

## Supplementary Table S1

Supplementary Table S1: Top 25 enriched pathways identified for DIRAGs higher reactive in seropositive versus seronegative RA in human IgG profiling. Out of 206 clean genesymbols, 101 were found Reactome pathway browser. Name of the pathway (link to Reactome pathway browser), found and total entities, their respective p-value and FDR and found and total reactions are given. The genesymbol found in Reactome and the overrepresentation analysis of the complete 16k chip serving as reference for the respective pathway is given (continued on page 2).

Pathway name	found/total entities	entities p-value	entities FDR (BH)	found/total reactions	GeneSymbols found	found/total entities (16k)	rank (16k)
<a href="#">Endosomal/vacuolar pathway</a>	14/82	$3.18 * 10^{-10}$	$1.99 * 10^{-7}$	3/4	HLA-C	74/82	1
<a href="#">Antigen Presentation: Folding, assembly and peptide loading of class I MHC</a>	14/102	$4.98 * 10^{-9}$	$1.56 * 10^{-6}$	13/16	HLA-C	84/102	2
<a href="#">Interferon alpha/beta signaling</a>	17/184	$3.64 * 10^{-8}$	$6.95 * 10^{-6}$	2/20	HLA-C, IRF5	120/186	41
<a href="#">ER-Phagosome pathway</a>	16/164	$4.45 * 10^{-8}$	$6.95 * 10^{-6}$	4/10	HLA-C, PSMB11, PSMD14	122/173	3
<a href="#">Interferon gamma signaling</a>	19/250	$1.16 * 10^{-7}$	$1.45 * 10^{-5}$	2/15	GBP6, HLA-C, IRF5	138/250	572
<a href="#">Antigen processing-Cross presentation</a>	16/186	$2.38 * 10^{-7}$	$2.48 * 10^{-5}$	8/23	HLA-C, PSMB11, PSMD14	127/195	22
<a href="#">Interferon Signaling</a>	21/392	$6.44 * 10^{-6}$	$5.74 * 10^{-4}$	6/66	EIF4G2, GBP6, HLA-C, IRF5, KPNA3	205/394	1102
<a href="#">Carboxyterminal post-translational modifications of tubulin</a>	7/52	$4.17 * 10^{-5}$	0.003	6/6	TUBA1B, TUBB2B	15/55	1589
<a href="#">RHO GTPases activate IQGAPs</a>	6/36	$4.65 * 10^{-5}$	0.003	5/5	IQGAP2, TUBA1B, TUBB2B	17/36	577
<a href="#">Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane</a>	5/22	$4.79 * 10^{-5}$	0.003	1/2	TUBA1B, TUBB2B	9/22	693
<a href="#">Transport of connexons to the plasma membrane</a>	5/23	$5.89 * 10^{-5}$	0.003	1/3	TUBA1B, TUBB2B	9/23	761
<a href="#">Recycling pathway of L1</a>	6/55	$4.50 * 10^{-4}$	0.023	6/14	MSN, TUBA1B, TUBB2B	30/55	368

<a href="#">The role GTSE1 in G2/M progression after G2 checkpoint</a>	7/83	$7.00 \times 10^{-4}$	0.034	4/10	PSMB11, PSMD14, TUBA1B, TUBB2B	53/83	87
<a href="#">Gap junction assembly</a>	5/41	$8.24 \times 10^{-4}$	0.036	3/16	TUBA1B, TUBB2B	11/41	1485
<a href="#">Post-chaperonin tubulin folding pathway</a>	4/25	0.001	0.042	9/9	TUBA1B, TUBB2B	11/25	610
<a href="#">Immunoregulatory interactions between a lymphoid and a non-lymphoid cell</a>	14/316	0.001	0.056	7/43	HLA-C	95/316	2008
<a href="#">HSP90 chaperone cycle for steroid hormone receptors (SHR)</a>	6/70	0.002	0.056	4/12	FKBP5, TUBA1B, TUBB2B	27/72	1322
<a href="#">Formation of tubulin folding intermediates by CCT/TriC</a>	4/30	0.002	0.068	2/2	TUBA1B, TUBB2B	17/30	250
<a href="#">Gap junction trafficking</a>	5/52	0.002	0.073	3/20	TUBA1B, TUBB2B	18/52	1291
<a href="#">Separation of Sister Chromatids</a>	10/194	0.002	0.073	5/8	ANAPC3, CDCA5, PPP2R1A, PSMB11, PSMD14, TUBA1B, TUBB2B	100/195	877
<a href="#">Cytokine signaling in Immune system</a>	31/1055	0.003	0.087	23/639	EIF4G2, GBP6, HLA-C, HNRPDL, IL17, IRF5, KPNA3, MSN, NFKB2, PPP2R1A, PSMB11, PSMD14	479/1092	2005
<a href="#">Gap junction trafficking and regulation</a>	5/56	0.003	0.089	3/24	TUBA1B, TUBB2B	19/56	1366
<a href="#">Class I MHC mediated antigen processing and presentation</a>	17/464	0.003	0.092	26/48	ANAPC3, HLA-C, PSMB11, PSMD14	240/473	1377
<a href="#">Mitotic Anaphase</a>	10/208	0.004	0.1	6/11	ANAPC3, CDCA5, PPP2R1A, PSMB11, PSMD14, TUBA1B, TUBB2B	124/249	1106
<a href="#">Cooperation of Prefolding and TriC/CCT in actin and tubulin folding</a>	4/37	0.004	0.101	4/6	TUBA1B, TUBB2B	22/37	185