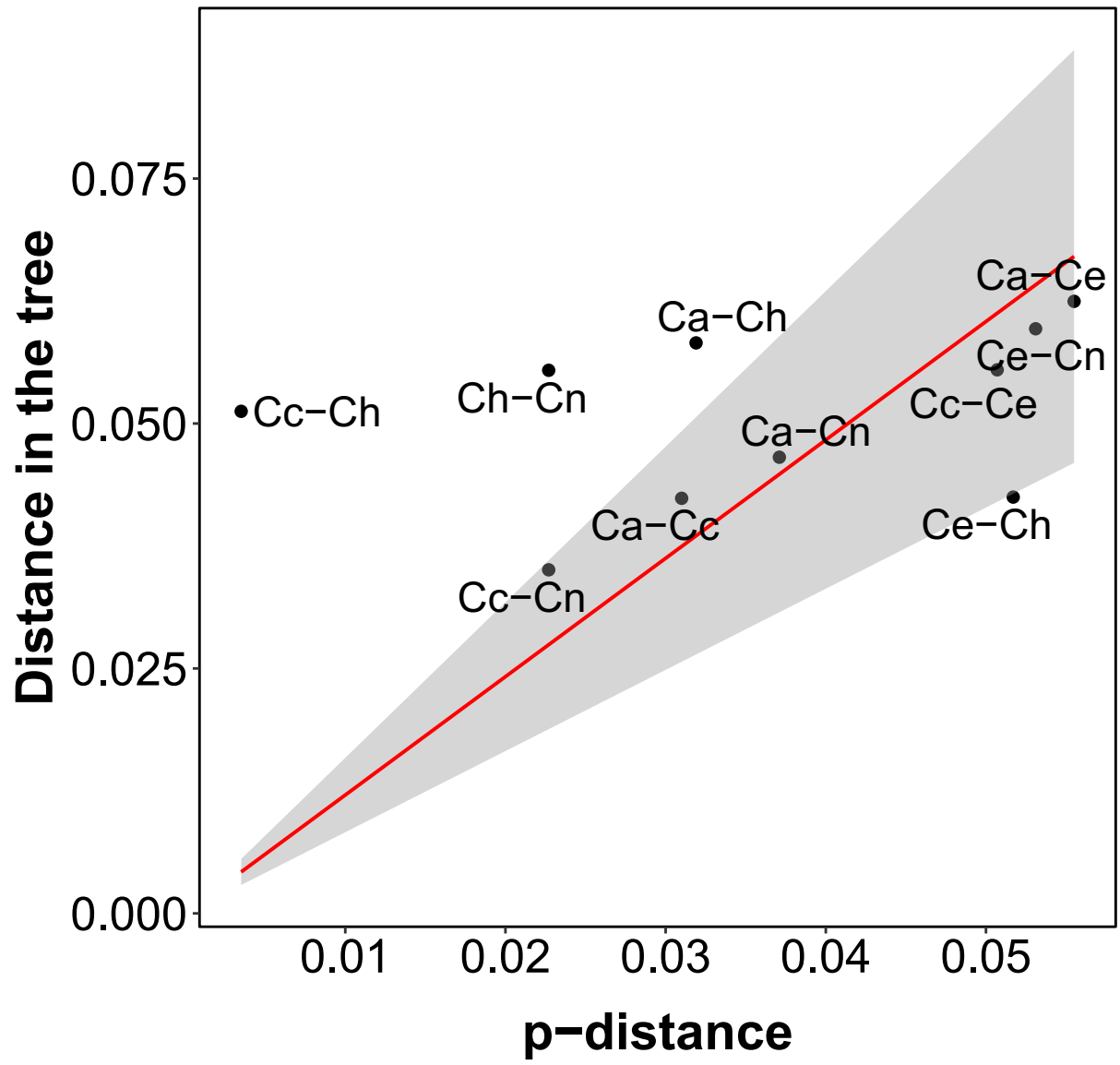
COX1



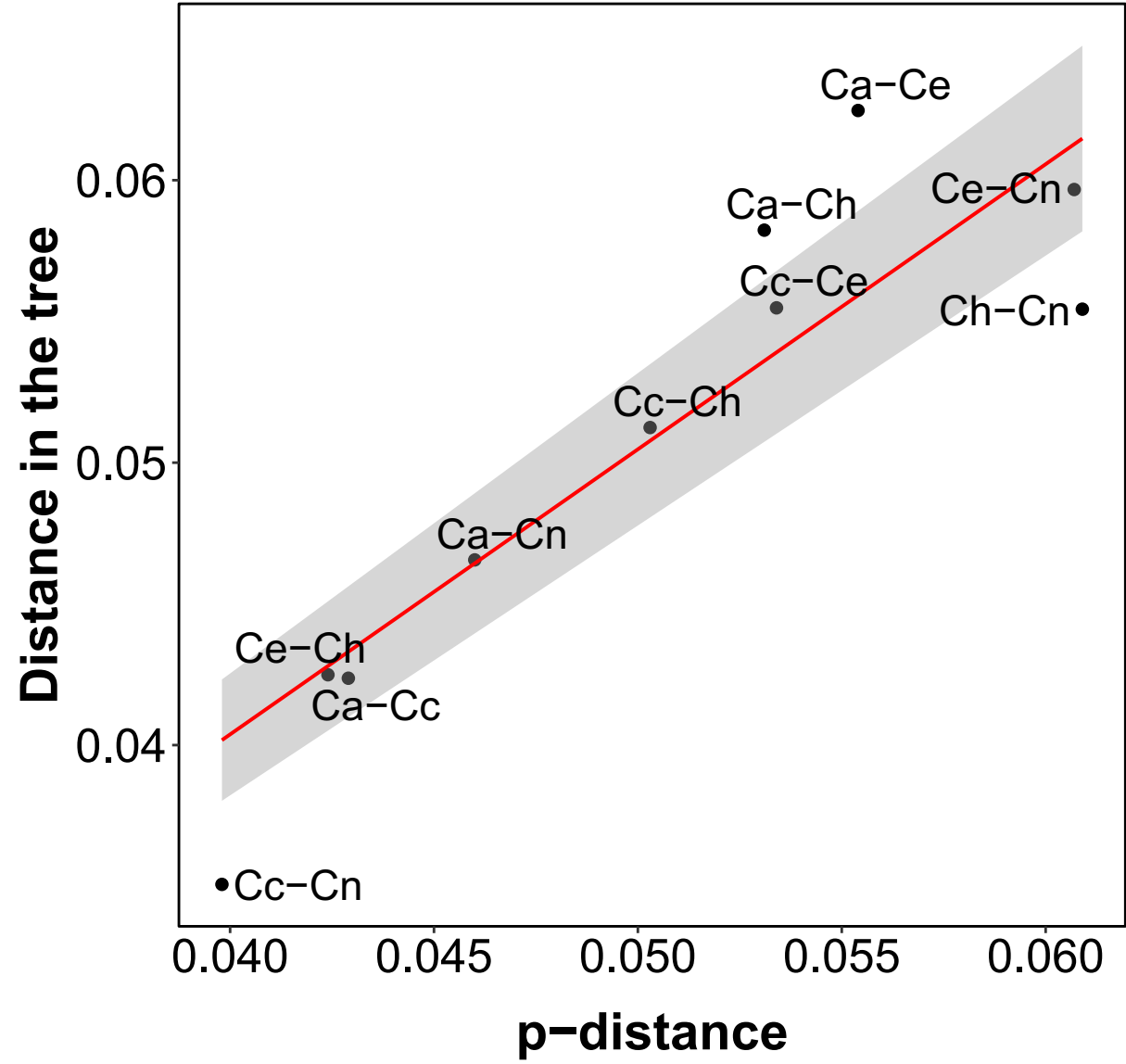
COX2



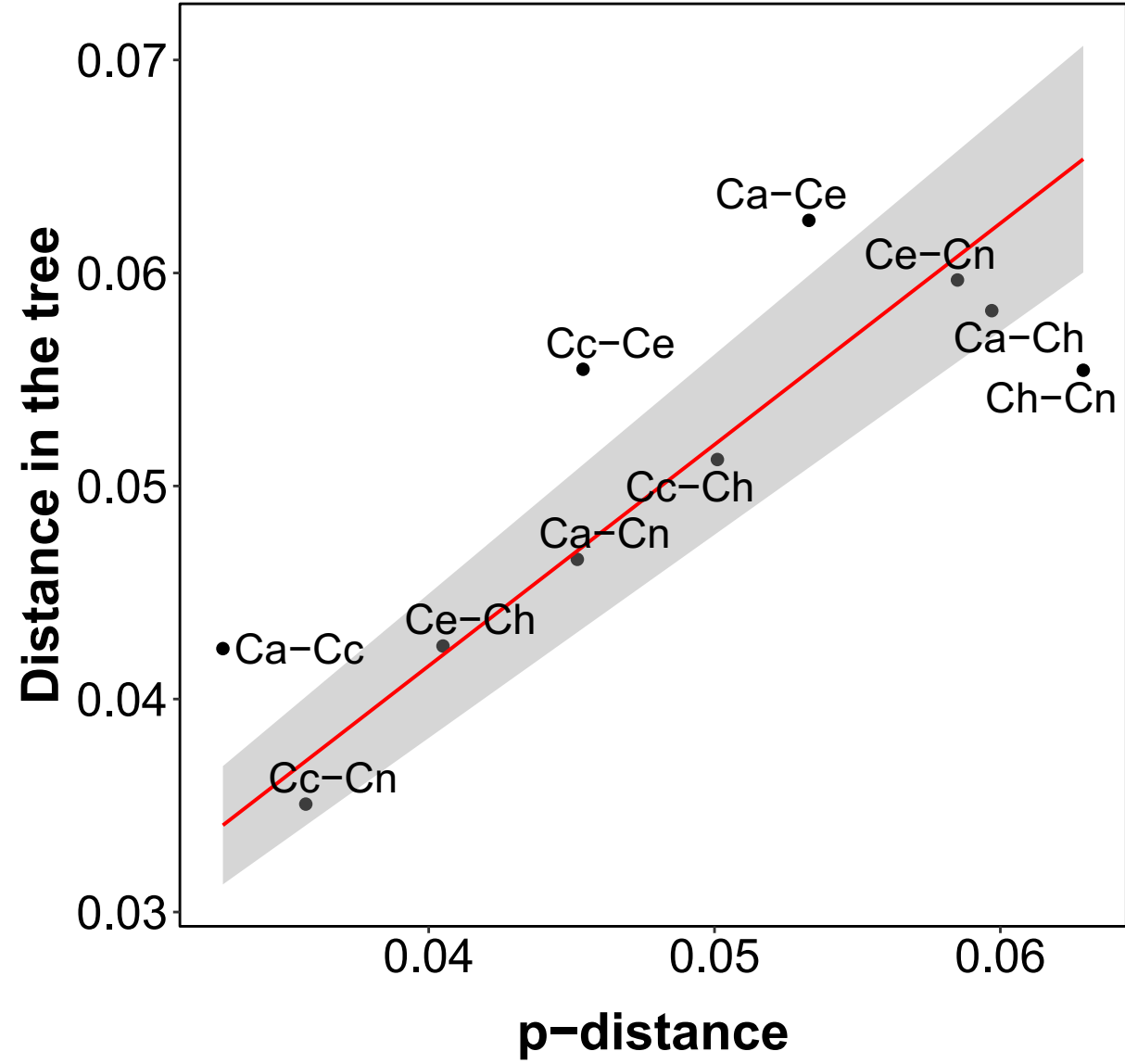
COX3



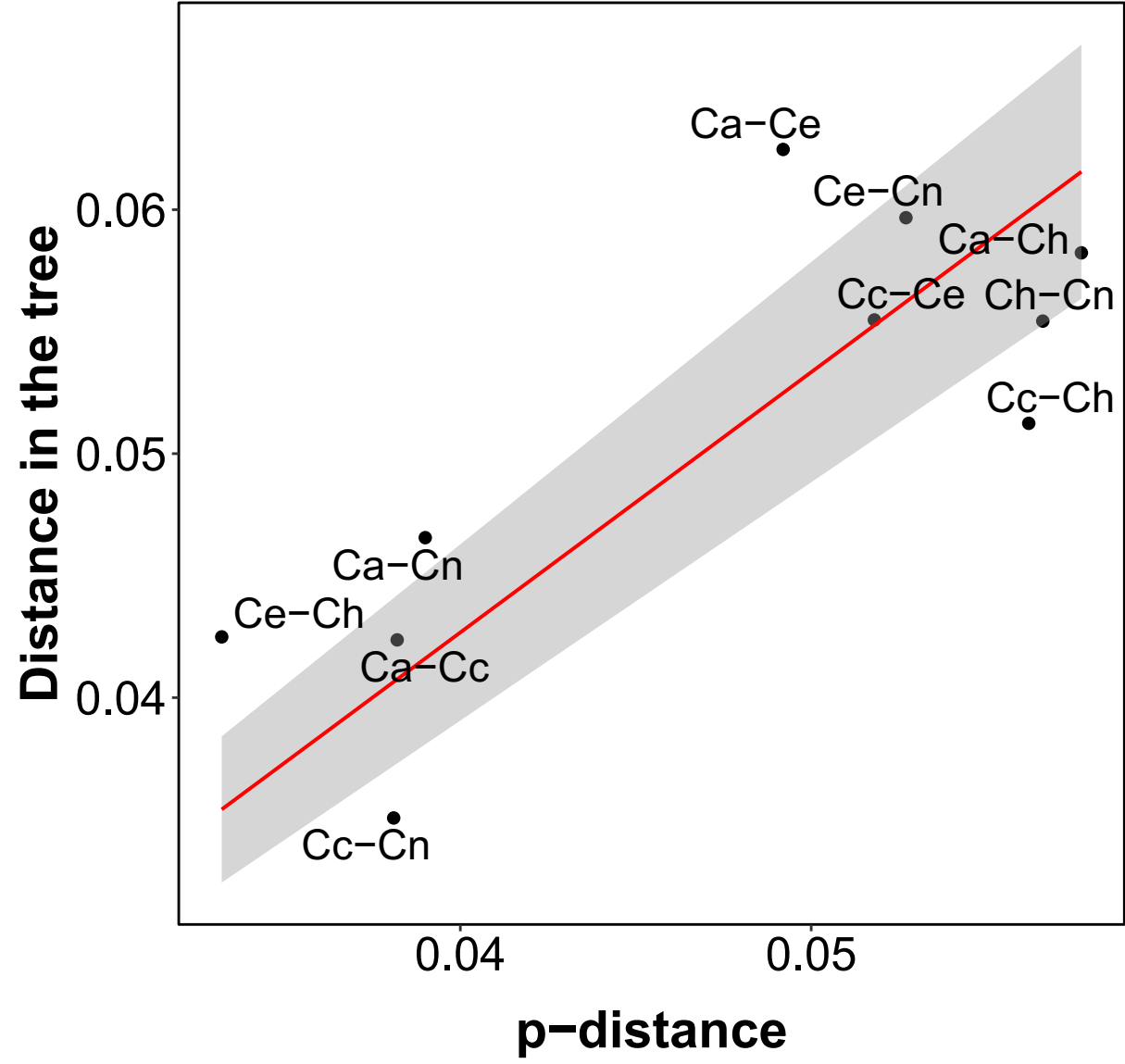
CYTB



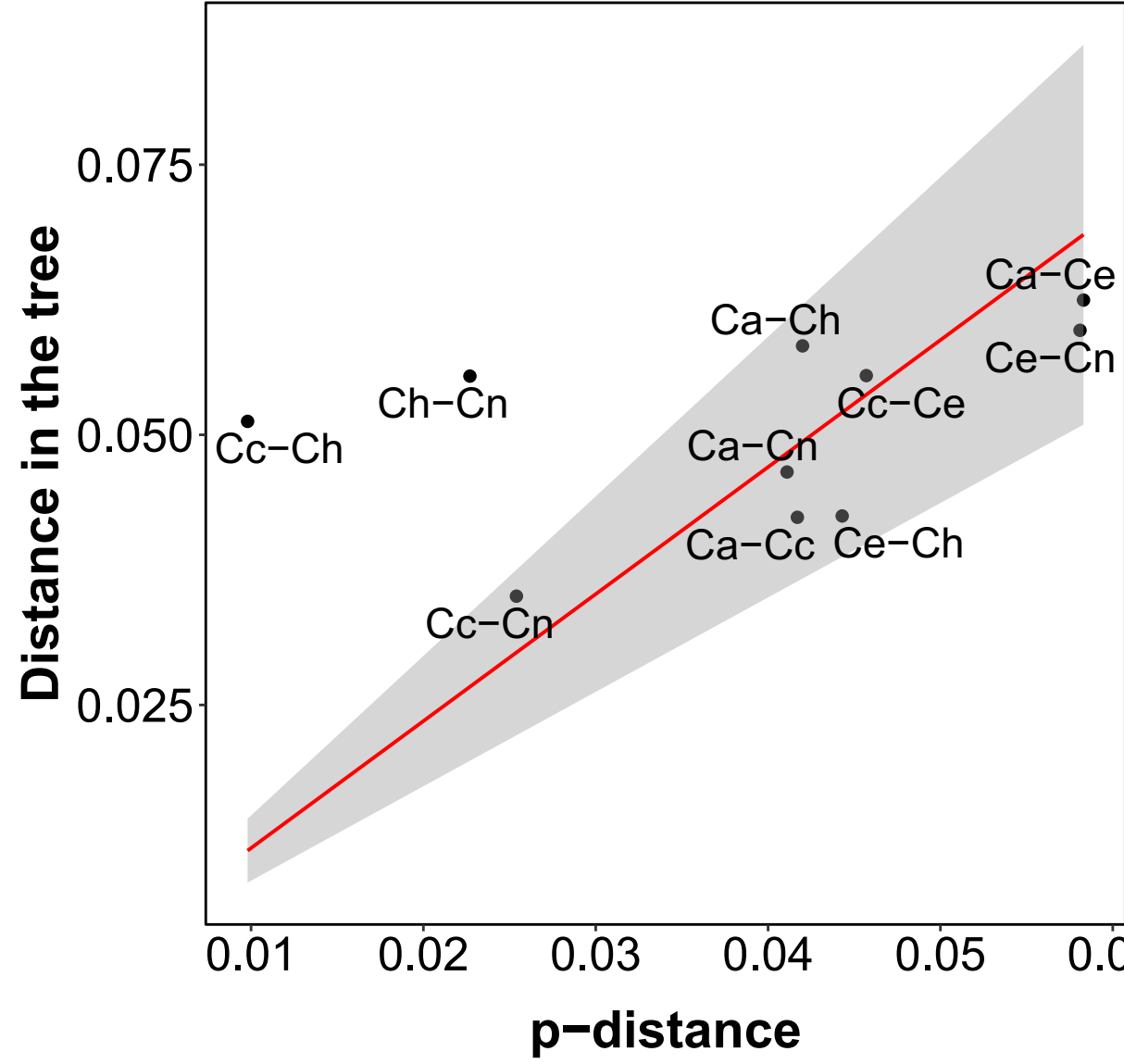
ND1



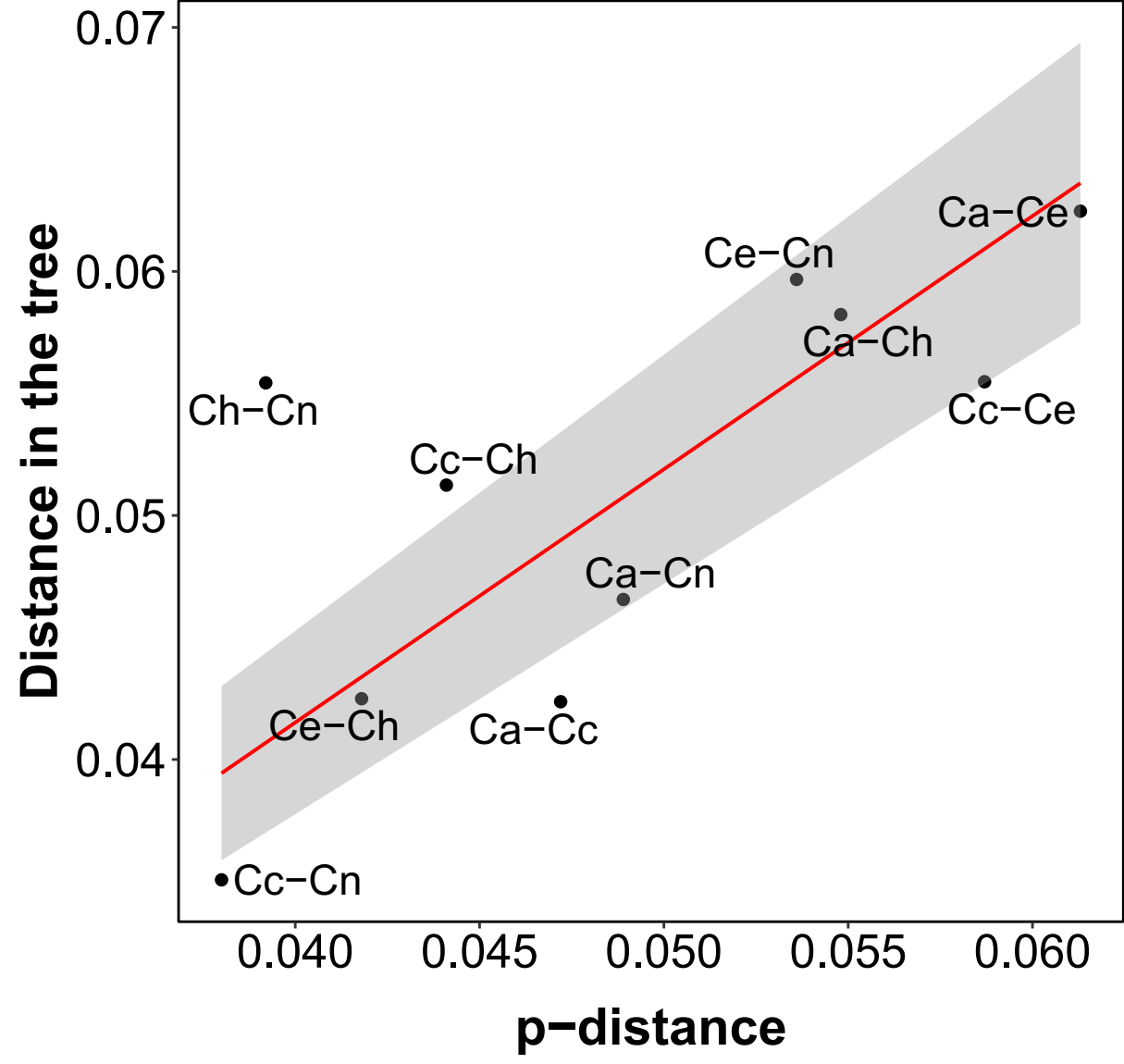
ND2



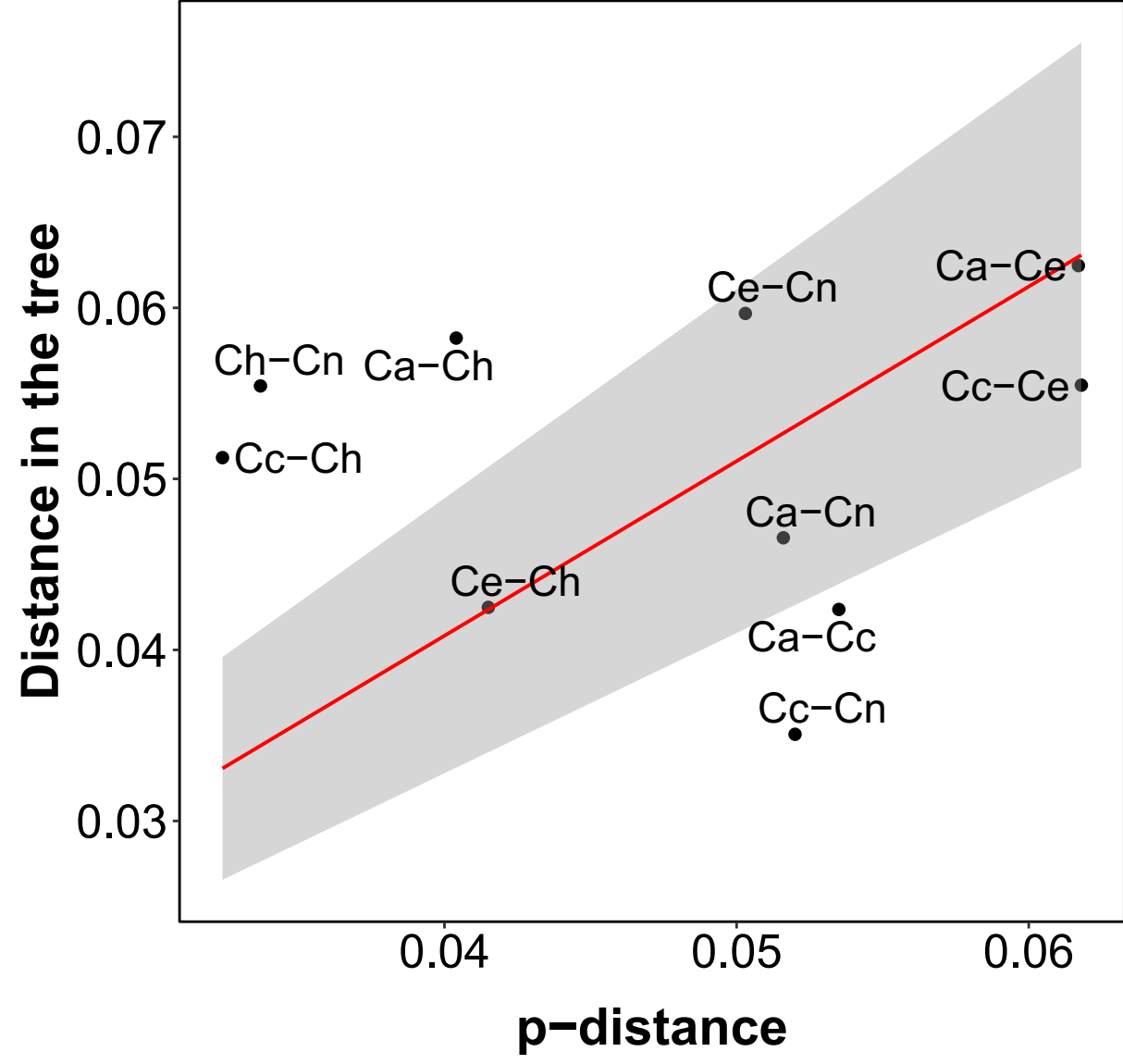
ND3



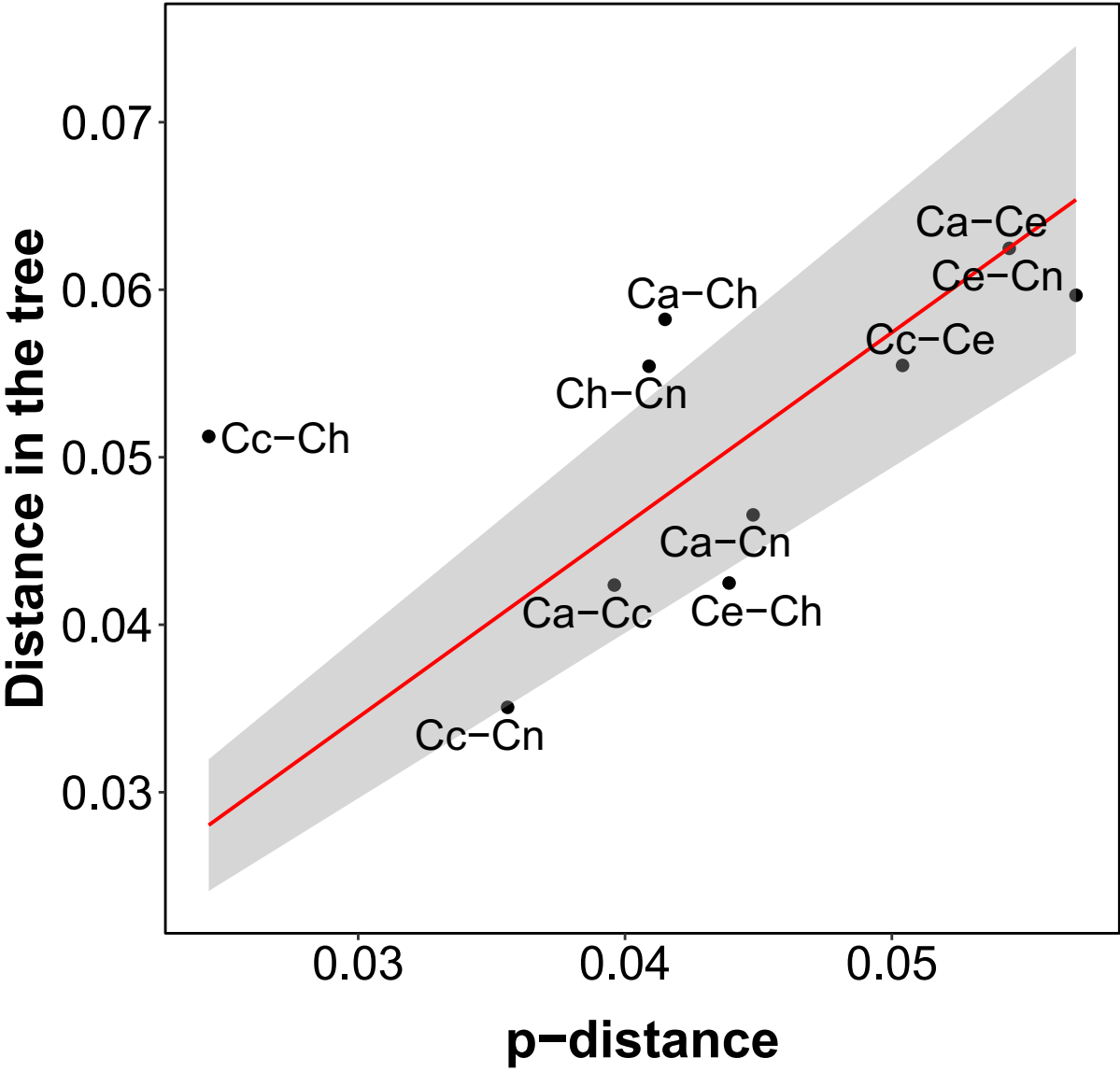
ND4



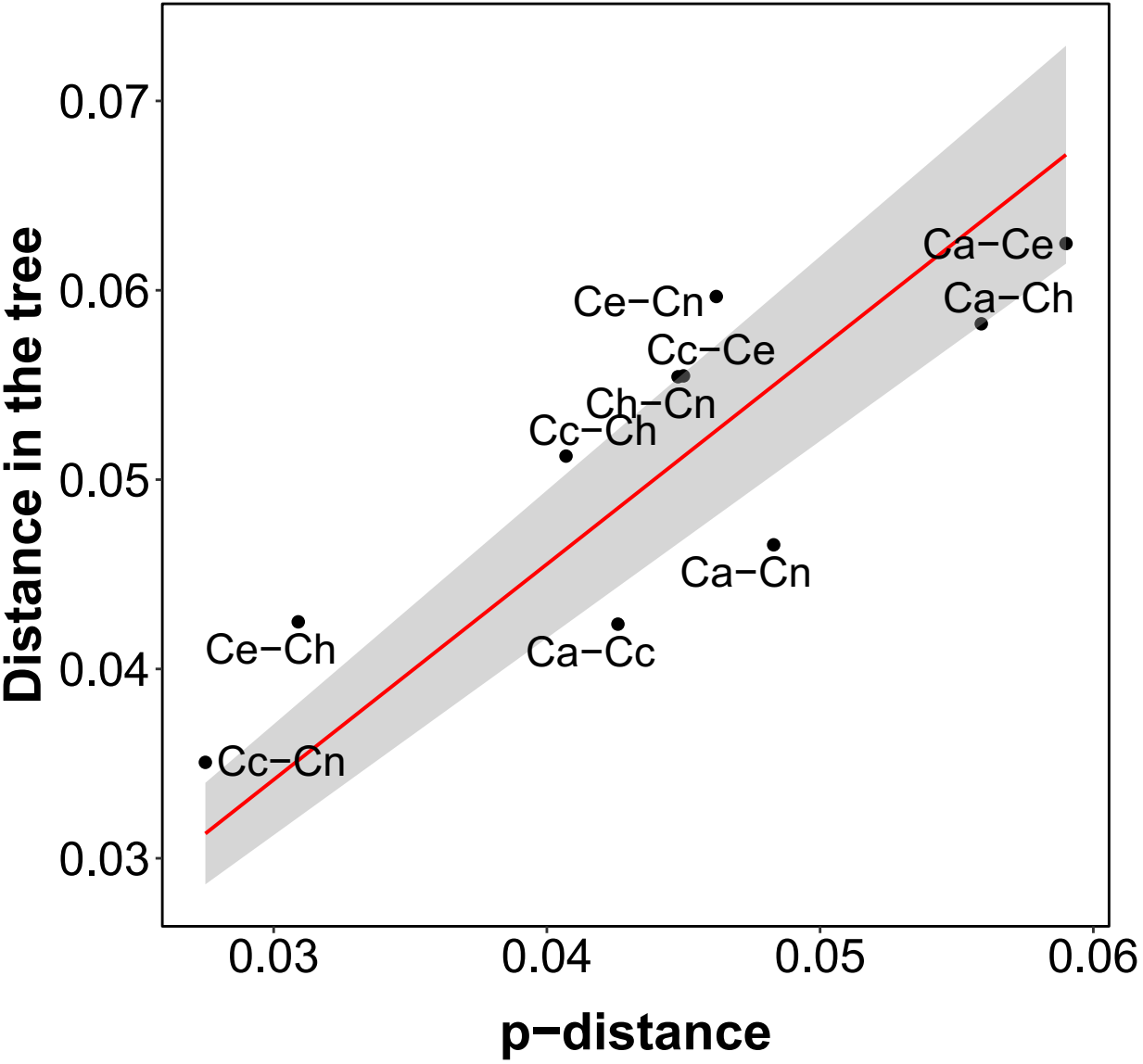
ND4L



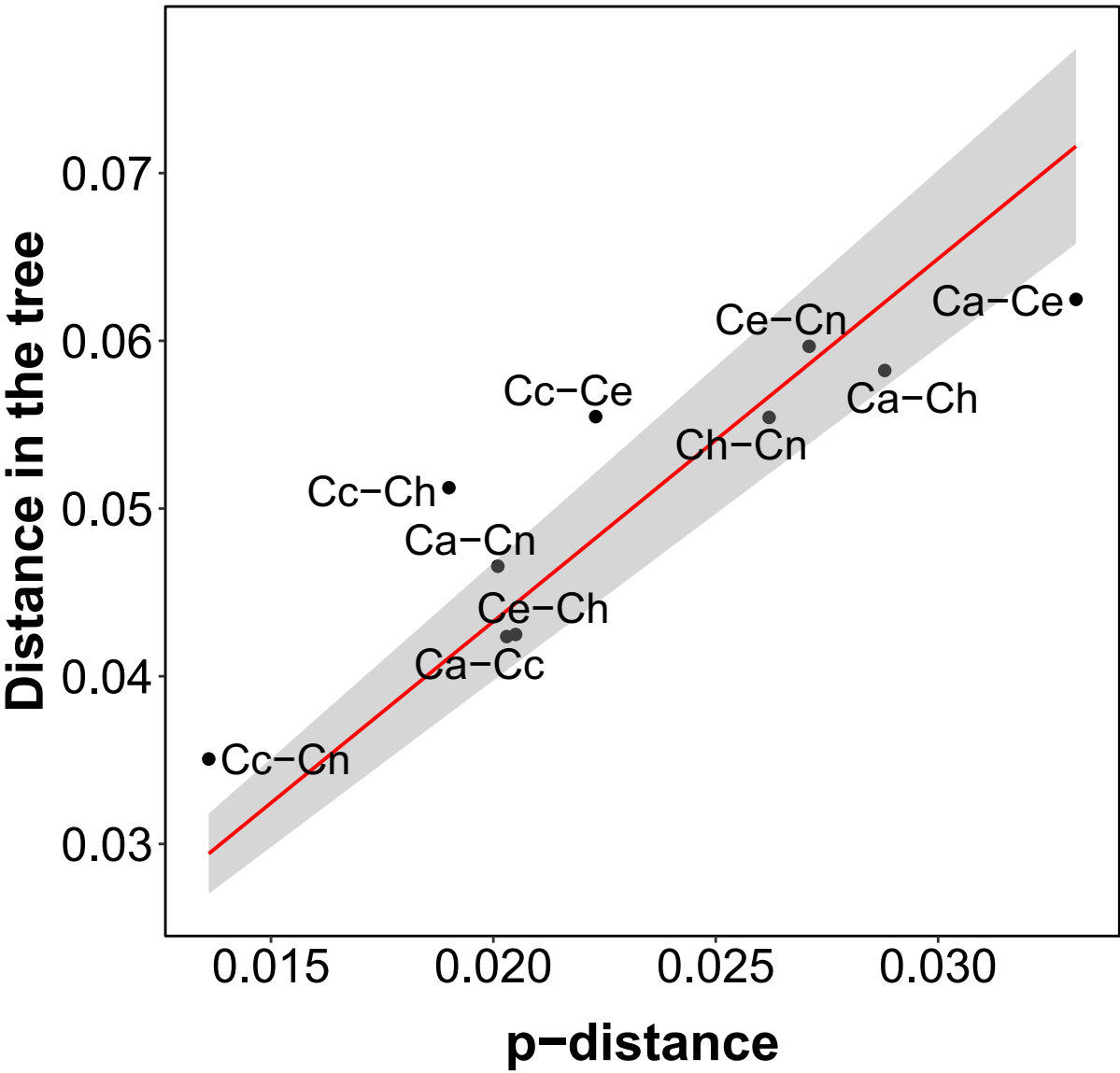
ND5



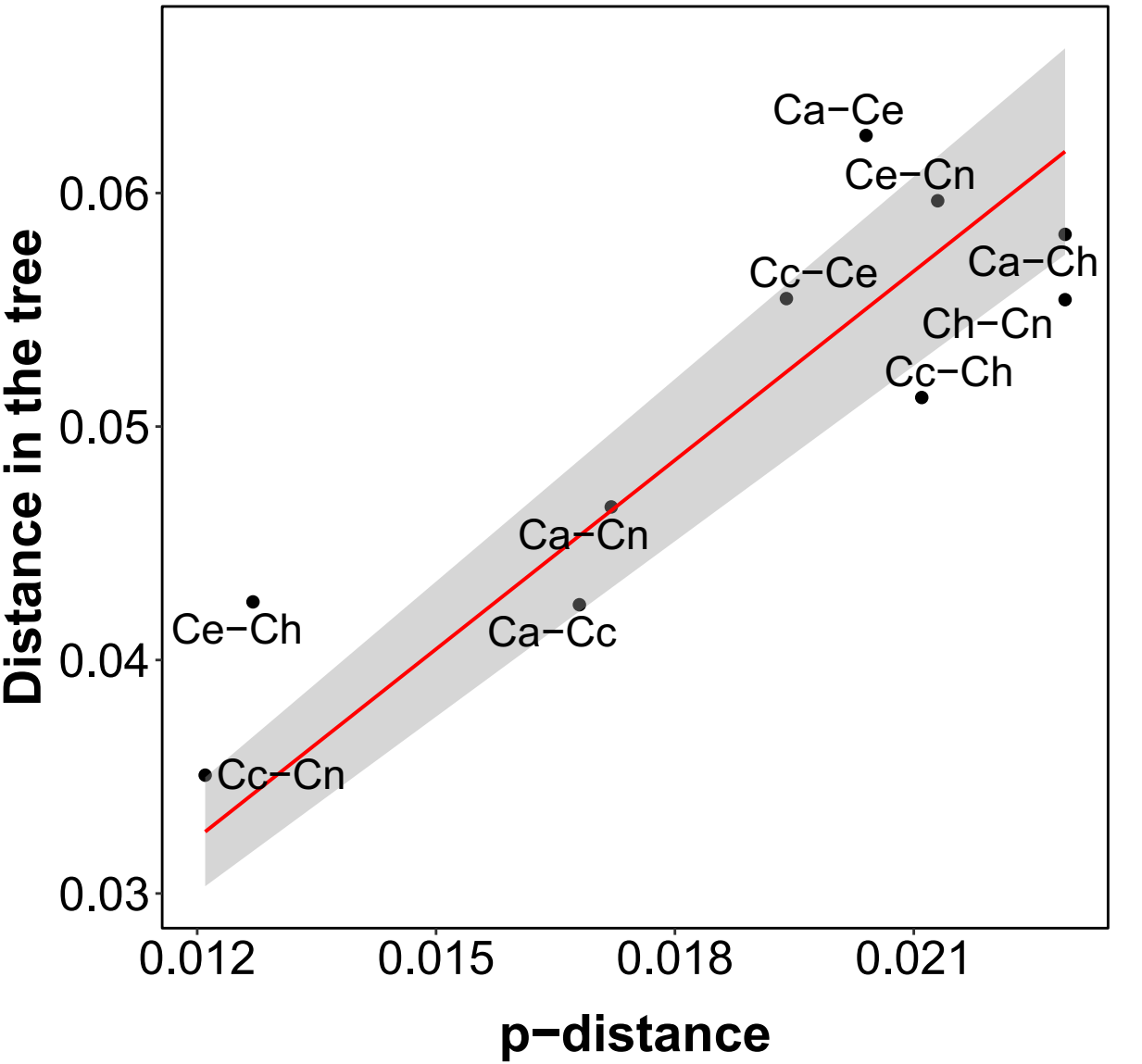
ND6



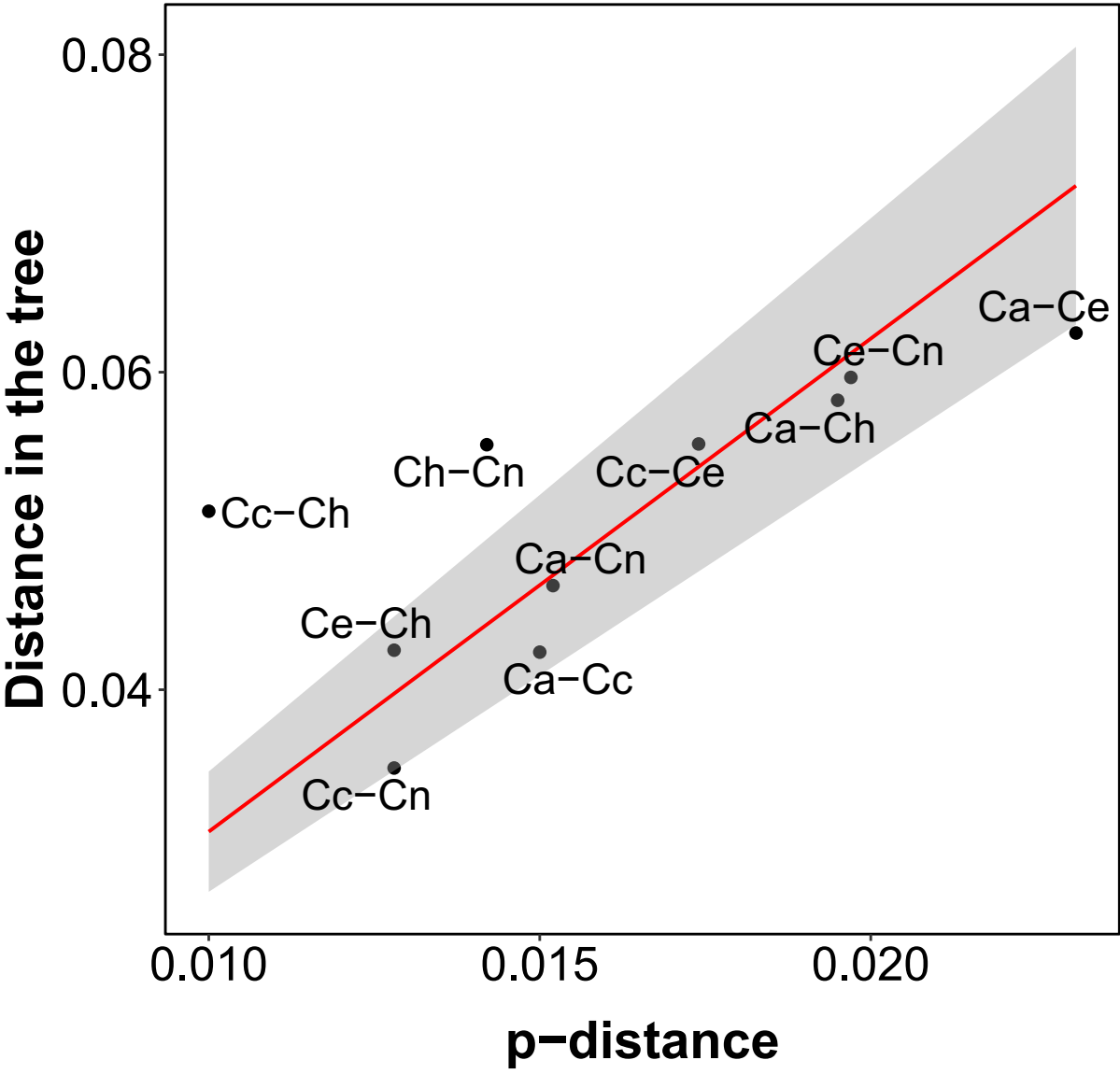
12S rRNA



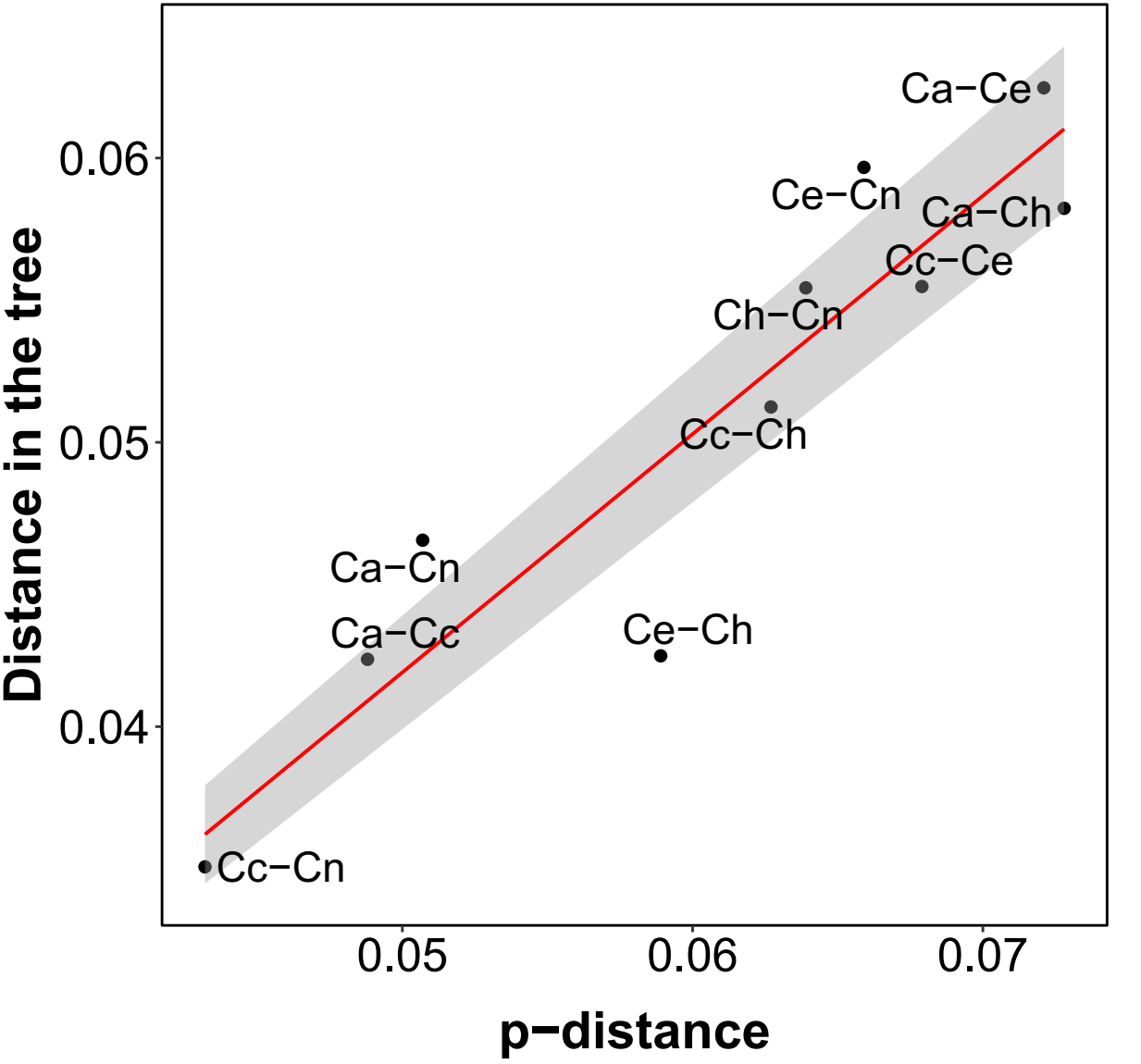
16S rRNA



tRNA



CR



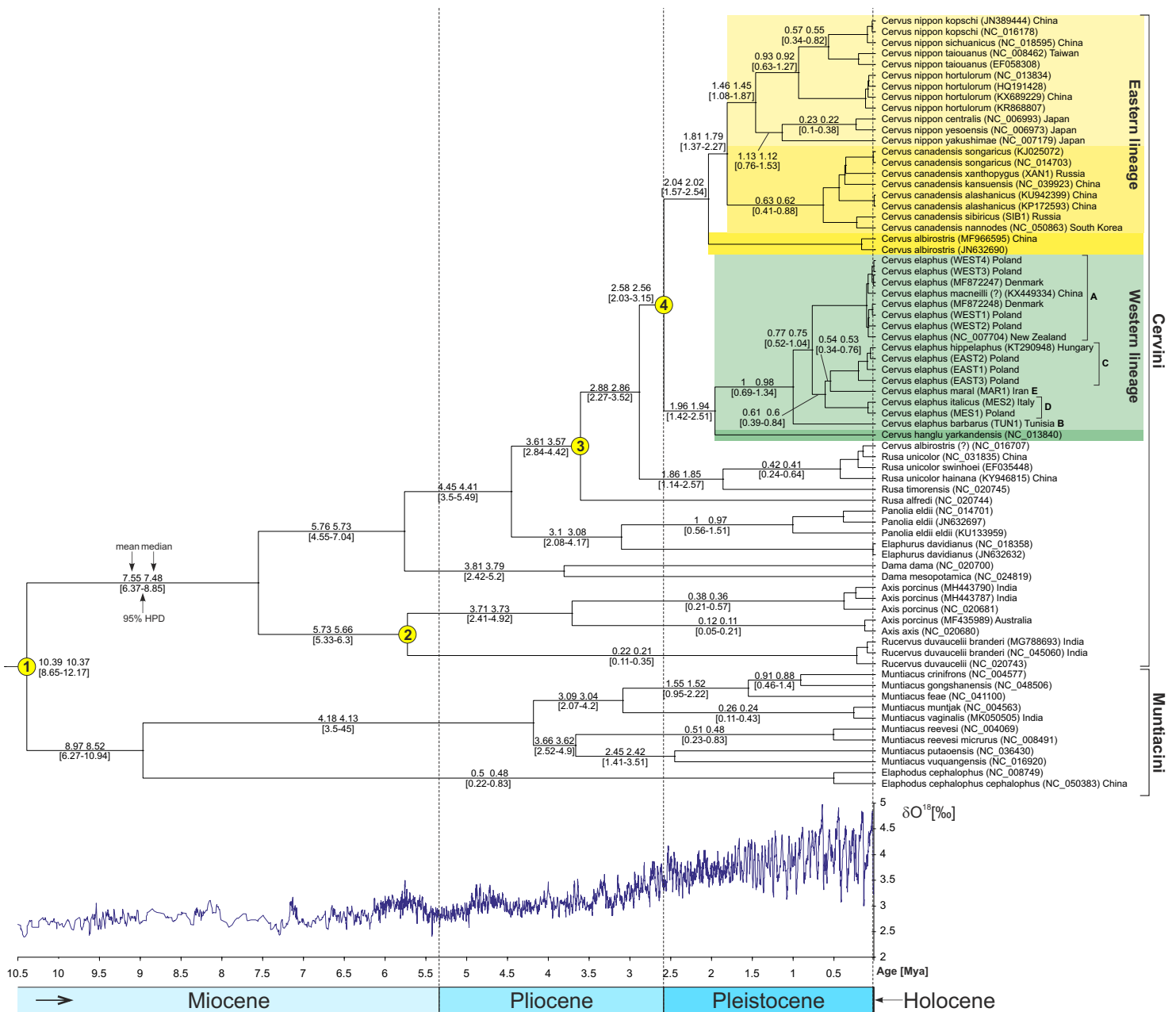






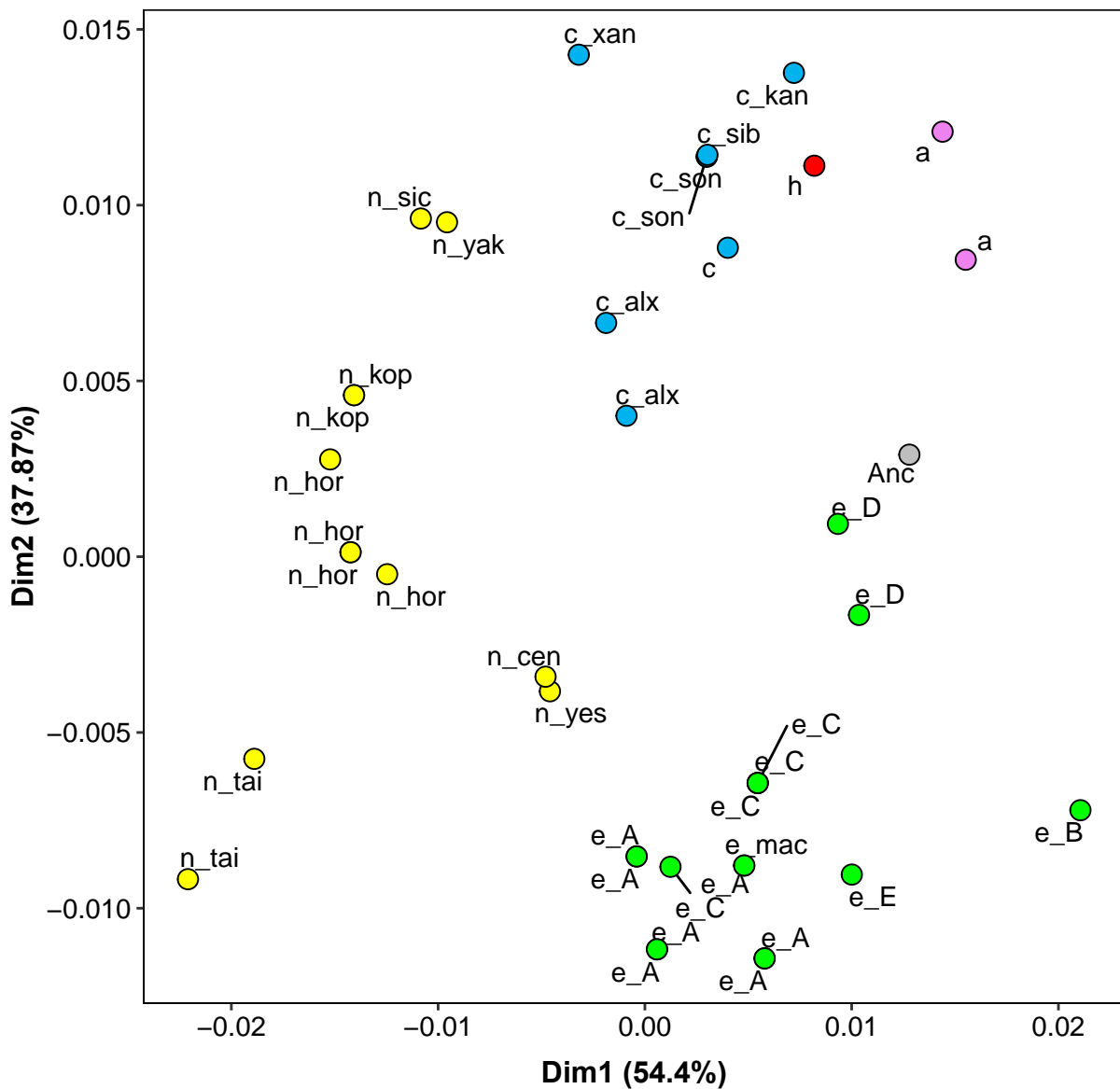


Figure S4. The chronogram for Muntiacini and Cervini with the oxygen isotopic curve (Zachos *et al.*, 2001). Mean and median as well as 95% Highest Posterior Density (HPD) of individual node ages are shown at selected branches. Letters (A-E) next to *Cervus elaphus* clades refer to intraspecific phylogeographic haplogroups. Calibration points were marked by yellow circles: 1 - the split of *Cervinae* into Cervini and Muntiacini based on previous molecular estimations (Świsłocka *et al.* 2020) and the oldest representative of Muntiacini (Dong 2007); 2 - the split of *Axis* and *Rucervus* based on the oldest fossils of *Axis* (Deng 2006; Vislobokova 2011); 3 - the divergence of *Rusa* and *Cervus* clade assumed according to the oldest *Rusa* (Vislobokova 2012); 4 - the separation of two *Cervus* clades: *C. elaphus* + *C. hanglu* and *C. canadensis* + *C. nippon* + *C. albirostris* according to the fossil *C. nestii* (Bellucci *et al.* 2014), probably belonging to the lineage of *C. elaphus* + *C. hanglu* (Croitor 2018; Croitor 2020).

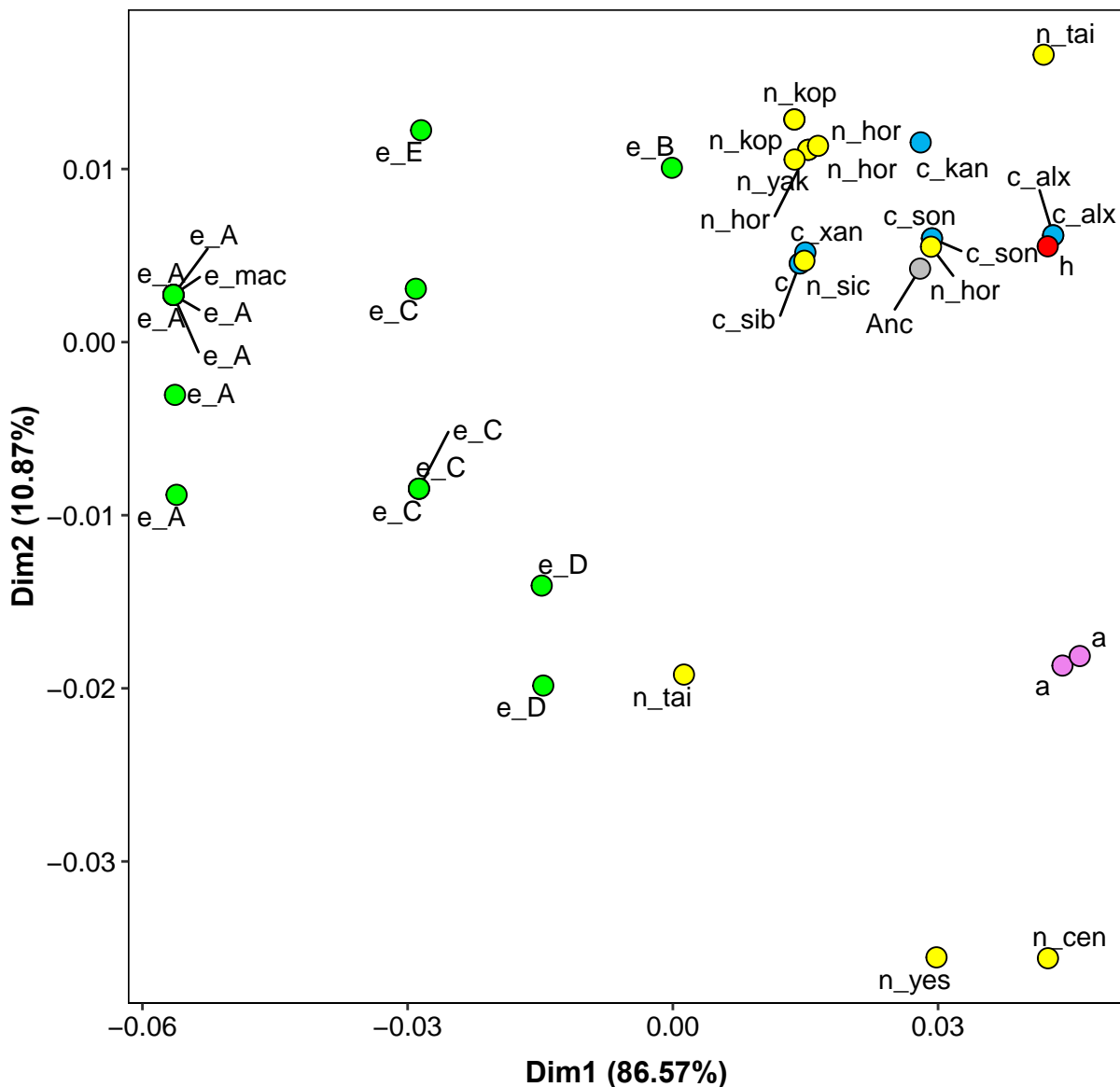
Figure S5. Correspondence analysis plots obtained for the nucleotide composition of selected genes showing a similar composition in *C. hanglu* and the Eastern lineage deer. *Cervus* taxa: a - *C. albirostris*; c - *C. canadensis*; c_ala - *C. canadensis alashanicus*; c_kan - *C. canadensis kansuensis*; c_sib - *C. canadensis sibiricus*; c_son - *C. canadensis songaricus*; c_xan - *C. canadensis xanthopygus*; e_A - *C. elaphus* haplogroup A; e_B - *C. elaphus* haplogroup B; e_C - *C. elaphus* haplogroup C; e_D - *C. elaphus* haplogroup D; e_E - *C. elaphus* haplogroup E; e_mac - *C. elaphus macneilli*; h - *C. hanglu yarkandensis*; n_cen - *C. nippon centralis*; n_hor - *C. nippon hortulorum*; n_kop - *C. nippon kopschi*; n_sic - *C. nippon sichuanicus*; n_tai - *C. nippon taiouanus*; n_yak - *C. nippon yakushimae*; n_yes - *C. nippon yesoensis*; Anc - *Cervus* common ancestor .

-  *C. albirostris*
-  *C. canadensis*
-  *C. elaphus*
-  *C. hanglu*
-  *C. nippon*
-  *Cervus* ancestor

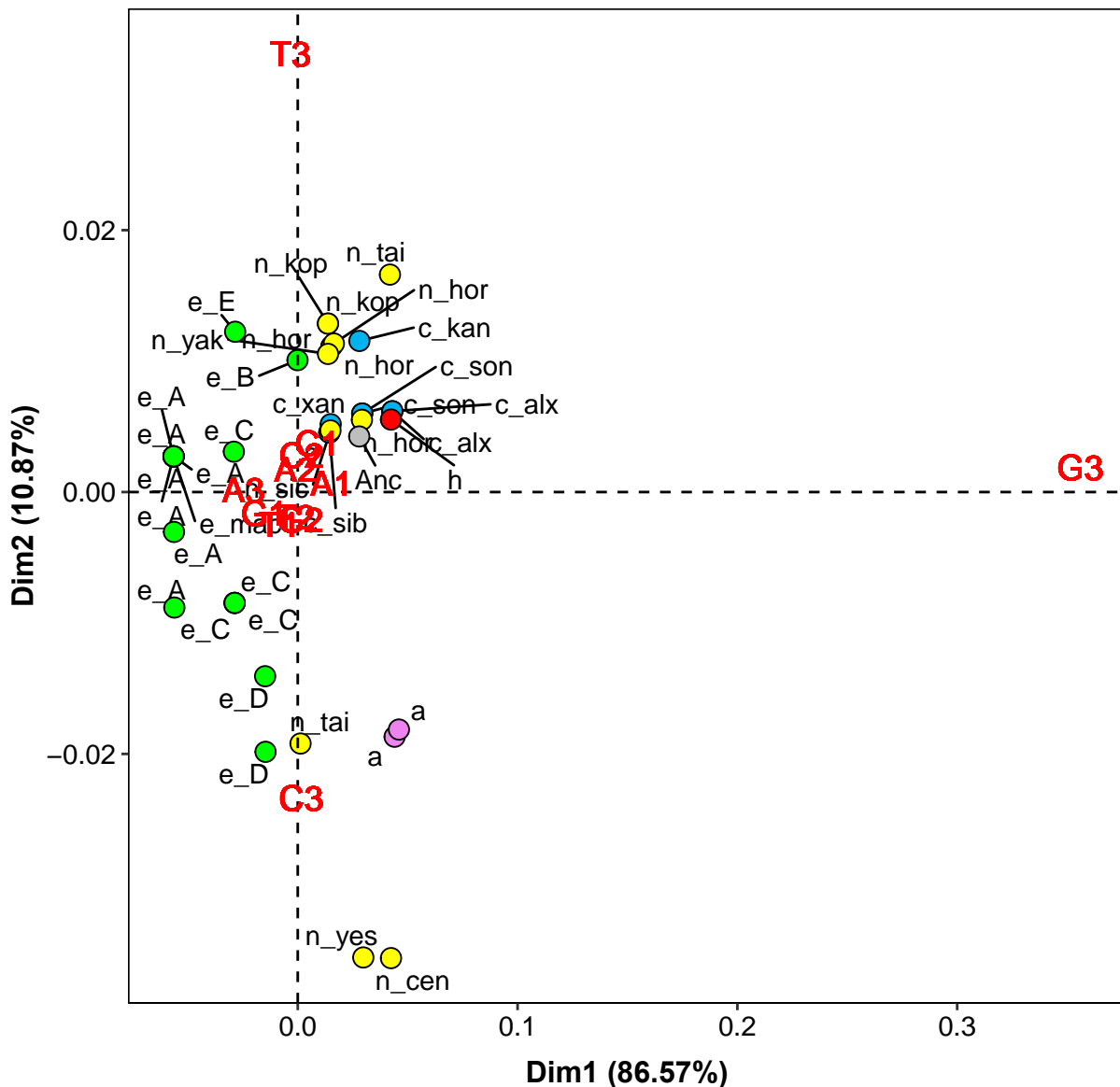
COX1



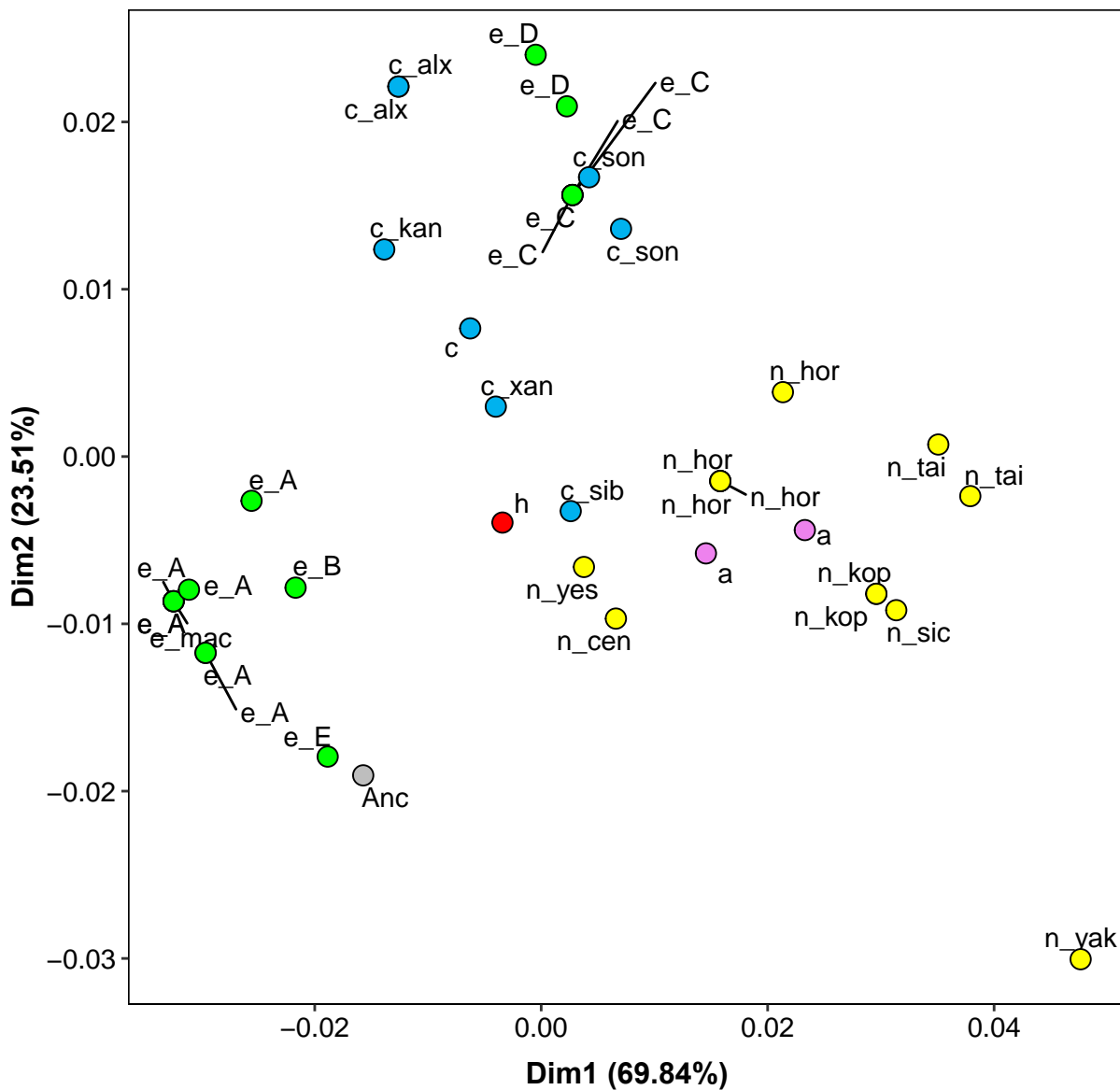
COX3



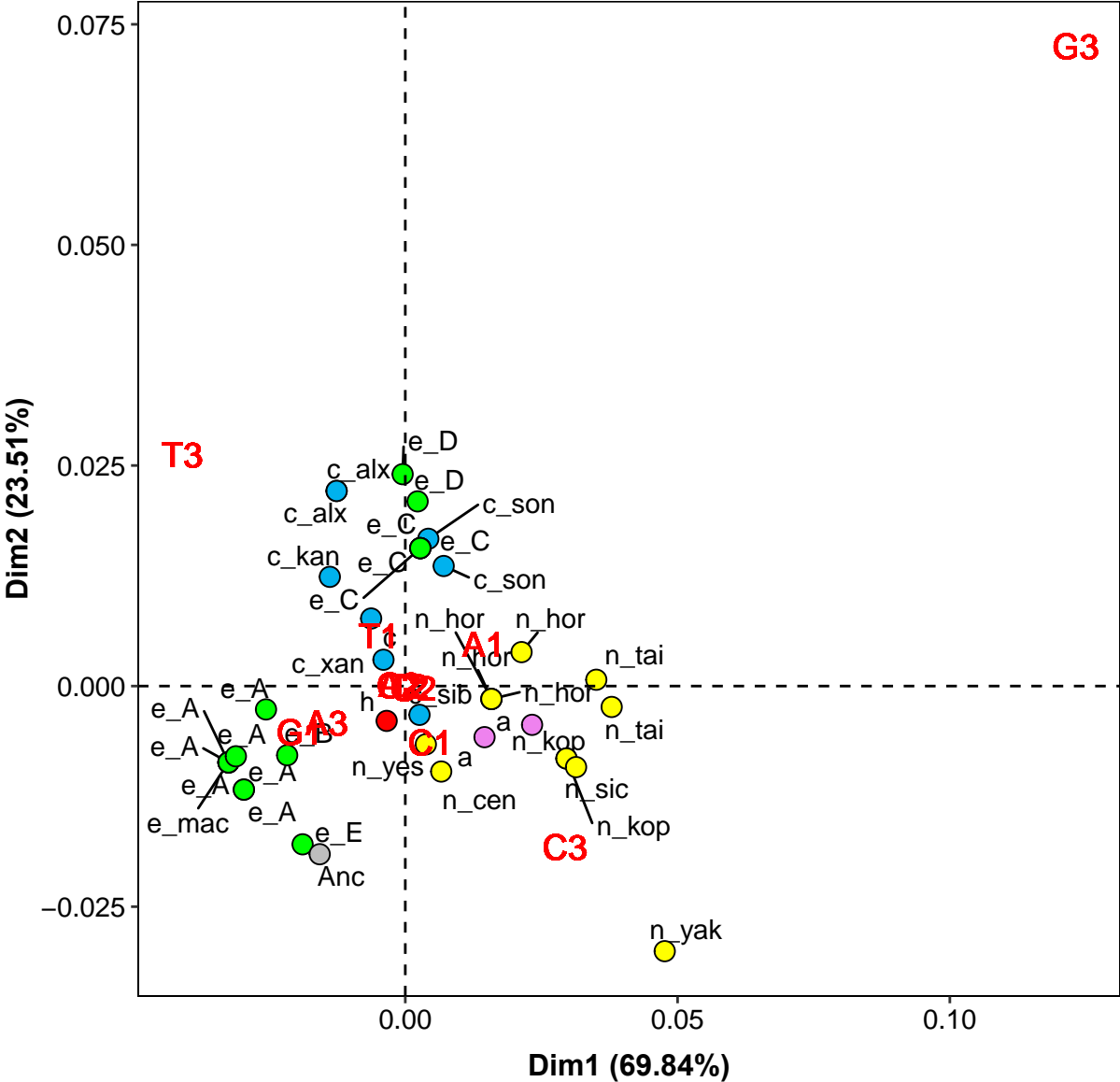
COX3



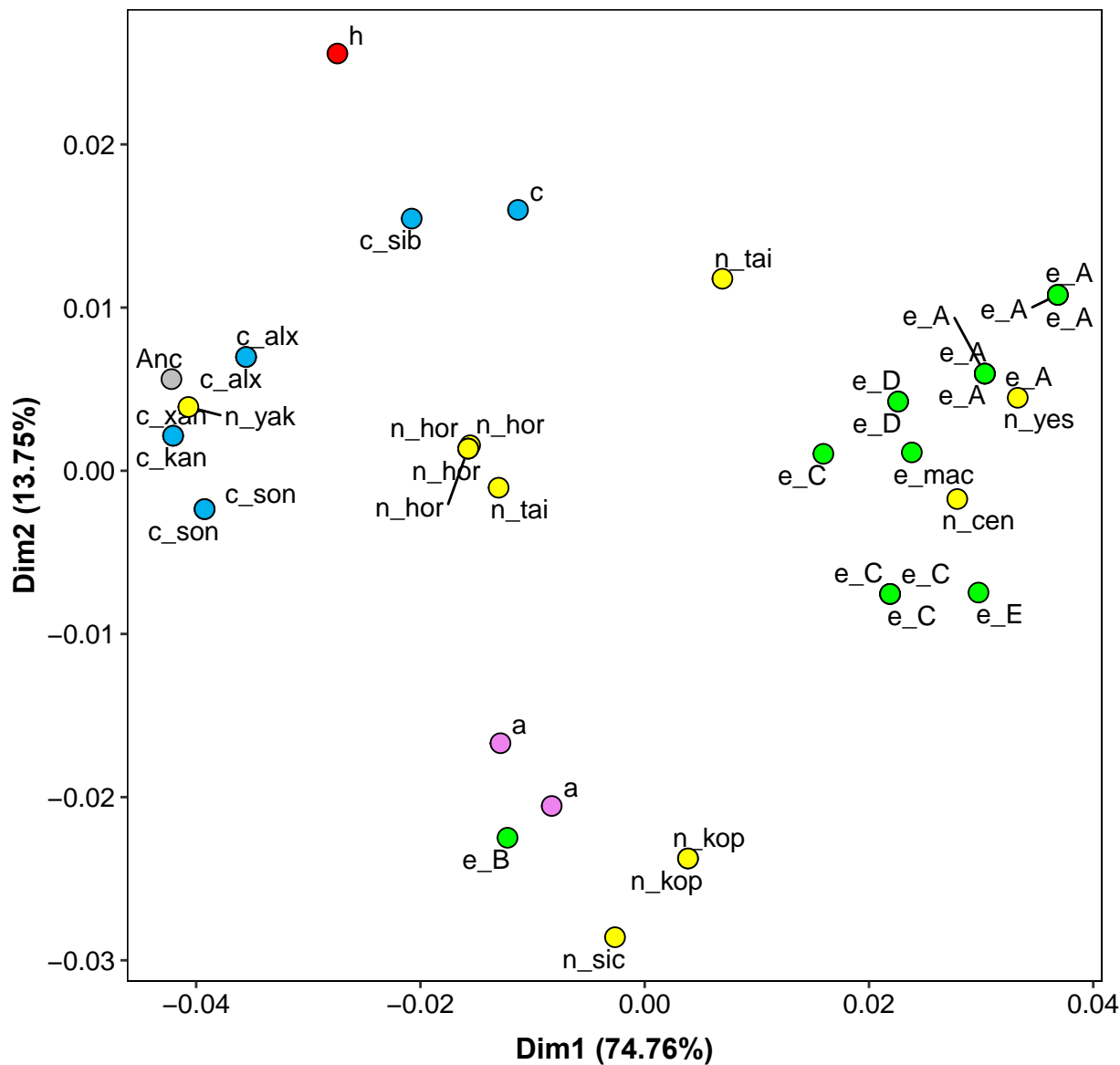
CYTB

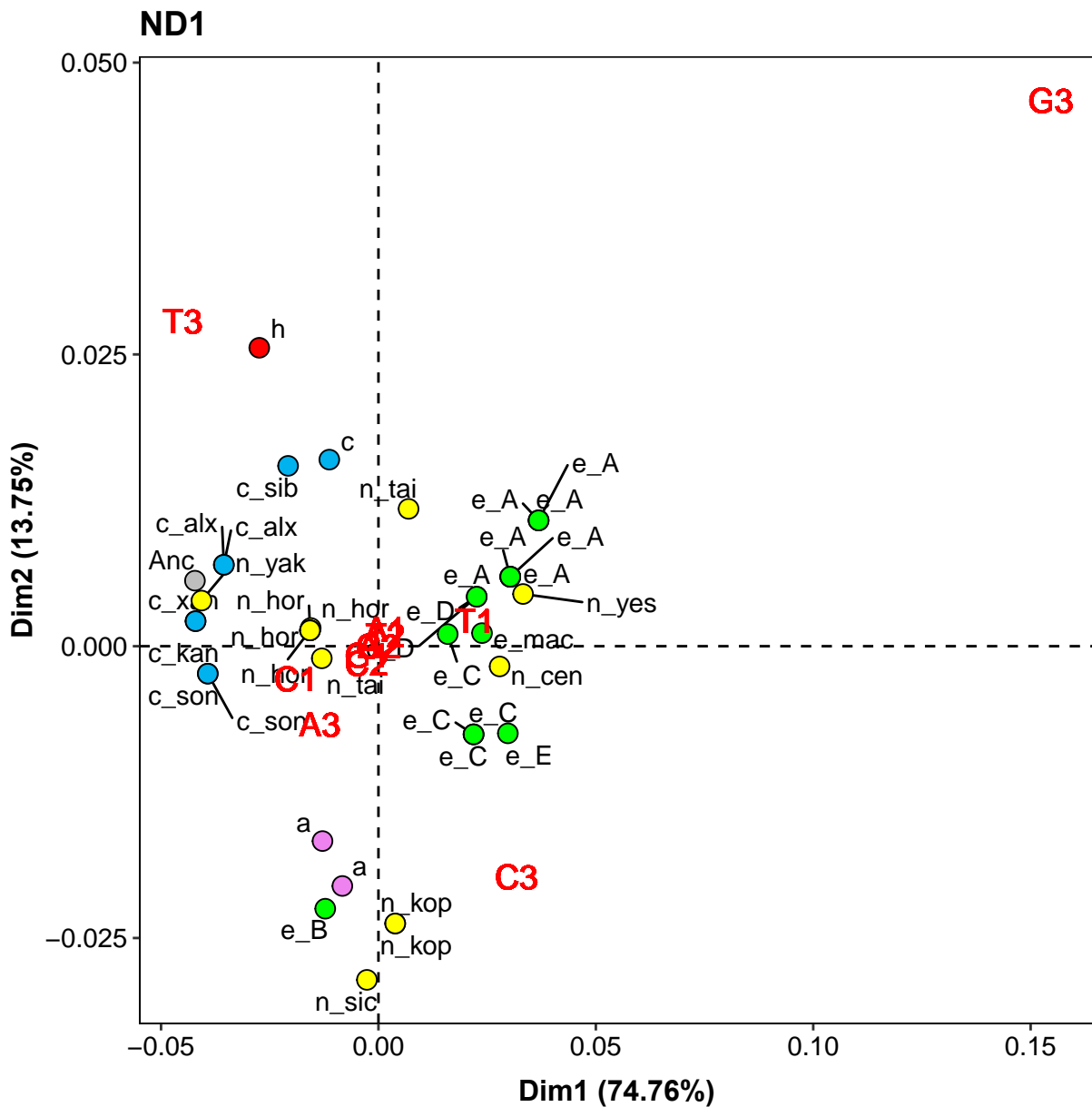


CYTB

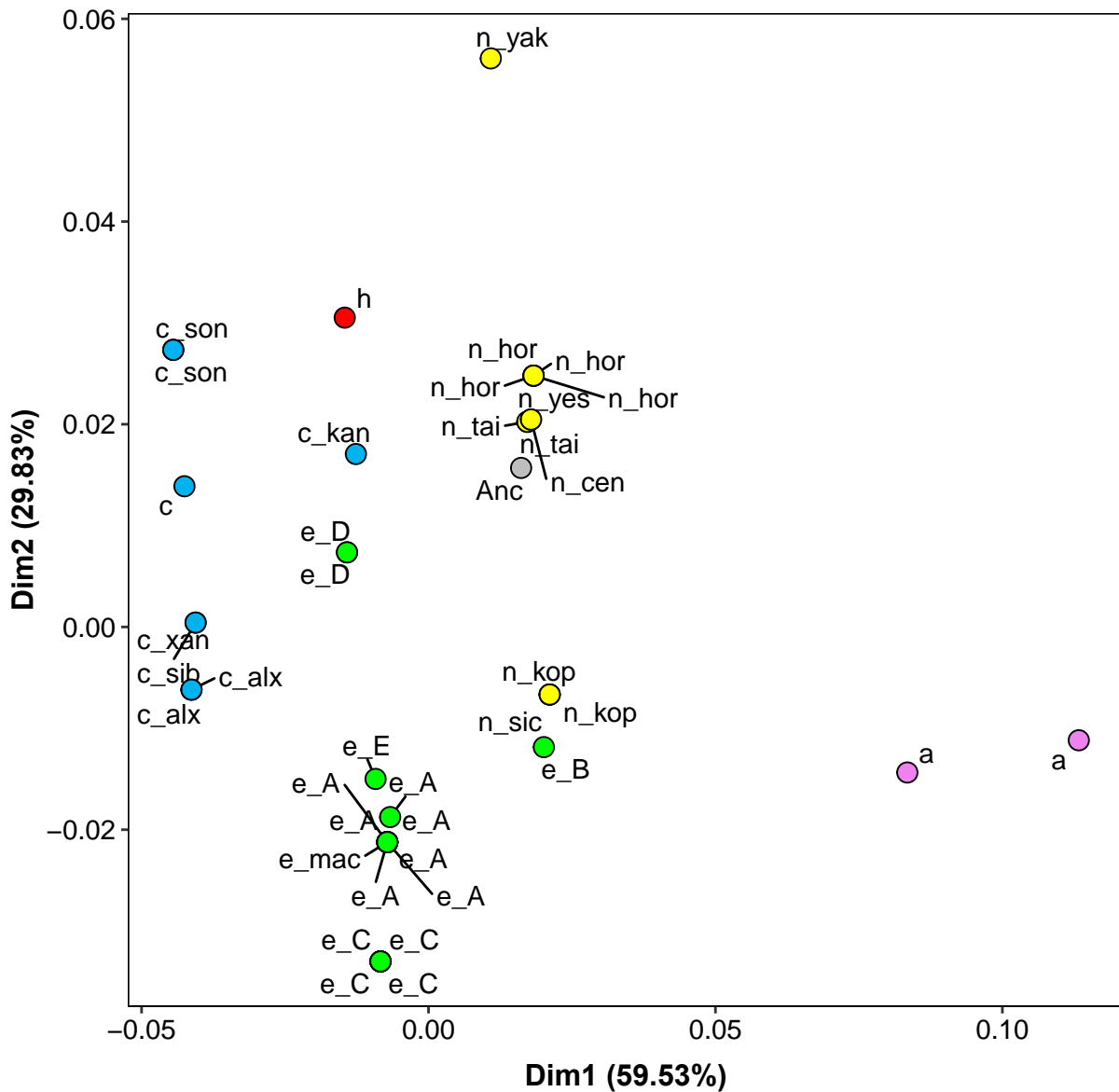


ND1

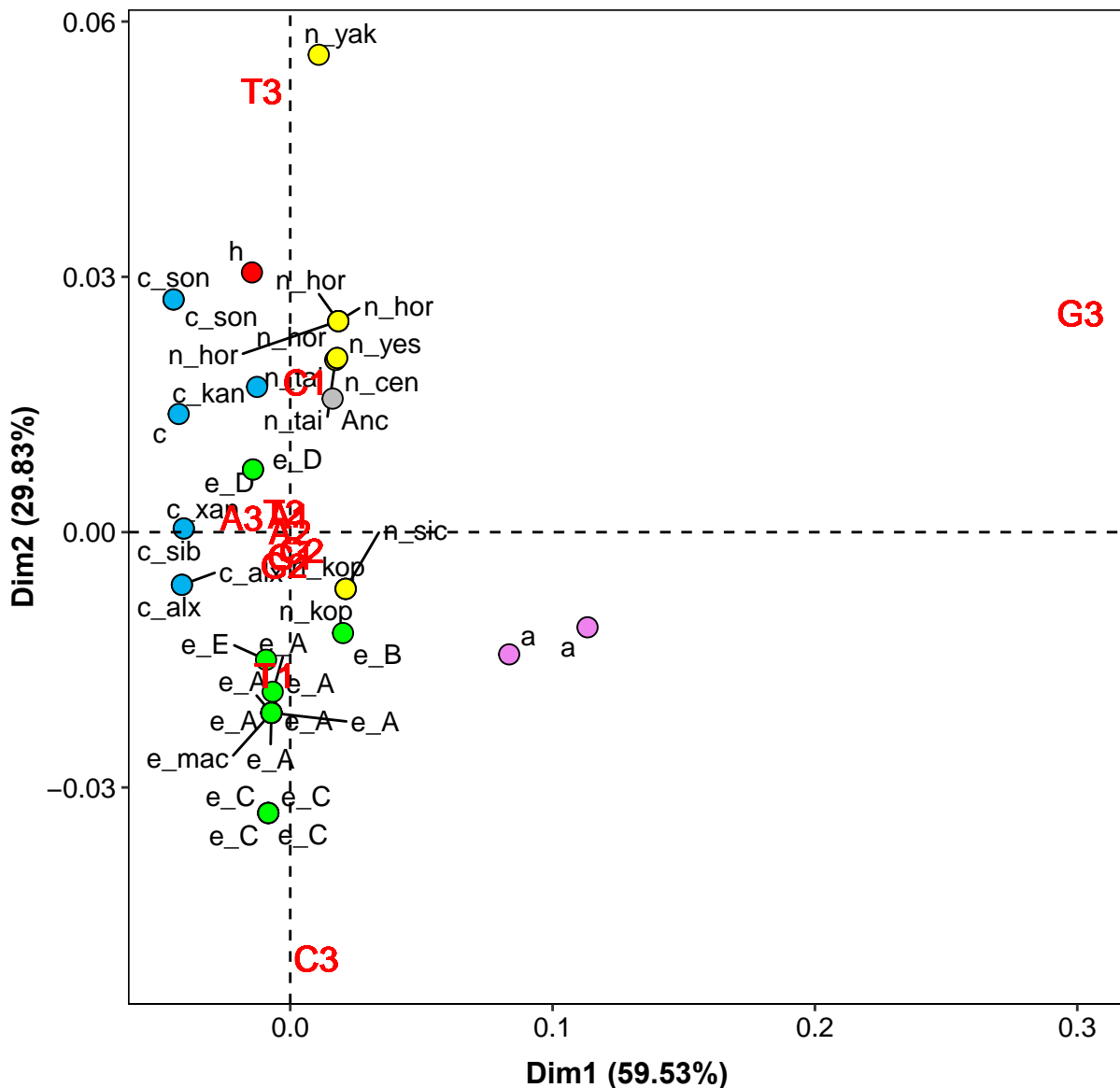




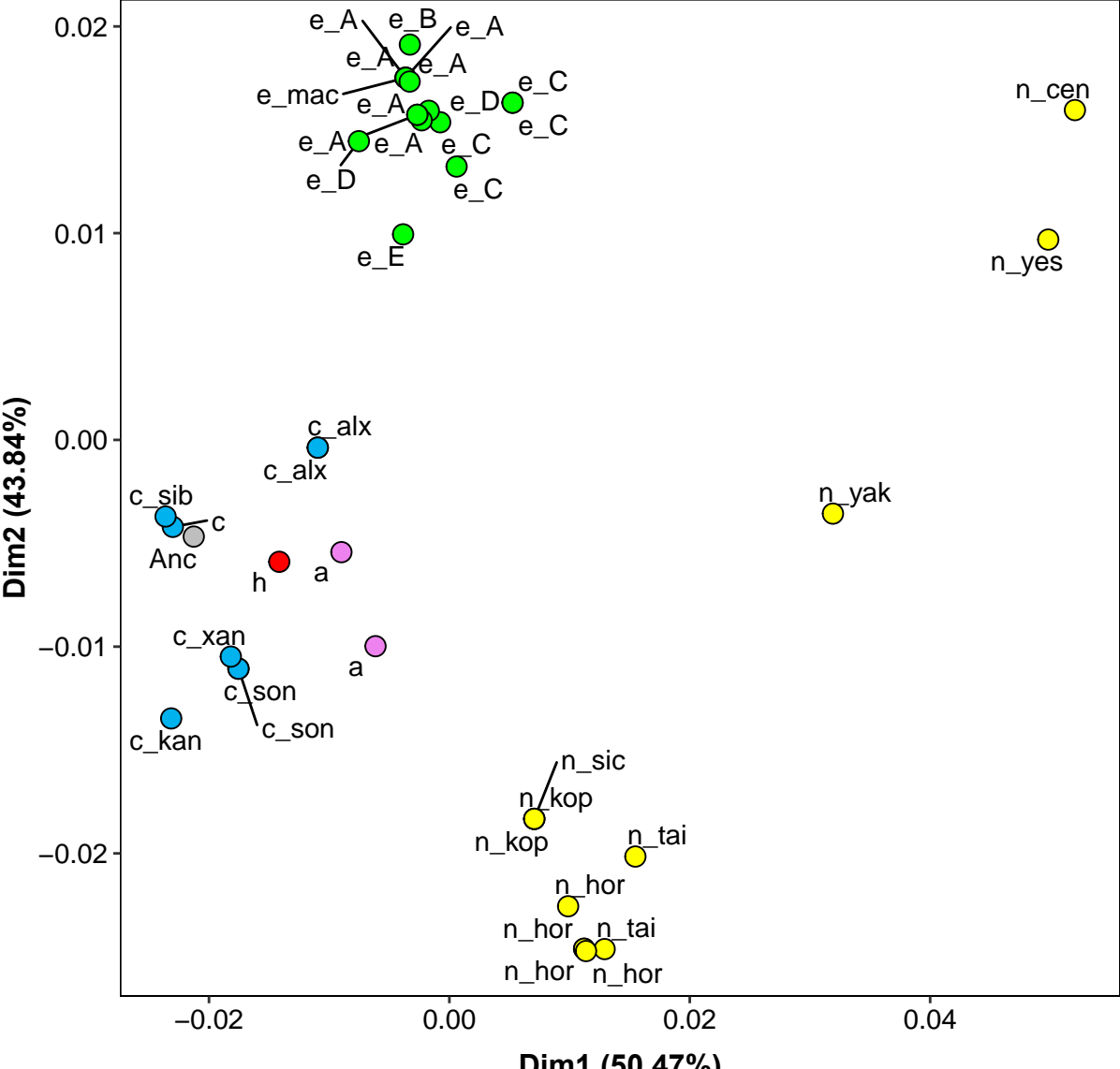
ND3



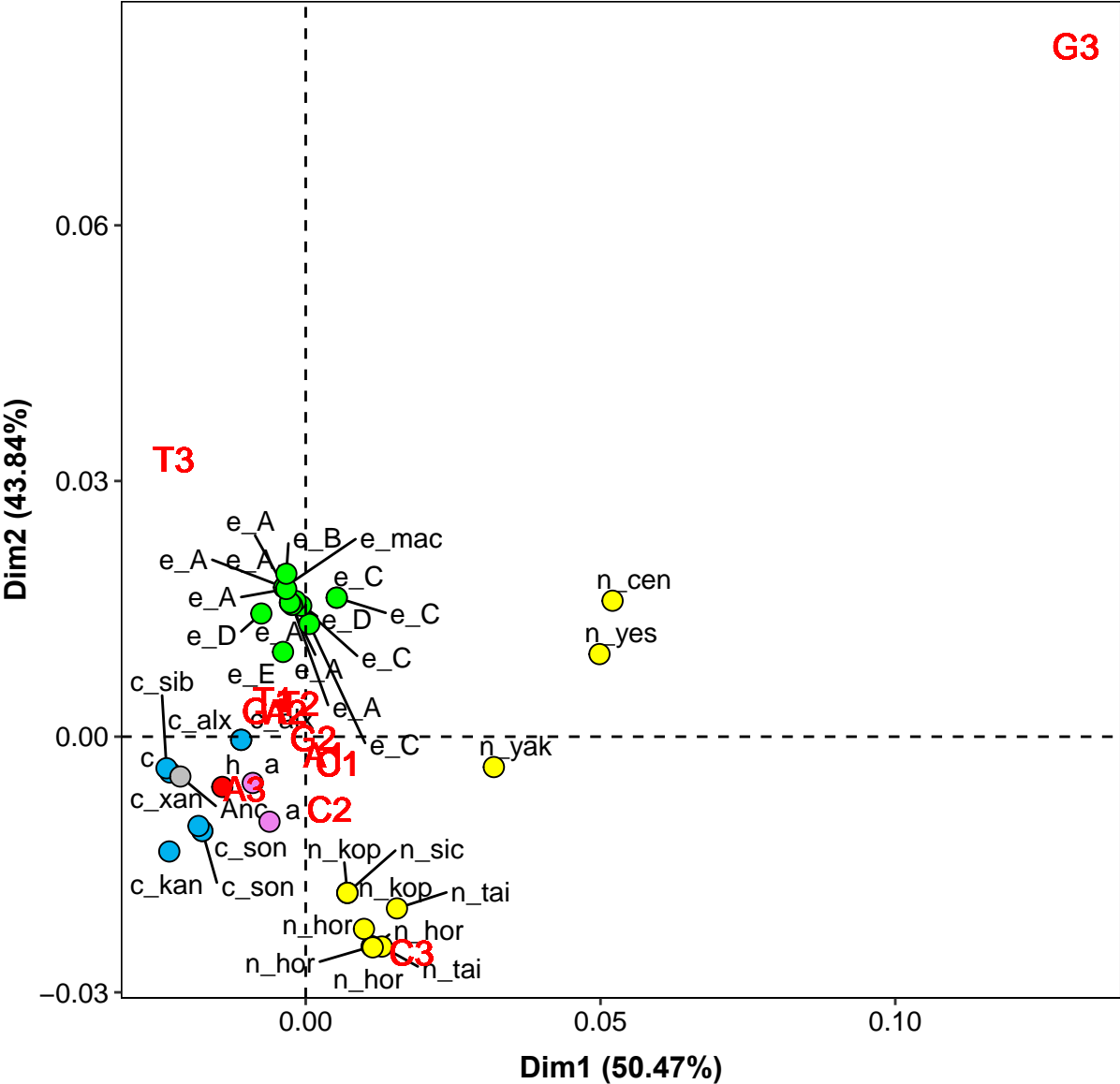
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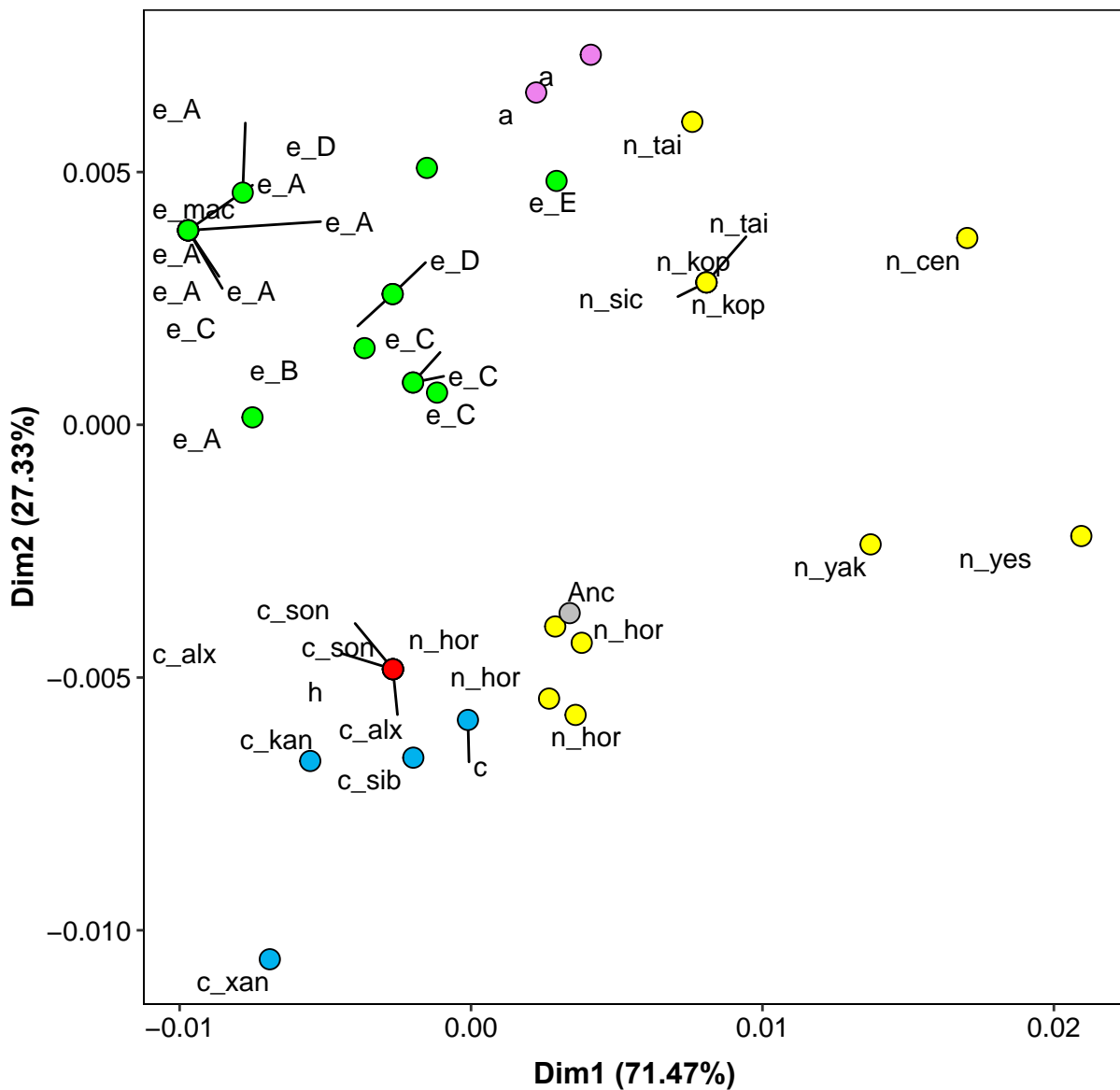
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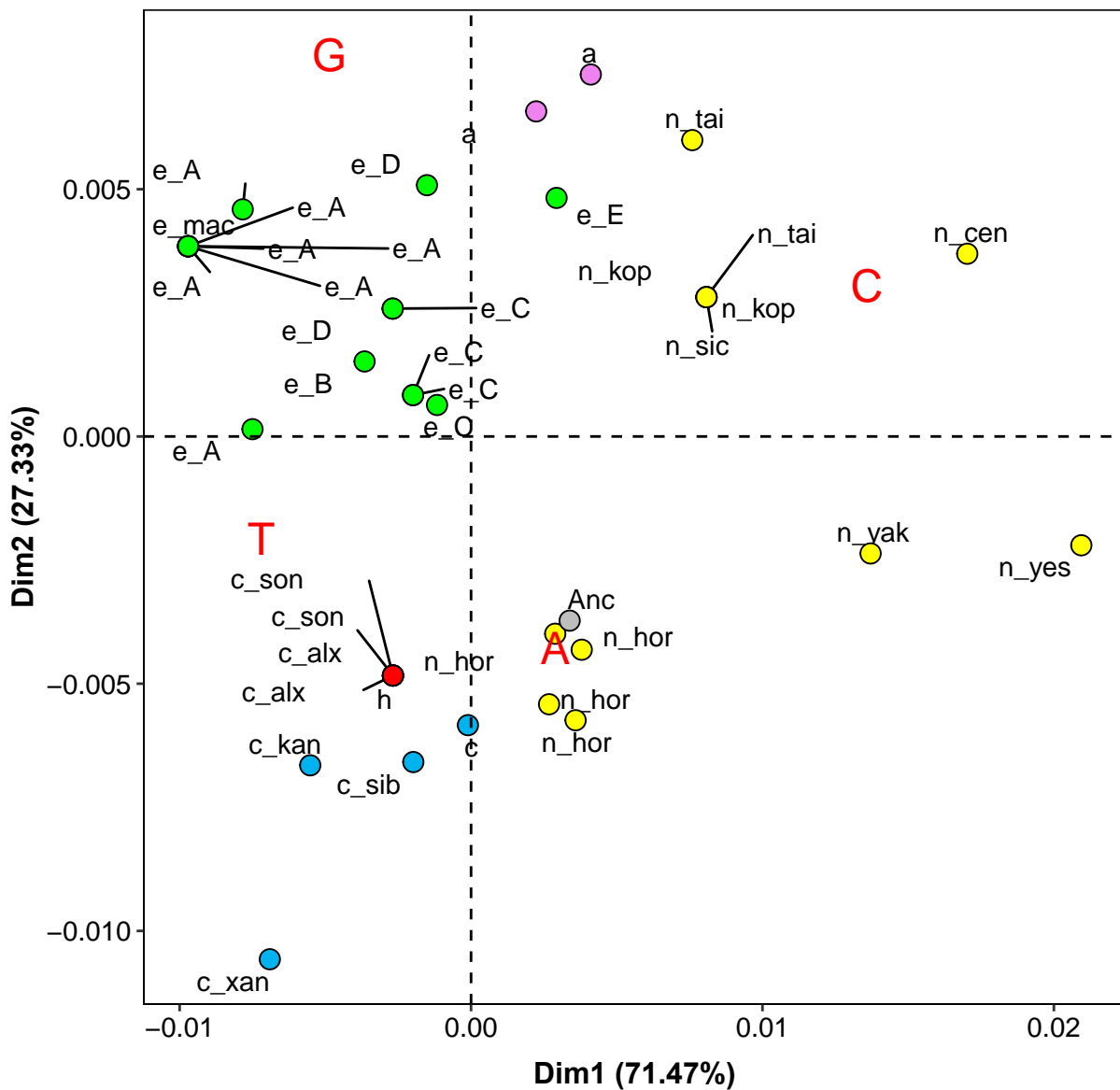
ND5



tRNA



tRNA



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