Supplementa Data

Supplemental Figure 1. Microarray analysis of gene expression in her-2 induced tumors. *A*. Total RNA was isolated from wild type and GnT-V knockout tumor tissues and used for detection of transcript levels of GnT-V by RT-PCR. T1-3 represents three tumor tissues collected from three different mice with *GnT-V* wild-type and knockout background, respectively. *B*. Heat map of 142 transcripts differentially expressed between wild-type and GnT-V knockout tumors was generated from the microarray data. The red color indicates high expression level, while blue indicates low expression level relative to wild-type. The top four Ingenuity Pathways Analysis (IPA)-picked molecular and cellular functions where altered transcripts involved are indicated on the left bottom. The number in parentheses indicates the number of transcripts in each.

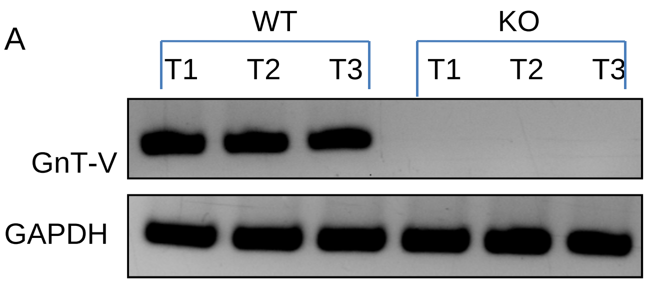
Supplemental Figure 2. qRT-PCR validation of the transcript levels showing largest changes as detected by microarray analysis. *A*, Total RNA was isolated from wild-type and GnT-V knockout tumors and used for detection of transcript levels as indicated. For each transcript, the values are normalized to control (GAPDH or RPL4) and expressed as mean ± SD (n=3). *B*, Fold-change (KO/WT) of gene expression detected by qRT-PCR was calculated.

Supplemental Figure 3. CpG island analysis of the promoter areas of the Pcdhβ gene cluster. The presence of CpG islands was analyzed around TSS sites (-1000 to +1000) in most altered genes of Pcdhβ cluster using the CpGplot program. Ratios of observed to expected CpG dinucleotide frequency were set up > 0.60 (top panel) with percentage of CG > 50% (middle panel) and length >50 bps (bottom panel). TSS: transcription starting site. Cdh1 was chosen as control.

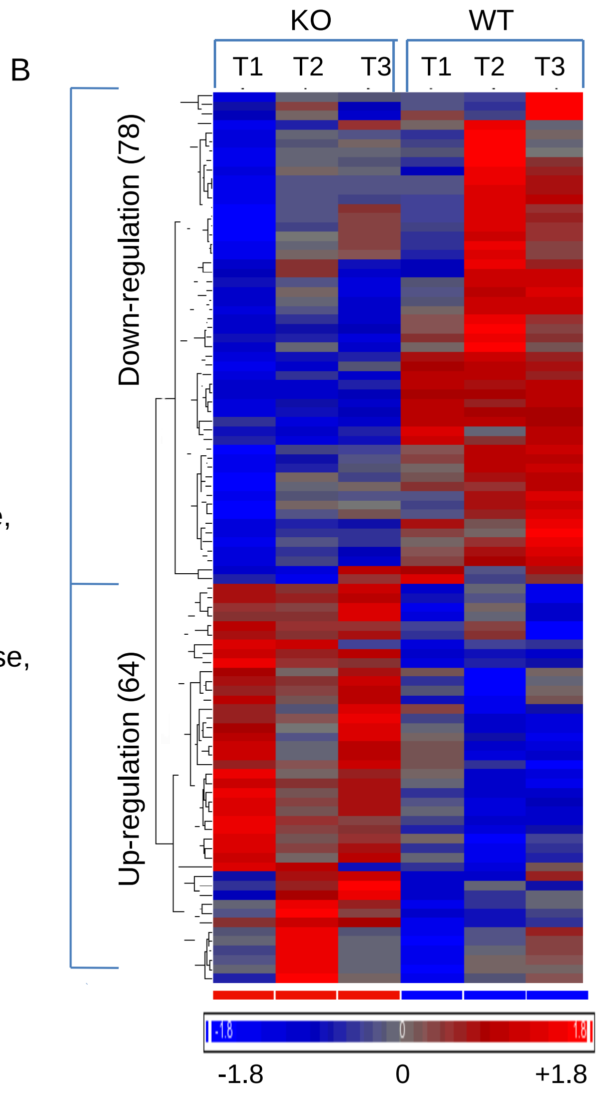
Supplemental Figure 4. Impaired her-2 mediated signaling in GnT-V null tumors. Mammary tumor sections from 10-week old tumor tissues were fixed and immunostained with anti-her-2/neu (top panel) and anti-p-PKB (bottom panel).

Supplemental Figure 5. Confirmation of overexpression of Pcdhβ4 and 19 in her-2 wild-type tumor cells and MDA-MB231 cells. *A*, Total RNA was isolated from control and Pcdhβ4 or 19 transfected tumor cells and used for detection of transcript levels of Pcdhβ 4 (in Pcdhβ4-transfected cells) and Pcdhβ19 (in Pcdhβ19-transfected cells). For each transcript, the values are normalized to control (GAPDH or RPL4) and expressed as mean ± SD (n=3). *B*, MDA-MB231 cells were grown on chamberslides, fixed, and stained for expression of Pcdhβ using anti-c-myc-tag antibody. *C*, Her-2 tumor cells with Pcdhβ4 expression were grown on chamberslides, fixed, and stained with anti-Pcdhβ4 antibody. Nuclei were counterstained by Dapi.

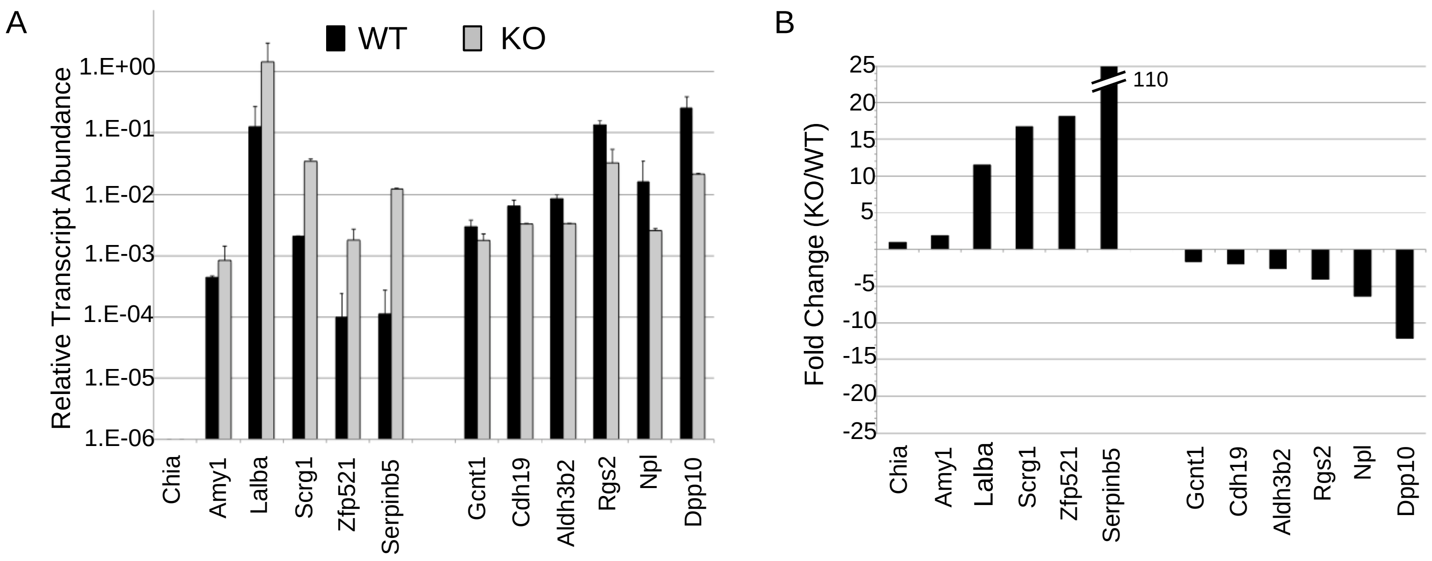
Supplemental Figure 6. Tumor growth in NOD/SCID mice was inhibited by expression of Pcdhβ genes. *A*, Pcdhβ19-transfected MDA-MB231 tumor cells ($2x10^6$) were injected into mammary fat pads of SCID mice (n=4) and secondary tumor growth was observed for 10 weeks. *: $p<0.05$. H&E staining of secondary tumor tissues formed after injecting Pcdhβ4-transfected her-2 tumor cells (*B*) and Pcdhβ19-transfected MDA-MB231 cells (*C*) into the mammary fat pads of SCID mice. Arrows indicate mitotic cells.



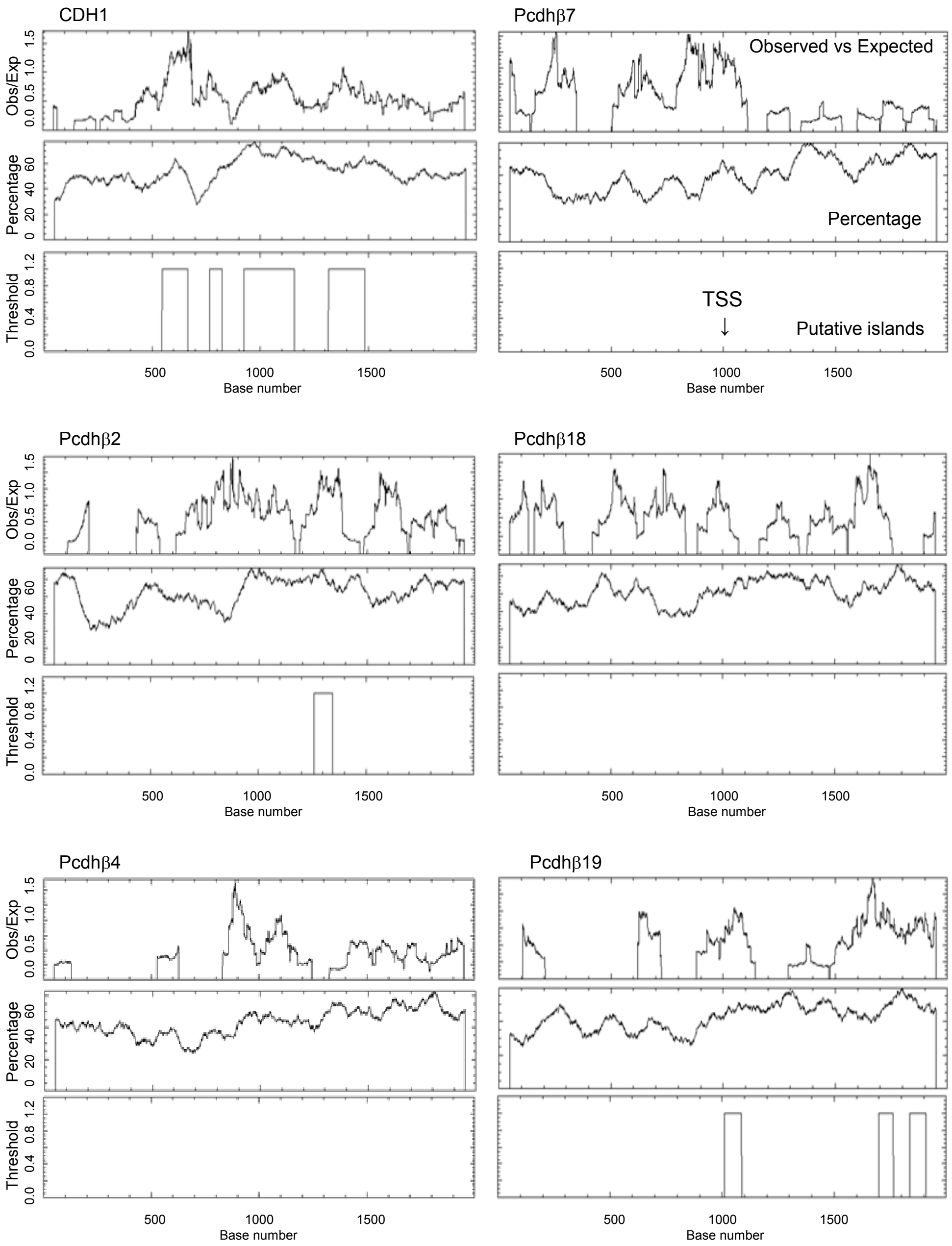
Antimicrobial Response, Inflammatory Response, RNA Damage and Repair (22)
Neurological Disease, Organismal Injury and Abnormalities, Cellular Compromise (14)
Antigen Presentation, Humoral Immune Response, Inflammatory Response (14)
Cell-To-Cell Signaling and Interaction, Cellular Development, Cellular Movement (12)



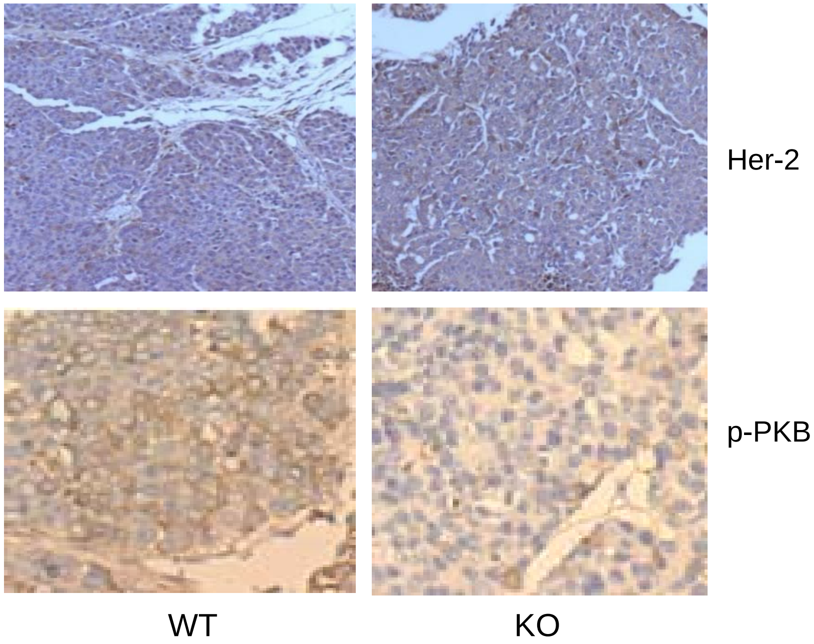
Guo et al, Fig. S1



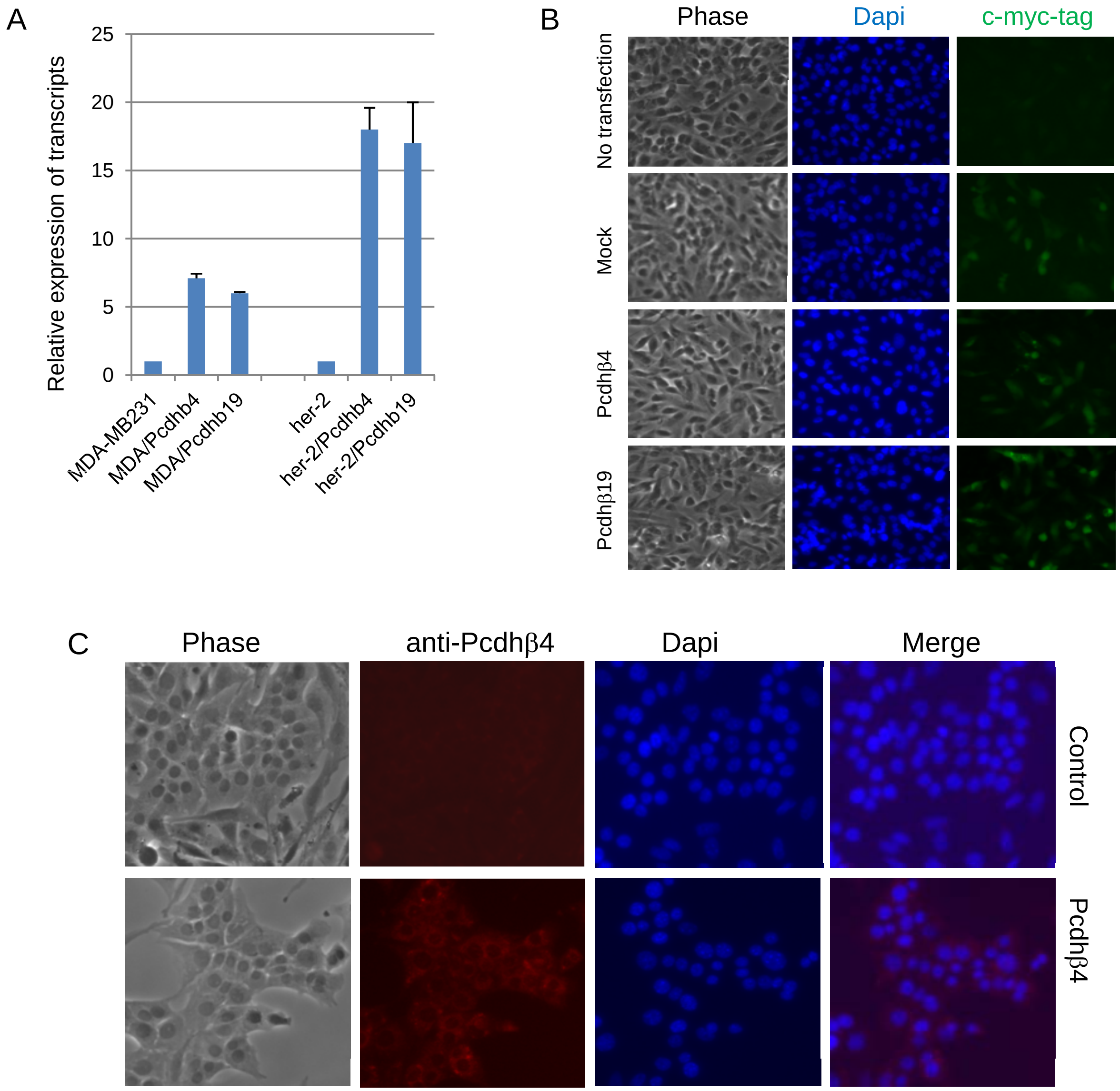
Guo et al, Fig.S2



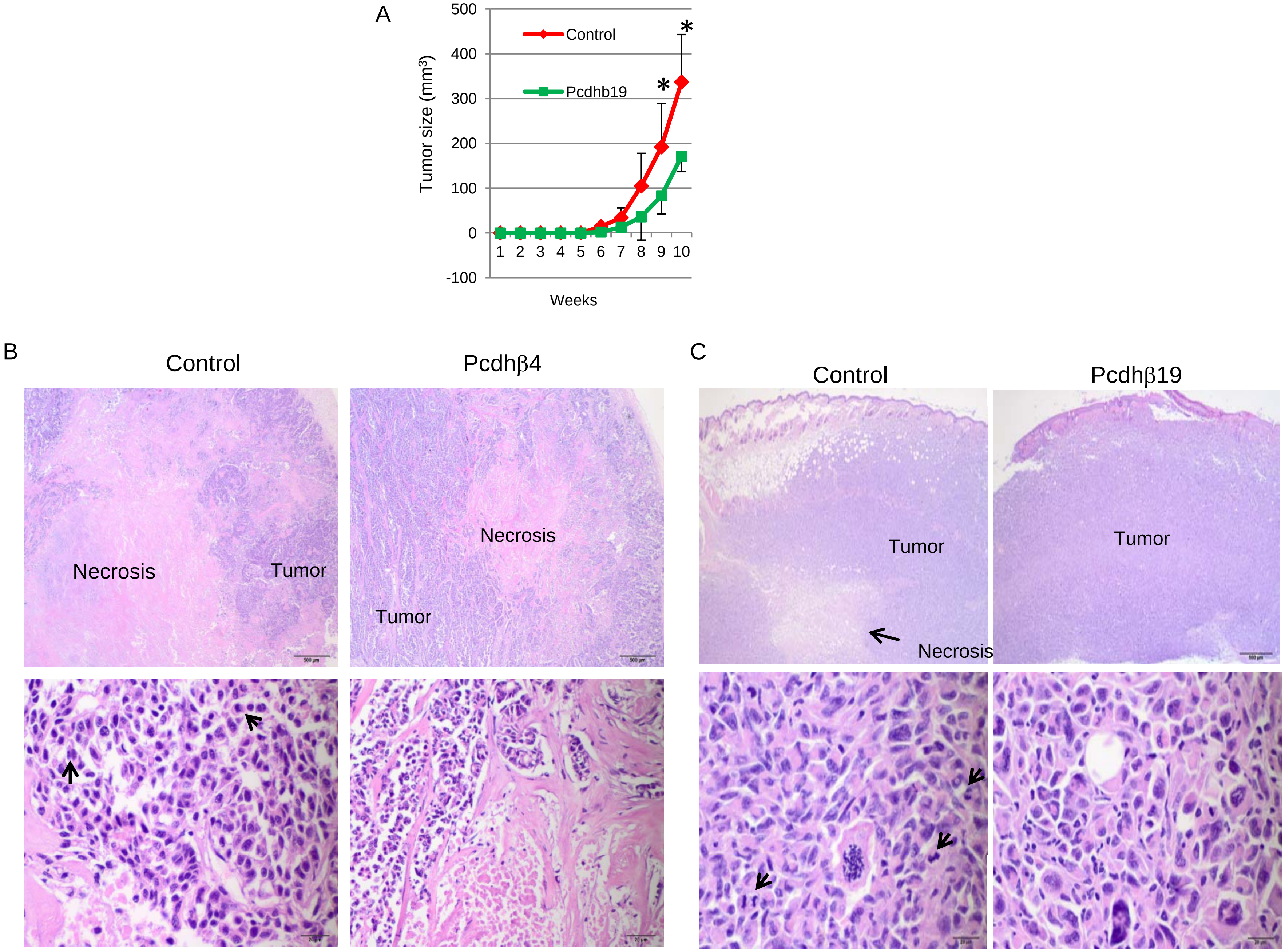
Guo et al, Fig.S3



Guo et al, Fig.S4



Guo et al. Fig. S5



Guo et al. Fig. S6

Table S1. Sequences of primers used in qRT-PCR

Gene	Symbol	Accession number	Forward primer (5' -3')	Reverse primer (5' - 3')
Mouse				
Aldehyde dehydrogenase 3 family, member B2	Aldh3b2	NM_001177438	gcttaatgacctccgttaccc	cctatggcccagcttatcag
Amylase 1, salivary	Amy1	NM_007446	gctcaagctggacaaagca	agggaactccaggaaagtcc
Cadherin 19, type 2	Cdh19	NM_001081386	gcccagacagtgccatattt	gagcacatgggtctgtgttg
Chitinase, acidic	Chia	NM_023186	gaaccgccagaccttcatta	caggtccagtccatcaaacc
Dipeptidylpeptidase 10	Dpp10	NM_199021	tgatggcagaggaagtgga	gcctccactgagcctatcc
Glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	NM_173442	cgaaggccatgtttccaacgg	tccgaagacgcacacagagc
Lactalbumin, alpha	Lalba	NM_010679	cggactcttccagatcagtga	gccacagatgttctccgact
N-acetylneuraminate pyruvate lyase	Npl	NM_028749	catcatgacgctggtctctg	gtaaactcctgggtggctttc
Regulator of G-protein signaling 2	Rgs2	NM_009061	atgggctggctgcattc	gtcttcacaagccaaccagaa
Scrapie responsive gene 1	Scrg1	NM_009136	atccttgggctaactttgctg	ctgtagcaggagaggcgact
Serine/cysteine peptidase inhibitor, clade B, member 5	Serpinb5	NM_009257	tgctgcctactttgttggaa	tgctgattctgaaaggacattc
Zinc finger protein 521	Zfp521	NM_145492	ctcttgcagcatttgctcag	ctgctggtgactgtccatgt
Protocadherin beta 1	Pcdhb1	NM_053126	cacagcaaagtcttggtgga	ctggacaccgaggagattgt
Protocadherin beta 2	Pcdhb2	NM_053127	cagcccacctggtagatgtt	ctccagtcaggcacacttca
Protocadherin beta 3	Pcdhb3	NM_053128	aactctcacagccctggatg	aagaccaggatgtggacctg
Protocadherin beta 4	Pcdhb4	NM_053129	tgtcacagcaaaggcaagtt	ctctgaaccagacacccaca
Protocadherin beta 5	Pcdhb5	NM_053130	tcgaaacaggcaactgattcct	gacagagtaccgagtaggca
Protocadherin beta 6	Pcdhb6	NM_053131	cattgtcccagagctaccagt	tttgaaatctgttgtcccagag
Protocadherin beta 7	Pcdhb7	NM_053132	tcagagttcagcatttcaaagc	atgaggtcccattgagtgct
Protocadherin beta 8	Pcdhb8	NM_053133	ctctggctgactgctctattcc	cgcaccactgacatccac
Protocadherin beta 9	Pcdhb9	NM_053134	atgagcaacacggtgaagattc	ctttctccatgatgaggaaatgca
Protocadherin beta 10	Pcdhb10	NM_053135	tccttaaacccatgatctcca	gtgcggactttccttcactt
Protocadherin beta 11	Pcdhb11	NM_053136	tctatgaggtgcagattctcga	ccctggcagagactgtaacaa
Protocadherin beta 12	Pcdhb12	NM_053137	agcctccctgggtgattact	ccctgctctactgacatccac
Protocadherin beta 13	Pcdhb13	NM_053138	gtgcaagacaaggcaagtga	aattgatcctgaacccacctc
Protocadherin beta 14	Pcdhb14	NM_053139	gcaagtgaccgccattatct	acggaatacgtgatggttgc
Protocadherin beta 15	Pcdhb15	NM_053140	tggagcgtcttgggctag	gtccctctctcggtttcctc
Protocadherin beta 16	Pcdhb16	NM_053141	gcccagcaggaagctcattt	tgcagtcgttagagggaagc
Protocadherin beta 17	Pcdhb17	NM_053142	gcatggatgtgcaatctgag	ccctgacacatgcagcaa
Protocadherin beta 18	Pcdhb18	NM_053143	caggttctgagcttggacgt	ttgctaggttcgccacaaat
Protocadherin beta 19	Pcdhb19	NM_053144	gacaaggcaagtcctgcttc	agtctcccagcctcagagtg
Protocadherin beta 20	Pcdhb20	NM_053145	gcgagtgctgaatctttgc	tttgccagattagccacaaa
Protocadherin beta 21	Pcdhb21	NM_053146	tgtgccagaagaaatggaga	ccagatcacccacatccata
Protocadherin beta 22	Pcdhb22	NM_053147	ctttctcttgctgggagtgg	ctgggtgtttcctccatcac
Cadherin 1	Cdh1	NM_009864	ggccaagcagcaatacatcct	tgtggaagggacaagagacc
RAS guanyl releasing protein 1	Rasgrp1	NM_011246	tgtcacagctccatctccag	ttcaccttcccatcttccag
Neuronal PAS domain protein 3	Npas3	NM_013780	cctccaccaaacacctcagt	cctgtcagctccacttgtga
Reversion-inducing-cysteine-rich protein with kazal motifs	Reck	NM_016678	gcacagaatggacgcactta	acttgtggttttggcacaca
Eph receptor A4	Epha4	NM_007936	taccccgcgaatgaagttac	atcacgttgcacacctggta
Mannoside N-acetylglucosaminyltransferase V	Mgat5	NM_145128	ccctggaagttgtcctctca	tcctctgccagtgccttaat
Glyceraldehyde-3-phosphate dehydrogenase[a]	Gapdh	NM_008084	tgcgacttcaacagcaactc	atgtaggccatgaggtccac
Ribosomal protein L4[a]	Rpl4	NM_024212	gacagccctatgccgtcagtg	gccacagctctgccagtacc
Human				
Protocadherin beta 6	Pcdhb6	NM_018939	ccaacccttcgaaataaacg	aaatccaaagcctttctcagc
Protocadherin beta 8	Pcdhb8	NM_019120	atcaccgtcactgacttaggg	ccagcacggtcatattgaga

Protocadherin beta 13	Pcdhb13	NM_018933	ggatgccaaagggaggac	ccagtatctgaggctgtggttatt
Mannoside N-acetylglucosaminyltransferase V	Mgat5	NM_002410	gagcagatcctggacctcag	gctgtcatgactccagcgta
Glyceraldehyde-3-phosphate dehydrogenase[a]	Gapdh	NM_002046	tggacctgacctgccgtctag	cctccgacgcctgcttcac

[a] Normalization control gene

Table S2. Sequences of primers used in methylation-specific PCR (MS-PCR)

Gene	Symbol	Accession number		Forward primer (5’ -3’)	Reverse primer (5’ - 3’)
Protocadherin beta 2	Pcdhb2	NM_053127	U	TTAGGTTGGGTTTATAATTAGGTGT	TTCCCTTTAAAAATAACTCACAAT
			M	GTTTAGGTTGGGTTTATAATTAGGC	CCCTTTAAAAATAACTCGCGAT
Protocadherin beta 3	Pcdhb3	NM_053128	U	AGTTGAAAGTTTTGGAAAATTTTGT	AATTAAACTAATCTCTAACTACTCTTCCCA
			M	GTTGAAAGTTTTGGAAAATTTCGT	AATTAAACTAATCTCTAACTACTCTTCCCG
Protocadherin beta 13	Pcdhb13	NM_053138	U	AGTAAGAATTTTTTAGTGTTTTTAGATTTT	AATTAATCATACAAATTCCCAAT
			M	AGAATTTTTTAGCGTTTTTAGATTTC	AAATTAATCGTACAAATTCCCGAT
Protocadherin beta 19	Pcdhb19	NM_053144	U	GGAGATTTGTTTTTTAGTGAATTGT	CAAAAAAATTATCATTTACATCCATA
			M	GGAGATTTGTTTTTTAGTGAATCGT	ACGAAAAAATTATCATTTACATCCG
Cadherin 1	Cdh1	NM_009864	U	TTTTTAGTTAATTAGTGGTGTTGG	CACTAAACTCAAATACAATCAAA
			M	GTTTTTAGTTAATTAGCGGCGTC	ACACTAAACTCGAATACGATCGAA

U: unmethylated; M: methylated

Table S3. Differential expression of genes detected by microarray

Gene Symbol	RefSeq	p-value	Fold-change (KO/WT)
B930036N10Rik	AK047216	0.098114	6.55705
Vmn2r96	NM_001104547	0.08262	6.3862
	---	0.071774	6.32384
Scrg1	NM_009136	0.023531	3.86718
	---	0.022472	3.79211
Serpinb5	NM_009257	0.082417	3.75104
ENSMUSG00000072618	ENSMUST00000100713	0.016753	3.72366
2310057J18Rik	NM_026336	0.232719	3.67941
Chia	NM_023186	0.302765	3.50042
Lalba	NM_010679	0.151283	3.24237
	---	0.053444	3.23159
Zfp521	NM_145492	0.020746	3.12831
E330013P04Rik	NR_026942	0.36213	3.11411
Amy1	NM_007446	0.290835	2.93382
Smoc1	NM_001146217	0.027821	2.88559
1700040L02Rik	BC087900	0.004049	2.81943
Cldn8	NM_018778	0.045599	2.66327
Fermt1	NM_198029	0.317376	2.6539
Vtcn1	NM_178594	0.022682	2.55331
Rbp1	NM_011254	0.103652	2.54128
Casp12	NM_009808	0.017624	2.50816
	---	0.037019	2.49757
Kcnj15	NM_019664	0.257777	2.47567
Nqo1	NM_008706	0.020957	2.4185
	---	0.048788	2.41597
Rnasel	NM_011882	0.136777	2.39604
Lect1	NM_010701	0.077178	2.39435
Pcdhb6	NM_053131	0.094767	2.38506
Nxf7	NM_130888	0.219268	2.38275
Smr3a	NM_011422	0.392494	2.36647
Cyp2d22	NM_019823	0.099721	2.35066
Pcdhb11	NM_053136	0.116768	2.33405
Cytip	NM_139200	0.039081	2.33386
Scrn1	NM_027268	0.026819	2.32697
Zfp239	NM_001001792	0.130009	2.29707
	---	0.021262	2.29063
Odam	NM_027128	0.372451	2.26607
Crisp1	NM_009638	0.095797	2.25761
	---	0.080433	2.23904

	---	0.163611	2.23747
	---	0.009639	2.23546
Arntl2	NM_172309	0.12843	2.22943
Pcdhb18	NM_053143	0.021566	2.21905
	---	0.036855	2.21008
	---	0.030372	2.20457
Pip	NM_008843	0.386624	2.1838
Pcdhb7	NM_053132	0.049552	2.15923
Fam150b	NM_001159743	0.064585	2.14069
Cst10	NM_021405	0.374166	2.13611
Cd14	NM_009841	0.000607	2.13547
Slc38a3	NM_023805	0.00921	2.13304
Pcdhb2	NM_053127	0.048118	2.11683
Muc15	NM_172979	0.043913	2.11666
Tubb2b	NM_023716	0.05763	2.1079
	---	0.121762	2.08922
	---	0.037103	2.077
Thsd4	NM_001040426	0.041443	2.06645
OTTMUSG00000015351	ENSMUST00000099395	0.09831	2.05147
Pcdhb4	NM_053129	0.038903	2.04059
	---	0.009093	2.03234
Pcdhb19	NM_053144	0.020934	2.02627
Ddo	NM_027442	0.017712	2.01305
Nox4	NM_015760	0.255613	2.01048
Cldn2	NM_016675	0.099988	2.00173
	---	0.288824	-2.00321
Prom1	NM_008935	0.051685	-2.01073
	---	0.034671	-2.01378
Slc38a1	NM_134086	0.33995	-2.01623
EG546714	XR_033405	0.235945	-2.0251
EG240327	NM_001033767	0.302275	-2.02514
	---	0.002031	-2.03624
	---	0.075336	-2.04699
3632451O06Rik	NM_026142	0.318044	-2.04823
	---	0.028619	-2.0569
H2-Q6	NM_207648	0.339281	-2.07207
Fam125b	BC059907	0.138111	-2.07544
	---	0.02368	-2.07973
Masp1	NM_008555	0.32383	-2.08409
H2-T22	NM_010397	0.323309	-2.10938
Mgat5	NM_145128	0.00044	-2.11392
Ifi44	NM_133871	0.333874	-2.12046
Hspa1a	NM_010479	0.010781	-2.13604

Kcnj13	NM_001110227	0.012275	-2.13735
4930503L19Rik	NM_172967	0.123851	-2.14255
Irf7	NM_016850	0.285127	-2.14528
ENSMUSG00000074338	ENSMUST00000098753	0.070983	-2.14572
Xaf1	NM_001037713	0.24696	-2.14863
Oas2	NM_145227	0.299249	-2.16678
Fndc3c1	NM_001007580	0.38789	-2.1785
	---	0.01239	-2.1894
	---	0.343579	-2.20348
Prrg3	NM_001081135	0.293288	-2.21033
Zic3	NM_009575	0.082876	-2.21726
Sv2c	NM_029210	0.034726	-2.22967
	---	0.088689	-2.23248
Aldh3b2	ENSMUST00000100032	0.056715	-2.23401
3110007F17Rik	BC027572	0.134285	-2.2395
Eno2	NM_013509	4.32E-05	-2.24011
Gbp3	NM_018734	0.214679	-2.25156
Ablim3	NM_198649	0.020009	-2.25541
Tox3	NM_172913	0.040529	-2.26008
Ak3l1	NM_009647	0.003423	-2.26087
	---	0.126934	-2.26874
A2m	NM_175628	0.316066	-2.28987
Igfbp4	NM_010517	0.027816	-2.30083
Rasgrp1	NM_011246	0.015876	-2.32995
3110007F17Rik	BC027572	0.085889	-2.34447
3110007F17Rik	BC027572	0.086488	-2.34842
	---	0.087033	-2.41889
Cnksr2	NM_177751	0.062454	-2.42852
Apol9b	NM_173743	0.109329	-2.43259
Osbpl6	NM_145525	0.126167	-2.4537
Ifit3	NM_010501	0.35072	-2.46503
Prol1	NM_008644	0.232442	-2.47301
Adcy8	NM_009623	0.206611	-2.48208
Ifit1	NM_008331	0.264036	-2.50971
H2afy2	NM_207000	0.107156	-2.56499
Mkx	NM_177595	0.022573	-2.66449
Ifi202b	NM_008327	0.005126	-2.69043
D17H6S56E-5	L78788	0.195089	-2.69761
Usp18	NM_011909	0.250999	-2.71902
Apol9b	NM_173743	0.117611	-2.72568
Ifi27l2a	NM_029803	0.116437	-2.72604
	---	0.088632	-2.73829
EG545886	AB256662	0.20286	-2.75787

Tspan1	NM_133681	0.089039	-2.76683
Ldlrad3	NM_178886	0.050311	-2.8352
LOC100044501	XM_001472232	0.119105	-2.87802
1700055N04Rik	AK081788	0.03032	-2.96093
Cdh19	NM_001081386	0.028015	-3.07028
Mfsd4	NM_001114662	0.026284	-3.09621
	---	0.2319	-3.14342
Abpa	NM_009596	0.151376	-3.32643
Gcnt1	NM_173442	0.00149	-3.37106
	---	0.000949	-3.4074
	---	0.250398	-3.45319
Apoc1	NM_007469	0.068058	-3.61227
Npl	NM_028749	0.000753	-3.64734
	---	0.091361	-3.74479
Rgs2	NM_009061	0.003417	-3.81328
Dpp10	NM_199021	0.01564	-4.71333
Hhipl2	BC034362	0.000242	-6.52572

---: unindentified genes, KO: Knockout, WT: Wild-type

Table S4. Genes showing top fold-changes by microarray analyses

Gene	Symbol	Accession number	p-value (KO/ WT)	Fold-change (KO/ WT)
Scrapie responsive gene 1	SCRG1	NM_009136	0.0235309	3.867
Serine (or cysteine) peptidase inhibitor	SERPINB5	NM_009257	0.0824169	3.751
Chitinase, acidic	CHIA	NM_023186	0.302765	3.500
Lactalbumin, alpha	LALBA	NM_010679	0.151283	3.242
Zinc finger protein 521	ZNF521	NM_145492	0.0207462	3.128
Amylase 2a1, pancreatic	AMY2A	NM_001042712	0.359697	2.934
RIKEN cDNA 1700040L02 gene	C10ORF107	BC087900	0.00404911	2.819
Claudin 8	CLDN8	NM_018778	0.0455989	2.663
Fermitin family homolog 1 (Drosophila)	FERMT1	NM_198029	0.317376	2.654
V-set domain containing T cell activation inhibitor 1	VTCN1	NM_178594	0.0226818	2.553
Dipeptidylpeptidase 10	DPP10	NM_199021	0.0156397	-4.713
Regulator of G-protein signaling 2	RGS2	NM_009061	0.00341655	-3.813
N-acetylneuraminate pyruvate lyase	NPL	NM_028749	0.000753106	-3.647
Glucosaminyl (N-acetyl) transferase 1, core 2	GCNT1	NM_173442	0.00148991	-3.371
Cadherin 19, type 2	CDH19	NM_001081386	0.0280145	-3.070
Aldehyde dehydrogenase 3 family, member B2	ALDH3B2	ENSMUST00000100032	0.0567148	-2.961
Low density lipoprotein receptor class A domain	LDLRAD3	NM_178886	0.0503106	-2.835
Tetraspanin 1	TSPAN1	NM_133681	0.0890391	-2.767
Interferon, alpha-inducible protein 27 like 2A	IFI27L2	NM_029803	0.116437	-2.726
Ubiquitin specific peptidase 18	USP18	NM_011909	0.250999	-2.719

KO: Knockout, WT: Wild-type

Table S5. Fold changes of major N-glycan-related enzymes and galectins

Gene	Symbol	Accession number	p-value (KO/ WT)	Fold-change
Mannoside acetylglucosaminyltransferase 1	Mgat1	NM_001110148	0.74	1.01
Mannoside acetylglucosaminyltransferase 2	Mgat2	NM_146035	0.35	-1.05
Mannoside acetylglucosaminyltransferase 3	Mgat3	NM_010795	0.42	-1.04
Mannoside acetylglucosaminyltransferase 4, isoenzyme A	Mgat4a	NM_173870	0.94	1.01
Mannoside acetylglucosaminyltransferase 4, isoenzyme B	Mgat4b	NM_145926	0.01	-1.2
Mannoside acetylglucosaminyltransferase 5	Mgat5	NM_145128	0.0004	-2.1
Mannoside acetylglucosaminyltransferase 5, isoenzyme b	Mgat5b	NM_172948	0.05	1.07
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide1	B4galt1	NM_022305	0.42	-1.15
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide2	B4galt2	NM_017377	0.56	-1.08
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide3	B4galt3	NM_020579	0.68	1.02
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide4	B4galt4	NM_019804	0.43	-1.12
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide5	B4galt5	NM_019835	0.13	-1.31
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly peptide6	B4galt6	NM_019737	0.73	1.05
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3gnt1	NM_175383	0.30	1.04
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	B3gnt2	NM_016888	0.83	-1.03
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	B3gnt3	NM_028189	0.39	1.10
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	B3gnt4	NM_198611	0.45	1.10
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	B3gnt5	NM_001159407	0.10	-1.22
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	B3gnt6	NM_001081167	0.36	1.09
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	B3gnt7	NM_145222	0.12	-1.10
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	B3gnt8	NM_146184	0.03	-1.66
ST3 beta-galactoside alpha-2,3-sialyltransferase 1	St3gal1	NM_009177	0.14	-1.58
ST3 beta-galactoside alpha-2,3-sialyltransferase 2	St3gal2	NM_009179	0.42	1.11
ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	NM_009176	0.16	-1.27
ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	NM_009178	0.02	1.35
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	NM_011375	0.98	-1.01
ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	NM_018784	0.96	-1.00
Beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	NM_145933	0.52	-1.06
Beta galactoside alpha 2,6 sialyltransferase 2	St6gal2	NM_172829	0.38	1.16
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	St8sia1	NM_011374	0.27	-1.27
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	St8sia2	NM_009181	0.96	1.00
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	St8sia3	NM_009182	0.83	-1.02
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	St8sia4	NM_009183	0.03	-1.24
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	St8sia5	NM_153124	0.20	1.18
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	St8sia6	NM_145838	0.64	-1.07
Glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	NM_173442	0.001	-3.37
Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	Gcnt2	NM_023887	0.98	-1.00
Glucosaminyl (N-acetyl) transferase 3, mucin type	Gcnt3	NM_028087	0.53	-1.10
Fucosyltransferase 1	Fut1	NM_008051	0.32	-1.16
Fucosyltransferase 2	Fut2	NM_018876	0.23	-1.13
Fucosyltransferase 4	Fut4	NM_010242	0.15	1.16
Fucosyltransferase 7	Fut7	NM_013524	0.88	1.00
Fucosyltransferase 8	Fut8	NM_016893	0.19	1.28
Fucosyltransferase 9	Fut9	NM_010243	0.38	1.23
Fucosyltransferase 10	Fut10	NM_134161	0.43	-1.08
Fucosyltransferase 11	Fut11	NM_028428	0.34	1.10
Mannosidase 1, alpha	Man1a	NM_008548	0.68	1.11
mannosidase, alpha, class 1A, member 2	Man1a2	NM_010763	0.02	1.17
mannosidase, alpha, class 1C, member 1	Man1c1	NM_207237	0.68	1.06
mannosidase 2, alpha 1	Man2a1	NM_008549	0.17	1.16
mannosidase 2, alpha 2	Man2a2	NM_172903	0.02	-1.35
Lectin, galactose binding, soluble 1	Lgals1	NM_008495	0.47	1.08
Lectin, galactose binding, soluble 2	Lgals2	NM_025622	0.62	1.03
Lectin, galactose binding, soluble 3	Lgals3	NM_001145953	0.95	1.00
Lectin, galactose binding, soluble 4	Lgals4	NM_010706	0.38	-1.09
Lectin, galactose binding, soluble 7	Lgals7	NM_008496	0.69	-1.06
Lectin, galactose binding, soluble 8	Lgals8	NM_018886	0.69	1.02
Lectin, galactose binding, soluble 9	Lgals9	NM_010708	0.24	-1.96
Lectin, galactose binding, soluble 12	Lgals12	NM_019516	0.94	-1.02

KO: Knockout, WT: Wild-type

Table S6. Fold changes for major growth factor receptors and integrins

Gene	Symbol	Accession number	p-value	Fold-change (KO/ WT)
Growth factor receptors				
Epidermal growth factor receptor	Egfr	NM_207655	0.226926	1.08447
v-erb-b2 erythroblastic leukemia viral oncogene homolog	Erbb2	NM_001003817	0.453444	-1.08611
v-erb-b2 erythroblastic leukemia viral oncogene homolog 3	Erbb3	NM_010153	0.0898661	1.1808
v-erb-a erythroblastic leukemia viral oncogene homolog 4	Erbb4	NM_010154	0.957624	1.01974
Fibroblast growth factor receptor 1	Fgfr1	NM_010206	0.055296	1.42813
Fibroblast growth factor receptor 2	Fgfr2	NM_010207	0.120927	-1.46872
Fibroblast growth factor receptor 3	Fgfr3	NM_008010	0.963771	-1.00325
Fibroblast growth factor receptor 3	Fgfr4	NM_008011	0.336899	1.07013
Transforming growth factor, beta receptor I	Tgfbr1	NM_009370	0.0286279	1.18104
Transforming growth factor, beta receptor II	Tgfbr2	NM_009371	0.579646	-1.13361
Transforming growth factor, beta receptor III	Tgfbr3	NM_011578	0.873379	1.01872
Platelet derived growth factor receptor, alpha polypeptide	Pdgfra	NM_011058	0.547481	1.11775
Platelet derived growth factor receptor, beta polypeptide	Pdgfrb	NM_001146268	0.686129	-1.03521
Insulin-like growth factor I receptor	Igf1r	NM_010513	0.114178	1.63282
Insulin-like growth factor 2 receptor	Igf2r	NM_010515	0.473084	1.07524
Integrins				
Integrin beta 1 (fibronectin receptor beta)	Itgb1	NM_010578	0.0115619	1.28233
Integrin beta 2	Itgb2	NM_008404	0.261101	-1.05837
Integrin beta 3	Itgb3	NM_016780	0.862831	1.04203
Integrin beta 4	Itgb4	NM_001005608	0.800576	1.01401
Integrin beta 5	Itgb5	NM_001145884	0.30287	1.14265
Integrin beta 6	Itgb6	NM_001159564	0.515293	1.14611
Integrin beta 7	Itgb7	NM_013566	0.0909787	-1.08144
Integrin beta 8	Itgb8	NM_177290	0.186688	1.18508
Integrin alpha 1	Itga1	NM_001033228	0.356648	-1.27442
Integrin alpha 2	Itga2	NM_008396	0.198102	1.29557
Integrin alpha 3	Itga3	NM_013565	0.600712	1.05675
Integrin alpha 4	Itga4	NM_010576	0.439389	-1.12907
Integrin alpha 5 (fibronectin receptor alpha)	Itga5	NM_010577	0.0302691	-1.2422
Integrin alpha 6	Itga6	NM_008397	0.290547	-1.1494
Integrin alpha 7	Itga7	NM_008398	0.399622	-1.04407
Integrin alpha 8	Itga8	NM_001001309	0.530318	1.12615
Integrin alpha 9	Itga9	NM_133721	0.215066	-1.25473
Integrin alpha 10	Itga10	NM_001081053	0.212197	-1.04209
Integrin alpha 11	Itga11	NM_176922	0.155082	-1.16072

KO: Knockout, WT: Wild-type