

Appendix

Table S1. The rank scores of 25 genes in common that are upregulated with training

rank scores

gene abbreviation	full gene name	ACC	HC
astl	astacin like metalloendopeptidase	2.9782302	2.6145406
c9	complement C9	2.4242568	2.9751272
cacna2d4	calcium voltage-gated channel auxiliary subunit alpha2delta 4	2.5569508	3.471862
card6	caspase recruitment domain family member 6	2.9706614	2.433023
cd40	CD40 molecule	2.4512355	3.8273673
dmrtb1	DMRT like family B with proline rich C-terminal 1	2.6347992	3.5000591
dnai2	dynein axonemal intermediate chain 2	2.026856	3.2761416
dnase1l2	deoxyribonuclease 1 like 2	3.3436997	3.72264
entpd8	ectonucleoside triphosphate diphosphohydrolase 8	2.0840733	2.364991
ghrh	growth hormone releasing hormone	2.8068497	2.369232
hmox1	heme oxygenase 1	2.5849724	2.5780656
impdh2	inosine monophosphate dehydrogenase 2	2.0824804	2.2658856
inhbb	inhibin beta B subunit	2.61479	2.8082063
mbnl3	muscleblind like splicing regulator 3	3.1857593	2.489401
mnx1	motor neuron and pancreas homeobox 1	3.6334696	4.335227
nkx6-1	NK6 homeobox 1	2.2450445	3.0883238
prrl5l	proline rich 15 like	2.5259113	4.2262025
rps7	ribosomal protein S7	3.7486062	3.9771392
senp8	SUMO/sentrin peptidase family member, NEDD8 specific	3.3826416	2.3196073
sftpa1	surfactant protein A1	2.1839666	5.2199636
skp2	S-phase kinase associated protein 2	2.2981544	3.0969088
steap3	STEAP3 metalloredutase	2.4964416	2.7268634
tbx5	T-box 5	2.2913268	3.3157961
trim7	tripartite motif containing 7	2.114829	2.5109558
znf217	zinc finger protein 217	2.3345547	2.2881632

Table S2. The GSEA results in mouse brain showing the effect of region x training. (NES, normalized enrichment score; p, significance; FDR q, significance when corrected for multiple testing).

	region:training			ACC, trained vs control			HC, trained vs control		
Gene Set Name	NES	p	FDR q	NES	p	FDR q	NES	p	FDR q
<u>REACTOME COLLAGEN CHAIN TRIMERIZATION</u>	2.35	0.0000	0.0000	-1.96	0.0000	0.1332	1.87	0.0000	0.2134
<u>HALLMARK PROTEIN SECRETION</u>	-2.34	0.0000	0.0000	1.78	0.0000	0.4323	-1.78	0.0000	0.2595
<u>GOBP TRANSEPITHELIAL TRANSPORT</u>	2.25	0.0000	0.0050	-1.82	0.0000	0.3015	1.62	0.0151	0.3531
<u>GOMF EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT CONFERRING TENSILE STRENGTH</u>	2.25	0.0000	0.0053	-2.00	0.0000	0.1305	1.85	0.0000	0.2265
REACTOME_COLLAGEN_DEGRADATION	2.15	0.0000	0.0227	-2.00	0.0000	0.1740	1.68	0.0044	0.2923
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES	2.13	0.0000	0.0237	-2.13	0.0000	0.0744	1.92	0.0000	0.1715

Table 3. The GSEA results in mouse blood showing the effect of training. (NES, normalized enrichment score; p, significance; FDR q, significance when corrected for multiple testing).

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 WikiPathways pathway	<u>WP B CELL RECEPTOR SIGNALING PATHWAY</u>	2.51	0.0000	0.0000
Hallmark	<u>HALLMARK OXIDATIVE PHOSPHORYLATION</u>	2.32	0.0000	0.0000
C2 PID pathway	<u>PID BCR 5PATHWAY</u>	2.42	0.0000	0.0000
C2 KEGG pathway	<u>KEGG B CELL RECEPTOR SIGNALING PATHWAY</u>	2.37	0.0000	0.0000
C5 GO Biological Process	<u>GOBP ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY</u>	2.33	0.0000	0.0000
C5 GO Biological Process	<u>GOBP GOLGI VESICLE TRANSPORT</u>	2.29	0.0000	0.0002
C2 Reactome pathway	<u>REACTOME SIGNALING BY THE B CELL RECEPTOR BCR</u>	2.27	0.0000	0.0005
C5 GO Biological Process	<u>GOBP B CELL RECEPTOR SIGNALING PATHWAY</u>	2.25	0.0000	0.0009
C2 PID pathway	<u>PID ATM PATHWAY</u>	2.25	0.0000	0.0010
C2 Reactome pathway	<u>REACTOME TCR SIGNALING</u>	2.23	0.0000	0.0012
C2 PID pathway	<u>PID TNF PATHWAY</u>	2.22	0.0000	0.0014
Hallmark	<u>HALLMARK ALLOGRAFT REJECTION</u>	2.19	0.0000	0.0017
C5 GO Biological Process	<u>GOBP INTRA GOLGI VESICLE MEDIATED TRANSPORT</u>	2.19	0.0000	0.0018
C2 WikiPathways pathway	<u>WP IL3 SIGNALING PATHWAY</u>	2.19	0.0000	0.0019
C2 Reactome pathway	<u>REACTOME HIV INFECTION</u>	2.19	0.0000	0.0021
Hallmark	<u>HALLMARK MTORC1 SIGNALING</u>	2.19	0.0000	0.0021
C2 Reactome pathway	<u>REACTOME INTRA GOLGI TRAFFIC</u>	2.20	0.0000	0.0022
C2 Reactome pathway	<u>REACTOME TRANSLOCATION OF SLC2A4 GLUT4 TO THE PLASMA MEMBRANE</u>	2.19	0.0000	0.0022
C5 GO Biological Process	<u>GOBP IMMUNE RESPONSE REGULATING CELL SURFACE RECEPTOR SIGNALING PATHWAY</u>	2.17	0.0000	0.0026
C5 GO Biological Process	<u>GOBP T CELL RECEPTOR SIGNALING PATHWAY</u>	2.17	0.0000	0.0027
C2 Reactome pathway	<u>REACTOME SIGNALING BY TGF BETA RECEPTOR COMPLEX</u>	2.16	0.0000	0.0032
C2 Reactome pathway	<u>REACTOME ER TO GOLGI ANTEROGRADE TRANSPORT</u>	2.15	0.0000	0.0034
C2 PID pathway	<u>PID TCR PATHWAY</u>	2.14	0.0000	0.0037
C2 Reactome pathway	<u>REACTOME GENERATION OF SECOND MESSENGER MOLECULES</u>	2.14	0.0000	0.0038
C5 GO Cellular Component	<u>GOCC ENDOPLASMIC RETICULUM PROTEIN CONTAINING COMPLEX</u>	2.14	0.0000	0.0039

C5 GO Cellular Component	<u>GOCC FICOLIN 1 RICH GRANULE</u>	2.14	0.0000	0.0039
C5 GO Biological Process	<u>GOBP IMMUNE RESPONSE REGULATING SIGNALING PATHWAY</u>	2.13	0.0000	0.0039
C2 Reactome pathway	<u>REACTOME FC EPSILON RECEPTOR FCERI SIGNALING</u>	2.13	0.0000	0.0040
C2 WikiPathways pathway	<u>WP STEROL REGULATORY ELEMENTBINDING PROTEINS SREBP SIGNALING</u>	2.13	0.0000	0.0041
C2 Reactome pathway	<u>REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC</u>	2.13	0.0000	0.0041
C2 Reactome pathway	<u>REACTOME INTRA GOLGI AND RETROGRADE GOLGI TO ER TRAFFIC</u>	2.12	0.0000	0.0042
C2 PID pathway	<u>PID RAC1 PATHWAY</u>	2.11	0.0000	0.0043
C5 GO Cellular Component	<u>GOCC FICOLIN 1 RICH GRANULE LUMEN</u>	2.10	0.0000	0.0043
C5 GO Biological Process	<u>GOBP GOLGI TO VACUOLE TRANSPORT</u>	2.11	0.0000	0.0044
Hallmark	<u>HALLMARK MYC TARGETS V1</u>	2.12	0.0000	0.0044
C2 Reactome pathway	<u>REACTOME NEUTROPHIL DEGRANULATION</u>	2.09	0.0000	0.0044
C5 GO Biological Process	<u>GOBP RETROGRADE VESICLE MEDIATED TRANSPORT GOLGI TO ENDOPLASMIC RETICULUM</u>	2.10	0.0000	0.0044
C2 KEGG pathway	<u>KEGG NATURAL KILLER CELL MEDIATED CYTOTOXICITY</u>	2.11	0.0000	0.0044
C2 Reactome pathway	<u>REACTOME HOST INTERACTIONS OF HIV FACTORS</u>	2.10	0.0000	0.0044
C2 Reactome pathway	<u>REACTOME G2 M CHECKPOINTS</u>	2.10	0.0000	0.0045
C2 Reactome pathway	<u>REACTOME DEUBIQUITINATION</u>	2.10	0.0000	0.0045
C2 Reactome pathway	<u>REACTOME TNF SIGNALING</u>	2.09	0.0000	0.0046

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF RESPONSE TO ENDOPLASMIC RETICULUM STRESS</u>	2.08	0.0000	0.0050
C5 GO Biological Process	<u>GOBP CELLULAR RESPIRATION</u>	2.08	0.0000	0.0051
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 3 INTERLEUKIN 5 AND GM-CSF SIGNALING</u>	2.08	0.0000	0.0051
C2 WikiPathways pathway	<u>WP MODULATORS OF TCR SIGNALING AND T CELL ACTIVATION</u>	2.08	0.0000	0.0052
C2 PID pathway	<u>PID PDGFRB PATHWAY</u>	2.08	0.0000	0.0052
C2 Reactome pathway	<u>REACTOME CLEC7A DECTIN 1 SIGNALING</u>	2.08	0.0000	0.0052
C2 Reactome pathway	<u>REACTOME COSTIMULATION BY THE CD28 FAMILY</u>	2.07	0.0000	0.0053
C2 Reactome pathway	<u>REACTOME ANTIGEN ACTIVATES B CELL RECEPTOR BCR LEADING TO GENERATION OF SECOND MESSENGERS</u>	2.07	0.0000	0.0053
C2 PID pathway	<u>PID FAS PATHWAY</u>	2.07	0.0000	0.0054
C5 GO Cellular Component	<u>GOCC VESICLE TETHERING COMPLEX</u>	2.07	0.0000	0.0054

C2 KEGG pathway	<u>KEGG SPLICEOSOME</u>	2.07	0.0000	0.0054
C5 GO Biological Process	<u>GOBP NATURAL KILLER CELL MEDIATED IMMUNITY</u>	2.06	0.0000	0.0054
C2 WikiPathways pathway	<u>WP TNFALPHA SIGNALING PATHWAY</u>	2.07	0.0000	0.0054
C5 GO Biological Process	<u>GOBP MEMBRANE RAFT ORGANIZATION</u>	2.06	0.0000	0.0055
C2 Reactome pathway	<u>REACTOME ANTIGEN PROCESSING CROSS PRESENTATION</u>	2.06	0.0000	0.0055
C5 GO Biological Process	<u>GOBP POST GOLGI VESICLE MEDIATED TRANSPORT</u>	2.07	0.0000	0.0055
C2 KEGG pathway	<u>KEGG FC GAMMA R MEDIATED PHAGOCYTOSIS</u>	2.06	0.0000	0.0055
C2 Reactome pathway	<u>REACTOME REGULATION OF TNFR1 SIGNALING</u>	2.06	0.0000	0.0055
C5 GO Molecular Function	<u>GOMF PROTEIN N TERMINUS BINDING</u>	2.06	0.0000	0.0055
C2 PID pathway	<u>PID IL12 2PATHWAY</u>	2.06	0.0000	0.0056
C2 Reactome pathway	<u>REACTOME COOPERATION OF PREFOLDIN AND TRIC CT IN ACTIN AND TUBULIN FOLDING</u>	2.06	0.0000	0.0056
C2 Reactome pathway	<u>REACTOME PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA</u>	2.05	0.0000	0.0056
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL ACTIVITY OF SMAD2 SMAD3 SMAD4 HETEROTRIMER</u>	2.05	0.0000	0.0056
C2 Reactome pathway	<u>REACTOME HSP90 CHAPERONE CYCLE FOR STEROID HORMONE RECEPTORS SHR IN THE PRESENCE OF LIGAND</u>	2.05	0.0000	0.0057
C2 Reactome pathway	<u>REACTOME COPI INDEPENDENT GOLGI TO ER RETROGRADE TRAFFIC</u>	2.04	0.0000	0.0064
C2 WikiPathways pathway	<u>WP 4HYDROXYTAMOXIFEN DEXAMETHASONE AND RETINOIC ACIDS REGULATION OF P27 EXPRESSION</u>	2.04	0.0000	0.0064
C2 WikiPathways pathway	<u>WP TCELL ACTIVATION SARSCOV2</u>	2.04	0.0000	0.0064
C2 WikiPathways pathway	<u>WP TCELL ANTIGEN RECEPTOR TCR PATHWAY DURING STAPHYLOCOCCUS AUREUS INFECTION</u>	2.04	0.0000	0.0064
C2 WikiPathways pathway	<u>WP INTERACTIONS OF NATURAL KILLER CELLS IN PANCREATIC CANCER</u>	2.04	0.0000	0.0065
C2 PID pathway	<u>PID P38 ALPHA BETA PATHWAY</u>	2.04	0.0000	0.0065
C2 PID pathway	<u>PID CD8 TCR PATHWAY</u>	2.03	0.0000	0.0066
C2 PID pathway	<u>PID PI3KCI PATHWAY</u>	2.03	0.0000	0.0068
C2 Reactome pathway	<u>REACTOME PROTEIN LOCALIZATION</u>	2.03	0.0000	0.0069
C5 GO Cellular Component	<u>GOCC SPLICEOSOMAL SNRNP COMPLEX</u>	2.03	0.0000	0.0071
C5 GO Cellular Component	<u>GOCC NUCLEAR PERIPHERY</u>	2.02	0.0000	0.0073
C2 KEGG pathway	<u>KEGG PATHOGENIC ESCHERICHIA COLI INFECTION</u>	2.02	0.0000	0.0073
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF B CELL ACTIVATION</u>	2.02	0.0000	0.0075
C5 GO Biological Process	<u>GOBP REGULATION OF TRANSLATIONAL INITIATION</u>	2.02	0.0000	0.0076
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL REGULATION BY RUNX3</u>	2.01	0.0000	0.0079

C5 GO Biological Process	<u>GOBP_OXIDATIVE_PHOSPHORYLATION</u>	2.01	0.0000	0.0079
C5 GO Biological Process	<u>GOBP_RETROGRADE_TRANSPORT_ENDOSOME_TO_GOLGI</u>	2.01	0.0000	0.0081
C2 WikiPathways pathway	<u>WP_PATHOGENIC_ESCHERICHIA_COLI_INFECTION</u>	2.01	0.0000	0.0081

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 WikiPathways pathway	<u>WP_IL1_SIGNALING_PATHWAY</u>	2.01	0.0000	0.0083
C2 WikiPathways pathway	<u>WP_MRNA_PROCESSING</u>	2.01	0.0000	0.0084
C2 Reactome pathway	<u>REACTOME_TNFR1_INDUCED_NFKAPPAB_SIGNALING_PATHWAY</u>	2.00	0.0000	0.0086
C2 Reactome pathway	<u>REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION</u>	2.00	0.0000	0.0088
C5 GO Molecular Function	<u>GOMF_RIBOSOME_BINDING</u>	2.00	0.0000	0.0089
C2 Reactome pathway	<u>REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT</u>	2.00	0.0000	0.0089
C2 Reactome pathway	<u>REACTOME_SIGNALING_BY_NOTCH4</u>	2.00	0.0000	0.0090
C2 WikiPathways pathway	<u>WP_MICROGLIA_PATHOGEN_PHAGOCYTOSIS_PATHWAY</u>	1.99	0.0000	0.0090
C5 GO Biological Process	<u>GOBP_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL</u>	1.99	0.0000	0.0090
C2 Reactome pathway	<u>REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION</u>	2.00	0.0000	0.0090
C2 BioCarta pathway	<u>BIOCARTA_PROTEASOME_PATHWAY</u>	1.99	0.0019	0.0091
C5 GO Biological Process	<u>GOBP_MACROAUTOPHAGY</u>	1.99	0.0000	0.0091
C2 WikiPathways pathway	<u>WP_HEPATITIS_B_INFECTION</u>	1.99	0.0000	0.0091
C2 KEGG pathway	<u>KEGG_TYPE_II_DIABETES_MELLITUS</u>	1.99	0.0000	0.0092
C2 WikiPathways pathway	<u>WP_TGFBETA_SIGNALING_PATHWAY</u>	1.99	0.0000	0.0092
C5 GO Molecular Function	<u>GOMF_SNORNA_BINDING</u>	1.99	0.0018	0.0092
C2 BioCarta pathway	<u>BIOCARTA_HCMV_PATHWAY</u>	1.99	0.0000	0.0092
C2 WikiPathways pathway	<u>WP_THYMIC_STROMAL_LYMPHOPOIETIN_TSLP_SIGNALING_PATHWAY</u>	1.99	0.0000	0.0092
C2 KEGG pathway	<u>KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY</u>	1.99	0.0000	0.0092
C5 GO Biological Process	<u>GOBP_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OXIDATIVE_STRESS</u>	1.99	0.0000	0.0093
C5 GO Cellular Component	<u>GOCC_MEDIATOR_COMPLEX</u>	1.98	0.0000	0.0094
C2 Reactome pathway	<u>REACTOME_S_PHASE</u>	1.98	0.0000	0.0094
C5 GO Biological Process	<u>GOBP_PROTEIN_LOCALIZATION_TO_CHROMOSOME</u>	1.98	0.0000	0.0095
C5 GO Biological Process	<u>GOBP_ENDOPLASMIC_RETICULUM_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT</u>	1.98	0.0000	0.0096

C2 Reactome pathway	<u>REACTOME DOWNSTREAM SIGNALING EVENTS OF B CELL RECEPTOR BCR</u>	1.98	0.0000	0.0097
C2 WikiPathways pathway	<u>WP IL5 SIGNALING PATHWAY</u>	1.98	0.0000	0.0097
C2 WikiPathways pathway	<u>WP LEPTIN SIGNALING PATHWAY</u>	1.98	0.0018	0.0099
C5 GO Molecular Function	<u>GOMF RIBONUCLEOPROTEIN COMPLEX BINDING</u>	1.98	0.0000	0.0099
C2 BioCarta pathway	<u>BIOCARTA FCER1 PATHWAY</u>	1.97	0.0000	0.0100
C2 WikiPathways pathway	<u>WP TCELL RECEPTOR TCR SIGNALING PATHWAY</u>	1.97	0.0000	0.0100
C2 WikiPathways pathway	<u>WP TYROBP CAUSAL NETWORK IN MICROGLIA</u>	1.97	0.0000	0.0100
C5 GO Molecular Function	<u>GOMF SIGNAL SEQUENCE BINDING</u>	1.97	0.0000	0.0100
C2 Reactome pathway	<u>REACTOME FCERI MEDIATED NF KB ACTIVATION</u>	1.97	0.0000	0.0101
C2 Reactome pathway	<u>REACTOME COPI MEDIATED ANTEROGRADE TRANSPORT</u>	1.97	0.0000	0.0102
C2 WikiPathways pathway	<u>WP PROLACTIN SIGNALING PATHWAY</u>	1.97	0.0000	0.0103
C5 GO Molecular Function	<u>GOMF ISOPEPTIDASE ACTIVITY</u>	1.97	0.0000	0.0103
C2 Reactome pathway	<u>REACTOME CRISTAE FORMATION</u>	1.97	0.0000	0.0103
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL REGULATION BY RUNX1</u>	1.97	0.0000	0.0103
C2 Reactome pathway	<u>REACTOME MYD88 INDEPENDENT TLR4 CASCADE</u>	1.97	0.0000	0.0103
C2 Reactome pathway	<u>REACTOME INFLAMMASOMES</u>	1.96	0.0000	0.0104
C5 GO Molecular Function	<u>GOMF INOSITOL PHOSPHATE PHOSPHATASE ACTIVITY</u>	1.96	0.0000	0.0104
C5 GO Biological Process	<u>GOBP REGULATION OF RESPONSE TO ENDOPLASMIC RETICULUM STRESS</u>	1.96	0.0000	0.0104

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 Reactome pathway	<u>REACTOME DOWNREGULATION OF SMAD2 3 SMAD4 TRANSCRIPTIONAL ACTIVITY</u>	1.96	0.0000	0.0105
C5 GO Biological Process	<u>GOBP ACTIVATION OF IMMUNE RESPONSE</u>	1.96	0.0000	0.0107
C2 BioCarta pathway	<u>BIOCARTA STRESS PATHWAY</u>	1.96	0.0000	0.0108
C2 Reactome pathway	<u>REACTOME DEATH RECEPTOR SIGNALLING</u>	1.95	0.0000	0.0110
C5 GO Molecular Function	<u>GOMF NUCLEAR RECEPTOR COACTIVATOR ACTIVITY</u>	1.95	0.0000	0.0110
C2 Reactome pathway	<u>REACTOME FLT3 SIGNALING</u>	1.95	0.0000	0.0110
C5 GO Biological Process	<u>GOBP T CELL ACTIVATION</u>	1.95	0.0000	0.0111
Hallmark	<u>HALLMARK PI3K AKT MTOR SIGNALING</u>	1.96	0.0000	0.0111
C5 GO Molecular Function	<u>GOMF TRANSLATION ELONGATION FACTOR ACTIVITY</u>	1.95	0.0000	0.0111
C2 WikiPathways pathway	<u>WP GASTRIC CANCER NETWORK 2</u>	1.95	0.0000	0.0111
C5 GO Biological Process	<u>GOBP LEUKOCYTE DEGRANULATION</u>	1.95	0.0000	0.0111
C5 GO Biological Process	<u>GOBP NUCLEOLAR LARGE RRNA TRANSCRIPTION BY RNA POLYMERASE I</u>	1.95	0.0000	0.0111

C5 GO Biological Process	<u>GOBP MEMBRANE LIPID CATABOLIC PROCESS</u>	1.95	0.0000	0.0112
C2 Reactome pathway	<u>REACTOME METALLOPROTEASE DUBS</u>	1.95	0.0000	0.0112
C5 GO Biological Process	<u>GOBP LYMPHOCYTE COSTIMULATION</u>	1.95	0.0019	0.0112
C2 Reactome pathway	<u>REACTOME ASPARAGINE N LINKED GLYCOSYLATION</u>	1.95	0.0000	0.0113
C2 KEGG pathway	<u>KEGG CHRONIC MYELOID LEUKEMIA</u>	1.95	0.0000	0.0113
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL REGULATION BY TP53</u>	1.95	0.0000	0.0114
C5 GO Molecular Function	<u>GOMF MANNOSIDASE ACTIVITY</u>	1.95	0.0019	0.0114
C2 WikiPathways pathway	<u>WP TOLLLIKE RECEPTOR SIGNALING PATHWAY</u>	1.95	0.0000	0.0114
C5 GO Biological Process	<u>GOBP PROTEIN K11 LINKED UBIQUITINATION</u>	1.95	0.0000	0.0115
C5 GO Biological Process	<u>GOBP LEUKOCYTE MEDIATED CYTOTOXICITY</u>	1.94	0.0000	0.0116
C2 Reactome pathway	<u>REACTOME NEGATIVE REGULATION OF MAPK PATHWAY</u>	1.94	0.0000	0.0116
C5 GO Biological Process	<u>GOBP REGULATION OF B CELL DIFFERENTIATION</u>	1.94	0.0019	0.0116
C5 GO Molecular Function	<u>GOMF UBIQUITIN LIKE PROTEIN BINDING</u>	1.94	0.0000	0.0117
C5 GO Biological Process	<u>GOBP PROTEIN LOCALIZATION TO ENDOSOME</u>	1.94	0.0000	0.0118
C5 GO Cellular Component	<u>GOCC MITOCHONDRIAL PROTEIN CONTAINING COMPLEX</u>	1.94	0.0000	0.0119
C2 Reactome pathway	<u>REACTOME MRNA SPLICING</u>	1.94	0.0000	0.0119
C2 Reactome pathway	<u>REACTOME RHOA GTPASE CYCLE</u>	1.94	0.0000	0.0119
C5 GO Biological Process	<u>GOBP ALPHA BETA T CELL PROLIFERATION</u>	1.94	0.0000	0.0119
C5 GO Biological Process	<u>GOBP TRANSLATIONAL INITIATION</u>	1.94	0.0000	0.0120
C2 Reactome pathway	<u>REACTOME COPII MEDIATED VESICLE TRANSPORT</u>	1.93	0.0000	0.0121
C2 Reactome pathway	<u>REACTOME RNA POLYMERASE II TRANSCRIBES SNRNA GENES</u>	1.93	0.0000	0.0121
C5 GO Biological Process	<u>GOBP ORGANELLE DISASSEMBLY</u>	1.93	0.0000	0.0121
C5 GO Biological Process	<u>GOBP CYTOSOLIC TRANSPORT</u>	1.94	0.0000	0.0121
C5 GO Biological Process	<u>GOBP MITOPHAGY</u>	1.93	0.0018	0.0121
C2 KEGG pathway	<u>KEGG NEUROTROPHIN SIGNALING PATHWAY</u>	1.93	0.0000	0.0121
C2 PID pathway	<u>PID IL6 7 PATHWAY</u>	1.93	0.0000	0.0121
C5 GO Cellular Component	<u>GOCC INTRINSIC COMPONENT OF ENDOPLASMIC RETICULUM MEMBRANE</u>	1.94	0.0017	0.0121
C2 Reactome pathway	<u>REACTOME SWITCHING OF ORIGINS TO A POST REPLICATIVE STATE</u>	1.93	0.0000	0.0121
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF TELOMERASE RNA LOCALIZATION TO CAJAL BODY</u>	1.93	0.0038	0.0121
C2 WikiPathways pathway	<u>WP ATM SIGNALING PATHWAY</u>	1.94	0.0017	0.0121

Group	Gene Set Name	NES	p	FDR q
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		post, trained vs control		
C2 WikiPathways pathway	<u>WP INTERFERON TYPE I SIGNALING PATHWAYS</u>	1.93	0.0000	0.0121
C2 Reactome pathway	<u>REACTOME OVARIAN TUMOR DOMAIN PROTEASES</u>	1.93	0.0000	0.0126
C5 GO Biological Process	<u>GOBP INTRACELLULAR PROTEIN TRANSMEMBRANE TRANSPORT</u>	1.93	0.0036	0.0126
C2 Reactome pathway	<u>REACTOME SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION</u>	1.93	0.0000	0.0126
C2 PID pathway	<u>PID FCER1 PATHWAY</u>	1.92	0.0000	0.0128
C2 PID pathway	<u>PID P53 REGULATION PATHWAY</u>	1.92	0.0000	0.0128
C2 Reactome pathway	<u>REACTOME TRANSCRIPTION OF THE HIV GENOME</u>	1.92	0.0000	0.0128
C2 WikiPathways pathway	<u>WP ELECTRON TRANSPORT CHAIN OXPHOS SYSTEM IN MITOCHONDRIA</u>	1.92	0.0000	0.0128
C2 Reactome pathway	<u>REACTOME CTLA4 INHIBITORY SIGNALING</u>	1.92	0.0000	0.0129
C5 GO Cellular Component	<u>GOCC AZUROPHIL GRANULE LUMEN</u>	1.92	0.0000	0.0129
C5 GO Molecular Function	<u>GOMF MODIFICATION DEPENDENT PROTEIN BINDING</u>	1.92	0.0000	0.0129
C2 WikiPathways pathway	<u>WP MITOCHONDRIAL IMMUNE RESPONSE TO SARS COV2</u>	1.92	0.0000	0.0129
C2 Reactome pathway	<u>REACTOME PTEN REGULATION</u>	1.92	0.0000	0.0129
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF OXIDATIVE STRESS INDUCED CELL DEATH</u>	1.92	0.0018	0.0129
C2 Reactome pathway	<u>REACTOME PARASITE INFECTION</u>	1.92	0.0000	0.0129
C2 PID pathway	<u>PID IL2 STAT5 PATHWAY</u>	1.92	0.0019	0.0129
C2 PID pathway	<u>PID INSULIN GLUCOSE PATHWAY</u>	1.92	0.0000	0.0129
C2 PID pathway	<u>PID IL2 1PATHWAY</u>	1.92	0.0000	0.0130
C5 GO Biological Process	<u>GOBP REGULATION OF ALPHA BETA T CELL ACTIVATION</u>	1.91	0.0000	0.0130
C5 GO Biological Process	<u>GOBP REGULATION OF ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY</u>	1.92	0.0000	0.0130
C5 GO Biological Process	<u>GOBP GOLGI ORGANIZATION</u>	1.91	0.0000	0.0130
C2 Reactome pathway	<u>REACTOME SIGNALING BY BRAF AND RAF1 FUSIONS</u>	1.91	0.0000	0.0130
C2 Reactome pathway	<u>REACTOME REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU RICH ELEMENTS</u>	1.92	0.0000	0.0130
C2 Reactome pathway	<u>REACTOME CYTOSOLIC SENSORS OF PATHOGEN ASSOCIATED DNA</u>	1.92	0.0000	0.0130
C2 Reactome pathway	<u>REACTOME FCGAMMA RECEPTOR FCGR DEPENDENT PHAGOCYTOSIS</u>	1.92	0.0000	0.0131
C5 GO Cellular Component	<u>GOCC INNER MITOCHONDRIAL MEMBRANE PROTEIN COMPLEX</u>	1.91	0.0000	0.0131
C5 GO Cellular Component	<u>GOCC SPLICEOSOMAL COMPLEX</u>	1.91	0.0000	0.0131
C2 Reactome pathway	<u>REACTOME TOLL LIKE RECEPTOR 9 TLR9 CASCADE</u>	1.92	0.0000	0.0131

C2 Reactome pathway	<u>REACTOME DEGRADATION OF BETA CATENIN BY THE DESTRUCTION COMPLEX</u>	1.91	0.0000	0.0131
C2 Reactome pathway	<u>REACTOME SIGNALING BY CTNNB1 PHOSPHO SITE MUTANTS</u>	1.91	0.0019	0.0131
C2 WikiPathways pathway	<u>WP DNA IRDAMAGE AND CELLULAR RESPONSE VIA ATR</u>	1.91	0.0000	0.0131
C2 Reactome pathway	<u>REACTOME CELL CYCLE CHECKPOINTS</u>	1.91	0.0000	0.0131
C5 GO Biological Process	<u>GOBP AEROBIC RESPIRATION</u>	1.91	0.0000	0.0131
C5 GO Cellular Component	<u>GOCC U2 TYPE SPLICEOSOMAL COMPLEX</u>	1.91	0.0000	0.0131
C2 KEGG pathway	<u>KEGG INSULIN SIGNALING PATHWAY</u>	1.91	0.0000	0.0132
C2 Reactome pathway	<u>REACTOME ABERRANT REGULATION OF MITOTIC EXIT IN CANCER DUE TO RB1 DEFECTS</u>	1.91	0.0019	0.0132
C5 GO Cellular Component	<u>GOCC LUMENAL SIDE OF MEMBRANE</u>	1.91	0.0000	0.0133
C2 WikiPathways pathway	<u>WP TNFRELATED WEAK INDUCER OF APOPTOSIS TWAK SIGNALING PATHWAY</u>	1.91	0.0000	0.0135
C5 GO Biological Process	<u>GOBP FATTY ACID BETA OXIDATION</u>	1.90	0.0000	0.0140
C2 Reactome pathway	<u>REACTOME PEROXISOMAL PROTEIN IMPORT</u>	1.90	0.0000	0.0141
C2 Reactome pathway	<u>REACTOME RUNX1 REGULATES GENES INVOLVED IN MEGAKARYOCYTE DIFFERENTIATION AND PLATELET FUNCTION</u>	1.90	0.0000	0.0141
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY</u>	1.90	0.0000	0.0142

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP PROTEASOMAL PROTEIN CATABOLIC PROCESS</u>	1.90	0.0000	0.0142
C2 Reactome pathway	<u>REACTOME TOLL LIKE RECEPTOR TLR1 TLR2 CASCADE</u>	1.90	0.0000	0.0143
C2 Reactome pathway	<u>REACTOME DEFECTIVE INTRINSIC PATHWAY FOR APOPTOSIS</u>	1.90	0.0000	0.0143
C5 GO Cellular Component	<u>GOCC SITE OF DOUBLE STRAND BREAK</u>	1.90	0.0000	0.0149
C5 GO Biological Process	<u>GOBP PROTEIN K63 LINKED DEUBIQUITINATION</u>	1.89	0.0017	0.0149
C2 KEGG pathway	<u>KEGG PANCREATIC CANCER</u>	1.89	0.0000	0.0150
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION</u>	1.89	0.0019	0.0150
C5 GO Molecular Function	<u>GOMF RNA POLYMERASE CORE ENZYME BINDING</u>	1.89	0.0000	0.0150
C2 Reactome pathway	<u>REACTOME REGULATION OF RUNX3 EXPRESSION AND ACTIVITY</u>	1.89	0.0000	0.0151
C2 WikiPathways pathway	<u>WP CARDIAC HYPERTROPHIC RESPONSE</u>	1.89	0.0017	0.0151
C5 GO Biological Process	<u>GOBP REGULATION OF HISTONE METHYLATION</u>	1.89	0.0000	0.0151

C2 Reactome pathway	<u>REACTOME ONCOGENIC MAPK SIGNALING</u>	1.89	0.0000	0.0151
C2 Reactome pathway	<u>REACTOME REGULATION OF SIGNALING BY CBL</u>	1.89	0.0000	0.0152
C2 Reactome pathway	<u>REACTOME RESPIRATORY ELECTRON TRANSPORT ATP SYNTHESIS BY CHEMIOSMOTIC COUPLING AND HEAT PRODUCTION BY UNCOUPLING PROTEINS</u>	1.89	0.0000	0.0153
C2 WikiPathways pathway	<u>WP PROTEASOME DEGRADATION</u>	1.89	0.0000	0.0154
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 1 SIGNALING</u>	1.89	0.0000	0.0154
C2 Reactome pathway	<u>REACTOME SYNTHESIS OF DNA</u>	1.89	0.0000	0.0155
C2 WikiPathways pathway	<u>WP IL2 SIGNALING PATHWAY</u>	1.89	0.0000	0.0155
C5 GO Cellular Component	<u>GOCC MAGNESIUM DEPENDENT PROTEIN SERINE THREONINE PHOSPHATASE COMPLEX</u>	1.89	0.0038	0.0156
C2 KEGG pathway	<u>KEGG ANTIGEN PROCESSING AND PRESENTATION</u>	1.89	0.0000	0.0156
C5 GO Biological Process	<u>GOBP VACUOLAR TRANSPORT</u>	1.89	0.0000	0.0156
C2 PID pathway	<u>PID CERAMIDE PATHWAY</u>	1.88	0.0000	0.0158
C5 GO Biological Process	<u>GOBP REGULATION OF LYMPHOCYTE ACTIVATION</u>	1.88	0.0000	0.0158
C5 GO Biological Process	<u>GOBP ESTABLISHMENT OF PROTEIN LOCALIZATION TO ORGANELLE</u>	1.88	0.0000	0.0159
C2 WikiPathways pathway	<u>WP NAD METABOLISM IN ONCOGENEINDUCED SENESCENCE AND MITOCHONDRIAL DYSFUNCTIONASSOCIATED SENESCENCE</u>	1.88	0.0000	0.0159
C5 GO Biological Process	<u>GOBP B CELL ACTIVATION</u>	1.88	0.0000	0.0159
C5 GO Molecular Function	<u>GOMF HEAT SHOCK PROTEIN BINDING</u>	1.88	0.0000	0.0159
C2 Reactome pathway	<u>REACTOME UB SPECIFIC PROCESSING PROTEASES</u>	1.88	0.0000	0.0159
C5 GO Cellular Component	<u>GOCC PHOSPHATASE COMPLEX</u>	1.88	0.0000	0.0161
C5 GO Molecular Function	<u>GOMF PHOSPHATASE BINDING</u>	1.88	0.0000	0.0162
C2 Reactome pathway	<u>REACTOME TELOMERE EXTENSION BY TELOMERASE</u>	1.88	0.0000	0.0162
C2 Reactome pathway	<u>REACTOME INTEGRIN SIGNALING</u>	1.88	0.0019	0.0163
C5 GO Molecular Function	<u>GOMF PROTEIN PHOSPHORYLATED AMINO ACID BINDING</u>	1.88	0.0000	0.0166
C5 GO Cellular Component	<u>GOCC SITE OF DNA DAMAGE</u>	1.88	0.0000	0.0166
C5 GO Cellular Component	<u>GOCC VESICLE LUMEN</u>	1.88	0.0000	0.0167
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF HISTONE MODIFICATION</u>	1.87	0.0000	0.0169
C5 GO Cellular Component	<u>GOCC CHAPERONE COMPLEX</u>	1.87	0.0000	0.0169
C5 GO Cellular Component	<u>GOCC OUTER MITOCHONDRIAL MEMBRANE PROTEIN COMPLEX</u>	1.87	0.0000	0.0169
C2 BioCarta pathway	<u>BIOCARTA BCR PATHWAY</u>	1.87	0.0000	0.0169
C2 Reactome pathway	<u>REACTOME HIV LIFE CYCLE</u>	1.87	0.0000	0.0169

C5 GO Biological Process	<u>GOBP REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS</u>	1.87	0.0000	0.0169
C2 Reactome pathway	<u>REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS</u>	1.87	0.0000	0.0169

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 WikiPathways pathway	<u>WP COPPER HOMEOSTASIS</u>	1.87	0.0000	0.0170
C5 GO Molecular Function	<u>GOMF PHOSPHOLIPID TRANSFER ACTIVITY</u>	1.87	0.0056	0.0170
C2 WikiPathways pathway	<u>WP TRANSLATION INHIBITORS IN CHRONICALLY ACTIVATED PDGFRA CELLS</u>	1.87	0.0000	0.0171
C2 Reactome pathway	<u>REACTOME AUTOPHAGY</u>	1.87	0.0000	0.0174
C5 GO Biological Process	<u>GOBP RNA SPLICING VIA TRANSESTERIFICATION REACTIONS</u>	1.87	0.0000	0.0174
C2 Reactome pathway	<u>REACTOME UNFOLDED PROTEIN RESPONSE UPR</u>	1.87	0.0000	0.0174
C2 KEGG pathway	<u>KEGG T CELL RECEPTOR SIGNALING PATHWAY</u>	1.87	0.0000	0.0175
C2 Reactome pathway	<u>REACTOME ASSOCIATION OF TRIC CCT WITH TARGET PROTEINS DURING BIOSYNTHESIS</u>	1.87	0.0000	0.0176
C2 Reactome pathway	<u>REACTOME RRNA MODIFICATION IN THE NUCLEUS AND CYTOSOL</u>	1.87	0.0000	0.0176
C2 Reactome pathway	<u>REACTOME DNA REPLICATION</u>	1.87	0.0000	0.0176
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 1 FAMILY SIGNALING</u>	1.86	0.0000	0.0177
C2 Reactome pathway	<u>REACTOME UCH PROTEINASES</u>	1.86	0.0000	0.0177
C5 GO Biological Process	<u>GOBP CHAPERONE MEDIATED PROTEIN FOLDING</u>	1.86	0.0036	0.0177
C2 PID pathway	<u>PID VEGFR1 2 PATHWAY</u>	1.86	0.0000	0.0177
C2 WikiPathways pathway	<u>WP DNA IRDOUBLE STRAND BREAKS AND CELLULAR RESPONSE VIA ATM</u>	1.86	0.0035	0.0178
C2 WikiPathways pathway	<u>WP REGUCALCIN IN PROXIMAL TUBULE EPITHELIAL KIDNEY CELLS</u>	1.86	0.0019	0.0178
C2 KEGG pathway	<u>KEGG PROTEIN EXPORT</u>	1.86	0.0000	0.0179
C2 WikiPathways pathway	<u>WP TCA CYCLE AKA KREBS OR CITRIC ACID CYCLE</u>	1.86	0.0018	0.0179
C2 Reactome pathway	<u>REACTOME THE CITRIC ACID TCA CYCLE AND RESPIRATORY ELECTRON TRANSPORT</u>	1.86	0.0000	0.0179
C2 KEGG pathway	<u>KEGG PARKINSONS DISEASE</u>	1.86	0.0000	0.0179
C5 GO Biological Process	<u>GOBP RNA SPLICING</u>	1.86	0.0000	0.0180
C2 KEGG pathway	<u>KEGG UBIQUITIN MEDIATED PROTEOLYSIS</u>	1.86	0.0000	0.0180
C5 GO Biological Process	<u>GOBP PROTEIN TRANSMEMBRANE TRANSPORT</u>	1.86	0.0000	0.0180
C2 BioCarta pathway	<u>BIOCARTA NTHI PATHWAY</u>	1.86	0.0018	0.0180
C5 GO Molecular Function	<u>GOMF UNFOLDED PROTEIN BINDING</u>	1.86	0.0000	0.0182

C2 Reactome pathway	<u>REACTOME PROTEIN FOLDING</u>	1.86	0.0017	0.0182
C5 GO Biological Process	<u>GOBP REGULATION OF LEUKOCYTE DEGRANULATION</u>	1.86	0.0037	0.0183
C5 GO Biological Process	<u>GOBP RESPIRATORY ELECTRON TRANSPORT CHAIN</u>	1.86	0.0000	0.0183
C5 GO Biological Process	<u>GOBP GRANULOCYTE ACTIVATION</u>	1.86	0.0000	0.0184
C5 GO Biological Process	<u>GOBP FC EPSILON RECEPTOR SIGNALING PATHWAY</u>	1.86	0.0019	0.0184
C2 Reactome pathway	<u>REACTOME MAPK6 MAPK4 SIGNALING</u>	1.86	0.0000	0.0184
C5 GO Cellular Component	<u>GOCC VESICLE COAT</u>	1.85	0.0000	0.0185
C5 GO Biological Process	<u>GOBP ANTIGEN PROCESSING AND PRESENTATION</u>	1.85	0.0000	0.0189
C5 GO Cellular Component	<u>GOCC PRESPLICEOSOME</u>	1.85	0.0073	0.0189
C5 GO Biological Process	<u>GOBP FC RECEPTOR MEDIATED STIMULATORY SIGNALING PATHWAY</u>	1.85	0.0054	0.0192
C5 GO Cellular Component	<u>GOCC VACUOLAR MEMBRANE</u>	1.85	0.0000	0.0193
C5 GO Cellular Component	<u>GOCC SM LIKE PROTEIN FAMILY COMPLEX</u>	1.85	0.0000	0.0193
C5 GO Biological Process	<u>GOBP ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN</u>	1.85	0.0018	0.0193
C5 GO Biological Process	<u>GOBP TOLL LIKE RECEPTOR SIGNALING PATHWAY</u>	1.85	0.0000	0.0193
C5 GO Biological Process	<u>GOBP REGULATION OF PROTEIN DEPHOSPHORYLATION</u>	1.85	0.0000	0.0193
C5 GO Cellular Component	<u>GOCC CUL4 RING E3 UBIQUITIN LIGASE COMPLEX</u>	1.85	0.0000	0.0193
C5 GO Biological Process	<u>GOBP CELLULAR RESPONSE TO DSRNA</u>	1.85	0.0000	0.0193

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 Reactome pathway	<u>REACTOME ANTIGEN PROCESSING UBIQUITINATION PROTEASOME DEGRADATION</u>	1.84	0.0000	0.0194
C5 GO Molecular Function	<u>GOMF RNA POLYMERASE BINDING</u>	1.85	0.0000	0.0194
C5 GO Biological Process	<u>GOBP B CELL DIFFERENTIATION</u>	1.85	0.0000	0.0194
C2 WikiPathways pathway	<u>WP VEGFAVEGFR2 SIGNALING PATHWAY</u>	1.85	0.0000	0.0194
C2 Reactome pathway	<u>REACTOME THE ROLE OF NEF IN HIV 1 REPLICATION AND DISEASE PATHOGENESIS</u>	1.85	0.0039	0.0195
C5 GO Biological Process	<u>GOBP VIRAL RNA GENOME REPLICATION</u>	1.85	0.0018	0.0195
C2 Reactome pathway	<u>REACTOME RAB REGULATION OF TRAFFICKING</u>	1.84	0.0000	0.0197
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF PROTEIN DEPHOSPHORYLATION</u>	1.84	0.0018	0.0197
C5 GO Biological Process	<u>GOBP TRANSPORT OF VIRUS</u>	1.84	0.0019	0.0197
C5 GO Biological Process	<u>GOBP RESPONSE TO LECTIN</u>	1.84	0.0000	0.0197
C5 GO Biological Process	<u>GOBP PROTEIN INSERTION INTO ER MEMBRANE</u>	1.84	0.0018	0.0197
C5 GO Biological Process	<u>GOBP ATP METABOLIC PROCESS</u>	1.84	0.0000	0.0197
C2 WikiPathways pathway	<u>WP TLR4 SIGNALING AND TOLERANCE</u>	1.84	0.0019	0.0197

C2 BioCarta pathway	<u>BIOCARTA ERAD PATHWAY</u>	1.84	0.0020	0.0198
C2 Reactome pathway	<u>REACTOME DECTIN 1 MEDIATED NONCANONICAL NF KB SIGNALING</u>	1.84	0.0000	0.0198
C5 GO Biological Process	<u>GOBP REGULATION OF T CELL ACTIVATION</u>	1.84	0.0000	0.0198
C2 WikiPathways pathway	<u>WP HOSTPATHOGEN INTERACTION OF HUMAN CORO NAVIRUSES INTERFERON INDUCTION</u>	1.84	0.0000	0.0198
C2 Reactome pathway	<u>REACTOME NUCLEOTIDE BINDING DOMAIN LEUCINE R ICH REPEAT CONTAINING RECEPTOR NLR SIGNALING PATHWAYS</u>	1.84	0.0000	0.0198
C5 GO Molecular Function	<u>GOMF POLYUBIQUITIN MODIFICATION DEPENDENT PR OTEIN BINDING</u>	1.84	0.0000	0.0198
C5 GO Cellular Component	<u>GOCC AZUROPHIL GRANULE</u>	1.84	0.0000	0.0198
C5 GO Biological Process	<u>GOBP REGULATION OF CELLULAR RESPIRATION</u>	1.84	0.0000	0.0198
C5 GO Molecular Function	<u>GOMF ADP BINDING</u>	1.84	0.0000	0.0199
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF FIBROBLAST PROLIF ERATION</u>	1.84	0.0056	0.0199
C5 GO Cellular Component	<u>GOCC SMALL SUBUNIT PROCESSOME</u>	1.84	0.0018	0.0199
C2 Reactome pathway	<u>REACTOME REGULATION OF CHOLESTEROL BIOSYNTHESIS BY SREBP SREBF</u>	1.84	0.0000	0.0199
C2 PID pathway	<u>PID FOXO PATHWAY</u>	1.84	0.0000	0.0200
C2 Reactome pathway	<u>REACTOME SEPARATION OF SISTER CHROMATIDS</u>	1.83	0.0000	0.0200
C2 Reactome pathway	<u>REACTOME APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1</u>	1.84	0.0000	0.0200
C2 Reactome pathway	<u>REACTOME C TYPE LECTIN RECEPTORS CLRS</u>	1.83	0.0000	0.0200
C5 GO Molecular Function	<u>GOMF PROTEIN SELF ASSOCIATION</u>	1.84	0.0017	0.0201
C5 GO Molecular Function	<u>GOMF PROTEIN PHOSPHATASE BINDING</u>	1.84	0.0000	0.0201
C5 GO Cellular Component	<u>GOCC PROTON TRANSPORTING ATP SYNTHASE COMPLEX</u>	1.84	0.0019	0.0201
C2 Reactome pathway	<u>REACTOME RHO GTPASES ACTIVATE WASPS AND WAVES</u>	1.83	0.0020	0.0201
C5 GO Biological Process	<u>GOBP GOLGI TO ENDOSOME TRANSPORT</u>	1.83	0.0056	0.0201
C2 Reactome pathway	<u>REACTOME TP53 REGULATES METABOLIC GENES</u>	1.83	0.0000	0.0201
C2 BioCarta pathway	<u>BIOCARTA RELA PATHWAY</u>	1.83	0.0037	0.0203
C5 GO Biological Process	<u>GOBP REGULATION OF PROGRAMMED NECROTIC CELL DEATH</u>	1.83	0.0018	0.0204
C5 GO Molecular Function	<u>GOMF UBIQUITIN BINDING</u>	1.83	0.0000	0.0204
C5 GO Biological Process	<u>GOBP PROTEIN LOCALIZATION TO CHROMOSOME TELL OMERIC REGION</u>	1.83	0.0000	0.0204
C5 GO Cellular Component	<u>GOCC PROTEASOME COMPLEX</u>	1.83	0.0035	0.0204

C2 Reactome pathway	<u>REACTOME DNA REPLICATION PRE INITIATION</u>	1.83	0.0000	0.0204
C5 GO Molecular Function	<u>GOMF TRANSLATION REGULATOR ACTIVITY NUCLEIC ACID BINDING</u>	1.83	0.0000	0.0204

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 Reactome pathway	<u>REACTOME METABOLISM OF POLYAMINES</u>	1.83	0.0018	0.0204
C2 Reactome pathway	<u>REACTOME ORC1 REMOVAL FROM CHROMATIN</u>	1.83	0.0018	0.0204
C2 Reactome pathway	<u>REACTOME ANTIGEN PRESENTATION FOLDING ASSEMBLY AND PEPTIDE LOADING OF CLASS I MHC</u>	1.83	0.0056	0.0204
C2 KEGG pathway	<u>KEGG TOLL LIKE RECEPTOR SIGNALING PATHWAY</u>	1.83	0.0000	0.0204
C2 KEGG pathway	<u>KEGG CYTOSOLIC DNA SENSING PATHWAY</u>	1.83	0.0036	0.0205
C2 Reactome pathway	<u>REACTOME DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS</u>	1.83	0.0019	0.0205
C5 GO Molecular Function	<u>GOMF TRANSLATION FACTOR ACTIVITY RNA BINDING</u>	1.83	0.0000	0.0205
C2 Reactome pathway	<u>REACTOME TP53 REGULATES TRANSCRIPTION OF DNA REPAIR GENES</u>	1.83	0.0018	0.0206
C5 GO Biological Process	<u>GOBP PROTEIN K48 LINKED UBIQUITINATION</u>	1.83	0.0000	0.0206
C2 Reactome pathway	<u>REACTOME RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF HSCS</u>	1.83	0.0000	0.0207
C2 Reactome pathway	<u>REACTOME MTOR SIGNALLING</u>	1.83	0.0035	0.0208
C2 Reactome pathway	<u>REACTOME MITOTIC G2 G2 M PHASES</u>	1.82	0.0000	0.0209
C2 Reactome pathway	<u>REACTOME CITRIC ACID CYCLE TCA CYCLE</u>	1.82	0.0037	0.0209
C2 WikiPathways pathway	<u>WP COHESIN COMPLEX CORNELIA DE LANGE SYNDROME</u>	1.82	0.0018	0.0212
C2 Reactome pathway	<u>REACTOME NEGATIVE REGULATION OF NOTCH4 SIGNALING</u>	1.82	0.0000	0.0212
C2 Reactome pathway	<u>REACTOME STABILIZATION OF P53</u>	1.82	0.0020	0.0213
C5 GO Biological Process	<u>GOBP ALPHA BETA T CELL ACTIVATION</u>	1.82	0.0000	0.0215
C2 WikiPathways pathway	<u>WP PI3KAKTMTOR SIGNALING PATHWAY AND THERAPEUTIC OPPORTUNITIES</u>	1.82	0.0018	0.0217
C2 Reactome pathway	<u>REACTOME TGF BETA RECEPTOR SIGNALING ACTIVATES SMADS</u>	1.82	0.0037	0.0220
C2 Reactome pathway	<u>REACTOME M PHASE</u>	1.82	0.0000	0.0220
C5 GO Biological Process	<u>GOBP REGULATION OF PHAGOCYTOSIS</u>	1.82	0.0000	0.0220
C2 PID pathway	<u>PID IL12 STAT4 PATHWAY</u>	1.82	0.0017	0.0222
C2 WikiPathways pathway	<u>WP EUKARYOTIC TRANSCRIPTION INITIATION</u>	1.82	0.0018	0.0222
C5 GO Biological Process	<u>GOBP SELECTIVE AUTOPHAGY</u>	1.82	0.0000	0.0222
C2 WikiPathways pathway	<u>WP ANDROGEN RECEPTOR SIGNALING PATHWAY</u>	1.82	0.0000	0.0223

C5 GO Biological Process	<u>GOBP PROTEIN TARGETING TO PEROXISOME</u>	1.81	0.0019	0.0223
C2 Reactome pathway	<u>REACTOME DEGRADATION OF DVL</u>	1.81	0.0000	0.0226
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF CELL ACTIVATION</u>	1.81	0.0000	0.0229
C2 KEGG pathway	<u>KEGG LYSOSOME</u>	1.81	0.0000	0.0230
C2 Reactome pathway	<u>REACTOME REGULATION OF HMOX1 EXPRESSION AND ACTIVITY</u>	1.81	0.0017	0.0230
C5 GO Biological Process	<u>GOBP CELL KILLING</u>	1.81	0.0000	0.0232
C2 BioCarta pathway	<u>BIOCARTA CSK PATHWAY</u>	1.81	0.0000	0.0235
C5 GO Biological Process	<u>GOBP CELL DEATH IN RESPONSE TO OXIDATIVE STRESS</u>	1.81	0.0000	0.0235
C5 GO Cellular Component	<u>GOCC RNA POLYMERASE COMPLEX</u>	1.81	0.0017	0.0236
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF LEUKOCYTE CELL CELL ADHESION</u>	1.81	0.0000	0.0236
C2 Reactome pathway	<u>REACTOME SIGNALING BY INTERLEUKINS</u>	1.81	0.0000	0.0237
C2 PID pathway	<u>PID TGFBR PATHWAY</u>	1.81	0.0000	0.0239
C2 WikiPathways pathway	<u>WP T CELL RECEPTOR AND COSTIMULATORY SIGNALING</u>	1.81	0.0056	0.0241
C2 Reactome pathway	<u>REACTOME RAF INDEPENDENT MAPK1 3 ACTIVATION</u>	1.80	0.0038	0.0242
C5 GO Biological Process	<u>GOBP RRNA TRANSCRIPTION</u>	1.80	0.0000	0.0242
C5 GO Molecular Function	<u>GOMF MACROMOLECULE TRANSMEMBRANE TRANSPORTER ACTIVITY</u>	1.80	0.0037	0.0243
C2 PID pathway	<u>PID MYC PATHWAY</u>	1.80	0.0038	0.0243

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP CHROMATIN DISASSEMBLY</u>	1.80	0.0057	0.0243
C5 GO Biological Process	<u>GOBP NUCLEAR EXPORT</u>	1.80	0.0000	0.0243
C2 PID pathway	<u>PID NFAT 3PATHWAY</u>	1.80	0.0000	0.0244
C2 PID pathway	<u>PID CD8 TCR DOWNSTREAM PATHWAY</u>	1.80	0.0018	0.0244
C5 GO Molecular Function	<u>GOMF PEPTIDASE ACTIVATOR ACTIVITY</u>	1.80	0.0000	0.0244
C2 Reactome pathway	<u>REACTOME GOLGI TO ER RETROGRADE TRANSPORT</u>	1.80	0.0000	0.0244
C2 BioCarta pathway	<u>BIOCARTA TCR PATHWAY</u>	1.80	0.0035	0.0245
C2 Reactome pathway	<u>REACTOME CDT1 ASSOCIATION WITH THE CDC6 ORC ORIGIN COMPLEX</u>	1.80	0.0000	0.0245
C2 Reactome pathway	<u>REACTOME INHIBITION OF DNA RECOMBINATION AT TELOMERE</u>	1.80	0.0053	0.0245
C5 GO Biological Process	<u>GOBP NUCLEAR TRANSPORT</u>	1.80	0.0000	0.0245
C2 KEGG pathway	<u>KEGG CITRATE CYCLE TCA CYCLE</u>	1.80	0.0000	0.0246
C2 Reactome pathway	<u>REACTOME CELL CYCLE MITOTIC</u>	1.80	0.0000	0.0246

C2 KEGG pathway	<u>KEGG OXIDATIVE PHOSPHORYLATION</u>	1.80	0.0000	0.0246
C2 Reactome pathway	<u>REACTOME DEGRADATION OF GLI1 BY THE PROTEASOME</u>	1.80	0.0000	0.0248
C5 GO Cellular Component	<u>GOCC COPI COATED VESICLE</u>	1.80	0.0037	0.0249
C5 GO Cellular Component	<u>GOCC TRANSCRIPTION ELONGATION FACTOR COMPLEX</u>	1.80	0.0018	0.0251
C2 Reactome pathway	<u>REACTOME MITOTIC METAPHASE AND ANAPHASE</u>	1.80	0.0000	0.0251
C5 GO Biological Process	<u>GOBP MAST CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE</u>	1.80	0.0000	0.0252
C2 WikiPathways pathway	<u>WP HEMATOPOIETIC STEM CELL GENE REGULATION BY GABP ALPHABETA COMPLEX</u>	1.79	0.0000	0.0252
C2 WikiPathways pathway	<u>WP NETRINUNC5B SIGNALING PATHWAY</u>	1.80	0.0018	0.0252
C5 GO Biological Process	<u>GOBP IMMUNOGLOBULIN PRODUCTION</u>	1.79	0.0000	0.0252
C5 GO Biological Process	<u>GOBP ATP BIOSYNTHETIC PROCESS</u>	1.79	0.0000	0.0252
C2 WikiPathways pathway	<u>WP TYPE II DIABETES MELLITUS</u>	1.79	0.0055	0.0252
C5 GO Biological Process	<u>GOBP REGULATION OF TRANSLATION IN RESPONSE TO STRESS</u>	1.79	0.0073	0.0252
C5 GO Biological Process	<u>GOBP SPLICEOSOMAL COMPLEX ASSEMBLY</u>	1.79	0.0000	0.0252
C5 GO Biological Process	<u>GOBP ACTIVATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY INVOLVED IN APOPTOTIC PROCESS</u>	1.79	0.0000	0.0252
C5 GO Biological Process	<u>GOBP CELLULAR RESPONSE TO PROSTAGLANDIN ESTIMULUS</u>	1.79	0.0075	0.0253
C5 GO Biological Process	<u>GOBP FC RECEPTOR SIGNALING PATHWAY</u>	1.79	0.0034	0.0253
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 17 SIGNALING</u>	1.79	0.0000	0.0253
C2 Reactome pathway	<u>REACTOME RNA POLYMERASE III TRANSCRIPTION INITIATION FROM TYPE 1 PROMOTER</u>	1.79	0.0000	0.0253
C5 GO Biological Process	<u>GOBP ENDOCRINE HORMONE SECRETION</u>	-2.22	0.0000	0.0253
C5 GO Biological Process	<u>GOBP REGULATION OF CELLULAR AMIDE METABOLIC PROCESS</u>	1.79	0.0000	0.0255
C2 WikiPathways pathway	<u>WP ATM SIGNALING IN DEVELOPMENT AND DISEASE</u>	1.79	0.0000	0.0257
C5 GO Biological Process	<u>GOBP ATP SYNTHESIS COUPLED ELECTRON TRANSPORT</u>	1.79	0.0000	0.0258
C5 GO Biological Process	<u>GOBP ENERGY DERIVATION BY OXIDATION OF ORGANIC COMPOUNDS</u>	1.79	0.0000	0.0259
C2 Reactome pathway	<u>REACTOME CYCLIN A CDK2 ASSOCIATED EVENTS AT S PHASE ENTRY</u>	1.79	0.0000	0.0260
C5 GO Biological Process	<u>GOBP HISTONE H4 K16 ACETYLATION</u>	1.79	0.0053	0.0262
C5 GO Biological Process	<u>GOBP REGULATION OF PROTEIN STABILITY</u>	1.79	0.0000	0.0262
C5 GO Biological Process	<u>GOBP MRNA PROCESSING</u>	1.79	0.0000	0.0262
C5 GO Biological Process	<u>GOBP REGULATION OF HISTONE MODIFICATION</u>	1.79	0.0000	0.0262
C5 GO Biological Process	<u>GOBP LYSOSOMAL TRANSPORT</u>	1.79	0.0000	0.0263

C2 Reactome pathway	<u>REACTOME HIV ELONGATION ARREST AND RECOVERY</u>	1.79	0.0019	0.0263
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Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C2 Reactome pathway	<u>REACTOME DEGRADATION OF AXIN</u>	1.78	0.0000	0.0263
C2 WikiPathways pathway	<u>WP ESTROGEN SIGNALING PATHWAY</u>	1.79	0.0055	0.0264
C2 Reactome pathway	<u>REACTOME INACTIVATION OF CSF3 G CSF SIGNALING</u>	1.79	0.0037	0.0264
C2 Reactome pathway	<u>REACTOME FCERI MEDIATED CA 2 MOBILIZATION</u>	1.78	0.0074	0.0264
C2 PID pathway	<u>PID MTOR 4PATHWAY</u>	1.79	0.0017	0.0264
C2 KEGG pathway	<u>KEGG PEROXISOME</u>	1.79	0.0000	0.0264
C5 GO Biological Process	<u>GOBP TRANSCRIPTION BY RNA POLYMERASE I</u>	1.78	0.0035	0.0264
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF ALPHA BETA T CELL ACTIVATION</u>	1.78	0.0053	0.0264
Hallmark	<u>HALLMARK PEROXISOME</u>	1.78	0.0000	0.0264
C5 GO Biological Process	<u>GOBP TELOMERASE RNA LOCALIZATION</u>	1.78	0.0000	0.0264
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF HISTONE METHYLATION</u>	1.78	0.0000	0.0265
C5 GO Biological Process	<u>GOBP REGULATION OF GOLGI ORGANIZATION</u>	1.78	0.0037	0.0265
C2 Reactome pathway	<u>REACTOME THE ROLE OF GTSE1 IN G2 M PROGRESSION AFTER G2 CHECKPOINT</u>	1.78	0.0018	0.0269
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF HISTONE MODIFICATION</u>	1.78	0.0000	0.0271
C5 GO Biological Process	<u>GOBP DNA TEMPLATED TRANSCRIPTION INITIATION</u>	1.78	0.0000	0.0273
C5 GO Biological Process	<u>GOBP GENERATION OF PRECURSOR METABOLITES AND ENERGY</u>	1.78	0.0000	0.0274
C5 GO Cellular Component	<u>GOCC RNA POLYMERASE II HOLOENZYME</u>	1.78	0.0000	0.0276
C5 GO Biological Process	<u>GOBP RNA EXPORT FROM NUCLEUS</u>	1.78	0.0019	0.0277
C2 BioCarta pathway	<u>BIOCARTA IL2RB PATHWAY</u>	1.78	0.0074	0.0283
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF LEUKOCYTE DEGRANULATION</u>	1.77	0.0114	0.0284
C2 Reactome pathway	<u>REACTOME RHOB GTPASE CYCLE</u>	1.77	0.0000	0.0284
C5 GO Biological Process	<u>GOBP REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS</u>	1.77	0.0018	0.0284
C5 GO Biological Process	<u>GOBP MACROPHAGE ACTIVATION INVOLVED IN IMMUNE RESPONSE</u>	1.77	0.0057	0.0284
C5 GO Biological Process	<u>GOBP ELECTRON TRANSPORT CHAIN</u>	1.78	0.0000	0.0284
C2 Reactome pathway	<u>REACTOME REGULATION OF TP53 ACTIVITY THROUGH METHYLATION</u>	1.77	0.0036	0.0284
C5 GO Biological Process	<u>GOBP INTERMEMBRANE LIPID TRANSFER</u>	1.77	0.0019	0.0284

C5 GO Biological Process	<u>GOBP LEUKOCYTE CELL CELL ADHESION</u>	1.77	0.0000	0.0284
C5 GO Molecular Function	<u>GOMF PROTEIN TRANSMEMBRANE TRANSPORTER ACTIVITY</u>	1.77	0.0037	0.0284
C2 Reactome pathway	<u>REACTOME SEALING OF THE NUCLEAR ENVELOPE NE BY ESCRT III</u>	1.77	0.0155	0.0285
C5 GO Biological Process	<u>GOBP PATTERN RECOGNITION RECEPTOR SIGNALING PATHWAY</u>	1.77	0.0000	0.0285
C2 Reactome pathway	<u>REACTOME REGULATION OF PTEN STABILITY AND ACTIVITY</u>	1.77	0.0018	0.0285
C2 Reactome pathway	<u>REACTOME ROLE OF PHOSPHOLIPIDS IN PHAGOCYTOSIS</u>	1.77	0.0018	0.0286
C5 GO Biological Process	<u>GOBP PROTEIN LOCALIZATION TO NUCLEUS</u>	1.77	0.0000	0.0286
C2 Reactome pathway	<u>REACTOME CELLULAR RESPONSE TO CHEMICAL STRESS</u>	1.77	0.0000	0.0286
C2 WikiPathways pathway	<u>WP EPO RECEPTOR SIGNALING</u>	1.77	0.0036	0.0287
C2 WikiPathways pathway	<u>WP METABOLIC REPROGRAMMING IN COLON CANCER</u>	1.77	0.0000	0.0288
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF LYMPHOCYTE ACTIVATION</u>	1.77	0.0000	0.0289
C5 GO Biological Process	<u>GOBP VERY LONG CHAIN FATTY ACID METABOLIC PROCESS</u>	1.77	0.0036	0.0290
C2 Reactome pathway	<u>REACTOME MITOCHONDRIAL PROTEIN IMPORT</u>	1.77	0.0017	0.0290
C5 GO Molecular Function	<u>GOMF EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT</u>	-2.16	0.0000	0.0290
C2 WikiPathways pathway	<u>WP IL4 SIGNALING PATHWAY</u>	1.77	0.0054	0.0291
C5 GO Molecular Function	<u>GOMF BASAL TRANSCRIPTION MACHINERY BINDING</u>	1.77	0.0000	0.0291

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF IMMUNE EFFECTOR PROCESS</u>	1.77	0.0000	0.0291
C2 Reactome pathway	<u>REACTOME BETA CATENIN PHOSPHORYLATION CASCADE</u>	1.77	0.0057	0.0292
C5 GO Cellular Component	<u>GOCC PROTEASOME CORE COMPLEX</u>	1.77	0.0000	0.0292
C2 Reactome pathway	<u>REACTOME CELLULAR RESPONSE TO HYPOXIA</u>	1.77	0.0000	0.0292
C2 Reactome pathway	<u>REACTOME TNFR2 NON CANONICAL NF KB PATHWAY</u>	1.77	0.0017	0.0292
C2 PID pathway	<u>PID PI3K/AKT PATHWAY</u>	1.77	0.0018	0.0294
C2 KEGG pathway	<u>KEGG PROTEASOME</u>	1.77	0.0019	0.0295
C2 Reactome pathway	<u>REACTOME CELLULAR SENESCENCE</u>	1.76	0.0000	0.0296
C5 GO Biological Process	<u>GOBP PROTEASOME MEDIATED UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS</u>	1.76	0.0000	0.0296

C5 GO Biological Process	<u>GOBP REGULATION OF B CELL ACTIVATION</u>	1.76	0.0017	0.0298
C5 GO Biological Process	<u>GOBP PROTEIN MONOUBIQUITINATION</u>	1.76	0.0017	0.0300
C2 WikiPathways pathway	<u>WP OXIDATIVE PHOSPHORYLATION</u>	1.76	0.0019	0.0302
C2 Reactome pathway	<u>REACTOME REGULATION OF TP53 ACTIVITY</u>	1.76	0.0000	0.0302
C2 WikiPathways pathway	<u>WP CORI CYCLE</u>	1.76	0.0056	0.0302
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF TRANSLATION</u>	1.76	0.0000	0.0304
C5 GO Molecular Function	<u>GOMF NUCLEAR LOCALIZATION SEQUENCE BINDING</u>	1.76	0.0078	0.0304
C5 GO Biological Process	<u>GOBP REGULATION OF B CELL PROLIFERATION</u>	1.76	0.0000	0.0304
C2 BioCarta pathway	<u>BIOCARTA CERAMIDE PATHWAY</u>	1.76	0.0019	0.0305
C5 GO Biological Process	<u>GOBP LEUKOCYTE PROLIFERATION</u>	1.76	0.0000	0.0305
C5 GO Biological Process	<u>GOBP RIBONUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS</u>	1.76	0.0000	0.0305
C5 GO Biological Process	<u>GOBP ATP SYNTHESIS COUPLED PROTON TRANSPORT</u>	1.76	0.0055	0.0305
C5 GO Molecular Function	<u>GOMF ELECTRON TRANSFER ACTIVITY</u>	1.76	0.0000	0.0305
C2 Reactome pathway	<u>REACTOME DAP12 SIGNALING</u>	1.76	0.0018	0.0305
C2 PID pathway	<u>PID PS1 PATHWAY</u>	1.76	0.0035	0.0305
C5 GO Biological Process	<u>GOBP FIBROBLAST APOPTOTIC PROCESS</u>	1.76	0.0019	0.0305
C5 GO Biological Process	<u>GOBP REGULATION OF IMMUNOGLOBULIN PRODUCTION</u>	1.76	0.0000	0.0306
C5 GO Biological Process	<u>GOBP CELLULAR LIPID CATABOLIC PROCESS</u>	1.76	0.0000	0.0307
C5 GO Cellular Component	<u>GOCC TRAPP COMPLEX</u>	1.76	0.0073	0.0307
C2 Reactome pathway	<u>REACTOME CYTOPROTECTION BY HMOX1</u>	1.76	0.0000	0.0307
C2 Reactome pathway	<u>REACTOME APC C MEDIATED DEGRADATION OF CELL CYCLE PROTEINS</u>	1.76	0.0000	0.0307
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS</u>	1.76	0.0017	0.0308
C5 GO Biological Process	<u>GOBP ORGANELLE INHERITANCE</u>	1.75	0.0059	0.0310
C5 GO Biological Process	<u>GOBP ESTABLISHMENT OF PROTEIN LOCALIZATION TO ENDOPLASMIC RETICULUM</u>	1.75	0.0052	0.0311
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL REGULATION BY VENTX</u>	1.75	0.0068	0.0311
C5 GO Biological Process	<u>GOBP CERAMIDE CATABOLIC PROCESS</u>	1.75	0.0036	0.0311
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF ALPHA BETA T CELL ACTIVATION</u>	1.75	0.0053	0.0312
C5 GO Biological Process	<u>GOBP RECEPTOR CATABOLIC PROCESS</u>	1.75	0.0000	0.0312
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF KINASE ACTIVITY</u>	1.75	0.0000	0.0312
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF PEPTIDYL LYSINE ACETYLATION</u>	1.75	0.0073	0.0312
C2 WikiPathways pathway	<u>WP IL7 SIGNALING PATHWAY</u>	1.75	0.0074	0.0312
C5 GO Biological Process	<u>GOBP MITOCHONDRIAL TRANSMEMBRANE TRANSPORT</u>	1.75	0.0000	0.0312

C2 KEGG pathway	<u>KEGG_ALLOGRAFT_REJECTION</u>	1.75	0.0018	0.0313
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Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Cellular Component	<u>GOCC_PHOTORECEPTOR_INNER_SEGMENT</u>	-2.13	0.0000	0.0315
C2 Reactome pathway	<u>REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT</u>	1.75	0.0000	0.0317
C2 Reactome pathway	<u>REACTOME_DUAL_INCISION_IN_TC_NER</u>	1.75	0.0018	0.0318
C2 PID pathway	<u>PID_IFNG_PATHWAY</u>	1.75	0.0056	0.0318
C2 Reactome pathway	<u>REACTOME_MAP2K_AND_MAPK_ACTIVATION</u>	1.75	0.0018	0.0318
C5 GO Cellular Component	<u>GOCC_COPI_COATED_VESICLE_MEMBRANE</u>	1.75	0.0056	0.0321
C2 Reactome pathway	<u>REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING</u>	1.75	0.0073	0.0321
C2 PID pathway	<u>PID_MET_PATHWAY</u>	1.75	0.0018	0.0322
C2 Reactome pathway	<u>REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS</u>	1.75	0.0036	0.0322
C2 Reactome pathway	<u>REACTOME_RAF_ACTIVATION</u>	1.75	0.0019	0.0324
C2 PID pathway	<u>PID_ECADHERIN_NASCENT_AJ_PATHWAY</u>	1.75	0.0018	0.0324
C2 Reactome pathway	<u>REACTOME_RHO_GTPASES_ACTIVATE_NADPH_OXIDASES</u>	1.74	0.0058	0.0327
C2 Reactome pathway	<u>REACTOME_PURINERGIC_SIGNALING_IN_LEISHMANIASIS_INFECTION</u>	1.74	0.0091	0.0327
C5 GO Biological Process	<u>GOBP_RNA_LOCALIZATION</u>	1.74	0.0000	0.0328
C5 GO Biological Process	<u>GOBP_LATE_ENDOSOME_TO_LYSOSOME_TRANSPORT</u>	1.74	0.0038	0.0328
C5 GO Biological Process	<u>GOBP_REGULATION_OF_SUPEROXIDE_ANION_GENERATION</u>	1.74	0.0133	0.0328
C2 Reactome pathway	<u>REACTOME_PROGRAMMED_CELL_DEATH</u>	1.74	0.0000	0.0328
C2 BioCarta pathway	<u>BIOCARTA_RHO_PATHWAY</u>	1.74	0.0072	0.0328
C2 BioCarta pathway	<u>BIOCARTA_MTOR_PATHWAY</u>	1.74	0.0076	0.0328
C5 GO Biological Process	<u>GOBP_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION</u>	1.74	0.0000	0.0328
C5 GO Biological Process	<u>GOBP_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE</u>	1.74	0.0000	0.0328
C5 GO Molecular Function	<u>GOMF_PHOSPHOTYROSINE_RESIDUE_BINDING</u>	1.74	0.0034	0.0328
C5 GO Biological Process	<u>GOBP_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS</u>	1.74	0.0000	0.0329
C5 GO Biological Process	<u>GOBP_PROTEIN_FOLDING</u>	1.74	0.0000	0.0329
C2 Reactome pathway	<u>REACTOME_TOLL LIKE RECEPTOR CASCADES</u>	1.74	0.0000	0.0329
C5 GO Biological Process	<u>GOBP_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS</u>	1.74	0.0000	0.0329
C5 GO Molecular Function	<u>GOMF_LIPID_TRANSFER_ACTIVITY</u>	1.74	0.0018	0.0329
C2 KEGG pathway	<u>KEGG_PRIMARY_IMMUNODEFICIENCY</u>	1.74	0.0018	0.0329
C5 GO Biological Process	<u>GOBP_PROTEIN_IMPORT</u>	1.74	0.0000	0.0330

C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF DNA REPAIR</u>	1.74	0.0072	0.0331
C5 GO Biological Process	<u>GOBP PEROXISOMAL TRANSPORT</u>	1.74	0.0074	0.0331
C2 PID pathway	<u>PID ERBB1 DOWNSTREAM PATHWAY</u>	1.74	0.0000	0.0332
C5 GO Biological Process	<u>GOBP RESPONSE TO ENDOPLASMIC RETICULUM STRESS</u>	1.74	0.0000	0.0332
C2 WikiPathways pathway	<u>WP EBSTEINBARR VIRUS LMP1 SIGNALING</u>	1.74	0.0104	0.0332
C5 GO Molecular Function	<u>GOMF MITOGEN ACTIVATED PROTEIN KINASE BINDING</u>	1.74	0.0078	0.0333
C5 GO Biological Process	<u>GOBP DOUBLE STRAND BREAK REPAIR VIA NONHOMOLOGOUS END JOINING</u>	1.74	0.0017	0.0334
C2 BioCarta pathway	<u>BIOCARTA HIVNEF PATHWAY</u>	1.74	0.0000	0.0334
C2 PID pathway	<u>PID IGF1 PATHWAY</u>	1.74	0.0093	0.0337
C5 GO Biological Process	<u>GOBP REGULATION OF PATTERN RECOGNITION RECEPTOR SIGNALING PATHWAY</u>	1.74	0.0000	0.0339
C5 GO Molecular Function	<u>GOMF NON MEMBRANE SPANNING PROTEIN TYROSINE KINASE ACTIVITY</u>	1.74	0.0017	0.0339
C2 KEGG pathway	<u>KEGG HUNTINGTONS DISEASE</u>	1.74	0.0000	0.0341
C5 GO Biological Process	<u>GOBP REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS</u>	1.74	0.0000	0.0341

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP PROTEIN TRANSMEMBRANE IMPORT INTO INTRACELLULAR ORGANELLE</u>	1.74	0.0054	0.0341
C5 GO Biological Process	<u>GOBP RIBONUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS</u>	1.73	0.0036	0.0342
C2 PID pathway	<u>PID AR NONGENOMIC PATHWAY</u>	1.73	0.0019	0.0342
C2 WikiPathways pathway	<u>WP WNT SIGNALING PATHWAY</u>	1.73	0.0072	0.0346
C5 GO Biological Process	<u>GOBP CARDIOLIPIN METABOLIC PROCESS</u>	1.73	0.0150	0.0347
C5 GO Molecular Function	<u>GOMF UBIQUITIN LIKE PROTEIN LIGASE BINDING</u>	1.73	0.0000	0.0348
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF INTERLEUKIN 2 PRODUCTION</u>	1.73	0.0091	0.0348
C2 BioCarta pathway	<u>BIOCARTA TOLL PATHWAY</u>	1.73	0.0074	0.0348
C2 Reactome pathway	<u>REACTOME RAB GEFS EXCHANGE GTP FOR GDP ON RABS</u>	1.73	0.0000	0.0348
C5 GO Biological Process	<u>GOBP TRANSCRIPTION BY RNA POLYMERASE III</u>	1.73	0.0036	0.0348
C2 Reactome pathway	<u>REACTOME CLASS I PEROXISOMAL MEMBRANE PROTEIN IMPORT</u>	1.73	0.0093	0.0348
C2 KEGG pathway	<u>KEGG INOSITOL PHOSPHATE METABOLISM</u>	1.73	0.0035	0.0349

C5 GO Cellular Component	<u>GOCC PROTON TRANSPORTING TWO SECTOR ATPASE COMPLEX</u>	1.73	0.0018	0.0349
C5 GO Cellular Component	<u>GOCC PERICENTRIOLAR MATERIAL</u>	1.73	0.0074	0.0349
C5 GO Biological Process	<u>GOBP CELLULAR RESPONSE TO EXOGENOUS DSRNA</u>	1.73	0.0039	0.0349
C2 Reactome pathway	<u>REACTOME MITOCHONDRIAL BIOGENESIS</u>	1.73	0.0018	0.0352
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY</u>	1.73	0.0053	0.0353
C5 GO Cellular Component	<u>GOCC U2 SNRNP</u>	1.73	0.0036	0.0353
C2 WikiPathways pathway	<u>WP MEASLES VIRUS INFECTION</u>	1.73	0.0000	0.0353
C5 GO Biological Process	<u>GOBP RRNA METABOLIC PROCESS</u>	1.73	0.0000	0.0353
C2 Reactome pathway	<u>REACTOME PHOSPHORYLATION OF THE APC_C</u>	1.73	0.0054	0.0354
C2 PID pathway	<u>PID CXCR4 PATHWAY</u>	1.73	0.0017	0.0354
C2 WikiPathways pathway	<u>WP CELL CYCLE</u>	1.73	0.0000	0.0354
C2 Reactome pathway	<u>REACTOME TELOMERE MAINTENANCE</u>	1.73	0.0017	0.0354
C2 Reactome pathway	<u>REACTOME SIGNALING BY NOTCH</u>	1.73	0.0000	0.0354
C2 WikiPathways pathway	<u>WP TRANSLATION FACTORS</u>	1.73	0.0036	0.0355
C5 GO Biological Process	<u>GOBP ENDOSOMAL TRANSPORT</u>	1.73	0.0000	0.0355
C2 KEGG pathway	<u>KEGG NON SMALL CELL LUNG CANCER</u>	1.73	0.0017	0.0355
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS</u>	1.73	0.0000	0.0355
C5 GO Molecular Function	<u>GOMF UBIQUITIN LIKE PROTEIN SPECIFIC PROTEASE ACTIVITY</u>	1.72	0.0000	0.0362
C2 Reactome pathway	<u>REACTOME ACTIVATION OF GENE EXPRESSION BY SREBF SREBP</u>	1.72	0.0018	0.0362
C2 BioCarta pathway	<u>BIOCARTA GH PATHWAY</u>	1.72	0.0074	0.0362
C2 Reactome pathway	<u>REACTOME AUF1 HNRNP D0 BINDS AND DESTABILIZES MRNA</u>	1.72	0.0020	0.0363
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF TRANSFERASE ACTIVITY</u>	1.72	0.0000	0.0363
C2 Reactome pathway	<u>REACTOME GLYCOPHINGOLIPID METABOLISM</u>	1.72	0.0089	0.0363
C5 GO Biological Process	<u>GOBP CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE</u>	1.72	0.0000	0.0363
C5 GO Biological Process	<u>GOBP MYELOID LEUKOCYTE MEDIATED IMMUNITY</u>	1.72	0.0034	0.0364
C5 GO Biological Process	<u>GOBP ACTIVATION OF INNATE IMMUNE RESPONSE</u>	1.72	0.0000	0.0364
C2 Reactome pathway	<u>REACTOME PLATELET ACTIVATION SIGNALING AND AGGREGATION</u>	1.72	0.0000	0.0364
C5 GO Biological Process	<u>GOBP REGULATION OF HISTONE H3 K9 METHYLATION</u>	1.72	0.0129	0.0364
C5 GO Biological Process	<u>GOBP AUTOPHAGY OF MITOCHONDRION</u>	1.72	0.0000	0.0365
C5 GO Biological Process	<u>GOBP PROTEIN POLYUBIQUITINATION</u>	1.72	0.0000	0.0365

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Biological Process	<u>GOBP MITOTIC INTRA S DNA DAMAGE CHECKPOINT SIGNALING</u>	1.72	0.0060	0.0366
C5 GO Biological Process	<u>GOBP DNA DOUBLE STRAND BREAK PROCESSING</u>	1.72	0.0055	0.0368
C2 Reactome pathway	<u>REACTOME CD28 CO STIMULATION</u>	1.72	0.0125	0.0368
C5 GO Biological Process	<u>GOBP COPII COATED VESICLE CARGO LOADING</u>	1.72	0.0113	0.0368
C5 GO Biological Process	<u>GOBP NUCLEOBASE BIOSYNTHETIC PROCESS</u>	1.72	0.0096	0.0369
C2 PID pathway	<u>PID ATR PATHWAY</u>	1.72	0.0075	0.0369
C2 Reactome pathway	<u>REACTOME REGULATION OF TP53 ACTIVITY THROUGH PHOSPHORYLATION</u>	1.72	0.0017	0.0369
C5 GO Biological Process	<u>GOBP PROTEIN QUALITY CONTROL FOR MISFOLDED OR INCOMPLETELY SYNTHESIZED PROTEINS</u>	1.72	0.0055	0.0370
C5 GO Biological Process	<u>GOBP REGULATION OF PROTEIN CATABOLIC PROCESS</u>	1.72	0.0000	0.0370
C5 GO Molecular Function	<u>GOMF S ACYLTRANSFERASE ACTIVITY</u>	1.72	0.0093	0.0370
C5 GO Biological Process	<u>GOBP CELLULAR RESPONSE TO BIOTIC STIMULUS</u>	1.72	0.0000	0.0370
C5 GO Biological Process	<u>GOBP TUMOR NECROSIS FACTOR MEDIATED SIGNALING PATHWAY</u>	1.72	0.0017	0.0370
C5 GO Biological Process	<u>GOBP LEUKOCYTE MEDIATED IMMUNITY</u>	1.72	0.0000	0.0370
C5 GO Biological Process	<u>GOBP ERAD PATHWAY</u>	1.72	0.0017	0.0371
C2 PID pathway	<u>PID TXA2PATHWAY</u>	1.72	0.0018	0.0371
C2 Reactome pathway	<u>REACTOME RHOC GTPASE CYCLE</u>	1.72	0.0000	0.0371
Hallmark	<u>HALLMARK REACTIVE OXYGEN SPECIES PATHWAY</u>	1.72	0.0018	0.0371
C2 Reactome pathway	<u>REACTOME PROCESSING OF DNA DOUBLE STRAND BREAK ENDS</u>	1.72	0.0017	0.0371
C2 WikiPathways pathway	<u>WP APOPTOSIS</u>	1.72	0.0000	0.0371
C2 KEGG pathway	<u>KEGG VASOPRESSIN REGULATED WATER REABSORPTION</u>	1.71	0.0037	0.0373
C5 GO Biological Process	<u>GOBP RNA POLYADENYLATION</u>	1.71	0.0035	0.0373
C2 BioCarta pathway	<u>BIOCARTA LONGEVITY PATHWAY</u>	1.71	0.0073	0.0374
C2 KEGG pathway	<u>KEGG NOTCH SIGNALING PATHWAY</u>	1.71	0.0036	0.0375
C2 Reactome pathway	<u>REACTOME G1 S DNA DAMAGE CHECKPOINTS</u>	1.71	0.0052	0.0376
C5 GO Biological Process	<u>GOBP FC GAMMA RECEPTOR SIGNALING PATHWAY</u>	1.71	0.0037	0.0376
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF TRANSLATIONAL INITIATION</u>	1.71	0.0072	0.0377
C5 GO Biological Process	<u>GOBP REGULATION OF HISTONE H3 K4 METHYLATION</u>	1.71	0.0037	0.0378
C5 GO Molecular Function	<u>GOMF PROMOTER SPECIFIC CHROMATIN BINDING</u>	1.71	0.0017	0.0378
C2 Reactome pathway	<u>REACTOME CD28 DEPENDENT PI3K AKT SIGNALING</u>	1.71	0.0098	0.0378

C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE</u>	1.71	0.0018	0.0378
C5 GO Biological Process	<u>GOBP FATTY ACID CATABOLIC PROCESS</u>	1.71	0.0000	0.0379
C5 GO Cellular Component	<u>GOCC SPECIFIC GRANULE LUMEN</u>	1.71	0.0073	0.0379
C5 GO Biological Process	<u>GOBP REGULATION OF DEPHOSPHORYLATION</u>	1.71	0.0000	0.0380
C2 Reactome pathway	<u>REACTOME TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM</u>	1.71	0.0017	0.0381
C5 GO Cellular Component	<u>GOCC UBIQUITIN LIGASE COMPLEX</u>	1.71	0.0000	0.0382
C2 Reactome pathway	<u>REACTOME DNA DOUBLE STRAND BREAK RESPONSE</u>	1.71	0.0056	0.0382
C5 GO Biological Process	<u>GOBP REGULATION OF T CELL RECEPTOR SIGNALING PATHWAY</u>	1.71	0.0000	0.0385
C5 GO Molecular Function	<u>GOMF PEPTIDASE ACTIVATOR ACTIVITY INVOLVED IN APOPTOTIC PROCESS</u>	1.71	0.0038	0.0385
C2 Reactome pathway	<u>REACTOME REGULATION OF RAS BY GAPS</u>	1.71	0.0018	0.0385
C5 GO Molecular Function	<u>GOMF ENZYME ACTIVATOR ACTIVITY</u>	1.71	0.0000	0.0386
C5 GO Molecular Function	<u>GOMF OXIDOREDUCTASE ACTIVITY ACTING ON THE CH₂ GROUP OF DONORS</u>	1.71	0.0109	0.0387
C2 Reactome pathway	<u>REACTOME GPVI MEDIATED ACTIVATION CASCADE</u>	1.71	0.0145	0.0387

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		post, trained vs control		
C5 GO Biological Process	<u>GOBP REGULATION OF MYELOID LEUKOCYTE MEDIATED IMMUNITY</u>	1.71	0.0000	0.0388
C2 Reactome pathway	<u>REACTOME FOXO MEDIATED TRANSCRIPTION</u>	1.71	0.0018	0.0388
C2 Reactome pathway	<u>REACTOME IRE1ALPHA ACTIVATES CHAPERONES</u>	1.71	0.0000	0.0388
C2 BioCarta pathway	<u>BIOCARTA KERATINOCYTE PATHWAY</u>	1.70	0.0055	0.0390
C5 GO Biological Process	<u>GOBP HISTONE UBIQUITINATION</u>	1.70	0.0035	0.0391
C2 WikiPathways pathway	<u>WP KIT RECEPTOR SIGNALING PATHWAY</u>	1.70	0.0000	0.0391
C2 Reactome pathway	<u>REACTOME RETROGRADE TRANSPORT AT THE TRANS GOLGI NETWORK</u>	1.70	0.0090	0.0391
C5 GO Biological Process	<u>GOBP VACUOLE ORGANIZATION</u>	1.70	0.0017	0.0391
C5 GO Biological Process	<u>GOBP REGULATION OF NUCLEASE ACTIVITY</u>	1.70	0.0092	0.0391
C2 Reactome pathway	<u>REACTOME RRNA PROCESSING</u>	1.70	0.0000	0.0391
C2 WikiPathways pathway	<u>WP VASOPRESSINREGULATED WATER REABSORPTION</u>	1.70	0.0056	0.0392
C5 GO Biological Process	<u>GOBP ESTABLISHMENT OF PROTEIN LOCALIZATION TO TELOMERE</u>	1.70	0.0097	0.0393
C2 KEGG pathway	<u>KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM</u>	1.70	0.0017	0.0394
C2 Reactome pathway	<u>REACTOME DAP12 INTERACTIONS</u>	1.70	0.0058	0.0394

C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF PROTEOLYSIS INVOLVED IN CELLULAR PROTEIN CATABOLIC PROCESS</u>	1.70	0.0000	0.0394
C5 GO Cellular Component	<u>GOCC ENDOLYSOSOME</u>	1.70	0.0055	0.0394
C5 GO Biological Process	<u>GOBP TAIL ANCHORED MEMBRANE PROTEIN INSERTION INTO ER MEMBRANE</u>	1.70	0.0075	0.0395
Hallmark	<u>HALLMARK UNFOLDED PROTEIN RESPONSE</u>	1.70	0.0017	0.0395
C2 Reactome pathway	<u>REACTOME DEADENYLATION DEPENDENT MRNA DECA</u> <u>Y</u>	1.70	0.0018	0.0396
C2 KEGG pathway	<u>KEGG ENDOMETRIAL CANCER</u>	1.70	0.0092	0.0396
C2 PID pathway	<u>PID EPO PATHWAY</u>	1.70	0.0037	0.0397
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS</u>	1.70	0.0000	0.0400
C5 GO Biological Process	<u>GOBP T CELL PROLIFERATION</u>	1.70	0.0000	0.0400
C5 GO Biological Process	<u>GOBP REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS</u>	1.70	0.0000	0.0401
C2 PID pathway	<u>PID NCADHERIN PATHWAY</u>	1.70	0.0055	0.0401
C2 BioCarta pathway	<u>BIOCARTA IL7 PATHWAY</u>	1.70	0.0078	0.0401
C2 PID pathway	<u>PID SMAD2 3NUCLEAR PATHWAY</u>	1.70	0.0017	0.0403
C2 Reactome pathway	<u>REACTOME HIV TRANSCRIPTION INITIATION</u>	1.70	0.0051	0.0405
C2 Reactome pathway	<u>REACTOME NONHOMOLOGOUS END JOINING NHEJ</u>	1.70	0.0057	0.0405
C5 GO Molecular Function	<u>GOMF GTPASE BINDING</u>	1.70	0.0000	0.0405
C5 GO Cellular Component	<u>GOCC ORGANELLE INNER MEMBRANE</u>	1.70	0.0000	0.0409
C5 GO Biological Process	<u>GOBP NCRNA TRANSCRIPTION</u>	1.69	0.0051	0.0412
C5 GO Biological Process	<u>GOBP TRANSLATIONAL ELONGATION</u>	1.69	0.0056	0.0412
C2 Reactome pathway	<u>REACTOME SIGNALING BY CSF3 G CSF</u>	1.69	0.0071	0.0412
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF PROTEIN CATABOLIC PROCESS</u>	1.69	0.0000	0.0416
C5 GO Biological Process	<u>GOBP MATURATION OF LSU RRNA</u>	1.69	0.0130	0.0416
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION</u>	1.69	0.0037	0.0417
C2 BioCarta pathway	<u>BIOCARTA TGFB PATHWAY</u>	1.69	0.0055	0.0417
C5 GO Cellular Component	<u>GOCC MEMBRANE COAT</u>	1.69	0.0036	0.0417
C2 BioCarta pathway	<u>BIOCARTA TNFR1 PATHWAY</u>	1.69	0.0056	0.0417
C2 BioCarta pathway	<u>BIOCARTA GLEEVEC PATHWAY</u>	1.69	0.0072	0.0417
C5 GO Biological Process	<u>GOBP TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER</u>	1.69	0.0000	0.0417

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		

C2 PID pathway	<u>PID_RHOA_REG_PATHWAY</u>	1.69	0.0053	0.0418
C2 WikiPathways pathway	<u>WP_PRION_DISEASE_PATHWAY</u>	1.69	0.0130	0.0420
C2 WikiPathways pathway	<u>WP_DNA_DAMAGE_RESPONSE_ONLY_ATM_DEPENDENT</u>	1.69	0.0032	0.0421
C2 Reactome pathway	<u>REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21</u>	1.69	0.0018	0.0423
C5 GO Biological Process	<u>GOBP_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING</u>	1.69	0.0000	0.0424
C2 Reactome pathway	<u>REACTOME_TRANSLATION</u>	1.69	0.0000	0.0425
C5 GO Biological Process	<u>GOBP_ER_NUCLEUS_SIGNALING_PATHWAY</u>	1.69	0.0018	0.0426
C2 Reactome pathway	<u>REACTOME_APOPTOSIS</u>	1.69	0.0000	0.0427
C5 GO Biological Process	<u>GOBP_PEPTIDYL_LYSINE_METHYLATION</u>	1.69	0.0000	0.0427
C5 GO Biological Process	<u>GOBP_MAST_CELL_ACTIVATION</u>	1.68	0.0017	0.0428
C2 Reactome pathway	<u>REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION</u>	1.69	0.0210	0.0428
C5 GO Biological Process	<u>GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I</u>	1.69	0.0286	0.0429
C2 KEGG pathway	<u>KEGG_CELL_CYCLE</u>	1.68	0.0000	0.0429
C5 GO Biological Process	<u>GOBP_RESPONSE_TO_PROSTAGLANDIN_E</u>	1.69	0.0071	0.0429
Hallmark	<u>HALLMARK_MYC_TARGETS_V2</u>	1.69	0.0074	0.0429
C5 GO Biological Process	<u>GOBP_PHOSPHOLIPID_CATABOLIC_PROCESS</u>	1.69	0.0054	0.0429
C2 Reactome pathway	<u>REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1</u>	1.69	0.0113	0.0429
C5 GO Biological Process	<u>GOBP_NATURAL_KILLER_CELL_ACTIVATION</u>	1.68	0.0017	0.0429
C2 Reactome pathway	<u>REACTOME_CONSTITUTIVE_SIGNALING_BY_AKT1_E17K_IN_CANCER</u>	1.69	0.0055	0.0429
C5 GO Molecular Function	<u>GOMF_MHC_CLASS_I_PROTEIN_BINDING</u>	1.69	0.0092	0.0429
C2 Reactome pathway	<u>REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION</u>	1.69	0.0167	0.0429
C2 Reactome pathway	<u>REACTOME_RESPIRATORY_ELECTRON_TRANSPORT</u>	1.69	0.0017	0.0430
C5 GO Biological Process	<u>GOBP_PROTEIN_STABILIZATION</u>	1.69	0.0000	0.0430
C2 Reactome pathway	<u>REACTOME_SIGNALING_BY_TGFB_FAMILY_MEMBERS</u>	1.68	0.0034	0.0431
C5 GO Biological Process	<u>GOBP_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE</u>	1.68	0.0073	0.0431
C5 GO Biological Process	<u>GOBP_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION</u>	1.68	0.0000	0.0432
C2 BioCarta pathway	<u>BIOCARTA_IL2_PATHWAY</u>	1.68	0.0145	0.0432
C5 GO Cellular Component	<u>GOCC_PML_BODY</u>	1.68	0.0000	0.0432
C2 Reactome pathway	<u>REACTOME_RHO_GTPASE_EFFECTORS</u>	1.68	0.0000	0.0432
C2 WikiPathways pathway	<u>WP_FOLLICLE_STIMULATING_HORMONE_FSH_SIGNALING_PATHWAY</u>	1.68	0.0071	0.0432
C5 GO Molecular Function	<u>GOMF_GTPASE_ACTIVATOR_ACTIVITY</u>	1.68	0.0000	0.0432

C2 WikiPathways pathway	<u>WP GLYCOGEN SYNTHESIS AND DEGRADATION</u>	1.68	0.0092	0.0432
C5 GO Cellular Component	<u>GOCC PROTEIN ACETYLTRANSFERASE COMPLEX</u>	1.68	0.0000	0.0433
C5 GO Biological Process	<u>GOBP PHAGOCYTOSIS</u>	1.68	0.0016	0.0433
C5 GO Biological Process	<u>GOBP INNATE IMMUNE RESPONSE ACTIVATING SIGNAL TRANSDUCTION</u>	1.68	0.0092	0.0433
C2 PID pathway	<u>PID CASPASE PATHWAY</u>	1.68	0.0036	0.0433
C2 Reactome pathway	<u>REACTOME NUCLEAR ENVELOPE REASSEMBLY</u>	1.68	0.0000	0.0433
C5 GO Cellular Component	<u>GOCC ENDOPEPTIDASE COMPLEX</u>	1.68	0.0037	0.0434
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF DNA TRANSCRIPTION INITIATION</u>	1.68	0.0018	0.0434
C2 Reactome pathway	<u>REACTOME ZBP1 DAI MEDIATED INDUCTION OF TYPE I IFNS</u>	1.68	0.0092	0.0434
C2 PID pathway	<u>PID TRAIL PATHWAY</u>	1.68	0.0132	0.0434
C5 GO Cellular Component	<u>GOCC NUCLEAR SPECK</u>	1.68	0.0000	0.0435

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C5 GO Biological Process	<u>GOBP B CELL PROLIFERATION</u>	1.68	0.0018	0.0435
C2 Reactome pathway	<u>REACTOME PROTEIN UBIQUITINATION</u>	1.68	0.0018	0.0435
C5 GO Biological Process	<u>GOBP IMPORT INTO NUCLEUS</u>	1.68	0.0017	0.0436
C2 KEGG pathway	<u>KEGG GRAFT VERSUS HOST DISEASE</u>	1.68	0.0147	0.0436
C5 GO Cellular Component	<u>GOCC SPECIFIC GRANULE</u>	1.68	0.0000	0.0438
C5 GO Biological Process	<u>GOBP RUFFLE ORGANIZATION</u>	1.68	0.0000	0.0439
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS</u>	1.68	0.0017	0.0442
C5 GO Cellular Component	<u>GOCC TERTIARY GRANULE LUMEN</u>	1.68	0.0000	0.0442
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF IMMUNE SYSTEM PROCESS</u>	1.68	0.0000	0.0442
C2 Reactome pathway	<u>REACTOME TICAM1 RIP1 MEDIATED IKK COMPLEX RECRUITMENT</u>	1.68	0.0095	0.0446
C5 GO Biological Process	<u>GOBP PROTEIN DESTABILIZATION</u>	1.68	0.0075	0.0446
C5 GO Molecular Function	<u>GOMF ISOPRENOID BINDING</u>	-2.09	0.0000	0.0446
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 10 SIGNALING</u>	1.68	0.0137	0.0446
C2 Reactome pathway	<u>REACTOME REGULATION OF PTEN GENE TRANSCRIPTION</u>	1.68	0.0018	0.0446
C2 KEGG pathway	<u>KEGG LEISHMANIA INFECTION</u>	1.67	0.0036	0.0446
C5 GO Biological Process	<u>GOBP RIBONUCLEOPROTEIN COMPLEX BIOGENESIS</u>	1.68	0.0000	0.0447
C2 Reactome pathway	<u>REACTOME CROSS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS ENDOSOMES</u>	1.67	0.0053	0.0447

C5 GO Biological Process	<u>GOBP RESPIRATORY BURST</u>	1.67	0.0037	0.0447
C2 BioCarta pathway	<u>BIOCARTA PTEN PATHWAY</u>	1.67	0.0108	0.0447
C5 GO Cellular Component	<u>GOCC GOLGI ASSOCIATED VESICLE</u>	1.67	0.0019	0.0448
C5 GO Molecular Function	<u>GOMF HSP70 PROTEIN BINDING</u>	1.67	0.0018	0.0448
C5 GO Cellular Component	<u>GOCC ENDOSOME MEMBRANE</u>	1.67	0.0000	0.0448
C5 GO Biological Process	<u>GOBP CELLULAR RESPONSE TO MOLECULE OF BACTERIAL ORIGIN</u>	1.67	0.0000	0.0448
C5 GO Cellular Component	<u>GOCC IMMUNOLOGICAL SYNAPSE</u>	1.67	0.0038	0.0448
C5 GO Biological Process	<u>GOBP MYELOID CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE</u>	1.67	0.0000	0.0449
C5 GO Biological Process	<u>GOBP MONOVALENT INORGANIC ANION HOMEOSTASIS</u>	1.67	0.0221	0.0451
C2 WikiPathways pathway	<u>WP HEAD AND NECK SQUAMOUS CELL CARCINOMA</u>	1.67	0.0035	0.0451
C2 KEGG pathway	<u>KEGG N GLYCAN BIOSYNTHESIS</u>	1.67	0.0112	0.0453
C2 Reactome pathway	<u>REACTOME OXIDATIVE STRESS INDUCED SENESCENCE</u>	1.67	0.0018	0.0453
C2 Reactome pathway	<u>REACTOME SIGNALING BY WNT</u>	1.67	0.0000	0.0453
Hallmark	<u>HALLMARK IL2 STAT5 SIGNALING</u>	1.67	0.0016	0.0453
C5 GO Biological Process	<u>GOBP REGULATION OF CARBOHYDRATE CATABOLIC PROCESS</u>	1.67	0.0112	0.0454
C5 GO Biological Process	<u>GOBP COTRANSLATIONAL PROTEIN TARGETING TO MEMBRANE</u>	1.67	0.0114	0.0455
C5 GO Biological Process	<u>GOBP REGULATION OF LEUKOCYTE PROLIFERATION</u>	1.67	0.0000	0.0455
C5 GO Cellular Component	<u>GOCC PRERIBOSOME</u>	1.67	0.0035	0.0455
C5 GO Biological Process	<u>GOBP REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS</u>	1.67	0.0000	0.0457
C5 GO Biological Process	<u>GOBP REGULATION OF TRANSCRIPTION OF NUCLEOLAR LARGE RRNA BY RNA POLYMERASE I</u>	1.67	0.0057	0.0457
C2 Reactome pathway	<u>REACTOME TRANSCRIPTIONAL REGULATION BY SMALL RNAS</u>	1.67	0.0071	0.0458
C2 Reactome pathway	<u>REACTOME GOLGI ASSOCIATED VESICLE BIOGENESIS</u>	1.67	0.0071	0.0458
C2 WikiPathways pathway	<u>WP MICRORNAS IN CARDIOMYOCYTE HYPERTROPHY</u>	1.67	0.0000	0.0458
C5 GO Biological Process	<u>GOBP REGULATION OF OXIDATIVE STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY</u>	1.67	0.0055	0.0459
C5 GO Biological Process	<u>GOBP T CELL SELECTION</u>	1.67	0.0035	0.0460

Group	Gene Set Name	NES	p	FDR q
		post, trained vs control		
C5 GO Molecular Function	<u>GOMF TRANSLATION REGULATOR ACTIVITY</u>	1.67	0.0000	0.0460
C5 GO Biological Process	<u>GOBP MONONUCLEAR CELL DIFFERENTIATION</u>	1.67	0.0000	0.0460

C5 GO Biological Process	<u>GOBP MRNA SPLICE SITE SELECTION</u>	1.67	0.0107	0.0461
C5 GO Biological Process	<u>GOBP INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE</u>	1.67	0.0017	0.0461
C5 GO Biological Process	<u>GOBP NCRNA PROCESSING</u>	1.67	0.0000	0.0461
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF CELL ADHESION MEDIATED BY INTEGRIN</u>	1.67	0.0096	0.0462
C5 GO Cellular Component	<u>GOCC INTRINSIC COMPONENT OF ORGANELLE MEMBRANE</u>	1.67	0.0000	0.0462
C2 Reactome pathway	<u>REACTOME TRAF6 MEDIATED NF KB ACTIVATION</u>	1.67	0.0147	0.0463
C5 GO Biological Process	<u>GOBP RIBOSE PHOSPHATE BIOSYNTHETIC PROCESS</u>	1.66	0.0017	0.0465
C5 GO Molecular Function	<u>GOMF NUCLEOCYTOPLASMIC CARRIER ACTIVITY</u>	1.66	0.0055	0.0467
C2 Reactome pathway	<u>REACTOME CYCLIN A B1 B2 ASSOCIATED EVENTS DURING G2 M TRANSITION</u>	1.66	0.0112	0.0467
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF ALPHA BETA T CELL DIFFERENTIATION</u>	1.66	0.0054	0.0468
C2 PID pathway	<u>PID CDC42 PATHWAY</u>	1.66	0.0053	0.0468
C5 GO Biological Process	<u>GOBP FATTY ACYL COA METABOLIC PROCESS</u>	1.66	0.0200	0.0468
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF MAP KINASE ACTIVITY</u>	1.66	0.0087	0.0468
C2 WikiPathways pathway	<u>WP FBXL10 ENHANCEMENT OF MAPERK SIGNALING IN DIFFUSE LARGE BCELL LYMPHOMA</u>	1.66	0.0184	0.0468
C5 GO Cellular Component	<u>GOCC CATALYTIC STEP 2 SPLICEOSOME</u>	1.66	0.0017	0.0469
C2 WikiPathways pathway	<u>WP CHEMOKINE SIGNALING PATHWAY</u>	1.66	0.0000	0.0469
C5 GO Molecular Function	<u>GOMF PHOSPHATIDYLINOSITOL KINASE ACTIVITY</u>	1.66	0.0153	0.0470
C5 GO Cellular Component	<u>GOCC GOLGI APPARATUS SUBCOMPARTMENT</u>	1.66	0.0000	0.0474
C5 GO Biological Process	<u>GOBP POSITIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS</u>	1.66	0.0000	0.0474
C5 GO Molecular Function	<u>GOMF GENERAL TRANSCRIPTION INITIATION FACTOR BINDING</u>	1.66	0.0089	0.0474
C5 GO Biological Process	<u>GOBP PROTEIN LOCALIZATION TO PHAGOPHORE ASSEMBLY SITE</u>	1.66	0.0199	0.0475
C5 GO Cellular Component	<u>GOCC U12 TYPE SPLICEOSOMAL COMPLEX</u>	1.66	0.0143	0.0476
C5 GO Molecular Function	<u>GOMF PROTEIN TRANSPORTER ACTIVITY</u>	1.66	0.0107	0.0476
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS</u>	1.66	0.0000	0.0476
C5 GO Molecular Function	<u>GOMF CYSTEINE TYPE ENDOPEPTIDASE REGULATOR ACTIVITY INVOLVED IN APOPTOTIC PROCESS</u>	1.66	0.0091	0.0476
C5 GO Biological Process	<u>GOBP MATURATION OF SSU RRNA</u>	1.66	0.0095	0.0476
C2 BioCarta pathway	<u>BIOCARTA EIF4 PATHWAY</u>	1.66	0.0108	0.0476
C2 WikiPathways pathway	<u>WP AGERAGE PATHWAY</u>	1.66	0.0017	0.0477

C5 GO Cellular Component	<u>GOCC GOLGI ASSOCIATED VESICLE MEMBRANE</u>	1.66	0.0035	0.0477
C2 KEGG pathway	<u>KEGG RNA DEGRADATION</u>	1.66	0.0053	0.0477
C5 GO Biological Process	<u>GOBP ANTIGEN PROCESSING AND PRESENTATION OF EXOGENOUS ANTIGEN</u>	1.66	0.0074	0.0478
C2 PID pathway	<u>PID INSULIN PATHWAY</u>	1.66	0.0108	0.0478
C2 WikiPathways pathway	<u>WP NOTCH SIGNALING</u>	1.66	0.0107	0.0478
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA</u>	1.66	0.0219	0.0482
C2 PID pathway	<u>PID P38 MK2 PATHWAY</u>	1.66	0.0134	0.0482
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF PROTEIN ACETYLATION</u>	1.66	0.0150	0.0482
C2 Reactome pathway	<u>REACTOME E3 UBIQUITIN LIGASES UBIQUITINATE TARGET PROTEINS</u>	1.66	0.0093	0.0486
C5 GO Molecular Function	<u>GOMF PHOSPHOPROTEIN BINDING</u>	1.66	0.0018	0.0486
C5 GO Biological Process	<u>GOBP ESTABLISHMENT OF PROTEIN LOCALIZATION TO CHROMOSOME</u>	1.66	0.0146	0.0487
C5 GO Cellular Component	<u>GOCC MICROBODY</u>	1.65	0.0000	0.0489

Group	Gene Set Name	NES	p	FDR q
C5 GO Biological Process	<u>GOBP REGULATION OF IMMUNE EFFECTOR PROCESS</u>	1.65	0.0000	0.0490
C2 WikiPathways pathway	<u>WP NUCLEOTIDE EXCISION REPAIR</u>	1.65	0.0127	0.0491
C2 Reactome pathway	<u>REACTOME DNA REPAIR</u>	1.65	0.0000	0.0491
C5 GO Biological Process	<u>GOBP REGULATION OF DNA REPAIR</u>	1.65	0.0000	0.0492
C2 Reactome pathway	<u>REACTOME INTERLEUKIN 12 SIGNALING</u>	1.65	0.0000	0.0492
C5 GO Biological Process	<u>GOBP LEUKOCYTE HOMEOSTASIS</u>	1.65	0.0017	0.0495
C2 Reactome pathway	<u>REACTOME BBSOME MEDIATED CARGO TARGETING TO CILIUM</u>	1.65	0.0127	0.0497
C5 GO Biological Process	<u>GOBP NEGATIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS</u>	1.65	0.0108	0.0498
C2 KEGG pathway	<u>KEGG RENAL CELL CARCINOMA</u>	1.65	0.0052	0.0498
C5 GO Biological Process	<u>GOBP HISTONE METHYLATION</u>	1.65	0.0000	0.0498
C5 GO Biological Process	<u>GOBP REGULATION OF GENERATION OF PRECURSOR METABOLITES AND ENERGY</u>	1.65	0.0000	0.0498
C5 GO Cellular Component	<u>GOCC TERTIARY GRANULE</u>	1.65	0.0000	0.0498
C2 BioCarta pathway	<u>BIOCARTA CTCF PATHWAY</u>	1.65	0.0209	0.0499
C2 WikiPathways pathway	<u>WP FACTORS AND PATHWAYS AFFECTING INSULINLIKE GROWTH FACTOR IGF1AKT SIGNALING</u>	1.65	0.0129	0.0499
C5 GO Biological Process	<u>GOBP REGULATION OF TRANSCRIPTION BY RNA POLYMERASE I</u>	1.65	0.0035	0.0500
C5 GO Biological Process	<u>GOBP COENZYME A METABOLIC PROCESS</u>	1.65	0.0168	0.0500

