Supplementary Data

Supplemental Table 1: List of 144 Genes that Positively Correlated with the KYN/TRP Ratio. The first 71 listed genes, in **bold**, indicate interferon-stimulated genes. Gene ontology (GO) of the remaining 73 genes that correlated with the KYN/TRP ratio revealed genes associated with cell movement, including microtubules and motile cilia; notably, increased kynurenine has been associated with increased expression of cytoskeletal proteins that enhance cell motility in mice.[1] The GO analysis also revealed genes involved in muscle tissue generation and organization, as well as embryo implantation.

Gene	r_s	p
ACVRL1	0.267	0.023
ATF3	0.344	0.003
BST2	0.397	0.001
C1QA	0.300	0.010
C1QB	0.326	0.005
C1QC	0.294	0.012
CDK1	0.294	0.012
CRYM	0.282	0.016
DHX58	0.262	0.026
EPSTI1	0.274	0.020
ETV7	0.321	0.006
EXOC3L1	0.297	0.011
FBXO6	0.247	0.037
GBP1	0.261	0.027
GBP1P1	0.295	0.012
HBQ1	0.304	0.009
HERC6	0.263	0.026
HES4	0.385	0.001
HESX1	0.233	0.049
HIST1H2BO	0.272	0.021
HIST1H4H	0.307	0.009
IFI27	0.367	0.002
IFI35	0.290	0.013
IFI44	0.244	0.039
IFI44L	0.299	0.011
IFI6	0.342	0.003
IFIT1	0.238	0.044
IFIT1B	0.233	0.049
IFIT3	0.254	0.031
IFITM1	0.284	0.016
IFITM3	0.234	0.048
IRF7	0.319	0.007
ISG15	0.315	0.007
KLHDC7B	0.356	0.002

LAP3	0.283	0.016
LGALS3BP	0.290	0.014
LRRC2	0.406	<0.001
LY6E	0.267	0.024
MDK	0.238	0.044
MOV10	0.356	0.002
MS4A4A	0.297	0.011
MT2A	0.402	<0.001
MX1	0.242	0.041
NEXN	0.295	0.012
NRN1	0.252	0.033
OAS1	0.330	0.005
ODF3B	0.317	0.007
PARP10	0.299	0.011
PARP12	0.265	0.024
PTTG1	0.256	0.030
RMI2	0.360	0.002
RTP4	0.307	0.009
SCO2	0.370	0.001
SERPING1	0.268	0.023
SGIP1	0.266	0.024
SIGLEC1	0.237	0.045
SPATS2L	0.286	0.015
STAT2	0.236	0.046
TIMM10	0.335	0.004
TK1	0.344	0.003
TMCC2	0.319	0.006
TMEM45A	0.265	0.024
TPX2	0.248	0.036
TREX1	0.355	0.002
TRHDE-AS1	0.238	0.044
UBE2L6	0.269	0.022
UBQLNL	0.260	0.027
USP18	0.268	0.023
USP41	0.270	0.022
XAF1	0.302	0.010
ZNF684	0.251	0.033
ABCC13	0.288	0.014
AC007016.3	0.267	0.023
AC067945.3	0.371	0.001
AC068831.16	0.246	0.038
AC074338.4	0.275	0.019
ACOD1	0.298	0.011

AL137860.1	0.258	0.029
ANO7P1	0.372	0.001
AP000662.4	0.297	0.011
AP001627.1	0.250	0.034
BISPR	0.309	0.008
CDH6	0.238	0.044
CKAP2L	0.328	0.005
CRAT37	0.332	0.004
CTA-384D8.31	0.277	0.018
CTA-384D8.35	0.281	0.017
CTA-384D8.36	0.350	0.003
CTD-2047H16.2	0.287	0.015
CTD-2095E4.5	0.233	0.049
CTD-2521M24.13	0.248	0.036
CTD-2521M24.4	0.341	0.003
CTD-2521M24.8	0.359	0.002
CTD-2561J22.5	0.304	0.009
FAM155B	0.294	0.012
GAPDHP66	0.263	0.026
GTSE1	0.252	0.033
HBM	0.369	0.001
HCG9	0.289	0.014
HMP19	0.267	0.024
IFITM9P	0.305	0.009
KLC3	0.311	0.008
LA16c-17H1.3	0.273	0.020
LARP1P1	0.279	0.018
LIF	0.390	0.001
LINC01296	0.251	0.033
LLNLR-271C9.1	0.267	0.023
MAFA	0.254	0.032
MTND3P10	0.265	0.024
MTND4LP14	0.245	0.038
MTND4P26	0.254	0.032
MYBL2	0.272	0.021
NRIR	0.263	0.025
OLFM5P	0.232	0.049
OR2B6	0.242	0.040
OR51AB1P	0.375	0.001
OR52B3P	0.248	0.036
RABGAP1L-IT1	0.270	0.022
RNY3P8	0.279	0.018
RP1-221C16.8	0.255	0.031

RP1-71H24.1	0.330	0.005
RP1-99E18.2	0.245	0.038
RP11-20D14.6	0.350	0.003
RP11-273G15.2	0.334	0.004
RP11-288L9.1	0.411	0.000
RP11-288L9.4	0.234	0.048
RP11-54O7.17	0.348	0.003
RP11-560F18.1	0.262	0.026
RP11-609D21.3	0.315	0.007
RP11-77H9.8	0.234	0.048
RP3-449M8.9	0.246	0.037
RP3-467D16.3	0.459	0.000
RP4-718J7.4	0.235	0.047
RUNDC3A	0.322	0.006
RUNDC3A-AS1	0.272	0.021
SMTNL1	0.249	0.035
TEKT1	0.260	0.027
THEM5	0.236	0.046
TMEM56	0.237	0.045
TPRG1-AS1	0.247	0.037
TROAP	0.319	0.006
UNC93B3	0.285	0.015
XK	0.233	0.049
ZDHHC4P1	0.276	0.019

Supplemental Table 2: List of 81 Genes that Positively Correlated with the QA/KA Ratio. The first 38 listed genes, in **bold**, indicate interferon-stimulated genes.

Gene	r_s	p
ATF3	0.250	0.034
BCL2L14	0.345	0.003
C2orf66	0.301	0.010
CCL2	0.370	0.001
CCL8	0.495	<0.001
CCNA1	0.260	0.028
CCNB2	0.268	0.023
CDCA2	0.239	0.043
CDK1	0.311	0.008
CXCL10	0.278	0.018
DLGAP5	0.283	0.016
DTL	0.278	0.018
E2F8	0.390	0.001
EMP1	0.283	0.016
EPHB2	0.261	0.027
IGHV4-59	0.257	0.029
IGHV4-61	0.243	0.040
IGKV1-17	0.284	0.015
IGKV1D-33	0.248	0.036
IL10	0.254	0.031
KCTD14	0.270	0.022
KLHDC7B	0.327	0.005
LAMP3	0.250	0.034
LAP3	0.233	0.049
LIF	0.340	0.004
MCM10	0.327	0.005
MELK	0.276	0.019
MOXD1	0.258	0.029
MS4A4A	0.345	0.003
MT1E	0.249	0.035
NKAIN1	0.259	0.028
PBK	0.273	0.020
RMI2	0.236	0.046
RRM2	0.293	0.013
RUFY4	0.255	0.030
SDC1	0.279	0.018
SLC12A8	0.410	<0.001
SOCS1	0.276	0.019
AC006160.5	0.342	0.003

AP001626.1	0.259	0.028
C1orf226	0.245	0.038
CAV1	0.246	0.037
CDC20P1	0.256	0.030
CDC42P3	0.420	<0.001
CDC45	0.265	0.025
CEP55	0.296	0.012
CKAP2L	0.289	0.014
CTA-384D8.31	0.283	0.016
DLGAP1	0.238	0.044
IGFL2	0.370	0.001
IGKJ3	0.266	0.024
IGKV1-33	0.255	0.031
IGKV1-6	0.267	0.024
IGKV1-8	0.259	0.028
IGKV1D-8	0.269	0.023
IGKV2-40	0.245	0.038
IGKV2D-40	0.248	0.036
IGKV3D-20	0.242	0.041
IGLJ6	0.256	0.030
IGLJ7	0.308	0.009
IGLV1-40	0.253	0.032
IGLV1-50	0.251	0.034
IGLV2-28	0.288	0.014
IGLV3-1	0.236	0.046
IGLV5-37	0.319	0.006
IGLV6-57	0.271	0.022
IQGAP3	0.241	0.041
LIPM	0.272	0.021
MAP6	0.267	0.023
MT2P1	0.262	0.026
PTGFR	0.233	0.049
RGS13	0.278	0.018
RP11-10L7.1	0.334	0.004
RP11-239E10.2	0.276	0.019
RP11-439M11.1	0.260	0.027
RP11-466G12.3	0.237	0.045
SKA1	0.318	0.007
TICRR	0.235	0.047
TMEM178B	0.370	0.001
TTK	0.334	0.004
TYMSOS	0.396	0.001

Reference

1. Moffett JR, Arun P, Puthillathu N, et al. Quinolinate as a Marker for Kynurenine Metabolite Formation and the Unresolved Question of NAD(+) Synthesis During Inflammation and Infection*. Front Immunol* 2020;11:31.