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A Bioinformatics Approach to
Synthetic Lethal Interactions in
Cancer with Gene Expression
Data

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a thesis submitted for the degree of
Doctor of Philosophy
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New Zealand.

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Abstract

Introduction

Synthetic lethal genetic interactions are re-emerging as an important concept in the post-genomics era due to their potential for use in precision medicine against cancers. Synthetic lethal drug design exploits the functional redundancy of genes disrupted in cancers (including tumour suppressors) to develop specific treatments against them. *CDH1*, which encodes E-cadherin, is a tumour suppressor gene with loss of function in breast and stomach cancers. Experimental screens have identified candidate synthetic lethal interactions with *CDH1*, which can be further supported with bioinformatics analysis. Furthermore, gene expression data enables investigation of synthetic lethal pathways and [the structure of synthetic lethal genes](#).

Methods

[A computational methodology](#), the Synthetic Lethal Prediction Tool (SLIPT) was developed to detect synthetic lethal interactions in gene expression data. The application of this methodology is demonstrated on interactions with *CDH1* in breast and stomach cancer data from The Cancer Genome Atlas (TCGA) project. Synthetic lethal genes and pathways were further investigated with unsupervised clustering, gene set over-representation analysis, metagenes, and permutation resampling. In particular, analyses focused on comparing SLIPT gene candidates to an experimental short interfering RNA (siRNA) screen. Network analysis methods were applied to the most supported pathways to test for pathway structure between synthetic lethal candidates. Simulation and modelling was used to assess the statistical performance of SLIPT, including simulated data with correlation structures [from](#) graph structures.

Results

Many candidate synthetic lethal partners of *CDH1* were detected in TCGA breast cancer. These genes clustered into several distinct groups, with distinct biological functions and elevated expression in different clinical subtypes. While the number of genes detected by both SLIPT and siRNA was not significant, these contained significantly enriched pathways. In particular, $G_{\alpha i}$ signalling, cytoplasmic microfibres, and extracellular fibrin clotting were robustly supported by both approaches, which is consistent with the known cytoskeletal and cell signalling roles of E-cadherin. Many of these pathways were replicated in stomach cancer data. The pathways supported only by SLIPT included regulation of immune signalling and translation, which were not expected to be detected in an isogenic cell line model but are still candidates for further investigation.

Synthetic lethal candidates detected by SLIPT and siRNA were compared within the graph structures of the candidate synthetic lethal pathways. **SLIPT genes** had lower centrality and were **consistently** upstream of siRNA candidates, specifically in the $G_{\alpha i}$ signalling pathway.

A statistical model of synthetic lethality was used to simulate gene expression data with known synthetic lethal partners for a gene. The SLIPT methodology had high statistical performance when detecting few synthetic lethal partners, which diminished with more synthetic lethal partners or lower sample size. The SLIPT methodology performed better than Pearson correlation or the χ^2 -test. In particular, it performed well with high specificity for datasets containing thousands of genes, or genes positively correlated with the query gene (as expected to occur in gene expression data). SLIPT was robust across correlation structures, including those derived from complex pathway structures, and often distinguished synthetic lethal genes from those positively or negatively correlated with them.

Thus this thesis has developed, evaluated, and applied a bioinformatics approach for the discovery of synthetic lethal genes from gene expression data. This approach has been demonstrated to detect biologically informative and clinically relevant candidate synthetic lethal partners for *CDH1* in breast and stomach cancers.

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どうもありがとうございます。頑張った!もうすぐ行きます。また来月！

Contents

Acronyms	xvi
1 Introduction and Literature Review	1
1.1 Cancer Research in the Post-Genomic Era	1
1.1.1 Cancer is a Global Health Issue	2
1.1.1.1 The Genetics and Molecular Biology of Cancers	3
1.1.2 The Genomics Revolution in Cancer Research	3
1.1.2.1 High-Throughput Technologies	4
1.1.2.2 Bioinformatics and Genomic Data	5
1.1.3 Genomics Projects	5
1.1.3.1 The Cancer Genome Project	6
1.1.3.2 The Cancer Genome Atlas Project	6
1.1.4 Genomic Cancer Medicine	8
1.1.4.1 Cancer Genes and Driver Mutations	8
1.1.4.2 Precision Cancer Medicine	9
1.1.4.3 Molecular Diagnostics and Pan-Cancer Medicine	9
1.1.4.4 Targeted Therapeutics and Pharmacogenomics	10
1.1.5 Systems and Network Biology	11
1.2 Synthetic Lethal Cancer Medicine	12
1.2.1 Synthetic Lethal Genetic Interactions	13
1.2.2 Synthetic Lethal Concepts in Genetics	13
1.2.3 Synthetic Lethality in Model Systems	15
1.2.3.1 Synthetic Lethal Pathways and Networks	15
1.2.3.2 Evolution of Synthetic Lethality	16
1.2.4 Synthetic Lethality in Cancer	17
1.2.5 Clinical Impact of Synthetic Lethality in Cancer	17
1.2.6 High-throughput Screening for Synthetic Lethality	20
1.2.6.1 Synthetic Lethal Screens	21
1.2.7 Computational Prediction of Synthetic Lethality	22
1.2.7.1 Bioinformatics Approaches to Genetic Interactions	22
1.2.7.2 Comparative Genomics	24
1.2.7.3 Analysis and Modelling of Protein Data	26
1.2.7.4 Differential Gene Expression	27
1.2.7.5 Data Mining and Machine Learning	28
1.2.7.6 Mutual Exclusivity and Bimodality	31
1.2.7.7 Rationale for Further Development	32

1.3	E-cadherin as a Synthetic Lethal Target	33
1.3.1	The <i>CDH1</i> gene and its Biological Functions	33
1.3.2	Hereditary Diffuse Gastric (and Lobular Breast) Cancer	34
1.3.3	Cell Line Models of <i>CDH1</i> Null Mutations	35
1.4	Summary and Research Direction of Thesis	35
1.4.1	Thesis Aims	36
2	Methods and Resources	38
2.1	Bioinformatics Resources for Genomics Research	38
2.1.1	Public Data and Software Packages	38
2.1.1.1	Cancer Genome Atlas Data	39
2.1.1.2	Reactome and Annotation Data	40
2.2	Data Handling	40
2.2.1	Normalisation	40
2.2.2	Sample Triage	40
2.2.3	Metagenes and the Singular Value Decomposition	42
2.2.4	Candidate Triage and Integration with Screen Data	43
2.3	Techniques	44
2.3.1	Statistical Procedures and Tests	44
2.3.2	Gene Set Over-representation Analysis	45
2.3.3	Clustering	45
2.3.4	Heatmap	45
2.3.5	Modelling and Simulations	46
2.3.5.1	Receiver Operating Characteristic Curves	47
2.3.6	Resampling Analysis	47
2.4	Pathway Structure Methods	48
2.4.1	Network and Graph Analysis	48
2.4.2	Sourcing Graph Structure Data	49
2.4.3	Constructing Pathway Subgraphs	50
2.4.4	Network Analysis Metrics	50
2.5	Implementation	51
2.5.1	Computational Resources and Linux Utilities	51
2.5.2	R Language and Packages	51
2.5.3	High Performance and Parallel Computing	54
3	Methods Developed During Thesis	56
3.1	A Synthetic Lethal Detection Methodology	56
3.2	Synthetic Lethal Simulation and Modelling	58
3.2.1	A Model of Synthetic Lethality in Expression Data	59
3.2.2	Simulation Procedure	63
3.3	Detecting Simulated Synthetic Lethal Partners	66
3.3.1	Binomial Simulation of Synthetic Lethality	66
3.3.2	Multivariate Normal Simulation of Synthetic Lethality	68
3.3.2.1	Multivariate Normal Simulation with Correlated Genes	70
3.3.2.2	Specificity with Query-Correlated Pathways	78
3.4	Graph Structure Methods	80

3.4.1	Upstream and Downstream Gene Detection	80
3.4.1.1	Permutation Analysis for Statistical Significance	81
3.4.2	Simulating Gene Expression from Graph Structures	82
3.5	Customised Functions and Packages Developed	86
3.5.1	Synthetic Lethal Interaction Prediction Tool	86
3.5.2	Data Visualisation	87
3.5.3	Extensions to the iGraph Package	88
3.5.3.1	Sampling Simulated Data from Graph Structures	89
3.5.3.2	Plotting Directed Graph Structures	89
3.5.3.3	Computing Information Centrality	89
3.5.3.4	Testing Pathway Structure with Permutation Testing .	90
3.5.3.5	Metapackage to Install iGraph Functions	90
4	Synthetic Lethal Analysis of Gene Expression Data	91
4.1	Synthetic Lethal Genes in Breast Cancer	92
4.1.1	Synthetic Lethal Pathways in Breast Cancer	93
4.1.2	Expression Profiles of Synthetic Lethal Partners	96
4.1.2.1	Subgroup Pathway Analysis	100
4.2	Comparing Synthetic Lethal Gene Candidates	101
4.2.1	Primary siRNA Screen Candidates	101
4.2.2	Comparison with Correlation	102
4.2.3	Comparison with Primary Screen Viability	105
4.2.4	Comparison with Secondary siRNA Screen Validation	107
4.2.5	Comparison to Primary Screen at Pathway Level	108
4.2.5.1	Resampling Genes for Pathway Enrichment	110
4.2.6	Integrating Synthetic Lethal Pathways and Screens	116
4.3	Synthetic Lethal Pathway Metagenes	117
4.4	Replication in Stomach Cancer	119
4.4.1	Synthetic Lethal Genes and Pathways	120
4.4.2	Synthetic Lethal Expression Profiles	120
4.4.3	Comparison to Primary Screen	125
4.4.3.1	Resampling Analysis	128
4.4.4	Metagene Analysis	131
4.5	Discussion	132
4.5.1	Strengths of the SLIPT Methodology	132
4.5.2	Synthetic Lethal Pathways for E-cadherin	133
4.5.3	Replication and Validation	134
4.5.3.1	Integration with siRNA Screening	134
4.5.3.2	Replication across Tissues	135
4.6	Summary	135
5	Synthetic Lethal Pathway Structure	137
5.1	Synthetic Lethal Genes in Reactome Pathways	137
5.1.1	The PI3K/AKT Pathway	138
5.1.2	The Extracellular Matrix	140
5.1.3	G Protein Coupled Receptors	141

5.1.4	Gene Regulation and Translation	141
5.2	Network Analysis of Synthetic Lethal Genes	143
5.2.1	Gene Connectivity and Vertex Degree	143
5.2.2	Gene Importance and Centrality	145
5.2.2.1	Information Centrality	145
5.2.2.2	PageRank Centrality	146
5.3	Relationships between Synthetic Lethal Genes	148
5.3.1	Detecting Upstream or Downstream Synthetic Lethality	148
5.3.2	Resampling for Synthetic Lethal Pathway Structure	151
5.4	Discussion	153
5.5	Summary	155
6	Simulation and Modelling of Synthetic Lethal Pathways	156
6.1	Synthetic Lethal Detection Methods	157
6.1.1	Performance of SLIPT and χ^2 across Quantiles	157
6.1.1.1	Correlated Query Genes affects Specificity	160
6.1.2	Alternative Synthetic Lethal Detection Strategies	162
6.1.2.1	Correlation for Synthetic Lethal Detection	162
6.1.2.2	Testing for Bimodality with BiSEp	164
6.2	Simulations with Graph structures	165
6.2.1	Performance over Graph structures	166
6.2.1.1	Simple Graph structures	166
6.2.1.2	Constructed Graph structures	169
6.2.2	Performance with Inhibitions	169
6.2.3	Synthetic Lethality across Graph structures	176
6.2.4	Performance within a Large Simulated Dataset	179
6.3	Simulations in More Complex Graph structures	182
6.3.1	Simulations over Pathway-based Graphs	183
6.3.2	Pathway Structures in a Large Simulated Dataset	185
6.4	Discussion	188
6.4.1	Simulation Procedure	188
6.4.2	Comparing Methods with Simulated Data	189
6.4.3	Design and Performance of SLIPT	190
6.4.4	Simulations from Graph structures	192
6.5	Summary	193
7	Discussion	194
7.1	Synthetic Lethality and <i>CDH1</i> Biology	194
7.1.1	Established Functions of <i>CDH1</i>	195
7.1.2	The Molecular Role of <i>CDH1</i> in Cancer	195
7.2	Significance	196
7.2.1	Synthetic Lethality in the Genomic Era	196
7.2.2	Clinical Interventions based on Synthetic Lethality	198
7.3	Future Directions	199
7.4	Conclusions	200

Bibliography	203
A Sample Quality	227
A.1 Sample Correlation	227
A.2 Replicate Samples in TCGA Breast Cancer Data	230
B Software Used for Thesis	234
C Mutation Analysis in Breast Cancer	244
C.1 Synthetic Lethal Genes and Pathways	244
C.2 Synthetic Lethal Expression Profiles	245
C.3 Comparison to Primary Screen	249
C.3.1 Resampling Analysis	251
C.4 Compare SLIPT genes	252
D Metagene Analysis	254
D.1 Pathway Signature Expression	254
D.2 Synthetic Lethal Reactome Metagenes	258
E Intrinsic Subtyping	259
F Synthetic Lethal Genes in Pathways	261
G Network Analysis for Mutation SLIPT	270
H Pathway Structure for Mutation SLIPT	273
I Performance of SLIPT and χ^2	275
I.1 Correlated Query Genes affects Specificity	281
J Simulations on Graph Structures	287
J.1 Simulations from Inhibiting Graph Structures	288
J.2 Simulation across Graph Structures	291
J.3 Simulations within a Large Simulated Dataset	295
J.4 Simulations from Complex Graph Structures	296
J.5 Simulations from Complex Inhibiting Graphs	299
J.6 Simulations from Pathway Graph Structures	305

List of Tables

1.1	Methods for predicting genetic interactions	23
1.2	Methods for predicting synthetic lethality in cancer	23
2.1	Excluded samples by batch and clinical characteristics.	42
2.2	R installations used during thesis	52
2.3	R Packages used during thesis	52
2.4	R packages developed during thesis	54
4.1	Candidate synthetic lethal gene partners of <i>CDH1</i> from SLIPT	93
4.2	Candidate synthetic lethal gene partners of <i>CDH1</i> from mtSLIPT	94
4.3	Pathways for <i>CDH1</i> partners from SLIPT	95
4.4	Pathways for clusters of <i>CDH1</i> partners from SLIPT	99
4.5	ANOVA for synthetic lethality and correlation with <i>CDH1</i>	105
4.6	Comparison of Synthetic Lethal Interaction Prediction Tool (SLIPT) genes against secondary short interfering RNA (siRNA) screen	108
4.7	Pathways for <i>CDH1</i> partners from SLIPT and siRNA	109
4.8	Pathways for <i>CDH1</i> partners from SLIPT	112
4.9	Pathways for <i>CDH1</i> partners from SLIPT and siRNA primary screen .	113
4.10	Pathways for <i>CDH1</i> partners from mtSLIPT and siRNA primary screen	115
4.11	Examples of candidate metagenes synthetic lethal for <i>CDH1</i> from SLIPT	118
4.12	Synthetic lethal gene partners of <i>CDH1</i> from SLIPT in stomach cancer	121
4.13	Pathways for <i>CDH1</i> partners from SLIPT in stomach cancer	122
4.14	Pathways for clusters of <i>CDH1</i> partners in stomach SLIPT	124
4.15	Pathways for <i>CDH1</i> partners from SLIPT and siRNA	127
4.16	Pathways for <i>CDH1</i> partners from SLIPT in stomach cancer	129
4.17	Pathways for <i>CDH1</i> partners from SLIPT in stomach and siRNA	130
4.18	Synthetic lethal metagenes against <i>CDH1</i> in stomach cancer	131
5.1	ANOVA for synthetic lethality and vertex degree	144
5.2	ANOVA for synthetic lethality and information centrality	146
5.3	ANOVA for synthetic lethality and PageRank centrality	148
5.4	Resampling for pathway structure of synthetic lethal detection methods	152
B.1	Computers used during thesis	234
B.2	Linux utilities and applications used during thesis	235
B.3	Complete list of R packages used during this thesis	235
C.1	Pathways for <i>CDH1</i> partners from mtSLIPT	244

C.2	Pathways for clusters of <i>CDH1</i> partners from mtSLIPT	247
C.3	Pathways for <i>CDH1</i> partners from mtSLIPT and siRNA	250
C.4	Pathways for <i>CDH1</i> partners from mtSLIPT	251
D.1	Candidate synthetic lethal metagenes against <i>CDH1</i> from mtSLIPT . .	258
E.1	Comparison of intrinsic subtypes	259
G.1	ANOVA for synthetic lethality and vertex degree	272
G.2	ANOVA for synthetic lethality and information centrality	272
G.3	ANOVA for synthetic lethality and PageRank centrality	272
H.1	Resampling for pathway structure of synthetic lethal detection methods	274

List of Figures

1.1	Synthetic genetic interactions	14
1.2	Synthetic lethality in cancer	18
2.1	Read count density	41
2.2	Read count sample mean	42
3.1	Framework for synthetic lethal prediction	57
3.2	Synthetic lethal prediction adapted for mutation	58
3.3	A model of synthetic lethal gene expression	60
3.4	Modelling synthetic lethal gene expression	61
3.5	Synthetic lethality with multiple genes	62
3.6	Simulating gene function	64
3.7	Simulating synthetic lethal gene function	64
3.8	Simulating synthetic lethal gene expression	65
3.9	Performance of binomial simulations	67
3.10	Comparison of statistical performance	67
3.11	Performance of multivariate normal simulations	69
3.12	Simulating expression with correlated gene blocks	71
3.13	Simulating expression with correlated gene blocks	72
3.14	Synthetic lethal prediction across simulations	74
3.15	Performance with correlations	75
3.16	Comparison of statistical performance with correlation structure	76
3.17	Performance with query correlations	77
3.18	Statistical evaluation of directional criteria	78
3.19	Performance of directional criteria	79
3.20	Simulated graph structures	83
3.21	Simulating expression from a graph structure	84
3.22	Simulating expression from graph structure with inhibitions	85
3.23	Demonstration of violin plots with custom features	88
3.24	Demonstration of annotated heatmap	88
3.25	Simulating graph structures	90
4.1	Synthetic lethal expression profiles of analysed samples	97
4.2	Comparison of SLIPT with siRNA	103
4.3	Comparison of SLIPT and siRNA genes with correlation	103
4.4	Comparison of SLIPT and siRNA genes with correlation	104
4.5	Comparison of SLIPT and siRNA genes with screen viability	106

4.6	Comparison of SLIPT genes with siRNA screen viability	106
4.7	Resampled intersection of SLIPT and siRNA candidate genes	111
4.8	Synthetic lethal expression profiles of stomach samples	123
4.9	Comparison of SLIPT in stomach to siRNA	126
5.1	Synthetic lethality in the PI3K cascade	139
5.2	Synthetic lethality in the GPCRs	142
5.3	Synthetic lethality and vertex degree	144
5.4	Synthetic lethality and centrality	146
5.5	Synthetic lethality and PageRank	147
5.6	Structure of synthetic lethality resampling	150
6.1	Performance of χ^2 and SLIPT across quantiles	159
6.2	Performance of χ^2 and SLIPT across quantiles with more genes	160
6.3	Performance of χ^2 and SLIPT across quantiles with query correlation .	161
6.4	Performance of negative correlation and SLIPT	163
6.5	Simple graph structures	166
6.6	Performance of simulations on a simple graph	167
6.7	Performance of simulations is similar in simple graphs	168
6.8	Performance of simulations on a pathway	170
6.9	Performance of simulations on a simple graph with inhibition	171
6.10	Performance is higher on a simple inhibiting graph	173
6.11	Performance of simulations on a constructed graph with inhibition . .	174
6.12	Performance is affected by inhibition in graphs	175
6.13	Detection of synthetic lethality within a graph structure	177
6.14	Performance on a simple graph improves with more genes	180
6.15	Performance on an inhibiting graph improves with more genes . . .	181
6.16	Performance of simulations on the PI3K cascade	185
6.17	Performance on pathways improves with more genes	187
A.1	Correlation analysis and sample removal	228
A.2	Correlation profiles of removed samples	229
A.3	Replicate excluded samples	230
A.4	Replicate samples with all remaining	231
A.5	Replicate samples with some excluded	232
C.1	Synthetic lethal expression profiles of analysed samples	246
C.2	Comparison of mtSLIPT to siRNA	249
C.3	Compare mtSLIPT and siRNA genes with correlation	252
C.4	Compare mtSLIPT and siRNA genes with correlation	252
C.5	Compare mtSLIPT and siRNA genes with siRNA viability	253
D.1	Pathway metagene expression profiles	256
D.2	Expression profiles for estrogen receptor related genes	257
F.1	Synthetic lethality in the PI3K/AKT pathway	261
F.2	Synthetic lethality in the PI3K/AKT pathway in cancer	262

F.3	Synthetic lethality in Elastic Fibre Formation	263
F.4	Synthetic lethality in Fibrin Clot Formation	264
F.5	Synthetic lethality in the Extracellular Matrix	265
F.6	Synthetic lethality in the GPCR Downstream	266
F.7	Synthetic lethality in the Translation Elongation	267
F.8	Synthetic lethality in the Nonsense-mediated Decay	268
F.9	Synthetic lethality in the 3' UTR	269
G.1	Synthetic lethality and vertex degree	270
G.2	Synthetic lethality and centrality	271
G.3	Synthetic lethality and PageRank	271
H.1	Structure of synthetic lethality resampling	273
I.1	Performance of χ^2 and SLIPT across quantiles	275
I.2	Performance of χ^2 and SLIPT across quantiles	277
I.3	Performance of χ^2 and SLIPT across quantiles with more genes	279
I.4	Performance of χ^2 and SLIPT across quantiles with query correlation	281
I.5	Performance of χ^2 and SLIPT across quantiles with query correlation	283
I.6	Performance of χ^2 and SLIPT across quantiles with query correlation and more genes	285
J.1	Performance of simulations on a simple graph	287
J.2	Performance of simulations on an inhibiting graph	288
J.3	Performance of simulations on a constructed graph with inhibition	289
J.4	Performance of simulations on a constructed graph with inhibition	290
J.5	Detection of synthetic lethality within a graph structure	291
J.6	Detection of synthetic lethality within an inhibiting graph	293
J.7	Detection of synthetic lethality within an inhibiting graph	294
J.8	Performance of simulations including a simple graph	295
J.9	Performance of simulations on a branching graph	296
J.10	Performance of simulations on a complex graph	297
J.11	Performance of simulations on a large graph	298
J.12	Performance of simulations on a branching graph with inhibition	299
J.13	Performance of simulations on a branching graph with inhibition	300
J.14	Performance of simulations on a complex graph with inhibition	301
J.15	Performance of simulations on a complex graph with inhibition	302
J.16	Performance of simulations on a large constructed graph with inhibition	303
J.17	Performance of simulations on a large constructed graph with inhibition	304
J.18	Performance of simulations on the $G_{\alpha i}$ signalling pathway	305
J.19	Performance of simulations including the PI3K cascade	306
J.20	Performance of simulations including the $G_{\alpha i}$ signalling pathway	307

Acronyms

ANOVA	Analysis of Variance
AUROC	Area Under the Receiver Operating Characteristic (curve)
BioPAX	Biological Pathway Exchange
BiSEp	Bimodal Subsetting Expression
cDNA	Complementary DNA (from mRNA)
CNV	Copy Number Variation
CPM	Counts Per Million mapped reads
CPU	Central Processing Unit
CRAN	Comprehensive R Archive Network
DAISY	Data Mining Synthetic Lethal Identification Pipeline
DNA	Deoxyribonucleic Acid
EMT	Epithelial-Mesenchymal Transition
ER	Estrogen Receptor
FDR	False Discovery Rate
GO	Gene Ontology
GPCR	G Protein Coupled Receptor
HDGC	Hereditary Diffuse Gastric Cancer
HPC	High Performance Computing
ICGC	International Cancer Genome Consortium
mRNA	Messenger RNA
mtSLIPT	Synthetic Lethal Interaction Prediction Tool (against mutation)
NeSI	New Zealand eScience Infrastructure
NGS	Next-Generation Sequencing
NMD	Nonsense-Mediated Decay
PAM50	Prediction Analysis of Microarray 50
PARP	Poly-ADP-Ribose Polymerase
PCR	Polymerase Chain Reaction
PI3K	Phosphoinositide 3-kinase
PPI	Protein-Protein Interaction
PR	Progesterone Receptor
RNA	Ribonucleic Acid
RNAi	RNA Interference
ROC	Reciever Operating Characteristic (curve)
RSEM	RNA-Seq by Expectation Maximization (normalisation)
SGA	Synthetic Gene Array (technique)

SGI	Synthetic Genetic Interaction
shRNA	Short Hairpin RNA
siRNA	Short Interfering RNA
SL	Synthetic Lethal
SLIPT	Synthetic Lethal Interaction Prediction Tool
Slurm	Simple Linux Utility for Resource Management
SOCKS	Socket Secure
SR	Synthetic Rescue (or viability)
SS	Synthetic Suppression
SSL	Synthetic Sick
TCGA	The Cancer Genome Atlas (genomics project)
UCSC	University of California, Santa Cruz
UTR	Untranslated Region (of mRNA)

Chapter 1

Introduction and Literature Review

This thesis presents research into genetic interactions using genomics data and bioinformatics approaches. Chapter 1 introduces recent developments in genomics and bioinformatics, particularly in their application to cancer research. Studies of synthetic lethal interactions, which have fundamental importance in genetics in model organisms and renewed relevance in cancer biology specifically, will be discussed and reviewed in detail. A bioinformatic approach to synthetic lethal interactions enables a wider exploration of the function of genes and proteins in cancer cells, in contrast with candidate gene and experimental screening approaches. Synthetic lethal drug design aims to develop treatments with specificity against loss of function mutations in tumour suppressor genes, such as *CDH1* (which encodes E-cadherin) and was the focus of the analysis in this thesis. The role of *CDH1* in cellular and cancer biology is therefore also briefly reviewed.

1.1 Cancer Research in the Post-Genomic Era

Genomic technologies are expected to significantly impact on the clinical treatment of cancers, along with wider applications of genetics (Goodwin *et al.*, 2016; Roychowdhury and Chinnaian, 2016). These technologies enable focused genetic investigations on candidate genes selected from bioinformatic analyses of genomic data. Facilitated by rapidly developing technologies, large-scale projects have investigated populations (1000 Genomes, 2010), cancers (Dickson, 1999; Zhang *et al.*, 2011), and functional genomics (Kawai *et al.*, 2001; ENCODE, 2004). However, genomic technologies **such as microarrays or genome sequencing** have yet to be widely adopted in healthcare or oncology (Roychowdhury and Chinnaian, 2016; Waldron, 2016). Bioinformatics analysis for interpretation of genomic data is one of the main approaches to address

this disparity (Goodwin *et al.*, 2016). Here, I outline the cancer genomics projects and findings which have led to the availability of genomics data used in this thesis, and recent findings in cancer research which demonstrate potential applications of using this data.

1.1.1 Cancer is a Global Health Issue

Cancers are the second leading cause of death globally (WHO, 2017), with an estimated annual incidence of 14.1 million cases and annual mortality of 8.2 million people (Ferlay *et al.*, 2015). Breast and stomach cancers are among the most prevalent cancers. Breast cancer is the most common cancer in women and has an estimated annual incidence of 1.6 million cases and mortality of 520,000 people. Stomach cancer has an estimated annual incidence of 950,000 cases and a mortality of 723,000 people. Cancer is also a major health concern here in New Zealand, with 19,100 people (including 2500 cases of breast cancer and 370 cases of stomach cancer) diagnosed annually (Hanna, 2003). New Zealand has among the highest incidence (age-standardised per capita) of cancer in the world (Ferlay *et al.*, 2015).

While environmental factors often play a role, genetics is an important contributor to cancer risk. Most cancers occur more frequently with age and family history. Cancers arise from dysregulated cellular growth or differentiation. These can occur through genetic mutations or alterations in gene regulation or expression which generally accumulate as the disease develops. Therefore, early diagnosis is important to ensure patient survival and quality of life. Identification of patients with genetic variants or family histories at a high-risk of particular cancers is an important health issue. These high-risk individuals are regularly monitored for some cancers and are sometimes offered preventative surgery (Guilford *et al.*, 2010; Scheuer *et al.*, 2002).

Chemotherapy is a treatment for many advanced stage cancers, designed to inhibit rapidly growing cells. However, this approach often has severe adverse effects, a narrow therapeutic window, and is not suitable for chemopreventative application in many cases (Kaelin, Jr, 2009). Patients at high-risk of cancers are offered surveillance and preventative surgery but these approaches are not completely effective at preventing cancers and can severely impact on quality of life (Guilford *et al.*, 2010). Alternative chemoprevention and treatment strategies based on molecular biology and other fields are being investigated, including targeted molecular therapeutics (Bozovic-Spasojevic *et al.*, 2012).

1.1.1.1 The Genetics and Molecular Biology of Cancers

Cancers involve dysregulation of genes, including somatic and hereditary mutations, which may predispose individuals to high-risk cancers and familial cancer syndromes (American Cancer Society, 2017; Guilford *et al.*, 1998; Stratton *et al.*, 2009; NCI, 2015; Vogelstein *et al.*, 2013). The occurrence of somatic mutations **throughout our lifespan** increases the risk of cancer with age. An association of cancer incidence with the stem cell divisions in which mutations could occur across tissue types, suggests that cancers may be inseparably coupled with aging (Tomasetti and Vogelstein, 2015).

Hanahan and Weinberg (2000) proposed the “hallmarks of cancer”, molecular and cellular traits shared across cancers. These form the basis of a rational approach to categorising the complex changes that occur in cancer. These traits include limitless replication potential, signals for indefinite growth, and invasive or metastatic capabilities. Cancers also evade apoptosis and the immune system, and sustain angiogenesis and energy metabolism (Hanahan and Weinberg, 2011). To achieve this, cancer cells change their genomes and the tumour microenvironment. Genomic instability has a role in the survival and proliferation of cancer cells and the progression of disease, as these malignant characteristics are acquired. Identifying the genetic mechanisms involved in the acquisition of these traits is important for understanding and effectively inhibiting cancer.

1.1.2 The Genomics Revolution in Cancer Research

Genomic technologies have transformed genetics research, including the study of health and disease (Goodwin *et al.*, 2016; Lander, 2011). Genomics enables systematic, unbiased studies across all of the genes in the genome. Cancer genomics investigations have been widely applied to different tissues across molecular profiles (Bamford *et al.*, 2004; Weinstein *et al.*, 2013; Zhang *et al.*, 2011). Genome sequencing technologies continue to improve and become feasible in a wider range of applications.

Genomics has been used in many investigations (Goodwin *et al.*, 2016) but relatively few of the potential applications in healthcare have been realised yet (Roychowdhury and Chinnaiyan, 2016; Tran *et al.*, 2012). Cancer genomics, in particular, could have numerous benefits across diagnostics, prognosis, management, and treatment (Roychowdhury and Chinnaiyan, 2016). While direct impact of genomics on the clinic has been limited thus far, the cancer genes and therapeutic targets identified have begun to be introduced in the clinic (Stratton *et al.*, 2009).

1.1.2.1 High-Throughput Technologies

These investigations have been enabled by recent developments in genomics technologies, including microarrays and more recently “Next-Generation Sequencing” (NGS), which can both be used to generate high-throughput expression data. Microarray are a high-throughput molecular technique, reducing the cost, time, and labour required to study genes at the “genome” scale (Schena, 1996). Microarray can detect genotype or expression across many genes, making it feasible to perform on a statistically informative number of samples. Microarray are manufactured with probes which measure binding of nucleotides which either detect the presence of a sequence such as a single nucleotide polymorphism (SNP) or quantify sequences for DNA copy number, gene expression, or DNA CpG methylation. In addition to being more versatile, with higher-throughput than polymerase chain reaction (PCR) based techniques, microarrays are considered cost-effective, particularly when scaled up to a large number of probes.

The introduction of massively parallel sequencing technologies has further expanded high-throughput molecular studies and the availability of genomics data. NGS enables rapid *de novo* genome and transcriptome sequencing, in addition to **quantifying** gene expression (Goodwin *et al.*, 2016). However, the cost of sequencing for gene expression studies is still considerably higher than a microarray study, limiting feasible sample sizes, and NGS studies have large compute requirements to handle the raw data. In many cases, the benefits of NGS technologies outweigh the additional cost. NGS technologies have the advantage of greater potential accuracy and sensitivity than microarrays. NGS has a wider dynamic range than microarrays and are not limited to genes with an already characterised sequence or functions (Tarazona *et al.*, 2011).

NGS is highly adaptable to different applications, including DNA sequencing (obtaining the base sequence for the exome or whole genome) or RNA-Seq (Goodwin *et al.*, 2016; Tran *et al.*, 2012; Waldron, 2016). RNA-Seq of the transcriptome is a common adaptation where RNA is reverse transcribed and sequenced from the resulting complementary DNA (cDNA). This is utilised to quantify the levels of RNA and identify which regions of DNA are expressed. Subsets of the nucleic acid may be extracted for sequencing such as the coding regions of DNA (for the “exome”), mRNA, or micro RNA. These “omics” technologies (Roychowdhury and Chinnaiyan, 2016; Waldron, 2016) are applicable across a wide range of biomolecules to generate “molecular profiles” of a cell or sample (Perou *et al.*, 2000).

NGS technologies continue to be refined (Goodwin *et al.*, 2016) with Illumina (the platform used to generate data in this project) and competitors continuing to improve products and decrease costs. As such, RNA-Seq for examining transcriptomes or expression studies is a growing field and will continue to be generated for a range of samples. The technology may yet improve (Goodwin *et al.*, 2016) with developments in speed and accuracy (e.g., semi-conductor platforms) or long reads, single molecule sequences (e.g., Pacific Biosciences, Oxford Nanopore, and Quantum Biosystems Japan). Due to the benefits of sequencing and the availability of public data, this thesis has focused on gene expression data generated by RNA-Seq. RNA-Seq data is publicly available from large-scale cancer genomics projects and the methods analysis developed for RNA-Seq data could be applied to future genomics technologies.

1.1.2.2 Bioinformatics and Genomic Data

Genomic technologies have generated data at a scale which requires computational, mathematical, and statistical expertise to handle this data effectively (Markowetz, 2017; Tran *et al.*, 2012), in addition to an understanding of the biological context and research questions. The interdisciplinary field of “bioinformatics”, which draws upon these skills, focuses specifically on making inferences from genomics data or developing the tools to do so. Gene expression analysis is the focus of many bioinformatics research groups, drawing upon statistical approaches to appropriately handle microarray and RNA-Seq data along with making biological inferences from a large number of statistical tests.

Bioinformatics is often confused with the broader field “computational biology” (Markowetz, 2017), which focuses on modelling and simulating aspects of biology and is not necessarily limited to genetics or data analysis. In practice, many researchers identify with both bioinformatics and computational biology or use techniques in both fields. This thesis uses many of these approaches, mainly in bioinformatics, to address biological research questions pertaining to synthetic lethal interactions.

1.1.3 Genomics Projects

Genomic projects have also been applied to various organisms, functional genetics (Kawai *et al.*, 2001; ENCODE, 2004), and human populations focusing on variability between individuals and health or disease risk (HapMap, 2003; 1000 Genomes, 2010). International projects and consortiums have begun to release data gathered using common agreed upon protocols across laboratories. These include many genomics projects including cancer genomics projects discussed below. The quality, consistency, and

accessibility of these international projects is appealing, particularly for gene expression datasets where the more recent, larger projects have switched from microarray to RNA-Seq technologies.

1.1.3.1 The Cancer Genome Project

The cancer genome project was among the first genomics investigations into cancer (Dickson, 1999), using the human genome sequence (Collins and Barker, 2007; Lander *et al.*, 2001), the cancer research literature, and sequencing the genes of cancers themselves. The main aim of the Cancer Genomes Project was to discover “cancer genes”, which are frequently mutated in cancers by comparing cancer and normal tissue samples. These include both “oncogenes” (which drive cancer growth) and “tumour suppressors” (which protect against cancers) that are functionally activated and inactivated in cancers respectively. This project is ongoing and continues to maintain the [Catalogue Of Somatic Mutations In Cancer](#) (COSMIC), a database of cancer genes (COSMIC, 2016). It includes 1,257,487 samples with 4,175,8787 gene mutations curated from 23,870 publications, including 29,112 whole genomes (COSMIC, 2016).

1.1.3.2 The Cancer Genome Atlas Project

The Cancer Genome Atlas (TCGA) network initially set out to demonstrate utility in a pilot project on brain (McLendon *et al.*, 2008), ovarian (Bell *et al.*, 2011), and squamous cell lung (Hammerman *et al.*, 2012) cancers. The project then expanded, aiming to analyse 500 samples each for 20-25 tumour tissue types. TCGA has since exceeded that goal, with data available for 33 cancer types including 10 “rare” cancers, a total of over 10,000 samples (TCGA, 2017). The TCGA projects set out to generate a molecular “profile” of the tumour (and some matched normal tissue) samples: genotype, somatic mutations, gene expression, micro RNA, DNA copy number, DNA methylation, and protein levels. Data which cannot be used to identify the patients are publicly available

The Cancer Genome Atlas pilot projects (Bell *et al.*, 2011; Hammerman *et al.*, 2012; McLendon *et al.*, 2008) serve to demonstrate the power of applying genomic technologies to cancer research at such a scale. TCGA demonstrated the potential discovery of the molecular basis of cancer with these tissues, including describing the recurrently mutated genes in each cancer, identifying differentially methylated regions, and proposing transcriptional subtypes for ovarian cancers. The molecular aberrations in each cancer represent potential therapeutic targets in some cases and some were shown to have an impact on patient survival.

The TCGA breast cancer analysis (Koboldt *et al.*, 2012) consisted of 802 samples with exomes, copy number variants, RPPA protein quantification, and DNA methylation, mRNA, and micro RNA arrays, with 97 whole genomes sequenced. Four main molecular classes were identified to subtype the samples, despite considerable heterogeneity between samples. Recurrent mutations across more than 10% of samples were identified in the *TP53*, *PIK3CA*, and *GATA3* genes. In a further analysis of 817 breast cancer samples including 127 invasive lobular breast and 88 mixed type samples (Ciriello *et al.*, 2015), 3 molecular subtypes of lobular breast cancer were identified. Lobular breast cancer was also characterised by recurrent mutations in the *CDH1*, *PTEN*, *TBX2*, and *FOXA1* genes.

TCGA stomach cancer analysis of 295 samples (Bass *et al.*, 2014) identified molecular subtypes of stomach cancers characterised by: the Epstein-Barr virus, microsatellite instability, genomic instability, and chromosomal instability. Aberrations in *PD-L1*, *PIK3CA*, and *JAK2* were also identified in stomach cancers which may present therapeutic targets.

TCGA has identified various genes as recurrent, driver mutations across cancer types which are likely to have a role in driving the development of these cancers and present a molecular target that could be applied across tissue types. In addition to disregarding the tissue-based distinction between colon and rectal cancers based on molecular similarity (Muzny *et al.*, 2012), TCGA has observed differences within tumour types and proposed molecular subtyping for breast, clear cell renal, papillary renal, stomach, skin, bladder, and prostate cancers (Abeshouse *et al.*, 2015; Akbani *et al.*, 2015; Bass *et al.*, 2014; Ciriello *et al.*, 2015; Creighton *et al.*, 2013; Hammerman *et al.*, 2012; Koboldt *et al.*, 2012; Linehan *et al.*, 2016; Muzny *et al.*, 2012; Weinstein *et al.*, 2014).

The “Pan Cancer” TCGA project (Hoadley *et al.*, 2014; Weinstein *et al.*, 2013) analysed 3527 samples across 12 tissue types. This project performed a comprehensive analysis of molecular data across cancer types to identify molecular similarities and differences. These included recurrent *TP53*, *BRCA1* and *BRCA2* mutations, HER2 over-expression, and microsatellite instability across cancer types. The Pan Cancer project has identified 11 molecular subtypes across these tissues, with only 5 of these corresponding to tissue cancer types due to molecular similarities shared across cancer types (Hoadley *et al.*, 2014). The project further supports the genomic stratification of cancer patients, demonstrated in breast cancer (Parker *et al.*, 2009; Pereira *et al.*,

2016; Perou *et al.*, 2000), and there being core molecular characteristics across cancers (Hanahan and Weinberg, 2000, 2011).

While these findings contribute to further understanding cancer biology within and across tissue types, the main objective of such projects is to publicly release data to analyse in future investigations (McLendon *et al.*, 2008; TCGA, 2017; Weinstein *et al.*, 2013). These serve as a vast resource of common and rare cancer types and are publicly available for further analysis (cBioPortal, 2017; TCGA, 2017; Zhang *et al.*, 2011).

1.1.4 Genomic Cancer Medicine

Cancer genomics has substantial potential for impacts in cancer medicine: from diagnosis to treatment (Roychowdhury and Chinnaiyan, 2016; Tran *et al.*, 2012). Beyond direct use of genomes or RNA-Seq in clinical laboratories to more precisely diagnose cancers based on molecular features, genomic studies also generate prognostic biomarkers to better predict patient outcomes and inform development of novel treatments such as targeted therapeutics. These are likely to have a more immediate patient benefit considering the cost of routine genomes sequencing for diagnostics.

1.1.4.1 Cancer Genes and Driver Mutations

There are two main classes of “cancer genes” (Futreal *et al.*, 2001). Oncogenes are activated in cancers either by gain of function mutations in proto-oncogenes, amplification of DNA, or elevated gene expression. Their normal functions are typically to regulate stem cells or to promote cellular growth, with recurrent mutations that are typically concentrated to particular gene regions (“hotspots”). Conversely, tumour suppressor genes are those inactivated in cancer either by loss of function mutations, deletion of DNA copies, or reduced gene expression, including hypermethylation. Their normal functions are typically to regulate cell division (e.g., *TP53*), DNA repair (e.g., *BRCA1*), and cell signalling (e.g., *PIK3CA* and *PTEN*). Detecting these cancer genes has accelerated with genomic technologies, as demonstrated by COSMIC and TCGA (COSMIC, 2016; Weinstein *et al.*, 2013). Recurrent mutations, DNA copy number variants, differential gene expression, or differential DNA methylation are all indicative of cancer genes (Mattison *et al.*, 2009), which can be detected in genomics data (Pereira *et al.*, 2016; Weinstein *et al.*, 2013).

Distinguishing important “driver” mutations in cancer genes from “passenger mutation” mutations is challenging due to patient variation, tumour heterogeneity, and genomic instability producing many variant gene sequences (Stratton *et al.*, 2009; Tran *et al.*, 2012). Driver mutations can be identified by whether they co-occur or are mutu-

ally exclusive with mutations in other genes in cancers, are recurrently mutated across a significant proportion of samples for a specific tissue type, or if mutations are recurrent across different cancer tissue types (cBioPortal, 2017; Pereira *et al.*, 2016; COSMIC, 2016; Weinstein *et al.*, 2013; Zhang *et al.*, 2011). Approximately 140 driver mutations have been identified, including many novel genes in particular cancers from genomic studies, with 2–8 typically occurring in each tumour usually affecting cell fate, survival, or genomes maintenance (Vogelstein *et al.*, 2013). There remains a need to translate the identification of many cancer genes and driver mutations to patient benefit by repurposing or designing of therapeutic interventions against these molecular targets.

1.1.4.2 Precision Cancer Medicine

The importance of genomics is emphasised in translational cancer research in contrast with current strategies of healthcare based on what works well for the majority of the population. Cancers could eventually be treated by their genomic features (Roychowdhury and Chinnaiyan, 2016), particularly grouping patients by the mutation, expression, or DNA methylation profiles of their cancers, which is already done in part (Parker *et al.*, 2009). Identifying actionable molecular targets is a key aspect of “precision medicine”, the rationale to target molecular subtypes with separate treatment strategies (Glaire *et al.*, 2017). To this end many driver mutations and gene expression signatures for distinguishing cancers have been identified. Some oncogenic driver mutations have effective pharmacological inhibitors designed against them (**such as vemurafenib against BRAF^{V600E} and herceptin against ERBB2**) but there remain many cancer genes and mutations, particularly tumour suppressors, for which there is not yet a targeted therapy.

1.1.4.3 Molecular Diagnostics and Pan-Cancer Medicine

Molecular features such as mutations or gene expression signatures have been proposed to diagnose tumour subtypes. In breast cancer, several distinct “intrinsic subtypes” have been identified, distinguished by molecular mechanisms, with differences in malignancy and patient outcome (Parker *et al.*, 2009; Perou *et al.*, 2000). Conversely, common molecular mechanisms may be shared between cancers across tissue types as discovered by the “Pan Cancer” TCGA project, which combined molecular profiles across tissue types (Weinstein *et al.*, 2013). Molecular subtypes could feasibly be included in clinical testing as a panel of biomarkers for diagnosis, monitoring drug response, or predicting risk of recurrence. As these molecular subtypes and genetic

aberrations specific to cancers have been identified, there is an increasingly clear need for further development of treatments that target them.

Gene expression can be used to characterise breast cancers. The “intrinsic subtypes” identified were characterised by estrogen receptor, *HER2*, and basal, epithelial signalling (Perou *et al.*, 2000). The expression profiles were similar across independent samples of the same tumour or the same patient and therefore represent the molecular state of a tumour. The molecular intrinsic subtypes “luminal A”, “luminal B”, “*HER2*-enriched”, “basal-like”, and “normal-like” have been replicated across microarray studies (Hu *et al.*, 2006), with their relevance to prognosis demonstrated, and a 50-gene subtype predictor developed (Parker *et al.*, 2009; Sørlie *et al.*, 2001). Despite specific differences in subtyping, there is widespread agreement that distinguishing luminal, *HER2*-enriched, and triple negative tumours has prognostic importance for patients (Dai *et al.*, 2015). The “Pan Cancer” The Cancer Genome Atlas project (discussed in Section 1.1.3.2) demonstrates the importance of molecular similarities and differences between cancers across cancer tissue types (Weinstein *et al.*, 2013).

Gatza *et al.* (2010) used gene signatures for 18 cellular pathways in breast cancer to define subtypes with distinct molecular pathway activity. A “metagene” is a measure of pathway activation (derived from eigenvectors or principal components) which gives a consistent signal of gene expression (Anjomshoaa *et al.*, 2008; Huang *et al.*, 2003; Nagalla *et al.*, 2013). Unsupervised hierarchical clustering defined subtypes with common pathway activity, despite variation in mutations. These intrinsic subtypes and provide finer molecular stratification with a functional basis (Gatza *et al.*, 2014; Parker *et al.*, 2009). The subtypes with shared pathway activity have similar molecular characteristics (e.g., DNA copy number) and clinical properties including prognosis.

1.1.4.4 Targeted Therapeutics and Pharmacogenomics

Targeted therapies with specificity against a molecular target are examples of precision cancer medicine. Molecular targets can be tested in laboratory conditions with RNA interference (RNAi) or pharmacological agents (Fece de la Cruz *et al.*, 2015). Identification of molecular targets is important for developing novel anti-cancer treatments along with validation and drug testing. For oncogenic mutations, the recurrent mutant variant or over-expressed gene can be directly inhibited, however, oncogenes with high homology to other genes or tumour suppressor genes are not amenable to direct targeting (Kaelin, Jr, 2009). Targeted anticancer therapeutics can exploit complex interactions to distinguish normal and cancerous cells which may benefit from studies of gene regulation or interaction networks (Hopkins, 2008). Targeted therapeutics have

already been successfully applied as monoclonal antibodies against oncogenes, such as HER2 in breast cancer (Miles, 2001).

1.1.5 Systems and Network Biology

Driver mutations in oncogenes and tumour suppressor genes do not occur in isolation. Genetic interactions, regulatory and cellular signalling, and metabolic reactions are inter-related and may each be perturbed by aberrations in gene function occurring in cancers. These relationships can be represented by biological networks of connected pairs of genes with a relationship. Due to the complexity of a cell, these molecular networks are very large, consisting of thousands of nodes comprised by genes or proteins.

The properties of large networks were first studied by constructing random networks by randomly linking a fixed number of nodes (Erdős and Rényi, 1959, 1960). Despite the random nature of these networks, properties such as their connectivity were well characterised. The vertex degree (number of partners for each node) of their random networks followed a Poisson distribution, however this property does not hold in nature. Thus natural networks are non-random or not formed in this way (Barabási and Oltvai, 2004).

This work formed the foundation for studying complex networks (van Steen, 2010), which model features of observed networks not found in Erdő and Rényi's random networks (Erdős and Rényi, 1959, 1960). The small world property, made popular by findings in social networks (Travers and Milgram, 1969), is the remarkably short path lengths between any nodes in a network. A small world network is well-connected with a characteristic path length (the average length of shortest paths between all pairs of nodes) proportional to the logarithm of the number of nodes. Watts and Strogatz (1998) developed a model of random rewiring of a regular network to construct random networks with the small world property and a high clustering coefficient. While these properties are more representative of networks occurring in nature, their model was limited by the degree distribution which converges to a Poisson distribution as it is rewired (Barrat and Weigt, 2000). The vertex degree distribution of naturally occurring networks often follows a power law distribution with most nodes having far fewer connections than average and a small subset of highly connected network 'hubs' (Barabási and Albert, 1999).

Barabási and Albert (1999) constructed a network model in an entirely different way to randomly generate scale-free networks which have a power law degree distribution.

They constructed random networks by preferential attachment, modelling growth of a network by sequentially adding nodes with links to existing nodes. The scale-free nature of the random networks was ensured by adding new nodes with an increasing probability of attachment to an existing node if it had a higher degree. These networks successfully captured the scale-free nature of many observed networks with short characteristic path length and low eccentricity resulting in super small worlds (Barabási and Albert, 1999).

High-throughput technologies such as siRNA screens, two-hybrid screens, microarrays and massively parallel sequencing have generated genome-scale data and enabled analysis of biological networks (Barabási and Oltvai, 2004; Boone *et al.*, 2007; Goodwin *et al.*, 2016). Molecular networks are biological networks consisting of biological molecules including genes, transcripts (with non-coding and micro RNAs), or proteins related by known interactions and gene regulatory or metabolic pathways. Many types of molecular networks can be constructed, depending on the biological application (Barabási and Oltvai, 2004). Synthetic genetic interactions **occurring between mutations in different genes** are relatively unexplored within molecular networks and may lead to better understanding of the role of gene functions in cellular function and disease. High-throughput screens in humans, mammals, and non-model organisms are costly and labour-intensive (Fece de la Cruz *et al.*, 2015). Computational approaches with effective predictive models are therefore a more feasible alternative to study the connectivity of a biological network in a complex metazoan cell at the genome-scale.

1.2 Synthetic Lethal Cancer Medicine

Synthetic lethality has vast potential to improve cancer medicine by expanding application of targeted therapeutics to include inactivation of tumour suppressors and genes that are difficult to target directly. Synthetic lethal interactions are also studied for gene function and drug mode-of-action in model organisms. This Section introduces the concept of synthetic lethality as it was originally conceived and how it has been adopted conceptually in cancer research. Detecting these interactions at scale and interpreting them is the focus of this thesis, hence I start with an overview of the concepts involved, initial work on the interaction, and the rationale for applications to cancer. Specific investigations into synthetic lethality in cancer, detection by experimental screening, and prediction by computational analysis will then be reviewed.

1.2.1 Synthetic Lethal Genetic Interactions

Genetic interactions are a core concept of molecular biology, discovered among earliest investigations of Mendelian genetics, and have received revived interest with new technologies and potential applications. Biological epistasis is the effect of an allele at one locus “masking” the phenotype of another locus (Bateson and Mendel, 1909). Statistical epistasis is where there is significant disparity between the observed and expected phenotype of a double mutant, compared to the respective phenotypes of single mutant and the wild-type (Fisher, 1919). Fisher’s definition lends itself to quantitative traits and more broadly encompasses synthetic genetic interactions (SGIs). These have become popular for studies in yeast genetics and cancer drug design (Boone *et al.*, 2007; Kaelin, Jr, 2005).

SGIs are substantial deviations of growth or viability from the expected null mutant phenotype (of an organism or cell) assuming additive (deleterious) effects of the single mutant. The double mutant does not necessarily have either of the single mutant phenotypes (as shown for cellular growth phenotypes in Figure 1.1). Most SGIs are more viable than either single mutant or less viable than the expected double mutant. Mutations are “synergistic” in negative SGI with more deviation from the wild-type than expected. Formally, “synthetic sick” (SSL) and “synthetic lethal” (SL) interactions are negative SGIs giving growth inhibition and complete inviability respectively. In cancer research, synthetic lethality more broadly describes any negative SGI with specific inhibition of a mutant cell, including SSL interactions. Mutations are “alleviating” in positive SGI with less deviation from the wild-type than expected. For viability, “suppression” (SS) and “rescue” (SR) are positive SGIs giving at least partial restoration of wild-type growth from single mutant with growth impairment and lethal phenotypes respectively. Negative SGIs were markedly more common than positive SGIs in a number of studies in model systems (Boucher and Jenna, 2013; Tong *et al.*, 2004).

1.2.2 Synthetic Lethal Concepts in Genetics

Synthetic lethal genes are generally regarded to arise due to functional redundancy (Boone *et al.*, 2007). Due to the functional level of SGIs, synthetic lethal genes do not need to directly interact, nor be expressed in the same cell or at the same developmental stage: serving related functions is sufficient to affect cell (or organism) viability and be relevant to drug-mode-of-action cancer biology. Combined loss of genes performing an essential or important function in a cell are therefore deleterious. Synthetic lethal

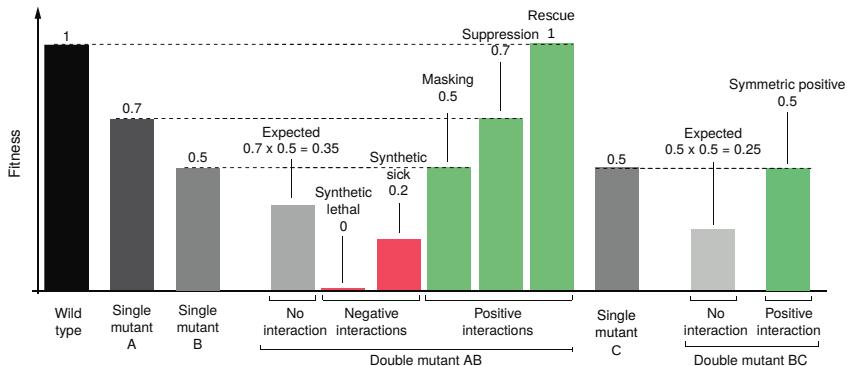


Figure 1.1: Synthetic genetic interactions. Impact of various negative and positive SGIs: negative interactions involve deleterious (sick) or inviable (lethal) phenotypes whereas positive interactions involve restoring viability by masking or suppressing the other mutation or complete rescue of the wild-type phenotype. Figure adapted from (Costanzo *et al.*, 2011) concerning growth viability fitness in yeast.

gene pairs are therefore pairwise essential with “induced essentiality”: each synthetic lethal gene becomes essential to the cell upon loss of the other (Ashworth *et al.*, 2011; Kaelin, Jr, 2005).

Since synthetic lethal gene partners can be affected by extracellular stimuli such as chemicals, essentiality of synthetic lethal genes can be induced by the environment of a cell. An environmental stress condition may inhibit one or the other synthetic lethal gene, such as exposure to chemicals, in which case the synthetic lethal partner gene is “conditionally essential” (Hillenmeyer, 2008). Thus the evolutionary rationale for the abundance of SGIs (compared to the surprisingly low number of essential genes) in Eukaryotic genomes can be attributed to genetic functional redundancy and network robustness of a cell which are advantageous to survival.

Biological functions are typically performed by a pathway of genes (or their products). Synthetic lethal genes occur within the same biological pathway and between them (Boone *et al.*, 2007; Costanzo *et al.*, 2010; Kelley and Ideker, 2005). Many genes of the same pathway may be **interchangeable** as synthetic lethal partners of a particular gene. Therefore biological pathways can exhibit induced essentiality with loss of the synthetic lethal partner gene and synthetic lethality may occur at pathway level or in a gene regulation network.

1.2.3 Synthetic Lethality in Model Systems

Genetic high-throughput screens have identified unexpected, functionally informative, and clinically relevant synthetic lethal interactions; including synthetic lethal partners of genes recurrently mutated in cancer or attributed to familial early-onset cancers (Lord *et al.*, 2015). While screening presents an appealing strategy for synthetic lethal discovery, computational approaches are becoming popular as an alternative or complement to experimental methods to overcome inherent bias and limitations of experimental screens. An array of recently developed computational methods (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015; Tiong *et al.*, 2014; Wang and Simon, 2013; Wappett, 2014) show the need for synthetic lethal discovery in the fundamental genetics and translational cancer research community. However, many existing computational methods are not suitable for queries of genomic data for interacting partners of a particular gene, as (1) they have been applied pairwise across the genomes, (2) they do not have software released to apply the methodology, or (3) they lack statistical measures of error for further analysis. A robust prediction of gene interactions is an effective and practical approach at a scale of the entire genome for ideal translational applications, analysis of biological systems, and constructing functional gene networks.

1.2.3.1 Synthetic Lethal Pathways and Networks

SGIs are common in genomes, four-fold more interactions were detected with synthetic gene array (SGA) mating screens than protein-protein interactions detected with yeast-2-hybrid (Tong *et al.*, 2004). The SGI network was scale-free and had a low average shortest path length, as expected for a complex biological network (Barabási and Oltvai, 2004). Highly connected “hub” genes with the highest number of links (vertex degree) are functionally important with many negative SGI hubs involved in cell cycle regulation, and many positive SGI hubs involved in translation (Baryshnikova *et al.*, 2010b; Costanzo *et al.*, 2010). Negative SGIs were far more common than positive SGIs, with synthetic gene loss being more likely to be deleterious to cell than advantageous, which indicates that synthetic lethality may be comparably easier to detect than other SGIs.

Essential pathways are highly buffered, with five-fold more interactions than other SGIs, consistent with strong selection for survival, as found with conditional and partial mutations in essential genes (Davierwala *et al.*, 2005). This SGI network had scale-free topology and rarely shared interactions with the protein-protein interaction network. These networks are related by an “orthogonal” relationship: shared partners in one

network tend to be themselves connected directly in the other network. Essential genes were likely to have closely related functions, whereas non-essential networks were relatively more inclined to have SGIs between distinct biological pathways.

1.2.3.2 Evolution of Synthetic Lethality

There is poor conservation of specific SGIs between *S. cerevisiae* and *S. pombe* with 29% of the interactions tested in both distantly related species being conserved between them (Dixon *et al.*, 2008). The remaining interactions show high species-specific differences, however, many of the species-specific interactions were still conserved between biological pathways, protein complexes, or protein-protein interaction modules. Similarly, conservation of pathway redundancy was also found between Eukaryotes (*S. cerevisiae*) and prokaryotes (*E. coli*) (Butland *et al.*, 2008). Negative SGIs were more likely to be conserved between biological pathways, whereas positive SGIs were more likely to be conserved within a pathway or protein complex (Roguev *et al.*, 2008).

A modest 5% of interactions were conserved between unicellular (*S. cerevisiae*) and multicellular (*C. elegans*) organisms. However, the nematode SGI network had similar scale-free topology and modularity despite differences in methodology: metazoan synthetic lethal screens with RNA interference (RNAi) are incomplete knockouts, whereas screening null mutations is feasible in yeast (Bussey *et al.*, 2006). The nematode SGI screen identified network hubs with important interactions to orthologues of known human disease genes (Lehner *et al.*, 2006). Despite the lack of direct conservation of SGIs between yeasts and nematode worms, genetic redundancy was consistent with an “induced essentiality” model of SGIs where gene functions are conserved with network restructuring over evolutionary change (Tischler *et al.*, 2008).

While nematode models are more closely related to human cells which are also screened with RNAi, cancer cells can present growth and viability phenotypes more comparable to yeast models. Therefore findings from both SGA and RNAi models are relevant to understanding human and cancer cells. RNAi has also been applied to human and mouse cancer cells with short interfering RNA (siRNA) in cell culture and genetic screening experiments. These findings suggest that SGI network “rewiring” is a concern for identifying specific synthetic lethal interactions in cancer as specific synthetic lethal genes may vary between genetic backgrounds. Thus it is expected at a pathway approach will be more robust in the context of evolution, patient variation, tumour heterogeneity, or disease progression.

1.2.4 Synthetic Lethality in Cancer

Loss of function occurs in many genes in cancers, including tumour suppressors, yet few interventions target such mutations compared to targeted therapies for gain of function mutation in oncogenes (Kaelin, Jr, 2005). Synthetic lethality is a powerful design strategy for therapies selective against loss of gene function with potential for application against a range of genes and diseases (Fece de la Cruz *et al.*, 2015; Kaelin, Jr, 2009). When genes are disrupted in cancers, the induced essentiality of synthetic lethal partners presents a vulnerability that may be exploited for anti-cancer therapy. Since synthetic lethality affects cellular viability by indirect functional relationships between genes, it is suitable for indirectly targeting mutations in cancers via synthetic lethal partners with targeted therapeutics. These treatments could be highly specific against cancer cells (with the target mutation) over non-cancer cells (with a functional compensating gene). Analogous to “oncogene addiction”, where cancer cells adapt to particular oncogenic growth signals and become reliant on them to remain viable (Luo *et al.*, 2009; Weinstein, 2000), synthetic lethal partners of inactivated tumour suppressors are required to maintain cancer cell viability and proliferation. As such cancers are subject to “non-oncogene addiction” and these genes are feasible anti-cancer drug targets.

The synthetic lethal approach to cancer medicine is most amenable to loss of function mutations in tumour suppressor genes, where it would feasibly be effective against any loss of function mutation across the tumour suppressor with a viable synthetic lethal partner gene (as shown in Figure 1.2). However, the approach may also be suitable for cases where cancer cells have mutations where the normal function of the gene is disrupted such as if it were over-expressed (“synthetic dosage lethality”) or if an oncogenic mutation interfered with the function of the proto-oncogene. Thus synthetic lethality makes it feasible to target a range of cancer-specific mutations with targeted therapeutic, including inactivated tumour suppressor genes. synthetic lethality may also enable distinguishing highly homologous oncogenes by functional differences by targeting their synthetic lethal partners.

1.2.5 Clinical Impact of Synthetic Lethality in Cancer

The synthetic lethal interaction of *BRCA1* or *BRCA2* with *PARP1* in breast cancer is an example of how gene interactions are important in cancer and these discovery of these interactions has lead to translation to the clinic. These genetic interactions enable specific targeting of mutations in *BRCA1* or *BRCA2* tumour suppressor genes

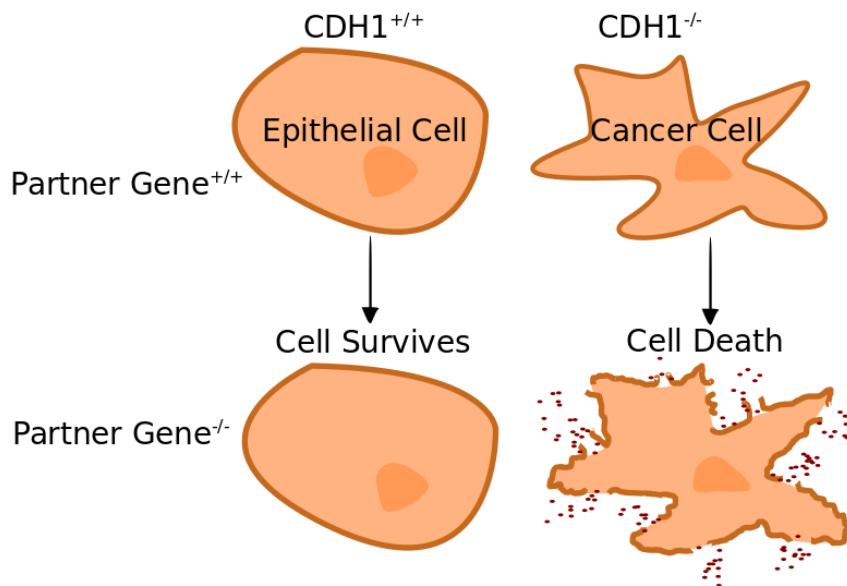


Figure 1.2: **Synthetic lethality in cancer.** Rationale of exploiting synthetic lethality for specificity against a tumour suppressor gene (e.g., *CDH1*) while other cells are spared under the inhibition of a partner gene.

with PARP inhibitors by inducing synthetic lethality in breast cancer (Farmer *et al.*, 2005). PARP inhibitors were one of the first targeted therapeutic against a tumour suppressor mutation to exhibit success in clinical trials.

BRCA1/BRCA2 and *PARP1* genes demonstrate the application of the synthetic lethal approach to cancer therapy (Ashworth, 2008; Kaelin, Jr, 2005). *BRCA1* and *BRCA2* are homologous DNA repair genes, widely known as tumour suppressors; mutation carriers have substantially increased risk of breast (risk by age 70 of 57% for *BRCA1* and 59% for *BRCA2*) and ovarian (risk by age 70 of 40% for *BRCA1* and 18% for *BRCA2*) cancers (Chen and Parmigiani, 2007). The *BRCA1* or *BRCA2* genes, which usually repair DNA or destroy the cell if it cannot be repaired, have inactivating somatic mutations in some familial and sporadic cancers. Poly-ADP-ribose polymerase (PARP) genes are tumour suppressor genes involved in base excision DNA repair. Loss of PARP activity results in single-stranded DNA breaks. However, *PARP1*^{-/-} knockout mice are viable and healthy indicating low toxicity from PARP inhibition (Bryant *et al.*, 2005).

Bryant *et al.* (2005) showed that *BRCA2* cells were sensitive to PARP inhibition by siRNA of *PARP1* or drug inhibition (which targets *PARP1* and *PARP2*) using Chinese hamster ovary cells, MCF7 and MDA-MB-231 breast cell lines. This effect

was sufficient to kill mouse tumour xenografts and showed high specificity to *BRCA2* deficient cells in culture and xenografts. Farmer *et al.* (2005) replicated these results in embryonic stem cells and showed that *BRCA1* cells were also sensitive to PARP inhibition relative to the wild-type with siRNA and drug experiments in cell culture and drug activity against *BRCA1* or *BRCA2* deficient embryonic stem cell mouse xenografts. They found evidence that PARP inhibition causes DNA lesions, usually repaired in wild-type cells, which lead to chromosomal instability, cell cycle arrest, and induction of apoptosis in *BRCA1* or *BRCA2* deficient cells. The combined loss of DNA repair pathways gives a plausible mechanism for an effective anti-cancer treatment.

Thus PARP inhibitors could be applied with clinical use against *BRCA1* or *BRCA2* mutations in both hereditary and sporadic cancers (Ashworth, 2008; Kaelin, Jr, 2005). PARP inhibition has been found to be effective in ovarian cancer patients carrying *BRCA1* or *BRCA2* mutations and some patients without these mutations, suggesting synthetic lethality between PARP and other DNA repair pathways (Ström and Helleday, 2012). This supports the potential for PARP inhibition as a chemopreventative alternative to prophylactic surgery for high-risk individuals with *BRCA1* or *BRCA2* mutations (Ström and Helleday, 2012). Hormone-based therapy has also been suggested as a chemopreventative in such high-risk individuals and aromatase inhibitors have completed phase I clinical trials for this purpose (Bozovic-Spasojevic *et al.*, 2012). Ström and Helleday (2012) also postulate increased efficacy of PARP inhibitors in the hypoxic DNA-damaging tumour micro-environment.

A PARP inhibitor, olaparib, showed fewer adverse effects than cytotoxic chemotherapy and anti-tumour activity in various clinical trials against *BRCA1* or *BRCA2* deficient familial or sporadic breast, ovarian, and prostate cancers (Audeh *et al.*, 2010; Fong *et al.*, 2009, 2010; Tutt *et al.*, 2010). This treatment has a favourable therapeutic window and similarly low toxicity between mutation carriers of *BRCA1* or *BRCA2* mutations and sporadic cases. These PARP inhibitors have been FDA approved for some cancers (McLachlan *et al.*, 2016), are effective against germline and sporadic *BRCA1* or *BRCA2* mutations, and are a potential prevention alternative to prophylactic surgery for high-risk mutation carriers Ström and Helleday (2012).

This demonstrates the clinical impact of a well characterised system of synthetic lethality with known cancer risk genes. Synthetic lethality has the benefit of being effective against inactivation of tumour suppressor genes by any means, broader than targeting a specific oncogenic mutation (Kaelin, Jr, 2005). The targeted therapy is

effective in both sporadic and hereditary *BRCA1* or *BRCA2* deficient tumours acting against an oncogenic molecular aberration across several tissues.

1.2.6 High-throughput Screening for Synthetic Lethality

RNA interference (RNAi) technologies have enabled extensive investigations of genetic redundancy in mammalian experimental models including testing experimentally for synthetic lethality (Fraser, 2004). Synthetic lethal RNAi screens are performed, using short interfering RNA (siRNA) or short hairpin RNA (shRNA) to target specific genes in isogenic cells. Identifying synthetic lethality is crucial for studying gene function, drug mechanisms, and to design novel therapies (Lum *et al.*, 2004). Candidate selection of synthetic lethal gene pairs relevant to cancer has shown some success but is limited because interactions are difficult to predict; they can occur between seemingly unrelated pathways in model organisms (Costanzo *et al.*, 2011). While biologically informed hypotheses have had some success in synthetic lethal discovery (Bitler *et al.*, 2015; Bryant *et al.*, 2005; Farmer *et al.*, 2005), interactions occurring indirectly between distinct pathways would be missed (Boone *et al.*, 2007; Costanzo *et al.*, 2011). Scanning the entire genomes for interactions against a clinically relevant gene is an emerging strategy being explored with high-throughput screens (Fece de la Cruz *et al.*, 2015) and computational approaches (Boucher and Jenna, 2013; van Steen, 2012).

Experimental screening for synthetic lethality is an appealing strategy for wider discovery of functional interactions *in vivo* despite many potential sources of error which must be considered. The synthetic lethal concept has both genetic and pharmacological screening applications to cancer research. Genetic screens, with RNAi to discover the specific genes involved, inform development of targeted therapies with a known mode of action, anticipated mechanisms of resistance, and biomarkers for treatment response. RNAi is a transient knockdown of gene expression more similar to the effect of drugs than complete gene loss and is more representative of disease than model organisms (Bussey *et al.*, 2006). The RNAi gene knockdown process has inherent toxicity to some cells, potential off-target effects, and issues with a high false positive rate. Therefore, it is important to validate any candidates in a secondary screen and replicate knockdown experiments with a number of independent shRNAs. Genetic screens have potential for quantitative gene disruption experiments to selectively target over-expressed genes in cancer via synthetic dosage lethality. While powerful for understanding fundamental cellular function, analysis of isogenic cell lines is inherently limited by assuming only a single mutation differs between them and cannot account for diverse genetic

backgrounds or tumour heterogeneity (Fece de la Cruz *et al.*, 2015). Genetic screens can thus identify targets to develop, or can repurpose targeted therapies for disease, but alone will not directly identify a lead compound to develop for the market or for clinical translation.

Chemical screens are immediately applicable to the clinic, as they are directly screening for selective lead compounds with suitable pharmacological properties. However, chemical screens lack a known mode of action, may affect many targets, and screen a narrow range of genes with existing drugs. With either approach there are still many challenges to translating candidates into the clinic. Identifying specific target genes may contribute to overcoming such challenges, which can be approached with genetic screens and computational alternatives. Screening methods have proven a fruitful area of research, despite being costly, laborious, and having many different sources of error. These limitations suggest a need for complementary computational approaches to synthetic lethal discovery.

1.2.6.1 Synthetic Lethal Screens

Synthetic lethal screens have been conducted for cancer genes in a variety of cancers. These have found synthetic lethality of *PIM1* over-expression with *PLK1* inhibition in prostate cells (van der Meer *et al.*, 2014), *FH* null mutations (involved in hereditary leiomyomatosis and renal cell cancer) with inhibition of adenylate cyclases (Boettcher *et al.*, 2014), and *WEE1* inhibitor treatment with knockdown of checkpoint kinases, Fanconi anaemia, and homologous recombination in colorectal cells (Aarts *et al.*, 2015). These results include genes that have been found to be co-expressed in cancers, are consistent with those identified in the literature, and that were successfully validated with RNAi and drug experiments. These findings demonstrate that synthetic lethal screening can identify partner genes with clinical relevance as biomarkers, therapeutic targets, or conferring sensitivity to existing treatments. These are of particular importance for familial cancer syndromes **where treatments with adverse effects are unsuitable for outwardly healthy patients with high cancer risk** (Boettcher *et al.*, 2014; Telford *et al.*, 2015).

Heredity diffuse gastric cancer (HDGC) is a cancer syndrome involving predisposition to early-onset malignant stomach and breast cancers that has been attributed to inactivating mutations in E-cadherin, encoded by *CDH1* (as discussed in Section 1.3). Telford *et al.* (2015) performed an RNAi screen on MCF10A breast cells for synthetic lethality with *CDH1*. In conjunction with a drug compound screen, inhibitors of JAK, HDAC, PI3K, aurora kinase, and tyrosine kinases were demonstrated to be synthetic

lethal with *CDH1*. Therefore the synthetic lethal strategy shows potential to achieve clinical impact against HDGC by the identification of compounds suitable for use in chemoprevention.

The examples above show that high-throughput screens are an effective approach to discover synthetic lethality in cancer. Screens have the power to test mode of action of drugs, find unexpected synthetic lethal interactions between pathways, or identify effective treatment strategies without prior knowledge of a mechanism. However, synthetic lethal screens are costly, labour-intensive, error-prone, and biased towards genes with effective RNAi knockdown libraries. Off-target effects and inconsistent replication synthetic lethality across different cell lines, tissues, or laboratories, are also problematic. Therefore there is a need for replication, validation, and alternative approaches to identify synthetic lethal candidates. In addition, varied conditions across experimental screens and differences between RNAi and drug screens makes meta-analysis extremely challenging.

Genome-scale synthetic lethal experiments (across gene pairs) are not feasible, even in model organisms, and these studies typically focus on specific gene candidates or the partners of a gene of interest. Therefore a computational approach is more suitable for this task and may also augment existing experimental screens.

1.2.7 Computational Prediction of Synthetic Lethality

1.2.7.1 Bioinformatics Approaches to Genetic Interactions

Prediction of gene interaction networks is a feasible alternative to high-throughput screening, and has both biological importance and clinical relevance. There are many existing methods to predict gene networks (Boucher and Jenna, 2013; van Steen, 2012), as shown in Table 1.1. However, many of these methods have limitations, including the requirement for existing SGI data, several data inputs, and reliability of gene function annotation. Many of the existing methods also assume conservation of individual interactions between species, which has been found not to hold in yeast studies (Dixon *et al.*, 2008). Tissue specificity is important in gene regulation and gene expression, which are used as predictors of genetic interaction. However, tissue specificity of genetic interactions cannot be explored in yeast studies and has not been considered in many studies of multicellular model organisms, human networks, or cancers. Similarly, investigation into tissue specificity of PPIs, an important predictor of genetic interactions, is difficult given that high-throughput two-hybrid screens occur out of cellular context for multicellular organisms (Brückner *et al.*, 2009).

Table 1.1: Methods for predicting genetic interactions

Method	Input Data	Species	Source	Tool Offered
Between Pathways Model	PPI, SGI	<i>S. cerevisiae</i>	Kelley and Ideker (2005)	
Within Pathways Model	PPI, SGI	<i>S. cerevisiae</i>	Kelley and Ideker (2005)	
Decision Tree	PPI, expression, phenotype	<i>S. cerevisiae</i>	Wong <i>et al.</i> (2004)	2 Hop
Logistic Regression	SGI, PPI, co-expression, phenotype	<i>C. elegans</i>	Zhong and Sternberg (2006)	Gene Orienteer
Network Sampling	SGI, PPI, GO	<i>S. cerevisiae</i>	Le Meur and Gentleman (2008) Le Meur <i>et al.</i> (2014)	SLGI(R)
Random Walk	GO, PPI, expression	<i>S. cerevisiae</i> <i>C. elegans</i>	Chipman and Singh (2009)	
Shared Function	Co-expression, PPI, text mining, phylogeny	<i>C. elegans</i>	Lee <i>et al.</i> (2010b)	WormNet
Logistic Regression	Co-expression, PPI, phenotype	<i>C. elegans</i>	Lee <i>et al.</i> (2010a)	GI Finder
Jaccard Index	GO, SGI, PPI, phenotype	Eukarya	Hoechndorf <i>et al.</i> (2013)	
Machine Learning			Pandey <i>et al.</i> (2010)	MNMC
Machine Learning Meta-Analysis			Wu <i>et al.</i> (2014)	MetaSL
Flux Variability Analysis				
Flux Balance Analysis	Metabolism	<i>E. coli</i> <i>M. pneumoniae</i>	Güell <i>et al.</i> (2014)	
Network Simulation				

Table 1.2: Methods for predicting synthetic lethality in cancer

Method	Input Data	Source	Tool Offered
Network Centrality	protein-protein interactions	Kranthi <i>et al.</i> (2013)	
Differential Expression	Expression Mutation	Wang and Simon (2013)	
Comparative Genomic	Yeast synthetic gene interactions	Heiskanen and Aittokallio (2012)	
Chemical-Genomic	Homology		
Comparative Genomic	Yeast synthetic gene interactions Homology	Deshpande <i>et al.</i> (2013)	
Machine Learning		Discussed by Babyak (2004) and Lee and Marcotte (2009)	
Differential Expression	Expression	Tiong <i>et al.</i> (2014)	
Literature Database		Li <i>et al.</i> (2014)	Syn-Lethality
Meta-Analysis	Meta-Analysis Machine Learning	Wu <i>et al.</i> (2014)	MetaSL
Pathway Analysis		Zhang <i>et al.</i> (2015)	
Protein Domains	Homology	Kozlov <i>et al.</i> (2015)	
Data-Mining	Expression	Jerby-Arnon <i>et al.</i> (2014)	
Machine Learning	Somatic mutation and DNA CNV siRNA in cell lines	Ryan <i>et al.</i> (2014) Crunkhorn (2014) Lokody (2014)	DAISY (method)
Genome Evolution	Expression	Lu <i>et al.</i> (2013)	
Hypothesis Test	DNA CNV	Lu <i>et al.</i> (2015)	
Machine Learning	Known SL		
Bimodality	Expression DNA CNV Somatic Mutation	Wappett (2014) Wappett <i>et al.</i> (2016)	BiModal Subsetting ExPression (BiSEp)
Directional Chi-Square	Expression (microarray) Somatic mutation	Kelly, S. T., Guilford, P. J., and Black, M. A. Dissertation (Kelly, 2013) and developed here	SLIPT

There are existing computational methods for predicting synthetic lethal gene pairs in humans, with a specific emphasis on cancer (shown in Table 1.2). While these

demonstrate the power and need for predictions of synthetic lethality in human and cancer contexts, limitations of previous methods could be met with a different approach. Existing computational approaches to synthetic lethal prediction are often difficult to interpret or replicate for new genes, or are reliant on data types not available for a wider range of genes to test.

1.2.7.2 Comparative Genomics

A comparative genomic approach by Deshpande *et al.* (2013) used the results of well characterised high-throughput mutation screens in *S. cerevisiae* as candidates for synthetic lethality in humans (Baryshnikova *et al.*, 2010a; Costanzo *et al.*, 2010, 2011; Tong *et al.*, 2001, 2004). Yeast synthetic lethal partners were compared to human orthologues to find cancer relevant synthetic lethal candidate pairs with direct therapeutic potential. Proposed as a complementary approach to siRNA screens, approximately 24,000 of the 116,000 negative SGI in yeast (Costanzo *et al.*, 2011) were matched to human orthologues, with over 500 involving a cancer gene (Futreal *et al.*, 2004). Under strict criteria of one-to-one orthologues, large effect size and significant interaction in yeast data, 1522 interactions were identified with 70 involving cancer genes. Of the 21 gene interactions tested with pairs of siRNA in IMR1 fibroblast cells, 6 exhibited synthetic lethal effects. The two strongest interactions (*SMARCB1* with *PSMA4* and *ASPSCR1* with *PSMC2*) were successfully validated by protein analysis of human cells and replication with tetrad analysis for yeast orthologues.

Another approach to systematic synthetic lethality discovery specific to human cancer (in contrast to the plethora of yeast synthetic lethality data) was to build a database as done by Li *et al.* (2014). In their relational database, called “Syn-lethality”, they have curated both known experimentally discovered synthetic lethal pairs in humans (113 pairs) from the literature and those predicted from synthetic lethality between orthologous genes in *S. cerevisiae* yeast (1114 pairs). This knowledge-based database is the first dedicated to human cancer synthetic lethal interactions and integrates gene function annotation, pathway and molecular mechanism data with experimental and predicted synthetic lethal gene pairs. This combination of data sources is intended to tackle the trade-off between more conclusive synthetic lethal experiments in yeast and more clinically relevant synthetic lethal experiments in human cancer models, such as RNAi, especially when high-throughput screens are costly and prone to false positives in either system and are difficult to replicate across gene backgrounds. This database centralises a wealth of knowledge scattered in the literature including cancer relevant genes, including the previously mentioned interactions of *BRCA1* and *BRCA2* with

PARP1, and *TP53* with *WEE1* and *PLK1*, although the computational methodology was not released and was limited to 647 human genes. Their future directions were promising, such as constructing networks of known synthetic lethality, applying known synthetic lethality to cancer treatment, data mining, replicating the approach for synthetic lethality in model organisms, signalling pathways, and developing a complete global network in human cancer or yeast (both of which are still incomplete with experimental data), some of which has been implemented in “SynLethDB” (Guo *et al.*, 2016).

Machine learning approaches have also been explored for synthetic lethal discovery (Babyak, 2004; Lee and Marcotte, 2009). Due to concerns that these may be subject to overfitting or noise, Wu *et al.* (2014) developed a meta-analysis method. They focused on synthetic lethal gene pairs relevant to developing selective drugs against human cancer, building upon their previous database (Li *et al.*, 2014). Their “metaSL” approach utilises genomic, proteomic and annotation data and had a high statistical performance in yeast data with an area under receiver operating characteristic (AUROC) of 0.871 (as described in Section 2.3.5.1). They predicted orthologous synthetic lethal partners in human data **that** were not experimentally validated but some were relevant to cancer such as *EGFR* with *PRKCZ*.

Computational approaches scale-up across the genome at a lower cost than experimental screens (Wu *et al.*, 2014). Wu *et al.* (2014) provided their most supported interactions online but the method is not available for analysis of other genes. Syn-Lethality (Li *et al.*, 2014) and MetaSL (Wu *et al.*, 2014) demonstrate the value of computational approaches to synthetic lethality but omitted many genes of importance in cancer, such as *CDH1*. Accordingly, there remains a need to enable biological researchers to query further genes and do so in a particular tissue or genetic background.

There is also concern for analyses based on yeast data that many synthetic lethal interactions may not be conserved between species (Dixon *et al.*, 2009), although interactions between pathways may be more comparable. It is unsurprising that many of the interactions identified were not experimentally validated. There have been many gene duplications in the separate evolutionary histories of humans and yeast which may lead to differences in genetic redundancy. Yeast cells are not an ideal human cancer model because they do not have tissue specificity, multicellular gene regulation, or orthologues to several known cancer genes such as p53 (Guaragnella *et al.*, 2014). Although these studies have tried to anticipate these issues with stringent criteria such as requiring one-to-one orthologues (Deshpande *et al.*, 2013; Heiskanen and Aittokallio,

2012; Kranthi *et al.*, 2013), there remains the possibility that changes in gene function may affect whether these are solely redundant such as if functions had co-evolved without sequence homology. Many genes will also be excluded since they lack homologues in yeast, the corresponding experimental data, or having paralogues in either species. Thus conservation of yeast interactions is not an ideal strategy and analysis of human data directly for comparison with human experimental data will be the focus of this thesis.

1.2.7.3 Analysis and Modelling of Protein Data

Kranthi *et al.* (2013) took a network approach to discovery of synthetic lethal candidate selection applying the concept of “centrality” to a human PPI network involving interacting partners of known cancer genes. The effect of removing pairs of genes on connectivity of the network was used as a surrogate for viability which is supported by observations that the PPI and synthetic lethal networks are orthogonal in *S. cerevisiae* studies (Tong *et al.*, 2004). They showed that the human cancer protein interaction network derived protein interactions and cancer gene databases (Futreal *et al.*, 2004; Higgins *et al.*, 2007; Keshava Prasad *et al.*, 2009), consisting of 1539 proteins and 6471 interactions, exhibits the power law distribution expected of a scale-free synthetic lethal network with high connectivity (average vertex degree of 23.67 and network efficiency of 0.2952). Their top 100 candidate interactions included interactions of the tumour suppressor *TP53* with *BRCA1*, *CDKNA1*, *CDKNA2*, *MET*, and *RB1* which have been detected by prior studies. The gene pairs were often observed to be in the same or a plausible compensatory pathway. This demonstrated that network structure is important in the biological functions of cancers and could be exploited for targeting *TP53* loss of function mutations.

However, the approach of Kranthi *et al.* (2013) was limited to known cancer genes and is not applicable to genes that do not have PPI data. Other nucleotide sequencing data types are more commonly available for cancer studies at a genomic scale. Of further concern is that the results were enriched for p53 synthetic lethal partners, which is relevant to many cancers but this genome-wide approach did not detect many other cancer genes due to the extent of multiple testing. This enrichment may be due to the known drastic effect of removing p53 itself from the network as a highly connected, master regulator, and cancer driving tumour suppressor gene. The focus on cancer genes is useful for translation into therapeutics but does not account for variable genetic backgrounds or effect of removing an individual protein on the cellular network.

Focusing on the potential for synthetic lethality to be an effective anti-cancer drug target, Zhang *et al.* (2015) used modelling of signalling pathways to identify synthetic lethal interactions between known drug targets and cancer genes by simulating gene knockdowns. A computational approach was applied to avoid the limitations of experimental RNAi screens such as scale, instability of knockdown, and off-target effects. This ‘hybrid’ method of a data-driven model and known signalling pathways showed potential to predict cell death in single and combination gene knockouts. They used time series protein phosphorylation data (Lee *et al.*, 2012) for 28 signalling proteins and Gene Ontology (GO) pathways (Ashburner *et al.*, 2000; Blake *et al.*, 2015). This approach successfully detected many known essential genes in the human gene essentiality database, known synthetic lethal partners in the Syn-Lethality database (Li *et al.*, 2014), and predicted novel synthetic lethal gene pairs.

These novel results contained many *TP53* and AKT synthetic lethal partners (Zhang *et al.*, 2015), genes known to be important in many cancers. However, these genes also have a severe impact on the signalling pathways in an essentiality analysis of single gene disruptions and large phenotypic changes in cancer (Zhang *et al.*, 2015). This approach is amenable to detect functionally related pathways and protein complexes across the molecular function, cellular component, and biological process annotations provided by Gene Ontology. The results were consistent with the experimental results in the literature but the novel synthetic lethal interactions have yet to be validated. While the mathematical reasoning and algorithms are given, the code was not released to replicate the findings or apply the methodology beyond the signalling pathways analysed by Zhang *et al.* (2015). While this is an interesting approach, the analysis of this thesis will focus on gene expression and RNAi data, the widespread availability of which allows testing of a broader range of candidate gene pairs.

1.2.7.4 Differential Gene Expression

Differential gene expression has been explored to predict synthetic lethal pairs in cancer which would be widely applicable due to the availability of public gene expression data for many samples and cancer types. Wang and Simon (2013) found differentially expressed genes (by the t-test, adjusted by False discovery rate (FDR)) between tumours with or without functional p53 mutations in TCGA (McLendon *et al.*, 2008) and Cancer Cell Line Encyclopaedia (CCLE) (Barretina *et al.*, 2012) RNA-Seq gene expression data as candidate synthetic lethal partner pathways of p53. They identified 2, 8, and 21 candidate synthetic lethal partner genes in 3 microarray datasets from the NCI60 cell lines, 31 partner genes from the CCLE RNA-Seq data (Barretina *et al.*, 2012), and

50 in TCGA RNA-Seq data (Muzny *et al.*, 2012). *PLK1* was replicated across 4 of these analyses and 17 other genes were replicated across 2 analyses (including *MTOR*, *PLK4*, *MAST2*, *MAP3K4*, *AURKA*, *BUB1* and 6 CDK genes) with many playing a role in cell cycle regulation. This was supported by a drug sensitivity experiment on the NCI60 cell lines which found that cells lacking functional p53 were more sensitive to paclitaxel (which targets *PLK1*, *AURKA*, and *BUB1*). This demonstrated the potential of gene expression as a surrogate for gene function, and the use of public genomic data to predict synthetic lethal gene pairs in cancer. Wang and Simon (2013) advocated for pre-screening of expression profiles to augment future RNAi screens, however, their analyses were limited to kinase genes and focused on currently druggable targets, lacking wider application of synthetic lethal prediction methodology. This approach may not be feasible or applicable in cancer genes with a lower mutation rate than p53.

Tiong *et al.* (2014) also investigated gene expression as a predictor of synthetic lethal pairs with colorectal cancer microarrays from a Han Chinese population with a sample size of 70 tumours and 12 normal tissue samples. Simultaneously differential expressed “tumour dependent” gene pairs (which includes co-expression) between cancer and normal tissue were used to rank 663 candidate synthetic lethal interactions identified in cell line siRNA experiments. Of the top 20 gene pairs, 17 were tested for differential expression at the protein level with immunohistochemistry staining and correlation with clinical characteristics, with 11 pairs exhibiting synergistic effects. Some of the predicted synthetic lethal pairs were consistent with the literature (including *TP53* with *S6K1* and partners of *KRAS*, *PTEN*, *BRCA1*, and *BRCA2*) and two novel synthetic lethal interactions (*TP53* with *CSNK1E* and *CTNNB1*) were validated in pre-clinical models. This serves as a valuable proof-of-concept for integration of *in silico* approaches to synthetic lethal discovery in cancer, demonstrating its utility to triage and identify synthetic lethal partners of p53 applicable to colorectal tissues. Although the experimental work was the focus of the paper, these findings show that bioinformatically identified synthetic lethal candidates can be validated in patient tissue samples to find those applicable to colorectal cancers (including in a non-Caucasian population).

1.2.7.5 Data Mining and Machine Learning

Recognising the utility of synthetic lethality to drug inhibition and specificity of anti-cancer treatments, Jerby-Arnon *et al.* (2014) also saw the need for effective prediction of gene essentiality and synthetic lethality to augment experimental studies. They developed the “DAta mIning SYnthetic lethal identification pipeline” (DAISY), a data-

driven approach for genome-wide analysis of synthetic lethality in public cancer genomics data from TCGA and CCLE (Barretina *et al.*, 2012). DAISY is intended to predict the candidate synthetic lethal partners of a query gene such as genes recurrently mutated in cancer.

Jerby-Arnon *et al.* (2014) combined a computational approach to triage candidates with a conventional RNAi screen to validate synthetic lethal partners. They screened a selection of computationally predicted candidates and randomly selected genes with RNAi against *VHL* loss of function mutation in RCC4 renal cell lines. The computational method had a high AUROC of 0.779 and predictions were enriched 4-fold for validated RNAi hits over randomly selected genes. This approach detected known synthetic lethal pairs such as *BRCA1* or *BRCA2* genes with *PARP1*, and *MSH2* with *DHFR*. The synthetic lethal candidates identified with both RNAi screening and computational prediction formed an extensive network of 2077 genes with 2816 synthetic lethal interactions, and a similar network of 3158 genes with 3635 synthetic dosage lethal interactions (for synthetic lethality with over-expression). Each network was scale-free, as expected of a biological network, and was enriched for known cancer genes and for essential genes in mice which could be harnessed for predicting prognosis and drug response.

The DAISY methodology (Jerby-Arnon *et al.*, 2014) compares the results of analysis of several data types to predict synthetic lethality, namely: DNA copy number and somatic mutation for TCGA patient samples and CCLE cell lines. The cell lines were also analysed with gene expression and gene essentiality (shRNA screening) profiles. Genes were classed as inactivated by copy number deletion, somatic loss of function mutation, or low expression and tested for synthetic lethal gene partners which are either essential in screens or not deleted with copy number variants. Co-expression is also used for synthetic lethality prediction based on studies in yeast (Costanzo *et al.*, 2010; Kelley and Ideker, 2005). Copy number, gene expression, and essentiality analyses were stringently compared by adjusting each for multiple tests with Bonferroni correction and only taking candidates identified in all analyses. The predictions performed well and an RNAi screen, for the example of *VHL* in renal cancer, validated predicted synthetic lethal partners of *VHL* demonstrating the feasibility of combining approaches to synthetic lethal discovery in cancer and using computational predictions to enable more efficient high-throughput screening. While DAISY performed well statistically, co-expression and shRNA functional examination contributed less to this than the mutation and copy number analysis (AUROC 0.683 alone). However, this

methodology was very stringent, missing potentially valuable synthetic lethal candidates. Additionally, the software for the procedure has not been publicly released for replication.

Although the DAISY procedure performed well and has been well received by the scientific community (Crunkhorn, 2014; Lokody, 2014; Ryan *et al.*, 2014), showing a need for such methodology, there has not yet been widespread adoption of this approach. Co-expression analysis may exclude some synthetic lethal interactions, where inverse correlation could occur (Lu *et al.*, 2015). In the interests of a large sample size, tissue types were not tested separately despite tissue-specific synthetic lethality being likely since gene function (and by extension expression, isoforms, and clinical characteristics) in cancers may often be tissue-dependent. Some data forms and analyses used, such as gene essentiality, may not be available for all cancers, genes, or tissues, and may not be reproduced.

Lu *et al.* (2015) propose an alternative computational prediction of synthetic lethality based on machine learning methods and a “cancer genome evolution” hypothesis. Using DNA copy number and gene expression data from TCGA patient samples, a cancer genomes evolution model assumes that synthetic lethal gene pairs behave in two distinct ways in response to an inactive synthetic lethal partner gene, either a “compensation” pattern where the other synthetic lethal partner is overactive or a “co-loss underrepresentation” pattern where the other synthetic lethal partner is less likely to be lost, since loss of both genes would cause death of the cancer cell. During the genomes evolution of cancers, the cell becomes addicted to the remaining synthetic lethal partner due to induced gene essentiality. These patterns would explain why DAISY detects only a small number of synthetic lethal pairs, compared to the large number expected based on model organism studies (Boone *et al.*, 2007), and the disparity between screening and computationally predicted synthetic lethal candidates due to testing different classes of synthetic lethal gene pairs.

Lu *et al.* (2015) compared a genome-wide computational model of genomes evolution and gene expression patterns to the experimental data (Laufer *et al.*, 2013; Vizeacoumar *et al.*, 2013). This more simple model performed well, with an AUROC of 0.751 (lower than DAISY), and did not rely on data from cell lines which may not represent patient disease. Lu *et al.* (2015) predicted 591,000 human synthetic lethal partners with a probability score threshold of 0.81, giving a precision of 67% and 14-fold enrichment of synthetic lethal true positives compared to randomly selected gene pairs. Discovery of such a vast number of cancer-relevant synthetic lethal interactions

in humans would not be feasible experimentally and is a valuable resource for research and clinical applications. These predictions are not limited by assuming co-expression of synthetic lethal partners or evolutionary conservation with model organisms enabling wider synthetic lethal discovery. However, there remains a lack of basis for an expectation of how many synthetic lethal partners a particular gene will have, how many pairs there are in the human genomes, and whether pathways or correlation structure would influence predicted synthetic lethal partners.

Large scale, computational approaches have yet to determine whether synthetic lethal interactions are tissue-specific, since Lu *et al.* (2015) used pan cancer data for 14136 patients with 31 cancer types. Experimental data used for comparison was a small training dataset specific to colorectal cancer, and based on screens for other phenotypes, which may limit performance of the model or application to other cancers. Proposed expansion of the computational approach to mutation, micro RNA, or epigenetic modulation of gene function and tumour micro-environment or heterogeneity suggests that synthetic lethal discovery could be widely applied to the current challenges in cancer genomics. This approach was also based on machine learning methodology and was not supported by a software release for the community to develop, contribute to, or reproduce beyond the gene pairs given in the supplementary results.

1.2.7.6 Mutual Exclusivity and Bimodality

Wappett *et al.* (2016) demonstrated a multi-omic approach to identify synthetic lethality in cancer with a strategy to detect bimodal patterns in molecular profiles. They released this solution as the BiSEp R package (Wappett, 2014) which aims to detect subtle bimodal and non-normal patterns in expression data. Since loss of gene function is not consistently genetic, Wappett *et al.* (2016) advocate for the use of gene expression (loss of mRNA) and deletion (loss of copy number) data in addition to mutations. The BiSEp procedure was demonstrated on an analysis of 881 cell lines from CCLE (Barretina *et al.*, 2012), 442 cell lines from COSMIC (Forbes *et al.*, 2015), and RNA-Seq by Expectation Maximization (RSEM) normalised RNA-Seq data for 178 TCGA lung patient samples (Collisson *et al.*, 2014). BiSEp was demonstrated to have significant enrichment of validated tumour suppressor, synthetic lethal gene pairs (detecting 76 experimentally supported gene pairs) and was improved (detecting 420) with expression data, rather than relying on detecting loss of gene function by mutation or deletion. Wappett *et al.* (2016) identified interactions with genes relevant to

cancer with support in experimental screens including *ERCC4* with *XRCC1*, *BRCA1* with *PARP3*, and *SMARCA1* with *SMARCA4*.

Wappett *et al.* (2016) demonstrated that analysis of genomics data, particularly expression data, is relevant to augment the identification of synthetic lethal interactions with screening experiments. They further showed that this is applicable in both genetically homogeneous cell lines and heterogeneous cell population from patient samples. These approaches are limited however, to genes that exhibit bimodal expression patterns which does not commonly occur, particularly in normalised gene expression data. Other approaches may need to be considered for gene, such as *CDH1* which were not identified by BiSEp.

Srihari *et al.* (2015) used a computational analysis to identify synthetic lethal candidate genes from mutually exclusive alterations in cancers. This analysis focused on synthetic lethality with “DNA damage response genes” in cancers, including *CDH1*, using TCGA expression and copy number data across several cancers. The 718 genes that were identified as frequently altered in cancer were enriched among essential genes in cell lines deficient in DNA damage response genes which demonstrates “induced essentiality” in a cancer model. These were tested by `underMutExSL`, a hypergeometric test, for synthetic lethality. Of the DNA damage response genes examined, *CDH1* exhibited the most mutually exclusive alterations with other frequently altered genes in breast cancers, including related genes in focal adhesion such as *PTK2*. These results indicate that *CDH1* may be particularly subject to “non-oncogene addiction” in breast cancers and that computational analysis is valuable to rationally identify these putative synthetic lethal genes. These results were limited to frequently altered genes in cancer and could be improved with an approach that expands to consider synthetic lethal genes that are not themselves altered in cancers or further investigation into synthetic lethal pathways.

1.2.7.7 Rationale for Further Development

Many of the approaches discussed here aimed to identify the strongest synthetic lethal pairs across the yeast or human genomes (Deshpande *et al.*, 2013; Lu *et al.*, 2015; Wappett *et al.*, 2016; Wu *et al.*, 2014), which may not be an ideal strategy to identify interactions in particular functions or relevance to particular cancers. These demonstrate a need for computational approaches to prioritise candidate gene pairs for validation. This thesis will focus on the interactions with *CDH1* with importance in breast and stomach cancers, although these partners may be applicable in other cancers. As such,

this thesis presents a query-based method, amenable to identification of candidate partners for a selected gene of functional or translational importance such as *CDH1*.

1.3 E-cadherin as a Synthetic Lethal Target

E-cadherin is a transmembrane protein (encoded by *CDH1*) with several well-characterised functions in the cytoskeleton and cell-to-cell signalling. Here I outline the characterised functions of E-cadherin and its importance in cancer biology. *CDH1* is a tumour suppressor gene, with loss of function occurring in both familial (germline mutations) and sporadic (somatic mutations) cancers. As such, *CDH1* inactivation is a prime example of a genetic event that could be targeted by synthetic lethality. Drugs against *CDH1*-deficient cancers would be applicable for chemoprevention of HDGC and treatment of sporadic cancers carrying somatic *CDH1* mutations.

1.3.1 The *CDH1* gene and its Biological Functions

CDH1 is implicated in hereditary and sporadic lobular breast cancers and diffuse gastric cancers (Berx *et al.*, 1996; Berx and van Roy, 2009; De Leeuw *et al.*, 1997; Guilford *et al.*, 1998; Masciari *et al.*, 2007; Semb and Christofori, 1998; Vos *et al.*, 1997). E-cadherin is normally expressed in epithelial tissues and loss of *CDH1* function has been implicated in breast cancer progression and metastasis (Becker *et al.*, 1994; Berx *et al.*, 1995; Christofori and Semb, 1999).

The primary function of *CDH1* is cell-cell adhesion at the adherens junction, maintaining the cytoskeleton and mediating molecular signals between cells. The function of the adherens complex is particularly important for cell structure and regulation because it interacts with actin and microtubule cytoskeletons. The cytoskeletal role of E-cadherin includes maintaining cellular polarity (Jeanes *et al.*, 2008). E-cadherin is not essential to cellular viability but loss in epithelial cells does lead to defects in cytoskeletal structure and proliferation. In addition to a central role in the adherens complex, E-cadherin is involved in many other cellular functions and thus *CDH1* is regarded as a highly pleiotropic gene (Kroepil *et al.*, 2012).

As a transmembrane signalling protein E-cadherin also interacts with the extracellular environment and other cells, most notably forming adherens junctions between cells (Chen *et al.*, 2014; Tunggal *et al.*, 2005) and regulating of epithelial tissues by intercellular communication (Jeanes *et al.*, 2008). The signals mediated by adherens junctions are also passed on to intracellular signalling pathways. One such example is the regulation of β -catenin which interacts with both the actin cytoskeleton and acts

as a transcription factor via the WNT pathway (Jeanes *et al.*, 2008). Similarly, the Hippo and PI3K/AKT pathways are also mediated in part by E-cadherin (De Santis *et al.*, 2009; Kim *et al.*, 2011). E-cadherin shares several downstream pathways with cell-surface proteins, such as integrins, and thus indirectly interacts with them.

The key roles of E-cadherin in maintaining cellular structure and regulating growth are consistent with *CDH1* being a tumour suppressor gene. E-cadherin loss in breast cancers has been shown to cause increased proliferation, lymph node invasion, and metastasis with poor cell-cell contact (Berx and van Roy, 2009). Thus the *CDH1* gene is an established invasion suppressor, with a key role in the epithelial-mesenchymal transition (EMT), an established mechanism of cancer progression (Hanahan and Weinberg, 2011). EMT is important during development and wound healing but such changes in cellular differentiation also occur in cancers.

1.3.2 Hereditary Diffuse Gastric (and Lobular Breast) Cancer

CDH1 loss of function mutations also cause familial cancers, including diffuse gastric cancer and lobular breast cancer (Graziano *et al.*, 2003; Guilford *et al.*, 2010, 1999; Oliveira *et al.*, 2009). Individuals carrying a null mutation in *CDH1* have a syndromic predisposition to early-onset of these cancers, including hereditary diffuse gastric cancer (HDGC) (Guilford *et al.*, 1998). Due to carrying a dysfunctional allele, these individuals are prone to carcinogenic lesions in the breast or stomach **when** the remaining functional allele is inactivated. **Thus familial cancers occur** more frequently and at an earlier age than in individuals with two functional *CDH1* alleles. The loss of the second allele is most often through hypermethylation suppressing expression rather than mutation (Grady *et al.*, 2000; Graziano *et al.*, 2003; Machado *et al.*, 2001; Oliveira *et al.*, 2009), although loss of heterozygosity may also occur (Guilford *et al.*, 2010).

HDGC is an autosomal dominant cancer syndrome with incomplete penetrance. The “lifetime” (until age 80 years) risk for mutation carriers of diffuse gastric cancer is 70% in males and 56% in females (Hansford *et al.*, 2015; van der Post *et al.*, 2015). In addition, the lifetime risk of lobular breast cancer is 42% in female mutation carriers (Hansford *et al.*, 2015). HDGC represents less than 1% of gastric cancers (Ferlay *et al.*, 2015), however, it is a serious health issue for several hundred families globally. E-cadherin is also mutated in 13% of sporadic gastric cancers (Ferlay *et al.*, 2015).

While diagnostic testing for *CDH1* genotype has enabled more effective management of HDGC and improved patient outcomes, there are still limited options for clinical interventions (Guilford *et al.*, 2010). Individuals with a family history of HDGC are

recommended to be tested for *CDH1* mutations in late adolescence and are offered prophylactic stomach surgery at the age of 20 years. Another option is annual endoscopic screening to diagnose early stage stomach cancers with surgical intervention once they are detected (Oliveira *et al.*, 2013). However, these early stage cancers are difficult to detect and may be missed in regular screening. Thus patients carrying germline *CDH1* mutations either have surgery which has a significant impact on quality of life and risk of complications or remain at risk of developing stomach cancer. There are similar concerns for female mutations carriers for the management of high-risk lobular breast cancer. An effective treatment against *CDH1* mutant cancers would potentially have significant therapeutic and preventative applications for many patients.

1.3.3 Cell Line Models of *CDH1* Null Mutations

Previous work published by members of our research group used a model of homozygous *CDH1*^{-/-} null mutation in non-malignant MCF10A breast cells to show that loss of *CDH1* alone was not sufficient to induce EMT (Chen *et al.*, 2014). However, *CDH1*-deficient cells did manifest changes in morphology, migration, and weaker cell adhesion (Chen *et al.*, 2014). This *CDH1*^{-/-} MCF10A model has been used in a genome-wide screen of 18,120 genes using siRNA and a complementary drug screen using 4057 known drugs to identify synthetic lethal partners to E-cadherin (Telford *et al.*, 2015). One of the most supported pathways from the siRNA screen was the G protein coupled receptor (GPCR) signalling cascades, which were highly enriched in a Gene Ontology (GO) analysis validated with Pertussis toxin which targets G_{αi} signalling (Clark, 2004).

1.4 Summary and Research Direction of Thesis

Genomic technologies have immense potential for understanding of genetics and improving healthcare, including the identification of cancer genes for diagnosis, biomarkers, and therapeutic targets. This has been demonstrated by the identification of many driver genes, tumour subtypes, and the development of targeted therapies against oncogenes (e.g., *BRAF*^{V600E}) and tumour suppressors (e.g., *BRCA1*). Synthetic lethality is important for studying cellular functions and exploiting them for biomarker identification and cancer treatment. Synthetic lethal interactions present a means to target loss of function mutations and dysregulation of tumour suppressor genes via interacting partners with redundant (or compensating) functions.

Discovery of synthetic lethal partners of *CDH1* could identify molecular mechanisms driving the growth of *CDH1*-deficient tumours and therapeutic targets or chemopre-

ventative agents for management of HDGC. The clinical potential of the synthetic lethal approach has been demonstrated by the use of olaparib against *BRCA1* and *BRCA2* mutations (Lord *et al.*, 2015; McLachlan *et al.*, 2016). There is still a need to systematically identify synthetic lethal partners for other genes, such as *CDH1*.

Effective screening and prediction of synthetic lethal interactions are crucial for developing precision cancer medicines. Therefore, I will develop a computational statistical procedure to identify synthetic lethal interactions. This will assist the development of novel precision medicine targeted to particular molecular aberrations. To address the concerns raised by recent computational approaches to synthetic lethal discovery in cancer (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015; Wappett *et al.*, 2016), this query-based method uses gene expression data that is widely available for many samples in different cancers. To further determine the limitations and implications of synthetic lethal predictions, modelling and simulation was performed upon the statistical behaviour of synthetic lethal gene pairs in genomics data. Comparison of synthetic lethal gene candidates from public data analysis and experimental candidates, pathway analysis, and networks structure will also be presented to investigate the relationships between synthetic lethal candidates. Release of the R code used for simulation, prediction, and analysis will enable adoption of the methodology by the research community and comparison to existing methods.

1.4.1 Thesis Aims

This thesis aims to develop and demonstrate a method to identify synthetic lethal gene pairs using public gene expression data. Chapter 3 describes this synthetic lethal detection methodology (SLIPT), the methods developed to evaluate it, and the release of R software packages. This chapter also documents the simulation procedures and network analysis that were developed to support the use of SLIPT and perform analyses throughout this thesis.

To demonstrate the SLIPT methodology for analysis of RNA-Seq gene expression data, an analysis was performed in Chapter 4 to identify candidate synthetic lethal gene partners of *CDH1* in public breast and stomach cancer data (Bass *et al.*, 2014; Koboldt *et al.*, 2012). This analysis demonstrates the biological relevance of candidate synthetic lethal partners by identifying synthetic lethal pathways and makes comparisons to an experimental siRNA screen (Telford *et al.*, 2015).

To assess the importance of synthetic lethal genes within pathways, network analysis was also performed using graph structures in Chapter 5. Chapter 5 also used

pathway structure to identify directional relationships between SLIPT and siRNA synthetic lethal candidates and explore the disparity between them. The SLIPT methodology was supported by simulation-based investigations in Chapters 3 and 6 to evaluate performance of SLIPT with known synthetic lethal genes in simulated data. Graph structures were used in Chapter 6 to investigate the effect of pathway correlation structures on synthetic lethal detection with SLIPT in simulated data, including complex correlation structures within biological pathways.

Chapter 2

Methods and Resources

In this Chapter, I will outline the various existing resources and methods that were used throughout this project. This includes public data repositories, stable and development releases of software packages (primarily using the R programming environment), and custom implementation of bioinformatic methods and statistical concepts with Shell or R scripts developed for this purpose. The methods and packages that have been developed specifically for this project will be covered in Chapter 3 with supporting data and demonstration of their use .

2.1 Bioinformatics Resources for Genomics Research

2.1.1 Public Data and Software Packages

Various bioinformatics resources, such as databases and methods, have become integral parts of genetics and genomics research. Reference genomes, genotyped variants, gene expression, and epigenetics profiles are among the most commonly used resources. Gene expression data, in particular, is widely available from microarray and RNA-Seq projects, driven by data sharing, data mining, and the wider initiatives for publicly available data for enabling the scientific community to further utilise the data generated beyond a single research group or consortium (Rung and Brazma, 2013). These datasets are a valuable resource to examine the changes in gene expression occurring in cancers and the variation between samples. The potential for integrating findings from publicly available genomic data with experimental investigations has expanded with RNA-Seq datasets, including large-scale cancer genomics projects (Zhang *et al.*, 2011). This thesis presents such an investigation, enabled by the release of these datasets and tools developed to handle them.

It is now common practice for bioinformatics researchers to release open-source code or provide software packages to enable replication of the findings or further applications of the methods (Stajich and Lapp, 2006). This is part of a wider movement in software and data analysis, including the development of Linux and the R programming environment (R Core Team, 2016). In addition to the R packages hosted on comprehensive R archive network (CRAN) (CRAN, 2017), many packages specifically developed for applications in bioinformatics are hosted on the Bioconductor repositories (Gentleman *et al.*, 2004), and numerous packages in various stages of development are hosted on GitHub (<https://github.com/>). Packages from each of these resources have been used throughout this project and are cited wherever possible. Several R packages have been developed during this thesis project and publicly released on GitHub or will be released in conjunction with a publication.

2.1.1.1 Cancer Genome Atlas Data

Molecular profile data for normal and tumour samples were downloaded from publicly available sources, using the TCGA (TCGA, 2017) and the International Cancer Genome Consortium (ICGC) web portals (Zhang *et al.*, 2011). These include gene expression (RNA-Seq), somatic mutations, and clinical data. The versions were downloaded on the 6th of August 2015 (Release 19) and the 2nd of May 2016 (Release 20) for breast and stomach cancer respectively via the ICGC data portal (<https://dcc.icgc.org/>).

The TCGA project (Koboldt *et al.*, 2012) used widely adopted tools: “Bowtie” for alignment (Langmead *et al.*, 2009), “mapsplice” to detect splice sites (Wang *et al.*, 2010), and the RSEM approach to quantify reads as a measure of gene expression (Li *et al.*, 2010). These are widely acceptable tools for processing RNA-Seq data which were used to produce the raw counts of mapped reads (tier 1) and normalised expression data (tier 3) publicly downloaded from ICGC and TCGA respectively.

Raw count and RSEM normalised TCGA expression data from Illumina RNA-Seq protocols were downloaded for 1177 breast samples (113 normal, 1057 primary tumour, and 7 metastases) for 20,501 genes. TCGA breast somatic mutation data for 981 samples (976 primary tumours and 5 metastases) across 25,836 genes were downloaded. These included 969 samples (964 primary tumours and 5 metastases) with corresponding RNA-Seq expression data and 19,166 genes mapped from Ensembl identifiers to gene symbols. Of these genes, 16,156 had corresponding gene expression information. Unless otherwise stated, the raw counts were used for further processing rather than the RSEM normalised data (provided by TCGA tier 3). Somatic mutations

were reported if there were non-synonymous substitutions, frameshifts, or truncations (by premature stop codons) detected which would likely disrupt the wild-type gene function.

Raw count TCGA expression data (TCGA tier 1) from Illumina RNA-Seq was downloaded for 450 stomach samples (35 normal, 415 primary tumour) for 20,501 genes. TCGA stomach mutation data was also used for 289 samples across 25,807 genes, corresponding to 19,436 genes with expression data.

2.1.1.2 Reactome and Annotation Data

Pathway analysis was performed for human pathway annotation from the Reactome database (version 52) with pathway gene sets derived from the `reactome.db` R package. Entrez identifiers were mapped to gene symbols or aliases to match to TCGA expression and mutation data using the `org.Hs.eg.db` R package. Gene expression for breast cancer from Gatza and colleagues were also used (Gatza *et al.*, 2011; Gatza *et al.*, 2014). The gene symbols for each pathway were matched to the expression data and to construct a matrix of category membership using the `safe` R package (Barry, 2016).

2.2 Data Handling

2.2.1 Normalisation

Apart from the Prediction Analysis of Microarray 50 (PAM50) subtyping procedure (Parker *et al.*, 2009), which required RSEM normalised data (J.S. Parker personal communication), the analysis of the RNA-Seq data presented here was based on raw read count data. After some samples were removed for consistency (based on a Euclidean distance correlation matrix as described in Section 2.2.2), raw read counts were log-scaled and the final dataset was normalised as Counts per Million mapped reads (CPM), weighted by variance modelling, using the `voom` function (Law *et al.*, 2014) in the `limma` R package (Ritchie *et al.*, 2015). This procedure adjusts the data to account for differences in read count by sequencing depth between samples and length between genes.

2.2.2 Sample Triage

The TCGA breast RNA-Seq data were assessed for batch effects using a correlation matrix of the log-transformed raw counts for which a heatmap (Euclidean distance, complete linkage) is shown in Appendix Figure A.1. While no major batch effects were detectable between the samples, 9 samples were excluded due to poor correlation

with the remaining samples, as detailed in Table 2.1. These samples showed unusual density plots compared to the rest of the dataset, and exhibited low mean read count in Figures 2.1 and 2.2. A heatmap showing key clinical properties of these excluded samples and their correlation with the remainder of the samples is shown in Appendix Figure A.2, and a full correlation heatmap (Figure A.1) shows these samples as relatively poorly correlated outliers in the bottom rows and left columns. In addition to the clustering analysis (in Appendix A.1), replicate tumour samples were also examined for sample quality in Appendix A.2. After removal of these samples, the TCGA dataset used for analysis consisted of the remaining 1168 samples (from 1040 patients): 1049 tumour samples, 112 normal tissue for matched samples, and 7 metastases.

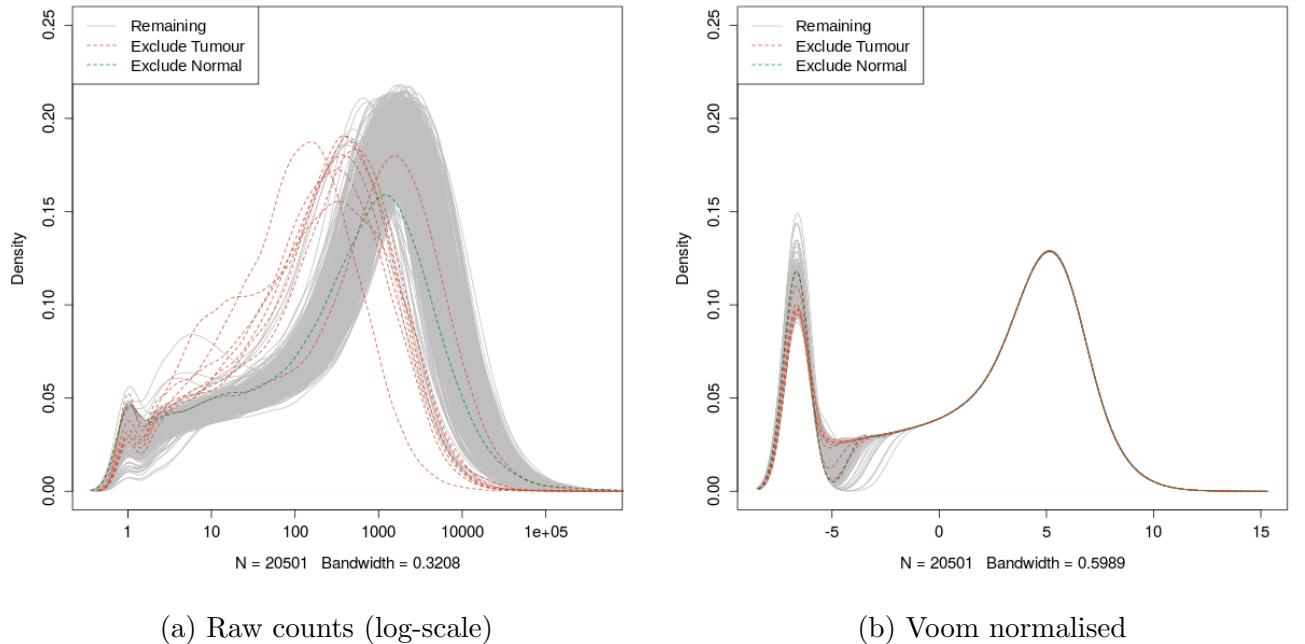


Figure 2.1: **Read count density.** Sample density plots of raw counts on log-scale and voom normalised showing samples removed due to quality concerns.

Similarly, a correlation matrix of log-transformed raw counts was used to evaluate sample quality for TCGA stomach RNA-Seq. A tumour sample (patient 4294) was removed due to similar quality concerns leaving a final dataset for 449 samples (from 417 patients): 414 tumour samples and 35 normal tissue samples.

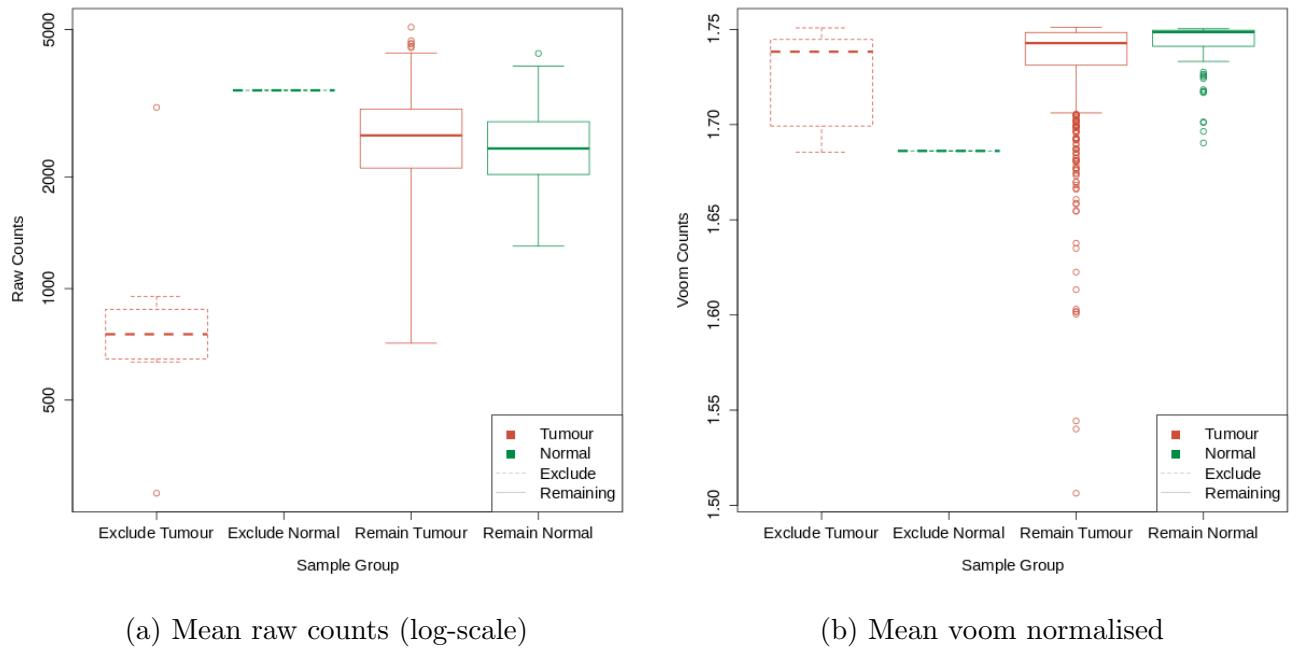


Figure 2.2: **Read count sample mean.** Boxplots of sample means for raw counts on log-scale and voom normalised show removed tumour samples with low mean read count.

Table 2.1: Excluded samples by batch and clinical characteristics.

Tissue Source	Type	Batch	Plate	Patient	Samples	p53	Subtype	Treatment (History)	Clinical Subtypes (Stage)
A7 Christiana	Tumour	47	A227	A0DB	1 of 3	NA	Luminal A	Mastectomy (no)	ER+ Ductal (2)
A7 Christiana	Tumour	96	A220	A13D	1 of 3	Wildtype	Luminal A	Mastectomy (no)	ER+ Ductal (2)
A7 Christiana	Tumour	96	A227	A13E	1 of 3	NA	Basal	Lumpectomy (no)	ER- Ductal (2)
A7 Christiana	Tumour	142	A277	A26E	1 of 3	NA	Basal	Lumpectomy (no)	ER+ Ductal (2)
A7 Christiana	Tumour	47	A277	A0DC	1 of 2	NA	Luminal A	Mastectomy (yes)	ER+ Lobular (3)
A7 Christiana	Tumour	142	A220	A26I	1 of 2	Mutant	Basal	Lumpectomy (yes)	ER- Ductal (2)
AC Intl Genom	Tumour	177	A18M	A2QH	2 of 2	Mutant	Basal	Radical Mastectomy (no)	ER- Metaplastic (2)
AC Intl Genom	Tumour	177	A220	A2QH	2 of 2	Mutant	Basal	Radical Mastectomy (no)	ER- Metaplastic (2)
GI ABS IUPUI	Normal	177	A16F	A2C8	1 of 1	NA	Luminal A	Radical Mastectomy and Neoadjuvant (no)	ER+ Ductal (2)

2.2.3 Metagenes and the Singular Value Decomposition

A “metagene” offers a one-dimensional summary of pathway (expression) activation or inactivation by dimension reduction of a matrix, avoiding negatively correlated genes averaging out the signal of a mean-based centroid (Huang *et al.*, 2003). Constructing pathway metagenes used gene sets for Reactome and the Gatzka signatures (Gatzka *et al.*, 2011, 2014) as specified above (in Section 2.1.1.2). The singular-value decomposition ($X = U^T DV$) was performed on a data matrix X of m genes (in the gene set) \times

n samples, U an $m \times m$ matrix of eigenvectors of the matrix XX^T which gives an eigenvector for each gene, D is a rectangular diagonal matrix of “singular values” which weight the eigenvectors, and V is an $n \times n$ matrix of eigenvectors of the matrix X^TX which gives an eigenvector for each sample. The leading eigenvector (first column of V) corresponding to the largest singular value was used as a metagene for the pathway gene set. To ensure consistent directionality of metagene signals, the median of the gene set in each sample was calculated and correlated against the metagene with the (arbitrary) metagene sign adjusted as needed to conform with the majority of the gene set (i.e., positive correlation between metagene and the median-based centroid). To ensure that genes and pathways were weighted equally, metagenes were derived from a z-transformed (mean 0, standard deviation 1) dataset of gene expression and samples were scaled (by fractional ranking) for each metagene so that they were comparable on a $[0, 1]$ scale.

2.2.4 Candidate Triage and Integration with Screen Data

Candidate triage in combination with the experimental data was intended to integrate findings of the SLIPT analysis with an ongoing experiment project (Chen *et al.*, 2014; Telford *et al.*, 2015). The first procedure to compare the SLIPT gene candidates for *CDH1* with an siRNA experimental screen (Telford *et al.*, 2015) was a direct comparison of the overlapping candidates, presented in a Venn diagram and tested with the χ^2 test. Since these candidates modestly overlapped at the gene level (even when excluding genes not contained in both datasets), further gene set over-representation analysis was performed for pathways specific to each detection approach and the intersection of the two.

The pathway composition of the intersection was further verified by a permutation resampling analysis (as described in Section 2.3.6): the same number of genes detected by SLIPT were sampled randomly from the universe of genes tested by both approaches. These samplings were performed over 1 million iterations and the pathway over-representation was compared for each of the 1652 Reactome pathways. These over-representation scores (χ^2) were compared the observed over-representation in the intersection of the SLIPT candidates, with the proportion of resamplings with higher χ^2 values used for empirical p-values of pathway composition. The χ^2 test was used as an appropriation of Fisher’s exact test on a hypergeometric distribution for resampling to computationally scale pathway over-representation tests across iterations. Pathways for which no resamplings were occurred as high as the observed were reported

as $p < 10^{-6}$. These empirical p-values were adjusted for multiple comparisons (FDR). Intersection size was not assumed to be constant during resampling so that it could also be used to evaluate significance of enrichment or depletion (of siRNA candidate among SLIPT candidate genes).

2.3 Techniques

Various statistical, computational, and bioinformatics techniques were performed throughout this thesis. This Section describes these techniques and gives the parameters used unless otherwise specified. Where relevant, the R package implementation which provided the technique will be acknowledged.

2.3.1 Statistical Procedures and Tests

As described in Sections 2.3.4 and 2.2.3, the z-transform has been used to generate z-scores in various analyses in this thesis. Each row (i) of the dataset (x_i) was transformed into a scores vector (z_i) using the mean (\bar{x}_i) and standard deviation (s_i) of the data such that:

$$z_i = \frac{\mathbf{x}_i - \bar{x}_i}{s_i}$$

This generates data where each row (gene) has a mean of 0 and standard deviation of 1. Where plotted as a heatmap, any data more than 3 standard deviations above or below the mean was plotted as 3 or -3 respectively.

Where specified, the Fisher's exact test, χ^2 test, and correlation were used to measure associations between variables, as implemented in the **stats** R package (R Core Team, 2016). Unless otherwise specified, Pearson correlation was used for correlation analyses (r) and coefficient of determination (R^2). Where these comparisons are discussed in more detail, Fisher's exact test and χ^2 tests are supported by a table or Venn diagram, rendered with the **limma** R package (Ritchie *et al.*, 2015). In some analyses, correlation is further supported by a scatter plot and a line of best fit derived by least squares linear regression.

The **t.test** function (R Core Team, 2016) has also been used to implement the t-test to compare pairs of data. Where relevant, an analysis of variance (ANOVA) has been performed to report significance of multivariate predictors of outcomes, or least squares linear regression performed for the adjusted coefficient of determination (R^2) and F-statistic p-value to evaluate the fit of the predictor variables. For some analyses these are supported by boxplot or violin plot visualisation (Adler, 2005), rendered in R (R Core Team, 2016).

Multiple comparisons were accounted for with the Benjamini-Hochberg procedure to control the FDR unless otherwise specified (Benjamini and Hochberg, 1995). This procedure adjusts p-values to achieve an average of the proportion of false-positives among significant tests below a threshold, α . The more stringent Holm-Bonferroni (Holm, 1979) was also applied in some cases to adjust for multiple comparisons and control the family-wise error rate which adjusts p-values so that the probability that any one of the tests is a false-positive (type-1 error) below a threshold, α .

2.3.2 Gene Set Over-representation Analysis

Gene set enrichment over-representation analysis was performed to test whether there was an enrichment of a gene set (e.g., a biological pathway) among a group of input genes. Such input genes may be predicted synthetic lethal candidates or a subset defined by clustering (in Section 2.3.3) or comparison with experimental candidates (in Section 2.2.4). Initially, these tests were performed using the GeneSetDB web tool (Araki *et al.*, 2012) hosted by the University of Auckland on the Reactome pathways (Croft *et al.*, 2014). Since the GeneSetDB tool used an older version of Reactome (version 40), it was difficult to directly compare with the results of other analysis (in Sections 2.2.4 and 2.3.6) performed on version 52 (as described in Section 2.1.1.2). Thus an implementation of the hypergeometric test in R (R Core Team, 2016) was used to test for over-representation against Reactome (version 52) pathways. Pathways containing less than 10 genes or more than 500 (as performed in GeneSetDB by Araki *et al.*, 2012) were excluded before adjusting for multiple comparisons.

2.3.3 Clustering

The clustering analysis used unsupervised hierarchical clustering with complete linkage (distance calculated from the furthest possible pairing). For correlation matrices or multivariate normal parameters (e.g., Σ), the distance metric used was Euclidean distance. For empirical or simulated gene and pathway expression data correlation distance was used, calculated by $distance = 1 - cor(t(x))$ where cor is Pearson correlation and $t(x)$ is the transpose of the expression matrix.

2.3.4 Heatmap

Standardised z-scores of the data were used to plot heatmaps on an appropriate scale. Raw (log-scale) read counts or voom normalised counts per gene (as specified) were plotted as normalised z-scores on a $[-3, +3]$ blue-red scale. Similarly, correlations

were plotted on a $[-1, +1]$ blue-red scale. Heatmap dendograms were generated using the linkage method and distance specified for the clustering performed in Section 2.3.3. The `gplots` R package (Warnes *et al.*, 2015) was used to generate many of the heatmaps throughout this thesis, along with a customised heatmap function (released as `heatmap.2x`, detailed in Table 2.4 and Section 3.5.2). Where clearly specified, data have been split into subsets with clustering performed separately on each subset with these plotted alongside each other.

2.3.5 Modelling and Simulations

Statistical modelling and simulations were used to test various synthetic lethal detection procedures on simulated data. This involved constructing a statistical model of how synthetic lethality would appear in (continuous normally distributed) gene expression data. Where presented (in Section 3.2.1), the assumptions of the model are stated clearly. The model allows sampling from a multivariate normal distribution (using the `mvtnorm` R package (Genz and Bretz, 2009; Genz *et al.*, 2016)) to generate simulated data with known underlying synthetic lethal partners (detailed in Section 3.2.2). I can test whether statistical procedures, including those developed in this thesis (presented in Section 3.1), are capable of detecting synthetic lethal partners within the simulated data. This multivariate normal simulation procedure also enables the inclusion of correlation structure which is either given as correlated blocks of genes or derived from pathway structures (as detailed in Section 3.4.2).

When this multivariate normal distribution is sampled once and the procedure to add known synthetic lethal partners is performed, it generates a simulated dataset. Performing this simulation procedure and testing with a synthetic lethal detection procedure iteratively, these simulations can be used to assess the statistical performance of the detection procedure. The number of iterations (`Reps`) will be given for each simulation result. Typically, these are performed 1000 or 10,000 times depending on the computational feasibility of doing so on larger datasets.

Several measures of statistical performance were used to assess the simulations. The following measures used the final classification of the detection procedure, statistical significance for χ^2 , significance and directional criteria met for SLIPT (in Section 3.1), and an arbitrary threshold: $r < -0.2$ and $r > +0.2$ for negative correlation and correlation respectively. The significance thresholds (of FDR adjusted $p < 0.05$) were applied for SLIPT and χ^2 as used throughout thesis. The thresholds for correlation were used to classify a meaningful number of genes (several hundred) to test the methodology.

This threshold does not affect the statistical performance from which the main conclusions are drawn. Sensitivity (or “true positive rate”) was measured as the proportion of known synthetic lethal partners predicted to be synthetic lethal. Specificity (or “true negative rate”) was measured as the proportion of known non-synthetic lethal partners predicted not to be synthetic lethal. The “false positive rate” was measured here as the proportion of known non-synthetic lethal partners out of all putative partners predicted by the detection procedure. Statistical “accuracy” is the proportion of true predictions for a detection procedure, which is both the correctly predicted known synthetic lethal partners and correctly negative known non-synthetic lethal partners.

2.3.5.1 Receiver Operating Characteristic Curves

A more general procedure to measure the statistical performance of a simulation is the receiver operating characteristic (ROC) curve which does not assume a threshold for classification of synthetic lethality but demonstrates the achievable range of sensitivity and specificity for a model (Akobeng, 2007; Fawcett, 2006; Zweig and Campbell, 1993). These curves (implemented with the `ROCR` R package (Sing *et al.*, 2005)) plot the true positive rate (sensitivity) against the false positive rate (1-specificity) as the prediction threshold is varied. An ideal detection method will have a true positive rate of 1 and a false positive rate of 0, hence the Area Under the ROC curve (AUC or area under receiver operating characteristic (AUROC)) is a measure of statistical performance for a detection procedure accounting for this trade-off. AUROC values typically range from 0.5 (the value expected by random chance) to 1 for an optimal detection method, however it is possible for an AUROC below 0.5 for a poor detection method that performs worse than random chance. In cancer biology, it has been suggested that an AUROC of approximately 0.8 is a predictive biomarker suitable for publication (Hajian-Tilaki, 2013) but predictors with lower AUROC values may still be informative depending on the context. In this thesis, the AUROC values varied widely across simulation parameters and were primarily used for comparisons across these parameters, although they can also be used to refine thresholds for optimal classification.

2.3.6 Resampling Analysis

Resampling analyses (e.g., “permutation” analysis) are used to statistically test the significance of an observation without assuming the underlying distribution of expected test statistics (Collingridge, 2013). Instead these are derived from randomly shuffling test statistics or randomly sampling predicted candidates. For the purposes of this

thesis, this involved randomly sampling genes from those tested to be analysed as putative synthetic lethal candidates. This was performed both for testing the significance of pathway composition in the intersection with experimental gene candidates (Section 2.2.4) and for assessing the significance of pathway structure among synthetic lethal candidates (Section 3.4.1.1).

These were analysed to compare the observed synthetic lethal genes against values derived from randomly sampling the same number of genes as were observed to be synthetic lethal from among the genes tested. Sampling iteratively across many resampling procedures, these resampling-based values form a null distribution that could be expected if the null hypothesis were true. Thus the proportion of resampling-based values across these iterations that are greater than or equal to that observed, forms an empirically derived p-value to test significance.

Resampling was performed for comparison (in Section 2.2.4) with fixed experimental screen candidates (Telford *et al.*, 2015) both resampling the number of genes overlapping with the screen candidates and test statistics for pathway enrichment. Resampling analysis was also applied to shortest paths and network metrics (in Section 3.4.1.1) to test significance of directional relationships between synthetic lethal candidate genes within pathway structures.

The number of iterations determines the accuracy of these p-values. For pathway composition (in Section 2.2.4), a million iterations were performed using high performance computing (as detailed in Section 2.5.3) to provide sufficient accuracy after adjusting for multiple comparisons across pathways. For the purposes of network analysis (in Section 3.4.1.1), a thousand iterations were sufficient to reject the null hypothesis for the majority of pathways tested before adjusting for multiple comparisons, and thus further iterations were not performed.

2.4 Pathway Structure Methods

2.4.1 Network and Graph Analysis

Networks are important in considering the structure of relationships in molecular biology, including gene regulation, kinase cellular signalling, and metabolic pathways (Barabási and Oltvai, 2004). Network theory is an interdisciplinary field which combines the approaches of computer science with the metrics and fundamental principles of graph theory, an area of pure mathematics dealing with relationships between sets of discrete elements. The vast amounts of molecular and cellular data from high-

throughput technologies have enabled the application of network-based and genomes-wide bioinformatics analysis to examine the complexity of a cell at the molecular level and understand aberrations in cancer. This thesis uses various metrics and analysis procedures developed in Graph and Network theory to analyse graph structure of biological pathways. Where feasible, these have been implemented using the `igraph` R package with such procedures described below (Csardi and Nepusz, 2006). Custom R functions were used to perform more complex analysis and visualisation of iGraph data (as described in Section 3.5.3).

Graph theory is a branch of pure mathematics which deals with the properties of sets of discrete objects (referred to as a ‘node’ or ‘vertex’) with some pairs are joined (by a ‘link’ or an ‘edge’). While a seemingly reductionist abstraction to mathematically study relationships, graph theory has applications in a wide range of fields, including the life sciences. Network theory is the sub-discipline of graph theory that deals with networks, which has become popular due to the vast potential for applications of networks (van Steen, 2010).

Applications vary depending on the situation modelled, particularly in how the edges between vertices are defined, whether they are directed or weighted, and whether multiple redundant edges between a pair of vertices (referred to as ‘parallel edges’) or edges connecting a vertex to itself (referred to as ‘loops’) are permitted in the model. Networks are defined such that the edges represent a relationship between the vertices and may be directed, weighted, or contain parallel edges or loops depending on the application (van Steen, 2010). Unless otherwise stated, graph structures and networks in this thesis will be unweighted and have no parallel edges or loops. Where a directional relationship is known or modelled, it will be represented with a directed edge in a directed graph.

2.4.2 Sourcing Graph Structure Data

Pathway Commons interaction data was sourced using the Biological PAthway eXchange (BioPAX) with the paxtools-4.3.0 Java application on October 6th 2015 (Cerami *et al.*, 2011; Demir *et al.*, 2013). This utility was used to import ‘sif’ format interaction data into R (R Core Team, 2016) and extract the human Reactome (version 52) dataset of interactions was imported (Croft *et al.*, 2014), matching those used for pathway enrichment analysis. These interactions were used to construct an adjacency matrix for the Reactome network and subnetworks corresponding to each relevant biological pathway.

2.4.3 Constructing Pathway Subgraphs

Subgraphs for each relevant pathway were constructed by matching the nodes in the complete Reactome network to the pathway gene sets (as derived in Section 2.1.1.2). A subgraph with adjacent nodes was constructed by adding nodes which have an edge with a gene in the pathway gene set. The pathways these adjacent nodes belong to were added to form a “meta-pathway” to account for the possibility for nodes within the pathway being linked by the surrounding graph structure.

2.4.4 Network Analysis Metrics

The existing network analysis measures applied in this thesis (as described below) used an implementation in the `igraph` R package to compute vertex degree, shortest paths, and centrality (Csardi and Nepusz, 2006). Additionally, custom features were developed for analysis of iGraph objects in R and released as `igraph.extensions` (as described in Section 3.5.3).

Vertex degree is the number of edges a node has and is a fundamental measure of the importance and connectivity of a network (van Steen, 2010). More connected nodes, such as network hubs, will have a higher vertex degree relative to other nodes. For the purposes of this thesis, vertex degree ignored edge direction with loops (edges with itself) and double edges to the same node excluded.

A fundamental concept in network analysis is a “shortest path”, that is the shortest route via edges between any two particular nodes in a network. These are computed by Dijkstra’s algorithm (Dijkstra, 1959) in the `igraph` R package (Csardi and Nepusz, 2006). Where applicable paths will only use directed edges in a particular direction. Shortests paths are a useful measure of how close nodes are in a network. This is used to compute information centrality, and for further analysis of pathway structure (as described in Section 3.4.1).

Network centrality is an alternative measure of the importance or influence of a node to the graph structure (Borgatti, 2005). Various strategies are used to derive centrality, typically based on how connected the node is or the impact of node removal on the connectivity of the network. One of the most notable is the “PageRank” algorithm, a refinement of eigenvector centrality based on the eigenvectors of the adjacency matrix (Brin and Page, 1998). This is implemented in the `igraph` R package (Csardi and Nepusz, 2006).

Another network centrality measure that has been previously applied to biological protein interaction networks (Kranthi *et al.*, 2013) is the “information centrality”.

The information centrality of a node is the relative impact on efficiency (transmission of information via shortest paths) of the network when the node is removed. The centrality (C) (Kranthi *et al.*, 2013) for node n in a graph G (containing N nodes) is defined as:

$$C_n = \frac{E(G) - E(G')}{E(G)}$$

where G' is the subgraph with the node removed and E is the efficiency (Latora and Marchiori, 2001), derived from shortest paths (d_{ij} between nodes i and j).

$$E(G) = \frac{2}{N(N-1)} \sum_{i < j \in G} \frac{1}{d_{ij}}$$

The efficiency of a network can be derived from shortest paths using the `igraph` R package and the network centrality computation for each node has been released as an R package (`info.centrality`) and included in the `igraph.extensions` package.

2.5 Implementation

2.5.1 Computational Resources and Linux Utilities

Several computers were used to process and store data during this thesis (as summarised in Appendix Table B.1), running different versions of Linux operating systems, including a personal laptop computer, laboratory desktop machine, departmental server, and the New Zealand eScience Infrastructure Intel Pan high-performance computing cluster (a supercomputer based at the University of Auckland). Each of these systems support a 64-bit architecture. Current workflows on local machines use Elementary OS (based on the Ubuntu versions given in Appendix Table B.1) and the ZSH shell. However, Ubuntu OS and the Bash were used at the inception of this project and Bash continues to be used for running scripts. Various Linux applications and command-line utilities were used on these machines (shown in Appendix Table B.2). As such, the workflows developed in this project should be backwards-compatible with Ubuntu Linux (and other derivatives). The majority of novel methodology and implementations were performed in R which is a cross-platform language, packages developed in R will be available for users of Linux, Mac, and Windows machines.

2.5.2 R Language and Packages

The R programming language has been used for the majority of this thesis. Current R installations across the machines used are given in Table 2.2. Local machines currently

run the latest version of the R (at the time of writing) and remote machines run the versions and modules as managed by the system administrator.

Various scripts and packages in this thesis were developed or run in previous versions of RStudio and R but these run without error in the current version of R (and the older versions on remote machines). The R packages which were used throughout this thesis (as detailed in Table 2.3 with versions specified) were installed from the comprehensive R archive network (CRAN) (CRAN, 2017), Bioconductor (Gentleman *et al.*, 2004, version 3.4; BiocInstaller 1.24.0), or GitHub (<https://github.com/>). These packages were not updated when they would change the functionality of scripts or functions in packages. In particular, imported data from annotation packages (used to define gene sets) have been saved as local files to continue using stable versions of these pathway data (across machines).

This is a summary of the key packages which (in addition to their dependencies) have been used throughout this project. Where a package implementation has been central to the methods applied, they are described in more detail in the relevant Section. A full table of packages used in this thesis can be found in Appendix Table B.3. The R packages developed during this thesis are given in Table 2.4 with the relevant Sections describing their implementation and use where appropriate, in addition to further details on these functions in Section 3.5.

Table 2.2: R installations used during thesis

	Viao Laptop	Lab Machine	Biochem Server	NeSI Pan Cluster
OS	Elementary OS Freya 0.3.2	Elementary OS Loki 0.4	Red Hat Enterprise Maipo 7.2	Cent OS Final 6.4
Programming	R	3.3.2	3.3.2	3.3.0-intel (module)
Development	RStudio	1.0.136	1.0.136	1.0.136 (server)

Table 2.3: R Packages used during thesis

Package	Version Used	Built	Repository
colorspace	1.3-2	3.3.1	CRAN
curl	2.3	3.3.1	CRAN
data.table	1.9.6	3.3.1	CRAN
dendextend	1.4.0	3.3.2	CRAN
DBI	0.5-1	3.3.1	CRAN
devtools	1.12.0	3.3.1	CRAN
dplyr	0.5.0	3.3.1	CRAN

ggplot2	2.2.1	3.3.1	CRAN
git2r	0.18.0	3.3.1	CRAN
gplots	3.0.1	3.3.1	CRAN
gtools	3.5.0	3.3.1	CRAN
igraph	1.0.1	3.3.1	CRAN
matrixcalc	1.0-3	3.3.1	CRAN
mclust	5.2.2	3.3.1	CRAN
mvtnorm	1.0-6	3.3.1	CRAN
org.Hs.eg.db	3.1.2	3.1.2	Bioconductor
openssl	0.9.6	3.3.1	CRAN
plyr	1.8.4	3.3.1	CRAN
purrr	0.2.2	3.3.1	CRAN
reactome.db	1.52.1	3.2.1	Bioconductor
RColorBrewer	1.1-2	3.3.1	CRAN
Rcpp	0.12.9	3.3.1	CRAN
ROCR	1.0-7	3.3.1	CRAN
roxygen2	6.0.1	3.3.2	CRAN
shiny	1.0.0	3.3.1	CRAN
snow	0.4-2	3.3.1	CRAN
testthat	1.0.2	3.3.2	CRAN
tidyverse	1.1.1	3.3.2	GitHub (hadley)
sm	2.2-5.4	3.3.1	CRAN
Unicode	9.0.0-1	3.3.2	CRAN
vioplot	0.2	3.3.1	CRAN
viridis	0.3.4	3.3.2	CRAN
xml2	1.1.1	3.3.2	CRAN
xtable	1.8-2	3.3.1	CRAN
zoo	1.7-14	3.3.1	CRAN
graphics	3.3.2	3.3.2	base
grDevices	3.3.2	3.3.2	base
cluster	2.0.5	3.3.1	base
Matrix	1.2-8	3.3.1	base
stats	3.3.2	3.3.2	base

Table 2.4: R packages developed during thesis

	Package Name	Description and GitHub Repository	Section
	<code>slipt</code>	Synthetic lethal detection by SLIPT (to accompany publication) https://github.com/TomKellyGenetics/slipt	3.1
visualisation	<code>vioplotx</code>	Customised violin plots (based on <code>vioplot</code>) https://github.com/TomKellyGenetics/vioplotx	
	<code>heatmap.2x</code>	Customised heatmaps (based on <code>gplots</code>) https://github.com/TomKellyGenetics/heatmap.2x	2.3.4
igraph.extensions	<code>igraph.extensions</code>	Meta-package to install the follow iGraph functions https://github.com/TomKellyGenetics/igraph.extensions	3.5.3
	<code>plot.igraph</code>	Custom plotting of directed graphs https://github.com/TomKellyGenetics/plot.igraph	2.4.4
	<code>info.centrality</code>	Computing information centrality from network efficiency https://github.com/TomKellyGenetics/info.centrality	3.4.2
	<code>pathway.structure.permutation</code>	Testing pathway structure with resampling analysis https://github.com/TomKellyGenetics/pathway.structure.permutation	3.4.1.1
	<code>graphsim</code>	Generating simulated expression from graph structures https://github.com/TomKellyGenetics/graphsim	3.4.2

2.5.3 High Performance and Parallel Computing

Another enabling technology for bioinformatics is parallel computing, performing independent operations using separate central processing unit (CPU) cores: this “multithreading” is widely used to decrease the time to compute results. Bioinformatics is particularly amenable to this since performing multiple iterations of a simulation or testing separate genes is often “embarrassingly parallel”, as CPUs completely independent of each other.

The New Zealand eScience Infrastructure (NeSI) is a High Performance Computing (HPC) organisation providing the Intel Pan cluster or “supercomputer” at the University of Auckland (NeSI, 2017). The cluster was used throughout this thesis project to optimise and perform computations which would have otherwise been infeasible. High performance computing on the Pan cluster was used extensively in this project including for resampling analysis (in Sections 2.3.6 and 3.4.1.1), calculating information centrality (in Section 2.4.4), and in simulations (in Sections 2.3.5, 3.2, and 3.4.2)

Scripts and data were transferred between the Pan cluster and University of Otago computing resources by `rsync` or the Globus file transfer service (Globus, 2017). R scripts (R Core Team, 2016) were run in parallel with the “simple network of workstations” `snow` R package Tierney *et al.* (2015). This utilised the “message passing

interface” (Yu, 2002) when it was feasible with memory requirements to run in parallel across multiple compute nodes, otherwise Socket Secure (SOCKS) was used to access multiple cores within an instance of R and pass input data to them. R jobs were submitted to queue for available resources and run on the Pan cluster via the Simple Linux Utility for Resource Management (Slurm) workload manager (Slurm, 2017). Slurm array job submission and independent running of different parameters (with arguments passed to R from the shell) were used to run memory-intensive job or scripts across many parameters simultaneously. In some cases, this submission was automated across a range of parameters with Bash scripts.

Chapter 3

Methods Developed During Thesis

In this Chapter, I outline the rationale and development of various methods used throughout this thesis to examine synthetic lethality in gene expression data, graph structures, models and simulations. Firstly, the Synthetic Lethal Interaction Prediction Tool (SLIPT), a bioinformatics approach to triage synthetic lethal candidate genes, will be described. This is one of the main research outputs of this thesis project and is supported by comparisons to an experimental screen from a related project and evaluation of performance on simulated data. These supporting findings will be covered in further chapters but simulation data is included to support the use and design of SLIPT. This includes the construction of a statistical model of synthetic lethality in (continuous multivariate Gaussian) gene expression data, which enables testing SLIPT upon simulated data with known synthetic lethal partners. Another key component of this simulation pipeline is the generation of simulated data from a known graph structure or simulated biological pathway (as applied in Chapter 6). The development of this simulation procedure and other statistical treatment of graph and network structures will also be covered. Various R packages have been developed to support this project, including the `slipt` package to implement the SLIPT methodology. Additional R packages for handling graph structures, simulations, and custom plotting features will be described as research outputs of this thesis, methods applied throughout, and contributions of open-source software.

3.1 A Synthetic Lethal Detection Methodology

The SLIPT methodology identifies gene expression patterns consistent with synthetic lethal interactions, between a query gene and a panel of candidate interacting partners. Gene expression is scored “low”, “medium”, or “high”, sorting samples by tertiles ($^{1/3}$ -

quantiles) for each gene. Genes with insufficient expression across all samples are excluded by requiring that the first tertile of raw counts is above zero. A χ^2 test is then performed between the query gene and each candidate partner. The p-values for the χ^2 test are corrected for multiple testing using False discovery rate (FDR) error control to reduce false positives (Benjamini and Hochberg, 1995). Significance is called for FDR adjusted $p < 0.05$. A synthetic lethal interaction is predicted (as shown in Figure 3.1) when (i) the χ^2 test is significant; (ii) observed low-query, low-candidate samples are less frequent than expected; and (iii) observed low-query, high-candidate and high-query, low-candidate samples are more frequent than expected.

The synthetic lethal prediction procedure has also been performed with somatic mutation data for the query gene. This is intended for a **known query gene** which is recurrently mutated, with the majority of mutations disrupting gene function (e.g., null or frameshift mutations). A synthetic lethal interaction is predicted (as shown in Figure 3.2) when (i) the χ^2 test is significant; (ii) observed mutant-query, low-candidate samples are less frequent than expected; and (iii) observed mutant-query,

		Candidate Gene		
		Low	Medium	High
Query Gene (e.g. <i>CDH1</i>)	Low	Observed less than expected		Observed more than expected
	Medium			
	High	↓ Observed more than expected		

Figure 3.1: Framework for synthetic lethal prediction. SLIPT was designed to identify candidate interacting genes from gene expression data using the χ^2 test against a query gene. Samples are sorted into low, medium, and high expression quantiles for each gene to test for a directional shift. A sample being low in both genes of a synthetic lethal pair is unlikely, since loss of both genes will be deleterious, and is expected to be statistically under-represented in a gene expression dataset. I expect a corresponding (symmetric) increase in frequency of sample with low-high gene pairs. Synthetic lethal candidate partners of a gene were identified by running this procedure on all possible partner genes, selecting those with an FDR-adjusted χ^2 -derived $p < 0.05$, and meeting the directional criteria. Since synthetic lethal genes are partners of each other, commutatively, the symmetric direction criteria were defined such that detected synthetic lethal genes are partners of each other.

		Candidate Gene		
		Low	Medium	High
Query Gene (e.g. <i>CDH1</i>)	Mutation	Observed less than expected		→ Observed more than expected
	Wild-type	↓ Observed more than expected		

Figure 3.2: **Synthetic lethal prediction adapted for mutation.** SLIPT was also adapted to identify candidate interacting genes using (somatic) mutation data of the query gene in the χ^2 test. Samples are sorted into low, medium, and high expression quantiles for each candidate gene and tested for a directional shift against mutation status of the query gene. A sample having low expression or mutation for the synthetic lethal pair is expected to be unlikely with a corresponding increase in frequency of sample with mutant-high or wild-type-low gene pairs. Synthetic lethal (mtSLIPT) candidate partners of a gene were identified from running this procedure on all possible partner genes, selecting those with an FDR-adjusted χ^2 -derived $p < 0.05$, and meeting the directional criteria.

high-candidate and wild-type-query, low-candidate samples are more frequent than expected. .

The SLIPT methodology can be performed on expression data, including pathway metagenes (as generated in Section 2.2.3). The application of the SLIPT methodology on public gene expression data will be supported with simulation results (in Section 3.3 and Chapter 6), including comparison to other statistical methods. SLIPT results for *CDH1* were compared experimental screen results in a breast cell line (Telford *et al.*, 2015). Primary screen results are discussed in Section 4.2 and secondary screen results are presented in Section 4.2.4.

3.2 Synthetic Lethal Simulation and Modelling

A statistical model of synthetic lethality was developed to generate simulated data and to evaluate the SLIPT procedure. This Section describes the synthetic lethal model and the simulation procedure for generating gene expression data with known synthetic lethal partners. Simulation results, to support usage of the SLIPT methodology throughout this thesis, will be presented in Section 3.3. The simulation procedure will

also be applied in Chapter 6, including in combination with simulations from graph structures (as described in Section 3.4.2).

3.2.1 A Model of Synthetic Lethality in Expression Data

A conceptual model of synthetic lethality was devised (as shown in Figure 3.3), which was used to build a statistical model of synthetic lethal gene expression and to simulate expression data for assessing various potential synthetic lethal prediction methods, including SLIPT. In the model, synthetic lethality occurs between genes with related functions leading to a cell death phenotype when these functions are inactivated.

This model suggests that synthetic lethality is detectable in measures of gene inactivation across a sample population, namely mutation, DNA copy number, DNA methylation, and expression levels. While any of these mechanisms of gene inactivation could lead to synthetic lethality, expression data is readily available and changes in other mechanisms are likely to impact on the amount of expressed RNA that is detectable. Functional relationships between genes could manifest in expression data in several ways, including coexpression, mutual exclusivity and directional shifts. Co-expression is overly simplistic (Lu *et al.*, 2015) and has previously performed poorly as a predictor of synthetic lethality (Jerby-Arnon *et al.*, 2014), although this will still be tested with correlation measures in later simulations. The alternative hypothesis is that synthetic lethality will result in a detectable shift in the number of samples which exhibit low or high expression of either gene. This model does not preclude mutual exclusivity, compensating expression, or co-loss under-representation which may occur between synthetic lethal genes (Lu *et al.*, 2015; Wappett *et al.*, 2016).

The first condition of the synthetic lethal model is that if there are only two synthetic lethal genes (e.g., *CDH1* and one SL partner), then they will not both be non-functional in the same sample (in an ideal model). Gene function is thus determined for each sample in a model of synthetic lethality with the proportion of samples which are functional or non-functional for a gene being arbitrary. Whether a gene is functional can similarly be modelled by an arbitrary threshold of continuous and normally distributed gene expression data to define gene function (as shown in Figure 3.4). For the purposes of modelling synthetic lethality in cancer expression data, a threshold of the 30th percentile of the expression levels was used because approximately 30% of samples analysed had *CDH1* inactivation (mutations) in breast cancer (Koboldt *et al.*, 2012). This was generalised for a model of the proportion of samples inactivated for each gene. The threshold of the 0.3 quantile was used in simulations derived from this

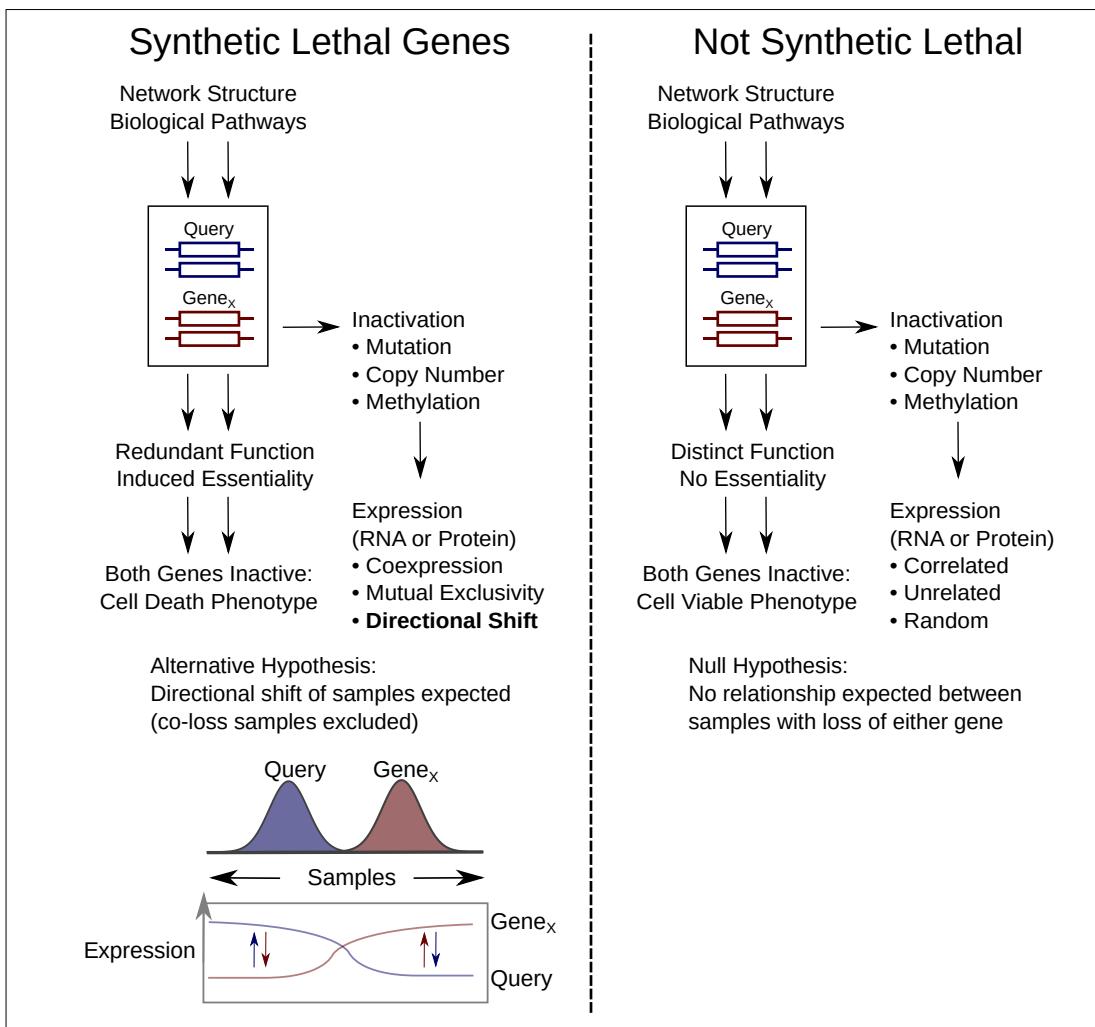


Figure 3.3: **A model of synthetic lethal gene expression.** A conceptual model of synthetic lethal interactions between a Query gene and partner gene (G_X). Genes that are synthetic lethal may not both be non-functional in the same sample without another gene compensating for the loss of function. This is most likely to be detectable as low gene expression, whether they are lost by mutation, deletion, DNA methylation, or suppressing regulatory signals. This could manifest as coexpression, mutual exclusivity, or directional shifts in sample frequency. Thus the alternative hypothesis (H_A) is that synthetic lethal genes will have a reduced frequency of co-loss samples while the null hypothesis (H_0) is that non-synthetic lethal gene pairs would show no such relationship, even if they may be correlated for other means such as pathway relationships. In this model synthetic lethal genes may compensate for the loss of each other but this is not assumed, only that loss of both is unfavourable to cell viability and probability of detecting samples with combined gene loss.

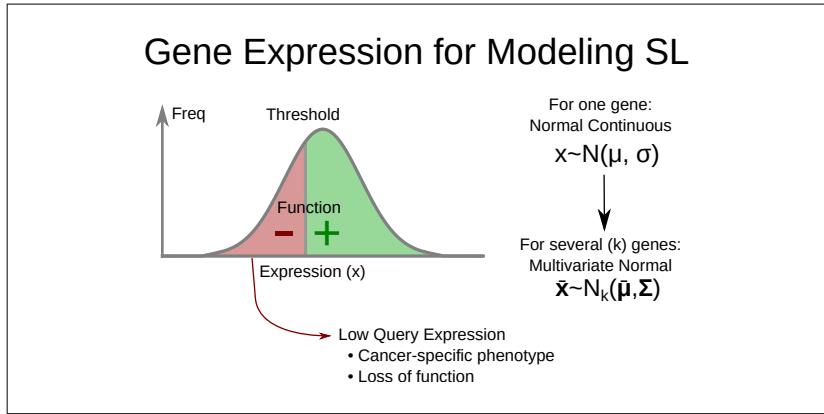


Figure 3.4: Modelling synthetic lethal gene expression. When modelling synthetic lethal interactions between a Query gene and partner genes (G_X and G_Y) above, cellular viability requires that at least one of genes is not inactivated. As a model of loss of function, genes are regarded as non-functional with expression below a threshold for the purposes of modelling synthetic lethality. Tumour suppressor genes with loss of function also have cancer specific phenotypes (although these thresholds are not assumed to be the same). Expression is modelled by normally (Gaussian) distributed continuous data, such as (log-scale) data from RNA (microarray or RNA-Seq), protein, or pathway metagenes. This rationale generalises to several genes on a multivariate normal distribution.

model throughout this thesis. In this ideal case, no samples lowly expressing both of these genes are expected to be observed. While this was not the case, that is to be expected as it is unlikely that only two genes will have an exclusive synthetic lethal partnership.

A synthetic lethal pair of genes is unlikely to act in isolation, therefore higher-order synthetic lethal interactions (i.e., 3 or more genes) must be considered in the model as shown in Figure 3.5. Even when testing pairwise interactions, it is important to model higher level interactions that may interfere. If there are additional synthetic lethal partners, there are two possibilities for adding these: 1) that they are independent partners of the query genes interacting pairwise (and not with each other) or 2) that an additional partner gene interacts with both of the synthetic lethal genes already in the system and any of the three (or more) are required to be functional for the cell to survive.

The signal (in terms of gene expression data) will be weaker for this latter case and this model has the more stringent assumption that all synthetic lethal partner genes interact with each other: that only one of these must be expressed to satisfy

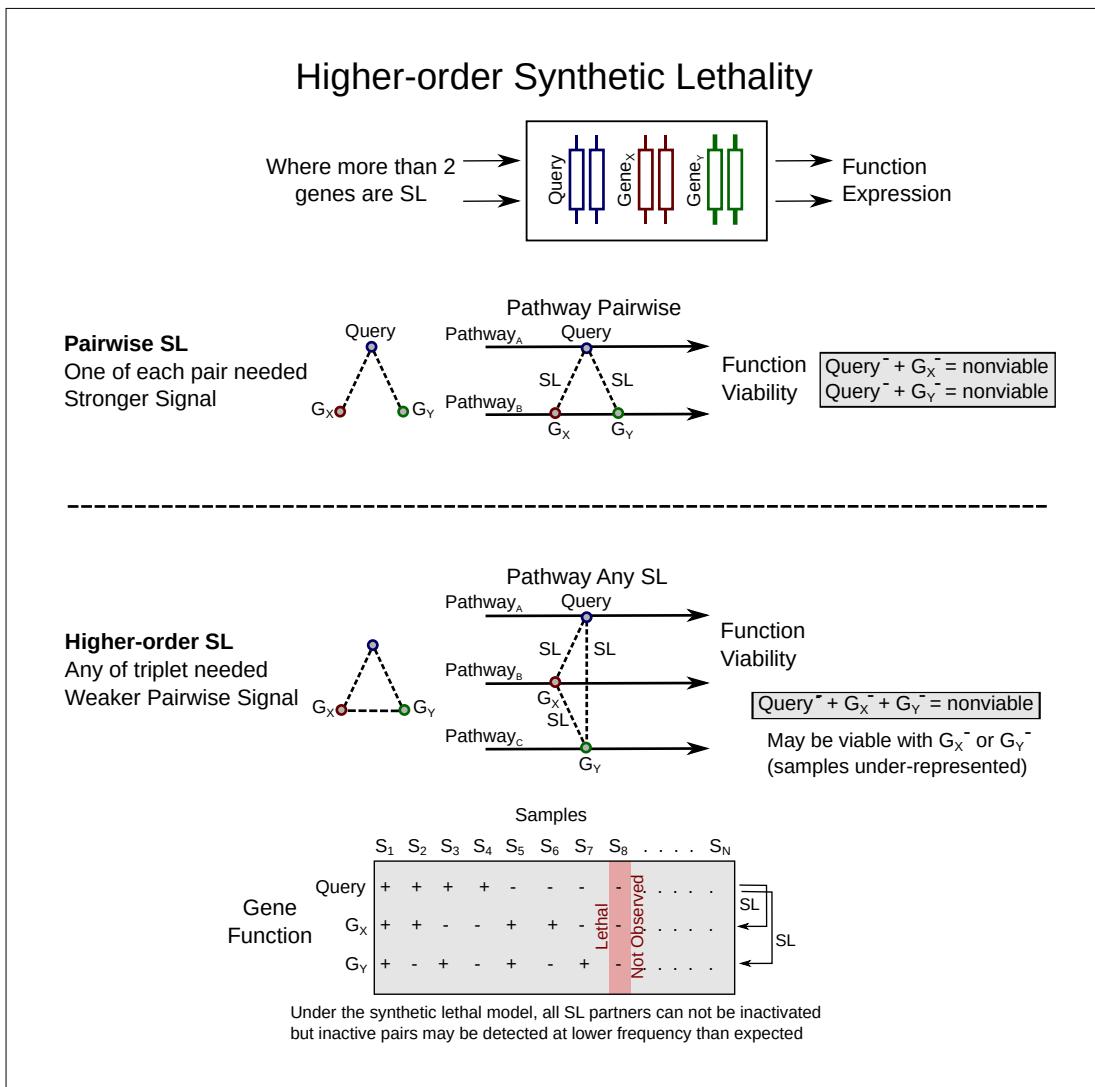


Figure 3.5: **Synthetic lethality with multiple genes.** Higher order synthetic lethal interactions may occur between 3 or more genes, affecting the simulated expression (or synthetic lethal predictions) even if undetected when observed pairwise. Consider interactions between a Query gene and two partner genes (G_x and G_y). They may interact with the Query pairwise (inviolate when either gene pair is lost) or form a higher-order interaction such as the “synthetic lethal triplet” if any of the genes provide an essential function (inviolate only when all are lost). Either is plausible with the potential pathway structures. A synthetic lethal triple has 8 potential combinations of gene function but one is not expected to be observed (due to inviability), however pairwise inactivation may be observed if additional partner genes are functional. The proportion of these combinations varies depending on the functional threshold.

the model of synthetic lethality. In this model, any of the synthetic lethal genes in a higher-order interaction are able to perform the essential function of the others, allowing for higher-level synthetic lethal partners to compensate for loss of a synthetic lethal gene pair. While samples that express low levels of the synthetic lethal gene pairs will be under-represented, they may not be completely absent from the dataset, due to these higher-level interactions. In the example of three synthetic lethal genes (shown in Figure 3.5), only one of the genes involved in the higher-order synthetic lethal interaction is required for cell viability. For synthetic lethal pairs, only a subset of these samples will be inviable (i.e., removed from simulated data), leading to an under-representation.

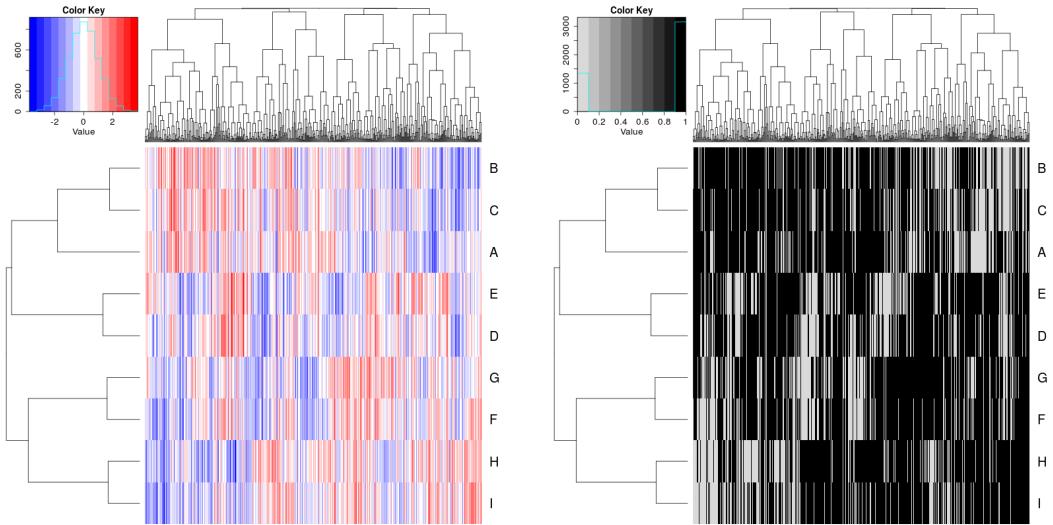
Samples were not actually removed from a simulated dataset, rather the expression and function of the query gene is generated across samples separately from the pool of potential partner genes. The query gene data was matched to simulated samples (as shown in Figure 3.7) satisfying the synthetic lethal condition with the procedure described in Section 3.2.2. This was performed to maintain a comparable sample size across simulations and to preserve the (multivariate) normal distribution of the data.

3.2.2 Simulation Procedure

Simulations were developed to generate normal distributions of expression data and define gene function with a threshold cut-off. While gene function was used as an intermediary step in modelling synthetic lethal genes in expression data, the normal distribution was sampled for simulated data to represent normalised empirical gene expression data for which SLIPT (and other methods) will be applicable.

Sampling a distribution for expression profiles has the advantage of enabling simulating correlation structures with the multivariate normal distribution, using the `mvtnorm` R package (Genz and Bretz, 2009; Genz *et al.*, 2016). The parameter Σ , the covariance matrix ($\Sigma_{ij} = \sigma_{X_i X_j}$), defines the correlation structure between the simulated genes (rows i and j in data matrix X) being sampled. With a diagonal of one ($\Sigma_{ii} = \sigma_{X_i}^2 = 1$), this Σ matrix simulates genes with a standard deviation of one and the covariance parameters between them are the correlations between each gene. In Figure 3.6, an example of such a simulated multivariate normal dataset is shown with the functional threshold applied.

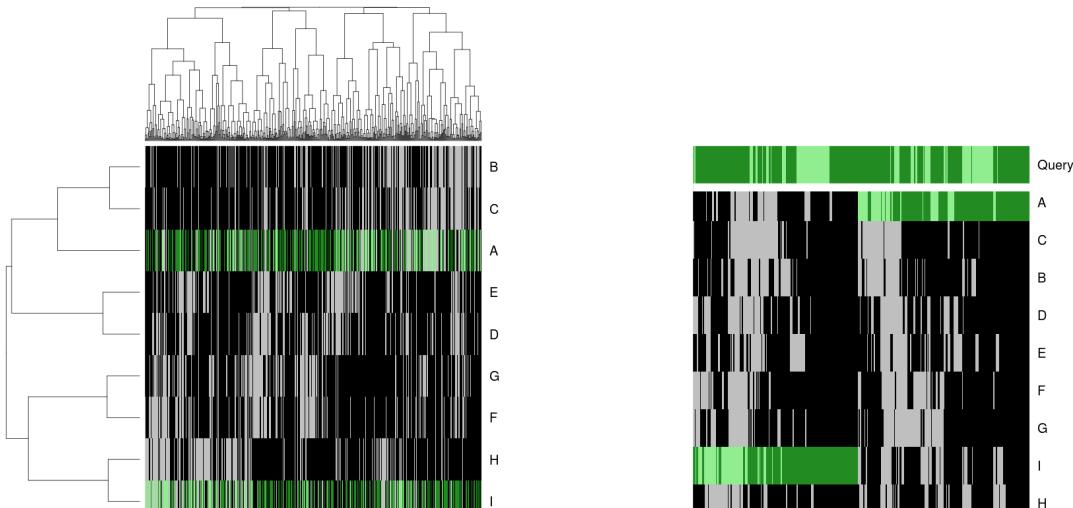
Once a simulated dataset has been generated, the samples were compared by gene function (as derived from a functional threshold). The known underlying synthetic lethal partners were selected within the dataset and a query gene was generated by



(a) Simulated expression matrix

(b) Corresponding gene function calls

Figure 3.6: **Simulating gene function.** A simulated dataset with samples (columns) and genes A–I (rows) was transformed from a continuous (coloured blue–red) scale to a discrete matrix of gene function (black for functional levels and grey for non-functional).



(a) Simulated gene function with SL genes (b) Query gene added with SL condition

Figure 3.7: **Simulating synthetic lethal gene function.** In a discrete simulated gene function dataset (shaded for functional levels and pale otherwise) with samples (columns) and genes (rows), genes A and I were SL partners of a “Query” gene. A partner was selected (highlighted in green) randomly in each sample for simulating synthetic lethality, then ordered such that the query gene or an SL partner were functional in each sample.

sampling from the normal distribution. These were matched (as shown for two synthetic lethal partners in Figure 3.7) such that the synthetic lethal condition was met: at least one of the synthetic lethal partner genes and the query gene are functional in any particular cell. The samples are ordered by functional data (without assuming correlation of underlying expression values) with the query gene in one direction and the remaining dataset ordered by the selected synthetic lethal partner.

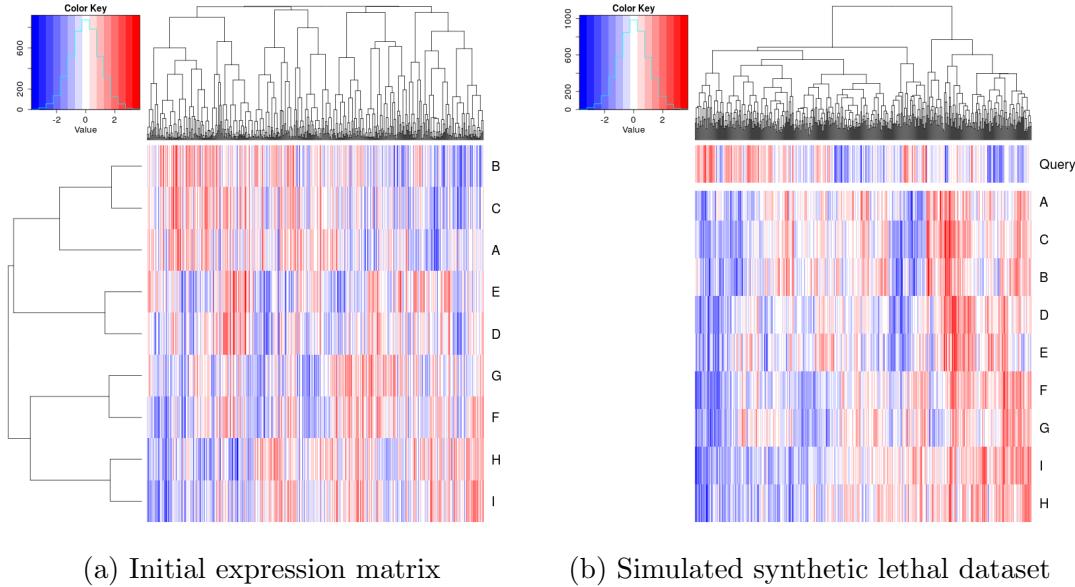


Figure 3.8: **Simulating synthetic lethal gene expression.** A simulated continuous expression dataset (blue–red scale) with samples (columns) and genes A–I (rows) was matched to a query gene such that at least one synthetic lethal partner was above a functional threshold when the query gene was below it which satisfied the synthetic lethal model.

This procedure produces a simulated dataset where samples with a non-functional query gene have at least one functional partner gene. Similarly, the query gene is functional in all samples where all of the synthetic lethal partner genes are non-functional. In this procedure, a dataset has been generated with known synthetic lethal partners (as shown in Figure 3.8) with few assumptions about the relationships between the each synthetic lethal pair (allowing compensating functions from higher-order interactions). This procedure has been designed to have the most stringent (least detectable) synthetic lethal relationships, where higher-order interactions are possible for the purposes of testing pairwise detection procedures such as SLIPT.

3.3 Detecting Simulated Synthetic Lethal Partners

The synthetic lethal detection methodology (SLIPT), as described in Section 3.1, was evaluated with simulated data containing known synthetic lethal partners, generated using the procedure described in Section 3.2.2. Simulations were performed to demonstrate the methodology and support its use throughout this thesis. These simulations were performed by sampling from statistical distributions, including the multivariate normal distribution with correlated blocks of genes, generated by Σ matrices such as those shown. A more complex multivariate normal sampling procedure based on pathway graph structures, as described in Section 3.4.2, was used for further investigations in Chapter 6.

3.3.1 Binomial Simulation of Synthetic Lethality

The synthetic lethal simulation procedure (described in Section 3.2.2) initially used gene function, sampled directly from a binomial distribution using the binomial probability of observing functional gene levels ($p = 0.3$) in one observation ($n = 1$) for each samples:

$$X \sim \text{Binomial}(n, p)$$

for a binary matrix X of gene function with n trials and a probability of p . Once a query gene with synthetic lethal partners has been added, these functional levels were passed directly into SLIPT as “low” and “high” samples.

The simulation procedure was performed with 20,000 total genes (as occurs in expression datasets) with a variable number of true synthetic lethal partners and 500, 1000, 2000, or 5000 samples. Each ROC curve was derived from the results of 10,000 replicate simulations. The statistical performance (as shown in Figure 3.9) of the χ^2 -derived p-value declined towards random predictions (an AUROC of 0.5) with more underlying synthetic lethal partners to detect. However, increased sample size somewhat mitigated this decline, as expected with a statistical predictor, particularly for moderate numbers of synthetic lethal partners.

Simulations using this binomial model of synthetic lethality were simplistic but informed the development of more complex simulations including expression and correlation structures. It did not represent the data that SLIPT will be applied to but the binomial simulations demonstrated that SLIPT is able to distinguish small numbers of synthetic lethal partners in a simulated system with behaviours expected with respect to sample size. This supported further development of the synthetic lethal model

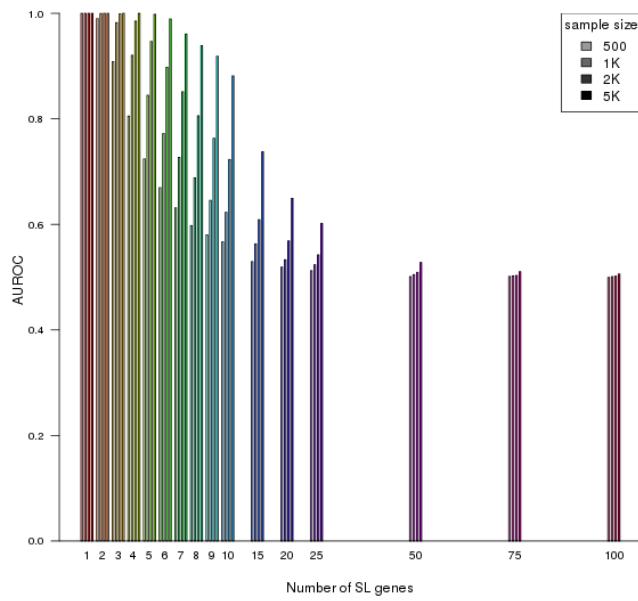


Figure 3.9: **Performance of binomial simulations.** Gene function was simulated by binomial sampling and tested for synthetic lethality by SLIPT. Statistical performance declined with additional synthetic lethal partners but this was mitigated by increased sample sizes.

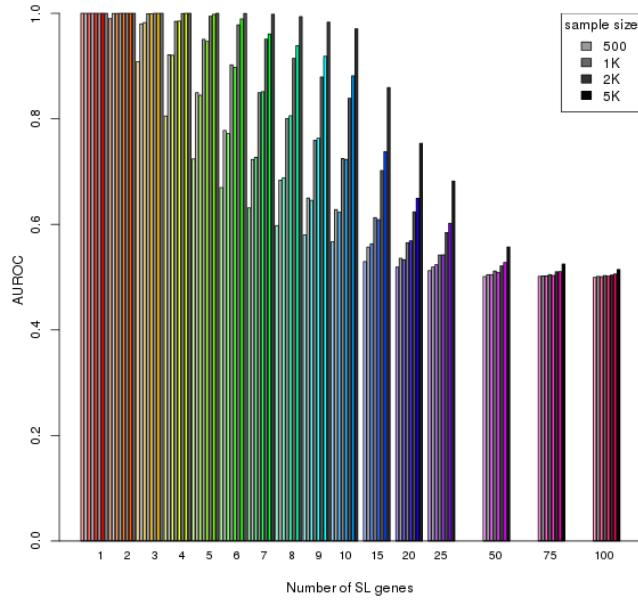


Figure 3.10: **Comparison of statistical performance.** Binomial simulation of synthetic lethality (in colour) in comparison to multivariate normal simulations (in greyscale), in which SLIPT consistently had higher performance across parameters.

and simulation pipeline (as described in Section 3.2) using the multivariate normal distribution.

The multivariate normal simulation procedure more closely recapitulates the (normalised) expression data that SLIPT was intended for and enables the methodology procedure to be tested without requiring modifications (in Section 3.3.2). Sampling continuous expression values from a normal distribution enabled the expression threshold for gene function to differ from the categorical “low” and “high” expression binning performed by SLIPT (as discussed in Section 3.2.1). The SLIPT procedure does not assume a known threshold for expression and instead uses expression as an estimate of gene function which does not compromise the statistical performance of the SLIPT in the multivariate normal simulation. The performance was an improvement over the binomial simulation procedure (shown in Figure 3.10) across simulation parameters in an equivalent simulation (without correlation structure). This multivariate normal model is also more refined since it defines the synthetic lethal condition, to ensure that at least one synthetic lethal partner was active in query-deficient samples, without disrupting the proportion of samples with each gene being functional.

3.3.2 Multivariate Normal Simulation of Synthetic Lethality

The multivariate normal simulation procedure was initially performed using the `mvttnorm` R package (Genz and Bretz, 2009; Genz *et al.*, 2016) (as described in Section 3.2) without correlation structure. Expression `data (X)` was sampled from multivariate normal distribution with a mean ($\mu = 0$), standard deviation ($\sigma = 1$), and no correlation between genes ($r = 0$):

$$X \sim \text{Normal}(\bar{\mu}, \Sigma).$$

Once a query gene with synthetic lethal partners has been added, the simulated expression values were tested by SLIPT, as described in Section 3.1.

The statistical accuracy of SLIPT as a binary classifier was high across simulations of a full dataset of 20,000 genes (shown in Figure 3.11a). Using the χ^2 -derived p-value as a threshold for prediction, this was largely due to high specificity: the majority of non-synthetic lethal genes were distinguished from the underlying synthetic lethal genes. Thus the SLIPT methodology performed better with larger datasets with more expected negatives and the results of simulations of smaller numbers of genes (e.g., the graph structures analysed in Section 6.2.1) can be applied to larger datasets, where they are expected to perform comparably or better with a lower false negative rate

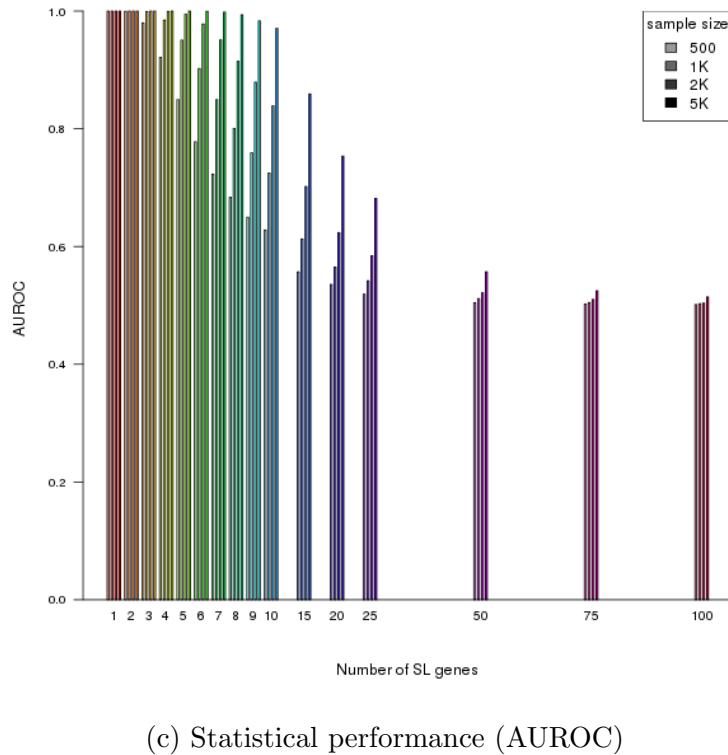
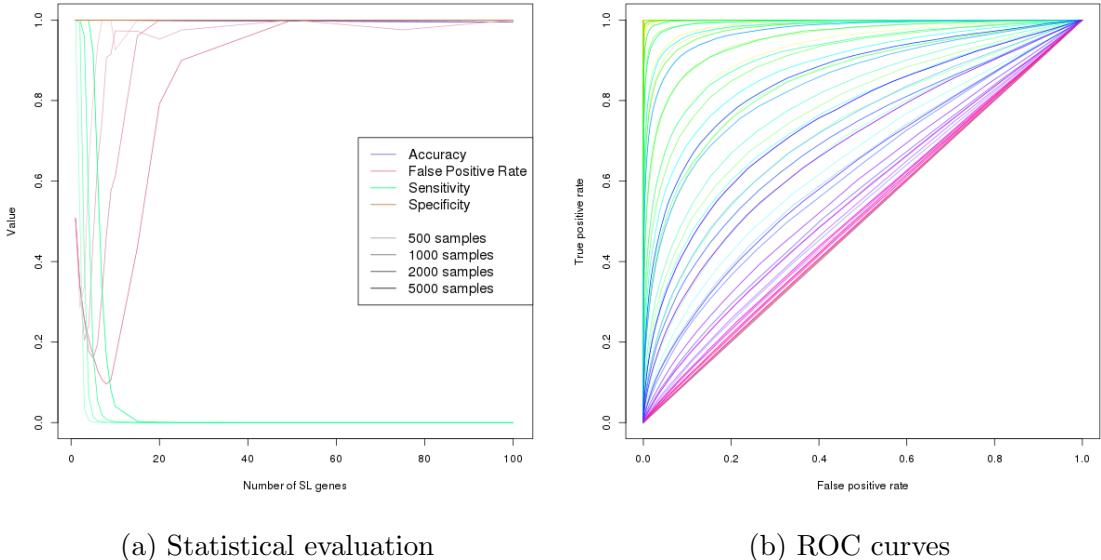


Figure 3.11: Performance of multivariate normal simulations. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution (without correlation structure). Performance of SLIPT declined with increasing numbers of synthetic lethal partners but this was mitigated by increased sample sizes (in darker colours). This occurred as the sensitivity decreased with a greater number of true positives to detect, which lead to a trade-off in accuracy as seen in a trough for false positive rate and the ROC curves.

(as shown in Sections 6.2.4 and 6.3.2). Accordingly, key results will be supported by replication with larger numbers of non-synthetic lethal genes added to the simulations.

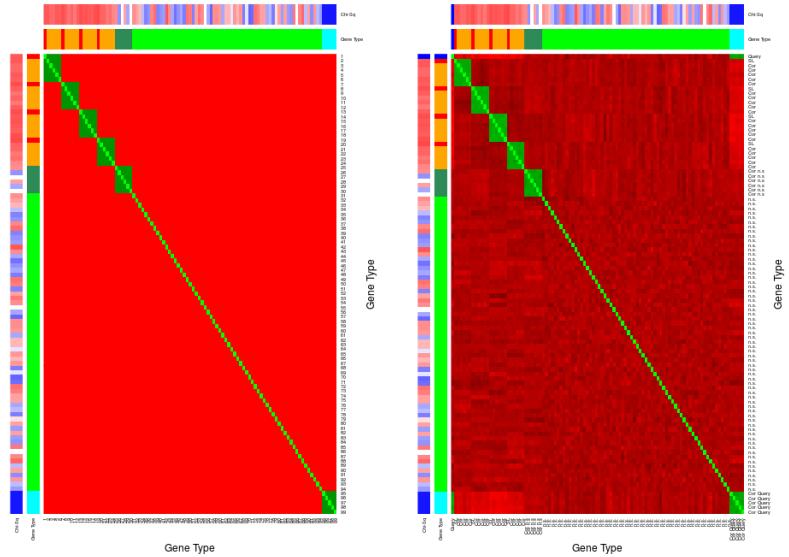
The sensitivity of SLIPT as a binary classifier of synthetic lethality (as shown in Figure 3.11a) declined with higher numbers of synthetic lethal genes to detect, although this is somewhat mitigated by higher sample sizes. The minority of true synthetic lethal partners are more difficult to distinguish when there are more of them (with a weaker expression signal from each). While a reduction of the false positive rate could be achieved for moderate numbers of underlying synthetic lethal partners, the number of partners to be detected in analyses of expression data is unknown. However, this simulation procedure is amenable to assessing the performance of SLIPT across simulation parameters, graph structures, and comparisons to other approaches (as presented in Chapter 6).

Not all of the genes detected by SLIPT were true synthetic lethal genes but they were among the strongest candidates and SLIPT had higher performance with fewer underlying synthetic lethal genes to detect. These results support a focus on pathway analyses, in particular, the selection of pathways for further investigation. Pathway over-representation analysis was performed to detect functional groups recurrently detected by SLIPT since individually detected gene candidates were not necessarily synthetic lethal. The detection of functionally related genes (in Chapter 4) supports the role of a pathway in synthetic lethal relationships. The use of pathway metagenes can reduce the number of potential pathways, compared to genes, to help identify synthetic lethality. These approaches were both applied in Chapter 4 to identify the synthetic lethal pathways of *CDH1*. Pathways are also more likely to replicate across experimental models, as demonstrated by Dixon *et al.* (2008).

The ROC curves showed that SLIPT is subject to a near equal trade-off between sensitivity and specificity across threshold values (as shown in Figure 3.11b). The lower sensitivity and higher specificity with a binary classification (as shown in Figure 3.11a) results from stringent testing by SLIPT with FDR adjusted p-values. The area under these curves (AUROC) was used to compare statistical performance (as shown in Figure 3.11c), which had lower performance for more underlying synthetic lethal partners, and higher performance for larger sample size in multivariate normal simulations.

3.3.2.1 Multivariate Normal Simulation with Correlated Genes

Correlation structures were added to the simulation procedure (with the Σ matrix, as discussed in Section 3.2), using correlated blocks of genes (as shown in Figure 3.12a). These correlated blocks represent genes with correlated expression, such as co-regulation



(a) Input Σ matrix parameter (b) Simulated correlation matrix

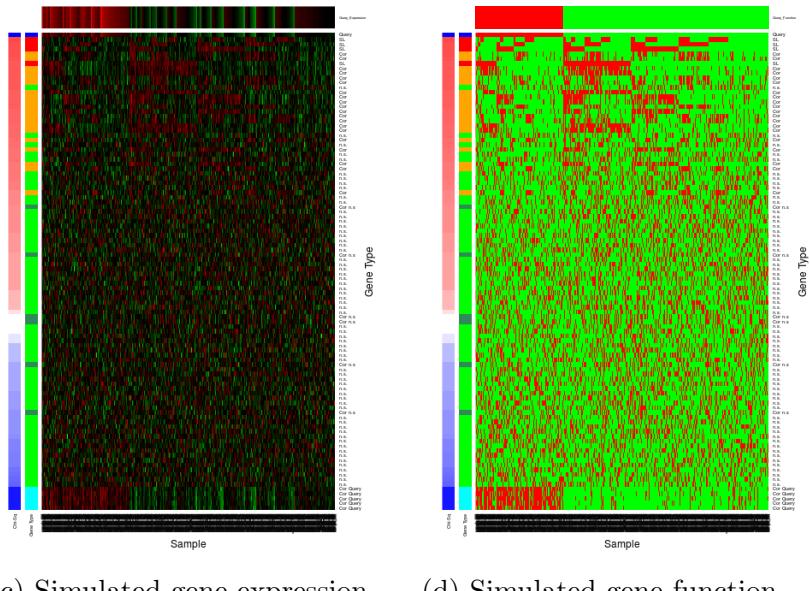


Figure 3.12: Simulating expression with correlated gene blocks. A Σ matrix (a) was used to generate 100 genes with a multivariate normal distribution, including correlated blocks of genes ($r = 0.8$) with correlation (b) similar to Σ , on a red-to-green scale. The annotation for genes gives the χ^2 (in blue for in the direction of SLIPT or red otherwise) and the gene category (blue for query, cyan for query-correlated, red for SL, orange for SL-correlated, forest green for non-synthetic lethal-correlated, and green for non-synthetic lethal). The simulated gene expression (c) and function (d) generated were ordered by χ^2 showing the functional structure of synthetic lethal genes and that they were among the strongest SLIPT results.

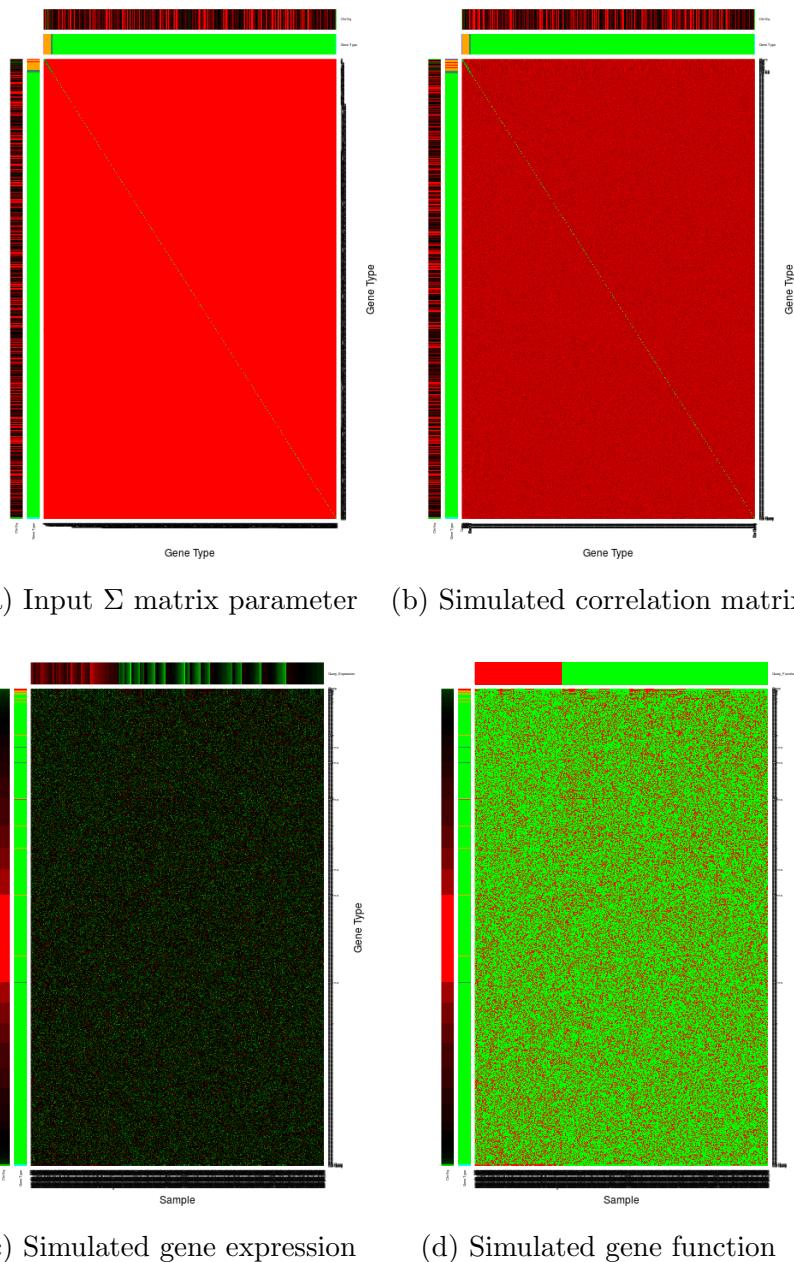


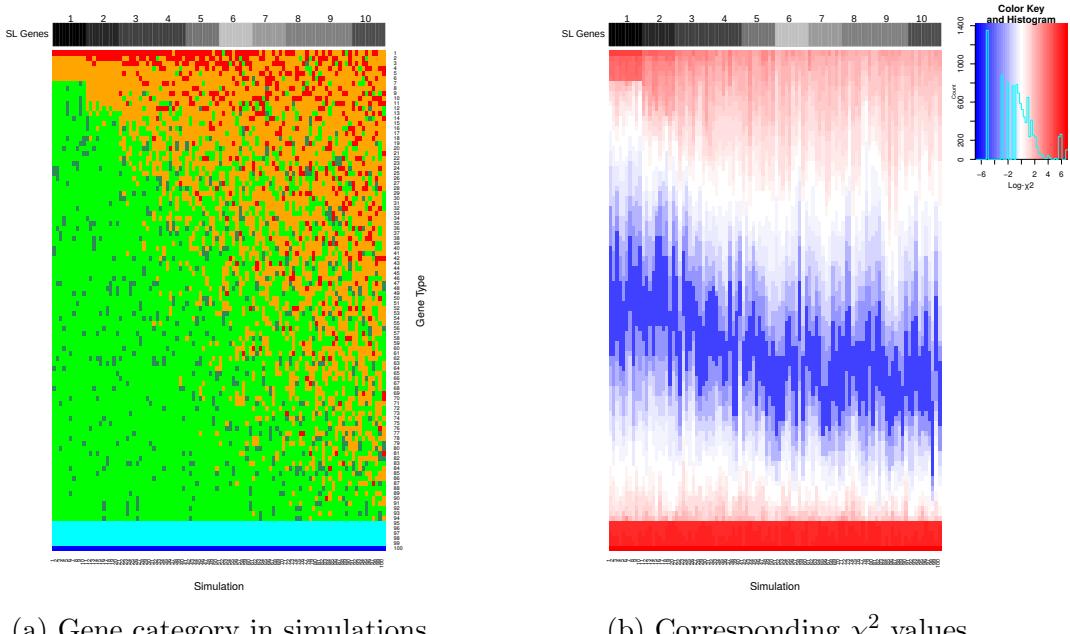
Figure 3.13: Simulating expression with correlated gene blocks. Using the Σ matrix (a), sampling 1000 genes from a multivariate normal distribution produced (b) correlated blocks of genes (correlated by $r = 0.8$) on a red-to-green scale. The simulated gene expression (c) and function (d) generated were ordered by χ^2 and SLIPT direction show that synthetic lethal genes are among the strongest SLIPT results with high specificity against many potential false positives. These are annotated for $\log\chi^2$ (on a red-to-green scale) and category (blue for query, cyan for query-correlated, red for SL, orange for SL-correlated, forest green for non-synthetic lethal-correlated, and green for non-synthetic lethal) for each gene.

or shared membership of biological pathways. The example (as shown in Figure 3.12) shows four synthetic lethal genes (out of 100), each with five correlated genes that are not themselves synthetic lethal partners of the query gene. These simulations address whether synthetic lethal genes are distinguishable from correlated partners. The Σ matrix produced a similar correlation structure (Figure 3.12b) and expression profiles (Figure 3.12c). Apart from correlated blocks of genes ($r = 0.8$), the remaining genes had small variations due to random sampling. The structure of the dataset, particularly between synthetic lethal genes and the query, was evident in the simulated gene expression (Figure 3.12c) and function (Figure 3.12d). When these genes were ordered by the SLIPT results, the synthetic lethal genes were highly ranked **and** the majority of them were distinguishable from highly correlated genes.

The use of correlation structure was applied to larger datasets, such as the 1000 genes shown in Figure 3.13. Synthetic lethal genes were highly ranked by SLIPT and were often distinguishable from correlated genes. As previously discussed in Section 3.3.2, these synthetic lethal genes were still detectable among a larger number of non-synthetic lethal genes, and the SLIPT methodology performed better on large datasets.

These plots (Figures 3.12 and 3.13) used similar correlated blocks with a non-synthetic lethal gene (true negative) and the query gene (which is not synthetic lethal with itself). Neither of these were synthetic lethal but they could potentially affect performance methodology, particularly the specificity, as correlated non-synthetic lethal genes may be distinguishable from synthetic lethal genes. The non-synthetic lethal correlated block of genes had no impact on synthetic lethal detection but the query correlated genes were important (as shown in Sections 3.3.2.2 and 6.1.1.1).

The simulations of gene expression data (with 100 genes) with correlations structure were used to examine the variation between detection in different samples and varying the number of underlying synthetic lethal partners. A small number of simulations (10 for each) are shown to demonstrate the variation between replicate simulations from iterative sampling from the same multivariate normal distribution (as shown in Figure 3.14). These simulations showed that synthetic lethal genes were highly ranked by SLIPT when there are few of them and these were relatively consistent across replicate simulations. However, they were less consistent for higher numbers of synthetic lethal partners to detect and were more difficult to distinguish from other genes, particularly those correlated with them. Similarly, the χ^2 values showed clear



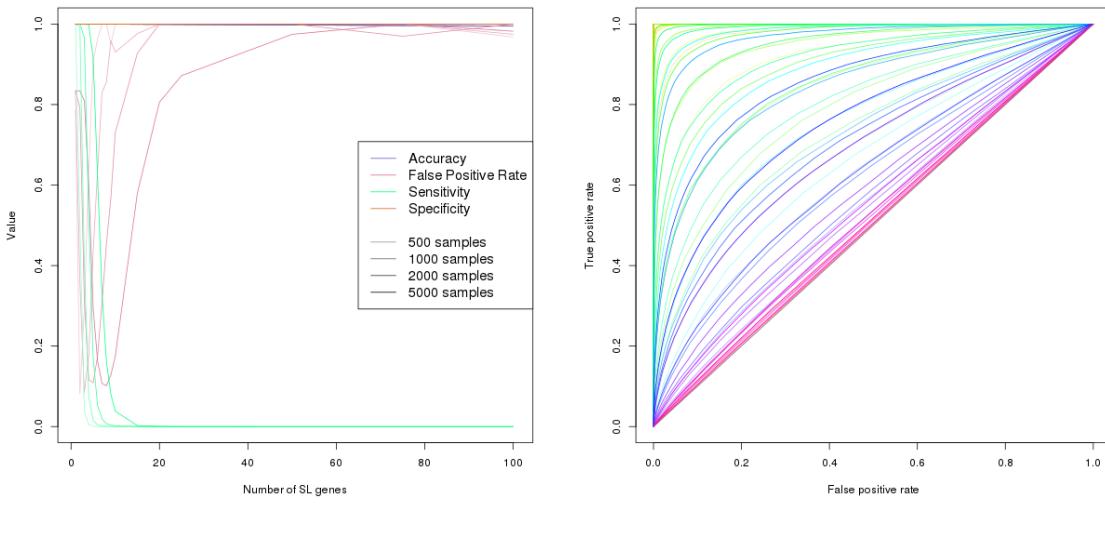
(a) Gene category in simulations

(b) Corresponding χ^2 values

Figure 3.14: Synthetic lethal prediction across simulations. The gene category (a) ordered by χ^2 and the SLIPT directional condition is shown across simulations (blue for query, cyan for query-correlated, red for SL, orange for SL-correlated, forest green for non-synthetic lethal-correlated, and green for non-synthetic lethal). For each number (1–10) of synthetic lethal partners, 10 simulations show that the increasing numbers of synthetic lethal partners became harder detect (i.e., red cells become interspersed in the columns of (a)). The $\log \chi^2$ values (b) showed a threshold for synthetic lethal and correlated genes when there are fewer of them, distinguishable from correlated genes in this case.

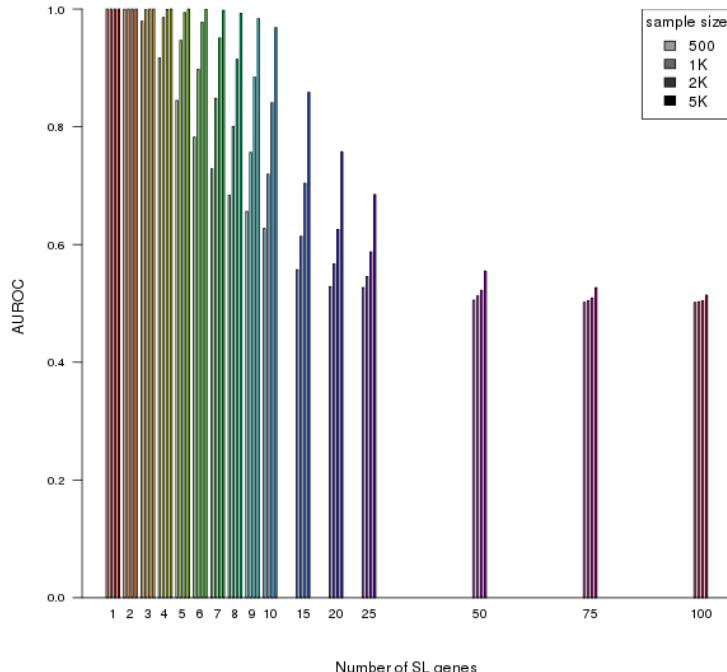
thresholds for synthetic lethal and correlated genes in simple simulations but these were more gradual for higher numbers of synthetic lethal partners.

While the synthetic lethal genes were detected in simple simulations (as shown in Figure 3.14), ROC analysis was performed to determine whether they were robustly detectable and to make further comparisons. These results (as shown in Figure 3.15) were similar to simulations without correlation structure. As a binary classifier, SLIPT had low sensitivity for higher numbers of synthetic lethal partners to detect and high specificity with the vast majority of non-synthetic lethal genes (for 20,000 genes). This was reflected in a similar reduction in statistical performance for higher numbers of synthetic lethal partners and a higher performance with higher sample size. Overall, the statistical performance was no different to simulations without correlation structure (as shown in Figure 3.16).



(a) Statistical evaluation

(b) ROC curves



(c) Statistical performance (AUROC)

Figure 3.15: Performance with correlations. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution (with correlation structure). Performance of SLIPT declines for more synthetic lethal partners but this is mitigated by increased sample sizes (darker colours). This generally occurs as the sensitivity decreases for a greater number of true positives to detect, leading to a trade-off in accuracy as seen in a trough for false positive rate and the ROC curves.

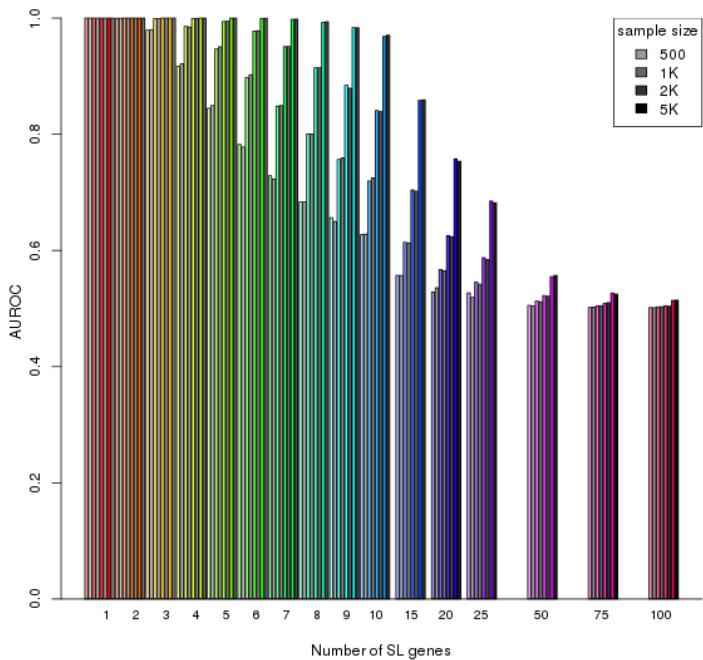


Figure 3.16: Comparison of statistical performance with correlation structure. Multivariate simulation of synthetic lethality with correlation structure (in colour) has comparable performance to simulation without correlations (in greyscale) with known synthetic lethal partners across parameters.

SLIPT was robust across correlation structures and is applicable to gene expression data, with pathway structures and correlations. These correlation structures were not intended to model specific biological pathways or represent them but showed potential impact of correlation structure on the performance of SLIPT using highly correlated ($r = 0.8$) gene blocks. More complex correlation structures, such as genes positively correlated with the query gene and derived from pathway graph structures (as described in 3.4.2) were examined further in Sections 3.3.2.2 and 6.2.1 respectively.

In particular, genes correlated with true synthetic lethal genes had little impact on the performance of SLIPT detection: synthetic lethal genes were as distinguishable from correlated genes as they are from true negative genes. Genes correlated with synthetic lethal partners did not interfere with the detection of true synthetic lethal genes, although they were often ranked next below them and may support synthetic lethal pathways by having related gene functions.

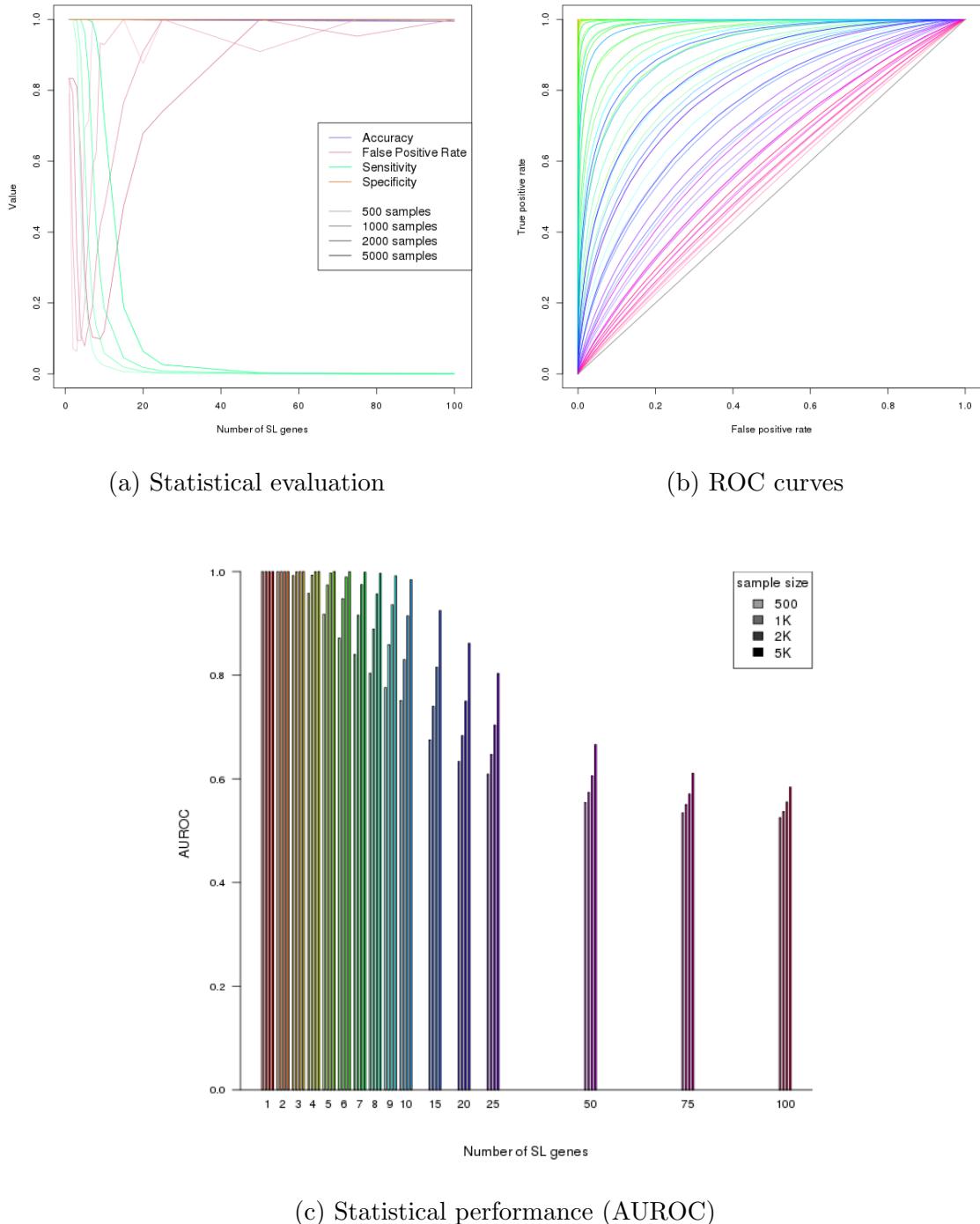


Figure 3.17: Performance with query correlations. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution (with correlation structure including correlated genes with non-synthetic lethal and query genes). Performance of SLIPT declined for more synthetic lethal partners and is mitigated by increased sample sizes (darker colours) but the sensitivity remains higher for a greater number of true positives with corresponding improvements in ROC curves.

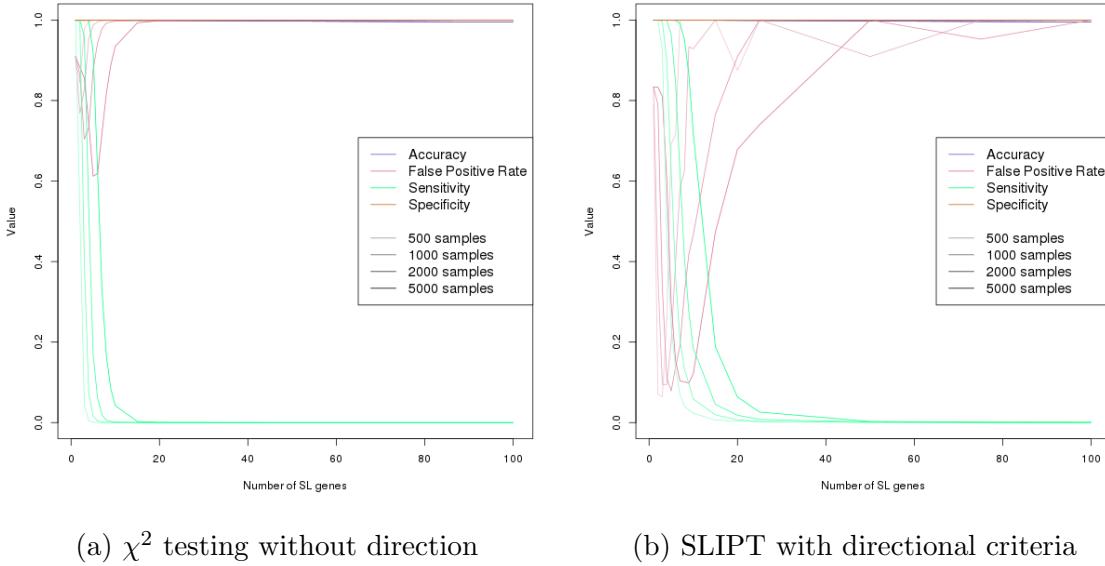
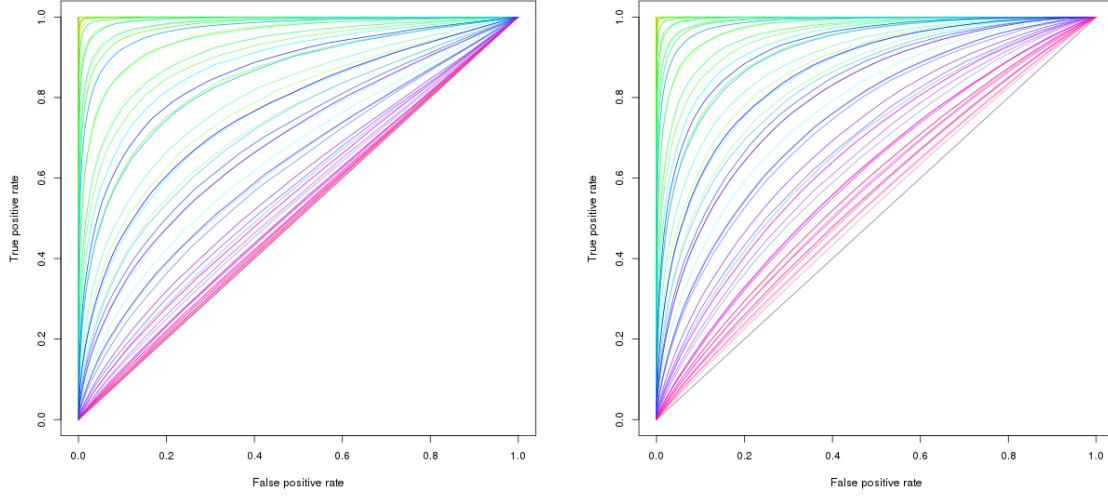


Figure 3.18: **Statistical evaluation of directional criteria.** A simulated multivariate normal dataset of 20,000 genes with correlation structures was tested by SLIPT with the directional condition and the χ^2 test. SLIPT exhibited a consistently higher sensitivity and lower false positive rate.

3.3.2.2 Specificity with Query-Correlated Pathways

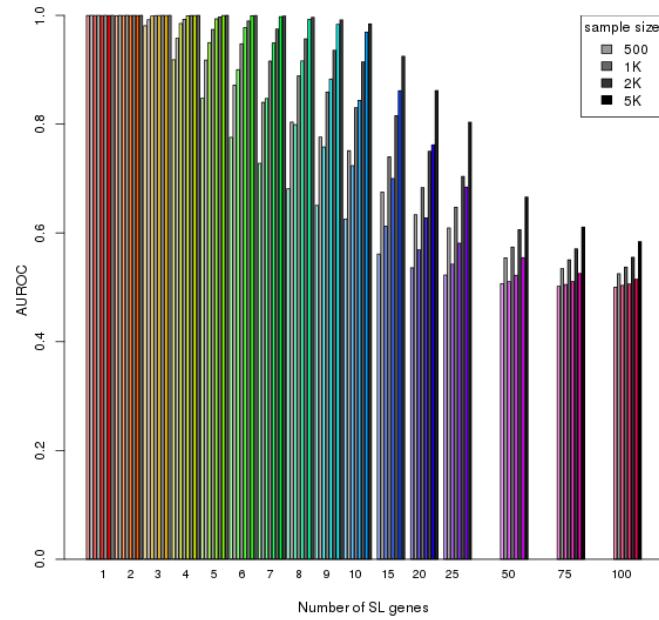
Correlation structures were also considered for non-synthetic lethal genes that were (positively) correlated genes with the query gene. Specifically, five highly correlated ($r = 0.8$) with the query gene were added (as described in Section 3.3.2.1). These simulations had similar performance (as shown in Figure 3.17) to those without these correlations with a higher specificity and a lower false positive rate (shown in Figure 3.17a).

The directional criteria of the SLIPT procedure was important in this case, enhancing its performance, particularly in distinguishing positively correlated non-synthetic lethal genes. The multivariate normal simulations were performed, with 20,000 genes, including all of the correlation structures discussed (with synthetic lethal, non-synthetic lethal, and query correlated genes). These simulations were compared for the direction SLIPT and the χ^2 testing. There was a considerably higher statistical performance with SLIPT, particularly increased sensitivity and lower false positive rate (as shown in Figure 3.18).



(a) χ^2 testing without direction

(b) SLIPT with directional criteria



(c) Statistical performance (AUROC)

Figure 3.19: Performance with directional criteria. A simulated multivariate normal dataset of 20,000 genes with correlation structures was tested by SLIPT and χ^2 test. SLIPT had higher performance across simulation parameters, clearly differing from random (grey diagonal) in ROC curves up to 100 SL genes (b). The performance (c) of SLIPT (in greyscale) was consistently higher than the χ^2 test (in color).

These results show that the performance of SLIPT is appropriate for the analysis of expression datasets, where positively correlated genes commonly occur, with the directional condition robustly improving the performance of SLIPT across simulation parameters (compared to the χ^2 test). Without assuming the underlying number of synthetic lethal genes, SLIPT will perform better than the χ^2 test alone, irrespective of the significance threshold as shown by ROC analysis (as shown in Figure 3.19). The directional SLIPT methodology outperformed the χ^2 test at detecting synthetic lethal partners with even up to 100 synthetic lethal genes.

Together these simulation results support the application of the SLIPT methodology as it has been performed throughout Chapters 4 and 5. The methodology and simulation procedure were explored further in Chapter 6, with comparison to other synthetic lethal detection approaches and the inclusion of graph structures.

3.4 Graph Structure Methods

Graph structures have been used in several ways in this project, including novel approaches to analysis and simulations. Procedures were developed for statistical and network analysis of gene states in pathway structures. Specifically, the relationships between siRNA and SLIPT genes were tested within biological pathways in Chapter 5. These graph structures were also used in Chapter 6 to derive correlation structure between simulated gene expression profiles to represent biological pathways.

3.4.1 Upstream and Downstream Gene Detection

Comparison of experimental and computational candidate synthetic lethal partner genes within pathway structures was performed to determine whether these sets of genes were related by pathway structure. Considering the differences in how these candidates were generated, it was unsurprising that they did not detect some identical genes within the candidate biological pathways. However, they could still be related by being upstream or downstream of each other.

Using the Reactome version 52 (Croft *et al.*, 2014), as described in Section 2.4.2, genes detected by each synthetic lethal discovery approach were mapped to the graph structure for each candidate pathway identified in Chapter 4 (with graphs defined as described in Section 2.4.3). To test whether siRNA candidate genes were upstream of SLIPT candidate genes, shortest paths were traced between each pair of these genes in a directed network. The paths where the siRNA candidate was upstream (“up”) and downstream (“down”) of a SLIPT candidate were scored. This procedure yielded

the total number of shortest paths which indicated that siRNA genes were upstream or downstream of the SLIPT genes and measured the difference between these to determine if there was an imbalance in a particular direction. While this difference was indicative of the number of paths between the gene candidate groups in either direction, it was not sufficient to statistically verify structure or relationships between siRNA and SLIPT genes. It was then combined with a permutation resampling procedure (as described in Section 3.4.1.1) to test for directional relationships.

Initially, this procedure excluded genes that were detected by both approaches since they would count in both directions. Upon further consideration, these genes were restored to account for that they may contribute unequally to each gene set if there are unequal numbers of genes above or below them in the pathway structure.

3.4.1.1 Permutation Analysis for Statistical Significance

A permutation procedure was developed to randomly assign members of the pathway to siRNA and/or SLIPT groups, with the same number of each candidate partner gene set as observed in the pathway. These permuted genes were measured for pathway structure between the permuted gene groups as performed for the observed candidates (as performed in Section 3.4.1). A distribution of pathway structure relationships expected by chance was generated by permuting iteratively over these pathways. The resulting null distribution was compared to the observed counts of relationships (in either direction). This procedure yielded a permutation p-value as the proportion of permutations which had a value greater than the observed value. The null hypothesis was that there was no relationship between these gene groups compared to genes that had been selected at random. Thus both the alternate hypotheses that the siRNA genes were either upstream of the SLIPT genes or that they are downstream of them were testable.

The permutation procedure does not assume the underlying distribution of the data under the null hypothesis and accounts for the total number of nodes, edges, siRNA, and SLIPT genes in each graph or networkpathway structure. The number of genes detected by both siRNA and SLIPT was not accounted for under the initial shortest path counts procedure that excluded them. Once they were included, it was ensured that the number of intersecting genes was equal to the number observed to test for pathway structure without changing the intersection size, the subject of prior analyses.

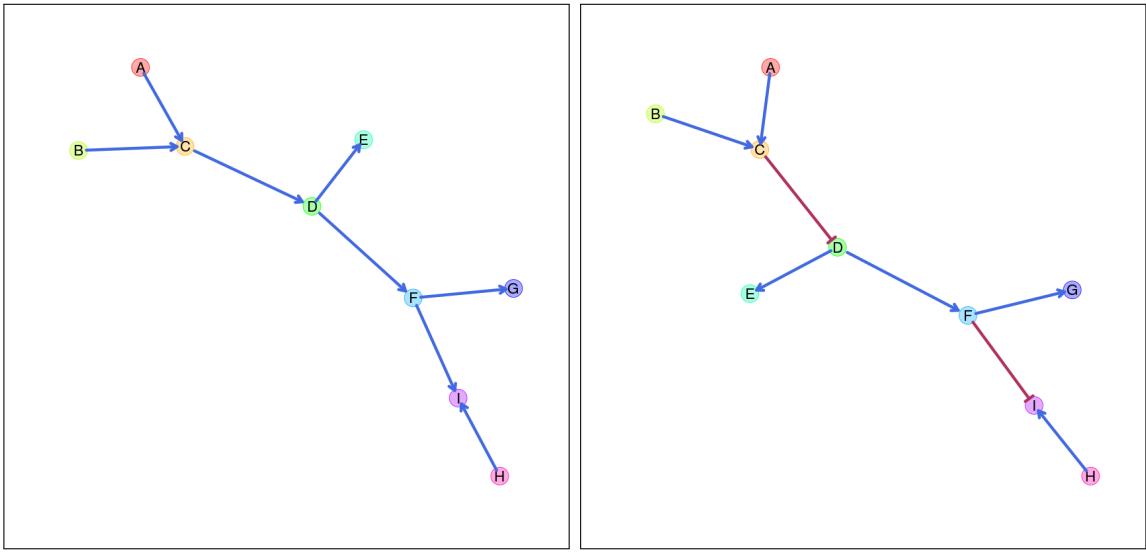
3.4.2 Simulating Gene Expression from Graph Structures

The simulation procedure was refined to generate expression data with correlation structure from a known graph structure. This enabled modelling of synthetic lethal partners within a biological pathway and the investigation of the impact of pathway structure on synthetic lethal prediction. Firstly, a simulated pathway was constructed as a graph structure, with the `igraph` R package Csardi and Nepusz (2006), with the state of the edges (i.e, whether they activate or inhibit downstream pathway members). This simulation procedure was intended for biological pathway members with correlated gene expression (higher than the background of genes in other pathways) but it may also be applicable to modelling protein levels (e.g, in a kinase regulation cascade) or substrates and products (e.g., in a metabolic pathway).

The graph structure was constructed [to be used to simulate data by](#) sampling a multivariate normal distribution using the `mvtnorm` R package (Genz and Bretz, 2009; Genz *et al.*, 2016). Throughout this Section, the simulation procedure will be demonstrated with the relatively simple constructed graph structure shown in Figure 3.20. This graph structure visualisation was specifically developed for (directed) iGraph objects in R and has been released in the `plot.igraph` package and `igraph.extensions` library (in Table 2.4 and Section 3.5.3). The `plot_directed` function enabled customisation of plot parameters for each node or edge and mixed (directed) edge types for indicating activation or inhibition. These inhibition links (which occur frequently in biological pathways) were demonstrated in Figure 3.20b.

The simulation procedure was designed to use such graph structures to inform development of a “Sigma” variance-covariance matrix (Σ) for sampling from a multivariate normal distribution (using the `mvtnorm` R package). Given a graph structure (or adjacency matrix), such as Figure 3.21a, a relation matrix was calculated based on distance such that nearer nodes are given higher weight than farther nodes. Throughout this thesis, a geometrically decreasing (relative) distance weighting was used, with each more distant node being related by $1/2$ compared to the next nearest, as shown in Figure 3.21b. An arithmetically decreasing (absolute) distance weighting is also supported in the `graphsim` R package release of this procedure.

A Σ matrix can be derived from this distance weighting matrix, creating a matrix (with a diagonal of 1) where each node has a variance and standard deviation of 1. Thus covariances between adjacent nodes were assigned by a correlation parameter and the remaining matrix based on weighting these correlations by the geometrically weighted distance matrix (or the nearest “positive definite” matrix for Σ weighted for



(a) Activating pathway structure (b) Pathway structure with inhibitions

Figure 3.20: **Simulated graph structures.** A constructed graph structure used as an example to demonstrate the simulation procedure. Activating links are denoted by blue arrows and inhibiting links by red edges.

negatively correlated inhibitions). Throughout this thesis, the correlation parameter was 0.8, unless otherwise specified (as used for the example in Figure 3.21c). This Σ matrix was then used to sample from a multivariate normal distribution such that each gene had a mean of 0, standard deviation 1, and covariance within the range [0, 1] such that they are correlations. This procedure generated a simulated (continuous normally distributed) expression profile for each node (as shown in Figure 3.21e) with corresponding correlation structure (Figure 3.21d). The simulated correlation structure closely resembled the expected correlation structure (Σ in 3.21c) even for the relatively modest sample size ($N = 100$) illustrated in 3.21. Once a simulated gene expression dataset has been generated (as in Figure 3.21e), then a discrete matrix of gene function was constructed with a functional threshold quantile to simulate functional relationships of synthetic lethality (as shown in Figure 3.4). Throughout this thesis, this threshold is the 0.3 quantile (as discussed in Section 3.2.1) which generates functional discrete matrices such as those used for synthetic lethal simulation in Section 3.2.2 (as shown Figure 3.21f).

The simulation procedure (depicted in Figure 3.21) can be used for pathways containing inhibition links (as shown in Figure 3.22) with several refinements. With the inhibition links (as shown in Figure 3.22a), distances were calculated in the same manner

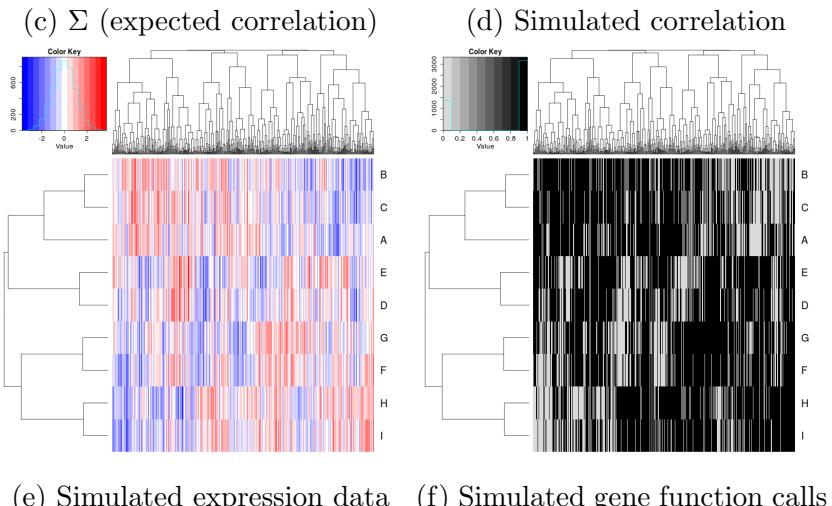
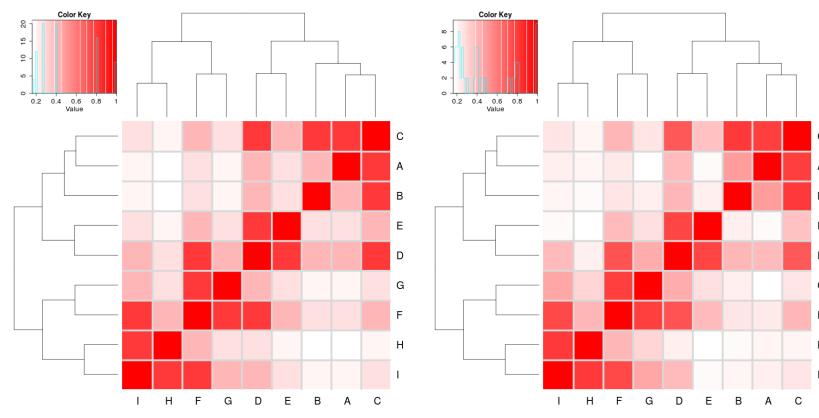
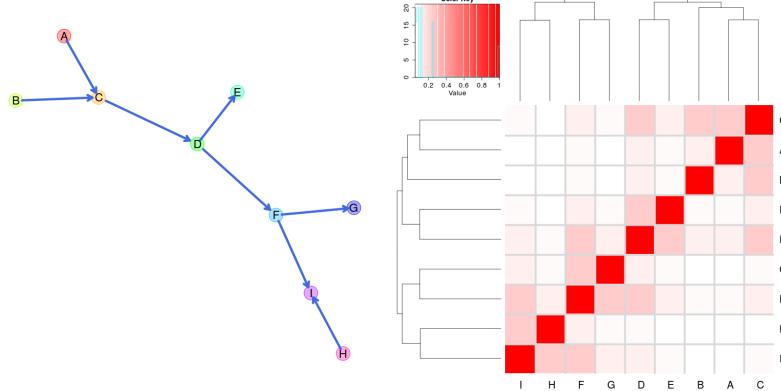


Figure 3.21: Simulating expression from a graph structure. An example graph structure that was used to derive a correlation structure from the relative distances between nodes and simulate continuous gene expression with sampling from the multivariate normal distribution.

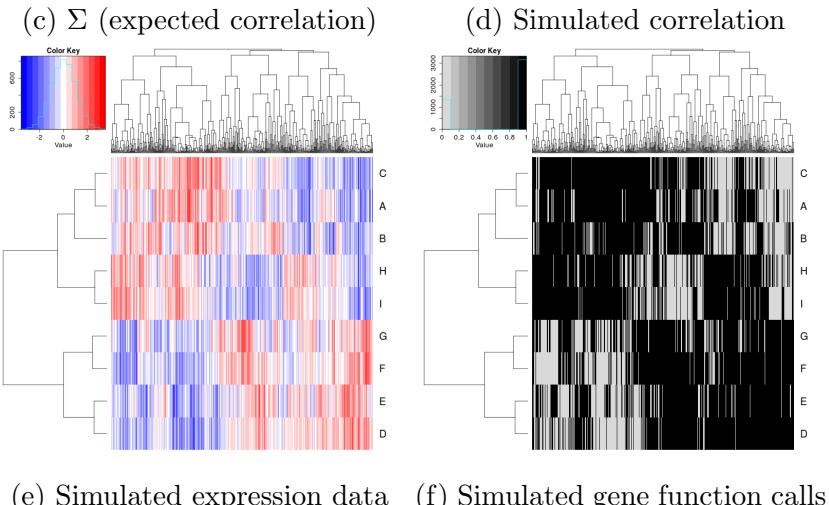
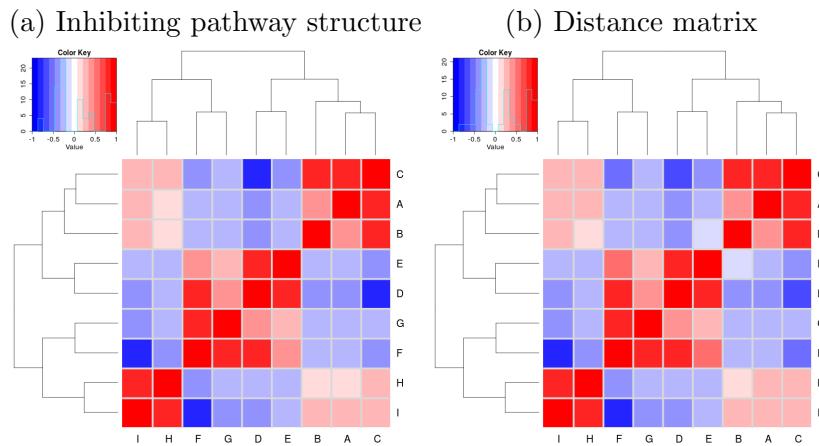
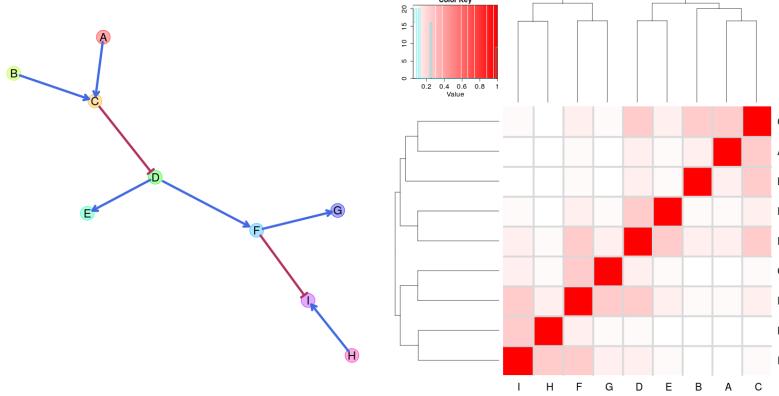


Figure 3.22: Simulating expression from graph structure with inhibitions. An example graph structure that was used to derive a correlation structure from the relative distances between nodes and simulate continuous gene expression with sampling from the multivariate normal distribution.

as before (Figure 3.22b) with inhibitions accounted for by iteratively multiplying downstream nodes by -1 to form blocks of negative correlations (as shown in Figures 3.22c and 3.22d). A multivariate normal distribution with these negative correlations can be sampled to generate simulated data (as shown in Figures 3.22e and 3.22f).

These simulated datasets could then be used for simulating synthetic lethal partners of a query gene within a graph network. The query gene was assumed to be separate from the graph network pathway and was added to the dataset using the procedure in Section 3.2.2. Thus I can simulate known synthetic lethal partner genes within a synthetic lethal partner pathway structure.

3.5 Customised Functions and Packages Developed

Various R packages (R Core Team, 2016) have been developed throughout this thesis using `devtools` (Wickham and Chang, 2016) and `roxygen` (Wickham *et al.*, 2017) to enable reproducibility of customised analysis and visualisation. Many of these have been documented, demonstrated in vignettes, and released on GitHub (<https://github.com/TomKellyGenetics>) to enable the research community to utilise them in their own analysis. These are summarised in Table 2.4, with the corresponding urls for their GitHub repository which contains instructions for installation with the `devtools` R package (Wickham and Chang, 2016) and links the relevant vignette(s).

3.5.1 Synthetic Lethal Interaction Prediction Tool

The statistical methodology for detection of synthetic lethality in gene expression data (SLIPT) is one of the main novel procedures developed in this thesis, as described in Section 3.1. The `slipt` R package has been prepared for release to accompany a publication demonstrating the applications of the methodology for identifying candidate interacting genes and pathways with *CDH1* in breast cancer (Koboldt *et al.*, 2012).

SLIPT can be used for analysis of any effectively continuous measure of gene activity (e.g., microarray, RNA-Seq, protein abundance, or pathway metagenes). Executing `slipt` is straightforward: the `prep_data_for_SL` function scores samples as “low”, “medium”, or “high” for each gene, then the `detect_SL` function tests a given query gene against all potential partners by performing the chi-squared test and directional conditions. This function returns a table summarising the observed and expected sample numbers used for the directional criteria, the χ^2 values, and corresponding p-values including adjusting for multiple comparisons. The `count_of_SL` and `table_of_SL` func-

tions serve to facilitate summary and extraction of the positive SLIPT hits, respectively, from the table of predictions of synthetic lethal partners.

The SLIPT methodology in this package release was used in later analyses rather than the corresponding source R code, including use on remote machines and upon simulated data. In particular, the functions in the package facilitate alterations to parameters, such as the proportion of samples called as exhibiting low or high gene activity (as shown in Section 6.1.1). This release supports reproducible research and enables wider use of SLIPT in future investigations into other disease genes.

3.5.2 Data Visualisation

Customised data visualisations in R (R Core Team, 2016) were developed to present data throughout this thesis. The `vioplotx` package provides an alternative visualisation (of continuous variables against categories) to the more familiar boxplot, showing variability of the data by the width of the plots. As demonstrated in Figure 3.23, this version enables separate plotting parameters for each violin with vector inputs for colour, shape, and size of various elements of the median point, central boxplot, borders, and fill colour for the violin. Scaling violin width to adjust violin area and splitting data by a second categorical variable is also enabled. This function is intended to be backwards compatible with the `vioplot` package (Adler, 2005) (applying scalar inputs across all violins) and `boxplot` (by enabling formula inputs as an S3 method). Each of these features has been demonstrated with examples in respective vignettes on the package GitHub repository (<https://github.com/TomKellyGenetics/vioplotx>).

The `heatmap.2x` function provides extensions for annotation colour bars for both the rows and columns (as shown in Figure 3.24). Multiple bars are enabled on both axes with matrix inputs (rather than single vector for `heatmap.2` (Warnes *et al.*, 2015)) which facilitates additional plotting of gene and sample characteristics for comparison with correlation matrices, expression profiles, or pathway metagenes. The annotation bar inputs correspond to their orientation on the plot, each colour bar is provided as a column for the row annotation on the left of the heatmap and as a row for the column annotation on top of the heatmap. Row and column annotation bars are labelled with the column or row names respectively. Additional parameters enable resizing of these annotation bar labels and control of reordering columns for when samples have been ordered in advance (e.g., ranked by a metagene or split into groups clustered separately). These features were used through this thesis and have been provided in a package GitHub repository (<https://github.com/TomKellyGenetics/heatmap.2x>).

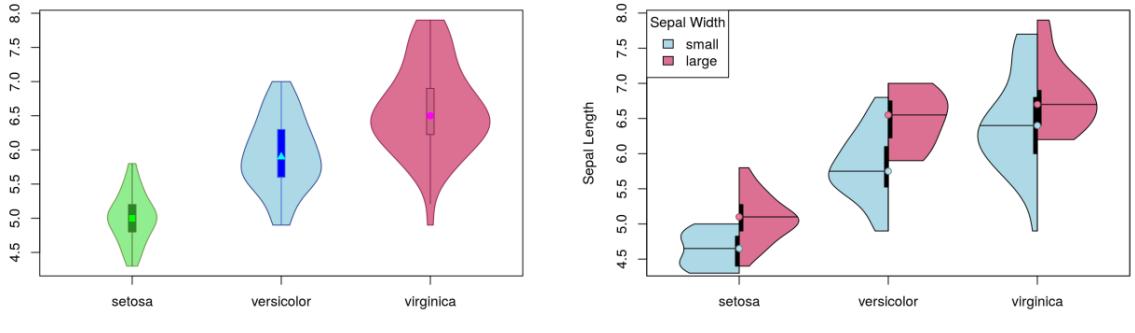


Figure 3.23: **Demonstration of violin plots with custom features.** An example of the `iris` dataset is plotted to show the custom features of the `vioplotx` package including (a) individual colour, shape and size parameters of each violin, scaling violin widths by area, and (b) splitting violins to compare subsets of data.

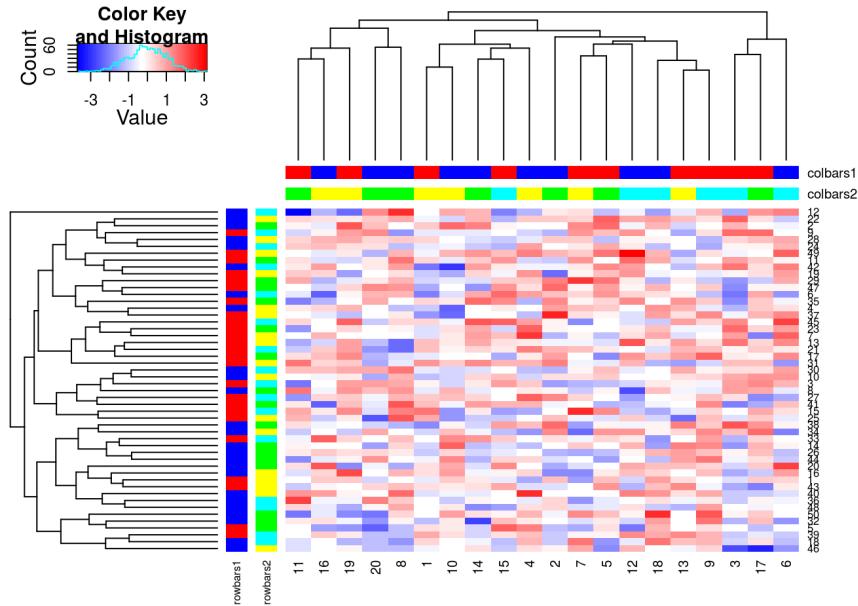


Figure 3.24: **Demonstration of annotated heatmap.** The example heatmap depicts the additional row and column annotation bars enabled by `heatmap.2x`, extending the features of `gplots` with backwards compatible inputs.

3.5.3 Extensions to the iGraph Package

The following features were developed during this thesis using “iGraph” data objects, building upon the `igraph` package (Csardi and Nepusz, 2006). These have been re-

leased as separate packages for each respective procedure and can be installed together as a collection of extensions to the `igraph` package (<https://github.com/TomKellyGenetics/igraph.extensions>).

3.5.3.1 Sampling Simulated Data from Graph Structures

The `graphsim` package implements the procedure for simulating gene expression from graph structures (as described in Section 3.4.2). By default, this derives a matrix with a geometrically decreasing weighting by distance (by shortest paths) between each pair of nodes. An absolute decreasing weighting is also available with the option `to` derive correlation structures from adjacency matrices or the number of links common partners (i.e., size of the shared “neighbourhood” (Hell, 1976)) between each pair of nodes. Functions to compute these are called directly by passing parameters to them when running the `generate_expression` or `make_sigma_mat` commands. This package enables simulating expression data directly from a graph structure (with the intermediate steps automated) or generating Σ parameters for `mvtnorm` from graph structures or matrices derived from them. These functions support assignment of activating or inhibiting relationships to each edge (with a `state` parameter).

3.5.3.2 Plotting Directed Graph Structures

The `plot.igraph` package provides the `plot_directed` function, specifically developed for directed graph structures, to plot activating or inhibiting for each edge (as described in Section 3.4.2). As shown in Figure 3.25, this function supports separate plotting parameters for each node, node label, and edge. This includes colours of node fill, border, label text, and edges and size of nodes, edge widths, arrowhead lengths, and font size of labels. The `state` parameter for assigning activating or inhibiting to each edge determines whether edges were depicted with 30° or 90° arrowheads. Colours are assigned separately so they may be customised. Vectorised parameters are applied across each node or edge, whereas scalar parameters apply the same plotting parameters across them. The default layout function is `layout.fruchterman.reingold` but any layout function supported by `plot` function in `igraph` (Csardi and Nepusz, 2006) was compatible, such as `layout.kamada.kawai` used to implement the Kamada–Kawai algorithm (Kamada and Kawai, 1989) for graph plots throughout this thesis.

3.5.3.3 Computing Information Centrality

The shortest paths of a network were computed by the `igraph` package (Csardi and Nepusz, 2006) which can be extended to calculate the network efficiency but was not provided by the package itself (as described in Section 2.4.4). The “information

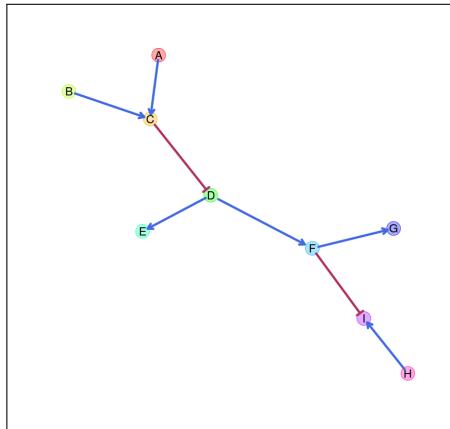


Figure 3.25: **Simulating graph structures.** An example graph structure which has been used throughout demonstrating the simulation procedure from graph structures. Activating links are denoted by blue arrows and inhibiting links by red edges.

centrality” of a vertex is computed as the relative change in the network efficiency when the vertex is removed. Information centrality is calculated iteratively for each node and the sum of information centrality for each vertex is the information centrality for the network. These metrics were released in the `info.centrality` package (<https://github.com/TomKellyGenetics/info.centrality>).

3.5.3.4 Testing Pathway Structure with Permutation Testing

A network-based procedure was developed to compare siRNA and SLIPT candidate genes in a pathway structure. Such pathway structure relationships were tested by computing the number of shortest paths between two different groups of nodes in either direction within a graph . This pathway relationship metric was implemented in the `pathway.structure.permutation` package (<https://github.com/TomKellyGenetics/pathway.structure.permutation>) with permutation testing (as described in Sections 3.4.1 and 3.4.1.1).

3.5.3.5 Metapackage to Install iGraph Functions

These features may be installed together with `igraph.extensions`, which can be accessed from a GitHub repository (<https://github.com/TomKellyGenetics/igraph.extensions>). This meta-package installs `igraph` (Csardi and Nepusz, 2006) and the packages described in Section 3.5.3 including their dependencies for matrix operations and statistical procedures: `Matrix`, `matrixcalc`, and `mvtnorm` (Bates and Maechler, 2016; Genz and Bretz, 2009; Genz *et al.*, 2016; Novomestky, 2012).

Chapter 4

Synthetic Lethal Analysis of Gene Expression Data

Having developed a statistical synthetic lethal detection methodology, SLIPT, it was next applied to publicly available cancer gene expression datasets. The analysis presented in this Chapter focuses on breast cancer for which TCGA expression data (Koboldt *et al.*, 2012) from a patient cohort and siRNA screen data, from experiments conducted in MCF10A cells (Telford *et al.*, 2015), were available. Stomach cancer data (Bass *et al.*, 2014) was used to replicate findings in an independent dataset, with this cancer chosen because it also occurs in syndromic HDGC patients. The TCGA data also has the advantages of having other clinical and molecular profiles, including somatic mutation across many of the same samples, in addition to a considerable sample size for RNA-Seq expression data generated with common TCGA procedures to minimise batch effects.

Synthetic lethal candidate partners for *CDH1* were identified at both the gene and pathway level. SLIPT gene candidates were analysed by cluster analysis for common expression profiles across samples and relationships with clinical factors and mutations in key breast cancer genes. These genes were also compared to the gene candidates from primary and secondary (validation) screens conducted by Telford *et al.* (2015) on isogenic cell lines. For comparison, the SLIPT methodology was also applied using mutation data for *CDH1* against expression of candidate partners (as described in Section 3.1) which may better represent the null mutations in HDGC patients and the experimental cell model (Chen *et al.*, 2014). Pathways were analysed by overrepresentation analysis (with resampling for comparisons with siRNA data) and supported by a metagene analysis of pathways gene signatures. The pathways metagene

expression profiles were used to replicate known relationships between clinical and molecular characteristics for breast cancer and to demonstrate application of SLIPT directly on metagenes to detect synthetic lethal pathways.

4.1 Synthetic Lethal Genes in Breast Cancer

The SLIPT methodology (as described in Section 3.1) was applied to the normalised TCGA breast cancer gene expression dataset ($n = 1168$). As shown in Table 4.1, the most significant genes had strong evidence of expression-based association with *CDH1* (high χ^2 values) with fewer samples exhibiting low expression of both genes than expected statistically. Eukaryotic translation genes were among the highest scoring gene candidates, including initiation factors, elongation factors, and ribosomal proteins. These are clearly necessary for cancer cells to grow and proliferate, with sustained gene expression needed to maintain growth signalling pathways and resist apoptosis or immune factors, translation genes may be subject to non-oncogene addiction for *CDH1*-deficient cells.

While these are among the strongest synthetic lethal candidates, translational genes are **crucial** to the viability of healthy cells and dosing for a selective synthetic lethal effect against these may be difficult compared to other biological functions which may also be supported among the SLIPT candidate genes. Furthermore, few known biological functions of *CDH1* were among the strongest SL candidates, so the remaining candidate genes may also be informative since they are likely to contain these expected functions in addition to novel relationships for *CDH1*. Thus further pathway level analyses were also conducted to examine biological functions over-represented among synthetic candidate genes and to identify synthetic lethal pathways.

The modified mtSLIPT methodology (as described in Section 3.1) was also applied to the normalised TCGA breast cancer gene expression dataset, against somatic loss of function mutations in *CDH1*. As shown in Table 4.2, the most significant genes also had strong evidence of expression associated with *CDH1* mutations (high χ^2 values) with fewer samples with *CDH1* exhibiting low expression each candidate gene than expected statistically. These genes were not as strongly supported as the expression analysis (in Table 4.1), however, nor were as many genes detected. This is perhaps unsurprising due to the lower sample size with matching somatic mutation data and the lower frequency of *CDH1* mutations compared to low expression defined by $1/3$ quantiles.

Table 4.1: Candidate synthetic lethal gene partners of *CDH1* from SLIPT

Gene	Observed*	Expected*	χ^2 value	p-value	p-value (FDR)
<i>TRIP10</i>	62	130	162	5.65×10^{-34}	1.84×10^{-31}
<i>EEF1B2</i>	56	130	158	3.10×10^{-33}	9.45×10^{-31}
<i>GBGT1</i>	61	131	156	1.08×10^{-32}	3.14×10^{-30}
<i>ELN</i>	81	130	149	3.46×10^{-31}	8.82×10^{-29}
<i>TSPAN4</i>	78	130	146	1.63×10^{-30}	3.79×10^{-28}
<i>GLIPR2</i>	72	130	146	1.68×10^{-30}	3.86×10^{-28}
<i>RPS20</i>	73	131	145	1.89×10^{-30}	4.28×10^{-28}
<i>RPS27A</i>	80	130	143	5.53×10^{-30}	1.18×10^{-27}
<i>EEF1A1P9</i>	63	130	141	1.91×10^{-29}	3.74×10^{-27}
<i>C1R</i>	73	130	141	2.05×10^{-29}	3.97×10^{-27}
<i>LYL1</i>	73	130	140	2.99×10^{-29}	5.74×10^{-27}
<i>RPLP2</i>	71	130	139	4.88×10^{-29}	9.07×10^{-27}
<i>C10orf10</i>	73	130	138	6.72×10^{-29}	1.20×10^{-26}
<i>DULLARD</i>	74	131	138	9.29×10^{-29}	1.61×10^{-26}
<i>PPM1F</i>	64	130	136	1.61×10^{-28}	2.65×10^{-26}
<i>OBFC2A</i>	69	130	136	2.49×10^{-28}	3.93×10^{-26}
<i>RPL11</i>	70	130	136	2.56×10^{-28}	3.97×10^{-26}
<i>RPL18A</i>	70	130	135	3.08×10^{-28}	4.70×10^{-26}
<i>MFNG</i>	76	131	133	7.73×10^{-28}	1.12×10^{-25}
<i>RPS17</i>	77	131	133	8.94×10^{-28}	1.29×10^{-25}
<i>MGAT1</i>	73	130	132	1.44×10^{-27}	2.03×10^{-25}
<i>RPS12</i>	72	130	128	8.57×10^{-27}	1.12×10^{-24}
<i>C10orf54</i>	73	130	127	1.37×10^{-26}	1.75×10^{-24}
<i>LOC286367</i>	72	130	126	2.20×10^{-26}	2.70×10^{-24}
<i>GMFG</i>	70	130	126	2.20×10^{-26}	2.70×10^{-24}

Strongest candidate synthetic lethal partners for *CDH1* of 5165 genes detected by SLIPT in TCGA breast cancer expression data

* Observed and expected numbers of samples which had low expression of both genes

The mtSLIPT candidates had more genes involved in cell and gene regulation, particularly DNA and RNA binding factors. The strongest candidates also included microtubule (*KIF12*), microfibril (*MFAP4*), and cell adhesion (*TENC1*) genes consistent with the established cytoskeletal role of *CDH1*. The elastin gene (*ELN*) was notably strongly supported by both expression and mutation SLIPT analysis of *CDH1* supporting interactions with extracellular proteins and the tumour microenvironment.

4.1.1 Synthetic Lethal Pathways in Breast Cancer

Translational pathways were strongly over-represented in SLIPT partners, as shown in Table 4.3. These include ribosomal subunits, initiation, peptide elongation, and

Table 4.2: Candidate synthetic lethal gene partners of *CDH1* from mtSLIPT

Gene	Observed*	Expected*	χ^2 value	p-value	p-value (FDR)
<i>TFAP2B</i>	8	36.7	89.5	3.60×10^{-20}	8.37×10^{-17}
<i>ZNF423</i>	15	36.7	78.8	7.89×10^{-18}	1.22×10^{-14}
<i>CALCOCO1</i>	11	36.7	76.8	2.09×10^{-17}	2.59×10^{-14}
<i>RBM5</i>	13	36.7	75.7	3.65×10^{-17}	4.00×10^{-14}
<i>BTG2</i>	7	36.7	71.7	2.72×10^{-16}	1.81×10^{-13}
<i>RXRA</i>	6	36.7	70.5	5.00×10^{-16}	2.97×10^{-13}
<i>SLC27A1</i>	11	36.7	70.3	5.42×10^{-16}	2.97×10^{-13}
<i>MEF2D</i>	12	36.7	69.6	7.86×10^{-16}	3.95×10^{-13}
<i>NISCH</i>	12	36.7	69.6	7.86×10^{-16}	3.95×10^{-13}
<i>AVPR2</i>	9	36.7	69.2	9.36×10^{-16}	4.58×10^{-13}
<i>CRY2</i>	13	36.7	68.9	1.07×10^{-15}	4.98×10^{-13}
<i>RAPGEF3</i>	13	36.7	68.9	1.07×10^{-15}	4.98×10^{-13}
<i>NRIP2</i>	10	36.7	68.2	1.58×10^{-15}	7.18×10^{-13}
<i>DARC</i>	12	36.7	66.4	3.76×10^{-15}	1.54×10^{-12}
<i>SFRS5</i>	12	36.7	66.4	3.76×10^{-15}	1.54×10^{-12}
<i>NOSTRIN</i>	5	36.7	65.1	7.40×10^{-15}	2.70×10^{-12}
<i>KIF13B</i>	12	36.7	63.4	1.69×10^{-14}	5.16×10^{-12}
<i>TENC1</i>	10	36.7	62.5	2.67×10^{-14}	7.40×10^{-12}
<i>MFAP4</i>	12	36.7	60.5	7.17×10^{-14}	1.67×10^{-11}
<i>ELN</i>	13	36.7	59.7	1.07×10^{-13}	2.32×10^{-11}
<i>SGK223</i>	14	36.7	59	1.51×10^{-13}	3.05×10^{-11}
<i>KIF12</i>	11	36.7	58.8	1.74×10^{-13}	3.34×10^{-11}
<i>SELP</i>	11	36.7	58.8	1.74×10^{-13}	3.34×10^{-11}
<i>CIRBP</i>	9	36.7	58.7	1.83×10^{-13}	3.41×10^{-11}
<i>CTDSP1</i>	9	36.7	58.7	1.83×10^{-13}	3.41×10^{-11}

Strongest candidate synthetic lethal partners for *CDH1* of 3743 genes detected by mtSLIPT in TCGA in breast cancer expression and mutation data

* Observed and expected numbers of *CDH1* mutant TCGA breast tumours with low expression of partner genes

termination. Regulatory processes involving mRNA including 3' untranslated region (UTR) binding, L13a-mediated translational silencing, and nonsense-mediated decay were also implicated. These are consistent with protein translation being subject to “non-oncogene addiction” (Luo *et al.*, 2009), as a core process that is dysregulated to sustain cancer proliferation and survival (Gao and Roux, 2015).

Immune pathways, including the adaptive immune system and responses to infectious diseases were also strongly implicated as synthetic lethal with loss of E-cadherin. This is consistent with the alterations of immune response being a hallmark of cancer Hanahan and Weinberg (2000), since evading the immune system is necessary for cancer

survival. Either of these systems are potential means to target *CDH1*-deficient cells, although these were not detected in an isolated cell line experimental screen (Telford *et al.*, 2015) and the differences between the findings in patient data are described in more detail in Section 4.2.5.

Table 4.3: Pathways for *CDH1* partners from SLIPT

Pathways Over-represented	Pathway Size	SL Genes	p-value (FDR)
Eukaryotic Translation Elongation	86	81	1.3×10^{-207}
Peptide chain elongation	83	78	5.6×10^{-201}
Eukaryotic Translation Termination	83	77	1.2×10^{-196}
Viral mRNA Translation	81	76	1.2×10^{-196}
Formation of a pool of free 40S subunits	93	81	3.7×10^{-194}
Nonsense Mediated Decay independent of the Exon Junction Complex	88	77	5.3×10^{-187}
L13a-mediated translational silencing of Ceruloplasmin expression	103	82	9.6×10^{-183}
3' -UTR-mediated translational regulation	103	82	9.6×10^{-183}
GTP hydrolysis and joining of the 60S ribosomal subunit	104	82	1.9×10^{-181}
Nonsense-Mediated Decay	103	80	6.2×10^{-176}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	103	80	6.2×10^{-176}
Adaptive Immune System	412	167	6.5×10^{-174}
Eukaryotic Translation Initiation	111	82	5.7×10^{-173}
Cap-dependent Translation Initiation	111	82	5.7×10^{-173}
SRP-dependent cotranslational protein targeting to membrane	104	79	2.0×10^{-171}
Translation	141	91	6.1×10^{-170}
Infectious disease	347	146	1.6×10^{-166}
Influenza Infection	117	81	1.9×10^{-163}
Influenza Viral RNA Transcription and Replication	108	77	1.9×10^{-160}
Influenza Life Cycle	112	77	2.5×10^{-156}

Gene set over-representation analysis (hypergeometric test) for Reactome pathways in SLIPT partners for *CDH1*.

It is also notable that the pathways over-represented in SLIPT candidate genes have strongly significant over-representation of Reactome pathways based on the hypergeometric test (as described in Section 2.3.2). Even after adjusting stringently for multiple testing, biologically related pathways were supported together. These pathways are further supported by testing for synthetic lethality against *CDH1* mutations (mtSLIPT) with many of these pathways also among the most strongly supported in this analysis (shown in Appendix Table C.1). This mutation-based analysis more closely represents the null *CDH1* mutations in HDGC (Guilford *et al.*, 1998) and the experimental MCF10A cell model (Chen *et al.*, 2014). There was still support for translational and immune pathways not detected in the isolated experimental system. GPCRs also among the most strongly supported pathways, supporting the experimental findings of Telford *et al.* (2015) for these intracellular signalling pathways already being targeted for other diseases.

4.1.2 Expression Profiles of Synthetic Lethal Partners

Due to the sheer number of gene candidates (e.g., 5165 for SLIPT), investigations proceeded into correlation structure and pathways over-representation. These analyses also examined expression patterns of synthetic lethal gene candidates. This serves to explore the functional similarity of the synthetic lethal partners of *CDH1*, with the eventual aim to assess their utility as drug targets. As shown in Figure 4.1 (which clusters *CDH1* lowly expressing samples separately), there were several large clusters of genes among the expression profiles of the *CDH1* synthetic lethal candidate partners. The clustering suggests co-regulation of genes or pathways correlation between partner gene candidates. A number of candidates from an experimental RNAi screen study performed by Telford *et al.* (2015) were also identified by this approach. In addition, novel gene candidates were also identified, which had not been observed to affect viability in isogenic cell line experiments.

In these expression profiles, a gene with a moderate or high signal across samples exhibiting low *CDH1* expression would represent a potential drug target. However, it appears that several molecular subtypes of cancer have elevation of different clusters of synthetic lethal candidates in samples with low *CDH1*. This clustering suggests that different targets (or combinations) could be effective in different patients, suggesting potential utility for stratification. In particular, ER negative, basal-like subtype, and “normal-like” tumours (Dai *et al.*, 2015; Eroles *et al.*, 2012; Parker *et al.*, 2009) have elevation of genes specific to particular clusters, indicative of some synthetic lethal interactions being specific to a particular molecular subtype or genetic background. Thus synthetic lethal drug therapy against these subtypes may be ineffective if it were designed against genes in another cluster.

A similar correlation structure was observed among the candidates tested against *CDH1* mutation (mtSLIPT), as shown in Appendix Figure C.1. This clustering analysis similarly identified several major clusters of putative synthetic lethal partner genes. In this case, many partner genes had consistently high expression across most of the (predominantly lobular subtype) *CDH1* breast cancer samples. However, a major exception to this in the *CDH1* expression analysis were the normal tissue samples which were excluded from the mutation data (as they were not tested for tumour-specific genotypes). This supports synthetic lethal interventions being more applicable to *CDH1* mutant tumours. There was still considerable correlation structure, particularly among *CDH1* wild-type samples, sufficient to distinguish gene clusters. In contrast, the predominantly ductal *CDH1* wild-type basal-like subtype and ER negative samples had

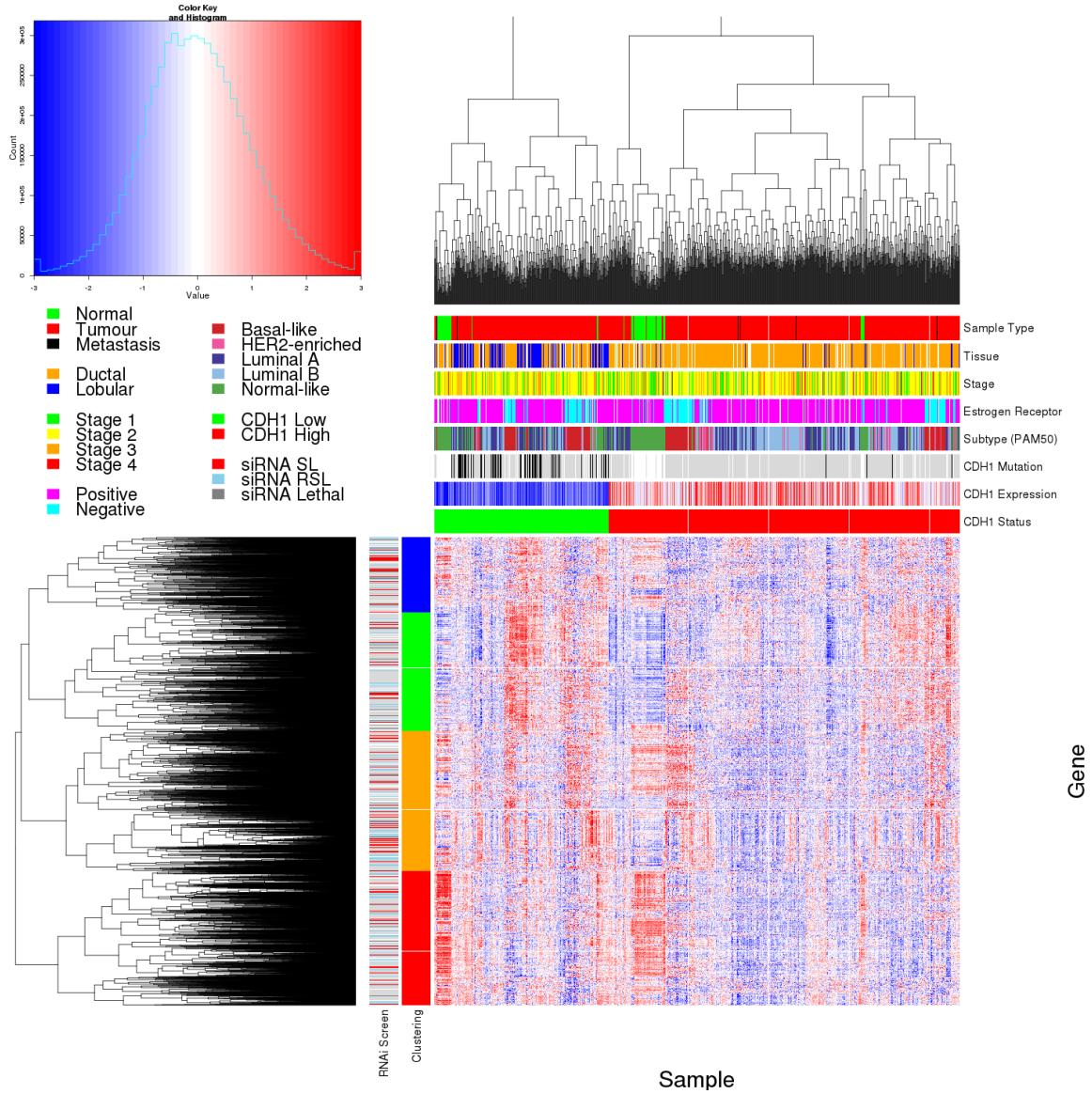


Figure 4.1: Synthetic lethal expression profiles of analysed samples. Gene expression profile heatmap (correlation distance, complete linkage) of all samples (separated by the 1/3 quantile of *CDH1* expression) analysed in TCGA breast cancer dataset for gene expression of 5165 candidate partners of E-cadherin (*CDH1*) from SLIPT prediction (with FDR adjusted $p < 0.05$). Deeply clustered, inter-correlated genes form several main groups, each containing genes that were SL candidates or lethal in an siRNA screen (Telford *et al.*, 2015). Screen results for synthetic lethal (SL), the reverse effect (RSL), or lethal cell viability are shown as reported by Telford *et al.* (2015). Clusters had different sample groups highly expressing the synthetic lethal candidates in *CDH1* low samples, notably ‘normal-like’, ‘basal-like’, and Estrogen receptor (ER) negative samples have elevated expression in one or more distinct clusters showing complexity and variation among candidate synthetic lethal partners. *CDH1* low samples also contained most of samples with *CDH1* mutations (shown in black). Negative values for mutation and screen data are shown in light grey, with missing data in white.

depleted expression among most candidate synthetic lethal partners. This is consistent with synthetic lethal interventions only being effective in lobular ER positive breast cancers in which they are a more common, as recurrent (driver) mutation. However, the remaining samples are still informative for synthetic lethal analysis (by SLIPT) as it requires highly expressing *CDH1* samples for comparison.

The *CDH1* mutant samples (as shown in Figure 4.1) were predominantly among the low *CDH1* expressing samples, clustering throughout them with similar expression profiles to other samples exhibiting low *CDH1* expression. Thus the molecular profiles of *CDH1* low samples were indistinguishable from *CDH1* mutant samples, with the exception of normal samples (that do not have somatic mutation data available). Many of the *CDH1* mutant samples (in Appendix Figure C.1) had among the lowest *CDH1* expression, and some of the synthetic lethal partners were also highly expressed in low expressing *CDH1* wild-type samples, despite these not being considered as “inactivated” by mtSLIPT analysis.

Together these results support the use of low *CDH1* expression as a strategy for detecting *CDH1* inactivation. This has the benefit of increasing sample size (including samples such as normal tissue which do not have somatic mutation data available) and increasing the expected number of mutually inactive (low-low) samples for the directional criteria of (mt)SLIPT which enables it to better distinguish significant deviations below this (as discussed in Section 6.1). This also circumvents the assumption that all (detected) mutations are inactivating (although synonymous mutations were excluded from the analysis), which may not be the case for several highly expressing *CDH1* mutant samples that do not cluster together in Figure 4.1 or Appendix Figure C.1. One of these exhibits among the lowest expression for many predicted synthetic lethal partners and would not be vulnerable to inactivation of these genes. As such, correctly genotyping inactivating mutations will be essential in clinical practice for synthetic lethal targeting of tumour suppressor genes, particularly for other genes such as *TP53* where oncogenic and tumour suppressor mutations (with different molecular consequences) are both common. Using expression as a measure of gene function also avoids the assumption that mutations are somatic, rather than germline, and that gene inactivation occurs by detectable mutations, rather than other mechanisms, such as epigenetic changes. These factors may also account for some of the lowly expressing *CDH1* wild-type samples clustering with similar profiles to mutant samples.

Table 4.4: Pathways for clusters of *CDH1* partners from SLIPT

Pathways Over-represented in Cluster 1	Pathway Size	Cluster Genes	p-value (FDR)
Collagen formation	67	10	4.0×10^{-11}
Extracellular matrix organisation	238	21	1.8×10^{-9}
Collagen biosynthesis and modifying enzymes	56	8	1.8×10^{-9}
Uptake and actions of bacterial toxins	22	5	9.5×10^{-9}
Elastic fibre formation	37	6	1.9×10^{-8}
Muscle contraction	62	7	2.4×10^{-7}
Fatty acid, triacylglycerol, and ketone body metabolism	117	10	4.9×10^{-7}
XBP1(S) activates chaperone genes	51	6	6.6×10^{-7}
IRE1alpha activates chaperones	54	6	1.2×10^{-6}
Neurotoxicity of clostridium toxins	10	3	1.3×10^{-6}
Retrograde neurotrophin signalling	10	3	1.3×10^{-6}
Assembly of collagen fibrils and other multimeric structures	40	5	1.9×10^{-6}
Collagen degradation	58	6	2.0×10^{-6}
Arachidonic acid metabolism	41	5	2.1×10^{-6}
Synthesis of PA	26	4	3.0×10^{-6}
Signalling by NOTCH	80	7	3.3×10^{-6}
Signalling to RAS	27	4	3.7×10^{-6}
Integrin cell surface interactions	82	7	4.2×10^{-6}

Pathways Over-represented in Cluster 2	Pathway Size	Cluster Genes	p-value (FDR)
Eukaryotic Translation Elongation	86	75	1.1×10^{-181}
Viral mRNA Translation	81	72	9.8×10^{-179}
Peptide chain elongation	83	72	1.9×10^{-175}
Eukaryotic Translation Termination	83	72	1.9×10^{-175}
Formation of a pool of free 40S subunits	93	75	1.9×10^{-171}
Nonsense Mediated Decay independent of the Exon Junction Complex	88	72	9.9×10^{-168}
L13a-mediated translational silencing of Ceruloplasmin expression	103	75	3.0×10^{-159}
3' -UTR-mediated translational regulation	103	75	3.0×10^{-159}
Nonsense-Mediated Decay	103	75	3.0×10^{-159}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	103	75	3.0×10^{-159}
SRP-dependent cotranslational protein targeting to membrane	104	75	3.2×10^{-158}
GTP hydrolysis and joining of the 60S ribosomal subunit	104	75	3.2×10^{-158}
Eukaryotic Translation Initiation	111	75	4.5×10^{-151}
Cap-dependent Translation Initiation	111	75	4.5×10^{-151}
Influenza Infection	117	75	1.4×10^{-145}
Influenza Viral RNA Transcription and Replication	108	72	5.7×10^{-145}
Translation	141	81	8.0×10^{-143}
Influenza Life Cycle	112	72	2.3×10^{-141}

Pathways Over-represented in Cluster 3	Pathway Size	Cluster Genes	p-value (FDR)
Adaptive Immune System	412	90	6.1×10^{-61}
Chemokine receptors bind chemokines	52	27	6.7×10^{-56}
Generation of second messenger molecules	29	21	6.5×10^{-55}
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	64	29	6.5×10^{-55}
TCR signalling	62	27	8.9×10^{-51}
Peptide ligand-binding receptors	161	40	1.5×10^{-45}
Translocation of ZAP-70 to Immunological synapse	16	14	3.1×10^{-43}
Costimulation by the CD28 family	51	22	4.0×10^{-43}
PD-1 signalling	21	15	4.0×10^{-41}
Class A/1 (Rhodopsin-like receptors)	258	50	6.7×10^{-41}
Phosphorylation of CD3 and TCR zeta chains	18	14	1.3×10^{-40}
Interferon gamma signalling	74	24	5.0×10^{-39}
GPCR ligand binding	326	57	1.8×10^{-38}
Cytokine Signalling in Immune system	268	48	8.9×10^{-37}
Downstream TCR signalling	45	18	1.8×10^{-35}
G _{αi} signalling events	167	33	2.2×10^{-33}
Cell surface interactions at the vascular wall	99	21	1.3×10^{-26}
Interferon Signalling	164	28	1.7×10^{-26}

Table 4.4: Pathways for clusters of *CDH1* partners from SLIPT

Pathways Over-represented in Cluster 4	Pathway Size	Cluster Genes	p-value (FDR)
Extracellular matrix organisation	238	48	8.0×10^{-41}
Class A/1 (Rhodopsin-like receptors)	258	47	2.8×10^{-36}
GPCR ligand binding	326	54	2.1×10^{-34}
G _{αs} signalling events	83	22	1.4×10^{-31}
GPCR downstream signalling	472	68	1.1×10^{-29}
Haemostasis	423	61	3.3×10^{-29}
Platelet activation, signalling and aggregation	180	31	7.1×10^{-28}
Binding and Uptake of Ligands by Scavenger Receptors	40	14	9.9×10^{-27}
RA biosynthesis pathways	22	11	2.5×10^{-26}
Response to elevated platelet cytosolic Ca ²⁺	82	19	3.0×10^{-26}
Developmental Biology	420	57	3.5×10^{-26}
G _{αi} signalling events	167	28	7.3×10^{-26}
Platelet degranulation	77	18	1.6×10^{-25}
Gastrin-CREB signalling pathways via PKC and MAPK	171	28	2.5×10^{-25}
Muscle contraction	62	16	4.7×10^{-25}
G _{αq} signalling events	150	25	3.2×10^{-24}
Retinoid metabolism and transport	34	12	5.0×10^{-24}
Phase 1 - Functionalisation of compounds	67	16	6.5×10^{-24}

Pathway over-representation analysis for Reactome pathways with the number of genes in each pathways (Pathway Size), number of genes within the pathways identified (Cluster Genes), and the pathway over-representation p-value (adjusted by FDR) from the hypergeometric test.

4.1.2.1 Subgroup Pathway Analysis

Synthetic lethal gene candidates for *CDH1* from SLIPT analysis of RNA-Seq gene expression data were also used for pathway over-representation analyses (as described in Section 2.3.2). The correlation structure in the expression of candidates synthetic lethal genes in *CDH1* low tumours (lowest 1/3rd quantile of expression) was examined for distinct biological pathways in subgroups of genes elevated in different clusters of samples. These genes were highly expressed in different samples with their clinical factors including ER status and intrinsic subtypes, from the PAM50 procedure (Parker *et al.*, 2009) shown in Figure 4.1.

As shown by the most over-represented pathways in Table 4.4, each correlated cluster of candidate synthetic lethal partners of *CDH1* contains functionally different genes. Cluster 1 contains genes with less evidence of over-represented pathways than other clusters, corresponding to less correlation between genes within the cluster, and to it being a relatively small group. While there is some indication that collagen biosynthesis, microfibril elastic fibres, extracellular matrix, and metabolic pathways may be over-represented in Cluster 1, these results are mainly based on small pathways containing few synthetic lethal genes. Genes in Cluster 2 exhibited low expression in

normal tissue samples compared to tumour samples (as shown in Figure 4.1) and show compelling evidence of over-representation of post-transcriptional gene regulation and protein translation processes. Similarly, Cluster 3 has over-representation of immune signalling pathways (including chemokines, secondary messenger, and TCR signalling) and downstream intracellular signalling cascades such as GPCR and $G_{\alpha i}$ signalling events. While pathways over-representation was weaker among genes in Cluster 4, they contained intracellular signalling pathways and were highly expressed in normal samples (in contrast to Cluster 2). Cluster 4 also involved extracellular factors and stimuli such as extracellular matrix, platelet activation, ligand receptors, and retinoic acid signalling.

Based on these results, potential synthetic lethal partners of *CDH1* include processes known to be dysregulated in cancer, such as translational, cytoskeletal, and immune processes. Intracellular signalling cascades such as the GPCRs and extracellular stimuli for these pathways were also implicated in potential synthetic lethality with *CDH1*.

Similar translational, cytoskeletal, and immune processes were identified among SLIPT partners with respect to *CDH1* mutation, shown in Appendix Table C.2. While GPCR signalling was replicated in mtSLIPT analysis, there was also stronger over-representation for NOTCH, ERBB2, and PI3K/AKT signalling in mutation analysis consistent with these signals being important for proliferation of *CDH1*-deficient tumours. The GPCR and PI3K/AKT pathways are of particular interest as pathways with oncogenic mutations that can be targeted and downstream effects on translation (a strongly supported process across analyses). Extracellular matrix pathways (e.g., elastic fibre formation) were also supported across analyses (in Table 4.4 and Appendix Table C.2) consistent with the established cell-cell signalling role of *CDH1* and the importance of the tumour microenvironment for cancer proliferation.

4.2 Comparing Synthetic Lethal Gene Candidates

4.2.1 Primary siRNA Screen Candidates

Gene candidates were compared between computational (SLIPT in TCGA breast cancer data) and experimental (the primary siRNA screen performed by Telford *et al.* (2015)) approaches in Figure 4.2. The number of genes detected by both methods did not produce a significant overlap but these may be difficult to compare due to vast differences between the detection methods. There were similar issues in the comparison

of mtSLIPT genes tested against *CDH1* mutations (in Appendix Figure C.2), despite excluding genes not tested by both methods in either test. However, these intersecting genes may still be functionally informative or amenable to drug triage as they were replicated across both methods and pathways over-representation differed between the sections of the Venn diagram (as shown in Figure 4.2).

4.2.2 Comparison with Correlation

Another potential means to triage drug target candidates is by correlation of expression profiles with *CDH1*. Correlation with *CDH1* was compared to SLIPT and siRNA results in Figure 4.3. The genes not detected by SLIPT (including siRNA candidates) included genes with non-significant SLIPT p-values. As expected, these genes were distributed around a correlation of zero. Genes with higher correlation with *CDH1* (either direction) **were more significant**. The majority of SLIPT candidates had negative correlations, particularly genes detected by both approaches, although these were typically weak correlations and are unlikely to be sufficient to detect such genes on their own. This is supported by simulation results in Section 6.1.

There were not **many** strong positive correlations with *CDH1* among siRNA candidates, consistent with previous findings that co-expression was not predictive of synthetic lethality (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015). Negative correlation may not be indicative of synthetic lethality either as many siRNA candidates also had positive **correlation with *CDH1***. The SLIPT methodology has **therefore been** shown to detect genes with both positive and negative correlations, although it does appear to preferentially detect negatively correlated genes to some extent. These findings were replicated with the mtSLIPT approach against *CDH1* mutation (in Appendix Figure C.3), although the range of the χ^2 p-values differs due to lower sample size for mutation analysis.

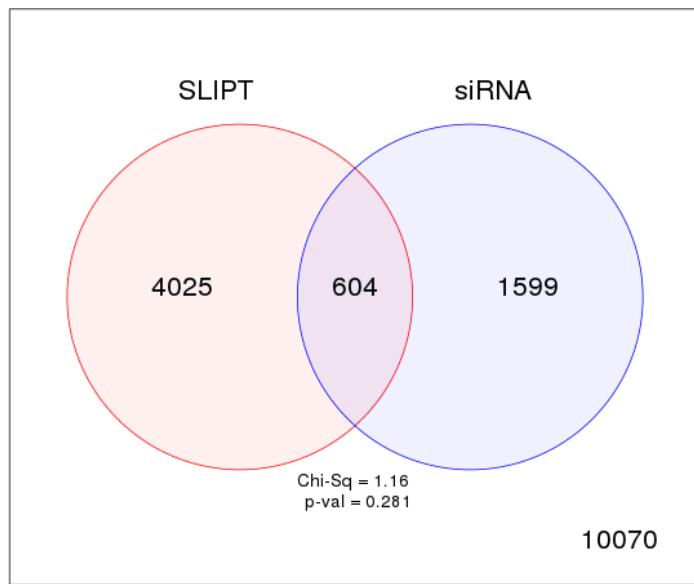


Figure 4.2: Comparison of SLIPT with siRNA. Testing the overlap of gene candidates for E-cadherin synthetic lethal partners between computational (SLIPT) and experimental screening (siRNA) approaches. The χ^2 test suggests that the overlap is no more than would be expected by chance ($p = 0.281$). Only genes tested by both methods were included.

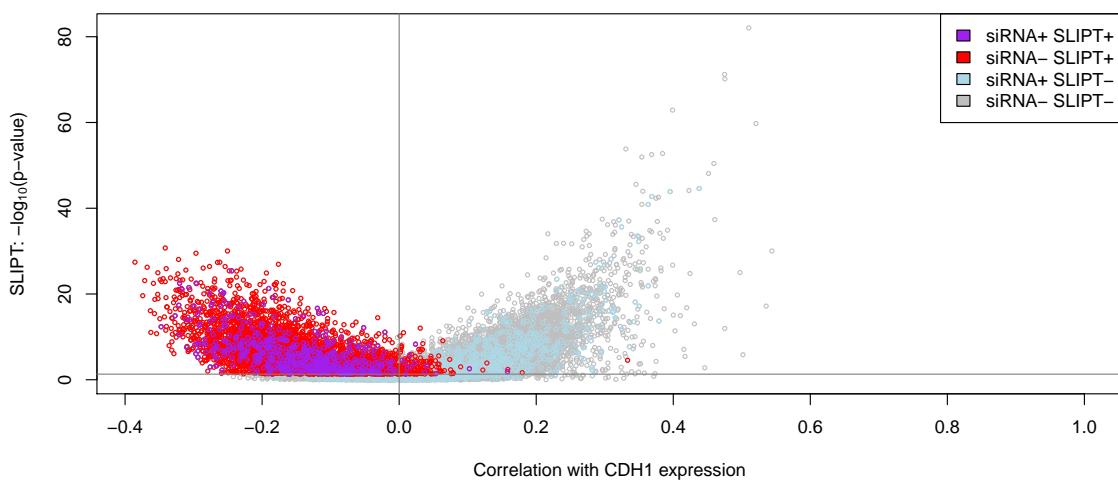


Figure 4.3: Comparison of SLIPT and siRNA genes with correlation. The χ^2 p-values for genes tested by SLIPT (in TCGA breast cancer) expression analysis were compared against Pearson correlation of gene expression with *CDH1*. Genes detected by SLIPT or siRNA are coloured according to the legend.

The apparent tendency for genes detected by SLIPT or siRNA to have negative correlations with *CDH1* expression was not due to the smaller number of genes in these groups. The distribution of *CDH1* correlations differed across these gene groups (as shown by Figure 4.4 and Appendix Figure C.4) and tended to be lower in SLIPT candidates (as supported by analysis of variance (ANOVA) in Table 4.5). However, these are relatively weak correlations and further triage of gene candidates by correlation is not suitable. The genes detected both SLIPT and siRNA did not differ from SLIPT genes and the number of positively correlated SLIPT genes was very small. The use of correlation itself is also less effective than SLIPT to predict synthetic lethal partners in the first place (as shown in Section 6.1.2.1).

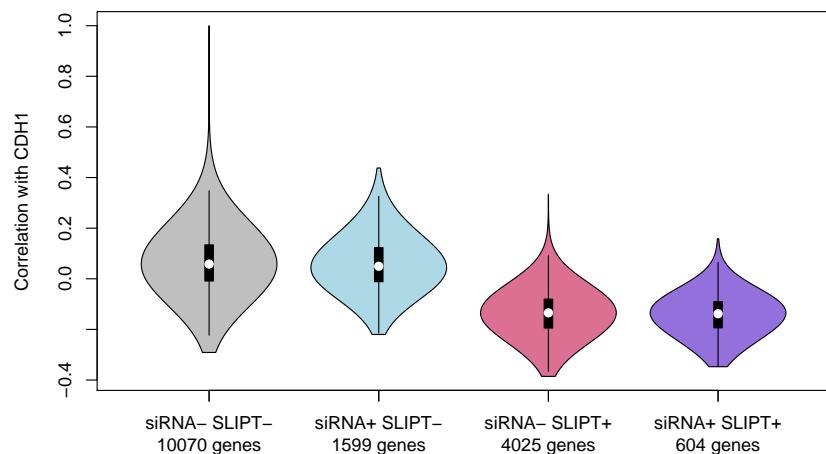


Figure 4.4: Comparison of SLIPT and siRNA genes with correlation. Genes detected as candidate synthetic lethal partners by SLIPT (in TCGA breast cancer) expression analysis and experimental screening (with siRNA) were compared against Pearson correlation of gene expression with *CDH1*. There were significant differences in correlation between gene groups (as shown in Table 4.5).

Table 4.5: ANOVA for synthetic lethality and correlation with *CDH1*

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.027	0.027	2.8209	0.09306
SLIPT	1	134.603	134.603	14115.9824	<0.0001
siRNA×SLIPT	1	0.000	0.000	0.0073	0.93212

Analysis of variance for correlation with *CDH1* against synthetic lethal detection approaches (with an interaction term). Only genes tested by both methods were included in this analysis.

4.2.3 Comparison with Primary Screen Viability

A similar comparison of SLIPT results was made with the viability ratio (*CDH1*^{-/-} mutant to wild-type) of MCF10A cells in the primary siRNA screen performed by Telford *et al.* (2015). The significance and viability thresholds used for SLIPT and siRNA detection of synthetic lethal candidate partners of *CDH1* are shown in Figure 4.5. Not all of the genes below the viability thresholds were necessarily selected to be candidate partners, however, as additional criteria were used in each case: directional criteria as for SLIPT (in Section 3.1) and minimum wild-type viability for siRNA (Telford *et al.*, 2015).

There does not appear to be a clear relationship between SLIPT and siRNA candidates. The genes detected by one approach but not the other were numerous in Figure 4.2 and Appendix Figure C.2. The genes detected by one approach are not necessarily near the thresholds for the other. In this respect, the SLIPT approach with patient data and the siRNA cell line experiments are independent means to identify synthetic lethal candidates. While genes detected by both approaches were not necessarily more strongly supported by either, the genes with a viability closer to 1 (no synthetic lethal effect) in siRNA included those with more significant SLIPT p-values, whereas more extreme viability ratios tended to be less significant (as shown by Figure 4.5). However, it should be noted that genes with more moderate viability ratios were more common and SLIPT was capable (despite adjusting for multiple testing) of detecting significant genes with extreme viability ratios, particularly those considerably lower than 1. Lower viability ratios were used by Telford *et al.* (2015) to detect synthetic lethal candidates in the primary screen. However, there was little support for SLIPT candidates differing with respect to viability ratio (as shown in Figures 4.6 and C.5) and the vast majority of SLIPT candidate genes did not have different viability in the primary screen to genes not identified by SLIPT.

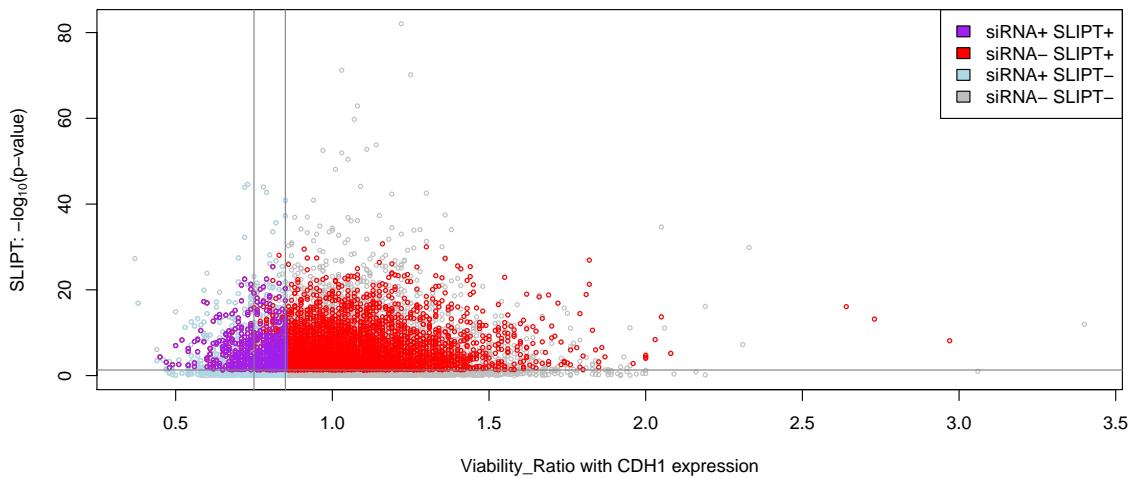


Figure 4.5: Comparison of SLIPT and siRNA genes with screen viability. The χ^2 p-values (log-scale) for genes tested by SLIPT (in TCGA breast cancer) were compared against the viability ratio of *CDH1* mutant and wild-type cells in the primary siRNA screen. Genes detected by SLIPT or siRNA are coloured according to the legend. Lines show the thresholds of significance with SLIPT ($p < 0.05$) and of viability (ratio < 0.75 or < 0.85) used by Telford *et al.* (2015).

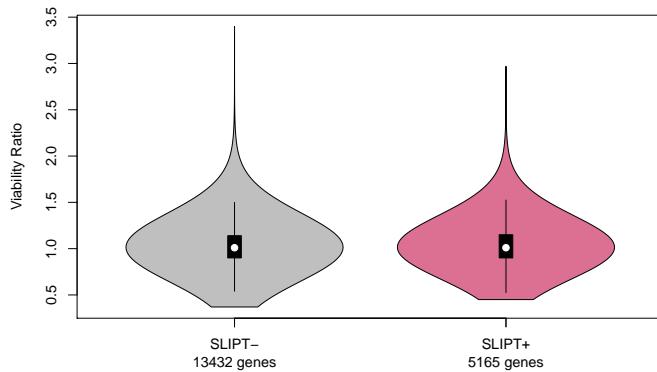


Figure 4.6: Comparison of SLIPT genes with siRNA screen viability. Genes detected as candidate synthetic lethal partners by SLIPT (in TCGA breast cancer) expression analysis were compared against the viability ratio of *CDH1* mutant and wild-type cells in the primary siRNA screen. The genes identified by SLIPT had a higher viability ratio (by t-test: $t = 2.1553$, $p = 0.03117$), although the effect size was relatively small (mean SLIPT- 1.029, mean SLIPT+ 1.037).

4.2.4 Comparison with Secondary siRNA Screen Validation

It should be noted that genes with a lower viability ratio were not necessarily the most strongly supported by experimental screening. The primary screen (with 4 pooled siRNAs for each gene) has been used for the majority of comparisons in this thesis because the genome-wide panel of target genes screened enables a large number of genes to be compared with SLIPT results from gene expression and somatic mutation analysis. A secondary screen was also performed by Telford *et al.* (2015) on the isogenic MCF10A breast cell lines to validate the individual (i.e., non-pooled) siRNAs separately, with the strongest candidates being those exhibiting synthetic lethal viability ratios replicated across independently targeting siRNAs. The strongest candidates from the primary screen were subject to a further secondary screen for validation by independent replication with 4 gene knockdowns with different targeting siRNAs. This was performed for the top 500 candidates (with the lowest viability ratio) from the primary screen: 482 of these genes were also tested by SLIPT in breast cancer.

The secondary screen results show that SLIPT candidate genes were significantly ($p = 7.49 \times 10^{-3}$ by Fisher's exact test) more likely to be validated with detection by more independently targeting siRNAs in the secondary screen. Gene detected by SLIPT are thus informative of more robust partner genes, in addition to providing support that these interactions are consistent with expression profiles from heterogeneous patient samples across genetic backgrounds. As shown in Table 4.6, there is significant association between SLIPT candidates and stronger validations of siRNA candidates. Since there were more SLIPT- genes among those not validated and more SLIPT+ genes among those validated with several siRNAs, this supports the use of SLIPT as a synthetic lethal discovery procedure which may augment such screening experiments.

While the individual genes detected by either approach do not necessarily match (and are potentially false-positives), the biological functions important in *CDH1*-deficient cancers and potential mechanisms for specific targeting of them can be further supported by pathways analysis of the genes detected by either method. The genes detected by both approaches may therefore be more informative at the pathway level, where it is less likely for a pathway to be consistently detected by chance. As the SLIPT candidates differ from the siRNA candidates (in addition to those detected by both approaches which were more likely to be validated), they can provide information about additional mechanisms by which *CDH1*-deficient cancers proliferate, and vulnerabilities that may be exploited against them by using the synthetic lethal pathways.

Table 4.6: Comparison of SLIPT genes against secondary siRNA screen

		Secondary Screen					Total	
		siRNAs*	0/4	1/4	2/4	3/4	4/4	
SLIPT+	Observed	70	46	31	8	2	157	
	Expected	85	44	10	4	2		
SLIPT-	Observed	190	90	31	10	4	325	
	Expected	175	91	42	12	4		
		Total	280	136	52	18	6	482

* Number of siRNAs (targeting the same gene) to successfully reproduce synthetic lethality in MCF10A cells (Telford *et al.*, 2015)

4.2.5 Comparison to Primary Screen at Pathway Level

These pathway over-representation analyses (performed as described in Section 2.3.2) correspond to genes separated into SLIPT or siRNA screen candidates unique to either method, or detected by both (Table 4.7). The SLIPT-specific gene candidates were involved most strongly with translational and immune regulatory pathways, although extracellular matrix pathways were also supported. These pathways were largely consistent with those identified in Table 4.3 and in the clustering analysis (Table 4.4). The genes detected only by the siRNA screen had over-representation of cell signalling pathways, including many containing genes known to be involved in cancer (e.g., MAPK, PDGF, ERBB2, and FGFR), with the detection of Class A GPCRs supporting the independent analyses by Telford *et al.* (2015). The intersection of computational and experimental synthetic lethal partners of *CDH1* had stronger evidence for over-representation of GPCR pathways and more specific subclasses, such as visual phototransduction ($p = 6.9 \times 10^{-10}$) and G_{αs} signalling events ($p = 1.7 \times 10^{-7}$), than other signalling pathways.

The pathways analysis for mtSLIPT against *CDH1* mutations (in Table C.3) had similar results to SLIPT, particularly for mtSLIPT-specific pathways. The specific pathways composition of the intersection of these analyses differed from SLIPT against low *CDH1* expression. However, signalling pathways were also detected, including GPCRs, NOTCH, EERB2, PDGF, and SCF-KIT. These findings indicate the signalling pathways are among the most suitable vulnerability to exploit in targeting *CDH1*-deficient tumours as they can be detected in both a patient cohort (with TCGA

Table 4.7: Pathways for *CDH1* partners from SLIPT and siRNA

Predicted only by SLIPT (4025 genes)	Pathway Size	Genes Identified	p-value (FDR)
Eukaryotic Translation Elongation	80	75	1.5×10^{-182}
Peptide chain elongation	77	72	2.9×10^{-176}
Viral mRNA Translation	75	70	4.9×10^{-172}
Eukaryotic Translation Termination	76	70	5.9×10^{-170}
Formation of a pool of free 40S subunits	87	74	9.5×10^{-166}
Nonsense Mediated Decay independent of the Exon Junction Complex	81	70	1.2×10^{-160}
L13a-mediated translational silencing of Ceruloplasmin expression	97	75	3.8×10^{-155}
3' -UTR-mediated translational regulation	97	75	3.8×10^{-155}
GTP hydrolysis and joining of the 60S ribosomal subunit	98	75	6.0×10^{-154}
Nonsense-Mediated Decay	96	73	5.2×10^{-150}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	96	73	5.2×10^{-150}
SRP-dependent cotranslational protein targeting to membrane	97	73	7.8×10^{-149}
Eukaryotic Translation Initiation	105	75	4.7×10^{-146}
Cap-dependent Translation Initiation	105	75	4.7×10^{-146}
Translation	133	83	4.0×10^{-142}
Influenza Viral RNA Transcription and Replication	102	71	2.9×10^{-137}
Influenza Infection	111	74	3.7×10^{-137}
Influenza Life Cycle	106	71	2.3×10^{-133}
Infectious disease	326	125	4.2×10^{-120}
Extracellular matrix organisation	189	77	5.4×10^{-95}

Detected only by siRNA screen (1599 genes)	Pathway Size	Genes Identified	p-value (FDR)
Class A/1 (Rhodopsin-like receptors)	282	44	1.3×10^{-27}
GPCR ligand binding	363	52	5.8×10^{-26}
$G_{\alpha q}$ signalling events	159	26	6.7×10^{-23}
Gastrin-CREB signalling pathways via PKC and MAPK	180	27	2.0×10^{-21}
$G_{\alpha i}$ signalling events	184	27	5.3×10^{-21}
Downstream signal transduction	146	23	7.6×10^{-21}
Signalling by PDGF	172	25	4.0×10^{-20}
Peptide ligand-binding receptors	175	25	8.5×10^{-20}
Signalling by ERBB2	146	22	1.3×10^{-19}
DAP12 interactions	159	23	2.6×10^{-19}
DAP12 signalling	149	22	2.7×10^{-19}
Organelle biogenesis and maintenance	264	33	5.5×10^{-19}
Signalling by NGF	266	33	8.2×10^{-19}
Downstream signalling of activated FGFR1	134	20	1.1×10^{-18}
Downstream signalling of activated FGFR2	134	20	1.1×10^{-18}
Downstream signalling of activated FGFR3	134	20	1.1×10^{-18}
Downstream signalling of activated FGFR4	134	20	1.1×10^{-18}
Signalling by FGFR	146	21	1.3×10^{-18}
Signalling by FGFR1	146	21	1.3×10^{-18}
Signalling by FGFR2	146	21	1.3×10^{-18}

Intersection of SLIPT and siRNA screen (604 genes)	Pathway Size	Genes Identified	p-value (FDR)
Visual phototransduction	54	9	6.9×10^{-10}
$G_{\alpha s}$ signalling events	48	7	1.6×10^{-7}
Retinoid metabolism and transport	24	5	1.7×10^{-7}
Acyl chain remodelling of PS	10	3	6.5×10^{-6}
Transcriptional regulation of white adipocyte differentiation	51	6	6.5×10^{-6}
Chemokine receptors bind chemokines	22	4	6.5×10^{-6}
Signalling by NOTCH4	11	3	6.9×10^{-6}
Defective EXT2 causes exostoses 2	11	3	6.9×10^{-6}
Defective EXT1 causes exostoses 1, TRPS2 and CHDS	11	3	6.9×10^{-6}
Platelet activation, signalling and aggregation	146	12	6.9×10^{-6}
Phase 1 - Functionalisation of compounds	41	5	1.3×10^{-5}
Amine ligand-binding receptors	13	3	1.7×10^{-5}
Acyl chain remodelling of PE	14	3	2.4×10^{-5}
Signalling by GPCR	300	23	2.4×10^{-5}
Molecules associated with elastic fibres	29	4	2.6×10^{-5}
DAP12 interactions	128	10	2.6×10^{-5}
Cytochrome P ₄₅₀ - arranged by substrate type	30	4	3.2×10^{-5}
GPCR ligand binding	147	11	3.8×10^{-5}
Acyl chain remodelling of PC	16	3	4.0×10^{-5}
Response to elevated platelet cytosolic Ca ²⁺	66	6	4.2×10^{-5}

expression data) and experimentally tested by inhibition with siRNA or drugs (Telford *et al.*, 2015). However, it is possible that the siRNA screen, that was conducted in an isolated experimental system of MCF10A cell lines, was pre-disposed to preferentially detect kinase signalling pathways (which are amenable to pharmacological inhibition and clinical application). Nevertheless, the other pathways identified by SLIPT may still be informative of the role of *CDH1* loss of function in cancers or mechanisms by which further gene loss leads to specific inviability.

4.2.5.1 Resampling Genes for Pathway Enrichment

A high number of significantly over-represented pathways were detected between SLIPT in TCGA expression data and siRNA genes despite relatively few genes being detected by both approaches. These strongly supported pathways are not unexpected, since synthetic lethal pathways are more robustly conserved (Dixon *et al.*, 2008) and the computational approach using patient samples from complex tumour micro-environment has considerably different strengths to an experimental screen (Telford *et al.*, 2015) based on genetically homogenous cell line models in an isolated laboratory environment. For instance, it is unlikely for immune signalling to be detected in an isolated cell culture system.

While many pathways were highly over-represented in the genes detected by both SLIPT and siRNA, some of these pathways were also highly over-represented in the siRNA candidate genes and these may not reflect the results of SLIPT in expression data. A resampling approach (as described in Section 2.3.6) was used to assess whether SLIPT and the siRNA candidate genes had more frequently over-represented pathways than expected by chance. This resampling procedure tests whether pathways were over-represented in the genes detected by both approaches beyond that expected from any subset of siRNA candidates. Thus resampling can determine whether SLIPT independently supports these putative synthetic lethal pathways (without assuming an underlying test statistic distribution).

A resampling approach is also applicable to testing whether the number of genes detected by each approach significantly intersected. As shown in Figure 4.7, resampling did not find evidence of significant depletion or over-representation for experimental synthetic lethal candidate genes in the computationally predicted synthetic lethal partners of *CDH1*, and thus the observed overlap may be due to chance. This is consistent with previous findings (as shown in Figure 4.2) and does not preclude pathways relationships being supported by resampling.

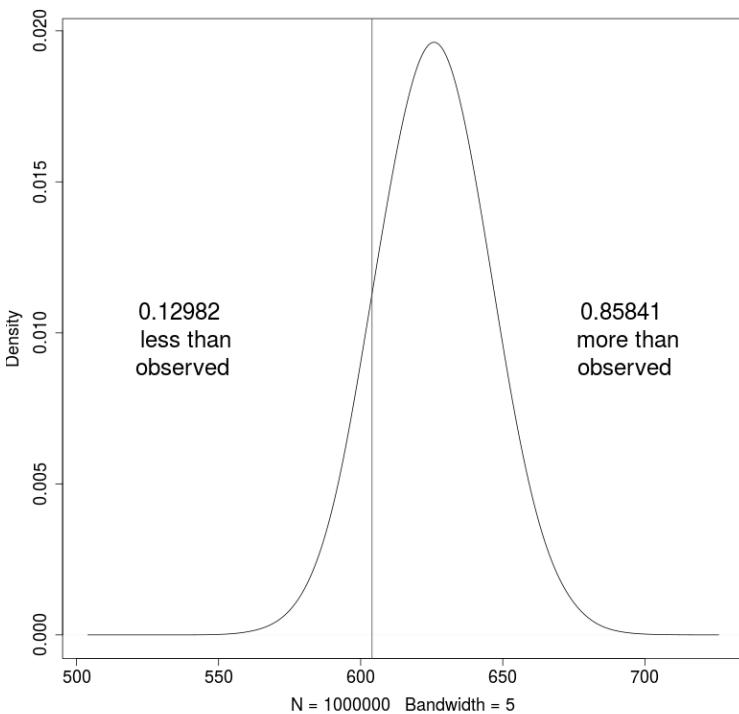


Figure 4.7: Resampled intersection of SLIPT and siRNA candidate genes. Resampling analysis of intersect size from genes detected by SLIPT and siRNA screening approaches over 1 million replicates. The proportion of expected intersection sizes for random samples below or above the observed intersection size respectively, lacking significant over-representation or depletion of siRNA screen candidates within the SLIPT predictions for *CDH1*.

A permutation analysis was performed to resample the genes tested by both approaches to investigate whether the observed pathways over-representation could have occurred in a randomly selected sample of genes from the experimental candidates, that is, whether the pathways predictions from SLIPT could be expected by chance (as described in Sections 2.2.4 and 2.3.6). While the number of siRNA candidate genes also detected by SLIPT was not statistically significant ($p = 0.281$), this may be due to the vastly different limitations of the approaches and the correlation structure of gene expression not being independent (as assumed for multiple testing procedures). The intersection may still be functionally relevant to *CDH1*-deficient cancers, such as the pathways data in Table 4.7. The resampling analysis for pathways was compared to the pathways over-representation for SLIPT predicted synthetic lethal partners in Table 4.8. Similarly, the pathways resampling for intersection between SLIPT predictions

and experimental screen candidates was compared to pathways over-representation in Table 4.9 for intersection with siRNA data.

The pathways resampling approach for SLIPT-specific gene candidates (Table 4.8) largely recapitulates the parametric gene set over-representation analysis for all SLIPT genes, detecting evidence of synthetic lethal pathways for *CDH1* in translational, immune, and cell signalling pathways including $G_{\alpha i}$ signalling, GPCR downstream signalling, and chemokine receptor binding. While the immune and signal transduction pathways were not significantly over-represented in the resampling analysis, the results for the two approaches were largely consistent for translation and post-transcriptional gene regulation, supporting gene set over-representation of the SLIPT-specific pathways

Table 4.8: Pathways for *CDH1* partners from SLIPT

Reactome Pathway	Over-representation	Permutation
Eukaryotic Translation Elongation	1.3×10^{-207}	$< 1.241 \times 10^{-5}$
Peptide chain elongation	5.6×10^{-201}	$< 1.241 \times 10^{-5}$
Viral mRNA Translation	1.2×10^{-196}	$< 1.241 \times 10^{-5}$
Eukaryotic Translation Termination	1.2×10^{-196}	$< 1.241 \times 10^{-5}$
Formation of a pool of free 40S subunits	3.7×10^{-194}	$< 1.241 \times 10^{-5}$
Nonsense Mediated Decay independent of the Exon Junction Complex	5.3×10^{-187}	$< 1.241 \times 10^{-5}$
L13a-mediated translational silencing of Ceruloplasmin expression	9.6×10^{-183}	$< 1.241 \times 10^{-5}$
3' -UTR-mediated translational regulation	9.6×10^{-183}	$< 1.241 \times 10^{-5}$
GTP hydrolysis and joining of the 60S ribosomal subunit	1.9×10^{-181}	$< 1.241 \times 10^{-5}$
Nonsense-Mediated Decay	6.2×10^{-176}	$< 1.241 \times 10^{-5}$
Nonsense Mediated Decay enhanced by the Exon Junction Complex	6.2×10^{-176}	$< 1.241 \times 10^{-5}$
Adaptive Immune System	6.5×10^{-174}	0.15753
Eukaryotic Translation Initiation	5.7×10^{-173}	$< 1.241 \times 10^{-5}$
Cap-dependent Translation Initiation	5.7×10^{-173}	$< 1.241 \times 10^{-5}$
SRP-dependent cotranslational protein targeting to membrane	2.0×10^{-171}	$< 1.241 \times 10^{-5}$
Translation	6.1×10^{-170}	$< 1.241 \times 10^{-5}$
Infectious disease	1.6×10^{-166}	0.23231
Influenza Infection	1.9×10^{-163}	$< 1.241 \times 10^{-5}$
Influenza Viral RNA Transcription and Replication	1.9×10^{-160}	$< 1.241 \times 10^{-5}$
Influenza Life Cycle	2.5×10^{-156}	$< 1.241 \times 10^{-5}$
<i>Extracellular matrix organisation</i>	1.1×10^{-152}	0.071761
GPCR ligand binding	1.1×10^{-143}	0.55801
Class A/1 (Rhodopsin-like receptors)	1.5×10^{-142}	0.58901
<i>GPCR downstream signalling</i>	7.6×10^{-140}	0.098357
Haemostasis	1.9×10^{-134}	0.27059
Developmental Biology	2.0×10^{-123}	0.52737
Metabolism of lipids and lipoproteins	3.3×10^{-120}	0.724
Cytokine Signalling in Immune system	2.6×10^{-119}	0.39661
Peptide ligand-binding receptors	3.7×10^{-109}	0.61102
$G_{\alpha i}$ signalling events	8.9×10^{-100}	$< 1.241 \times 10^{-5}$

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR).

Significant pathways are marked in bold (FDR < 0.05) and italics (FDR < 0.1).

Table 4.9: Pathways for *CDH1* partners from SLIPT and siRNA primary screen

Reactome Pathway	Over-representation	Permutation
Visual phototransduction	6.9×10^{-10}	0.91116
G_{αs} signalling events	1.6×10^{-7}	0.012988
Retinoid metabolism and transport	1.7×10^{-7}	0.20487
Transcriptional regulation of white adipocyte differentiation	6.5×10^{-6}	0.38197
Acylic chain remodelling of PS	6.5×10^{-6}	0.58485
Chemokine receptors bind chemokines	6.5×10^{-6}	0.97255
<i>Defective EXT2 causes exostoses 2</i>	6.9×10^{-6}	0.056437
<i>Defective EXT1 causes exostoses 1, TRPS2 and CHDS</i>	6.9×10^{-6}	0.056437
Signalling by NOTCH4	6.9×10^{-6}	0.15497
Platelet activation, signalling and aggregation	6.9×10^{-6}	0.53358
Phase 1 - Functionalisation of compounds	1.3×10^{-5}	0.24836
Amine ligand-binding receptors	1.7×10^{-5}	0.3195
Acylic chain remodelling of PE	2.4×10^{-5}	0.7307
Signalling by GPCR	2.4×10^{-5}	0.9939
Molecules associated with elastic fibres	2.6×10^{-5}	0.0072929
DAP12 interactions	2.6×10^{-5}	0.78273
Cytochrome P ₄₅₀ - arranged by substrate type	3.2×10^{-5}	0.87019
GPCR ligand binding	3.8×10^{-5}	0.99417
Acylic chain remodelling of PC	4.0×10^{-5}	0.65415
Response to elevated platelet cytosolic Ca ²⁺	4.2×10^{-5}	0.55461
<i>Arachidonic acid metabolism</i>	4.4×10^{-5}	0.060298
Defective B4GALT7 causes EDS, progeroid type	4.9×10^{-5}	0.15497
Defective B3GAT3 causes JDSSDHD	4.9×10^{-5}	0.15497
Elastic fibre formation	4.9×10^{-5}	0.0019227
HS-GAG degradation	6.2×10^{-5}	0.017747
Bile acid and bile salt metabolism	6.2×10^{-5}	0.15497
Netrin-1 signalling	7.1×10^{-5}	0.95056
Integration of energy metabolism	7.1×10^{-5}	0.0019287
DAP12 signalling	7.9×10^{-5}	0.67835
GPCR downstream signalling	8.1×10^{-5}	0.88678
Diseases associated with glycosaminoglycan metabolism	8.7×10^{-5}	0.017747
Diseases of glycosylation	8.7×10^{-5}	0.017747
Signalling by Retinoic Acid	8.7×10^{-5}	0.13592
Signalling by Leptin	8.7×10^{-5}	0.15497
Signalling by SCF-KIT	8.7×10^{-5}	0.73399
Opioid Signalling	8.7×10^{-5}	0.99417
Signalling by NOTCH	0.0001	0.26453
Platelet homeostasis	0.0001	0.55912
Signalling by NOTCH1	0.00011	0.13797
Class B/2 (Secretin family receptors)	0.00011	0.4659
Diseases of Immune System	0.00013	0.15497
Diseases associated with the TLR signalling cascade	0.00013	0.15497
A tetrasaccharide linker sequence is required for GAG synthesis	0.00013	0.33566
Nuclear Receptor transcription pathways	0.00016	0.22735
Formation of Fibrin Clot (Clotting Cascade)	0.00016	0.0054639

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR). Significant pathways are marked in bold (FDR < 0.05) and italics (FDR < 0.1).

in Table 4.8. In particular, some of the most significantly over-represented pathways had higher observed χ^2 values than any of the 1 million random permutations. Similar pathways were also replicated by permutation analysis for mtSLIPT candidate partners against *CDH1* mutation (shown in Appendix Table C.4). For the genes detected by SLIPT, the permutation approach detected many of the most strongly over-represented pathways.

The permutation approach was also applied to the intersection between computational and experimental candidates. This permutation analysis **tested whether** detection of pathways was independent of their pre-existing status as experimental candidates. In contrast to the SLIPT pathways (in Table 4.8), the pathways results for these candidate partners (in Table 4.9) differed considerably between over-representation and resampling analyses.

Namely, many of the over-represented pathways were not significant in the resampling analysis, including visual phototransduction and retinoic acid signalling, and were likely over-represented in the intersection due to over-representation in the siRNA candidates rather than additional support from SLIPT. Of the highest over-represented pathways in the intersection, only $G_{\alpha s}$ signalling events were supported by both over-representation and resampling analyses. Other pathways supported by both analyses were cytoplasmic elastic fibre formation, associated HS-GAG protein modification pathways, energy metabolism, and the fibrin clotting cascade.

Many of the pathways supported in the intersection by permutation analysis were also replicated in the mtSLIPT analysis of partners tested with *CDH1* mutation (in Table 4.10), including $G_{\alpha s}$, elastic fibres, HS-GAG, and energy metabolism. While there were differences between the pathways identified by over-representation analysis, those replicated by permutation were highly concordant, supporting the combined use of these pathways approaches to identify synthetic lethal gene functions and targets.

While this indicates that $G_{\alpha s}$ and GPCR class A/1 signalling events were significantly detected by both approaches, GPCR signalling pathways overall were not. It is likely that GPCRs were primarily over-represented in the intersection with the experimental candidates due to strong over-representation of these pathways in experimental candidates, rather than detection by SLIPT, which may be driven by these more specific constituent pathways.

Several pathways, including some immune functions and neurotransmitters, were supported by the resampling analysis (in Table 4.9 and Appendix Table 4.10) when the initial pathways over-representation test was not significant. These functions appear

Table 4.10: Pathways for *CDH1* partners from mtSLIPT and siRNA primary screen

Reactome Pathway	Over-representation	Permutation
Visual phototransduction	1.2×10^{-9}	0.86279
G_{αs} signalling events	2.9×10^{-7}	0.023066
Retinoid metabolism and transport	2.9×10^{-7}	0.299
Acyl chain remodelling of PS	1.1×10^{-5}	0.42584
Transcriptional regulation of white adipocyte differentiation	1.1×10^{-5}	0.53928
Chemokine receptors bind chemokines	1.1×10^{-5}	0.95259
<i>Signalling by NOTCH4</i>	1.2×10^{-5}	0.079229
Defective EXT2 causes exostoses 2	1.2×10^{-5}	0.22292
Defective EXT1 causes exostoses 1, TRPS2 and CHDS	1.2×10^{-5}	0.22292
Platelet activation, signalling and aggregation	1.2×10^{-5}	0.48853
Serotonin receptors	1.4×10^{-5}	0.34596
Nicotinamide salvaging	1.4×10^{-5}	0.70881
Phase 1 - Functionalization of compounds	2×10^{-5}	0.31142
Amine ligand-binding receptors	2.5×10^{-5}	0.34934
Acyl chain remodelling of PE	3.8×10^{-5}	0.42615
Signalling by GPCR	3.8×10^{-5}	0.93888
Molecules associated with elastic fibres	3.9×10^{-5}	0.017982
DAP12 interactions	3.9×10^{-5}	0.71983
Beta defensins	3.9×10^{-5}	0.91458
Cytochrome P ₄₅₀ - arranged by substrate type	4.7×10^{-5}	0.83493
GPCR ligand binding	5.7×10^{-5}	0.95258
Acyl chain remodelling of PC	6.1×10^{-5}	0.42584
Response to elevated platelet cytosolic Ca ²⁺	6.4×10^{-5}	0.54046
Arachidonic acid metabolism	6.7×10^{-5}	0.026696
Defective B4GALT7 causes EDS, progeroid type	7.3×10^{-5}	0.24921
Defective B3GAT3 causes JDSSDHD	7.3×10^{-5}	0.24921
Hydrolysis of LPC	7.3×10^{-5}	0.80663
Elastic fibre formation	7.4×10^{-5}	0.0058768
HS-GAG degradation	9.4×10^{-5}	0.0083179
<i>Bile acid and bile salt metabolism</i>	9.4×10^{-5}	0.079905
Netrin-1 signalling	0.00011	0.92216
Integration of energy metabolism	0.00011	0.011152
Dectin-2 family	0.00012	0.10385
Platelet sensitization by LDL	0.00012	0.34596
DAP12 signalling	0.00012	0.62787
Defensins	0.00012	0.77542
GPCR downstream signalling	0.00012	0.79454
<i>Diseases associated with glycosaminoglycan metabolism</i>	0.00013	0.065927
<i>Diseases of glycosylation</i>	0.00013	0.065927
Signalling by Retinoic Acid	0.00013	0.22292
Signalling by Leptin	0.00013	0.34596
Signalling by SCF-KIT	0.00013	0.70881
Opioid Signalling	0.00013	0.96053
Signalling by NOTCH	0.00015	0.26884

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR). Significant pathways were marked in bold (FDR < 0.05) and italics (FDR < 0.1).

to have been detected by both approaches more than expected by chance but must be interpreted with caution since they were still not common enough to be detected in pathways over-representation analysis.

4.2.6 Integrating Synthetic Lethal Pathways and Screens

Based on these results, it appears that computational and experimental approaches to synthetic lethal screening for *CDH1* lead to a broader functional characterisation, and many candidate partners, when combined, despite different strengths and limitations. Compared to candidate gene approaches, experimental genome-wide screens are an appealing unbiased strategy for identifying synthetic lethal interactions. Since these screens are costly, laborious, and specific to genetic background, computational analysis can augment candidate triage to either reduce the initial panel of screened genes or prioritise validation.

GPCR pathways were detected among both computational and experimental synthetic lethal candidates, with more support in the experimental screen (Table 4.9). The homogeneous cell line model may be more likely to detect particular pathways. For instance, SLIPT identified immune pathways, not expected to be detected in isolated cell culture. GPCR signalling was supported in experimental models Telford *et al.* (2015) with some of these pathways replicated in varied genetic backgrounds of patient samples. These pathways require further investigation such as identification of more specific pathways, higher order interactions, and modes of resistance.

The pathways composition across computational and experimental synthetic lethal candidates was informative with over-representation (Table 4.7) and was supported by resampling analysis (Table 4.9), despite a modest intersection of genes between them (Figure 4.2). Either approach may be significant for a pathway in this intersection without being supported by the other: resampling analysis may support pathways that were not over-represented due to small effect sizes, thus both tests are required to identify candidate pathways. The pathways detected by both over-representation and resampling are the strongest candidates for further investigation, such as $G_{\alpha s}$ signalling, a strong candidate in prior analyses with a role in the regulation of translation in cancer Gao and Roux (2015), another function supported by SLIPT analysis.

The predicted synthetic lethal partners occurred across functionally distinct pathways, including characterised functions of *CDH1*. This diversity is consistent with the wide ranging role of *CDH1* in cell-cell adhesion, cell signalling, and the cytoskeletal structure of epithelial tissues. Pathway structure may be relevant to identifying poten-

tial drug targets from gene expression signatures, indicating downstream effector genes and mechanisms leading to cell inviability. These distinct synthetic lethal gene clusters and pathways may further lead to the elucidation of drug resistance mechanisms.

4.3 Synthetic Lethal Pathway Metagenes

Metagenes are a one-dimensional summary of the activity for each biological pathway. The direction of metagenes (derived by the singular value matrix decomposition as described in Section 2.2.3) reflects overall activation of the pathways. This has been verified by examining the expression patterns of previously published gene signatures (Gatza *et al.*, 2011, 2014) in Appendix D. Pathway metagenes for Reactome pathways were used for testing synthetic lethal pathways. Since the metagenes values are higher when the pathways as a whole is activated, they are suitable for SLIPT analysis using low metagene levels to represent less activated pathways.

The TCGA breast cancer expression data was used to generate pathway metagenes for each collection of genes in a pathway from the Reactome database (Croft *et al.*, 2014). These metagenes were tested against the expression of *CDH1* by SLIPT to directly detect synthetic lethal pathways. These synthetic lethal metagenes differed to the over-represented pathways among synthetic lethal gene candidates. However, there were some similarities to previous findings, as shown in Table 4.11. In particular, translational pathways were replicated as observed in Table 4.3. While the specific pathways differ, immune pathways (e.g., NF- κ B) were also supported by metagene synthetic lethal analysis.

Signalling pathways were more strongly supported by mtSLIPT analysis of metagene pathways expression against *CDH1* mutation, as shown in Table D.1, although these results were generally less statistically significant than expression analyses. Signalling pathways detected as synthetic lethal metagenes include G $_{\alpha z}$, insulin-related growth factor (IGF), GABA receptor, G $_{\alpha s}$, S6K1 and various toxin responses mediated by GPCRs. Metabolic processes including processing of carbohydrates and fatty acids were also implicated across these analyses.

The metagene analyses differ more between expression and *CDH1* mutation than previous analyses, with more specific signalling pathways identified in the mutation analysis. This supports the usage of a complete null mutant model in experimental testing for synthetic lethality of signalling pathways against *CDH1* inactivation rather than a knockdown in expression. However, low expression of partners has been used in either case to be applicable to dose-dependent pharmacological inhibition and across

Table 4.11: Examples of candidate metagenes synthetic lethal for *CDH1* from SLIPT

Pathway	ID	Observed	Expected	χ^2 value	p-value	p-value (FDR)
Glycogen storage diseases	3229121	68	130	176	6.62×10^{-37}	1.82×10^{-34}
Myoclonic epilepsy of Lafora	3785653	68	130	176	6.62×10^{-37}	1.82×10^{-34}
Diseases of carbohydrate metabolism	5663084	68	130	176	6.62×10^{-37}	1.82×10^{-34}
Arachidonic acid metabolism	2142753	81	130	157	8.13×10^{-33}	1.49×10^{-30}
Translation initiation complex formation	72649	70	130	152	7.08×10^{-32}	1.17×10^{-29}
Synthesis of 5-eicosatetraenoic acids	2142688	68	130	151	1.25×10^{-31}	1.88×10^{-29}
SRP-dependent cotranslational protein targeting to membrane	1799339	69	130	150	2.01×10^{-31}	2.76×10^{-29}
L13a-mediated translational silencing of Ceruloplasmin expression	156827	72	130	148	5.91×10^{-31}	6.44×10^{-29}
3' -UTR-mediated translational regulation	157279	72	130	148	5.91×10^{-31}	6.44×10^{-29}
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	72662	70	130	147	1.14×10^{-30}	9.28×10^{-29}
Formation of the ternary complex, and subsequently, the 43S complex	72695	70	130	147	1.14×10^{-30}	9.28×10^{-29}
Ribosomal scanning and start codon recognition	72702	70	130	147	1.14×10^{-30}	9.28×10^{-29}
Eukaryotic Translation Elongation	156842	72	130	146	1.19×10^{-30}	9.28×10^{-29}
Nonsense Mediated Decay independent of the Exon Junction Complex	975956	71	130	146	1.24×10^{-30}	9.28×10^{-29}
Viral mRNA Translation	192823	70	130	146	1.51×10^{-30}	1.04×10^{-28}
Eukaryotic Translation Termination	72764	70	130	146	1.51×10^{-30}	1.04×10^{-28}
NF-kB is activated and signals survival	209560	71	130	145	1.90×10^{-30}	1.19×10^{-28}
Peptide chain elongation	156902	72	130	145	1.91×10^{-30}	1.19×10^{-28}
Influenza Life Cycle	168255	70	130	145	1.95×10^{-30}	1.19×10^{-28}
Formation of a pool of free 40S subunits	72689	73	130	145	2.01×10^{-30}	1.19×10^{-28}
Nonsense-Mediated Decay	927802	71	130	145	2.44×10^{-30}	1.34×10^{-28}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	975957	71	130	145	2.44×10^{-30}	1.34×10^{-28}
GTP hydrolysis and joining of the 60S ribosomal subunit	72706	72	130	145	2.58×10^{-30}	1.37×10^{-28}
Influenza Viral RNA Transcription and Replication	168273	72	130	144	4.01×10^{-30}	2.07×10^{-28}
Signalling by NOTCH1 HD Domain Mutants in Cancer	2691230	79	130	143	5.99×10^{-30}	2.82×10^{-28}

Strongest candidate synthetic lethal partners for *CDH1* by SLIPT with observed and expected numbers of TCGA breast cancer samples with low expression of both *CDH1* and the metagene. The most significant 26 pathways are reported to show the diversity of candidate synthetic lethal metagene and demonstrate the highly significant results of SLIPT when performed on pathway metagenes.

genes where mutations have different functional consequences, including variants of unknown significance.

These results show an alternative pathways-based approach to detecting synthetic lethal gene functions interacting with *CDH1*. The use of synthetic lethal metagenes replicates support for these pathways independent of pathways size (as genes are weighted equally). Having verified that the direction of metagenes recapitulates the activity of a pathway, these demonstrate that many of the pathways previously identified (from SLIPT candidate genes) are synthetic lethal pathways, with their activity dependent on synthetic lethal genes, rather than containing synthetic lethal genes as inhibitors or peripheral regulators of the pathways.

The synthetic lethal analysis against low *CDH1* expression supports prior findings in translational and immune pathways even if they were not able to be detected in an

experimental screen (Telford *et al.*, 2015). Together these findings support the role of *CDH1* loss in cancer disrupting cell signalling with wider effects on protein translation and metabolism necessary for the proliferation of cancer cells. This is consistent with the GPCR pathways, such as G_{as} signalling, being supported by SLIPT gene candidates and the experimental primary siRNA screen, as shown by resampling in Section 4.2.5.1.

4.4 Replication in Stomach Cancer

CDH1 is also important in stomach cancer biology as a driver tumour suppressor gene, including as a germline mutation in many cases of hereditary diffuse gastric cancer. The synthetic lethal analysis of genes and pathways (previously identified for TCGA breast cancer data) was replicated in TCGA stomach cancer.

While the sample size was lower for TCGA stomach cancer (particularly for mutations), the results serve to support the findings in breast cancer in an independent patient cohort and tissue samples. The molecular profiling, including RNA-Seq expression, were performed by TCGA using the sample procedures as for breast cancer and the findings reported here were performed using data analysis techniques identical to those presented previously. These procedures should ensure as close a comparison as feasible across both of the cancer types most relevant to HDGC and recurrent *CDH1* mutations.

The strongest SLIPT genes for stomach cancer (shown in Table 4.12) did not necessarily directly correspond to those observed in breast cancer (shown in Table 4.1). However, several gene functions were replicated in stomach cancer. Together, these gene candidates indicate widespread functions of *CDH1* and strongly detectable synthetic lethality with many genes, using a strategy that can be applied across cancer types. More specifically, the signalling genes included GPCR signalling genes, which was one of the most supported synthetic lethal pathways in breast cancer analysis and the experimental screen (Telford *et al.*, 2015). These findings were further supported by the pathways over-represented in SLIPT candidates from TCGA stomach cancer (shown in Appendix Table 4.13) which replicated the translational and immune pathways observed in TCGA breast cancer (shown in Table 4.3) and further supported GPCR signalling pathways, including the class A/1 receptors. The extracellular matrix was also detected at the pathway level in stomach cancer, including elastic fibres, glycosylation, collagen, and integrin cell-surface interactions. While fewer pathways were supported by resampling for the intersection of SLIPT and experimental screen candidate partners in stomach cancer than breast cancer, many of those detected (shown in

Appendix Table 4.17) replicate those detected in breast cancer (shown in Table 4.9). The pathways detected by both permutation and over-representation analysis were more likely to be replicated across stomach and breast cancer than those detected by over-representation alone, supporting the use of this procedure to detect synthetic lethal pathways applicable across cancer types. These pathways include $G_{\alpha s}$ signalling and elastic fibre formation as discussed for breast cancer (in Section 4.2.5.1).

4.4.1 Synthetic Lethal Genes and Pathways

The strongest SLIPT genes for stomach cancer (shown in Table 4.12) did not necessarily directly correspond to those observed in breast cancer (shown in Table 4.1). However, several gene functions were replicated in stomach cancer. Cell membrane genes including *EMP3*, *GYPC*, *LGALS1*, *PRR24*, and *FUNCD2* were among the strongest SL candidates. Similarly, cell signalling genes including *PLEKHO1*, *RARRES2*, *VEGFB*, *HSPB2*, and *CREM* were detected in stomach cancers. It is notable that several of these genes (*EMP3*, *PLEKHO1*, and *FUNCD2*) have a known role in cancer. Together these genes support the roles of *CDH1* in cell membrane and signalling functions (of epithelial tissues) which are perturbed in both breast and stomach cancers.

These findings were further supported by the pathways over-represented in SLIPT candidates from TCGA stomach cancer (shown in Table 4.13) which were replicated the translational and immune pathways observed in TCGA breast cancer (shown in Table 4.3). There was further support for GCPR signalling pathways including the class A/1 receptors in *CDH1*-deficient stomach cancers, in addition to cell signalling and translation pathways important in tumour growth across breast and stomach cancer.

4.4.2 Synthetic Lethal Expression Profiles

The expression profiles of candidate synthetic lethal partners detected by SLIPT in stomach cancer were plotted against clinical characteristics as described for breast cancer data in Section 4.1.2 (shown in Figure 4.8). As expected the majority of *CDH1* mutant samples had low expression of *CDH1* and were the diffuse type of stomach cancer.

The SLIPT partners of *CDH1* exhibited similar clustering in stomach cancer to breast cancer, replicating the diverse roles of elevated partner genes in different clinical samples. Specifically (as shown in Figure 4.8), the diffuse type stomach cancers had higher expression of the candidate synthetic lethal partners (where *CDH1* has a role as a driver mutation), despite an unbiased clustering. This is consistent with compensating expression of synthetic lethal partners under loss of *CDH1*, as suggested by Lu *et al.*

Table 4.12: Synthetic lethal gene partners of *CDH1* from SLIPT in stomach cancer

Gene	Observed*	Expected*	χ^2 value	p-value	p-value (FDR)
<i>PRAF2</i>	17	50.4	121	3.54×10^{-25}	1.45×10^{-21}
<i>EMP3</i>	17	50.4	115	5.06×10^{-24}	1.48×10^{-20}
<i>PLEKHO1</i>	22	50.4	112	2.14×10^{-23}	4.75×10^{-20}
<i>SELM</i>	20	50.4	111	5.13×10^{-23}	8.09×10^{-20}
<i>GYPC</i>	20	50.4	110	5.77×10^{-23}	8.45×10^{-20}
<i>COX7A1</i>	18	50.4	109	1.15×10^{-22}	1.39×10^{-19}
<i>TNFSF12</i>	20	50.4	106	4.06×10^{-22}	4.38×10^{-19}
<i>SEPT4</i>	17	50.4	106	6.58×10^{-22}	5.91×10^{-19}
<i>LGALS1</i>	19	50.4	105	6.64×10^{-22}	5.91×10^{-19}
<i>RARRES2</i>	27	50.4	105	8.02×10^{-22}	6.85×10^{-19}
<i>VEGFB</i>	16	50.4	104	1.19×10^{-21}	9.74×10^{-19}
<i>PRR24</i>	22	50.4	102	2.96×10^{-21}	2.02×10^{-18}
<i>SYNC</i>	19	50.4	102	3.73×10^{-21}	2.39×10^{-18}
<i>MAGEH1</i>	17	50.4	100	9.52×10^{-21}	5.01×10^{-18}
<i>HSPB2</i>	23	50.4	99.6	1.19×10^{-20}	5.82×10^{-18}
<i>SMARCD3</i>	19	50.4	99	1.59×10^{-20}	7.57×10^{-18}
<i>CREM</i>	13	50.4	98.1	2.48×10^{-20}	1.13×10^{-17}
<i>GNG11</i>	20	50.4	97.3	3.68×10^{-20}	1.59×10^{-17}
<i>GNAI2</i>	17	50.4	96.4	5.75×10^{-20}	2.36×10^{-17}
<i>FUNDC2</i>	22	50.4	95.9	7.39×10^{-20}	2.91×10^{-17}
<i>CNRIP1</i>	21	50.4	95.3	1.0×10^{-19}	3.66×10^{-17}
<i>CALHM2</i>	22	50.4	93.1	2.94×10^{-19}	1.06×10^{-16}
<i>ARID5A</i>	18	50.4	92.7	3.47×10^{-19}	1.22×10^{-16}
<i>ST3GAL3</i>	27	50.4	92.2	4.49×10^{-19}	1.56×10^{-16}
<i>LOC339524</i>	21	50.4	92.1	4.8×10^{-19}	1.59×10^{-16}

Strongest candidate synthetic lethal partners for *CDH1* of 4365 genes detected by SLIPT in TCGA stomach cancer expression data

* Observed and expected numbers of samples which had low expression of both genes

Table 4.13: Pathways for *CDH1* partners from SLIPT in stomach cancer

Pathways Over-represented	Pathway Size	SL Genes	p-value (FDR)
Extracellular matrix organization	241	104	7.5×10^{-140}
Hemostasis	445	138	1.8×10^{-121}
Developmental Biology	432	125	9.2×10^{-107}
Axon guidance	289	94	1.5×10^{-102}
Eukaryotic Translation Termination	84	49	1.9×10^{-99}
GPCR ligand binding	373	108	3.8×10^{-99}
Viral mRNA Translation	82	48	3.3×10^{-98}
Formation of a pool of free 40S subunits	94	51	3.3×10^{-98}
Eukaryotic Translation Elongation	87	49	1.6×10^{-97}
Peptide chain elongation	84	48	7.2×10^{-97}
Class A/1 (Rhodopsin-like receptors)	289	90	2.7×10^{-96}
Nonsense Mediated Decay independent of the Exon Junction Complex	89	49	3.0×10^{-96}
Infectious disease	349	100	2.6×10^{-94}
GTP hydrolysis and joining of the 60S ribosomal subunit	105	52	3.4×10^{-94}
L13a-mediated translational silencing of Ceruloplasmin expression	104	51	2.8×10^{-92}
3' -UTR-mediated translational regulation	104	51	2.8×10^{-92}
Neuronal System	272	84	8.4×10^{-92}
SRP-dependent cotranslational protein targeting to membrane	105	51	9.5×10^{-92}
Eukaryotic Translation Initiation	112	52	2.0×10^{-90}
Cap-dependent Translation Initiation	112	52	2.0×10^{-90}

Gene set over-representation analysis (hypergeometric test) for Reactome pathways in SLIPT partners for *CDH1*.

(2015). The pathways composition of gene clusters for stomach cancer (shown in Table 4.14) was also highly concordant with breast cancer findings (shown in Table 4.4). These included replicated of translation (Cluster 1), immune functions (Cluster 2), G_{αs} signalling (Cluster 3), and further support for the roles of GPCRs and the extracellular matrix (Cluster 4) in the synthetic lethal partners and functions of *CDH1*, replicated across stomach and breast cancers. Clusters 1 and 4, which had particularly high expression of SLIPT candidate partner genes in the diffuse subtype, also had the most significant over-representation of pathways.

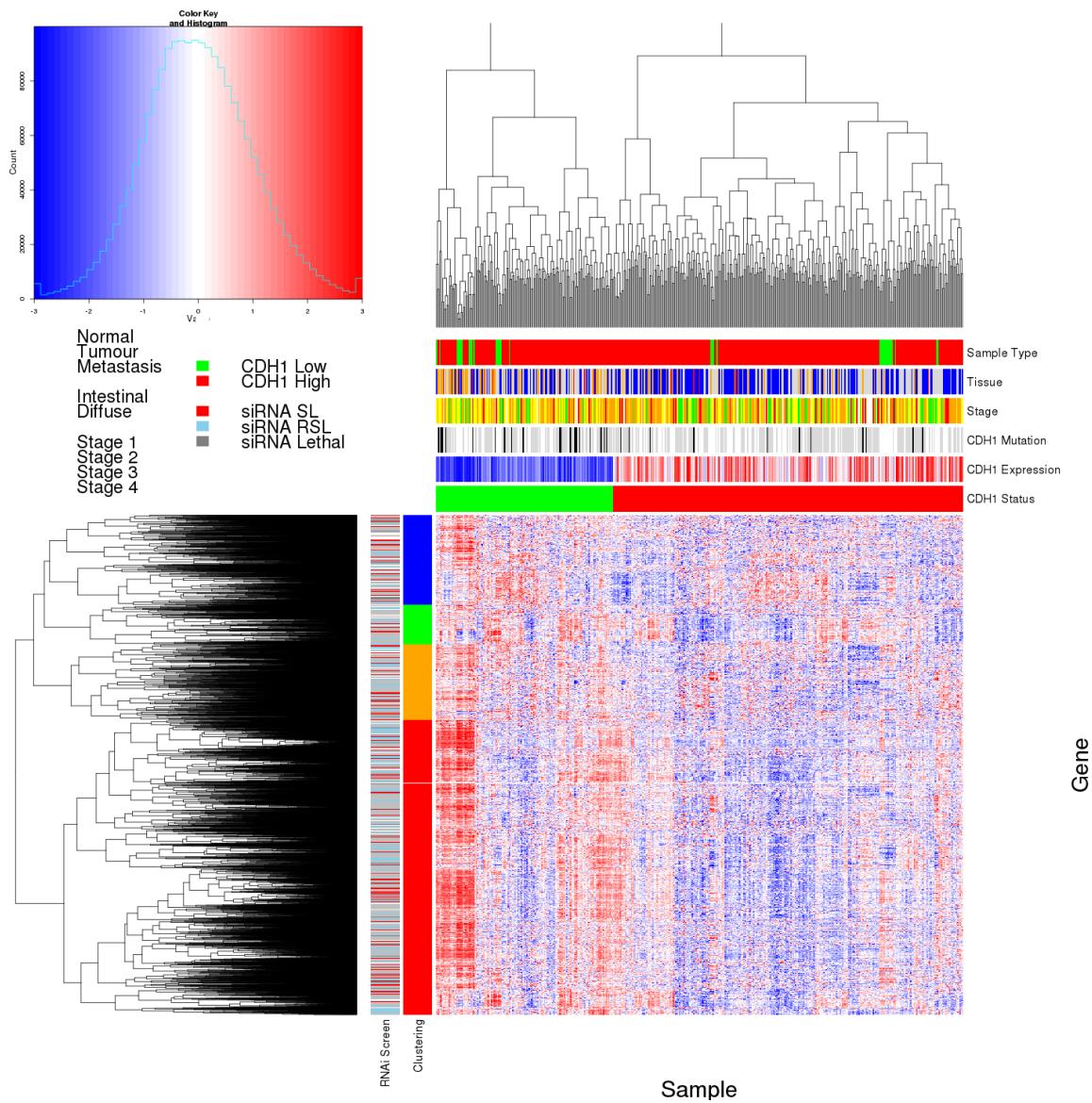


Figure 4.8: Synthetic lethal expression profiles of analysed samples. Gene expression profile heatmap (correlation distance) of all samples (separated by the $1/3$ quantile of *CDH1* expression) analysed in TCGA stomach cancer dataset for gene expression of 4365 candidate partners of E-cadherin (*CDH1*) from SLIPT prediction (with significant FDR adjusted $p < 0.05$). Deeply clustered, inter-correlated genes form several main groups, each containing genes that were SL candidates or toxic in an siRNA screen Telford *et al.* (2015). Clusters had different sample groups highly expressing the synthetic lethal candidates in *CDH1* low samples. Notably, diffuse and *CDH1* mutant samples had elevated expression in one or more distinct clusters, although there was less complexity and variation among candidate synthetic lethal partners than in breast data. *CDH1* low samples also contained most of samples with *CDH1* mutations.

Table 4.14: Pathways for clusters of *CDH1* partners in stomach SLIPT

Pathways Over-represented in Cluster 1	Pathway Size	Cluster Genes	p-value (FDR)
Viral mRNA Translation	82	48	1.3×10^{-97}
Formation of a pool of free 40S subunits	94	51	1.3×10^{-97}
Eukaryotic Translation Elongation	87	49	4.8×10^{-97}
Peptide chain elongation	84	48	1.4×10^{-96}
Eukaryotic Translation Termination	84	48	1.4×10^{-96}
GTP hydrolysis and joining of the 60S ribosomal subunit	105	52	7.9×10^{-94}
Nonsense Mediated Decay independent of the Exon Junction Complex	89	48	3.1×10^{-93}
L13a-mediated translational silencing of Ceruloplasmin expression	104	51	5.1×10^{-92}
3' -UTR-mediated translational regulation	104	51	5.1×10^{-92}
SRP-dependent cotranslational protein targeting to membrane	105	51	1.7×10^{-91}
Eukaryotic Translation Initiation	112	52	3.3×10^{-90}
Cap-dependent Translation Initiation	112	52	3.3×10^{-90}
Translation	142	56	3.6×10^{-85}
Nonsense-Mediated Decay	104	48	1.2×10^{-84}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	104	48	1.2×10^{-84}
Influenza Viral RNA Transcription and Replication	109	48	4.1×10^{-82}
Influenza Life Cycle	113	48	3.4×10^{-80}
Influenza Infection	118	48	6.4×10^{-78}

Pathways Over-represented in Cluster 2	Pathway Size	Cluster Genes	p-value (FDR)
Immuno-regulatory interactions between a Lymphoid and a non-Lymphoid cell	65	12	1.3×10^{-15}
Phosphorylation of CD3 and TCR zeta chains	18	6	1.7×10^{-12}
Generation of second messenger molecules	29	7	2.7×10^{-12}
PD-1 signalling	21	6	7.4×10^{-12}
TCR signalling	62	9	4.3×10^{-11}
Translocation of ZAP-70 to Immunological synapse	16	5	1.1×10^{-10}
Interferon alpha/beta signalling	68	9	1.6×10^{-10}
Initial triggering of complement	17	5	1.6×10^{-10}
IKK complex recruitment mediated by RIP1	19	5	5.1×10^{-10}
TRIF-mediated programmed cell death	10	4	6.2×10^{-10}
Creation of C4 and C2 activators	11	4	1.3×10^{-9}
RHO GTPases Activate NADPH Oxidases	11	4	1.3×10^{-9}
Interferon Signalling	175	15	2.3×10^{-9}
Chemokine receptors bind chemokines	52	7	4.0×10^{-9}
Interferon gamma signalling	74	8	1.6×10^{-8}
TRAF6 mediated induction of TAK1 complex	15	4	1.6×10^{-8}
Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	16	4	2.7×10^{-8}
Downstream TCR signalling	45	6	3.5×10^{-8}

Pathways Over-represented in Cluster 3	Pathway Size	Cluster Genes	p-value (FDR)
Uptake and actions of bacterial toxins	22	4	3.5×10^{-6}
Neurotoxicity of clostridium toxins	10	3	3.5×10^{-6}
Activation of PPARC1A (PGC-1alpha) by phosphorylation	10	3	3.5×10^{-6}
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	28	4	1.4×10^{-5}
Assembly of the primary cilium	149	10	2.5×10^{-5}
Serotonin Neurotransmitter Release Cycle	15	3	2.5×10^{-5}
Glycosaminoglycan metabolism	114	8	3.3×10^{-5}
Platelet homeostasis	54	5	3.3×10^{-5}
Norepinephrine Neurotransmitter Release Cycle	17	3	3.3×10^{-5}
Acetylcholine Neurotransmitter Release Cycle	17	3	3.3×10^{-5}
G _{αs} signalling events	100	7	5.5×10^{-5}
GABA synthesis, release, reuptake and degradation	19	3	5.6×10^{-5}
deactivation of the beta-catenin transactivating complex	39	4	6.7×10^{-5}
Dopamine Neurotransmitter Release Cycle	20	3	6.7×10^{-5}
IRS-related events triggered by IGF1R	83	6	7.1×10^{-5}
Generic Transcription Pathway	186	11	7.1×10^{-5}
Termination of O-glycan biosynthesis	21	3	7.4×10^{-5}
Kinesins	22	3	8.5×10^{-5}

Pathway over-representation analysis for Reactome pathways with the number of genes in each pathway (Pathway Size), number of genes within the pathway identified (Cluster Genes), and the pathway over-representation p-value (adjusted by FDR) from the hypergeometric test.

Table 4.14: Pathways for clusters of *CDH1* partners in stomach SLIPT

Pathways Over-represented in Cluster 4	Pathway Size	Cluster Genes	p-value (FDR)
Extracellular matrix organization	241	97	8.8×10^{-126}
Axon guidance	289	75	8.3×10^{-72}
Hemostasis	445	101	8.3×10^{-72}
Developmental Biology	432	95	3.0×10^{-67}
Response to elevated platelet cytosolic Ca^{2+}	84	37	5.8×10^{-67}
Platelet degranulation	79	36	5.8×10^{-67}
Degradation of the extracellular matrix	104	39	6.7×10^{-63}
Platelet activation, signalling and aggregation	186	52	6.6×10^{-62}
ECM proteoglycans	66	31	8.1×10^{-61}
Neuronal System	272	64	5.1×10^{-60}
Signalling by PDGF	173	47	9.7×10^{-57}
Integrin cell surface interactions	82	31	1.9×10^{-53}
Collagen biosynthesis and modifying enzymes	56	26	1.1×10^{-52}
Collagen formation	67	28	1.4×10^{-52}
Class A/1 (Rhodopsin-like receptors)	289	61	2.3×10^{-52}
GPCR ligand binding	373	73	2.8×10^{-52}
Elastic fibre formation	38	22	4.7×10^{-52}
Non-integrin membrane-ECM interactions	53	24	7.0×10^{-49}

Pathway over-representation analysis for Reactome pathways with the number of genes in each pathway (Pathway Size), number of genes within the pathway identified (Cluster Genes), and the pathway over-representation p-value (adjusted by FDR) from the hypergeometric test.

4.4.3 Comparison to Primary Screen

The number of genes detected by both SLIPT in TCGA stomach cancer data and siRNA in breast cell lines (shown in Figure 4.9) was also not a significant overlap (as observed for breast cancer in Figure 4.2). SLIPT against *CDH1* in stomach cancer detected fewer genes due to low sample size and mutation frequency compared to the breast cancer analysis. This smaller overlap can also be attributed to the tissue-specific differences between the stomach cancers and the breast cells used for the experimental model (Chen *et al.*, 2014). Nevertheless, many genes were detected across SLIPT in stomach cancers and the experimental screen (Telford *et al.*, 2015) and the pathways detected were consistent with prior observations in breast cancer. Despite differences in the specific genes detected, the functions of *CDH1* were conserved across epithelial cancers in different tissues and synthetic lethal inhibition of interacting pathways may be effective against molecular targets such as *CDH1* inactivation across tissue types.

However, the pathways composition of SLIPT-specific genes and those replicated with the siRNA primary screen (Telford *et al.*, 2015) were highly concordant between the pathways identified by SLIPT in TCGA stomach cancer (shown in Table 4.15) and pathways previously identified in TCGA breast cancer (shown in Table 4.7). In both cases, translation and immune pathways were highly over-represented in SLIPT-specific genes, which I would not expect to be detected by siRNA screening in cell

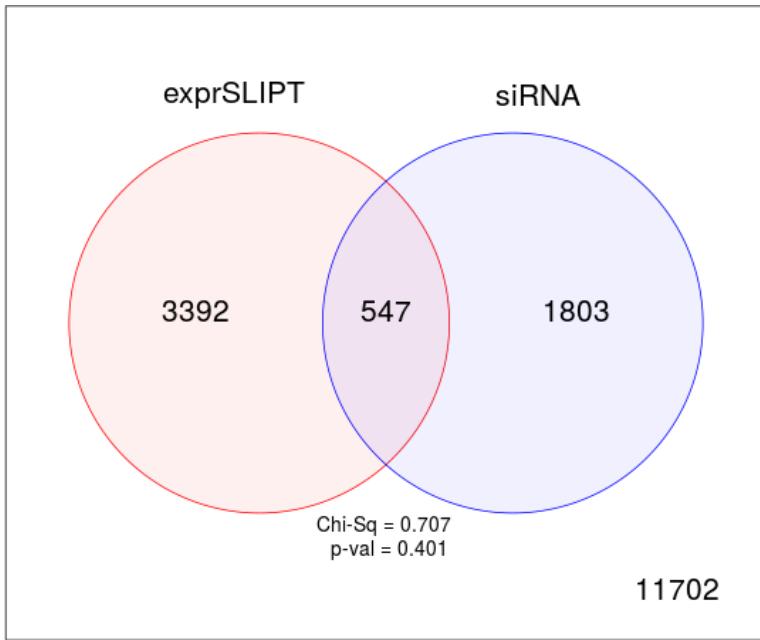


Figure 4.9: Comparison of SLIPT in stomach to siRNA. The overlap of gene candidates for E-cadherin synthetic lethal partners between computational (SLIPT) and experimental screening (siRNA) approaches. The χ^2 test suggests that the overlap is no more than would be expected by chance ($p = 0.281$).

lines, as discussed in Section 4.2.5. In addition, the extracellular matrix was supported by in stomach cancer. While the pathways identified by specifically by SLIPT in stomach cancer or siRNA screening were similar to those observed for breast cancer (in Table 4.7), the pathways over-represented in the intersection for stomach cancer SLIPT candidates and the siRNA primary screen (Telford *et al.*, 2015) also had a clear over-representation of signalling pathways, although they differed from those observed in breast cancer SLIPT candidates. GPCR signalling was supported in genes detected in both TCGA stomach cancer and screening, including $G_{\alpha q}$, $G_{\alpha s}$, serotonin receptors, and class A signalling (shown in more detail in Table 4.17). In addition MAPK and NOTCH signalling pathways were detected. These replicate the findings in breast cancer and show consistent detection of signalling pathways in stomach cancer despite less genes being detected by SLIPT and patient samples differing from the tissue in which the experiments were conducted.

Table 4.15: Pathways for *CDH1* partners from SLIPT and siRNA

Predicted only by SLIPT (3392 genes)	Pathway	Size	Genes Identified	p-value (FDR)
Extracellular matrix organization		238	90	3.4×10^{-107}
Eukaryotic Translation Termination		79	46	7.6×10^{-91}
Viral mRNA Translation		77	45	1.2×10^{-89}
Eukaryotic Translation Elongation		82	46	5.8×10^{-89}
Peptide chain elongation		79	45	2.1×10^{-88}
Nonsense Mediated Decay independent of the Exon Junction Complex		84	46	9.4×10^{-88}
Formation of a pool of free 40S subunits		89	47	3.3×10^{-87}
GTP hydrolysis and joining of the 60S ribosomal subunit		100	48	3.2×10^{-83}
Axon guidance		284	84	3.9×10^{-82}
Developmental Biology		426	111	4.2×10^{-82}
L13a-mediated translational silencing of Ceruloplasmin expression		99	47	1.4×10^{-81}
3' -UTR-mediated translational regulation		99	47	1.4×10^{-81}
SRP-dependent cotranslational protein targeting to membrane		99	47	1.4×10^{-81}
Nonsense-Mediated Decay		99	47	1.4×10^{-81}
Nonsense Mediated Decay enhanced by the Exon Junction Complex		99	47	1.4×10^{-81}
Hemostasis		438	112	1.2×10^{-80}
Eukaryotic Translation Initiation		107	48	8.0×10^{-80}
Cap-dependent Translation Initiation		107	48	8.0×10^{-80}
Infectious disease		338	90	1.6×10^{-76}
Neuronal System		267	77	1.6×10^{-76}

Detected only by siRNA screen (1803 genes)	Pathway	Size	Genes Identified	p-value (FDR)
Class A/1 (Rhodopsin-like receptors)		282	62	8.1×10^{-50}
GPCR ligand binding		363	71	4.9×10^{-46}
Peptide ligand-binding receptors		175	38	7.9×10^{-38}
G _{αi} signalling events		184	37	1.1×10^{-34}
Gastrin-CREB signalling pathway via PKC and MAPK		180	35	1.4×10^{-32}
G _{αq} signalling events		159	32	4.8×10^{-32}
DAP12 interactions		159	29	1.4×10^{-27}
Downstream signal transduction		146	26	2.4×10^{-25}
DAP12 signalling		149	26	6.4×10^{-25}
VEGFA-VEGFR2 Pathway		91	19	8.1×10^{-24}
Signalling by PDGF		172	27	5.7×10^{-23}
Signalling by ERBB2		146	24	1.4×10^{-22}
Signalling by VEGF		99	19	2.0×10^{-22}
Visual phototransduction		85	17	1.3×10^{-21}
Downstream signalling of activated FGFR1		134	22	1.3×10^{-21}
Downstream signalling of activated FGFR2		134	22	1.3×10^{-21}
Downstream signalling of activated FGFR3		134	22	1.3×10^{-21}
Downstream signalling of activated FGFR4		134	22	1.3×10^{-21}
Signalling by FGFR		146	23	2.0×10^{-21}
Signalling by FGFR1		146	23	2.0×10^{-21}

Intersection of SLIPT and siRNA screen (547 genes)	Pathway	Size	Genes Identified	p-value (FDR)
Class A/1 (Rhodopsin-like receptors)		282	25	3.9×10^{-9}
Platelet activation, signalling and aggregation		182	17	3.9×10^{-9}
Response to elevated platelet cytosolic Ca ²⁺		82	9	5.5×10^{-8}
Platelet homeostasis		53	7	5.7×10^{-8}
Nucleotide-like (purinergic) receptors		16	4	1.8×10^{-7}
Platelet degranulation		77	8	2.8×10^{-7}
Peptide ligand-binding receptors		175	14	3.8×10^{-7}
Molecules associated with elastic fibres		34	5	7.1×10^{-7}
Amine ligand-binding receptors		35	5	8.6×10^{-7}
G _{αi} signalling events		184	14	9.8×10^{-7}
GPCR ligand binding		363	27	1.1×10^{-6}
Elastic fibre formation		38	5	1.5×10^{-6}
G _{αq} signalling events		159	12	1.9×10^{-6}
Serotonin receptors		12	3	3.8×10^{-6}
P2Y receptors		12	3	3.8×10^{-6}
Signal amplification		16	3	2.3×10^{-5}
Gastrin-CREB signalling pathway via PKC and MAPK		180	12	2.3×10^{-5}
Complement cascade		33	4	2.4×10^{-5}
Glycosaminoglycan metabolism		110	8	2.5×10^{-5}
Glycogen breakdown (glycogenolysis)		17	3	2.7×10^{-5}

4.4.3.1 Resampling Analysis

Similarly, resampling for SLIPT specific candidates (shown in Table 4.16) replicated many of the most highly over-represented pathways in stomach cancer. These include translational, immune, GPCR signalling, and elastic fibres, consistent with previous analyses in breast cancer (shown in Tables 4.8 and C.4).

While fewer pathways were supported by resampling for the intersection of SLIPT and experimental screen (Telford *et al.*, 2015) candidate partners in stomach cancer than breast cancer, many of those detected (shown in Table 4.17) replicate those detected in breast cancer (shown in Table 4.9). The pathways detected by both permutation and over-representation were more likely to be replicated across stomach and breast cancer than those detected by over-representation alone, supporting the use of this procedure to detect synthetic lethal pathways applicable across cancer types. The include $G_{\alpha s}$ signalling and elastic fibre formation as discussed for breast cancer (in Section 4.2.5.1).

Table 4.16: Pathways for *CDH1* partners from SLIPT in stomach cancer

Reactome Pathway	Over-representation	Permutation
<i>Extracellular matrix organization</i>	7.5×10^{-140}	0.070215
Hemostasis	1.8×10^{-121}	0.25804
Developmental Biology	9.2×10^{-107}	0.53032
Axon guidance	1.5×10^{-102}	0.6704
Eukaryotic Translation Termination	1.9×10^{-99}	$> 1.031 \times 10^{-5}$
GPCR ligand binding	3.8×10^{-99}	0.54914
Viral mRNA Translation	3.3×10^{-98}	$> 1.031 \times 10^{-5}$
Formation of a pool of free 40S subunits	3.3×10^{-98}	$> 1.031 \times 10^{-5}$
Eukaryotic Translation Elongation	1.6×10^{-97}	$> 1.031 \times 10^{-5}$
Peptide chain elongation	7.2×10^{-97}	$> 1.031 \times 10^{-5}$
Class A/1 (Rhodopsin-like receptors)	2.7×10^{-96}	0.58174
Nonsense Mediated Decay independent of the Exon Junction Complex	3×10^{-96}	$> 1.031 \times 10^{-5}$
Infectious disease	2.6×10^{-94}	0.25484
GTP hydrolysis and joining of the 60S ribosomal subunit	3.4×10^{-94}	$> 1.031 \times 10^{-5}$
L13a-mediated translational silencing of Ceruloplasmin expression	2.8×10^{-92}	$> 1.031 \times 10^{-5}$
3' -UTR-mediated translational regulation	2.8×10^{-92}	$> 1.031 \times 10^{-5}$
Neuronal System	8.4×10^{-92}	0.53433
SRP-dependent cotranslational protein targeting to membrane	9.5×10^{-92}	$> 1.031 \times 10^{-5}$
Eukaryotic Translation Initiation	2.0×10^{-90}	$> 1.031 \times 10^{-5}$
Cap-dependent Translation Initiation	2.0×10^{-90}	$> 1.031 \times 10^{-5}$
Nonsense-Mediated Decay	7.4×10^{-90}	$> 1.031 \times 10^{-5}$
Nonsense Mediated Decay enhanced by the Exon Junction Complex	7.4×10^{-90}	$> 1.031 \times 10^{-5}$
Adaptive Immune System	8.1×10^{-88}	0.14116
Translation	1.3×10^{-87}	$> 1.031 \times 10^{-5}$
Platelet activation, signalling and aggregation	1.3×10^{-86}	0.28959
Influenza Infection	1×10^{-82}	$> 1.031 \times 10^{-5}$
Influenza Viral RNA Transcription and Replication	2.4×10^{-82}	$> 1.031 \times 10^{-5}$
Influenza Life Cycle	2×10^{-80}	$> 1.031 \times 10^{-5}$
Response to elevated platelet cytosolic Ca ²⁺	4.9×10^{-78}	0.50817
Signalling by NGF	1.6×10^{-75}	0.38518
Rho GTPase cycle	5.1×10^{-75}	0.14864
Signalling by PDGF	7.4×10^{-74}	0.40493
<i>Signalling by Rho GTPases</i>	5.1×10^{-73}	0.077217
Glycosaminoglycan metabolism	1.4×10^{-68}	0.52984
G _{αi} signalling events	1.8×10^{-66}	0.9254
Metabolism of carbohydrates	1.1×10^{-65}	0.39501
G_{αs} signalling events	2.7×10^{-65}	0.0050293
Potassium Channels	2.7×10^{-65}	0.53359

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR).

Significant pathways were marked in bold (FDR < 0.05) and italics (FDR < 0.1).

Table 4.17: Pathways for *CDH1* partners from SLIPT in stomach and siRNA

Reactome Pathway	Over-representation	Permutation
Platelet activation, signalling and aggregation	3.9×10^{-9}	0.49557
Class A/1 (Rhodopsin-like receptors)	3.9×10^{-9}	0.98432
Response to elevated platelet cytosolic Ca ²⁺	5.5×10^{-8}	0.54349
Platelet homeostasis	5.7×10^{-8}	0.45017
Nucleotide-like (purinergic) receptors	1.8×10^{-7}	0.36966
Peptide ligand-binding receptors	3.8×10^{-7}	0.91294
Molecules associated with elastic fibres	7.1×10^{-7}	0.0025868
Amine ligand-binding receptors	8.6×10^{-7}	0.43303
G _{αi} signalling events	9.8×10^{-7}	0.99626
GPCR ligand binding	1.1×10^{-6}	0.97733
Elastic fibre formation	1.5×10^{-6}	0.0025868
G _{αq} signalling events	1.9×10^{-6}	0.86089
P2Y receptors	3.8×10^{-6}	0.18795
Serotonin receptors	3.8×10^{-6}	0.37853
Signal amplification	2.3×10^{-5}	0.47856
Gastrin-CREB signalling pathway via PKC and MAPK	2.3×10^{-5}	0.98567
Complement cascade	2.4×10^{-5}	$> 3.4628 \times 10^{-6}$
Glycosaminoglycan metabolism	2.5×10^{-5}	0.38953
Glycogen breakdown (glycogenolysis)	2.7×10^{-5}	0.83772
Defective B4GALT7 causes EDS, progeroid type	4.9×10^{-5}	0.10792
Defective B3GAT3 causes JDSSDHD	4.9×10^{-5}	0.10792
Role of LAT2/NTAL/LAB on calcium mobilization	5.6×10^{-5}	0.35373
Cell surface interactions at the vascular wall	5.6×10^{-5}	0.47642
G_{αs} signalling events	6×10^{-5}	0.019858
Signalling by NOTCH	6×10^{-5}	0.19008
A tetrasaccharide linker sequence is required for GAG synthesis	0.00017	0.47642
Extracellular matrix organization	0.00018	0.0047308
Collagen formation	0.00018	0.19245
Effects of PIP2 hydrolysis	0.0002	0.37779
Syndecan interactions	0.0002	0.37779
Diseases associated with glycosaminoglycan metabolism	0.00023	0.01028
Diseases of glycosylation	0.00023	0.01028
<i>Chondroitin sulfate/dermatan sulfate metabolism</i>	0.00023	0.085541
Integrin alphaIIb beta3 signalling	0.00028	0.76936
Keratan sulfate biosynthesis	0.00034	0.68744
Rho GTPase cycle	0.00034	0.15675
Creation of C4 and C2 activators	0.00035	0.12275
Abacavir transport and metabolism	0.00035	0.12443
Amine compound SLC transporters	0.00037	0.69773
FCER1 mediated NF-κB activation	0.00037	0.69846
Fc epsilon receptor (FCER1) signalling	0.00056	0.43303
Defective EXT2 causes exostoses 2	0.00067	0.16053
Defective EXT1 causes exostoses 1, TRPS2 and CHDS	0.00067	0.16053
<i>Collagen biosynthesis and modifying enzymes</i>	0.00071	0.052911
Keratan sulfate/keratin metabolism	0.00073	0.46533
G alpha (12/13) signalling events	0.00078	0.59164
SEMA3A-Plexin repulsion signalling by inhibiting Integrin adhesion	0.00084	0.038504
Signal attenuation	0.00084	0.37779
Eicosanoid ligand-binding receptors	0.0011	0.11117
SOS-mediated signalling	0.0011	0.25387

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR). Significant pathways were marked in bold (FDR < 0.05) and italics (FDR < 0.1).

4.4.4 Metagene Analysis

Metagene analysis (as conducted in Section 4.3) was also performed for TCGA stomach cancer expression data, using Reactome pathways. These results (as shown in Table 4.18) provided further support for signalling and extracellular processes as synthetic lethal pathways across stomach and breast cancer. Namely, cell-cell communication, VEGF signalling, and various GPCR pathways were detected. These results support the role of extracellular processes in proliferation of *CDH1*-deficient cancers and interactions of *CDH1* with the extracellular environment that was not tested in the cell line experimental screen in addition to the signalling pathways that were identified.

Table 4.18: Synthetic lethal metagenes against *CDH1* in stomach cancer

Pathway	ID	Observed	Expected	χ^2 value	p-value	p-value (FDR)
Cell-Cell communication	1500931	18	50.4	110	7.43×10^{-23}	1.53×10^{-20}
VEGFR2 mediated vascular permeability	5218920	19	50.4	109	1.36×10^{-22}	2.49×10^{-20}
Sema4D in semaphorin signalling	400685	20	50.4	104	1.62×10^{-21}	2.12×10^{-19}
Ion transport by P-type ATPases	936837	17	50.4	100	8.29×10^{-21}	8.06×10^{-19}
Sialic acid metabolism	4085001	19	50.4	95.3	9.95×10^{-20}	7.82×10^{-18}
Synthesis of pyrophosphates in the cytosol	1855167	26	50.4	94	1.86×10^{-19}	1.23×10^{-17}
Keratan sulfate/keratin metabolism	1638074	25	50.4	93.5	2.36×10^{-19}	1.44×10^{-17}
Ion channel transport	983712	19	50.4	92.8	3.37×10^{-19}	1.99×10^{-17}
Keratan sulfate biosynthesis	2022854	26	50.4	91.4	6.79×10^{-19}	3.62×10^{-17}
Arachidonic acid metabolism	2142753	22	50.4	90.6	9.81×10^{-19}	5.07×10^{-17}
RHO GTPases activate CIT	5625900	22	50.4	87	5.80×10^{-18}	2.66×10^{-16}
Stimuli-sensing channels	2672351	25	50.4	85.8	1.03×10^{-17}	4.58×10^{-16}
Synthesis of PI	1483226	19	50.4	85.6	1.15×10^{-17}	4.89×10^{-16}
G-protein activation	202040	19	50.4	85.3	1.34×10^{-17}	5.53×10^{-16}
NrCAM interactions	447038	22	50.4	84.3	2.1×10^{-17}	8.27×10^{-16}
Inwardly rectifying K^+ channels	1296065	24	50.4	83.5	3.19×10^{-17}	1.22×10^{-15}
Calcitonin-like ligand receptors	419812	20	50.4	82.2	6.07×10^{-17}	2.13×10^{-15}
Prostacyclin signalling through prostacyclin receptor	392851	24	50.4	81.8	7.27×10^{-17}	2.5×10^{-15}
Presynaptic function of Kainate receptors	500657	26	50.4	79.7	2.00×10^{-16}	6.34×10^{-15}
ADP signalling through P2Y purinoceptor 12	392170	23	50.4	79.2	2.57×10^{-16}	7.71×10^{-15}
regulation of FZD by ubiquitination	4641263	22	50.4	78.8	3.15×10^{-16}	9.3×10^{-15}
Toxicity of tetanus toxin (TeNT)	5250982	27	50.4	78.7	3.36×10^{-16}	9.75×10^{-15}
Gap junction degradation	190873	21	50.4	78.5	3.66×10^{-16}	1.04×10^{-14}
Nephrin interactions	373753	25	50.4	78.2	4.21×10^{-16}	1.14×10^{-14}
GABA synthesis, release, reuptake and degradation	888590	26	50.4	77	7.69×10^{-16}	1.95×10^{-14}

Strongest candidate synthetic lethal partners for *CDH1* by SLIPT with observed and expected numbers of TCGA stomach cancer samples with low expression of both genes.

4.5 Discussion

4.5.1 Strengths of the SLIPT Methodology

Synthetic lethal discovery with SLIPT applied statistical procedures to identify putative partner genes from gene expression data. The χ^2 -values were also used for pathways or permutation analyses. This approach could be applied to other disease genes or pair-wise across the genomes, although previous genome-wide approaches were unable to find informative candidate genes for E-cadherin (Lu *et al.*, 2015). Synthetic lethal discovery in cancer has focused on genes with severe cellular mutant phenotypes, such as essential genes or the oncogenes *TP53* and *AKT* (Lu *et al.*, 2015; Tiong *et al.*, 2014; Wang and Simon, 2013). Other cancer genes, such as *CDH1*, required more focused investigations (Srihari *et al.*, 2015; Telford *et al.*, 2015). Prior computational approaches for synthetic lethal discovery, in cancer, vary widely (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015; Tiong *et al.*, 2014; Wappett *et al.*, 2016). There is no consensus as to which approach is more appropriate, and the methods are difficult to compare, as many do not make predictions from similar data or have a released code implementation.

The query-based approach demonstrated by SLIPT analysis is suitable for wider application on expression data in concert with experimental screens. This approach has identified biologically plausible synthetic lethal pathways for *CDH1*, triaged candidates from experimental screening (Telford *et al.*, 2015), and replicates gene and pathways across breast and stomach cancer datasets. SLIPT avoids the assumptions underlying the design of some approaches, such as co-expression of synthetic candidates or that interacting gene pairs will have known (annotated) similarities in function. Since functional redundancy does not require genes to be expressed at the same time (Lu *et al.*, 2015), the SLIPT approach does not assume co-expression of synthetic lethal genes which may enrich for synthetic lethal genes in established coregulated pathways. The interpretation of synthetic lethality for SLIPT was similar to methods based on ‘co-loss under-representation’, ‘compensation’, or ‘simultaneous differential expression’ (Lu *et al.*, 2015; Tiong *et al.*, 2014; Wang and Simon, 2013).

Genomics analyses are prone to false-positives and require statistical caution, particularly with gene-pairs which scale up the number of multiple tests drastically. Thus analyses throughout this thesis have focused on querying for partners of a particular gene of interest. Experimental screens for synthetic lethality are also error-prone (Fec de la Cruz *et al.*, 2015; Lord *et al.*, 2015; Lu *et al.*, 2015), especially with false-positives,

raising the need for integrated analysis of genetic interactions in the genomes, or statistical modelling of the discovery of synthetic lethal partners of a particular query gene (in Section 3.3 and Chapter 6). Simulations based on the model also supported the design decisions underlying SLIPT analysis and its strengths over other approaches.

4.5.2 Synthetic Lethal Pathways for E-cadherin

Specific genes were difficult to replicate across experiments. This is consistent with gene expression profiles for synthetic lethal partners reflecting the complexity of biological pathways (Perou *et al.*, 2000), which are subject to higher-order interactions and do not consistently compensate for loss of gene function across all samples (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015). The large number of synthetic lethal partners detected may stem from synthetic lethal detection being error-prone, and indicates that identifying genes relevant for clinical application could be difficult without a supporting biological pathway rationale. As such, investigations into the genes identified by SLIPT, the correlation structure between them, and those which were validated by experimental screening (Telford *et al.*, 2015), focused at the pathway level throughout this chapter and comparisons across analyses were mainly made at the pathway level.

The synthetic lethal partners identified by SLIPT had many distinct functions and were highly expressed in different patient subgroups (Figure 4.1). Ductal breast cancers had higher expression of synthetic lethal partners, suggesting treatment may be more effective in these tumours. Conversely, there was consistently low expression of SL partners in ER negative tumours, that have poor prognosis, which could inform other treatment strategies. Synthetic lethal partner expression varies between patients which suggests that these different tumour classes could react differently to the same treatment and that the expression of synthetic lethal partners could be a clinically important biomarker. Treatment of different pathway and gene combinations in different patients is likely to be the most effective approach to target genes compensating for *CDH1* gene loss without acquired resistance as well (Lord *et al.*, 2015).

The synthetic lethal partners of *CDH1* identified by SLIPT were involved in a diverse range of biological functions and differed to those detected experimentally. This discrepancy may be accounted for by gene expression analyses detecting both synthetic lethal partners, as screened for experimentally by Telford *et al.* (2015), and their upstream regulators or downstream targets (that were not detected by siRNA). Hence SLIPT may be capturing the wider pathways and mechanisms involved in synthetic lethality with *CDH1* inactivation. In particular, GPCR phosphorylation cascades,

which regulate gene expression and translation in cancers (Gao and Roux, 2015), were predicted to be synthetic lethal with *CDH1*. The most consistently supported pathways included elastic fibres in the extracellular matrix, GPCR signalling, and translation, which present vulnerabilities for *CDH1*-deficient cancer cells from extracellular stimuli to the core growth mechanisms of a cell.

The diversity in synthetic lethal functions is consistent with the wide ranging role of *CDH1* in cell-cell adhesion, cell signalling, and the cytoskeletal structure of epithelial tissues. Pathway structure may be relevant to identifying potential drug targets from gene expression signatures, indicating downstream effector genes and mechanisms leading to cell inviability. Identification of distinct synthetic lethal gene clusters may lead to the elucidation of drug resistance mechanisms. While these pathways are indicative of the main functions of E-cadherin and synthetic lethal partners, it remains to identify the genes within these pathways that are the most actionable or supported across SLIPT analysis in patient samples and detected by experiments in preclinical models (Chen *et al.*, 2014; Telford *et al.*, 2015). The specific genes within key pathways will be discussed in Chapter 5, along with further investigations in the context of pathway structure. These synthetic lethal pathways have potential clinical implications, particularly those supported in pre-clinical models and in patient expression data. However, further validation of gene candidates will be necessary to ensure that these are able to be reproduced in further pre-clinical studies, they are applicable to tumours *in vivo*, and that effective inhibitory agents can be repurposed or designed against them. While these pathways have important clinical implications, the synthetic lethal predictions also need statistical modelling and simulation of synthetic lethality in genomics expression data to ensure that the candidates detected are reliable.

4.5.3 Replication and Validation

4.5.3.1 Integration with siRNA Screening

The pathways composition across computational and experimental synthetic lethal candidates was identified by over-representation (Table 4.7), and supported by resampling analysis (Table 4.9), despite a modest intersection of genes between them (Figure 4.2). Either approach may identify a pathway without being supported by the other: resampling analysis may support pathways that were not over-represented due to small effect sizes, thus both tests are required for a candidate pathway. The pathways detected by both over-representation and resampling are the strongest candidates for further investigation. The pathway structure analyses in Chapter 5 will focus on these pathways

detected by both over-representation and resampling. Particularly, those replicated across datasets or with pathway metagenes.

The SLIPT approach was shown to be predictive of which siRNA primary screen candidate partners of *CDH1* were validated in a secondary screen (as shown in Section 4.2.4). These results further support SLIPT for identifying robust synthetic lethal candidates which can be validated and as a triage approach for interpreting screening experiments.

4.5.3.2 Replication across Tissues

Synthetic lethal partners identified by SLIPT were replicated across breast and stomach cancer. These were particularly concordant at the pathway level, as expected between tissues, since synthetic lethal pathways have higher conservation between species (Dixon *et al.*, 2008). These findings support gene functions conserved across *CDH1*-deficient cancers in breast and stomach tissues, presenting vulnerabilities that could be applied against molecular targets in both cancers. In addition, these analyses serve as a replication across independent patient cohorts from breast and stomach cancers, decreasing the likelihood of the synthetic lethal pathways detected being false positives or artifacts of either dataset.

Synthetic lethal pathways were also replicated across expression analyses of TCGA patient samples in heterogeneous tumours and homogeneous cell line isolates. This further **suggests** that the subset of synthetic lethal functions detectable in experimental models (Chen *et al.*, 2014; Telford *et al.*, 2015) would be **applicable to** tumours of patients with *CDH1*-deficient cancers. There are many gene functions replicated across breast cancer gene expression analyses. Many of these were also replicated with mutation analysis and with stomach cancer or cell line expression data.

4.6 Summary

I have developed a simple, interpretable, computational approach to predict synthetic lethal partners from gene expression data. This approach has been applied to robustly detect synthetic lethal pathways for E-cadherin (the *CDH1* gene) in TCGA breast cancer molecular **profiles**. **Comparisons** were made to experimental screening (Telford *et al.*, 2015) in cell lines and **the analysis was replicated in** TCGA stomach cancer molecular profiles. The pathways replicated across several analyses included extracellular matrix pathways (e.g., elastic fibres formation), cell signalling (including GPCRs), and core gene regulation and translational processes crucial for the growth and proliferation of cancer cells. These pathways are **subject to** non-oncogene addiction for

CDH1-deficient cells, which presents vulnerabilities that could be exploited for specific treatment against *CDH1* mutations in cancers. There was also support for synthetic lethality with *CDH1* in cell adhesion and cytoskeletal processes, supporting the finding that synthetic lethality occurs within biological pathways (Boone *et al.*, 2007; Kelley and Ideker, 2005).

While translational and immune pathways detected by SLIPT were not supported by primary siRNA screening (Telford *et al.*, 2015), these were replicated across various analyses. Due to the differences between an experimental cell line model (Chen *et al.*, 2014; Fece de la Cruz *et al.*, 2015) and patient molecular profiles (Bass *et al.*, 2014; Koboldt *et al.*, 2012), these would not be expected to be completely concordant as some pathways are difficult to test in an isolated experimental system. Nevertheless, many of the genes and pathways detected by SLIPT are suitable to inform further investigations and triage of therapeutic targets against *CDH1*-deficient tumours.

Thus synthetic lethal pathways have been identified using TCGA patient molecular profiles and experimental screening results. Some of these were robustly replicated across these datasets and against *CDH1* mutation or expression analysis. However, there remains the need to identify actionable genes within these pathways, relationships with experimental candidates, and how these pathways may affect viability when lost. The results of the TCGA breast cancer analysis will be further examined in the context of pathway structure and relationships in the following Chapter.

Chapter 5

Synthetic Lethal Pathway Structure

Having identified key pathways implicated in synthetic lethal genetic interactions with *CDH1* (in Chapter 4), the synthetic lethal genes within these pathways were investigated for their relationships with respect to pathway structure. This chapter will focus on the Reactome biological pathways detected across analyses in Chapter 4. Specifically, investigations were performed to determine whether synthetic lethal candidates, detected by SLIPT or siRNA, exhibited differences with respect to metrics of pathway structure of network connectivity and importance (as described in Sections 2.4.4 and 3.5.3). The relationships between synthetic lethal candidates, detected by either approach, were also examined to determine whether SLIPT candidate genes were upstream or downstream siRNA candidate genes by resampling (as described in Sections 3.4.1 and 3.4.1.1). Together these investigations into structural relationships demonstrate how a combination of network biology and statistical techniques can be performed with genes identified by a bioinformatics analysis.

5.1 Synthetic Lethal Genes in Reactome Pathways

The graph structure for Reactome pathways was obtained from Pathway Commons via BioPAX (as described in Section 2.4.2). The pathways describe the (directional) relationships between biomolecules, including genes that encode proteins in biological pathways. These relationships include cell signalling (e.g., kinase phosphorylation cascades), gene regulation (e.g., transcription factors, chromatin modifiers, RNA binding proteins), and metabolism (e.g., the product of an enzyme being the substrate of another). Together these relationships describe the known functional pathways in a human cell with a reasonable resolution, from a curated database supported by publications documenting pathway relationships.

Pathway structures from the Reactome network (as described in Section 2.4.3) were used to derive the graph structure of each biological pathway. The synthetic lethal candidate genes for notable pathways discussed in Chapter 4, including candidate synthetic lethal pathways of *CDH1*, were examined to show the SLIPT and siRNA candidates within these pathways. The synthetic lethal genes considered here are those candidates detected by SLIPT (as described in Section 3.1) in TCGA breast cancer expression and mutation data (Koboldt *et al.*, 2012) in comparison to the candidate gene partners from the siRNA screening in breast cell lines (Telford *et al.*, 2015).

5.1.1 The PI3K/AKT Pathway

The phosphoinositide 3-kinase (PI3K) cascade signalling pathway is important in cancer because it is involved in mediating signals between the GPCRs and regulation of protein translation, which have both been strongly implicated to be synthetic lethal pathways with loss of *CDH1* function (Chapter 4). These pathways are all subject to dysregulation in cancer (Courtney *et al.*, 2010; Dorsam and Gutkind, 2007; Gao and Roux, 2015). Thus the PI3K cascade will be examined along with the most supported synthetic lethal pathways (as identified in Chapter 4).

The PI3K pathway is well characterised and has an established direction of signal transduction from extracellular stimuli (and membrane bound receptors) to the inner mechanisms of the cell, namely, the regulation of protein translation. The production of proteins is necessary for the growth of the cell so it is reasonable to suggest that these processes may be subject to (non-oncogene) addiction in some cancer cells which rely upon them for sustained protein production and cell growth. This is also supported by the oncogenes *PIK3CA* and *AKT1* being involved with the PI3K cascade and the related PI3K/AKT pathway, which may be subject to oncogene addiction when these proto-oncogenes are activated.

The PI3K cascade was not supported across SLIPT in TCGA breast expression data and the siRNA primary screen by over-representation (in Section 4.2.5) or resampling (in Section 4.2.5.1) but genes within this pathway were detectable by either approach (as shown in Figure 5.1). While few genes were identified by both approaches, they include genes that are highly connected in the PI3K cascade and are hubs to information transmission such as *FGF9*, *PDE3B*, and *PDE4A*. The key upstream genes *PIK3CA* and *PIK3CG* were detected by siRNA whereas the downstream *PIK3R1* and *AKT2* genes were detected by SLIPT. Genes detected by either method were also prevalent in the PI3K, PDE, and AMPK modules, in addition to the downstream translation factors

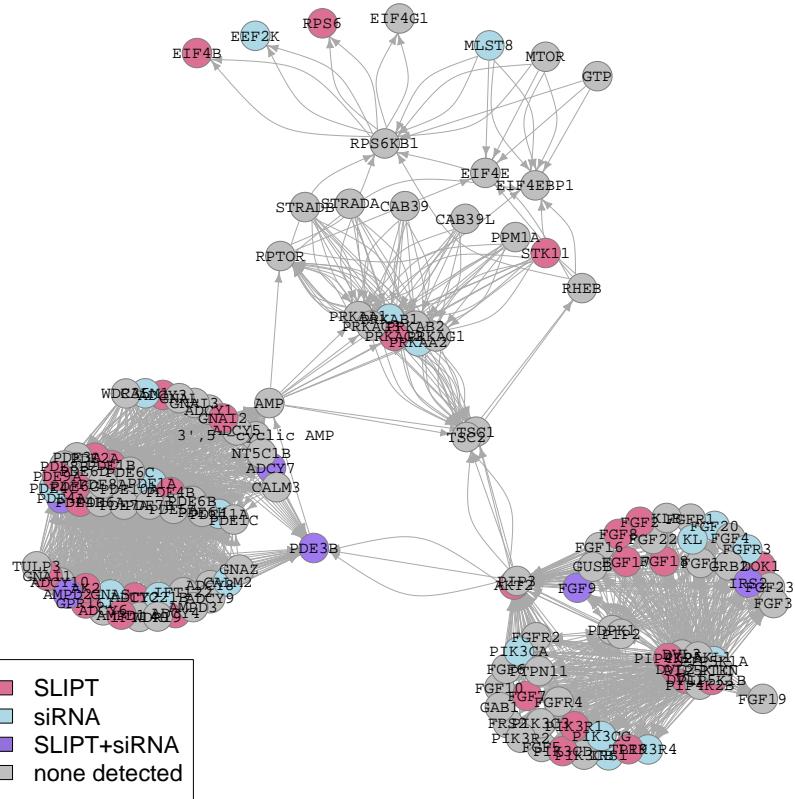


Figure 5.1: **Synthetic lethality in the PI3K cascade.** The Reactome PI3K Cascade pathway with synthetic lethal candidates coloured as shown in the legend.

and ribosomal genes (*EIF4B*, *EEF2K*, and *RPS6*). Together these suggest that there may be further structure between the SLIPT and siRNA candidate partners of *CDH1* in pathways as illustrated by PI3K. As such, pathway structure will be investigated to detect differences in the upstream and downstream gene candidates detected by either method. Pathway structure may account for the disparity between SLIPT and siRNA genes, even in pathways such as PI3K where they did not significantly intersect. For instance, SLIPT gene partners may be downstream of siRNA candidates rather than replicating them directly.

This disparity between SLIPT and siRNA gene candidates synthetic lethal partners of CDH1 (i.e., a high number of genes detected by either approach with few detected by both) was replicated in the related PI3K/AKT pathway and the “PI3K/AKT in cancer” pathway (shown in Appendix Figures F.1 and F.2). Many synthetic lethal candi-

dates were at the upstream core of these pathway networks and the downstream extremities. It is particularly notable that many genes important in cell signalling and gene regulation were detected by either synthetic lethal detection approach. These include *AKT1*, *AKT2*, and *AKT3*, the Calmodulin signalling genes *CALM1* and *CAMK4*, and the forkhead family transcription factors *FOXO1* (a tumour suppressor) and *FOXO4* (an inhibitor of EMT).

5.1.2 The Extracellular Matrix

The extracellular pathways “elastic fibre formation” and “fibrin clot formation” (shown in Appendix Figures F.3 and F.4 respectively) were both supported across analyses (in Chapter 4). These pathways were identified by both SLIPT (for TCGA breast cancer) and siRNA gene candidates as they had significant over-representation and resampling analyses.

Particularly for elastic fibres (Appendix Figure F.3), the vast majority of genes were detected by either approach, in addition to a significant proportion of genes detected by both approaches (as determined in Section 4.2.5). The genes detected by both approaches also appeared to have a non-random distribution in the network, with *TFGB1*, *ITGB8*, and *MFAP2* exhibiting high connectivity, and having a central role in their respective pathway modules. In addition to a structural role in the extracellular matrix and connective tissue (including the tumour microenvironment), these proteins including Furin, TGF β , and BMP, are also involved in responses to endocrine signals and interact with the cellular receptors for signalling pathways. Therefore it is plausible that *CDH1*-deficient tumours will be subject to non-oncogene addiction to the extracellular environment and growth signals arising from this pathway. The pathway structure also indicated that the genes detected by siRNA (or by both approaches) may be downstream of those detected by SLIPT, in addition to whether connectivity or centrality is higher for synthetic lethal candidates than other genes in the pathway.

Genes detected as synthetic lethal partners of *CDH1* by SLIPT or siRNA screening were also common in the Fibrin clot formation pathway (shown in Appendix Figure F.4). This is consistent with the established pleiotropic role of *CDH1* in regulating fibrin clotting. It is also notable that the genes detected by either method appear to be highly connected such as *C1QBP*, *KNG1*, *F8*, *F10*, *F12*, *F13A*, and *PROC* (including many of the coagulation factors). Synthetic lethal candidates also include *SERPINE2* and *PRCP*, which only affect downstream genes, in addition to *PROCR* and *VWF*, which are only affected by upstream genes.

Many of these genes are involved in the Extracellular Matrix pathway (shown in Appendix Figure F.5), including many of the synthetic lethal candidates discussed for elastic fibres. The number of SLIPT candidate genes outnumbers those identified by siRNA, as expected from an isolated cell model. However, the endocrine response genes (e.g., *TGFB1* and *LTBP4*) which are potentially artifacts of the cell line growth process were replicated with SLIPT analysis in patient tumours (TCGA breast cancer data). There is also additional support for synthetic lethal genes (e.g., *ITGB2*, *MFAP2*, and *SPARC*) being highly connected networks hubs of the pathway. The complexity of the extracellular matrix pathway lends credence to the need for formal network analysis approaches to interpret the pathway structure of synthetic lethal candidates. Furthermore, statistical approaches are needed to determine whether the apparent structural relationships between synthetic lethal candidates could have occurred by chance

5.1.3 G Protein Coupled Receptors

G protein coupled receptor (GPCR) pathways are highly complex (as shown in Figure 5.2 and Appendix Figure F.6). Many genes in these pathways were synthetic lethal as detected by either SLIPT or siRNA screening, including genes frequently detected by both approaches, consistent with these pathways being supported by prior analyses (in Sections 4.2.5 and 4.2.5.1). Synthetic lethal candidates include the Phosphodiesterase (PDE) and Calmodulin genes (as discussed in Section 5.1.3) in addition to others such as the regulators of RGS, chemokine receptors (CXCR), Janus Kinase (JAK), and the Ras Homolog Family (RHO) genes. These are important regulatory signalling pathways necessary for cellular growth and cancer proliferation. Thus the GPCR pathways (and downstream PI3K/AKT signals) are a potentially actionable vulnerability against *CDH1*-deficient cancers, particularly since many existing drug targets are in these signalling pathways, some of which have been experimentally validated (Telford *et al.*, 2015). While statistically significant numbers of genes in pathways were detected by both approaches (in Sections 4.2.5 and 4.2.5.1), the complexity of GPCR networks (containing hundreds of genes) further support the needs for a rational network-based approach to the relationships between SLIPT and experimental candidates.

5.1.4 Gene Regulation and Translation

While very few synthetic lethal genes were detected in translational pathways in an experimental screen against *CDH1* (Telford *et al.*, 2015), these were highly overrepresented in translational elongation (as shown in Appendix Figure F.7). These

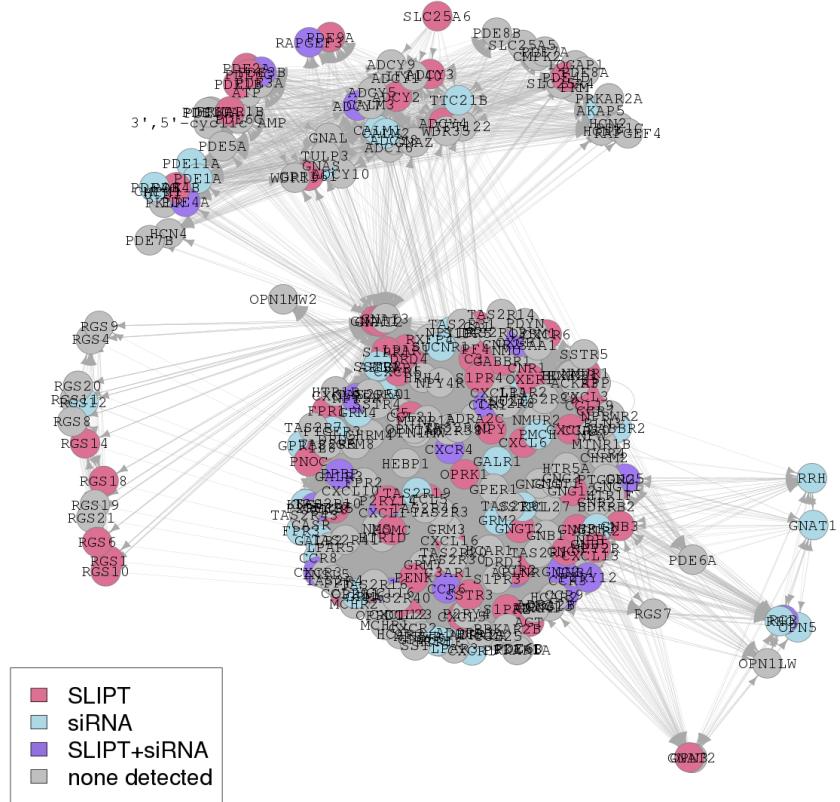


Figure 5.2: Synthetic lethality in the GPCRs. The Reactome $G_{\alpha i}$ pathway with synthetic lethal candidates, coloured as shown in the legend.

SLIPT genes include many ribosomal proteins and the regulatory “elongation factors” which may be subject to responses in the upstream signalling pathways. This observation further indicates that pathway structure may be used to identify relationships between synthetic lethal candidates detected by SLIPT and siRNA. The computational approach with SLIPT may exhibit the ability to detect downstream genes in the core translational processes, which experimental screening did not identify. The experimental screening may similarly detect upstream regulatory genes less sensitive to inactivation, that is, genes that are less likely to be indiscriminately lethal to both genotypes at high doses of inactivation.

Many of these SLIPT candidate genes are also among the nonsense-mediated decay (NMD) pathway (shown in Appendix Figure F.8) or 3' untranslated region (UTR) mediated translational regulation (shown in Appendix Figure F.9). While genes in

these pathways were also supported by experimental screening with siRNA, there were differences in which genes were detected within the pathway structures. In particular, *UPF1* was detected in the siRNA screen and is the focal downstream gene for the entire NMD pathway showing that (in this case) siRNA genes are downstream effectors of those detected by SLIPT. 3' UTR mediated translational regulation has a similar structure with two modules connected solely by *RPL13A*, giving an example of SLIPT candidate genes with high connectivity, although there were many ribosomal proteins detected by SLIPT. However, the detection of *EIF3K*, a regulatory elongation factor (not essential to ribosomal function) was replicated across SLIPT and siRNA screening, while the majority of the elongation factors were not detected by either approach. Regulatory genes, being more amenable to experimental validation, also support further investigation into pathway structure. The SLIPT candidates may support experimental candidates in biological pathways by detecting downstream genes, which may not be detectable by experimental screening with high dose inhibitors. This difference between the approaches may explain the greater number of SLIPT candidate partners of *CDH1* than those experimentally identified.

5.2 Network Analysis of Synthetic Lethal Genes

To demonstrate the network properties of synthetic lethal candidates in a pathway, a network analysis was performed on the genes detected as synthetic lethal partners of *CDH1* with the SLIPT computational approach and the siRNA screen (Telford *et al.*, 2015) in G_{ai} signalling, a GPCR pathway. This pathway was used to demonstrate deeper network analysis approaches to synthetic lethal candidates within complex pathways, as it was supported across analyses (in Chapter 4), with significant over-representation in both SLIPT and siRNA screening, and the genes differed considerably between synthetic lethal detection methods (shown in Appendix Figure 5.2). These network metrics were used to measure whether the network properties differed between groups of genes detected by either or both approaches. These analyses serve to test both whether synthetic lethal gene candidates had higher connectivity or importance in a network and whether either detection approach is biased towards genes with different network properties.

5.2.1 Gene Connectivity and Vertex Degree

Vertex degree (the number of connections) for each gene is a fundamental property of a network. The vast majority of genes had a relatively modest number of connections,

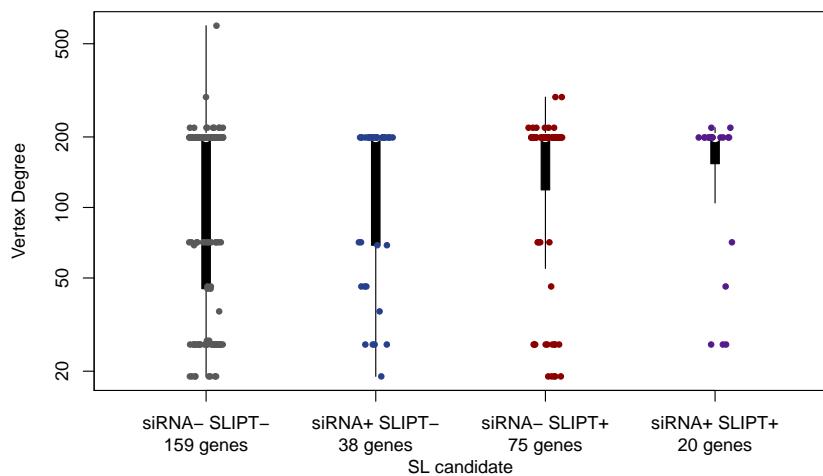


Figure 5.3: Synthetic lethality and vertex degree. The number of connected genes (vertex degree) was compared (on a log-scale) across genes detected by SLIPT and siRNA screening in the Reactome $G_{\alpha i}$ signalling pathway. There were no differences in vertex degree between the groups (shown in Table 5.1), although genes detected by siRNA included those with the fewest connections.

Table 5.1: ANOVA for synthetic lethality and vertex degree

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	21	20.8	0.0030	0.9561
SLIPT	1	16215	16215	2.3722	0.1246
siRNA×SLIPT	1	17	17	0.0025	0.9603

Analysis of variance for vertex degree against synthetic lethal detection approaches (with an interaction term)

each with only a few genes in the $G_{\alpha i}$ pathway (shown in Figure 5.3) having pathway relationships with a high number of genes, consistent with the scale-free property of biological networks (Barabási and Oltvai, 2004). The number of connections was similar between gene groups (by synthetic lethal detection). Genes detected by siRNA included those with the fewest connections, despite there being fewer genes that were detected by either approach. There was no statistically significant effect of either computational or experimental synthetic lethal detection method on vertex degree, as determined by analysis of variance (ANOVA) (shown by Table 5.1).

The results for the $G_{\alpha i}$ pathway were very similar when testing synthetic lethality against *CDH1* mutation (mtSLIPT). In either case, there was no significant evidence that SLIPT or mtSLIPT-specific genes had higher connectivity than those detected by siRNA screening (shown in Appendix Figure G.1 and Appendix Table G.1). Thus synthetic lethal detection does not discriminate among genes by their connectivity in this pathway network, nor is either approach constrained to detecting highly connected genes. Both approaches have been demonstrated to detect genes with many and very few connections in the $G_{\alpha i}$ signalling pathway.

5.2.2 Gene Importance and Centrality

5.2.2.1 Information Centrality

Information centrality is a measure of the importance of nodes in a network in terms of how vital they are to the transmission of information throughout the network. This applies well to biological pathways, particularly gene regulation and cell signalling. The nodes with the highest information centrality are not necessarily the most connected, as they may also include nodes that pass signals between highly connected network hubs. Information centrality therefore provides a distinct metric for the connectivity of a gene in a pathway, which has the added benefit of being directly related to the disruption of pathway function were it to be inactivated or removed. Information centrality has also been suggested to be indicative of the essentiality of genes or proteins (Kranthi *et al.*, 2013).

Within the $G_{\alpha i}$ pathway, the information centrality across gene groups detected by either synthetic lethal approach did not differ significantly (shown by Figure 5.4 and Table 5.2). Genes detected by SLIPT span the complete range of PageRank centrality values for this pathway. These findings were very similar for mtSLIPT against *CDH1* mutation (shown in Appendix Figure G.2 and Appendix Table G.2). Thus neither method was unable to detect synthetic lethal genes in the $G_{\alpha i}$ pathway with particular centrality constraints but they were also not detecting genes with higher centrality than expected by chance.

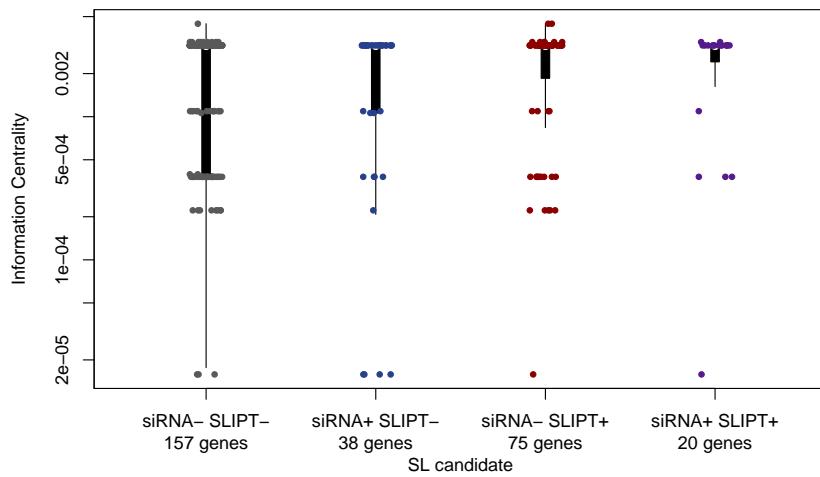


Figure 5.4: Synthetic lethality and centrality. The information centrality was compared (on a log-scale) across genes detected by SLIPT and siRNA screening in the Reactome $G_{\alpha i}$ pathway. Genes detected by SLIPT or siRNA did not have higher centrality than other genes (shown in Table 5.2). Genes detected by SLIPT spanned the range of centrality values.

Table 5.2: ANOVA for synthetic lethality and information centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.00000000	2.7000×10^{-9}	0.0016	0.96783
SLIPT	1	0.00000548	5.4831×10^{-6}	3.3253	0.06926
siRNA×SLIPT	1	0.00000002	1.8800×10^{-8}	0.0114	0.91511

Analysis of variance for information centrality against synthetic lethal detection approaches (with an interaction term)

5.2.2.2 PageRank Centrality

PageRank centrality is another network analysis procedure to infer a hierarchy of gene importance from a network using connections and structure (Brin and Page, 1998). In contrast to the information centrality approach of removing nodes, PageRank uses the eigenvalue properties of the adjacency matrix to rank genes according to the number of connections and paths they are involved in.

This distinction is immediately clear within the $G_{\alpha i}$ pathway (shown in Figure 5.5), which differs considerably from the information centrality scores (as shown in Figure 5.4). Genes detected by either synthetic lethal approach did not include those with the highest PageRank centrality. There was a significant association between genes

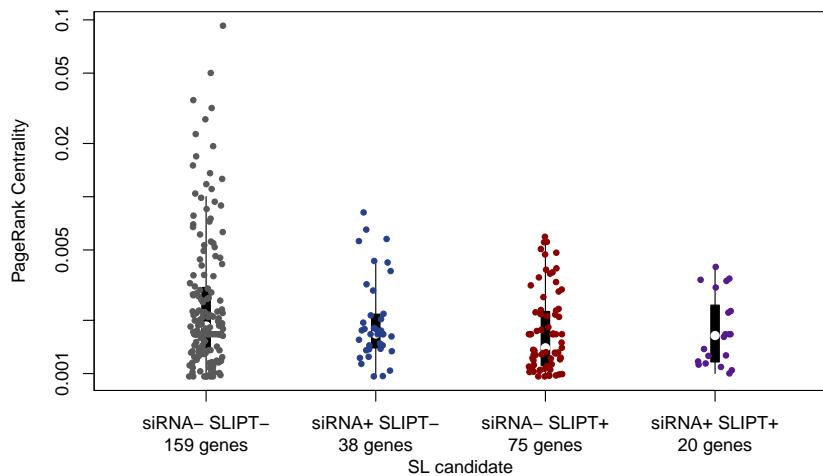


Figure 5.5: Synthetic lethality and PageRank. The PageRank centrality was compared (on a log-scale) across genes detected by SLIPT and siRNA screening in the Reactome $G_{\alpha i}$ pathway. Genes detected by either synthetic lethal detection approach had a more restricted range of centrality values but only SLIPT genes had a significant association with centrality (shown in Table 5.3).

detected by SLIPT (which had a lower median) with PageRank centrality (shown by Table 5.3).

The genes detected by SLIPT span the range of centrality values of siRNA showing that both approaches were capable of detecting genes of moderately high centrality (as shown for information centrality) and that the lower centrality of SLIPT candidates in the $G_{\alpha i}$ pathway may be due to synthetic lethal partners being less critical to the pathway, rather than a limitation of the methodology. While it is expected that some synthetic lethal genes will be important to the function of the pathway, it is possible that genes with high centrality were avoided if they are essential to cellular viability.

There was not a significant association between siRNA candidates and PageRank centrality. The significant result for SLIPT was not replicated when testing synthetic lethality against *CDH1* mutation (shown in Appendix Figure G.3 and Appendix Table G.3). However, this may be due to fewer genes being detected by mtSLIPT and siRNA.

Table 5.3: ANOVA for synthetic lethality and PageRank centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.0001059	1.0589×10^{-4}	2.1021	0.14818
SLIPT	1	0.0002881	2.8808×10^{-4}	5.7188	0.01743
siRNA×SLIPT	1	0.0000477	4.7704×10^{-5}	0.9470	0.33131

Analysis of variance for PageRank centrality against synthetic lethal detection approaches (with an interaction term)

5.3 Relationships between Synthetic Lethal Genes

The network analyses so far have tested whether synthetic lethal candidate genes were more connected or important within a pathway structure, such as the $G_{\alpha i}$ pathway. However these metrics do not ascertain whether there were relationships between SLIPT and siRNA candidate partners of *CDH1*. In particular, it is plausible that they may be upstream or downstream of **one another** within a pathway.

The direction of a biological pathway is important, particularly those involved in cell signalling which respond to extracellular stimuli and transmit these signals via intermediary proteins to regulate core functions and responses of the cell. These pathways regulate **processes** such as gene expression and protein translation, which are important in the proliferation of cancers (Gao and Roux, 2015). Therefore it is important to determine which synthetic lethal candidates were upstream or downstream in the context of a biological pathway. In particular, pathway structure may be used to identify relationships between SLIPT and siRNA gene candidates.

A pathway structure method was devised to use network structures to identify directional relationships between individual SLIPT and siRNA genes. This pathway structure methodology was applied (as described in Section 3.4.1) to detect the direction of shortest paths between SLIPT and siRNA gene candidates. This is used to demonstrate the methodology on the PI3K and $G_{\alpha i}$ pathways, to develop a statistical test for pathway structure **between** SLIPT and siRNA gene candidates using resampling (as described in Section 3.4.1.1), and to apply this test for pathway structure among synthetic lethal gene candidates to the pathways identified in Chapter 4 and discussed in Section 5.1.

5.3.1 Detecting Upstream or Downstream Synthetic Lethality

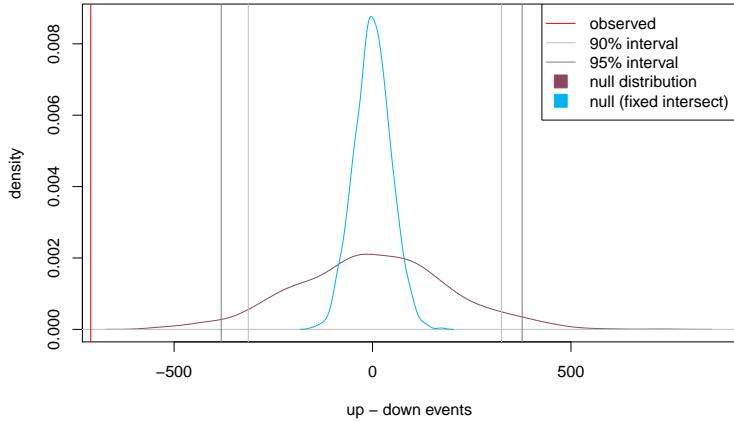
Shortest paths in a pathway network were used to devise a strategy to detect pathway structure between SLIPT and siRNA gene candidates partners of *CDH1* (as described

in Section 3.4.1). Thus I can determine whether individual SLIPT genes have upstream or downstream siRNA candidates (scored as “up” or “down” events respectively). This procedure enables the detection of directional relationships between SLIPT and siRNA gene candidates (e.g., if genes detected by siRNA are more likely to be downstream of genes detected by SLIPT in the same pathway).

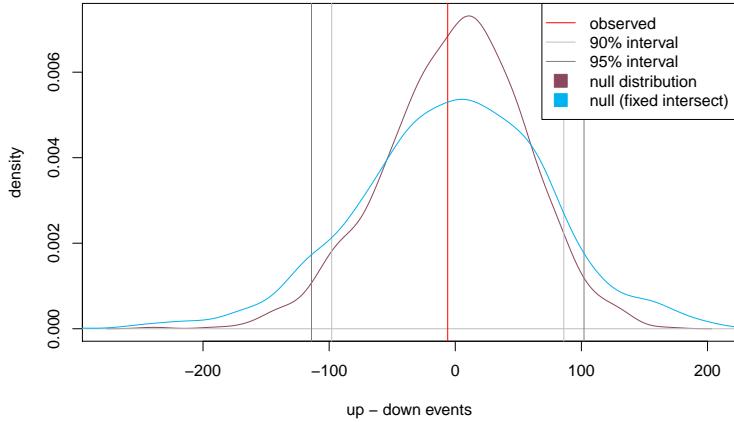
The total number of gene candidate pairs in either direction can be compared within a pathway network to assess the overall directional relationships in a pathway. This directionality is detectable by the difference between the number of SLIPT candidate genes with upstream and downstream siRNA gene partners. However, this measure alone is not sufficient to determine whether there is evidence of pathway structure between SLIPT and siRNA gene candidates partners of *CDH1* in a pathway network. Nevertheless, it does serve to measure the magnitude (and direction) of the consensus of directional relationships (upstream and downstream) between SLIPT and siRNA gene candidates partners. This measure of pathway structure can be used for testing for statistical significance of pathway structure by resampling, using a permutation procedure to test whether these relationships are detectable among randomly selected gene groups rather than the detected SLIPT and siRNA gene candidates partners (as described in Sections 2.3.6 and 3.4.1.1).

This resampling procedure was performed for the $G_{\alpha i}$ and PI3K pathways to generate a null distribution for the difference in the number of “up events” and “down events” for these pathway structures (as shown in Figures 5.1 and 5.2). The resulting null distributions (as shown in Figure 5.6) were used to detect whether genes detected by SLIPT had significantly more upstream or downstream siRNA candidates in either pathway. It can be seen that siRNA genes were significantly downstream of SLIPT candidate genes by resampling for the $G_{\alpha i}$ signalling pathway (Figure 5.6a). This demonstrates that pathway relationships can be detected between synthetic lethal candidates by this procedure and that siRNA genes were downstream of gene detected by SLIPT in an example of GPCR signalling expanding on support for synthetic lethality in this pathway (as shown in Chapter 4). These structural relationships may also account for why each **of** the computational and experimental approaches did not detect many of the same specific genes because they are detecting different parts of the pathway.

In contrast, there was **no** significant evidence of such pathway structure between siRNA and SLIPT candidate genes when resampling within the PI3K cascade pathway (as shown in Figure 5.6b). This indicates that such relationships may be pathway spe-



(a) Resampling in $G_{\alpha i}$ signalling



(b) Resampling in the PI3K cascade

Figure 5.6: Structure of synthetic lethality resampling. A null distribution with 10,000 iterations of the number of siRNA genes upstream or downstream of SLIPT genes (depicted as the difference of these) in each pathway. To assess significance, the observed events (with shortest paths) were compared to the 90% and 95% intervals for the null distribution (shown in blue). Genes detected by both methods were not fixed to the same number as observed for the alternative null distribution (shown in red), although the significance of the observed number of events (red) was changed in either case. The genes detected by both approaches were included in computing the number of shortest paths (in either direction) between SLIPT and siRNA genes. The permutations show (a) significant pathway relationships for $G_{\alpha i}$ signalling and (b) non-significant relationships for the PI3K cascade.

specific rather than a general property of these synthetic lethal detection methods. These results were robustly reproducible, with similar findings (as shown in Appendix Figure H.1) for each pathway when testing for synthetic lethality against *CDH1* mutation (mtSLIPT).

The number of genes detected by both approaches was fixed (to the number observed) for deriving p-values for pathway relationships (as described in Section 3.4.1.1). These genes were included in the analysis because they can be disproportionately upstream (or downstream) of more siRNA genes than SLIPT genes, which may lead to them having different proportions of genes detected by either approach upstream (or downstream) of them. However, allowing the number of jointly detected genes to vary during resampling (as shown in Figure 5.6 and Appendix Figure H.1) or excluding these jointly detected genes did not alter the findings of this approach. Furthermore, expanding the range of shortest paths to consider links in related pathways (using the “meta-pathways” constructed in Section 2.4.3) also had little effect on the null distribution generated, despite increasing the computational complexity of the procedure.

5.3.2 Resampling for Synthetic Lethal Pathway Structure

The permutation procedure (as described in Section 3.4.1.1) that was performed in Section 5.3.1 for the $G_{\alpha i}$ and PI3K pathways was also applied to other pathways identified in Chapter 4 and discussed in Section 5.1. In addition to the cell signalling pathways (PI3K/AKT and GCPRs demonstrated in Section 5.3.1), the pathways tested include extracellular matrix (with constituent elastic fibre and fibrin pathways), and translational pathways (with NMD and 3'UTR regulation).

The resampling results across these pathways (as shown in Table 5.4) had limited support for association between pathway structure and detection of synthetic lethal genes, with the majority of these being non-significant (as shown for PI3K in Figure 5.6b), with the exception of $G_{\alpha i}$ signalling (as shown in Figure 5.6a). However, the exact distribution for these pathways will differ depending on their structure, the number of genes they contain, and the proportion of synthetic lethal candidates among them (including a higher frequency of genes detected by both methods for the pathways identified in Section 4.2.5.1). This resampling is therefore an appropriate procedure to use to detect structural relationships across pathways as it does not assume an underlying test statistic distribution.

Pathway structure was supported for the NMD pathway (which is consistent with siRNA being downstream in Appendix Figure F.8). However, this observation rests

Table 5.4: Resampling for pathway structure of synthetic lethal detection methods

Pathway	Graph		Candidates		Observed				Permutation p-value		p-value (FDR)
	Nodes	Edges	SLIPT	siRNA	Up ¹	Down ²	Up–Down	Up/Down	Up–Down	Down–Up	Down–Up
PI3K Cascade	138	1495	38	25	122	128	-6	0.953	0.5326	0.4606	0.6734
PI3K/AKT Signalling in Cancer	275	12882	98	44	779	679	100	1.147	0.3255	0.6734	0.6734
G_{αi} Signalling	292	22003	95	58	836	1546	-710	0.541	0.9971	0.0029	0.0145
GPCR downstream	1270	142071	312	160	9755	9261	494	1.053	0.3692	0.6305	0.6734
Elastic fibre formation	42	175	24	7	1	2	-1	0.500	0.5461	0.3865	0.6734
Extracellular matrix	299	3677	127	29	547	455	92	1.202	0.3351	0.6636	0.6734
Formation of Fibrin	52	243	18	5	12	17	-5	0.706	0.6198	0.3564	0.6734
Nonsense-Mediated Decay	103	102	74	2	0	74	-74	0	1.0000	< 0.0001	< 0.0010
3'-UTR-mediated translational regulation	107	2860	77	1	0	0	0		0.4902	0.5027	0.6734
Eukaryotic Translation Elongation	92	3746	76	0	0	0	0		0.4943	0.4933	0.6734

Pathways in the Reactome network tested for structural relationships between SLIPT and siRNA genes by resampling. The raw p-value (computed without adjusting for multiple comparisons over pathways) is given for the difference in upstream and downstream paths from SLIPT to siRNA gene candidate partners of *CDH1* with significant pathways highlighted in bold. Sampling was performed only in the target pathway and shortest paths were computed within it. Loops or paths in either direction that could not be resolved were excluded from the analysis. The genes detected by both SLIPT and siRNA (or resampling for them) were included in the analysis and the number of these were fixed to the number observed.

¹ The number of paths where the siRNA candidate was upstream of a SLIPT candidate

² The number of paths where the siRNA candidate was downstream of a SLIPT candidate

upon a single gene and was not replicated when testing synthetic lethality (mtSLIPT) against *CDH1* mutation (as shown in Appendix Table H.1) nor was it supported by the related 3'UTR regulation and translational elongation pathways.

There does not appear to be a consensus on the directionality of SLIPT and siRNA candidates across pathways as distinct pathways showed stronger tendency for siRNA genes to be either upstream or downstream. Even related pathways such as PI3K and PI3K/AKT signalling showed directional events in opposite directions. The strongest pathway (among those tested) with support for directional pathways structure is G_{αi} signalling (as shown in Figure 5.6a). In contrast to the other pathways G_{αi} signalling showed significant downstream siRNA genes for SLIPT from a large number of shortest paths (in Table 5.4). This would indicate that SLIPT detects upstream regulators of genes experimentally validated by siRNA in this pathway. **This result was also** the strongest result in mtSLIPT results (Appendix Table H.1), although it was not significant after adjusting for multiple testing in this case.

There is insufficient evidence to determine whether there is pathway structure, that genes were detected upstream or downstream by either method, between the SLIPT and siRNA candidates in many of the synthetic lethal pathways (identified in Chapter 4). In particular, directional structure among synthetic lethal candidates for *CDH1* was not strongly supported in most of the signalling pathways (with the exception of G_{αi} signalling) upon which the rationale for pathway structure hypotheses were based. While there is statistically significant over-representation of many of these pathways

in genes detected by both SLIPT and siRNA (as described in Chapter 4), many of these did not show relationships with respect to pathway structure. Despite the design of a robust resampling approach to test relationships between gene groups, the detection of structural relationships between SLIPT and siRNA gene candidates did not generalise across pathways (and was specific to a few). Such structural relationships may apply more broadly to gene networkss as different biological pathways were more over-represented among SLIPT and siRNA gene candidates. Furthermore, pathway structure did not account for the discrepancy between SLIPT and siRNA gene candidates which did not significantly intersect, such as the PI3K cascade.

5.4 Discussion

These investigations used a pathway network that encapsulates protein complexes and functional modules. The Reactome network uses curated, experimentally identified pathways to map relationships between genes and does not have the limitation of relying solely on protein binding or text-mining which are prone to false positives (Croft *et al.*, 2014). While it is not documented whether these relationships are activating or inhibiting, the Reactome network (Croft *et al.*, 2014) was sufficient to test pathway relationships with directional information.

Synthetic lethal genes and pathways (for *CDH1* loss in cancer) were identified across gene expression and mutation datasets in Chapter 4. The investigations in [this chapter](#) considered synthetic lethal gene candidates within pathway structures, including whether the discrepancy between individual SLIPT and siRNA candidate genes could be accounted for, within a synthetic lethal pathway. Pathways with replicated synthetic lethal genes across SLIPT and siRNA candidates in breast and stomach cancer data, were investigated, including pathways from the extracellular microenvironment to core translational pathways and the signalling pathways between them.

Examining synthetic lethal gene candidates in the context of pathway structures may provide additional mechanisms by which the function of particular genes is subject to induced essentiality and support for them belonging to a synthetic lethal pathway. Gene candidates with characterised functions important to cellular viability are ideal for triage of targets specific to *CDH1*-deficient tumours and for further experimental validation in preclinical models. This chapter presents computational methods using pathway structure to detect genes with importance in a pathway and to compare the differences between SLIPT and siRNA candidate genes with pathway relationships (e.g., one group being downstream of the other). The differences between these computa-

tional and experimental screening approaches could feasibly lead to differences in which genes within a synthetic lethal pathway are identified. Genes detected by synthetic lethal detection strategies included those of biological importance within synthetic lethal pathways, those which are actionable drug targets, and those with functional implications for the biological growth mechanisms or vulnerabilities of *CDH1*-deficient tumours. It appeared that genes detected by both approaches were highly connected (or of importance) in the network structure of some pathways, and that there may be some structure with SLIPT and siRNA candidates tending to appear upstream or downstream of each other.

The complexity of biological pathways meant that relationships between gene candidates were difficult to discern without formal mathematical and computational approaches, which were used to analyse these networks. Network analysis techniques were applied to formalise and quantify the connectivity or importance of genes within pathways in the $G_{\alpha i}$ pathway. These network metrics support the application of synthetic lethal detection across pathways (and the findings using pathways as gene sets in Chapter 4) as neither synthetic lethal detection approach was pre-disposed towards genes of higher importance or connectivity and neither approach was insensitive to genes of lower importance or connectivity. SLIPT did not detect genes with a significantly more crucial role in the $G_{\alpha i}$ pathway, as inferred by pathway connectivity and centrality measures. However, SLIPT genes had significantly lower centrality in the $G_{\alpha i}$ pathway by PageRank centrality (as shown in Section 5.2.2.2), and so the highest scoring genes may be essential to cellular viability rather than synthetic lethal.

Pathway structure between individual SLIPT and siRNA candidate genes within a pathway was measured with the direction of shortest paths in graph structures. This enabled the detection of a consensus of directionality for the pathway across pairs of genes detected by either method. This pathway structure methodology is generally applicable to comparison of node groups (which may intersect), including genes in biological pathways and their detection by different methodologies. While the pathway structure measure alone was not able to detect structural relationships between gene groups (e.g., SLIPT and siRNA gene candidates), it was able to determine whether these relationships were statistically significant by resampling. This approach successfully detected a relationship between SLIPT and siRNA candidate genes in the $G_{\alpha i}$ signalling pathway, despite there being few differences between these genes with respect to other network metrics.

5.5 Summary

Analyses of biological pathways, network metrics, and statistical procedures devised specifically for this purpose were applied to Reactome pathway structures to test whether structural relationships existed between synthetic lethal candidates. In particular, the differences between the computational (SLIPT) and experimental (siRNA) synthetic lethal candidate partners of *CDH1* were examined (in the pathways discussed in Chapter 4).

There were few detectable structural relationships between SLIPT and siRNA gene candidates, with respect to network connectivity or centrality measures **with the notable exception of $G_{\alpha i}$ signalling**. Since network analyses were unable to ascertain whether the candidates detected by either method stratified into upstream and downstream genes, a statistical resampling procedure was applied for shortest path analysis between pairs of SLIPT and siRNA gene candidates. This approach did not detect many structural relationships in the synthetic lethal pathways identified in Chapter 4. Overall, support for pathway structure between SLIPT and siRNA gene candidates was weak and the direction was inconsistent across pathways. Therefore pathway structure does not appear to generally account for the differences between the SLIPT and siRNA gene candidates. However, it may apply in specific pathways, as demonstrated with $G_{\alpha i}$ signalling. It was possible to detect some pathway relationships between candidate genes in synthetic lethal pathways, in addition to the significantly over-represented genes shared between SLIPT and siRNA (as identified in Chapter 4).

The resampling procedure demonstrated in this chapter is more widely applicable to gene states in network structures and may be of further utility in the analysis of biological pathways or networks. This approach was able to quantify structural relationships that were otherwise difficult to interpret and to conclusively exclude many potential relationships. In this respect, the network resampling methodology may also be applicable to triage of therapeutic targets for experimental validation.

Chapter 6

Simulation and Modelling of Synthetic Lethal Pathways

Simulation and modelling of synthetic lethality in gene expression was revisited in greater detail in this chapter, building upon the results which supported the use of SLIPT (in Section 3.3). In Chapter 3, a procedure for generating simulated data with underlying (known) synthetic lethal partners of a query gene, such as *CDH1*, was developed (as described in Section 3.2.2) by sampling from a multivariate normal distribution based on a statistical model of synthetic lethality in gene expression data (as described in Section 3.2.1). This simulation framework was applied to simulated data (in Section 3.3), including simple correlation structures to assess the statistical performance of the SLIPT methodology and support its use as a computational approach for detecting synthetic lethal candidates from expression data throughout this thesis (Chapters 4 and 5).

While this basic framework provided some support for the use of SLIPT, further investigations with simulations were conducted to assess the strengths and limitations of the SLIPT methodology, compare it to alternative statistical approaches to synthetic lethal detection, and assess its performance under more complex correlation structures. Together these simulation investigations assess the performance of the SLIPT methodology, including on pathway graph structures (e.g., those discussed in Chapter 5). These results can indicate whether the SLIPT methodology robustly detects known synthetic lethal partners (and how it compares to other bioinformatics strategies) or is suitable for wider genomics applications.

These simulation investigations continued to utilise the multivariate normal simulation procedure (as applied in Section 3.3) with further refinements. The SLIPT

methodology (and the χ^2 test) were applied across a range of parameters (including altering the quantiles for detecting synthetic lethal direction) and compared to correlation as a predictor of synthetic lethality. These simulations included thousands of non-synthetic lethal genes and correlations with the query gene (as performed in Section 3.3).

A refined simulation procedure was developed specifically to extend the methodology described in Section 3.2 to utilise pathway graph structures for the correlation structures of simulated datasets (as described in Section 3.4.2). This methodology can be applied to simulated correlation structures across simple graph structures to test specific network modules or use pathway structures based on biological pathways. Thus graph structure and simulation approaches were combined to test whether a gene locus in a pathway affects detection by SLIPT and whether SLIPT performance is affected by pathway structure. The simulation procedure based on graph structures was applied in a computational pipeline across many parameter combinations using high-performance computing resources (as discussed in Section 2.5.3) and the core simulation functions have been released as a software package for wider use to test bioinformatics and statistical methods on graph structures (as described in Section 3.5.3).

6.1 Synthetic Lethal Detection Methods

The SLIPT methodology (as it has been applied throughout Chapters 4 and 5) was compared to alternative computational approaches for detecting synthetic lethality in simulated gene expression data. As discussed in Section 3.3, this procedure enabled testing the ability of SLIPT to detect known synthetic lethal partner genes by sampling from a statistical model of synthetic lethality. While comprehensive benchmarking has not been performed, several approaches to synthetic lethal detection are considered (e.g., Pearson correlation, the χ^2 test, and testing for bimodality) to evaluate the strengths of the SLIPT methodology, including modifications to the parameters of SLIPT. The following comparisons of simulations of computational detection of synthetic lethality with different statistical rationales were performed to show the strengths of SLIPT, evaluate whether it is appropriate for further application in genomics research, and identify limitations which may be addressed with further developments.

6.1.1 Performance of SLIPT and χ^2 across Quantiles

Simulated datasets with synthetic lethal partner genes were generated using the multivariate normal simulation procedure (as described in Section 3.2.2) with performance

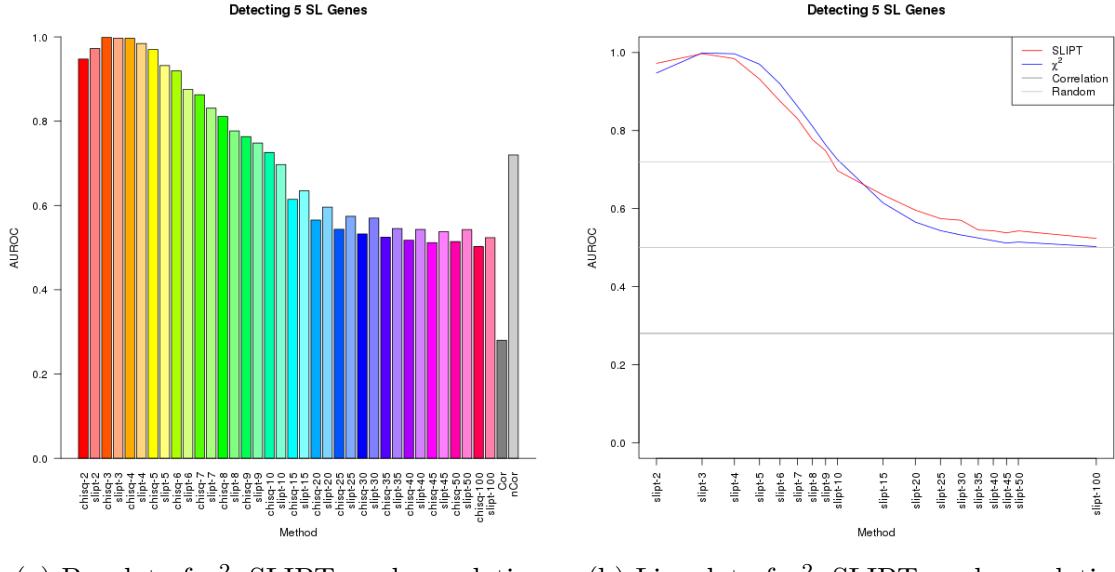
assessed using AUROC analysis (as described in Section 2.3.5). Synthetic lethal detection was compared for modifications to the SLIPT methodology (as described in Section 3.1), namely that the quantiles used to define low and high expression were varied. Rather than $1/3$ (as used throughout this thesis) the samples below the lowest $1/n$ quantile and above the highest $1/n$ quantile were used for SLIPT (and the χ^2 -test) to detect samples that exhibited low and high expression levels respectively. The quantiles tested ranged from two, splitting at the $1/2$ quantile (the median), to 100, using the lowest (1%) and highest (99%) percentiles.

This enabled testing of the threshold for low expression of genes which is most able to distinguish synthetic lethal genes, even with higher-order synthetic lethal interactions (as discussed in Section 3.2.1). Both SLIPT with the directional criteria for synthetic lethality and significance of the equivalent χ^2 test were performed for each quantile. Pearson correlation was also tested on simulated continuous expression data for synthetic lethal **detection**. Both positive and negative correlations **were considered** separately as predictors of synthetic lethality for comparison with χ^2 based approaches, using discrete categories of gene function deriving from quantiles.

The results presented throughout this Section use the example of five synthetic lethal partners to illustrate the differences in performance between the standard SLIPT procedure (slipt-3) to n quantiles (slipt- n), the χ^2 -test on the same quantiles, and positive or negative correlation. However, similar results across different numbers of known synthetic lethal genes are shown in Appendix I. The synthetic lethal detection procedures were compared with 10,000 simulations of a small dataset of 100 genes and 1000 samples without correlation structure between genes (as performed in Section 3.3.2).

As shown in Figure 6.1, the $1/3$ -quantiles previously used have optimal performance and SLIPT has a comparable or higher performance than the χ^2 -test alone across quantiles. Pearson correlation was also tested as a predictor of synthetic lethality (i.e., whether highly positive or negative correlations with the query gene detected synthetic lethal partners). Positive correlation performed worse than random (with an AUROC lower than 0.5) as thus coexpression of genes was not predictive of synthetic lethality in simulated data. Conversely, negative correlation was predictive of synthetic lethality, consistent with synthetic lethal gene activity being mutually exclusive. However, neither correlation approach performed as well as the optimal quantiles for the SLIPT procedure or the χ^2 -test.

These results are shown in both a bar graph and lineplot to show the individual results of each parameter, and to compare SLIPT with the χ^2 -test side-by-side across



(a) Barplot of χ^2 , SLIPT, and correlation (b) Lineplot of χ^2 , SLIPT, and correlation

Figure 6.1: Performance of χ^2 and SLIPT across quantiles. Synthetic lethal detection (of 5 genes) with quantiles as on the axes. The barplot uses the same hues for each quantile (grey for correlation) and darker for χ^2 (and positive correlation). The line plot (with log-scale quantiles) is coloured according to the legend. SLIPT and χ^2 perform similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation had higher performance than positive correlation but not optimal quantiles for SLIPT or χ^2 .

quantiles. Similarly, these plots are given for detecting a range of known synthetic lethal partners in the simulations in Appendix Figures I.1 and I.2. These demonstrate that the findings shown for five synthetic lethal genes are robust across different numbers of underlying synthetic lethal genes.

The synthetic lethal detection procedures were also tested with 1000 simulations of a larger dataset of 20,000 genes and 1000 samples. While fewer simulations gives a less accurate ROC result, this is sufficient to replicate the above findings with a feasible number of genes in a human gene expression dataset and assess the impact of a higher proportion of non-synthetic lethal genes (potential false positives). Simulated datasets of this size were also used in Section 3.3.2 to test the specificity in a number of genes similar to that in experimental datasets for cancer genomes. As shown in Figure 6.2, the above findings were replicated in simulations of a larger dataset with 20,000 genes.

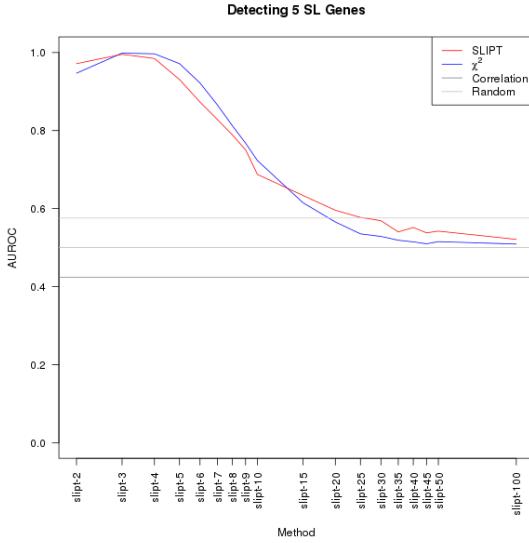


Figure 6.2: Performance of χ^2 and SLIPT across quantiles with more genes. Synthetic lethal detection (of 5 genes in 20,000) with quantiles as in axis labels. The line plot (with log-scale quantiles) is coloured according to the legend. As for simulations with fewer genes, SLIPT and χ^2 perform similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation had higher performance than positive correlation but not optimal quantiles for SLIPT or χ^2 .

These were also robustly replicated across varying numbers of underlying synthetic lethal genes (as shown in Appendix Figure I.3).

6.1.1.1 Correlated Query Genes affects Specificity

As discussed in Section 3.3.2.2, positively correlated genes (with the query gene) have an impact on the performance of synthetic lethal detection. SLIPT was able to distinguish these correlated genes from synthetic lethal partners and hence is likely to have a higher specificity in datasets which include positively correlated genes with the query gene (as expected in gene expression data). The synthetic lethal detection procedures were compared with 10,000 simulations of a small dataset of 100 genes (with 5 correlated with the query gene) and 1000 samples otherwise without correlation structure between genes. As shown in Figure 6.3a, this specificity is reflected in the increased AUROC performance values for SLIPT (in contrast to Figure 6.1). This specificity can be attributed to the directional criteria (as described in Section 3.1) since the χ^2 -test alone performs comparatively poorly with positively correlated genes.

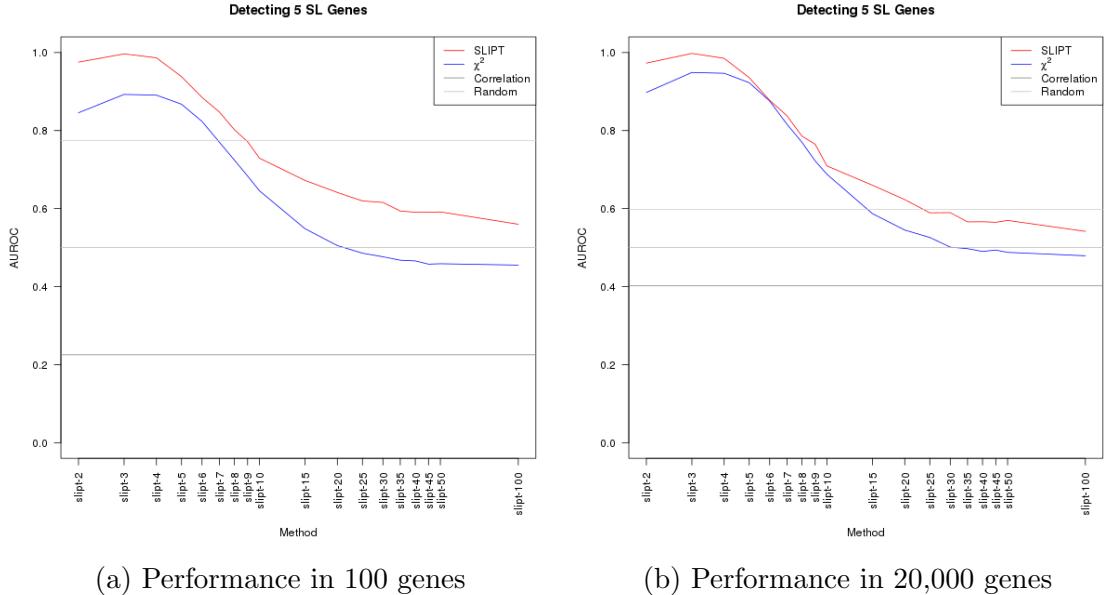


Figure 6.3: Performance of χ^2 and SLIPT across quantiles with query correlation. Synthetic lethal detection (of 5 genes with query correlated genes) with quantiles as in axis labels. Query correlated genes composed 5% of the dataset: (a) 5 out of 100 genes and (b) 1000 out of 20,000. The line plot (with log-scale quantiles) is coloured according to the legend. SLIPT performs consistently higher than χ^2 due to higher specificity. Negative correlation performed modestly.

The synthetic lethal detection procedures were also compared with 1000 simulations of a larger dataset of 20,000 genes (with 1000 correlated with the query gene) and 1000 samples otherwise without correlation structure between genes. This simulation increases the number of genes (and proportion of negative genes) to those comparable with a human gene expression dataset while maintaining a comparable 5% of positively correlated genes. As shown in Figure 6.3b, SLIPT outperformed χ^2 or negative correlation and was optimal at the $1/3$ -quantile. The difference between SLIPT and χ^2 was less pronounced in a larger dataset, with many weakly correlated genes. The greater specificity of SLIPT than the χ^2 -test, to distinguish positively correlated non-synthetic lethal genes, was not as evident with a large number of negative genes (as potential false positives). However, specificity is important in large-scale genomics analysis with many potential false positives. SLIPT with $1/3$ -quantiles (as performed throughout Chapters 4 and 5), had higher performance than other quantile thresholds,

particularly with positive correlations (replicating the Section 3.3.2.2), across different numbers of underlying synthetic lethal genes (as shown in Figures I.5 and I.6).

Together these results support the use of SLIPT, particularly the use of quantiles as thresholds for gene function and specific use of $1/3$ -quantiles which performed well compared to other quantiles. Of particular concern in the design of SLIPT for expression data is whether the samples sizes are sufficient when the data are divided into quantiles. The SLIPT methodology further performed better for $1/3$ -quantiles (and other moderate values) than χ^2 or correlation as a predictor of synthetic lethality. These results were irrespective of sample size or p-value threshold since the results replicated across sample sizes and the AUROC values were independent significance thresholds. Using a moderate number of quantiles for SLIPT ensures that there are a sufficient number of samples expected below and above them so that deviations from these are statistically detectable. These quantiles were also optimal for the χ^2 test which uses the same expected values as the SLIPT directional conditions.

6.1.2 Alternative Synthetic Lethal Detection Strategies

The SLIPT approach (and χ^2) to detect synthetic lethality from binning expression to estimate gene function also outperformed correlations, which use continuous data directly. Correlation performing poorly as a synthetic lethal detection strategy is consistent with there not necessarily being a relationship between synthetic lethal partners, which can be in distinct biological pathways, expressed at different times or in different cell types. Nevertheless, correlation is among the alternative detection methods considered in further detail.

The BiSEp R package (Wappett, 2014) for using bimodality to detect synthetic lethality (Wappett *et al.*, 2016) was also considered, along with a linear regression approach. These statistical methods span a range of computational approaches to detecting synthetic lethality and serve to compare alternatives to SLIPT, supporting its design and application. However, these comparisons are able to provide supporting data from statistical modelling and simulations for the viability of the SLIPT methodology for synthetic lethal discovery in cancer (as demonstrated in Chapter 4) and further applications.

6.1.2.1 Correlation for Synthetic Lethal Detection

As expected from prior results, negative (Pearson) correlation performed better than positive correlation at detecting synthetic lethality (shown in Section 6.1.1). However, neither correlation approach performed as well as SLIPT or the χ^2 test as a predictor

of synthetic lethal gene partners. It is notable that negative correlation still often performed considerably better than random chance.

Negative correlation was compared directly to the SLIPT methodology (as described in Section 3.1) across numbers of known synthetic lethal partners and sample size (ranging from 500 to 5000). This comparison used 1000 simulations of a dataset with 20,000 genes and synthetic lethal genes from within a network (sampled as in Section 3.4.2) with a 0.8 correlation between adjacent genes. In a direct comparison of SLIPT and negative correlation (shown in Figure 6.4), SLIPT consistently has higher performance in simulated data across parameter values and (inverse) correlation-based approaches perform modestly in comparison. Thus using thresholds to categorise expression data (as performed by SLIPT and χ^2) does not compromise the performance of these methods by losing continuous data that would be used for calculating correlations.

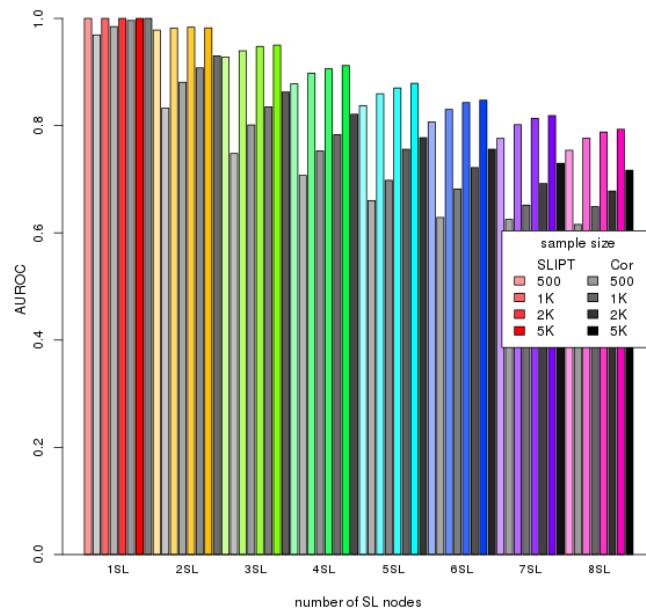


Figure 6.4: Performance of negative correlation and SLIPT. Synthetic lethal detection with SLIPT was compared to negative (Pearson) correlation across parameters. SLIPT consistently outperformed correlation. Both approaches had lower performance for more synthetic lethal partners and for lower sample sizes. 10,000 simulations were performed with correlation structure.

Both SLIPT and correlation had poorer performance with increasing numbers of the synthetic lethal genes to detect, while they had higher performance in higher sample sizes, as expected (as previously observed for SLIPT in Section 3.3). Thus the issue with detection of greater numbers of synthetic lethal genes is not specific to SLIPT but occurs across computational methods of synthetic lethal discovery in (simulated) expression data and likely stems from cryptic higher-order synthetic lethal interactions (as conservatively assumed in Section 3.2.1).

6.1.2.2 Testing for Bimodality with BiSEp

Extensive attempts were also made to compare SLIPT to the BiSEp methodology (Wappett *et al.*, 2016), a statistical approach to identify synthetic lethal gene pairs from mutually exclusive relationships using bimodal distributions. This synthetic lethal detection methodology is also designed for expression analysis in cancer and is readily available as an (open-source) R package (Wappett, 2014), a practice which facilitates adoption and testing of the methodology on the same datasets and simulations procedures as previously used for SLIPT.

The BiSEp package is designed for global testing of all potential gene pairs in the genomes for synthetic lethality rather than focusing on the search space of potential partners of the query gene. This approach was unable to detect synthetic lethal gene pairs in the TCGA breast cancer expression dataset (Koboldt *et al.*, 2012). However, this may be due to stringent thresholds under the multiple testing of millions of potential gene pairs.

For a direct comparison with the query-based SLIPT approach, the source code of the BiSEp R functions was modified to test solely for the partners of a specific gene. This approach was still unable to detect synthetic lethal partners of *CDH1* in TCGA breast cancer expression data (Koboldt *et al.*, 2012), even with the detection thresholds for bimodality and significance greatly relaxed from those the package defaults to.

To circumvent multiple testing issues, BiSEp only tests gene pairs for synthetic lethality between genes with a detectable bimodal distribution. However, even with relaxed thresholds, bimodal distributions were not detectable in the normalised TCGA data (Koboldt *et al.*, 2012). Such normalisation Ritchie *et al.* (2015) is standard practice for expression datasets generated from microarrays or RNA-Seq and therefore BiSEp may not be appropriate to apply to this data. However, it is noted that BiSEp may also use other data types such as DNA copy number or cell line data for which it may be more applicable (Wappett *et al.*, 2016).

Nevertheless, attempts were made to test BiSEp on simulated datasets with underlying synthetic lethal genes (using the procedures described in Sections 3.2.2 and 3.4.2). However, BiSEp was also unable to detect genes with bimodal distributions of genes (and thus unable to detect synthetic lethality) in a limited number of computationally intensive simulations. Therefore investigations on a wider range of parameters were not performed.

6.2 Simulations with Graph structures

The simulations of synthetic lethality performed in Section 3.3 included correlated blocks of genes as a rudimentary representation of pathway structure and co-regulated genes. The simulation procedure was enhanced here to account for more complex pathway structures by sampling from multivariate normal distributions with correlation structure derived from graph structures (as described in Section 3.4.2). This approach enabled the simulation of synthetic lethal pathways with known correlation structure and synthetic lethal partners (of a gene not in the pathway). Using this procedure, the performance of SLIPT was evaluated under simple controlled correlation structures and complex correlations, such as those derived from biological networks (e.g., those described in Chapter 5). The SLIPT methodology was tested in artificially constructed networks to evaluate the effect of pathway structure on synthetic lethal detection. These included large biologically feasible pathways to ensure that the SLIPT methodology is robust under complex correlation structures and applicable to such complex genomics data.

These simulations combine the approach of prior simulation analyses (in Sections 3.3 and 6.1) with the graph structures for biological pathways (as used in Chapter 5). This enabled testing whether subtle or large differences in pathway structure affect synthetic lethal detection, whether inhibiting relationships (or inverse correlations) between genes affects synthetic lethal detection, and whether synthetic lethal detection varies by which gene is synthetic lethal and which genes are closely linked within the pathway structure. In addition, large numbers of synthetic lethal genes and biologically feasible numbers of genes (with many non-synthetic lethal genes) were tested to replicate the findings of Sections 3.3 and 6.1 in correlated structures derived from pathway graphs, including examples of biological pathways from Reactome (Croft *et al.*, 2014).

Simple and more complex constructed graph structures were used to demonstrate the impact of pathway structure on the performance of SLIPT for synthetic lethal detection in simulations. In addition, more complex constructed graph structures were

compared to the PI3K and $G_{\alpha i}$ signalling pathways derived from Reactome which were used for simulation of pathway structures of biological complexity (as shown in Figure 5.1 and Appendix Figure 5.2).

6.2.1 Performance over Graph structures

6.2.1.1 Simple Graph structures

Simple pathway modules were used to test the effect of pathway structure on the performance of detecting synthetic lethal partners within graph structures. For an initial comparison, the graph structures (shown by Figure 6.5) were used where a gene has one upstream regulator and two downstream (Figure 6.5a) or a gene has two upstream regulators and one downstream gene (Figure 6.5b). SLIPT had a high performance in these simulations, detecting randomly selected synthetic lethal partners in both of these small simple networks (shown in Figure 6.6 and Appendix Figure J.1).

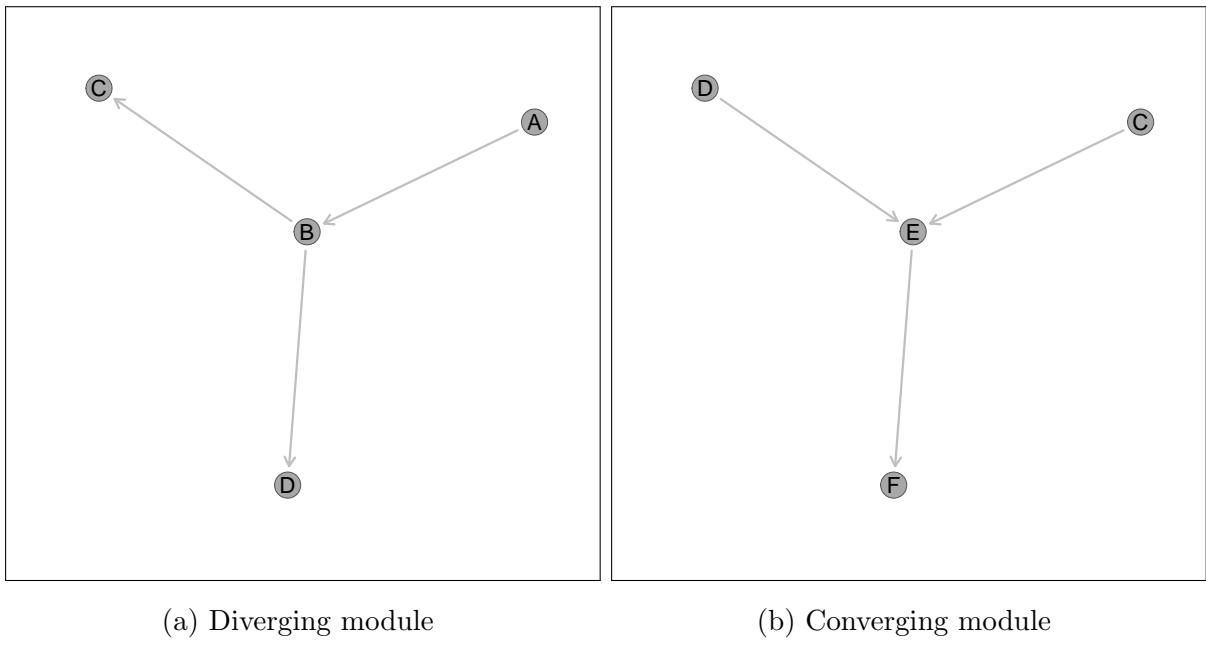


Figure 6.5: **Simple graph structures.** These simple graph structures **were** used to demonstrate the simulation procedure. These are examples of a pathway **diverging** (a) or **converging** (b) which enabled testing the importance of direction in pathway structures. These are used with both activating and inhibiting relationships as shown.

As previously observed (in Section 3.3), performance declined with higher numbers of synthetic lethal genes and lower sample sizes. However, the sensitivity of SLIPT as a binary classifier was high. Synthetic lethal partners are often distinguishable **from** non-

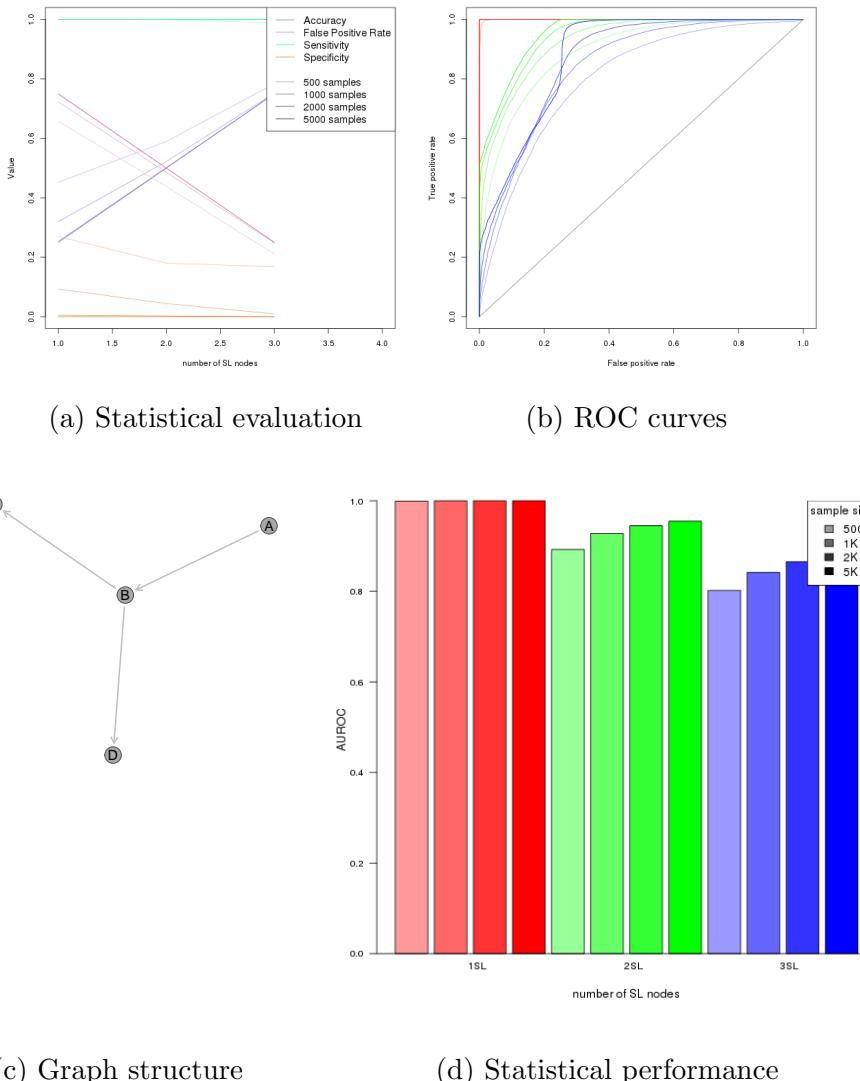
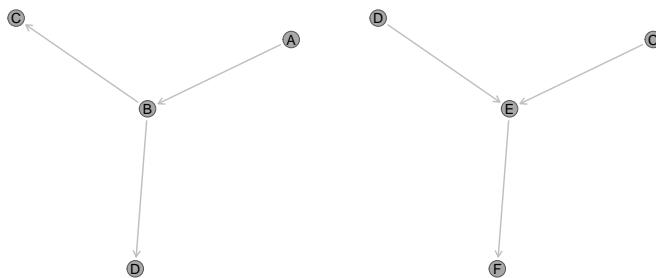


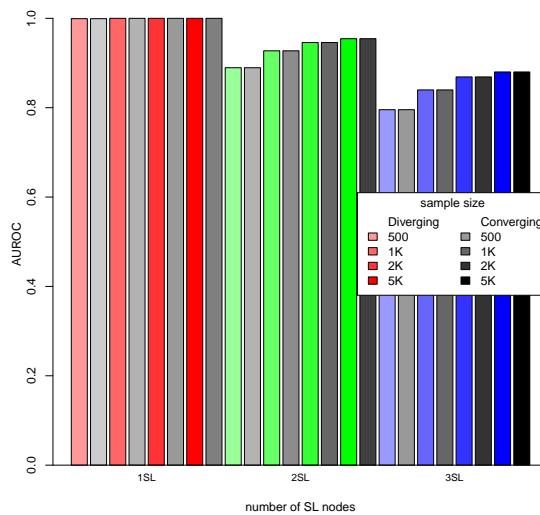
Figure 6.6: Performance of simulations on a simple graph. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution generated from a diverging graph structure. Performance of SLIPT declines for more synthetic partners but this is mitigated by increased sample sizes (in darker colours). This manifests as a decline in specificity and the false positive rate. For each parameter value, 10,000 simulations were used. Colours of the ROC curves in Figure 6.6b correspond to the parameters in Figure 6.6d.

synthetic lethal genes, even in simple highly correlated networks. The small number of genes and their high correlation has an impact on the ROC curves for higher numbers of synthetic lethal partners which are skewed compared to those observed previously. Specificity cannot be tested if all potential partner genes are synthetic lethal, which limits the number of synthetic lethal genes that can be tested.

These results were consistent between the pathway modules of diverging (as shown in Figure 6.7a) and converging signals (as shown in Figure 6.7b). The AUROC performance and underlying curves were strikingly similar between these graph structures (as shown in Figure 6.6 and Appendix Figure J.1). Thus the performance of SLIPT was not perturbed by pathway structure, specifically the direction of pathway relationships since these graph structures also demonstrate pathways in opposite direction. In a direct comparison (shown in Figure 6.7c), the performance of simulations did not differ across parameter values in these simple graphs and therefore SLIPT is robust to pathway direction.



(a) Diverging module (b) Converging module



(c) Performance between graph structures

Figure 6.7: Performance of simulations is similar in simple graphs. The AUROC values for simulations of multivariate normal distributions based on each graph structure yielded indistinguishable performance across parameter values in 10,000 simulations.

6.2.1.2 Constructed Graph structures

A more complex graph structure was used to examine the performance of detecting synthetic lethal partners with SLIPT in simulated expression data with pathway correlation structures. For a simple chain of genes representing a very linear pathway (shown in Figure 6.8), the above findings were generally replicated. SLIPT had high performance across parameter values in small networks but was still lower for higher numbers of synthetic lethal genes and lower sample sizes.

When detecting synthetic lethal genes with SLIPT as a binary classifier, the performance differences were primarily due to changes in specificity, as the small numbers of synthetic lethal genes still had highly significant p-values. Despite lower specificity and performance in ROC curves, the accuracy increased and false positive rate decreased desirably with higher numbers of synthetic lethal genes due to the high sensitivity and the high proportion of synthetic lethal genes detected. Therefore the use of adjusted p-values for SLIPT as a binary classifier appears to be appropriate for detecting synthetic lethal partners, even in strongly correlated pathways, at least in these small-scale test cases.

An artifact of these small test cases led to the skewed ROC curves (as discussed in Section 6.2.1.1), which may be the result of the low number of non-synthetic lethal genes to identify as true negatives, affecting the accuracy of specificity. This issue does not occur in larger, more complex graph structures, even with modest total numbers of genes and high correlations (as shown in Section 6.3). This issue is unlikely to occur in large expression datasets with many non-synthetic lethal genes, as shown previously (in Section 3.3 and 6.2.1.1) and with graph structures in larger datasets (in Section 6.2.4).

6.2.2 Performance with Inhibitions

Simulations of synthetic lethality in expression data were also performed with correlation structures derived from graphs containing inhibiting relationships (as are commonplace in biological pathways) which produce negative correlations. As shown in Figure 6.9, these were not an issue for detection by SLIPT. Rather, the SLIPT procedure performs well on simple graph modules with highly negative correlations. With SLIPT as a binary classifier, it had higher specificity, higher accuracy, and lower false positive rate in an inhibitory graph than the same graph with activating relationships (as shown by Figure 6.6).

The ROC curves for an inhibiting graph also showed consistently high specificity, irrespective of detection threshold, with only the upper extreme of the curve exhibit-

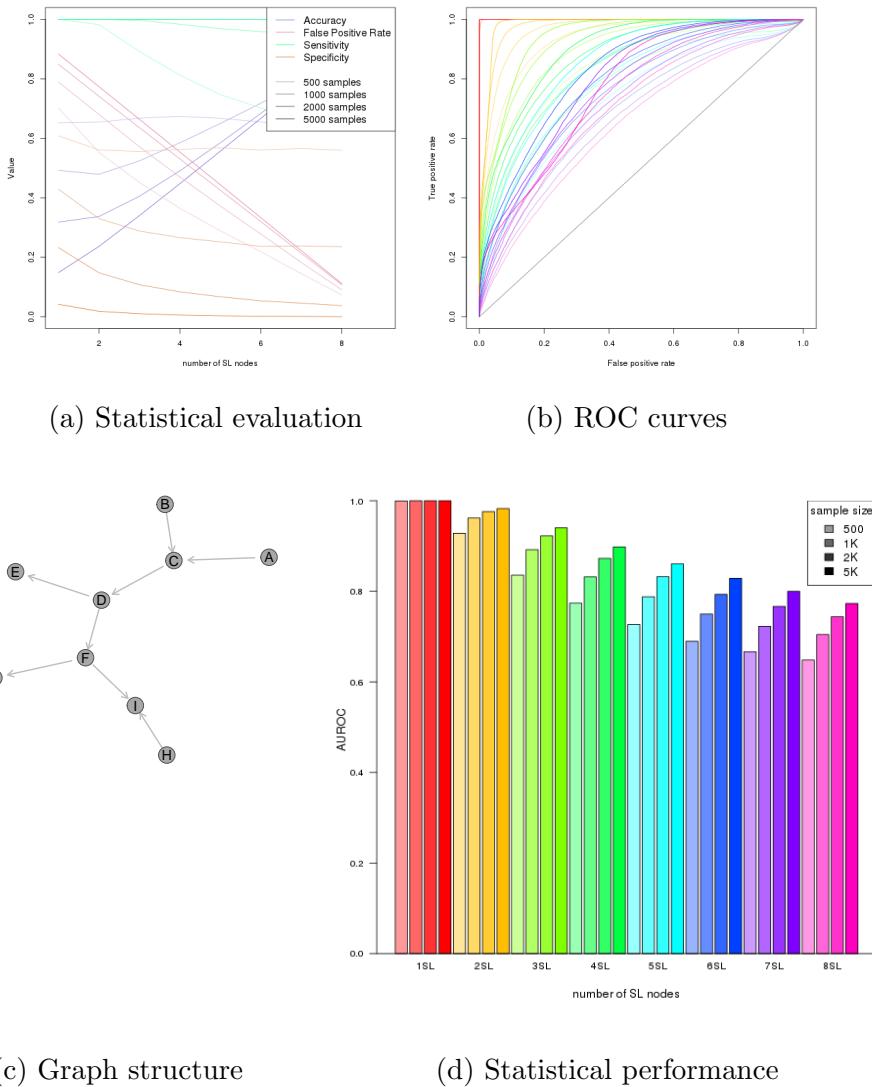


Figure 6.8: Performance of simulations on a pathway. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution generated from a pathway structure. Performance of SLIPT declines for more synthetic partners and lower sample sizes (in darker colours). For each parameter value, 10,000 simulations were used. Colours of the ROC curves in Figure 6.8b correspond to the parameters in Figure 6.8d.

ing a skew below random performance (as shown in Figure 6.9). Nevertheless, SLIPT had high performance across parameter values, particularly avoiding issues with higher numbers of synthetic lethal partners (as observed in Section 6.2.1.1). However, performance was marginally lower for higher numbers of synthetic lethal genes to detect and lower sample sizes, consistent with previously observations. Negatively correlated simulated datasets are also unperturbed by minor differences in graph structure, such as

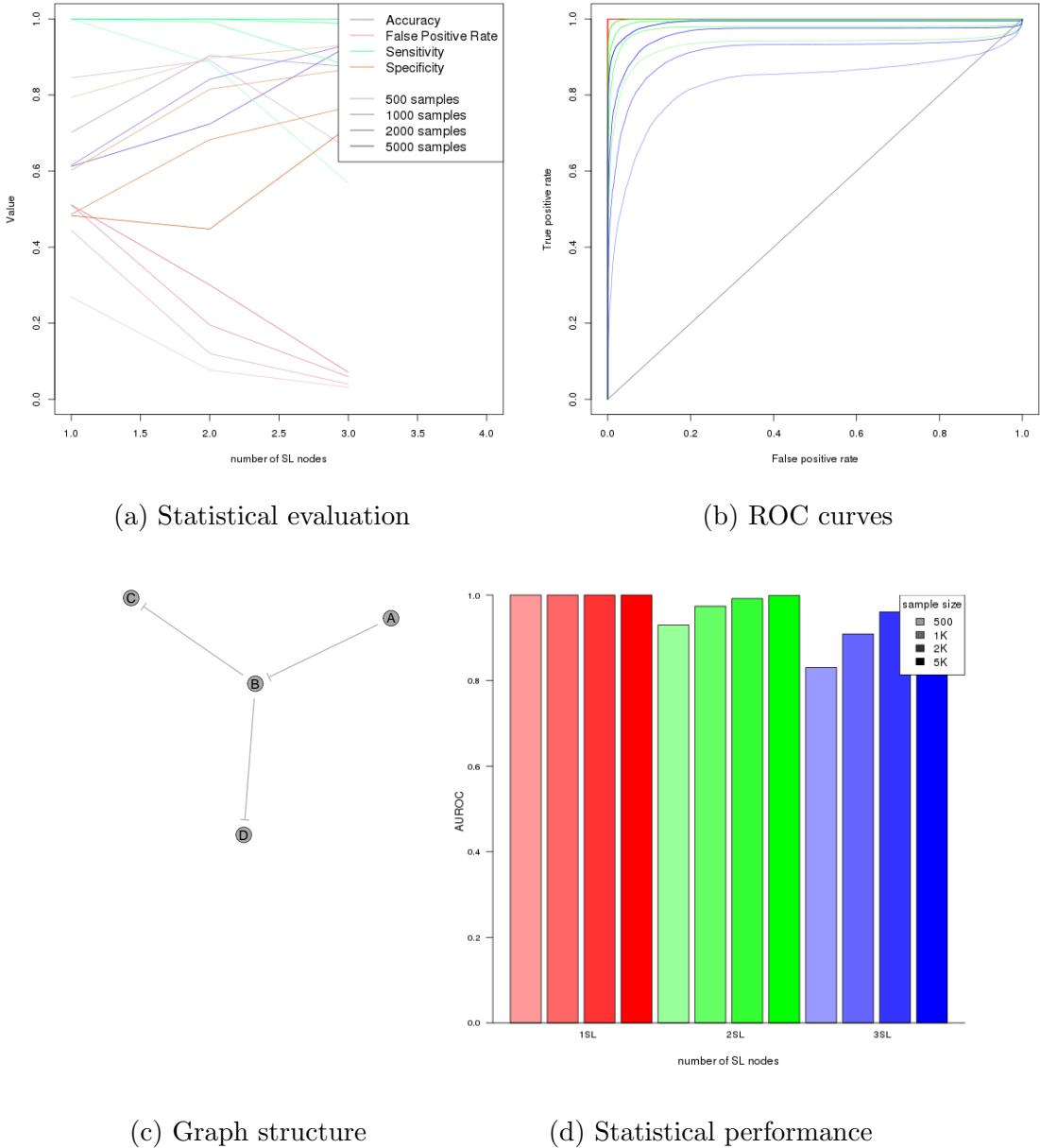


Figure 6.9: **Performance of simulations on a simple graph with inhibition.** Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution generated from an inhibiting graph. Performance of SLIPT declined for more synthetic partners and lower sample sizes. For each parameter value, 10,000 simulations were used. Colours of the ROC curves in Figure 6.9b correspond to the parameters in Figure 6.9d.

changing in the direction of the graph module. As observed for activating relationships in these graph modules, the performance was highly concordant between the graph modules (shown by similar results in Figures 6.9 and J.2).

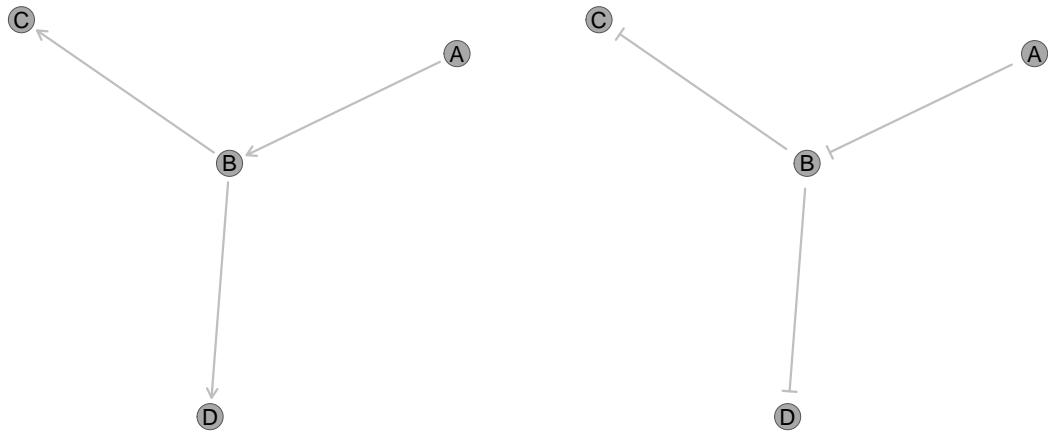
Detection of synthetic lethality by SLIPT in simulated data with inhibiting relationships outperforms simulations with activating relationships in the same graph structure (as shown in Figure 6.10). Thus SLIPT was robust in gene expression datasets with inverse correlations and performed well in them, at least in simple test cases. These relationships occur frequently in biological pathways and therefore the findings inferred from graph structures without inhibiting relationships are a conservative estimate of performance.

The SLIPT methodology appears to perform better in biological pathways (which contain negative correlations) than the graph structures discussed previously (in Section 6.2.1). This may be due to negative correlations which lead to synthetic lethal partners and inversely correlated genes which are positively correlated with the query gene. As previously shown, the SLIPT methodology performed well with specificity against positively correlated query genes (in Sections 3.3.2.2 and 6.1.2.1).

Similarly, more complex graph structures with entirely inhibiting relationships (negative correlations) also perform desirably with SLIPT as a binary classifier and had high performance across increasing numbers of synthetic lethal genes, particularly for sufficiently high sample sizes (as shown by Appendix Figure J.3). However, this was not necessarily the case for graph structures with a combination of activating and inhibiting relationships (i.e., containing positive and negative correlations). As shown by Appendix Figure J.4, such a mixed network structure did not necessarily have high performance across parameters as observed for purely inhibiting networks.

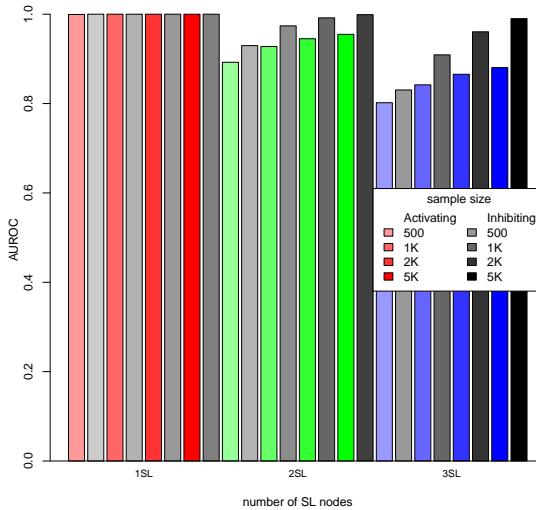
These still appeared to have desirably high sensitivity, high accuracy, and low false positive rate for detecting more synthetic lethal genes, despite poor specificity. The ROC curves were particularly skewed for high proportions of the network being synthetic lethal and may stem from low numbers of true negative genes to detect (as discussed in Section 6.2.1.1). In a direct comparison of performance (shown in Figure 6.12), the purely inhibiting graph had consistently higher performance than the activating one, as observed for simpler graphs (as shown in Figure 6.10).

In contrast, the combination of activating and inhibiting relationships had slightly lower performance across parameters compared to the same graph structure with activating relationships. Therefore correlation structure (e.g., the addition of negative correlations) can impact on the performance of SLIPT in a graph network in either direction. However, this may be an artifact of the simulation procedure as synthetic lethal genes from the correlation structure were randomly selected (without regard to



(a) Activating graph

(b) Inhibiting graph



(c) Performance between graph structures

Figure 6.10: **Performance is higher on a simple inhibiting graph.** The AUROC values for simulations of multivariate normal distributions based on inhibitions in the graph structure yielded consistently higher performance across parameter values in 10,000 simulations.

the relationships between them), with the query gene added to ensure that conditions for synthetic lethal relationships were met.

This system for simulating inhibitory pathways is not ideal since it can lead to synthetic lethal gene combinations, by randomly selecting them, which are unlikely to occur in biological pathways. These randomly selected synthetic lethal genes may

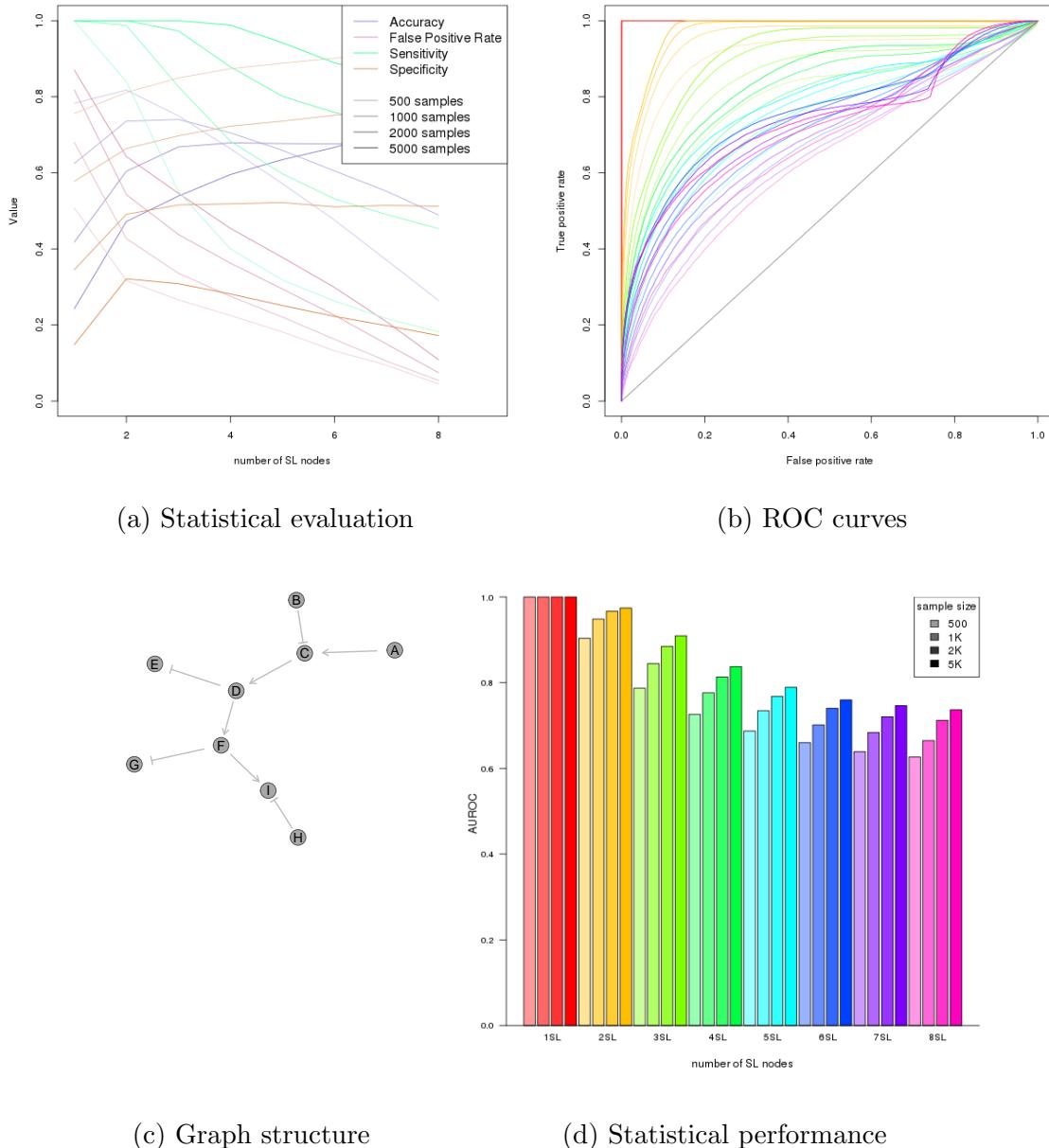
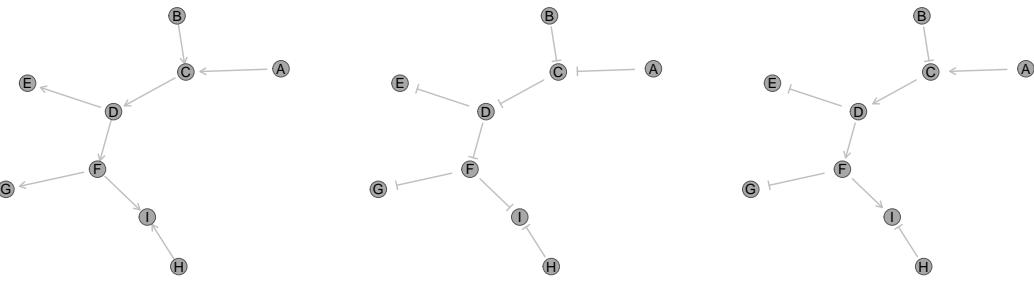


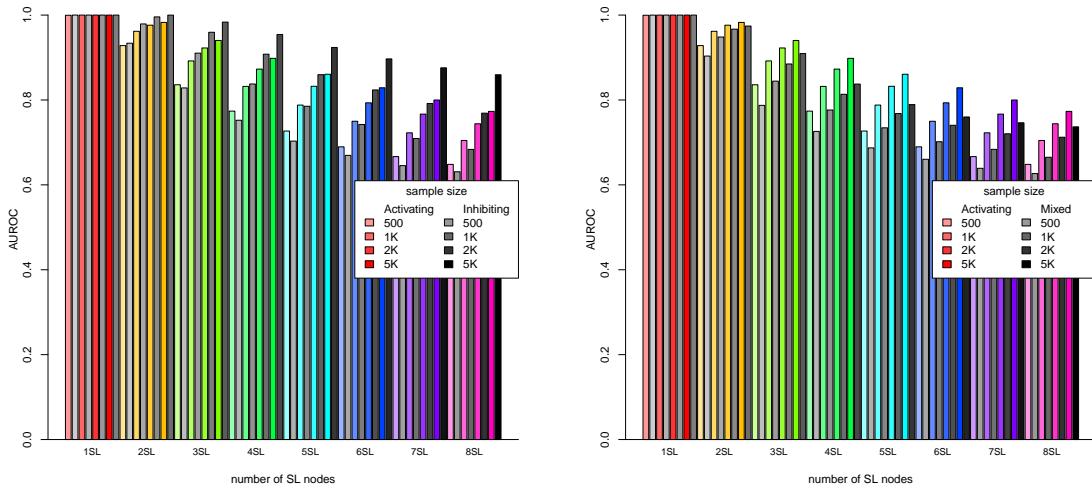
Figure 6.11: Performance of simulations on a constructed graph with inhibition.
 Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution generated from pathway structure with a combination of inhibitions. Performance of SLIPT declines for more synthetic partners and lower sample sizes. For each parameter value, 10,000 simulations were used.



(a) Activating graph

(b) Inhibiting graph

(c) Mixed Graph



(d) Performance between graphs (a) and (b) (e) Performance between graphs (a) and (c)

Figure 6.12: **Performance is affected by inhibition in graphs.** The AUROC values for simulations of multivariate normal distributions based on graph structure containing only inhibitions in the graph structure yielded consistently higher performance across parameter values in 10,000 simulations. A combination of activating and inhibiting relationships had lower performance but was more similar to the activating graph.

account for the detection results being suboptimal (i.e., difficult to detect synthetic lethal partners) compared to previous investigations. It is expected that inversely correlated synthetic partner genes will be highly expressed in a mutually exclusive manner such that at least one of them will be compensating for loss of the query gene in most samples, leading to a weak synthetic lethal signature in expression data in this case. Furthermore, this case may not be representative of biological data with synthetic lethal partners of tumour suppressor genes which are commonly inversely correlated

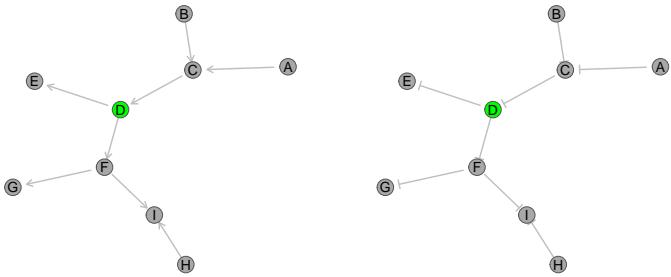
to the query gene (to some extent) and therefore it is unlikely that they are strongly negative correlated with each other, unless they are synthetic lethal partners of each other as well.

It is plausible that many synthetic lethal partner genes will serve to separately compensate for the loss of query gene function and be positively correlated with each other. Nonetheless, these simulations demonstrate that correlation structure (particularly negative correlations) have an impact on the detection of synthetic lethality. However, SLIPT was still able to perform well across graphs with different activating and inhibiting relationships, and the perturbations in performance were marginal, particularly those reducing performance compared to an activating network.

6.2.3 Synthetic Lethality across Graph structures

Synthetic lethal genes were distinguishable from highly correlated genes in simple cases (as shown by ROC analysis). However, correlated genes may lead to low specificity and high false positive rates. Negative correlations do not affect specificity this way but they may perturb the correlation structure between synthetic lethal partner genes, making it difficult to detect many of them with high sensitivity. Synthetic lethal genes have been selected randomly in simulations so far, which is a limited approach. To examine the impact of pathway relationships in more detail, specific genes were selected to be synthetic lethal within a network over replicate simulations. These simulations with a fixed synthetic lethal gene were performed to demonstrate their impact on the detection of other genes in the network.

For detection of a synthetic lethal gene in an activating graph structure (as shown in Figure 6.13a), the χ^2 values were clearly distinguishable from other genes (shown in Figure 6.13c). Simulations were performed for each gene being the synthetic lethal partner. For each synthetic lethal gene, it had the highest χ^2 value amongst 20,000 genes, including the highly correlated graph network (as shown in Appendix Figure J.5). Despite optimal performance for SLIPT detecting one synthetic lethal gene in a ROC curve (as shown in Figure 6.8), irrespective of detection threshold, the highly correlated genes would be detected as false positives by SLIPT as a binary classifier (as described in Section 3.1). In particular, the genes that were adjacent in the pathway to the synthetic lethal gene “D” had high test statistics which could be false positives (as shown in Figure 6.13c). This was not specific to example of gene “D”, with the neighbouring genes of each synthetic lethal having higher χ^2 values (as shown in Appendix Figure J.5).



(a) Activating graph

(b) Inhibiting graph

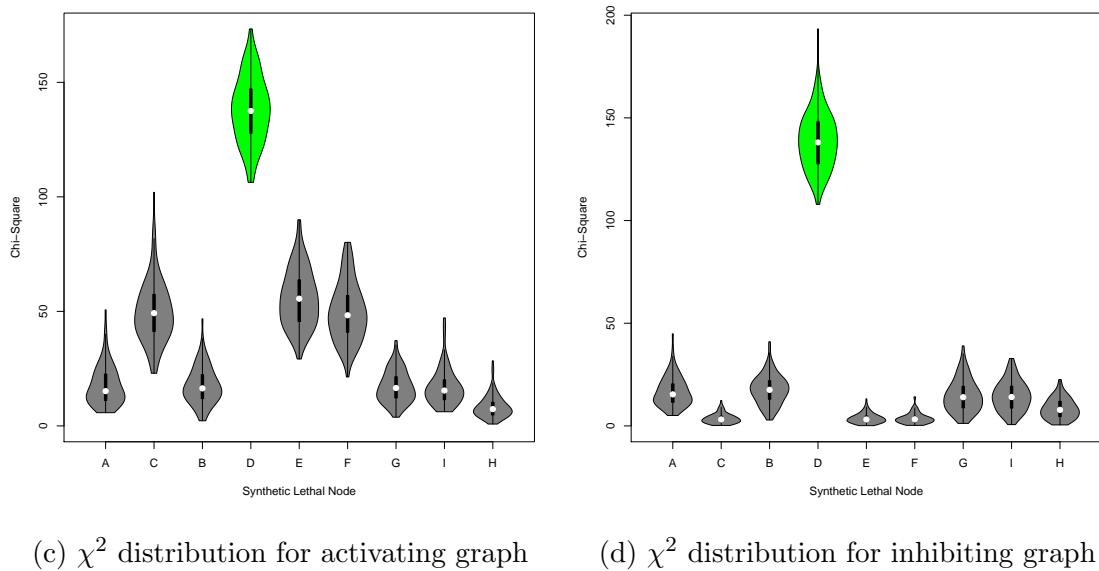


Figure 6.13: **Detection of synthetic lethality within a graph structure.** The gene “D” was designated to be synthetic lethal and the χ^2 value from SLIPT was computed for each gene across each graph structure. The χ^2 values were computed in 100 simulations of datasets of 20,000 genes including the graph structure and 1000 samples. Adjacent genes exhibited lower χ^2 values with inhibiting relationships.

The synthetic lethal signal propagates from the true synthetic lethal gene throughout the network. As such, the genes nearer to (i.e., more highly correlated with) the true synthetic lethal gene had higher test statistics and were more likely to be detected by SLIPT as false positives. The adjacent genes of synthetic lethal partners being false positives may account for the higher concordance of synthetic lethal pathways than genes between SLIPT in TCGA data (Koboldt *et al.*, 2012) and the siRNA screen (Telford *et al.*, 2015) than individual gene results (in Chapter 4). False positive genes

are more likely to be involved in a synthetic lethal pathway, being correlated with a true synthetic lethal gene. Synthetic lethal pathways are likely to contain many genes detected by SLIPT, giving a consensus in the pathway over-representation analysis. SLIPT is also able to detect true synthetic lethal partners or prioritise those most likely to be experimentally validated. Genes with the strongest support (i.e, higher χ^2 values and more significant p-values) are more likely to be the underlying synthetic lethal gene.

The immediately adjacent genes in an inhibiting graph (Figure 6.13b) did not have elevated χ^2 test statistics or a significant inverse effect (as shown in Figure 6.13d). Therefore true synthetic lethal partners were highly distinguishable from other genes with inhibiting relationships. This was shown for each gene in the graph structure as the synthetic lethal partner (shown in Appendix Figure J.6). These results support SLIPT as an appropriate approach to distinguish synthetic lethal partners in biological pathways (which frequently have inhibitions), including those relevant to cancer growth and inhibition.

The 2nd degree neighbours of the synthetic lethal gene still exhibited moderate χ^2 values (and are moderately correlated with the synthetic lethal gene). These genes could be false positives, as shown for an activating graph structure, although inhibitory relationships (i.e., negative correlations) lead to more differences in test statistics between correlated genes and underlying synthetic lethal partners (as shown in Appendix Figure J.6). Simulations in a graph containing a combination of activating and inhibiting relationships exhibits either of these χ^2 profiles, depending on which gene is synthetic lethal and the relationships between genes (as shown in Appendix Figure J.7). In this case, the synthetic lethal gene is distinguishable and inhibitory relationships make it easier to detect with SLIPT.

These results contrast with randomly selecting multiple synthetic lethal genes (as shown in Figure 6.12), where the performance of SLIPT was impeded by the inhibitory relationships between synthetic lethal partners. The randomly selected synthetic lethal genes, with negative correlations between them, which had poor performance due to an artifact in the simulation process resulting in biologically implausible synthetic lethal genes. The results with one synthetic lethal partner were sufficient to show the impact of synthetic lethal partners on neighbouring (correlated) genes. It is plausible that the synthetic lethal signatures in expression data would propagate similarly through a network from multiple synthetic lethal partners.

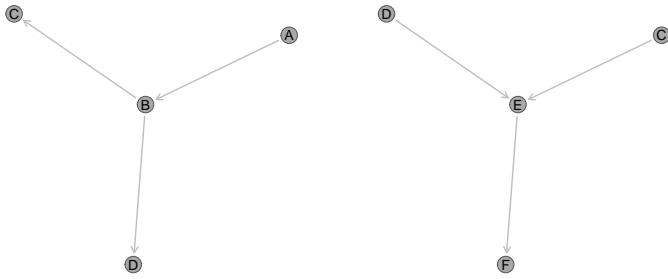
6.2.4 Performance within a Large Simulated Dataset

The performance of SLIPT with higher numbers of true partners to detect may have been affected by the high proportion of synthetic lethal partners (i.e., fewer true negatives) in small networks (as noted in Section 6.2.1.1). The performance of SLIPT increased with the addition of more non-synthetic lethal genes, particularly the specificity (as shown in Sections 3.3 and 6.1). Therefore, correlated genes from graph structures (as used in Section 6.2.1) were included in a larger simulated dataset to assess the performance of SLIPT for a synthetic lethal pathway in the context of thousands of genes, as occurs in expression datasets.

The simulations performed in Section 6.2.1.1 were replicated within a dataset of 20,000 genes with the remainder being composed of non-synthetic lethal genes without correlation structure. The specificity in a higher number of synthetic lethal genes did not affect performance in a simple graph structure (as shown in Appendix Figure J.8). For a graph of highly correlated genes within a gene expression dataset, SLIPT had high performance detecting of synthetic lethal genes in the network within a larger dataset. In this case, a reduction in sensitivity resulted in poorer performance. A high number of non-synthetic lethal genes were correctly identified, with a low false positive rate and high accuracy. Thus the use of stringent χ^2 p-value thresholds (adjusted by FDR) are suitable for testing for synthetic lethality in gene expression data across the number of genes in human and cancer data.

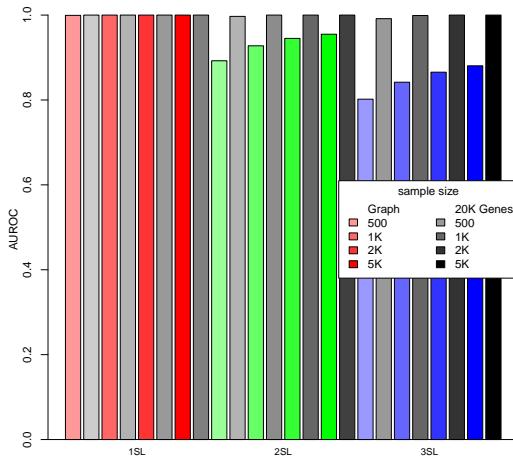
In a direct comparison with simulations in the graph structure alone (as performed in Section 6.2.1.1), detection of synthetic lethality with SLIPT performed consistently better in a larger dataset with many true negative genes to detect (as shown in Figure 6.14). The SLIPT methodology had a high specificity and low false positive rate, which is desirable. SLIPT is therefore applicable to large gene expression datasets, where these are important considerations since the number of negative genes often vastly outnumbers the number of positive genes to detect.

Performance was not necessarily higher with more non-synthetic lethal genes in an inhibiting graph structure. The performance of simulations of an entirely inhibiting graph structure did not improve within a larger dataset. Rather, the performance in the inhibiting graph structure was similar to simulations of the graph structure in isolation. Biological pathways commonly contain inhibiting relationships (and inverse correlations), although they are unlikely to occur across an entire pathway. In graph structures with inhibitions included in a larger dataset, the performance of synthetic lethal detection by SLIPT was sometimes higher than in graph structure simulated

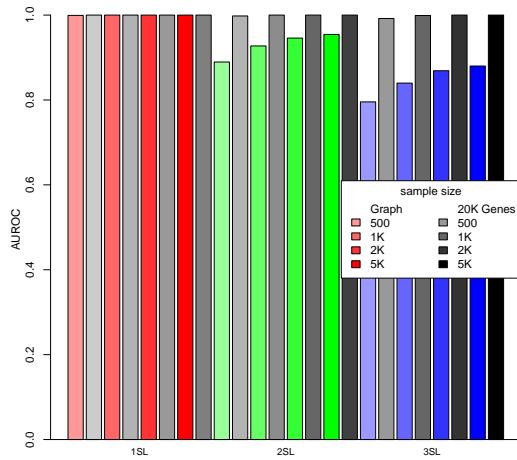


(a) Diverging module

(b) Converging module



(c) Performance in Diverging module



(d) Performance in Converging module

Figure 6.14: Performance on a simple graph improves with more genes. Simulations were performed with each of the graph structures to detect synthetic lethal partners within them. In either structure, performance of detection in a dataset containing on the graph structure (in colour) was lower than testing the graph structure within a larger dataset of non-synthetic lethal genes (without correlations).

alone (as shown in Figure 6.15). However, these did not perform as well as the equivalent graph structures without inhibitory relationships within a similar dataset. It is expected that the findings based on these simulations of genes with pathway structures in smaller datasets (as described in Section 6.2.1) will be relevant to larger datasets. The simulation results in these inhibiting graph structures perform comparably or **better** with more non-synthetic lethal genes to distinguish from them even with inhibitory relationships within the graph structure

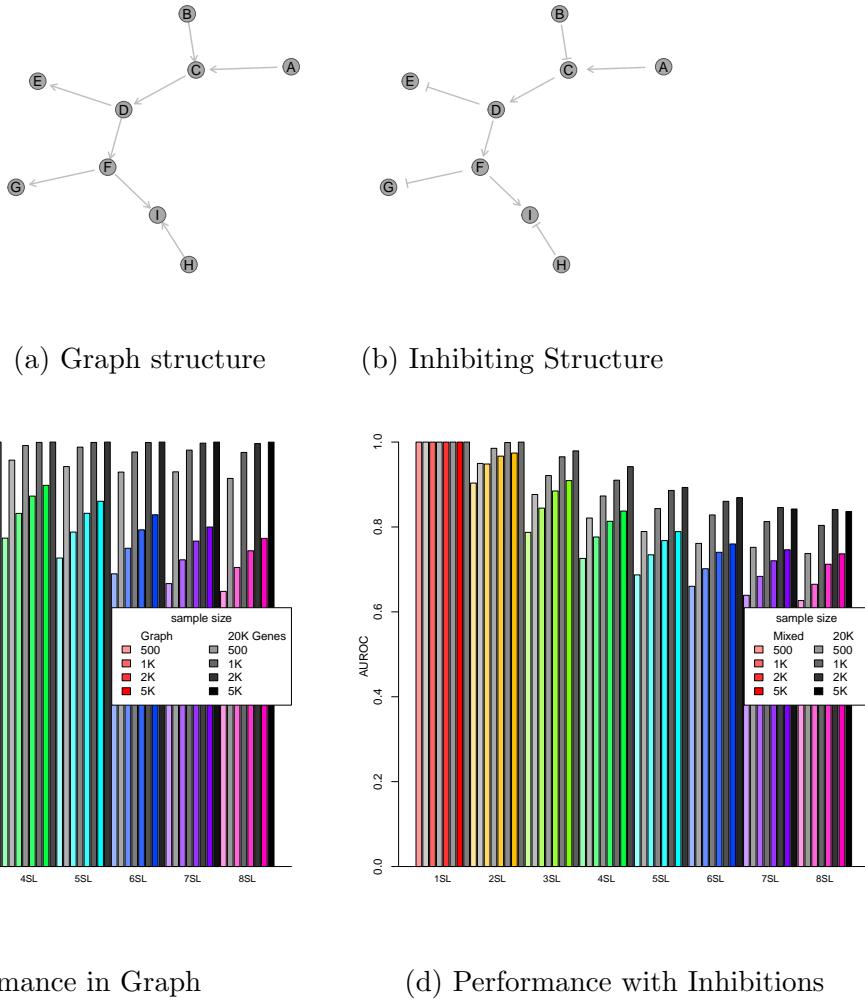


Figure 6.15: **Performance on an inhibiting graph improves with more genes.** Simulations were performed in a graph structure with activating and inhibiting relationships to detect synthetic lethal partners within them. In contrast to an activating graph, performance of detection in a dataset containing only the graph structure (in colour) was as much lower than testing the graph structure within a larger dataset of non-synthetic lethal genes (without correlations) in an inhibiting graph structure with negative correlations.

This poorer performance of inhibitory graph structures may be due to highly negatively correlated genes being false positives. These genes will be positively correlated with the query gene if they are negatively correlated with a synthetic lethal partner (i.e., within a synthetic lethal pathway). The SLIPT procedure performs well at distinguishing these positively correlated genes, as previously shown (in Sections 3.3.2.2

and 6.1.1.1). These false positives will also be a minority amongst a larger dataset of non-synthetic lethal genes without correlation to the query or synthetic lethal genes.

It is more likely that the poorer performance stems from negative correlations between synthetic lethal genes which makes them more difficult to individually detect (as observed in Section 6.2.2). As discussed in Section 6.2.3, this is likely an artifact of the simulation procedure selecting random synthetic lethal genes with strong inhibitory relationships between them. Therefore the poorer performance for inhibiting graphs within larger datasets is not cause for concern because the cases where SLIPT performs poorly are likely to be combinations of simulated synthetic lethal genes that are not likely to occur within biological pathways. This simulation procedure has included higher-order synthetic lethal to produce the weakest signal of synthetic lethality for individual partner genes which are still detectable by SLIPT.

6.3 Simulations in More Complex Graph structures

Investigations with simulations based on graph structures were extended to larger graphs, enabling more synthetic lethal genes within a pathway and modelling the complexity of a biological pathway. Sensitivity declines over a greater range for the number of synthetic lethal partners in a larger network with a trade-off with specificity (as shown in Appendix Figures J.9–J.11). However, the accuracy declined for greater numbers of synthetic lethal partners and the false positive rate peaks at intermediate values. In this range, differences between simulations varied with greater sample size. The AUROC results were similar between these more complex graph structures, although the larger graph (Appendix Figure J.11) differed in sensitivity and specificity for SLIPT as a binary classifier. This difference be due to different proportions of synthetic lethal and non-synthetic lethal genes to detect, since these graphs (as shown in Appendix Figures J.9 and J.10) had fewer genes.

While the graph structures (of similar size) were highly distinct, they had similar performance profiles across parameters. SLIPT is therefore robust across pathway structures and is more affected by the number or proportion of genes to detect. Findings from previous simulations in similar correlation structures (in Section 3.3) should be applicable to expression data with more complex correlation structures, such as those occurring in biological pathways. Specifically, synthetic lethal partners are distinguishable from closely correlated genes in the context of biological pathway networks, irrespective of thresholds (shown by ROC) and with the sensitivity and specificity of SLIPT as a binary classifier (as used in Chapters 4 and 5).

The findings for inhibitory graph structures were replicated with larger more complex graph structures with inhibiting relationships and more synthetic lethal genes to detect (shown in Appendix Figures J.12–J.15). In each graph structure, simulations entirely with inhibiting relationships (Appendix Figures J.12, J.14, and J.16) had higher performance than the equivalent graph with entirely activating relationships (Appendix Figures J.9, J.10, and J.11) or a combination of activating and inhibiting relationships (Appendix Figures J.13, J.15, and J.17). While the presence of negative correlations subtly affects the performance of SLIPT, the methodology is robust across the exact structures of genes and is therefore applicable to detecting synthetic lethal genes in a range of (synthetic lethal) biological pathways with different structural relationships.

6.3.1 Simulations over Pathway-based Graphs

Simulations of synthetic lethality in gene expression with correlation structures thus far have used simple blocks of correlated genes (as used in Section 3.3) or have been derived from constructed graph structures (as used in Section 6.2). These have been used to make inferences on the impact of correlation structure but it remains to be shown whether these findings are reproducible in the complexity of the biological network structure. Specifically, SLIPT was tested on simulated data with known underlying simulated synthetic lethal partners (as described in Section 3.2.2) with multivariate normal correlation structure derived from biological pathways (as described in Section 3.4.2).

The Reactome pathway structure for the PI3K cascade (as used in Chapter 5) was used to demonstrate the simulation procedure for detecting synthetic lethality in the graph structure of a biological pathway. This pathway has clear directionality, with related signalling pathways among those identified to be synthetic lethal candidates (in Chapter 4). The PI3K pathway has a relatively moderate size (138 genes) and complexity. It is therefore suitable for comparison to previous graph structures of a similar scale (50–100 genes) with the complexity of a biological pathway.

The performance of synthetic lethal detection with SLIPT, in simulated expression data based on the Reactome PI3K pathway (as shown in Figure 6.16), was concordant with previous findings. SLIPT had high performance when detecting a low number of synthetic lethal genes which decreased for high numbers of synthetic lethal genes or lower sample sizes. In particular, the performance of simulations in the PI3K pathway closely resembled the simulation results for constructed graphs of similar scale and complexity (as shown in Appendix Figures J.9 and J.10). Using thresholds based on

the χ^2 p-value (adjusted by FDR), simulations in the biological PI3K pathway had a higher sensitivity and lower specificity. While the performance decreased for more synthetic lethal genes to detect within the simulated PI3K pathway, this primarily involved a reduction in sensitivity to detect synthetic lethal genes rather than false positives, as the false positive rate decreased, the accuracy increased, and the specificity was relatively unperturbed (being more dependent on sample size). Thus SLIPT was stringent in an example of a biological graph structure and is appropriate for detection of synthetic lethal genes in complex correlation structures in gene expression data involving biological pathways.

These simulations were replicated in the more complex $G_{\alpha i}$ signalling pathway (of 292 genes), which was one of the most well supported synthetic lethal pathways with loss of *CDH1* in cancer (in Chapters 4 and 5). This pathway showed similar relationships between sensitivity, specificity, and false positive rate with number of synthetic lethal partners and sample size (as shown in Appendix Figure J.18). While the overall performance was lower than for smaller networks structures, many of the findings from previous networks were replicated in a larger more complex biological network. In the $G_{\alpha i}$ signalling pathway, SLIPT had high performance for detecting low numbers of synthetic lethal genes and was highly stringent against false positives for higher numbers of synthetic lethal genes.

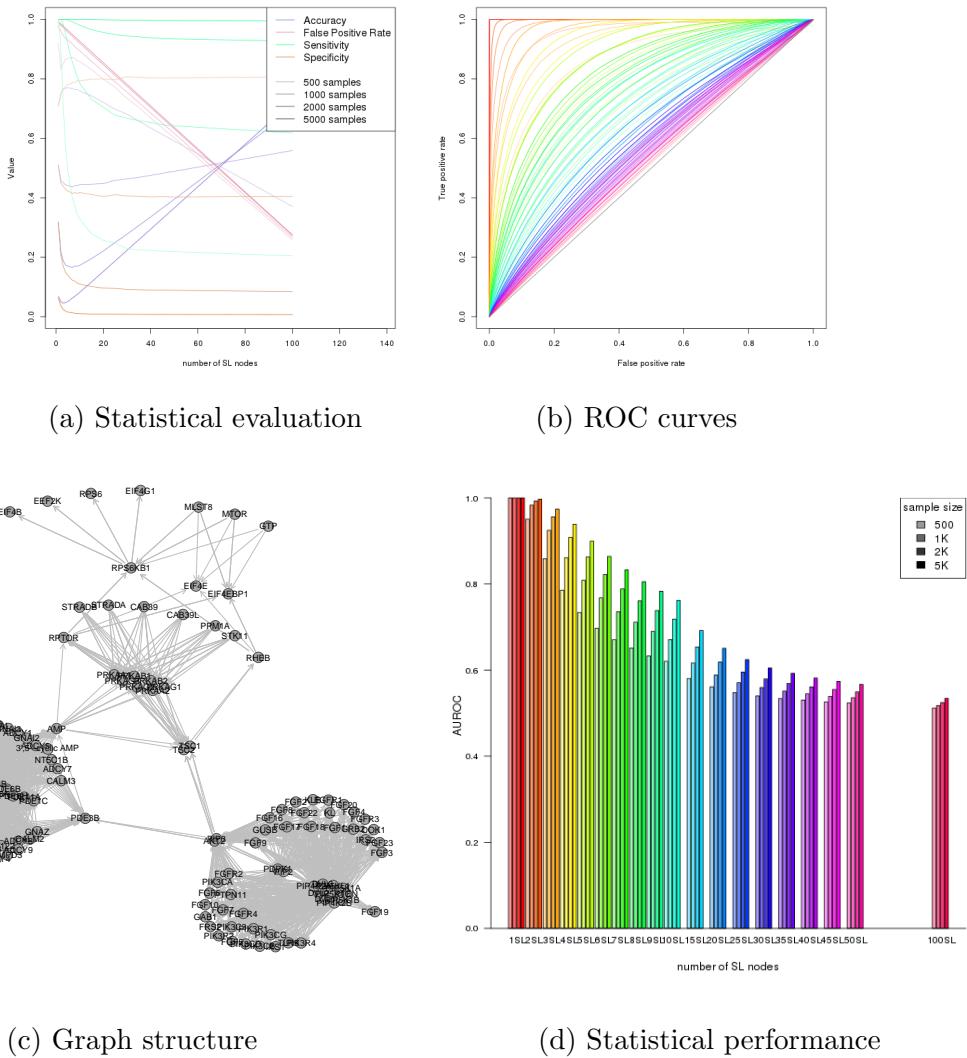


Figure 6.16: Performance of simulations on the PI3K cascade. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution based on the Reactome PI3K cascade. Performance of SLIPT was high across parameters for detecting synthetic lethality in the graph structure within a larger dataset. The performance decreased for a greater number of true positives to detect but the accuracy increased with a low false positive rate.

6.3.2 Pathway Structures in a Large Simulated Dataset

Simulations were also performed with graph structures from biological pathways included in a larger dataset to simulate gene expression data of the scale typical for human and cancer studies. These simulations (as discussed in Section 6.2.4) showed a higher specificity and therefore SLIPT had higher performance. The simulated PI3K

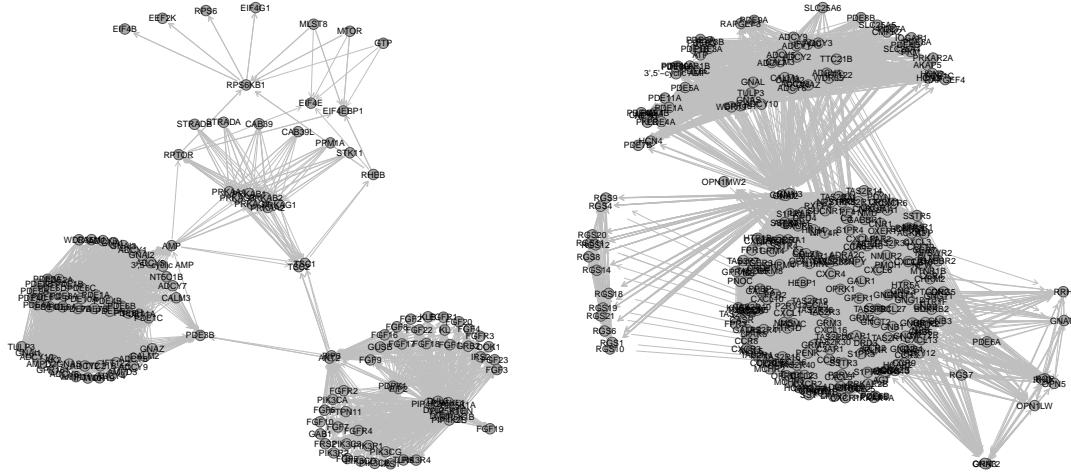
pathway (as shown in Appendix Figure J.19) was no exception, with high performance across parameter values, which remained high up to many genes. While the sensitivity decreased for high numbers of synthetic lethal genes to detect within the PI3K pathway, the SLIPT methodology remained accurate, with high specificity in a large simulated gene expression dataset.

Therefore the SLIPT methodology is a highly stringent approach suitable to be applied for detecting synthetic lethal genes and pathways within highly complex expression data with biological pathway structure. Even the poorly performing simulations were highly stringent, with low false positive rates, which are an important consideration *in* gene expression data with many non-synthetic lethal genes. The enrichment of true synthetic lethal partners among detected genes makes SLIPT valuable for triage of candidate synthetic lethal partners for further validation and for pathway analysis.

The performance of SLIPT in simulations of synthetic lethality within biological pathways was markedly higher in the context of a larger dataset of thousands of genes. As shown in a direct comparison with the graph structures alone (as shown in Figure 6.17c), performance was consistently higher across parameters in pathways of biological complexity from the Reactome database (Croft *et al.*, 2014) such as PI3K cascade and the $G_{\alpha i}$ signalling pathway (shown in Figure 6.17d and Appendix Figure J.20).

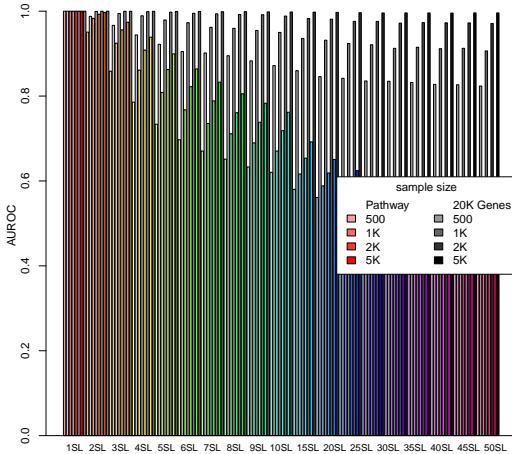
These biologically complex graph structures, based on the Reactome pathways, assumed activating relationships to test synthetic lethal detection with SLIPT in the context of complex correlation structures. Inhibiting relationships were not distinguished in the Reactome database (Croft *et al.*, 2014). However, these investigations with pathway-based graph structures indicate that the findings in constructed graphs (as used in Section 6.2) are relevant to gene expression data containing real correlated pathways. Furthermore, previous comparisons between simulations with inhibiting relationships indicated that the performance of synthetic lethal detection in an equivalent graph structure with inhibitory relationships will likely be higher.

Non synthetic lethal genes, inversely correlated with the underlying synthetic lethal partners, were distinguishable by SLIPT with high specificity. Synthetic lethal genes were detectable with reasonable performance in large scale simulated gene expression data and highly (positively) correlated genes in pathway structures. These findings serve as a conservative estimate for the performance of SLIPT to detect synthetic lethal genes within a synthetic lethal biological pathway in empirical data. Synthetic lethal genes are distinguishable from correlated genes, to varying extents, in simulations.

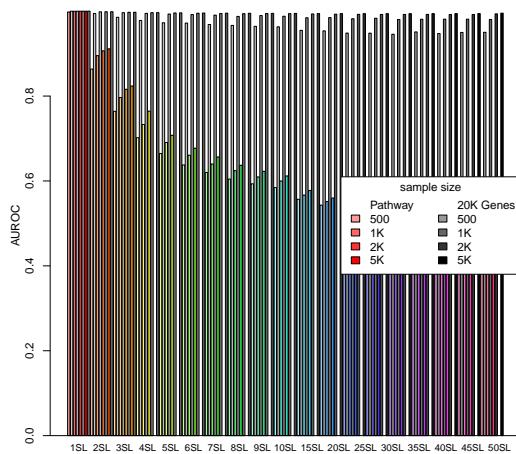


(a) The PI3K cascade (see Figure 5.1)

(b) $G_{\alpha i}$ signalling (see Figure 5.2)



(c) Performance in the PI3K cascade



(d) Performance in $G_{\alpha i}$ signalling

Figure 6.17: Performance on pathways improves with more genes. Simulations were performed in a graph structures for the PI3K cascade and $G_{\alpha i}$ signalling pathways structures to detect synthetic lethal partners within them. As for constructed graphs, performance of detection in a dataset containing only the graph structure (in colour) was as much lower than testing the graph structure within a larger dataset of non-synthetic lethal genes (without correlations) for both graphs of biological complexity.

False positives are also more likely to occur within the same (synthetic lethal) pathways. Therefore SLIPT is both effective at triage of synthetic lethal candidates within a

biological pathway and at identifying synthetic lethal pathways in high dimensional gene expression data.

6.4 Discussion

6.4.1 Simulation Procedure

Simulations were performed to assess the performance of the SLIPT methodology (as described in Section 3.1 and with modifications) when detecting known underlying synthetic lethal partners of a query gene. The simulation results supported the findings in empirical data (in Chapters 4 and 5) by addressing whether the methodology used to generate them was accurate or had desirable statistical performance in controlled simulated conditions. These investigations included adjusting parameters, such as the number of synthetic lethal genes that were known in simulated data, to assess the performance of the SLIPT methodology and characterise the datasets for which SLIPT performs well. Simulation and statistical modelling also enabled comparison of the SLIPT methodology to other approaches to synthetic lethal detection in expression data.

These simulations were based on a statistical model of synthetic lethality (as described in Section 3.2.1) which was designed stringently to ensure that if synthetic lethality was detectable in the simulated datasets, it would also be detectable by the same methodology in empirical expression data. The model of synthetic lethality made conservative assumptions, such as the low threshold of expression for gene function or the inclusion of cryptic higher-order synthetic lethality (when testing pairwise). These assumptions decrease the likelihood that synthetic lethality would be detectable in expression data. Thus it is reassuring that synthetic lethality was still detectable *under* many simulation parameters as the performance of SLIPT would be expected to be higher were these assumptions to be violated in empirical data.

The simulation procedure (as described in Section 3.2.2) was designed as a computational pipeline with arguments passes to scripts. The SLIPT methodology and simulation of expression from graph structures were both used as R (R Core Team, 2016) software packages, developed and released for this project (as described in Section 3.5). This design ensured that the simulations can be robustly applied across parameters with consistency between simulations apart from the differences discussed. The simulation procedure is also flexible to simulating other datasets, including synthetic lethal relationships and pathway correlation structures, should these be rele-

vant to future investigations or bioinformatics tool development. The computational pipeline is also compatible with parallel computing and made use of High Performance Computing (HPC) infrastructure provided by the New Zealand eScience Infrastructure (NeSI) using the Simple Linux Utility for Resource Management (Slurm) submission system (as described in Section 2.5.3). This parallel computing pipeline enabled extensive investigations into synthetic lethality in simulated data, including approximately 2 million cpu-hours on NeSI.

6.4.2 Comparing Methods with Simulated Data

Attempts were made to implement alternative synthetic lethal detection approaches such as Pearson correlation and the BiSEp R package (discussed in Section 6.1). However, these were less effective than SLIPT at detecting synthetic lethality in multivariate normal simulated data. While some of the published synthetic lethal detection methods (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015) did not provide reproducible software releases for direct comparison, some of the central assumptions used in their design were tested by the statistical methods considered for synthetic lethal detection in expression data.

BiSEp took considerably more time to compute predictions than SLIPT or χ^2 , which limited the number of simulations that were feasible and made it difficult to apply across parameters in the simulation pipeline (even when using supercomputing infrastructure as discussed in Section 2.5.3). The computationally intensive nature of the BiSEp procedure does not appear to be the issue for detecting synthetic lethal genes in TCGA data or simulations, although it has made more extensive simulations challenging. Rather, BiSEp was not suitable in either case since the TCGA data was normalised with `voom` (Ritchie *et al.*, 2015) and simulated data was generated by sampling from a multivariate normal distribution. In either case, even subtle bimodal signatures in expression data were not consistently detectable or sufficient to detect synthetic lethality.

The BiSEp methodology may perform better on other data types but it cannot be directly compared with the results for SLIPT throughout this thesis which have used normalised or (multivariate) normally distributed data. Since it requires bimodal distributions, BiSEp was not suitable for stringently normalised expression data nor would it be expected to perform on (ranked) pathway metagenes. Thus SLIPT represents a distinct approach more suitable for these data types whereas BiSEp may be applicable to other applications in which bimodal distributions are more frequent.

This investigation also demonstrated that implementing scientific software from other research groups is not a trivial exercise, even when released as an open-source R package. Therefore, the above results were used to evaluate SLIPT and compare it to other statistical rationales. A comprehensive comparison to other synthetic lethal detection approaches or further benchmarking is left to an impartial researcher to evaluate. Nevertheless, the SLIPT methodology was shown to be able to detect synthetic lethal genes in simulated data with comparable or better performance than a range of distinct statistical techniques and was appropriate for use throughout this thesis.

6.4.3 Design and Performance of SLIPT

The simulation procedure using sampling from a multivariate normal distribution was used throughout the simulation investigations in this thesis. This approach has the advantages of emulating the continuous normalised expression data used for gene expression analysis and enabled the simulation of correlation structures (as discussed in Section 3.3). These simulations scaled to datasets of comparable *size* to those used in gene expression analysis, with thousands of genes. The SLIPT methodology was shown to perform robustly, across large numbers of genes and simple correlation structures. This included high specificity against genes positively correlated with the query gene, for which the directional SLIPT methodology was more suited to distinguishing synthetic lethal genes *than* the χ^2 test without directional criteria on the number of samples observed.

The SLIPT and the χ^2 test , approaches using threshold-based discrete gene function, were compared across different quantiles to the Pearson correlation without loss of the continuous expression data. The $1/3$ -quantiles for SLIPT (as described in Section 3.1) were optimal for both SLIPT and the χ^2 alone, being optimal for the significance of synthetic lethal interactions and for the directional criteria of SLIPT (since this method outperformed the χ^2 test and was the most different at the $1/3$ -quantile). This difference was more pronounced with positively correlated genes (with the query gene), for which the specificity of SLIPT improved, and was replicated in large datasets with thousands of genes. These results were not simply due to sufficient samples for significant p-values, since the AUROC analysis was independent from significance thresholds. This indicated that the SLIPT methodology (as it has been used in Chapters 4 and 5) was optimal, with the $1/3$ -quantile having the highest performance, and *that* the parameters used to design it were appropriate.

Both discrete functional approaches (SLIPT and χ^2) were able to outperform negative correlation, which addressed the concern that arbitrary thresholds of low and high gene function (as used by SLIPT) may lose useful data by compressing the spectrum of gene expression into categorical data. However, this does not impede the performance of SLIPT if the quantiles used are optimal. The poorer performance of correlation-based detection of synthetic lethality was consistent with gene function for synthetic lethality being qualitative, that is expression must be sufficient for cell viability and higher expression is not necessary for function (as this is not the case for all genes). Furthermore, the finding that negative correlation outperforms positive correlation was also consistent with co-expression being a poor predictor of synthetic lethality compared to other approaches (Jerby-Arnon *et al.*, 2014), supporting the claims of Lu *et al.* (2015). Compared with SLIPT correlation approaches were not as suitable for detecting synthetic lethality in expression data. The correlation-based approaches made assumptions about the relationship between gene expression and function which do not necessarily hold for all genes. A linear model or regression approach may also be used to detect synthetic lethality from relationships between expression of genes, which may be improved with conditioning on known synthetic lethal partners with multivariate regression or Bayesian priors. Similarly, synthetic lethal detection could be performed by iteratively conditioning upon the strong candidate from previous analysis. These approaches may be able to better circumvent the issues of high-order synthetic lethality and multiple testing.

Nevertheless, the above findings were sufficient to assess the performance of SLIPT and present an effective straightforward approach to synthetic lethal detection in gene expression data. Further development with linear models, Bayesian inference approaches, or comparison to existing synthetic lethal approaches (e.g., machine learning) remain as future directions. Developing and testing more sophisticated statistical approaches to synthetic lethal detection may benefit from findings for the relatively simple SLIPT methodology. Similarly, further comparisons and benchmarking of SLIPT against other computational approaches to synthetic lethal detection in gene expression data is more suitable for an independent researcher and the `slipt` R package has been released (as described in Section 3.5) for this purpose, in addition to further application in research.

6.4.4 Simulations from Graph structures

The simple correlation structures (as used in Section 3.3) were expanded upon using the multivariate normal simulation procedure to produce correlation structures based on graph structures (as described in Section 6.2). These simulations enabled further investigations into the performance of SLIPT in the context of more complex correlation structures. The simulation of expression from network structures is widely applicable to simulating pathway expression data and as such the `graphsim` R package has been released (as described in Section 3.5).

These investigations show that SLIPT performs robustly across datasets with different correlation structures, including those derived from graphs with the complexity of biological pathways. The SLIPT methodology was able to detect synthetic lethal genes within synthetic lethal pathways across many graph structures. This methodology performed particularly well with synthetic lethal pathways in the context of a larger dataset with a high specificity, which supports SLIPT as a stringent approach to synthetic lethal detection in highly dimensional gene expression data. Together these results support the use of SLIPT in biological gene expression data, since it was able to detect synthetic lethal genes in highly complex correlation structures.

Similarly, the inclusion of inhibitory relationships in graph structures was shown to increase the performance in simple networks, supporting SLIPT being applicable to biological data in which these relationships are common. While these results were not replicated in more complex inhibitory graph structures, this is likely an artifact of the simulation procedure (which randomly selects combinations of synthetic lethal genes). When the simulations with a synthetic lethal gene were examined in more detail, the test statistics of the synthetic lethal gene were consistently higher and distinguishable from nearby genes in the graph structure. These differences were more pronounced with genes which had inhibitory relationships with synthetic lethal genes. While distinguishable from nearby genes in a pathway structure, the genes correlated with synthetic lethal partners had higher test statistics than more distant genes (similar to observations with correlated genes in Section 3.3).

In addition to being able to detect synthetic lethal genes in a pathway, the proximal genes in a pathway were most likely to be false positives and therefore SLIPT is also able to detect synthetic lethal pathways. SLIPT identifies genes which are likely to be constituent of a synthetic lethal pathway and is more likely to rank underlying synthetic lethal genes with greater significance. Together these findings support the use of SLIPT throughout this thesis, further application of SLIPT, and further development of such

strategies for synthetic lethal detection. Similarly, the simulation procedures developed and demonstrated for examining synthetic lethal detection in expression data using graph structures is amenable to further development. Investigations into pathway structure in expression data, such as predicting biological pathways from expression data or on the impact of pathways on differential expression analyses, could also be conducted with simulated data.

6.5 Summary

A statistical model and simulation procedure has been developed to test the performance of the SLIPT methodology in controlled conditions, using multivariate normal distributions. This simulation procedure has been developed into a computational pipeline which was able to test the statistical performance (using stringent assumptions) of SLIPT across many parameters and compare it to alternative synthetic lethal detection strategies. The SLIPT methodology performed well at detecting small numbers of synthetic lethal genes in simple systems. It did not perform as well in more complex systems but neither did alternative strategies. The SLIPT methodology performed well compared to Pearson correlation and the χ^2 test. Thus SLIPT is an effective detection method for synthetic lethal relationships in expression data despite its relatively simple design.

Simulations of more complex datasets were performed, including large numbers of genes, complex correlation structure derived from graph structures, and correlations with the query gene. SLIPT performed robustly across these, including correlation structures based on complex biological pathways. The performance of SLIPT improved in larger datasets, datasets with positive correlations with the query genes, and some graph structures which included inhibiting relationships, namely those datasets that were more representative of gene expression in biological data. SLIPT was both capable of recurrently detecting genes within a synthetic lethal pathway and distinguishing synthetic lethal genes from **those** correlated with them, even in highly complex correlation structures. Therefore SLIPT is a stringent synthetic lethal detection strategy and is applicable to gene expression as previously demonstrated for the partners of *CDH1* in breast and stomach cancer.

Chapter 7

Discussion

This thesis combines analysis of gene expression data from TCGA with experimental screening results (Telford *et al.*, 2015) to demonstrate synthetic lethal discovery for partners of *CDH1*. Together these findings further elucidate known and novel functions of *CDH1* in the cell, functional redundancy in cancer, and represent potential therapeutic targets against loss of *CDH1* function. Synthetic lethal candidate genes were further investigated for relationships within synthetic lethal pathways, and in the process a network-based approach to compare gene sets was developed.

The SLIPT synthetic lethal detection methodology was applied to gene expression data throughout this thesis and was evaluated with simulated data. A procedure was developed to stringently generate gene expression data from known synthetic lethal partners in simulated data. These simulations included simple and complex correlation structures, and modelling synthetic lethal genes within pathways. Together, these results demonstrate SLIPT as a robust widely applicable gene expression analysis procedure for discovery of synthetic lethal partner genes (for which an R package has been made available). The performance of SLIPT on simulated data also highlights the strengths and limitations of the procedure.

7.1 Synthetic Lethality and *CDH1* Biology

The *CDH1* tumour suppressor gene was the focus to demonstrate the novel SLIPT methodology for identifying synthetic lethal partners. This gene is important in sporadic breast and stomach cancers, in addition to familial syndromes, such as HDGC. The analysis of synthetic lethal partners of *CDH1* in breast and stomach cancers was enabled by the availability of molecular data (Bass *et al.*, 2014; Koboldt *et al.*, 2012)

and a synthetic lethal screen conducted in MCF10A breast cells (Chen *et al.*, 2014; Telford *et al.*, 2015).

Synthetic lethal interactions arise due to functional redundancy (Boone *et al.*, 2007; Fece de la Cruz *et al.*, 2015; Kaelin, Jr, 2005) and so the synthetic lethal partners of *CDH1* indicate the wide-ranging biological functions that E-cadherin is involved in. The diverse synthetic lethal pathways identified support the known pleiotropic nature of the *CDH1* gene (Kroepil *et al.*, 2012), across established functions of *CDH1*, candidates from an experimental screen (Telford *et al.*, 2015), and novel interactions identified for further investigation. The highly pleiotropic functions of E-cadherin was also consistent with *CDH1* being a tumour suppressor gene.

7.1.1 Established Functions of *CDH1*

CDH1 has established functions in cell-cell communication and maintaining the cytoskeleton, specifically with cell-cell adhesion by forming tight junctions and the adherens complex (Jeanes *et al.*, 2008). More recently, functions of *CDH1* in the extracellular matrix and fibrin clotting have also been identified (Cardiff *et al.*, 2011; Tunggal *et al.*, 2005; Wojtukiewicz *et al.*, 2016). Synthetic lethal interactions within the same biological pathway were expected (Boone *et al.*, 2007; Kelley and Ideker, 2005). Synthetic lethal interactions identified in these pathways are consistent with the known functions of *CDH1*, which are also potentially actionable targets against cancers.

7.1.2 The Molecular Role of *CDH1* in Cancer

The involvement of *CDH1* in the extracellular matrix is important in cancers as it indicates that *CDH1* loss may affect the tumour microenvironment, contributing to its role as a tumour and invasion suppressor. Furthermore, perturbations in the extracellular matrix and tumour microenvironment present a means by which to specifically inhibit (cancerous) *CDH1*-deficient cells, in addition to those identified by siRNA screening (Telford *et al.*, 2015). These may be further supported in further investigations with 3D cell culture, “organoid”, or mouse xenograft cancer models.

Many of the pathways involved in cell signalling, including GPCRs, were identified by SLIPT in addition to the experimental screen, supporting findings in cell line models (Telford *et al.*, 2015). These pathways are essential to the growth of *CDH1*-deficient cancers and present a potential vulnerability specific to these (cancerous) cells. Furthermore, the replication of synthetic lethality of *CDH1* with cell signalling pathways in TCGA data, across cancer types and genetic backgrounds, robustly supports these pathways being clinically applicable beyond the genetic background of the model sys-

tem of *CDH1*^{-/-} MCF10A cells (Chen *et al.*, 2014). While specific synthetic lethal genes were not consistently detected between the SLIPT analyses and siRNA screen (Telford *et al.*, 2015), they were sufficient to identify synthetic lethal pathways for further experimental investigation, which are more likely to be replicated between genetic backgrounds (Dixon *et al.*, 2008). Together these results demonstrate **that** computational methods, such as SLIPT, could be integrated with an experimental screen to triage potential therapeutic targets for further pre-clinical investigation.

The analysis of expression data with SLIPT is also indicative of biological mechanisms of synthetic lethality in pathways beyond those identified in screening experiments (Telford *et al.*, 2015). In particular, translation and regulatory pathways, involving 3' UTRs and NMD, were candidate synthetic lethal pathways with *CDH1* **identified** by SLIPT. These pathways represent downstream targets, regulated by the putative synthetic lethal signalling pathways, which cancer cells are dependent on to proliferate and evade host defense processes, such as apoptosis and immune responses (Gao and Roux, 2015).

7.2 Significance

7.2.1 Synthetic Lethality in the Genomic Era

An effective synthetic lethal discovery tool for bioinformatic analysis could have a wide range of applications in genetics research, including functional genomics, medical and agricultural applications. The SLIPT approach demonstrated in this thesis is widely applicable to other genes, cell types, and biological research questions. In addition to further query of cancer genes, synthetic lethal gene functions **also have** implications for genetic redundancy. Highly redundant genes, and the genetically robust systems they give rise to, are also relevant to evolutionary, developmental, and systems biology to understand how these change over time and play **a fundamental role in fundamental development** (Boone *et al.*, 2007; Nowak *et al.*, 1997; Tischler *et al.*, 2008).

Developmental genes in particular, are highly evolutionarily conserved and subject to high rates of redundancy (Fromental-Ramain *et al.*, 1996; Kockel *et al.*, 1997; Nowak *et al.*, 1997). These genes are often difficult to study with conventional functional genetics techniques since individual knockouts of redundant genes may not have a mutant phenotype. Identifying genes with a common function is therefore also important to characterise developmental genes. Synthetic lethal discovery methods, such as SLIPT,

represent a genomic approach to further systematic characterisation of gene function including highly redundant developmental genes.

Variants of unknown significance and modifier loci are a major concerns in human genetics, including “monogenic” and “rare” diseases. Many of these variants could be difficult to characterise individually due to synthetic lethal interactions, where additional loci contribute to the disease (or only compensate for some variants). Systematic identification of synthetic lethal interactions therefore also has applications in the study of these “oligogenic” diseases. There could also be similar applications in the study of heritability for traits including agricultural genomic selection.

Polypharmacology and network medicine are rationales that account for genetic redundancy by using drugs with multiple (known and specific) targets (Barabási *et al.*, 2011; Hopkins, 2008). Further characterisation of synthetic lethal genes could assist with the design of effective multi-target drugs or combination therapies in a range of therapeutic applications, including molecular targeted therapies against cancer for which combination therapies may alleviate acquired resistance against individual targeted therapies. Characterisation of genetic interactions and combination therapies also has the potential to expand pharmacogenomic investigations. Synthetic lethality may elucidate the impact of genotypes at multiple loci, which lead to adverse effects due to variants in synthetic lethal genes.

Redundant functions and synthetic lethal interactions also present a means to expand upon the concept of the “minimal” genome (Hutchison *et al.*, 2016). It is important to account for essential gene functions that are performed by redundant genes (or in combination with pleiotropic genes), rather than simply those that are perturbed by individual genes. An essential gene approach therefore is likely to produce an underestimate that does not account for synthetic lethal interactions.

Synthetic lethal interactions are fundamentally important throughout genetics. Further understanding of them in a genomic context, facilitated by methods such as SLIPT, would contribute towards deeper understanding of gene functions and their role in traits or diseases in the post-genomic era. Genes do not function in isolation and understanding them in the context of the complexity of a cell and across genetic backgrounds is essential to further characterise their functions and ensure that findings can be validated or applied beyond experimental systems.

7.2.2 Clinical Interventions based on Synthetic Lethality

Synthetic lethal discovery with SLIPT is of particular relevance to cancer for the discovery of synthetic lethal drug targets. The cancer research community relies on cell line and mouse models for screening and validation experiments (Fece de la Cruz *et al.*, 2015) which would benefit from integration with gene expression analysis, as demonstrated for *CDH1* and the screen conducted by Telford *et al.* (2015). Synthetic lethal drug design against cancer mutations, including gene loss or over-expression, could lead to a revolution in cancer therapy and chemoprevention. These therapeutics would enable personalised treatment for cancer patients and high risk individuals. The synthetic lethal strategy for cancer treatment has been shown to be clinically effective (Bryant *et al.*, 2005; Farmer *et al.*, 2005; McLachlan *et al.*, 2016). Many large-scale RNAi screens have been conducted recently, aiming to discover gene function and drug targets for similar application with other cancer genes, including cancers in other tissues (Fece de la Cruz *et al.*, 2015).

While SLIPT analysis and RNAi screens represent a significant step towards anti-cancer medicines, further validation is required to ensure that the synthetic lethal candidate genes and pathways identified for *CDH1* in breast and stomach cancer are applicable against *CDH1*-deficient cancers in the clinic. Validation with RNAi or pharmacological inhibitors is needed because false positives may occur in SLIPT analysis or siRNA screens. These candidates still need to be tested in pre-clinical models (cell lines and mouse xenografts) before proceeding to clinical trials. A therapeutic intervention will also require a targeted therapeutic to be developed or repurposed against a synthetic lethal partner. Drug targets could be triaged from synthetic lethal genes by functions known to be amenable to drugs, having protein structures with conserved specific sites that are not homologous to other genes, or those with existing drugs. Both structure-aided drug design and compound screening are viable ways to target synthetic lethal partners.

Targeted therapeutics designed based on synthetic lethal interactions could expand the applications of “precision medicine” against molecular targets. Synthetic lethality expands the range of cancer genes which can be (indirectly) targeted to include tumour suppressor genes with loss of function, such as *CDH1*. Oncogenes with disrupted functions that are over-expressed or highly homologous to non-cancerous proto-oncogenes, such as *MYC*, *EGFR* or *KRAS*, may also be targeted by synthetic lethality. Applications against tumour suppressor genes is particularly important, as these cannot be approached by careful dosing. Synthetic lethal drug design has the benefit of being

highly specific against a particular genotype (e.g., *CDH1*^{-/-}) with the potential for targeted therapies with a wide therapeutic index and few adverse effects, in contrast to many cancer treatment regimens (Hopkins, 2008; Kaelin, Jr, 2009). These properties are highly desirable for chemoprevention applications, such as treatment against *CDH1*-deficient in HDGC patients (Guilford *et al.*, 2010), as an alternative to monitoring or surgery.

7.3 Future Directions

While further validation and pre-clinical testing is required to translate the findings for *CDH1* to cancer therapy or prevention, there are also further avenues for research into the detection of synthetic lethality in gene expression and other genomics data. The SLIPT methodology is amenable to wider application against a range of genes for which loss of function is deleterious, including other cancer genes in breast cancer or other tissues. Synthetic lethal interactions are functionally informative, particularly for mode-of-action of known drug targets, and are also relevant for identifying functions of newly characterised genes in genomics studies and designing specific interventions against cells with loss of function in cancer and other diseases. Thus synthetic lethal detection using SLIPT in expression data could be further used for many other genes, including others relevant to human health and disease.

These investigations do not need to be limited to expression data. While expression as a measure of gene function has been the focus of this thesis, other genomics data could be used for a similar purpose for SLIPT analysis. These include DNA copy number, DNA methylation, histone activation, mutation status, protein abundance, and protein activation state. In particular, DNA copy number and mutations have been demonstrated by other approaches to synthetic lethal analysis (Jerby-Arnon *et al.*, 2014; Lu *et al.*, 2015; Srihari *et al.*, 2015; Wappett *et al.*, 2016), although some of these have not been released for wider application.

For some applications or genes, these molecular profiles may be more informative of gene function and synthetic lethal relationships. However, expression was the focus of the investigations thus far as a widely accepted measure of gene function which has widely available genomics data. SLIPT is compatible with each of these data types (if the thresholds are selected appropriately) and may perform better for some applications with these molecular profiles or a weighted combination of these. As demonstrated, SLIPT is also suitable for future investigations with pathway metagenes and other summary data as well.

It may also be possible to improve the performance of SLIPT with refinements to the statistical or computational approach. This thesis has focused on rational query-based approach which computes relatively quickly in R (R Core Team, 2016), and is relatively intuitive to interpret. These computations are compatible with parallel computing and the computational resources may be further reduced by using a different computing language. The `slipt` R package has been documented and released as open-source software (as described in Section 3.5) to facilitate further development, wider adoption, or comparison with other scientific software for similar purposes.

Alternative methods **may also** improve on the statistical performance of SLIPT. In particular, the sensitivity was generally **an issue** with higher numbers of synthetic lethal partners in simulated data. While approaches using continuous data such as Pearson correlation and linear regression did not perform as well as SLIPT, they could be improved. A least squares regression approach in particular, enables multiple measures of relationships such as the coefficients of the fitted curve and significance of the fit (computed from the residuals). A linear modelling approach using regression is also amenable to refinement such as extending from fitting a linear relationship to a polynomial or logistic regression. Another benefit to fitting linear models is that these would enable the conditioning of known synthetic lethal partners to identify subtle signatures of further interacting partners.

This approach could also be applied iteratively on the strongest candidates from previous synthetic lethal analyses in further rounds of prediction conditioned upon them. Similarly, synthetic lethal prediction could also be approached with a Bayesian framework (Friedman *et al.*, 2000; Imoto *et al.*, 2004; Jansen *et al.*, 2003) which is also amenable to Bayesian priors on known or previously predicted synthetic lethal partners. Either of these approaches has the potential to improve upon the synthetic lethal predictions which have been demonstrated as possible and biologically relevant by SLIPT.

7.4 Conclusions

Synthetic lethal interactions are important for understanding gene function and the development of highly specific targeted cancer treatments. In particular, synthetic lethality could expand the repertoire of applications for precision cancer medicine by indirectly targeting loss of function in tumour suppressor genes. Synthetic lethal discovery with experimental screening is error-prone and limited by the model systems in which it is performed. Thus there is a need for a bioinformatics tool to predict synthetic

lethal interactions from gene expression data, which would facilitate the rapid identification of synthetic lethal candidates, and augment functional genetic screens and triage of cancer drug targets. This thesis develops the Synthetic Lethal Interaction Prediction Tool (SLIPT) methodology as a statistically robust procedure to perform this analysis.

The SLIPT methodology has been demonstrated to identify biologically relevant genes and pathways. A comprehensive analysis of synthetic lethal partners of the *CDH1* gene was performed in TCGA breast cancer data (Koboldt *et al.*, 2012), with many of these findings replicated in stomach cancer data (Bass *et al.*, 2014). These genes clustered into several distinct groups, with distinct biological functions and elevated expression in different clinical subtypes. These analyses identified synthetic lethal candidates in the $G_{\alpha i}$ signalling, cytoplasmic microfibres, and extracellular fibrin clotting pathways. These pathways were supported by an siRNA screen performed by Telford *et al.* (2015) and were consistent with the known cytoskeletal and cell signalling roles of E-cadherin. SLIPT also identified synthetic lethal partners in novel pathways for *CDH1*, including the regulation of immune signalling and translational elongation, which extend the range of established functions of *CDH1* and present further biological mechanisms that can be investigated to exploit the vulnerabilities of *CDH1*-deficient cancers.

While some of these pathways are not expected to be detected in an isolated experimental cell line model, pathway structure may have accounted for this disparity. Thus synthetic lethal candidates detected by SLIPT and siRNA were compared within graph structures of the candidate synthetic lethal pathways. However, this did not generally account for differences between these approaches. Neither synthetic lethal detection methodology preferentially detected genes of more importance or connectivity in pathway structures using established network metrics, nor could it be generally established that SLIPT gene candidates were upstream or downstream of siRNA gene candidates in pathway structures across biological pathways. However, it could be shown that SLIPT genes had lower centrality and were upstream of siRNA candidates, specifically in the $G_{\alpha i}$ signalling pathway.

Pathway graph structures were also included in investigations with simulated data to ascertain whether the SLIPT procedure performed well in data with complex correlation structures derived based on biological pathways. A simulation procedure was developed based on a statistical model of synthetic lethality which generates multivariate normal data with known synthetic lethal partners and correlation structures.

The SLIPT methodology had high statistical performance, particularly when detecting few known synthetic lethal genes, with large sample sizes, and a background of many non-synthetic lethal genes to distinguish true partners from. This method had high specificity, performed better than Pearson correlation or the χ^2 -test, and had optimal performance across simulation parameter combinations for the thresholds used throughout this thesis. These findings were robust across correlation structures, including those derived from complex pathway structures containing strong positive and negative correlations between genes. Together, these findings support the release of the SLIPT software R packages and the application of the method to identify synthetic lethal genes within pathways and use candidate synthetic lethal genes to identify synthetic lethal pathways, as demonstrated in this thesis.

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Appendix A

Sample Quality

A.1 Sample Correlation

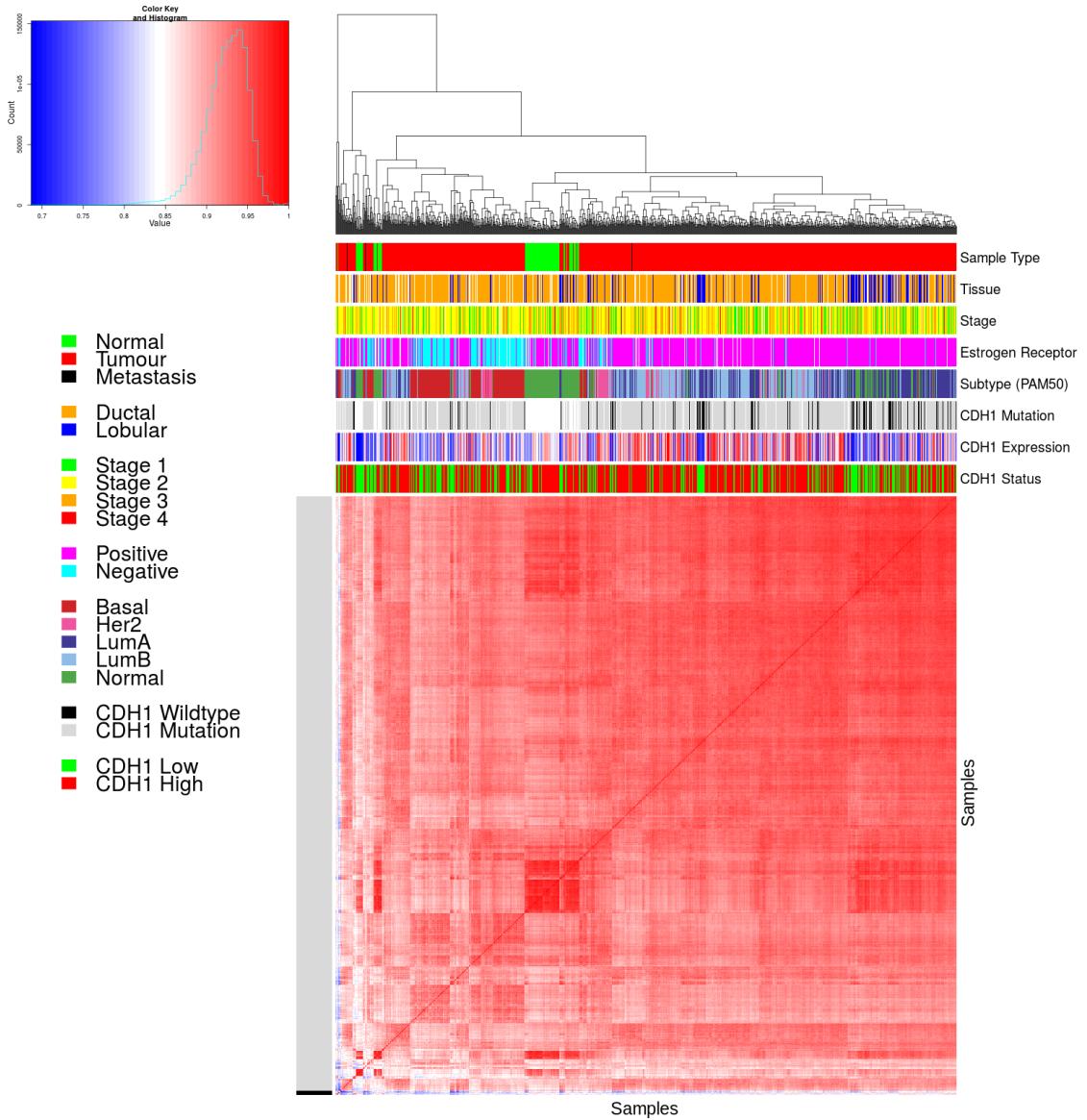


Figure A.1: Correlation analysis and sample removal. Correlation matrix heatmap (Euclidean distance) of all samples in TCGA breast cancer dataset against each other annotated for sample clinical data: sample type, tissue type, tumour stage, ER and intrinsic subtype (from the PAM50 method). *CDH1* somatic mutation, gene expression, and status for SLIPT prediction were also annotated. Discrete variables were coloured as displayed in the legend and continuous variables on a blue–red scale as shown in the colour key. Trimmed samples cluster at the bottom of the heatmap and the colour bars of the left show which were removed for quality concerns.

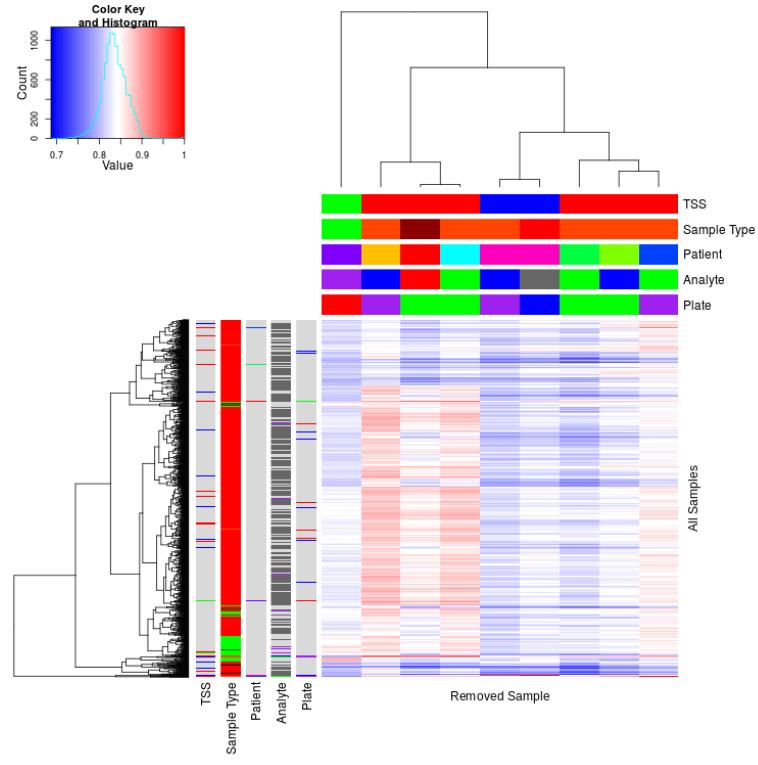


Figure A.2: Correlation profiles of removed samples. Heatmap (Euclidean distance) of samples in TCGA breast cancer dataset (left) clustered for all samples against removed samples (top): tissue source site (TSS), sample type with reds for tumour and greens for normal, patient (A2QH in pink), with varied analyte and plate. Excluded samples clustered at the bottom and annotation (left) show shared properties between samples in the dataset.

A.2 Replicate Samples in TCGA Breast Cancer Data

Replicate samples were picked where possible from the TCGA breast cancer gene expression data to examine for sample quality. Independent samples of the same tumour were expected to have very high Pearson correlation between their expression profiles unless there were issues with sample collection or preparation and were thus an indicator of sample quality. The log-transformed raw read counts for replicate samples were examined in Figures A.3–A.5. These were examined before normalisation which would be expected to increase sample concordance.

Another consideration was the samples which were removed for quality concerns (in Section 2.2.2). While these were selected by unbiased hierarchical clustering (See Figure A.1), many of the excluded (tumour) samples were performed in replicate despite relatively few replicate samples in the overall dataset. These samples correlate poorly with the rest of the dataset, in addition to correlation with replicate samples.

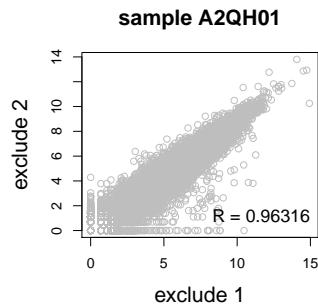


Figure A.3: **Replicate excluded samples.** Both tumour samples of patient A2QH were excluded as they were poorly correlated with other samples, although they were highly similar to each other as shown by Pearson correlation of log-raw counts.

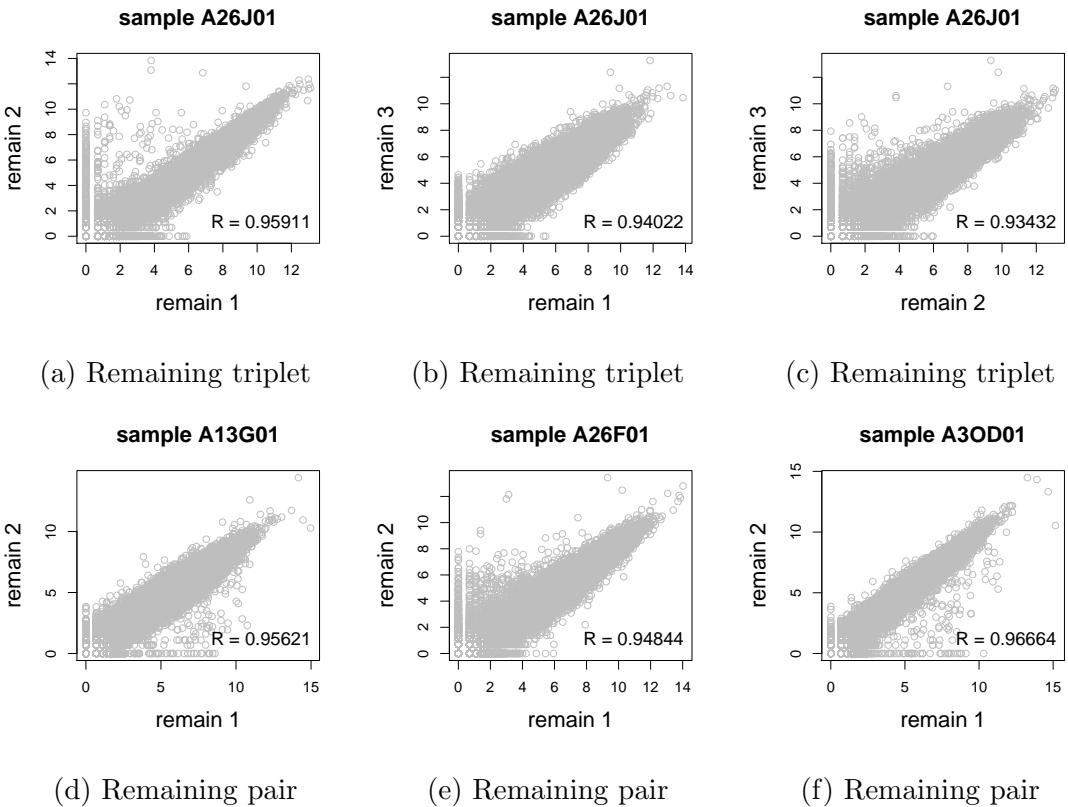


Figure A.4: **Replicate samples with all remaining.** Patient A26J was sampled 3 times and compared pairwise. Pairs of samples were also compared for other patients with replicate samples. In all cases, replicate samples remaining in the dataset were highly concordant, as shown by Pearson correlation of log-raw counts.

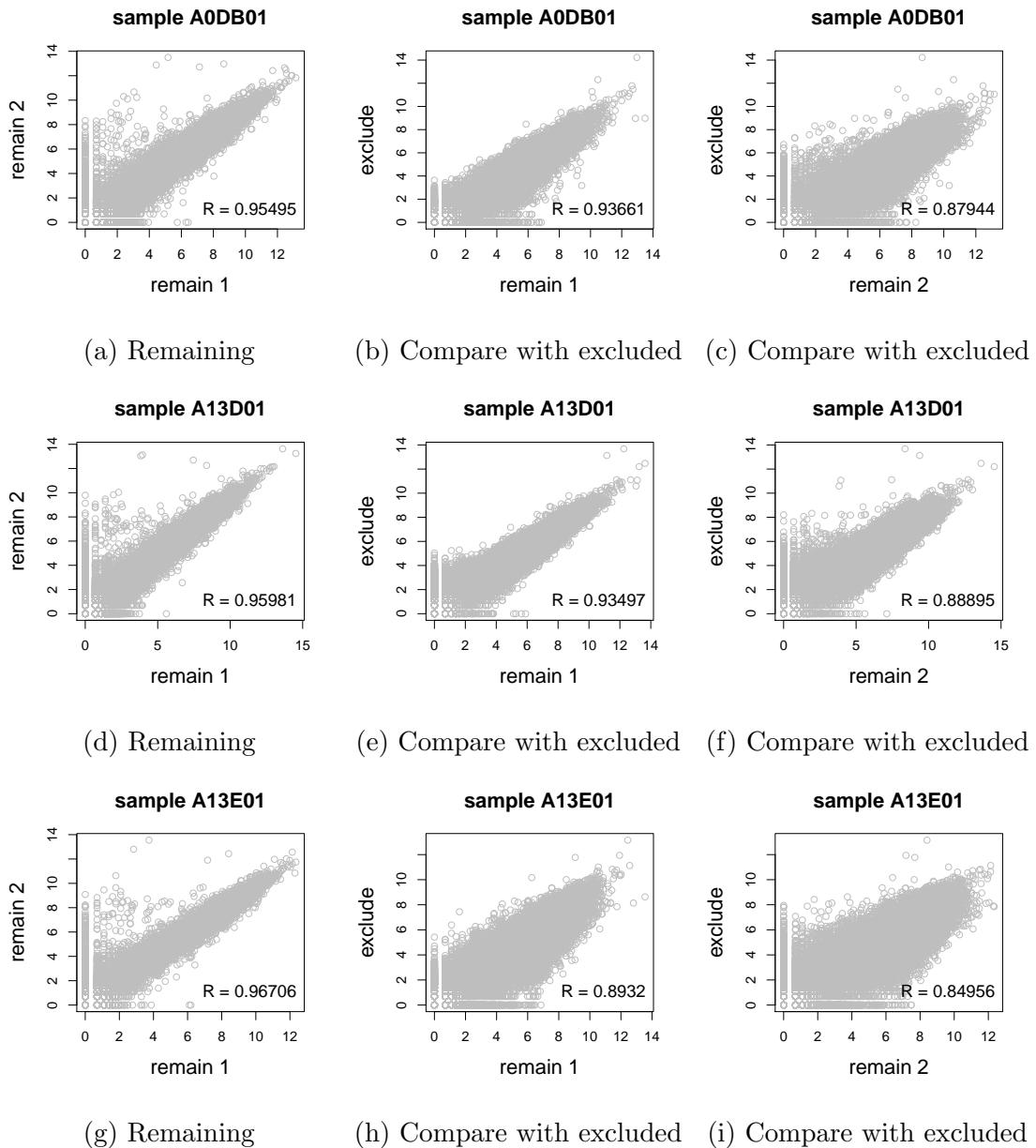


Figure A.5: Replicate samples with some excluded. (continued on next page)

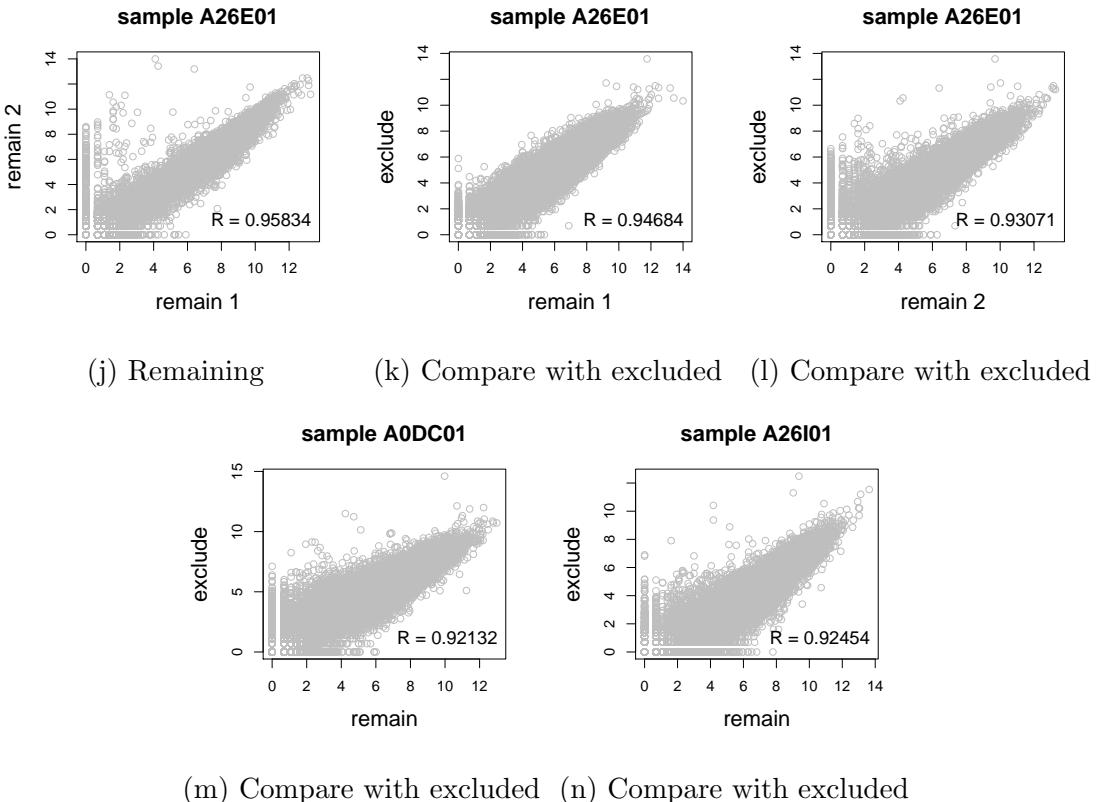


Figure A.5: **Replicate samples with some excluded.** Patients A0DB, A13D, A13E, and A26E were each sampled 3 times and compared pairwise. Pairs of samples were also compared for other patients with replicate samples. In all cases, the replicate samples remaining in the dataset more were highly concordant than those excluded from the analysis, as shown by Pearson correlation of log-log counts.

Appendix B

Software Used for Thesis

Table B.1: Computers used during thesis

	Viao Laptop	Lab Machine	Biochem Server	NeSI Pan Cluster
Operating System (OS)	Elementary OS Freya 0.3.2	Elementary OS Loki 0.4	Red Hat Enterprise Maipo 7.2	Cent OS Final 6.4
Upstream OS	Ubuntu LTS Trusty 14.04	Ubuntu LTS Xenial 16.04		
Linux Kernel	3.19.0-65-generic	4.4.0-36-generic	3.10.0-327.36.2.el7.x86_64	2.6.32-504.16.2.el6.x86_64
Shell: Bash	4.3.11(1)	4.3.46(1)	4.2.46(1)	4.2.1(1)
Shell: zsh	5.0.2	5.1.1	5.0.2	5.2

Table B.2: Linux utilities and applications used during thesis

		Viao Laptop	Lab Machine	Biochem Server	NeSI Pan Cluster
	OS	Elementary OS Freya 0.3.2	Elementary OS Loki 0.4	Red Hat Enterprise Maipo 7.2	Cent OS Final 6.4
	Linux Kernel	3.19.0-65-generic	4.4.0-36-generic	3.10.0-327.36.2.el7.x86_64	2.6.32-504.16.2.el6.x86_64
Scripting	Shell Bash	4.3.11(1)	4.3.46(1)	4.2.46(1)	4.2.1(1)
	Shell zsh	5.0.2	5.1.1	5.0.2	5.2
Programming	Python	2.7.6	2.7.12	2.7.5	
	Java	1.8.0_101	9-ea	1.8.0_101	
	C++	4.8.4	5.4.0	4.8.5	4.4.7
Text Editor	nano	2.2.6	2.5.3	2.3.1	2.0.9
	kile (L ^A T _E X)	2.1.3	2.1.3		
Version Control	git	1.9.1	2.11.0	1.7.1	1.8.3.1
Shell Utilities	sed	4.4.2	4.4.2	4.4.2	4.4.1
	grep	2.16-1	2.25-1	2.20	2.6.3
	nohup	8.21	8.25	8.22	8.4
Typesetting	T _E X	3.1415926	3.14159265		
	TexLive (L ^A T _E X)	2013	2015		
	PDFT _E X	2.5-1	2.6		
	pandoc	1.12.2.1	1.16.0.2		
Remote Computing	Slurm scheduler				16.05.6
	OpenSSH	7.2p2	7.2p2	6.6.1	5.3p1
	OpenSSL	1.0.2g	1.0.2g	1.0.01e-fips	1.0.01e-fips
	rsync	3.1.0p31	3.1.1p31	3.0.9p30	
	Globus Online Transfer			3.1	3.1
	Cisco AnyConnect VPN		3.1.05170		
Image Processing	Inkscape	0.48.4	0.91		
	GIMP	2.8.10	2.8.16		
	ImageMagick	6.7.7.10-6			

Table B.3: Complete list of R packages used during this thesis

Package	Repository	Laptop	Lab	Server	NeSI
base	base	3.3.2	3.3.2	3.3.1	3.3.0
abind	CRAN		1.4-5		1.4-3
acepack	CRAN		1.4.1		1.3-3.3
ade4	CRAN		1.7-5		
annaffy	Bioconductor		1.46.0		
AnnotationDbi	Bioconductor		1.36.0	1.36.0	1.34.4
apComplex	CRAN		2.40.0		
ape	CRAN		4		3.4
arm	CRAN		1.9-3		
assertthat	CRAN	0.1	0.1	0.1	0.1
backports	CRAN	1.0.5	1.0.4	1.0.5	1.0.2
base64	CRAN			2	2
base64enc	CRAN		0.1-3		0.1-3

beanplot	CRAN		1.2	1.2	1.2
BH	CRAN	1.60.0-2	1.62.0-1	1.62.0-1	1.60.0-2
Biobase	Bioconductor		2.34.0	2.34.0	2.32.0
BiocGenerics	Bioconductor		0.20.0	0.20.0	0.18.0
BiocInstaller	Bioconductor		1.24.0	1.20.3	1.22.3
BiocParallel	Bioconductor		1.8.1	1.8.1	
Biostrings	Bioconductor		2.42.1	2.42.0	
BiSEp	Bioconductor		2.0.1	2.0.1	2.0.1
bitops	CRAN	1.0-6	1.0-6	1.0-6	1.0-6
boot	base	1.3-18	1.3-18	1.3-18	1.3-18
brew	CRAN	1.0-6	1.0-6	1.0-6	1.0-6
broom	CRAN	0.4.1			
caTools	CRAN	1.17.1	1.17.1	1.17.1	1.17.1
cgdssr	CRAN		1.2.5		
checkmate	CRAN		1.8.2		1.7.4
chron	CRAN	2.3-47	2.3-48	2.3-50	2.3-47
class	base	7.3-14	7.3-14	7.3-14	7.3-14
cluster	base	2.0.5	2.0.5	2.0.5	2.0.4
coda	CRAN		0.19-1		0.18-1
codetools	base	0.2-15	0.2-15	0.2-15	0.2-14
colorRamps	CRAN		2.3		
colorspace	CRAN	1.2-6	1.3-2	1.3-2	1.2-6
commonmark	CRAN	1.1		1.2	
compiler	base	3.3.2	3.3.2	3.3.1	3.3.0
corpcor	CRAN		1.6.8	1.6.8	1.6.8
Cprob	CRAN		1.2.4		
crayon	CRAN	1.3.2	1.3.2	1.3.2	1.3.2
crop	CRAN		0.0-2	0.0-2	
curl	CRAN	1.2	2.3	2.3	0.9.7
d3Network	CRAN		0.5.2.1		
data.table	CRAN	1.9.6	1.10.0	1.10.1	1.9.6
data.tree	CRAN		0.7.0	0.7.0	
datasets	base	3.3.2	3.3.2	3.3.1	3.3.0
DBI	CRAN	0.5-1	0.5-1	0.5-1	0.5-1
dendextend	CRAN	1.4.0	1.4.0	1.4.0	

DEoptimR	CRAN	1.0-8	1.0-8	1.0-8	1.0-4
desc	CRAN	1.1.0		1.1.0	
devtools	CRAN	1.12.0	1.12.0	1.12.0	1.12.0
DiagrammeR	CRAN		0.9.0	0.9.0	
dichromat	CRAN	2.0-0	2.0-0	2.0-0	2.0-0
digest	CRAN	0.6.10	0.6.11	0.6.12	0.6.9
diptest	CRAN	0.75-7	0.75-7	0.75-7	
doParallel	CRAN	1.0.10	1.0.10	1.0.10	1.0.10
dplyr	CRAN	0.5.0	0.5.0	0.5.0	0.5.0
ellipse	CRAN		0.3-8	0.3-8	0.3-8
evaluate	CRAN		0.1	0.1	0.9
fdrtool	CRAN		1.2.15		
fields	CRAN		8.1		
flexmix	CRAN	2.3-13	2.3-13	2.3-13	
forcats	CRAN	0.2.0			
foreach	CRAN	1.4.3	1.4.3	1.4.3	1.4.3
foreign	base	0.8-67	0.8-67	0.8-67	0.8-66
formatR	CRAN		1.4	1.4	1.4
Formula	CRAN		1.2-1		1.2-1
fpc	CRAN	2.1-10	2.1-10	2.1-10	
futile.logger	CRAN		1.4.3	1.4.3	1.4.1
futile.options	CRAN		1.0.0	1.0.0	1.0.0
gdata	CRAN	2.17.0	2.17.0	2.17.0	2.17.0
geepack	CRAN		1.2-1		
GenomeInfoDb	Bioconductor		1.10.2	1.10.1	
GenomicAlignments	Bioconductor		1.10.0	1.10.0	
GenomicRanges	Bioconductor		1.26.2	1.26.1	
ggm	CRAN		2.3		
ggplot2	CRAN	2.1.0	2.2.1	2.2.1	2.1.0
git2r	CRAN	0.15.0	0.18.0	0.16.0	0.15.0
glasso	CRAN		1.8		
GO.db	Bioconductor		3.4.0	3.2.2	3.3.0
GOSemSim	Bioconductor		2.0.3	1.28.2	1.30.3
gplots	CRAN	3.0.1	3.0.1	3.0.1	3.0.1
graph	Bioconductor		1.52.0		

graphics	base	3.3.2	3.3.2	3.3.1	3.3.0
graphsim	GitHub TomKellyGenetics	0.1.0	0.1.0	0.1.0	0.1.0
grDevices	base	3.3.2	3.3.2	3.3.1	3.3.0
grid	base	3.3.2	3.3.2	3.3.1	3.3.0
gridBase	CRAN	0.4-7	0.4-7	0.4-7	0.4-7
gridExtra	CRAN	2.2.1	2.2.1	2.2.1	2.2.1
gridGraphics	CRAN		0.1-5		
gtable	CRAN	0.2.0	0.2.0	0.2.0	0.2.0
gtools	CRAN	3.5.0	3.5.0	3.5.0	3.5.0
haven	CRAN	1.0.0			
heatmap.2x	GitHub TomKellyGenetics	0.0.0.9000	0.0.0.9000	0.0.0.9000	0.0.0.9000
hgu133plus2.db	Bioconductor		3.2.3		
highr	CRAN		0.6	0.6	0.6
Hmisc	CRAN		4.0-2	4.0-2	3.17-4
hms	CRAN	0.2	0.3		
htmlTable	CRAN		1.8	1.9	
htmltools	CRAN	0.3.5	0.3.5	0.3.5	0.3.5
htmlwidgets	CRAN		0.8	0.8	
httpuv	CRAN	1.3.3		1.3.3	
httr	CRAN	1.2.1	1.2.1	1.2.1	1.1.0
huge	CRAN		1.2.7		
hunspell	CRAN		2.3		2
hypergraph	CRAN		1.46.0		
igraph	CRAN	1.0.1	1.0.1	1.0.1	1.0.1
igraph.extensions	GitHub TomKellyGenetics	0.1.0.9001	0.1.0.9001	0.1.0.9001	0.1.0.9001
influenceR	CRAN		0.1.0	0.1.0	
info.centrality	GitHub TomKellyGenetics	0.1.0	0.1.0	0.1.0	0.1.0
IRanges	Bioconductor		2.8.1	2.8.1	2.6.1
irlba	CRAN	2.1.1	2.1.2	2.1.2	2.0.0
iterators	CRAN	1.0.8	1.0.8	1.0.8	1.0.8
jpeg	CRAN		0.1-8		

jsonlite	CRAN	1.1	1.2	1.3	0.9.20
KEGG.db	Bioconductor		3.2.3		
kernlab	CRAN	0.9-25	0.9-25	0.9-25	
KernSmooth	base	2.23-15	2.23-15	2.23-15	2.23-15
knitr	CRAN		1.15.1	1.15.1	1.14
labeling	CRAN	0.3	0.3	0.3	0.3
lambda.r	CRAN		1.1.9	1.1.9	1.1.7
lattice	base	0.20-34	0.20-34	0.20-34	0.20-33
latticeExtra	CRAN		0.6-28		0.6-28
lava	CRAN		1.4.6		
lavaan	CRAN		0.5-22		
lazyeval	CRAN	0.2.0	0.2.0	0.2.0	0.2.0
les	CRAN		1.24.0		
lgtdl	CRAN		1.1.3		
limma	Bioconductor		3.30.7	3.30.3	
lme4	CRAN		1.1-12		1.1-12
lubridate	CRAN	1.6.0			
magrittr	CRAN	1.5	1.5	1.5	1.5
maps	CRAN		3.1.1		
markdown	CRAN		0.7.7	0.7.7	0.7.7
MASS	base	7.3-45	7.3-45	7.3-45	7.3-45
Matrix	base	1.2-7.1	1.2-7.1	1.2-8	1.2-6
matrixcalc	CRAN	1.0-3	1.0-3	1.0-3	1.0-3
mclust	CRAN	5.2	5.2.1	5.2.2	5.2
memoise	CRAN	1.0.0	1.0.0	1.0.0	1.0.0
methods	base	3.3.2	3.3.2	3.3.1	3.3.0
mgcv	base	1.8-16	1.8-16	1.8-17	1.8-12
mi	CRAN		1		
mime	CRAN	0.5	0.5	0.5	0.4
minqa	CRAN		1.2.4		1.2.4
mnormt	CRAN	1.5-5	1.5-5		1.5-4
modelr	CRAN	0.1.0			
modeltools	CRAN	0.2-21	0.2-21	0.2-21	
multtest	Bioconductor		2.30.0	2.30.0	
munsell	CRAN	0.4.3	0.4.3	0.4.3	0.4.3

mvtnorm	CRAN	1.0-5	1.0-5	1.0-6	1.0-5
network	CRAN		1.13.0		
nlme	base	3.1-128	3.1-128	3.1-131	3.1-128
nloptr	CRAN		1.0.4		1.0.4
NMF	CRAN	0.20.6	0.20.6	0.20.6	0.20.6
nnet	base	7.3-12	7.3-12	7.3-12	7.3-12
numDeriv	CRAN		2016.8-1		2014.2-1
openssl	CRAN	0.9.4	0.9.6	0.9.6	0.9.4
org.Hs.eg.db	Bioconductor		3.1.2		3.3.0
org.Sc.sgd.db	Bioconductor		3.4.0		
parallel	base	3.3.2	3.3.2	3.3.1	3.3.0
pathway.structure	GitHub				
.permutation	TomKellyGenetics	0.1.0	0.1.0	0.1.0	0.1.0
pbivnorm	CRAN		0.6.0		
PGSEA	Bioconductor		1.48.0		
pkgmaker	CRAN	0.22	0.22	0.22	0.22
PKI	CRAN		0.1-3		
plogr	CRAN		0.1-1	0.1-1	
plot.igraph	GitHub				
	TomKellyGenetics	0.0.0.9001	0.0.0.9001	0.0.0.9001	0.0.0.9001
plotrix	CRAN		3.6-4		
plyr	CRAN	1.8.4	1.8.4	1.8.4	1.8.3
png	CRAN		0.1-7		0.1-7
prabclus	CRAN	2.2-6	2.2-6	2.2-6	
praise	CRAN	1.0.0	1.0.0		1.0.0
pROC	CRAN		1.8	1.9.1	
prodlim	CRAN		1.5.7		
prof.tree	CRAN		0.1.0		
protoools	CRAN		0.99-2		
progress	CRAN			1.1.2	
psych	CRAN	1.6.12	1.6.12		
purrr	CRAN	0.2.2	0.2.2	0.2.2	0.2.2
qgraph	CRAN		1.4.1		
quadprog	CRAN		1.5-5	1.5-5	1.5-5
R.methodsS3	CRAN		1.7.1		1.7.1

R.oo	CRAN		1.21.0		1.20.0
R.utils	CRAN		2.5.0		
R6	CRAN	2.1.3	2.2.0	2.2.0	2.1.3
RBGL	CRAN		1.50.0		
RColorBrewer	CRAN	1.1-2	1.1-2	1.1-2	1.1-2
Rcpp	CRAN	0.12.7	0.12.9	0.12.9	0.12.7
RcppArmadillo	CRAN			0.7.700.0.0	0.6.700.6.0
RcppEigen	CRAN		0.3.2.9.0		0.3.2.8.1
RCurl	CRAN		1.95-4.8	1.95-4.8	1.95-4.8
reactome.db	Bioconductor		1.52.1	1.52.1	
reactometree	GitHub TomKellyGenetics		0.1		
readr	CRAN	1.0.0	1.0.0		
readxl	CRAN	0.1.1			
registry	CRAN	0.3	0.3	0.3	0.3
reshape2	CRAN	1.4.1	1.4.2	1.4.2	1.4.1
rgexf	CRAN		0.15.3	0.15.3	
rgl	CRAN			0.97.0	0.95.1441
Rgraphviz	CRAN		2.18.0		
rjson	CRAN		0.2.15		
RJSONIO	CRAN		1.3-0		
rmarkdown	CRAN		1.3	1.3	1
Rmpi	CRAN		0.6-6		0.6-5
rngtools	CRAN	1.2.4	1.2.4	1.2.4	1.2.4
robustbase	CRAN	0.92-7	0.92-7	0.92-7	0.92-5
ROCR	CRAN	1.0-7	1.0-7	1.0-7	1.0-7
Rook	CRAN		1.1-1	1.1-1	
roxygen2	CRAN	6.0.1	5.0.1	6.0.1	5.0.1
rpart	base	4.1-10	4.1-10	4.1-10	4.1-10
rprojroot	CRAN	1.2	1.1	1.2	
Rsamtools	Bioconductor		1.26.1	1.26.1	
rsconnect	CRAN		0.7		
RSSQLite	CRAN		1.1-2	1.1-2	1.0.0
rstudioapi	CRAN	0.6	0.6	0.6	0.6
rvest	CRAN	0.3.2			

S4Vectors	Bioconductor		0.12.1	0.12.0	0.10.3
safe	Bioconductor		3.14.0	3.10.0	
scales	CRAN	0.4.0	0.4.1	0.4.1	0.4.0
selectr	CRAN	0.3-1			
sem	CRAN		3.1-8		
shiny	CRAN	0.14		1.0.0	
slipt	GitHub TomKellyGenetics	0.1.0	0.1.0	0.1.0	0.1.0
sm	CRAN	2.2-5.4	2.2-5.4		
sna	CRAN		2.4		
snow	CRAN	0.4-1	0.4-2	0.4-2	0.3-13
sourcetools	CRAN	0.1.5		0.1.5	
SparseM	CRAN		1.74		1.7
spatial	base	7.3-11	7.3-11	7.3-11	7.3-11
splines	base	3.3.2	3.3.2	3.3.1	3.3.0
statnet.common	CRAN		3.3.0		
stats	base	3.3.2	3.3.2	3.3.1	3.3.0
stats4	base	3.3.2	3.3.2	3.3.1	3.3.0
stringi	CRAN	1.1.1	1.1.2	1.1.2	1.0-1
stringr	CRAN	1.1.0	1.1.0	1.2.0	1.0.0
Summarized Experiment	Bioconductor		1.4.0	1.4.0	
survival	base	2.39-4	2.40-1	2.40-1	2.39-4
tcltk	base	3.3.2	3.3.2	3.3.1	3.3.0
testthat	CRAN	1.0.2	1.0.2		1.0.2
tibble	CRAN	1.2	1.2	1.2	1.2
tidyverse	GitHub hadley	1.1.1			
timeline	CRAN		0.9		
tools	base	3.3.2	3.3.2	3.3.1	3.3.0
tpr	CRAN		0.3-1		
trimcluster	CRAN	0.1-2	0.1-2	0.1-2	
Unicode	CRAN	9.0.0-1	9.0.0-1	9.0.0-1	
utils	base	3.3.2	3.3.2	3.3.1	3.3.0

vioplot	CRAN		0.2		
vioplotx	GitHub				
	TomKellyGenetics	0.0.0.9000	0.0.0.9000		
viridis	CRAN	0.3.4	0.3.4	0.3.4	
visNetwork	CRAN		1.0.3	1.0.3	
whisker	CRAN	0.3-2	0.3-2	0.3-2	0.3-2
withr	CRAN	1.0.2	1.0.2	1.0.2	1.0.2
XML	base	3.98-1.3	3.98-1.1	3.98-1.5	3.98-1.4
xml2	CRAN	1.1.1		1.1.1	1.0.0
xtable	CRAN	1.8-2	1.8-2	1.8-2	1.8-2
XVector	Bioconductor		0.14.0	0.14.0	
yaml	CRAN		2.1.14	2.1.14	2.1.13
zlibbioc	CRAN		1.20.0	1.20.0	
zoo	CRAN	1.7-13	1.7-14		1.7-13

Appendix C

Mutation Analysis in Breast Cancer

C.1 Synthetic Lethal Genes and Pathways

SLIPT expression analysis (described in Section 3.1) on TCGA breast cancer data ($n = 969$) found the following genes and pathways, described in Sections 4.1 and 4.1.1.

Table C.1: Pathways for *CDH1* partners from mtSLIPT

Pathways Over-represented	Pathway Size	SL Genes	p-value (FDR)
Eukaryotic Translation Elongation	86	60	2.0×10^{-128}
Peptide chain elongation	83	59	2.0×10^{-128}
Eukaryotic Translation Termination	83	58	2.3×10^{-125}
Viral mRNA Translation	81	57	2.5×10^{-124}
Nonsense Mediated Decay independent of the Exon Junction Complex	88	59	8.6×10^{-124}
Nonsense-Mediated Decay	103	61	5.2×10^{-117}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	103	61	5.2×10^{-117}
Formation of a pool of free 40S subunits	93	58	1.6×10^{-116}
L13a-mediated translational silencing of Ceruloplasmin expression	103	59	1.3×10^{-111}
3' -UTR-mediated translational regulation	103	59	1.3×10^{-111}
GTP hydrolysis and joining of the 60S ribosomal subunit	104	59	6.2×10^{-111}
SRP-dependent cotranslational protein targeting to membrane	104	58	2.9×10^{-108}
Eukaryotic Translation Initiation	111	59	3.0×10^{-106}
Cap-dependent Translation Initiation	111	59	3.0×10^{-106}
Influenza Viral RNA Transcription and Replication	108	57	5.1×10^{-103}
Influenza Infection	117	59	1.5×10^{-102}
Translation	141	64	3.7×10^{-101}
Influenza Life Cycle	112	57	1.4×10^{-100}
GPCR downstream signalling	472	116	1.0×10^{-80}
Hemostasis	422	105	1.4×10^{-78}

Gene set over-representation analysis (hypergeometric test) for Reactome pathways in mtSLIPT partners for *CDH1*.

The genes and pathways identified in Tables 4.2 and C.1 were derived from comparing the expression profiles of potential partners to the mutation status of *CDH1*

(as shown in Figure 3.2). The following analysis was limited to the samples for which both expression and somatic mutation data were available from TCGA.

C.2 Synthetic Lethal Expression Profiles

Similar to the analysis of synthetic lethal partners against low *CDH1* expression in Section 4.1.2, the partners detected from *CDH1* mutation were also examined for their expression profiles and the pathway composition of gene clusters. Hierarchical clustering was performed on mtSLIPT partners for *CDH1* as shown in Figure C.1. Over-representation for Reactome pathways for each of the gene clusters identified is given in Table C.2.

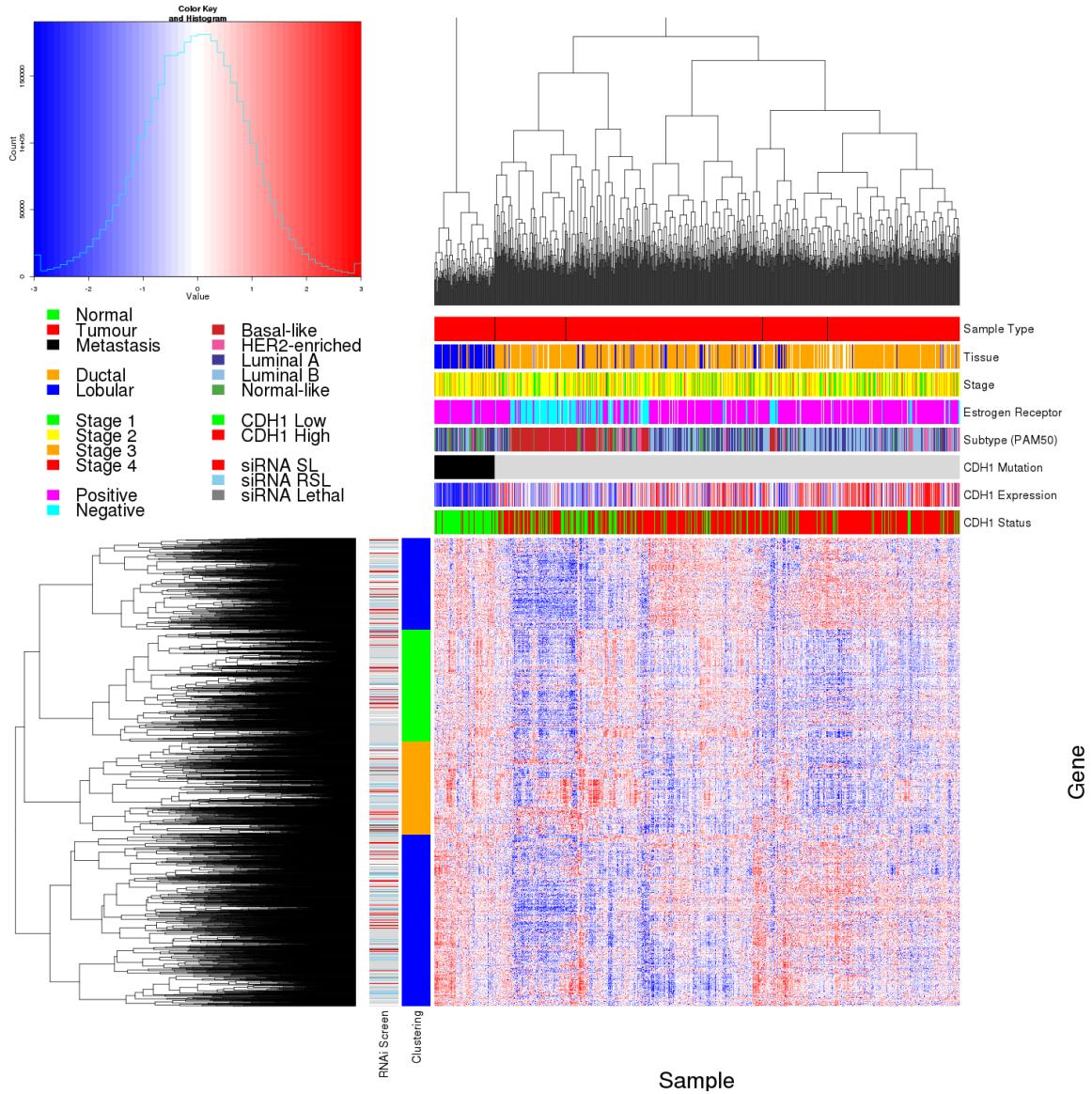


Figure C.1: Synthetic lethal expression profiles of analysed samples. Gene expression profile heatmap (correlation distance) of all samples (separated by *CDH1* somatic mutation status) analysed in TCGA breast cancer dataset for gene expression of 3743 candidate partners of E-cadherin (*CDH1*) from mtSLIPT prediction (with significant FDR adjusted $p < 0.05$). Deeply clustered, inter-correlated genes form several main groups, each containing genes that were SL candidates or toxic in an siRNA screen Telford *et al.* (2015). Clusters had different sample groups highly expressing the synthetic lethal candidates in *CDH1* mutant samples and often lowly expressing *CDH1* wild-type samples (which were not tested for), although many of the *CDH1* mutant samples had among the lowest *CDH1* expression. In contrast to the expression analysis the (predominantly *CDH1* wild-type) basal subtype and ER negative samples have depleted expression among most candidate synthetic lethal partners.

Table C.2: Pathways for clusters of *CDH1* partners from mtSLIPT

Pathways Over-represented in Cluster 1	Pathway Size	Cluster Genes	p-value (FDR)
Olfactory Signalling Pathway	57	8	7.1×10^{-9}
Assembly of the primary cilium	149	14	8.0×10^{-9}
Sphingolipid metabolism	62	8	9.6×10^{-9}
Signalling by ERBB4	133	12	5.1×10^{-8}
PI3K Cascade	65	7	4.9×10^{-7}
Circadian Clock	33	5	4.9×10^{-7}
Nuclear signalling by ERBB4	34	5	4.9×10^{-7}
Intraflagellar transport	35	5	4.9×10^{-7}
PI3K events in ERBB4 signalling	87	8	4.9×10^{-7}
PIP3 activates AKT signalling	87	8	4.9×10^{-7}
PI3K events in ERBB2 signalling	87	8	4.9×10^{-7}
PI-3K cascade:FGFR1	87	8	4.9×10^{-7}
PI-3K cascade:FGFR2	87	8	4.9×10^{-7}
PI-3K cascade:FGFR3	87	8	4.9×10^{-7}
PI-3K cascade:FGFR4	87	8	4.9×10^{-7}
Deadenylation of mRNA	22	4	5.6×10^{-7}
PI3K/AKT activation	90	8	5.6×10^{-7}
Cargo trafficking to the periciliary membrane	38	5	5.6×10^{-7}

Pathways Over-represented in Cluster 2	Pathway Size	Cluster Genes	p-value (FDR)
G _{as} signalling events	83	19	5.1×10^{-25}
Extracellular matrix organization	238	30	1.4×10^{-18}
Hemostasis	422	46	2.7×10^{-16}
Aquaporin-mediated transport	32	9	2.7×10^{-16}
Transcriptional regulation of white adipocyte differentiation	56	11	1.7×10^{-15}
Degradation of the extracellular matrix	102	15	1.7×10^{-15}
Integration of energy metabolism	84	13	8.8×10^{-15}
GPCR downstream signalling	472	48	2.8×10^{-14}
G _{az} signalling events	15	6	5.0×10^{-14}
Molecules associated with elastic fibres	33	8	5.4×10^{-14}
Phase 1 - Functionalization of compounds	67	11	5.6×10^{-14}
Platelet activation, signalling and aggregation	179	20	5.6×10^{-14}
Vasopressin regulates renal water homeostasis via Aquaporins	24	7	6.1×10^{-14}
Elastic fibre formation	37	8	$.03 \times 10^{-13}$
Calmodulin induced events	27	7	3.3×10^{-13}
CaM pathway	27	7	3.3×10^{-13}
cGMP effects	18	6	3.6×10^{-13}
G _{ai} signalling events	167	18	6.3×10^{-13}

Pathway over-representation analysis for Reactome pathways with the number of genes in each pathway (Pathway Size), number of genes within the pathway identified (Cluster Genes), and the pathway over-representation p-value (adjusted by FDR) from the hypergeometric test.

Table C.2: Pathways for clusters of *CDH1* partners from mtSLIPT

Pathways Over-represented in Cluster 3	Pathway Size	Cluster Genes	p-value (FDR)
Eukaryotic Translation Elongation	86	55	1.1×10^{-12}
Peptide chain elongation	83	54	1.3×10^{-12}
Viral mRNA Translation	81	53	1.6×10^{-11}
Eukaryotic Translation Termination	83	53	7.1×10^{-10}
Nonsense Mediated Decay independent of the Exon Junction Complex	88	54	1.0×10^{-98}
Formation of a pool of free 40S subunits	93	53	4.1×10^{-102}
Nonsense-Mediated Decay	103	54	3.9×10^{-98}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	103	54	3.9×10^{-98}
L13a-mediated translational silencing of Ceruloplasmin expression	103	53	1.2×10^{-95}
3' -UTR-mediated translational regulation	103	53	1.2×10^{-95}
SRP-dependent cotranslational protein targeting to membrane	104	53	4.3×10^{-95}
GTP hydrolysis and joining of the 60S ribosomal subunit	104	53	4.3×10^{-95}
Influenza Viral RNA Transcription and Replication	108	53	9.6×10^{-93}
Eukaryotic Translation Initiation	111	53	4.2×10^{-91}
Cap-dependent Translation Initiation	111	53	4.2×10^{-91}
Influenza Life Cycle	112	53	1.4×10^{-90}
Influenza Infection	117	53	6.2×10^{-88}
Translation	141	55	3.0×10^{-81}

Pathways Over-represented in Cluster 4	Pathway Size	Cluster Genes	p-value (FDR)
ECM proteoglycans	66	10	2.9×10^{-11}
deactivation of the beta-catenin transactivating complex	38	7	5.1×10^{-10}
Arachidonic acid metabolism	41	7	1.1×10^{-9}
G _{aq} signalling events	149	14	4.0×10^{-9}
HS-GAG degradation	21	5	4.5×10^{-9}
Uptake and actions of bacterial toxins	22	5	6.1×10^{-9}
Gastrin-CREB signalling pathway via PKC and MAPK	170	15	6.1×10^{-9}
RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription	64	8	6.1×10^{-9}
Non-integrin membrane-ECM interactions	53	7	1.5×10^{-8}
Syndecan interactions	25	5	1.5×10^{-8}
NOTCH1 Intracellular Domain Regulates Transcription	40	6	2.3×10^{-8}
Synthesis of Leukotrienes and Eoxins	15	4	3.2×10^{-8}
Signalling by NOTCH1	59	7	5.3×10^{-8}
Regulation of insulin secretion	44	6	6.0×10^{-8}
Metabolism of lipids and lipoproteins	471	37	8.2×10^{-8}
Signalling by NOTCH	80	8	1.2×10^{-7}
Platelet activation, signalling and aggregation	179	14	1.2×10^{-7}
Recruitment of mitotic centrosome proteins and complexes	64	7	1.2×10^{-7}

Pathway over-representation analysis for Reactome pathways with the number of genes in each pathway (Pathway Size), number of genes within the pathway identified (Cluster Genes), and the pathway over-representation p-value (adjusted by FDR) from the hypergeometric test.

C.3 Comparison to Primary Screen

The mutation synthetic lethal partners with *CDH1* were also compared to siRNA primary screen data (Telford *et al.*, 2015), as performed in Section 4.2.1. These were expected to be more concordant with the experimental results performed on a null mutant, however this was not the case at the gene level: less genes overlapped with experimental candidates in Figure C.2. This discrepancy was may be due to lower sample size for mutations in TCGA data or lower frequency (expected value) of *CDH1* mutations compared to low expression.

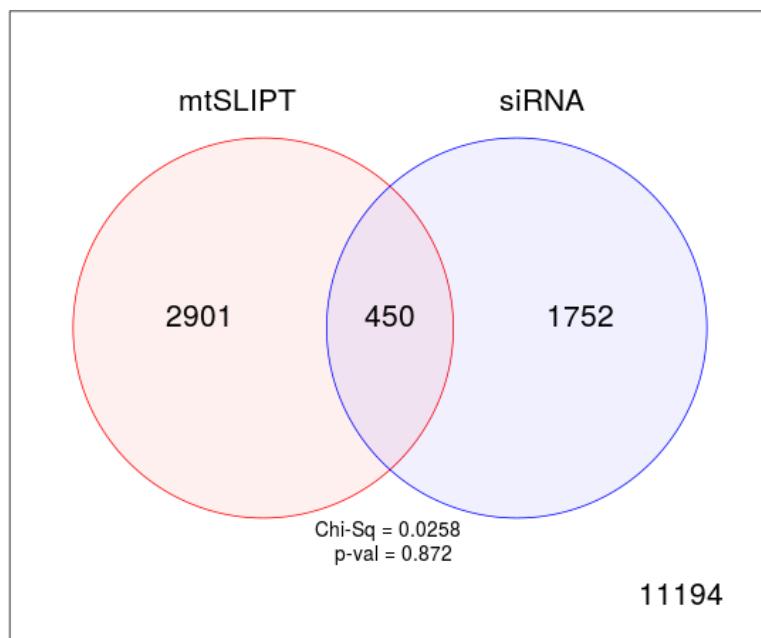


Figure C.2: **Comparison of mtSLIPT to siRNA.** Testing the overlap of gene candidates for E-cadherin synthetic lethal partners between computational (SLIPT) and experimental screening (siRNA) approaches. The χ^2 test suggests that the overlap is no more than would be expected by chance ($p = 0.281$).

Despite a lower sample size (and low number of a predicted partners) for mutation analysis, the pathway composition (Tables C.1 and C.3) was similar to expression analysis, as described in Section 4.2.5. In particular, the resampling analysis (Section C.3.1) supported many of the results of expression analysis (Section 4.2.5.1). Tables C.4 and 4.10 detected many of the same or functionally-related pathways.

Table C.3: Pathways for *CDH1* partners from mtSLIPT and siRNA

Predicted only by SLIPT (2901 genes)	Pathway Size	Genes Identified	p-value (FDR)
Eukaryotic Translation Elongation	87	57	2.8×10^{-120}
Peptide chain elongation	84	56	3.1×10^{-120}
Eukaryotic Translation Termination	84	55	2.8×10^{-117}
Viral mRNA Translation	82	54	4.1×10^{-116}
Nonsense Mediated Decay independent of the Exon Junction Complex	89	55	3.7×10^{-113}
Formation of a pool of free 40S subunits	94	55	2.8×10^{-109}
Nonsense-Mediated Decay	104	57	8.4×10^{-108}
Nonsense Mediated Decay enhanced by the Exon Junction Complex	104	57	8.4×10^{-108}
L13a-mediated translational silencing of Ceruloplasmin expression	104	56	3.4×10^{-105}
3' -UTR-mediated translational regulation	104	56	3.4×10^{-105}
GTP hydrolysis and joining of the 60S ribosomal subunit	105	56	1.4×10^{-104}
Eukaryotic Translation Initiation	112	56	2.8×10^{-100}
Cap-dependent Translation Initiation	112	56	2.8×10^{-100}
SRP-dependent cotranslational protein targeting to membrane	105	54	2.2×10^{-99}
Influenza Viral RNA Transcription and Replication	109	54	5.3×10^{-97}
Influenza Life Cycle	113	54	9.6×10^{-95}
Influenza Infection	118	55	1.7×10^{-94}
Translation	142	60	3.5×10^{-94}
Infectious disease	349	77	5.9×10^{-62}
Extracellular matrix organization	241	54	3.0×10^{-52}

Detected only by siRNA screen (1752 genes)	Pathway Size	Genes Identified	p-value (FDR)
Class A/1 (Rhodopsin-like receptors)	282	69	1.9×10^{-59}
GPCR ligand binding	363	78	2.7×10^{-54}
Peptide ligand-binding receptors	175	41	1.5×10^{-42}
G_{ai} signalling events	184	41	1.1×10^{-40}
Gastrin-CREB signalling pathway via PKC and MAPK	180	37	1.5×10^{-35}
G_{aq} signalling events	159	34	3.7×10^{-35}
DAP12 interactions	159	27	1.1×10^{-24}
VEGFA-VEGFR2 Pathway	91	19	1.0×10^{-23}
Downstream signal transduction	146	24	1.9×10^{-22}
Signalling by VEGF	99	19	2.6×10^{-22}
DAP12 signalling	149	24	4.2×10^{-22}
Organelle biogenesis and maintenance	264	34	4.3×10^{-20}
Downstream signalling of activated FGFR1	134	21	4.3×10^{-20}
Downstream signalling of activated FGFR2	134	21	4.3×10^{-20}
Downstream signalling of activated FGFR3	134	21	4.3×10^{-20}
Downstream signalling of activated FGFR4	134	21	4.3×10^{-20}
Signalling by ERBB2	146	22	5.3×10^{-20}
Signalling by FGFR	146	22	5.3×10^{-20}
Signalling by FGFR1	146	22	5.3×10^{-20}
Signalling by FGFR2	146	22	5.3×10^{-20}

Intersection of SLIPT and siRNA screen (450 genes)	Pathway Size	Genes Identified	p-value (FDR)
HS-GAG degradation	21	4	4.9×10^{-6}
Retinoid metabolism and transport	39	5	4.9×10^{-6}
Platelet activation, signalling and aggregation	186	13	4.9×10^{-6}
Signalling by NOTCH4	11	3	4.9×10^{-6}
G_{as} signalling events	100	8	5.0×10^{-6}
Defective EXT2 causes exostoses 2	12	3	5.0×10^{-6}
Defective EXT1 causes exostoses 1, TRPS2 and CHDS	12	3	5.0×10^{-6}
Class A/1 (Rhodopsin-like receptors)	289	18	2.2×10^{-5}
Signalling by PDGF	250	11	2.9×10^{-5}
Circadian Clock	34	4	2.9×10^{-5}
Signalling by ERBB4	139	9	4.3×10^{-5}
Role of LAT2/NTAL/LAB on calcium mobilization	99	7	4.4×10^{-5}
Peptide ligand-binding receptors	181	11	4.5×10^{-5}
Defective B4GALT7 causes EDS, progeroid type	19	3	4.5×10^{-5}
Defective B3GAT3 causes JDSSDHD	19	3	4.5×10^{-5}

C.3.1 Resampling Analysis

Table C.4: Pathways for *CDH1* partners from mtSLIPT

Reactome Pathway	Over-representation	Permutation
Eukaryotic Translation Elongation	3.2×10^{-128}	$< 7.035 \times 10^{-4}$
Peptide chain elongation	3.2×10^{-128}	$< 7.035 \times 10^{-4}$
Eukaryotic Translation Termination	3.7×10^{-125}	$< 7.035 \times 10^{-4}$
Viral mRNA Translation	4.1×10^{-124}	$< 7.035 \times 10^{-4}$
Nonsense Mediated Decay independent of the Exon Junction Complex	1.4×10^{-123}	$< 7.035 \times 10^{-4}$
Nonsense-Mediated Decay	8.4×10^{-117}	$< 7.035 \times 10^{-4}$
Nonsense Mediated Decay enhanced by the Exon Junction Complex	8.4×10^{-117}	$< 7.035 \times 10^{-4}$
Formation of a pool of free 40S subunits	2.6×10^{-116}	$< 7.035 \times 10^{-4}$
L13a-mediated translational silencing of Ceruloplasmin expression	2.0×10^{-111}	$< 7.035 \times 10^{-4}$
3' -UTR-mediated translational regulation	2.0×10^{-111}	$< 7.035 \times 10^{-4}$
GTP hydrolysis and joining of the 60S ribosomal subunit	9.9×10^{-111}	$< 7.035 \times 10^{-4}$
SRP-dependent cotranslational protein targeting to membrane	4.7×10^{-108}	$< 7.035 \times 10^{-4}$
Eukaryotic Translation Initiation	4.8×10^{-106}	$< 7.035 \times 10^{-4}$
Cap-dependent Translation Initiation	4.8×10^{-106}	$< 7.035 \times 10^{-4}$
Influenza Viral RNA Transcription and Replication	8.1×10^{-103}	$< 7.035 \times 10^{-4}$
Influenza Infection	2.4×10^{-102}	$< 7.035 \times 10^{-4}$
Translation	6.0×10^{-101}	$< 7.035 \times 10^{-4}$
Influenza Life Cycle	2.2×10^{-100}	$< 7.035 \times 10^{-4}$
Disease	2.1×10^{-90}	0.013347
GPCR downstream signalling	1.6×10^{-80}	0.095478
Hemostasis	2.1×10^{-78}	0.2671
Signalling by GPCR	1.2×10^{-73}	0.44939
<i>Extracellular matrix organization</i>	2.2×10^{-67}	0.054008
Metabolism of proteins	1.4×10^{-66}	0.9607
Signal Transduction	2.1×10^{-66}	0.48184
Developmental Biology	2.5×10^{-66}	0.54075
Innate Immune System	5.3×10^{-66}	0.9589
Infectious disease	9.6×10^{-66}	0.21075
Signalling by NGF	1.1×10^{-62}	0.43356
Immune System	2.8×10^{-62}	0.23052

Over-representation (hypergeometric test) and Permutation p-values adjusted for multiple tests across pathways (FDR).

Significant pathways were marked in bold (FDR < 0.05) and italics (FDR < 0.1).

C.4 Compare SLIPT genes

The mutation synthetic lethal partners with *CDH1* were also compared to siRNA primary screen data (Telford *et al.*, 2015), by correlation and siRNA viability as described in Sections 4.2.2 and 4.2.3.

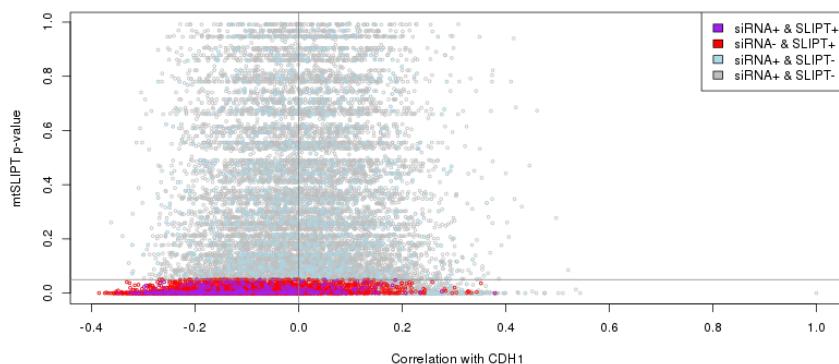


Figure C.3: Compare mtSLIPT and siRNA genes with correlation. The mtSLIPT p-values were compared against Pearson correlation of expression with *CDH1*. Genes detected by SLIPT or siRNA were coloured according to the legend.

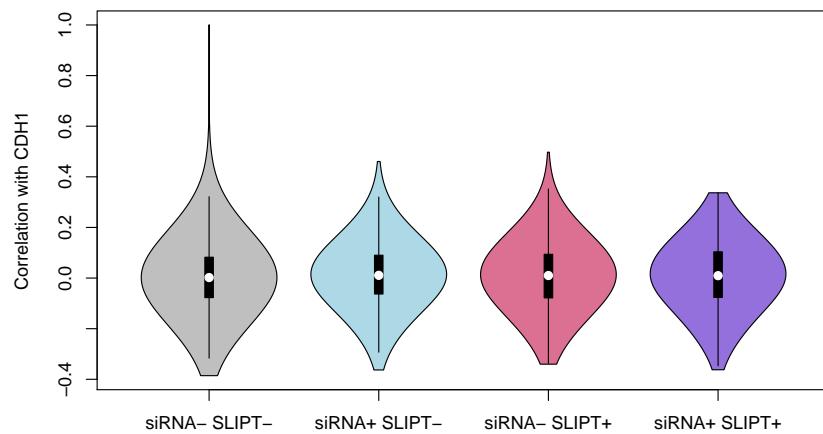


Figure C.4: Compare mtSLIPT and siRNA genes with correlation. Genes detected by mtSLIPT against *CDH1* mutation and siRNA screening were compared against Pearson correlation of expression with *CDH1*. There were no differences in correlation between the gene groups.

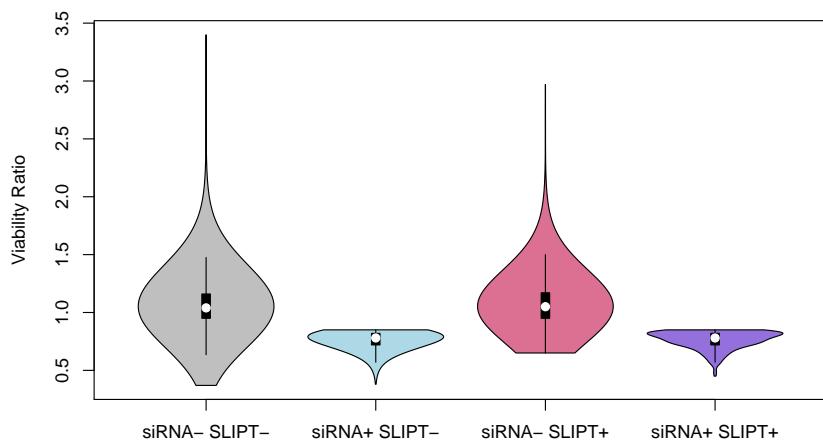


Figure C.5: Compare mtSLIPT and siRNA genes with siRNA viability. Genes detected as candidate synthetic lethal partners by mtSLIPT (in TCGA breast cancer) expression analysis against *CDH1* mutation and experimental screening (with siRNA) were compared against the viability ratio of *CDH1* mutant and wild-type cells in the primary siRNA screen. There were clear no differences in viability between genes detected by mtSLIPT and those not with the differences being primarily due to viability thresholds that were used to detect synthetic lethality by Telford *et al.* (2015).

Appendix D

Metagene Analysis

Well characterised gene signatures from previous publications in breast cancer (Gatza *et al.*, 2011, 2014) were used to demonstrate to utility of the metagene approach for use on a wider range of pathways as was performed with the Reactome (Croft *et al.*, 2014) pathways as an alternative approach to identification of synthetic lethal pathways. The direction of metagenes is arbitrary but they have been corrected to ensure the metagene increases in a direction which reflects overall activation of the pathways (as described in Section 2.2.3) which was verified by examining in the pathway signatures in breast cancer. Metagenes were derived for these pathways signatures (Gatza *et al.*, 2011, 2014), which were expected to have particular molecular properties in clinical and molecular subtypes (Parker *et al.*, 2009; Perou *et al.*, 2000). This was performed by examining the pathways expression of breast cancer gene signatures in TCGA expression data.

These gene signatures were used to establish that metagenes generated with this procedure reflect gene activity. The same metagene procedure (in Section 2.2.3) was applied to the Reactome pathways (Croft *et al.*, 2014). These Reactome metagenes were used for synthetic lethal analysis of pathways with SLIPT, directly using pathways activity for identifying synthetic lethal pathways with *CDH1*.

D.1 Pathway Signature Expression

Pathway metagenes (generated as described in Section 2.2.3) for gene signatures of key processes in breast cancer (Gatza *et al.*, 2011) were used to check that metagenes were generated in the correct direction to indicate pathways activation. Some of these gene signatures are plotted in Figure D.1 for comparison with clinical factors and somatic mutations. The “intrinsic subtypes” was computed by performing the PAM50 procedure Parker *et al.* (2009) for RNA-Seq data which was highly concordant ($\chi^2 =$

1305.9 , $p = 2.73 \times 10^{-268}$) with the subtypes provided by University of California, Santa Cruz (UCSC) (UCSC, 2012) for TCGA samples (Koboldt *et al.*, 2012) previously analysed by microarrays (as shown in Appendix E). Somatic mutations were reported for glinkrecurrent mutationrecurrently mutated genes in breast cancer, as reported by TCGA (Koboldt *et al.*, 2012), related genes, and those previously discussed to be important in hereditary breast cancers (*BRCA1*, *BRCA2*, and *CDH1*).

These gene signatures reflect intrinsic subtypes as expected. In particular, the estrogen and progesterone receptor signatures are low in the predominantly ER⁻ and Progesterone receptor (PR)⁻ basal-like subtype tumours. These tumours also had the highest frequency of *TP53* mutations and a corresponding reduction of p53 metagene activity, as expected for loss of a tumour suppressor. The luminal A and luminal B tumour subtypes are the most similar, which is reflected in these metagenes signatures, although they are distinguishable molecular subtypes as shown by elevated PI3K, AKT, RAS, and β -catenin signalling in luminal B tumours. However, these pathways were also elevated in basal-like and HER2-enriched subtypes and lowly expressed in the “normal-like” subtype (which contained the normal samples).

The direction of each metagene was consistent with the clinical characteristics, which formed a consensus of gene activity as shown for the PI3K and ER signatures (Gatza *et al.*, 2011) in Figure D.2. The expression of the majority of the genes were highly concordant with the metagene, being either positively or negatively correlated. These were generally consistent with established clinical and molecular subtypes of breast cancer and the recurrent mutations shown.

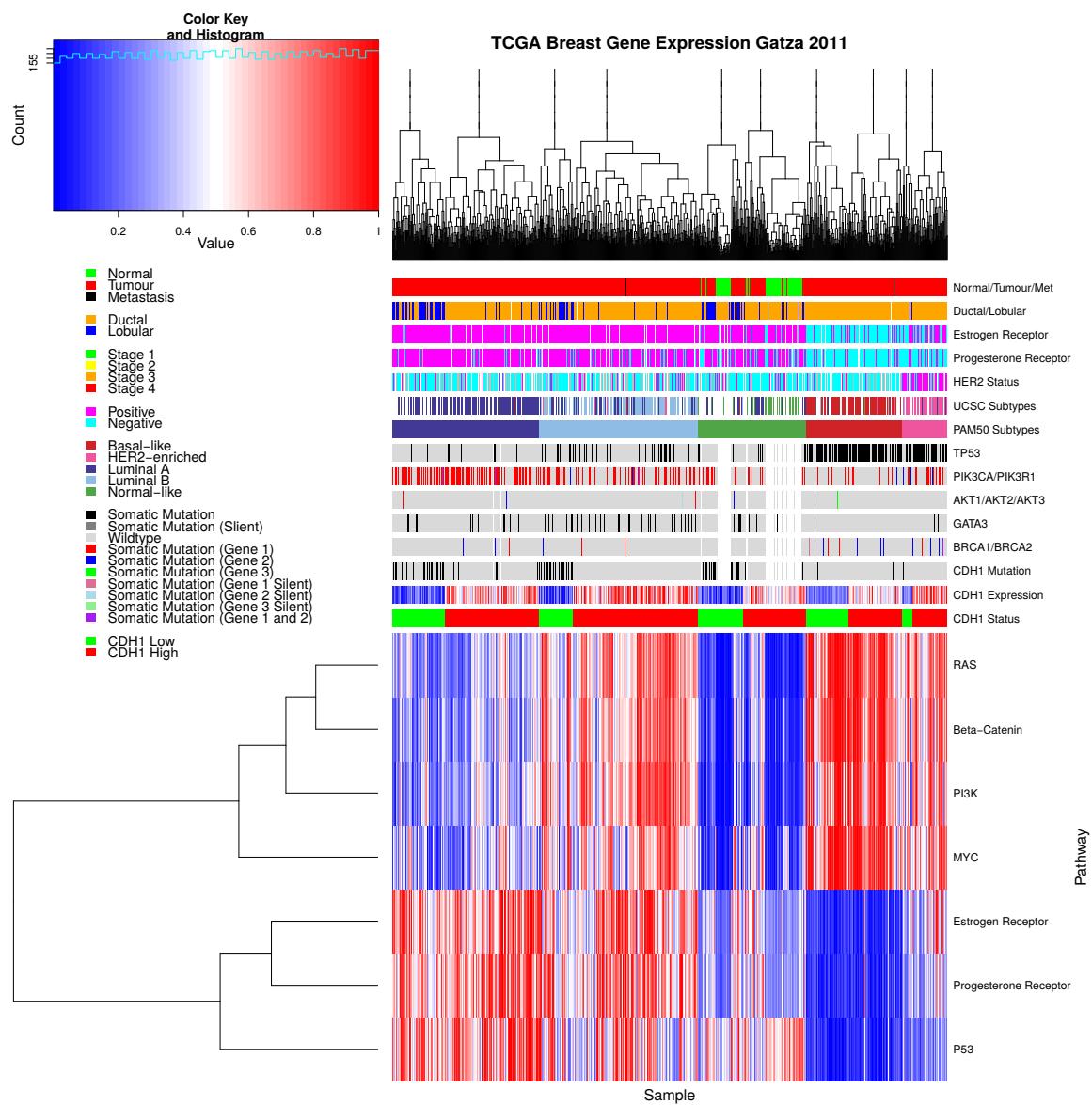


Figure D.1: Pathway metagene expression profiles. Expression profiles for metagene signatures from Gatza *et al.* (2011) in TCGA breast data, annotated for clinical factors (with sample types and histological results coloured according to the legend) and cancer gene mutations (Negative values for mutation are light grey with missing data in white). Intrinsic subtypes are shown as derived from microarray (UCSC) and RNA-Seq (PAM50) data (Koboldt *et al.*, 2012; Parker *et al.*, 2009). Samples were clustered independently for each intrinsic subtypes and by *CDH1* expression status. Pathway expression signatures are consistent with mutations and clinical subgroups.

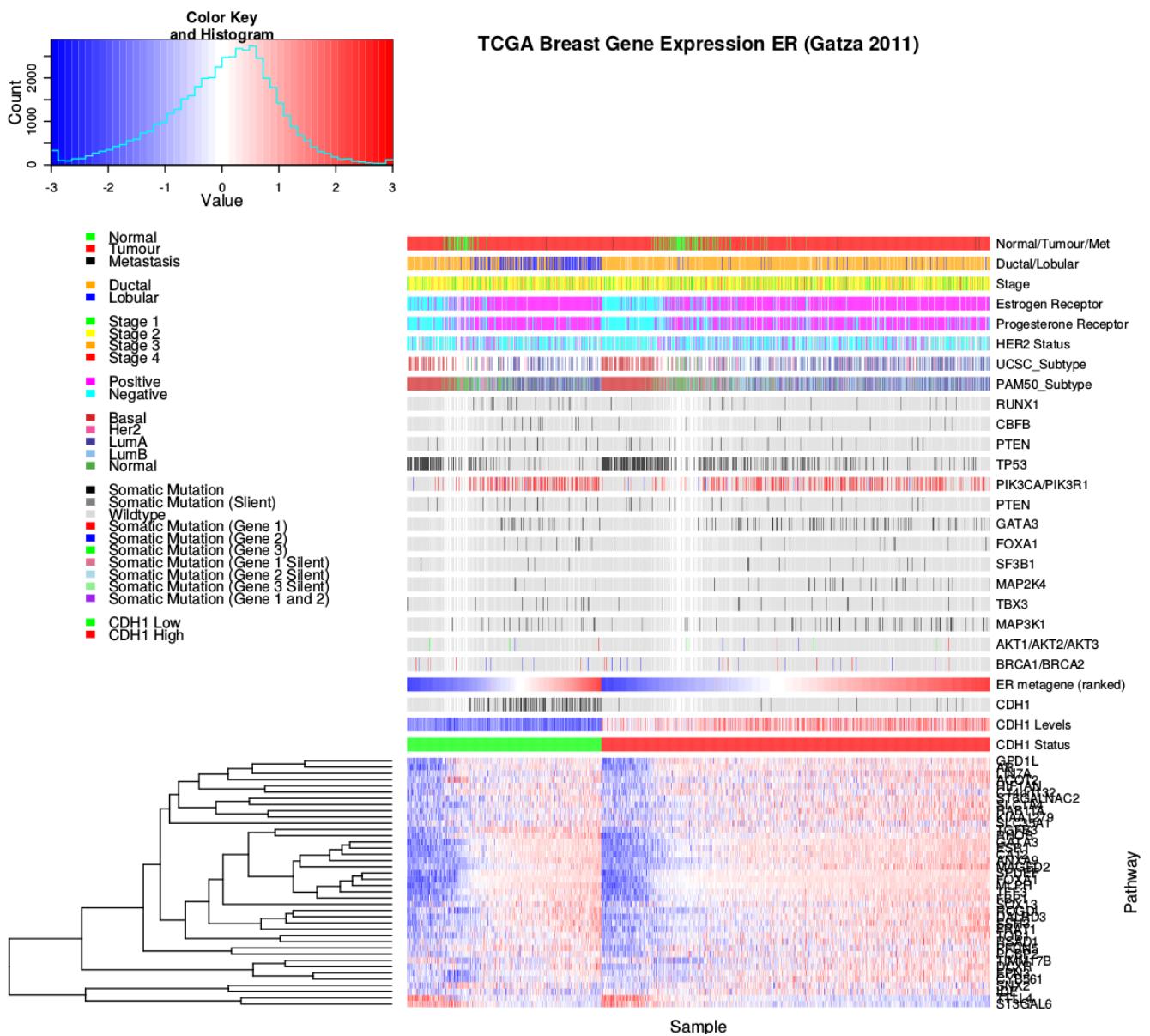


Figure D.2: **Expression profiles for estrogen receptor related genes.** Expression profiles the genes contained in the estrogen receptor (ER) gene signature from Gatza *et al.* (2011) in TCGA breast data, annotated for clinical factors and cancer gene mutations. Samples are separated by *CDH1* expression status and sorted by the metagene. In both cases, the majority of genes were consistent with the direction of the metagene, with very few exceptions being inversely correlated. Estrogen receptor (by antibody staining) negative samples had low metagene expression, as expected. These were more likely to be ductal and basal subtypes, lacking *CDH1* or *PIK3CA* mutations.

D.2 Synthetic Lethal Reactome Metagenes

Metagene analysis was performed for synthetic lethal pathways against *CDH1* mutation. These were described and compared to expression analysis in Section 4.3.

Table D.1: Candidate synthetic lethal metagenes against *CDH1* from mtSLIPT

Pathway	ID	Observed	Expected	χ^2 value	p-value	p-value (FDR)
Neurotoxicity of clostridium toxins	168799	8	36.7	79.4	5.71×10^{-18}	3.14×10^{-15}
Aquaporin-mediated transport	445717	8	36.7	76.3	2.73×10^{-17}	9.01×10^{-15}
Toxicity of botulinum toxin type G (BoNT/G)	5250989	8	36.7	76.3	2.73×10^{-17}	9.01×10^{-15}
ABC-family proteins mediated transport	382556	10	36.7	68.2	1.58×10^{-15}	1.86×10^{-13}
G _{αz} signalling events	418597	10	36.7	59.9	9.97×10^{-14}	5.48×10^{-12}
Regulation of IGF transport and uptake by IGFBPs	381426	9	36.7	56.3	5.88×10^{-13}	2.11×10^{-11}
GP1b-IX-V activation signalling	430116	8	36.7	55.7	8.20×10^{-13}	2.76×10^{-11}
GABA receptor activation	977443	12	36.7	55.1	1.07×10^{-12}	3.26×10^{-11}
Vasopressin regulates renal water homeostasis via Aquaporins	432040	9	36.7	54.1	1.77×10^{-12}	4.88×10^{-11}
Toxicity of botulinum toxin type D (BoNT/D)	5250955	14	36.7	53.4	2.54×10^{-12}	6.64×10^{-11}
Toxicity of botulinum toxin type F (BoNT/F)	5250981	14	36.7	53.4	2.54×10^{-12}	6.64×10^{-11}
STAT6-mediated induction of chemokines	3249367	16	36.7	52.2	4.72×10^{-12}	1.13×10^{-10}
Toxicity of botulinum toxin type B (BoNT/B)	5250958	14	36.7	50.8	9.5×10^{-12}	1.98×10^{-10}
S6K1 signalling	165720	12	36.7	50.2	1.24×10^{-11}	2.5×10^{-10}
G _{αs} signalling events	418555	11	36.7	49.2	2.08×10^{-11}	3.85×10^{-10}
RHO GTPases activate CIT	5625900	14	36.7	48.2	3.34×10^{-11}	5.9×10^{-10}
NADE modulates death signalling	205025	15	36.7	47.4	5.00×10^{-11}	8.32×10^{-10}
Keratan sulfate degradation	2022857	10	36.7	46.6	7.5×10^{-11}	1.15×10^{-9}
Signalling by Retinoic Acid	5362517	10	36.7	46.6	7.5×10^{-11}	1.15×10^{-9}
Adenylate cyclase inhibitory pathway	170670	14	36.7	45.9	1.11×10^{-10}	1.59×10^{-9}
Inhibition of adenylate cyclase pathway	997269	14	36.7	45.9	1.11×10^{-10}	1.59×10^{-9}
Fatty acids	211935	6	36.7	45.7	1.21×10^{-10}	1.72×10^{-9}
Ionotropic activity of Kainate Receptors	451306	13	36.7	44.6	2.03×10^{-10}	2.58×10^{-9}
Activation of Ca-permeable Kainate Receptor	451308	13	36.7	44.6	2.03×10^{-10}	2.58×10^{-9}
RA biosynthesis pathway	5365859	13	36.7	44.6	2.03×10^{-10}	2.58×10^{-9}

Strongest candidate synthetic lethal partners for *CDH1* by mtSLIPT with observed and expected numbers of mutant *CDH1* TCGA breast cancer tumours with low expression of partner metagenes.

Appendix E

Intrinsic Subtyping

The intrinsic subtypes for TCGA breast cancer samples provided by UCSC (Koboldt *et al.*, 2012; UCSC, 2012) that were derived from microarray analysis have been compared to the PAM50 results for performing subtyping from RNA-Seq data (Parker *et al.*, 2009). As shown in Table E.1, these subtypes were highly concordant for samples which had both procedures performed upon them ($\chi^2 = 1305.9$, $p = 2.73 \times 10^{-268}$). The main exception were the luminal A samples some of which were reclassified as luminal B or “normal-like”.

Table E.1: Comparison of intrinsic subtypes

UCSC Subtype					
	Basal-like	HER2-enriched	Luminal A	Luminal B	Normal-like
	100	58	232	128	30
PAM50 Subtype					
	Basal-like	HER2-enriched	Luminal A	Luminal B	Normal-like
	208	94	314	334	227
UCSC Subtype					
PAM50 Subtype	Basal-like	HER2-enriched	Luminal A	Luminal B	Normal-like
Basal-like	96	4	2	2	1
HER2-enriched	0	47	5	3	0
Luminal A	1	0	141	1	0
Luminal B	2	7	49	121	0
Normal-like	1	0	35	1	29

The intrinsic subtypes of TCGA breast samples were compared between those provided by UCSC (Koboldt *et al.*, 2012) from microarray expression to those derived from RNA-Seq data (Parker *et al.*, 2009). Comparisons between these were limited to samples for which both data types were available.

The PAM50 subtypes could be more accurate given similarity of these subtypes and that the remainder of the subtypes were accurately recapitulated with RNA-Seq data. Furthermore, UCSC subtypes correctly identified 22/22 normal samples as “normal-like” and PAM50 subtyping in RNA-Seq data had a success rate of 112/113 (including all of those identified from microarrays). Therefore the PAM50 subtypes (performed on a larger cohort of samples) are appropriate to use for further interpretation, superseding the UCSC subtypes available for a limited set of samples.

Appendix F

Synthetic Lethal Genes in Pathways

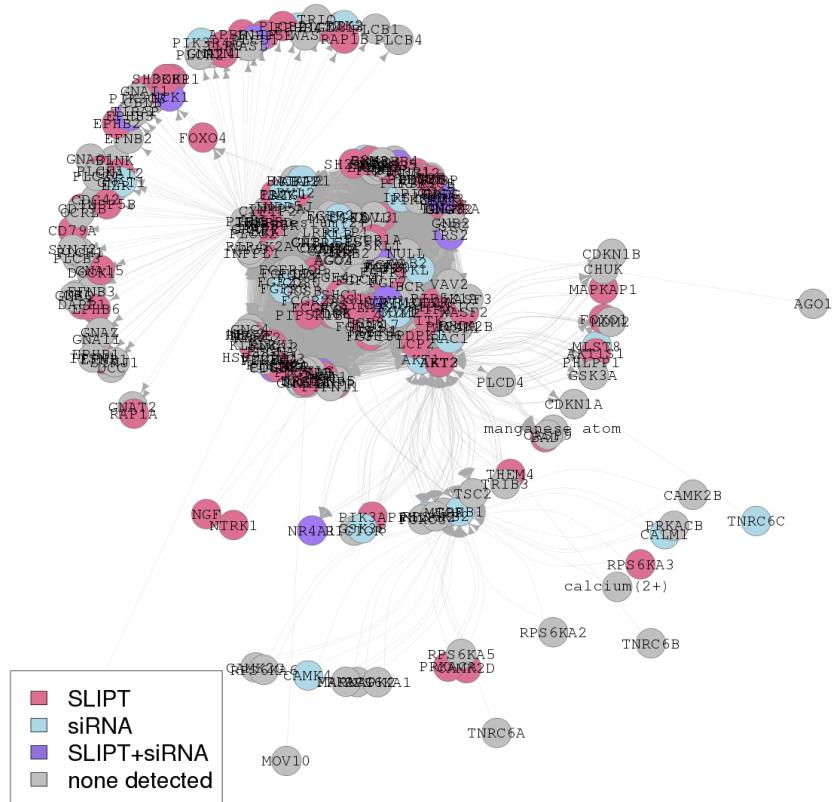


Figure F.1: **Synthetic lethality in the PI3K/AKT pathway.** The Reactome PI3K/AKT pathway with synthetic lethal candidates, coloured as shown in the legend.

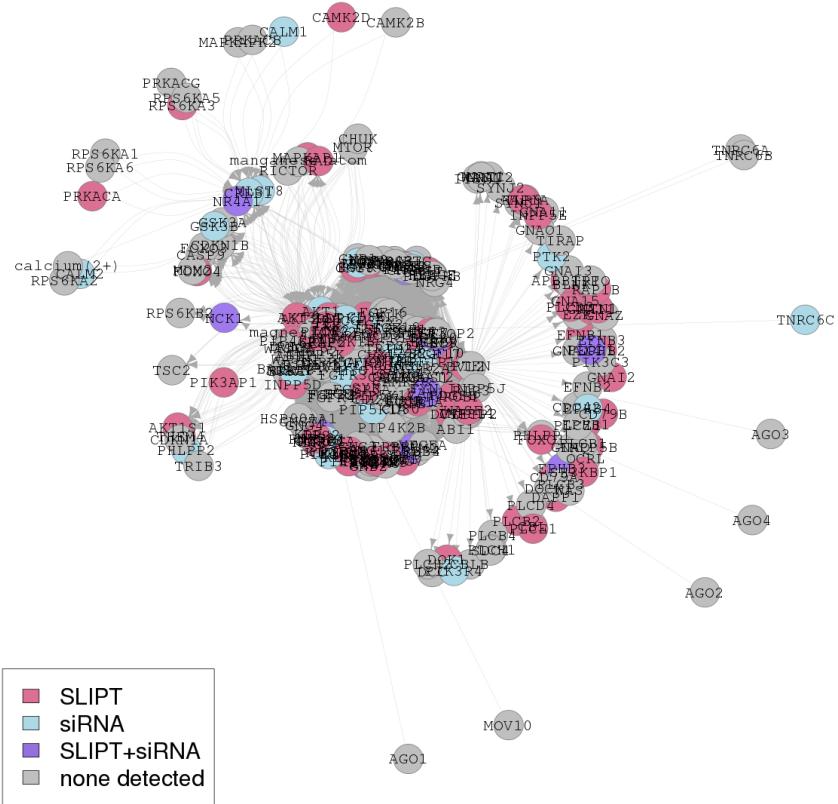


Figure F.2: **Synthetic lethality in the PI3K/AKT pathway in cancer.** The Reactome PI3K/AKT in cancer pathway with synthetic lethal candidates, coloured as shown in the legend.

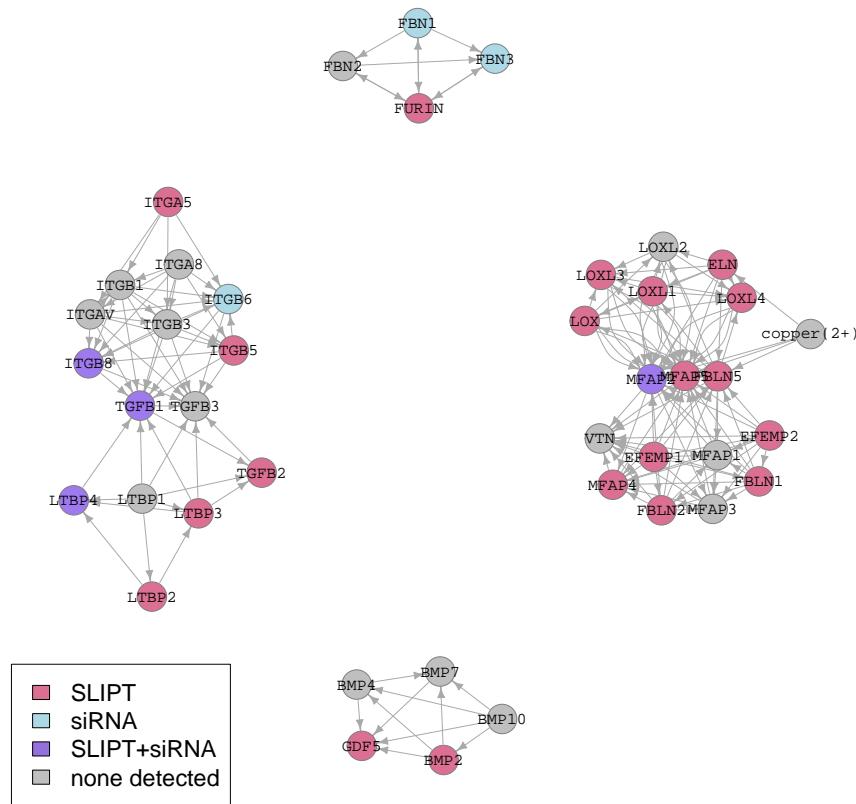


Figure F.3: **Synthetic lethality in Elastic Fibre Formation.** The Reactome Elastic Fibre Formation pathway with synthetic lethal candidates coloured as shown in the legend.

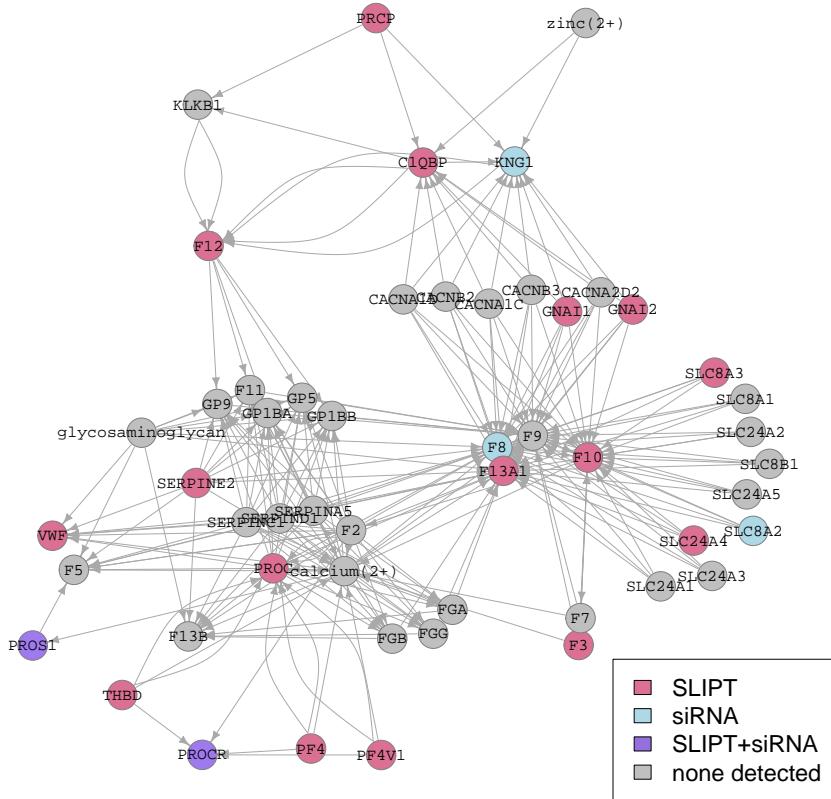


Figure F.4: **Synthetic lethality in Fibrin Clot Formation.** The Reactome Fibrin Clot Formation pathway with synthetic lethal candidates coloured as shown in the legend.

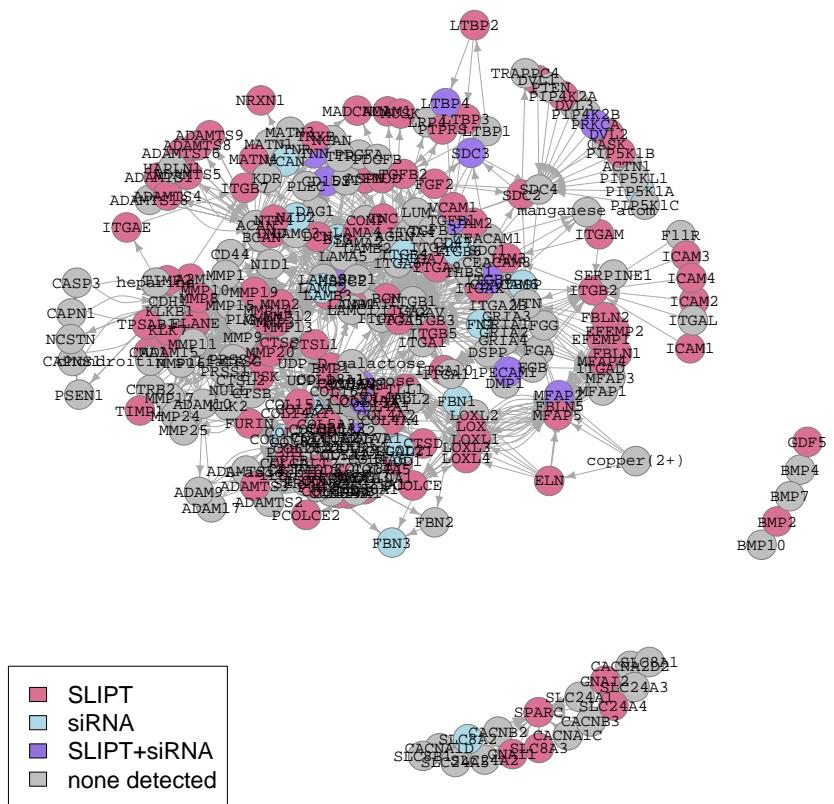


Figure F.5: **Synthetic lethality in the Extracellular Matrix.** The Reactome Extracellular Matrix pathway with synthetic lethal candidates, coloured as shown in the legend.

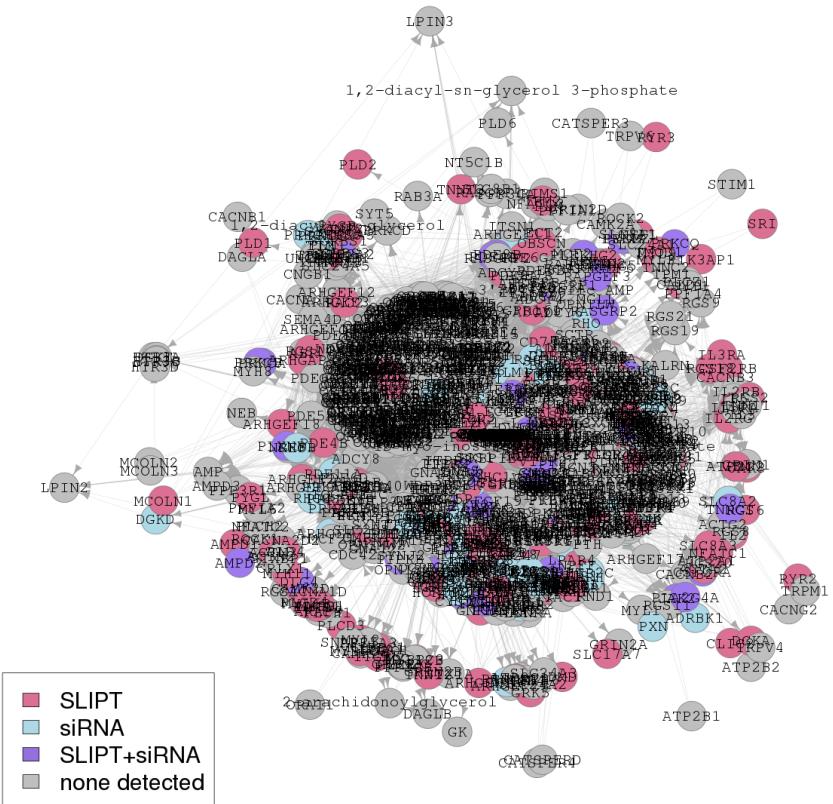


Figure F.6: **Synthetic lethality in the GPCR Downstream.** The Reactome GPCR Downstream pathway with synthetic lethal candidates, coloured as shown in the legend.

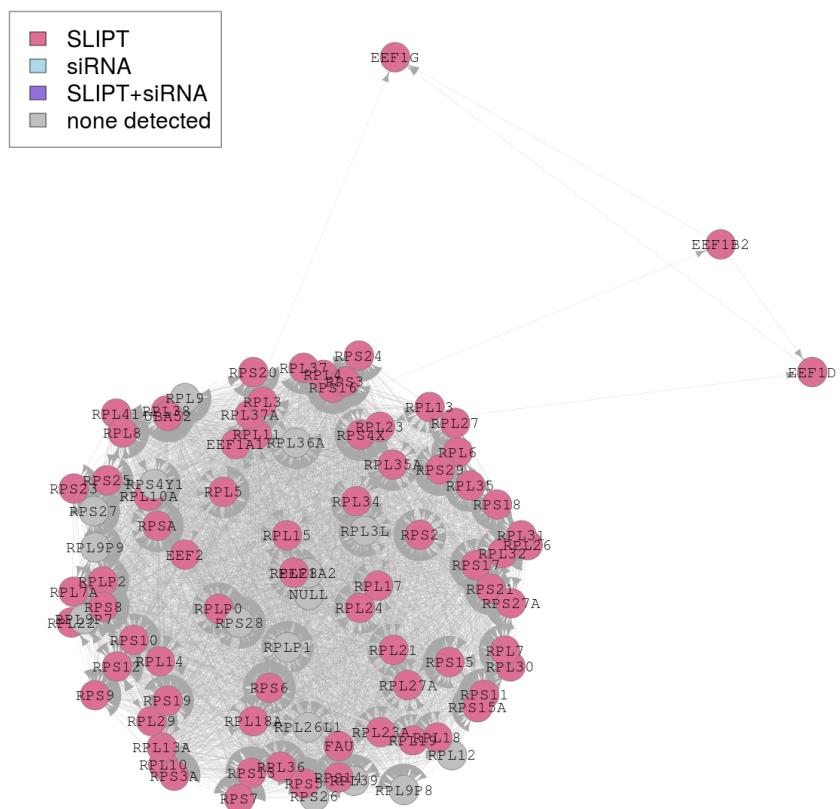


Figure F.7: **Synthetic lethality in the Translation Elongation**. The Reactome Translation Elongation pathway with synthetic lethal candidates, coloured as shown in the legend.

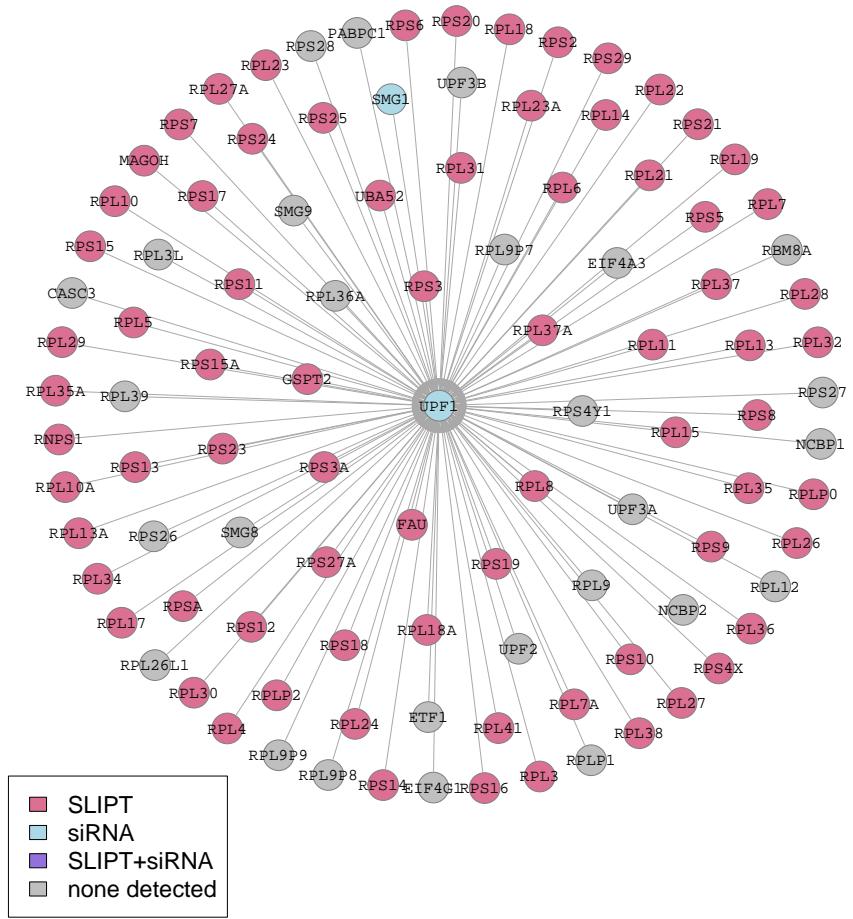


Figure F.8: **Synthetic lethality in the Nonsense-mediated Decay.** The Reactome NMD pathway with synthetic lethal candidates, coloured as shown in the legend.

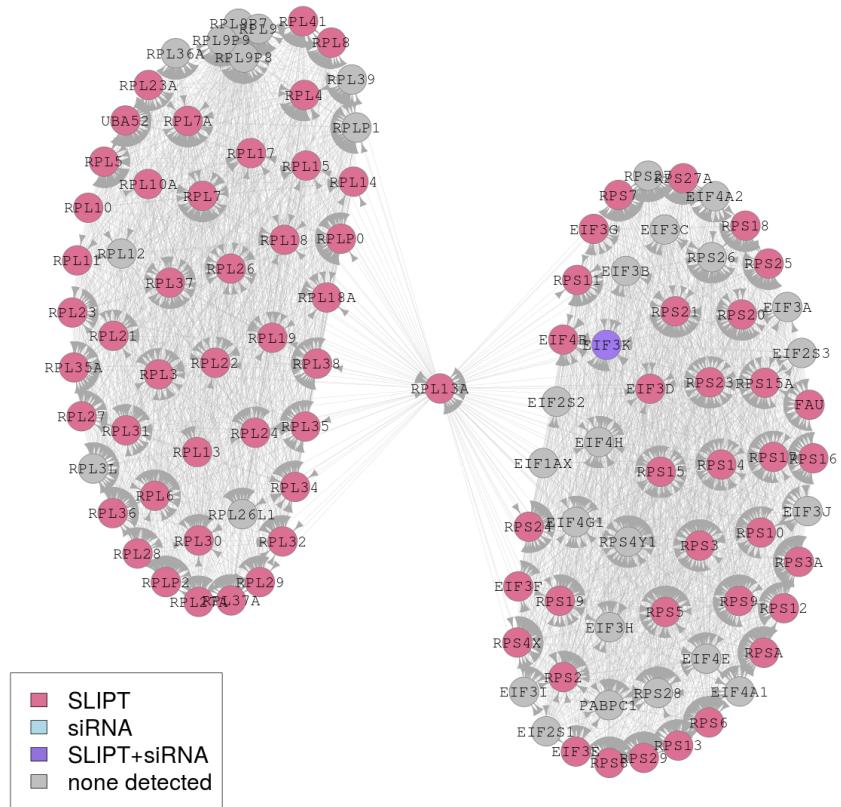


Figure F.9: **Synthetic lethality in the 3' UTR.** The Reactome 3' UTR pathway with synthetic lethal candidates, coloured as shown in the legend.

Appendix G

Network Analysis for Mutation SLIPT

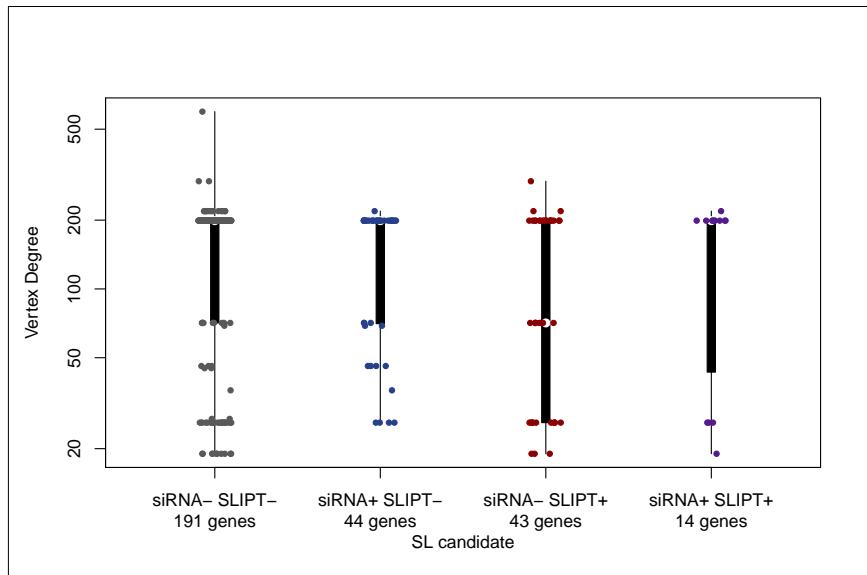


Figure G.1: **Synthetic lethality and vertex degree.** The number of connected genes (vertex degree) was compared (on a log-scale) across genes detected by mtSLIPT and siRNA screening in the Reactome $G_{\alpha i}$ pathway. There were no differences in vertex degree between the groups (shown in Table 5.1), although genes detected by siRNA included those with the fewest connections.

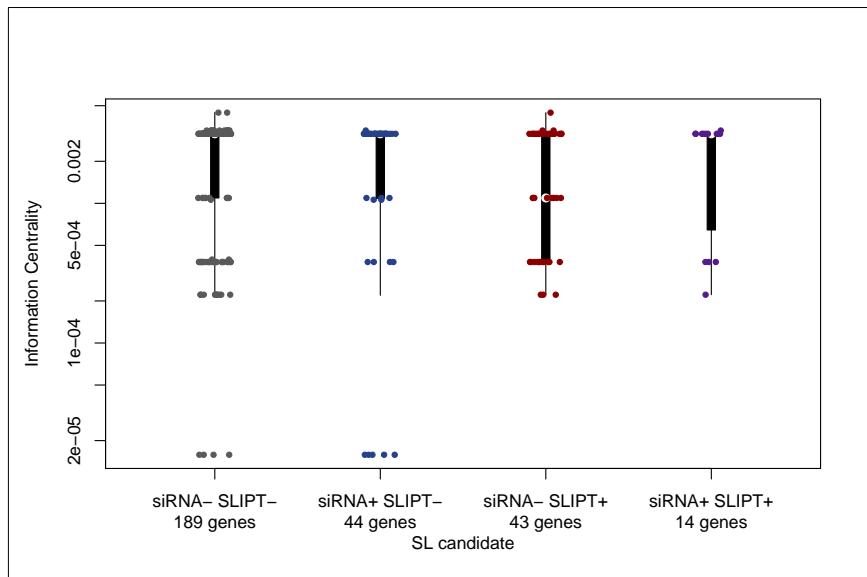


Figure G.2: Synthetic lethality and centrality. The information centrality was compared (on a log-scale) across genes detected by SLIPT and siRNA screening in the Reactome $G_{\alpha i}$ pathway. Genes detected by SLIPT or siRNA did not have higher centrality than other genes (shown in Table G.2). Genes detected by SLIPT spanned the range of centrality values.

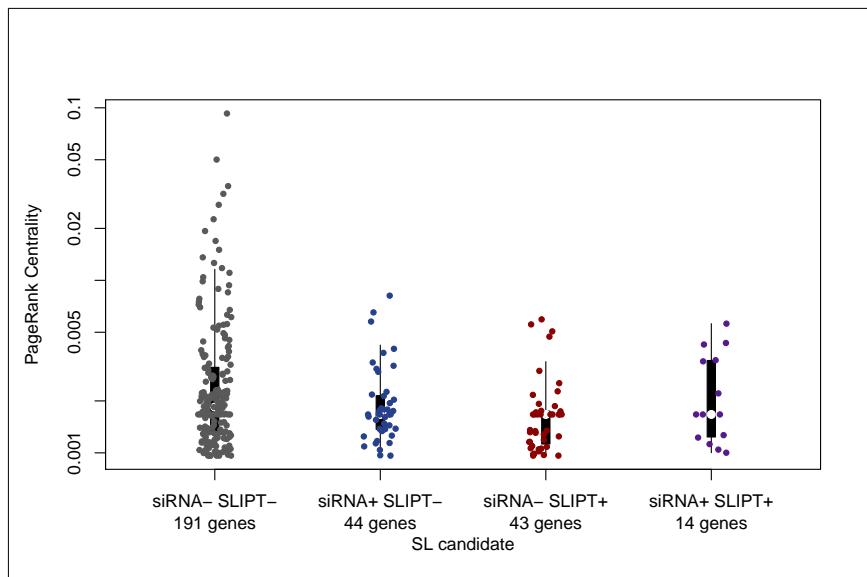


Figure G.3: Synthetic lethality and PageRank. The PageRank centrality was compared (on a log-scale) across genes detected by mtSLIPT and siRNA screening in the Reactome $G_{\alpha i}$ pathway. Genes detected by either synthetic lethal detection approach had a more restricted range of centrality values neither of these had a significant association with centrality (shown in Table G.3).

Table G.1: ANOVA for synthetic lethality and vertex degree

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	15	15.50	0.0134	0.9084
mtSLIPT	1	196	195.94	0.1689	0.6825
siRNA×mtSLIPT	1	9	9.17	0.0079	0.9294

Analysis of variance for vertex degree against synthetic lethal detection approaches (with an interaction term)

Table G.2: ANOVA for synthetic lethality and information centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.000256	0.0002561	0.1851	0.6685
mtSLIPT	1	0.003225	0.0032247	2.3308	0.1318
siRNA×mtSLIPT	1	0.001238	0.0012385	0.8952	0.3476

Analysis of variance for information centrality against synthetic lethal detection approaches (with an interaction term)

Table G.3: ANOVA for synthetic lethality and PageRank centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.0002038	2.0385×10^{-4}	1.1423	0.2892
mtSLIPT	1	0.0000208	2.0752×10^{-5}	0.1163	0.7342
siRNA×mtSLIPT	1	0.0000137	1.3743×10^{-5}	0.0770	0.7823

Analysis of variance for PageRank centrality against synthetic lethal detection approaches (with an interaction term)

Appendix H

Pathway Structure for Mutation SLIPT

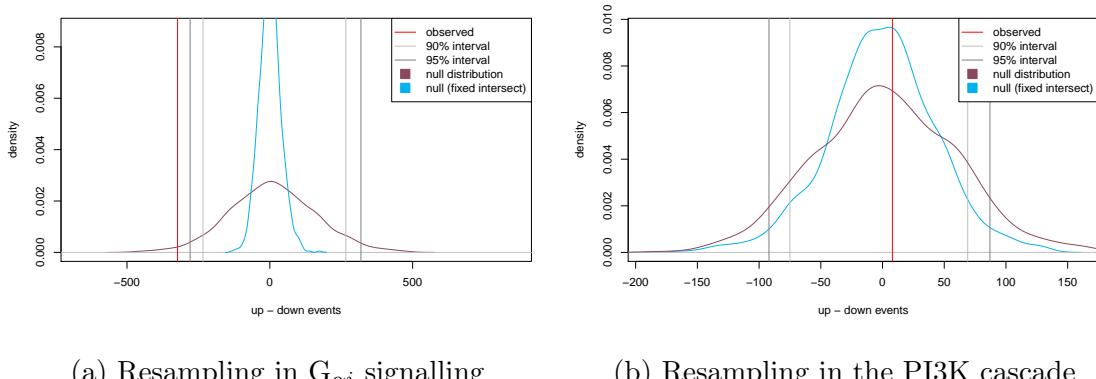


Figure H.1: **Structure of synthetic lethality resampling.** A null distribution with 10,000 iterations of the number of siRNA genes upstream or downstream of mtSLIPT genes (depicted as the difference of these) in each pathway. To assess significance, the observed events (with shortest paths) were compared to the 90% and 95% intervals for the null distribution (shown in blue). Genes detected by both methods were not fixed to the same number as observed for the alternative null distribution (shown in red), although the significance of the observed number of events (red) was changed in either case. The genes detected by both approaches were included in computing the number of shortest paths (in either direction) between SLIPT and siRNA genes. The permutations show (a) a significant pathway relationship for $G_{\alpha i}$ signalling and (b) a non-significant relationship for the PI3K cascade.

Table H.1: Resampling for pathway structure of synthetic lethal detection methods

PPathway	Graph		Candidates		Observed				Permutation p-value		p-value (FDR)
	Nodes	Edges	SLIPT	siRNA	Up ¹	Down ²	Up–Down	Up/Down	Up–Down	Down–Up	Down–Up
PI3K Cascade	138	1495	42	25	131	123	8	1.065	0.4473	0.5466	0.7263
PI3K/AKT Signalling in Cancer	275	12882	56	44	478	440	38	1.086	0.4163	0.5810	0.7263
G_{αi} Signalling	292	22003	57	58	543	866	-323	0.627	0.9507	0.0488	0.488
GPCR downstream	1270	142071	218	160	7632	6500	1132	1.174	0.1707	0.8291	0.8751
Elastic fibre formation	42	175	16	7	6	7	-1	0.857	0.5512	0.3681	0.7263
Extracellular matrix	299	3677	81	29	313	347	-34	0.902	0.5762	0.4215	0.7263
Formation of Fibrin	52	243	11	5	8	19	-11	0.421	0.7993	0.1800	0.6000
Nonsense-Mediated Decay	103	102	56	2	0	0	0		0.197	0.1373	0.6000
3'-UTR-mediated translational regulation	107	2860	56	1	52	1	51	52	0.1210	0.8751	0.8751
Eukaryotic Translation Elongation	92	3746	57	0	0	0	0		0.4952	0.4892	0.7263

Pathways in the Reactome network tested for structural relationships between mtSLIPT and siRNA genes by resampling. The raw p-value (computed without adjusting for multiple comparisons over pathways) is given for the difference in upstream and downstream paths from mtSLIPT to siRNA gene candidate partners of CDH1 with significant pathways highlighted in bold. Sampling was performed only in the target pathway and shortest paths were computed within it. Loops or paths in either direction that could not be resolved were excluded from the analysis. The genes detected by both mtSLIPT and siRNA (or resampling for them) were included in the analysis and the number of these were fixed to the number observed.

¹ The number of paths where the siRNA candidate was upstream of a mtSLIPT candidate

² The number of paths where the siRNA candidate was downstream of a mtSLIPT candidate

Appendix I

Performance of SLIPT and χ^2

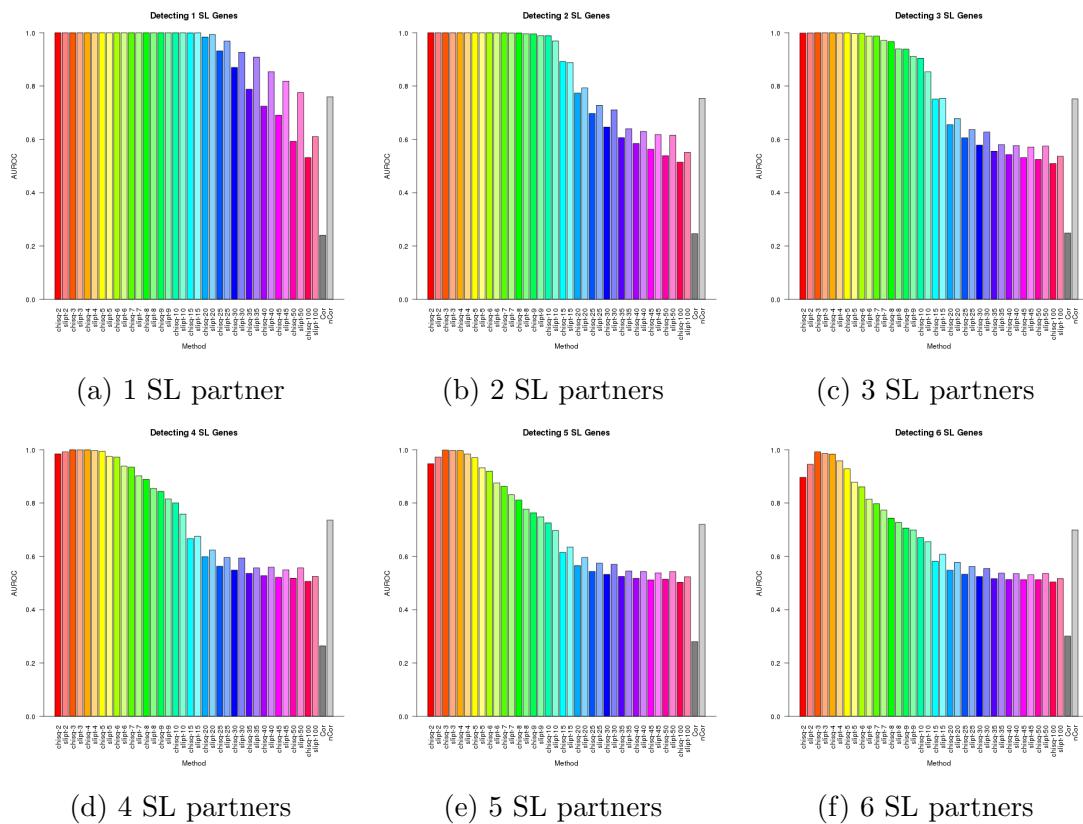


Figure I.1: Performance of χ^2 and SLIPT across quantiles. (continued on next page)

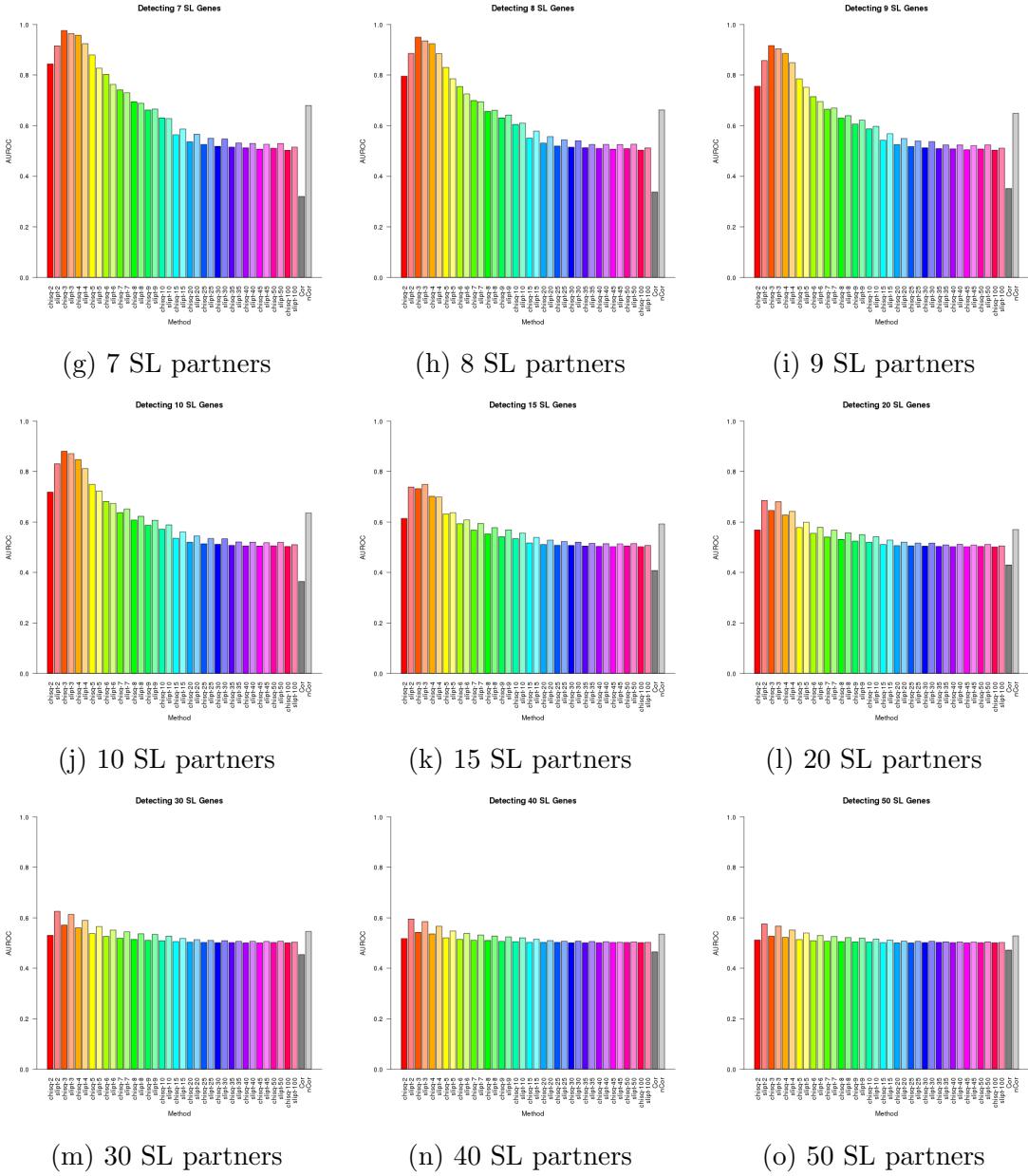


Figure I.1: Performance of χ^2 and SLIPT across quantiles. Synthetic lethal detection with quantiles as in axis labels. The barplots have the same hue for each quantile (grey for correlation) and darker for χ^2 (and positive correlation). SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 10,000 simulations of 100 genes and 1000 samples. SLIPT performed better than χ^2 for higher numbers of synthetic lethal genes and finer quantiles.

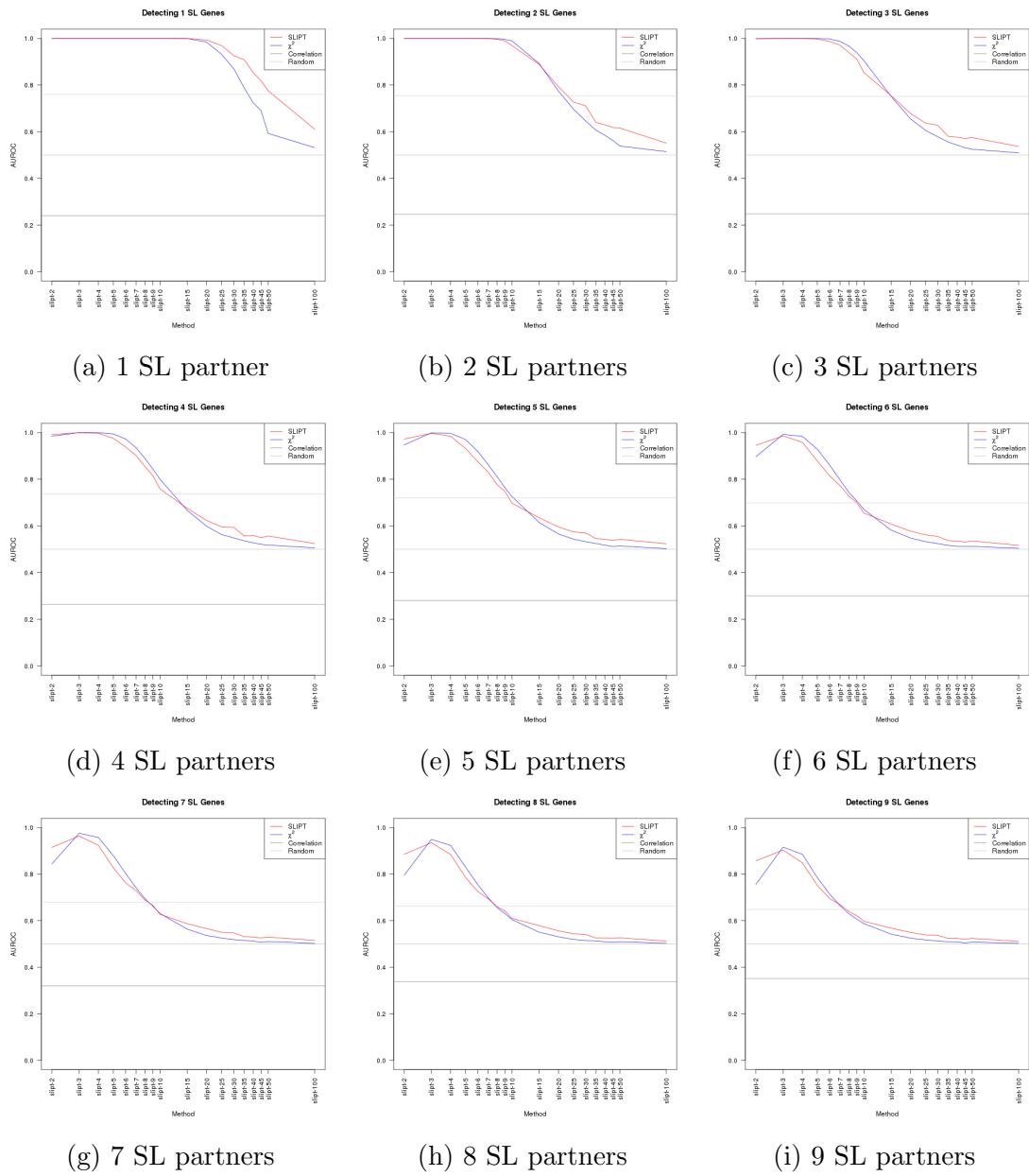


Figure I.2: Performance of χ^2 and SLIPT across quantiles. (continued on next page)

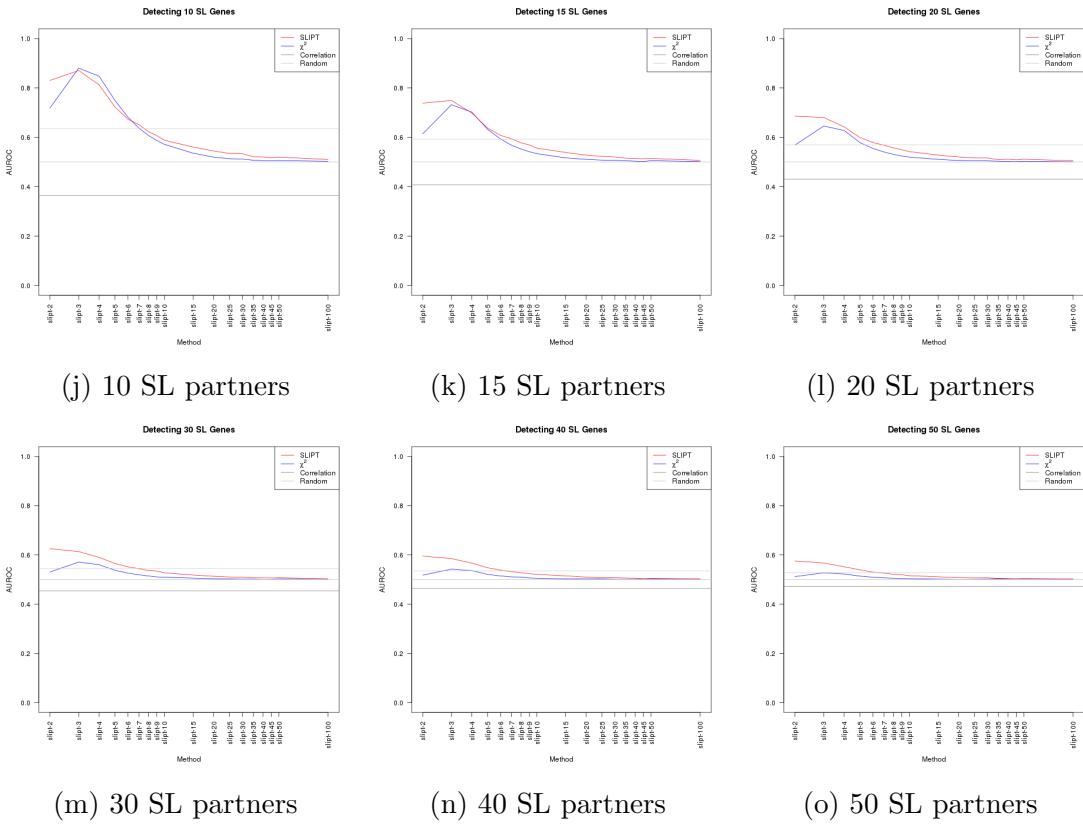


Figure I.2: Performance of χ^2 and SLIPT across quantiles. Synthetic lethal detection with quantiles as in axis labels. The line plots are coloured for SLIPT (red), χ^2 (blue) and correlation (grey), according to the legend. SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 10,000 simulations of 100 genes and 1000 samples. SLIPT performed better than χ^2 for higher numbers of synthetic lethal genes and finer quantiles.

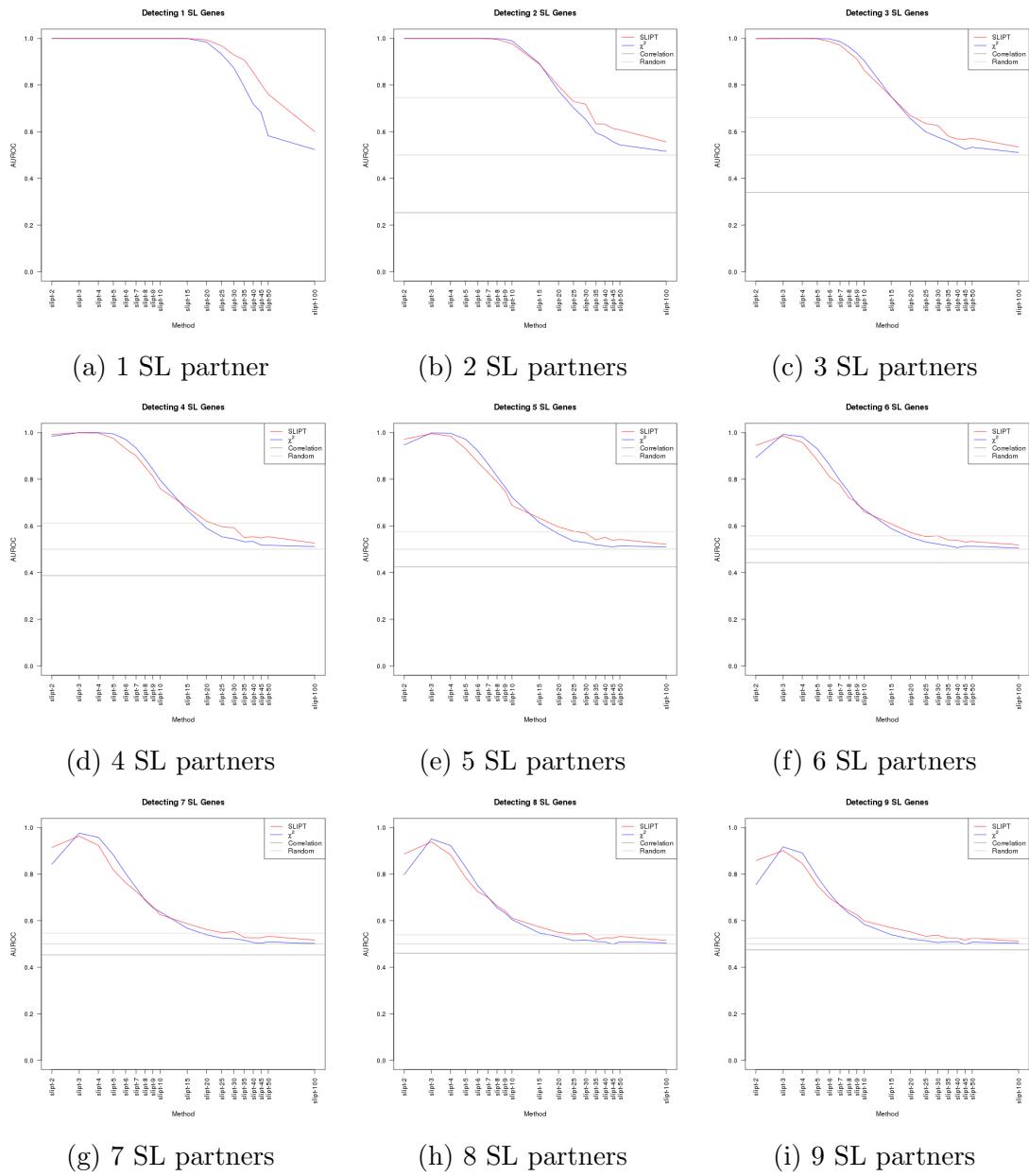


Figure I.3: Performance of χ^2 and SLIPT across quantiles with more genes.
 (continued on next page)

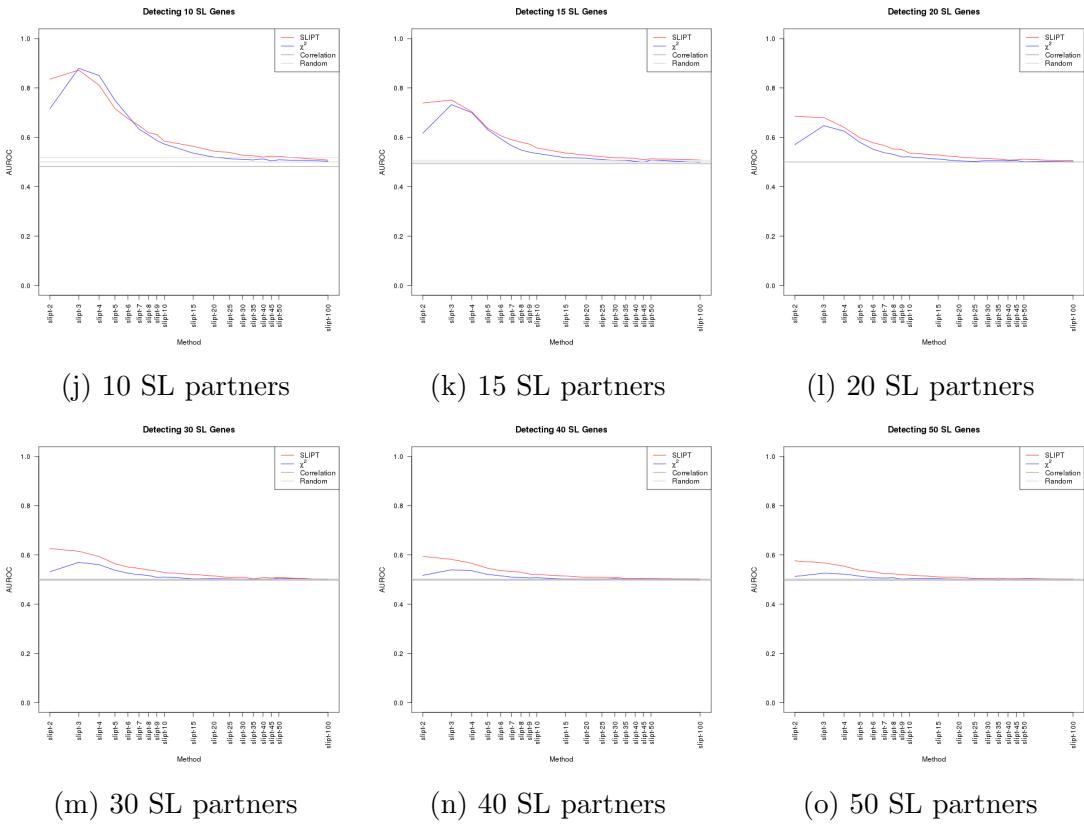


Figure I.3: Performance of χ^2 and SLIPT across quantiles with more genes.
 Synthetic lethal detection with quantiles as in axis labels. The line plots are coloured for SLIPT (red), χ^2 (blue) and correlation (grey), according to the legend. SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 1000 simulations of 20,000 genes and 1000 samples. SLIPT performed better than χ^2 for higher numbers of synthetic lethal genes and finer quantiles.

I.1 Correlated Query Genes affects Specificity

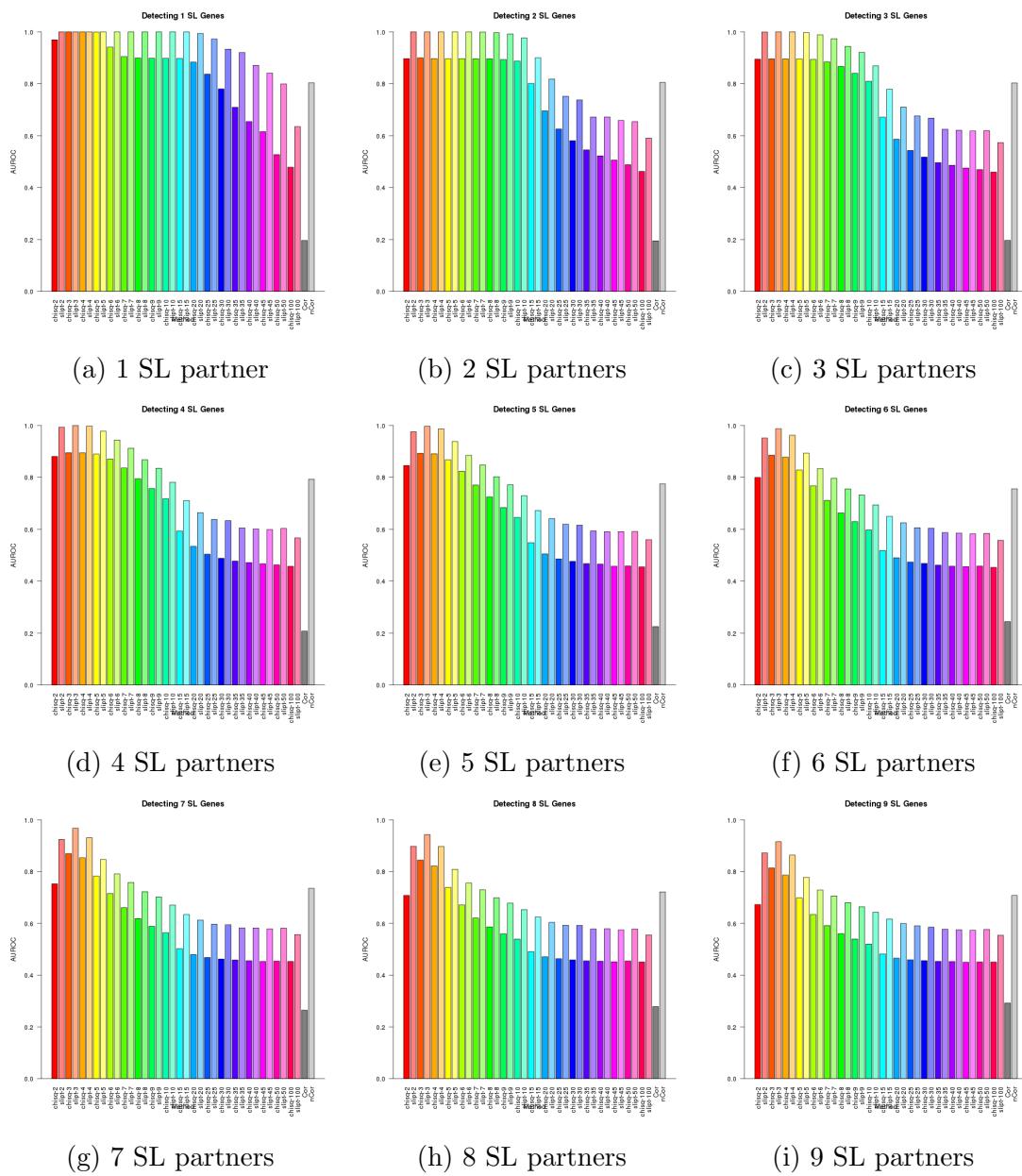


Figure I.4: Performance of χ^2 and SLIPT across quantiles with query correlation. (continued on next page)

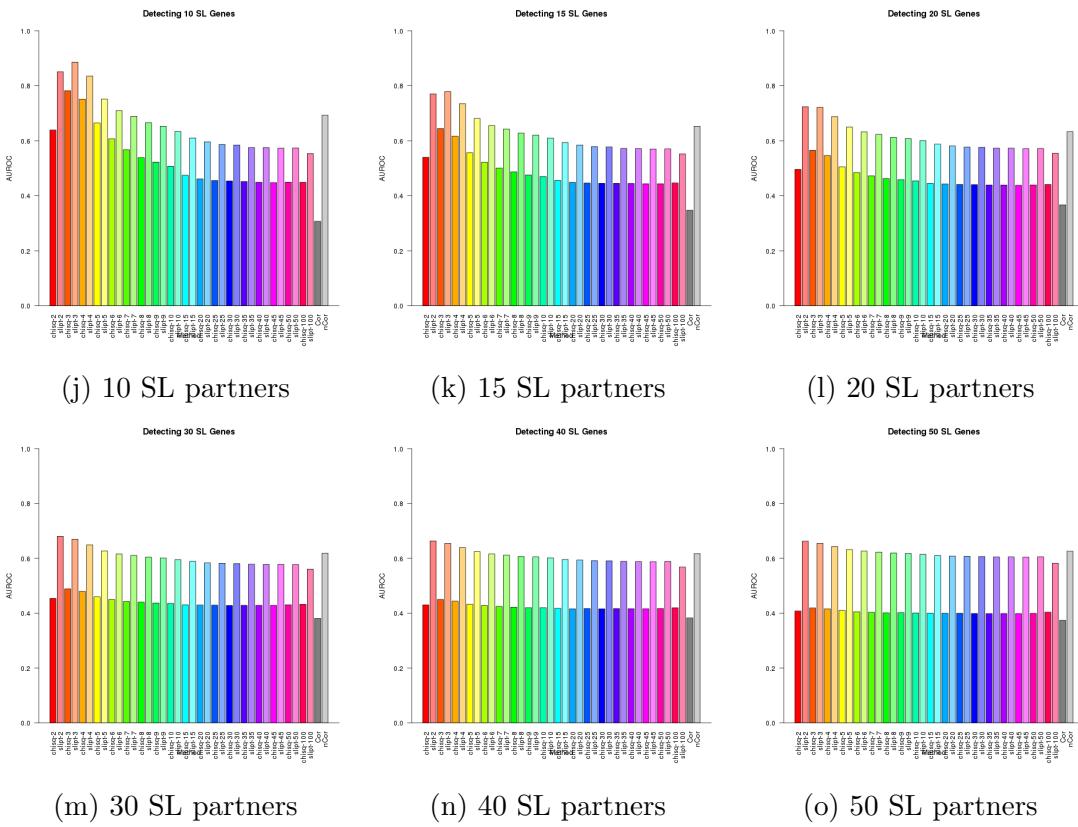


Figure I.4: Performance of χ^2 and SLIPT across quantiles with query correlation. Synthetic lethal detection with quantiles as in axis labels. The barplots have the same hue for each quantile (grey for correlation) and darker for χ^2 (and positive correlation). SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 10,000 simulations of 100 genes (including 10 correlated with the query) and 1000 samples. SLIPT performed consistently better than χ^2 with positively correlated genes.

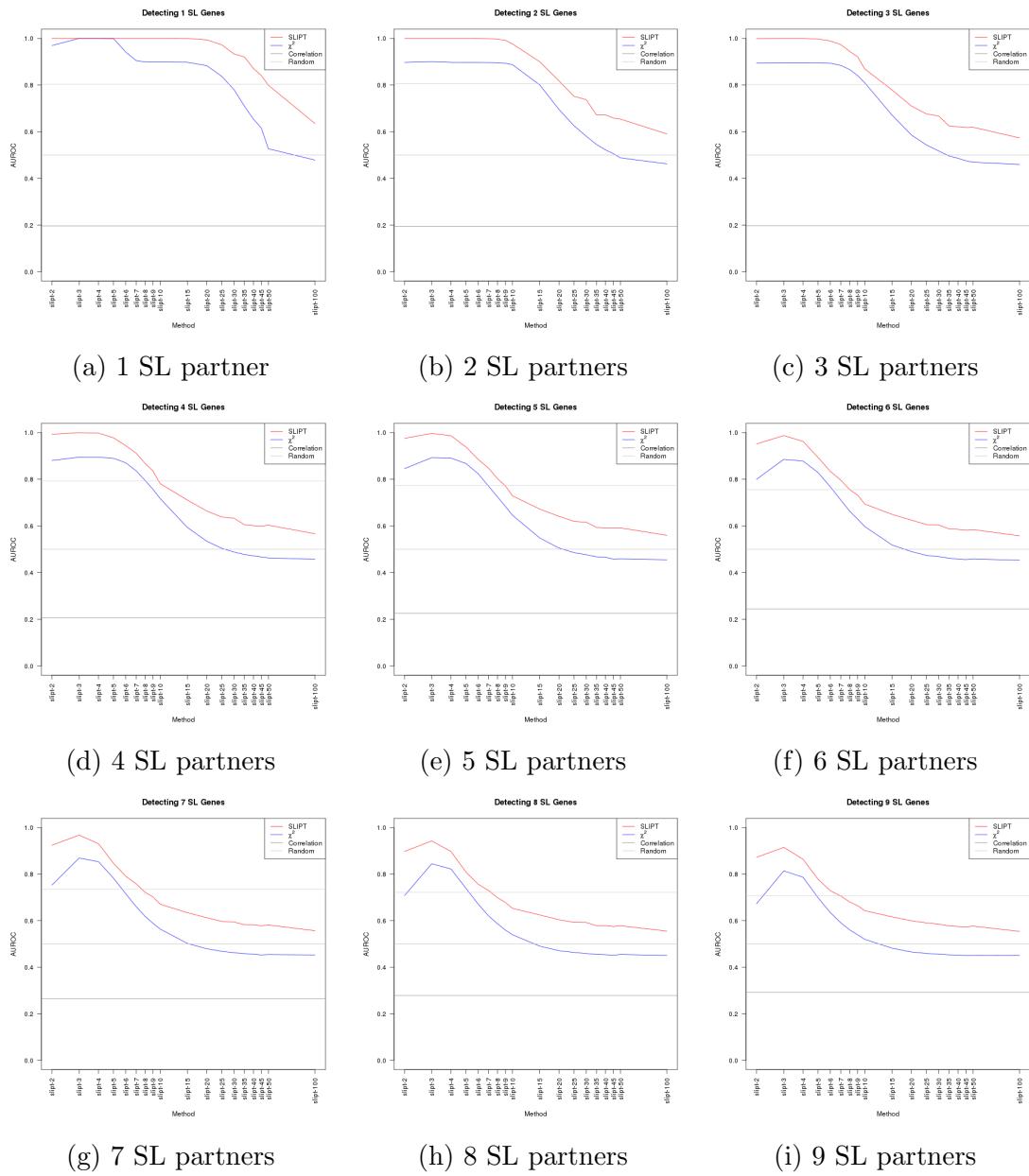


Figure I.5: **Performance of χ^2 and SLIPT across quantiles with query correlation.** (continued on next page)

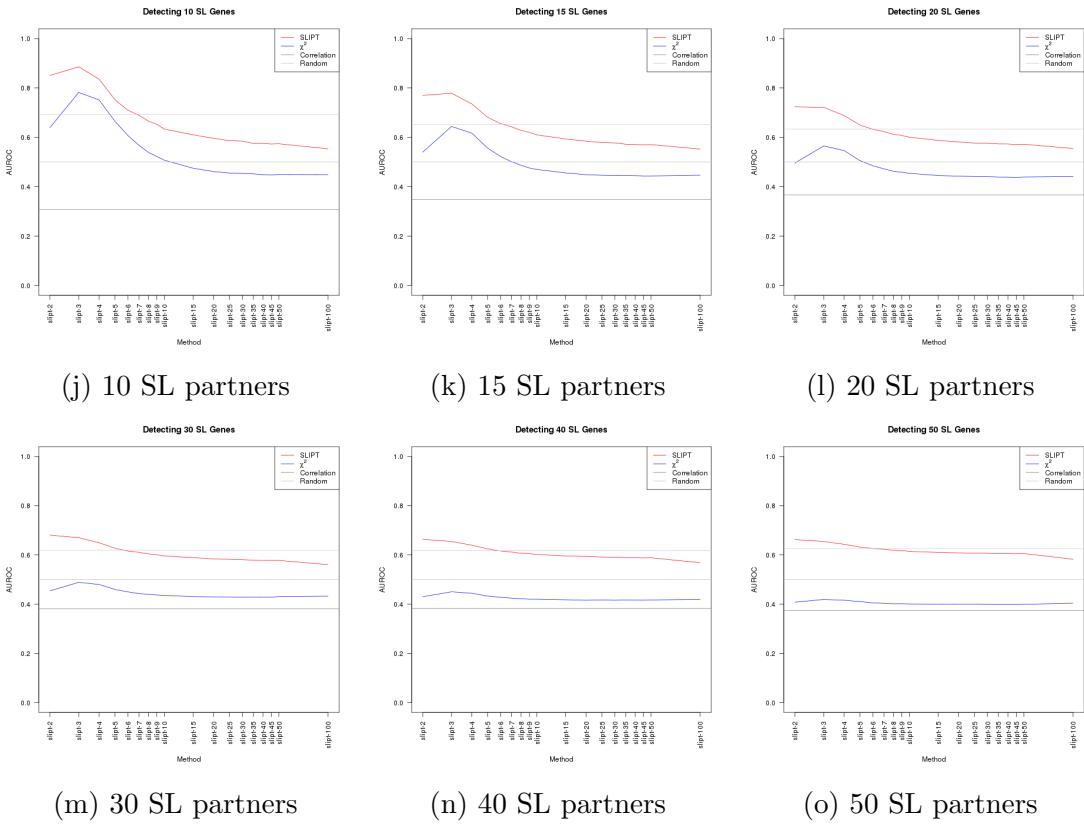


Figure I.5: Performance of χ^2 and SLIPT across quantiles with query correlation. Synthetic lethal detection with quantiles as in axis labels. The line plots are coloured for SLIPT (red), χ^2 (blue) and correlation (grey), according to the legend. SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 10,000 simulations of 100 genes (including 10 correlated with the query) and 1000 samples. SLIPT performed consistently better than χ^2 with positively correlated genes.

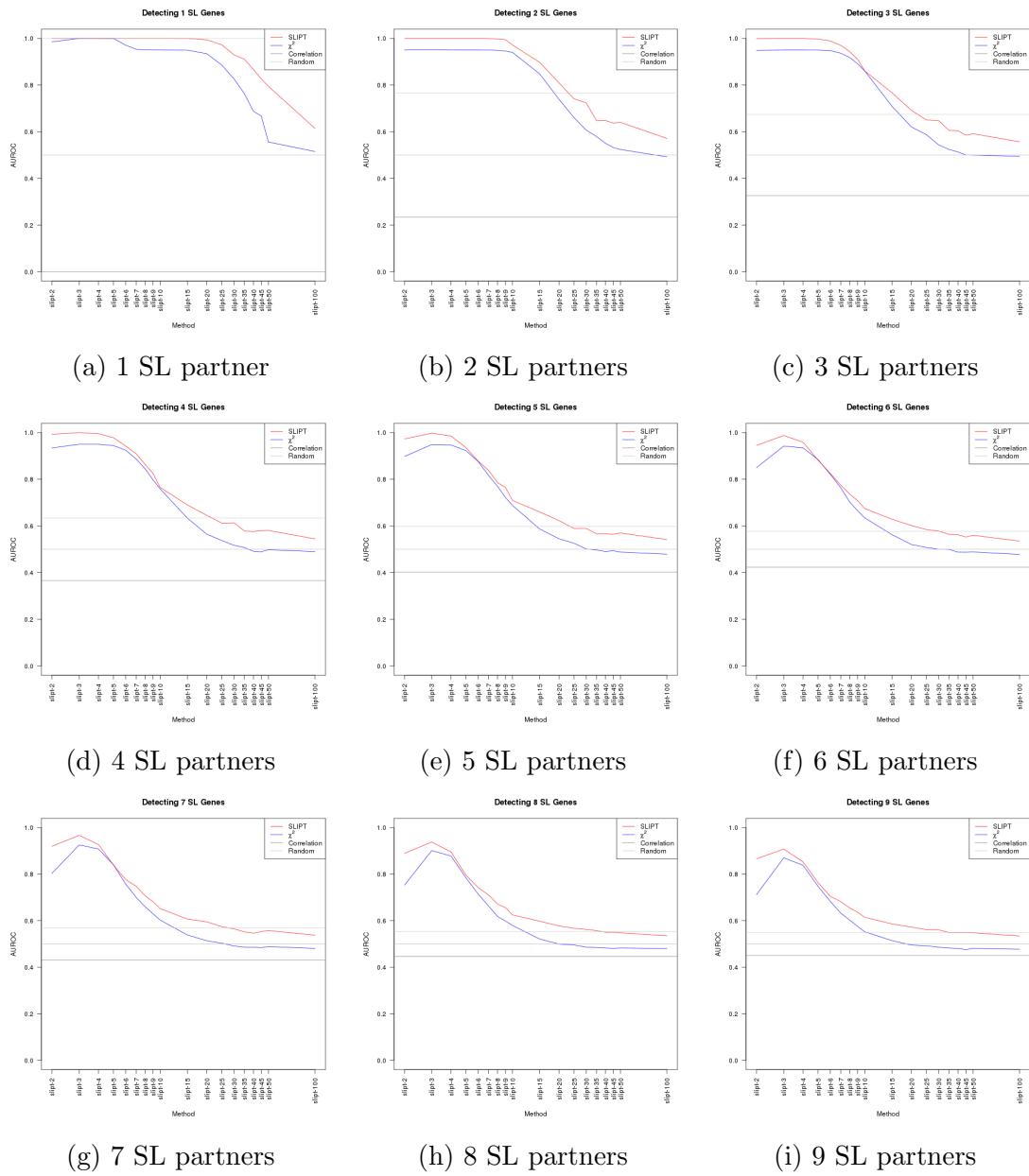


Figure I.6: Performance of χ^2 and SLIPT across quantiles with query correlation and more genes. (continued on next page)

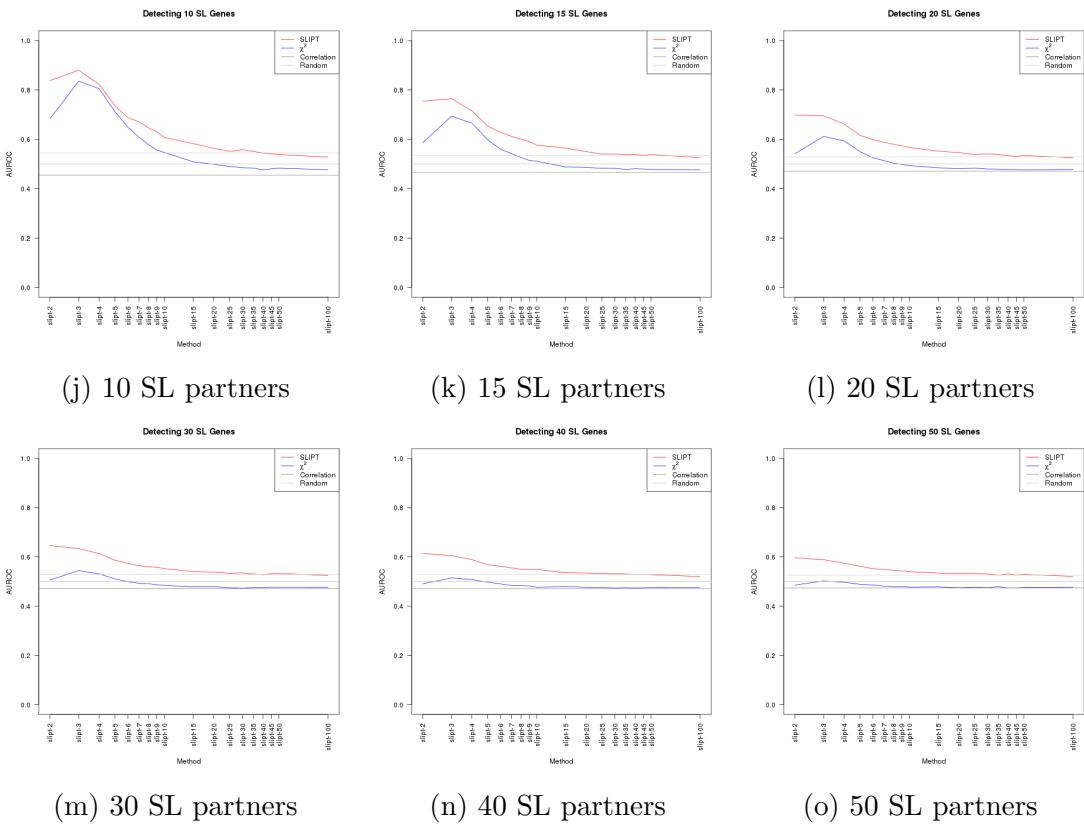


Figure I.6: Performance of χ^2 and SLIPT across quantiles with query correlation and more genes. Synthetic lethal detection with quantiles as in axis labels. The line plots are coloured for SLIPT (red), χ^2 (blue) and correlation (grey), according to the legend. SLIPT and χ^2 performed similarly, peaking at $1/3$ -quantiles and converging to random (0.5). Negative correlation was higher than positive but not optimal quantiles for SLIPT or χ^2 . These findings were robust across different numbers of underlying synthetic lethal genes in 1000 simulations of 20,000 genes (including 1000 correlated with the query) and 1000 samples. SLIPT performed consistently better than χ^2 with positively correlated genes.

Appendix J

Simulations on Graph Structures

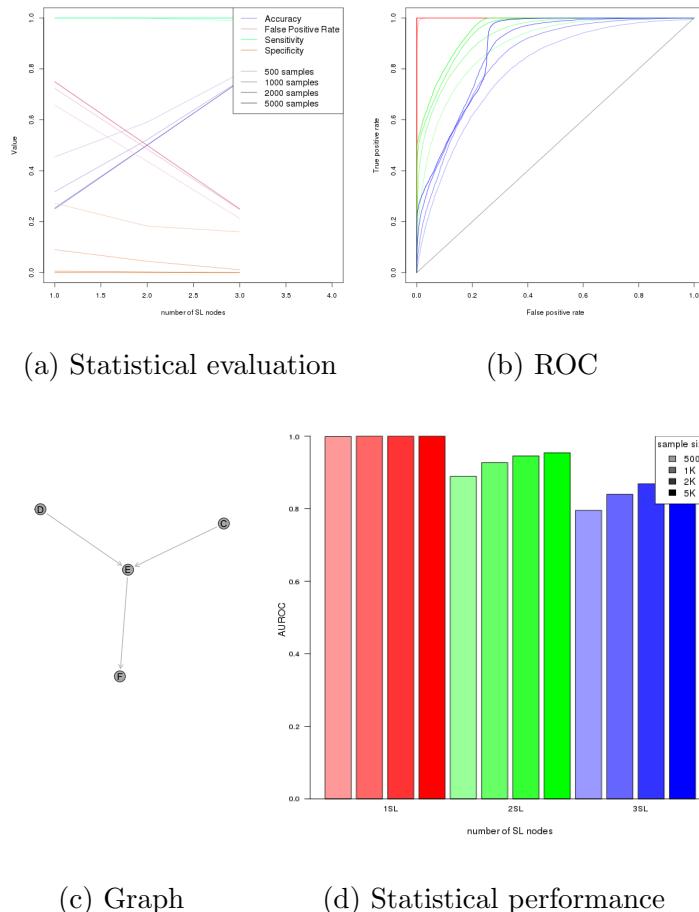


Figure J.1: **Performance of simulations on a simple graph.** Simulation of synthetic lethality was performed using a multivariate normal distribution from a converging graph. For each parameter, 10,000 simulations were used. Colours in Figure J.1b match Figure J.1d.

J.1 Simulations from Inhibiting Graph Structures

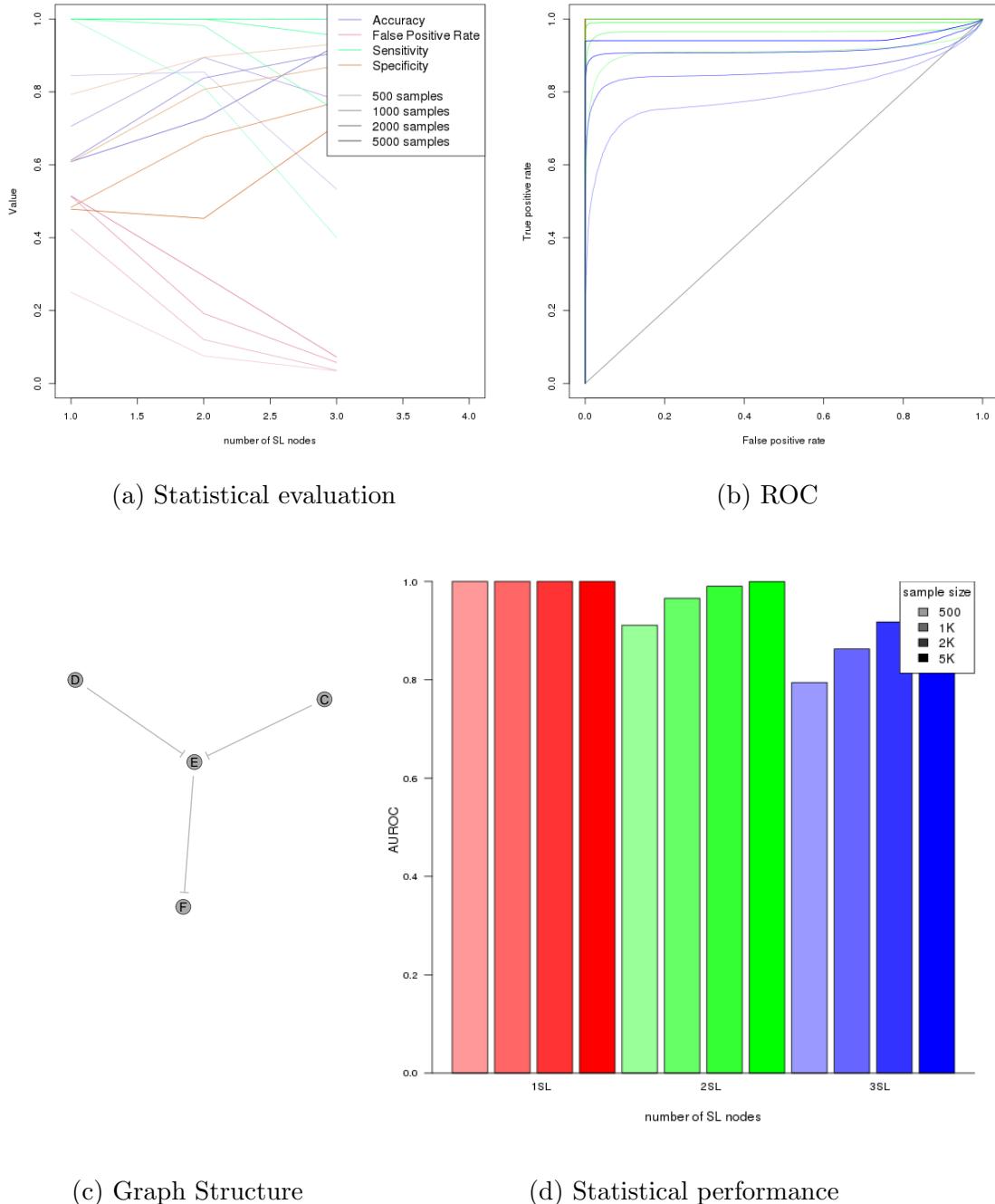
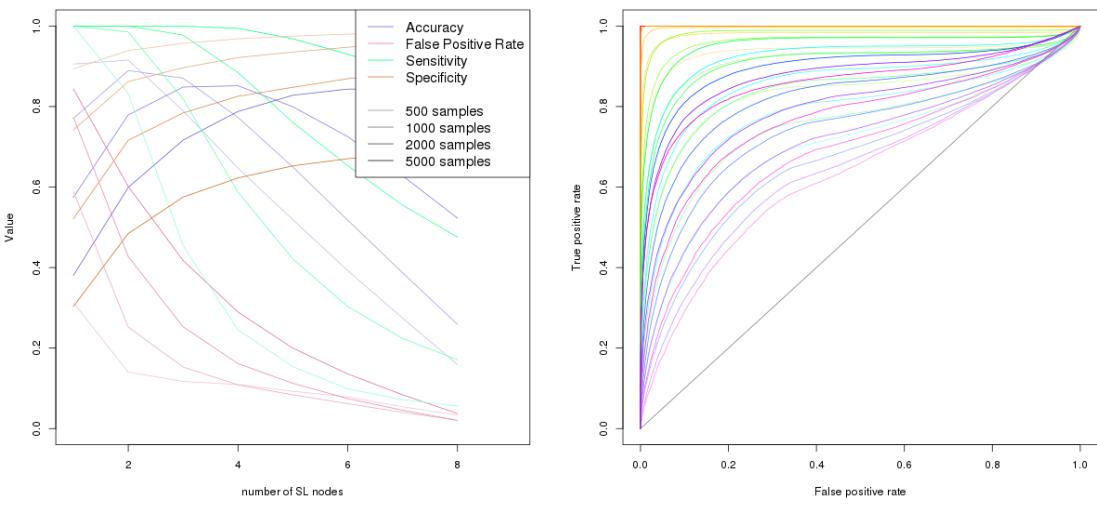
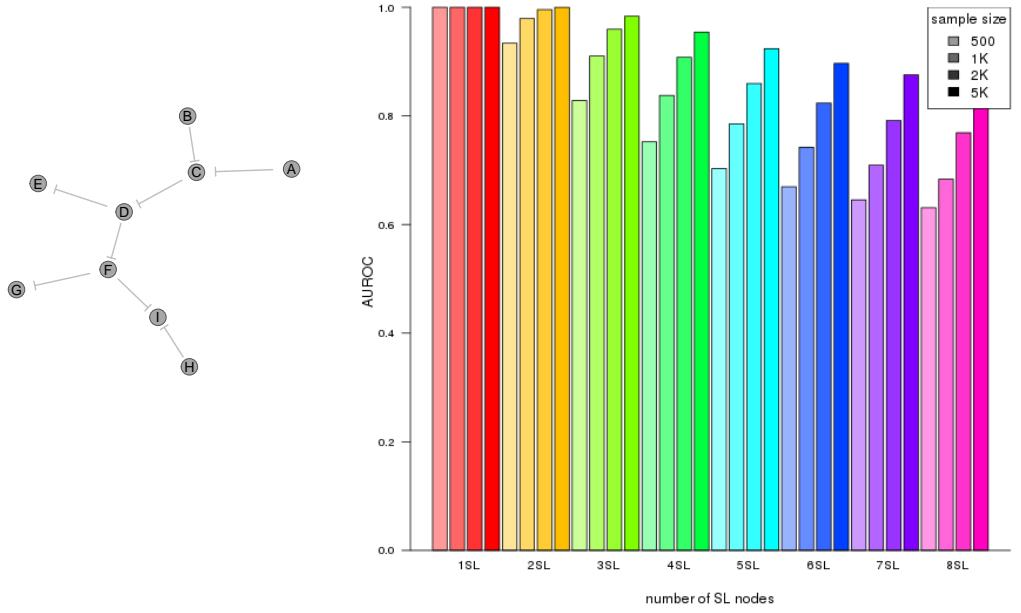


Figure J.2: **Performance of simulations on an inhibiting graph.** Simulation of synthetic lethality used a multivariate normal distribution from a converging graph. For each parameter, 10,000 simulations were used. Colours in Figure J.2b match Figure J.2d.



(a) Statistical evaluation

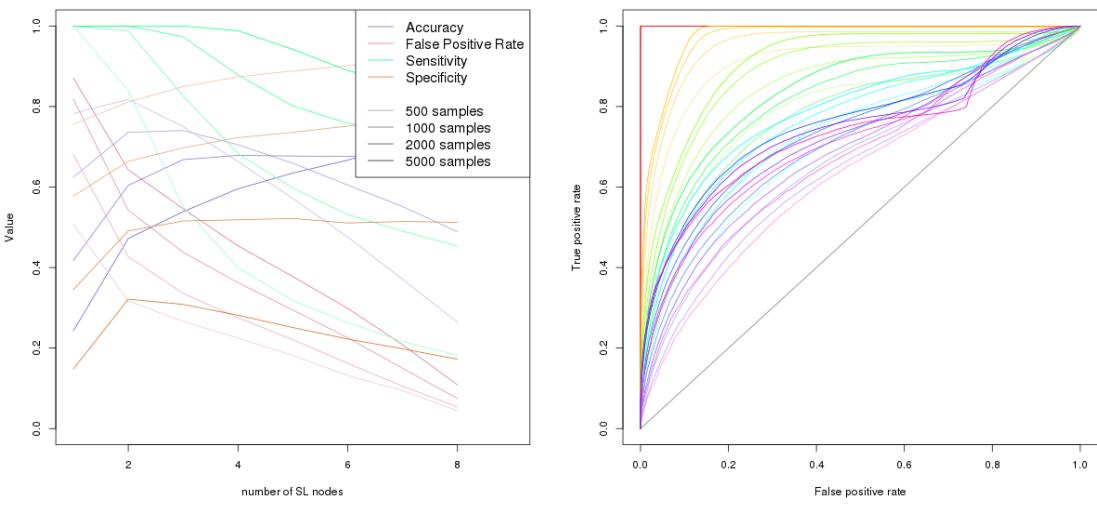
(b) ROC



(c) Graph Structure

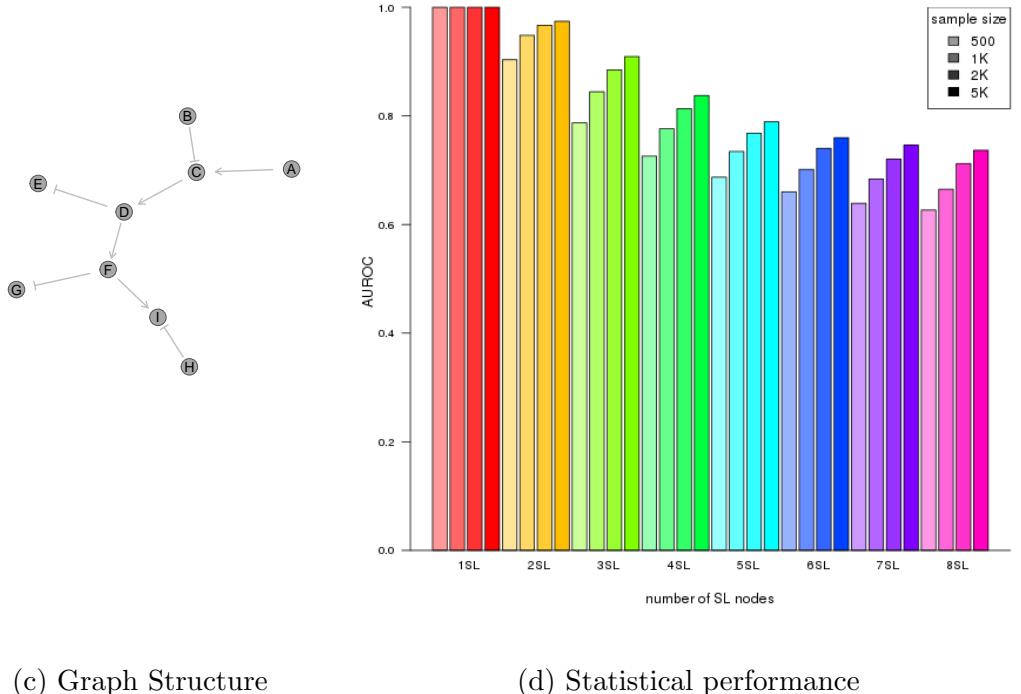
(d) Statistical performance

Figure J.3: Performance of simulations on a constructed graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a pathway with only inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.3b match Figure J.3d.



(a) Statistical evaluation

(b) ROC

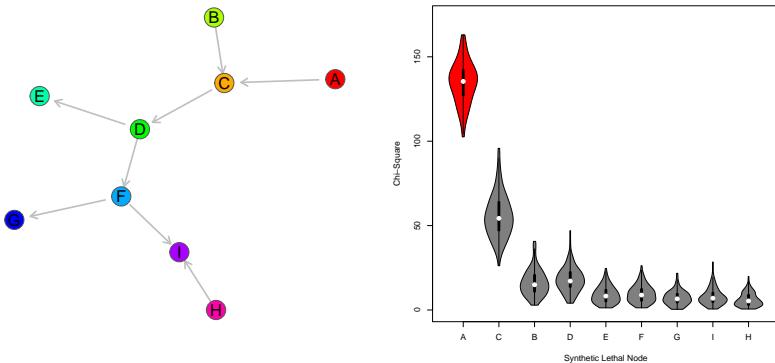


(c) Graph Structure

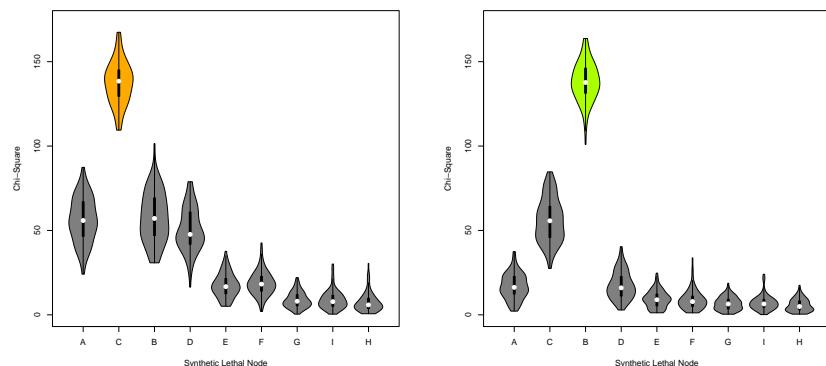
(d) Statistical performance

Figure J.4: Performance of simulations on a constructed graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a pathway with a combination of inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.4b match Figure J.4d.

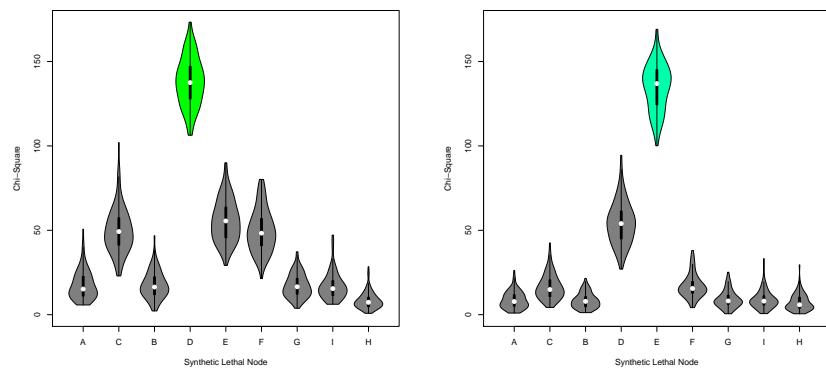
J.2 Simulation across Graph Structures



(a) Activating Graph Structure (b) χ^2 distribution for “A” SL



(c) Gene “B” SL (d) Gene “C” SL



(e) Gene “D” SL (f) Gene “E” SL

Figure J.5: **Detection of synthetic lethality within a graph Structure.** (continued on next page)

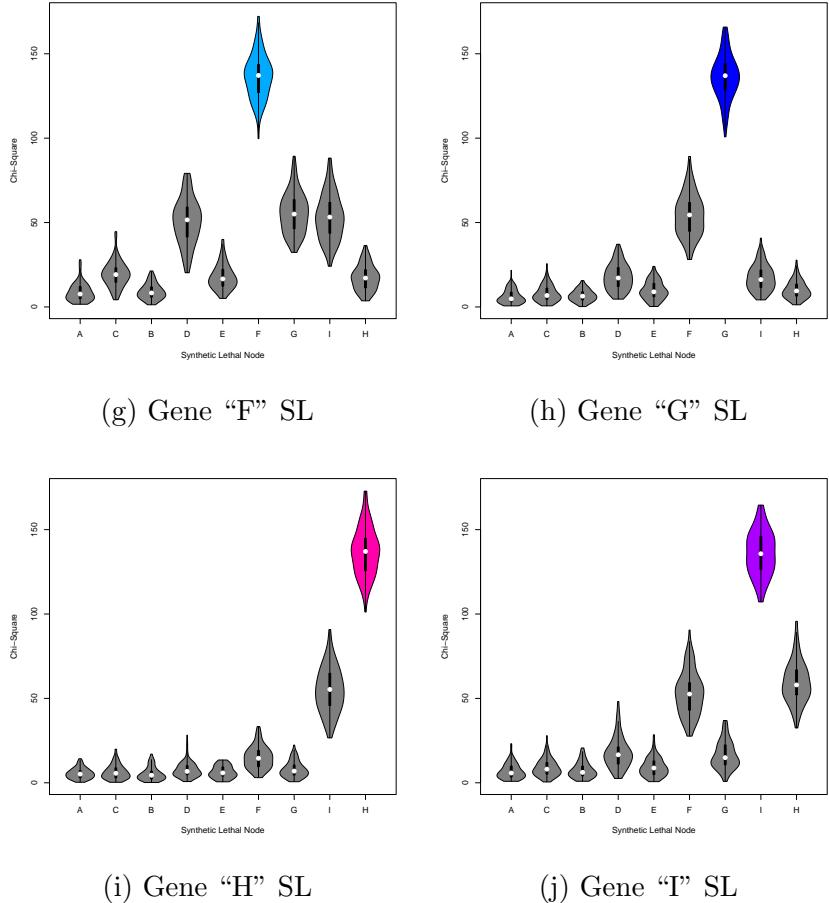
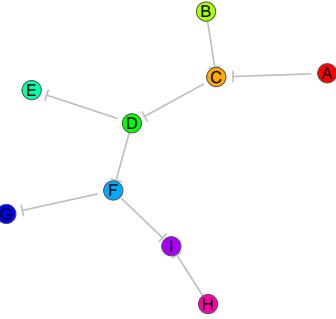
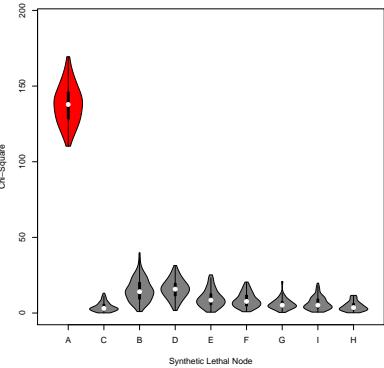


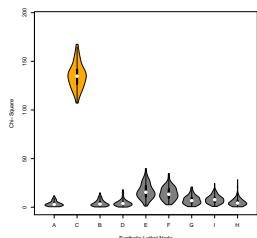
Figure J.5: Detection of synthetic lethality within a graph structure. Each gene was designated to be synthetic lethal separately and the χ^2 value from SLIPT was computed for each gene across the graph. For each synthetic lethal gene (highlighted in the respective colours), the χ^2 values were computed in 100 simulations of datasets of 20,000 genes including the graph structure and 1000 samples. For each synthetic lethal gene, the adjacent genes in the network also had elevated test statistics.



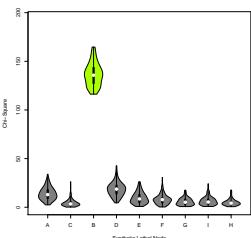
(a) Inhibiting Graph Structure



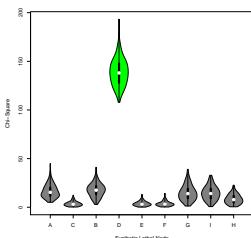
(b) χ^2 distribution for "A" SL



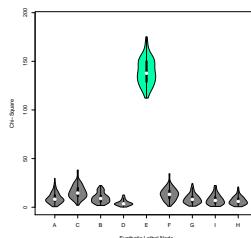
(c) Gene "B" SL



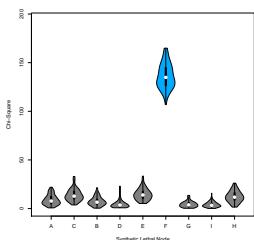
(d) Gene "C" SL



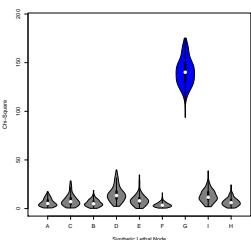
(e) Gene "D" SL



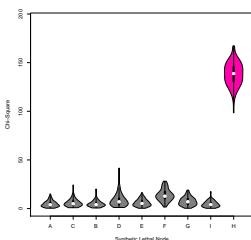
(f) Gene "E" SL



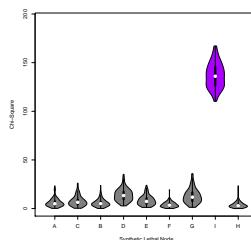
(g) Gene "F" SL



(h) Gene "G" SL

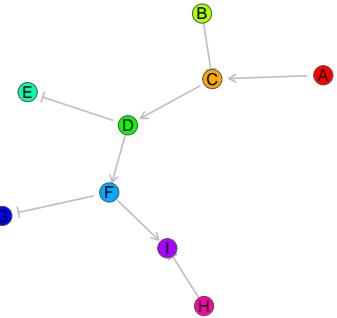


(i) Gene "H" SL

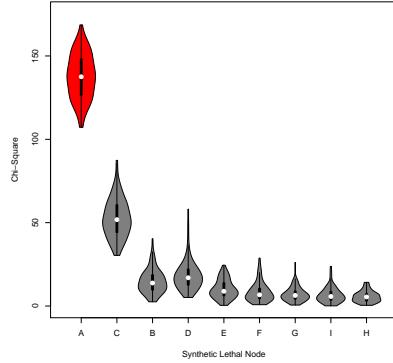


(j) Gene "I" SL

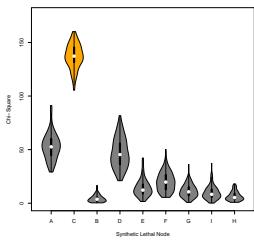
Figure J.6: Detection of synthetic lethality within an inhibiting graph. Each gene was designated to be synthetic lethal separately and the χ^2 value from SLIPT was computed for each gene across the graph structure with inhibiting relationships. For each synthetic lethal gene (highlighted in the respective colours), the χ^2 values were computed in 100 simulations of datasets of 20,000 genes including the graph structure and 1000 samples. For each synthetic lethal gene, the adjacent genes exhibited lower χ^2 values with inhibiting relationships.



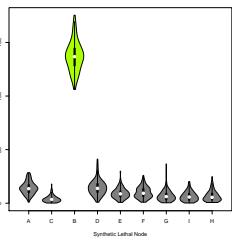
(a) Inhibiting Graph Structure



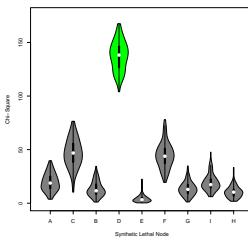
(b) χ^2 distribution for "A" SL



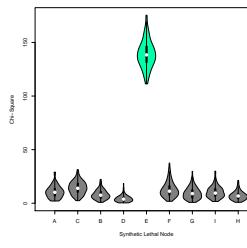
(c) Gene "B" SL



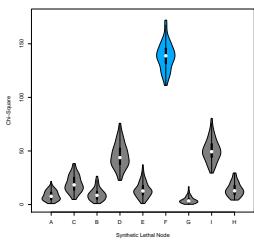
(d) Gene "C" SL



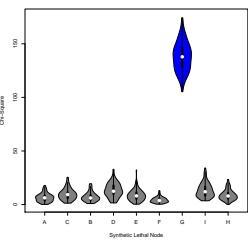
(e) Gene "D" SL



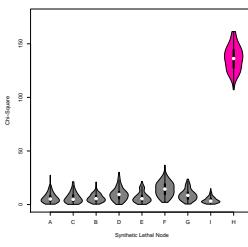
(f) Gene "E" SL



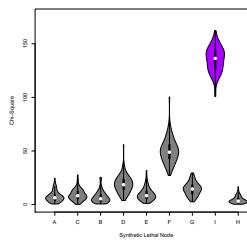
(g) Gene "F" SL



(h) Gene "G" SL



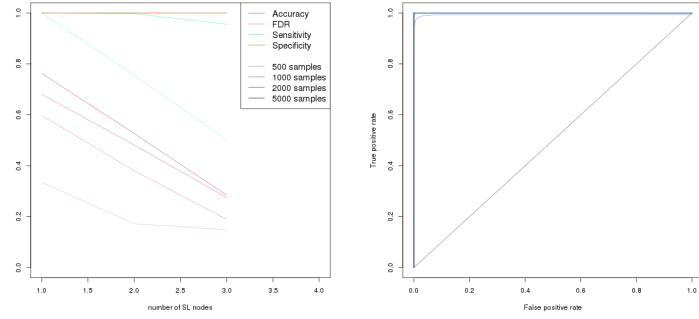
(i) Gene "H" SL



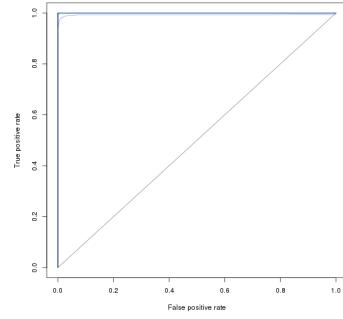
(j) Gene "I" SL

Figure J.7: Detection of synthetic lethality within an inhibiting graph. Each gene was designated to be synthetic lethal separately and the χ^2 value from SLIPT was computed for each gene across the graph structure with inhibiting and relationships. For each synthetic lethal gene (highlighted in the respective colours), the χ^2 values were computed in 100 simulations of datasets of 20,000 genes including the graph structure and 1000 samples.

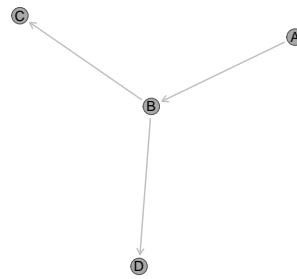
J.3 Simulations within a Large Simulated Dataset



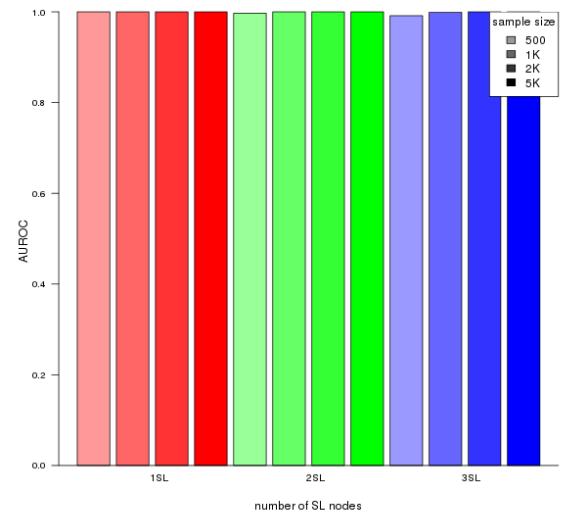
(a) Statistical evaluation



(b) ROC curves



(c) Graph Structure



(d) Statistical performance

Figure J.8: Performance of simulations including a simple graph. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution (without correlation structure apart from the graph shown). Performance of SLIPT was high across parameters for detecting synthetic lethality in the graph structure within a larger dataset. The sensitivity decreased for a greater number of true positives to detect but the specificity remained high with a low false positive rate.

J.4 Simulations from Complex Graph Structures

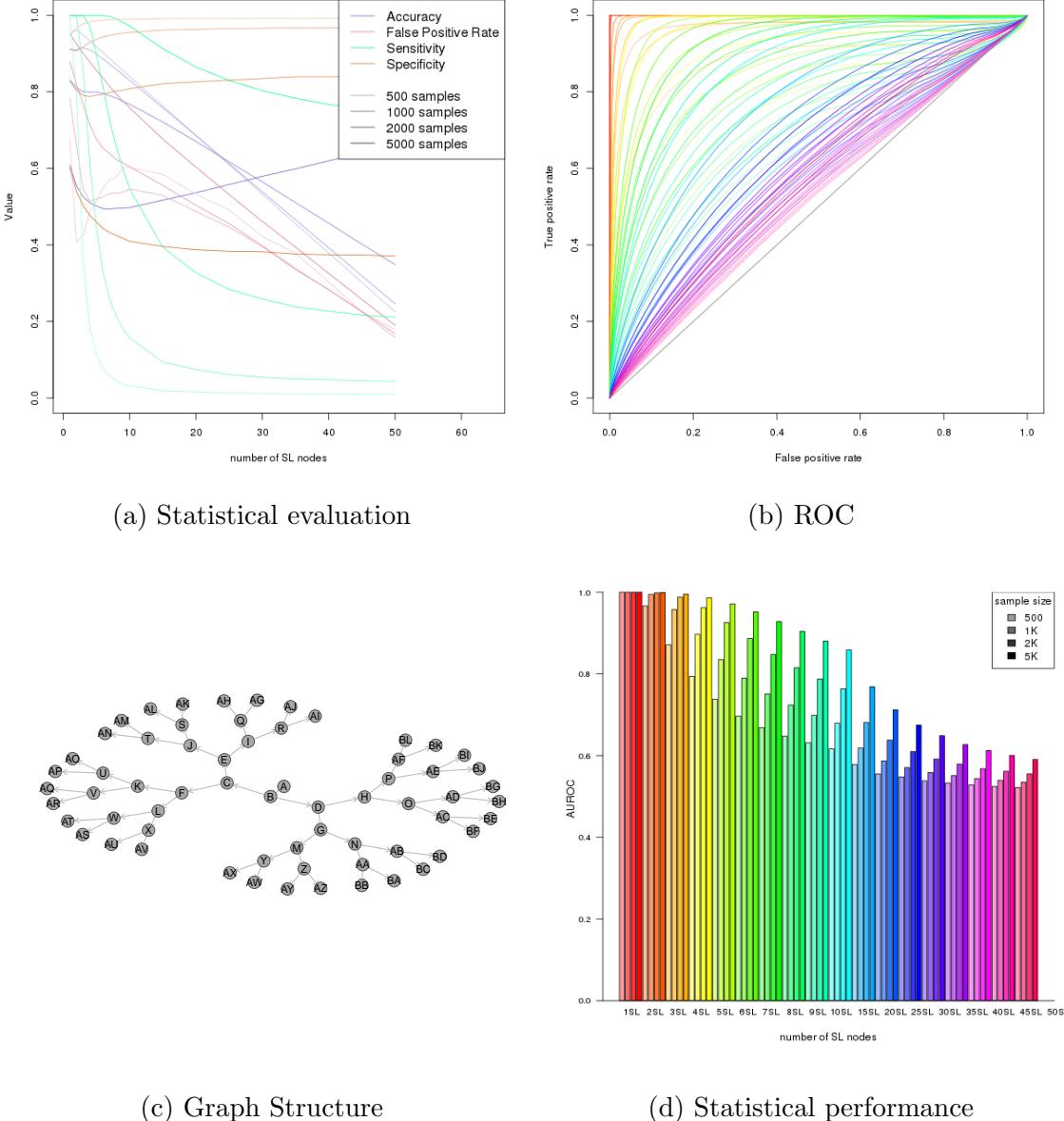
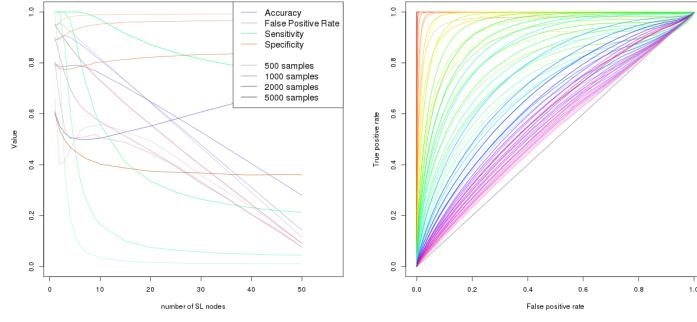
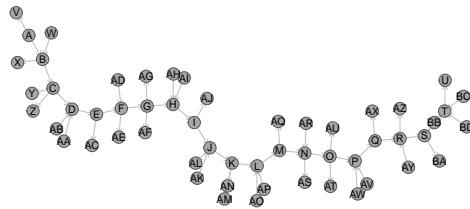


Figure J.9: Performance of simulations on a branching graph. Simulation of synthetic lethality used a multivariate normal distribution from a branching graph. For each parameter, 10,000 simulations were used. Colours in Figure J.9b match Figure J.9d.

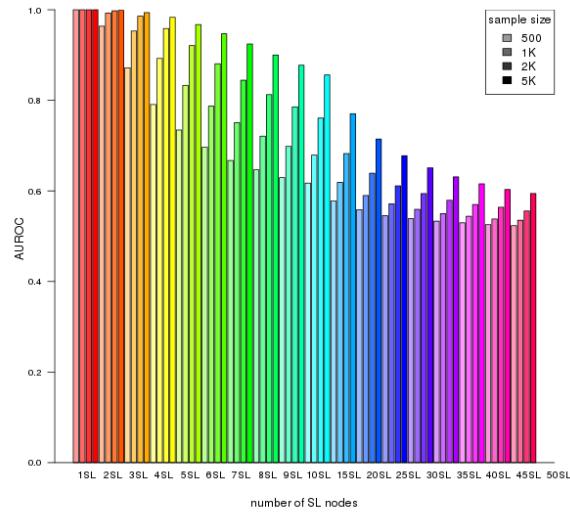


(a) Statistical evaluation

(b) ROC

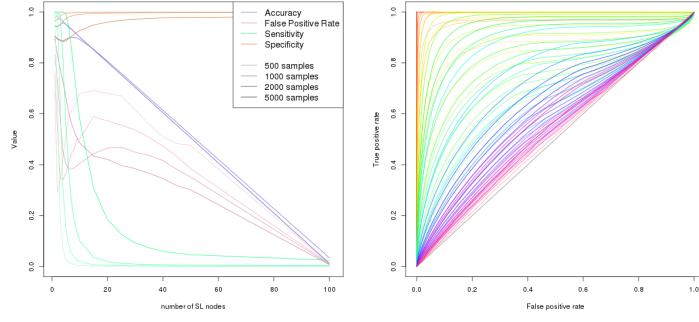


(c) Graph Structure



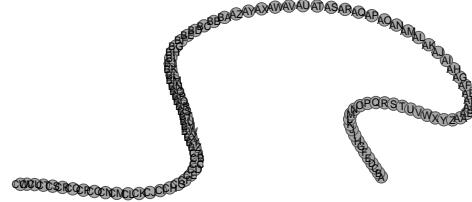
(d) Statistical performance

Figure J.10: **Performance of simulations on a complex graph.** Simulation of synthetic lethality used a multivariate normal distribution from a complex graph. For each parameter, 10,000 simulations were used. Colours in Figure J.10b match Figure J.10d.

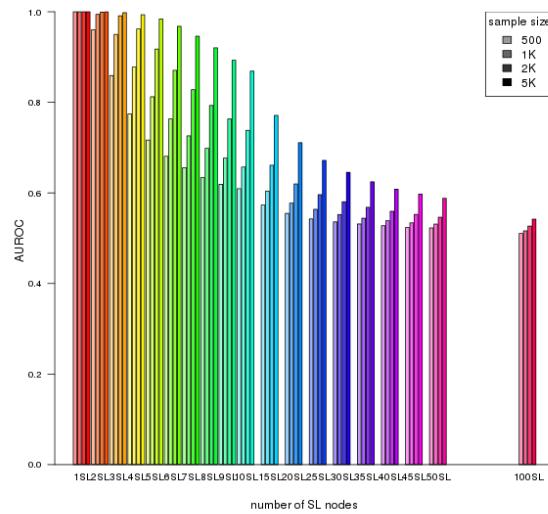


(a) Statistical evaluation

(b) ROC



(c) Graph Structure



(d) Statistical performance

Figure J.11: **Performance of simulations on a large graph.** Simulation of synthetic lethality used a multivariate normal distribution from a large graph. For each parameter, 10,000 simulations were used. Colours in Figure J.11b match Figure J.11d.

J.5 Simulations from Complex Inhibiting Graphs

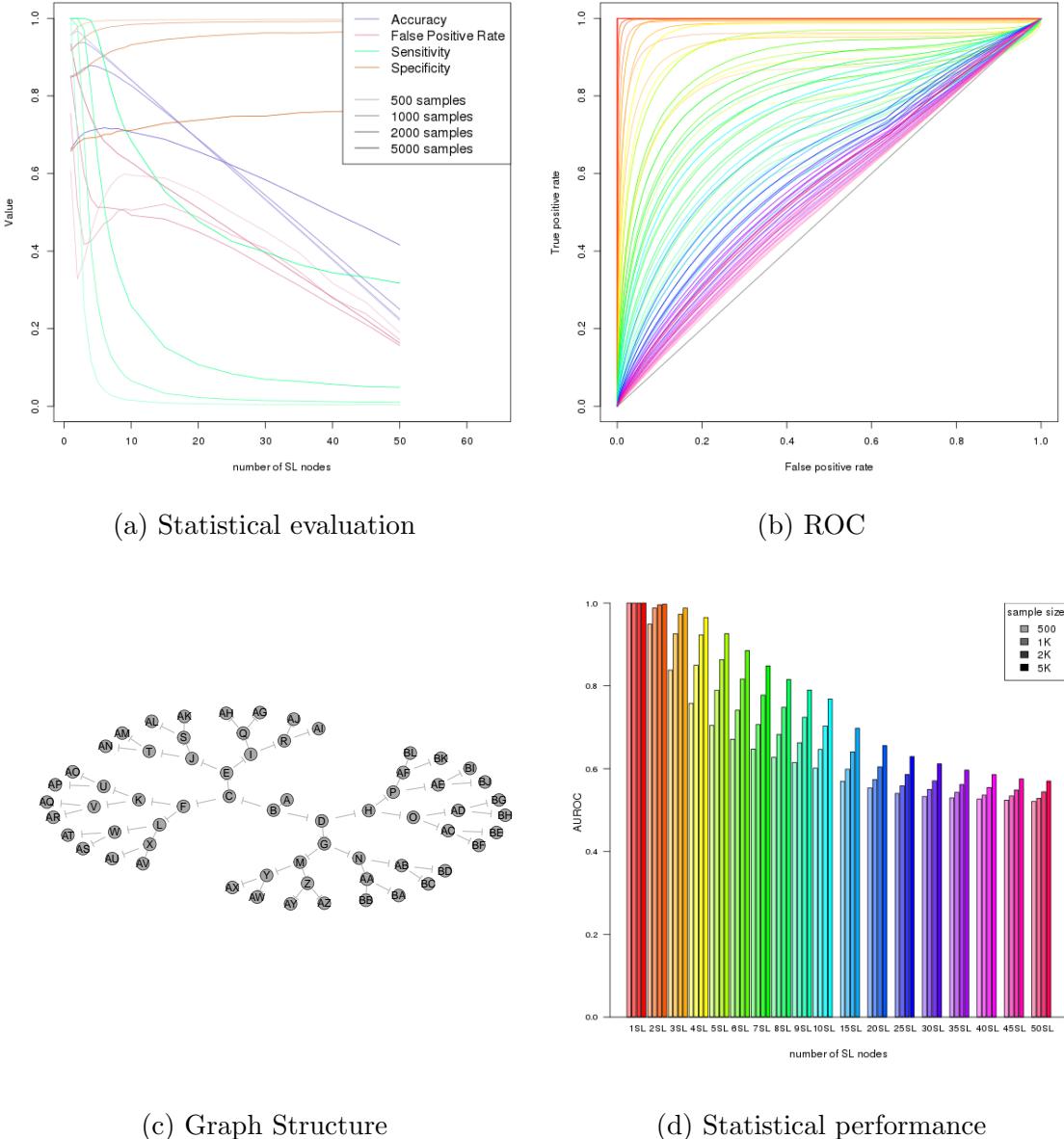
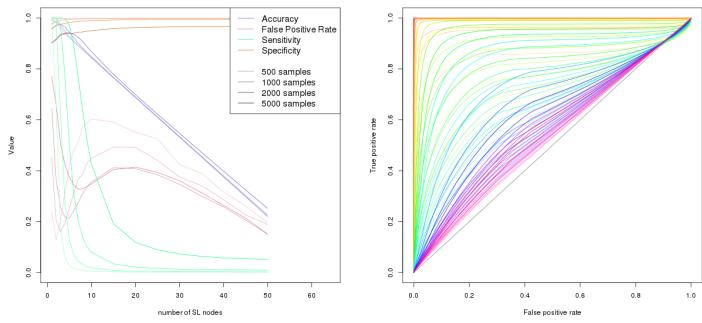
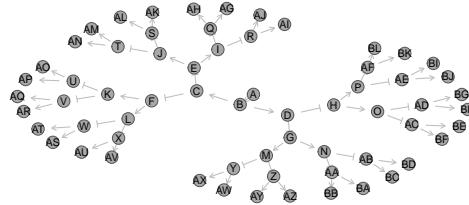


Figure J.12: Performance of simulations on a branching graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a branching graph with only inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.12b match Figure J.12d.

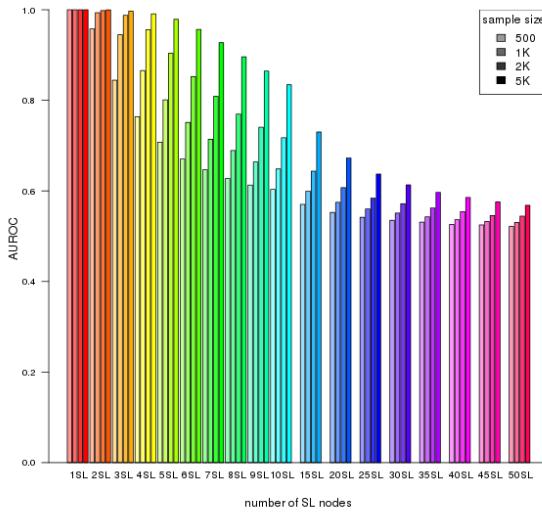


(a) Statistical evaluation

(b) ROC

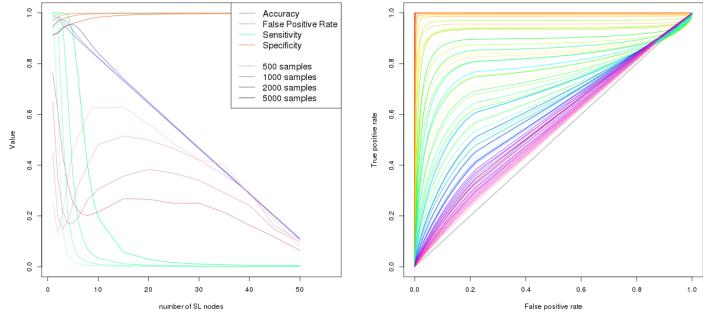


(c) Graph Structure



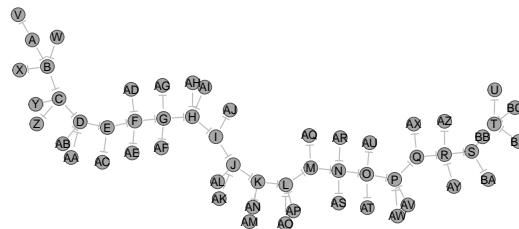
(d) Statistical performance

Figure J.13: Performance of simulations on a branching graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a branching graph with alternating inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.13b match Figure J.13d.

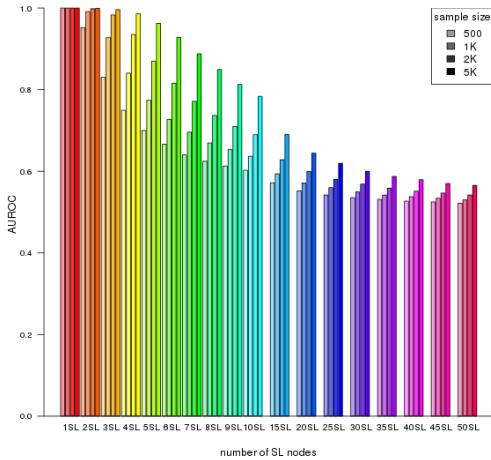


(a) Statistical evaluation

(b) ROC

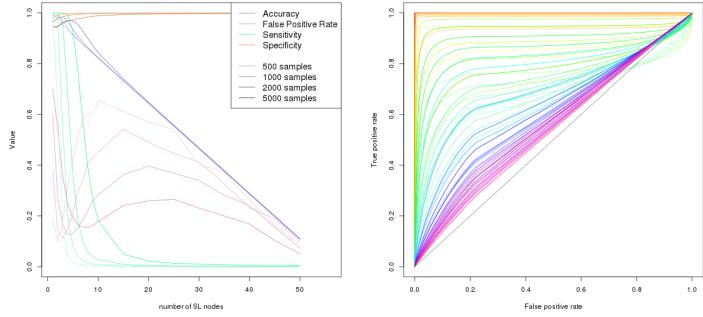


(c) Graph Structure



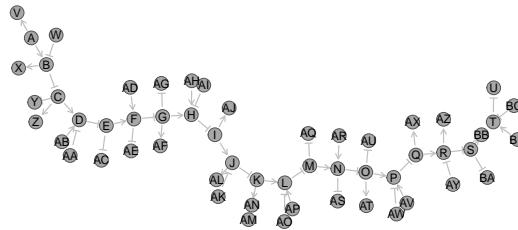
(d) Statistical performance

Figure J.14: Performance of simulations on a complex graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a complex graph with only inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.14b match Figure J.14d.

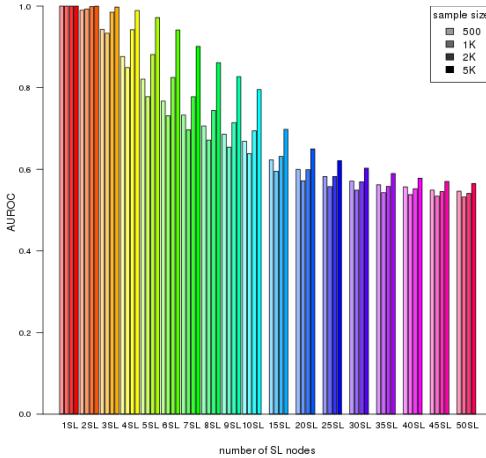


(a) Statistical evaluation

(b) ROC

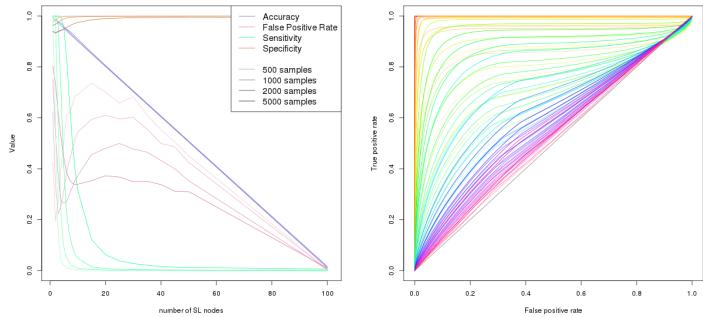


(c) Graph Structure



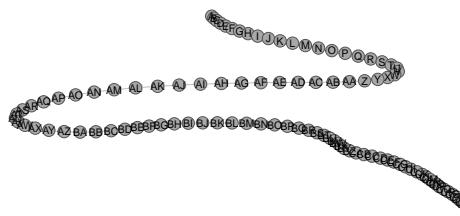
(d) Statistical performance

Figure J.15: Performance of simulations on a complex graph with inhibition.
 Simulation of synthetic lethality used a multivariate normal distribution from a complex graph with a combination of relationships. For each parameter, 10,000 simulations were used. Colours in Figure J.15b match Figure J.15d.

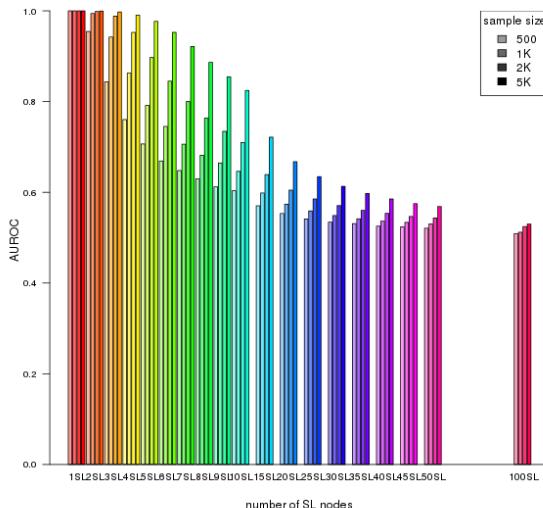


(a) Statistical evaluation

(b) ROC

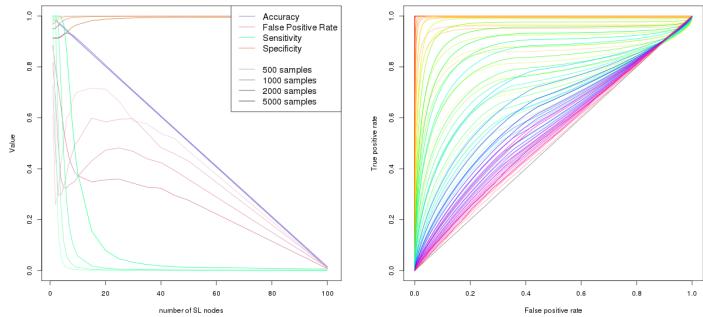


(c) Graph Structure



(d) Statistical performance

Figure J.16: **Performance of simulations on a large constructed graph with inhibition.** Simulation of synthetic lethality used a multivariate normal distribution from a large graph with only inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.16b match Figure J.16d.

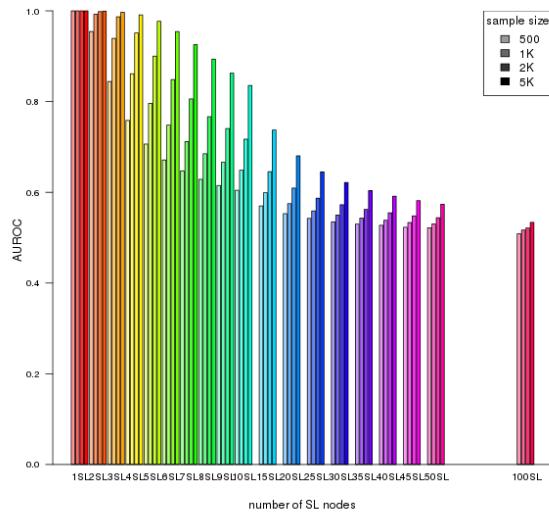


(a) Statistical evaluation

(b) ROC



(c) Graph Structure



(d) Statistical performance

Figure J.17: Performance of simulations on a large constructed graph with inhibition. Simulation of synthetic lethality used a multivariate normal distribution from a large graph with alternating inhibitions. For each parameter, 10,000 simulations were used. Colours in Figure J.17b match Figure J.17d.

J.6 Simulations from Pathway Graph Structures

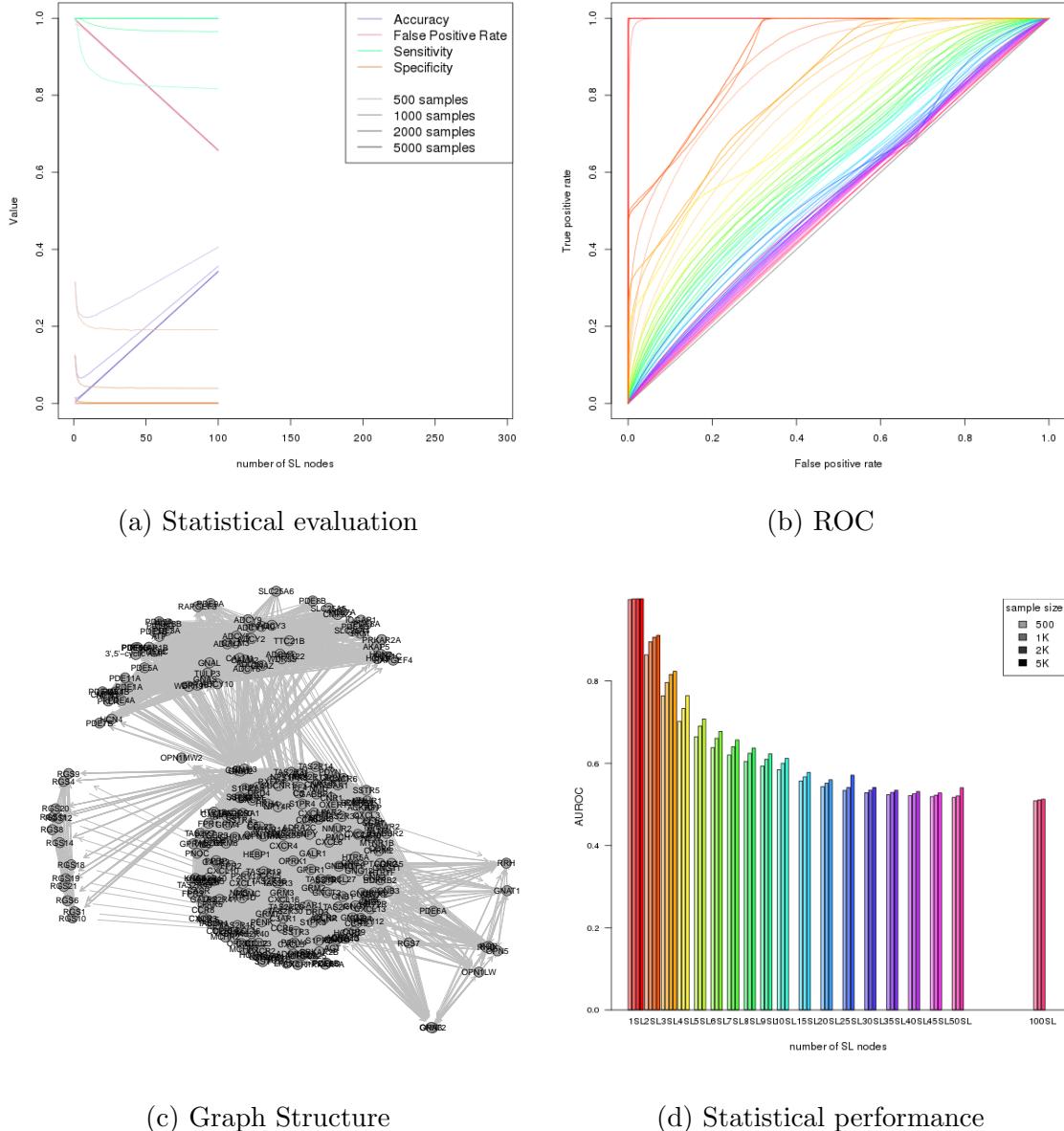


Figure J.18: Performance of simulations on the $G_{\alpha i}$ signalling pathway. Simulation of synthetic lethality used a multivariate normal distribution based on the Reactome $G_{\alpha i}$ signalling pathway. Performance of SLIPT was high across parameters for detecting synthetic lethality in the graph structure within a larger dataset. The performance decreased for a greater number of true positives to detect but the accuracy increased with a low false positive rate.

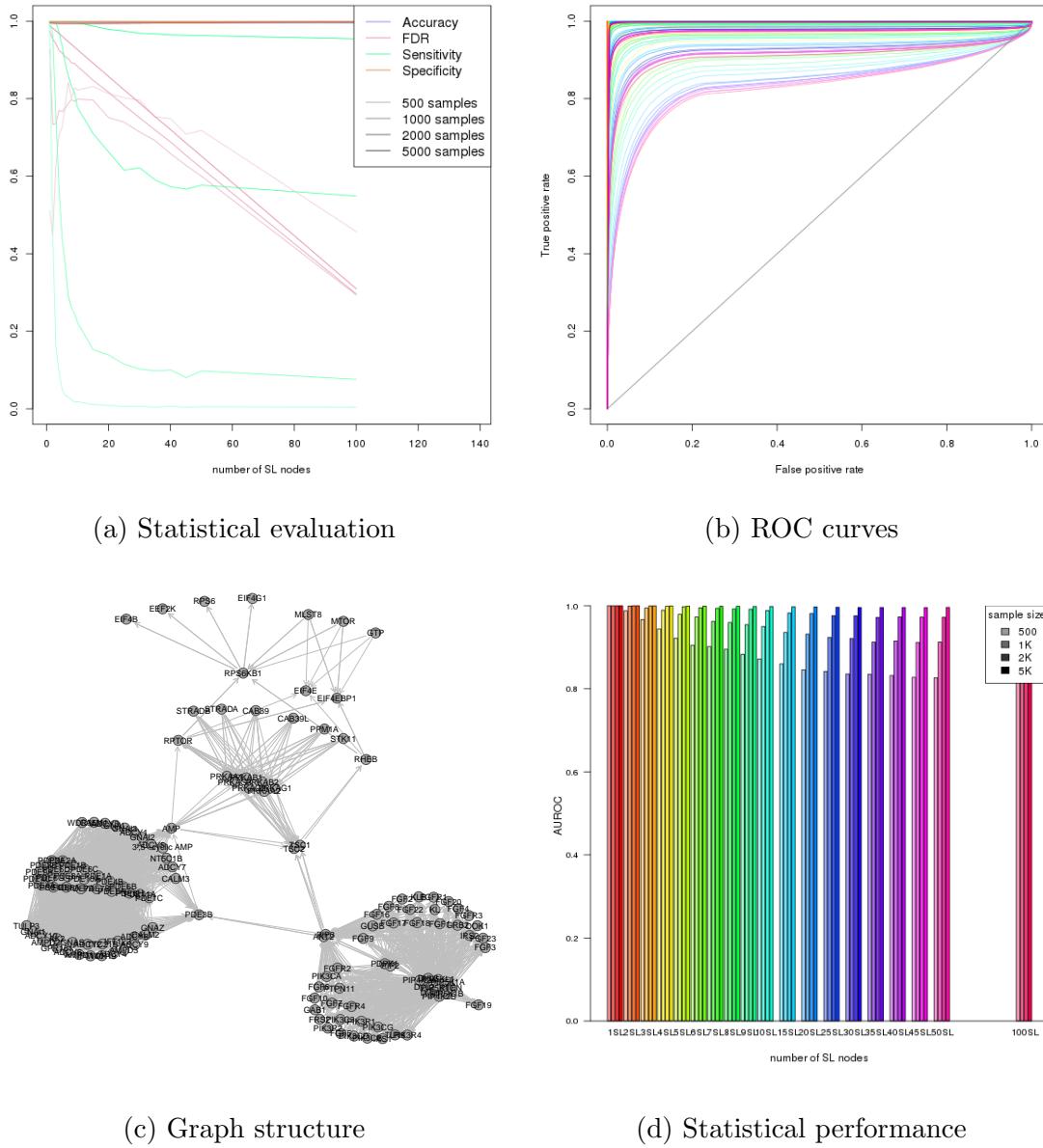


Figure J.19: Performance of simulations including the PI3K cascade. Simulation of synthetic lethality was performed by sampling from a multivariate normal distribution (without correlation structure apart from the Reactome PI3K cascade). Performance of SLIPT was high across parameters for detecting synthetic lethality in the graph structure within a larger dataset. The sensitivity decreases for a greater number of true positives to detect but the specificity remains high with a low false positive rate.

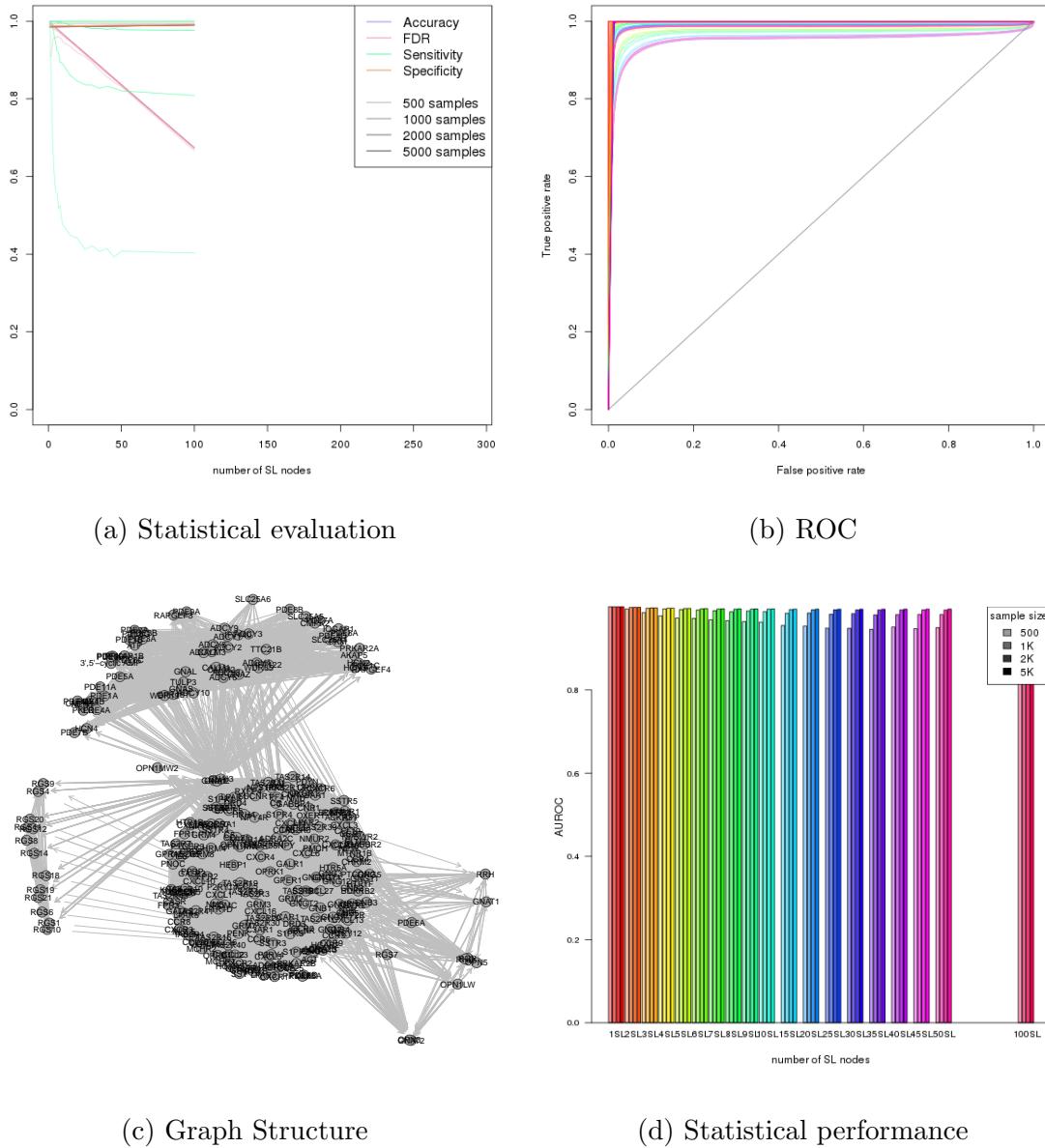


Figure J.20: Performance of simulations including the $G_{\alpha i}$ signalling pathway. Simulation of synthetic lethality used a multivariate normal distribution (without correlation structure apart from the Reactome $G_{\alpha i}$ signalling pathway. Performance of SLIPT was high across parameters for detecting synthetic lethality in the graph structure within a larger dataset. The sensitivity decreased for a greater number of true positives to detect but the specificity remained high with a low false positive rate.