Table SI. Sequences of primers used in the study.

Gene	Forward (5′-3′)	Reverse (5′-3′)
GLUT1	TCC ACG AGC ATC TTC GAG A	ATA CTG GAA GCA ACT GCC C
GLUT2	CTA CTC AAC CAG CAT TTT TC	AAC ACA TAA GGT CCA CAG AA
HK1	GCG CAG CTC CTG GCC TAT TAC	TGT TGG ATT AAA ATC CCG GGA
HK2	TCG CAT CTG CTT GCC TAC TTC	CTT CTG GAG CCC ATT GTC CGT
HK3	GAG TGT GTG AGC GGC ACC CC	GGT GGC CCG GAC GAA AGT GG
HK4	TGG ACC AAG GGC TTC AAG GC	CAT GTA GCA GGC ATT GCA GCC
SMCT1	CCT CAC CGC TAG CTT C	ATC TTC CAC CAT CAT AGG CA
HIF1A	CTC AAA GTC GGA CAG CCT CA	CCC TGC AGT AGG TTT CTG CT
ACTB	GTG GGG CGC CCC AGG CAC CA	CTC CTT AAT GTC ACG CAC GAT TTC

Table SII. Sequences of siRNAs used in the study.

siRNA	**Species**	**Sequences (5′-3′)**	**Company**
GLUT1	*Homo sapiens*	Sense: GAG ACU UCC AAA CCU GAC A Antisense: CAG GUU UGG AAG UCU C	Bioneer
GLUT2	*Homo sapiens*	Sense: UAU AAA UAU UUG UUG CAU CCU CAG G Antisense: CCU GAG GAU GCA ACA AAU AUU UAU A	MBiotech
HIF1A	*Homo sapiens*	Sense: GGG UAA AGA ACA AAA CAC A Antisense: UGU GUU UUG UUC UUU ACC C	Bioneer
Negative control	*Homo sapiens*	Sense: CCU ACG CCA CCA AUU UCG U Antisense: ACG AAA UUG GUG GCG UAG G	Bioneer

Table SIII. Transcripts upregulated by glucosamine in A549 cell line.

Gene ontology	**Gene symbols**	**Median fold change (range)**
Carbohydrate metabolism	*NDUFA4L2, PCK2, DHDH, SLC3A2, CYP4F12, C16orf7, GFPT1, SLC33A1, GBGT1, SLC16A4, HKDC1, PFKFB4, SLC2A6*	2.47 (2.04-7.65)
Nucleic acid, protein, and lipid biosynthesis	*PLA2G4C, CBS, C9orf95, CYP39A1, ASNS, HMGCS1, SLC6A6, CHST1, TPK1, SLC27A1, ANG, SC4MOL, UPP1, ABTB1, GMPPA, OSBP2, P4HA2, SC5DL, MVD, ACOT2, MOCOS, CERCAM, PYCR1, SPHK1, RETSAT, DAGLB, DCI, HSD17B14*	2.21 (2.01-5.17)
Glycosylation	*ALG5, TNIP1, CCNO, ALG12, SMPDL3A, UGCG*	2.06 (2.00-2.61)