**Supplementary Table 1:** Exonic candidate variants co-segregating with AD in the analyzed family members and likely being pathogenic.

| Gene name   | Chromosome | Start position | End position | ExonicFunc.refGene | ExonicFunc.aachange | Condel | P>0.3 | GERP>3 | PROVEAN_pred | SIFT_pred | LRT_pred | MetaSVM_pred | dANN>0.995 | SIFT scores | LRT scores | dANN scores | SiPhy > 10 | P>0.3 | Exonic variant
|-------------|------------|----------------|--------------|--------------------|---------------------|--------|-------|--------|--------------|-----------|----------|---------------|-----------|-------------|------------|-------------|-------------|---------|-------------|
| TSC22D1    | 10         | 112838908      | 112838908    | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| ADRA2A     | 10         | 112838908      | 112838908    | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| DDHD2      | 8          | 38107282       | 38107283     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| DAAM2      | 6          | 39869131       | 39869132     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| LIMCH1     | 4          | 41615578       | 41615579     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| GPR125     | 17         | 1149886        | 1149887      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| TBC1D14    | 4          | 6925579        | 6925580      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| WFS1       | 4          | 6293694        | 6293695      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| USP34      | 22         | 61566815       | 61566816     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| TSC22D1    | 10         | 112838908      | 112838908    | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| ADRA2A     | 10         | 112838908      | 112838908    | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| DDHD2      | 8          | 38107282       | 38107283     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| DAAM2      | 6          | 39869131       | 39869132     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| LIMCH1     | 4          | 41615578       | 41615579     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| GPR125     | 17         | 1149886        | 1149887      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| TBC1D14    | 4          | 6925579        | 6925580      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| WFS1       | 4          | 6293694        | 6293695      | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |
| USP34      | 22         | 61566815       | 61566816     | Exonic             |                     |        |       |        |              |           |          |               |           |             |            |             |              |        |             |

**Notes:**
- Exonic candidate variants with an *ExonicFunc.refGene* score of 7 are considered likely pathogenic.
- Exonic variant frequencies and allele counts are provided for each candidate variant.
- SIFT, LRT, and dANN scores above specific thresholds indicate deleteriousness.
- MetaSVM and CADD scores over specific thresholds also indicate potential pathogenicity.
- SiPhy scores over 10 indicate evidence for pathogenicity in the analyzed family members.
- AD-PPI interactions are noted for genes involved in the disease pathway.