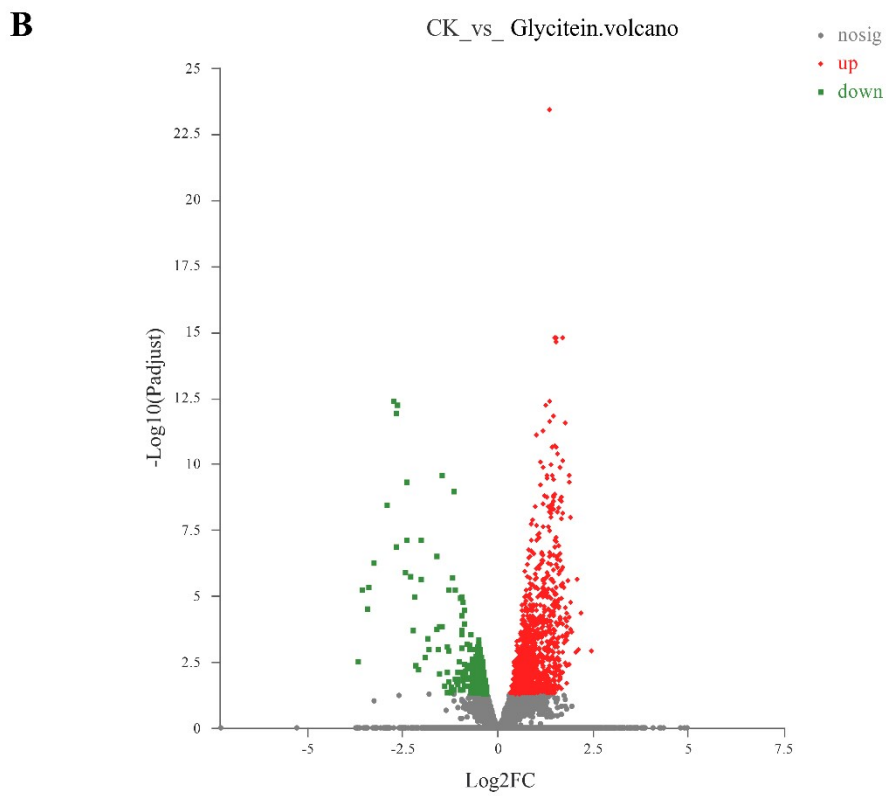
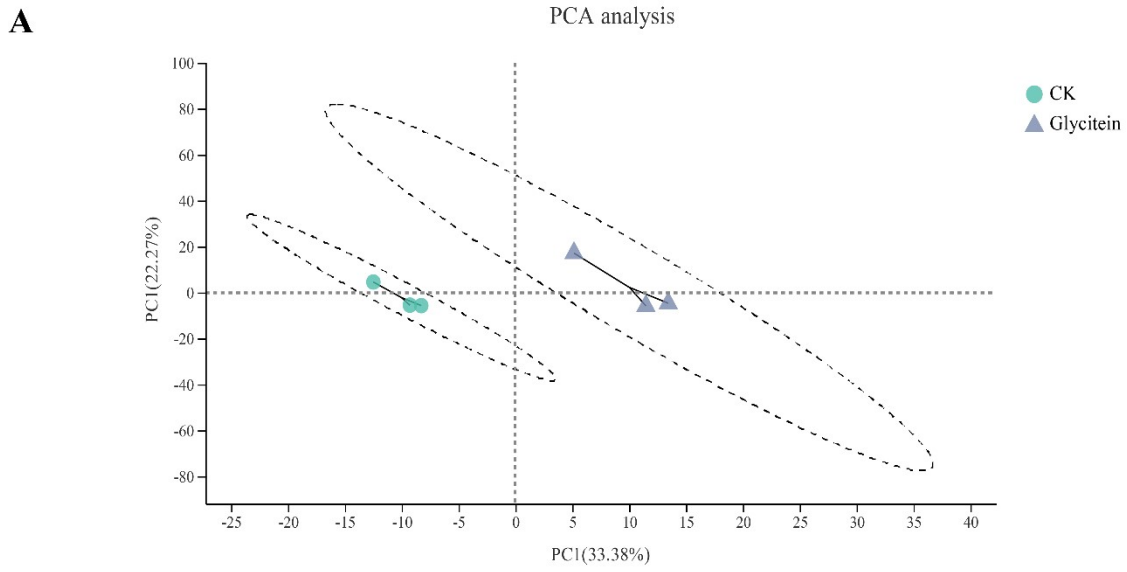


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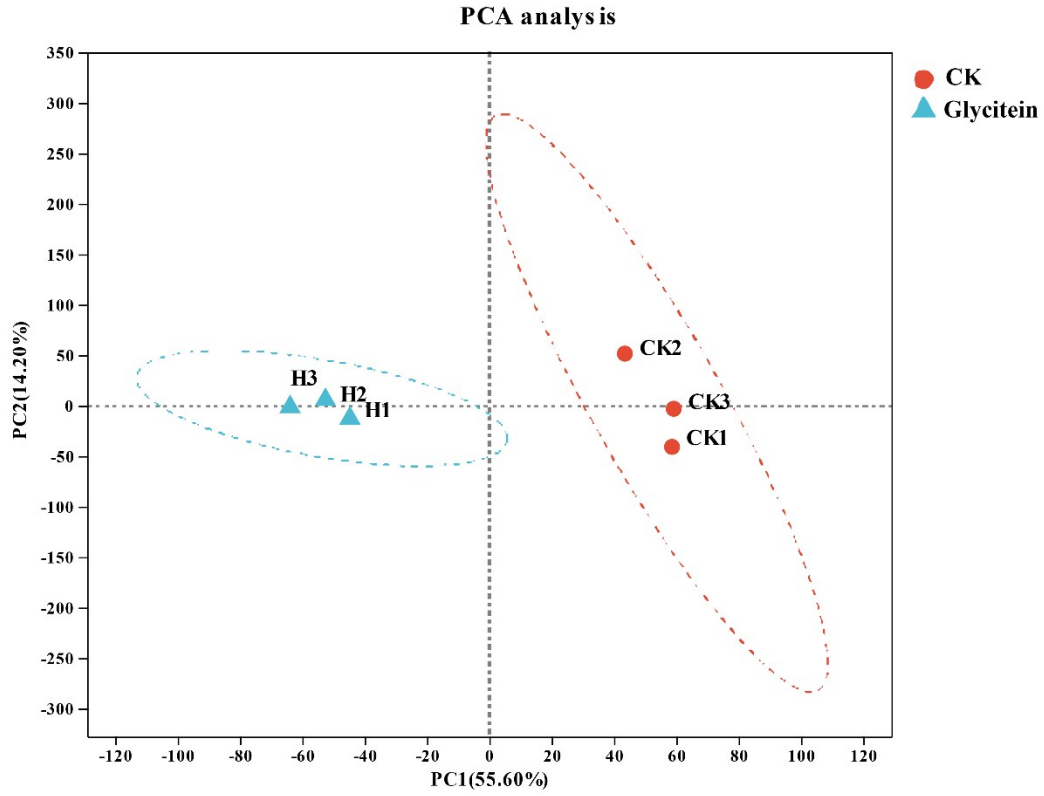
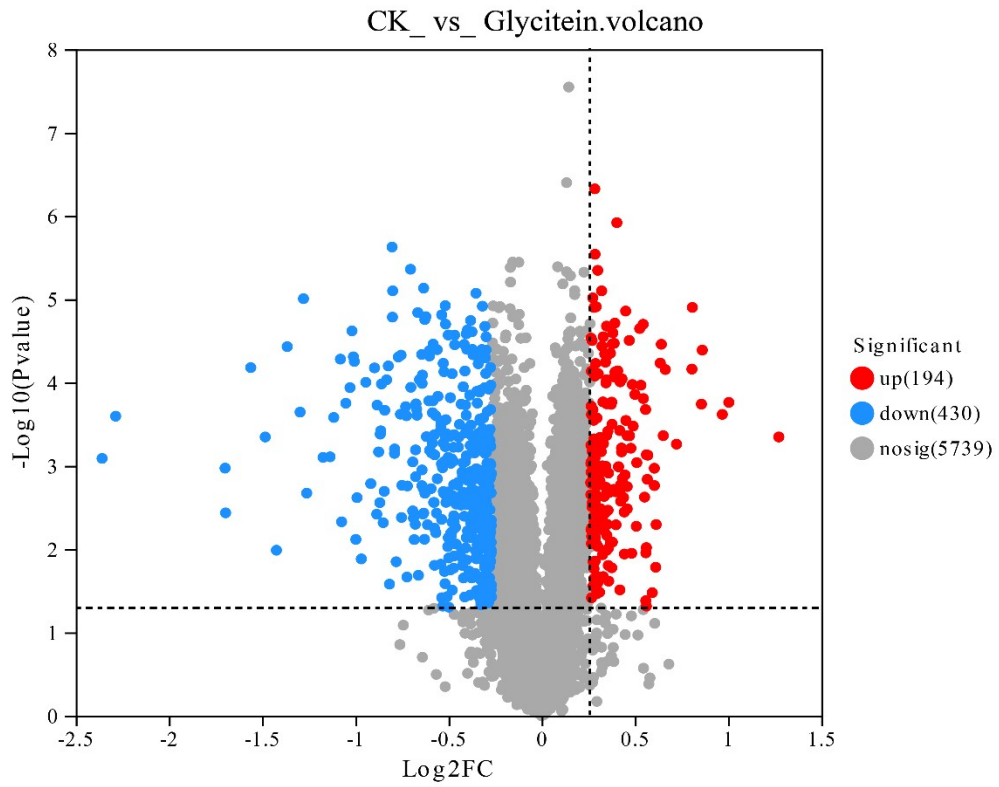
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3 Fig.S1. (A) PCA analysis and (B) Volcano plot of DEGs based on transcriptomic data.

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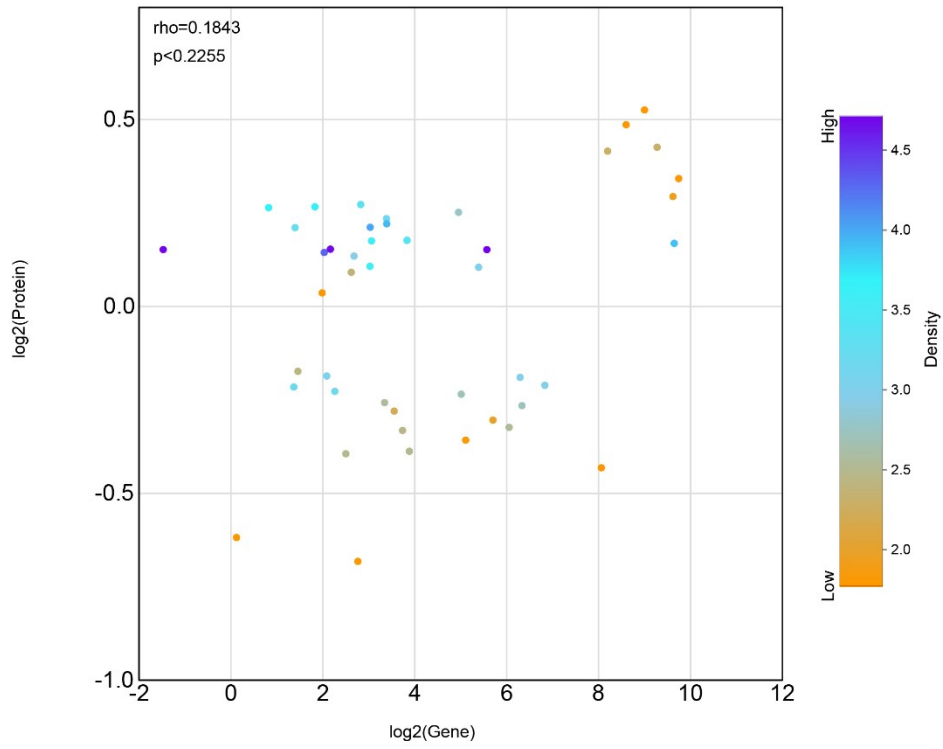
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A**B**

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8 Fig.S2. (A) PCA analysis and (B) Volcano plot of DEPs based on proteomics data.

Expression Correlation



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10 Fig. S3. Quantification relationship of transcriptomic and proteomic.

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Table S1 Core DEGs related to reproductive process

Gene name	Gene description	FC	Padjust	Regulate
<i>ptr-4</i>	PaTched Related family	2.339	3.36E ⁻⁰⁵	up
<i>plx-2</i>	Plexin-2	2.049	1.07E ⁻⁰⁵	up
<i>exc-9</i>	Uncharacterized protein	2.12	0.043634	up
<i>unc-10</i>	Rab-3-interacting molecule unc-10	2.015	0.000156	up
<i>unc-7</i>	Innexin	2.09	0.006792	up
<i>acn-1</i>	Inactive angiotensin-converting enzyme-related protein	2.025	0.000112	up
<i>eat-2</i>	Neuronal acetylcholine receptor subunit eat-2	2.647	0.027780	up
<i>col-81</i>	COLlagen	0.085	2.07E ⁻⁰⁷	down
<i>Y73F8A.35</i>	Uncharacterized protein	2.245	0.029226	up
<i>nphp-4</i>	NePHronoPhthisis (human kidney disease) homolog	2.167	0.016330	up
<i>ptr-18</i>	PaTched Related family	2.242	0.000732	up
<i>osm-8</i>	Osmotic avoidance abnormal protein 8	3.336	0.000156	up
<i>glf-1</i>	GaLactoFuranose synthesis (UGM, UDP-galactopyranose mutase)	2.928	0.003286	up
<i>adt-1</i>	A disintegrin and metalloproteinase with thrombospondin motifs adt-1	2.586	0.004114	up
<i>try-5</i>	TRYpsin-like protease	2.186	0.002742	up

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Table S2 Core DEGs related to locomotion

Gene name	Gene description	FC	Padjust	Regulate
<i>unc-10</i>	Rab-3-interacting molecule unc-10	2.015	0.000156	up
<i>osm-12</i>	Bardet-Biedl syndrome 7 protein homolog	2.551	0.030322	up
<i>sol-1</i>	Suppressor of lurcher protein 1	2.274	0.010961	up
<i>unc-7</i>	Innexin	2.09	0.006792	up
<i>glr-1</i>	Glutamate receptor 1	3.331	0.002016	up
<i>F23H12.5</i>	Uncharacterized protein	2.189	0.001504	up
<i>T14B4.19</i>	Uncharacterized protein	3.467	0.000713	up
<i>odr-10</i>	Serpentine receptor class r-10	2.268	0.036127	up
<i>pros-1</i>	Homeobox protein prospero homolog 1	2.154	0.000128	up
<i>sup-9</i>	Two pore potassium channel protein sup-9	2.138	0.031110	up

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Table S3 Core DEGs related to response to stimulus

Gene name	Gene description	FC	Padjust	Regulate
<i>abu-8</i>	Activated in Blocked Unfolded protein response	2.714	0.012093	up
<i>cyp-35A3</i>	CYtochrome P450 family	0.253	0.000424	down
<i>skpo-2</i>	ShK domain and PerOxidase domain containing protein	2.633	0.001361	up
<i>hot-2</i>	Homolog of Odr-2 (Two)	2.171	0.018906	up
<i>abu-10</i>	Activated in Blocked Unfolded protein response	2.569	0.0008	up
<i>abu-11</i>	Activated in Blocked Unfolded protein response	2.087	0.003284	up
<i>cyp-35C1</i>	CYtochrome P450 family	0.466	2.86E ⁻⁰⁶	down
<i>cyp-35A5</i>	CYtochrome P450 family	0.468	0.009969	down
<i>cyp-35D1</i>	CYtochrome P450 family	0.433	0.01792867	down

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Table S4 Core DEGs related to cellular component

Gene name	Gene description	FC	Padjust	Regulate
<i>eva-1</i>	Protein eva-1	2.207	1.07E ⁻⁰⁶	up
<i>dnj-4</i>	DNaJ domain (prokaryotic heat shock protein)	0.447	0.002127	up

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Table S5 Core DEGs related to response to oxidative stress

Gene name	Gene description	FC	Padjust	Regulate
<i>skpo-2</i>	ShK domain and PerOxidase domain containing protein	2.633	0.001361	up
<i>C46A5.4</i>	Uncharacterized protein	2.429	4.43E ⁻⁰⁵	up

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47 Table S6 Core DEGs related to response to oxidative stress based on KEGG databases

Second Category	Number	Regulate	Genes
Amino acid metabolism	1	up	<i>ech-9</i>
Glycan biosynthesis and metabolism	4	up	<i>bus-17</i> , <i>B0205.4</i> , <i>bus-8</i> , <i>bgnt-1.3</i>
Lipid metabolism	5	up	<i>ech-9</i> , <i>ace-3</i> , <i>lipl-6</i> , <i>T19H12.6</i> , <i>F13H10.5</i>
Signal transduction	9	up	<i>cdh-8</i> , <i>K07E8.6</i> , <i>prkl-1</i> , <i>ctbp-1</i> , <i>pros-1</i> , <i>daam-1</i> , <i>phg-1</i> , <i>igcm-1</i> , <i>C49H3.16</i>
Aging	1	up	<i>lips-17</i>
Development and regeneration	1	up	<i>plx-2</i>
Endocrine system	3	up	<i>unc-10</i> , <i>sup-9</i> , <i>acn-1</i>
Glycan biosynthesis and metabolism	4	up	<i>bus-17</i> , <i>B0205.4</i> , <i>bus-8</i> , <i>bgnt-1.3</i>

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50 Table S7 Core DEPs based on GO pathway analysis

GO ID	GO Description	Proteins
GO:0016021	Integral component of membrane	LIN-15B, RPS-26, DPY-11, DHS-19, TXDC-12.1
GO:0016705	Oxidoreductase activity, acting on paired donors	FAT-2, FAT-3, MTRR-1
GO:0005615	Extracellular space	DDO-3, VIT-1, OST-1
GO:0005764	Lysosome	ASP-1
GO:0016671	Oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	MSRA-1
GO:0006950	Response to stress	DNJ-10, PDE-2, FAT-6
GO:0008610	Lipid biosynthetic process	LET-767, PMT-1
GO:0009605	Response to external stimulus	PRMT-1
GO:1904666	Regulation of ubiquitin protein ligase activity	APAT-3
GO:0006573	Valine metabolic process	ALH-8

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