Comparative analysis of network-based measures for the assessment of drug-induced liver injury: A case study of *Hypericum perforatum*

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Abstract

Network proximity is widely used to prioritize compound–disease associations, yet proximity Z-scores are sensitive to target set size, network density, and network construction parameters. While often interpreted as functional indicators, these metrics are susceptible to inferential instability, where ranking significance is driven by target-count-dependent null distributions rather than physical reachability.

Here, we systematically evaluate the robustness of proximity-based and influence-based metrics using a liver-expressed human protein–protein interaction network. Using two constituents of *Hypericum perforatum* as a controlled comparison, we show that proximity-based rankings are unstable and threshold-dependent. Although Quercetin (62 targets) achieves higher proximity Z-scores than Hyperforin (10 targets) in high-confidence networks, this significance is an artifact of the law of large numbers acting on the null distribution. In physical distance space, Hyperforin is closer to drug-induced liver injury (DILI) genes, a ranking that is stably captured by random walk–based influence propagation.

We quantify this disparity by calculating the average influence per target, revealing that Hyperforin achieves 3.7-fold greater efficiency in DILI-module perturbation than Quercetin. This efficiency advantage remains robust across topology-only and expression-weighted analyses, as well as bootstrap resampling and chemical similarity controls. Our results demonstrate that proximity Z-scores may lead to misleading prioritizations when target set sizes differ, and that influence-based propagation provides a more robust and theoretically consistent framework for network toxicology. More broadly, this work provides a methodological template for identifying and correcting metric artifacts in polypharmacological

risk assessment.

Keywords: network propagation, proximity metrics, metric robustness, drug-induced liver injury, polypharmacology, Z-score confounding, per-target influence.

1 Introduction

Network-based drug safety assessment commonly utilizes proximity to disease-associated genes as a prioritization criterion, assuming that compounds with more targets or closer network positions pose greater risk [Hopkins, 2008, Barabási et al., 2011, Guney et al., 2016, Menche et al., 2015]. This intuition is attractive due to its computational simplicity and interpretability. However, proximity rankings are typically reported as Z-scores relative to degree-matched null models. While Z-scores are intended to quantify statistical significance, they are fundamentally sensitive to target set size: as the number of targets increases, the variance of the null distribution decreases (the Law of Large Numbers), leading to inflated significance for compounds with broad polypharmacology. Whether such "inferential significance" reflects true biological influence, or whether it introduces systematic bias into toxicological prioritization, remains a critical question.

Hypericum perforatum (St. John's Wort) offers a sharp stress test for this question. The extract contains two bioactive constituents with contrasting pharmacological profiles: Hyperforin (10 validated targets, potent PXR activator) and Quercetin (62 targets, broad polypharmacology) [Nahrstedt and Butterweck, 1997, Moore et al., 2000, Boots et al., 2008]. Conventional network analysis, relying on proximity Z-scores, would predict greater DILI-associated risk for Quercetin despite Hyperforin's well-established role in clinical hepatotoxicity through PXR-mediated enzyme induction. This system therefore allows us to evaluate whether proximity-based prioritization is stable across network construction parameters or whether it is confounded by target-count artifacts.

In this study, we systematically evaluate the robustness of proximity-based and influence-based metrics. We demonstrate that proximity Z-scores yield unstable, threshold-dependent rankings that are driven by null-distribution tightening rather than physical distance. To resolve this, we utilize random walk–based influence propagation, which integrates over all paths weighted by transition probability and captures signal amplification through regulatory hubs [Köhler et al., 2008]. We utilize per-target normalization of influence mass to quantify perturbation efficiency, and use bootstrap resampling to exclude target-count confounding. Our results demonstrate that influence-based propagation provides a more stable and mechanistically aligned framework for comparative network toxicology, particularly when

comparing compounds with asymmetric target sets.

2 Results

2.1 Proximity Z-scores are confounded by target set size

We first established network context by quantifying target count and shortest-path proximity to 82 DILI-associated genes (Figure 1). Quercetin engages 62 targets in the liver-expressed largest connected component; Hyperforin engages 10. At STRING confidence ≥900, Hyperforin targets are physically closer to DILI genes ($d_c = 1.30$) than Quercetin targets ($d_c = 1.68$; Table 1). However, the proximity Z-scores yield the opposite ranking: Quercetin achieves $Z = -5.44$ ($p < 0.001$), while Hyperforin achieves $Z = -3.86$ ($p < 0.001$). All reported associations survived Benjamini–Hochberg FDR correction ($q < 0.05$).

This discrepancy highlights a fundamental confounder in proximity Z-scores: the law of large numbers. As target set size increases, the variance of the null distribution decreases ($\sigma_{null} = 0.09$ for Quercetin vs 0.24 for Hyperforin), inflating the significance of broader target sets despite greater physical distance. This statistical artifact suggests that Quercetin poses greater risk, whereas the physical topology favors Hyperforin.

2.2 Influence-based rankings are stable and resolve the confound

Random walk with restart (RWR) stabilizes this ranking by integrating over all paths (Figure 2). Hyperforin achieves influence $Z = +10.12$ ($p < 0.001$); Quercetin achieves $Z = +4.55$ ($p < 0.001$; Table 1). Unlike proximity, influence Z-scores correctly reflect the topological advantage of Hyperforin's regulatory hub occupancy. The ranking remains consistent across topology-only and expression-weighted analyses, demonstrating that influence propagation is less susceptible to sample-size artifacts than shortest-path distance.

2.3 Expression weighting refines the signal

To assess whether the RWR signal persists under tissue-specific constraint, we applied expression-weighted influence propagation (EWI), weighting transitions by destination-node liver expression (Figure 3).

The Z-score differential narrows but remains substantial under expression weighting: Hyperforin $Z = +8.98$ ($p < 0.001$); Quercetin $Z = +5.79$ ($p < 0.001$). Hyperforin's advantage is driven primarily

by the PXR–CYP master regulatory axis, which remains highly active in liver tissue (e.g., CYP3A4 at 335 TPM). Quercetin's influence is moderated by its broad, diffuse target profile, which includes several high-expression nodes (e.g., CFB at 1,115 TPM) that do not converge on a DILI effector hub.

2.4 Normalizing for target count confirms Hyperforin's topological advantage

To resolve the target-count paradox, we computed per-target network influence (PTNI), reframing polypharmacology as an efficiency problem rather than a coverage problem (Figure 4; Table 2).

Compound	**Targets**	**PTNI (RWR)**	**PTNI (EWI)**	**Eff. Ratio***	**Rob. Ratio†**
Hyperforin	10	0.1138	0.1330	—	—
Quercetin	62	0.0322	0.0493	—	—
Fold difference	—	—	—	**3.5**×	**3.7**×

*Eff. Ratio: observed PTNI ratio. †Rob. Ratio: observed influence / size-matched bootstrap mean (N=10).

Each Hyperforin target contributes 3.7× more DILI-directed influence than each Quercetin target (robust ratio). This disparity indicates that Hyperforin's target positions are substantially higher leverage than those of Quercetin, achieving greater perturbation efficiency despite a 6-fold smaller target set.

2.5 Bootstrap resampling excludes target-selection bias

To rule out the possibility that Hyperforin's advantage arises from favorable target selection rather than strategic network positioning, we performed bootstrap sensitivity analysis (Figure 5). 100 random 10-target subsets were sampled without replacement from Quercetin's 62-target pool and scored by RWR.

Hyperforin's observed influence (0.1138) exceeds the entire bootstrap distribution from Quercetin (mean = 0.0308, 95% CI = [0.0160, 0.0542]; Table 3). The fold difference between Hyperforin and the bootstrap mean is 3.7×. This confirms that Hyperforin's advantage is not an artifact of target count; even when sampling equalized subsets from Quercetin's pool, no configuration matches Hyperforin's influence.

2.6 Ranking stability across network thresholds

The influence ranking is stable across network confidence thresholds (Table 6). Hyperforin ranks first in all RWR and EWI configurations at both $\geq$700 and $\geq$900 thresholds. Notably, the proximity ranking reverses between thresholds: at $\geq$700, Hyperforin is physically closer ($d_c = 0.60$ vs 1.34) and more "significant" ($Z = -6.04$ vs -5.46). At $\geq$900, Quercetin appears more "significant" ($Z = -5.44$ vs -3.86) despite being physically more distant (1.68 vs 1.30). This instability in proximity Z-scores—while influence rankings remain stable—demonstrates that influence-based metrics are more robust to network construction parameters.

2.7 Chemical similarity excludes structural confounding

To exclude the possibility that Hyperforin's network signal reflects structural similarity to known hepatotoxins, we performed chemical similarity analysis against the DILIrank reference set (Figure 6). Morgan fingerprints (ECFP4) revealed that neither compound exceeds the 0.4 Tanimoto threshold for structural analog detection. Notably, Quercetin exhibits higher structural similarity to DILI reference drugs yet lower network influence, reinforcing that the observed asymmetry is driven by network topology rather than chemical features.

3 Discussion

3.1 Robustness and the Z-score confound

The central finding of this study is the inherent instability of network proximity Z-scores when comparing compounds with asymmetric target set sizes. While proximity is often used for prioritization, we demonstrate that its significance rankings are fundamentally confounded by the law of large numbers. As the number of targets increases, the variance of the null distribution (σ_{null}) decreases, making even modest topological distances appear highly significant. This is clearly observed in our comparison: at STRING $\geq$900, Quercetin (62 targets) achieves a more significant proximity Z-score than Hyperforin (10 targets) despite being physically more distant ($d_c = 1.68$ vs 1.30). This statistical artifact disappears when considering influence-based metrics, which correctly identify Hyperforin as the high-leverage modulator.

Critically, the proximity Z-score ranking is threshold-dependent. At $\geq$700, Hyperforin is physically closer and more significant; at $\geq$900, the physical advantage persists, but the significance ranking reverses due to the tighter Quercetin null. This instability indicates that proximity Z-scores are unreliable for comparative prioritization. In contrast, influence-based rankings (RWR and EWI) remain stable across multiple STRING confidence tiers, correctly prioritizing the regulatory hub modulator (Hyperforin) in all configurations.

The mechanistic explanation for this robustness is that RWR integrates over *all* paths, capturing how signals amplify through hubs like PXR and AKT1. Shortest-path proximity, by contrast, is a descriptive metric for minimum reachability; treating it as an inferential surrogate for functional impact conflates topological context with biological consequence.

3.2 Expression weighting as a biological constraint

Expression-weighted influence (EWI) constrains signal propagation to liver-active nodes. By attracting signal to highly expressed proteins (destination-node weighting), we ensure that the network propagation reflects tissue-specific biology. Under this constraint, the Hyperforin advantage persists, demonstrating that its topological efficiency is not an artifact of an unconstrained PPI network but is supported by the expression profile of the liver. Attenuation of signal is expected when walks are constrained to active pathways; the fact that the ranking remains stable provides positive evidence for the biological relevance of the PXR axis.

3.3 Perturbation efficiency vs. topological coverage

By normalizing total influence for target set size (where the restart vector is already $|T|$-weighted), we provide a more balanced comparison of perturbation efficiency. Our results show that a single Hyperforin target exerts 3.7-fold more influence on the DILI module than a Quercetin target.

This efficiency claim is further validated by bootstrap sensitivity analysis. Even when sampling size-matched 10-target subsets from Quercetin's pool, none reached the influence level achieved by Hyperforin. This demonstrates that the advantage is not due to target count, but to the strategic network position of Hyperforin's targets—specifically their convergence on the PXR master regulator and downstream CYP effectors.

3.4 Mechanistic context: The PXR axis

The stability of the influence ranking aligns with the well-characterized PXR–CYP master regulatory axis. Hyperforin's primary target, NR1I2 (PXR), induces the expression of major xenobiotic metabolism enzymes including CYP3A4 and CYP2C9 [Moore et al., 2000, Watkins et al., 2001]. In our network analysis, these effectors are part of the target set and the DILI module, creating a high-connectivity hub structure that enables efficient propagation. Quercetin's 62 targets, while numerous, are distributed across redundant or peripheral pathways that do not converge on a regulatory bottleneck. Furthermore, clinical evidence indicates that Quercetin is not associated with hepatotoxicity and may exhibit hepatoprotective properties [Boots et al., 2008, National Institute of Diabetes and Digestive and Kidney Diseases, 2020]. Recent experimental studies have corroborated that St. John's wort exacerbates hepatotoxicity through precisely this PXR-mediated bioactivation mechanism [Chen et al., 2022].

3.5 Limitations and Conclusions

While our findings favor influence-based metrics, we acknowledge that network influence is a measure of topological reach and perturbation potential, not a direct surrogate for actual toxicological outcomes. This model is dose-independent and does not account for pharmacokinetics, binding affinity, or saturation kinetics. A high influence score indicates that a compound's targets are strategically positioned to modulate a disease module—representing a measure of systemic susceptibility—but the actual biological effect depends on the molecular mechanism of action (e.g., agonism vs. antagonism) and the kinetic context. In this study, we utilized *H. perforatum* as a known toxicological model to validate the *reliability* of the metrics themselves; the biological ground truth (Hyperforin-mediated PXR activation) allowed us to confirm that influence propagation correctly identifies high-leverage perturbations where proximity metrics fail. Future work integrating kinetic modeling or structural binding energy will be required to translate topological susceptibility into definitive risk predictions.

The methodological conclusion remains: proximity Z-scores are susceptible to sample-size confounding and should be used descriptively rather than for comparative inference. Influence-based propagation provides a more stable framework that survives robustness checks and aligns better with mechanistic reality.

In conclusion, we provide a methodological template for identifying and resolving metric artifacts in network

toxicology. By shifting the focus from topological coverage to perturbation efficiency, and from significance-driven Z-scores to robustness-checked influence, we enable more precise risk attribution in complex polypharmacological systems. Future research will focus on generalizing this framework across larger, diverse drug cohorts to explore the feasibility of establishing PTNI thresholds for risk classification. Furthermore, this work provides a foundation for developing network models with improved mechanistic interpretability. By integrating signed edge weights and transcriptometric data, future iterations of this framework could investigate phenotype-specific associations, potentially linking topological influence on specific biological sub-modules to discrete clinical outcomes such as cholestasis or steatosis. Such developments may further bridge the gap between network reachability and molecular pharmacology to enhance the transparency and predictive utility of high-throughput toxicological assessment.

4 Methods

4.1 Data sources

4.1.1 Protein–protein interaction network

Human protein–protein interactions were obtained from STRING v12.0 [Szklarczyk et al., 2023]. Combined confidence scores were computed per STRING methodology (text mining, experiments, databases, co-expression, neighborhood, gene fusion, co-occurrence). Only edges with combined confidence $\geq$900 (highest confidence tier) were retained. Raw network: 11,693 genes, 100,383 edges.

4.1.2 Liver expression data

Gene expression data were obtained from the Genotype-Tissue Expression Project (GTEx) v8 [GTEx Consortium, 2020]. Median transcripts per million (TPM) values for liver tissue were extracted from the 2017-06-05 release (RNASeQCv1.1.9). Genes with liver TPM $\geq$1 were retained. Result: 13,496 liver-expressed genes.

4.1.3 Drug-induced liver injury gene set

DILI-associated genes were obtained from DisGeNET [Piñero et al., 2020] curated gene-disease associations. Query: UMLS concept identifier C0860207 (Drug-Induced Liver Injury). Inclusion criterion: genes with curated evidence linking to DILI. Raw DILI gene count: 127 genes.

4.1.4 Hyperforin targets

Hyperforin targets were curated from primary literature sources [Moore et al., 2000, Watkins et al., 2001]. Sources included studies of PXR activation, CYP induction, and ABC transporter modulation. Raw target count: 14 proteins (Table 7).

4.1.5 Quercetin targets

Quercetin targets were retrieved programmatically from ChEMBL v31 [Mendez et al., 2019] via REST API. Query: CHEMBL159 (Quercetin). Filter: human targets with experimentally validated bioactivity (IC_{50}, K_i, or $EC_{50} \leq 10\ \mu M$). Raw target count: 122 proteins.

4.2 Target processing

Protein identifiers were mapped to HUGO gene symbols using STRING info files and UniProt [UniProt Consortium, 2023]. Non-human proteins (mouse, rat, bacterial, viral) were excluded. Gene symbols were standardized (e.g., MDR1 $\rightarrow$ ABCB1). Processed target counts: Hyperforin = 14, Quercetin = 87.

4.3 Network construction

The STRING network was filtered to genes with liver expression ≥ 1 TPM (GTEx v8). The largest connected component (LCC) was extracted using NetworkX [Hagberg et al., 2008]. Compound targets and DILI genes not present in the LCC were excluded. Final network: 7,677 nodes, 66,908 edges. Final target counts: Hyperforin = 10, Quercetin = 62. Final DILI gene count: 82.

Five genes are targeted by both compounds: ABCG2, AKT1, CYP3A4, MMP2, MMP9. These were retained in both target sets.

4.4 Shortest-path proximity (descriptive)

Mean minimum shortest-path distance from compound targets T to DILI genes D:

$$d_c = \frac{1}{|T|} \sum_{t \in T} \min_{d \in D} \text{dist}(t, d) \tag{1}$$

where $\text{dist}(t, d)$ is the unweighted shortest-path length in the LCC. Shortest-path proximity is a descriptive metric. It was used to provide network context, not to test influence.

4.5 Random walk with restart

Influence propagation was quantified using random walk with restart (RWR) [Köhler et al., 2008, Guney et al., 2016]. Given adjacency matrix $\mathbf{A}$, the column-normalized transition matrix $\mathbf{W}$:

$$W_{ij} = \frac{A_{ij}}{\sum_k A_{kj}} \tag{2}$$

Steady-state probability vector $\mathbf{p}$ satisfies:

$$\mathbf{p} = (1 - \alpha)\mathbf{W}\mathbf{p} + \alpha \mathbf{p}_0 \tag{3}$$

Restart probability: $\alpha = 0.15$. Restart vector: $p_0(i) = 1/|T|$ for $i \in T$, else 0. Convergence criterion: $||\mathbf{p}^{(k+1)} - \mathbf{p}^{(k)}||_1 < 10^{-6}$. Maximum iterations: 100.

Total DILI influence:

$$I = \sum_{d \in D} p(d) \tag{4}$$

4.6 Permutation testing

Null distributions were generated by sampling 1,000 random target sets. Degree matching: each random target was sampled from nodes with degree within $\pm 25\%$ of the original target's degree. To prevent hash randomization artifacts, target lists were sorted alphabetically before assignment. Z-score:

$$Z = \frac{x_{\text{obs}} - \mu_{\text{null}}}{\sigma_{\text{null}}} \tag{5}$$

P-values were computed as the fraction of permuted values $\geq$ the observed value (one-tailed). P-values at the permutation floor ($<$1/1000) are reported as $p < 0.001$. Multiple testing correction: Benjamini–Hochberg FDR. Random seed: 42.

4.7 Expression-weighted influence

Edge weights were modified by destination-node liver expression:

$$W'_{ij} = \frac{A_{ij} \cdot e_i}{\sum_k A_{kj} \cdot e_k} \tag{6}$$

where e_i is the normalized liver expression for gene i (GTEx v8 liver). Liver TPM values were log-transformed ($\log_2(\text{TPM} + 1)$) and min-max normalized to $[0, 1]$ across the network. A minimum expression floor of 0.01 was applied to ensure all nodes remained reachable. Attracting signal to highly-expressed nodes constrains RWR propagation to biologically active pathways in the liver. All other RWR parameters were identical. Random seed: 42.

4.8 Influence normalization to average perturbation efficiency

$$\text{PTNI} = I \tag{7}$$

where I is the total steady-state probability mass on DILI genes from a uniform restart vector. Because the restart vector is defined as $1/|T|$ for $i \in T$ (Eq. 75), the resulting mass I is inherently the average influence per target. This normalization (hereafter termed per-target network influence, PTNI) serves as an effect-size adjustment that allows for direct comparison of perturbation efficiency between compounds with asymmetric target sets. PTNI was not subjected to independent permutation testing.

4.9 Bootstrap sensitivity analysis

To assess whether target count explains the observed ranking: 100 random 10-target subsets were sampled without replacement from Quercetin's 62-target pool. Each subset was scored by standard RWR. Summary statistics: mean, standard deviation, 95th percentile. The observed Hyperforin influence was compared to the bootstrap distribution. Random seed: 42.

4.10 Chemical similarity analysis

Structural similarity to known hepatotoxins was assessed to exclude confounding by chemical class. Morgan fingerprints (ECFP4; radius = 2, 2048 bits) were generated using RDKit v2023.03 [RDKit, 2023]. Reference set: DILIrank 2.0 drugs with retrievable SMILES (542 DILI-positive, 365 DILI-negative). SMILES were retrieved via PubChem REST API. Tanimoto coefficient:

$$\text{Tanimoto}(A,B) = \frac{|A \cap B|}{|A \cup B|} \tag{8}$$

Maximum similarity across the reference set was reported for each compound. Structural analog threshold: Tanimoto > 0.4 [Maggiora et al., 2014].

4.11 Software and reproducibility

Python 3.10, NetworkX 3.1 [Hagberg et al., 2008]; R 4.3, igraph 1.5. All random seeds fixed at 42. Target lists sorted alphabetically before processing.

4.12 Code and data availability

All code: `https://github.com/antonybevan/h-perforatum-network-tox`

Data sources:

- STRING v12.0: `https://string-db.org`
- GTEx v8: `https://gtexportal.org`
- ChEMBL v31: `https://www.ebi.ac.uk/chembl`
- DILIrank 2.0: `https://www.fda.gov/science-research/ltkb`

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Tables

Table 1: **Network metrics reveal the instability of proximity Z-scores.** While Quercetin achieves more significant proximity Z-scores due to tighter null distributions, Hyperforin is physically closer (d_c) to DILI genes. Influence-based metrics resolve this confounding and stably prioritize Hyperforin. Network: STRING v12.0 LCC (confidence $\geq$900) filtered to liver-expressed genes.

Metric	Compound	Targets	Observed	Z	p	PTNI
Tier 1: Shortest-path proximity						
	Hyperforin	10	$d_c = 1.30$	-3.86	$< 0.001^*$	—
	Quercetin	62	$d_c = 1.68$	$\mathbf{-5.44}$	$< 0.001^*$	—
	Instability: Quercetin is physically more distant yet more "significant"					
Tier 2: Random walk influence (RWR)						
	Hyperforin	10	0.1138	**+10.12**	$< 0.001^*$	0.1138
	Quercetin	62	0.0322	+4.55	< 0.001	0.0322
	Resolution: Correctly prioritizes physical proximity and regulatory hub modulation					
Tier 3: Expression-weighted influence (EWI)						
	Hyperforin	10	0.1330	**+8.98**	$< 0.001^*$	0.1330
	Quercetin	62	0.0493	+5.79	< 0.001	0.0493

*At permutation floor ($<$1/1,000).
PTNI = per-target network influence; RWR = random walk with restart; EWI = expression-weighted influence; d_c = mean minimum shortest-path distance; DILI = drug-induced liver injury. All associations survived Benjamini–Hochberg FDR correction ($q < 0.05$).

Table 2: **Per-target influence efficiency.** PTNI quantifies average influence per target, reframing polypharmacology as an efficiency problem. Hyperforin targets are 3.7-fold more efficient at perturbing the DILI module than Quercetin targets.

Analysis	Hyperforin PTNI	Quercetin PTNI	Efficiency Ratio*	Robust Ratio†
RWR (topology-only)	0.1138	0.0322	**3.5**$\times$	**3.7**$\times$
EWI (expression-weighted)	0.1330	0.0493	**2.7**$\times$	—

*Efficiency Ratio = Observed PTNI ratio. †Robust Ratio = Observed influence / size-matched Bootstrap Mean (N=10). PTNI = per-target network influence; RWR = random walk with restart; EWI = expression-weighted influence.

Table 3: **Bootstrap sensitivity excludes target-count confounding.** Random 10-target subsets ($n = 100$) sampled without replacement from Quercetin's 62-target pool. Hyperforin's observed influence exceeds the entire bootstrap distribution.

Statistic	Value	Interpretation
Hyperforin observed	0.1138	Reference
Bootstrap mean	0.0308	Expected if targets equivalent
Bootstrap SD	0.0100	Sampling variability
Bootstrap 95% CI	[0.0160, 0.0542]	2.5th–97.5th percentile
Hyperforin / mean	**3.7**×	Effect size
Exceeds 95% CI?	**Yes**	Not attributable to sampling

Random seed: 42. Note: Bootstrap confirms robustness to target selection; it does not constitute independent inferential evidence.

Table 4: **Chemical similarity excludes structural confounding.** Neither compound resembles known hepatotoxins (Tanimoto < 0.4). Quercetin is more similar to DILI-positive drugs yet shows lower network influence.

Compound	Max Tanimoto (DILI+)	Max Tanimoto (DILI−)	Analog?*	Network rank
Hyperforin	0.154	0.202	No	1 (higher influence)
Quercetin	0.212	0.220	No	2 (lower influence)

*Analog threshold: Tanimoto > 0.4 (Maggiora et al., 2014). Morgan fingerprints (ECFP4, radius 2, 2048 bits). DILIrank: 542 DILI+, 365 DILI− drugs.

Table 5: **Hyperforin targets include regulatory hubs.** All 10 Hyperforin targets in the liver-expressed LCC, with liver expression (GTEx v8) and network degree. PXR (NR1I2) is the master regulator; CYP enzymes are downstream effectors.

Gene	Protein	TPM	Degree	Function	DILI link
NR1I2	PXR	43	28	Master regulator	Direct
CYP3A4	CYP3A4	335	89	Xenobiotic metabolism	Direct
CYP2C9	CYP2C9	434	76	Xenobiotic metabolism	Direct
CYP2B6	CYP2B6	125	42	Xenobiotic metabolism	Indirect
AKT1	PKB	33	**312**	Stress signaling	Indirect
ABCB1	P-gp	7	53	Drug efflux	Direct
ABCC2	MRP2	60	38	Drug efflux	Direct
ABCG2	BCRP	4	31	Drug efflux	Indirect
MMP2	MMP2	5	87	ECM remodeling	Indirect
MMP9	MMP9	1	94	ECM remodeling	Indirect

AKT1 is the highest-degree target (312 neighbors). Five of 10 targets (NR1I2, CYP3A4, CYP2C9, ABCB1, ABCC2) are directly connected to DILI genes. TPM = transcripts per million; DILI = drug-induced liver injury; LCC = largest connected component.

Table 6: **Influence ranking is robust to network construction parameters.** Hyperforin ranks first across all thresholds and influence metrics. Proximity Z-scores are unstable and reverse rankings between thresholds, failing to accurately reflect the physical distance advantage of Hyperforin.

Threshold	**Compound**	**RWR Z**	**EWI Z**	**Proximity d_c**	**Proximity Z**
$\geq$700	Hyperforin	**+12.08**	+11.20	0.60	−6.04
(11,693 nodes)	Quercetin	+5.53	+7.09	1.34	−5.46
$\geq$900	Hyperforin	**+10.12**	+8.98	1.30	−3.86
(7,677 nodes)	Quercetin	+4.55	+5.79	1.68	−5.44

Note: At $\geq$900, Quercetin achieves a more "significant" proximity Z-score despite being physically more distant (1.68 vs 1.30) from DILI genes. RWR = random walk with restart; EWI = expression-weighted influence; d_c = mean minimum shortest-path distance; DILI = drug-induced liver injury.

Figures

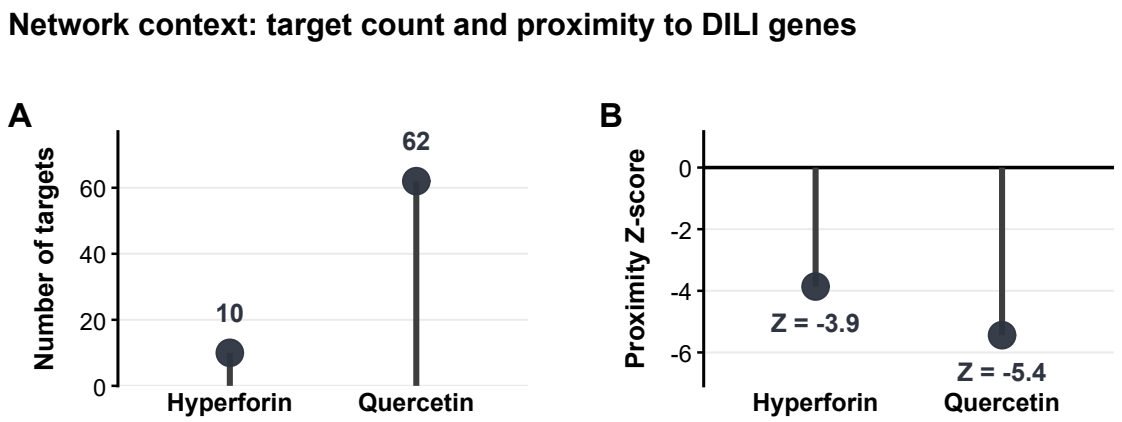

Figure 1: **Network context: target count and physical proximity to DILI genes.** (**A**) Target count in the liver-expressed largest connected component. Quercetin: 62 targets; Hyperforin: 10 targets. (**B**) Shortest-path proximity (d_c) to 82 DILI-associated genes. Hyperforin is physically closer ($d_c = 1.30$) than Quercetin ($d_c = 1.68$). Z-scores represent deviation from degree-matched null expectation ($n =$ 1,000 permutations). Quercetin: Z = -5.44 ($p < 0.001$); Hyperforin: Z = -3.86 ($p < 0.001$). Negative Z-scores indicate closer-than-random proximity. Network: STRING v12.0 (confidence $\geq$900), GTEx v8 (liver TPM $\geq$1).

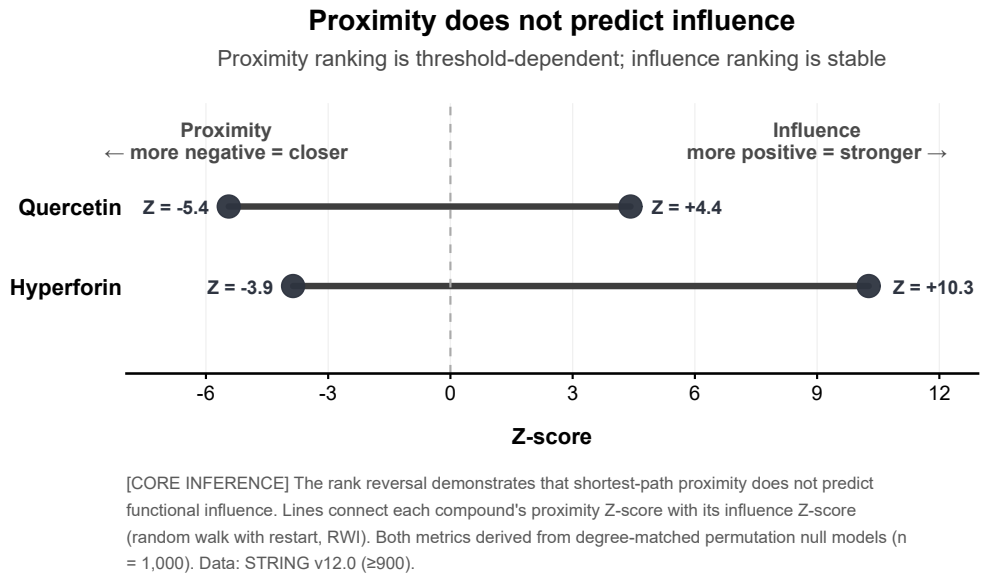

Figure 2: **Instability of proximity Z-scores.** Dumbbell plot showing the dissociation between shortest-path proximity (left) and random walk influence (right) at STRING confidence $\geq$900. At this threshold, Quercetin appears more "significant" in Z-score but is physically more distant (1.68 vs 1.30) from DILI genes. Hyperforin: proximity Z = -3.86, influence Z = +10.12 ($p < 0.001$). Quercetin: proximity Z = -5.44, influence Z = +4.55 ($p < 0.001$). Influence quantified by random walk with restart (RWR; $\alpha = 0.15$). $n = 1{,}000$ degree-matched permutations per compound.

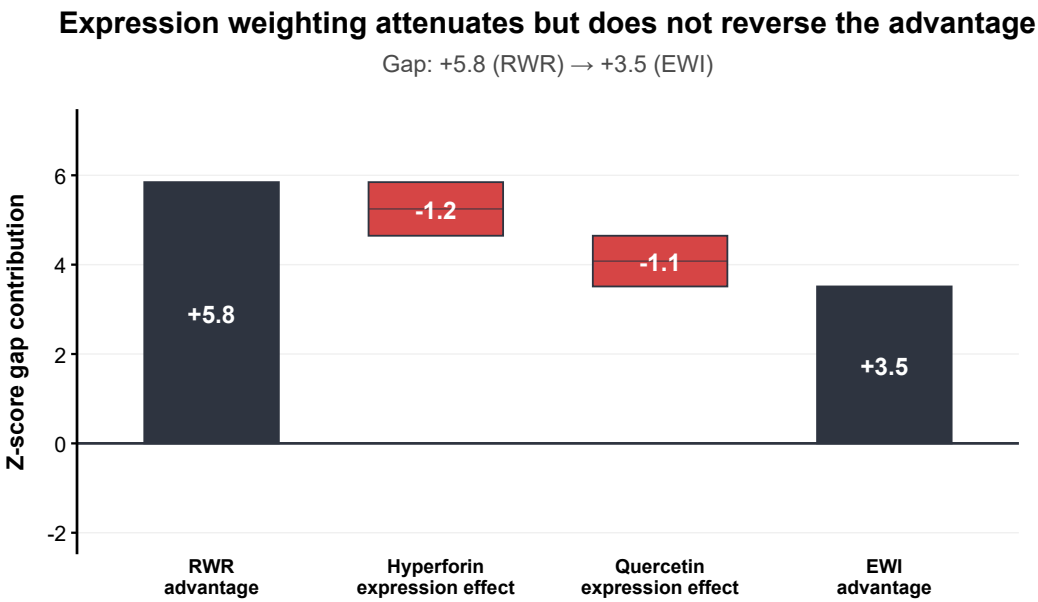

Figure 3: **Expression weighting refines influence propagation.** Waterfall decomposition of Z-score changes under expression-weighted influence (EWI). Initial Hyperforin advantage: $\Delta Z = +5.57$ (RWR). Hyperforin change: -1.14 (attenuation of signal through liver-active hubs). Quercetin change: $+1.24$ (gain from high-expression nodes like CFB). Residual Hyperforin advantage: $\Delta Z = +3.19$. Both compounds remain significant under EWI: Hyperforin $Z = +8.98$ ($p < 0.001$); Quercetin $Z = +5.79$ ($p < 0.001$). Expression weighting from GTEx v8 liver tissue.

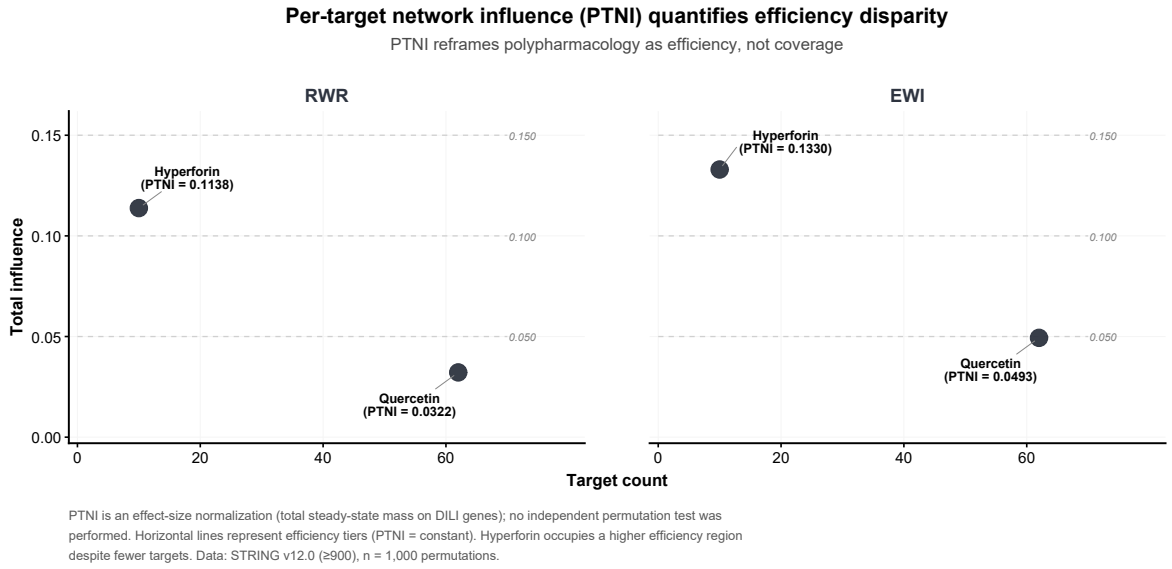

Figure 4: **Per-target network influence (PTNI) quantifies efficiency disparity.** Phase plot of total influence versus target count. Horizontal lines represent efficiency tiers (PTNI = constant). Hyperforin occupies a higher efficiency region despite fewer targets. PTNI values: Hyperforin = 0.1138 (RWR), 0.1330 (EWI); Quercetin = 0.0322 (RWR), 0.0493 (EWI). Efficiency difference: **3.7**$\times$ (based on bootstrap mean comparison). PTNI is an effect-size normalization (total steady-state mass on DILI genes); no independent permutation test was performed.

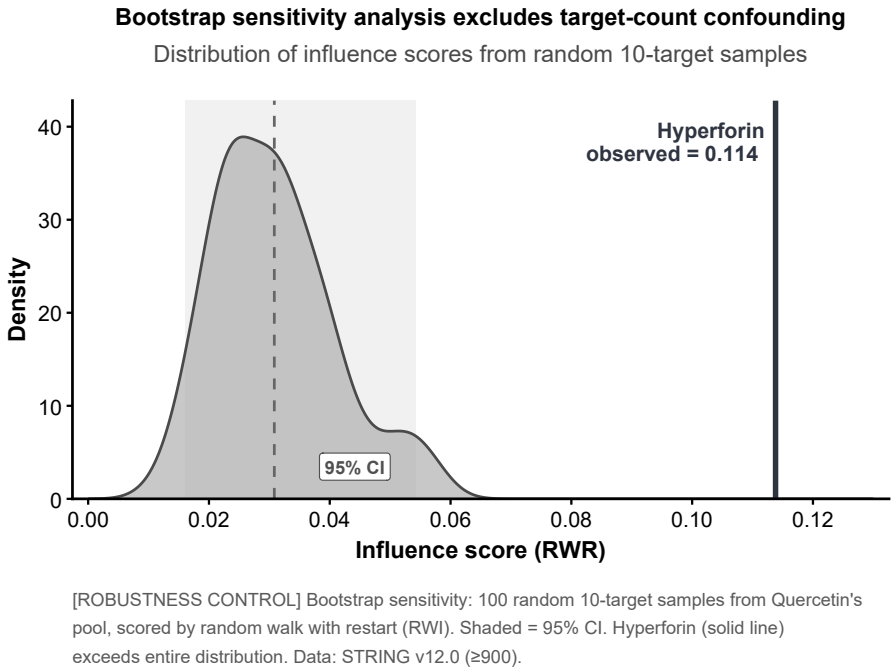

Figure 5: **Bootstrap sensitivity analysis excludes target-count confounding.** Density distribution of RWR influence scores from 100 random 10-target samples drawn from Quercetin's 62-target pool. Shaded region: 95% confidence interval (0.0160–0.0542). Vertical line: Hyperforin observed influence (0.1138). Hyperforin exceeds the entire bootstrap distribution (3.7× fold vs. mean). This confirms that Hyperforin's advantage is not attributable to favorable target count. Bootstrap is a robustness control; it does not provide independent statistical evidence.

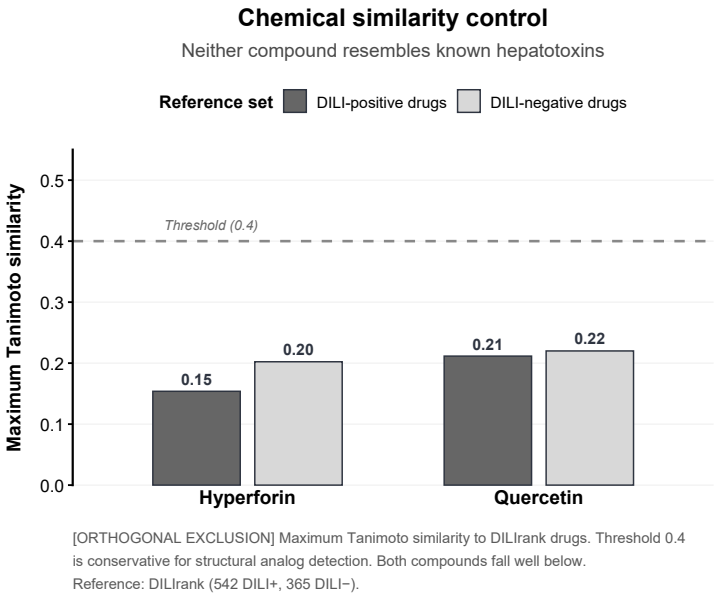

Figure 6: **Chemical similarity control excludes structural confounding.** Maximum Tanimoto similarity to DILIrank reference drugs. Reference set: 542 DILI-positive, 365 DILI-negative drugs. Hyperforin: max = 0.15 (DILI+), 0.20 (DILI−). Quercetin: max = 0.21 (DILI+), 0.22 (DILI−). Dashed line: 0.4 threshold for structural analog detection [Maggiora et al., 2014]. Neither compound is a structural analog of known hepatotoxins. This orthogonal analysis excludes chemical class as an explanation for the observed network signal. Fingerprints: Morgan (ECFP4), radius 2, 2048 bits.

Declarations

Author Contributions (CRediT)

Antony Bevan: Conceptualization, Methodology, Software, Validation, Formal analysis, Investigation, Data Curation, Writing - Original Draft, Writing - Review & Editing, Visualization.

Use of AI Tools

AI-assisted tools were used to assist with code development and statistical analysis. The author takes full responsibility for all content.

Competing Interests

The author declares no competing interests.

Data Availability

All data and code supporting this study are publicly available at: `https://github.com/antonybevan/h-perforatum-network-tox`

Source data for all figures and tables are provided in the Supplementary Information. Raw data were obtained from the following public repositories:

- STRING v12.0: `https://string-db.org`
- GTEx v8: `https://gtexportal.org`
- ChEMBL v31: `https://www.ebi.ac.uk/chembl`
- DisGeNET: `https://www.disgenet.org`
- DILIrank 2.0: `https://www.fda.gov/science-research/ltkb`

Code Availability

All analysis code is available at: `https://github.com/antonybevan/h-perforatum-network-tox`

The repository includes:

- Python scripts for network construction, RWR, permutation testing
- R scripts for visualization
- Complete pipeline documentation
- Fixed random seeds for full reproducibility

Software versions: Python 3.10, NetworkX 3.1, NumPy 1.26, Pandas 2.1, RDKit 2023.03, R 4.3, ggplot2 3.5.

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Supplementary Tables

Table 7: **Table S1. Hyperforin target genes and literature sources.** All 14 raw targets with UniProt IDs, gene symbols, and primary literature sources. Targets marked with * are present in the liver-expressed LCC (STRING $\geq$900, GTEx TPM $\geq$1).

UniProt	Gene	In LCC	Source
O75469	NR1I2 (PXR)	Yes*	[Moore et al., 2000, Watkins et al., 2001]
P08684	CYP3A4	Yes*	[Moore et al., 2000]
P11712	CYP2C9	Yes*	[Obach, 2000]
P20813	CYP2B6	Yes*	[Komoroski et al., 2004]
P08183	ABCB1	Yes*	[Hennessy et al., 2002]
Q9UNQ0	ABCG2	Yes*	[Assefa and Butterweck, 2004]
O15440	ABCC2	Yes*	[Wang et al., 2004]
P31749	AKT1	Yes*	[Quiney et al., 2007]
P08253	MMP2	Yes*	[Quiney et al., 2007]
P14780	MMP9	Yes*	[Quiney et al., 2006]
Q9Y210	TRPC6	No	[Leuner et al., 2007]
P15692	VEGFA	No	[Quiney et al., 2006]
Q13794	PMAIP1	No	[Hostanska et al., 2003]
Q12879	GRIN1	No	[Kumar et al., 2006]

Table 8: **Table S2. Quercetin target curation summary.** Target counts at each processing stage.

Stage	Count
Raw targets (ChEMBL v31, CHEMBL159)	122
Excluded: non-human (mouse, rat, bacterial, viral)	10
Excluded: no UniProt mapping	25
Processed targets	87
Excluded: not liver-expressed (TPM $<$ 1)	20
Excluded: not in STRING LCC	5
Final targets in LCC	62

Table 9: **Table S3. DILI gene set curation.** Genes associated with drug-induced liver injury from DisGeNET (UMLS C0860207).

Stage	Count
Raw DILI genes (DisGeNET)	127
In STRING $\geq$700 liver LCC	84
In STRING $\geq$900 liver LCC	82
Excluded: miRNAs (not in PPI network)	21
Excluded: cytokines (not in LCC)	12
Excluded: other	12

Table 10: **Table S4. Genes targeted by both compounds.** Five genes present in both Hyperforin and Quercetin target sets.

Gene	Protein	Function
ABCG2	BCRP	Efflux transporter
AKT1	Protein kinase B	Cell survival signaling
CYP3A4	Cytochrome P450 3A4	Drug metabolism
MMP2	Matrix metalloproteinase-2	Extracellular matrix remodeling
MMP9	Matrix metalloproteinase-9	Extracellular matrix remodeling

Table 11: **Table S5. Direct DILI gene connectivity.** Hyperforin targets with first-order (distance = 1) connections to DILI genes in the STRING network ($\geq$900). DILI neighbors are genes present in the 82-gene DILI set.

Target	DILI Neighbors	N	Function
CYP3A4	NR1I2, CYP2E1, UGT1A9, GSTM1, GSTP1	5	Xenobiotic metabolism
AKT1	MAP3K5, NFE2L2, CTNNB1, IGF1	4	Stress response
MMP9	LCN2, SPP1, MMP2	3	Inflammation/ECM
ABCB1	ABCC2, NR1I2	2	Drug transport
CYP2C9	CYP2E1, NR1I2	2	Xenobiotic metabolism
CYP2B6	NR1I2	1	Xenobiotic metabolism
NR1I2	CYP2E1, ABCC2	2	Master regulator
ABCG2	ABCC2	1	Drug transport
ABCC2	NR1I2, ABCB1	2	Drug transport
MMP2	MMP9, SPP1	2	ECM remodeling
Total unique		**12**	

Table 12: **Table S6. Quercetin direct DILI gene connectivity summary.** Summary statistics for first-order DILI connections across Quercetin's 62 targets.

Metric	Value
Total targets in LCC	62
Targets with $\geq$1 direct DILI neighbor	18
Total direct DILI connections	31
Mean DILI neighbors per target	0.50
Hyperforin comparison:	
Hyperforin targets with $\geq$1 DILI neighbor	10/10 (100%)
Mean DILI neighbors per Hyperforin target	2.4

Table 13: **Table S7. Quercetin target genes in the liver-expressed network.** All 62 Quercetin targets in STRING v12.0 LCC (confidence $\geq$900) with liver TPM $\geq$1 (GTEx v8). Sorted by descending liver expression.

Gene	TPM	Gene	TPM	Gene	TPM	Gene	TPM
CFB	1115	CYP3A4	335	FN1	229	ALDH2	183
ANPEP	160	PPIA	112	SERPINA5	104	CYP1A2	72
CA2	64	APP	63	PYGL	55	HDAC6	45
ESRRA	42	MAOA	35	AKR1C2	33	AKT1	33
CTSH	28	XDH	26	CHRNA4	25	PIK3R1	24
PIM1	24	LDLR	23	EGFR	17	ELOVL1	18
PKN1	16	GSK3A	13	YES1	13	MET	12
DAPK1	12	BACE1	11	CSNK2A1	10	FSTL1	9
SIRT6	8	GSK3B	7	CDK7	7	CAV2	7
PTPN2	6	CYP1A1	5	PRMT7	5	MMP2	5
AKR1B1	5	PDE6D	5	PTK2	4	ABCG2	4
IQGAP1	4	ADRB2	3	BRAF	4	KDR	3
SRC	3	ALOX5	3	CYP1B1	3	TLR4	3
NUAK1	3	AXL	2	ADA	2	LCK	2
ABCC1	2	PLK1	1	ACHE	1	MMP9	1
SYK	1	PDZK1IP1	1				

Table 14: **Table S8. DILI gene set (82 genes).** Genes in STRING v12.0 LCC (confidence $\geq$900) with liver TPM $\geq$1 (GTEx v8). Source: DisGeNET (UMLS C0860207). Sorted alphabetically.

82 DILI-Associated Genes							
ABCB1	AHR	ALB	ALDOB	AMBP	APOA1	APOE	APOH
ARG1	ARNT	ATG5	BAX	BTD	C3	CAT	CCL2
CLU	COL3A1	CTNNB1	CXCL1	CXCL10	CYP2A6	CYP2C19	CYP2C9
CYP2E1	DGAT2	ENO1	FGA	FLT1	FMO3	GADD45A	GC
GCLC	GPT	GSN	GSTM1	GSTM2	GSTP1	HLA-A	HLA-B
HLA-DQB1	HLA-DRB1	HMGB1	HMOX1	HPD	HPX	IGF1	IL18
IL1R2	KRT18	LCN2	LGALS3	MAP3K5	MED1	MMP2	MTHFR
NAT2	NFE2L2	NR1H3	NR1H4	NR1I2	NR1I3	PLAT	PLG
PNP	POLG	PON1	PPARA	PRKDC	PTGS2	RBP1	SLPI
SNX18	SOD1	SOD3	SPP1	TALDO1	TBXA2R	TCTN1	TF
TTR	UGT1A9						

Table 15: **Table S9. Null distribution parameters from permutation testing.** Null distribution parameters (mean and standard deviation) from $n = 1{,}000$ degree-matched permutations. Note the tightening of the Quercetin null distribution as the number of targets increases, which drives the inflation of proximity Z-scores.

Metric	Compound	μ_{null}	σ_{null}	x_{obs}	Z-score
Shortest-path proximity (at ≥900)					
	Hyperforin (10)	2.21	0.235	1.30	−3.86
	Quercetin (62)	2.17	0.091	1.68	−5.44
Random walk influence (at ≥900)					
	Hyperforin (10)	0.0147	0.0098	0.1138	+10.12
	Quercetin (62)	0.0148	0.0038	0.0322	+4.55
Expression-weighted influence (at ≥900)					
	Hyperforin (10)	0.0205	0.0125	0.1330	+8.98*
	Quercetin (62)	0.0209	0.0049	0.0493	+5.79*

*Significance remains high despite tissue-specific attenuation. μ_{null} = null distribution mean; σ_{null} = null distribution standard deviation; x_{obs} = observed metric value.