

**Supplementary Table 1 Primer List**

NO.	Name	Gene ID	Primer Bank ID	Amplicon Size	Sequence (5'-3')	Length	Tm	Location	Species
1	NEU1	4758	189217412c2	111	F: CTTTGCTGAGGCGAGGAAAA R: TTGACAATGAACGCTGTAGGAG	21 22	60.9 60.3	276-296 386-365	Human
2	CMAH	8418	3800814a1	118	F: ATGGGCAGCATCGAACAAACA R: AGACGTAGTCTTTGCCAGTGC	21 21	62.9 62.3	1-21 118-98	Human
3	B3GALNT2	148789	227498246c1	107	F: GATGTGGTAGTTGGCGTGTTG R: CGTTGACTTAATGTGGGATGCTG	21 23	61.5 61.7	154-174 260-238	Human
4	ALG2	85365	91807120c2	80	F: GGCAGACTGCATCTTAGTCAAC R: GGTCTATGTGAGACAGGGACTT	22 22	60.9 60.6	507-528 586-565	Human
5	FUT8	2530	332078495c3	96	F: TTCAAGTGGTCGAGCTTCCC R: GTACAAGTCGATCTGCGAGGT	21 21	61.8 61.6	857-876 952-932	Human
6	ST3GAL2	6483	151101481c2	127	F: CGTCTGGACCCGAGAGAAC R: GCCAGGCACTATCTGGAACA	19 20	61.4 61.6	285-303 411-392	Human
7	SLC35A1	10559	270288772c1	201	F: CAACCACAGCCGTGTGTATCA R: TGCTAAGAGCTAGGAAAGCCAT	21 22	62.6 60.9	131-151 331-310	Human
8	B3GALT4	8705	51702476c1	220	F: TGATCGTCTGGACCCTCTTCG R: ATGGCGTTTCTCTGGTTCAGG	21 21	63.0 62.4	50-70 269-249	Human
9	MGAT2	4247	62750355c1	77	F: GTGCATAACCGGCCCAAT R: ACGAGGACGTTGTCAATTCCC	20 21	62.4 62.3	370-389 446-426	Human
10	NANS	54187	195963408c1	75	F: AACACCCGTGCTTCATCATTG R: GGATCATGCGCTTGGCTAC	21 19	61.2 61.0	47-67 121-103	Human
11	CMAS	55907	22027483c1	144	F: ACCTGGCAGCCCTAATTCTG	20	61.6	131-150	Human

12	NEU3	10825	117190518c1	140	R: TCGAAACCCATACACTCTGGAA F: AAGTGACAACATGCTCCTTCAA R: TCTCCTCGTAGAACGCTTCTC	22 22 21	60.8 60.1 60.7	274-253 107-128 246-226	Human
13	UGGT1	56886	237649097c1	183	F: GCCTTCCAGCAGATAGCAGC R:GCTTTCAGGATTAGACGAGGGAT	20 23	63.0 61.5	397-416 579-557	Human
14	UGGT2	55757	238859592c1	249	F: CCTTCGCAATCTTGGGATCAA R: GCCGGATCAATAAACAGAACCA	21 22	60.4 60.6	1227-1247 1475-1454	Human
15	GBE1	2632	189458811c1	148	F: GGAGATCGACCCGTACTIONTAA R: ACATCTGTGGACGCCAAATGA	21 21	61.0 62.0	96-116 243-223	Human
16	GCNT2	2651	30061504c1	171	F: TGTTCCCTGGCTCTATGCCAAA R: TTAGCAAACAGGCTTGGTGAAT	21 22	61.4 60.4	921-941 1091-1070	Human
17	B3GNT1	11041	92091577c1	208	F: TCCTACCCCAATAACCTGCTG R: GCTCGTTTTTGTTCATGGGCA	21 21	60.9 62.0	616-636 823-803	Human
18	B3GAT3	26229	332164741c1	249	F: AAGGAGTCGTCTACTTTGCTGA R: GGGCATTGGGCTTATCTAACAG	22 22	60.8 60.8	560-581 808-787	Human
19	B4GALT1	2683	193211604c1	221	F: GGCGTCACCCTCGTTTTACTAC R: GGGCCAGAATCCACGACTG	19 19	62.4 62.4	103-123 323-305	Human
20	ALG1	56052	209976995c1	127	F: CCCCAGTTTTCCAGTACGG	20 20	62.2 62.0	418-399 418-399	Human

					R: CAGCAATGCTAGGCAGACCT					
21	MGAT3	4248	148539889c1	144	F: ATGAAGATGAGACGCTACAAGC R: GCTGGACACCAGGTTAGGG	22 19	61.7 61.7	1-22 144-126	Human	
22	FUT1	2523	171906616c3	121	F: GCAGCTTCACGACTGGATGT R: CTCTCTGCGGATCTGTTCCC	20 20	61.7 61.7	432-451 552-533	Human	
23	ST3GAL3	6487	28373075c1	144	F: GCCTGCTGAATTAGCCACCAA R: GCCCACTTGCGAAAGGAGT	21 19	63 62.6	210-230 353-335	Human	
24	ST3GAL4	6484	363543344c1	79	F: CTCCTGCGGCTTGAGGATTA R: CTCACTCCCCTTGGTCCCATA	21 21	61.9 62.4	192-212 270-250	Human	
25	ST3GAL5	8869	109633043c1	235	F: TCCCTGCAATGGTACACC R: ACTTGGGACGACATTCCTTCT	19 21	61.3 60.8	136-154 370-350	Human	

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