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Figure legends

Fig.1. IMS32 showed distinct Schwann cell phenotypes such as spindle-shaped morphology (**A-C**) and immunoreactivity to S100 protein (**D-F**) under normal ([Glc-5.6] (**A,D**)) and high ([Glc-30] (**B,E**) and [Glc-56](**C,F**)) glucose conditions.

Fig. 2. Relative mRNA expressions of AR and SDH in IMS32 determined by Northern blot analysis. (**A**) The picture of the blot hybridized with alkaline-phosphatase-labeled cDNA probes (**top**). Marker molecular masses for calibration are indicated on the left. mRNA for AR and SDH were detected as single bands corresponding to the molecular weight of around 1.4 kb and 2.4 kb, respectively. The blot showed more intense signals for AR mRNA in [Glc-30], [Glc-56] and [NaCl-50] than that in [Glc-5.6], and more intense signals for SDH mRNA in [Glc-56] and [NaCl-50] than that in [Glc-5.6]. A methylene blue (MB)-stained image of the duplicate membrane (**bottom**) showed that relatively equal amounts of RNA were loaded. (**B**) The mRNA expressions of AR (**top**) and SDH (**bottom**) in [Glc-30], [Glc-56] and [NaCl-50] relative to those in [Glc-5.6]. Values represent the mean + SEM of 4 experiments. * $P < 0.05$ (by Bonferroni Dunn post-hoc analysis) as compared with [Glc-5.6].

Fig.3. Relative protein expression of AR in IMS32 determined by Western blot analysis. (**A**) The picture of the blot incubated with a polyclonal anti-AR antibody (**top**). Marker molecular masses for calibration are indicated on the left. The expression band of AR was identified as the level a molecular size of around 36 kDa. The blot showed more intense signals for AR protein in [Glc-30], [Glc-56] and [NaCl-50] than that in [Glc-5.6]. The blot incubated with a monoclonal anti- β -actin antibody (**bottom**) showed that there was no significant difference in the signal intensity among each experimental group. (**B**) The protein expression of AR in [Glc-30], [Glc-56] and [NaCl-50] relative to that in

[Glc-5.6]. Values represent the mean + SEM of 3 experiments. *P<0.05 as compared with [Glc-5.6].

Fig.4. Immunocytochemical localization of AR protein in the cytoplasm of IMS32. The photomicrographs showed more intense immunoreactivity for AR in [Glc-30] (**B**) than that in [Glc-5.6] (**A**).

Fig.5. Intracellular contents of sorbitol (**top**) and fructose (**bottom**) determined by gas-chromatography. Values expressed as nmol /mg protein represent the mean + SEM of 4 experiments. *P<0.01 as compared with [Glc-5.6] or [Glc-30/SNK].

Fig.6. Relative mRNA expressions of serum amyloid A3 (SAA3), angiopoietin-like 4 (ANGPTL4) and ecotropic viral integration site 3 (Evi3) in IMS32 determined by semi-quantitative RT-PCR. (**A**) The pictures of gel electrophoresis showing more intense signals for SAA3, ANGPTL4 and Evi3 mRNA in [Glc-30] and [Glc-30/SNK] than those in [Glc-5.6]. (**B**) The mRNA expressions of SAA3, ANGPTL4 and Evi3 in [Glc-30] and [Glc-30/SNK] relative to those in [Glc-5.6]. Values represent the mean + SEM of 4 experiments. *P<0.05 as compared with [Glc-5.6].

Fig.7. Relative mRNA expression of aldehyde reductase (AKR1A4) in IMS32 determined by Northern blot analysis. (**A**) The picture of the blot hybridized with an alkaline-phosphatase-labeled cDNA probe (**top**). mRNA for AKR1A4 was detected as a single band corresponding to the molecular weight of around 1.7 kb. The blot showed a less intense signal for AKR1A4 mRNA in [Glc-30] than that in [Glc-5.6] or [Glc-30/SNK]. A methylene blue (MB)-stained image (28S ribosomal RNA) of the duplicate membrane (**bottom**) showed that a relatively equal amount of RNA was loaded. (**B**) The mRNA expression of AKR1A4 in [Glc-30] and [Glc-30/SNK] relative to that in [Glc-

5.6]. Values represent the mean + SEM of 4 experiments. *P<0.05 as compared with [Glc-5.6] or [Glc-30/SNK].

Fig.8. mRNA expression of SAA3, ANGPTL4, Evi3 and AKR1A4 in the peripheral nerves of an adult mouse: RT-PCR analysis. The pictures of gel electrophoresis showed the PCR products from cDNA of adult mouse DRG associated with spinal nerve bundles, IMS32 cells, and PCR reactions without a template cDNA, respectively.

Table 1

Altered gene expression in IMS32 under the high glucose ([Glc-30]) versus normal glucose ([Glc-5.6]) condition

GenBank Accession No.	Gene	Molecular Function	Ratio ([Glc-30]/[Glc-5.6])
[Up-regulated]			
AK003182	Myosin light chain, alkali, fast skel.	calcium ion binding (cytoskeleton organization and biogenesis)	2.04
NM_008182	Glutathione S-transferase alpha 2	glutathione transferase activity (detoxification of lipid aldehydes)	2.46
NM_009426	Thyrotropin-releasing hormone (TRH)	thyrotropin-releasing hormone activity	2.04
NM_011315	Serum amyloid A3 (SAA3)	acute-phase response protein activity, lipid transporter activity	2.61
NM_020581	Angiopoietin-like 4 (ANGPTL4)	inhibiting lipoprotein lipase activity, angiogenesis	2.3
NM_023557	RIKEN cDNA 2210409D01	unknown	3.35
NM_144731	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyl transferase (GALNT7)	polypeptide N-acetylgalactosaminyltransferase activity, transferase activity, transferring glycosyl groups	2.43
NM_144876	RIKEN cDNA D930050H05	unknown	3.21
NM_145492	Ecotropic viral integration site3 (Evi-3)	a retroviral integration site in murine B-cell lymphoma	3.13
NM_146720	Olfactory receptor 421 (Olfr421)	olfactory receptor function	2.05
[Down-regulated]			
AK019076	Adult male tongue cDNA (RAPI GTPase activating protein 1H)	unknown	0.37
NM_008474	Type II 65kd keratin (KRT-2-16)	structural constituent of cytoskeleton	0.44
NM_007392	Alpha 2 actin	structural constituent of cytoskeleton	0.49
NM_007810	Cytochrome P450, 19, aromatase (Cyp19)	monooxygenase activity, oxidoreductase activity	0.45
NM_008522	Lactoferrin	ferric iron binding	0.43
NM_008826	Phosphofructokinase	6-phosphofructokinase activity (glycolysis)	0.49
NM_009075	Ribose 5-phosphate isomerase	ribose-5-phosphate isomerase activity (pentose-phosphate shunt)	0.44
NM_010266	Guanine deaminase	hydrolase activity	0.43
NM_011144	Peroxisome proliferation activated receptor alpha (PPAR α)	transcription factor activity (regulation of fatty acid metabolism)	0.45
NM_013549	Histone2, H2AA1	unknown	0.34
NM_013713	Keratin associated protein 15	unknown (differentiation of epithelial cells?)	0.29
NM_018873	P140 protein	controlling actin cytoskeleton organization	0.42
NM_019467	Allograft inflammation factor 1 (AIF1)	a potential modulator of macrophage activation	0.43
NM_019752	Serine protease (Prss25)	serine-type endopeptidase activity (proteolysis, apoptosis)	0.37
NM_020009	FK506 binding protein associated protein 1 (FRAP1)	inositol/phosphatidylinositol kinase activity	0.27
NM_021473	Aldo-keto reductase (AKR1A4)	aldehyde reductase activity, oxidoreductase activity	0.39
NM_023115	Protocadherin 15 (PCDH15)	calcium ion binding (homophilic cell adhesion)	0.19
NM_024464	RIKEN cDNA 2010319C14	unknown	0.24
NM_025692	RIKEN cDNA 5730525G14	unknown	0.28

Fig.1

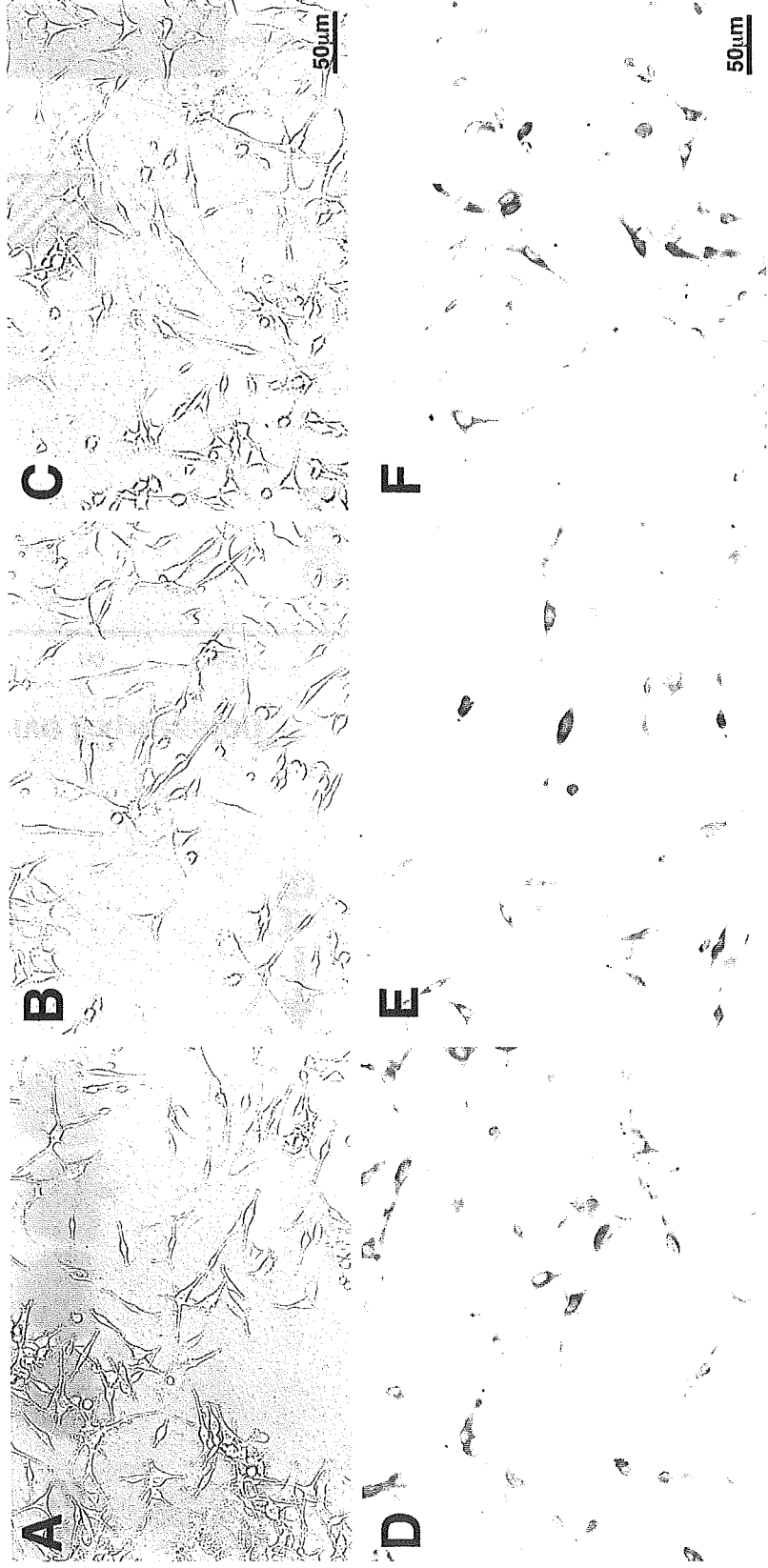
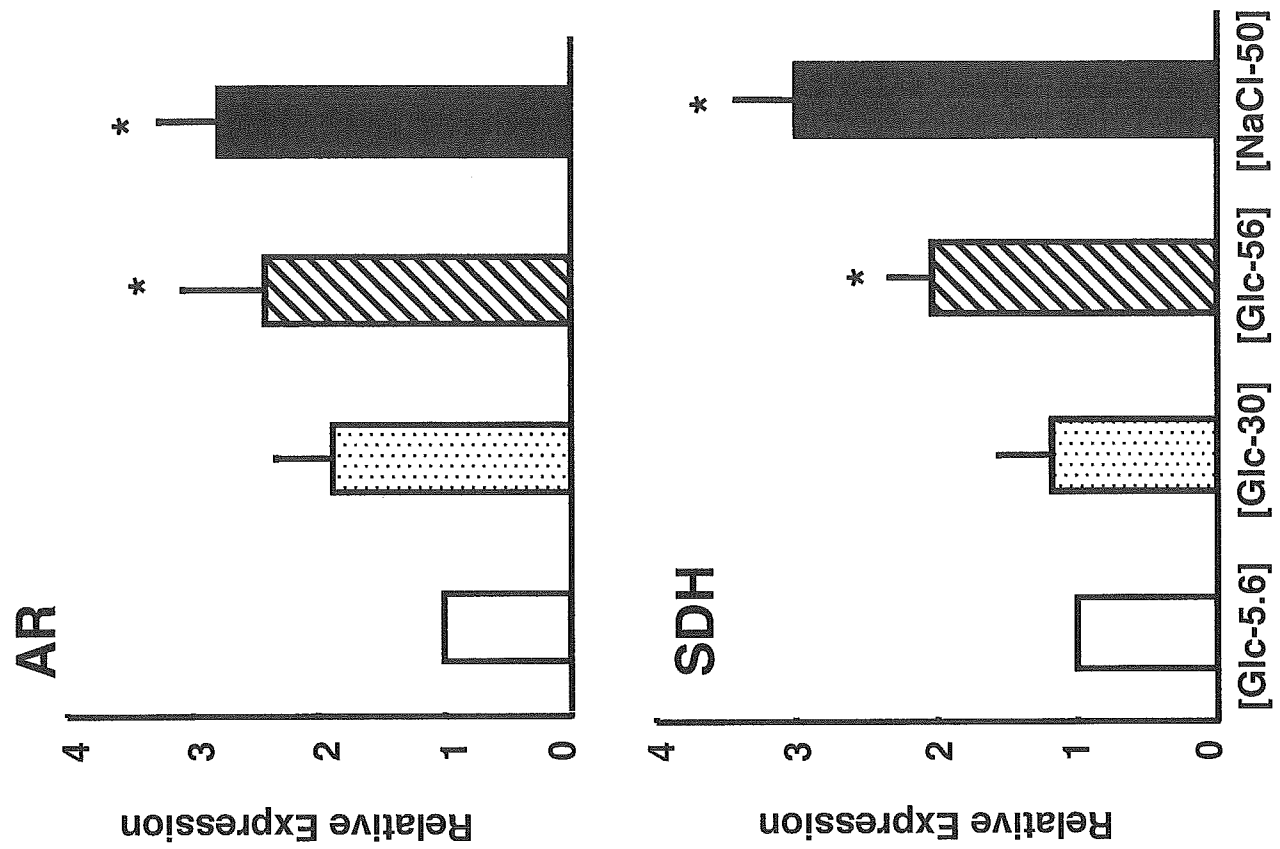
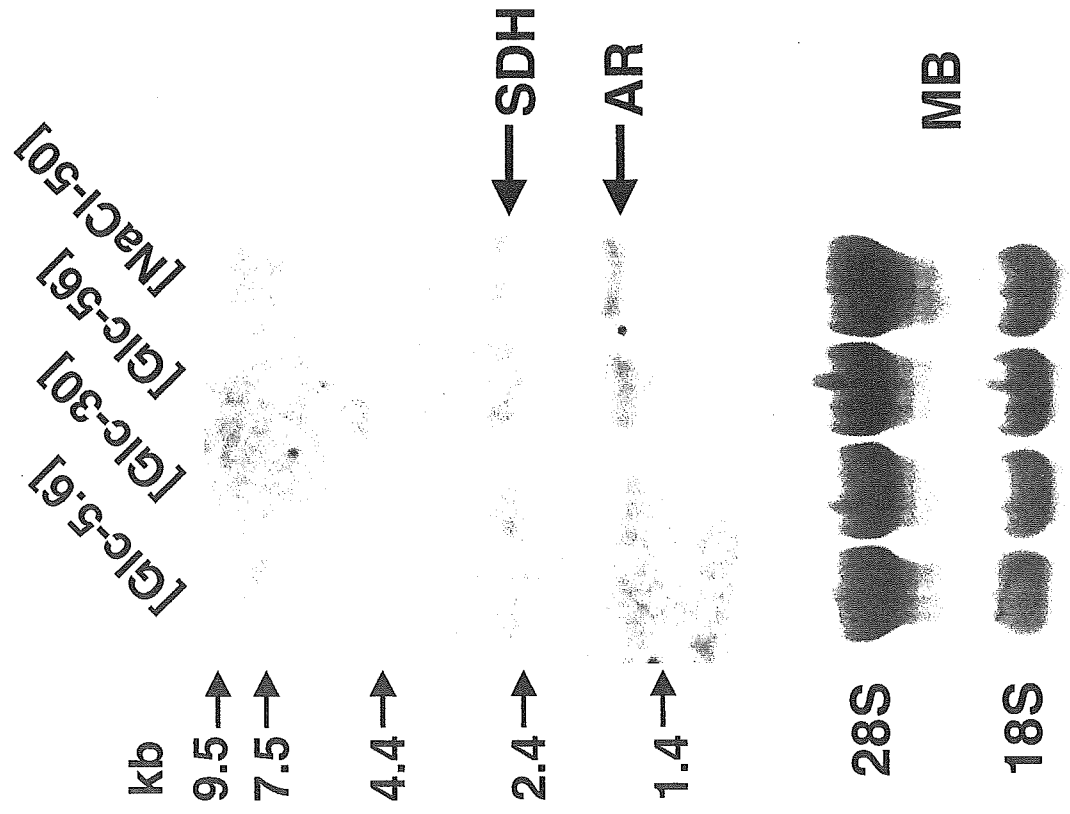


Fig.2

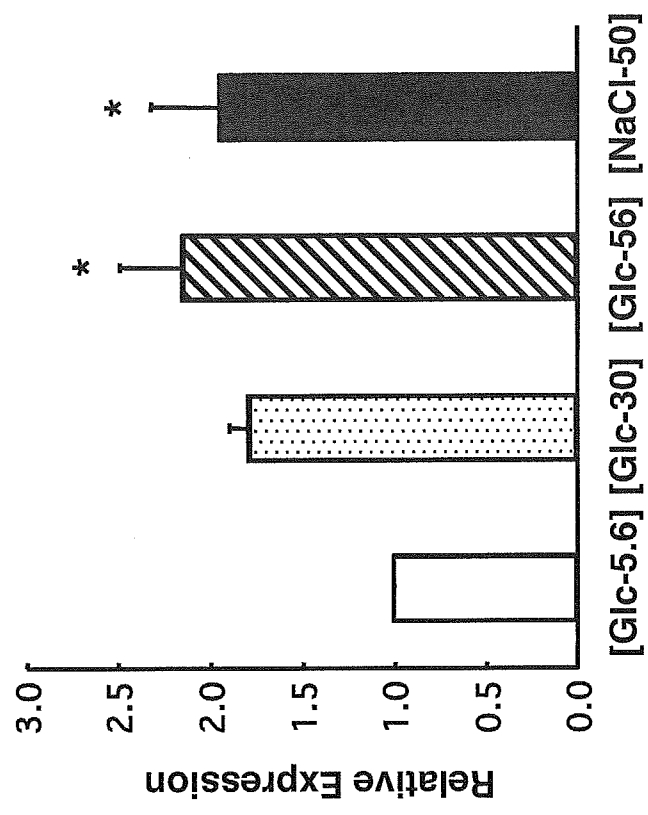


B



A

B



A

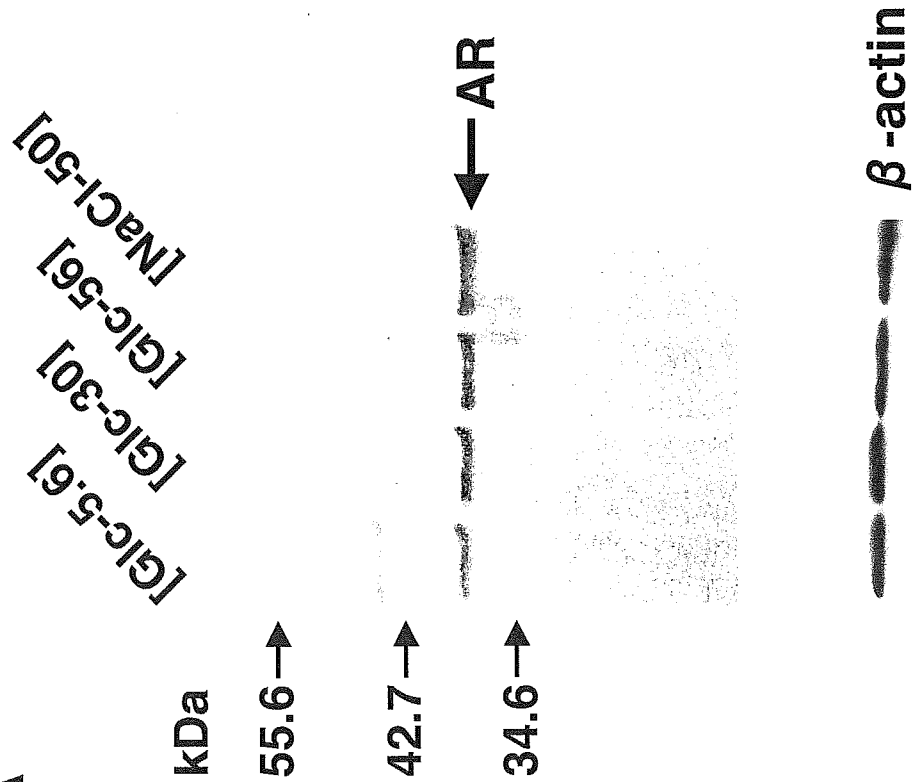


Fig.4



Fig. 3

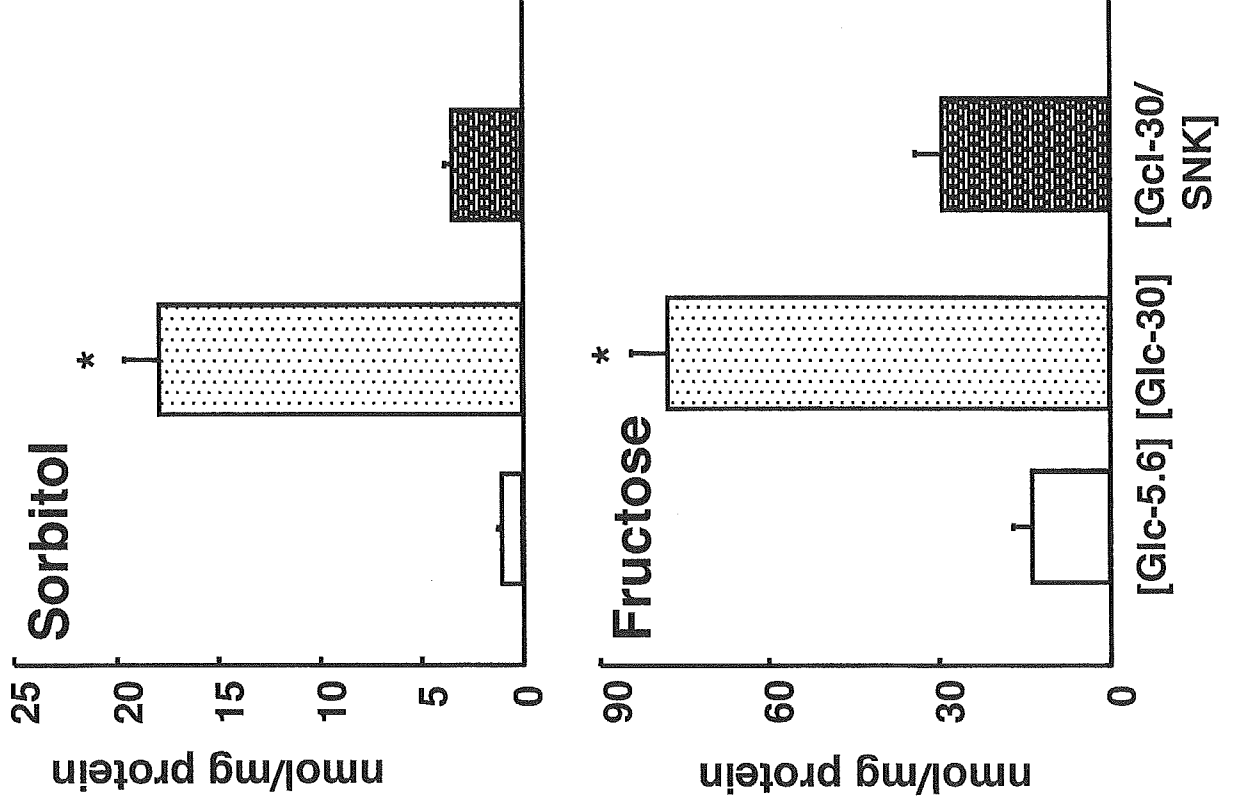


Fig.6

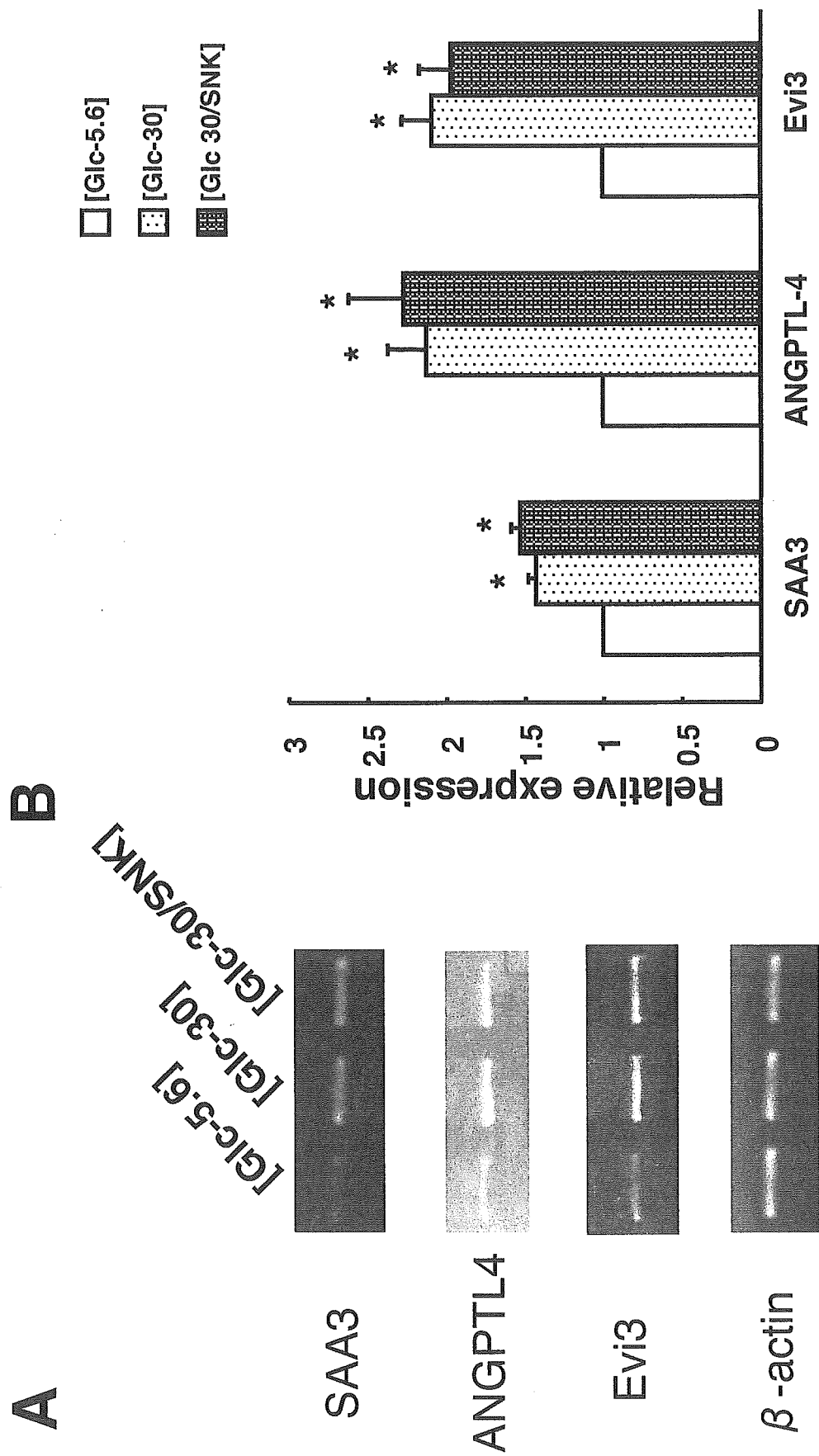


Fig.7

