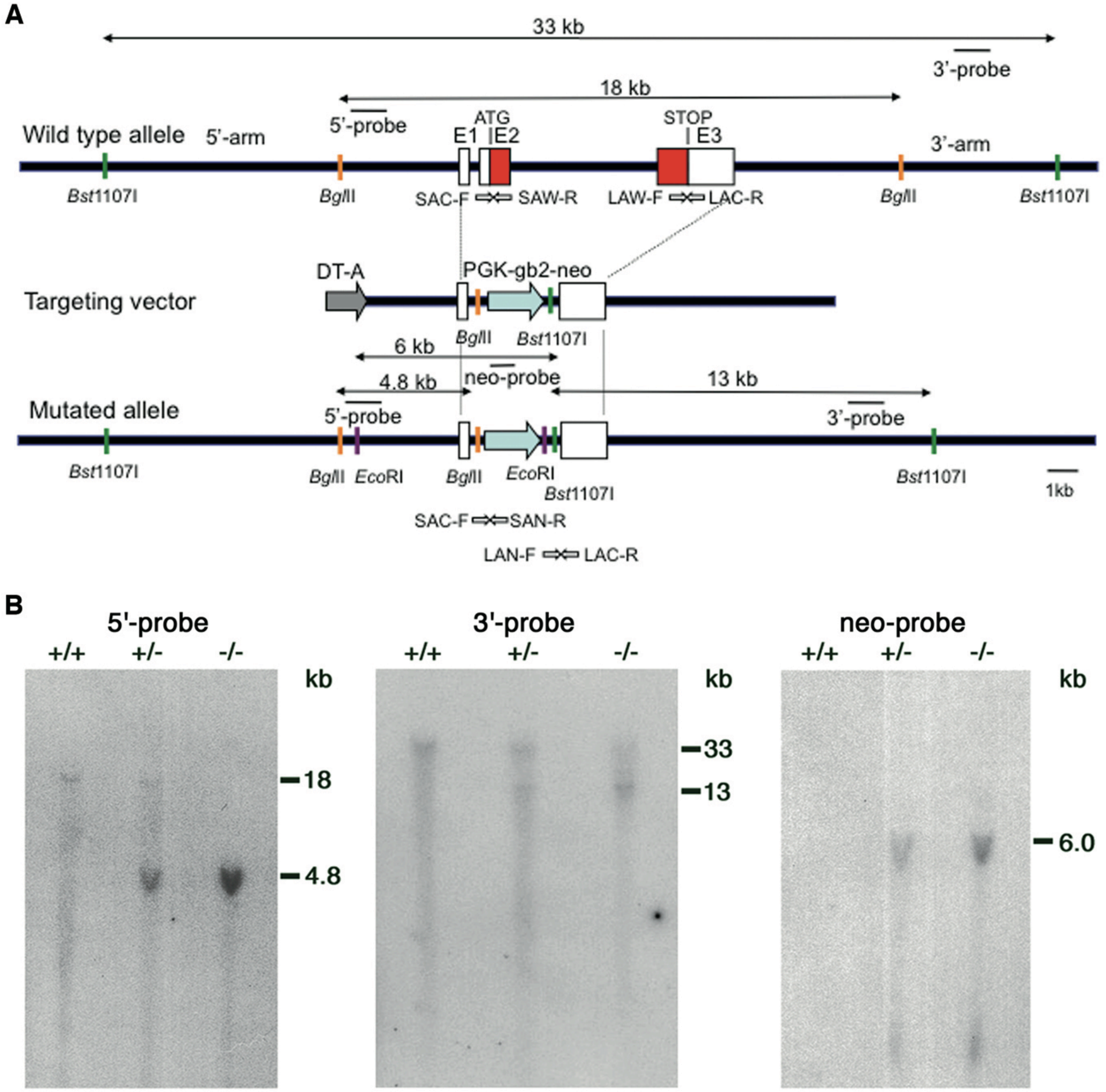
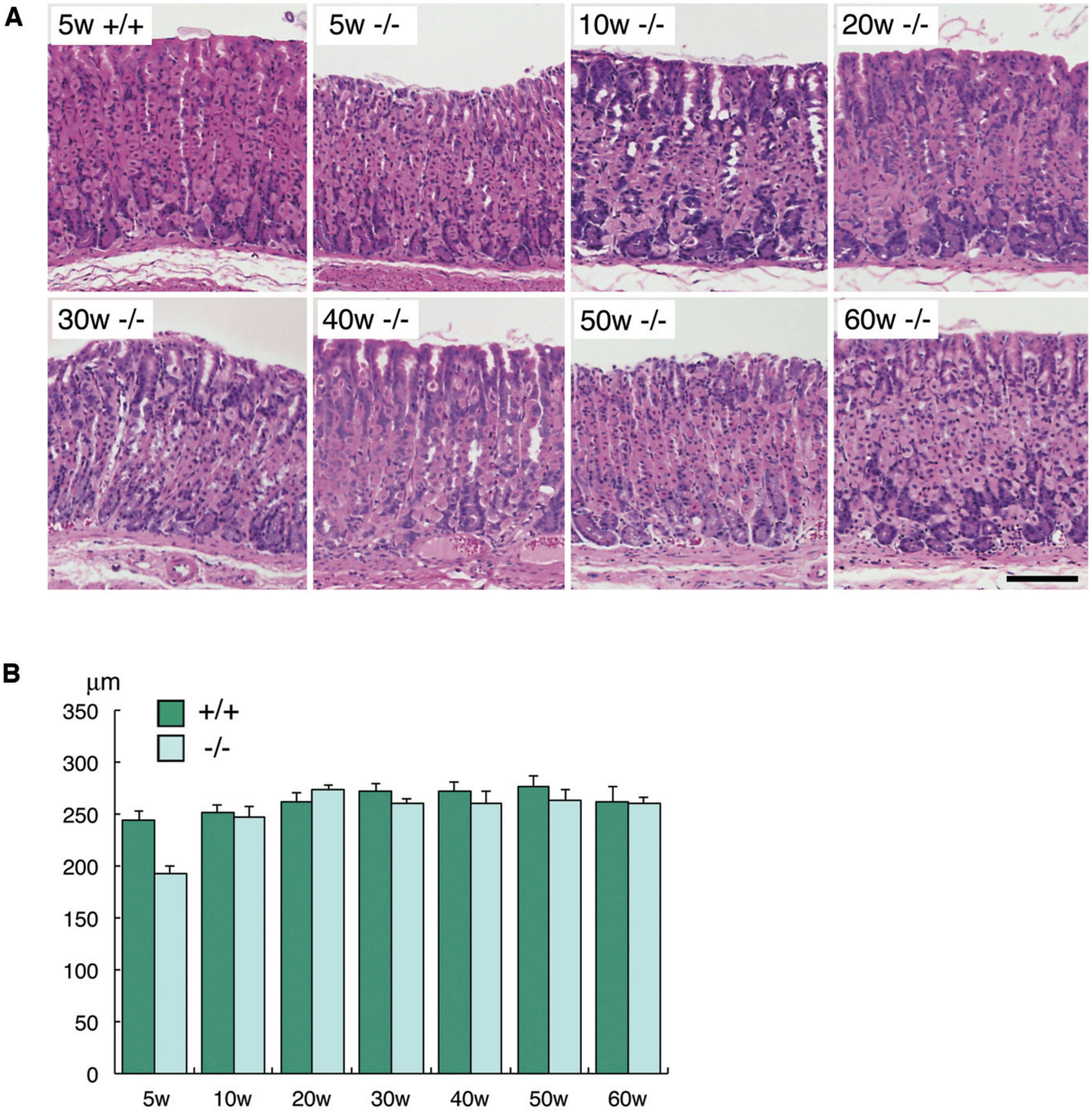


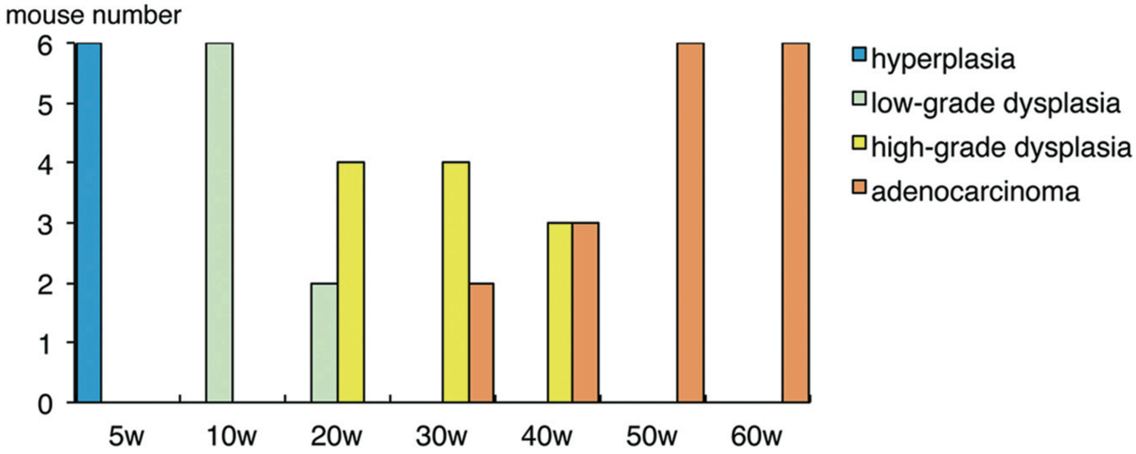
Supplemental Figure 1

Strategy for homologous recombination of *A4gnt* gene. (**A**) Wild type *A4gnt* allele (top), targeting vector containing neomycin-resistance (PGK-gb2-neo) and diphtheria toxin A (DT-A) cassettes (middle), and predicted mutant allele generated by homologous recombination (bottom) are shown. *A4gnt* inactivation was achieved by replacing genomic DNA sequences harboring exons 2 (E2) and 3 (E3), which correspond to the entire *A4gnt* coding region, with the neomycin-resistance gene. (**B**) Southern blot analysis of the *Bgl*II, *Bst*11071, and *Eco*RI-digested genomic DNA obtained from F6 *A4gnt*$^{+/+}$, *A4gnt*$^{+/-}$, and *A4gnt*$^{-/-}$ mice hybridized with 5'-, 3'-, and neo-probes, respectively, as shown in A.

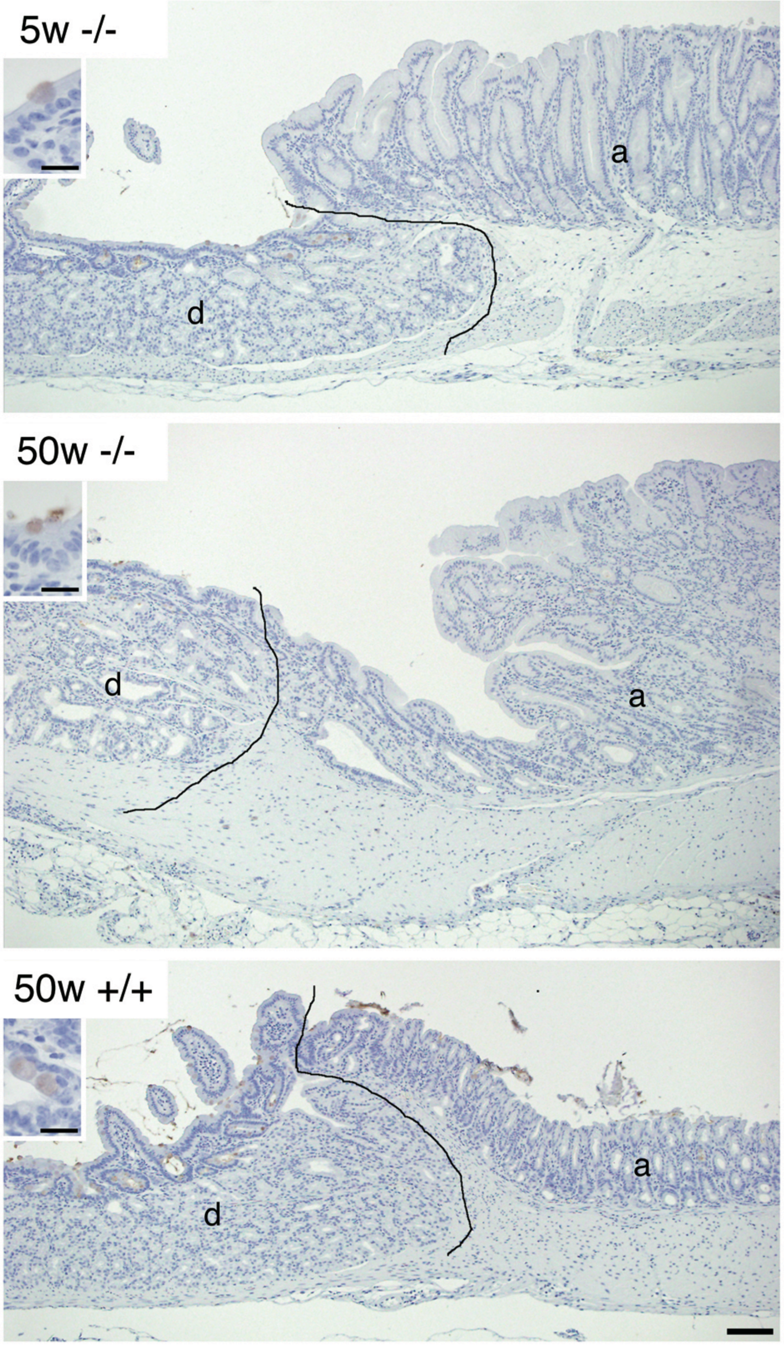


Supplemental Figure 2

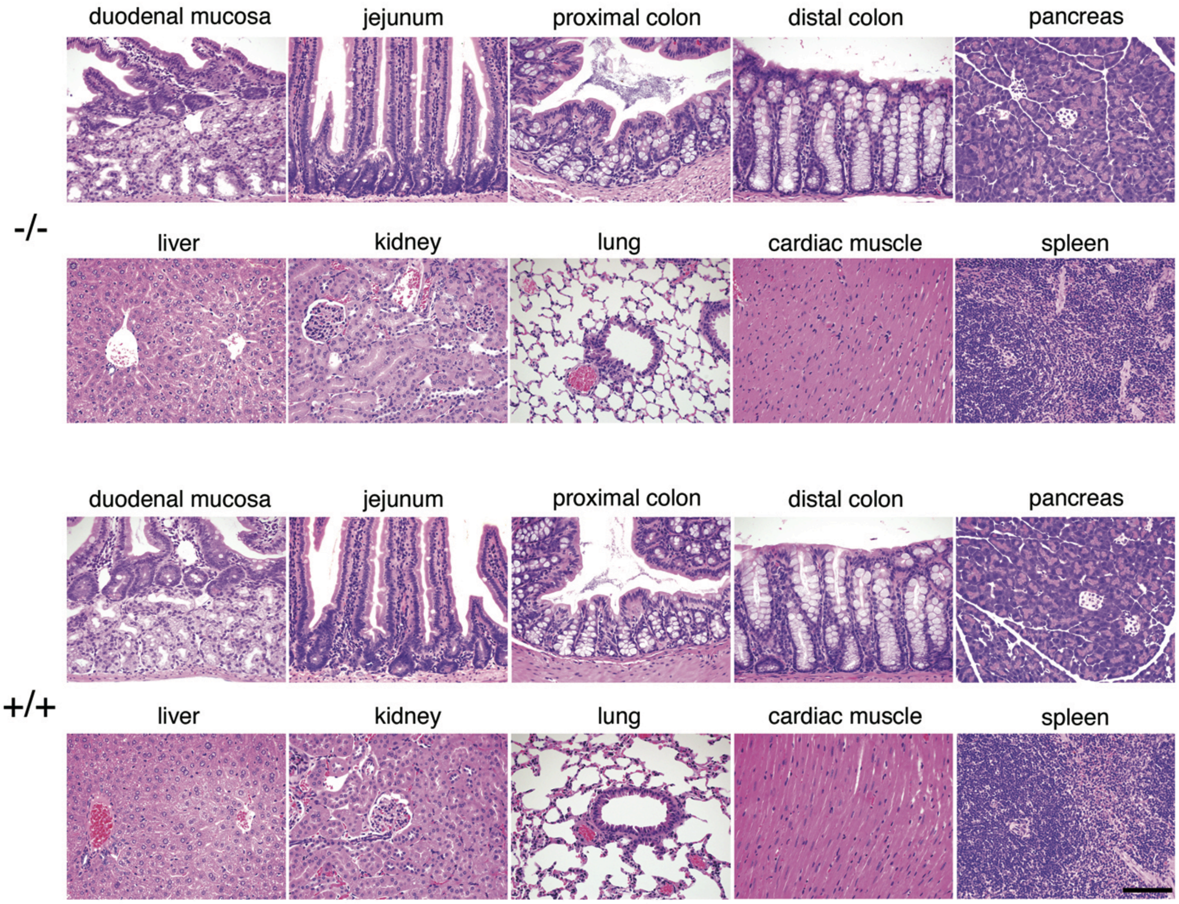
Histology of the fundic mucosa of the gastric corpus during development. (**A**) No significant differences are noted in the histology of 5-week-old (5w) *A4gnt*$^{+/+}$ mice and various ages of *A4gnt*$^{-/-}$ mice. HE staining. Scale bar = 100 µm. (**B**) Comparison of mucosal thickness of the fundic mucosa between *A4gnt*$^{+/+}$ and *A4gnt*$^{-/-}$ mice at different ages. No significant differences are noted between them. Each group consists of 6 mice, and data represent the mean ± SEM.



Supplemental Figure 3
Incidence of gastric pathology seen in *A4gnt*-deficient mice during development. Each group consists of 6 mice in total.

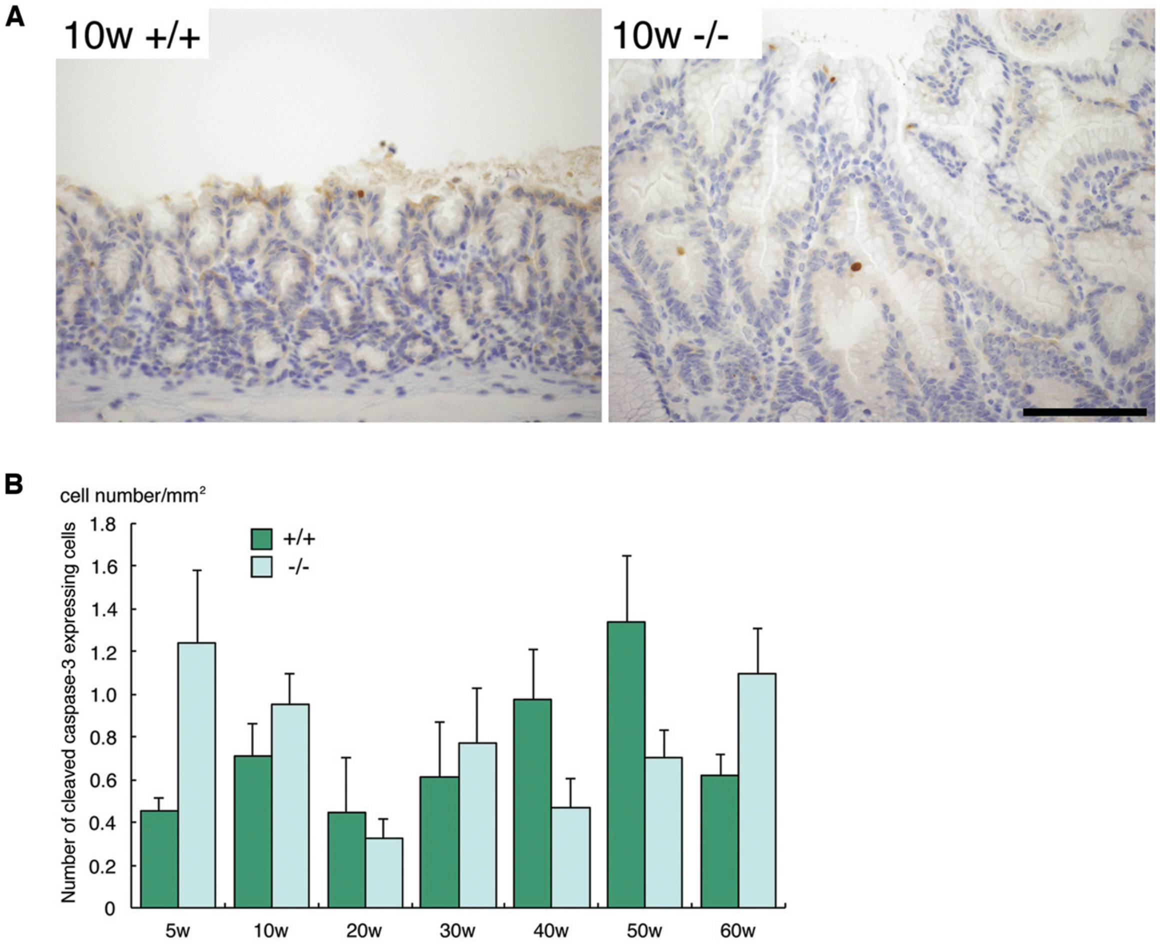


Supplemental Figure 4
Immunohistochemistry for goblet cell-specific MUC2 in the gastro-duodenal mucosa. Line indicates the border between antrum (a) and duodenum (d). Although MUC2 is expressed in goblet cells of the duodenum (inset), neither *A4gnt*$^{-/-}$ nor *A4gnt*$^{+/+}$ mice exhibit goblet cells expressing MUC2 in the gastric mucosa. Immunohistochemistry with the anti-MUC2 antibody. Scale bar = 100 μm (Scale bar in inset = 20 μm).

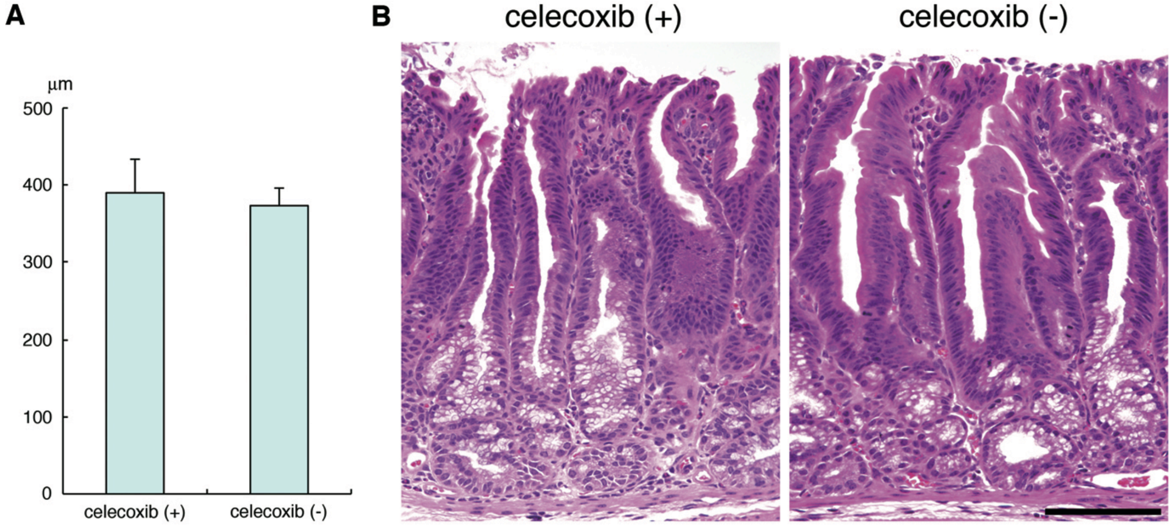


Supplemental Figure 5

Histology of tissues other than stomach of *A4gnt*$^{-/-}$ and *A4gnt*$^{+/+}$ mice. No significant histological differences were noted between *A4gnt*$^{-/-}$ and *A4gnt*$^{+/+}$ mice. HE staining. Scale bar = 100 μm.



Supplemental Figure 6
Immunohistochemistry for pre-apoptotic cells expressing cleaved caspase-3 in the gastric mucosa. (**A**) Expression of cleaved caspase-3 in the gastric mucosa of 10-week-old (10w) *A4gnt*$^{+/+}$ and *A4gnt*$^{-/-}$ mice. Scale bar = 100 μm. (**B**) Comparison of number of cleaved caspase-3-positive cells in the gastric mucosa of *A4gnt*$^{+/+}$ and *A4gnt*$^{-/-}$ mice. No significant differences were noted between genotypes. Each group consists of 6 mice, and data represent the mean ± SEM. Immunohistochemistry with anti-cleaved caspase-3 antibody.



Supplemental Figure 7
No effects of celecoxib treatment on the progression of gastric dysplasia. (**A**) Mucosal thickness of tumorous portion of 10-week-old (10w) *A4gnt*$^{-/-}$ mice treated with celecoxib (celecoxib (+); n = 4) and without celecoxib (celecoxib (-); n = 3). No significant difference was noted between these groups (P = 0.7775). Data represent the mean ± SEM. (**B**) Histology of 10w *A4gnt*$^{-/-}$ mice. Gastric pathology reveals low-grade dysplasia irrespective of celecoxib treatment. HE staining. Scale bar = 100 μm.

Supplemental Table 1
MUC6 and αGlcNAc expression in human differentiated type early gastric adenocarcinoma

Patient no.	Age	Sex	Histology[A]	MUC6[B]	αGlcNAc[B]
1	72	F	pap	1	0
2	78	M	tub	3	0
3	73	M	tub	2	1
4	69	F	tub	1	0
5	84	M	tub	2	0
6	86	M	pap = tub	1	0
7	76	F	tub > pap	3	2
8	83	F	tub	1	0
9	66	M	tub	2	0
10	73	M	tub	0	0
11	77	F	tub	1	0
12	80	F	tub > pap	2	1
13	72	M	tub	1	0
14	72	F	tub	2	0
15	78	F	tub	2	0
16	90	M	tub	3	0
17	87	M	tub	0	0
18	80	F	tub	3	0
19	78	M	tub	3	1
20	73	M	tub	0	0
21	71	F	tub	2	1
22	85	M	tub	1	0
23	68	F	tub	0	0
24	73	F	tub	2	1
25	79	F	tub	3	2
26	82	M	tub	0	0
27	75	M	tub	2	1
28	67	M	tub	3	1
29	79	F	tub	3	0
30	81	F	tub	3	1
31	88	M	tub	2	1

32	77	M	tub	2	1
33	88	F	tub	3	1
34	76	F	tub	1	0
35	70	M	tub	1	2
36	85	F	tub	3	0
37	84	M	pap = tub	3	2
38	52	F	tub	3	3
39	62	M	tub	0	0
40	58	M	tub	2	1
41	78	M	tub	1	0
42	80	M	tub	1	1
43	67	M	pap	3	1
44	73	M	tub > pap	2	0
45	78	M	tub	2	1
46	72	M	tub	2	1
47	85	M	tub	2	1
48	78	F	tub	3	1
49	71	M	tub	1	1
50	85	M	tub	1	1
51	82	M	tub	1	1
52	70	M	tub	2	1
53	86	M	tub	2	1
54	71	F	tub	1	1

[A] pap, papillary adenocarcinoma; tub, tubular adenocarcinoma. [B] Expression level scores for MUC6 and αGlcNAc are the ratio of the number of immunoreactive carcinoma cells to the total number of carcinoma cells examined; negative (0; no positive cells), weak (1; less than one-third of carcinoma cells positive), moderate (2; less than two-thirds of carcinoma cells positive), or strong (3; greater than two-thirds of carcinoma cells positive).

Supplemental Table 2

MUC6 and αGlcNAc expression in human tubular adenoma

Patient no.	Age	Sex	MUC6[A]	αGlcNAc[A]
1	67	M	0	0
2	73	F	0	0
3	74	M	1	0
4	76	M	2	1
5	59	M	1	0
6	87	M	1	0
7	73	M	0	0
8	84	M	0	0
9	79	F	0	0
10	80	F	2	0
11	72	M	0	0
12	71	M	1	1

[A] Expression level scores for MUC6 and αGlcNAc are the ratio of the number of immunoreactive adenoma cells to the total number of adenoma cells examined; negative (0; no positive cells), weak (1; less than one-third of adenoma cells positive), moderate (2; less than two-thirds of adenoma cells positive), or strong (3; greater than two-thirds of adenoma cells positive).

Supplemental Table 3

Genes consistently upregulated in the gastric mucosa of *A4gnt*$^{-/-}$ mice compared with *A4gnt*$^{+/+}$ mice at 5 weeks, 10 weeks, and 50 weeks of age

Probe ID	Fold change [5w -/-]/[5w +/+]	Fold change [10w -/-]/[10w +/+]	Fold change [50w -/-]/[50w +/+]	Gene name or genomic coordinates[A]	Gene symbol
A_51_P339793	108.8554	18.04302	16.828148	interleukin 1 receptor-like 1	*Il1rl1*
A_51_P475748	42.465908	2.7003295	4.0593624	involucrin	*Ivl*
A_55_P2009172	40.32854	8.3914585	2.029321	proline rich Gla (G-carboxyglutamic acid) 1	*Prrg1*
A_55_P2053439	37.32095	2.9804704	4.4126067	involucrin	*Ivl*
A_51_P246166	33.515827	224.96194	13.4086485	extracellular proteinase inhibitor	*Expi*
A_52_P119060	30.864937	13.675353	13.280033	acid phosphatase, prostate	*Acpp*
A_51_P255699	30.52678	7.0349813	101.58765	matrix metallopeptidase 3	*Mmp3*
A_52_P481957	29.328596	5.860716	3.7123177	gremlin 1	*Grem1*
A_51_P363187	26.513502	4.342503	33.988472	chemokine (C-X-C motif) ligand 1	*Cxcl1*
A_51_P254855	26.483452	4.598041	14.97036	prostaglandin-endoperoxide synthase 2	*Ptgs2*
A_51_P120830	24.509007	45.985104	97.81254	matrix metallopeptidase 10	*Mmp10*
A_51_P208603	23.017057	6.268397	6.4395814	deiodinase, iodothyronine, type II	*Dio2*
A_52_P251450	20.962683	8.710728	4.1299257	claudin 2	*Cldn2*
A_51_P239750	19.9938	13.459662	42.481365	inhibin beta-A	*Inhba*
A_51_P375783	19.132261	62.436523	2.7987473	proline-rich acidic protein 1	*Prap1*
A_51_P207591	17.903147	2.6637433	6.2556705	annexin A8	*Anxa8*
A_55_P2105958	16.41052	2.26625	3.5621502	transient receptor potential cation channel, subfamily A, member 1	*Trpa1*
A_55_P2014555	16.037077	2.9448986	2.243025	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	*Lrp8*
A_51_P354126	15.572688	11.971171	56.858353	regenerating islet-derived 3 gamma	*Reg3g*
A_55_P1985850	14.7717905	2.1635928	3.2635214	tissue inhibitor of metalloproteinase 1	*Timp1*
A_52_P474152	13.959233	7.994658	5.0199714	one cut domain, family member 3	*Onecut3*
A_66_P106231	13.779977	7.000856	4.5840807	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	*Nccrp1*
A_51_P346938	13.761934	5.329399	11.975477	leucine-rich alpha-2-glycoprotein 1	*Lrg1*
A_55_P1988310	13.212998	21.981241	23.338263	ring finger protein 183	*Rnf183*
A_51_P468260	13.034508	9.364333	4.3005533	S100 protein, beta polypeptide, neural	*S100b*
A_51_P213099	12.358411	80.22766	28.152596	netrin G1	*Ntng1*
A_51_P286737	10.460151	3.6093533	8.422346	chemokine (C-C motif) ligand 2	*Ccl2*
A_55_P2062469	10.458267	2.6583183	3.3134046	collagen, type XII, alpha 1	*Col12a1*
A_55_P2059352	10.311763	2.7662852	4.473892	collagen, type XVIII, alpha 1	*Col18a1*
A_55_P2394308	10.056791	6.101755	59.28317	follistatin	*Fst*
A_52_P496956	9.788273	2.5936964	3.468764	acyl-CoA synthetase bubblegum family member 1	*Acsbg1*
A_55_P2000022	9.496661	6.277022	5.8845143	coiled-coil domain containing 151	*Ccdc151*

A_51_P267783	9.238376	2.8356814	21.00276	interleukin 11	*Il11*
A_51_P488196	9.175155	3.2968907	7.0126553	BMP-binding endothelial regulator	*Bmper*
A_52_P302433	9.14549	4.185033	3.6948094	plasminogen activator, urokinase	*Plau*
A_55_P2037977	9.128626	18.893513	7.4017334	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase, transferase B, alpha 1-3-galactosyltransferase)	*Abo*
A_55_P1978424	8.869025	2.0779033	3.7303872	B-cell leukemia/lymphoma 2 related protein A1d	*Bcl2a1d*
A_51_P484998	8.690184	5.990187	4.1379337	hepatocyte growth factor	*Hgf*
A_55_P2153762	8.576415	16.8689	7.425774	similar to Probable G-protein coupled receptor 110 precursor (G-protein coupled receptor PGR19)	*LOC640020*
A_55_P2124791	8.411672	2.6572852	3.8849788	collagen, type XVIII, alpha 1	*Col18a1*
A_51_P212782	7.9394307	2.135097	16.729721	interleukin 1 beta	*Il1b*
A_66_P122511	7.892535	11.403562	4.2317014	claudin 2	*Cldn2*
A_55_P1985433	7.8159003	4.3436084	5.5367303	neuregulin 1	*Nrg1*
A_51_P220343	7.807517	4.6231084	18.598877	WNT1 inducible signaling pathway protein 1	*Wisp1*
A_55_P1994194	7.5779834	4.565096	3.5150826	hephaestin	*Heph*
A_55_P2127179	7.5672035	13.685784	6.5855985	predicted gene 379	*Gm379*
A_55_P2079890	7.560748	2.20925	3.4260042	hypothetical protein LOC100044438	*LOC100044438*
A_52_P208521	7.49035	2.0367372	12.2553215	KH domain containing 1A	*Khdc1a*
A_51_P501844	6.926439	4.860692	3.8652124	cytochrome P450, family 26, subfamily b, polypeptide 1	*Cyp26b1*
A_52_P462657	6.838056	2.257277	5.548313	predicted gene 11545	*Gm11545*
A_51_P317031	6.7934837	3.9847658	3.7042112	coiled-coil domain containing 109B	*Ccdc109b*
A_55_P1990032	6.5348234	46.776062	72.16895	chemokine (C-X-C motif) ligand 5	*Cxcl5*
A_51_P438967	6.5066147	2.0625668	2.7900038	glycoprotein (transmembrane) nmb	*Gpnmb*
A_55_P2139019	6.332895	16.865944	3.5988076	chr4:119544729-119544788	
A_52_P161488	6.3190765	6.3812017	2.56603	C-type lectin domain family 4, member e	*Clec4e*
A_55_P2119969	6.2877526	5.5085287	5.231002	3-hydroxybutyrate dehydrogenase, type 2	*Bdh2*
A_55_P2349148	6.198005	5.660662	3.1074162	RIKEN cDNA 5830408B19 gene	*5830408B19 Rik*
A_52_P610987	6.137662	9.588543	3.324493	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	*Slc28a3*
A_51_P246653	6.113484	5.684571	8.0474415	C-type lectin domain family 7, member a	*Clec7a*
A_52_P187058	5.9484944	15.310313	2.8630395	neuronal pentraxin 2	*Nptx2*
A_52_P355169	5.8783603	2.247188	2.0971909	tenascin C	*Tnc*
A_55_P2019312	5.714482	7.0456853	3.5244591	carbonic anyhydrase 12	*Car12*
A_52_P151320	5.468907	4.185318	2.1383593	tumor necrosis factor, alpha-induced protein 8-like 1	*Tnfaip8l1*
A_51_P184484	5.45247	24.133825	54.36819	matrix metallopeptidase 13	*Mmp13*
A_51_P436652	5.422487	4.713999	6.310615	chemokine (C-C motif) ligand 7	*Ccl7*

A_66_P124179	5.3965354	2.920844	3.3299441	ATPase, H+ transporting, lysosomal V0 subunit D2	*Atp6v0d2*
A_51_P209183	5.3218703	2.1891258	3.0951712	chemokine (C-X-C motif) ligand 14	*Cxcl14*
A_55_P1968703	5.3012743	3.9493718	4.595417	glial cell line derived neurotrophic factor family receptor alpha 2	*Gfra2*
A_51_P419017	5.279587	3.3315887	4.07505	phosphodiesterase 10A	*Pde10a*
A_55_P1966862	5.2114367	6.832302	4.17279	protease, serine, 32	*Prss32*
A_55_P2041626	5.050223	8.95535	36.848663	carcinoembryonic antigen-related cell adhesion molecule 12	*Ceacam12*
A_51_P477682	4.9791613	4.596769	7.0353303	protease, serine, 12 neurotrypsin (motopsin)	*Prss12*
A_55_P2089233	4.900603	2.8594043	2.3204653	POU domain, class 2, associating factor 1	*Pou2af1*
A_52_P71686	4.898313	2.311828	3.4059558	ATPase, H+ transporting, lysosomal V0 subunit D2	*Atp6v0d2*
A_51_P312949	4.7913914	3.9421246	4.842753	tudor domain containing 12	*Tdrd12*
A_55_P2176145	4.776694	5.6309977	5.1584144	regulator of G-protein signaling 17	*Rgs17*
A_51_P111962	4.7729506	5.507646	5.4402704	brain expressed, associated with Nedd4	*mCG_21548*
A_51_P239737	4.721524	6.1587243	10.505018	polymeric immunoglobulin receptor	*Pigr*
A_55_P2108708	4.6978116	6.560133	3.6777716	potassium voltage-gated channel, Isk-related subfamily, gene 3	*Kcne3*
A_52_P381484	4.6270585	6.1649585	2.0763702	spondin 2, extracellular matrix protein	*Spon2*
A_66_P103229	4.596269	3.2895327	6.692847	forkhead box L1	*Foxl1*
A_55_P2163363	4.540224	9.920428	16.565998	C-type lectin domain family 2, member f	*Clec2f*
A_51_P268094	4.494428	4.8701158	3.617337	serine (or cysteine) peptidase inhibitor, clade E, member 2	*Serpine2*
A_55_P2095227	4.4232764	4.0505543	5.0472045	chr14:043798829-043798770	
A_51_P496720	4.3868775	5.2041774	2.0234892	DNA (cytosine-5-)-methyltransferase 3-like	*Dnmt3l*
A_66_P121976	4.370485	2.4876237	4.000378	solute carrier family 4, sodium bicarbonate transporter-like, member 11	*Slc4a11*
A_55_P2054315	4.350561	3.5078752	3.3419127	mast cell protease 2	*Mcpt2*
A_51_P336599	4.293927	7.3603244	3.4545023	potassium voltage-gated channel, Isk-related subfamily, gene 3	*Kcne3*
A_55_P2166486	4.292551	3.7719646	3.8657656	CD44 antigen	*Cd44*
A_52_P198898	4.2850637	5.7176557	2.826035	sterile alpha motif domain containing 5	*Samd5*
A_51_P288876	4.223978	4.6658635	3.131205	transmembrane protein 45a	*Tmem45a*
A_55_P2386236	4.168029	5.335945	6.2207265	carcinoembryonic antigen-related cell adhesion molecule 2	*Ceacam2*
A_66_P101724	4.157834	8.039657	5.600809	family with sequence similarity 124, member A	*Fam124a*
A_51_P204387	4.1206203	10.683636	4.2765713	transmembrane protein 63c	*Tmem63c*
A_55_P2082478	4.111748	4.5594473	2.243395	kinase D-interacting substrate 220	*Kidins220*
A_55_P2035932	4.0948243	7.1590276	2.7109919	fibroblast growth factor 7	*Fgf7*
A_55_P1952482	4.0767393	3.1532423	5.6134872	phosphatidylethanolamine binding protein 2	*Pbp2*
A_52_P476754	4.0595326	2.2905612	2.3995874	ubiquitin associated and SH3 domain containing, B	*Ubash3b*
A_52_P316474	4.010735	2.4362147	3.1057703	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	*St3gal4*
A_52_P460791	4.0006876	13.70317	8.451858	pancreatic polypeptide	*Ppy*

A_55_P2181464	3.9850924	3.6126964	3.6458092	chr14:56570528-56570469	
A_51_P125205	3.9665678	5.227955	3.1071799	aquaporin 1	*Aqp1*
A_52_P408025	3.9636962	4.2313223	2.048672	metallophosphoesterase domain containing 2	*Mpped2*
A_65_P01991	3.957407	2.2752674	3.2982357	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	*Prrg4*
A_51_P145132	3.9269564	2.058158	4.1684422	mast cell protease 4	*Mcpt4*
A_51_P464918	3.9209697	2.8023138	8.604254	Mediterranean fever	*Mefv*
A_55_P1971006	3.9209023	2.5317929	2.1410706	RIKEN cDNA 1190003J15 gene	*1190003J15 Rik*
A_55_P2057459	3.8836694	2.897407	2.9825723	mal, T-cell differentiation protein-like	*Mall*
A_51_P267700	3.8495371	4.668702	2.776761	gastrokine 3	*Gkn3*
A_51_P391805	3.845084	4.337127	2.7730143	dickkopf-like 1	*Dkkl1*
A_55_P2174582	3.826994	2.4580333	2.2587337	RIKEN cDNA 1190003J15 gene	*1190003J15 Rik*
A_55_P2185905	3.8200583	4.808805	9.85464	neuregulin 4	*Nrg4*
A_55_P2166501	3.8193817	6.106036	3.2531419	CD44 antigen	*Cd44*
A_51_P401501	3.7798593	9.102471	2.3136976	transmembrane protein 213	*Tmem213*
A_55_P2079560	3.6982658	3.686958	3.709846	paired-Ig-like receptor A3	*Pira3*
A_55_P1992572	3.6585865	4.7233405	3.2152956	bruno-like 4, RNA binding protein (Drosophila)	*Brunol4*
A_51_P252988	3.6501944	11.46058	7.1729236	intestine specific homeobox	*Isx*
A_55_P2037439	3.5694456	7.99447	2.9788554	DEP domain containing 1a	*Depdc1a*
A_51_P289392	3.568981	17.242565	5.0611615	NLR family, apoptosis inhibitory protein 1	*Naip1*
A_52_P386459	3.5045156	3.0840619	2.0481424	glycoprotein A33 (transmembrane)	*Gpa33*
A_55_P1983448	3.4974456	4.435087	2.7339725	S100 calcium binding protein A4	*S100a4*
A_55_P2144686	3.4936757	2.582149	4.8858175	deleted in malignant brain tumors 1	*Dmbt1*
A_52_P228236	3.4390159	2.2343917	3.82967	transferrin receptor	*Tfrc*
A_52_P585124	3.3824632	2.8814185	2.6539087	chemokine (C-X-C motif) receptor 4	*Cxcr4*
A_55_P2064043	3.3824599	4.154347	2.8989933	CD44 antigen	*Cd44*
A_51_P264769	3.3446188	17.77986	6.2861633	dentin matrix protein 1	*Dmp1*
A_55_P2077558	3.3421125	6.2950892	4.275178	superoxide dismutase 3, extracellular	*Sod3*
A_55_P2369191	3.293447	4.3249965	2.0421772	glycoprotein galactosyltransferase alpha 1, 3	*Ggta1*
A_66_P112551	3.2876196	15.1415415	7.717762	Src homology 2 domain containing F	*Shf*
A_51_P358787	3.2540321	4.886076	4.044832	olfactory receptor 48	*Olfr48*
A_55_P1970002	3.2463524	3.5412362	2.5621436	SH3-domain kinase binding protein 1	*Sh3kbp1*
A_55_P2069659	3.2303798	3.1532245	6.123646	RIKEN cDNA 9930013L23 gene	*9930013L23 Rik*
A_55_P2158653	3.2168972	4.235065	4.8055034	claudin 7	*Cldn7*
A_55_P1971951	3.1767805	4.667318	3.0802853	CD86 antigen	*Cd86*
A_51_P129464	3.1537979	5.249488	2.767066	stearoyl-Coenzyme A desaturase 2	*Scd2*

A_55_P2078365	3.121197	2.466859	2.643214	regulator of G-protein signaling 12	*Rgs12*
A_51_P446510	3.1031723	2.5701034	2.5334747	epithelial membrane protein 3	*Emp3*
A_55_P1988804	3.0937076	2.2888525	2.7037616	stomatin	*Stom*
A_55_P2092492	3.0768726	2.6273503	2.8973563	interleukin 18 receptor 1	*Il18r1*
A_55_P2017055	3.0692751	4.1533074	2.246626	potassium channel tetramerisation domain containing 12b	*Kctd12b*
A_55_P1983450	3.0618775	4.2305813	2.6725416	S100 calcium binding protein A4	*S100a4*
A_55_P2027737	3.0311253	3.5311415	3.4829314	interleukin 1 receptor-like 1	*Il1rl1*
A_51_P471791	3.0265265	2.9473836	2.0667272	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	*St8sia6*
A_55_P2117908	3.0211344	2.0594747	3.7714398	paired box gene 9	*Pax9*
A_66_P121053	2.9964995	2.232679	4.2295704	surfactant associated protein D	*Sftpd*
A_55_P2166488	2.9780235	6.545356	3.54756	CD44 antigen	*Cd44*
A_55_P2364768	2.9646604	2.2120132	3.1314359	mast cell protease, pseudogene 1	*Mcpt-ps1*
A_51_P101545	2.9527602	3.9909146	2.0535977	hepatocyte growth factor activator	*Hgfac*
A_55_P2111218	2.941948	10.474875	3.9793353	RIKEN cDNA 2310014H01 gene	*2310014H01 Rik*
A_55_P1959994	2.9234412	5.5276318	2.4088967	unc-5 homolog C (C. elegans)-like	*Unc5cl*
A_55_P1978216	2.910876	4.5108953	2.2254353	cDNA sequence AF251705	*AF251705*
A_55_P2085295	2.88163	2.65375	2.3444228	inverted formin, FH2 and WH2 domain containing	*Inf2*
A_52_P266132	2.8599234	2.8816583	2.2306962	fibrinogen-like protein 2	*Fgl2*
A_55_P2337074	2.8595603	8.930329	2.9344509	midline 1	*Mid1*
A_55_P2022287	2.8459647	3.1028605	2.75086	predicted gene 4693	*Gm4693*
A_51_P240614	2.8409855	2.1617136	2.9291058	transmembrane 4 superfamily member 1	*Tm4sf1*
A_52_P501816	2.8174417	3.2105157	7.0517917	solute carrier family 6 (neurotransmitter transporter), member 14	*Slc6a14*
A_52_P203948	2.8114343	7.3436375	9.218744	phospholipase A2, group IVE	*Pla2g4e*
A_52_P485850	2.800016	3.339669	2.9672072	maltase-glucoamylase	*Mgam*
A_51_P303424	2.7785494	3.2667406	2.273328	integrin alpha X	*Itgax*
A_55_P2005984	2.7359178	3.2365742	2.4174685	WAP four-disulfide core domain 15B	*Wfdc15b*
A_51_P312485	2.7317064	2.3871047	2.918276	formyl peptide receptor 1	*Fpr1*
A_55_P2070869	2.7129881	4.181558	8.699078	lipocalin 2	*Lcn2*
A_52_P329398	2.7030253	3.9665887	2.7412999	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	*Atp12a*
A_51_P187602	2.6953032	2.0242739	2.0282025	serine (or cysteine) peptidase inhibitor, clade B, member 5	*Serpinb5*
A_51_P261059	2.6860943	3.1090405	2.2886927	copine II	*Cpne2*
A_52_P467449	2.6685538	3.3605375	2.06748	arachidonate 12-lipoxygenase	*Alox12*
A_51_P490840	2.667767	16.902212	3.7275808	tripartite motif-containing 31	*Trim31*
A_65_P06446	2.6665523	2.5861025	3.373188	transferrin receptor	*Tfrc*
A_55_P2011425	2.6331496	2.5839086	2.3581674	ATPase, class V, type 10B	*Atp10b*

A_52_P278295	2.632551	2.21701	3.7787876	platelet endothelial aggregation receptor 1	*Pear1*
A_52_P110534	2.626383	5.0125523	2.895079	Ttk protein kinase	*Ttk*
A_55_P2111907	2.6220186	4.5825458	3.3802874	NADPH oxidase organizer 1	*Noxo1*
A_55_P2185900	2.6180248	3.825303	4.3170233	neuregulin 4	*Nrg4*
A_51_P505617	2.6118107	3.3851755	3.6509485	interleukin 18 receptor 1	*Il18r1*
A_52_P366462	2.5964735	3.6361988	2.1524127	peptide YY	*Pyy*
A_55_P2313971	2.5913818	2.592582	3.8155599	RIKEN cDNA 4930509E22 gene	*4930509E22 Rik*
A_55_P1957245	2.5304317	5.507398	5.217737	vomeronasal 2, receptor, pseudogene 134	*Vmn2r-ps134*
A_55_P2185794	2.5248103	3.181739	2.5704246	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	*Sirt6*
A_55_P1972099	2.510589	2.0184162	2.0148268	chr7:126930954-126931013	
A_66_P114333	2.497173	3.1980631	3.286152	toll-like receptor 12	*Tlr12*
A_55_P2068615	2.494084	5.3099775	2.0158947	predicted gene 1006	*Gm1006*
A_55_P2083297	2.4849243	2.8746436	4.2097116	Riken cDNA E230025N22 gene	*E230025N22 Rik*
A_55_P1989341	2.4759192	14.224058	8.006616	netrin G1	*Ntng1*
A_55_P2025687	2.4669096	4.954653	4.0731635	mucin 4	*Muc4*
A_55_P2076545	2.4556208	6.400982	4.159909	coagulation factor V	*F5*
A_55_P2081488	2.454901	6.3133316	3.7940142	peptidoglycan recognition protein 1	*Pglyrp1*
A_55_P2139077	2.4532204	4.9283476	2.3219576	family with sequence similarity 38, member B2	*Fam38b*
A_52_P637812	2.4437745	2.9834232	2.910139	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	*Prrg4*
A_52_P322141	2.4083807	2.6394145	2.348732	coiled-coil domain containing 88B	*Ccdc88b*
A_55_P1959521	2.3907259	3.966147	2.2136002	ets variant gene 4 (E1A enhancer binding protein, E1AF)	*Etv4*
A_55_P1990944	2.3745153	3.053328	4.2150455	caspase 1	*Casp1*
A_51_P509573	2.371454	2.2198088	2.6153333	chemokine (C-C motif) ligand 4	*Ccl4*
A_55_P1998578	2.3577201	2.3662388	2.0346575	interferon induced transmembrane protein 2	*Ifitm2*
A_51_P473498	2.3412426	5.9529824	2.5165498	G protein-coupled receptor 171	*Gpr171*
A_51_P294555	2.3232417	3.043258	3.7776625	interferon induced transmembrane protein 6	*Ifitm6*
A_52_P31510	2.2965605	4.175164	2.0107043	pancreatic and duodenal homeobox 1	*Pdx1*
A_51_P100537	2.296123	17.093004	6.2900953	cDNA sequence BC048599	*BC048599*
A_51_P159612	2.2891905	3.5301192	2.136038	heme binding protein 2	*Hebp2*
A_55_P1963920	2.2767463	3.5175803	3.3469288	RIKEN cDNA A430084P05 gene	*A430084P05 Rik*
A_51_P429335	2.2389476	3.3460639	2.7172966	protease, serine, 16 (thymus)	*Prss16*
A_51_P169671	2.2337706	63.43168	98.43204	regenerating islet-derived 3 beta	*Reg3b*
A_52_P502141	2.2255259	5.8179665	2.7660913	HECT domain containing 2	*Hectd2*
A_51_P212754	2.2228146	2.2439601	2.4901123	transforming growth factor, beta induced	*Tgfbi*
A_55_P1953400	2.2166774	7.907907	5.275395	ataxin 2 binding protein 1	*A2bp1*

A_55_P2173897	2.1921813	2.914203	7.2524743	phospholipase A2, group IID	*Pla2g2d*
A_55_P1975843	2.1623304	2.5292454	2.1713586	chrX:057679316-057679257	
A_51_P240421	2.1611543	4.864115	3.6678696	protocadherin beta 14	*Pcdhb14*
A_51_P167876	2.1594157	2.4465506	3.3625531	transferrin receptor	*Tfrc*
A_55_P2197338	2.1565514	3.267395	6.1630573	RIKEN cDNA 2010012P19 gene	*2010012P19Rik*
A_55_P2058528	2.1490283	3.9474115	5.138741	similar to Dr1 associated protein 1 (negative cofactor 2 alpha)	*LOC100045300*
A_52_P467389	2.1472034	2.9539373	3.0057373	solute carrier family 15, member 3	*Slc15a3*
A_51_P490337	2.1471944	9.338635	8.078616	transmembrane protein 190	*Tmem190*
A_52_P232813	2.1465344	4.85657	5.307726	chemokine (C-X-C motif) ligand 3	*Cxcl3*
A_65_P20641	2.1336348	4.02687	2.6628718	fatty acid desaturase 2	*Fads2*
A_51_P331288	2.1125202	15.8518305	17.780107	aldo-keto reductase family 1, member B7	*Akr1b7*
A_55_P2066778	2.0903127	2.041478	2.3805723	cDNA sequence AB124611	*AB124611*
A_55_P2046145	2.0812714	3.1065896	3.8064227	chr7:3813627-3813568	
A_51_P503822	2.0773177	13.119052	3.5860493	SLIT and NTRK-like family, member 6	*Slitrk6*
A_51_P441983	2.0650797	2.7857642	3.6149478	integrin alpha 2	*Itga2*
A_55_P1977850	2.0411682	4.9109006	3.985552	sal-like 1 (Drosophila)	*Sall1*
A_66_P106711	2.0321755	2.3555143	2.2794216	hedgehog interacting protein-like 1	*Hhipl1*

[A] Gene name or genomic coordinates are listed in descending order based on fold-change seen in 5-week-old mice.

Supplemental Table 4

Genes consistently down-regulated in the gastric mucosa of *A4gnt*$^{-/-}$ mice compared with *A4gnt*$^{+/+}$ mice at 5 weeks, 10 weeks, and 50 weeks of age

Probe ID	Fold change [5w -/-]/[5w +/+]	Fold change [10w -/-]/[10w +/+]	Fold change [50w -/-]/[50w +/+]	Gene name or genomic coordinates[A]	Gene symbol
A_52_P175634	69.617905	98.89128	170.88913	alpha-1,4-N-acetylglucosaminyltransferase	*A4gnt*
A_55_P1978885	18.664349	2.1616502	6.0932345	chr9:30750774-30750715	
A_55_P2019719	9.747809	13.8596325	5.058765	2'-5' oligoadenylate synthetase 2	*Oas2*
A_52_P240693	9.026816	2.984889	2.378706	aquaporin 12	*Aqp12*
A_51_P514449	8.831314	7.326146	4.374258	nuclear receptor subfamily 5, group A, member 2	*Nr5a2*
A_55_P1985960	8.283492	6.5468574	2.503002	spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1	*Speer1-ps1*
A_55_P1957198	8.14184	2.9518137	2.3740773	apolipoprotein B	*Apob*
A_52_P88529	7.799619	3.409648	2.081292	acid phosphatase-like 2	*Acpl2*
A_52_P441070	7.4608555	4.034466	2.4300113	apolipoprotein B	*Apob*
A_66_P128537	7.139144	5.885388	4.0252967	ISG15 ubiquitin-like modifier	*Isg15*
A_55_P2127433	6.7204776	3.0474904	3.2951117	tetraspan transmembrane protein, hair cell stereocilia	*Tmhs*
A_66_P106744	6.664032	9.199876	2.4834619	RIKEN cDNA 1700007E06 gene	*1700007E06Rik*
A_51_P447785	6.3458247	2.5110967	2.783086	cytochrome P450, family 2, subfamily c, polypeptide 55	*Cyp2c55*
A_55_P2082090	6.294879	2.6498988	3.510153	similar to laminin alpha 2 subunit precursor	*LOC631028*
A_55_P2044182	6.0641465	2.2043746	2.251651	predicted gene 572	*Gm572*
A_55_P2025944	5.8376384	6.009999	10.461195	hypothetical protein LOC100045186	*LOC100045186*
A_55_P2403325	5.830722	2.1799862	2.0665605	expressed sequence AI451458	*AI451458*
A_55_P1998115	5.769141	2.8360302	2.7915175	kallikrein B, plasma 1	*Klkb1*
A_55_P1967473	5.5221076	3.0430677	4.570679	EF hand calcium binding domain 1	*Efcab1*
A_55_P2115151	5.515672	4.5728793	4.0880833	acid phosphatase-like 2	*Acpl2*
A_66_P101942	5.392884	5.5256896	2.0881562	predicted gene 9706	*Gm9706*
A_55_P2155843	5.2206025	4.8609185	2.7526891	hypothetical protein LOC100041609	*LOC100041609*
A_55_P2243768	5.2167907	3.2432015	2.0870972	RIKEN cDNA D930030O05 gene	*D930030O05Rik*
A_51_P433789	5.0760846	5.0360947	2.1547031	anterior gradient homolog 3 (Xenopus laevis)	*Agr3*
A_52_P836852	5.052278	2.8413472	2.3573632	TXK tyrosine kinase	*Txk*
A_55_P2143494	5.015658	3.2440453	3.3350582	double C2, beta	*Doc2b*
A_55_P2062953	4.890367	4.3170834	2.5092907	anti-Mullerian hormone	*Amh*
A_52_P654534	4.8405495	4.3008857	5.969204	diencephalon/mesencephalon homeobox 1	*Dmbx1*
A_55_P1962219	4.8380384	3.0374596	4.521354	proline rich membrane anchor 1	*Prima1*
A_51_P418901	4.723558	3.0337803	12.857501	protease, serine, 2	*Prss2*
A_52_P108243	4.7114396	2.8639	4.0403724	phosphodiesterase 1C	*Pde1c*
A_66_P110633	4.699315	5.0265145	2.3343248	apolipoprotein L 9b	*Apol9b*

A_55_P1969977	4.6960034	3.0002713	7.346167	myosin XV	*Myo15*
A_55_P2283119	4.688037	2.4706745	2.205564	RIKEN cDNA A530020G20 gene	*A530020G20Rik*
A_51_P436491	4.4726896	2.104184	7.401797	leucine rich repeat and Ig domain containing 3	*Lingo3*
A_51_P242687	4.46968	2.9618895	2.2049327	otogelin	*Otog*
A_55_P1972763	4.285157	4.617988	2.654592	chr4:107569273-107569332	
A_55_P2075258	4.171309	3.3212957	3.1422641	chr5:24615868-24615927	
A_55_P2013554	4.0805154	3.2629929	10.255578	protease, serine, 1 (trypsin 1)	*Prss1*
A_52_P352735	4.062547	4.0145	2.8621237	coiled-coil domain containing 153	*Ccdc153*
A_52_P38627	4.0518184	4.3469377	6.158944	epidermal growth factor	*Egf*
A_55_P1966690	3.9891486	78.15409	10.850478	cytochrome P450, family 2, subfamily e, polypeptide 1	*Cyp2e1*
A_55_P2021423	3.973877	2.5033784	2.5965593	MORN repeat containing 3	*Morn3*
A_55_P1994144	3.932609	3.281036	3.406708	coiled-coil domain containing 154	*Ccdc154*
A_55_P2261188	3.9076505	2.5001767	2.5324566	expressed sequence AI661323	*AI661323*
A_52_P341598	3.738973	2.552005	2.278523	serine/threonine kinase 32B	*Stk32b*
A_55_P1978755	3.725242	3.540286	5.433422	zinc finger protein 606	*Zfp606*
A_52_P69194	3.6720798	3.9805193	4.07404	ribosomal modification protein rimK-like family member A	*Rimkla*
A_51_P234140	3.6681678	3.5172093	3.417965	cyclin-dependent kinase-like 1 (CDC2-related kinase)	*Cdkl1*
A_55_P2013555	3.6660914	3.2033186	8.203788	protease, serine, 1 (trypsin 1)	*Prss1*
A_51_P469789	3.6376154	14.00243	3.761718	alanine-glyoxylate aminotransferase	*Agxt*
A_55_P2114953	3.5843215	3.4473462	2.0795186	ubiquitin specific peptidase 18	*Usp18*
A_55_P2393021	3.5811067	2.7071588	2.147271	RIKEN cDNA A430106G13 gene	*A430106G13Rik*
A_52_P48569	3.5648406	19.185186	2.7900665	solute carrier family 38, member 4	*Slc38a4*
A_51_P317882	3.5336435	3.6752658	2.9736605	secreted and transmembrane 1B	*Sectm1b*
A_55_P2102828	3.5287359	3.3468935	3.744284	predicted gene 8620	*Gm8620*
A_55_P2042319	3.4098554	2.6181746	2.2737894	cytochrome P450, family 2, subfamily d, polypeptide 40	*Cyp2d40*
A_55_P1999389	3.385989	9.152632	2.4243402	RIKEN cDNA 1500009C09 gene	*1500009C09Rik*
A_55_P2322620	3.3615596	4.558795	7.94778	chr12:58600733-58600792	
A_52_P404341	3.350763	11.761279	3.2592666	tryptophan 2,3-dioxygenase	*Tdo2*
A_51_P446825	3.329451	3.7323987	2.3646924	RIKEN cDNA 6430573F11 gene	*6430573F11Rik*
A_55_P2269289	3.3155758	2.5966537	2.7866187	diacylglycerol kinase, gamma	*Dgkg*
A_55_P2114903	3.3139644	3.9367263	3.979192	similar to OTTMUSG00000015204 protein	*LOC100043972*
A_55_P2257765	3.3048997	2.173076	2.5381472	predicted gene 7111	*Gm7111*
A_55_P1957043	3.300169	3.2986293	3.4516296	spermatogenesis associated glutamate (E)-rich protein 8, pseudogene 1	*Speer8-ps1*
A_66_P139703	3.2977374	6.3534265	3.2054317	chr4:136855342-136855401	
A_55_P2165999	3.269722	4.1074004	4.099556	metaxin 3	*Mtx3*

A_51_P421876	3.2659795	3.3476624	2.5484295	interferon regulatory factor 7	*Irf7*
A_52_P607683	3.2230508	2.2741983	5.704616	protein phosphatase 1E (PP2C domain containing)	*Ppm1e*
A_55_P2422164	3.1917336	2.5477414	2.4069493	RIKEN cDNA C130093G08 gene	*C130093G08Rik*
A_55_P2304337	3.164833	5.6369863	2.4371796	RIKEN cDNA 5730407M17 gene	*5730407M17Rik*
A_52_P104658	3.154291	9.482327	7.746298	keratin 6A	*Krt6a*
A_51_P295967	3.132349	2.9620657	2.1036165	protein C	*Proc*
A_55_P2403759	3.1272635	2.0325806	2.2592983	RIKEN cDNA 1700092C02 gene	*1700092C02Rik*
A_51_P189082	3.1080735	7.899853	12.762648	aldo-keto reductase family 1, member C6	*Akr1c6*
A_52_P675039	3.0848243	5.517421	2.2018216	forkhead-associated (FHA) phosphopeptide binding domain 1	*Fhad1*
A_55_P2186450	3.0547674	2.144495	2.1411803	chr18:010931562-010931621	
A_55_P2152472	3.0360906	54.365692	451.57474	late cornified envelope 3A	*Lce3a*
A_55_P2101963	3.035331	5.216351	3.311585	chr4:148501451-148501392	
A_51_P277088	2.9902952	2.0000086	3.8357518	insulin-like growth factor binding protein, acid labile subunit	*Igfals*
A_55_P2070185	2.984676	5.8183875	3.3769975	chr16:049923474-049923415	
A_55_P1994862	2.9256082	3.4681036	2.717012	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	*Ddx60*
A_55_P2129999	2.922819	3.045527	3.332797	RIKEN cDNA G630018N14 gene	*G630018N14Rik*
A_55_P2168722	2.9168913	4.92359	3.068197	flavin containing monooxygenase 5	*Fmo5*
A_55_P1969861	2.9040885	5.37535	2.9969127	zeta-chain (TCR) associated protein kinase	*Zap70*
A_55_P1961241	2.9027498	5.8869405	2.1474974	hypothetical protein LOC100046627	*LOC100046627*
A_55_P1974957	2.8989904	5.1364756	6.969068	tenascin R	*Tnr*
A_51_P129360	2.883138	4.502601	2.493957	parathyroid hormone-like peptide	*Pthlh*
A_55_P1954116	2.8704832	4.6483746	5.493418	complement component 8, beta polypeptide	*C8b*
A_51_P115005	2.868447	3.6097386	2.6505487	endothelin 1	*Edn1*
A_51_P130475	2.8578	8.47853	5.915544	wingless-related MMTV integration site 4	*Wnt4*
A_55_P2076448	2.8512852	2.396818	5.580275	family with sequence similarity 70, member A	*Fam70a*
A_55_P2052106	2.8375547	2.9638727	2.1202786	cDNA sequence BC049762	*BC049762*
A_55_P2121682	2.8362813	3.9947944	8.906662	arachidonate 12-lipoxygenase, 12R type	*Alox12b*
A_55_P2038217	2.795665	3.7748418	3.6803858	ATPase type 13A4	*Atp13a4*
A_51_P410681	2.7849512	7.304712	2.857341	Iroquois related homeobox 5 (Drosophila)	*Irx5*
A_55_P2148809	2.7800798	2.328323	2.1126893	zonadhesin	*Zan*
A_66_P101938	2.779378	2.0724459	11.231365	late cornified envelope 1K	*Lce1k*
A_51_P155755	2.7746215	3.0372398	4.2952642	phospholipase D family, member 6	*Pld6*
A_55_P2043367	2.7434816	5.27052	3.6111085	apolipoprotein L 9a	*Apol9a*
A_55_P2041653	2.7412755	6.582833	2.3573625	RIKEN cDNA 1500009C09 gene	*1500009C09Rik*
A_52_P198435	2.6987414	4.07661	3.9634068	RAS, guanyl releasing protein 3	*Rasgrp3*

A_55_P1969201	2.6869857	4.5705433	2.012268	similar to cyclic nucleotide gated channel beta 1	*LOC100045481*
A_51_P187242	2.665125	4.091426	2.4789686	histamine receptor H2	*Hrh2*
A_51_P491667	2.6576226	3.879533	2.6860082	Der1-like domain family, member 3	*Derl3*
A_55_P2059357	2.654743	2.4435637	2.7360046	myosin VIIA	*Myo7a*
A_52_P670188	2.65241	2.7518213	3.801655	4short chain dehydrogenase/reductase family 9C, member 7"	*ENSMUST 00000047134*
A_51_P316951	2.6513083	3.0791056	3.251608	WAS/WASL interacting protein family, member 3	*Wipf3*
A_55_P2170349	2.6437652	2.1888363	17.558805	killer cell lectin-like receptor subfamily A, member 22	*Klra22*
A_51_P385928	2.6404085	2.4638376	2.721335	prominin 2	*Prom2*
A_55_P2152637	2.6360397	2.6853406	3.1794431	zinc finger protein of the cerebellum 4	*Zic4*
A_55_P1963198	2.6334143	5.1004233	2.2784588	chr4:3870130-3870189	
A_55_P2156304	2.629624	3.7813	3.322151	potassium inwardly-rectifying channel, subfamily J, member 16	*Kcnj16*
A_55_P2014540	2.6262608	2.3629048	4.097654	cDNA sequence BC068281	*BC068281*
A_55_P2065424	2.6223407	3.6431062	3.5894835	somatostatin receptor 2	*Sstr2*
A_51_P344461	2.6051419	2.684676	2.9131947	proline-rich transmembrane protein 2	*Prrt2*
A_55_P2036907	2.594594	2.7936947	2.2103353	MYCBP associated protein	*Mycbpap*
A_51_P254262	2.5889359	2.4038446	4.1287766	neurexophilin 3	*Nxph3*
A_55_P2375194	2.5888	2.8058608	2.5205612	RIKEN cDNA 4930513E20 gene	*4930513E20Rik*
A_52_P685999	2.5603049	2.221715	3.28242	methyltransferase like 7B	*Mettl7b*
A_51_P253652	2.5373654	4.413228	3.630743	RIKEN cDNA A830012C17 gene	*A830012C17Rik*
A_55_P2031471	2.5373378	4.4284987	3.54847	RUN and FYVE domain containing 4	*Rufy4*
A_52_P101303	2.537129	2.6999083	2.7981331	potassium inwardly-rectifying channel, subfamily J, member 15	*Kcnj15*
A_51_P344249	2.5251892	2.029561	3.6253493	amyloid beta (A4) precursor protein-binding, family B, member 1	*Apbb1*
A_55_P2000354	2.5106056	5.684259	2.6895401	regulator of G-protein signaling 11	*Rgs11*
A_52_P315423	2.5070715	2.0808964	5.5679073	predicted gene 3224	*Gm3224*
A_55_P2022703	2.4934494	2.8933446	2.6123157	RIKEN cDNA 1700086O06 gene	*1700086O06Rik*
A_55_P2119249	2.472909	2.3778121	2.468948	serine/arginine repetitive matrix 3	*Srrm3*
A_55_P1982533	2.4665916	2.3163536	4.150364	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	*Elovl4*
A_55_P2164469	2.4645364	2.5116844	4.7507024	predicted gene 11744	*Gm11744*
A_51_P109258	2.4625642	2.6944375	2.34968	cystin 1	*Cys1*
A_55_P1961458	2.4484296	3.5656228	2.1107302	spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1	*Speer1-ps1*
A_55_P2185650	2.4125268	5.3709173	3.1772823	hypothetical protein LOC100046774	*LOC100046774*
A_51_P238523	2.4096913	3.3824756	2.677545	shisa homolog 4 (Xenopus laevis)	*Shisa4*
A_51_P136781	2.4054327	2.1353943	5.494059	pancreatic lipase related protein 1	*Pnliprp1*
A_55_P2003596	2.3978195	2.6057258	2.029946	similar to AFG3(ATPase family gene 3)-like 2 (yeast)	*LOC100048880*
A_55_P1959595	2.3927915	3.4866228	2.940619	flavin containing monooxygenase 5	*Fmo5*

A_55_P2419296	2.3781612	4.7202663	2.1296027	RIKEN cDNA 1110006E14 gene	*1110006E14Rik*
A_51_P179480	2.3763509	2.4256299	2.0628242	RIKEN cDNA 4930539E08 gene	*4930539E08Rik*
A_55_P1952156	2.3752978	7.7286925	4.709601	predicted gene 9622	*Gm9622*
A_52_P799815	2.3496342	2.1731822	2.4961112	transmembrane protein 171	*Tmem171*
A_55_P2206496	2.3460329	2.616083	2.7450545	RIKEN cDNA 1810062O18 gene	*1810062O18Rik*
A_55_P2074688	2.342515	2.453441	2.7457414	homeobox C4	*Hoxc4*
A_51_P455997	2.3354275	4.550929	9.721073	maternally expressed 3	*Meg3*
A_55_P1976356	2.3314557	2.1373925	2.0969841	fibroblast growth factor 18	*Fgf18*
A_51_P259631	2.3184867	2.0630133	2.541594	testis-specific serine kinase substrate	*Tsks*
A_55_P2149993	2.315572	2.50327	3.214556	similar to Qtrt1 protein	*LOC100046124*
A_55_P1973906	2.3119156	3.0952754	2.2757118	transformation related protein 53 inducible nuclear protein 1	*Trp53inp1*
A_52_P508991	2.3059425	4.9949026	3.5920908	flavin containing monooxygenase 1	*Fmo1*
A_66_P101935	2.3058693	28.646694	50.540733	keratin 6B	*Krt6b*
A_51_P133422	2.2925918	2.5470982	2.2506332	chr1:43518753-43518812	
A_55_P2412349	2.2911625	5.340483	7.294453	expressed sequence AW111846	*AW111846*
A_51_P185939	2.2841284	3.898303	2.5588186	G protein-coupled estrogen receptor 1	*Gper*
A_55_P2227321	2.283089	2.7101114	3.2823646	protein tyrosine phosphatase, receptor type, D	*Ptprd*
A_55_P2037912	2.2820606	5.7306857	2.2286792	cytochrome P450, family 2, subfamily d, polypeptide 10	*Cyp2d10*
A_51_P194853	2.2796047	2.6522558	2.8009222	SEC14-like 4 (S. cerevisiae)	*Sec14l4*
A_66_P121117	2.2788296	81.131714	10.431781	serine (or cysteine) peptidase inhibitor, clade A, member 1D	*Serpina1d*
A_66_P112495	2.2654095	4.6652994	2.2419913	sodium channel, type IV, beta	*Scn4b*
A_55_P2275054	2.2620988	5.901138	3.772649	nebulin-related anchoring protein	*Nrap*
A_55_P2028680	2.2510238	5.406208	8.008241	sperm acrosome associated 3	*Spaca3*
A_55_P1963639	2.2179623	3.4109757	8.170499	syncollin	*Sycn*
A_51_P260504	2.2125053	2.0994198	3.0926218	Rho guanine nucleotide exchange factor (GEF) 4	*Arhgef4*
A_55_P2075125	2.2080781	4.693621	5.5485773	paired box gene 2	*Pax2*
A_51_P148314	2.2064638	2.5319595	2.0406468	family with sequence similarity 117, memberA	*Fam117a*
A_51_P390476	2.2046223	4.922365	8.692137	hyaluronoglucosaminidase 3	*Hyal3*
A_66_P116461	2.1951613	2.8915532	2.3907282	maestro	*Mro*
A_55_P2104567	2.1857524	2.118808	2.9269962	cancer susceptibility candidate 1	*Casc1*
A_55_P2076683	2.1854591	4.7379303	4.113056	chr3:108158404-108158463	
A_55_P2024416	2.178705	4.86757	2.8066473	G protein-coupled receptor 15	*Gpr15*
A_55_P2099677	2.1724074	5.5716205	27.5292	chr2:69344322-69344263	
A_55_P2105694	2.1705177	6.443371	3.6531854	RIKEN cDNA 2310007L24 gene	*2310007L24Rik*
A_55_P2180459	2.1651673	2.9543808	2.8404186	predicted gene 2740	*Gm2740*

A_55_P2039099	2.1634529	2.945253	2.1826553	zinc finger protein 605	*Zfp605*
A_52_P452667	2.1594257	2.2280958	2.6798513	prominin 2	*Prom2*
A_52_P398279	2.1411946	7.0604043	2.5051935	chrX:53748356-53748415	
A_55_P2033407	2.135424	11.112163	5.908484	maternally expressed 3	*Meg3*
A_55_P2073248	2.132126	2.8057606	2.8210328	solute carrier family 25, member 34	*Slc25a34*
A_55_P2008407	2.1289518	4.630198	2.8287225	protein phosphatase 1, regulatory (inhibitor) subunit 14c	*Ppp1r14c*
A_65_P10673	2.1233299	2.1186254	2.3254058	transmembrane protein 44	*Tmem44*
A_51_P504815	2.117331	6.25683	8.782637	stefin A3	*Stfa3*
A_55_P1980521	2.1159585	2.210358	2.4364064	coiled-coil domain containing 85A	*Ccdc85a*
A_55_P2168271	2.114876	4.7667108	3.507124	chr16:48122244-48122185	
A_55_P1978293	2.106203	2.9561448	2.0413923	MICAL C-terminal like	*Micalcl*
A_55_P2042860	2.1037173	2.884687	6.9709687	predicted gene 5409	*Gm5409*
A_66_P139387	2.095649	6.374597	8.616491	prolactin receptor	*Prlr*
A_55_P2042212	2.0948644	3.679959	3.4489555	family with sequence similarity 161, member A	*Fam161a*
A_51_P143682	2.0849307	3.7732687	2.5342736	zinc finger protein 318	*Zfp318*
A_55_P2078084	2.084257	3.3844528	37.269463	predicted gene 13011	*Gm13011*
A_51_P344552	2.0803668	6.2051096	3.5674796	insulin receptor substrate 4	*Irs4*
A_51_P442097	2.07939	2.127859	2.3077488	solute carrier family 41, member 3	*Slc41a3*
A_52_P432969	2.0779617	4.2566047	5.4205756	protocadherin 19	*Pcdh19*
A_52_P125363	2.0730822	2.4079685	3.5300598	retinol binding protein 2, cellular	*Rbp2*
A_51_P495825	2.0600588	9.326646	2.3692565	apolipoprotein F	*Apof*
A_55_P2179493	2.051778	3.916307	3.2805002	chr17:28313609-28313550	
A_55_P2183955	2.0483713	3.4760737	3.3979096	olfactory receptor 97	*Olfr97*
A_55_P2118794	2.048118	6.4778824	3.9257066	otopetrin 2	*Otop2*
A_55_P2103249	2.0454817	2.8221688	3.693729	chemokine (C-X-C motif) receptor 1	*Cxcr1*
A_52_P600535	2.0445523	3.3074	4.440018	zinc finger protein 39	*Zfp39*
A_51_P347529	2.0407958	5.5650277	4.0199337	NIMA (never in mitosis gene a)-related expressed kinase 5	*Nek5*
A_55_P2332731	2.0395868	2.0348902	2.8822937	RIKEN cDNA D130062J21 gene	*D130062J21Rik*
A_55_P2045911	2.0395539	5.8649383	3.0275378	RIKEN cDNA 4933400C05 gene	*4933400C05Rik*
A_55_P2178698	2.0364943	2.1730466	2.1509092	G protein-coupled receptor, family C, group 5, member D	*Gprc5d*
A_55_P2144716	2.029254	4.191942	3.3680723	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	*Hecw2*
A_55_P1999301	2.02237	127.669716	14.625855	cytochrome P450, family 2, subfamily e, polypeptide 1	*Cyp2e1*
A_51_P483544	2.0139387	2.839082	2.2761354	aminoadipate-semialdehyde synthase	*Aass*
A_55_P2106469	2.0107043	3.3125844	2.602018	chr5:122689502-122689443	
A_66_P110104	2.0089877	5.5174937	4.4077787	myosin XVIIIb	*Myo18b*

A_55_P2117699	2.0078306	16.546917	2.4449282	p21 protein (Cdc42/Rac)-activated kinase 7	*Pak7*
A_55_P2157165	2.0066955	8.428698	6.607814	olfactory receptor 1444	*Olfr1444*

[A] Gene name and genomic coordinates are listed in descending order based on fold-change seen in 5-week-old mice.

Supplemental Table 5

Primers and oligonucleotides used for generation of *A4gnt*-deficient mice

Name	**Sequence**
A4GNT3PRF5	5’-GCACCTTCCAAACTTTCCTCTTA-3’
A4GNT3PRR5	5’-ATGGGTAAAAGACAAAGCCACAT-3’
A4GNT5PRF4	5’-GTGCATCGCTCCCTTAATCTGTG-3’
A4GNT5RRR4	5’-CCAGTCAAACCTGCCCGGGTGCA-3’
A4GNTBIF1	5’-TTCTTTTTCATCTAAATCGGTAAGTGATATCCTTACTCATTTTCGTGCAGAACGACGGCCAGTGTTAACT-3’
A4GNTBIR1	5’-GAATGGGGTAGCCCAGGAAGCATCTACTCTTCCACAGTAGCAACATCTCTGTAAATTCTCTAGGATCGAT-3’
A4GNTCOF1	5’-TCGAGGGTTTGTCCACATGAAGAAGAGAGAAACGGGGAGTTTAAACGCTTGCTCCCTCCTGTGGAAATGGTTTTAGATCA-3’
A4GNTCOR1	5’-CTAGTGATCTAAAACCATTTCCACAGGAGGGAGCAAGCGTTTAAACTCCCCGTTTCTCTCTTCTTCATGTGGACAAACCC-3’
SAC-F	5’-ACGTGTGTCCTGATACCCTAGTGA-3’
SAN-R	5’-TCTCCTAGAGTTAACACTGGCCGT-3’
SAW-R	5’-AGATGATGGGCTGCTCAGGATAGA-3’
LAN-F	5’-TCGCCTTCTTGACGAGTTCTTCTG-3’
LAW-F	5’-GATGACAAGGATGTTACGGGTGTG-3’
LAC-R	5’-AGCACCTATCCCCTAGAGACAATG-3’