

**S10 Table. List of the statistically overrepresented Reactome pathways obtained per IC after ICA.** Only IC1, IC3 and IC6 among the computed six components shown enriched pathways. ID and description pathway is enclosed in the table. *Gene Ratio* indicates the number of genes annotated to a pathway within the specific list of differential genes among the 509 major contributors that are included in the database (185 for IC1, 229 for IC3 and 171 for IC6). *Bg Ratio* refers to the number of genes annotated to a pathway within the background (all differential genes included in the database which is a total of 1895 elements among 5084). Pathways are sorted based on the adj p-value obtained (FDR).

#IC	ID	Description	GeneRatio	BgRatio	p.adj
IC1	198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	17/185	34/1895	<0.001
	168256	Immune System	62/185	361/1895	<0.001
	1280218	Adaptive Immune System	34/185	165/1895	0.001
	373076	Class A/1 (Rhodopsin-like receptors)	16/185	52/1895	0.002
	500792	GPCR ligand binding	17/185	59/1895	0.002
	202433	Generation of second messenger molecules	8/185	17/1895	0.006
	388396	GPCR downstream signaling	20/185	95/1895	0.032
	202403	TCR signaling	10/185	32/1895	0.032
	168249	Innate Immune System	35/185	211/1895	0.032
	2022870	Chondroitin sulfate biosynthesis	5/185	9/1895	0.034
	5602498	MyD88 deficiency (TLR2/4)	4/185	6/1895	0.041
	5603041	IRAK4 deficiency (TLR2/4)	4/185	6/1895	0.041
	202430	Translocation of ZAP-70 to Immunological synapse	5/185	10/1895	0.048
	IC3	156842	Eukaryotic Translation Elongation	33/229	54/1895
192823		Viral mRNA Translation	32/229	51/1895	<0.001
72764		Eukaryotic Translation Termination	32/229	51/1895	<0.001
156902		Peptide chain elongation	32/229	53/1895	<0.001
975956		Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	32/229	53/1895	<0.001
72689		Formation of a pool of free 40S subunits	34/229	61/1895	<0.001
927802		Nonsense-Mediated Decay (NMD)	33/229	58/1895	<0.001
975957		Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	33/229	58/1895	<0.001
156827		L13a-mediated translational silencing of Ceruloplasmin expression	35/229	66/1895	<0.001
157279		3' -UTR-mediated translational regulation	35/229	66/1895	<0.001
72706		GTP hydrolysis and joining of the 60S ribosomal subunit	35/229	67/1895	<0.001
72613		Eukaryotic Translation Initiation	35/229	69/1895	<0.001
72737		Cap-dependent Translation Initiation	35/229	69/1895	<0.001
168255		Influenza Life Cycle	33/229	65/1895	<0.001
168254		Influenza Infection	33/229	66/1895	<0.001
168273		Influenza Viral RNA Transcription and Replication	32/229	63/1895	<0.001
1799339		SRP-dependent cotranslational protein targeting to membrane	32/229	66/1895	<0.001
72766		Translation	36/229	87/1895	<0.001
72649		Translation initiation complex formation	19/229	38/1895	<0.001
72662		Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	19/229	38/1895	<0.001
72702		Ribosomal scanning and start codon recognition	19/229	38/1895	<0.001
72695		Formation of the ternary complex, and subsequently, the 43S complex	18/229	35/1895	<0.001
5663205		Infectious disease	43/229	159/1895	<0.001
1643685		Disease	55/229	244/1895	<0.001
1489509		DAG and IP3 signaling	5/229	8/1895	0.023
167021		PLC-gamma1 signalling	5/229	8/1895	0.023
212718		EGFR interacts with phospholipase C-gamma	5/229	8/1895	0.023

	186763	Downstream signal transduction	13/229	44/1895	0.029
	909733	Interferon alpha/beta signaling	8/229	20/1895	0.029
	1251932	PLCG1 events in ERBB2 signaling	5/229	9/1895	0.037
	5654219	Phospholipase C-mediated cascade	5/229	9/1895	0.037
	5654221	Phospholipase C-mediated cascade; FGFR2	5/229	9/1895	0.037
	5654227	Phospholipase C-mediated cascade; FGFR3	5/229	9/1895	0.037
	5654228	Phospholipase C-mediated cascade; FGFR4	5/229	9/1895	0.037
	140877	Formation of Fibrin Clot (Clotting Cascade)	4/229	6/1895	0.044
	392499	Metabolism of proteins	45/229	253/1895	0.047
IC6	198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	12/171	34/1895	0.010
	72766	Translation	18/171	87/1895	0.046
	156827	L13a-mediated translational silencing of Ceruloplasmin expression	15/171	66/1895	0.046
	157279	3' -UTR-mediated translational regulation	15/171	66/1895	0.046
	113510	E2F mediated regulation of DNA replication	5/171	9/1895	0.046
	1640170	Cell Cycle	29/171	175/1895	0.046
	72706	GTP hydrolysis and joining of the 60S ribosomal subunit	15/171	67/1895	0.046
	69298	Association of licensing factors with the pre-replicative complex	4/171	6/1895	0.046
	72613	Eukaryotic Translation Initiation	15/171	69/1895	0.046
	72737	Cap-dependent Translation Initiation	15/171	69/1895	0.046