OBJECTIVE: To investigate genes that may be important in determining lung function in subjects with asthma. METHODS: A genome-wide association study has been performed in subjects with asthma from the COMPASS study (Bleecker et al, Lancet 370: 2118-25, 2007). To reduce population stratification, homogenous populations were identified based on geographic region, self-reported race, and genetic ancestry using HapMap reference data. Standard quality control measures were applied to the resulting genotype data. Genome-wide association studies (GWAS) for percent predicted FEV₁ and FEV₁/FVC was performed on the genetically homogenous population from Eastern Europe using PLINK. RESULTS: To date, GWAS has been performed on 587,020 SNPs in Eastern Europeans (n = 885). For percent predicted FEV₁, the top three SNPs were in or near SLITRK5 (SLIT and NTRK-like family, member 5) on chromosome 13 (p=1.2-2.3x10⁻⁶). Additional genes of interest for percent predicted FEV₁ include ADAM7 (A Disintegrin And Metalloprotease 7) (p=9.1x10⁻⁶) and ADRA1D (alpha-1D-adrenergic receptor) (p=1.1x10⁻⁵). For FEV₁/FVC ratio, the top three genes are FGF1 (fibroblast growth factor 1) (p=2.2x10⁻⁶), EPHA5 (ephrin type-A receptor 5) (p=2.8x10⁻⁶) and WNT3A (wingless-type MMTV integration site family, member 3A) (p=6.3x10⁻⁶). CONCLUSIONS: Evidence was found to suggest that genes involved in regulation of cellular growth (ADRA1D and FGF1) and asthma susceptibility (EPHA5) are associated with lung function in subjects with asthma.