

## Expanded View Figures

**Figure EV1. Quantitative description of the PPI network by resource.**

- A Number of nodes and interactions. The light dots represent the shared nodes and edges (in more than one resource), while the dark ones show their total numbers.
- B Causality: number of connections by direction and effect sign.
- C Coverage of the networks on various groups of proteins. Dots show the percentage of proteins covered by network resources for the following groups: cancer driver genes from COSMIC and IntOGen, kinases from kinase.com, phosphatases from Phosphatome.net, receptors from the Human Plasma Membrane Receptome (HPMR) and transcription factors from the TF census. Gray bars show the number of proteins in the networks.

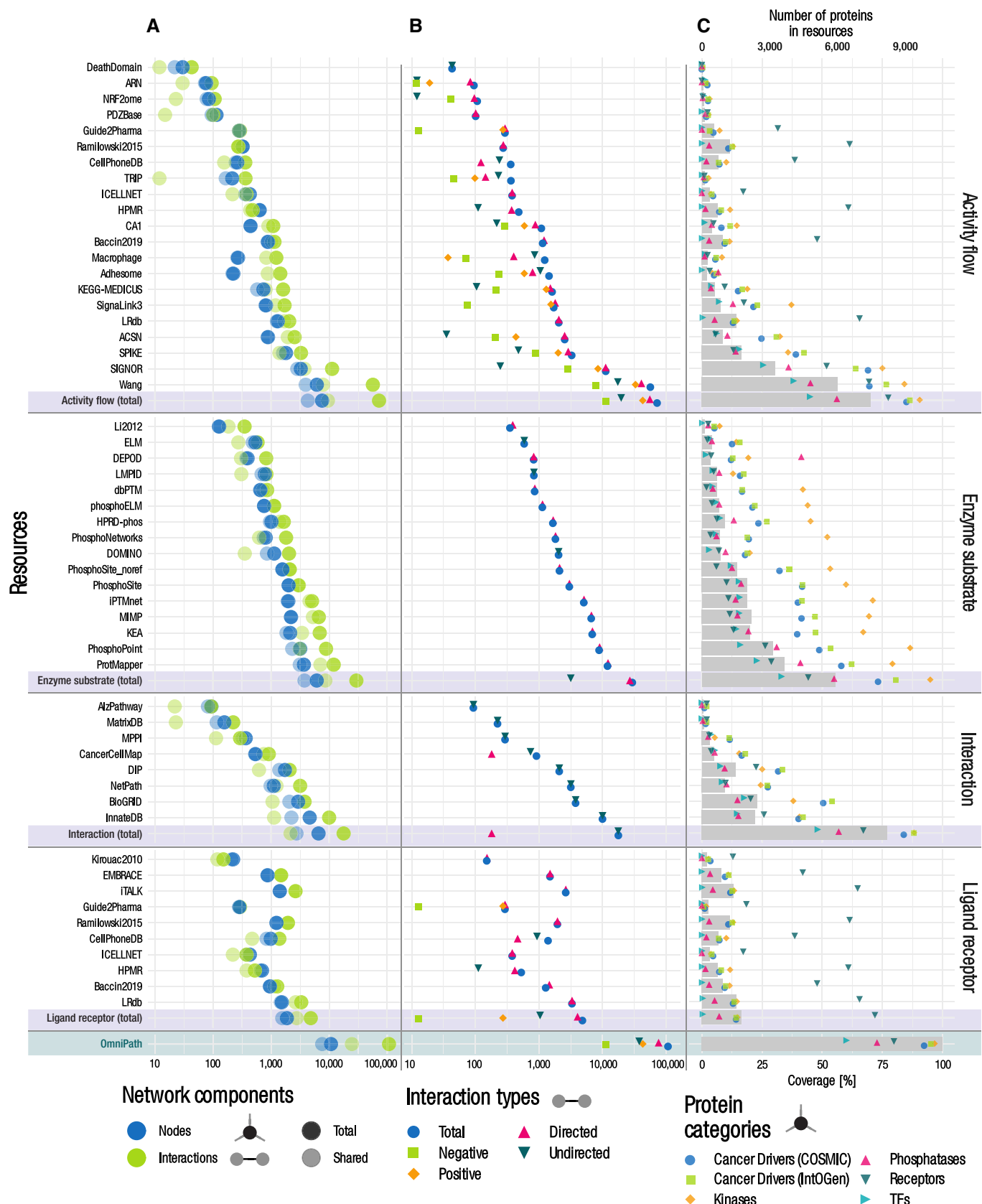


Figure EV1.

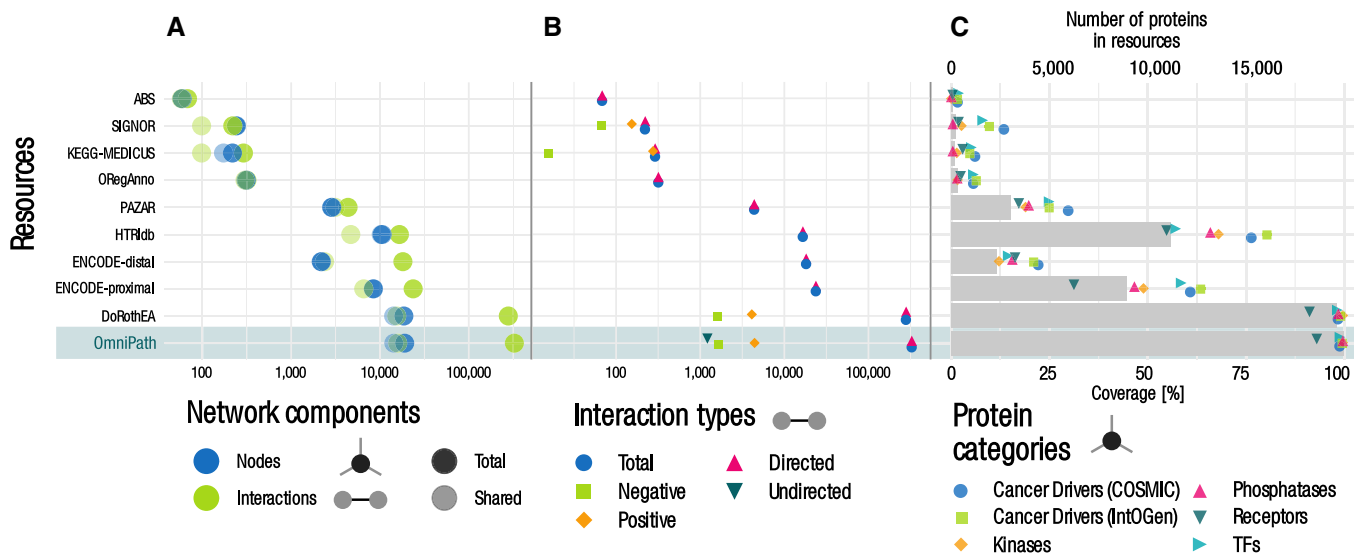


Figure EV2. Quantitative description of the transcriptional network by resource.

A–C Panels and notations are the same as on Fig EV1.

### Annotations in OmniPath

**mTOR is...**  
<http://omnipathdb.org/annotations?proteins=MTOR>

uniprot	genesymbol	source	label	value	record_id
P42345	MTOR	kinase.com	group	Atypical	94
P42345	MTOR	kinase.com	family	PIKK	94
P42345	MTOR	kinase.com	subfamily	FRAP	94
P42345	MTOR	HPA	organ	kidney	1204876
P42345	MTOR	HPA	tissue	cells in tubules	1204876
P42345	MTOR	HPA	level	Medium	1204876
P42345	MTOR	HPA	status	Approved	1204876
P42345	MTOR	HPA	prognostic	False	1204876
P42345	MTOR	HPA	favourable	False	1204876
P42345	MTOR	HPA	pathology	False	1204876
P42345	MTOR	DGIdb	category	SERINE THREONINE KINASE	4549
P42345	MTOR	DGIdb	category	TRANSCRIPTION FACTOR BINDING	4551
P42345	MTOR	DGIdb	category	PHOSPHATIDYLINOSITOL 3 KINASE	4552
P42345	MTOR	DGIdb	category	TUMOR SUPPRESSOR	4553
P42345	MTOR	DGIdb	category	KINASE	4554
P42345	MTOR	DGIdb	category	DRUGGABLE GENOME	4555
P42345	MTOR	DGIdb	category	DNA REPAIR	4556
P42345	MTOR	DGIdb	category	CLINICALLY ACTIONABLE	4556
P42345	MTOR	Signor	pathway	AML-BCRABL	313
P42345	MTOR	Signor	pathway	AML-FLT3	314
P42345	MTOR	Signor	pathway	AML-KIT 315	315
P42345	MTOR	Signor	pathway	Insulin Receptor	316
P42345	MTOR	Signor	pathway	MTOR Signaling	317
P42345	MTOR	Signor	pathway	AML_miRNA	318

parameters: [bit.ly/2m2U4Lt](http://bit.ly/2m2U4Lt) • examples: [bit.ly/2ku19nN](http://bit.ly/2ku19nN) • in pypath: [bit.ly/2k4IA9F](http://bit.ly/2k4IA9F)

Figure EV3. Example of the annotations query in the OmniPath web service.

For the protein mTOR a large variety of information is available from different databases. The “record\_id” binds together the fields of the record from the original resource. Each field has a “label” and a “value”.

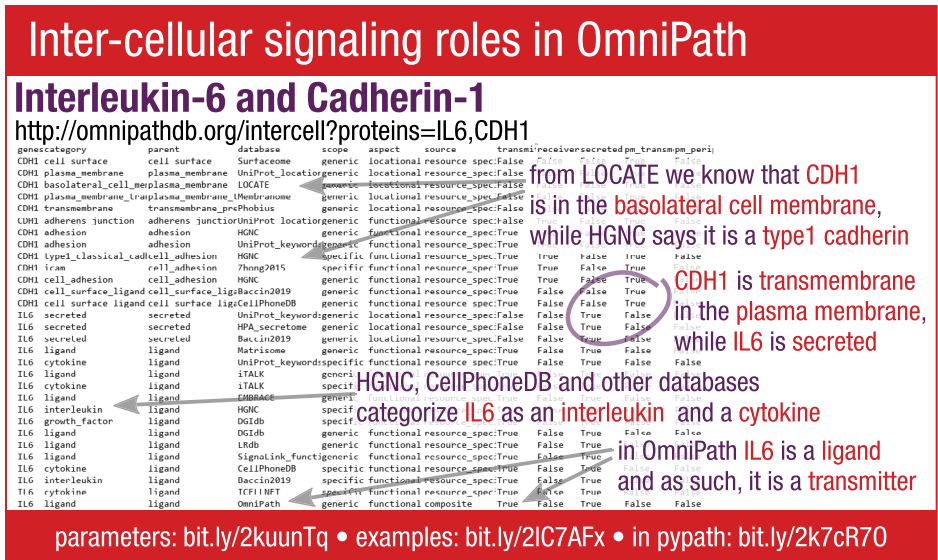
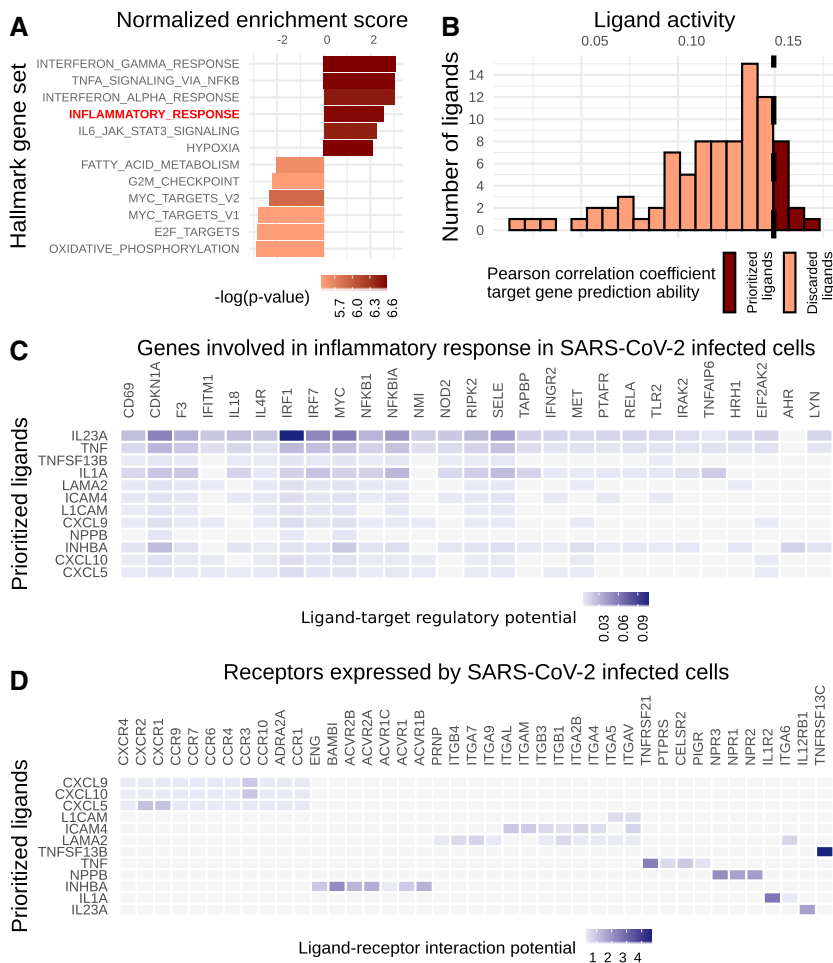


Figure EV4. Example of the intercell query in the OmniPath web service.

Each category has a parent category and a database of origin. The scope of a category is either “generic” (e.g., ligand) or “specific” (e.g., interleukin). The aspect is either “locational” or “functional”. Further attributes show whether the protein is a signal transmitter or a receiver, and whether it is secreted, or a transmembrane or peripheral protein of the plasma membrane.



**Figure EV5. OmniPath-based NicheNet analysis to predict over-expressed ligands in SARS-CoV-2 infection potentially affecting the expression of inflammatory response related genes in Calu3 cells.**

- A Most significantly enriched gene sets after SARS-CoV-2 infection on the Calu3 cell line. Inflammatory response is highlighted in red.
- B Results of NicheNet's ligand activity analysis: Number of over-expressed ligands after SARS-CoV-2 infection and their potential to predict the inflammatory response gene set based on the Pearson correlation coefficient. The top 12 ranked ligands, out of a total of 117 over-expressed ligands, were selected.
- C Regulatory potential of the top ranked ligands and target genes from the inflammatory response program based on NicheNet's prior knowledge model.
- D Ligand-receptor interaction potential based on NicheNet's prior knowledge model between the top ranked ligands and the receptors expressed in the Calu3 cell line.