



Supplementary Figure S1. PathwAX results showing the modulated pathways with the HYBRI treatment according to the gene array study. The top table and pie diagram summarize the significant pathways and its relation and distribution in different disease and processes. The table below shows the list of all enriched (blue) and depleted (red) pathways related to the genes entered in the database, sorted by increasing FDR (only top part shown). The pathways can also be restricted to a class by clicking on the top table. The network connectivity between the query genes and each pathway is represented in the matrix below. Each colored box represents a gene and mouseover shows the number of links to the pathway. The query genes linked to the pathway are represented by the green boxes and the genes that are part of the pathway are represented by the purple boxes. The greater the connectivity, the darker the tones of the boxes.

Supplementary Table S1. List of all the pathways related with the studied genes introduced to PathwAX database.

Pathway	Path-waySize	Cross-Talk	type	pValue	FWER
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NF-kappa B signaling pathway	103	26	enrichment	1.37e-18	3.51e-16
Chemokine signaling pathway	180	34	enrichment	1.53e-18	3.93e-16
Natural killer cell mediated cytotoxicity	94	27	enrichment	5.43e-18	1.40e-15
Leukocyte transendothelial migration	115	34	enrichment	1.22e-16	3.15e-14
Toll-like receptor signaling pathway	96	22	enrichment	4.25e-15	1.09e-12
Hematopoietic cell lineage	96	16	enrichment	9.97e-15	2.56e-12

PD-L1 expression and PD-1 checkpoint pathway in cancer	91	24	enrichment	4.13e-14	1.06e-11
Fc gamma R-mediated phagocytosis	90	28	enrichment	4.22e-14	1.08e-11
Cell adhesion molecules (CAMs)	158	17	enrichment	2.27e-13	5.82e-11
Leishmaniasis	75	22	enrichment	5.41e-13	1.39e-10
Focal adhesion	198	36	enrichment	9.62e-13	2.47e-10
Osteoclast differentiation	124	22	enrichment	1.14e-12	2.93e-10
Human cytomegalovirus infection	239	34	enrichment	1.44e-12	3.71e-10
B cell receptor signaling pathway	78	21	enrichment	2.60e-12	6.69e-10
Rap1 signaling pathway	215	32	enrichment	3.08e-12	7.92e-10
Axon guidance	180	26	enrichment	4.49e-12	1.15e-9
Primary immunodeficiency	40	11	enrichment	6.43e-12	1.65e-9
Tuberculosis	179	31	enrichment	9.75e-12	2.51e-9
Proteoglycans in cancer	206	37	enrichment	9.90e-12	2.54e-9
Regulation of actin cytoskeleton	121	20	enrichment	1.37e-11	3.51e-9
Th1 and Th2 cell differentiation	92	17	enrichment	3.71e-11	9.53e-9
T cell receptor signaling pathway	108	21	enrichment	1.07e-10	2.75e-8
Yersinia infection	127	26	enrichment	1.92e-10	4.92e-8
Kaposi sarcoma-associated herpesvirus infection	193	27	enrichment	2.08e-10	5.33e-8
Toxoplasmosis	116	23	enrichment	3.90e-10	1.00e-7
Cytokine-cytokine receptor interaction	266	12	enrichment	6.10e-10	1.57e-7
Salmonella infection	79	25	enrichment	6.17e-10	1.58e-7
MAPK signaling pathway	298	28	enrichment	1.08e-9	2.77e-7
Pertussis	72	20	enrichment	1.11e-9	2.85e-7
Human immunodeficiency virus 1 infection	227	32	enrichment	1.27e-9	3.25e-7
JAK-STAT signaling pathway	153	14	enrichment	8.16e-9	0.00000210

Hepatitis B	160	25	enrichment	1.26e-8	0.00000323
Th17 cell differentiation	110	21	enrichment	1.77e-8	0.00000456
Viral protein interaction with cytokine and cytokine receptor	83	8	enrichment	1.84e-8	0.00000472
Staphylococcus aureus infection	99	11	enrichment	1.99e-8	0.00000512
Platelet activation	129	24	enrichment	2.10e-8	0.00000539
Adherens junction	75	22	enrichment	4.14e-8	0.0000106
Herpes simplex virus 1 infection	336	25	enrichment	4.28e-8	0.0000110
Necroptosis	154	33	enrichment	1.04e-7	0.0000268
Phospholipase D signaling pathway	152	18	enrichment	2.23e-7	0.0000573
Bacterial invasion of epithelial cells	77	22	enrichment	3.55e-7	0.0000912
Ras signaling pathway	238	22	enrichment	3.75e-7	0.0000963
Fc epsilon RI signaling pathway	71	14	enrichment	6.81e-7	0.000175
Epstein-Barr virus infection	222	30	enrichment	7.67e-7	0.000197
Systemic lupus erythematosus	112	25	enrichment	0.00000134	0.000345
Apoptosis	137	24	enrichment	0.00000198	0.000509
Complement and coagulation cascades	86	10	enrichment	0.00000229	0.000590
Chagas disease (American trypanosomiasis)	105	16	enrichment	0.00000262	0.000673
MicroRNAs in cancer	163	20	enrichment	0.00000351	0.000901
PI3K-Akt signaling pathway	347	29	enrichment	0.00000357	0.000919
Measles	147	20	enrichment	0.00000504	0.00130
Viral carcinogenesis	206	32	enrichment	0.00000619	0.00159
Tight junction	169	27	enrichment	0.00000816	0.00210
Influenza A	167	23	enrichment	0.00000916	0.00235
Amoebiasis	100	13	enrichment	0.0000153	0.00393
Intestinal immune network for IgA production	48	6	enrichment	0.0000177	0.00454

Hepatitis C	158	21	enrich- ment	0.0000179	0.00461
Growth hormone synthesis, secretion and action	119	14	enrich- ment	0.0000267	0.00686
Phagosome	171	27	enrich- ment	0.0000269	0.00692
Pancreatic cancer	76	13	enrich- ment	0.0000297	0.00763
Relaxin signaling pathway	132	14	enrich- ment	0.0000462	0.0119
Endocytosis	245	27	enrich- ment	0.0000498	0.0128
Viral myocarditis	78	13	enrich- ment	0.0000541	0.0139
NOD-like receptor signaling pathway	177	20	enrich- ment	0.0000570	0.0146
TNF signaling pathway	116	11	enrich- ment	0.0000649	0.0167
Acute myeloid leukemia	69	11	enrich- ment	0.0000727	0.0187
Choline metabolism in cancer	97	12	enrich- ment	0.0000749	0.0193
Signaling pathways regulating pluripotency of stem cells	140	12	enrich- ment	0.0000818	0.0210
Hepatocellular carcinoma	176	18	enrich- ment	0.0000847	0.0218
Human T cell leukemia virus 1 infection	233	23	enrich- ment	0.000104	0.0268
Estrogen signaling pathway	133	20	enrich- ment	0.000105	0.0269
Malaria	53	6	enrich- ment	0.000113	0.0291
Pathways in cancer	168	12	enrich- ment	0.000137	0.0352
Neurotrophin signaling pathway	121	16	enrich- ment	0.000154	0.0396
Sphingolipid signaling pathway	124	15	enrich- ment	0.000182	0.0468