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Glossary

allele	A gene variant with a specific sequence and phenotype.
driver mutation	A mutation which promotes cancer growth.
E-cadherin	Epithelial cadherin (calcium-dependent adhesion), a cell-adhesion protein encoded by <i>CDH1</i> .
essential	A gene which is required to be functional or expressed for a cell or organism to be viable, grow or develop.
functional redundancy	Genes which perform a common function, also known as genetic redundancy.
gene expression	A measure of the relative expression of each gene from the mRNA extracted from (pooled) cells.
genome	All of the DNA sequence in the genome.
genomic	The use of data from all genes in the genome.
germline mutation	A mutation that occurred in germline cells and is passed between generation.
graph or network	A mathematical structure modelling or depicting the relationships between elements.
hereditary	A trait or disease which has a genetic cause and is inherited from family members.
intrinsic subtype	Distinguishing cancer by molecular and genetic features.
metagene	A consistent signal of expression for a collection of genes such as a biological pathway, derived from singular value decomposition.

microarray	A high-throughput technique to measure presence or abundance of nucleic acid sequences from binding to probes.
mutant	A variant or dysfunctional phenotype arising from a mutation in a gene.
mutation	A change in DNA sequence that disrupts gene function.
non-oncogene addiction	The dependence of a cancer cell on functioning non-mutant genes.
oncogene	A gene that potentially causes cancer, typically by over-expression or mutant gene variants.
pathway	A series of biomolecules that produces a particular product or biological function.
RNA-Seq	The generation of transcriptome data from sequencing RNA.
somatic mutation	A mutation that occurs in somatic cells, during a patient's lifespan.
sporadic cancer	Cancers which do occur in patients with a family history or carry a high-risk genetic variant.
synthetic lethal	Genetic interactions where inactivation of multiple genes is inviable (or deleterious) which are viable if inactivated separately.
tumour suppressor	A gene potentially causes cancer, typically by disruption of functions which protect the cell from cancer.
wild-type	A natural phenotype of a trait or the normally functional allele which encodes it.

Acronyms

ANOVA	Analysis of Variance.
DNA	Deoxyribonucleic Acid.
FDR	False Discovery Rate.
GPCR	G Protein Coupled Receptor.
HDGC	Hereditary Diffuse Gastric Cancer.
mRNA	Messenger RNA.
mtSLIPT	Synthetic Lethal Interaction Prediction Tool (against mutation).
PAM50	Prediction Analysis of Microarray 50.
PI3K	Phosphoinositide 3-kinase.
RNA	Ribonucleic Acid.
RNAi	RNA Interference.
siRNA	Short Interfering RNA.
SLIPT	Synthetic Lethal Interaction Prediction Tool.
TCGA	The Cancer Genome Atlas (genomics project).

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 [The Cancer Genome Atlas \(TCGA\) 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 [hereditary diffuse gastric cancer \(HDGC\)](#) 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 [pathways](#) 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 over-representation 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 [pathways](#) 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 Appendix Table C.1, 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 (False discovery rate (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* 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 4.2. These include ribosomal subunits, initiation, peptide elongation, and 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 4.2: 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.2). 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 trans-

lational and immune [pathways](#) not detected in the isolated experimental system. [G protein coupled receptors](#) 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, 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 [RNA interference \(RNAi\)](#) 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 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, estrogen receptor 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

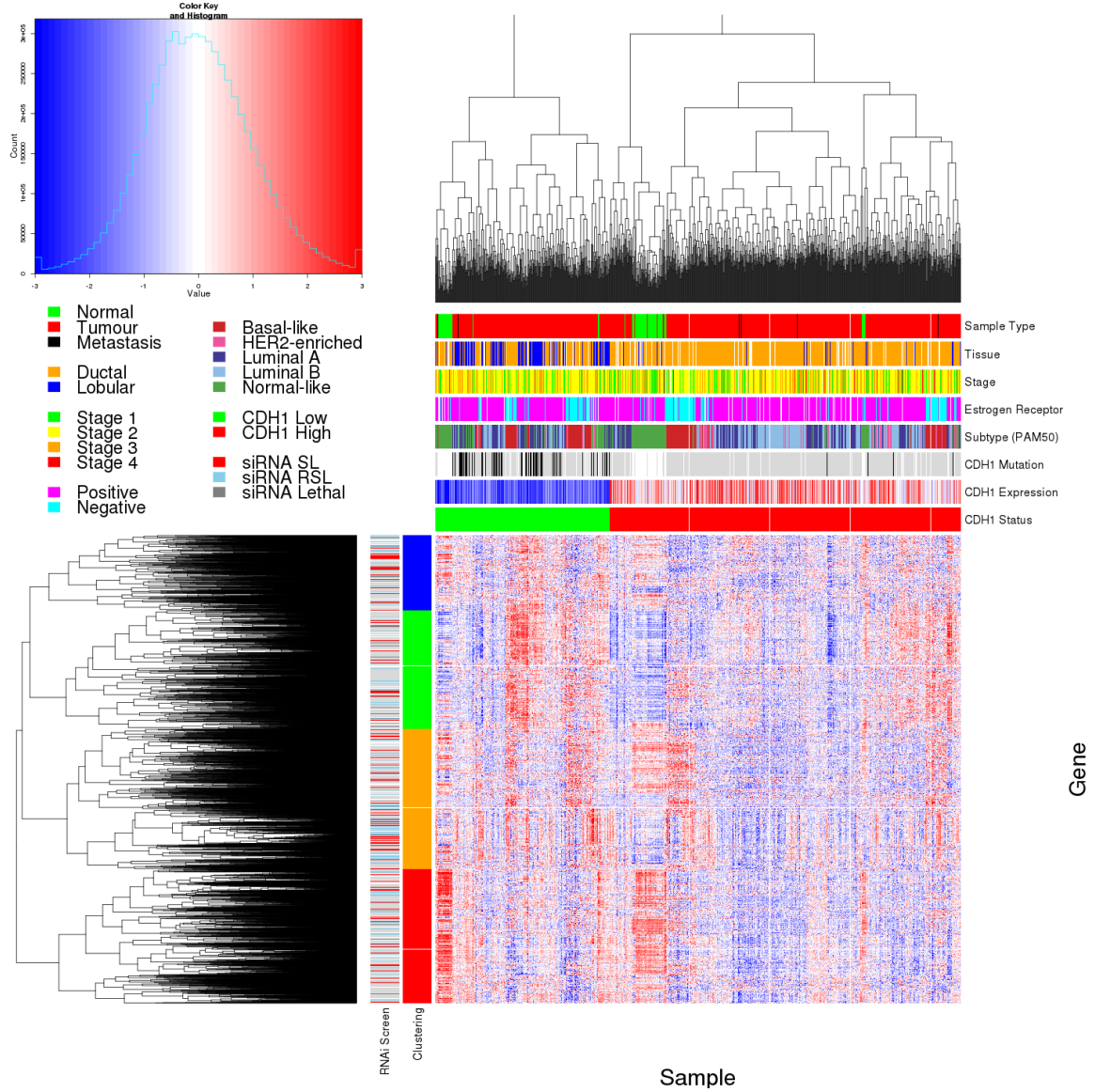


Figure 4.1: **Synthetic lethal expression profiles of analysed samples.** Gene expression profile heatmap (correlation distance, complete linkage) of all samples (separated by the $1/3$ quantile of *CDH1* expression) analysed in TCGA breast cancer dataset for gene expression of 5165 candidate partners 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 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.

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 to the [expression](#) analysis the (predominantly ductal *CDH1* [wild-type](#)) basal-like subtype and estrogen receptor negative samples had depleted [expression](#) among most candidate [synthetic lethal](#) partners. This is consistent with [synthetic lethal](#) interventions only being effective in lobular estrogen receptor 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 (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). Conversely, 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 commons. Using [expression](#) as a measure of gene

function also avoids the assumptions that **mutations** are **somatic**, rather than **germline mutation**, and that gene inactivation occurs by detectable **mutations**, rather than other mechanisms such as epigenetic changes. These may also account for some of the lowly expressing *CDH1* **wild-type** samples clustering with similar profiles to **mutant** samples.

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 **pathways** 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 $1/3^{\text{rd}}$ 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 estrogen receptor status and **intrinsic subtypes**, from the **Prediction Analysis of Microarray 50 (PAM50)** procedure (Parker *et al.*, 2009) shown in Figure 4.1.

As shown by the most over-represented **pathways** in Table 4.3, 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 (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 extracel-

Table 4.3: 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}
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 [pathways](#) over-representation p-value (adjusted by FDR) from the hypergeometric test.

lular 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.3. 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 4.3 and Appendix Table C.3) 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 (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, although there were exceptions to this trend and larger positive correlations than negative correlations. The majority of [SLIPT](#)

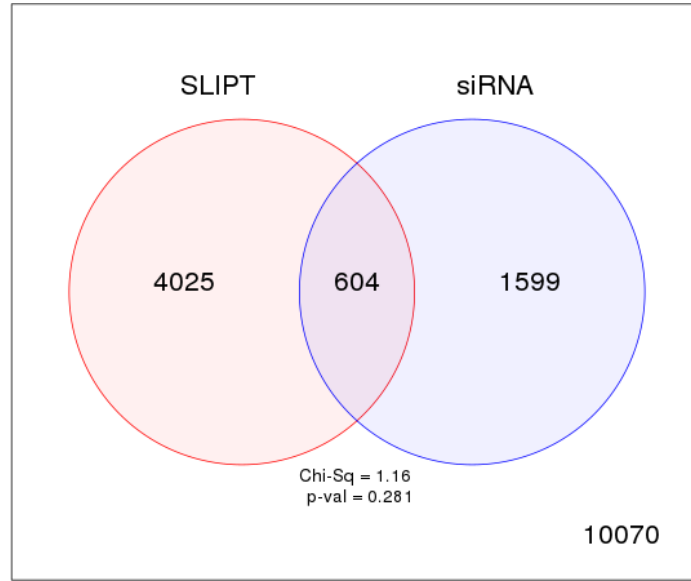


Figure 4.2: **Comparison of SLIPT with siRNA.** Testing the overlap of gene candidates for *E-cadherin* synthetic lethal partners between computational (SLIPT) and experimental screening (siRNA) approaches. The χ^2 test suggests that the overlap is no more than would be expected by chance ($p = 0.281$).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

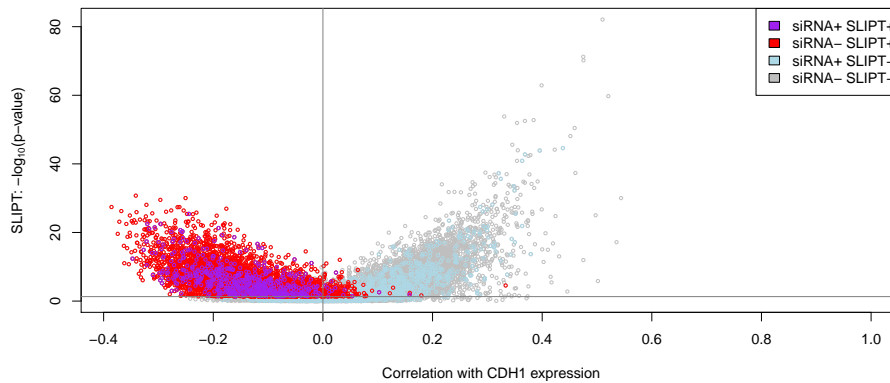


Figure 4.3: **Comparison of SLIPT and siRNA genes with correlation.** The χ^2 p-values for genes tested by SLIPT (in TCGA breast cancer) expression analysis were compared against Pearson correlation of gene expression with *CDH1*. Genes detected by SLIPT or siRNA are coloured according to the legend.

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 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 correlations. The SLIPT methodology has 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.

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 4.4). 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).

Table 4.4: 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.

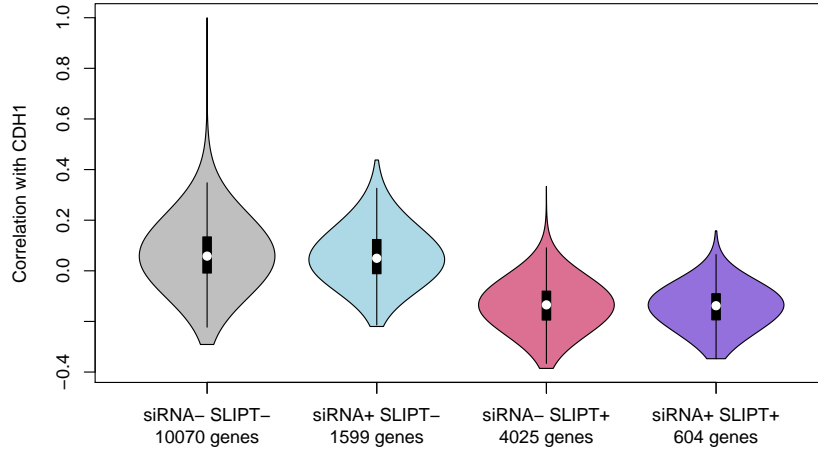


Figure 4.4: **Comparison of SLIPT and siRNA genes with correlation.** Genes detected as candidate **synthetic lethal** partners by SLIPT (in TCGA breast cancer) **expression** analysis and experimental screening (with siRNA) were compared against Pearson correlation of **gene expression** with *CDH1*.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

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. These 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

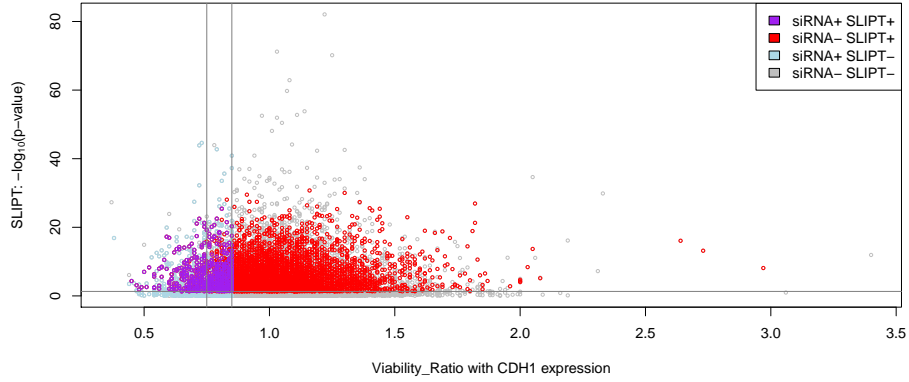


Figure 4.5: **Comparison of SLIPT and siRNA genes with screen viability.** The χ^2 p-values (log-scale) for genes tested by SLIPT (in TCGA breast cancer) were compared against the viability ratio of *CDH1* mutant and wild-type cells in the primary siRNA screen. Genes detected by SLIPT or siRNA are coloured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

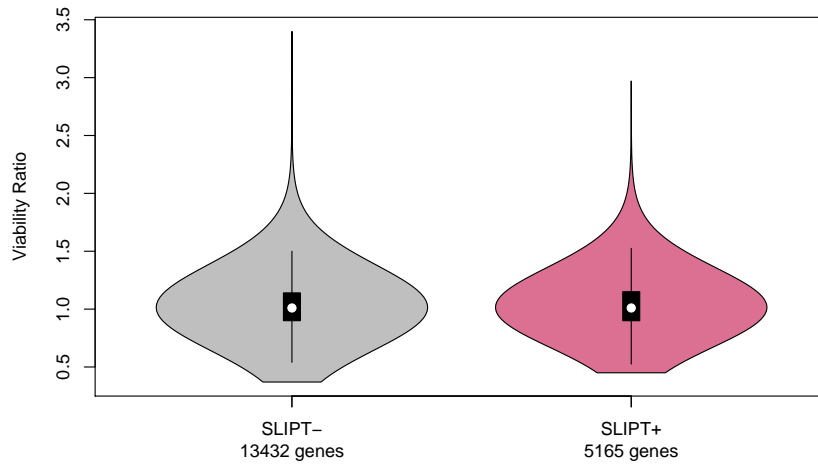


Figure 4.6: **Comparison of SLIPT genes with siRNA screen viability.** Genes detected as candidate synthetic lethal partners by SLIPT (in TCGA breast cancer) expression analysis were compared against the viability ratio of *CDH1* mutant and wild-type cells in the primary siRNA screen. There were clear no differences in viability between genes detected by SLIPT and those not detected. 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).

(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**.

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 **genomes**-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 more 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 4.5, 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.

Table 4.5: Comparison of SLIPT genes against secondary siRNA screen

		Secondary Screen					
siRNAs*		0/4	1/4	2/4	3/4	4/4	Total
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)

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 gene detected by either method. The genes detected by both approaches may therefore be more informative at the pathways level, where it is less likely for a pathways 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.

4.2.5 Comparison to Primary Screen at Pathway Level

These pathways 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 4.6). 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 4.2 and in the clustering analysis (Table 4.3). 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 com-

Table 4.6: 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 _{αs} signalling events	159	26	6.7×10^{-23}
Gastrin-CREB signalling pathways via PKC and MAPK	180	27	2.0×10^{-21}
G _{αi} 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}
DAPI2 interactions	159	23	2.6×10^{-19}
DAPI2 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 _{αs} 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}
DAPI2 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}

putational 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 $G_{\alpha s}$ signalling events ($p = 1.7 \times 10^{-7}$), than other signalling **pathways**.

The **pathways** analysis for **mtSLIPT** against *CDH1* **mutations** (in Table C.4) 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 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 (in Figure 4.2) and does not preclude **pathways** relationships being supported by resampling.

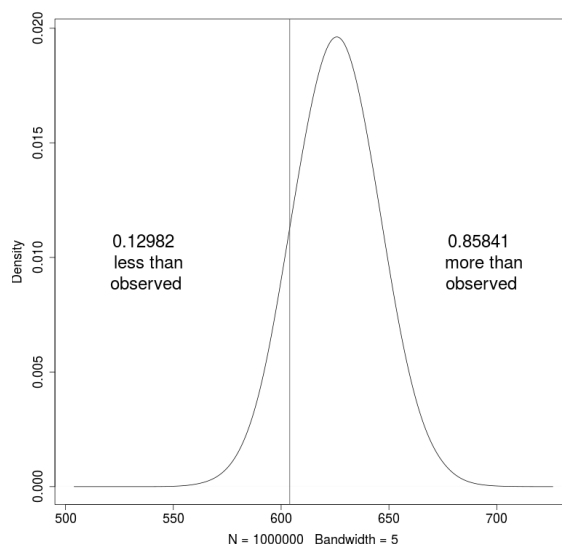


Figure 4.7: **Resampled intersection of SLIPT and siRNA candidate genes.** Resampling analysis of intersect size from genes detected by **SLIPT** and **siRNA** screening approaches over 1 million replicates. The proportion of expected intersection sizes for random samples below or above the observed 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 4.6. The resampling analysis for pathways was compared to the pathways over-representation for SLIPT predicted synthetic lethal partners in Table 4.7. Similarly, the pathways resampling for intersection between SLIPT predictions and experimental screen candidates was compared to pathways over-representation in Table 4.8 for intersection with siRNA data.

The pathways resampling approach for SLIPT-specific gene candidates (Table 4.7) 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 4.7: 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}	$< 1.241 \times 10^{-5}$
Extracellular matrix organisation	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
GPCR downstream signalling	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 4.8: Pathways for *CDH1* partners from SLIPT and siRNA primary screen

Reactome Pathway	Over-representation	Permutation
Visual phototransduction	6.9×10^{-10}	0.91116
G_{as} 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
Acyl 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
Acyl 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
Acyl 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
Syndecan interactions	0.00016	0.3974
Class A/1 (Rhodopsin-like receptors)	0.00016	0.99454
HS-GAG biosynthesis	0.0002	0.37199
Platelet degranulation	0.0002	0.39003
EPH-ephrin mediated repulsion of cells	0.00021	0.6193

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 4.7. 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.5). 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 for consistent detection of [pathways](#) was independent of their pre-existing status as experimental candidates. In contrast to the SLIPT [pathways](#) (in Table 4.7), the [pathways](#) results for these candidate partners (in Table 4.8) 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 C.6), 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 4.8 and Appendix Table C.6) when the initial [pathways](#) over-representation test was not significant. These functions appear

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 [genomes](#)-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 4.8). 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 4.6) and was supported by resampling analysis (Table 4.8), despite a modest intersection of genes between them (Figure 4.2). Either approach may be significant for a [pathways](#) 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 4.9. In particular, translational [pathways](#) were replicated as observed in Table 4.2. 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 4.9: 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 [pathways](#), 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 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 $G_{\alpha s}$ 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. The accompanying data for [SLIPT](#) analysis against *CDH1* expression is provided in Appendix F.

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 F.1) did not necessarily directly correspond to those observed in breast cancer (shown in Appendix 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 F.2) which replicated the translational and immune [pathways](#) observed in [TCGA](#) breast cancer (shown in Table 4.2) and further supported [GPCR](#) signalling [pathways](#), including the class A/1 receptors. The extracellular matrix was also detected at the [pathways](#) 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 F.6) replicate those detected in breast cancer (shown in Table 4.8). 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. The include $G_{\alpha s}$ signalling and elastic fibre formation as discussed for breast cancer (in Section 4.2.5.1).

4.5 Discussion

4.5.1 Strengths of the SLIPT Methodology

Synthetic lethal discovery with [SLIPT](#) used established statistical procedures to identify putative partner genes from [gene expression](#) data. Such use of the χ^2 -value is amenable to [pathways](#) or permutation analyses and could feasibly be applied to other disease gene or pair-wise across the [genomes](#), although previous [genomes](#)-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), with other cancer genes, such as *CDH1*, requiring more focused investigations. 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 they either do not have a released code implementation or do not make predictions solely from normalised [expression](#) data.

The query-based approach demonstrated by [SLIPT](#) analysis is suitable for wider application on [expression](#) data and for augmenting experimental studies such as high-throughput screens. This approach has identified biologically plausible [synthetic lethal pathways](#) for *CDH1*, triaged candidates from experimental screening (Telford *et al.*, 2015), and replicates genes and [pathways](#) across breast and stomach cancer datasets. In addition, [SLIPT](#) avoids critical 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.

The DAISY methodology Jerby-Arnon *et al.* (2014), which took a similar query-based approach with the [tumour suppressor](#) *VHL*, has been critiqued for being too stringent (Lu *et al.*, 2015) which impedes [pathways](#) analysis. Since [functional redundancy](#) does not require genes to be expressed at the same time, the [SLIPT](#) approach does not assume co-expression of [synthetic lethal](#) genes which may enrich for [syn-](#)

thetic lethal genes in established coregulated pathways. Rather, the interpretation of synthetic lethality for SLIPT was similar to other computational 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 where working with gene-pairs scale up the number of multiple tests drastically, at the expense of statistical power. Experimental screens for synthetic lethality are also error-prone (Fece de la Cruz *et al.*, 2015; Lord *et al.*, 2015; Lu *et al.*, 2015), especially with false-positives, raising the need for understanding the expected behaviour and number of functional relationships and genetic interactions in the genomes, or in discovery of synthetic lethal partners of a particular query gene. Thus analyses throughout this thesis have focused on querying for partners of a particular gene of interest. Statistical modelling and simulations (in Section 3.3 and Chapter 6) will further support 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 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; Kelly, 2013; Lu *et al.*, 2015). The predicted synthetic lethal partners of *CDH1* (with FDR correction) were investigated with gene expression profiles and clinical variables to find relationships in gene expression, gene function, and clinical characteristics. The large number of genes detected indicates that synthetic lethal detection is potentially error-prone, and that identifying genes relevant for clinical application will be difficult without a supporting biological pathways 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 pathways level throughout this Chapter. Similarly, comparisons across analyses were largely made at the pathways level, including comparisons between expression and mutation, breast and stomach TCGA datasets.

Potential synthetic lethal partners of *CDH1* identified by SLIPT had many distinct functions, with each gene cluster highly expressed in different patient subgroups (Figure 4.1). The expression profiles of the SL partners of *CDH1* predicted from TCGA breast cancer RNA-Seq data (expected to have compensating high or stable expression)

and their corresponding functional enrichment found in subgroups of genes, particularly among *CDH1* low breast tumours. Ductal breast cancers showed higher [expression](#) of [synthetic lethal](#) partners, suggesting treatment may be more effective in this tumour subtype. However, there was consistently low [expression](#) of SL partners in estrogen receptor negative tumours, although this is independent of tumour stage and consistent with poor prognosis in these patients and could inform other treatment strategies or prevent ineffective treatment further impacting quality of life in these patients. These results suggest that [synthetic lethal](#) partner [expression](#) varies between patients; that these different tumour classes would react differently to the same treatment; that treatment of different [pathways](#) and combinations in different patients is the most effective approach to target genes compensating for *CDH1* gene loss; and that the [expression](#) of synthetic partners could be a clinically important biomarker.

The [pathways](#) that [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 downstream targets (not detected by siRNA), 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 predicted [synthetic lethal](#) partners occurred across functionally distinct [pathways](#), including characterised functions of *CDH1*. The most consistently supported [pathways](#) included elastic fibres in the extracellular matrix, GPCR signalling, and translation presenting vulnerabilities for *CDH1* deficient cancer cells from extracellular stimuli to the core growth mechanisms of a cell.

This 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 further 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 into their relation to [pathway](#) structure. While these are important clinical implications, the [synthetic lethal](#) predictions lack enough confidence for direct translation into pre-clinical models or clinical applications leading to a need for statistical modelling and simulation of [synthetic lethality](#) in [genomics expression](#) data.

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.

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 informative with over-representation (Table 4.6) and supported by resampling analysis (Table 4.8), despite a modest intersection of genes between them (Figure 4.2). Either approach may be significant for a [pathways](#) 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 for a candidate [pathways](#).

The [pathways](#) detected by both over-representation and resampling are the strongest candidates for further investigation and 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 [pathways metagenes](#). In addition to GCPR [pathways](#) detected across these analyses, the [phosphoinositide 3-kinase \(PI3K\)](#) cascade will also be investigated in Chapter 5, this signalling [pathways](#) is a well characterised mediator between GCPR receptors and regulation of translation (Gao and Roux, 2015) (both detected throughout this Chapter) and exhibited unexpected behaviour with [pathways](#) the [metagenes](#) (in Section D). This [pathways](#) is activated by protein phosphorylation states and thus inactivation may not be detectable with [expression](#).

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

Furthermore, [synthetic lethal](#) partners identified by [SLIPT](#) were replicated across breast and stomach cancer. These were particularly concordant at the [pathways](#) 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 supports that the subset of [synthetic lethal](#) functions detectable in experimental models ([Chen *et al.*, 2014](#); [Telford *et al.*, 2015](#)) would be applicable 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. These [pathways](#) were more consistent across replication analyses than previous investigations with [TCGA microarray](#) data ([Kelly, 2013](#)).

4.6 Summary

We have developed a simple, interpretable, computational approach to predict [synthetic lethal](#) partners from [genomics](#) data. The analyses focus on [gene expression](#) data as it is widely available for applications in other cancers and other disease genes, particularly those with malignant loss of function.

This approach has been applied to robustly detect [synthetic lethal pathways](#) for [E-cadherin](#) (the *CDH1* gene) in [TCGA](#) breast cancer molecular profiles, with comparisons to experimental screening ([Telford *et al.*, 2015](#)) in cell lines and replication 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 translation processes crucial for the growth and proliferation of cancer cells. These [pathways](#) show evidence of [non-oncogene addiction](#) for *CDH1* deficient cells, which presents vulnerabilities that could

be exploited for specific treatment against *CDH1* mutations in HCGC and sporadic cancers. There was also support for synthetic lethal pathways with *CDH1* in cell adhesion and cytoskeletal processes to which *CDH1* belongs, 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. Furthermore, many 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 in combination with experimental screening.

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. While the genes identified between these analyses were less concordant the results of the TCGA breast cancer analysis will be used to test pathway structure relationships and further examine the synthetic lethal genes detected in the following Chapter.

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