

## Supplementary materials

### Comparative analysis of intestinal bacteria among venom secretion and non-secretion snakes

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**Supplementary Table 1. Basic information regarding the snakes used in this study.**

Breed	No.	Rearing pattern	Gender	Weight (Kg)	Length (metre)	Sample collection time
<i>Deinagkistrodon</i>	D1	Wild	Female	0.75	ND	2-Nov-17
<i>Deinagkistrodon</i>	D2	Breed	Female	0.6	ND	2-Nov-17
<i>Deinagkistrodon</i>	D3	Breed	Female	0.65	ND	2-Nov-17
<i>Deinagkistrodon</i>	D4	Breed	Male	0.25	ND	2-Nov-17
<i>Deinagkistrodon</i>	D5	Breed	Male	0.4	ND	10-Nov-17
<i>Deinagkistrodon</i>	D6	Breed	Male	0.4	ND	10-Nov-17
<i>Deinagkistrodon</i>	D7	Breed	Male	0.4	ND	10-Nov-17
<i>Deinagkistrodon</i>	D8	Breed	Female	0.45	ND	10-Nov-17
<i>Naja</i>	N1	Wild	Male	0.5	1.05	30-Sep-17
<i>Naja</i>	N2	Breed	Female	0.5	0.95	30-Sep-17
<i>Naja</i>	N3	Wild	Male	0.5	1.1	30-Sep-17
<i>Naja</i>	N4	Wild	Male	0.5	1.05	30-Sep-17
<i>Naja</i>	N5	Breed	Male	0.6	ND	2-Nov-17
<i>Naja</i>	N6	Breed	Male	0.6	ND	2-Nov-17
<i>Naja</i>	N7	Breed	Female	0.55	ND	2-Nov-17
<i>Naja</i>	N8	Breed	Male	0.45	ND	10-Nov-17
<i>Naja</i>	N9	Breed	Male	0.55	ND	10-Nov-17
<i>Naja</i>	N10	Breed	Male	1.4	ND	10-Nov-17
<i>Naja</i>	N11	Breed	Male	1.3	ND	10-Nov-17
<i>Naja</i>	N12	Breed	Male	ND	ND	16-Nov-17
<i>Naja</i>	N13	Breed	Male	ND	ND	16-Nov-17
<i>Naja</i>	N14	Breed	Male	ND	ND	16-Nov-17
<i>Ptyas mucosa</i>	P1	Breed	Male	1.25	2.1	30-Sep-17
<i>Ptyas mucosa</i>	P2	Breed	Male	1.2	ND	10-Nov-17
<i>Ptyas mucosa</i>	P3	Breed	Male	1.2	ND	10-Nov-17
<i>Ptyas mucosa</i>	P4	Breed	Female	0.9	ND	10-Nov-17
<i>Ptyas mucosa</i>	P5	Breed	Male	ND	ND	16-Nov-17
<i>Ptyas mucosa</i>	P6	Breed	Male	ND	ND	16-Nov-17
<i>Ptyas mucosa</i>	P7	Breed	Female	ND	ND	16-Nov-17

D, N, and P represents *Deinagkistrodon*, *Naja*, and *Ptyas mucosa*, respectively. ND represents not detected.

**Supplementary Table 2. Basic statistical results for high-throughput 16S rRNA gene sequencing.**

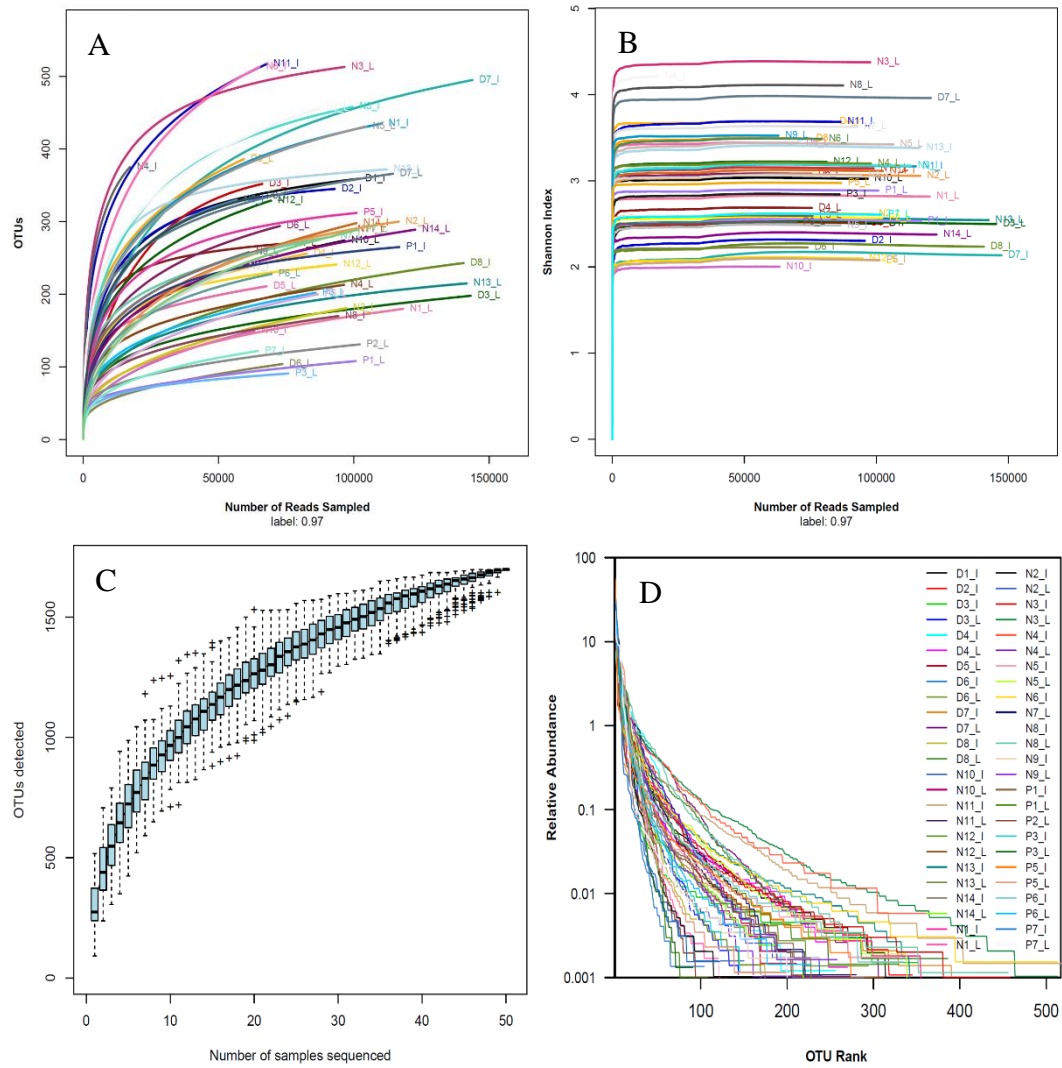
Sample ID	Reads	OTU (0.97)	Coverage	Ace	Chao	Shannon	Simpson
D1_I	102324	359	99.95%	382.52	406.05	2.47	0.23
D2_I	95640	345	99.97%	356.66	360.12	2.19	0.25
D3_I	95438	352	99.92%	381.02	372.07	2.54	0.14
D3_L	145406	198	99.96%	306.01	321.75	2.44	0.14
D4_I	83510	256	99.92%	376.01	343.65	3.65	0.05
D4_L	75579	270	99.97%	281.70	285.81	2.67	0.17
D5_L	70757	211	99.94%	285.85	286.25	3.38	0.08
D6_I	73958	104	99.95%	255.95	201.50	2.18	0.17
D6_L	75368	294	99.90%	363.89	373.64	3.03	0.10
D7_I	147420	495	99.93%	570.46	581.67	2.06	0.26
D7_L	120619	366	99.95%	415.68	416.83	3.93	0.04
D8_I	140727	243	99.95%	312.66	318.68	2.23	0.21
D8_L	74611	386	99.83%	498.60	500.77	3.72	0.05
N1_I	63319	150	99.91%	310.06	245.06	2.00	0.22
N1_L	96753	274	99.92%	412.41	363.52	3.01	0.12
N2_I	86450	517	99.83%	626.55	636.28	3.95	0.04
N2_L	99001	289	99.93%	362.72	354.17	3.14	0.09
N3_I	81141	329	99.88%	416.86	404.48	3.22	0.07
N3_L	94750	241	99.96%	267.62	280.18	2.05	0.27
N4_I	116403	372	99.97%	386.74	418.50	3.29	0.09
N4_L	142531	215	99.97%	257.68	253.33	2.51	0.16
N5_I	102463	298	99.91%	474.23	402.65	3.07	0.07
N5_L	122811	289	99.94%	365.00	369.16	2.37	0.19
N6_I	114964	435	99.93%	495.37	491.84	3.09	0.11
N7_L	120256	180	99.95%	313.84	270.05	2.77	0.09
N8_I	98403	181	99.93%	359.84	277.13	2.57	0.11
N8_L	116670	300	99.95%	347.65	334.88	3.05	0.07
N9_I	113063	458	99.92%	512.36	512.60	3.09	0.13
N9_L	97692	513	99.95%	540.12	550.12	4.35	0.03
N10_I	17370	375	99.59%	427.31	420.18	4.18	0.04
N10_L	97971	213	99.95%	334.51	278.62	3.16	0.07
N11_I	86405	330	99.89%	370.55	370.23	2.64	0.16
N11_L	106417	431	99.91%	511.92	511.72	3.38	0.09
N12_I	79430	513	99.82%	611.88	605.38	3.47	0.07
N12_L	92712	280	99.93%	397.39	339.09	3.62	0.04
N13_I	94335	170	99.95%	288.77	243.50	3.05	0.07
N13_L	87453	456	99.88%	567.30	544.06	4.09	0.03
N14_I	69778	238	99.86%	387.08	346.94	2.50	0.13

N14_L	62933	258	99.88%	404.24	350.04	3.49	0.06
P1_I	116923	265	99.97%	287.72	298.48	2.52	0.18
P1_L	100767	108	99.97%	237.25	156.00	2.88	0.09
P2_L	102193	131	99.96%	228.85	177.87	2.57	0.14
P3_I	86101	202	99.93%	320.85	277.14	2.83	0.10
P3_L	75856	91	99.97%	113.40	133.00	2.59	0.13
P5_I	101218	312	99.96%	334.33	341.64	2.06	0.34
P5_L	86702	200	99.93%	278.29	254.03	2.97	0.07
P6_I	65208	335	99.92%	370.04	368.28	2.91	0.11
P6_L	69632	228	99.93%	277.83	269.44	2.51	0.16
P7_I	64615	122	99.94%	205.15	189.36	1.98	0.19
P7_L	101834	289	99.91%	387.01	391.69	2.60	0.11

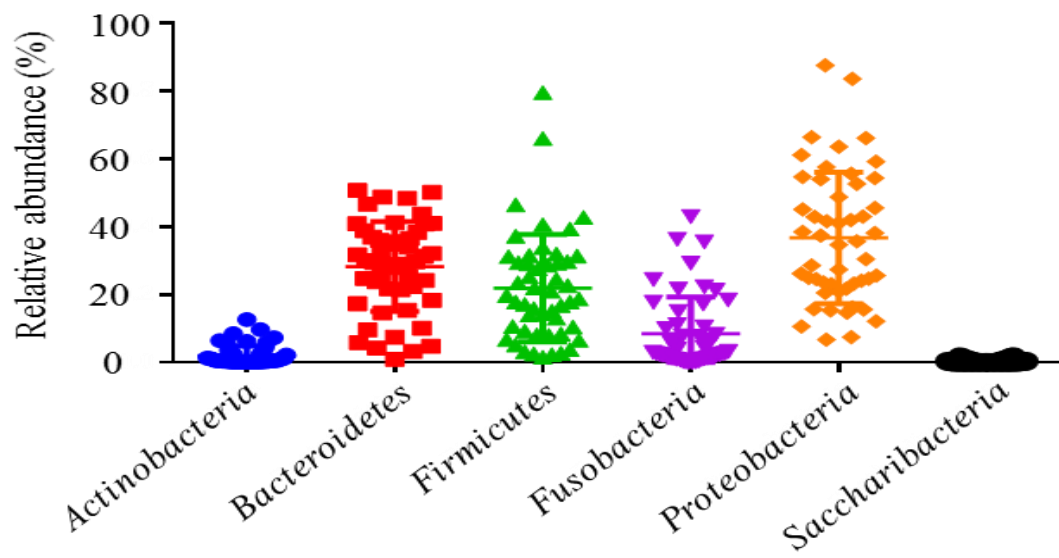
D, N, and P represents *Deinagkistrodon*, *Naja*, and *Ptyas mucosa*, respectively. I and L represent ileum and large intestinal samples, respectively.

### Supplementary Figure 1. Basic analysis of sequenced data.

A, rarefaction curves of sequenced samples. B, the Shannon-Wiener curves of sequenced samples. C, Specaccum analysis of sequenced samples. D, Rank-abundance distribution curve of sequenced samples.



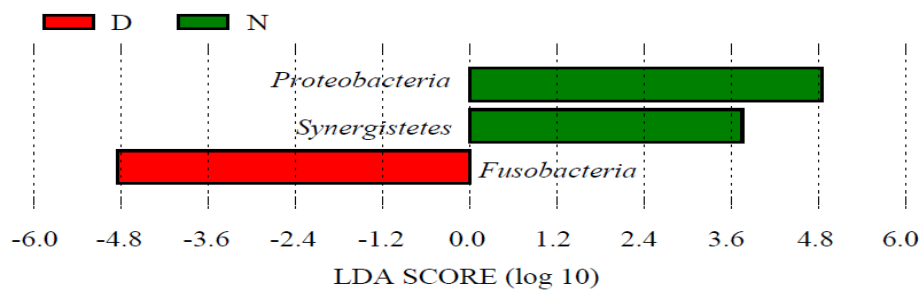
Supplementary Figure 2. Distribution of the core bacterial phyla.



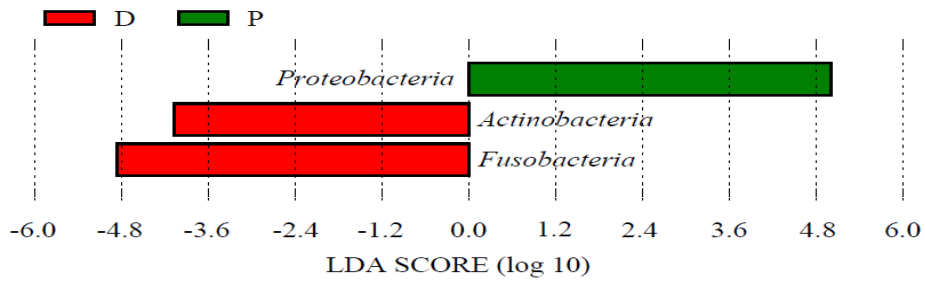
**Supplementary Figure 3. Significantly different bacterial phyla between snake breeds.**

A, different bacterial phyla between *Deinagkistrodon* to *Naja* samples; B, different bacterial phyla between *Deinagkistrodon* to *Ptyas mucosa* samples; C, different bacterial phyla between *Naja* to *Ptyas mucosa* samples.

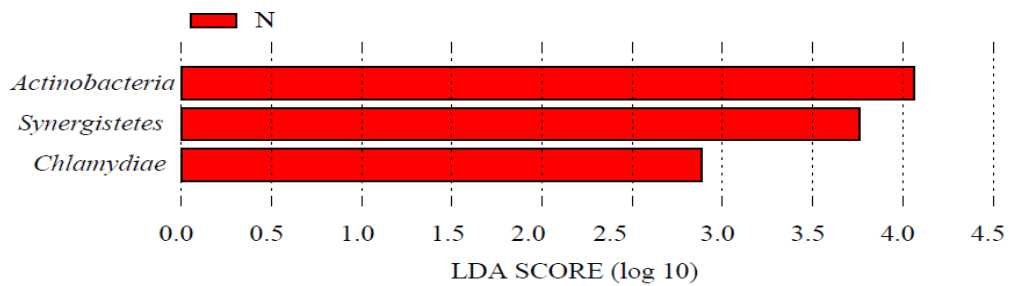
**A**



**B**



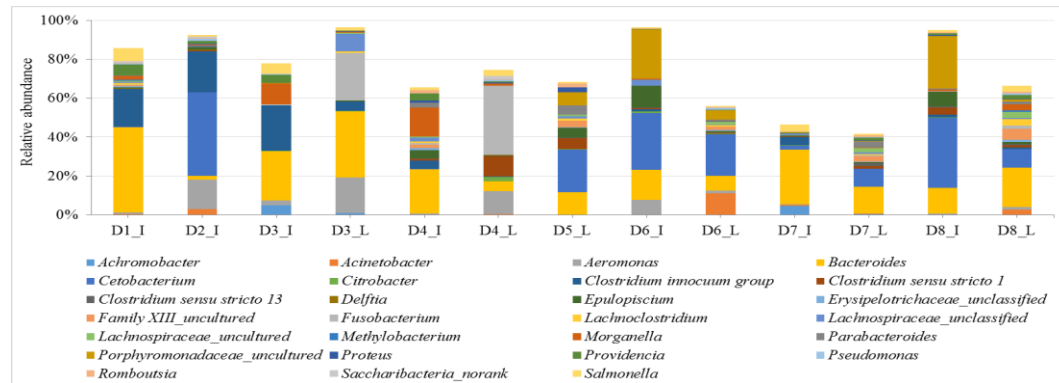
**C**



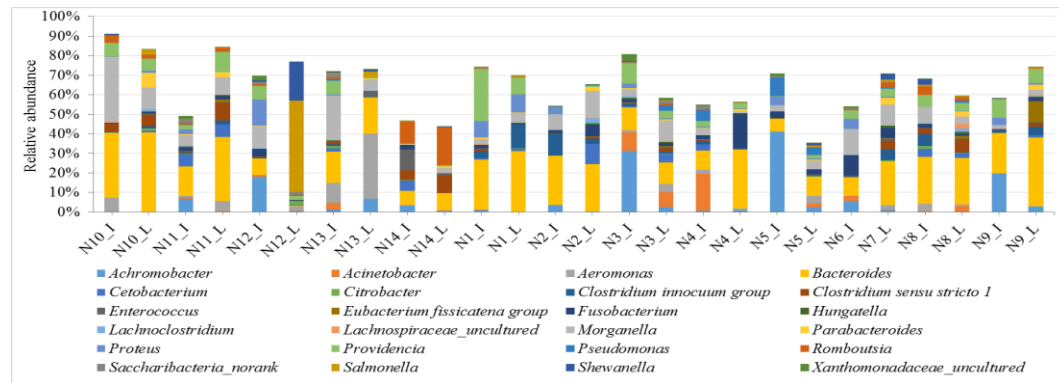
**Supplementary Figure 4. Distribution of the core bacterial genus.**

A, core bacterial genus in *Deinagkistrodon* samples; B, core bacterial genus in *Naja* samples; C, core bacterial genus in *Ptyas mucosa* samples.

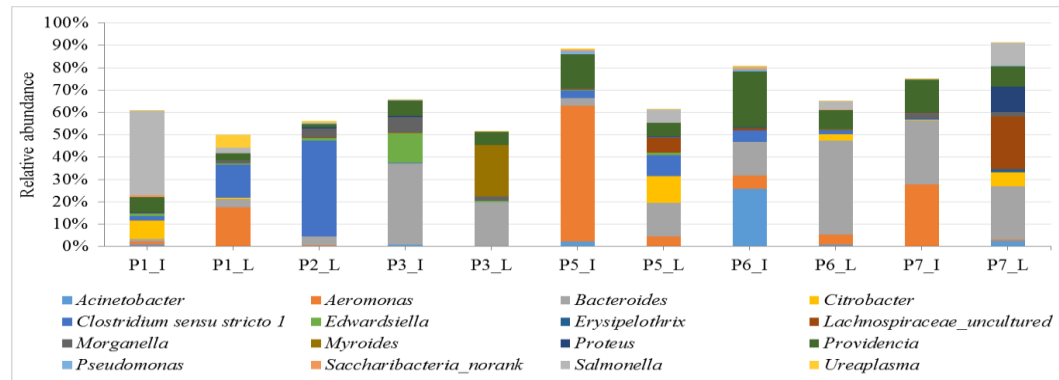
**A**



**B**



**C**

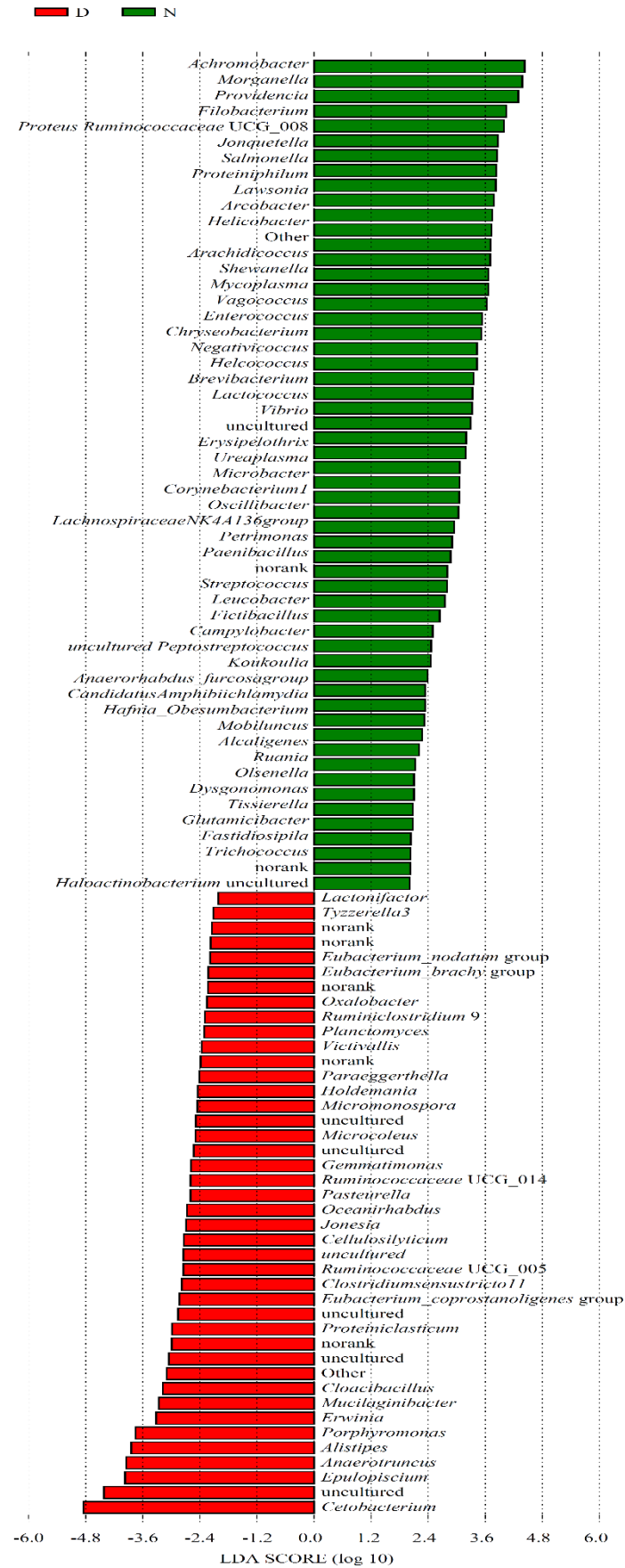




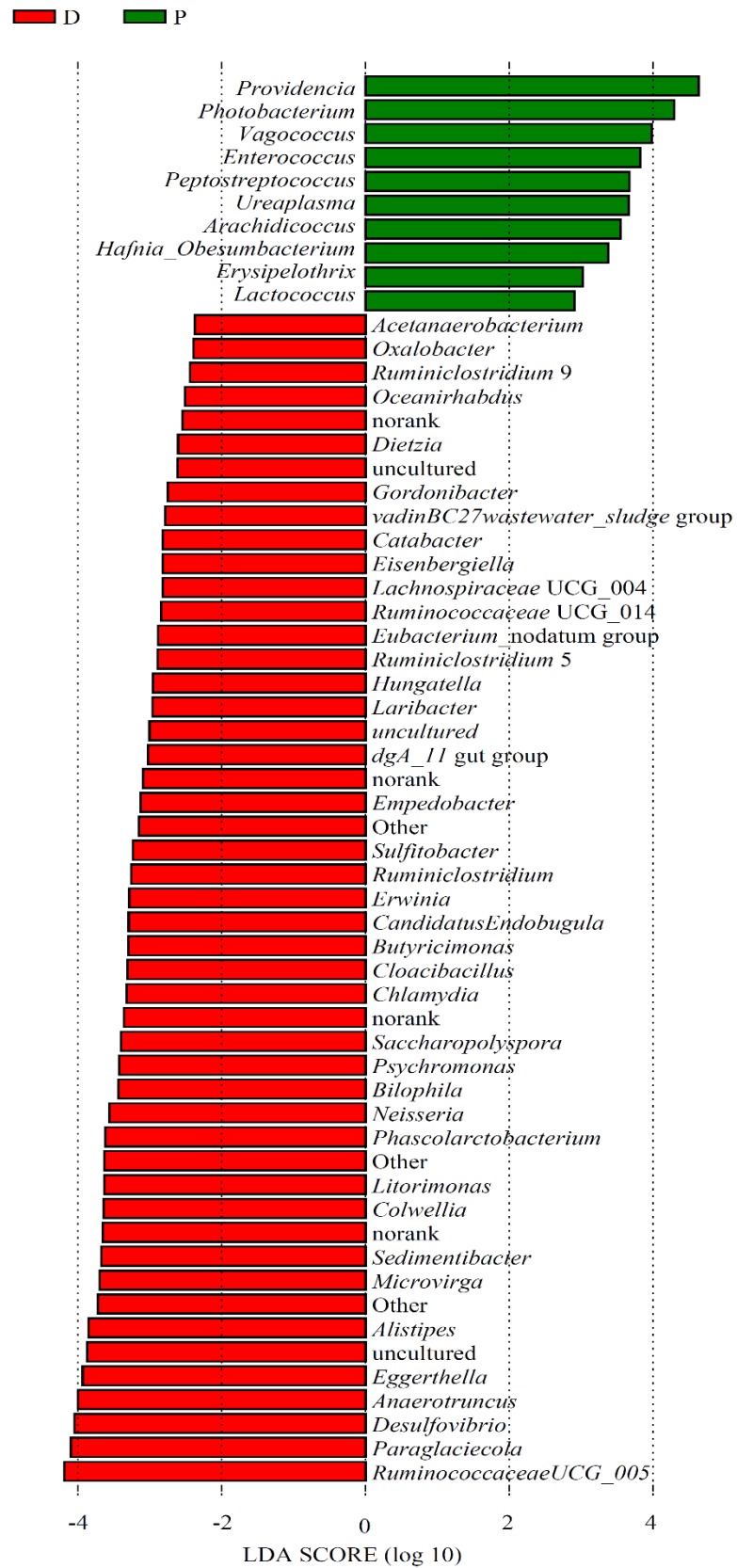
**Supplementary Figure 5. Significantly different bacterial genus between snake breeds.**

A, different bacterial genus between *Deinagkistrodon* to *Naja* samples; B, different bacterial genus between *Deinagkistrodon* to *Ptyas mucosa* samples; C, different bacterial genus between *Naja* to *Ptyas mucosa* samples.

A



B



C

