

Supplementary Table S4

Supplementary Table S4: The enriched pathways for antigens **positively (A)** and the **top 20 negatively (B)** correlated with CDAI. Out of the 429 antigenic proteins found significantly correlated with CDAI of both seropositive and seronegative RA patients, 153 positively correlated and 276 negatively correlated proteins were subjected separately to Reactome pathway analysis. Names (linked to Reactome pathway browser), found and total entities, ratio, their p-value and FDRs are given, the number of found & total reactions, as well the respective ratio are given.

A) POSITIVELY CORRELATED	Entities	Entities	Entities	Entities	Entities	Reactions	Reactions	Reactions
Pathway name	found	Total	ratio	pValue	FDR	found	total	ratio
RNA Polymerase I Transcription Initiation	<u>4</u>	50	0.003	2.86E-03	3.37E-01	4	6	0
RUNX1 regulates expression of components of tight junctions	<u>2</u>	8	0.001	3.99E-03	3.37E-01	2	6	0
Metabolism of RNA	<u>18</u>	785	0.052	4.49E-03	3.37E-01	70	187	0.014
Epigenetic regulation of gene expression	<u>6</u>	139	0.009	5.85E-03	3.37E-01	6	34	0.002
Cyclin A/B1/B2 associated events during G2/M transition	<u>3</u>	32	0.002	6.31E-03	3.37E-01	3	25	0.002
RNA Polymerase I Transcription Termination	<u>3</u>	33	0.002	6.86E-03	3.37E-01	3	4	0
Nef mediated downregulation of MHC class I complex cell surface expression	<u>2</u>	11	0.001	7.38E-03	3.37E-01	3	4	0
Formation of the HIV-1 Early Elongation Complex	<u>3</u>	34	0.002	7.44E-03	3.37E-01	5	5	0
Formation of the Early Elongation Complex	<u>3</u>	34	0.002	7.44E-03	3.37E-01	3	3	0
mRNA Capping	<u>3</u>	35	0.002	8.05E-03	3.37E-01	11	11	0.001
Glycolysis	<u>5</u>	110	0.007	9.42E-03	3.37E-01	3	24	0.002
Activation of PPARGC1A (PGC-1alpha) by phosphorylation	2	13	0.001	1.02E-02	3.37E-01	2	2	0

B) NEGATIVELY CORRELATED	Entities	Entities	Entities	Entities	Entities	Reactions	Reactions	Reactions
Pathway name	found	Total	ratio	pValue	FDR	found	total	ratio
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	<u>37</u>	103	0.007	1.11E-16	1.57E-14	13	16	0.001
Endosomal/Vacuolar pathway	<u>36</u>	82	0.005	1.11E-16	1.57E-14	3	4	0
Class I MHC mediated antigen processing & presentation	<u>51</u>	474	0.031	1.11E-16	1.57E-14	28	48	0.004
ER-Phagosome pathway	<u>44</u>	173	0.011	1.11E-16	1.57E-14	4	10	0.001
Interferon Signaling	<u>50</u>	394	0.026	1.11E-16	1.57E-14	25	71	0.005
Antigen processing-Cross presentation	<u>44</u>	195	0.013	1.11E-16	1.57E-14	8	23	0.002
Interferon alpha/beta signaling	<u>45</u>	188	0.012	1.11E-16	1.57E-14	6	24	0.002
Interferon gamma signaling	<u>43</u>	250	0.017	1.11E-16	1.57E-14	2	16	0.001
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	<u>37</u>	316	0.021	2.11E-15	2.64E-13	10	44	0.003
Cytokine Signaling in Immune system	<u>70</u>	1,092	0.072	1.37E-14	1.54E-12	67	710	0.052
Adaptive Immune System	<u>59</u>	1,005	0.067	7.67E-11	7.83E-09	82	264	0.019
Immune System	<u>99</u>	2,684	0.178	1.26E-06	1.19E-04	238	1,625	0.119
AUF1 (hnRNP D0) binds and destabilizes mRNA	<u>8</u>	56	0.004	6.34E-05	5.51E-03	3	4	0
Regulation of mRNA stability by proteins that bind AU-rich elements	<u>10</u>	93	0.006	8.41E-05	6.73E-03	12	26	0.002
ROS sensing by NFE2L2	<u>8</u>	60	0.004	1.02E-04	7.62E-03	3	8	0.001

HIV Infection	<u>17</u>	263	0.017	1.94E-04	1.26E-02	35	160	0.012
Regulation of activated PAK-2p34 by proteasome mediated degradation	<u>7</u>	50	0.003	2.05E-04	1.26E-02	2	2	0
APC/C:Cdc20 mediated degradation of Securin	<u>8</u>	68	0.005	2.36E-04	1.26E-02	3	3	0
Vpu mediated degradation of CD4	<u>7</u>	53	0.004	2.90E-04	1.26E-02	2	5	0
p53-Independent G1/S DNA damage checkpoint	<u>7</u>	54	0.004	3.24E-04	1.26E-02	2	4	0