Table 1: Lysosomal-related genes SNV variants found in the Lower Grade Glioma dataset. The dbSNP codes, pathogenicity classification and allele frequencies are shown in the columns.

| **Lower Grade Glioma, TCGA-LGG** | | | |
| --- | --- | --- | --- |
| **Gene** | **dbSNP** | **Prediction** | **gnomAD Allele Frequency** |
| *CTSA* | rs375345060 | Deleterious | 0.0000159 |
| *FUCA1* | rs750020102 | Probably damaging | 0.0000309 |
| *FUCA1* | rs749269943 | Probably damaging, deleterious | 0.0000636 |
| *GAA* | rs753483808 | Possibly damaging, deleterious | 0.000148 |
| *GAA* | rs752421149 | Probably damaging, deleterious | 0.00002 |
| *GLB1* | rs375582374 | Probably damaging, deleterious | 0.0000161 |
| *GUSB* | rs747572640 | Possibly damaging, deleterious1 | 0.00000795 |
| *HGSNAT* | rs193066451 | Splice donor, deleterious2 | 0.0000403 |
| *HYAL1* | rs781788934 | Possibly damaging | 0.000016 |
| *IDS* | rs368513342 | Possibly damaging | 0.0000115 |
| *MAN2B1* | rs148661421 | Possibly damaging, deleterious | 0.0000239 |
| *MAN2B1* | rs754036398 | Probably damaging, deleterious | 0.00000398 |
| *MANBA* | rs150554352 | Possibly damaging, deleterious | 0.00222 |
| *MCOLN1* | rs151300825 | Probably damaging, deleterious | 0.000012 |
| *NPC1* | rs765729815 | Probably damaging3 | 0.000004 |
| *PSAP* | rs1165032545 | Probably damaging, deleterious | 0.00000398 |
| *SUMF1* | rs1249221556 | Possibly damaging, deleterious | 0.0000119 |

1 Reported in MPS VII studies (Vervoort *et al.*, 1996; Tomatsu *et al.*, 2009).

2 Reported in MPS IIIC studies (Fan *et al.*, 2006; Hrebícek *et al.*, 2006; Feldhammer *et al.*, 2009).

3 Reported in Niemann-Pick type C studies (Garver *et al.*, 2010; Macías-Vidal *et al.*, 2011; Koens *et al.*, 2016).