

Supplementary Table 1. Genomic risk loci detected from NAFLD GWAS results

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 2. Lead SNPs identified from independent significant SNPs of NAFLD GWAS

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 3. Independent significant SNPs identified from NAFLD GWAS

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 4. Candidate SNPs identified from NAFLD GWAS

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 5. Functional consequences of SNPs on genes

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 6. Prioritized genes from NAFLD GWAS by functional mapping

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>

Supplementary Table 7. FUMA annotation pathway categories

<https://docs.google.com/spreadsheets/d/1oMwzQtdBc8bbug1JgCO8z2OFzPcRgm44V-vlUTGsYDU/edit?usp=sharing>
