

# Network analysis for the discovery of common oncogenic biomarkers in liver cancer experimental models

Loraine Kay D. Cabral<sup>1,2,\*</sup>, Pablo J. Giraudi<sup>1</sup>, Gianluigi Giannelli<sup>3</sup>, Francesco Dituri<sup>3</sup>, Roberto Negro<sup>3</sup>, Claudio Tiribelli<sup>1</sup> and Caecilia H. C. Sukowati<sup>1,4</sup>

<sup>1</sup> Fondazione Italiana Fegato ONLUS, AREA Science Park, Campus Basovizza, 34149 Trieste, Italy

<sup>2</sup> Doctoral School in Molecular Biomedicine, University of Trieste, 34127 Trieste, Italy

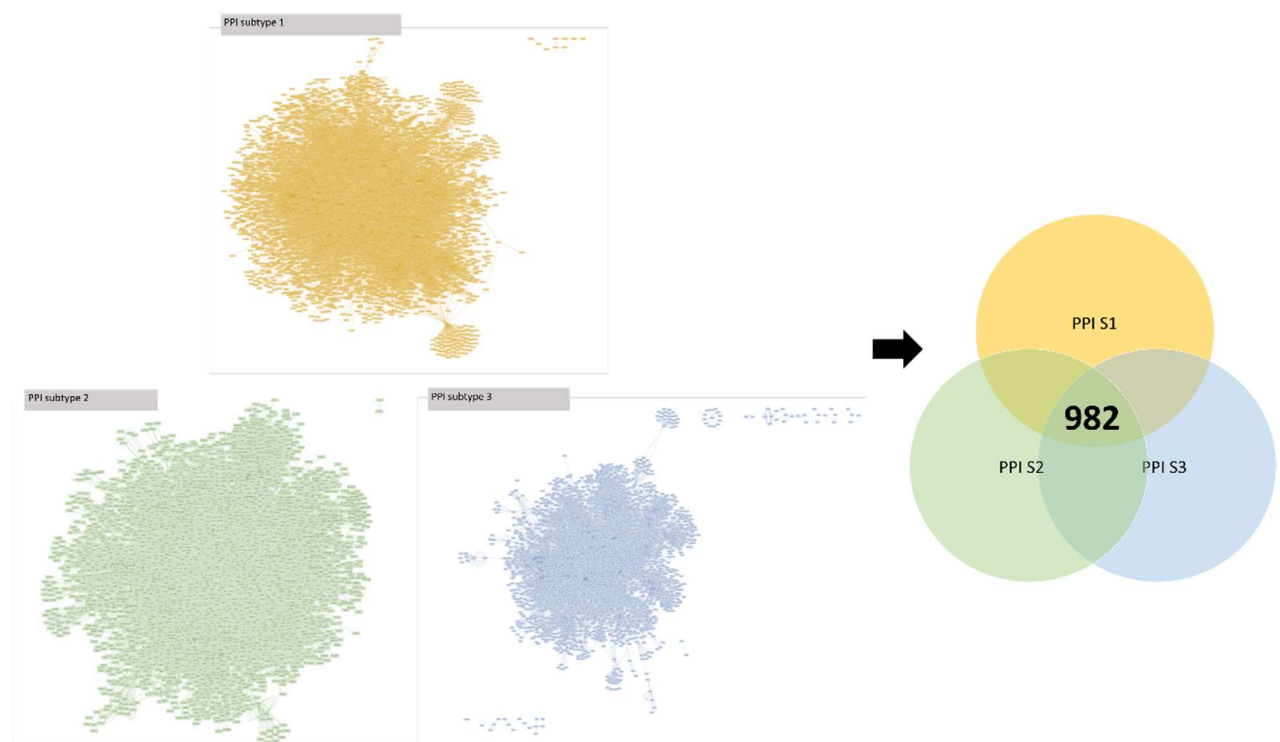
<sup>3</sup> National Institute of Gastroenterology “S. De Bellis” Research Hospital, 70013 Bari, Italy

<sup>4</sup> Eijkman Research Center for Molecular Biology, National Research and Innovation Agency of Indonesia (BRIN), B.J. Habibie Building, Jl. M.H. Thamrin No. 8, Jakarta Pusat 10340, Indonesia

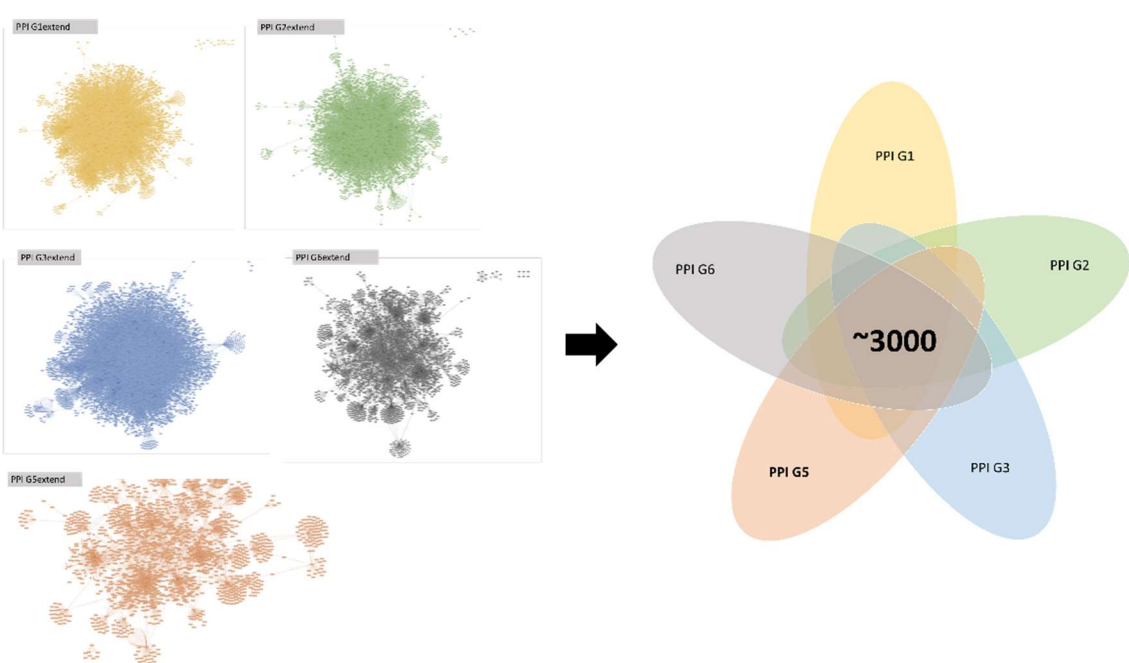
\* Correspondence: caecilia.sukowati@fegato.it

Supplemental Data

Hoshida *et al.* datasets



Boyault *et al.* datasets



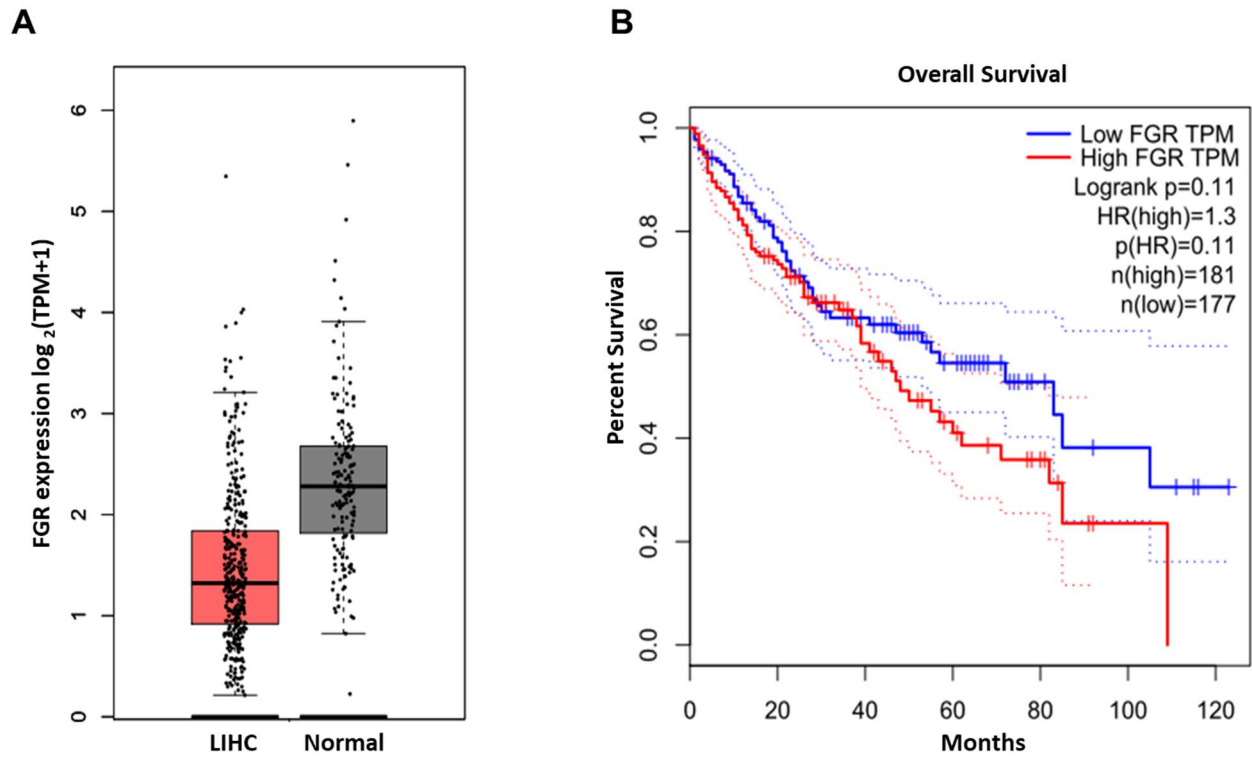
**Figure S1.** Protein-protein interaction (PPI) analysis of the different HCC subtypes and groups from published datasets.

	5-AZA						SOR						siR-PD-L1					
	H		S1		S2		H		S1		S2		H		S1		S2	
	IHH	HLE	HLF	JHH6	HepG2	HuH7	IHH	HLE	HLF	JHH6	HepG2	HuH7	IHH	HLE	HLF	JHH6	HepG2	HuH7
AURKA	3.00	106	146	138	196	3.26 **	139	0.27 *	183	0.99	0.17 **	104	0.33 **	0.61	0.46 **	0.57 **	0.87	0.24 **
FGR	0.04	0.48 **	0.37 *	2.84	0.01 *	151	0.31	125	0.06 *	4.91 ***	0.93	144	0.24 **	0.49 *	0.14 ***	0.11 ***	0.21 ***	0.36 *
EGFR	199	140 **	2.74	5.14	0.77	1.8	2.67	2.61	2.86 **	13.01 *	0.62	124	0.42 **	0.91 *	0.29 *	0.77	0.73	0.82
HGFR	0.75	165	5.04	191	189	3.3	159	3.06	5.56	4.28 *	0.32 *	0.33	0.49 **	0.76	0.32 **	1.19	0.84	0.77
YAP1	0.91	135	2.80 *	108	155	2.00	22.36	135	2.00	3.40	0.50	106	0.41	0.37	0.69 **	0.81	0.68	1.13
FOS	158 *	0.97	129	145	130	0.85	4.18	0.20 *	0.29 *	0.86	0.16 **	0.17	0.38 **	0.73 **	0.39 **	0.34	0.80	0.82
ASV1	151	2.01	2.79	5.80 *	2.41 **	0.42	3.99	3.09 *	2.41 *	2.16	0.41 *	105	0.56 **	0.92	0.35 **	1.13	105	0.72
PRKCA	0.67	114	3.47	2.36 *	108	0.93	3.18	3.30	2.80 **	4.28	158	137	0.61	0.73 **	0.27 **	106	0.65 **	0.58
YES1	0.48	124	4.71	0.97	103	155	196	2.60 *	2.76	6.26 *	0.36 *	0.40	0.46 **	0.77	0.33 *	121	0.66 **	0.68
FYN	148	114	8.11	3.55 *	130	0.97	2.63	3.32 *	4.08 **	4.03 **	0.67	0.78	0.58 **	108	0.45 *	124	104	0.95
cCBL	168	190	0.68	4.09	2.27	121	150	3.01	0.82	7.95	0.47	1.12	0.40 *	1.17	0.32	0.30	0.53 *	0.70 *
cJun	128	2.23	9.81 ***	6.87 **	2.43	0.35 **	3.00	1.15	5.44	7.17 *	2.68	0.59	0.28 **	182	0.02 ***	0.90	0.48	102
EP515	3.32	2.84	103	4.57 **	3.28	3.06	2.57	2.09	2.43	29.21	0.62	0.05	0.56	107	0.03 **	0.97	0.18	0.91 **
MDM2	186	2.28 **	3.04	135	4.88 *	1.13	7.16	104	165	3.65 *	0.85	0.04	0.92	0.64	0.02 **	0.32 *	0.09	102 **
PLZF	0.33	0.49	140	176	0.01 **	104	161	148	0.09	0.42	191	0.68	0.64	3.20 ***	0.02 **	0.08 **	0.88 **	0.13
DCUN1L1	0.56	2.33	3.99	2.18	147	2.45	1.11	2.87	4.73	14.08 **	0.64	0.06 *	0.45	0.85	0.26 *	0.97	0.38	0.77 **



\*  $p < 0.05$   
 \*\*  $p < 0.01$   
 \*\*\*  $p < 0.001$

**Figure S2.** Mean mRNA expression data from at least three independent replicates showing the dysregulation of proto-oncogene upon treatment from the cell lines investigated. Statistical analysis to evaluate the difference between means vs control/untreated cells is indicated in the corresponding p-value (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).



**Figure S3.** The relevance of FGR in clinical samples of LIHC. **(A)** The distribution of FGR in tumoral samples compared to non-tumoral tissues. **(B)** The association of FGR expression in the overall survival of patients. Datasets were taken from TCGA and GTEx databases and visualized by GEPIA online tool. LIHC - Liver hepatocellular carcinoma.