

| U4atac<br>HGVS | Chr | Pos       | ClinVar<br>variation ID | ClinVar classification       | U4 nt | Matching<br>ref base | Function<br>score | Category    | Region                |
|----------------|-----|-----------|-------------------------|------------------------------|-------|----------------------|-------------------|-------------|-----------------------|
| n.8C>A         | 2   | 121530887 | 692040                  | Likely pathogenic            |       |                      |                   |             | Stem II               |
| n.13C>T        | 2   | 121530892 | 218083                  | Pathogenic                   |       |                      |                   |             | Stem II               |
| n.16G>A        | 2   | 121530895 | 218082                  | Pathogenic/Likely pathogenic |       |                      |                   |             | Stem II               |
| n.29T>G        | 2   | 121530908 | 977869                  | Likely pathogenic            |       |                      |                   |             | 5' stem loop          |
| n.30G>A        | 2   | 121530909 | 30180                   | Likely pathogenic            |       |                      |                   |             | 5' stem loop          |
| n.35A>C        | 2   | 121530914 | 2674599                 | Likely pathogenic            | 30    | Y                    | -0.617            | UKB/AllofUs | 5' stem loop / k-turn |
| n.37G>A        | 2   | 121530916 | 218084                  | Pathogenic/Likely pathogenic | 32    | Y                    | -1.267            | UKB/AllofUs | 5' stem loop / k-turn |
| n.40C>T        | 2   | 121530919 | 599282                  | Pathogenic                   | 35    | N                    |                   |             | 5' stem loop / k-turn |
| n.46G>T        | 2   | 121530925 | 977856                  | Likely pathogenic            | 41    | N                    |                   |             | 5' stem loop / k-turn |
| n.46G>A        | 2   | 121530925 | 636959                  | Pathogenic                   | 41    | N                    |                   |             | 5' stem loop / k-turn |
| n.48G>A        | 2   | 121530927 | 218085                  | Pathogenic/Likely pathogenic | 43    | Y                    | -0.173            | UKB/AllofUs | 5' stem loop / k-turn |
| n.50G>C        | 2   | 121530929 | 30182                   | Likely pathogenic            | 45    | Y                    | -0.864            | UKB/AllofUs | 5' stem loop / k-turn |
| n.51G>A        | 2   | 121530930 | 30178                   | Pathogenic/Likely pathogenic | 46    | Y                    | -0.507            | UKB/AllofUs | 5' stem loop / k-turn |
| n.53C>G        | 2   | 121530932 | 30183                   | Pathogenic/Likely pathogenic | 48    | N                    |                   |             | 5' stem loop          |
| n.55G>A        | 2   | 121530934 | 30179                   | Pathogenic                   | 50    | Y                    | -0.331            | UKB/AllofUs | 5' stem loop          |
| n.111G>A       | 2   | 121530990 | 30181                   | Pathogenic                   |       |                      |                   |             | 3' stem loop          |
| n.114G>C       | 2   | 121530993 | 977780                  | Pathogenic                   | 116   | Y                    | -0.154            | unobserved  | 3' stem loop          |
| n.116A>C       | 2   | 121530995 | 1373455                 | Pathogenic                   | 118   | Y                    | -0.814            | UKB/AllofUs | Sm protein binding    |
| n.116A>G       | 2   | 121530995 | 870579                  | Likely pathogenic            | 118   | Y                    | -0.872            | UKB/AllofUs | Sm protein binding    |
| n.116A>T       | 2   | 121530995 | 812960                  | Likely pathogenic            | 118   | Y                    | -0.169            | UKB/AllofUs | Sm protein binding    |
| n.117A>G       | 2   | 121530996 | 1525441                 | Pathogenic                   | 119   | Y                    | -0.725            | UKB/AllofUs | Sm protein binding    |
| n.120T>G       | 2   | 121530999 | 977779                  | Pathogenic                   | 122   | Y                    | -0.737            | unobserved  | Sm protein binding    |
| n.124delG      | 2   | 121531002 | 1224468                 | Likely pathogenic            | 126   | N                    |                   |             | Sm protein binding    |
| n.124G>T       | 2   | 121531003 | 2813456                 | Pathogenic                   | 126   | N                    |                   |             | Sm protein binding    |
| n.124G>A       | 2   | 121531003 | 39443                   | Pathogenic/Likely pathogenic | 126   | N                    |                   |             | Sm protein binding    |
| n.23C>T        | 2   | 121530902 | 1133987                 | Likely benign                |       |                      |                   |             | loop region           |
| n.41G>A        | 2   | 121530920 | 1629605                 | Likely benign                | 36    | N                    |                   |             | loop region           |
| n.42C>T        | 2   | 121530921 | 1160662                 | Likely benign                | 37    | N                    |                   |             | loop region           |
| n.43A>G        | 2   | 121530922 | 1633266                 | Likely benign                | 38    | N                    |                   |             | loop region           |
| n.45A>C        | 2   | 121530924 | 1632468                 | Likely benign                | 40    | N                    |                   |             | loop region           |
| n.58C>T        | 2   | 121530937 | 1170904                 | Benign                       |       |                      |                   |             | loop region           |
| n.65C>T        | 2   | 121530944 | 1631270                 | Likely benign                |       |                      |                   |             | Stem I                |
| n.87C>T        | 2   | 121530966 | 1168718                 | Benign/Likely benign         |       |                      |                   |             | 3' stem loop          |
| n.93G>A        | 2   | 121530972 | 1601357                 | Benign                       |       |                      |                   |             | 3' stem loop          |
| n.109T>A       | 2   | 121530988 | 1628512                 | Likely benign                |       |                      |                   |             | 3' stem loop          |
| n.117dup       | 2   | 121530994 | 1159385                 | Likely benign                |       |                      |                   |             | Sm protein binding    |

**Supplementary Table 2. List of variants in *RNU4ATAC* in ClinVar.** The equivalent residue of *RNU4-2* was determined for variants in the 5' stem loop / k-turn and Sm protein binding site (see **Methods**). Function scores are included where an equivalent nucleotide could be determined and the reference base at that position is the same across *RNU4-2* and *RNU4ATAC*.