**Supplementary Table 1: Coordinate of intervals not excluded from linkage to ADH in family.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Chromosome** | **Start-SNP** | **End-SNP** | **Max LOD score** | **Size Mb** |
| Chr1 | rs12119876 | rs983494 | 1 | 0.24 |
| Chr2 | rs7568276 | rs13031576 | 2.1 | 73.12 |
| Chr2 | rs28442891 | rs10865490 | 1 | 0.68 |
| Chr2 | rs6728560 | rs12327907 | -1 | 1.27 |
| Chr2 | rs4556933 | rs11682905 | -1 | 0.73 |
| Chr2 | rs10930013 | rs984971 | -1 | 1.15 |
| Chr2 | rs11676513 | rs3769405 | -1 | 0.41 |
| Chr7 | rs10952119 | rs1405315 | 0 | 3.11 |
| Chr8 | rs830517 | rs16938353 | -1 | 0.34 |
| Chr8 | rs11988829 | rs4739611 | -1 | 0.45 |
| Chr8 | rs11776128 | rs2515226 | -1 | 0.16 |
| Chr9 | rs10963660 | rs2017761 | -1 | 0.39 |
| Chr9 | rs7034200 | rs13297783 | -1 | 0.17 |
| Chr11 | rs7131051 | rs11039836 | 2.1 | 28.62 |
| Chr11 | rs10902007 | rs4590891 | 1 | 30.19 |
| Chr14 | rs12887411 | rs2775254 | -1 | 0.16 |
| Chr14 | rs10130129 | rs4982381 | -1 | 0.16 |
| Chr16 | rs258282 | rs9925937 | 2.1 | 11.33 |
| Chr16 | rs2471453 | rs11639758 | -1 | 1.06 |
| Chr16 | rs4783944 | rs13329802 | -1 | 0.24 |
| Chr16 | rs2305691 | rs2432560 | -1 | 1.36 |
| Chr16 | rs8047671 | rs11647295 | -1 | 0.19 |
| Chr16 | rs2626643 | End | 2.1 | 9.98 |
| Chr19 | rs10411991 | rs7258236 | 0 | 6.09 |
| Chr19 | rs3746317 | rs7245564 | -1 | 0.30 |
| Chr19 | rs1669265 | rs11084803 | <-1 | 0.85 |
| Chr20 | Start | rs6116236 | <-1 | 0.10 |
| Chr20 | rs508396 | end | <-1 | 0.24 |
| **Total size (Mb):** | **173.1** |
| **Size relative to genome:** | **5.8%** |

**Supplementary Figure 1.** Result of parametric linkage analysis in family with p.R3095C mutation. Exome variants located in linkage intervals (marked with gray box) in with LOD score below -2 were excluded from the analysis.

