

User Guide

Online Component of CORGI

Welcome to the online user guide for CORGI. This resource has been designed to be reasonably intuitive for those familiar with browsing the internet. Hyperlinks, action buttons and search facilities are provided to aid navigation around this site.

CORGI is freely available to all users, however there is a registration process that should be completed before entering the main site.

CORGI presently contains information on over 100 genotype-phenotype comparisons, more than 150 linkage and association reports for chromosomes and includes information on over 1000 genes. Submission of additional information on these topics is welcomed either via the customised web forms for automated entry directly to the database, or by uploading files for bulk submissions. PLEASE CHECK that publications are not already present in the database as there are no validation mechanisms currently in place to check for user inputs to gene copy number, methylation or mitochondrial DNA tables. Data is periodically checked for duplicates by the database administrator.

CORGI is composed of modular components that deal with chromosome, gene, and experiment centred records. This resource provides the framework and background information to be of major benefit to the renal research community. The continued success of CORGI will be capitalised by the submission of regular contributor-driven data.

Chromosomes: Unique chromosome maps have been created to illustrate linked or associated genomic regions based on published information. Interim phenotypes are highlighted on individual chromosome maps by means of a grey box with darker colour indicating progressively more hits in a particular region. A specialised database has been developed to store information on complex chromosomal abnormalities that demonstrate consistent renal involvement. More detailed information is available from the comprehensive literature review and we welcome the addition of further information from your research projects.

Archiving and tracking mechanisms have also been developed for renal-related mitochondrial mutations, gene copy number variations, and epigenetic studies.

Genes: At present the candidate gene directory focuses on association studies for diabetic nephropathy. We plan to develop this information to incorporate candidate genes for other renal diseases - If you are keen to update this section, then please get in touch ☺. Customised web forms are available to all users for the submission of new association reports for candidate genes (please enter as much information as possible) and this section may be searched by gene name, symbol, SNP, outcome or

the first author of any publication. Summary information is also presently recorded for published meta-analyses.

Experimental: An efficient information management system has been incorporated to deal with the volume of data emerging from higher-throughput genotyping technologies. The CORE system incorporated for this section of CORGI was originally developed for [T1DBase](#) (GDxBase) and was generously provided by Dr Luc Smink and Barry Healy ([JDRF/WTDIL, UK](#)). This extensive bioinformatics tool provides visual and text-based results on collated gene-based information from a variety of disparate resources. A specialised system is used to store SNP, population and genotype-based information across or within the sample collections presently held in CORGI. Submission of as much data as possible will maximise the outcomes from genetic investigations; please contact us to discuss how inclusion of your data may be most easily facilitated. All genotyping information – regardless of outcome – is welcomed to prevent duplication of effort, downstream comparisons and allow platform-dependent comparisons to be performed.

If you require further assistance, please [contact us](#).