

Pulmonary Toxicity and Proteomic Analysis in Bronchoalveolar Lavage Fluids and Lungs of Rats Exposed to Copper Oxide Nanoparticles

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Supplementary Information

A

File

Reference Image Selection

Mask Of Disinterest

Alignment

Filtering

Experiment Design Setup

View Results

Progenesis Stats

Spot Picking

Report

Image QC

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Spot Picking

Report

Image: Rat lung tissue_pH4-7 spots

실물 위

다시 실행

Image: Rat lung tissue_pH4-7 spots

Filter spots

You can filter out spots that you do not wish to include in your analysis by using the criteria below:

Average norm. vol.

<=

0

Spot area

<=

1368

Inside selected area

☒

Delete 0 Matching Spots

Delete 783 Non-Matching Spots

Tips

For best results, you should aim to delete any false spots without deleting any of the real spots.

The types of spots to filter out may include:

- Spots in damaged areas
- Spots on the edge of the gel
- Spots outside of the gel e.g. on the scanner bed

Normalisation

Note that all remaining spots will be used in the normalisation calculation. If deleting a substantial number of spots, you should review the normalisation afterwards.

B

File

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Image: Rat lung tissue_pH6-9 spots

실물 위

다시 실행

Image: Rat lung tissue_pH6-9 spots

Filter spots

You can filter out spots that you do not wish to include in your analysis by using the criteria below:

Average norm. vol.

<=

1545153

Spot area

<=

2219

Inside selected area

☒

Delete 0 Matching Spots

Delete 638 Non-Matching Spots

Tips

For best results, you should aim to delete any false spots without deleting any of the real spots.

The types of spots to filter out may include:

- Spots in damaged areas
- Spots on the edge of the gel
- Spots outside of the gel e.g. on the scanner bed

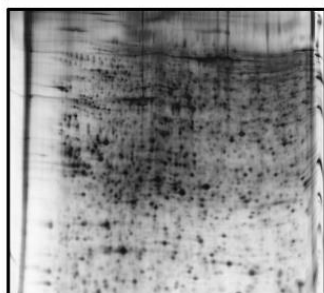
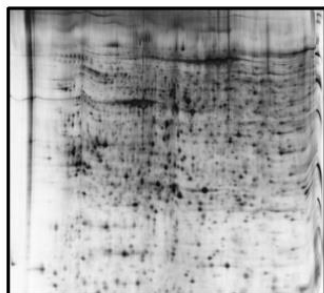
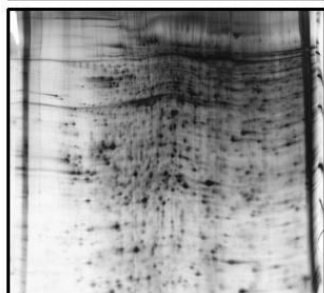
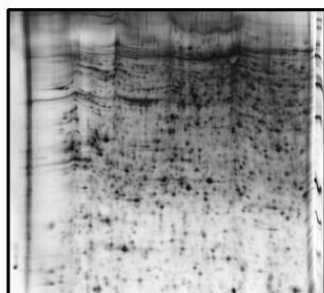
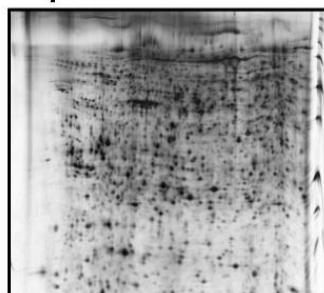
Normalisation

Note that all remaining spots will be used in the normalisation calculation. If deleting a substantial number of spots, you should review the normalisation afterwards.

C

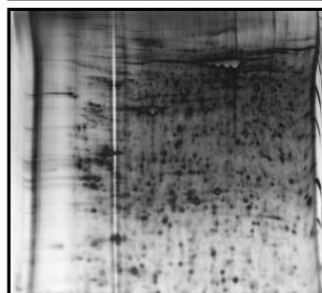
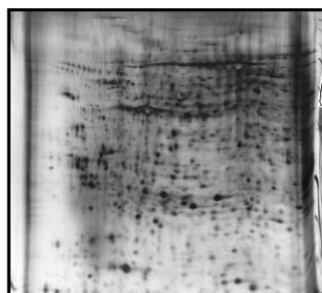
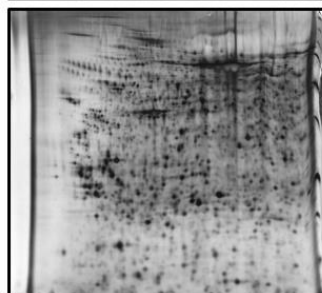
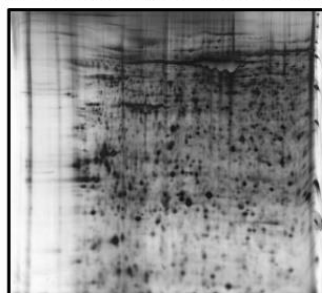
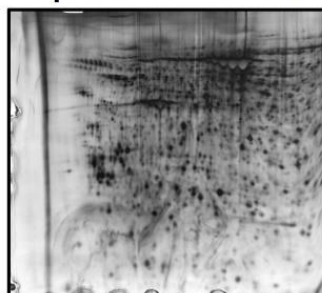
Control

pl 4 → 7



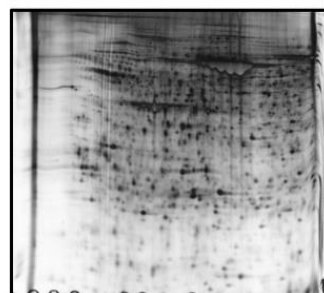
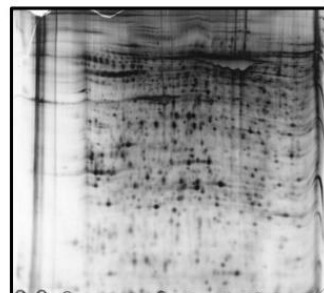
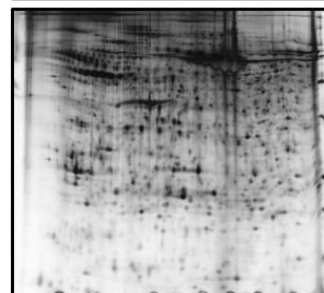
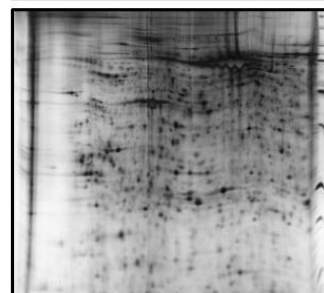
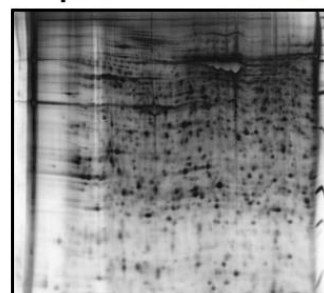
0.15mg/kg BW

pl 4 → 7



1.5mg/kg BW

pl 4 → 7



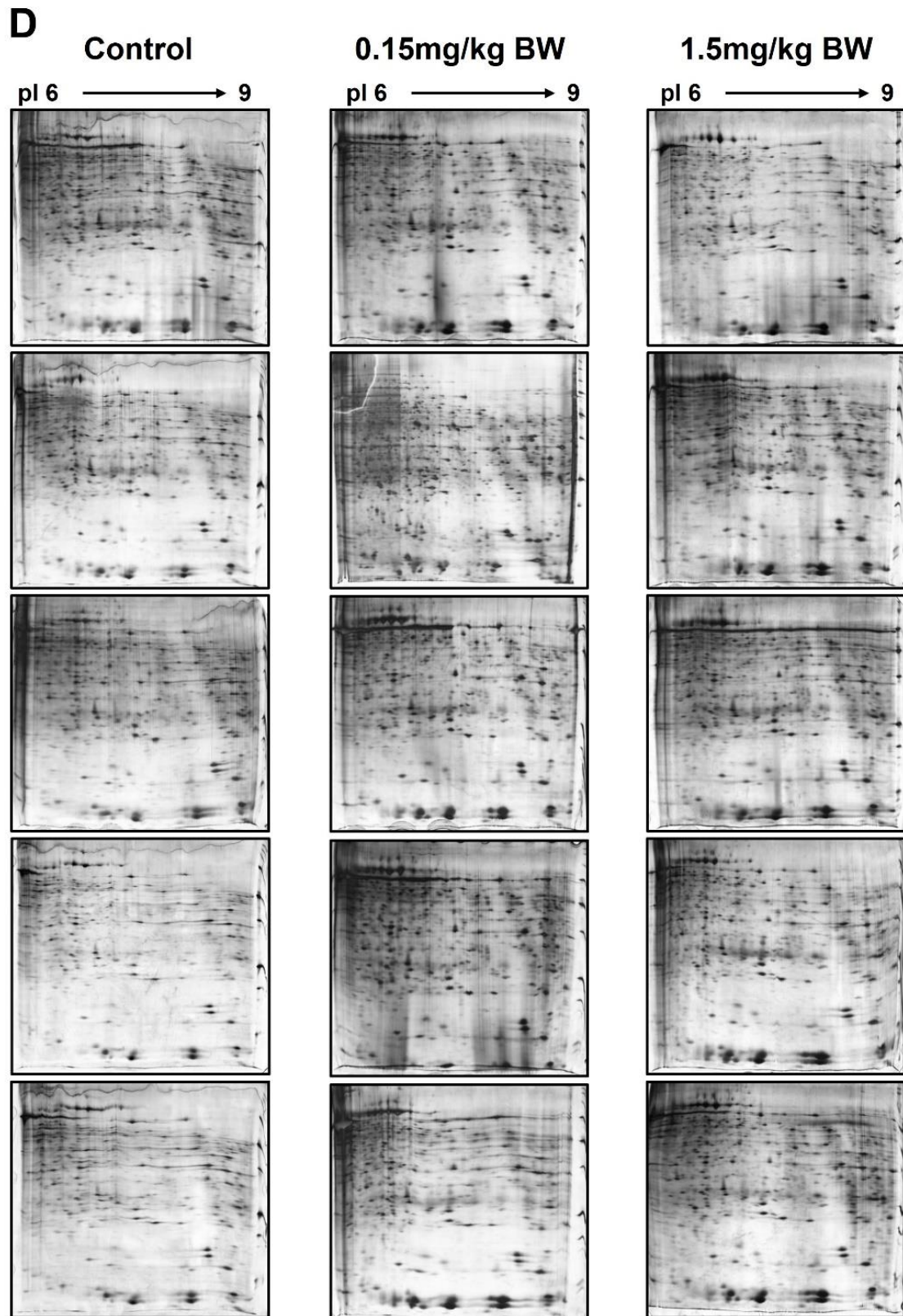


Figure S1. Supplementary image and original gel data: Gel image data. After separation on SDS-PAGE gels, the proteins were visualized by silver staining. The silver-stained gels were scanned using a 3600×4900 dpi instrument and the image files were transformed into a TIFF format with linear grayscale values. The computer analysis of the 2DE-image was carried out

using Progenesis SameSpot image analysis software. Two different ranges of pI strips (4-7, and 6-9), showed 783 (**A**) and 638 (**B**) protein spots present in the gels, respectively. **Original gel data, (C)** Original gels (pI 4-7) and (**D**) Original gels (pI 6-9).

Table S1. Identification of proteins via UPLC-ESI-MS^E

Spot No.	Accession No.	Protein name	Sequence coverage (%)	Matched peptides	Theoretical peptides	mW (Da)	pI (pH)	Products	Products RMS Mass Error (ppm)	Products RMS RT Error (min)	Protein ID
1	P17425	Hydroxymethylglutaryl CoA synthase cytoplasmic	10.2	3	40	57397	5.48	28	33	0.0208	3100
2	F7FIH7	Protein LOC100909412	37	11	19	20904	5.54	60	23.29	0.0213	8626
3	Q6GX84	Fidgetin like protein 1	7.8	4	60	74150	6.61	29	37.15	0.0231	2479
4	M0RBF1	Complement C3	30.1	138	139	186205	6.02	1204	21.84	0.0229	9870
5	D3ZDK8	Uncharacterized protein	23.5	4	12	11016	4.55	28	33.29	0.0184	19936
6	P02091	Hemoglobin subunit beta 1	47.6	10	13	15969	8.25	196	23.11	0.0193	3033
7	F1LZT6	Protein Asap2 Fragment	6.6	6	75	103093	6.36	53	30.3	0.0247	26089
8	F1LWD5	Protein 1700056E22Rik	9.4	3	11	25323	10.14	35	22.6	0.0205	19533
9	M3ZCQ3	Protein LOC100910765	79.3	14	8	12132	6.61	84	18.24	0.0211	24625
10	Q3B8N7	TSC22 domain family protein 4	13.2	6	30	40016	7.41	40	39.47	0.022	6850
11	O35817	A kinase anchor protein 14	4.8	7	48	55721	10.19	40	27.83	0.0351	297
12	D3Z8I7	Protein Gstt3	19.5	8	17	23366	9.26	51	16.59	0.016	15387
13	P01946	Hemoglobin subunit alpha 1 2	48.6	19	10	15318	8.03	300	19.78	0.0178	3032
14	F1LQ93	Collagen alpha 1 IX chain	11.2	5	57	93768	9.84	42	33.38	0.0269	19366
15	P29457	Serpin H1	22.5	9	33	46488	9.19	67	35	0.0254	6338
16	Q07936	Annexin A2	45.1	19	31	38653	7.7	198	22.96	0.0188	406
17	P18420	Proteasome subunit alpha type 1	31.9	12	25	29498	6.15	77	29.13	0.0236	5508

Proteins were identified based on the search on the UniProt website (<http://www.uniprot.org>) from the Rattus norvegicus (Rat) database (28,063 entries).