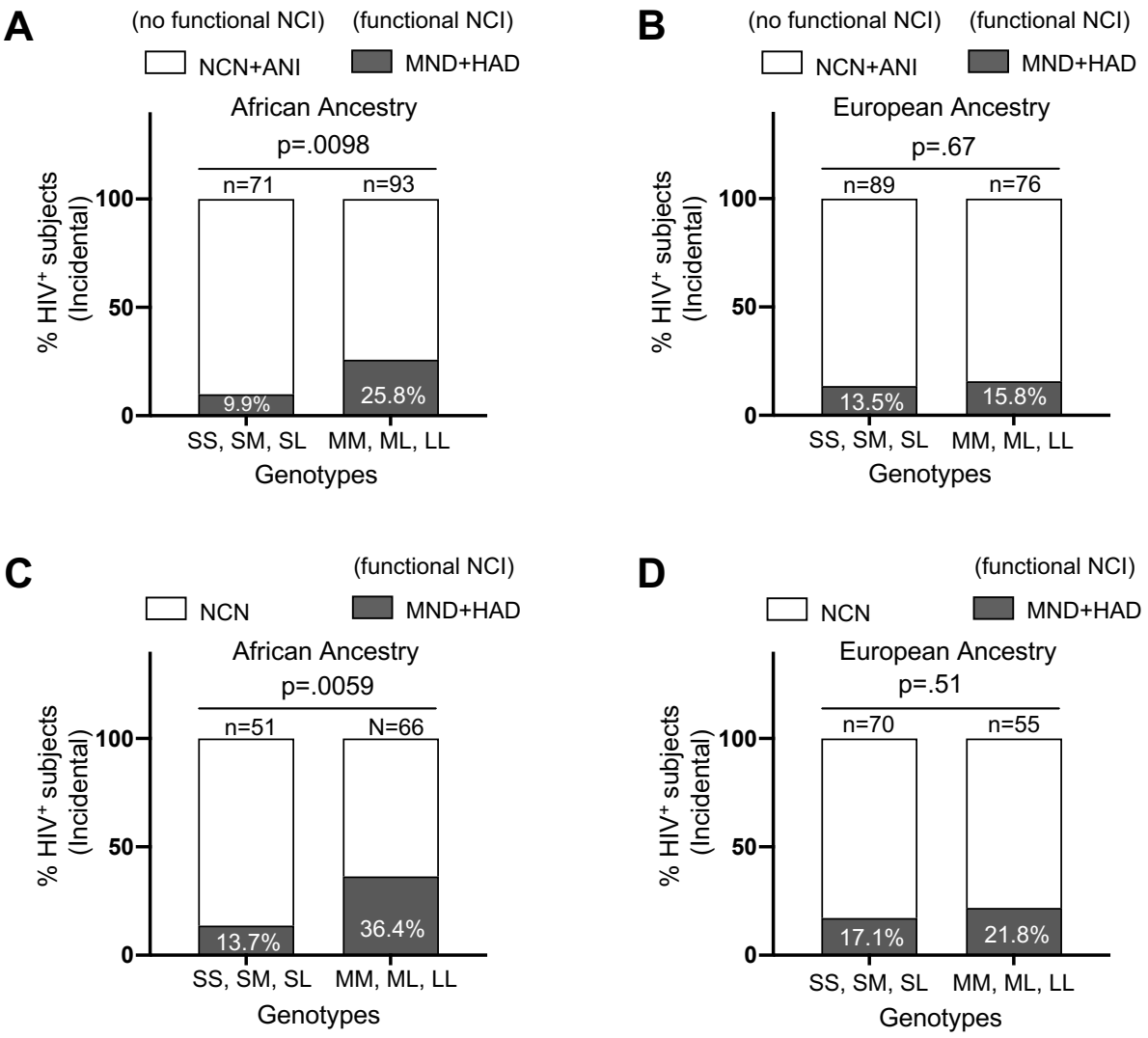


**Supplemental Figure 1**

**Supplemental Figure 1: PLWH of African ancestry with one or more short HO-1 $(GT)_n$ alleles have significantly decreased risk of functional HIV NCI in the absence of contributing co-morbidity factors.** Genetic ancestry clusters (i.e., African, European, or admixed Hispanic ancestry) were assigned to each PLWH in the CHARTER cohort using ancestry-informative nuclear DNA SNP variant analysis. In PLWH with functional HIV NCI without contributing co-morbidities determined to be of African ancestry (**A**), but not in individuals of European ancestry **(B)**, the presence of at least one short 'S' HO-1 $(GT)_n$ allele associated with lower functional HIV NCI (MND and HAD) vs. no functional HIV NCI (NCN and ANI), by an odds ratio of 0.31 (95% CI; .12 – .78) (chi-squared test, p=.010). Subgroup analyses in genetically assigned ancestry clusters were similarly performed by comparing function HIV NCI groups MND and HAD with NCN alone (**C** and **D**), with similar results showing in PLWH of African ancestry the presence of at least one short 'S' HO-1 $(GT)_n$ allele associated with lower functional HIV NCI (MND and HAD) vs. no functional HIV NCI (NCN), by an odds ratio of 0.28 (95% CI; .11 – .69) (chi-squared test, p=.006).