

Supplementary Information

Supplementary Table S1:

(A) Significantly up-regulated and/or carbonylated proteins in SW480 cell line (GO molecular function).

GO molecular function	Protein	PC	
Binding (GO:0005488)	Pre-mRNA-processing factor 19	+	
	Cellular retinoic acid-binding protein 2	-	
	ATP synthase subunit beta, mitochondrial	-	
Receptor activity (GO:0004872)	ATP synthase subunit beta, mitochondrial	-	
Enzyme regulator activity (GO:0030234)	Serpin B3	-	
	Serpin H1	-	
Structural molecule activity (GO:0005198)	Stomatin-like protein 2, mitochondrial	-	
	Peroxiredoxin-2	-	
Catalytic activity (GO:0003824)	Pre-mRNA-processing factor 19	+	
	Protein-glutamine gamma-glutamyltransferase 2	-	
	4-trimethylaminobutyraldehyde dehydrogenase	-	
	ATP synthase subunit beta, mitochondrial	-	
	Serpin B3	-	
	Serpin H1	-	
	Antioxidant activity (GO:0016209)	Peroxiredoxin-2	-
	Transporter activity (GO:0005215)	ATP synthase subunit beta, mitochondrial	-

(B) Significantly up-regulated and/or carbonylated proteins in SW620 cell line (GO molecular function).

GO molecular function	Protein	PC
Translation regulator activity (GO:0045182)	Spliceosome RNA helicase DDX39B	-
	Eukaryotic translation initiation factor 5A-1	-
Binding (GO:0005488)	Obg-like ATPase 1	-
	Spliceosome RNA helicase DDX39B	-
	Fatty acid-binding protein, epidermal	+
	Eukaryotic translation initiation factor 5A-1	-
	Rho GDP-dissociation inhibitor 1	+
	Calponin-3	+
	Heterogeneous nuclear ribonucleoprotein H3	+
Enzyme regulator activity (GO:0030234)	Rho GDP-dissociation inhibitor 1	+
	Serine/threonine-protein phosphatase	+
Structural molecule activity (GO:0005198)	Calponin-3	
	Heterogeneous nuclear ribonucleoprotein H3	+
Catalytic activity (GO:0003824)	Alpha-enolase	+
	Obg-like ATPase 1	-
	Spliceosome RNA helicase DDX39B	-
	Phosphoserine aminotransferase	+
	26S protease regulatory subunit 8	+
	Phosphoglycerate kinase 1	-
	Inorganic pyrophosphatase	+
	Protein phosphatase methylesterase 1	+
	Rho GDP-dissociation inhibitor 1	+
	L-lactate dehydrogenase B chain	+
	Methylthioribose-1-phosphate isomerase	+
	Serine/threonine-protein phosphatase 2A activator	+
	Ornithine aminotransferase, mitochondrial	+

Supplementary Table S2:

(A) Significantly up-regulated and/or carbonylated proteins in SW480 cell line (GO biological process).

GO biological process	Protein	PC
Immune system process (GO:0002376)	Peroxiredoxin-2	-
	Annexin A2*	-
Developmental process (GO:0032502)	Cellular retinoic acid-binding protein 2	-

Cellular process (GO:0009987)	Prohibitin	-
	Cellular retinoic acid-binding protein 2	-
Metabolic process (GO:0008152)	Pre-mRNA-processing factor 19	+
	Serpin B3	-
	Serpin H1	-
	T-complex protein 1 subunit eta	+
	Annexin A2*	-
	Cellular retinoic acid-binding protein 2	-
	4-trimethylaminobutyraldehyde dehydrogenase	-
	Peroxiredoxin-2	-
	60 kDa heat shock protein, mitochondrial	-
	ATP synthase subunit beta, mitochondrial	-
	Prohibitin	-
	Protein-glutamine gamma-glutamyltransferase 2	+
	Biological regulation (GO:0065007)	Serpin B3
Serpin H1		-
Cellular component organization or biogenesis (GO:0071840)	T-complex protein 1 subunit eta	+
Localization (GO:0051179)	Cellular retinoic acid-binding protein 2	-
	ATP synthase subunit beta, mitochondrial	-

(B) Significantly up-regulated and/or carbonylated proteins in SW620 cell line (GO biological process).

GO biological process	Protein	PC
Developmental process (GO:0032502)	Fatty acid-binding protein, epidermal	+
	Annexin A2*	+
Cellular process (GO:0009987)	Fatty acid-binding protein, epidermal	+
	Rho GDP-dissociation inhibitor 1	+
	Methylthioribose-1-phosphate isomerase	+
	Serine/threonine-protein phosphatase 2A	
	activator	+
Multicellular organismal process (GO: 0032501)	Calponin-3	+
Metabolic process (GO:0008152)	Alpha-enolase	+
	Annexin A2*	+
	Obg-like ATPase 1	-
	Spliceosome RNA helicase DDX39B	-

	Phosphoserine aminotransferase	+
	26S protease regulatory subunit 8	+
	Phosphoglycerate kinase 1	-
	Fatty acid-binding protein, epidermal	+
	Eukaryotic translation initiation factor 5A-1	-
	Inorganic pyrophosphatase	+
	Protein phosphatase methylesterase 1	+
	Rho GDP-dissociation inhibitor 1	+
	Nucleophosmin	+
	Heterogeneous nuclear ribonucleoprotein H3	+
	L-lactate dehydrogenase B chain	+
	Methylthioribose-1-phosphate isomerase	+
	Ornithine aminotransferase, mitochondrial	+
	Serine/threonine-protein phosphatase 2A activator	+
	Spliceosome RNA helicase DDX39B	-
	Eukaryotic translation initiation factor 5A-1	-
	Rho GDP-dissociation inhibitor 1	+
Biological regulation (GO:0065007)	Serine/threonine-protein phosphatase 2A activator	+
Cellular component organization or biogenesis (GO:0071840)	Serine/threonine-protein phosphatase 2A activator	+
Localization (GO:0051179)	Fatty acid-binding protein, epidermal	+

Supplementary Table S3:

(A) Significantly up-regulated and/or carbonylated proteins in SW480 cell line (GO pathway).

GO pathway	Protein	PC
mRNA splicing (P00058)	Pre-mRNA-processing factor 19	+
ATP synthesis (P02721)	ATP synthase subunit beta, mitochondrial	-

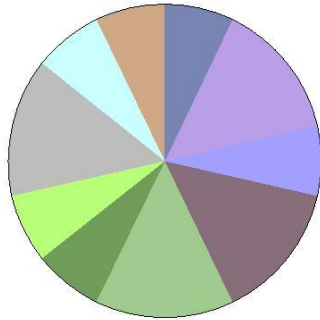
(B) Significantly up-regulated and/or carbonylated proteins in SW620 cell line (GO pathway).

GO pathway	Protein	PC
Fructose galactose metabolism (P02744)	Fructose-bisphosphate aldolase A	+
Serine glycine biosynthesis (P02776)	Phosphoserine aminotransferase	+
Vitamin B6 metabolism (P02787)	Phosphoserine aminotransferase	+
Pentose phosphate pathway (P02762)	Transaldolase	+
PLP biosynthesis (P02759)	Phosphoserine aminotransferase	+
Glycolysis (P00024)	Alpha-enolase	+
	Phosphoglycerate kinase 1	-
	Fructose-bisphosphate aldolase A	+
Ubiquitin proteasome pathway (P00060)	26S protease regulatory subunit 8	+

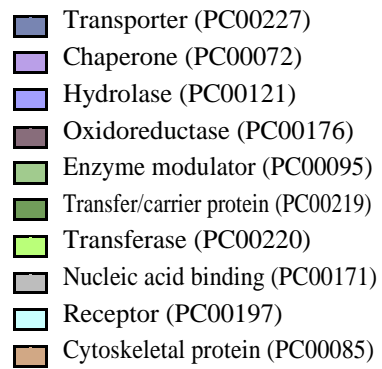
*Annexin A2 is up-regulated in SW480 but more carbonylated in SW620.

**Supplementary Figures:
Supplementary Figure 1:**

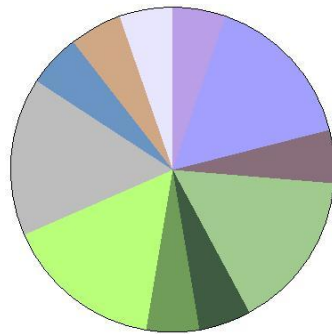
(A)



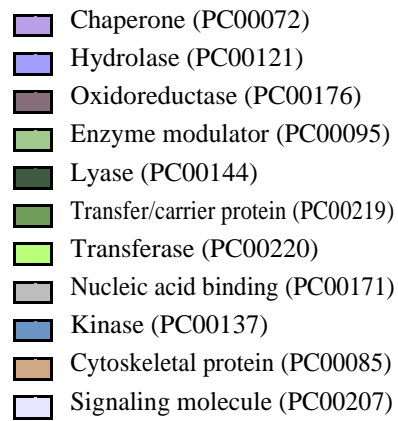
Total=14



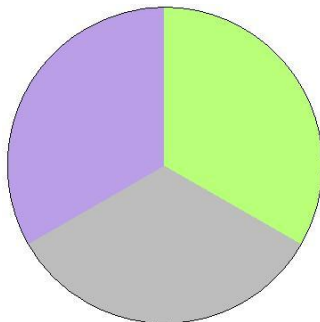
(B)



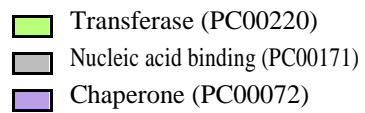
Total=19



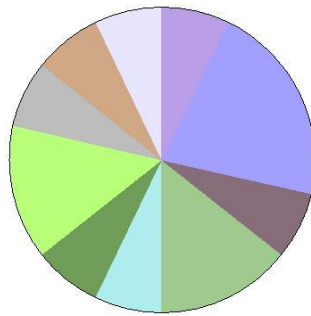
(C)



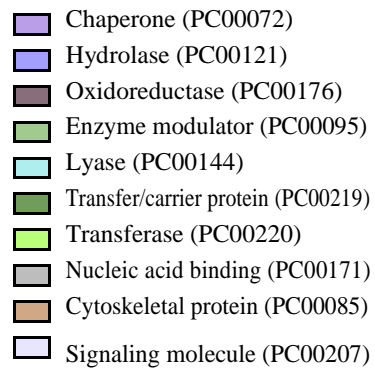
Total=3



(D)



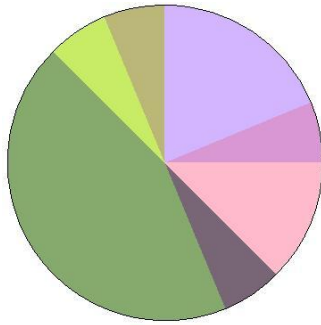
Total=14



- (A)** Groups of significantly up-regulated proteins in SW480 cell line (GO protein class).
- (B)** Groups of significantly up-regulated proteins in SW620 cell line (GO protein class).
- (C)** Groups of significantly carbonylated proteins in SW480 cell line (GO protein class).
- (D)** Groups of significantly carbonylated proteins in SW620 cell line (GO protein class).

Supplementary Figure 2:

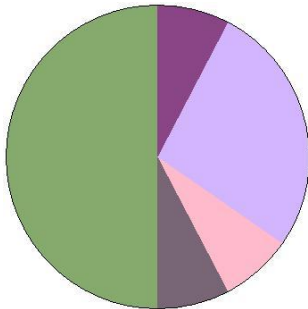
(A)



Total=16

- Binding (GO:0005488)
- Receptor activity (GO:0004872) Enzyme
- regulator activity (GO:0030234)
- Structural molecule activity (GO:0005198)
- Catalytic activity (GO:0003824) Antioxidant
- activity (GO:0016209) Transporter activity
- (GO:0005215)

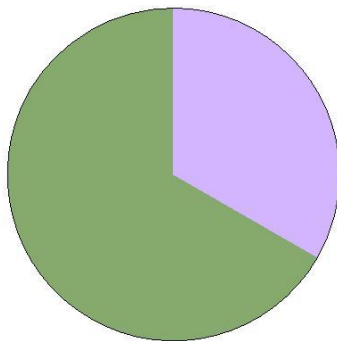
(B)



Total=26

- Translation regulator activity (GO:0045182)
- Binding (GO:0005488)
- Enzyme regulator activity (GO:0030234)
- Structural molecule activity (GO:0005198)
- Catalytic activity (GO:0003824)

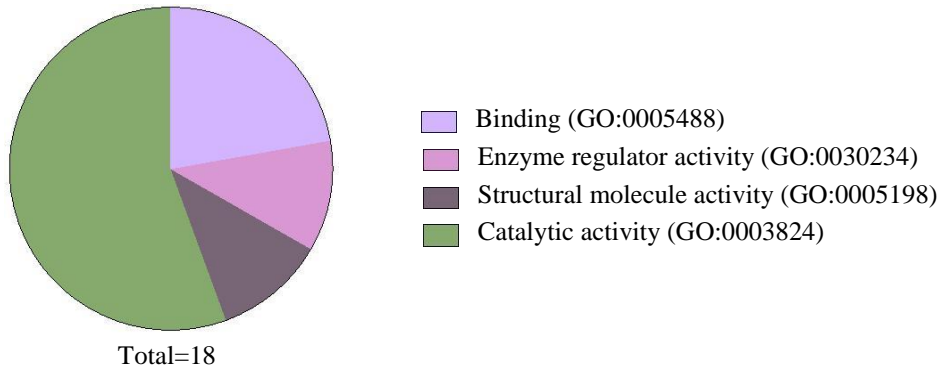
(C)



Total=3

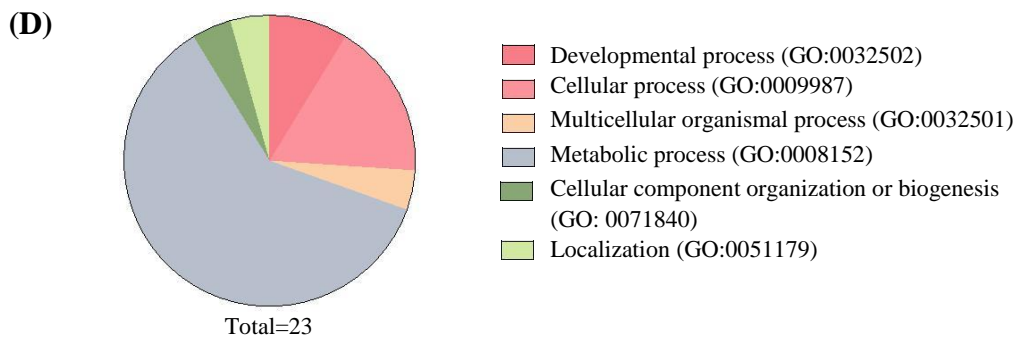
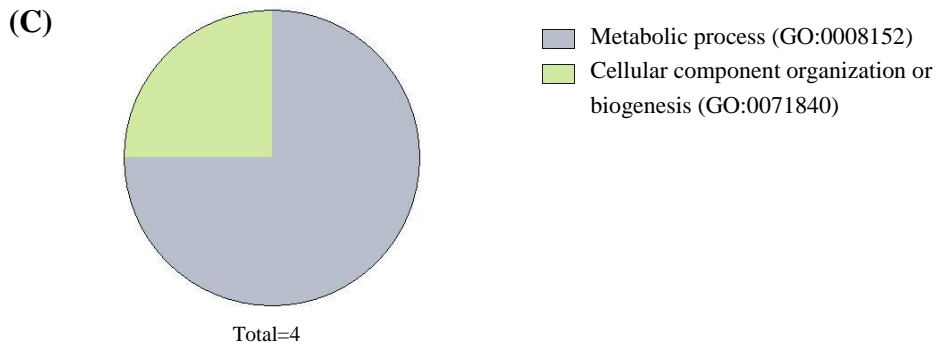
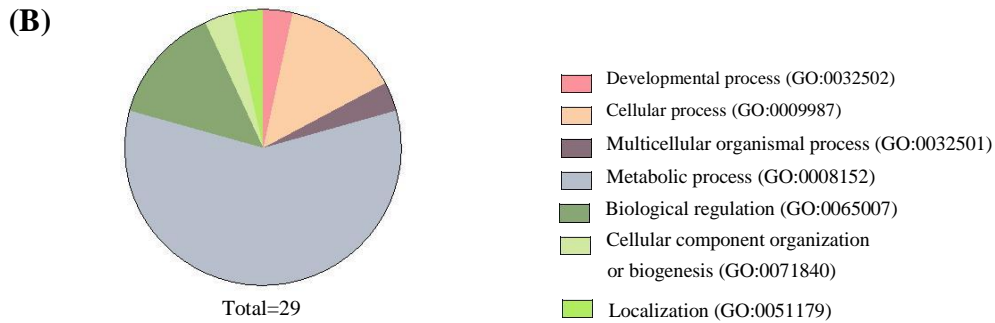
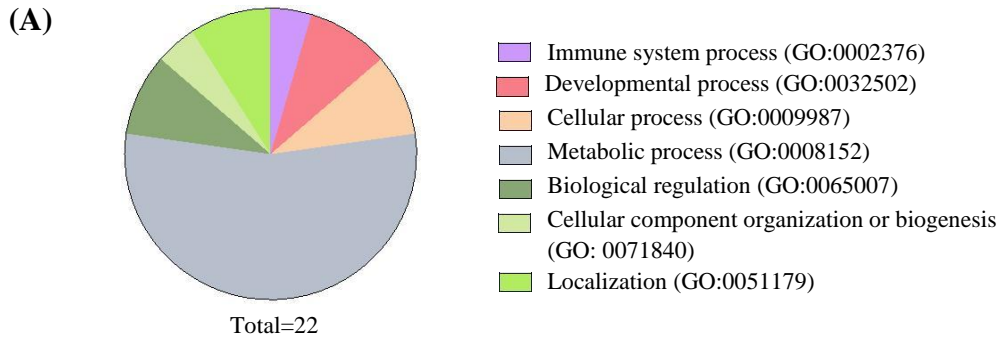
- Binding (GO:0005488) Catalytic
- activity (GO:0003824)

(D)



- (A) Groups of significantly up-regulated proteins in SW480 cell line (GO molecular function).
- (B) Groups of significantly up-regulated proteins in SW620 cell line (GO molecular function).
- (C) Groups of significantly carbonylated proteins in SW480 cell line (GO molecular function).
- (D) Groups of significantly carbonylated proteins in SW620 cell line (GO molecular function).

Supplementary Figure 3:



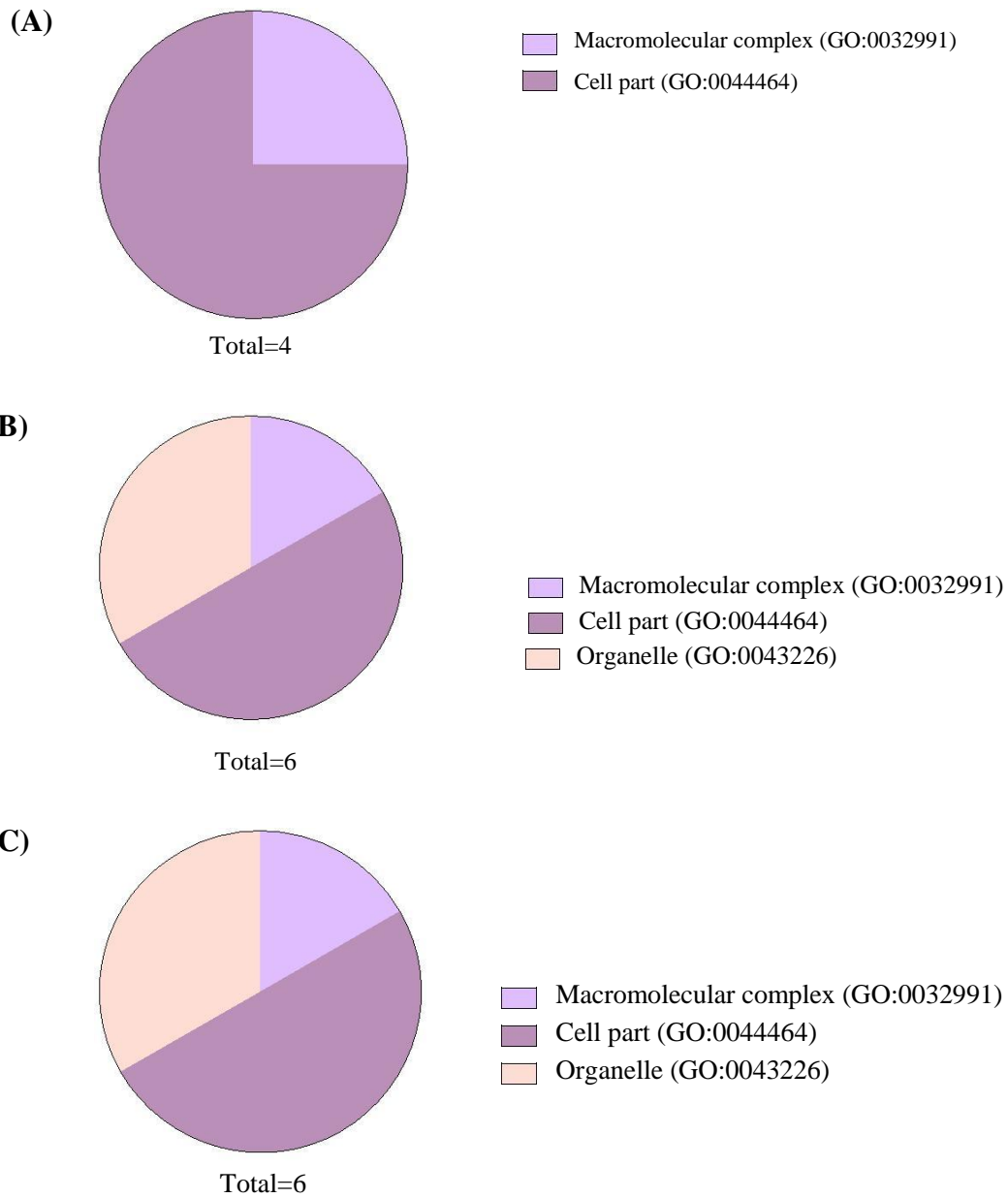
(A) Groups of significantly up-regulated proteins in SW480 cell line (GO biological process).

(B) Groups of significantly up-regulated proteins in SW620 cell line (GO biological process).

(C) Groups of significantly carbonylated proteins in SW480 cell line (GO biological process).

(D) Groups of significantly carbonylated proteins in SW620 cell line (GO biological process).

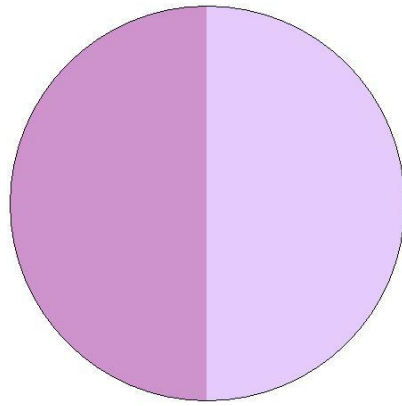
Supplementary Figure 4:



- (A)** Groups of significantly up-regulated proteins in SW480 cell line (GO cellular component).
- (B)** Groups of significantly up-regulated proteins in SW620 cell line (GO cellular component).
- (C)** Groups of significantly carbonylated proteins in SW620 cell line (GO cellular component).

Supplementary Figure 5:

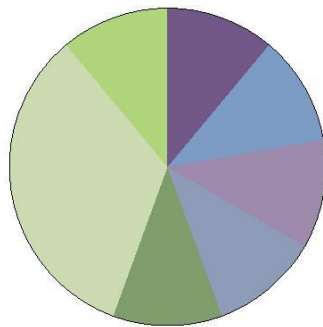
(A)



- mRNA splicing (P00058)
- ATP synthesis (P02721)

Total=2

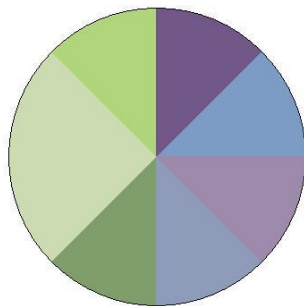
(B)



- Fructose galactose metabolism (P02744)
- Serine glycine biosynthesis (P02776)
- Vitamin B6 metabolism (P02787)
- Pentose phosphate pathway (P02762)
- PLP biosynthesis (P02759)
- Glycolysis (P00024)
- Ubiquitin proteasome pathway (P00060)

Total=9

(C)



- Fructose galactose metabolism (P02744)
- Serine glycine biosynthesis (P02776)
- Vitamin B6 metabolism (P02787)
- Pentose phosphate pathway (P02762)
- PLP biosynthesis (P02759)
- Glycolysis (P00024)
- Ubiquitin proteasome pathway (P00060)

Total=8

- (A) Groups of significantly up-regulated proteins in SW480 cell line (GO pathway).
(B) Groups of significantly up-regulated proteins in SW620 cell line (GO pathway).
(C) Groups of significantly carbonylated proteins in SW620 cell line (GO pathway).