SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Mass spectrometry characterization of MC α2(I) glycopeptides [76-90]. Deconvoluted mass spectrum over the mass range 1200 – 2000 Da showing peptides and glycopeptides containing Hyl 87 formed by in-gel trypsin digestion of the MC α-2(I). The spectrum was obtained by averaging the MS scans over the chromatographic elution time of all observed species. The ions indicated with an asterisk represent non-related co-eluting species. MC, collagen from MC3T3-E1 cell culture; α-2(I), type I collagen alpha-2 chain; Lys, lysine; Hyl, hydroxylysine; G-Hyl, galactosylhydroxylysine; GG-Hyl, glucosylgalactosylhydroxylysine.

Supplemental Figure 2. mRNA expression of *Lox* family (*Lox*, *Loxl*, *Loxl3*, and *Loxl4*) relative to *Col1A2*, in the Sh clones (Sh1-1,-2,and -3) and controls (MC and EV). Note that the expressions of the *Lox* family genes in the Sh clones are not statistically different from those of the controls, MC and EV. *Lox*, lysyl oxidase; *Loxl*, lysyl oxidase like; MC, MC3T3-E1; EV, MC cell-derived clone stably transfected with empty vector; Sh, MC cell-derived clones stably suppressing LH3. Error bar indicates mean ± SD from three independent analyses.

Supplemental Table 1. Sricholpech *et al*.

Supplemental Table 1 The tryptic peptides and their modifications considered for the site-specific, relative quantitation of glycosylation .

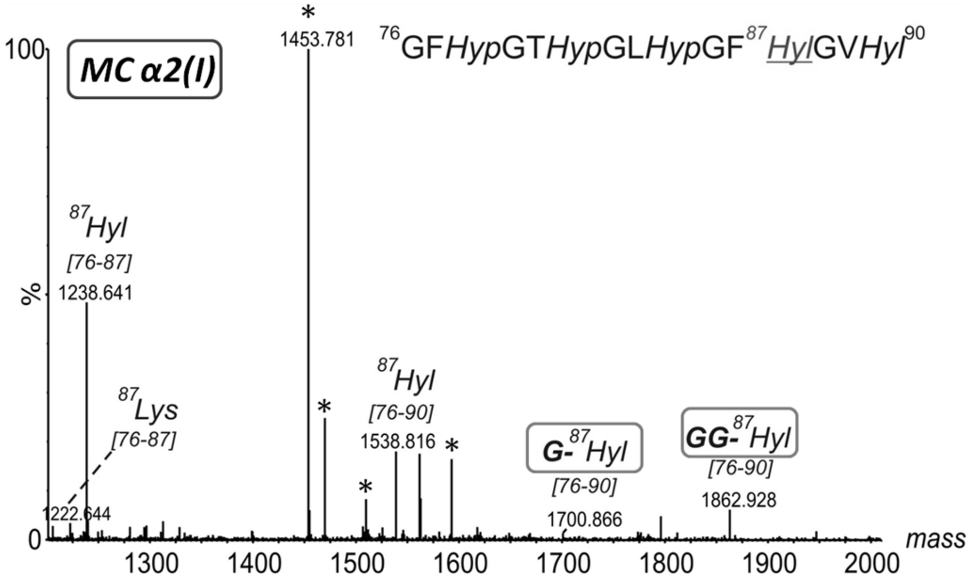
Chain/Residue [a]	**Peptide** [a]	**Modifications** [b]	**MW(exp)**	**MW (theor)**	**Mass accuracy (ppm)**	**Retention time (min)** [c]
α-1(I), K87	[76-90]	2×HYP, HYL	1495.779	1495.757	14.7	37.5
	[76-90]	2×HYP, M_{ox}, HYL	1511.755	1511.752	1.7	31.7
	[76-90]	2×HYP, G-HYL	1657.792	1657.809	10.5	37.1
	[76-90]	2×HYP, M_{ox}, G-HYL	1673.824	1673.804	11.7	31.2
	[76-90]	2×HYP, GG-HYL	1819.870	1819.862	4.2	36.2
	[76-90]	2×HYP, M_{ox}, GG-HYL	1835.889	1835.857	17.7	31.1
α-1(I), K174	[145-174]	3×HYP	2575.222	2575.230	3.2	46.3
	[145-174]	3×HYP, HYL	2591.268	2591.225	16.8	46.0
	[145-183]	3×HYP	3398.671	3398.624	13.7	44.6
	[145-183]	2×HYP, HYL	3398.671	3398.624	13.7	46.6
	[145-183]	3×HYP, HYL	3414.643	3414.619	6.9	44.1
	[145-183]	2×HYP, G-HYL	3560.767	3560.677	25.2	46.2
	[145-183]	3×HYP, G-HYL	3576.733	3576.672	16.9	43.9
	[145-183]	3×HYP, GG-HYL	3738.823	3738.725	26.1	43.7
α-2(I), K87	[76-87]	3×HYP	1221.572	1221.603	25.1	51.3
	[76-87]	3×HYP, HYL	1237.578	1237.598	16.2	51.2
	[76-90]	3×HYP, 2×HYL	1537.810	1537.778	20.5	48.8
	[76-90]	3×HYP, HYL, G-HYL	1699.804	1699.831	16.1	48.3
	[76-90]	3×HYP, HYL, GG-HYL	1861.885	1861.883	1.1	47.1
α-2(I), K174	[145-174]	3×HYP	2588.296	2588.251	17.4	52.7
	[145-174]	3×HYP, HYL	2604.302	2604.246	21.5	52.5
	[145-192]	3×HYP, HYL	4184.977	4185.052	17.9	55.7
	[145-192]	4×HYP, HYL	4200.992	4201.047	12.9	55.4
	[145-192]	3×HYP, G-HYL	4347.011	4347.104	23.7	56.5
	[145-192]	4×HYP, G-HYL	4363.177	4363.099	17.8	54.8
	[145-192]	3×HYP, GG-HYL	4509.125	4509.157	7.1	56.2
	[145-192]	4×HYP, GG-HYL	4525.063	4525.152	19.6	54.6
α-2(I), K219	[193-219]	3×HYP	2447.276	2447.229	19.3	55.3
	[193-219]	3×HYP, HYL	2463.288	2463.224	26.1	55.0
	[193-237]	6×HYP, HYL	4037.128	4037.045	20.4	59.9
	[193-237]	6×HYP, G-HYL	4199.140	4199.098	9.9	59.6
	[193-237]	6×HYP, GG-HYL	4361.170	4361.151	4.3	59.3

[a] – Residue number is determined relative to N-helical cross-linking site, Lys 87;

[b] – M_{ox} – oxidized methionine (+16 Da), HYP – hydroxyproline, HYL – hydroxylysine, G-HYL – galactosylhydroxylysine, GG-HYL – glucosylgalactosylhydroxylysine

[c] – retention time was determined from a single LC-MS run, based on a gradient from 2 to 40% solvent B over 90 min.

Supplemental Figure 1. Sricholpech *et al*.



Supplemental Figure 2. Sricholpech *et al*.