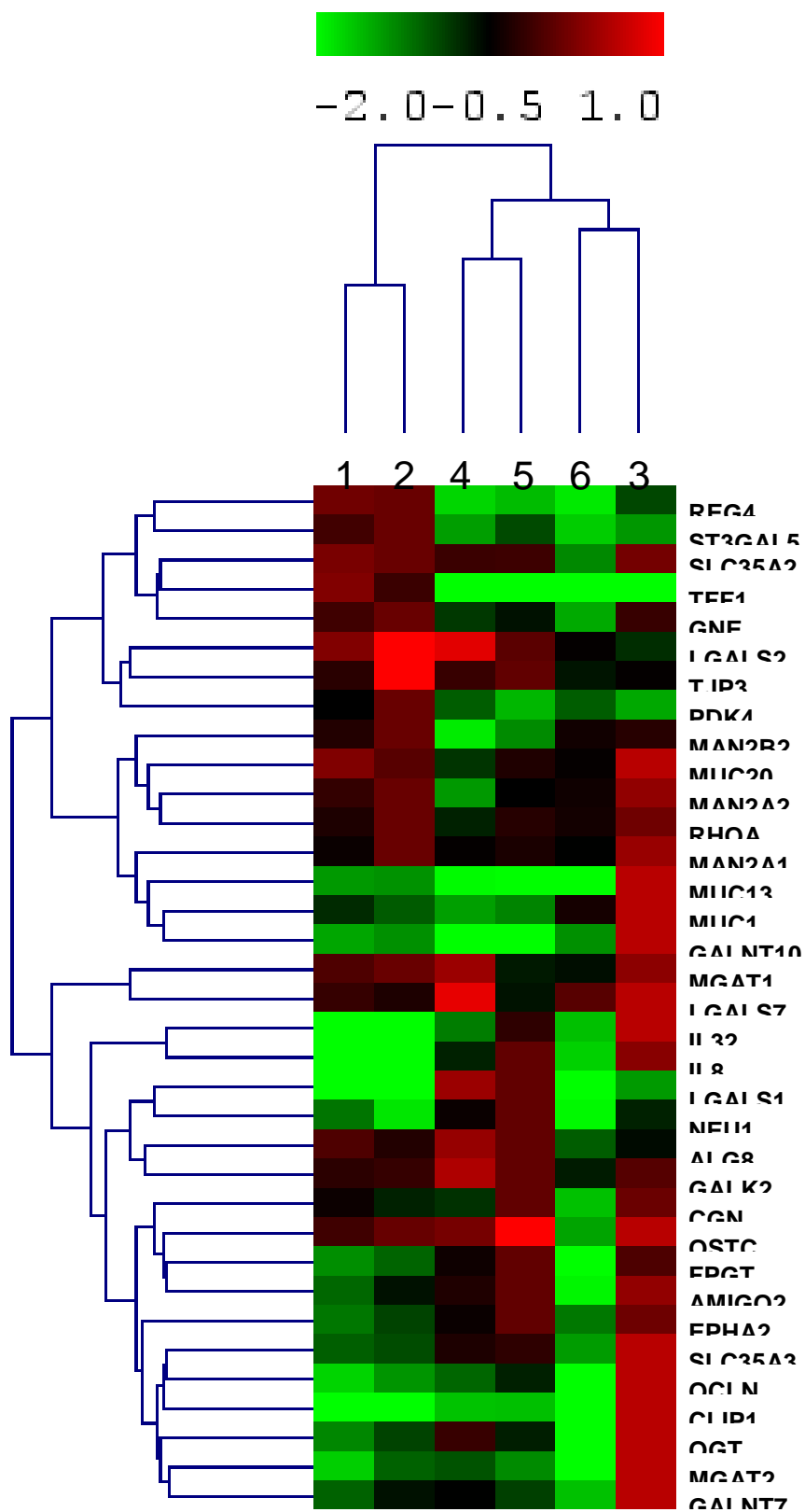


Supplementary Figure 1 Heatmap of RNA expression in E12-infected and uninfected E12 samples analysed by microarray. E12 untreated (E12/Con, 1-3) and E12 infected (E12/Hp, 4-6) samples separated into two clusters. Unsupervised clustering of samples was carried out in GeneSpring and used all probes after pre-filtering weak signals. The normalised signal values for each gene are represented as colour bars (yellow - median, red - higher, blue - lower).



Supplementary Figure 2 Heatmap of RNA expression in E12-infected and uninfected E12 samples analysed by qRT-PCR. The heatmap was created with TMeV, part of the TM4 Microarray Software Suite ^[69].

Supplementary Table 1 Primers used for qRT-PCR

Gene			
Symbol	Source	Forward primer	Reverse primer
<i>IL32</i>	Primer3	GGACAAGGAGGAG	TTGAGGATTGGGGTTCAG
		CTGACAC	AG
<i>REG4</i>	Primer3	AGCCTGGCTAAATC	TGGGCCAATGCTAAAGT
		TGCTCA	TTC
<i>IL8</i>	Primer3	GTGCAGTTTTGCCA	AAATTTGGGGTGGAAAG
		AGGAGT	GTT
<i>LGALS1</i>	PrimerBank	TCGCCAGCAACCTG	GCACGAAGCTCTTAGCG
		AATCTC	TCA
<i>LGALS2</i>	Primer3	TGAAGATCACAGGC	TGAAATGCAGGTTCAGC
		AGCATC	TTG
<i>NEU1</i>	PrimerBank	GGAGGCTGTAGGGT	CACCAGACCGAAGTCGT
		TTGGG	TC
<i>SLC35A2</i>	PrimerBank	GAATGCCTCCCTCA	CCTTTGAGCACTTCCGCC
		TCCTCAG	AT
<i>MUC1</i>	Primer3	AGACGTCAGCGTGA	GACAGCCAAGGCAATGA
		GTGATG	GAT
<i>MUC13</i>	Primer3	CAGAGACAGCCAG	CGGAGGCCAGATCTTTA
		ATGCAAA	CTG
<i>MUC20</i>	Primer3	GTGCAGGTGAAAAT	ACGCAGTAAGGAGACCT
		GGAGGT	GGA

<i>TFF1</i>	PrimerBank	CCCCGTGAAAGACA GAATTGT	GGTGTCGTCGAAACAGC AG
<i>MGAT1</i>	PrimerBank	CGCAAGTTCCAGGG CTACTAC	CTTCAGCAGCGGATAGG TGG
<i>ALG8</i>	PrimerBank	GCTCGGGGTGACTC TTCTC	AGCCAGTTTCGGTGTACT TCA
<i>OSTC</i>	PrimerBank	GCCAGTAGCTTTCTT GGCCTA	GATCGGTCCAGGATTATG AAACC
<i>ST3GAL5</i> ¹		CCCTGAACCAGTTC GATGTT	CATTGCTTGAAGCCAGTT GA
<i>RHOA</i>	PrimerBank	GATTGGCGCTTTTGG GTACAT	AGCAGCTCTCGTAGCCAT TTC
<i>GNE</i>	PrimerBank	GGAGCAAAGAGAT GGTTCGAG	ACGTGTTTAACTGCACGA AAGT
<i>SLC35A3</i>	PrimerBank	CAGTGGCTGTCCCT AGTAATTTT	AGAACTGCCATGAGTCC TACA
<i>GALK2</i>	PrimerBank	GCTTGGTGACGCTC ACAGT	GCCAATGTAACGCTCAC TCTT
<i>FPGT</i>	PrimerBank	GATGCCTATGGTGA CTTTCTGC	GCCTCATTTCTACCAACT CTGAC
<i>CGN</i>	PrimerBank	TGGAGTCCAGATTC GCTTCAT	CCCGTAGGTACTGGCTCT TG
<i>TJP3</i>	PrimerBank	GCTTTGGCATTGCG ATCTCTG	GATGTGGTCGCCTGTCTG TAG

<i>OCN</i>	PrimerBank	ACAAGCGGTTTTAT CCAGAGTC	GTCATCCACAGGCGAAG TTAAT
<i>EPHA2</i>	PrimerBank	TGGCTCACACACCC GTATG	GTCGCCAGACATCACGTT G
<i>MAN2A2</i>	PrimerBank	AGACCCAACACATC CTCAATAGC	ACTGCCGCTCTCTTTTGG AC
<i>MAN2B2</i>	PrimerBank	ACGCCGCCAATGTC TACAC	CAGCCGGAAAACTCCT GCT
<i>MAN2A1</i>	PrimerBank	CAGTGCGATCTTCT GTGTGGT	GCAAACGCTCCAAATGG TCTAT
<i>CLIP1</i>	PrimerBank	ATAGGCAAGAACG ATGGTTCG	GAAGGTCGGGTAAATAT GCCC
<i>LGALS7</i>	Primer3	TCCATGTAAACCTG CTGTGC	GCTCCTTGCTGTTGAAGA CC
<i>AMIGO2</i>	PrimerBank	AGCATTTCCACGGG CAGTTT	CCGTCTTCAGCTTATTGG ACGA
<i>PK4</i>	PrimerBank	GGAGCATTTCTCGC GCTACA	ACAGGCAATTCTTGTCGC AAA
<i>MGAT2</i>	PrimerBank	GTGCATAACCGGCC CGAATA	ACGAGGACGTTGTCAAT TCCC
<i>OGT</i>	PrimerBank	CAGTAGCTTGGAGT AATCTTGGC	GGTGACAGCCTTTTCAAA GTGAT
<i>GALNT1</i>		GAGCTGGTCGCCGA	CCCTTCCCGTTTCTTGGTT
<i>0</i>	PrimerBank	GATTG	C

		TGCTGGAGGAGATT	GCACAGGATCATGGTAG
<i>GALNT7</i>	PrimerBank	CCCAGAA	GTGAA
		GGAGAAACTGCTGC	GGAAAAAGGAGGTCTTC
<i>RPLP0</i>	²	CTCATA	TCG
		AGGGATCAAGATCA	GCCCACCAGCTAGAAGA
<i>UAP1</i>	qPrimerDepot	GCTCCA	AGA
		GCAAATTCCATGGC	TCGCCCCACTTGATTTTG
<i>GAPDH</i>	¹	ACCGT	G
		CCTGTACGCCAACA	ATACTCCTGCTTGCTGAT
<i>ACTB</i>	³	CAGTGC	CC

Primer3: **Untergasser A**, Cutcutache I, Koressaar T, Ye J, Faircloth BC, Remm M, Rozen SG. Primer3 – new capabilities and interfaces. *Nucleic Acids Res* 2012; **40**: e115.

PrimerBank: **Wang X**, Spandidos A, Wang H, Seed, B. PrimerBank: a PCR primer database for quantitative gene expression analysis. *Nucleic Acids Res* 2012; **40**: D1144–D1149.

qPrimerDepot: **Cui W**, Taub DD, Gardner K. qPrimerDepot: a primer database for quantitative real time PCR. *Nucleic Acids Res* 2007; **35**: D805–D809.

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²**Dydenborg AB**, Herring E, Auclair J, Tremblay E, Beaulieu JF. Normalizing genes for quantitative RT-PCR in differentiating human intestinal epithelial

cells and adenocarcinomas of the colon. *Am J Physiol Gastrointest Liver Physiol* 2006; **290**: G1067-74

³**Lindén SK**, Sheng YH, Every AL, Miles KM, Skoog EC, Florin TH, Sutton P, McGuckin MA. (2009) MUC1 limits *Helicobacter pylori* infection both by steric hindrance and by acting as a releasable decoy. *PLoS Pathog* 2009; **5**: e1000617.

Supplementary Table 2 Differentially expressed genes associated with *H. pylori* infection of E12 cells by microarray analysis - all 276 genes (FDR<0.05, fold change >2)

Gene symbol	P-value	Fold change	Gene name
Upregulated			
<i>CLIP1</i>	0.0025	5.42	CAP-GLY domain containing linker protein 1
<i>C10orf118</i>	0.0031	5.21	chromosome 10 open reading frame 118
<i>TOP1</i>	0.0352	5.09	topoisomerase (DNA) I
<i>LARS</i>	0.0054	5.02	leucyl-tRNA synthetase
<i>CDC27</i>	0.0073	4.95	cell division cycle 27 homolog (S. cerevisiae)
<i>STIP1</i>	0.0042	3.92	stress-induced-phosphoprotein 1
<i>MALAT1</i>	0.0077	3.82	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
<i>IL32</i>	0.0021	3.54	interleukin 32
<i>SLC39A6</i>	0.0204	3.33	solute carrier family 39 (zinc), member 6
<i>AHNAK2</i>	0.0070	3.25	AHNAK nucleoprotein 2
<i>HSP90AB1</i>	0.0014	3.24	heat shock protein 90kDa alpha (cytosolic), B1
<i>ACTR2</i>	0.0035	3.20	ARP2 actin-related protein 2 homolog (yeast)
<i>EIF4G1</i>	0.0349	3.16	eukaryotic translation initiation factor 4 gamma, 1
<i>ACBD3</i>	0.0253	3.14	acyl-CoA binding domain containing 3
<i>CCND1</i>	0.0222	3.09	cyclin D1

<i>PI3</i>	0.0014	3.05	peptidase inhibitor 3, skin-derived
<i>C12orf35</i>	0.0128	3.01	chromosome 12 open reading frame 35
<i>EZR</i>	0.0462	2.85	ezrin
<i>AFAP1-AS</i>	0.0030	2.83	AFAP1 antisense RNA (non-protein coding)
<i>THRAP3</i>	0.0261	2.80	thyroid hormone receptor associated protein 3
<i>CARS</i>	0.0066	2.80	cysteinyI-tRNA synthetase
<i>ATF3</i>	0.0034	2.78	activating transcription factor 3
<i>ENO1</i>	0.0058	2.75	enolase 1, (alpha)
<i>TCEB3</i>	0.0141	2.74	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)
<i>ACTB</i>	0.0344	2.70	actin, beta
<i>BCLAF1</i>	0.0069	2.69	BCL2-associated transcription factor 1
<i>KIAA0494</i>	0.0031	2.63	KIAA0494
<i>PIP4K2A</i>	0.0101	2.61	Phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
<i>LUZP1</i>	0.0400	2.59	leucine zipper protein 1
<i>KIF21A</i>	0.0256	2.58	kinesin family member 21A
<i>DEGS1</i>	0.0106	2.57	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)
<i>FNDC3B</i>	0.0015	2.53	fibronectin type III domain containing 3B
<i>PSPC1</i>	0.0110	2.53	paraspeckle component 1
<i>SAE1</i>	0.0046	2.49	SUMO1 activating enzyme subunit 1

<i>SRPRB</i>	0.0028	2.48	signal recognition particle receptor, B subunit
<i>MSTO1</i> /// <i>MSTO2P</i>	0.0014	2.46	misato homolog 1 (Drosophila) /// misato homolog 2 pseudogene
<i>NBPF10</i>	0.0274	2.45	neuroblastoma breakpoint family, member 10
<i>SERPINA3</i>	0.0023	2.42	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
<i>CEP350</i>	0.0024	2.42	centrosomal protein 350kDa
<i>ZNF800</i>	0.0121	2.37	zinc finger protein 800
<i>CCT2</i>	0.0045	2.34	chaperonin containing TCP1, subunit 2 (beta)
<i>PEA15</i>	0.0053	2.34	phosphoprotein enriched in astrocytes 15
<i>MAP4</i>	0.0386	2.34	microtubule-associated protein 4
<i>LGALS7/7B</i>	0.0115	2.31	lectin, galactoside-binding, soluble, 7/7B
<i>ANXA6</i>	0.0022	2.31	annexin A6
<i>PI4K2A</i>	0.0055	2.27	phosphatidylinositol 4-kinase type 2 alpha
<i>CXorf40A</i> <i>/40B</i>	0.0073	2.27	chromosome X open reading frame 40A / 40B
<i>YIF1B</i>	0.0024	2.26	Yip1 interacting factor homolog B (<i>S. cerevisiae</i>)
<i>USP6NL</i>	0.0073	2.26	USP6 N-terminal like
<i>UPP1</i>	0.0020	2.26	uridine phosphorylase 1
<i>CEP57</i>	0.0097	2.24	centrosomal protein 57kDa
<i>NBPF1 /10</i>	0.0224	2.23	neuroblastoma breakpoint family, member 1/10
<i>LARP1B</i>	0.0130	2.21	La ribonucleoprotein domain family, member 1B

<i>PHLDA1</i>	0.0051	2.19	pleckstrin homology-like domain, family A, member 1
<i>RRBP1</i>	0.0065	2.17	ribosome binding protein 1 homolog 180kDa (dog)
<i>TPM4</i>	0.0106	2.15	tropomyosin 4
<i>MTUS1</i>	0.0052	2.15	microtubule associated tumor suppressor 1
<i>GOT1</i>	0.0011	2.14	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
<i>TM7SF2</i>	0.0052	2.13	transmembrane 7 superfamily member 2
<i>CALD1</i>	0.0129	2.13	caldesmon 1
<i>PDZK1IP1</i>	0.0036	2.13	PDZK1 interacting protein 1
<i>FLOT1</i>	0.0116	2.13	flotillin 1
<i>ZMYM5</i>	0.0038	2.13	zinc finger, MYM-type 5
<i>GNG12</i>	0.0111	2.12	guanine nucleotide binding protein (G protein), gamma 12
<i>KIAA0100</i>	0.0430	2.10	KIAA0100
<i>C6orf106</i>	0.0132	2.10	chromosome 6 open reading frame 106
<i>RBM27</i>	0.0240	2.10	RNA binding motif protein 27
<i>HSP90B1</i>	0.0473	2.10	heat shock protein 90kDa beta (Grp94), member 1
<i>ATRX</i>	0.0337	2.09	alpha thalassemia/mental retardation syndrome X-linked
<i>FARSA</i>	0.0095	2.09	phenylalanyl-tRNA synthetase, alpha subunit
<i>RAD23A</i>	0.0279	2.08	RAD23 homolog A (<i>S. cerevisiae</i>)
<i>IWS1</i>	0.0091	2.08	IWS1 homolog (<i>S. cerevisiae</i>)

<i>NIPSNAP1</i>	0.0019	2.08	nipsnap homolog 1 (<i>C. elegans</i>)
<i>ARPC4</i>	0.0241	2.06	actin related protein 2/3 complex, subunit 4, 20kDa
<i>TRIB3</i>	0.0058	2.06	tribbles homolog 3 (<i>Drosophila</i>)
<i>DNMT3A</i>	0.0065	2.06	DNA (cytosine-5-)-methyltransferase 3 alpha
<i>ECE2</i>	0.0058	2.06	endothelin converting enzyme 2
<i>RHBDD2</i>	0.0067	2.05	rhomboid domain containing 2
<i>LCN2</i>	0.0014	2.04	lipocalin 2
<i>TCEAL3</i>	0.0014	2.04	transcription elongation factor A (SII)-like 3
<i>ZFR</i>	0.0095	2.04	zinc finger RNA binding protein
<i>ARF1</i>	0.0055	2.04	ADP-ribosylation factor 1
<i>COPE</i>	0.0027	2.01	coatamer protein complex, subunit epsilon
<i>HNRNPA3/A3P1</i>	0.0028	2.00	heterogeneous nuclear ribonucleoprotein A3 / A3 pseudogene 1
<i>SLFN5</i>	0.0290	2.00	schlafen family member 5
<i>FUS</i>	0.0087	2.00	fused in sarcoma
<i>FBXL6</i>	0.0059	2.00	F-box and leucine-rich repeat protein 6

Downregulated

<i>LOC150759</i>	0.0139	3.62	hypothetical LOC150759
<i>NCRNA00201</i>	0.0034	3.39	non-protein coding RNA 201
<i>PDK4</i>	0.0011	3.25	pyruvate dehydrogenase kinase, isozyme 4

<i>BCAT1</i>	0.0042	3.24	branched chain amino-acid transaminase 1, cytosolic
<i>PELI1</i>	0.0059	3.24	Pellino homolog 1 (Drosophila)
<i>CYP3A5</i>	0.0015	3.12	cytochrome P450, family 3, subfamily A, polypeptide 5
<i>HPGD</i>	0.0032	3.10	hydroxyprostaglandin dehydrogenase 15-(NAD)
<i>LRRC31</i>	0.0030	3.05	leucine rich repeat containing 31
<i>KIAA1984</i>	0.0082	2.97	KIAA1984
<i>HNRNPD</i>	0.0054	2.86	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
<i>IL28A</i>	0.0026	2.85	interleukin 28A (interferon, lambda 2)
<i>DDX60</i>	0.0026	2.84	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
<i>PHF14</i>	0.0021	2.82	PHD finger protein 14
<i>LOC100288092</i>	0.0025	2.82	Hypothetical protein LOC100288092
<i>ZNF207</i>	0.0027	2.82	zinc finger protein 207
<i>NCOA2</i>	0.0025	2.81	nuclear receptor coactivator 2
<i>AHSA2</i>	0.0064	2.72	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
<i>SLC2A13</i>	0.0052	2.69	solute carrier family 2 (facilitated glucose transporter), member 13
<i>TJP2</i>	0.0073	2.65	tight junction protein 2 (zona occludens 2)
<i>ELK4</i>	0.0125	2.64	ELK4, ETS-domain protein (SRF accessory protein 1)

<i>CHD2</i>	0.0053	2.63	chromodomain helicase DNA binding protein 2
<i>RUFY2</i>	0.0046	2.60	RUN and FYVE domain containing 2
<i>VAPA</i>	0.0075	2.56	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
<i>IQGAP2</i>	0.0026	2.56	IQ motif containing GTPase activating protein 2
<i>HMGCS2</i>	0.0022	2.56	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
<i>FNIP2</i>	0.0024	2.51	folliculin interacting protein 2
<i>INPP4B</i>	0.0056	2.51	inositol polyphosphate-4-phosphatase, type II, 105kDa
<i>NOV</i>	0.0027	2.48	nephroblastoma overexpressed gene
<i>PLSCR4</i>	0.0021	2.46	phospholipid scramblase 4
<i>DST</i>	0.0035	2.46	dystonin
<i>REG4</i>	0.0018	2.46	regenerating islet-derived family, member 4
<i>C11orf61</i>	0.0016	2.45	chromosome 11 open reading frame 61
<i>LRRFIP1</i>	0.0054	2.45	leucine rich repeat (in FLII) interacting protein 1
<i>SPATA13</i>	0.0032	2.43	spermatogenesis associated 13
<i>NAPEPLD</i>	0.0097	2.42	N-acyl phosphatidylethanolamine phospholipase D
<i>PLCB1</i>	0.0038	2.42	phospholipase C, beta 1 (phosphoinositide-specific)
<i>CTAGE5</i>	0.0132	2.41	CTAGE family, member 5
<i>PTGER4</i>	0.0061	2.40	prostaglandin E receptor 4 (subtype EP4)

<i>AKAP7</i>	0.0074	2.40	A kinase (PRKA) anchor protein 7
<i>HOXB8</i>	0.0051	2.40	homeobox B8
<i>INPP5F</i>	0.0052	2.38	inositol polyphosphate-5-phosphatase F
<i>ZNF148</i>	0.0082	2.38	zinc finger protein 148
<i>SRSF10</i>	0.0083	2.37	serine/arginine-rich splicing factor 10
<i>PPP1R9A</i>	0.0174	2.37	protein phosphatase 1, regulatory (inhibitor) subunit 9A
<i>IFIT2</i>	0.0024	2.37	interferon-induced protein with tetratricopeptide repeats 2
<i>ARL14</i>	0.0037	2.37	ADP-ribosylation factor-like 14
<i>DNAJC15</i>	0.0029	2.37	DnaJ (Hsp40) homolog, subfamily C, member 15
<i>ARHGAP5</i>	0.0075	2.36	Rho GTPase activating protein 5
<i>ZNF518A</i>	0.0021	2.36	zinc finger protein 518A
<i>HNMT</i>	0.0036	2.36	histamine N-methyltransferase
<i>ETNK1</i>	0.0268	2.35	ethanolamine kinase 1
<i>CAPN9</i>	0.0016	2.35	calpain 9
<i>TBL1XR1</i>	0.0200	2.33	transducin (beta)-like 1 X-linked receptor 1
<i>LOC439911</i>	0.0037	2.33	hypothetical LOC439911
<i>TUG1</i>	0.0084	2.33	taurine upregulated 1 (non-protein coding)
<i>ZNF532</i>	0.0104	2.32	zinc finger protein 532
<i>SLC44A1</i>	0.0092	2.32	solute carrier family 44, member 1
<i>IGF1R</i>	0.0028	2.31	insulin-like growth factor 1 receptor

<i>TACC1</i>	0.0055	2.30	transforming, acidic coiled-coil containing protein 1
<i>OCLN</i>	0.0057	2.30	occludin
<i>DLEU2</i>	0.0044	2.29	deleted in lymphocytic leukemia 2 (non-protein coding)
<i>PRKCA</i>	0.0033	2.29	protein kinase C, alpha
<i>CLK4</i>	0.0049	2.29	CDC-like kinase 4
<i>TMEM135</i>	0.0035	2.28	transmembrane protein 135
<i>HERC5</i>	0.0049	2.28	hect domain and RLD 5
<i>GAS5</i>	0.0032	2.27	growth arrest-specific 5 (non-protein coding)
<i>RASA2</i>	0.0054	2.27	RAS p21 protein activator 2
<i>FRY</i>	0.0017	2.27	furry homolog (Drosophila)
<i>SLC4A4</i>	0.0076	2.27	solute carrier family 4, sodium bicarbonate cotransporter, member 4
<i>DDX58</i>	0.0059	2.26	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
<i>GIPC2</i>	0.0015	2.26	GIPC PDZ domain containing family, member 2
<i>N4BP2L2</i>	0.0034	2.26	NEDD4 binding protein 2-like 2
<i>PELI2</i>	0.0028	2.25	pellino homolog 2 (Drosophila)
<i>DIAPH2</i>	0.0135	2.25	diaphanous homolog 2 (Drosophila)
<i>DICER1</i>	0.0185	2.25	dicer 1, ribonuclease type III
<i>ZNF862</i>	0.0027	2.25	zinc finger protein 862
<i>RBM4</i>	0.0011	2.25	RNA binding motif protein 4

<i>SLC1A1</i>	0.0037	2.25	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
<i>GLCCI1</i>	0.0173	2.25	glucocorticoid induced transcript 1
<i>C1orf63</i>	0.0175	2.24	chromosome 1 open reading frame 63
<i>RICTOR</i>	0.0018	2.24	RPTOR independent companion of MTOR, complex 2
<i>ACRC</i>	0.0067	2.24	acidic repeat containing
<i>MIER3</i>	0.0098	2.22	mesoderm induction early response 1, family member 3
<i>AMIGO2</i>	0.0039	2.22	adhesion molecule with Ig-like domain 2
<i>NCRNA00275</i>	0.0109	2.22	non-protein coding RNA 275
<i>LOC100288939</i>	0.0063	2.22	Similar to hCG1987955
<i>XIST</i>	0.0014	2.22	X (inactive)-specific transcript (non-protein coding)
<i>DIRAS2</i>	0.0044	2.21	DIRAS family, GTP-binding RAS-like 2
<i>GNAQ</i>	0.0017	2.21	guanine nucleotide binding protein (G protein), q polypeptide
<i>ATXN1</i>	0.0015	2.21	ataxin 1
<i>EXPH5</i>	0.0019	2.20	exophilin 5
<i>FRMD3</i>	0.0045	2.20	FERM domain containing 3
<i>BMPR2</i>	0.0056	2.20	bone morphogenetic protein receptor, type II (serine/threonine kinase)

<i>TRIM52</i>	0.0082	2.19	tripartite motif-containing 52
<i>CSNK1A1</i>	0.0150	2.19	Casein kinase 1, alpha 1
<i>KIAA1107</i>	0.0144	2.19	KIAA1107
<i>PRSS23</i>	0.0082	2.18	Protease, serine, 23
<i>CAMK2D</i>	0.0014	2.18	calcium/calmodulin-dependent protein kinase II delta
<i>FAM162A</i>	0.0029	2.18	family with sequence similarity 162, member A
<i>KLHL24</i>	0.0042	2.18	kelch-like 24 (Drosophila)
<i>RUFY3</i>	0.0065	2.18	RUN and FYVE domain containing 3
<i>MAGI1</i>	0.0026	2.18	membrane associated guanylate kinase, WW and PDZ domain containing 1
<i>FAM117B</i>	0.0182	2.18	family with sequence similarity 117, member B
<i>LTBP1</i>	0.0037	2.18	latent transforming growth factor beta binding protein 1
<i>EEA1</i>	0.0029	2.18	early endosome antigen 1
<i>SH3BP2</i>	0.0102	2.18	SH3-domain binding protein 2
<i>C6orf26</i> / <i>MSH5</i>	0.0048	2.18	chromosome 6 open reading frame 26 /mutS homolog 5 (E. coli)
<i>VPS13C</i>	0.0026	2.18	vacuolar protein sorting 13 homolog C (S. cerevisiae)
<i>GMFB</i>	0.0015	2.18	glia maturation factor, beta
<i>DPYSL2</i>	0.0023	2.17	dihydropyrimidinase-like 2
<i>SCAI</i>	0.0125	2.17	suppressor of cancer cell invasion

<i>ARHGAP32</i>	0.0041	2.17	Rho GTPase activating protein 32
<i>SMARCA1</i>	0.0065	2.16	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
<i>TIA1</i>	0.0027	2.16	TIA1 cytotoxic granule-associated RNA binding protein
<i>RSF1</i>	0.0071	2.16	remodeling and spacing factor 1
<i>PROS1</i>	0.0086	2.15	protein S (alpha)
<i>RABGGTB</i>	0.0026	2.15	Rab geranylgeranyltransferase, beta subunit
<i>NIN</i>	0.0065	2.14	ninein (GSK3B interacting protein)
<i>KRIT1</i>	0.0110	2.14	KRIT1, ankyrin repeat containing
<i>ZNF302</i>	0.0229	2.14	Zinc finger protein 302
<i>TXNDC16</i>	0.0061	2.13	thioredoxin domain containing 16
<i>ANK3</i>	0.0088	2.13	ankyrin 3, node of Ranvier (ankyrin G)
<i>KPNA5</i>	0.0110	2.13	karyopherin alpha 5 (importin alpha 6)
<i>GGPS1</i>	0.0048	2.13	geranylgeranyl diphosphate synthase 1
<i>C12orf28</i>	0.0083	2.13	chromosome 12 open reading frame 28
<i>PRPF4B</i>	0.0016	2.13	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
<i>FBXL17</i>	0.0084	2.13	F-box and leucine-rich repeat protein 17
<i>C5orf41</i>	0.0182	2.12	chromosome 5 open reading frame 41
<i>CDK19</i>	0.0044	2.12	cyclin-dependent kinase 19

<i>MMP28</i>	0.0011	2.12	matrix metallopeptidase 28
<i>THBS1</i>	0.0024	2.12	thrombospondin 1
<i>MIR21</i>	0.0043	2.12	microRNA 21
<i>FLJ31306</i>	0.0050	2.12	hypothetical LOC379025
<i>TIGD1</i>	0.0079	2.12	tigger transposable element derived 1
<i>CLMN</i>	0.0040	2.11	calmin (calponin-like, transmembrane)
<i>EIF5</i>	0.0108	2.11	eukaryotic translation initiation factor 5
<i>SLC35A3</i>	0.0169	2.11	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
<i>FAM172A</i>	0.0036	2.11	family with sequence similarity 172, member A
<i>SESTD1</i>	0.0021	2.10	SEC14 and spectrin domains 1
<i>DCUN1D4</i>	0.0057	2.10	DCN1, defective in cullin neddylation 1, domain containing 4 (<i>S. cerevisiae</i>)
<i>RTP4</i>	0.0024	2.10	receptor (chemosensory) transporter protein 4
<i>ATP8B1</i>	0.0027	2.10	ATPase, aminophospholipid transporter, class I, type 8B, member 1
<i>FNBP1</i>	0.0112	2.10	formin binding protein 1
<i>RAPGEF5</i>	0.0059	2.10	Rap guanine nucleotide exchange factor (GEF) 5
<i>SR140</i>	0.0026	2.09	U2-associated SR140 protein
<i>TFPI</i>	0.0020	2.09	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
<i>GRB14</i>	0.0022	2.09	growth factor receptor-bound protein 14

<i>GALNT12</i>	0.0033	2.09	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase (GalNAc-T12)	12
<i>LPCAT1</i>	0.0016	2.09	lysophosphatidylcholine acyltransferase 1	
<i>PHIP</i>	0.0045	2.08	pleckstrin homology domain interacting protein	
<i>RDH13</i>	0.0128	2.08	retinol dehydrogenase 13 (all-trans/9-cis)	
<i>ZMYM6</i>	0.0111	2.08	zinc finger, MYM-type 6	
<i>PAG1</i>	0.0025	2.07	phosphoprotein associated with glycosphingolipid microdomains 1	
<i>SEPSECS</i>	0.0127	2.07	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	
<i>NF1</i>	0.0064	2.07	neurofibromin 1	
<i>CNKSR3</i>	0.0060	2.06	CNKSR family member 3	
<i>LRIG2</i>	0.0110	2.06	Leucine-rich repeats and immunoglobulin-like domains 2	
<i>MTMR10</i>	0.0053	2.06	myotubularin related protein 10	
<i>SUN1</i>	0.0155	2.06	Sad1 and UNC84 domain containing 1	
<i>ABCA5</i>	0.0042	2.05	ATP-binding cassette, sub-family A (ABC1), member 5	
<i>FAR2</i>	0.0092	2.05	Fatty acyl CoA reductase 2	
<i>ZNF33A</i>	0.0073	2.05	zinc finger protein 33A	
<i>ATP10B</i>	0.0040	2.05	ATPase, class V, type 10B	
<i>SDCCAG1</i>	0.0102	2.05	serologically defined colon cancer antigen 1	
<i>STON2</i>	0.0272	2.05	stonin 2	

<i>MMAA</i>	0.0349	2.05	methylnmalonic aciduria (cobalamin deficiency) cblA type
<i>LOC100287896</i>	0.0066	2.04	Similar to cag
<i>FLJ44342</i>	0.0030	2.04	hypothetical LOC645460
<i>SMCHD1</i>	0.0043	2.04	structural maintenance of chromosomes flexible hinge domain containing 1
<i>GPATCH2</i>	0.0069	2.04	G patch domain containing 2
<i>SERPINB9</i>	0.0163	2.04	serpin peptidase inhibitor, clade B (ovalbumin), member 9
<i>CUL4B</i>	0.0189	2.04	cullin 4B
<i>SCIN</i>	0.0038	2.03	scinderin
<i>NR2C1</i>	0.0070	2.03	nuclear receptor subfamily 2, group C, member 1
<i>OPN3</i>	0.0053	2.03	opsin 3
<i>RAD50</i>	0.0014	2.03	RAD50 homolog (<i>S. cerevisiae</i>)
<i>MECOM</i>	0.0041	2.03	MDS1 and EVI1 complex locus
<i>VPS13B</i>	0.0058	2.03	vacuolar protein sorting 13 homolog B (yeast)
<i>ZBTB20</i>	0.0117	2.02	zinc finger and BTB domain containing 20
<i>TAF1D</i>	0.0030	2.02	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa
<i>FRMD4B</i>	0.0139	2.02	FERM domain containing 4B
<i>PHF3</i>	0.0050	2.02	PHD finger protein 3
<i>FUBP1</i>	0.0050	2.02	far upstream element (FUSE) binding protein 1

<i>DNAJB4</i>	0.0026	2.02	DnaJ (Hsp40) homolog, subfamily B, member 4
<i>KCTD12</i>	0.0060	2.01	potassium channel tetramerisation domain containing 12
<i>TC2N</i>	0.0056	2.01	tandem C2 domains, nuclear
<i>FAM190A</i>	0.0122	2.01	family with sequence similarity 190, member A
<i>GAB1</i>	0.0163	2.01	GRB2-associated binding protein 1
<i>IFIT3</i>	0.0030	2.00	interferon-induced protein with tetratricopeptide repeats 3

Supplementary Table 3 Glycosylation-related differentially expressed genes associated with *H. pylori* infection of E12 cells by microarray analysis – all 170 genes (FDR<0.05)

Gene symbol	P-value	Fold change	Gene name
Upregulated			
<i>LGALS7</i>	0.0115	2.31	lectin, galactoside-binding, soluble, 7
<i>UGGT1</i>	0.0059	1.98	UDP-glucose glycoprotein glucosyltransferase 1
<i>ST3GAL5</i>	0.0035	1.90	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
<i>PARM1</i>	0.0026	1.87	prostate androgen-regulated mucin-like protein 1
<i>ST6GALNAC4</i>	0.0036	1.79	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
<i>NAGK</i>	0.0016	1.79	N-acetylglucosamine kinase
<i>VSIG1</i>	0.0240	1.71	V-set and immunoglobulin domain containing 1
<i>EDEM2</i>	0.0032	1.69	ER degradation enhancer, mannosidase alpha-like 2
<i>MPDU1</i>	0.0029	1.69	mannose-P-dolichol utilization defect 1
<i>DPM2</i>	0.0015	1.61	dolichyl-phosphate mannosyltransferase

			polypeptide 2, regulatory subunit
<i>LMAN2</i>	0.0021	1.60	lectin, mannose-binding 2
<i>GMPPB</i>	0.0019	1.59	GDP-mannose pyrophosphorylase B
<i>ALG3</i>	0.0214	1.59	asparagine-linked glycosylation 3, alpha-1,3-mannosyltransferase homolog (<i>S. cerevisiae</i>)
<i>GALK2</i>	0.0027	1.57	galactokinase 2
<i>PAPSS2</i>	0.0120	1.54	3'-phosphoadenosine 5'-phosphosulfate synthase 2
<i>DDOST</i>	0.0094	1.53	dolichyl-diphosphooligosaccharide--protein glycosyltransferase
<i>MCAM</i>	0.0111	1.53	melanoma cell adhesion molecule
<i>B3GALT6</i>	0.0097	1.53	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6
<i>SLC35B1</i>	0.0025	1.51	solute carrier family 35, member B1
<i>GMPPA</i>	0.0031	1.49	GDP-mannose pyrophosphorylase A
<i>ALDOC</i>	0.0020	1.48	aldolase C, fructose-bisphosphate
<i>MPI</i>	0.0174	1.46	mannose phosphate isomerase
<i>MGAT2</i>	0.0191	1.46	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
<i>GNPDA1</i>	0.0097	1.46	glucosamine-6-phosphate deaminase 1
<i>MRC2</i>	0.0227	1.45	mannose receptor, C type 2
<i>COG1</i>	0.0048	1.44	component of oligomeric golgi complex 1

			dolichyl-phosphate (UDP-N-acetylglucosamine)	
<i>DPAGT1</i>	0.0041	1.42	N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	
<i>FUT4</i>	0.0039	1.41	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	
<i>B3GNT9</i>	0.0411	1.41	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	
<i>HABP4</i>	0.0207	1.40	hyaluronan binding protein 4	
<i>NEU1</i>	0.0031	1.40	sialidase 1 (lysosomal sialidase)	
<i>GALE</i>	0.0133	1.38	UDP-galactose-4-epimerase	
<i>LGALS1</i>	0.0065	1.38	lectin, galactoside-binding, soluble, 1	
<i>B4GALT7</i>	0.0021	1.37	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	
<i>TSTA3</i>	0.0019	1.37	tissue specific transplantation antigen P35B	
<i>NANS</i>	0.0155	1.36	N-acetylneuraminic acid synthase	
<i>VSIG2</i>	0.0024	1.35	V-set and immunoglobulin domain containing 2	
<i>B4GALT3</i>	0.0272	1.33	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	
<i>MANBAL</i>	0.0057	1.33	mannosidase, beta A, lysosomal-like	
<i>GLA</i>	0.0055	1.31	galactosidase, alpha	

<i>NPL</i>	0.0110	1.30	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)
<i>HS6ST1</i>	0.0283	1.30	heparan sulfate 6-O-sulfotransferase 1
<i>ST3GAL1</i>	0.0457	1.30	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
<i>PIGX</i>	0.0231	1.29	phosphatidylinositol glycan anchor biosynthesis, class X
<i>SLC35C2</i>	0.0248	1.27	solute carrier family 35, member C2
<i>ICAM3</i>	0.0092	1.27	intercellular adhesion molecule 3
<i>SLC35A2</i>	0.0070	1.27	solute carrier family 35 (UDP-galactose transporter), member A2
<i>BCAN</i>	0.0142	1.27	brevican
<i>ICAM1</i>	0.0187	1.26	intercellular adhesion molecule 1
<i>GALT</i>	0.0202	1.26	galactose-1-phosphate uridylyltransferase
<i>GNB1</i>	0.0146	1.25	guanine nucleotide binding protein (G protein), beta polypeptide 1
<i>PIGH</i>	0.0243	1.25	phosphatidylinositol glycan anchor biosynthesis, class H
<i>B4GALT2</i>	0.0050	1.24	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2
<i>MGAT1</i>	0.0095	1.24	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
<i>MUC5AC</i>	0.0110	1.23	mucin 5AC, oligomeric mucus/gel-forming

<i>B3GAT3</i>	0.0298	1.23	beta-1,3-glucuronyltransferase (glucuronosyltransferase I)	3
<i>MLEC</i>	0.0230	1.22	malectin	
<i>OS9</i>	0.0493	1.22	osteosarcoma amplified 9, endoplasmic reticulum lectin	
<i>COG4</i>	0.0065	1.22	component of oligomeric golgi complex	4
<i>POMGNT1</i>	0.0051	1.22	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	
<i>FUT1</i>	0.0082	1.21	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	
<i>SLC17A5</i>	0.0387	1.21	solute carrier family 17 (anion/sugar transporter), member 5	
<i>DAD1</i>	0.0320	1.21	defender against cell death	1
<i>PIGC</i>	0.0140	1.21	phosphatidylinositol glycan anchor biosynthesis, class C	
<i>HEXA</i>	0.0077	1.21	hexosaminidase A (alpha polypeptide)	
<i>SLC35B2</i>	0.0055	1.21	solute carrier family 35, member B2	
<i>ALG5</i>	0.0129	1.20	asparagine-linked glycosylation 5, dolichyl-phosphate beta-glucosyltransferase homolog (<i>S. cerevisiae</i>)	
<i>LEPRE1</i>	0.0075	1.18	leucine proline-enriched proteoglycan (leprecan)	1

<i>TFF1</i>	0.0147	1.18	trefoil factor 1
<i>IL8</i>	0.0099	1.17	interleukin 8
<i>TFF3</i>	0.0083	1.16	trefoil factor 3 (intestinal)
<i>AGA</i>	0.0345	1.16	aspartylglucosaminidase
<i>FUCA1</i>	0.0048	1.16	fucosidase, alpha-L- 1, tissue
<i>ALG2</i>	0.0026	1.16	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)
<i>SLC25A3</i>	0.0217	1.14	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
<i>LAMP3</i>	0.0241	1.14	lysosomal-associated membrane protein 3
<i>MOGS</i>	0.0071	1.13	mannosyl-oligosaccharide glucosidase
<i>GNB2L1</i>	0.0204	1.13	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
<i>GPI</i>	0.0207	1.11	glucose-6-phosphate isomerase
<i>CHST5</i>	0.0489	1.09	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5
<i>GUSB</i>	0.0346	1.08	glucuronidase, beta
<i>MAN2B1</i>	0.0414	1.07	mannosidase, alpha, class 2B, member 1
Downregulated			
<i>REG4</i>	0.0018	2.46	regenerating islet-derived family, member 4

<i>OGT</i>	0.0037	2.25	O-linked N-acetylglucosamine (GlcNAc) transferase (OGT)
<i>AMIGO2</i>	0.0039	2.22	adhesion molecule with Ig-like domain 2
<i>SLC35A3</i>	0.0169	2.11	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
<i>GALNT12</i>	0.0033	2.09	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)
<i>EXT1</i>	0.0256	1.99	exostosin 1
<i>MAN2A1</i>	0.0041	1.86	mannosidase, alpha, class 2A, member 1
<i>LY75</i>	0.0075	1.86	lymphocyte antigen 75
<i>PIGZ</i>	0.0072	1.82	phosphatidylinositol glycan anchor biosynthesis, class Z
<i>UGP2</i>	0.0320	1.79	UDPglucose pyrophosphorylase 2
<i>MANEA</i>	0.0225	1.79	mannosidase, endoalpha
<i>ALG13</i>	0.0138	1.78	asparaginelinked glycosylation 13 homolog (S. cerevisiae)
<i>PIGK</i>	0.0051	1.77	phosphatidylinositol glycan anchor biosynthesis, class K
<i>ST3GAL4</i>	0.0032	1.71	ST3 betagalactoside alpha2,3sialyltransferase 4
<i>B4GALNT3</i>	0.0129	1.71	beta1,4Nacetylgalactosaminyl transferase 3

<i>HMMR</i>	0.0039	1.70	hyaluronanmediated (RHAMM)	motility	receptor
<i>B4GALT6</i>	0.0134	1.69	UDPGal:betaGlcNAc galactosyltransferase, polypeptide 6	beta	1,4
<i>CD164</i>	0.0308	1.65	CD164 molecule, sialomucin		
<i>LGALS2</i>	0.0127	1.58	lectin, galactosidebinding, soluble, 2		
<i>MAN1A1</i>	0.0021	1.53	mannosidase, alpha, class 1A, member 1		
<i>MUC13</i>	0.0038	1.53	mucin 13, cell surface associated		
<i>B4GALT5</i>	0.0071	1.51	UDPGal:betaGlcNAc galactosyltransferase, polypeptide 5	beta	1,4
<i>ASAH1</i>	0.0118	1.50	Nacylsphingosine ceramidase) 1	amidohydrolase	(acid
<i>B3GNT5</i>	0.0041	1.49	UDPGlcNAc:betaGal beta1,3Nacetylglucosaminyltransferase 5		
<i>LMAN1</i>	0.0026	1.48	lectin, mannosebinding, 1		
<i>GALNT1</i>	0.0159	1.47	UDPNacetylalphaDgalactosamine:polypepti de Nacetylglactosaminyltransferase 1 (GalNAcT1)		
<i>MGAT4B</i>	0.0065	1.46	mannosyl beta1,4Nacetylglucosaminyltransferase, isozyme B	(alpha1,3)glycoprotein	
<i>COG3</i>	0.0110	1.46	component of oligomeric golgi complex 3		
<i>B3GNT2</i>	0.0102	1.44	UDPGlcNAc:betaGal		

			beta1,3Nacetylglucosaminyltransferase 2
<i>FPGT</i>	0.0142	1.44	fucose1phosphate guanylyltransferase
			glucosamine
<i>GNE</i>	0.0082	1.43	(UDPNacetyl)2epimerase/Nacetylmannosa mine kinase
<i>UGCG</i>	0.0083	1.43	UDPglucose ceramide glucosyltransferase
<i>ASAH2B</i>	0.0475	1.43	Nacylsphingosine amidohydrolase (nonlysosomal ceramidase) 2B
<i>HSPC159</i>	0.0053	1.42	Galectin-related protein
			UDPNacetylalphaDgalactosamine:polypepti
<i>GALNT10</i>	0.0238	1.42	de Nacetylglactosaminyltransferase 10 (GalNAcT10)
			mannosyl (alpha1,3)glycoprotein
<i>MGAT4A</i>	0.0375	1.42	beta1,4Nacetylglucosaminyltransferase, isozyme A
			phosphatidylinositol glycan anchor
<i>PIGF</i>	0.0032	1.41	biosynthesis, class F
<i>ATRN</i>	0.0069	1.40	attractin
			UDPNacetylalphaDgalactosamine:polypepti
<i>GALNT7</i>	0.0061	1.40	de Nacetylglactosaminyltransferase 7 (GalNAcT7)
<i>CLEC16A</i>	0.0202	1.38	Ctype lectin domain family 16, member A
<i>LGALS8</i>	0.0066	1.38	lectin, galactosidebinding, soluble, 8

<i>MUC20</i>	0.0040	1.35	mucin 20, cell surface associated
<i>CHSY1</i>	0.0482	1.34	chondroitin sulfate synthase 1
<i>GAL3ST1</i>	0.0092	1.34	galactose3O-sulfotransferase 1
<i>UGDH</i>	0.0046	1.33	UDP-glucose 6-dehydrogenase
<i>PKD2</i>	0.0161	1.32	polycystic kidney disease 2 (autosomal dominant)
<i>SLC35A1</i>	0.0063	1.31	solute carrier family 35 (CMP-sialic acid transporter), member A1
<i>MANBA</i>	0.0050	1.30	mannosidase, beta A, lysosomal
<i>GCNT2</i>	0.0364	1.30	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
<i>SLC35B3</i>	0.0083	1.30	solute carrier family 35, member B3
<i>GALNT2</i>	0.0136	1.30	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAcT2)
<i>HSPG2</i>	0.0095	1.30	heparan sulfate proteoglycan 2
<i>FUT11</i>	0.0308	1.29	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
<i>CD58</i>	0.0047	1.28	CD58 molecule
<i>UGGT2</i>	0.0446	1.28	UDP-glucose glycoprotein glucosyltransferase 2
<i>ST6GALNAC1</i>	0.0106	1.28	ST6 (alpha-N-acetylneuraminyl2,3-beta-galactosyl1,

			3)Nacetylgalactosaminide alpha2,6sialyltransferase 1
<i>GALM</i>	0.0284	1.28	galactose mutarotase (aldose 1epimerase)
<i>HGSNAT</i>	0.0051	1.27	heparanalphaglucoaminide Nacetyltransferase
<i>MAN2B2</i>	0.0411	1.26	mannosidase, alpha, class 2B, member 2
<i>MANEAL</i>	0.0068	1.26	mannosidase, endoalphanlike
<i>MGAT5</i>	0.0112	1.26	mannosyl (alpha1,6)glycoprotein beta1,6Nacetylglucosaminyltransferase
<i>EXTL2</i>	0.0151	1.26	exostoses (multiple)like 2
<i>SDCBP</i>	0.0059	1.24	syndecan binding protein (syntenin)
<i>UGT1A1, A4, A6, A8A10</i>	0.0205	1.23	UDP glucuronosyltransferase 1 family, polypeptide A1, A4, A6, A8A10
<i>OVGP1</i>	0.0396	1.23	oviductal glycoprotein 1, 120kDa
<i>COG5</i>	0.0268	1.23	component of oligomeric golgi complex 5
<i>POFUT1</i>	0.0175	1.22	protein Ofucosyltransferase 1
<i>HAS3</i>	0.0153	1.22	hyaluronan synthase 3
<i>MAN2A2</i>	0.0406	1.21	mannosidase, alpha, class 2A, member 2
<i>DGCR2</i>	0.0197	1.21	DiGeorge syndrome critical region gene 2
<i>FN3KRP</i>	0.0208	1.19	fructosamine 3 kinase related protein
<i>GLCE</i>	0.0444	1.18	glucuronic acid epimerase
<i>TFF2</i>	0.0263	1.17	trefoil factor 2

<i>CHPF2</i>	0.0250	1.17	chondroitin polymerizing factor 2
<i>UGT1A1, 1A31A10</i>	0.0368	1.16	UDP glucuronosyltransferase 1 family, polypeptide A1, 1A31A10
<i>UGT8</i>	0.0394	1.16	UDP glycosyltransferase 8
<i>HEXB</i>	0.0156	1.14	hexosaminidase B (beta polypeptide)
<i>POFUT2</i>	0.0182	1.12	protein Ofucosyltransferase 2
<i>PIGU</i>	0.0436	1.11	phosphatidylinositol glycan anchor biosynthesis, class U
<i>CHPF</i>	0.0418	1.11	chondroitin polymerizing factor
<i>B4GALT1</i>	0.0445	1.11	UDPGal:betaGlcNAc beta 1,4 galactosyltransferase, polypeptide 1
<i>UXS1</i>	0.0460	1.11	UDPGlucuronate decarboxylase 1
<i>NPC2</i>	0.0453	1.11	NiemannPick disease, type C2
<i>LDHA</i>	0.0352	1.09	lactate dehydrogenase A
<i>ALDOA</i>	0.0098	1.09	aldolase A, fructosebisphosphate
<i>EDEM1</i>	0.0307	1.08	ER degradation enhancer, mannosidase alphaslike 1
<i>ERLEC1</i>	0.0095	1.08	endoplasmic reticulum lectin 1
<i>LDHB</i>	0.0123	1.06	lactate dehydrogenase B
