Purpose: To elucidate the genetic risk factors for bilateral sensorineural hearing loss (SNHL) and to assess whether these genetic risk factors differ by sex or age group. Methods: We studied genome-wide associations of SNHL in FinnGen (R9) and Estonian Biobank in the general population and in sex and age-stratified subgroups. The study-specific results were combined through inverse variance-weighted genome-wide meta-analyses, encompassing a total of 531,059 individuals (N_{cases}=35,960). Age-stratified meta-analyses included 28,198 individuals diagnosed at the age of 55 years or older and 7,762 individuals diagnosed before the age of 55 years, with 495,099 controls. Sex-stratified meta-analyses included 313,501 females (N_{cases}=17,761) and 217,558 males (N_{cases}=18,199). Results: Altogether 32 loci (±1 Mb apart) were associated with SNHL at $p<5x10^{-8}$ in at least one of the study groups. Of these, 13 loci have not been previously reported in association with hearing impairment. Expectedly, most loci were discovered in the complete sample (N_{loci}=22). Age group and sex-specific analyses suggested that numerous loci are associated with SNHL in those diagnosed after the age of 55 years (N_{loci}=20) and in females (N_{loci}=15) compared with only few associations observed in those diagnosed before the age of 55 years (N_{loci}=3) and in males (N_{loci}=4). Significant effect size differences between age groups were observed at 6 loci and between sexes at 8 loci. Conclusions: GWAS revealed new novel genetic associations for sensorineural hearing loss as well as age- and sex-specific associations. That data provides a valuable baseline for further investigations.