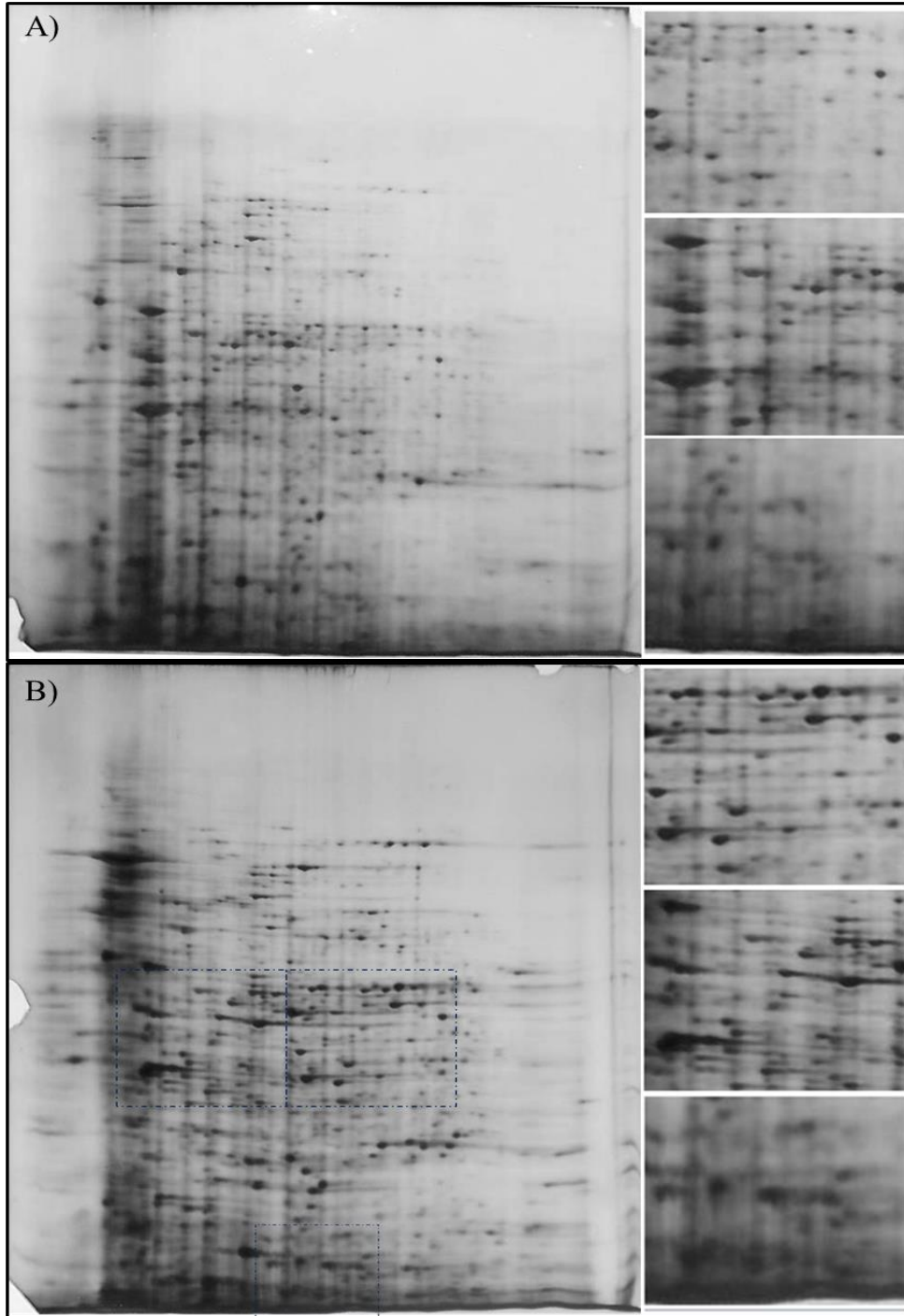
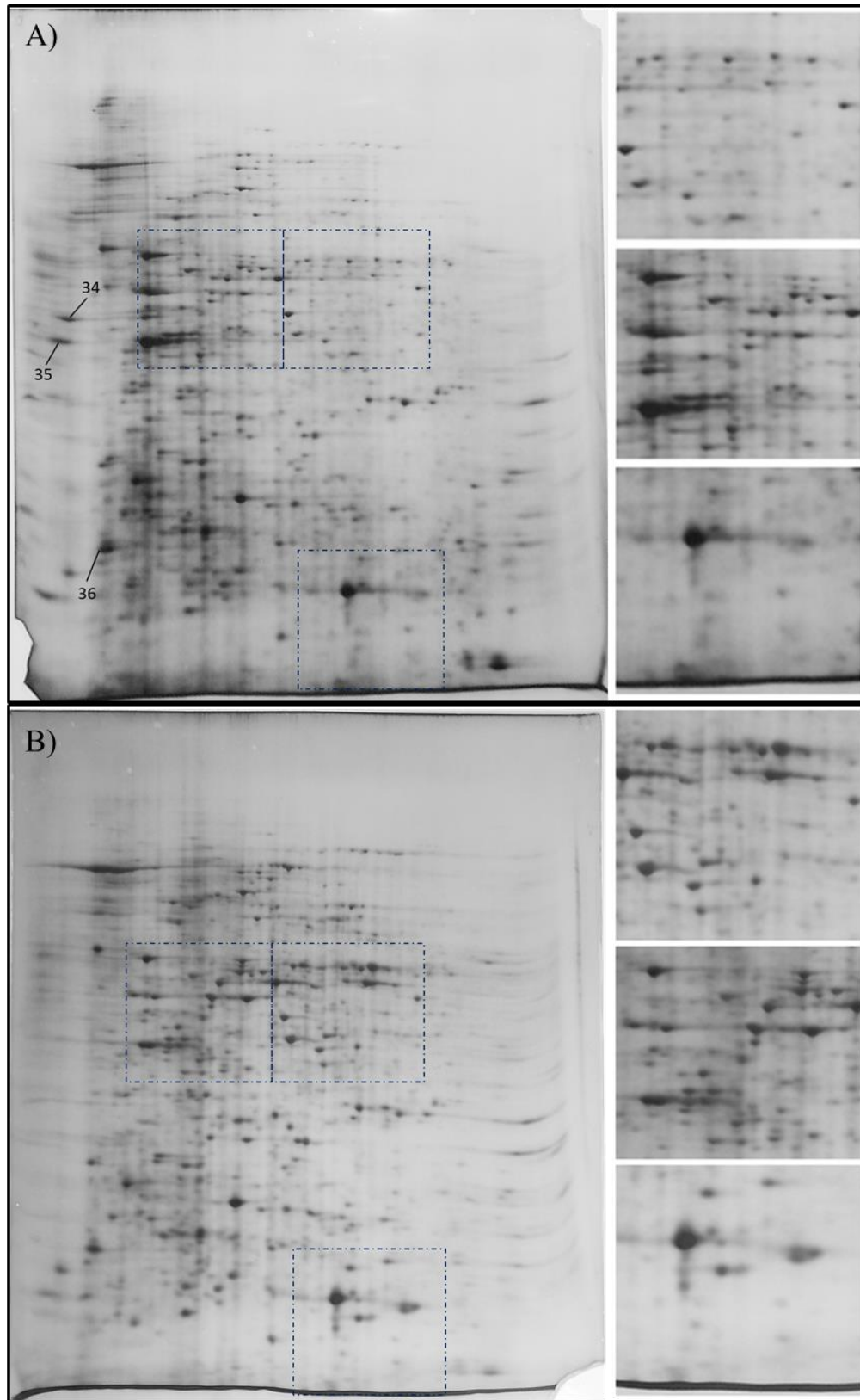


2D-SDS-PAGE IMAGES AND IDENTIFIED SPOTS

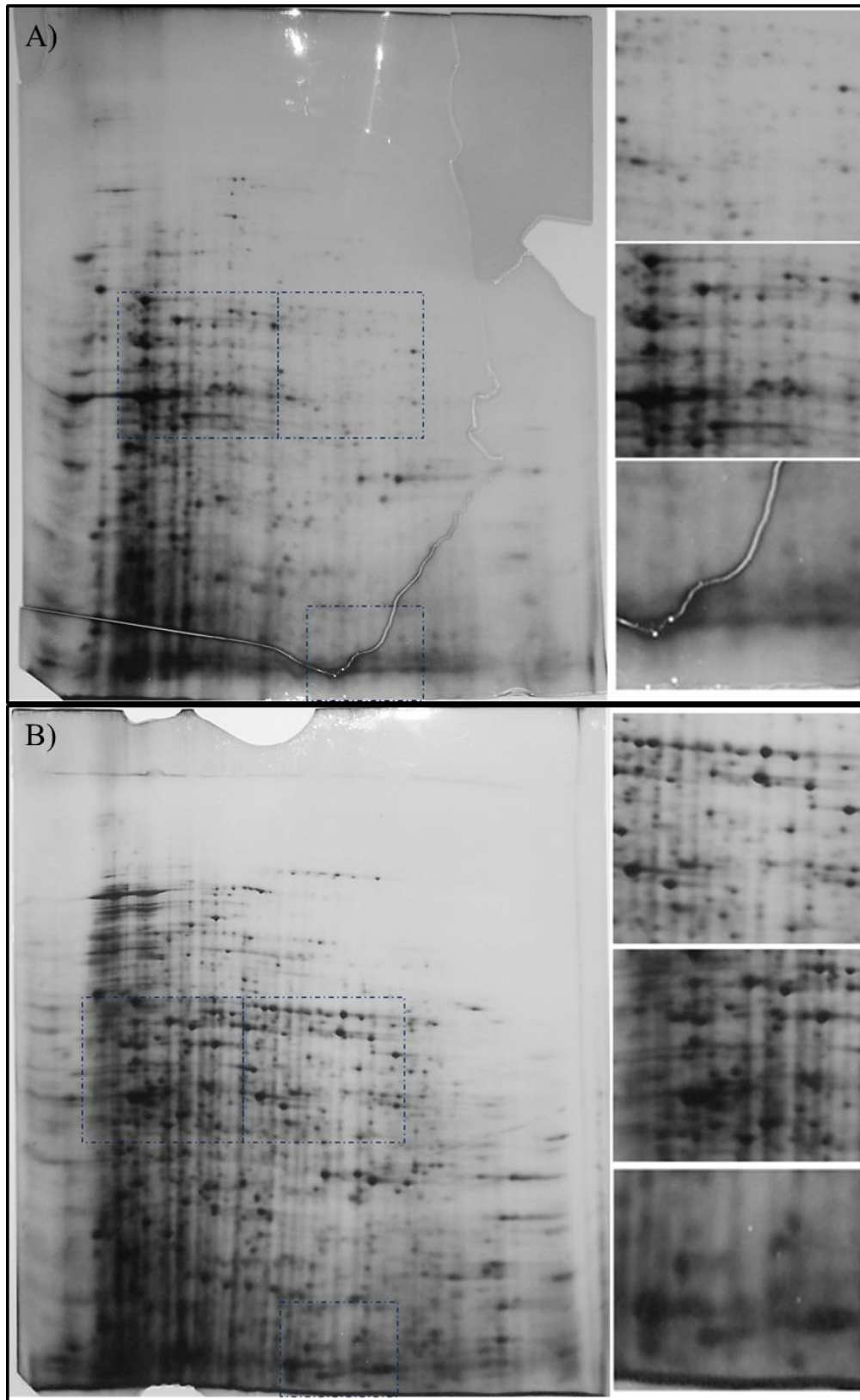
- A) *Leishmania infantum*-Visceral sample-239 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-121 (pH 3-10)



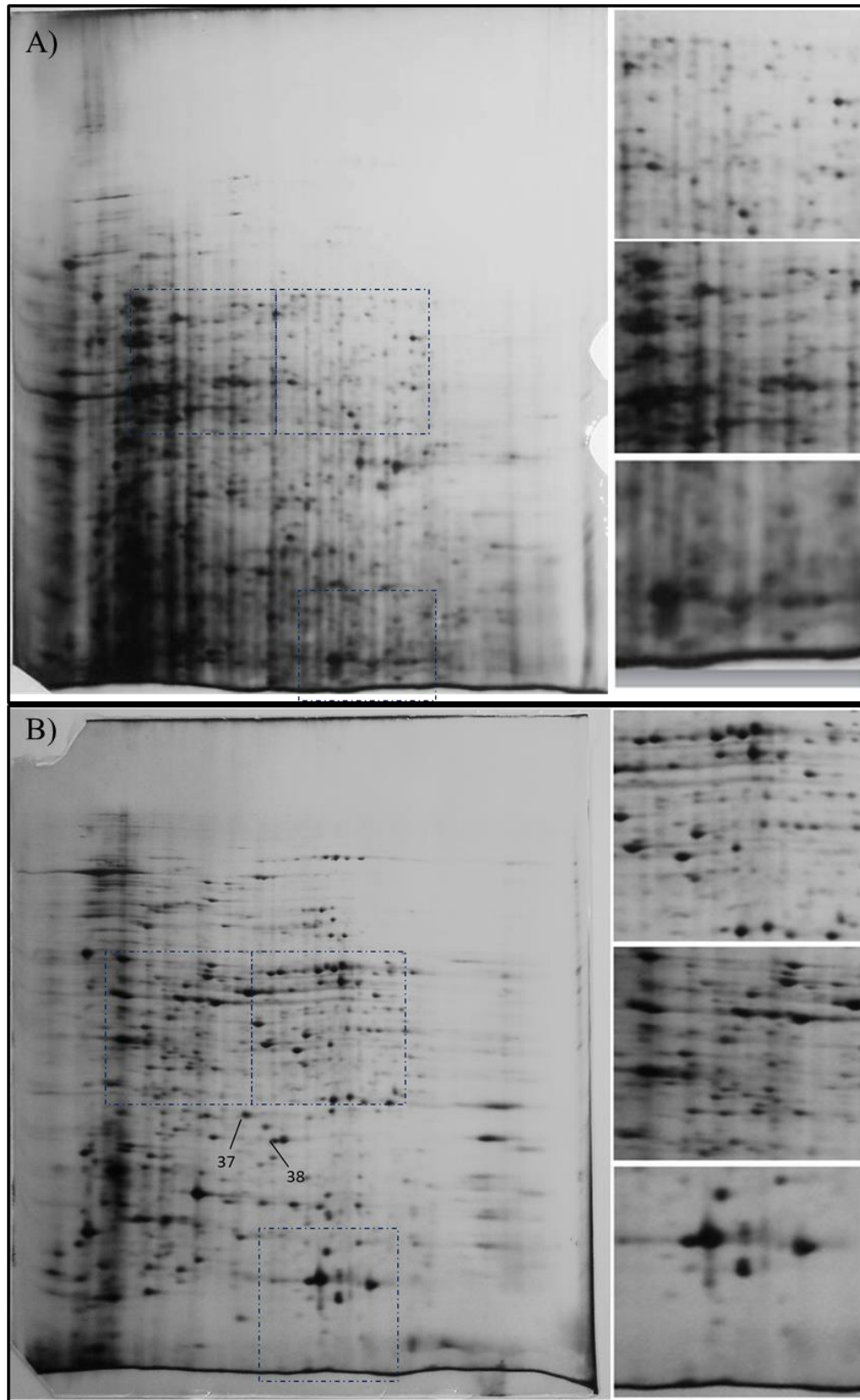
A) *Leishmania infantum*-Visceral sample-240 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-250 (pH 3-10)



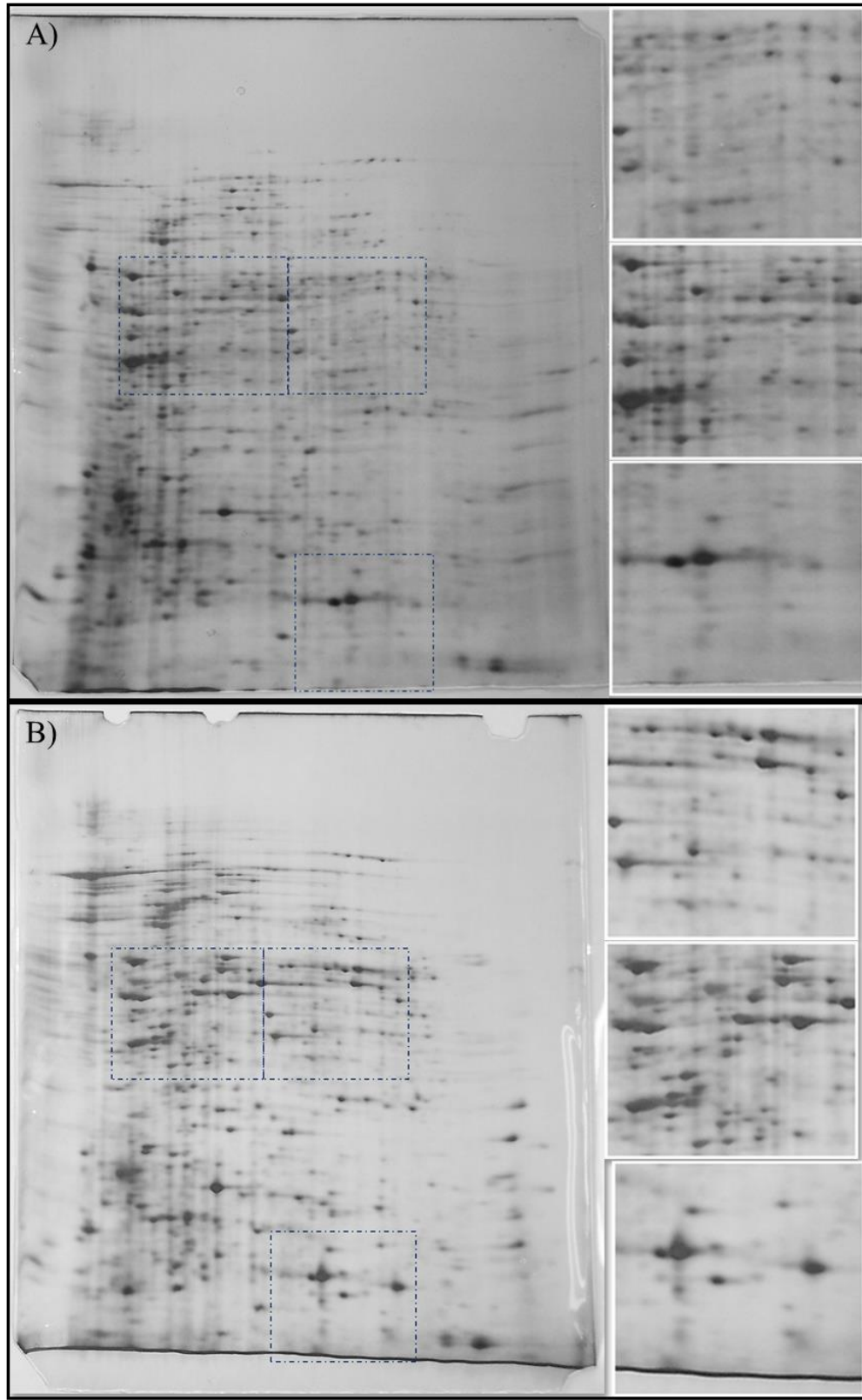
A) *Leishmania infantum*-Visceral sample-495 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-285 (pH 3-10)



A) *Leishmania infantum*-Visceral sample-628 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-259 (pH 3-10)

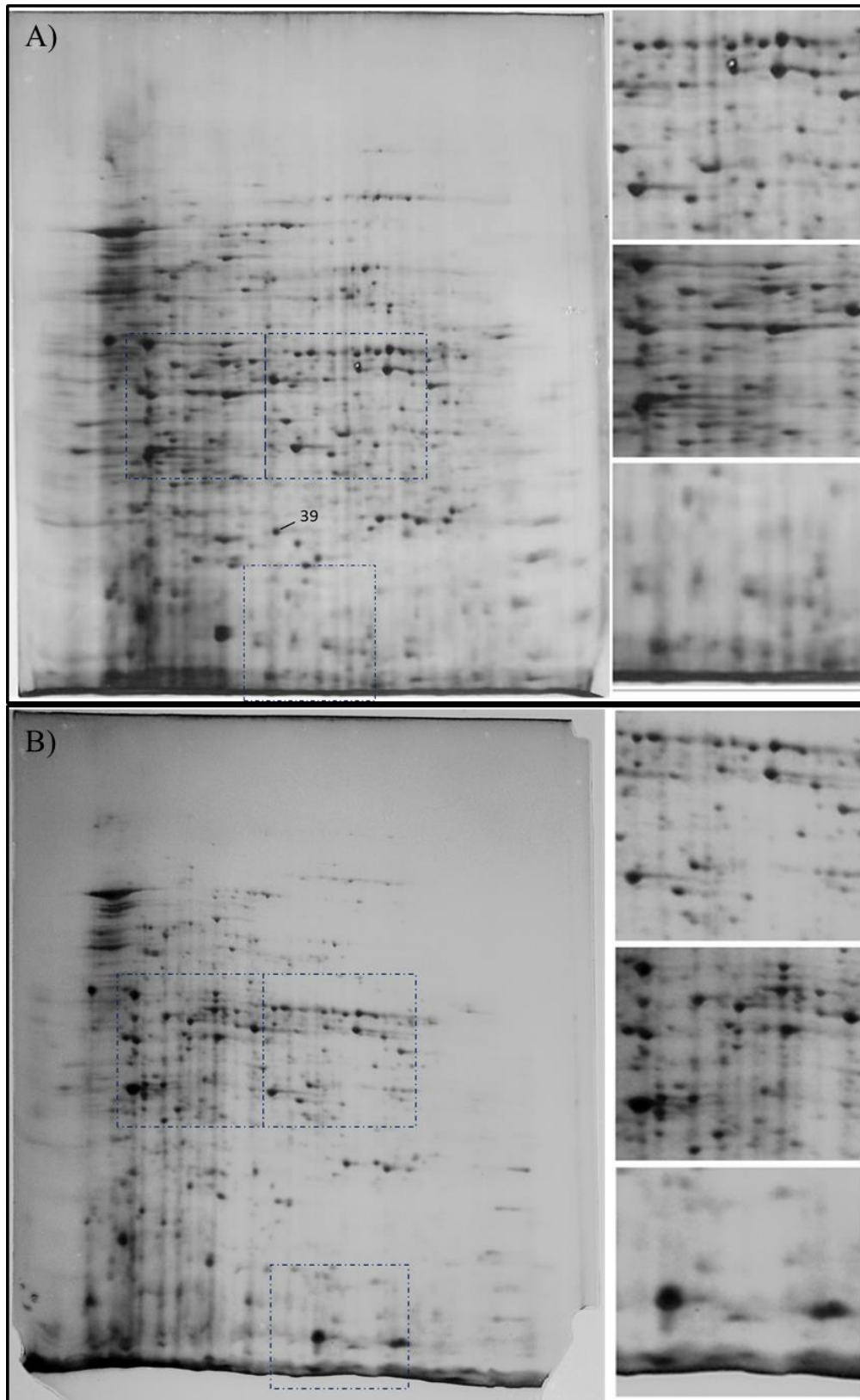


A) *Leishmania infantum* Visceral sample-Crt07 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-Cri08 (pH 3-10)



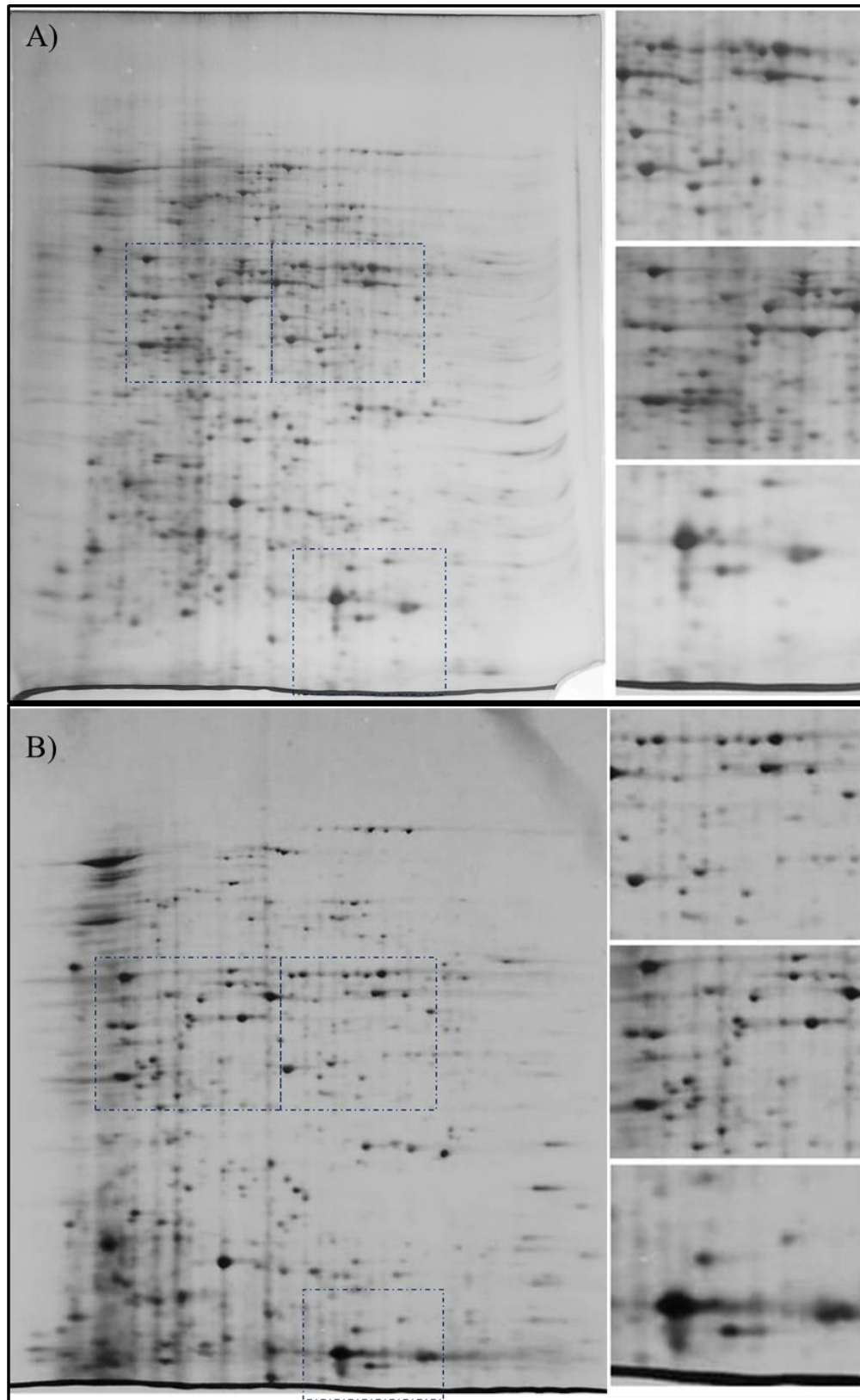
A) *Leishmania tropica*-Cutaneous sample-Crt02 (pH 3-10)

B) *Leishmania tropica*-Cutaneous sample-615 (pH 310)

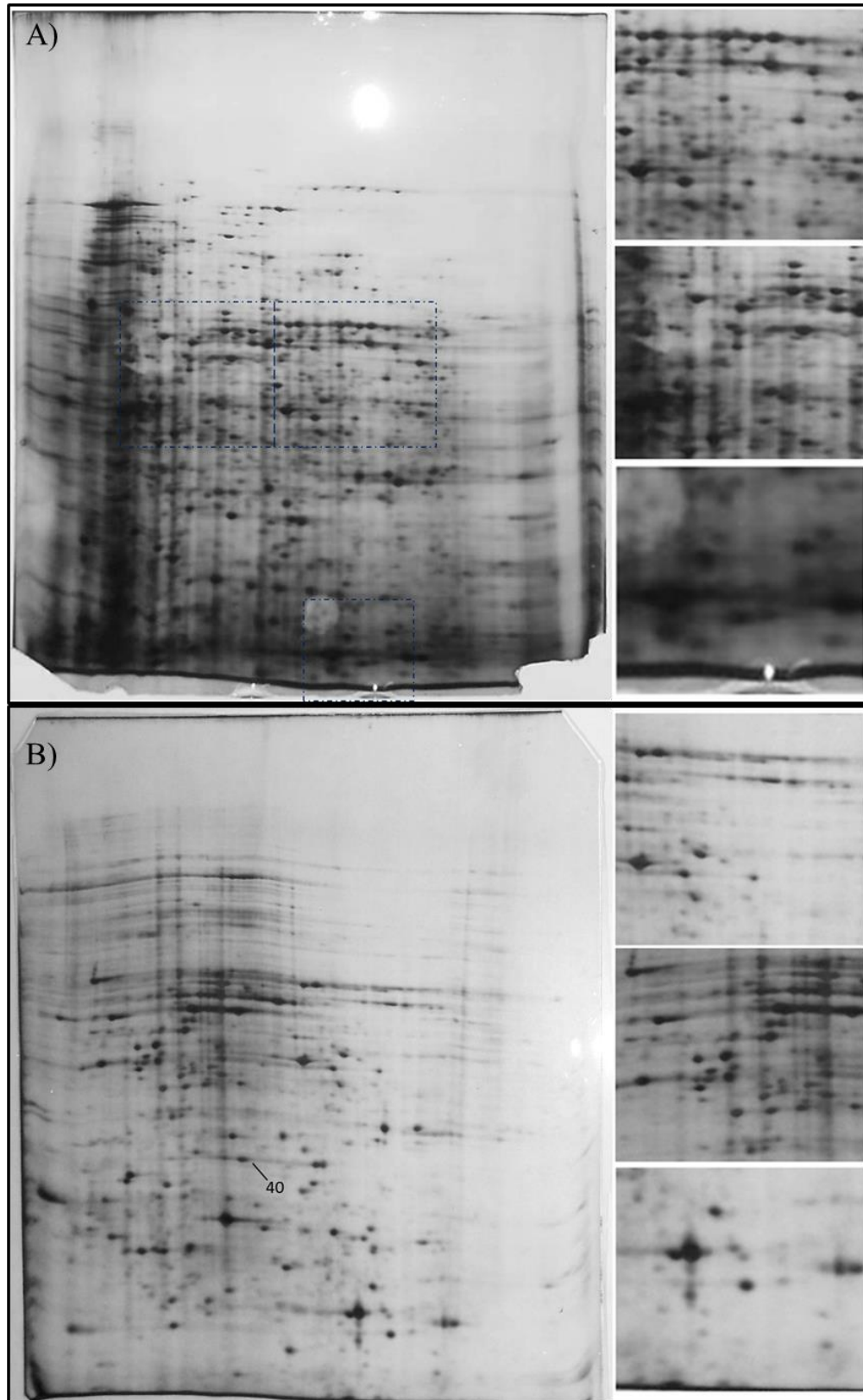


A) *Leishmania tropica*-Cutaneous sample-Crt03 (pH3-10)

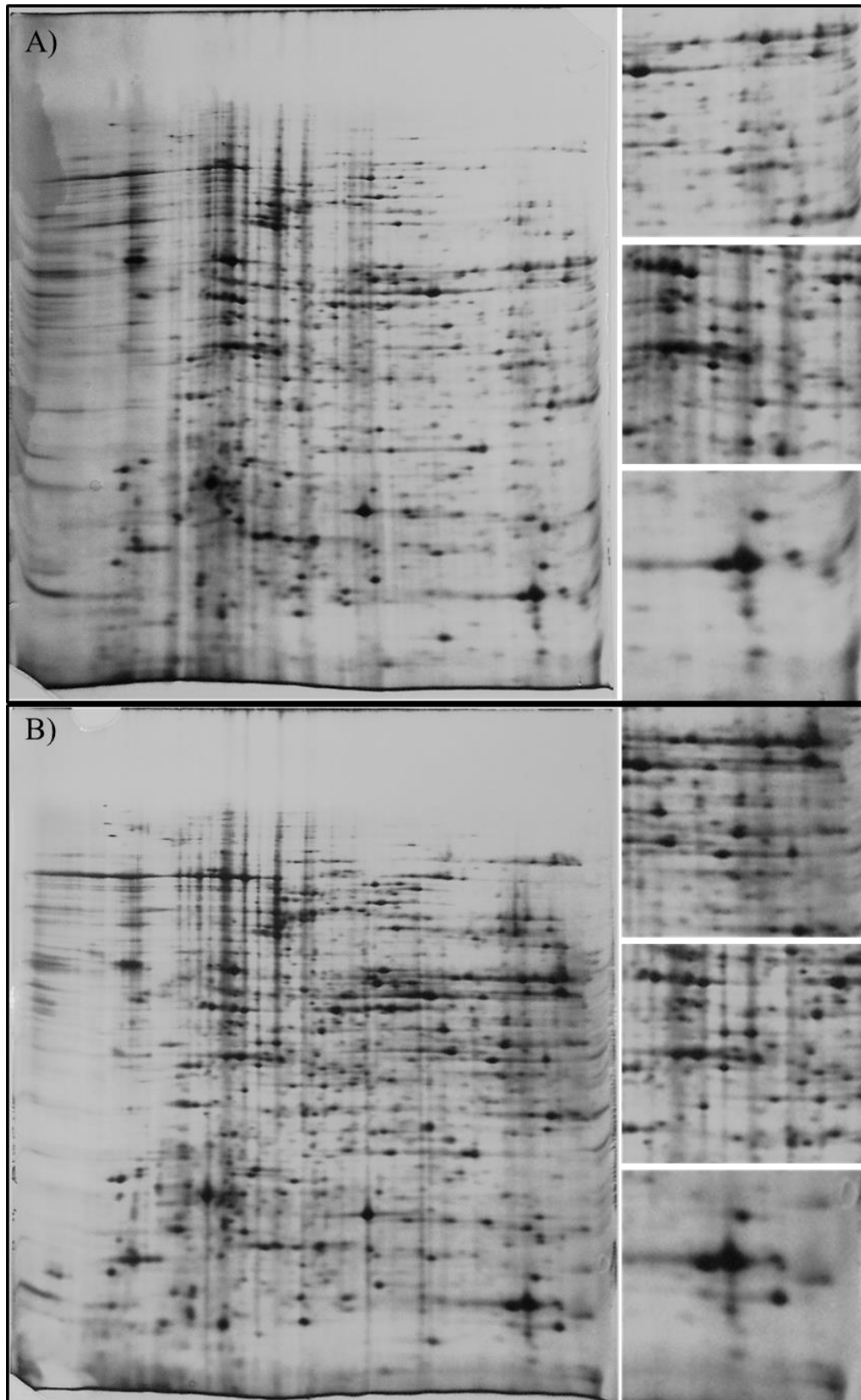
B) *Leishmania tropica*-Cutaneous sample-2FA (pH 3-10)



- A) *Leishmania tropica*-Cutaneous sample-Crt01 (pH 3-10)
B) *Leishmania infantum*-Cutaneous sample-285 (pH 5-8)

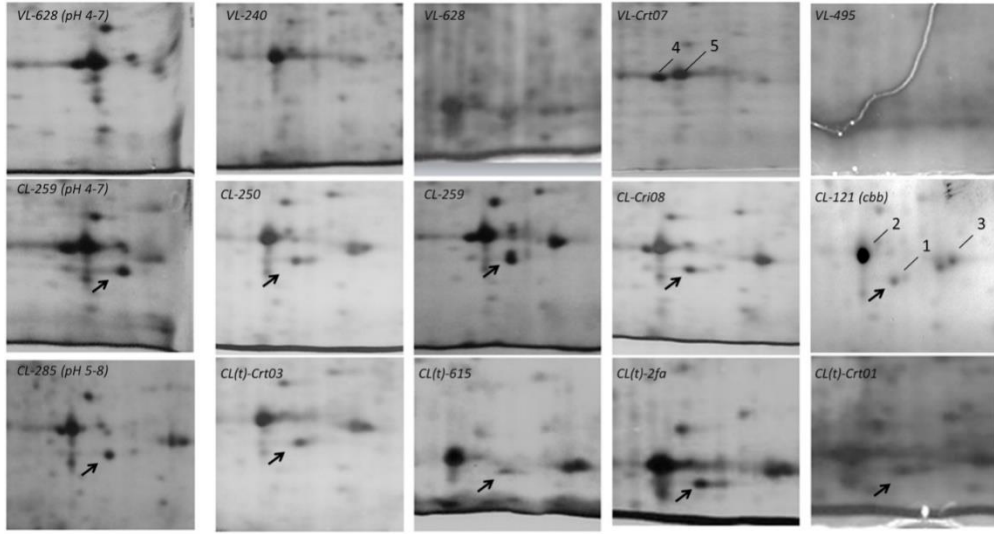


A) *Leishmania infantum*-Visceral sample-628 (pH 4-7)
B) *Leishmania infantum*-Cutaneous sample-259 (pH 4-7)

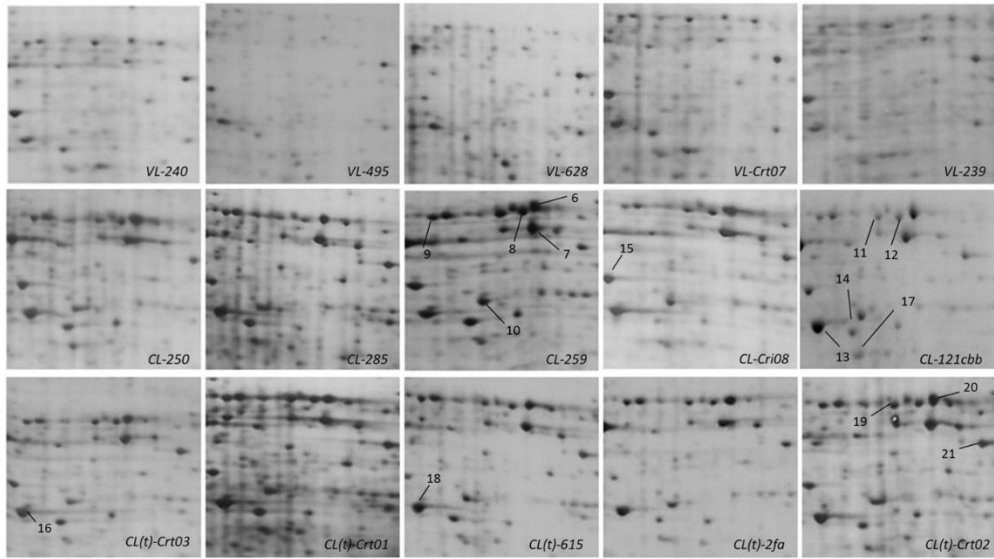


FOCUSED REGIONS

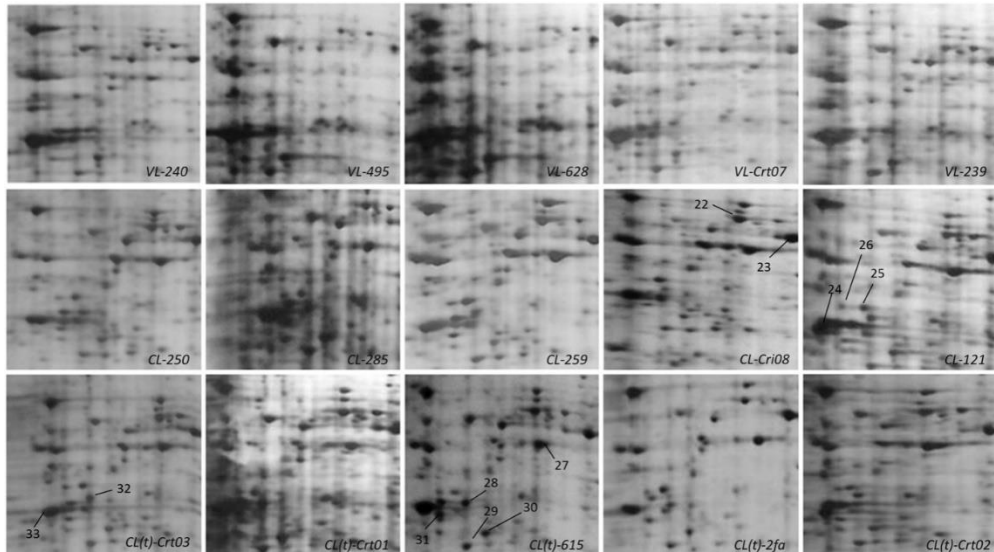
1st Region of Interest



2nd Region of Interest



3rd Region of Interest



LIST OF IDENTIFIED SPOTS

Spot #	Protein Name	MW	pI	PMF	MS/MS
1 (a)	Putative iron superoxide dismutase	21	6,4	-	2
2	Peroxidoxin	21	6,3	11	-
3	Peroxidoxin	21	6,3	8	2
4	Superoxide dismutase	21	6,4	-	2
5	Peroxidoxin	21	6,3	8	2
6 (b)	Pyruvate kinase	56	6,4	14	3
7 (d)	Putative succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor	53	7,9	6	4
8 (f)	Putative dihydrolipoamide dehydrogenase	51	6,4	-	2
9	Trypanothione reductase	53	5,8	-	1
10 (c)	Aspartate aminotransferase	46	6,5	8	2
11 (f)	Putative dihydrolipoamide dehydrogenase	51	6,4	9	-
12 (f)	Putative dihydrolipoamide dehydrogenase	51	6,4	9	-
13 (e)	Putative aldose 1-epimerase	42	5,9	-	2
14 (e)	Putative aldose 1-epimerase	42	5,9	6	-
15 (g)	Putative eukaryotic initiation factor 4a	45	5,8	9	2
16 (e)	Putative aldose 1-epimerase	42	5,8	9	1
17	Arginase	36	6,3	-	1
18 (e)	Putative aldose 1-epimerase	42	5,9	11	2
19 (f)	Putative dihydrolipoamide dehydrogenase	51	6,4	-	1
20 (b)	Pyruvate kinase	56	6,4	8	2
21	Metallo-peptidase, Clan ME, Family M16	55	6,6	10	-
22	Metallo-peptidase, Clan MA(E), Family M32	57	5,4	12	2
23	Putative eukaryotic initiation factor 4a	45	5,8	9	2
24	Heat shock protein 83-1	81	5,0	-	3
25 (h)	Putative N-acyl-L-amino acid amidohydrolase	44	5,1	5	2
26 (h)	Putative N-acyl-L-amino acid amidohydrolase	44	5,1	4	-
27 (i)	Enolase	46	5,3	13	3
28	Metallo-peptidase, Clan MA(E), family 32	57	5,4	12	1
29	Cytochrome c oxidase subunit IV	39	5,5	6	2
30	Metallo-peptidase, Clan MA(E), Family M32	57	5,4	11	2
31	Heat shock protein 83-1	81	5,0	-	2
32	Metallo-peptidase, Clan MA(E), family 32	57	5,4	16	2
33	Heat shock protein 83-1	81	5,0	-	3
34	Heat shock protein 83-1	81	5,0	-	2
35	Heat shock protein 83-2	80	5,0	10	2
36	Heat shock protein 70	50	5,2	4	2
37	Inosine-uridine preferring nucleoside hydrolase	34	5,8	4	-
38	Prostaglandin f2-alpha synthase, partial	30	6,7	5	1
39	Inosine-uridine preferring nucleoside hydrolase	34	5,8	5	-
40	Coproporphyrinogen III oxidase	35	5,3	6	2

Mw: Molecular weight; *pI*: Protein isoelectric point

PMF: Peptide mass fingerprinting (number of peptide *m/z* matches) by MALDI-TOF/TOF MS

MS/MS: Peptide fragmentation by MALDI-TOF/TOF MS