GENOTYPES PHENOTYPES Group 1 - CTR Group 2 - ATE Group 3 - ISO 1 Group 4 - ISO 10 Select informative 22 strains 22 strains 22 strains 22 strains ca 10 mice/strain ca 10 mice/strain ca 10 mice/strain ca 10 mice/strain SNPs from the isoproterenol isoproterenol mouse HapMap no treatment atenolol (10 mg/kg per day) (1 mg/kg per day) (10 mg/kg per day) collect phenotypic collect phenotypic collect phenotypic collect phenotypic 78922 SNPs values of 27 traits values of 27 traits values of 27 traits values of 27 traits Perform 105 separate GWAS using EMMA Perform quality check of the genome-wide association scans by QQ-plots Discard low quality plots from further analyses Catalogue all significant and suggestive SNPs using pre-defined thresholds of significance Examine allelic patterns underlying significant SNPs Manually impute significant SNPs with missing alleles Define significant and suggestive loci for each trait Check for replication Check for enrichment Manually scan the Manually scan databases of linkage with independent of cardiac genes in literature for studies, animal mutants and human phenotypic datasets potentially overlapping GWAS for potentially overlapping loci associated with cardiac traits functional and/or functional and/or genetic evidence of the MPD genetic evidence