Appendix 3. Non-HK human TM expressed genes grouped based on function*

Group no.	GO term	Description	I_A	I_B
1	GO:0005576	EXTRACELLULAR REGION	20 (20)	1892 (17826)
1	GO:0005615	EXTRACELLULAR SPACE	7 (20)	744 (17826)
3	GO:0005581	COLLAGEN	7 (10)	22 (17826)
3	GO:0005201	EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT	8 (10)	66 (17826)
3	GO:0031012	EXTRACELLULAR MATRIX	6 (10)	117 (17826)
3	GO:0005576	EXTRACELLULAR REGION	10 (10)	1892 (17826)
3	GO:0005515	PROTEIN BINDING	8 (10)	6581 (17826)
4	GO:0016021	INTEGRAL TO MEMBRANE	26 (37)	4218 (17826)
4	GO:0004930	G-PROTEIN COUPLED RECEPTOR ACTIVITY	9 (37)	362 (17826)
4	GO:0005886	PLASMA MEMBRANE	21 (37)	3059 (17826)
4	GO:0005887	INTEGRAL TO PLASMA MEMBRANE	12 (37)	1005 (17826)
4	GO:0007156	HOMOPHILIC CELL ADHESION	5 (37)	139 (17826)
4	GO:0007186	G-PROTEIN COUPLED RECEPTOR PROTEIN SIGNALING PATHWAY	5 (37)	291 (17826)
4	GO:0007155	CELL ADHESION	7 (37)	538 (17826)
4	GO:0004872	RECEPTOR ACTIVITY	11 (37)	1327 (17826)
4	GO:0016020	MEMBRANE	15 (37)	3852 (17826)
4	GO:0005509	CALCIUM ION BINDING	6 (37)	646 (17826)
7	GO:0005887	INTEGRAL TO PLASMA MEMBRANE	14 (16)	1005 (17826)
7	GO:0006865	AMINO ACID TRANSPORT	7 (16)	48 (17826)
7	GO:0015293	SYMPORTER ACTIVITY	6 (16)	113 (17826)
7	GO:0006810	TRANSPORT	7 (16)	482 (17826)
7	GO:0055085	TRANSMEMBRANE TRANSPORT	7 (16)	505 (17826)
7	GO:0005624	MEMBRANE FRACTION	6 (16)	482 (17826)
7	GO:0005886	PLASMA MEMBRANE	9 (16)	3059 (17826)
7	GO:0016020	MEMBRANE	7 (16)	3852 (17826)
7	GO:0004872	RECEPTOR ACTIVITY	5 (16)	1327 (17826)
11	GO:0000139	GOLGI MEMBRANE	10 (13)	361 (17827)

11	GO:0005794	GOLGI APPARATUS	11 (13)	835 (17827)
11	GO:0016757	TRANSFERASE ACTIVITY, TRANSFERRING GLYCOSYL GROUPS	5 (13)	151 (17827)
11	GO:0016020	MEMBRANE	12 (13)	3852 (17827)
11	GO:0016021	INTEGRAL TO MEMBRANE	12 (13)	4218 (17827)
12	GO:0006814	SODIUM ION TRANSPORT	10 (16)	119 (17826)
12	GO:0006811	ION TRANSPORT	12 (16)	519 (17826)
12	GO:0015293	SYMPORTER ACTIVITY	8 (16)	113 (17826)
12	GO:0005244	VOLTAGE-GATED ION CHANNEL ACTIVITY	6 (16)	150 (17826)
12	GO:0005215	TRANSPORTER ACTIVITY	6 (16)	299 (17826)
12	GO:0016324	APICAL PLASMA MEMBRANE	5 (16)	168 (17826)
12	GO:0055085	TRANSMEMBRANE TRANSPORT	6 (16)	505 (17826)
12	GO:0016021	INTEGRAL TO MEMBRANE	10 (16)	4218 (17826)
12	GO:0005887	INTEGRAL TO PLASMA MEMBRANE	6 (16)	1005 (17826)
12	GO:0006810	TRANSPORT	5 (16)	482 (17826)
12	GO:0005886	PLASMA MEMBRANE	9 (16)	3059 (17826)
12	GO:0016020	MEMBRANE	7 (16)	3852 (17826)
13	GO:0016021	INTEGRAL TO MEMBRANE	46 (49)	4218 (17826)
13	GO:0016020	MEMBRANE	42 (49)	3852 (17826)
13	GO:0005794	GOLGI APPARATUS	8 (49)	835 (17826)
13	GO:0000139	GOLGI MEMBRANE	6 (49)	361 (17826)
13	GO:0055085	TRANSMEMBRANE TRANSPORT	6 (49)	505 (17826)
14	GO:0006468	PROTEIN PHOSPHORYLATION	28 (33)	494 (17826)
14	GO:0005524	ATP BINDING	33 (33)	1489 (17826)
14	GO:0016740	TRANSFERASE ACTIVITY	29 (33)	1163 (17826)
14	GO:0000166	NUCLEOTIDE BINDING	32 (33)	1975 (17826)
14	GO:0004674	PROTEIN SERINE/THREONINE KINASE ACTIVITY	14 (33)	339 (17826)
14	GO:0004714	TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE ACTIVITY	6 (33)	35 (17826)
14	GO:0007169	TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHWAY	7 (33)	71 (17826)
14	GO:0004713	PROTEIN TYROSINE KINASE ACTIVITY	7 (33)	80 (17826)
14	GO:0004672	PROTEIN KINASE ACTIVITY	7 (33)	177 (17826)
14	GO:0007165	SIGNAL TRANSDUCTION	13 (33)	1105 (17826)

14	GO:0005887	INTEGRAL TO PLASMA MEMBRANE	12 (33)	1005 (17826)
14	GO:0005515	PROTEIN BINDING	26 (33)	6581 (17826)
14	GO:0004872	RECEPTOR ACTIVITY	12 (33)	1327 (17826)
14	GO:0005737	CYTOPLASM	14 (33)	4626 (17826)
14	GO:0005886	PLASMA MEMBRANE	9 (33)	3059 (17826)
14	GO:0005829	CYTOSOL	5 (33)	1320 (17826)
18	GO:0003700	SEQUENCE-SPECIFIC DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	15 (19)	950 (17826)
18	GO:0005634	NUCLEUS	19 (19)	5045 (17826)
18	GO:0045893	POSITIVE REGULATION OF TRANSCRIPTION, DNA-DEPENDENT	7 (19)	134 (17826)
18	GO:0003702	RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY	7 (19)	139 (17826)
18	GO:0003677	DNA BINDING	13 (19)	1767 (17826)
18	GO:0045944	POSITIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	7 (19)	319 (17826)
18	GO:0043565	SEQUENCE-SPECIFIC DNA BINDING	7 (19)	483 (17826)
18	GO:0006366	TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	5 (19)	180 (17826)
18	GO:0008134	TRANSCRIPTION FACTOR BINDING	5 (19)	221 (17826)
18	GO:0006355	REGULATION OF TRANSCRIPTION, DNA-DEPENDENT	8 (19)	1112 (17826)
18	GO:0016563	TRANSCRIPTION ACTIVATOR ACTIVITY	5 (19)	294 (17826)
18	GO:0005515	PROTEIN BINDING	14 (19)	6581 (17826)
22	GO:0046872	METAL ION BINDING	18 (18)	2847 (17826)
22	GO:0008270	ZINC ION BINDING	14 (18)	2016 (17826)
22	GO:0005515	PROTEIN BINDING	14 (18)	6581 (17826)
26	GO:0008270	ZINC ION BINDING	18 (19)	2016 (17826)
26	GO:0005622	INTRACELLULAR	17 (19)	1935 (17826)
26	GO:0046872	METAL ION BINDING	18 (19)	2847 (17826)
26	GO:0003677	DNA BINDING	13 (19)	1767 (17826)
26	GO:0005634	NUCLEUS	18 (19)	5045 (17826)
26	GO:0006355	REGULATION OF TRANSCRIPTION, DNA-DEPENDENT	11 (19)	1112 (17826)
26	GO:0003700	SEQUENCE-SPECIFIC DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	10 (19)	950 (17826)
26	GO:0045449	REGULATION OF TRANSCRIPTION	8 (19)	916 (17826)

* Groupings performed by classification tool within DAVID; groups containing ≥ 10 genes included

odds ratio	p-value	Genes
9,42	2.87E-03	GRP MYOC PLTP STC2 GDF15 NXPH4 SCRG1 ANGPTL2 FJX1 OLFML2B C2CD2 PCOLCE2 DKK3 OLFML3 C1
8,39	0,0098	GRP MYOC GDF15 SCRG1 ANGPTL2 FJX1 DKK3
567,19	1.72E-16	COL1A1 COL4A1 COL4A2 COL4A5 COL5A1 COL5A2 COL11A1
216,07	9.69E-16	COL1A1 COL4A1 COL4A2 COL4A5 COL5A1 COL5A2 COL6A2 COL11A1
91,42	1.38E-08	COL1A1 COL4A2 COL5A1 COL5A2 COL6A2 EMILIN1
9,42	1.69E-07	COL1A1 COL4A1 COL4A2 COL4A5 COL5A1 COL5A2 COL6A2 COL7A1 COL11A1 EMILIN1
2,17	0,01	COL1A1 COL4A1 COL4A2 COL4A5 COL5A1 COL6A2 COL7A1 EMILIN1
2,97	2.43E-06	ALCAM BAI2 CA12 CDH6 CDH11 FCGRT MR1 PCDH9 SECTM1 FZD7 TSPAN5 BTN2A2 GPNMB LPHN1 KIA
11,98	3.82E-05	BAI2 PTGER1 PTGER2 FZD7 GPRC5A GPR176 LPHN1 GPR162 CXCR7
3,31	5.72E-05	BAI2 CDH6 CDH11 FCGRT MR1 CD200 PCDH9 PTGER1 PTGER2 SECTM1 FZD7 GPRC5A RAMP1 GPR176 L
5,75	0,0004	CD200 PRRG1 PTGER1 PTGER2 TPBG SGCE GPRC5A RAMP1 GPNMB PROCR GPR176 LEPROT
17,33	0,0091	CDH6 CDH11 PCDH9 PVRL3 AMIGO2
8,28	0,01	BAI2 PTGER1 PTGER2 GPR176 LPHN1
6,27	0,01	ALCAM CDH6 CDH11 PCDH9 TPBG GPNMB AMIGO2
3,99	0,01	FCGRT PTGER1 PTGER2 GPRC5A RAMP1 PROCR GPR176 OR10H3 GPR162 CXCR7 NETO2
1,88	0,02	ALCAM CA12 PRRG1 TPBG TSPAN5 BTN2A2 GPNMB PROCR KIAA0922 TMEM158 LEPROT HEG1 NETO2 I
4,47	0,03	CDH6 CDH11 PCDH9 PRRG1 SGCE HEG1
15,52	3.07E-13	SCARB2 CD200 SLC1A1 SLC1A5 SLC6A8 SLC6A9 SLC7A1 SLC43A1 GPRC5A SLC7A6 SLC16A4 SLC16A3 GPF
162,48	6.94E-12	SLC1A5 SLC6A9 SLC7A1 SLC7A4 SLC43A1 SLC7A6 SLC7A11
59,16	4.11E-07	SLC1A1 SLC1A5 SLC6A8 SLC6A9 SLC16A4 SLC16A3
16,18	8.93E-05	SLC1A1 SLC1A5 SLC6A8 SLC6A9 SLC7A1 SLC7A4 SLC7A6
15,44	0,0001	SLC7A1 SLC7A4 SLC43A1 SLC7A6 SLC16A4 SLC16A3 SLC7A11
13,87	0,0022	SCARB2 SLC1A1 SLC1A5 SLC6A9 SLC16A4 SLC16A3
3,28	0,01	CD200 SLC7A1 SLC43A1 GPRC5A SLC7A6 SLC16A4 SLC16A3 GPR176 SLC7A11
2,02	0,06	SCARB2 SLC1A1 SLC1A5 SLC6A8 SLC6A9 SLC7A4 LEPROT
4,20	0,06	SCARB2 SLC1A5 SLC7A1 GPRC5A GPR176
37,99	2.63E-12	FKTN MAN1A1 MAN2A1 B3GALNT1 UST ST6GALNAC4 GALNT10 CHST7 XYLT1 GALNTL4

18,07	1.52E-10	FKTN MAN1A1 MAN2A1 B3GALNT1 UST ST6GALNAC4 DSE GALNT10 CHST7 XYLT1 GALNTL4
45,41	4.74E-05	B3GALNT1 GALNT10 XYLT1 GLT8D2 GALNTL4
4,27	0,0001	FKTN MAN1A1 MAN2A1 B3GALNT1 UST ST6GALNAC4 DSE GALNT10 CHST7 XYLT1 GLT8D2 GALNTL4
3,90	0,0002	FKTN MAN1A1 MAN2A1 B3GALNT1 UST ST6GALNAC4 DSE GALNT10 CHST7 XYLT1 GLT8D2 GALNTL4
93,62	8.79E-16	SCN1B SCN9A SCNN1A SLC5A2 SLC5A5 SLC6A8 SLC22A4 SLC4A4 SLC4A7 SLC23A2
25,76	5.06E-13	CACNB3 KCNJ2 KCNJ8 KCNS3 SCN1B SCN9A SCNN1A SLC5A2 SLC5A5 SLC6A8 SLC22A4 SLC23A2
78,88	2.38E-11	SLC5A2 SLC5A5 SLC6A8 SLC22A4 SLC4A4 SLC16A3 SLC4A7 SLC23A2
44,56	2.29E-06	CACNB3 KCNJ2 KCNJ8 KCNS3 SCN1B SCN9A
22,36	0,0001	SLC5A2 SLC5A5 SLC22A4 SLC4A4 SLC4A7 SLC23A2
33,16	0,0002	CACNB3 SCNN1A SLC22A4 SLC4A7 SLC23A2
13,24	0,0030	KCNS3 SCN9A SLC5A2 SLC5A5 SLC22A4 SLC16A3
2,64	0,01	KCNJ8 KCNS3 SCN1B SCN9A SCNN1A SLC5A2 SLC5A5 SLC6A8 SLC4A7 SLC23A2
6,65	0,01	KCNJ2 SLC6A8 SLC22A4 SLC4A4 SLC16A3 SLC23A2
11,56	0,01	CACNB3 SLC5A2 SLC5A5 SLC6A8 SLC4A4
3,28	0,01	KCNS3 SCNN1A SLC5A5 SLC22A4 SLC4A4 SLC16A3 SLC4A7 SLC23A2 KCTD12
2,02	0,06	CACNB3 KCNJ2 KCNJ8 SCN1B SCN9A SLC5A2 SLC6A8
3,97	1.05E-22	FKTN IFI27 PLXNA1 SECTM1 SLC2A3 SLC7A4 PTPLA FAM38A ARMCX2 UST TSPAN5 LHFP GLIPR1 KIAA09
3,97	1.44E-18	FKTN IFI27 SLC2A3 SLC7A4 PTPLA FAM38A ARMCX2 UST TSPAN5 LHFP GLIPR1 KIAA0922 FAM119B TME
3,49	0,01	FKTN SECTM1 UST D4S234E SCARA3 TMCO1 LEPROT TMEM22
6,05	0,01	FKTN UST D4S234E SCARA3 TMCO1 LEPROT
4,32	0,02	SLC2A3 SLC7A4 SLC43A1 SLC7A11 SLC2A10 SLC46A3
30,62	2.30E-36	AXL CDK6 DAPK1 EPHA4 EPHB4 EPHB6 GRK5 MET MST1R MYLK NPR2 PRKD1 PTK7 RPS6KA3 SGK1 TEK V
11,97	1.81E-33	ABL2 AXL CDK6 DAPK1 EPHA4 EPHB4 EPHB6 GRK5 MET MST1R MYLK NPR2 DDR2 PDGFRA PDGFRB PRK
13,47	9.01E-28	ABL2 AXL CDK6 DAPK1 EPHA4 EPHB4 GRK5 MET MST1R MYLK DDR2 PDGFRA PDGFRB PRKD1 RPS6KA3 S
8,75	5.95E-27	ABL2 AXL CDK6 DAPK1 EPHA4 EPHB4 EPHB6 GRK5 MET MST1R MYLK NPR2 DDR2 PDGFRA PDGFRB PRK
22,31	3.41E-13	DAPK1 PRKD1 RPS6KA3 SGK1 WEE1 STK19 AATK MELK NUAK1 SPEG MAP3K2 CHEK2 SRPK3 ZAK
92,60	3.71E-08	AXL EPHA4 EPHB4 DDR2 PTK7 TEK
53,26	4.40E-08	AXL EPHA4 EPHB4 EPHB6 MST1R DDR2 TEK
47,27	1.04E-07	ABL2 MET PDGFRA PDGFRB TEK WEE1 AATK
21,36	2.77E-05	ABL2 EPHB6 NPR2 RPS6KA3 TEK MAP3K2 TRIB2
6,36	3.17E-05	ABL2 AXL DAPK1 EPHA4 MET MST1R NPR2 DDR2 PDGFRB PRKD1 PTK7 RPS6KA3 TEK

6,45	0,0001	AXL EPHA4 EPHB4 EPHB6 MET MST1R DDR2 PDGFRA PDGFRB PRKD1 PTK7 TEK
2,13	0,0010	ABL2 AXL CDK6 DAPK1 EPHA4 EPHB4 EPHB6 GRK5 MET MST1R MYLK PDGFRB PRKD1 PTK7 SGK1 TEK W
4,88	0,0021	AXL EPHA4 EPHB4 EPHB6 MET MST1R NPR2 DDR2 PDGFRA PDGFRB PTK7 TEK
1,63	0,08	ABL2 CDK6 DAPK1 GRK5 PRKD1 RPS6KA3 SGK1 AATK IKBKE MELK MAP3K2 STK39 TRIB2 ZAK
1,59	0,24	GRK5 MET MST1R NPR2 PDGFRA PDGFRB PRKD1 SGK1 TEK
2,05	0,5	ABL2 MYLK PRKD1 RPS6KA3 MAP3K2
14,81	2.13E-13	AHR KLF5 E2F3 ELF4 ETS1 FOXF2 GATA2 MAF PLAGL2 SOX4 SOX9 SOX15 TCF4 TEAD3 HAND1
3,53	3.57E-08	AHR KLF5 E2F3 ELF4 ETS1 FOXF2 GATA2 MAF MITF PLAGL1 PLAGL2 SOX4 SOX9 SOX15 TCF4 TEAD3 UTF
49,01	5.16E-08	AHR E2F3 ETS1 FOXF2 SOX4 TCF4 HAND1
47,25	6.69E-08	KLF5 ETS1 MAF SOX9 SOX15 TEAD3 UTF1
6,90	1.25E-06	AHR KLF5 E2F3 ETS1 FOXF2 MITF PLAGL1 PLAGL2 SOX4 SOX15 TCF4 TEAD3 HAND1
20,59	2.20E-05	ELF4 GATA2 MITF PLAGL1 PLAGL2 SOX9 UTF1
13,60	0,0003	AHR ELF4 ETS1 FOXF2 GATA2 MAF TCF4
26,06	0,0009	AHR KLF5 ETS1 MAF HAND1
21,23	0,0026	AHR ETS1 FOXF2 GATA2 HAND1
6,75	0,0086	AHR KLF5 ELF4 GATA2 MAF MITF SOX4 SOX15
15,96	0,01	E2F3 ELF4 FOXF2 MITF SOX9
2,00	0,01	AHR KLF5 E2F3 ELF4 ETS1 FOXF2 GATA2 PLAGL1 SOX4 SOX9 TCF4 TEAD3 UTF1 HAND1
6,26	4.16E-12	RNF5 RNF113A ZNF239 PDLIM4 ZBED1 ZNHIT1 TRIM38 DZIP1 LIMCH1 PDZRN3 RNF115 APOBEC3C RNF
6,88	1.01E-07	RNF5 RNF113A ZNF239 PDLIM4 TRIM38 DZIP1 LIMCH1 PDZRN3 RNF115 APOBEC3C RNF220 RNF114 PL
2,11	0,01	RNF5 RNF113A PDLIM4 ZBED1 ZNHIT1 TRIM38 DZIP1 PDZRN3 RNF115 APOBEC3C RNF220 RNF114 SCN
8,38	1.38E-13	ZFHX3 KLF5 SP110 PLAGL1 PLAGL2 SALL2 SNAI2 NR2F1 ZNF22 ZNF187 ZNF217 ZNF239 ZNF264 ADNP2 I
8,24	5.02E-12	ZFHX3 KLF5 PLAGL1 PLAGL2 PMS2L3 SALL2 SNAI2 ZNF22 ZNF187 ZNF217 ZNF239 ZNF264 ADNP2 IKZF4
5,93	6.72E-11	ZFHX3 KLF5 SP110 PLAGL1 PLAGL2 SALL2 SNAI2 NR2F1 ZNF22 ZNF187 ZNF217 ZNF239 ZNF264 ADNP2 I
6,90	1.25E-06	KLF5 SP110 PLAGL1 PLAGL2 SALL2 SNAI2 ZNF22 ZNF217 ZNF239 ZNF264 IKZF4 ZNF430 ZNF528
3,35	1.76E-06	ZFHX3 KLF5 SP110 PLAGL1 PLAGL2 SALL2 SNAI2 NR2F1 ZNF22 ZNF187 ZNF217 ZNF239 ZNF264 ADNP2 I
9,28	2.40E-06	ZFHX3 KLF5 PMS2L3 SALL2 NR2F1 ZNF187 ZNF264 ADNP2 ZFHX4 ZNF430 ZNF528
9,88	1.00E-05	ZFHX3 KLF5 PLAGL2 SALL2 NR2F1 ZNF187 ZNF217 ADNP2 IKZF4 ZFHX4
8,19	0,002	SP110 PLAGL1 PLAGL2 SNAI2 ZNF22 ZNF217 ZNF239 IKZF4

ORF54 LY6G5C FAM172A FAM131A OLFML2A C3ORF64

A0922 TMEM158 PVRL3 OR10H3 GPR162 CXCR7 HEG1 NETO2 JAM3 FAM171A1 SLC46A3 AMIGO2

PHN1 PVRL3 OR10H3 GPR162 CXCR7 JAM3 AMIGO2

FAM171A1 SLC46A3

R176 LEPROT

22 SLC7A11 FAM119B TMEM158 D4S234E FAM18B CEND1 REEP2 SCARA3 TMCO1 CCDC109B TMEM45A FAM176B C14ORF132 CXCR7 POPDC3 TMEM
:M158 D4S234E FAM18B CEND1 REEP2 SCARA3 TMCO1 LEPROT CCDC109B TMEM45A FAM176B C14ORF132 POPDC3 TMEM135 TMEM185B DNAJC22

VEE1 STK19 IKBKE MELK NUAK1 SPEG MAP3K2 CHEK2 SRPK3 STK39 TRIB2 ZAK
D1 PTK7 RPS6KA3 SGK1 TEK WEE1 STK19 AATK IKBKE MELK NUAK1 SPEG MAP3K2 CHEK2 SRPK3 STK39 TRIB2 ZAK
SGK1 TEK WEE1 STK19 AATK IKBKE MELK NUAK1 SPEG MAP3K2 CHEK2 SRPK3 STK39 ZAK
D1 RPS6KA3 SGK1 TEK WEE1 STK19 AATK IKBKE MELK NUAK1 SPEG MAP3K2 CHEK2 SRPK3 STK39 TRIB2 ZAK

'EE1 STK19 AATK IKBKE MELK NUAK1 MAP3K2 CHEK2 STK39 ZAK

1 HAND1 ELL3

220 RNF114 ZBED5 SCNM1 PLEKHF2 ZCCHC24
EKHF2 ZCCHC24
M1 PLEKHF2

KZF4 ZFHX4 ZNF430 ZNF528
ZFHX4 ZNF430 ZNF528
KZF4 ZFHX4 ZNF430 ZNF528

KZF4 ZFHX4 ZNF430 ZNF528

l135 TMEM185B DNAJC22 ORAI2 TMEM22 SLC2A10 GDPD5 NETO2 GLT8D2 TMEM47 MBOAT2 C9ORF91 FAM171A1 SLC46A3 DPY19L4 SERINC2 FAM1
2 ORAI2 TMEM22 SLC2A10 GDPD5 NETO2 GLT8D2 MBOAT2 C9ORF91 FAM171A1 SLC46A3 DPY19L4 SERINC2 FAM155A

.55A