Abdominal aortic aneurysm (AAA) is a complex disease with both genetic and environmental risk factors. Together, 6 previously identified risk loci only explain a small proportion of the heritability of AAA. To identify additional AAA risk loci using data from all available genome-wide association studies (GWAS). Through a meta-analysis of 6 GWAS datasets and a validation study totalling 10,204 cases and 107,766 controls we identified 4 new AAA risk loci: 1q32.3 (SMYD2), 13q12.11 (LINC00540), 20q13.12 (near PCIF1/MMP9/ZNF335), and 21q22.2 (ERG). In various database searches we observed no new associations between the lead AAA SNPs and coronary artery disease, blood pressure, lipids or diabetes. Network analyses identified ERG, IL6R and LDLR as modifiers of MMP9, with a direct interaction between ERG and MMP9. The 4 new risk loci for AAA appear to be specific for AAA compared with other cardiovascular diseases and related traits suggesting that traditional cardiovascular risk factor management may only have limited value in preventing the progression of aneurysmal disease.