Supplementary file

UPLC-qToF-MS/MS analysis and anti-inflammatory activities of the soft coral *Litophyton savignyi* supported by bioactive molecular networking, network pharmacology, and molecular docking

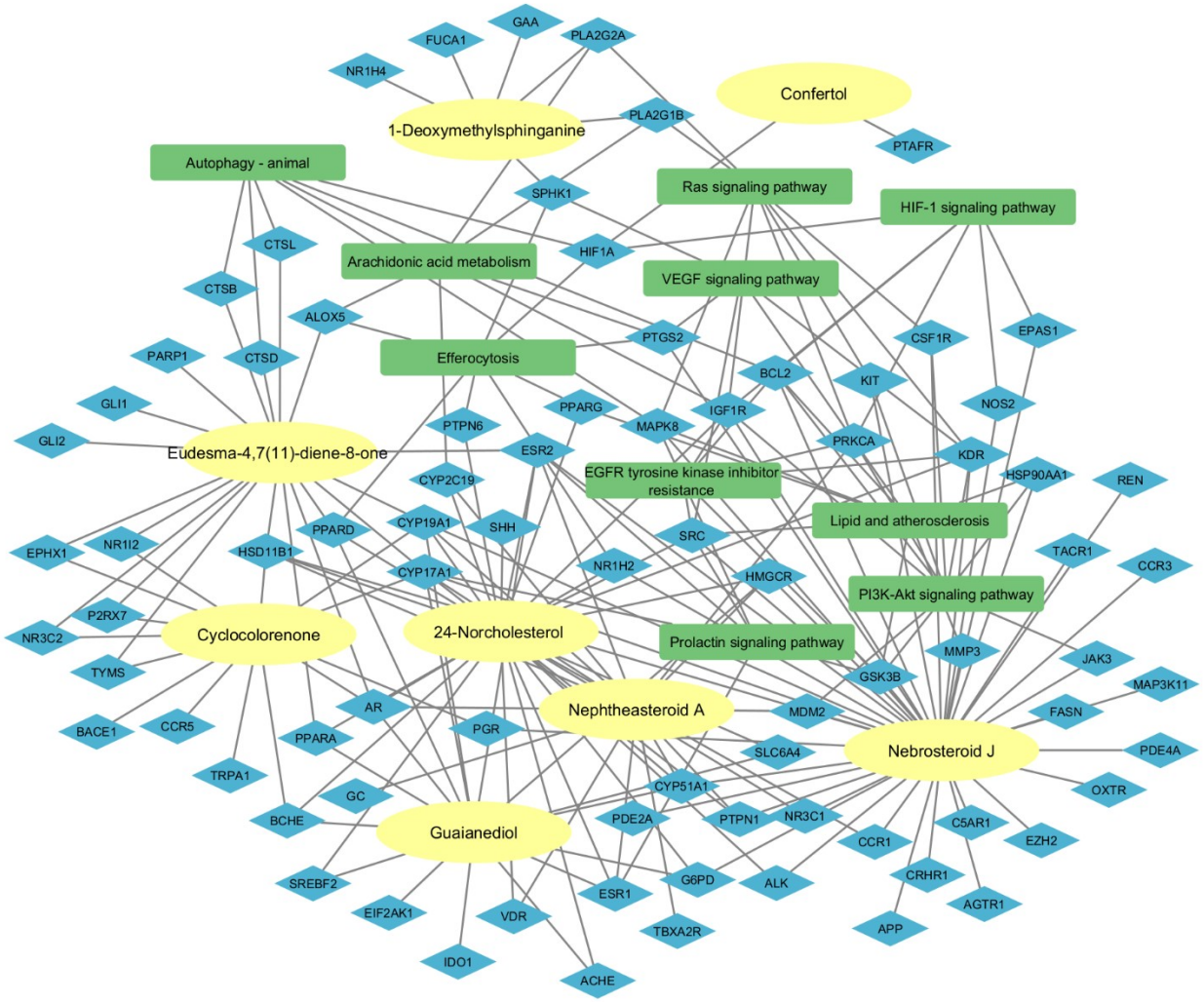

Figure S1. A network showing the connectivities between bioactive components, potential targets, and the top ranked signaling pathways.

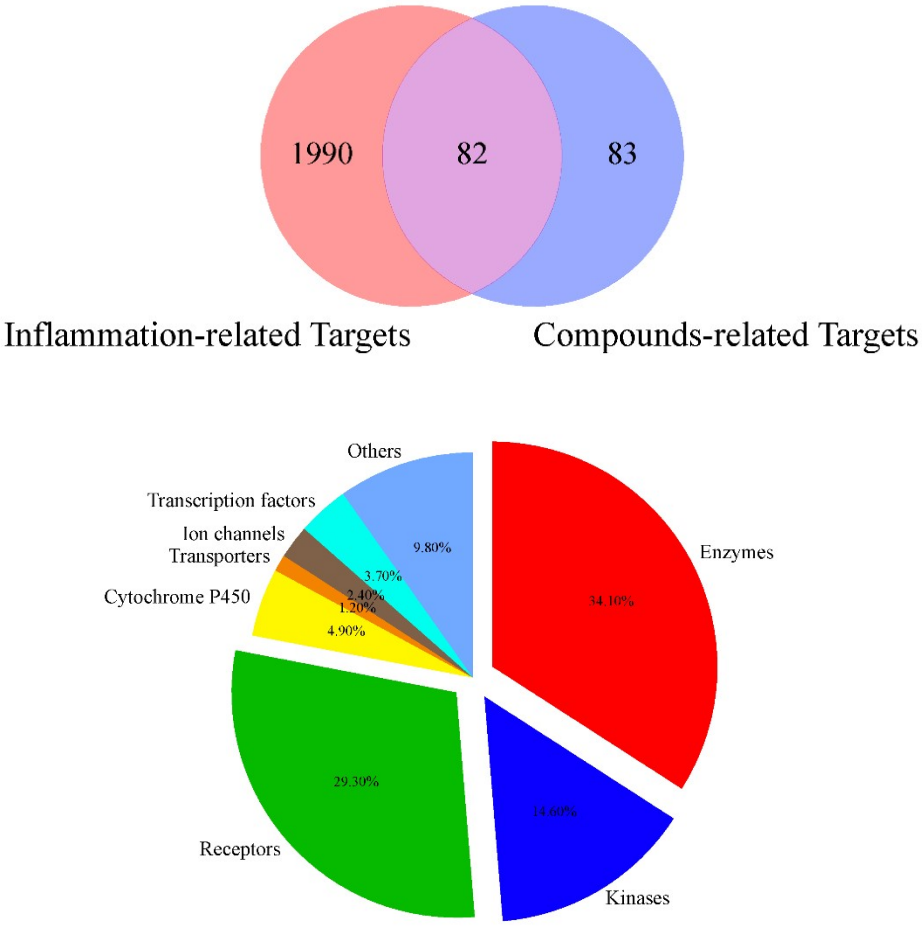

Figure S2. A Venn diagram showing the intersecting common targets between inflammation and the bioactive compounds in the hexane fraction (Top). A pie-chart showing the percentage of the intersecting targets where the majority of them are enzymes, receptors, and kinases (Bottom).

Table S1. Binding pocket grid parameters.

Protein	PDB ID	Grid Center			Grid Size			Grid Spacing (Å)
		X	Y	Z	X	Y	Z	
COX-2	6COX	23.049	23.526	46.984	50	50	50	0.375 (Default)

Table S2. Characteristics of GEO datasets used for hub gene validation.

Dataset	Platform	Assay type	Samples used	Species	Cell type	Groups used in study	Reference (PMID)
GSE2322	GPL96	[HG-U133A] Affymetrix Human Genome U133A Array	10	*H. sapiens*	In-vitro neutrophils	In-vitro control (n=5); In-vitro endotoxin (n=5)	16861384
GSE198326	GPL15207	[PrimeView] Affymetrix Human Gene Expression Array	6	*H. sapiens*	Macrophage	Control (n=3); LPS-induced (n=3)	29321478
GSE40885	GPL570	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	8	*H. sapiens*	Alveolar macrophage	Control (n=7); LPS-induced (n=7)	22952057

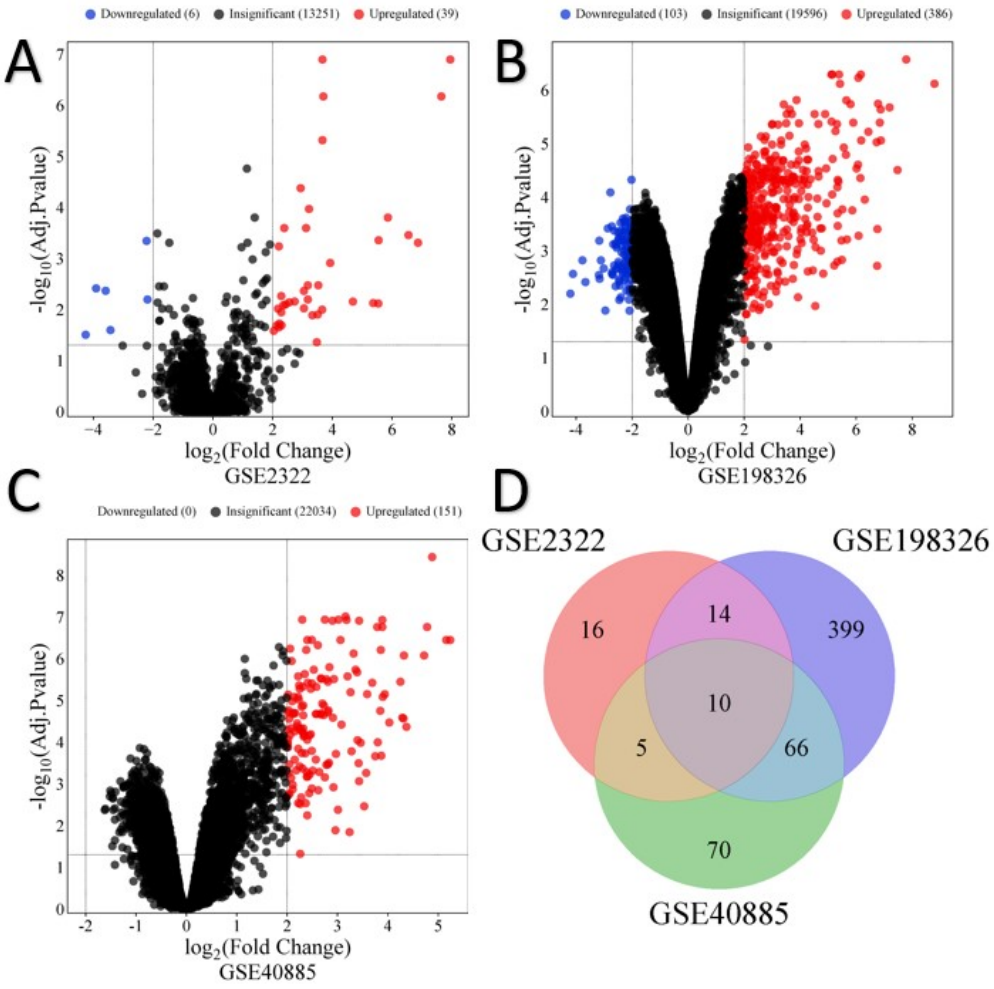

Figure S3. Differential expression analysis and hub gene overlap across selected GEO datasets. Volcano plots showing the distribution of significantly upregulated (red), downregulated (blue), and non-significant (black) genes in (A) GSE2322, (B) GSE198326, and (C) GSE40885, based on thresholds of $|\log_2 FC| > 2$ and adjusted P-value < 0.05. (D) Venn diagram illustrating the overlap of differentially expressed genes among the three datasets, with 10 common genes identified across all studies.

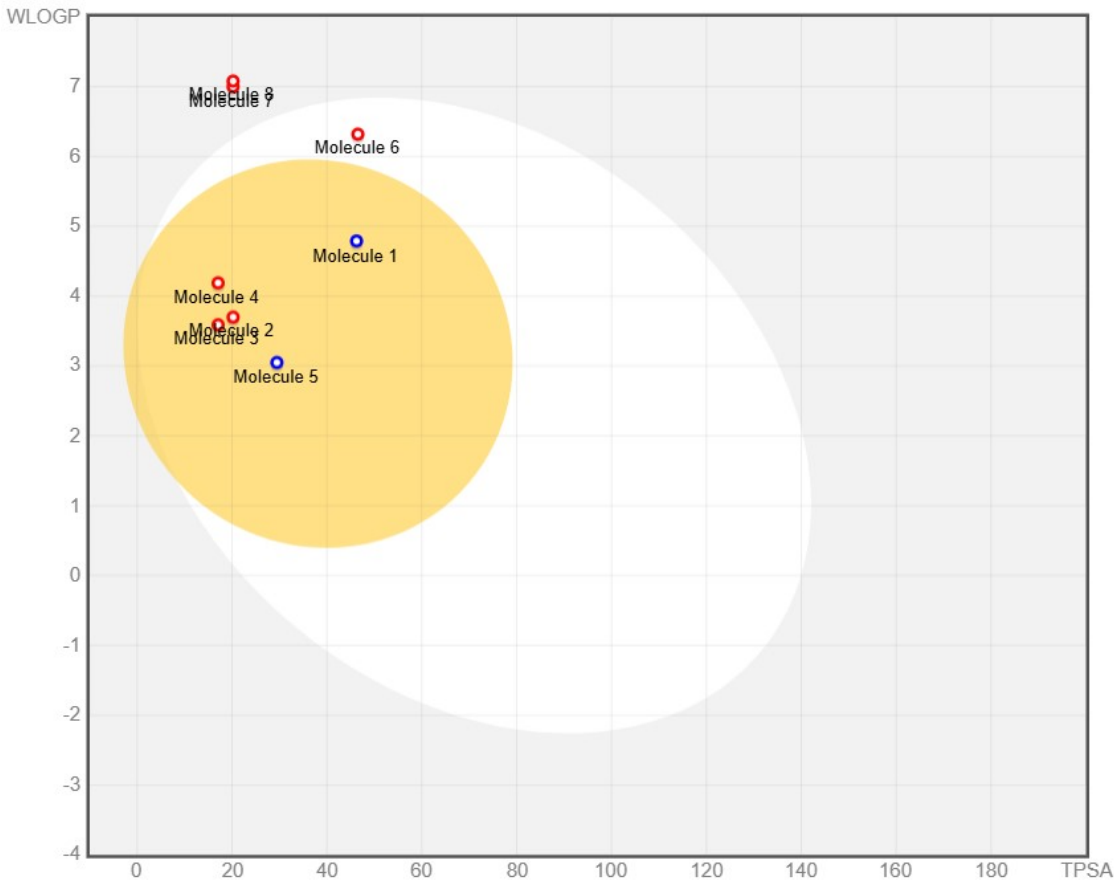

Figure S4. Boiled-EGG predictive model of *L. savignyi* bioactive compounds. Yellow zone indicates high BBB permeability; white zone indicates high GIT absorption; grey zone falls outside predicted absorption regions. Molecule 1: 1-Deoxymethylsphinganine; Molecule 2: Guaianediol; Molecule 3: Cyclocolorenone; Molecule 4: Eudesma-4,7(11)-diene-8-one; Molecule 5: Confertol; Molecule 6: Nebrosteroid J; Molecule 7: 24-Norcholesterol; Molecule 8: Nephtheasteroid A.