### **Abbreviations**

ASE allele-specific expression

ASW African ancestry in Southwest USA

BMI body mass index

bp base pairs

c-dSNP causal disease SNP c-eQTL causal eQTL SNP CD Crohn's disease

cDNA copy DNA

CEPH Centre d'Étude du Polymorphisme Humain

CEU Utah residents with Northern of Western European ancestry

CHB Han Chinese in Beijing, China

CHD Chinese in Metropolitan Denver, Colorado, USA

ChIP chromatin immunoprecipitation

cM centimorgan

CNV copy number variant

cRNA copy RNA cSNP causal SNP disease SNP DZ dizygotic

EBV Epstein-Barr virus

ENCODE encyclopedia of DNA elements eQTL expression quantitative trait locus

EST expressed sequence tag

FA factor analysis
FDR false discovery rate

GIH Gujarati Indians in Houston, Texas, USA GWAS genome-wide association study/studies

IVT in vitro transcription

JPT Japanese in Tokyo, Japan

kb kilobase

KCL King's College London

LCLs lymphoblastoid cell lines (EBV-transformed B-cells)

LCR locus control region
LD linkage disequilibrium
LR linear regression

LWK Luhya in Webuye, Kenya MAF minor allele frequency

Mb megabase

MCTA matched co-twin analysis

MEMN macrophage enriched metabolic network

MEX Mexican ancestry in Los Angeles, California, USA

miRNA microRNA

MKK Maasai in Kinyawa, Kenya

MS multiple sclerosis

MuTHER multiple tissue human expression resource

MZ monozygotic

NHGRI National Human Genome Research Institute

PCA principal component analysis

PT permutation threshold

QC quality control

QTL quantitative trait locus

RNA-seq RNA sequencing

RTC regulatory trait concordance

SAM sentrix array matrix

SNP single nucleotide polymorphism SRC Spearman rank correlation

SSAHA sequence search and alignment by hashing algorithm

T2D type 2 diabetes
TF transcription factor
TP true positives

TSI Toscans in Italy

TSS transcription start site

UGMS University of Geneva Medical School

UTR untranslated region

WTCCC Wellcome Trust Case Control Consortium
WTCHG Wellcome Trust Centre for Human Genetics

WTSI Wellcome Trust Sanger Institute

YRI Yoruban in Ibadan, Nigeria

# **List of Figures**

Figure 1.1 The process of eukaryotic gene expression	2
Figure 1.2. The haplotype structure of the human genome	10
Figure 1.3. Cis and trans effects on transcript levels.	13
Figure 1.4. Different trichome patterns among <i>Drosophila</i> species	18
Figure 1.5. Geographic distribution of lactose intolerance	19
Figure 1.6. Common disorders as quantitative traits	23
Figure 1.7. Interpreting GWAS results with eQTL data	25
Figure 2.1. Illumina II assay protocol	32
Figure 2.2. Direct hybridization assay overview and workflow	34
Figure 2.3. SNP-gene association example	38
Figure 3.1. Excess of regulatory variants among GWAS signals	49
Figure 3.2. Cis regulatory enrichment stratified by immunity relatedness	50
Figure 3.3. RTC score distribution following simulations	53
Figure 3.4. Properties of the RTC score when varying r <sup>2</sup>	54
Figure 3.5. Properties of the RTC score when varying D'	55
Figure 3.6. Properties of the RTC score when varying the median ${ m r}^2$ of the hotspot interval	56
Figure 3.7. Overrepresentation of immunity-related high RTC scoring <i>cis</i> signals	60
Figure 3.8. The RTC method compared to standard LD measurements in the observed data	64
Figure 3.9. The fraction of eQTL variance explained away by the dSNP versus the RTC score	65
Figure 4.1. P-value distribution of $cis$ eQTLs (10 $^{ ext{-}3}$ PT) after FA correction in the uncorrected data	74
Figure 4.2. Proportion of tissue shared and tissue-specific eQTLs from the SRC and SRC-FA analysis	75
Figure 4.3. Shared eQTLs ( $10^{-2}$ PT, SRC) have the same direction of effect (SRC rho) across tissues	78
Figure 4.4. Cumulative SRC rho distribution across tissues for tissue-specific and shared eQTLs	79
Figure 4.5. Distribution of independent cis eQTLs (10-3 PT, SRC) around the transcription start site	81
Figure 4.6. Fold change within twins and across tissues for LCL eQTLs ( $10^{-3}$ PT, SRC)	84
Figure 5.1. Distribution of RTC scores across tissues (GenCord)	89
Figure 5.2. Distribution of RTC scores across tissues for shared intervals-disease combinations	
(GenCord)	89

## **List of Tables**

Table 2.1. Summary of resources (samples, SNPs and transcripts) used throughout the thesis
Table 2.2. Factor analysis weight and noise prior values applied to each tissue. Analysis performed on
MuTHER pilot samples4
<b>Table 3.1. Candidate</b> <i>cis</i> <b>results.</b> Candidate genes (RTC score ≥ 0.9) for <i>cis</i> regulatory mediated GWAS effects
RTC applied on 976 GWAS SNPs from NHGRI and HapMap 3 CEU expression data in LCLs. The higher the
score, the more likely it is that the GWAS SNP and the eQTL for the gene shown are tagging the same
functional variant5
<b>Table 3.2. Candidate</b> <i>trans</i> <b>results.</b> Candidate <i>trans</i> genes likely involved in the same biological pathways,
relevant to the GWAS SNPs (GWAS SNP and the genes it affects in trans often reside on different
chromosomes, as indicated in the SNP Chr and Genes Chr fields respectively). Signals related to the same
hotspot interval separated by a horizontal line. Regulatory trans effects RTC applied in trans on 976
GWAS SNPs from NHGRI and HapMap 3 CEU expression data in LCLs. Table contains only the confident
results (RTC Score $\geq 0.9$ ) for the six immunity related intervals.
Table 3.3. Hotspot intervals with overlapping <i>cis</i> and <i>trans</i> effects as indicated by the high RTC score.
Candidate regulatory effects explaining GWAS signals were detected for two of the 15 intervals tested for
both <i>cis</i> and <i>trans</i> effects
Table 4.1. Successfully genotyped twin pairs (MZ and DZ) with available gene expression data. Number
of twin pairs per tissue sharing both genotypic and expression information $\epsilon$
Table 4.2. Cis eQTL associations detected with SRC analysis. Significant discoveries (number of genes with
eQTLs) are shown at different permutation thresholds for each tissue. Within each tissue, two
independent eQTL analyses were performed after separating related individuals in two subsets (Twin1,
Twin2)
Table 4.3. Replication of <i>cis</i> eQTL discoveries (number of significant genes per tissue at 10 <sup>-3</sup>
permutation threshold). Results from both the Spearman Rank Correlation (SRC) and Factor Analysis
(SRC-FA) are presented. Proportion of replicating signals calculated as the mean co-twin $\pi_1$ estimates
from the p-value distribution of same SNP-gene associations in the reciprocal twin set
Table 4.4. Cis eQTL associations detected with SRC-FA analysis. Number of genes with a significant eQTL
shown for each co-twin analysis per tissue at different permutation thresholds
Table 4.5. Recovery of SRC eQTLs (10-3 PT gene associations) with factor analysis correction. In each
tissue and for both co-twins, 80-90% of eQTLs detected before correction (standard analysis - Std) are
recovered with SRC-FA
Table 4.6. Tissue-shared and tissue-specific gene associations (10-3 PT), SRC analysis
Table 4.7. Tissue-shared and tissue-specific gene associations (10 <sup>-3</sup> PT), SRC-FA analysis
Table 4.8. Tissue-shared and tissue-specific interval-gene associations (10 $^{-3}$ PT), SRC analysis
Table 4.9. Continuous estimates of tissue sharing by enrichment of low p-values $(\pi_1)$ of reference
eQTLs (SNP-genes 10 <sup>-3</sup> PT) in the secondary tissues

Table	${\bf 5.1.}\ Number\ of\ nonredundant\ recombination\ hot spot\ intervals\ with\ co-localizing\ GenCord\ eQTLs$	
а	and GWAS SNPs. Unique count of intervals (#Intervals) and interval-disease combinations (#Intervals	
v	with multiple disease GWAS loci - #Interval-diseases) per tissue tested for causal regulatory effects with	
t	the RTC. A subset of intervals (Shared) harbour eQTLs detected in all three tissues	
Table	<b>5.2.</b> Tissue shared and tissue-specific interval-disease combinations with high RTC score. RTC	
r	results with a score ≥ 0.9 are overlapped and compared across tissues. The significant tissue-specific	
C	component ( $\sim$ 70% of results are found in one tissue only) implies that predicting causal regulatory	
$\epsilon$	effects for GWAS loci is highly dependent on the tissue where expression is determined91	
Table	<b>5.3. Candidate B-cell results.</b> Candidate genes (RTC score $\geq$ 0.9) for <i>cis</i> regulatory mediated GWAS	
$\epsilon$	effects. RTC applied on NHGRI GWAS SNPs and B-cell expression data from the GenCord92	
<b>Table 5.4. Candidate T-cell results.</b> Candidate genes (RTC score $\geq$ 0.9) for <i>cis</i> regulatory mediated GWAS		
$\epsilon$	effects. RTC applied on NHGRI GWAS SNPs and T-cell expression data from the GenCord95	
Table	<b>5.5. Candidate fibroblast results.</b> Candidate genes (RTC score $\geq$ 0.9) for <i>cis</i> regulatory mediated GWAS	
$\epsilon$	effects. RTC applied on NHGRI GWAS SNPs and fibroblast expression data from the GenCord <b>99</b>	

### **Appendix**

#### 1. Biopsy technique protocol

- 1. The lower abdominal biopsy site is cleaned. Local anesthetic with adrenaline is infiltrated into the pre-inked skin.
- 2. Stretching the skin perpendicular to the relaxed skin tension lines between thumb and finger either side of the area to be sampled, the punch blade is placed on the skin and rotated under gentle pressure by rolling it between the thumb and finger using a twisting drilling action.
- 3. One should penetrate to the level of the fat layer to achieve a full thickness skin biopsy specimen. The specimen should be weighed, cut in half, and stored immediately in liquid nitrogen
- 4. The specimen will either float up on the fat layer or can be gently lifted using a skin hook or gently applied forceps to allow specimen collection by cutting through the fat layer using a scalpel or sharp scissors.
- 5. Further fat can be obtained by careful dissection of the fat layer using forceps and scalpel. The fat sample should be weighed and immediately stored in liquid nitrogen.
- Haemostasis can be achieved with direct pressure and/or interrupted sutures.
   Both absorbent and non-absorbent sutures can be used in a layered closure for larger punch defects.
- 7. The resultant defect can be allowed to heal by secondary intention as an alternative method although optimal haemostasis and cosmesis as well as reduced healing time are usually seen with sutured wounds.