- Dgig_XM_0285548	33.0:like:SLC2A6/SLC2A8 NA lar_tr.HG3.0:like:SLC2A6/SLC2A8 NA ke:SLC2A6/SLC2A8 NA 3.0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA 0:like:SLC2A6/SLC2A8 NA
Horcal_Hcv1.av93.c5.g58.i1 Sugar_tr.HG3.2:like:SLC2A6/ Beraby_Baby_sb335635 Sugar_tr.HG3.2:like:SLC2A6/ Beraby_Baby_sb335636 Sugar_tr.HG3.2:like:SLC2A6/ Lampan_Lpan_4654_01 Sugar_tr.HG3.2:like:SLC2A6/ Lampan_Lpan_3980_01 Sugar_tr.HG3.2:like:SLC2A6/ Lampan_Lpan_3980_01 Sugar_tr.HG3.2:like:SLC2A6/ Coemet_Cmet_scaffold8678_01 Sugar_tr.HG3.2:like:SlC2A6/ Vmul_Simscaffold11049_01 Sugar_tr.HG3.2:like:SlC2A6/ Vmul_sbMO435893 Sugar_tr.HG3.2:like:SlC2A6/	SLC2A8 NA SLC2A8 NA SLC2A8 NA SLC2A8 NA SLC2A8 NA 6/SLC2A8 NA
Ctel_gnl_WGS_AMQN_CAPTEDRAFT_mRNA63779 Sugar_Cint_ENSCINT00000009501 Sugar_tr.HG3.8:like:SLC2A-Cint_ENSCINT000000034418 Sugar_tr.HG3.8:like:SLC2A-Tcas_TC013484_001 Sugar_tr.HG3.8:like:SLC2A-Tcas_TC030899_001 Sugar_tr.HG3.8:like:SLC2A-Tcas_TC012760_001 Sugar_tr.HG3.8:like:SLC2A-Tcas_TC012760_001 Sugar_tr.HG3.8:like:SLC2A-Tcas_TC0333331_001	
*Tcas_TC015809_001 Sugar_tr.HG3.8:like:SLC *Tcas_TC015809_001 Sugar_tr.HG3.8:like:SLC *Tcas_TC015809_001 Sugar_tr.HG3.8:like:SLC *Tcas_TC015809_001 Sugar_tr.HG3.8:like:SLC *Tcas_TC014872_001 Sugar_tr.HG3.8:like:SLC *Tcas_TC014877_001 Sugar_tr.HG3.8:like:SLC2A *Tcas_TC033857 001 Sugar_tr.HG3.20:like:SLC2A6/	SLC2A6/SLC2A8 NA 2A6/SLC2A8 NA
Dmel_FBtr0088073 Sugar_tr.HG3.13:like:SLC2A6/SLC2A8 100	NA
-Tcas_TC006802_001 Sugar_tr.H0	C2A8 NA A8 NA BLC2A8 NA 6/SLC2A8 NA ugar_tr.HG3.14:like:SLC2A6/SLC2A8 NA ugar_tr.HG3.15:like:SLC2A6/SLC2A8 NA ugar_tr.HG3.15:like:SLC2A6/SLC2A8 NA
Tcas_TC000733_001 Sugar_tr.HG3.15 Tcas_TC012290_001 Sugar_tr.HG3.15:like:STC012291_001 Sugar_tr.HG3.15:like:STC012291_001 Sugar_tr.HG3.15:like:STC032878_001 Sugar_tr.HG3.15:like:SLC0- Tcas_TC032878_001 Sugar_tr.HG3.15:like:SLC0- Tcas_TC033441_001 Sugar_tr.HG3.1- Tcas_TC009681_001 Sugar_tr.HG3.1- Tcas_TC009682_001 Sugar_tr.HG3.1-	ike:SLC2A6/SLC2A8 NA ike:SLC2A6/SLC2A8 NA is:SLC2A6/SLC2A8 NA
100 Tcas_TC008119_001 Sugar_tr.H	SLC2A6/SLC2A8 NA HG3.15:like:SLC2A6/SLC2A8 NA G3.15:like:SLC2A6/SLC2A8 NA Ltr.HG3.15:like:SLC2A6/SLC2A8 NA
Dmel_FBtr0077584 Sugar_tr.HG3.17:like:Sl Dmel_FBtr0452102 Sugar_tr.HG3.17:like:Sl Dmel_FBtr0081601 Sugar_tr.HG3.17:like:Sl Dmel_FBtr0077580 Sugar_tr.HG3.17:like:Sl Dmel_FBtr0077580 Sugar_tr.HG3.17:like:Sl Dmel_FBtr0077580 Sugar_tr.HG3.18:like:Sl Dmel_FBtr0077587 Sugar_tr.HG3.18:like:Sl	ike:SLC2A6/SLC2A8 NA IG3.17:like:SLC2A6/SLC2A8 NA 7:like:SLC2A6/SLC2A8 NA 1.17:like:SLC2A6/SLC2A8 NA
Tcas_TC001412_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC034160_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC034161_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC034161_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012232_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012233_001 Sugar_tr.HG3.18:like:SLC2A6/ Tcas_TC012230_001 Sugar_tr.HG3.18:like:SLC2A	SLC2A8 NA LC2A6/SLC2A8 NA SLC2A6/SLC2A8 NA SLC2A6/SLC2A8 NA S:SLC2A6/SLC2A8 NA
Tcas_TC001413_001 Sugar_tr.HG3.18:like:SL0 Tcas_TC034222_001 Sugar_tr.HG3.18:like:S Tcas_TC001414_001 Sugar_tr.HG3.18:like:S Tcas_TC012228_001 Sugar_tr.HG3.18: Tcas_TC012229_001 Sugar_tr.HG3.18: Tcas_TC012229_001 Sugar_tr.HG3.18: Tcas_TC012229_001 Sugar_tr.HG3.18: Tcas_TC012229_001 Sugar_tr.HG3.18: Tcas_TC012228_001 Sugar_tr.HG3.18: Tcas_TC01222	LC2A6/SLC2A8 NA LC2A6/SLC2A8 NA LC2A6/SLC2A8 NA :like:SLC2A6/SLC2A8 NA like:SLC2A6/SLC2A8 NA SLC2A6/SLC2A8 NA G3.18:like:SLC2A6/SLC2A8 NA SLC2A6/SLC2A8 NA SLC2A6/SLC2A8 NA
100 Tetwil_g23104.t1 Sugar_tr.HG3.6:SLC2A6/ 100 Tetwil_g23105.t1 Sugar_tr.HG3.6:SLC2A6/ -Emue_Em0005g1624a.t1 Sugar_tr.HG3.6:SLC2A6/S -Emue_Em0005g1617a.t1 Sugar_tr.HG3.6:SLC2A6/SL	SLC2A8 SLC2A6/SLC2A8 LC2A8 SLC2A6/SLC2A8 /SLC2A8 SLC2A6/SLC2A8 /SLC2A8 SLC2A6/SLC2A8 A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8
## Tetwil_g25976.t1 Sugar_tr.HG3.6:SLC2A6/	C2A6/SLC2A8 SLC2A6/SLC2A8 C2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8
*Aque_Aqu2.1.39896_001 Sugar_tr.HG3.6:S *Aque_Aqu2.1.20808_001 Sugar_tr.HG3.6:S *Aque_Aqu2.1.20810_001 Sugar_tr.HG3.6:SLC2A6/SLC2A8 Sugar_tr.HG3.6:SLC2A6/SLC2A6	6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 5:LC2A6/SLC2A8 6:LC2A6/SLC2A8 6:LC2A6/SLC2A8 6:LC2A6/SLC2A8 6:LC2A6/SLC2A8 6:LC2A6/SLC2A8
Tetwil_g15755.t2 Sugar_tr.HG3.6:SLC2A6/SL Tetwil_g18467.t1 Sugar_tr.HG3.6:SLC2A6 Tetwil_g13159.t1 Sugar_tr.HG3.6:SLC2A6 Tetwil_g18468.t1 Sugar_tr.HG3.6:SLC2A6 Tetwil_g18468.t1 Sugar_tr.HG3.6:SLC2A6 Tetwil_g18470.t1 Sugar_tr.HG3.6:SLC2A6 TrH2_TrispH2_007925-RA Sugar_tr.HG3.6:SLC2A6 Tool_HoiH23_PIH23_005098-RA Sugar_tr.HG3.6:SLC2A6 Tool_Hoon_g01114.t1 Sugar_tr.HG3.6:SLC2A6/SLC2A6	6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A6/SLC2A8 SLC2A6/SLC2A8 A8 SLC2A6/SLC2A8 A8 SLC2A6/SLC2A8 A8 SLC2A6/SLC2A8
+HoiH23_PIH23_005096-RA Sugar_tr.HG3.6:SLC2A6 +HoiH23_PIH23_005096-RA Sugar_tr.HG3.6:SLC2A6/SLC2A8	/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 HG3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 C2A6/SLC2A8 SLC2A6/SLC2A8 LC2A6/SLC2A8 SLC2A6/SLC2A8 IG3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8
Tadh_TriadT38377 Sugar_tr.HG3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A6/SLC2A6/SLC2A8 Sugar_tr.HG3.6:SLC2A6/SLC2A8 Sugar_tr.HG3.6:SLC2A6/	SLC2A6/SLC2A8 A8 SLC2A6/SLC2A8 B/SLC2A6/SLC2A8 B/SLC2A8 J/SLC2A8 SLC2A6/SLC2A8 SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8
100 Hhon_g01119.t1 Sugar_tr.HG3.6:SLC2A6/S	/SLC2A8 SLC2A6/SLC2A8 .8 SLC2A6/SLC2A8 .C2A6/SLC2A8 SLC2A6/SLC2A8 .C2A6/SLC2A8 SLC2A6/SLC2A8 .C2A6/SLC2A8 SLC2A6/SLC2A8 .C2A8 SLC2A6/SLC2A8 .C2A8 SLC2A6/SLC2A8 .C2A8 SLC2A6/SLC2A8 .C2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 .C2A6/SLC2A8 SLC2A6/SLC2A8
Gracom_Gcom_scaffold12669_01 Sugar_tr.HG3.6:SLC2A6/SLC2A8 SL Scil_scict013738.1 Sugar_tr.HG3.6:SLC2A6/SLC2A8 SL Gracom_Gcom_scaffold16020_01 Sugar_tr.HG3.6:SLC2A6/SL	C2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A
+ Hvul_g5135_1 Sugar_tr.HG3.6:SLC2A6/SLC2A8 NA + Hvul_g22836_1 Sugar_tr.HG3.6:SLC2A6/SLC2A8 Sugar_tr.HG3.6:SLC2A6/SLC2A	NA ugar_tr.HG3.6:SLC2A6/SLC2A8 NA LC2A8 NA i/SLC2A8 NA
-Hvul_g19557_1 Sugar_tr.HG3.61 -Hvul_g28044_1 Sugar_tr.HG3.61 -Hvul_g28044_1 Sugar_tr.HG3.61 -Hvul_g28053_1 Sugar_tr.HG3.61 -Hvul_g1428_1 Sugar_tr.HG3.61 -Hvul_g1428_1 Sugar_tr.HG3.61 -Hvul_g1428_1 Sugar_tr.HG3.6:SL	HG3.6:SLC2A6/SLC2A8 NA 6:SLC2A6/SLC2A8 NA 8:6:SLC2A6/SLC2A8 NA 6:3.6:SLC2A6/SLC2A8 NA 6:3.6:SLC2A6/SLC2A8 NA
Cint_ENSCINT0000003039 Sugar_tr.HG3.6:Signar	C2A6/SLC2A8 SLC2A8 2A6/SLC2A8 SLC2A8 6:SLC2A6/SLC2A8 SLC2A8 tr.HG3.6:SLC2A6/SLC2A8 SLC2A6 6:SLC2A6/SLC2A8 SLC2A6 6:SLC2A6/SLC2A8 SLC2A6 6:SLC2A6/SLC2A8 SLC2A6
Ctel_gnl_WGS_AMQN_CAPTEDRAFT_mF Plajan_Pjan_C564862_01 Sugar_tr.HG3.6:SL	NA1723 Sugar_tr.HG3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 ::SLC2A6/SLC2A8 SLC2A6/SLC2A8 ::SLC2A6/SLC2A8 SLC2A6/SLC2A8 :C2A6/SLC2A8 SLC2A6/SLC2A8 :C2A6/SLC2A8 SLC2A6/SLC2A8 :MRNA158645 Sugar_tr.HG3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 :A6/SLC2A8 SLC2A6/SLC2A8 :SLC2A8 SLC2A6/SLC2A8 :SLC2A8 SLC2A6/SLC2A8 :A6/SLC2A8 SLC2A6/SLC2A8 :SLC2A8 SLC2A6/SLC2A8
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*Exapal_XM_021057439.2 Sugar_tr.HG3.6:SLC2 *Exapal_XM_021041405.2 Sugar_tr.HG3.6:SLC2 *Spis_XP_022789882_1 Sugar_tr.HG3.6:SLC2A6/ *Spis_XP_022789884_1 Sugar_tr.HG3.6:SLC2A6/ *Spis_XP_022789889_1 Sugar_tr.HG3.6:SLC2A6/ *Spis_XP_022789889_1 Sugar_tr.HG3.6:SLC2A6/ *Spis_XP_022789905_1 Sugar_tr.HG3.6:SLC2A6/ *Spis_XP_022789904_1 Sugar_tr.HG3.6:SLC2A6/ *Adig_XM_015899588.1 Sugar_tr.HG3.6:SLC2A6/ *Adig_XM_015899587.1 Sugar_tr.HG3.6:SLC2A6/ *Adig_XM_015899587.1 Sugar_tr.HG3.6:SLC2A6/ *Adig_XM_015899587.1 Sugar_tr.HG3.6:SLC2A6/	2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A8 SLC2A6/SLC2A8 2A6/SLC2A8 SLC2A6/SLC2A8 2A6/SLC2A8 SLC2A6/SLC2A8 2A6/SLC2A8 SLC2A6/SLC2A8 2A6/SLC2A8 SLC2A6/SLC2A8 3LC2A6/SLC2A8 SLC2A6/SLC2A8 3LC2A6/SLC2A8 SLC2A6/SLC2A8 3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8 3.6:SLC2A6/SLC2A8 SLC2A6/SLC2A8
Adig_XM_015899539.1 Sugar_tr.HG3.6:S Adig_XM_015899540.1 Sugar_tr.HG3.6:S Adig_XM_015899582.1 Sugar_tr.HG3.6:S Adig_XM_015899582.1 Sugar_tr.HG3. Adig_XM_015899538.1 Sugar_tr.HG3. Adig_XM_015899538.1 Sugar_tr.HG3. Adig_XM_015899538.1 Sugar_tr.HG3. Adig_XM_015899538.1 Sugar_tr.HG3. Adig_XM_015899539.1 Sugar_tr.HG3.6:S Adig_XM_015899539.1 Sugar_tr.HG3.6:S Adig_XM_015899538.1 Sugar_tr.HG3.6:S Adig_XM_015899538.1	C2A6/SLC2A8 SLC2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 C2A6/SLC2A8 SLC2A6/SLC2A8 SLC2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A8 C2A6/SLC2A12 C2A6/SLC2A
Cgig_XM_034457498.1 Sugar_tr.HG3.3:SLC2A10/SLC2A12 Skow_XM_006812512.1 Sugar_tr.HG3.3:SLC2A10/SLC2A12 Spur_XM_030983482.1 Sugar_tr.HG3.3:SLC2A10/SLC2A12 Gracom_Gcom_C549996_01 Sugar_tr.HG3.3:SLC2A10/SLC2A12 Plajan_Pjan_scaffold11211_01 Sugar_tr.HG3.3:SLC2A12 Plajan_Pjan_scaffold11210_01 Sugar_tr.HG3.3:SLC2A12 Plajan_Pjan_scaffold11208_01 Sugar_tr.HG3.3:SLC2A12 Plajan_Pjan_scaffold11208_01 Sugar_tr.HG3.3:SLC2A12	2 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12 A10/SLC2A10/SLC2A12 A10/SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12 A10/SLC2A12 SLC2A10/SLC2A12
Drer_ENSDART00000053531 Sugar_tr.HG3	.3:SLC2A10/SLC2A12 SLC2A12 A10/SLC2A12 SLC2A12 SLC2A10/SLC2A12 SLC2A12 SLC2A10/SLC2A12 SLC2A12 B:SLC2A10/SLC2A12 SLC2A10
**Morvir_scaffold206.g20.t1 Sugar_tr.HG3.3:SLC2A1 **Dgig_XM_028550578.1 Sugar_tr.HG3.3:SLC2A10/SLC2 **Nvec_v1g222989 Sugar_tr.HG3.3:SLC2A10/SLC2 **Nvec_NVE3004 Sugar_tr.HG3.3:SLC2A10/SLC2 **Exapal_XM_028658294.1 Sugar_tr.HG3.3:SLC2A10/SlC2 **Nvec_NVE3005 Sugar_tr.HG3.3:SLC2A10/SlC2A10/SlC2A10/SlC2A10/SlC2A12 **Spis_XP_022796206_1 Sugar_tr.HG3.3:SlC2A10/SlC2A12 **Tadh_TriadT64243 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12	2A10/SLC2A12 SLC2A10/SLC2A12 0/SLC2A12 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 A12 SLC2A10/SLC2A12 2A10/SLC2A12 SLC2A10/SLC2A12 C2A12 SLC2A10/SLC2A12 C2A12 SLC2A10/SLC2A12 C2A10/SLC2A12 SLC2A10/SLC2A12
TrH2_TrispH2_008388-RA Sugar_tr.HG3.4:like:SLC2A10/Sl	C2A12/SLC2A13 NA 2/SLC2A13 NA 2/SLC2A13 NA 2/SLC2A13 NA 2/A12/SLC2A13 NA
Tetwil_g11852.t1 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ *Tetwil_g25435.t2 Sugar_tr.HG3.4:like: Tetwil_g24923.t2 Sugar_tr.HG3.4:like: Tetwil_g3204.t2 Sugar_tr.HG3.4:like: Tetwil_g6688.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g24923.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g24923.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g25435.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A10/SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g16688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g18688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g26688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g18688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g18688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g18688.t2 Sugar_tr.HG3.4:like:SLC2A12/ Tetwil_g24923.t2 Sugar_tr.HG3.4:like:	SLC2A13 NA :SLC2A10/SLC2A12/SLC2A13 NA :SLC2A10/SLC2A12/SLC2A13 NA :SLC2A10/SLC2A12/SLC2A13 NA :SLC2A10/SLC2A12/SLC2A13 NA :SLC2A10/SLC2A12/SLC2A13 NA :2A10/SLC2A12/SLC2A13 NA ::SLC2A10/SLC2A12/SLC2A13 NA ::SLC2A10/SLC2A12/SLC2A13 NA :AE:SLC2A10/SLC2A12/SLC2A13 NA :AE:SLC2A10/SLC2A12/SLC2A13 NA
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41 Aque_Aqu2.1.15232_001 Sugar_ti 95 Aque_Aqu2.1.19215_001 Sugar_ti	:HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A10/SLC2A12/SLC2A13 NA _tr.HG3.4:like:SLC2A13 NA
Mlei_ML1022.g60.i1 Sugar_tr.HG3.5:like:SLC Mlei_ML1022.g60.i1 Sugar_tr.HG3.5:like:SLC Horcal_Hcv1.av93.c1.g360.i2 Sugar_tr.H Mlei_ML0830.g25.i1 Sugar_tr.HG3.9:like:SLC2A13 NA Bolinf_Binf_sb1251917 Sugar_tr.HG3.9:like:SLC2A13 NA Bolinf_Binf_sb1251916 Sugar_tr.HG3.9:like:SLC2A13 NA Bolinf_Binf_sb1251918 Sugar_tr.HG3.9:like:SLC2A13 NA Bolinf_Binf_sb1169233 Sugar_tr.HG3.10:like:SLC2A13 NA Horcal_Hcv1.av93.c5.g790.i1 Sugar_tr.HG3.10:like:SLC2A13 NA	22413 NA G3.5:like:SLC2A13 NA G3.5:like:SLC2A13 NA WA WA WA WA WA WA WA
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**Scil_scict014873.3 Sugar_tr.HG3.7:SLC2A13 NA **Scil_scict014873.3 Sugar_tr.HG3.7:SLC2A13 NA **Gracom_Gcom_C555504_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15194_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15196_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15195_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15195_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15196_01 Sugar_tr.HG3.7:SLC2A13 NA **Plajan_Pjan_scaffold15196_01 Sugar_tr.HG3.7:SLC2A13 SLC2A13 **Aque_Aqu2.1.32928_001 Sugar_tr.HG3.7:SLC2A13 SLC2A13 **Tetwil_g6926.t2 Sugar_tr.HG3.7:SLC2A13 SLC2A13 **Emue_Em0006g1034a.t1 Sugar_tr.HG3.7:SLC2A13	A SLC2A13 SLC2A13 SLC2A13 SLC2A13
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Skow_XM_006820920.1 Sugar_tr.HG3.7:SLC2A13	13 SLC2A13 2A13 SLC2A13 3RNA168828 Sugar_tr.HG3.7:SLC2A13 SLC2A13 3 SLC2A13
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***Spury XM 793555.4 Stuger in HG3.7 SRUS** **Onli ENSONOTOCOMO2453 Stuger in HG3.7 SRUS** **Onli ENSONOTOCOMO2453 Stuger in HG3.7 SRUS** **Spury ENSONOTOCOMO2453 Stuger in HG3.7 SRUS** **Spury ENSONOTOCOMO2453 Stuger in HG3.7 SRUS** **Spury ENSONOTOCOMO2453 Stuger in HG3.7 SRUS** **Online ENSONOTOCOMO2453 Stuger in HG3.7 SRUS**	2015 ELAND 100 2017 2017 100 2017
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### Comment	
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