Figure 1

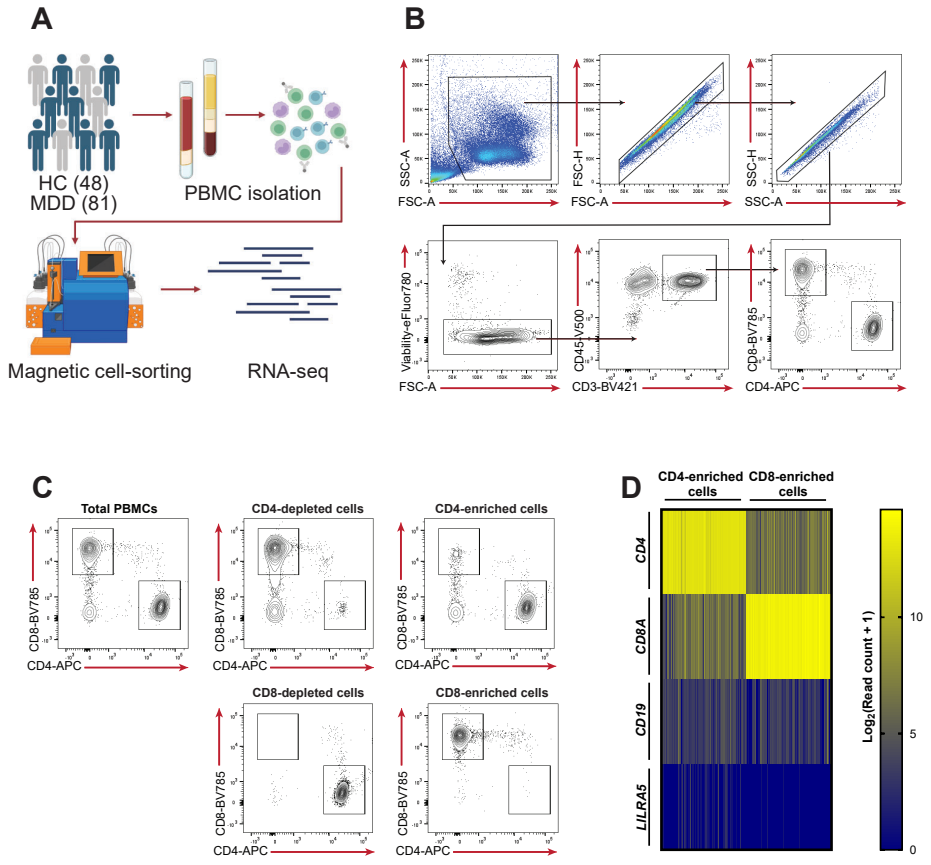
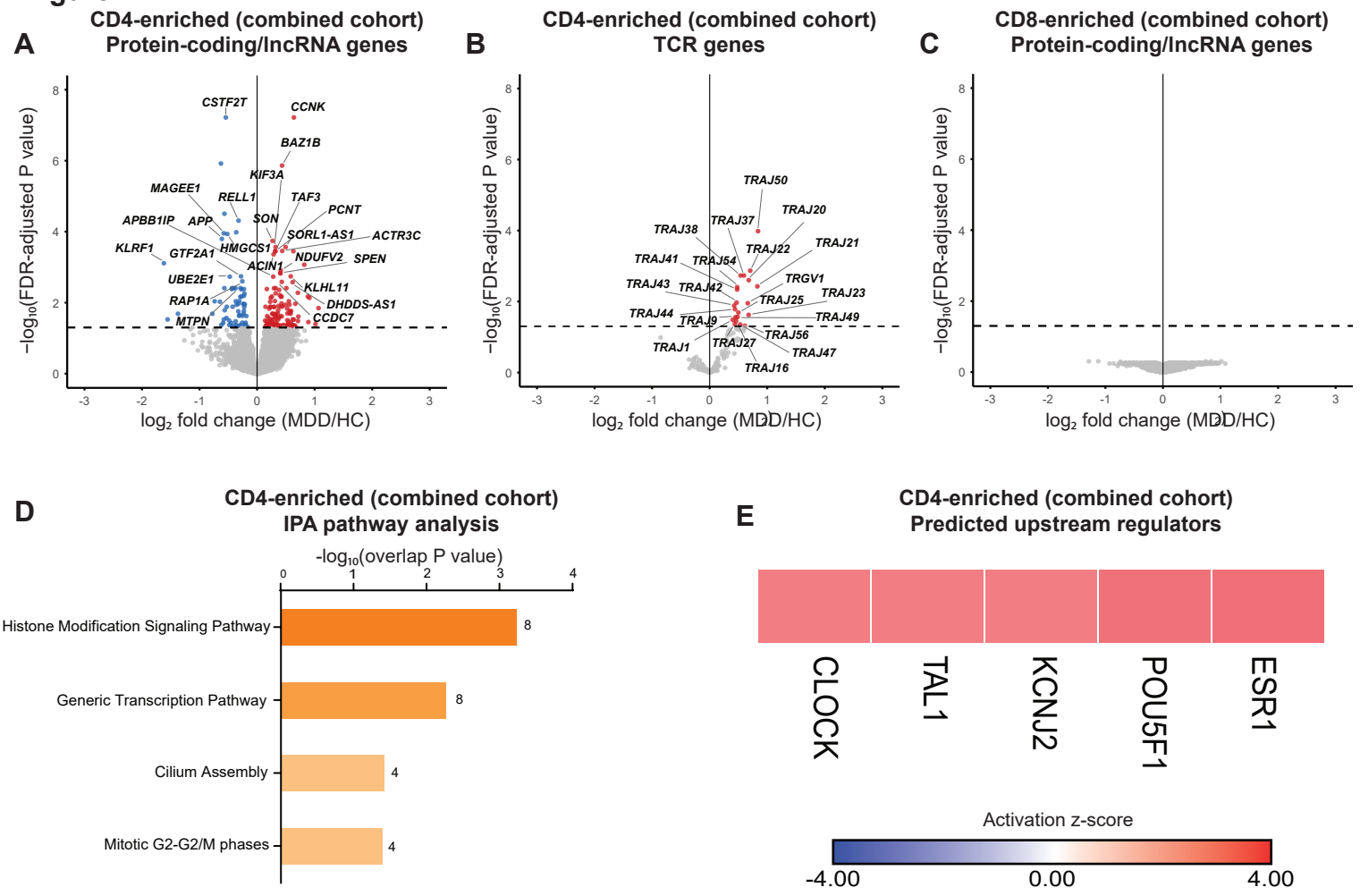

A
HC (48)
MDD (81)
PBMC isolation
Magnetic cell-sorting
RNA-seq
B
SSC-A
FSC-A
FSC-H
FSC-A
SSC-H
SSC-A
Viability-eFluor780
FSC-A
CD45-V500
CD3-BV421
CD8-BV785
CD4-APC
C
Total PBMCs
CD4-depleted cells
CD4-enriched cells
CD8-depleted cells
CD8-enriched cells
CD8-BV785
CD4-APC
D
CD4-enriched cells
CD8-enriched cells
CD4
CD8A
CD19
LILRA5
Log2(Read count + 1)
10
5
0

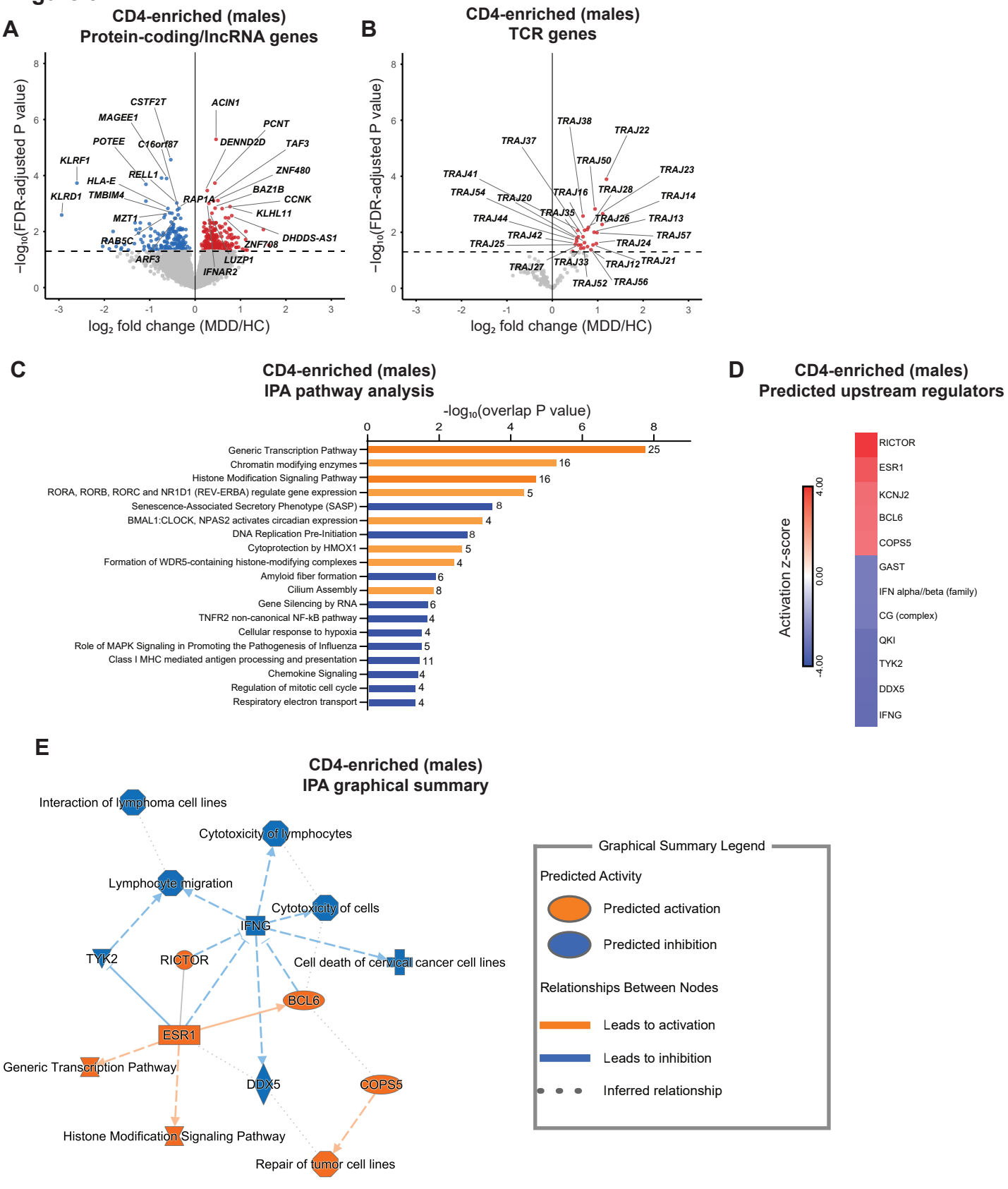
Figure 2


A
CD4-enriched (combined cohort)
Protein-coding/lncRNA genes
B
CD4-enriched (combined cohort)
TCR genes
C
CD8-enriched (combined cohort)
Protein-coding/lncRNA genes
−log10(FDR-adjusted P value)
log2 fold change (MDD/HC)
CSTF2T
CCNK
BAZ1B
KIF3A
MAGEE1
RELL1
TAF3
APBB1IP
APP
SON
PCNT
KLRF1
GTF2A1
HMGCS1
SORL1-AS1
ACTR3C
ACIN1
NDUFV2
SPEN
UBE2E1
KLHL11
RAP1A
DHDDS-AS1
MTPN
CCDC7
TRAJ50
TRAJ37
TRAJ20
TRAJ38
TRAJ22
TRAJ21
TRAJ41
TRAJ54
TRGV1
TRAJ43
TRAJ42
TRAJ25
TRAJ23
TRAJ44
TRAJ9
TRAJ49
TRAJ56
TRAJ1
TRAJ27
TRAJ47
TRAJ16

D
CD4-enriched (combined cohort)
IPA pathway analysis
-log10(overlap P value)
Histone Modification Signaling Pathway
Generic Transcription Pathway
Cilium Assembly
Mitotic G2-G2/M phases

E
CD4-enriched (combined cohort)
Predicted upstream regulators
CLOCK
TAL1
KCNJ2
POU5F1
ESR1
Activation z-score
-4.00
0.00
4.00

Figure 3


A
CD4-enriched (males)
Protein-coding/lncRNA genes
−log10(FDR-adjusted P value)
log2 fold change (MDD/HC)
CSTF2T
MAGEE1
POTEE
C16orf87
KLRF1
RELL1
HLA-E
KLRD1
TMBIM4
MZT1
RAB5C
ARF3
ACIN1
PCNT
DENND2D
TAF3
ZNF480
BAZ1B
RAP1A
CCNK
KLHL11
DHDDS-AS1
ZNF708
LUZP1
IFNAR2
B
CD4-enriched (males)
TCR genes
−log10(FDR-adjusted P value)
log2 fold change (MDD/HC)
TRAJ38
TRAJ22
TRAJ37
TRAJ50
TRAJ23
TRAJ41
TRAJ54
TRAJ20
TRAJ16
TRAJ28
TRAJ14
TRAJ35
TRAJ44
TRAJ26
TRAJ13
TRAJ42
TRAJ57
TRAJ25
TRAJ24
TRAJ27
TRAJ33
TRAJ12
TRAJ21
TRAJ52
TRAJ56
C
CD4-enriched (males)
IPA pathway analysis
-log10(overlap P value)
Generic Transcription Pathway 25
Chromatin modifying enzymes 16
Histone Modification Signaling Pathway 16
RORA, RORB, RORC and NR1D1 (REV-ERBA) regulate gene expression 5
Senescence-Associated Secretory Phenotype (SASP) 8
BMAL1:CLOCK, NPAS2 activates circadian expression 4
DNA Replication Pre-Initiation 8
Cytoprotection by HMOX1 5
Formation of WDR5-containing histone-modifying complexes 4
Amyloid fiber formation 6
Cilium Assembly 8
Gene Silencing by RNA 6
TNFR2 non-canonical NF-kB pathway 4
Cellular response to hypoxia 4
Role of MAPK Signaling in Promoting the Pathogenesis of Influenza 5
Class I MHC mediated antigen processing and presentation 11
Chemokine Signaling 4
Regulation of mitotic cell cycle 4
Respiratory electron transport 4
D
CD4-enriched (males)
Predicted upstream regulators
Activation z-score
4.00
0.00
-4.00
RICTOR
ESR1
KCNJ2
BCL6
COPS5
GAST
IFN alpha//beta (family)
CG (complex)
QKI
TYK2
DDX5
IFNG
E
CD4-enriched (males)
IPA graphical summary
Interaction of lymphoma cell lines
Cytotoxicity of lymphocytes
Lymphocyte migration
Cytotoxicity of cells
IFNG
TYK2
RICTOR
Cell death of cervical cancer cell lines
BCL6
ESR1
Generic Transcription Pathway
DDX5
COPS5
Histone Modification Signaling Pathway
Repair of tumor cell lines
Graphical Summary Legend
Predicted Activity
Predicted activation
Predicted inhibition
Relationships Between Nodes
Leads to activation
Leads to inhibition
Inferred relationship

Supplementary Figure 1

