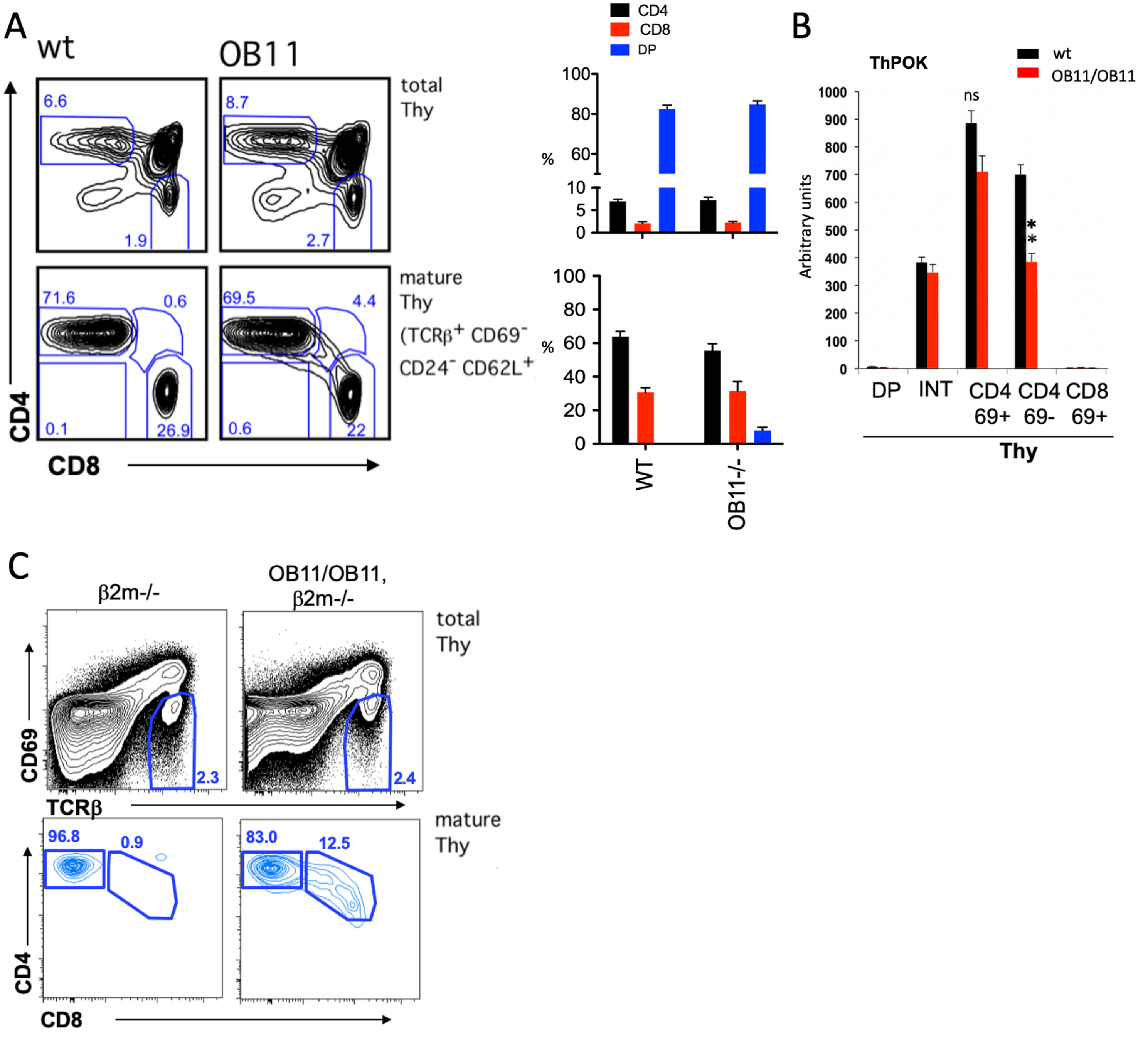
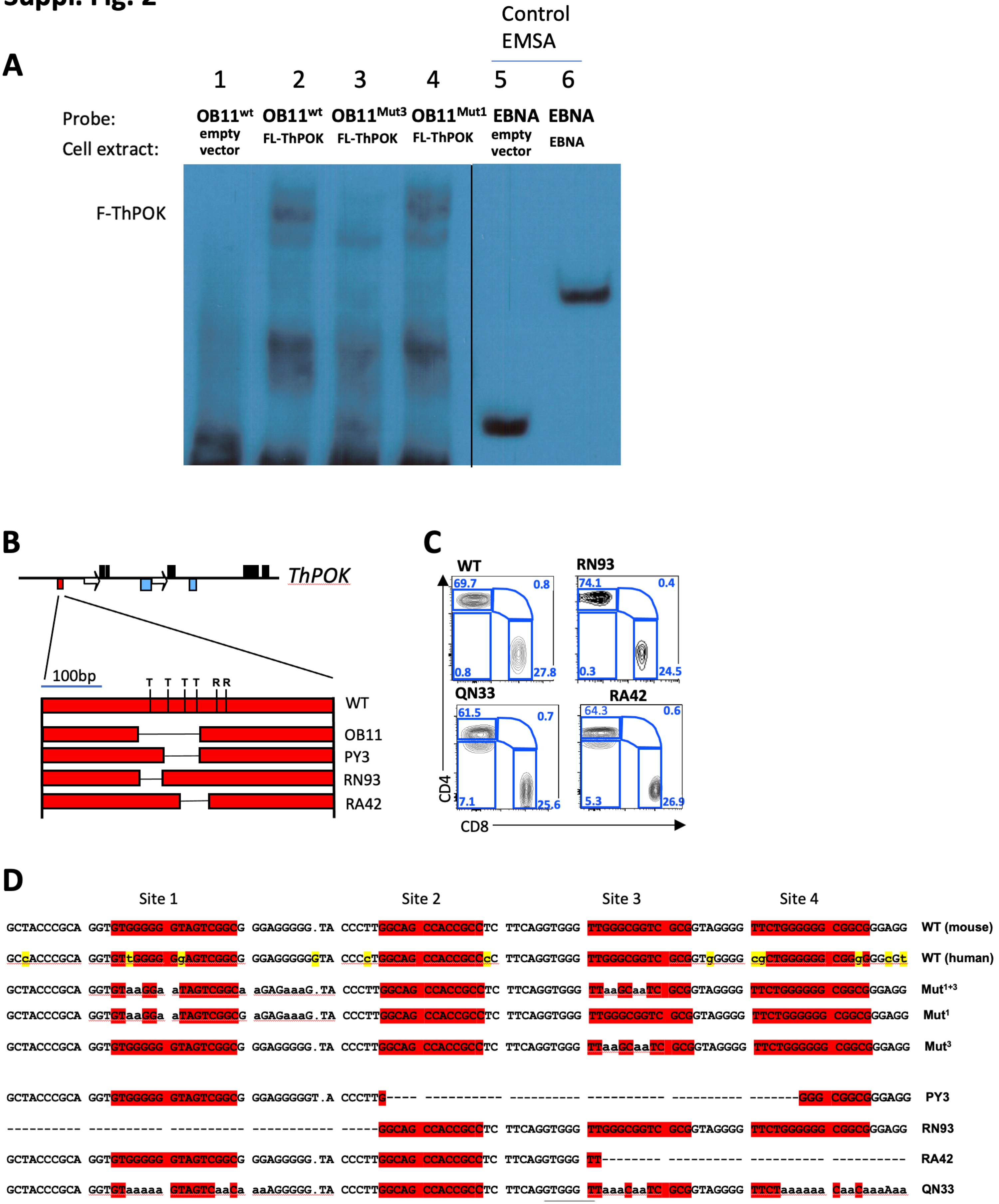
Suppl. Fig. 1

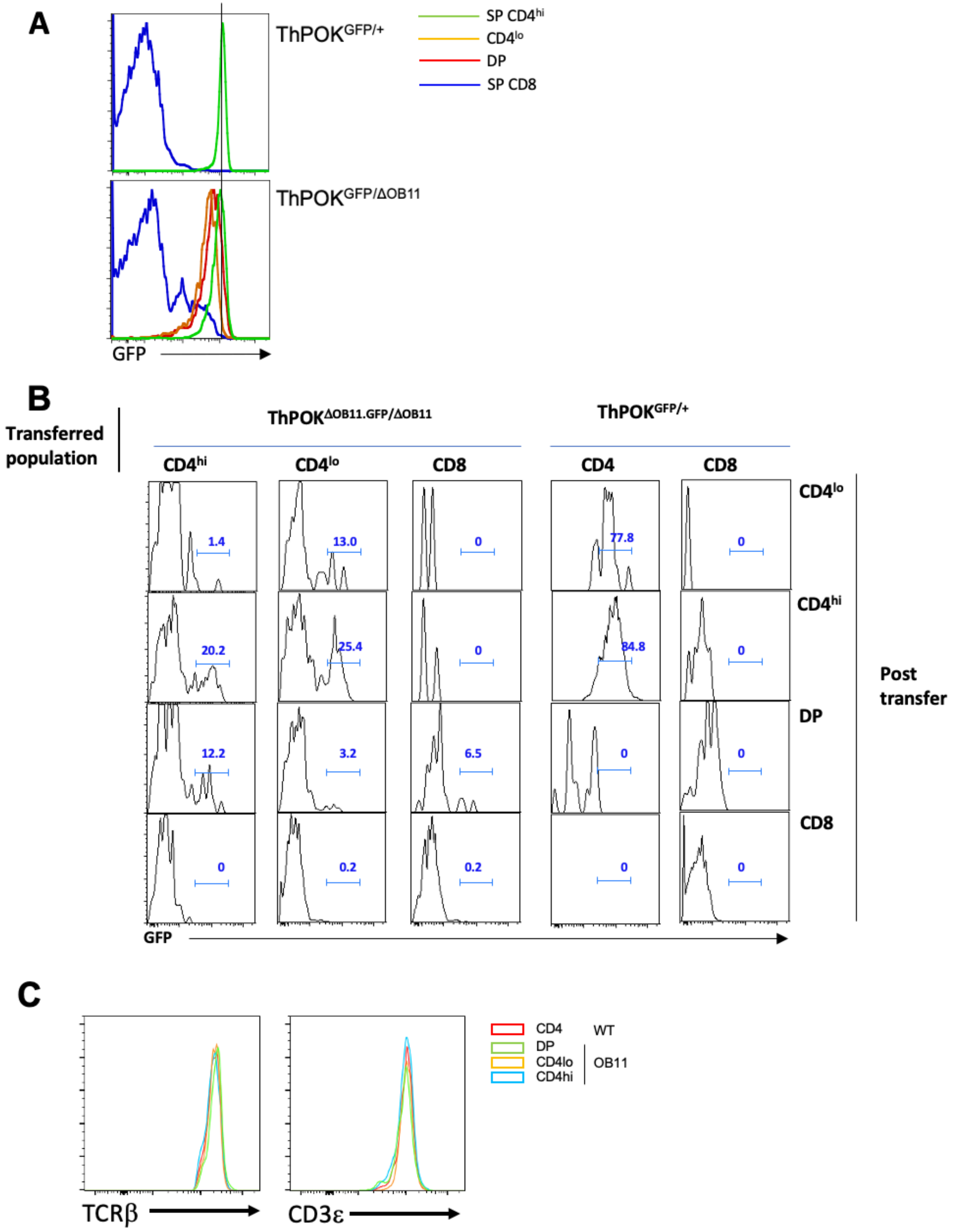


A
wt
OB11
total
Thy
6.6
1.9
8.7
2.7
mature
Thy
(TCRβ+ CD69- CD24- CD62L+
71.6
0.6
0.1
26.9
69.5
4.4
0.6
22
CD4
CD8
CD4
CD8
DP
100
80
60
10
5
0
%
100
80
60
40
20
0
%
WT
OB11-/-
B
ThPOK
wt
OB11/OB11
1000
900
800
700
600
500
400
300
200
100
0
Arbitrary units
ns
**
DP
INT
CD4 69+
CD4 69-
CD8 69+
Thy
C
β2m-/-
OB11/OB11, β2m-/-
total
Thy
CD69
TCRβ
2.3
2.4
96.8
0.9
83.0
12.5
mature
Thy
CD4
CD8

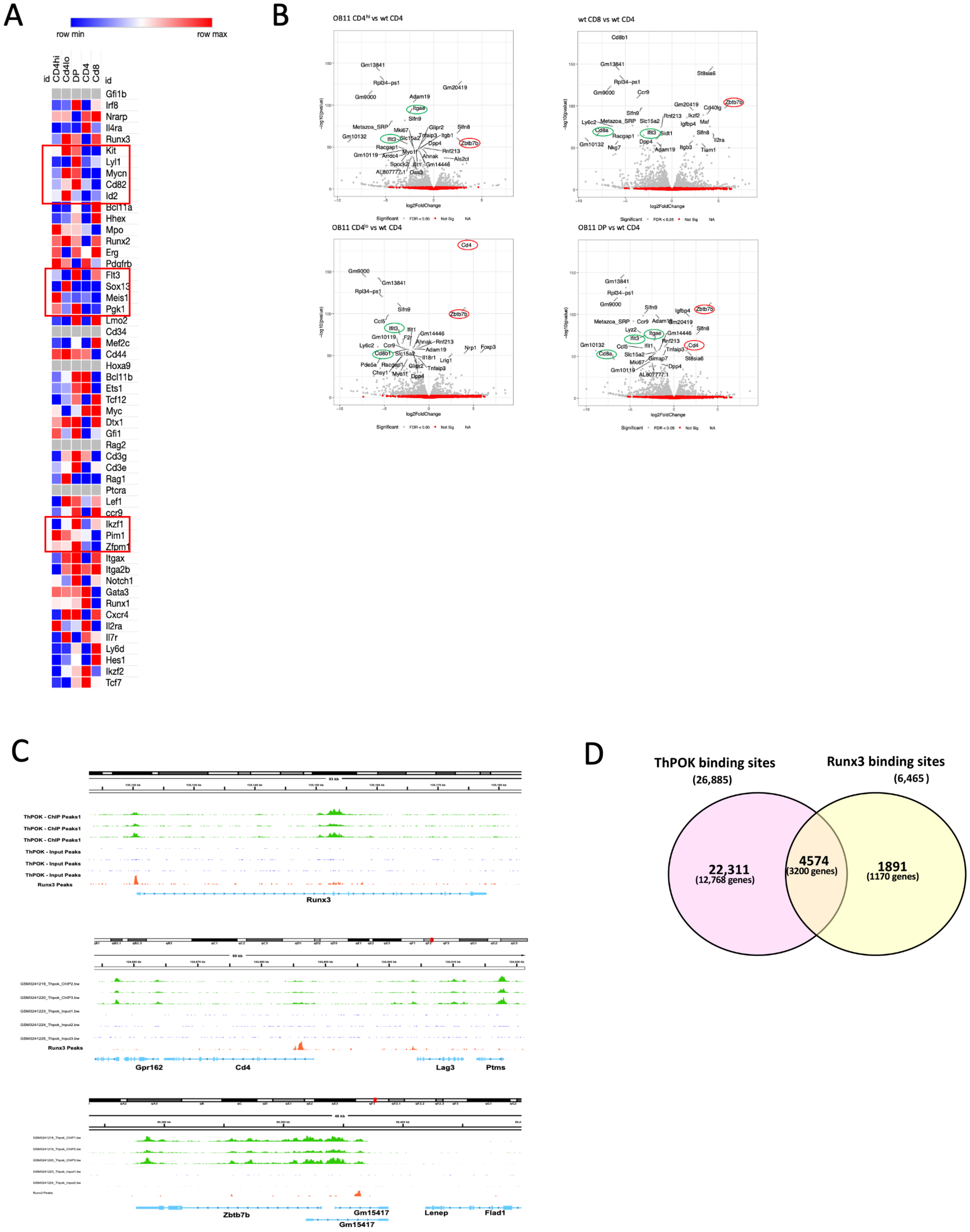
Suppl. Fig. 2


Control EMSA
A
1
2
3
4
5
6
Probe:
Cell extract:
OB11wt empty vector
OB11wt FL-ThPOK
OB11Mut3 FL-ThPOK
OB11Mut1 FL-ThPOK
EBNA empty vector
EBNA EBNA
F-ThPOK
B
ThPOK
100bp
T T T T R R
WT
OB11
PY3
RN93
RA42
C
WT
69.7
0.8
0.8
27.8
RN93
74.1
0.4
0.3
24.5
QN33
61.5
0.7
7.1
25.6
RA42
64.3
0.6
5.3
26.9
CD4
CD8
D
Site 1
Site 2
Site 3
Site 4
GCTACCCGCA GGTGTGGGGG GTAGTCGGCG GGAGGGGG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TTGGGCGGTC GCGGTAGGGG TTCTGGGGGG CGGCGGGAGG WT (mouse)
GCcACCCGCA GGTGTtGGGG GgAGTCGGCG GGAGGGGGGTA CCCcTGGCAG CCACCGCCcC TTCAGGTGGG TTGGGCGGTC GCGGTgGGGG cgCTGGGGGG CGGgGGGcGt WT (human)
GCTACCCGCA GGTGTaaGGa aTAGTCGGCa aGAGaaaG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TTaaGCaaTC GCGGTAGGGG TTCTGGGGGG CGGCGGGAGG Mut1+3
GCTACCCGCA GGTGTaaGGa aTAGTCGGCG aGAGaaaG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TTGGGCGGTC GCGGTAGGGG TTCTGGGGGG CGGCGGGAGG Mut1
GCTACCCGCA GGTGTGGGGG GTAGTCGGCG GGAGGGGG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TTaaGCaaTC GCGGTAGGGG TTCTGGGGGG CGGCGGGAGG Mut3
GCTACCCGCA GGTGTGGGGG GTAGTCGGCG GGAGGGGT.A CCCTTG---- ---------- ---------- ---------- ---------- -------GGG CGGCGGGAGG PY3
---------- ---------- ---------- ---------- -----GGCAG CCACCGCCTC TTCAGGTGGG TTGGGCGGTC GCGGTAGGGG TTCTGGGGGG CGGCGGGAGG RN93
GCTACCCGCA GGTGTGGGGG GTAGTCGGCG GGAGGGGG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TT-------- ---------- ---------- ---------- RA42
GCTACCCGCA GGTGTaaaaa GTAGTCaaCa aaAGGGGG.TA CCCTTGGCAG CCACCGCCTC TTCAGGTGGG TTaaaCaaTC GCGGTAGGGG TTCTaaaaaa CaaCaaaAaa QN33

Suppl. Fig. 3

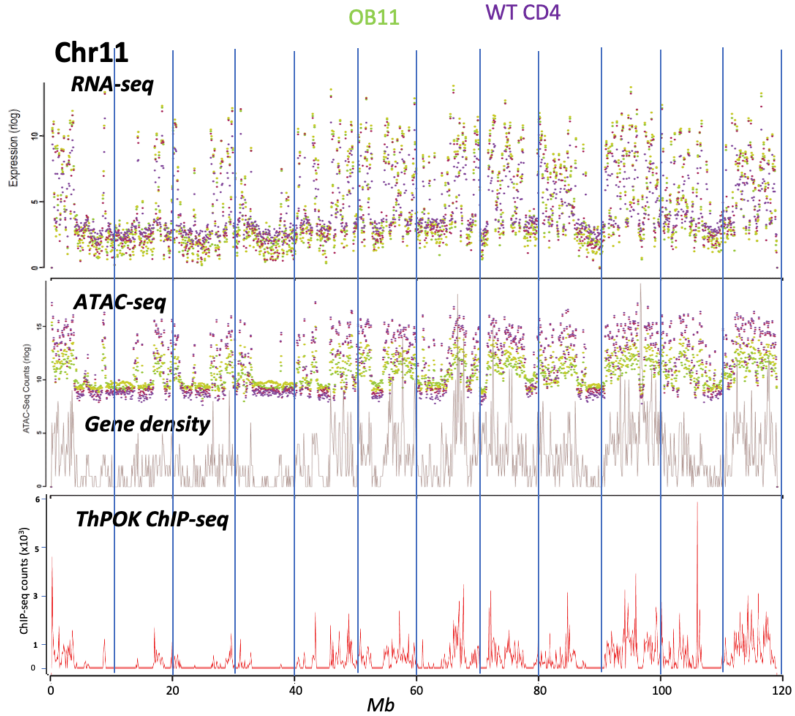

A
ThPOK$^{GFP/+}$
ThPOK$^{GFP/\Delta OB11}$
SP CD4^{hi}
CD4^{lo}
DP
SP CD8
GFP
B
Transferred population
ThPOK$^{\Delta OB11.GFP/\Delta OB11}$
ThPOK$^{GFP/+}$
CD4^{hi}
CD4^{lo}
CD8
CD4
CD8
CD4^{lo}
1.4
13.0
0
77.8
0
CD4^{hi}
20.2
25.4
0
84.8
0
DP
12.2
3.2
6.5
0
0
CD8
0
0.2
0.2
0
0
Post transfer
GFP
C
CD4
WT
DP
CD4lo
CD4hi
OB11
TCRβ
CD3ε

Suppl. Fig. 4


A
row min
row max
id
CD4hi
CD4lo
DP
CD4
Cd8
id
Gfi1b
Irf8
Nrarp
Il4ra
Runx3
Kit
Lyl1
Mycn
Cd82
Id2
Bcl11a
Hhex
Mpo
Runx2
Erg
Pdgfrb
Flt3
Sox13
Meis1
Pgk1
Lmo2
Cd34
Mef2c
Cd44
Hoxa9
Bcl11b
Ets1
Tcf12
Myc
Dtx1
Gfi1
Rag2
Cd3g
Cd3e
Rag1
Ptcra
Lef1
ccr9
Ikzf1
Pim1
Zfpm1
Itgax
Itga2b
Notch1
Gata3
Runx1
Cxcr4
Il2ra
Il7r
Ly6d
Hes1
Ikzf2
Tcf7
B
OB11 CD4hi vs wt CD4
wt CD8 vs wt CD4
OB11 CD4lo vs wt CD4
OB11 DP vs wt CD4
-log10(pvalue)
log2FoldChange
Significant
FDR < 0.05
Not Sig
NA
Gm13841
Rpl34-ps1
Gm9000
Gm20419
Adam19
Itgae
Slfn9
Slfn8
Metazoa_SRP
Mki67
Glipr2
Itgb1
Gm10132
Ifit3
Slc15a2
Tnfaip3
Dpp4
Zbtb7b
Racgap1
Rnf213
Gm10119
Arrdc4
Myo1f
Ahnak
Als2cl
Spock2
Ifit1
Gm14446
AL807777.1
Oas3
Cd8b1
St8sia6
Ccr9
Cd40lg
Ikzf2
Ly6c2
Igfbp4
Maf
Cd8a
Sidt1
Il2ra
Nkg7
Itgb3
Tiam1
Cd4
Ccl5
F2r
Ly6c2
Il18r1
Nrp1
Foxp3
Lrig1
Pde5a
Chsy1
Lyz2
Gimap7
Ifit1
C
ThPOK - ChIP Peaks1
ThPOK - Input Peaks
Runx3 Peaks
Runx3
GSM3241219_Thpok_ChIP2.bw
GSM3241220_Thpok_ChIP3.bw
GSM3241223_Thpok_Input1.bw
GSM3241224_Thpok_Input2.bw
GSM3241225_Thpok_Input3.bw
Gpr162
Cd4
Lag3
Ptms
GSM3241218_Thpok_ChIP1.bw
Zbtb7b
Gm15417
Lenep
Flad1
D
ThPOK binding sites
(26,885)
Runx3 binding sites
(6,465)
22,311
(12,768 genes)
4574
(3200 genes)
1891
(1170 genes)

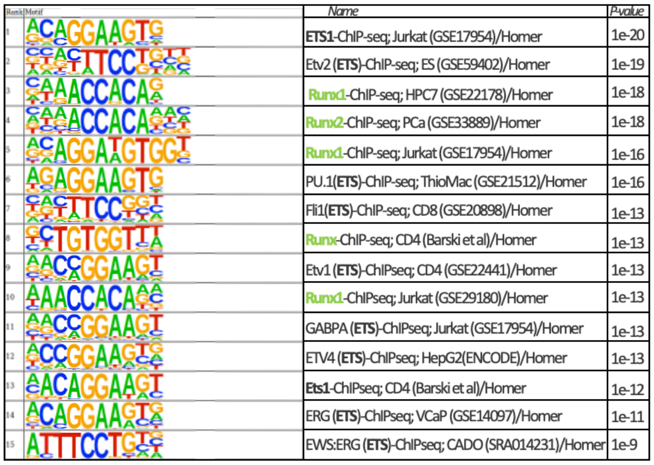
Suppl. Fig 5

A



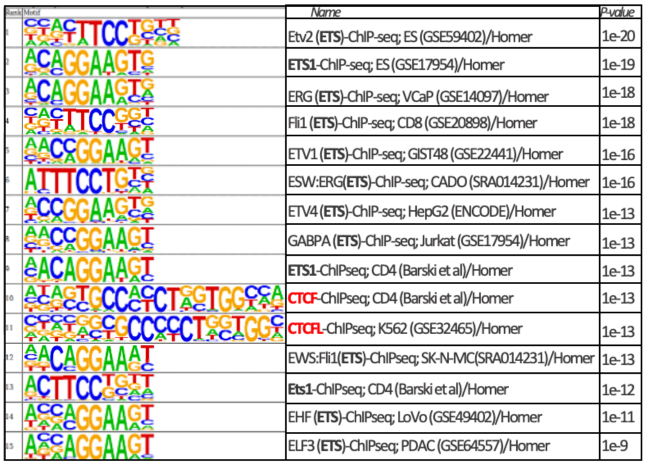
B

OB11 CD4^{lo}



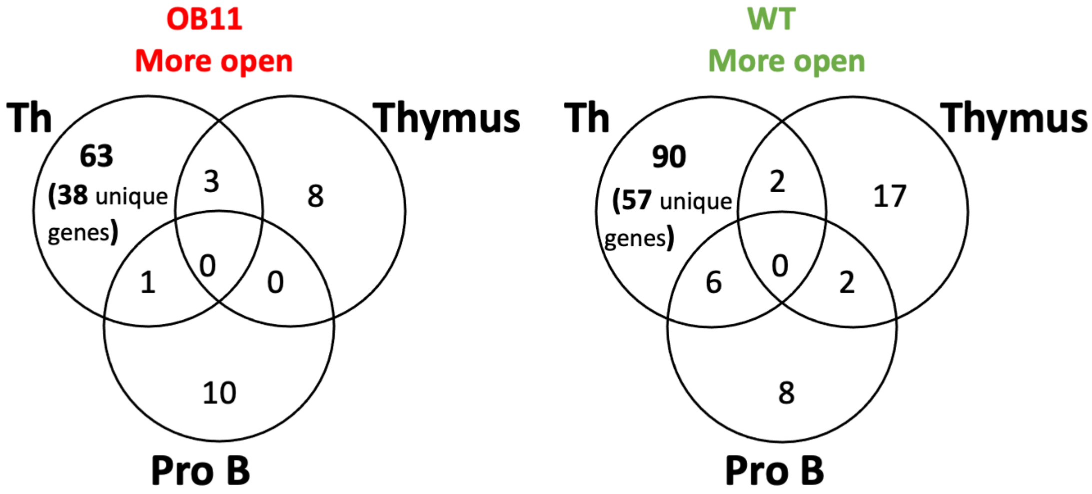
Rank	Motif	Name	P-value
1	ACAGGAAGTG	**ETS1**-ChIP-seq; Jurkat (GSE17954)/Homer	1e-20
2	CCACTTCCTGTT	Etv2 (**ETS**)-ChIP-seq; ES (GSE59402)/Homer	1e-19
3	CAAACCACAG	Runx1-ChIP-seq; HPC7 (GSE22178)/Homer	1e-18
4	CAAACCACAAAC	Runx2-ChIP-seq; PCa (GSE33889)/Homer	1e-18
5	ACAGGATGTGGT	Runx1-ChIP-seq; Jurkat (GSE17954)/Homer	1e-16
6	AGAGGAAGTG	PU.1(**ETS**)-ChIP-seq; ThioMac (GSE21512)/Homer	1e-16
7	CACTTCCGGT	Fli1(**ETS**)-ChIP-seq; CD8 (GSE20898)/Homer	1e-13
8	GCTGTGGTTA	Runx-ChIP-seq; CD4 (Barski et al)/Homer	1e-13
9	AACCGGAAGT	Etv1 (**ETS**)-ChIPseq; CD4 (GSE22441)/Homer	1e-13
10	AAACCACAAA	Runx1-ChIPseq; Jurkat (GSE29180)/Homer	1e-13
11	AACCGGAAGT	GABPA (**ETS**)-ChIPseq; Jurkat (GSE17954)/Homer	1e-13
12	ACCGGAAGTG	ETV4 (**ETS**)-ChIPseq; HepG2(ENCODE)/Homer	1e-13
13	AACAGGAAGT	**Ets1**-ChIPseq; CD4 (Barski et al)/Homer	1e-12
14	ACAGGAAGTG	ERG (**ETS**)-ChIPseq; VCaP (GSE14097)/Homer	1e-11
15	ATTTCCTGTG	EWS:ERG (**ETS**)-ChIPseq; CADO (SRA014231)/Homer	1e-9

WT

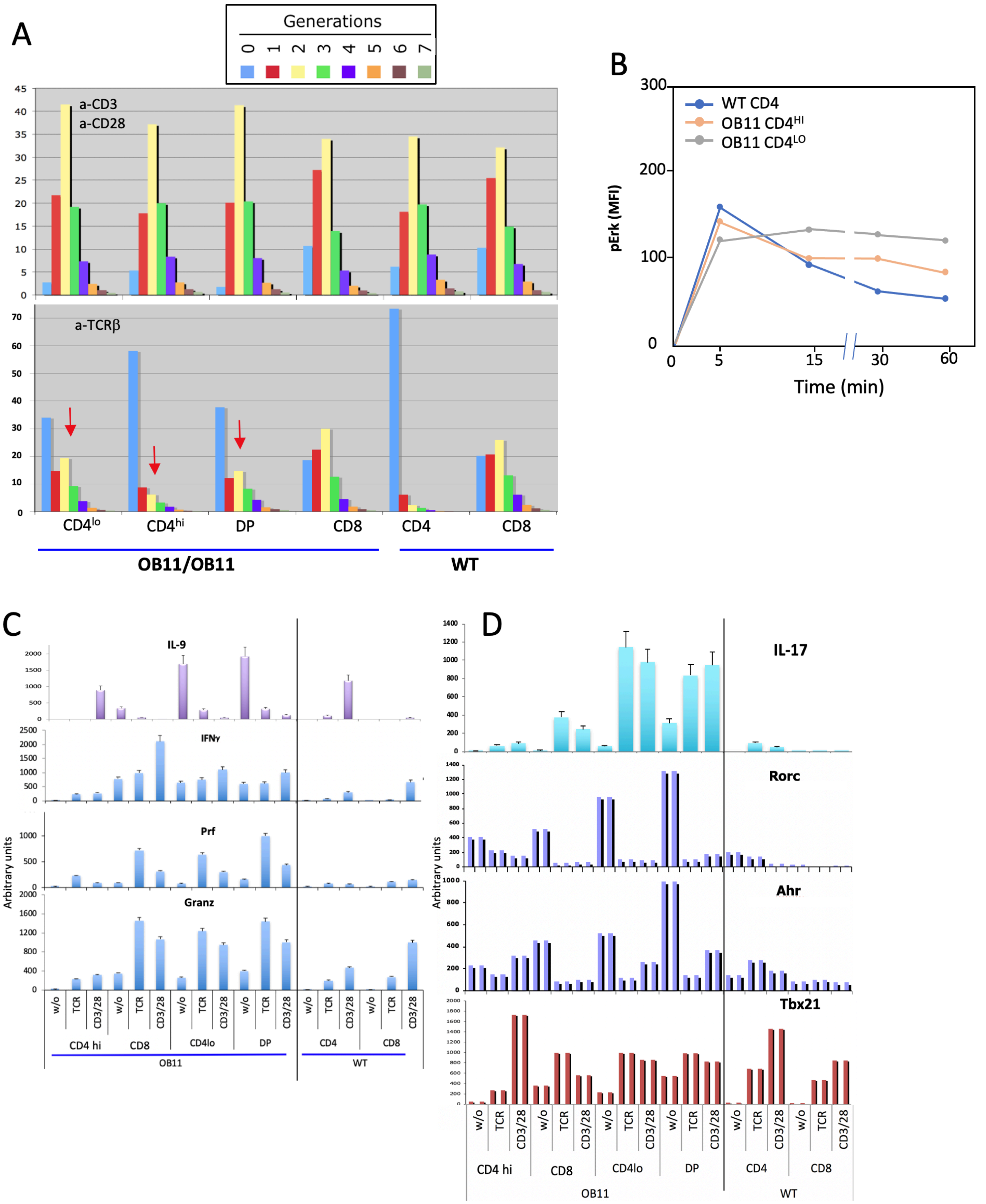


Rank	Motif	Name	P-value
1	CCACTTCCTGTT	Etv2 (**ETS**)-ChIP-seq; ES (GSE59402)/Homer	1e-20
2	ACAGGAAGTG	**ETS1**-ChIP-seq; ES (GSE17954)/Homer	1e-19
3	ACAGGAAGTG	ERG (**ETS**)-ChIP-seq; VCaP (GSE14097)/Homer	1e-18
4	CACTTCCGGT	Fli1 (**ETS**)-ChIP-seq; CD8 (GSE20898)/Homer	1e-18
5	AACCGGAAGT	ETV1 (**ETS**)-ChIP-seq; GIST48 (GSE22441)/Homer	1e-16
6	ATTTCCTGTG	ESW:ERG(**ETS**)-ChIP-seq; CADO (SRA014231)/Homer	1e-16
7	ACCGGAAGTG	ETV4 (**ETS**)-ChIP-seq; HepG2 (ENCODE)/Homer	1e-13
8	AACCGGAAGT	GABPA (**ETS**)-ChIP-seq; Jurkat (GSE17954)/Homer	1e-13
9	AACAGGAAGT	**ETS1**-ChIPseq; CD4 (Barski et al)/Homer	1e-13
10	ATAGTGCCACCTGGTGGCCA	CTCF-ChIPseq; CD4 (Barski et al)/Homer	1e-13
11	CCCCGGCGCCCCCTGGTGGC	CTCFL-ChIPseq; K562 (GSE32465)/Homer	1e-13
12	AACAGGAAAT	EWS:Fli1(**ETS**)-ChIPseq; SK-N-MC(SRA014231)/Homer	1e-13
13	ACTTCCTGTT	**Ets1**-ChIPseq; CD4 (Barski et al)/Homer	1e-12
14	ACCAGGAAGT	EHF (**ETS**)-ChIPseq; LoVo (GSE49402)/Homer	1e-11
15	ACCAGGAAGT	ELF3 (**ETS**)-ChIPseq; PDAC (GSE64557)/Homer	1e-9

C

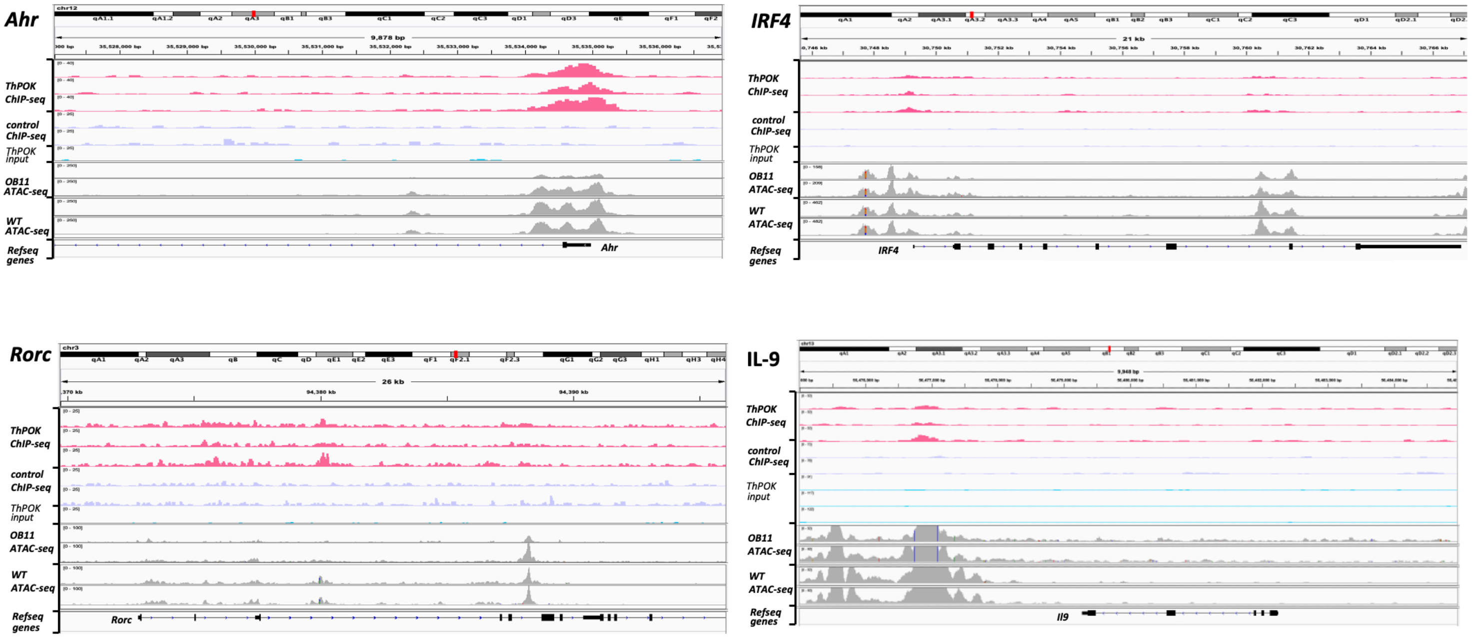


Suppl. Fig. 6


A
Generations
0 1 2 3 4 5 6 7
a-CD3
a-CD28
45 40 35 30 25 20 15 10 5 0
a-TCRβ
70 60 50 40 30 20 10 0
CD4lo
CD4hi
DP
CD8
CD4
CD8
OB11/OB11
WT
B
WT CD4
OB11 CD4HI
OB11 CD4LO
pErk (MFI)
300
200
100
0
0 5 15 30 60
Time (min)
C
IL-9
2000 1500 1000 500 0
IFNγ
2500 2000 1500 1000 500 0
Prf
1000 500 0
Granz
2000 1600 1200 800 400 0
Arbitrary units
w/o TCR CD3/28
CD4 hi
CD8
CD4lo
DP
CD4
CD8
OB11
WT
D
IL-17
1400 1200 1000 800 600 400 200 0
Rorc
1400 1200 1000 800 600 400 200 0
Ahr
1000 800 600 400 200 0
Tbx21
2000 1800 1600 1400 1200 1000 800 600 400 200 0
Arbitrary units
w/o TCR CD3/28
CD4 hi
CD8
CD4lo
DP
CD4
CD8
OB11
WT

Suppl. Fig. 6

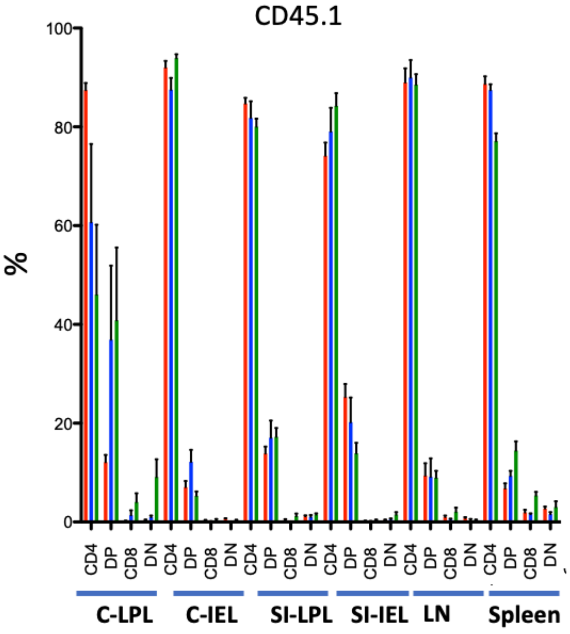
E



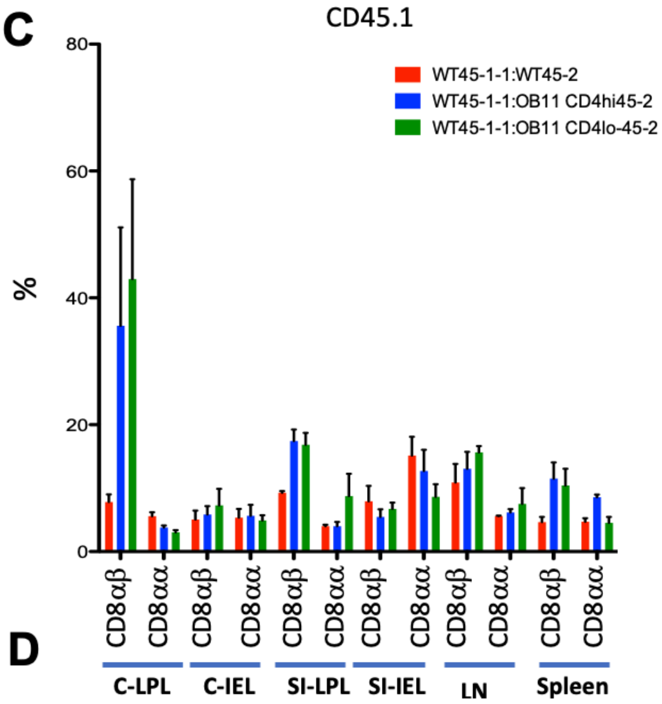
Ahr
chr12
9,878 bp
ThPOK ChIP-seq
control ChIP-seq
ThPOK input
OB11 ATAC-seq
WT ATAC-seq
Refseq genes
Ahr
IRF4
21 kb
ThPOK ChIP-seq
control ChIP-seq
ThPOK input
OB11 ATAC-seq
WT ATAC-seq
Refseq genes
IRF4
Rorc
chr3
26 kb
ThPOK ChIP-seq
control ChIP-seq
ThPOK input
OB11 ATAC-seq
WT ATAC-seq
Refseq genes
Rorc
IL-9
ThPOK ChIP-seq
control ChIP-seq
ThPOK input
OB11 ATAC-seq
WT ATAC-seq
Refseq genes
Il9

Suppl. Fig.7

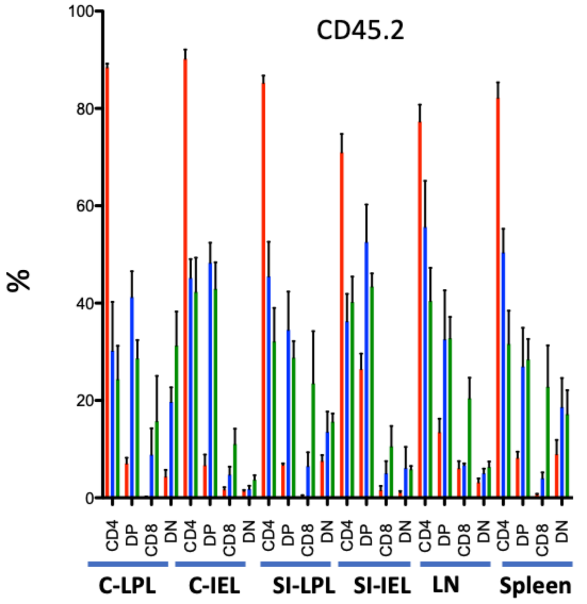
A



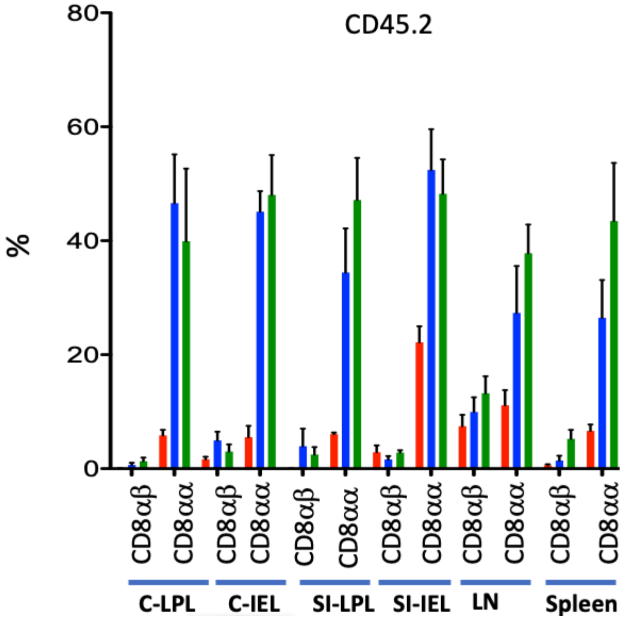
C



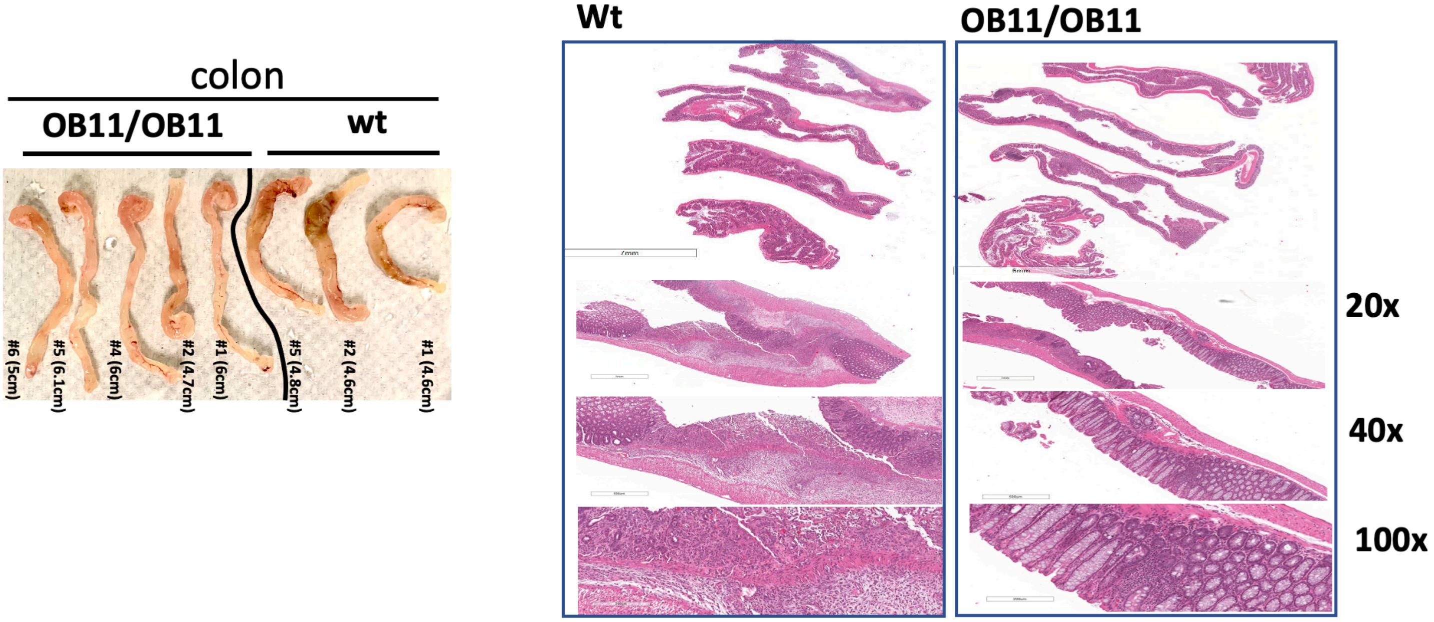
B



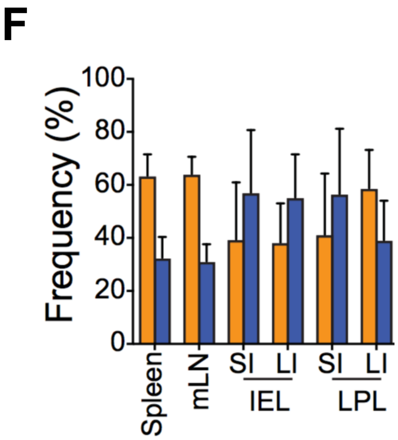
D



E



Suppl. Fig.7



Suppl. Table 1a

76 genes bound by ThPOK + Runx3, DN in all OB11 subsets

Akna
Amigo2
Arhgef1
Arid3b
Armc8
Atp1b1
Bbc3
Camk2d
Ccdc21 (=Cep85)
Ccr7
Cd27
Cd2ap
Cdk2
Celf1
Cflar
Chd3
Cnst
Dock4
Dopey1
Dusp7
Edem1
Enc1
Erc1
Fam3c
Gramd1a
Hjurp
Iqgap2
Kcnn4
Kidins220
Klhl3
Mat2a
Mllt3
Mob3c
Mpp7
Msl1
Mum1
Myo10
Naa16
Nrip1
Oxct1

Pag1
Phf1
Polg
Prkd2
Ptpn7
Ptpra
Pura
Rab27a
Rapgef6
Rasa1
Rasal3
Rasgrp1
Rassf2
Rbm38
Rgs14
Rock1
Sav1
Sfpq
Skil
Slc44a1
Smc6
Srpk1
Ssbp2
St6gal1
St8sia4
Tes
Tigit
Tmcc1
Tnfaip8l2
Trim24
Tspan32
Vamp1
Vps13d
Zbtb20
Zbtb37
Znrf1

136 genes bound by ThPOK +Runx3, UP in all OB11 subsets

2410006H16Rik
2700089E24Rik
5430417L22Rik
Actr2
Adcy3
Agl
Agpat4
Agrn
Ahnak
Ap1s2
Arhgap26
Arhgap30
Arl2bp
Arpc1b
Arrdc3
Atf7ip
Atp8b4
Atrnl1
AW112010
B4galt5
Birc5
Casc4
Ccdc102a
Ccdc117
Cct7
Cd72
Cd97
Cdt1
Celsr1
Cep152
Chmp4b
Chst11
Chsy1
Clic4
Cmah
Cmpk2
Cst7
Cxxc5
D4Wsu53e
D930015E06Rik

Daxx
Dazap2
Dennd4a
Dnajb1
Dnajb9
Dusp1
Eef1a1
Eef2
Ehd1
Ehd4
Eif4b
Eif5a
F2r
Fau
Fos
Gbp4
Ggt1
H2-Q4
H2-Q6
H2afy
Hipk1
Hmga1
Hspa5
Ifih1
Ifit3
Il2rb
Incenp
Irf9
Irs2
Junb
Klf11
Klk8
Lgals1
Ly9
Mafk
Map1lc3b
Mbnl1
Mex3a
Mical1
Mtap4

Naca
Ndc80
Ndufa10
Nfatc3
Nsmaf
Pabpc1
Pfkp

Plaur
Plekho2
Pmepa1
Ppp1r9b
Prf1
Psap
Ptp4a1
Ptp4a2
Rab8a
Rarg
Rnf157
Rpl10a
Rpl18a
Rpl21
Rpl27a
Rpl30
Rplp2
Rps12
Rras2
Runx3
Scarna2
Scpep1
Slbp
Slc16a6
Slc25a4
Sp140
Stat1
Stat2
Synj2
Tapbpl
Thy1
Tmem66

Topbp1
Tpx2
Tra2b
Traf4
Tspan3
Ubxn11
Usp18
Vasp
Vps13a
Xdh
Xrn2
Ywhae
Zbp1
Zc3h6
Zc3hav1
Zswim6

Suppl. Table 1b

132 genes bound by ThPOK only, DN in all OB11 subsets

1700020I14Rik
2010016I18Rik
2610035D17Rik
4930481A15Rik
Abhd14b
Acadvl
Actn4
Acvrl1
Afap1
Agtrap
Als2cl
App
Arhgap29
Arhgef11
Arsb
Atxn1
Aven
Axl
Bin1
Btg2
Cacnb1
Ccdc109b
Cd2
Cd200
Cd4
Cd5
Cd52
Cecr5
Chdh
Clec2d
Clip1
Cnn3
Coro7
Cpm
Cpt1a
Cyb5r4
Cyp2s1
Dapk1
Ddit4
Dgkd
Dhx40
Dst
Dtnb
Eea1
Eno1
Epas1
Epb4.1l1
Exoc3
Exoc6b
F2rl1
Fam177a
Fanci
Fkbp1a
Fmnl3
Fubp1
Galnt10
Galnt6
Ggt5
Gm4944
Gpatch4
Hadh
Hspa1b
Hspbap1
Igfbp4
Ikzf2
Il6st
Itgb3
Itpr2
L1cam
Lair1
Lats2
Ldlr
Lrig1
Ly6c1
Macf1
Mapk11
Me2
Mib2
Mical3
Micall1
Mns1
Mthfd2
Nacc2
Nav2
Nbeal1
Nek4
Npc1
Nrn1
Nrp1
Nup153
Nxpe3
Parp3
Pecam1
Polr1a
Ppm1j
Ptms
Ptpn13
Ptpn6
Pvr
Qser1
Rab6b
Rassf3
Rbm5
Rcan3
Rnf122
Rnf144a
Rpl29
Rpl34
Rps3a
Rsu1
S1pr1
Sfn
Sft2d2
Sh3bgrl3
Sipa1l2
Sit1
Slc30a4
Slfn8
Snapc1
St8sia1
St8sia6
Sytl2
Tbc1d30
Tcf7
Tecpr1
Tesc
Tgfbr2
Tnfaip8
Trio
Ttc28
Ttyh3
Vipr1

286 genes bound by ThPOK only, UP in all OB11 subsets

2310044G17Rik
2410001C21Rik
2700081O15Rik
8430419L09Rik
9430015G10Rik
A230050P20Rik
AA465934
Abcb1a
Acp5
Acsl5
Adam11
Adam19
Adar
Ahi1
Ak3
Anp32b
Anxa2
Anxa6
Apobec3
Arrdc4
Atp2b4
Atp6v1f
Atp6v1h
Bace1
Bai2
Baiap3
Baz1a
BC006779
Bcar3
Bend4
Bhlhe40
Bst2
C130039O16Rik
Cacna2d2
Camk2g
Ccl5
Ccna2
Ccr5
Ccr9
Ccrn4l
Cd274
Cdc20
Cdc25b
Cdk5rap1
Cdk5rap2
Cdk6
Cenpb
Cep250
Chst15
Coro2a
Csda
Ctsw
Cuedc2
Cxcl10
Cyth4
D17H6S56E-5
Ddx24
Ddx43
Ddx58
Ddx60
Dhx58
Dnaja4
Dock5
Dpp4
Dse
Dtx1
Dtx3l
Efhd2
Ehd3
Eif1
Eif2ak2
Eif3h
Eif3j2
Eml3
Eml5
Eno2
Eomes
Eps8l1
Fam107b
Fam111a
Fam129a
Fam179b
Fam73a
Fbxo32
Fcgr3
Ganc
Gatad2a
Gbp10
Gbp2
Gbp5
Gbp6
Gbp7
Gbp9
Gimap7
Glipr2
Gltscr2
Gm12250
Gm13212
Gm4902
Gpc1
Gpr68
Gramd1b
Gtf2i
Gzmb
H2-Oa
H2-Ob
H2-T23
Habp4
Herc6
Hip1r
Hist1h1b
Hist1h1c
Hist1h2af
Hist1h2al
Hist1h4a
Hist2h2bb
Hist4h4
Hmgb2
Hnrnpa1
Icam1
Id2
Ifi27l2a
Ifi47
Igtp
Ikzf3
Il18r1
Ildr1
Ipcef1
Iqgap1
Iqsec1
Irf1
Irf7
Irgc1
Irgm1
Irgm2
Isg15
Isg20
Itgb1
Jun
Kcna2
Kcnc1
Kcnk5
Kif23
Kif3c
Klhl6
Lax1
Lgals3
Lgals3bp
Limd1
Ltk
Magohb
Mast3
Mbd2
Mcm3
Mcm4
Mcm5
Mcm6
Med12
Mfap1a
Mki67
Mx1
Mx2
Myb
Myo1f
Nap1l1
Ncaph
Ncf1
Ncl
Nkg7
Nlrc3
Npc2
Nrg2
Nudc
Oas3
Oasl1
Oasl2
Orai2
Os9
Ostm1
Parp1
Parp14
Parp9
Pbxip1
Pctp
Pdcd6ip
Pde5a
Pfdn5
Pianp
Piga
Pik3ap1
Pim2
Plac8
Plcg2
Plekho1
Plxna1
Pmaip1
Pml
Pole3
Ppp1r15a
Prr13
Rab11fip1
Racgap1
Rbl2
Rcn1
Repin1
Rnf114
Rora
Rorc
Rpl10
Rpl11
Rpl17
Rpl24
Rpl28
Rpl3
Rpl31
Rpl32
Rpl34-ps1
Rpl41
Rpl6
Rps15a
Rps20
Rps24
Rps26
Rps27
Rps29
Rpsa
Rsad2
Rtp4
Runx2
S100a10
S100a11
S100a6
Sbno2
Scamp3
Scarna13
Sh3bp5
Shmt2
Sidt1
Slc2a3
Slc38a10
Slfn1
Slfn5
Slfn9
Smap2
Smchd1
Sorl1
Srgap3
Supt5h
Syde1
Syf2
Syn2
Tagap
Tapbp
Tbx21
Tdgf1
Tgtp1
Tgtp2
Tlr12
Tm6sf1
Tnfaip3
Tnfrsf14
Tnfsf14
Top2a
Tor3a
Trafd1
Trim12c
Trim25
Trim30a
Trp53i11
Tspyl3
Ttbk2
Tulp3
Uba7
Ubap2l
Uhrf1
Usp11
Usp24
Vcpip1
Wdtc1
Wipf1
Wipf2
Wnt5b
Xaf1
Zfp516
Zfp69
Zfp827

Suppl. Table 2a

David analysis: 76 genes DN in OB11, bound by ThPOK + Runx3

97	KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	7	3.723404	6.91E-04	LAT, PTPN6, PLCG1, FYN, RASGRP1, CD4, LCP2	83	101	7691	6.422164	0.105323
98	KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	7	3.723404	6.91E-04	LAT, PTPN6, PLCG1, FYN, RASGRP1, CD4, LCP2	83	101	7691	6.422164	0.105323
99	KEGG_PATHWAY	mmu04520:Adherens junction	6	3.191489	9.75E-04	PTPN6, TCF7, FYN, TGFBR1, TGFBR2, CTNNB1	83	72	7691	7.721888	0.145284
100	KEGG_PATHWAY	mmu04390:Hippo signaling pathway	8	4.255319	0.001086	TCF7, FRMD6, BBC3, TGFBR1, SAV1, TGFBR2, SCRIB, CTNNB1	83	151	7691	4.90928	0.160475
101	KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	9	4.787234	0.004096	CCR7, TNFRSF1B, IL2RA, CXCR5, CCR4, TGFBR1, TGFBR2, IL4RA, CD27	83	242	7691	3.446132	0.483603
102	KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	6	3.191489	0.005118	PRKCA, LAT, PTPN6, PLCG1, FYN, LCP2	83	105	7691	5.295009	0.562277
103	KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	6	3.191489	0.005118	PRKCA, LAT, PTPN6, PLCG1, FYN, LCP2	83	105	7691	5.295009	0.562277
104	KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	5	2.659574	0.005828	PRKCA, LAT, PLCG1, FYN, LCP2	83	68	7691	6.81343	0.609757
105	KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	5	2.659574	0.005828	PRKCA, LAT, PLCG1, FYN, LCP2	83	68	7691	6.81343	0.609757
106	KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	8	4.255319	0.007609	PRKCA, LAT, PLCG1, RAPGEF6, RGS14, DOCK4, LCP2, CTNNB1	83	214	7691	3.464024	0.707638
107	KEGG_PATHWAY	mmu04640:Hematopoietic cell lineage	5	2.659574	0.012647	IL2RA, ITGA6, IL4RA, CD2, CD4	83	85	7691	5.450744	0.871162
108	KEGG_PATHWAY	mmu05210:Colorectal cancer	4	2.12766	0.030557	TCF7, TGFBR1, TGFBR2, CTNNB1	83	64	7691	5.791416	0.993237
109	KEGG_PATHWAY	mmu04919:Thyroid hormone signaling pathway	5	2.659574	0.033108	PRKCA, ATP1B1, PLCG1, NCOA3, CTNNB1	83	114	7691	4.064151	0.995575
110	KEGG_PATHWAY	mmu04380:Osteoclast differentiation	5	2.659574	0.045176	CAMK4, FYN, TGFBR1, TGFBR2, LCP2	83	126	7691	3.677089	0.999414

David analysis: 132 genes UP in OB11, bound by ThPOK + Runx3

1	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich
2	GOTERM_BP_DIRECT	GO:0006412~translation	18	6.896552	1.77E-05	EEF1A1, RPL19, SLC25A4, RPL26, RPL27A, RPL36, EIF5A, EEF2, VARS, EIF4B, RPL30, RPS17, RPL	233	401	18082	3.483523
3	GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	12	4.597701	3.39E-05	COBLL1, ZC3HAV1, PFKP, EEF1G, DNAJB1, STAT1, TAGLN2, CLINT1, VASP, PLEC, DDX6, EHD4	233	189	18082	4.927311
4	GOTERM_BP_DIRECT	GO:0051607~defense response to virus	10	3.831418	3.12E-04	IFIT3, PRF1, IFIH1, ZC3HAV1, BCL2, LYST, OAS3, IFNGR1, STAT2, ZBP1	233	167	18082	4.647015
5	GOTERM_BP_DIRECT	GO:1901653~cellular response to peptide	4	1.532567	6.84E-04	PPP1R9B, KLF11, KLF4, KLF3	233	14	18082	22.1729
6	GOTERM_BP_DIRECT	GO:0006414~translational elongation	5	1.915709	0.003057	EEF1A1, RPLP2, EIF5A, EEF1G, EEF2	233	47	18082	8.255867
7	GOTERM_BP_DIRECT	GO:0034097~response to cytokine	6	2.298851	0.003869	IL12RB2, FOS, MCL1, BCL2, STAT1, JUNB	233	81	18082	5.74853
8	GOTERM_BP_DIRECT	GO:0032456~endocytic recycling	4	1.532567	0.003893	EHD1, ARL4C, EHD3, EHD4	233	25	18082	12.41682
9	GOTERM_BP_DIRECT	GO:0009615~response to virus	6	2.298851	0.00452	IFIT3, IFIH1, NPC2, ZC3HAV1, OAS3, EEF1G	233	84	18082	5.543225
10	GOTERM_BP_DIRECT	GO:0051260~protein homooligomerization	8	3.065134	0.0138	ANXA6, PRF1, EEF1A1, CHMP4B, ITPR3, EHD1, EHD3, EHD4	233	197	18082	3.151478
11	GOTERM_BP_DIRECT	GO:0051260~protein homooligomerization	8	3.065134	0.0138	ANXA6, PRF1, EEF1A1, CHMP4B, ITPR3, EHD1, EHD3, EHD4	233	197	18082	3.151478
12	GOTERM_BP_DIRECT	GO:0051056~regulation of small GTPase mediated signal transd	3	1.149425	0.021908	SIPA1L1, RAP1GAP2, ARHGAP26	233	18	18082	12.93419
13	GOTERM_BP_DIRECT	GO:0002376~immune system process	11	4.214559	0.026465	IFIT3, PRKCQ, IFIH1, NOD1, ZC3HAV1, PIK3CD, OAS3, SLAMF7, LY9, SEMA4A, ZBP1	233	383	18082	2.228869
14	GOTERM_BP_DIRECT	GO:0051591~response to cAMP	4	1.532567	0.027648	FOS, DUSP1, STAT1, JUNB	233	51	18082	6.086678
15	GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	6	2.298851	0.036342	ACTR2, PPP1R9B, TMSB10, IQSEC1, VASP, ARHGAP26	233	142	18082	3.279091
16	GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	7	2.681992	0.041883	IL12RB2, FOS, IL10RA, PLCG2, STAT1, JUNB, F2R	233	197	18082	2.757543

Suppl. Table 2b

DAVID analysis: 281 genes DN in OB11, bound by ThPOK only,

1	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fo
2	GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	12	4.33213	0.019527	PRKD2, MAST4, TNS1, SPSB1, TIAM1, DGKD, PINK1, MAPK11, ARHGAP29, MYO9A, LATS2, DAPK1	244	400	18082	2.
3	GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	8	2.888087	0.020154	IGF1R, S1PR1, ACTN4, TIAM1, CSF1, F2RL1, ITGB3, THBS1	244	203	18082	2.
4	GOTERM_BP_DIRECT	GO:0018105~peptidyl-serine phosphorylation	6	2.166065	0.033864	PRKD2, MAST4, MYO3B, MAPKAPK3, PINK1, LATS2	244	133	18082	3.
5	GOTERM_BP_DIRECT	GO:0016310~phosphorylation	15	5.415162	0.037551	ACVRL1, MYO3B, MAPKAPK3, CASK, PINK1, MAPK11, D8ERTD82E, LATS2, DAPK1, GALK2, IGF1R, PRKD2	244	612	18082	1.
6	GOTERM_CC_DIRECT	GO:0005769~early endosome	10	3.610108	0.002846	SH3GL3, CYTIP, NRP1, LDLR, ATP9A, MIB2, F2RL1, INPP5F, EEA1, RIN3	256	226	19662	3.
7	GOTERM_CC_DIRECT	GO:0016020~membrane	109	39.35018	0.014493	DYNC1LI2, IL6ST, F2RL1, CAPZA1, CASK, CD52, VIPR1, SLC26A11, SYP, KIF13A, PTGIR, S1PR1, TIAM1, UN	256	6998	19662	1.
35	KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	9	3.249097	0.006544	PRKD2, IGF1R, TIAM1, CSF1, SIPA1L2, MAPK11, ITGB2, ITGB3, THBS1	101	214	7691	3.
36	KEGG_PATHWAY	mmu05205:Proteoglycans in cancer	7	2.527076	0.048433	IGF1R, HIF1A, TIAM1, MAPK11, ITGB3, THBS1, ITPR2	101	203	7691	2.

DAVID analysis: 432 genes UP in OB11, bound by ThPOK only,

1	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	P	
2	GOTERM_BP_DIRECT	GO:0009615~response to virus	24	5.607477	1.43E-19	BST2, TBX21, RPS15A, RSAD2, CDK6, PIM2, CCL5, CXCL10, ISG20, DDX58, IFIT2, OASL2, IFI27L2A, DDX60,	387	84		
3	GOTERM_BP_DIRECT	GO:0006412~translation	43	10.04673	1.08E-17	RPL17, RPL36A, RBM3, EIF5, RPL15, RPL35, RPS15A, RPL38, RPS2, RPL39, RPS3, RPS26, RPS27, RPS28, RP	387	401		
4	GOTERM_BP_DIRECT	GO:0002376~immune system process	41	9.579439	7.42E-17	APOBEC3, HMGB2, PML, RSAD2, ISG20, B2M, NLRC5, OASL2, OASL1, ITCH, MX1, MX2, DHX58, SYK, CD7, TI	387	383		
5	GOTERM_BP_DIRECT	GO:0051607~defense response to virus	27	6.308411	2.01E-15	APOBEC3, A230050P20RIK, RNASEL, SLFN9, PML, RSAD2, PMAIP1, CXCL10, ISG20, NLRC5, ISG15, OASL2,	387	167		
6	GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	13	3.037383	1.16E-12	APOBEC3, A230050P20RIK, RNASEL, BST2, FAM111A, RSAD2, CCL5, ISG20, ISG15, OASL1, EIF2AK2, MX2,	387	32		
7	GOTERM_BP_DIRECT	GO:0045087~innate immune response	34	7.943925	3.39E-11	APOBEC3, HMGB2, PML, RSAD2, ISG20, B2M, NLRC5, OASL2, OASL1, ITCH, MX1, MX2, DHX58, TEC, SYK, TL	387	400		
8	GOTERM_BP_DIRECT	GO:0035458~cellular response to interferon-beta	9	2.102804	2.07E-06	IRGM1, GBP6, IRGM2, IRF1, IFI47, TGTP1, TGTP2, GBP2, AIM2	387	41		
36	GOTERM_CC_DIRECT	GO:0005840~ribosome	36	8.411215	1.19E-23	RPL17, RPL36A, RPL15, RPS15A, RPL38, RPS2, RPL39, RPS3, PRMT3, RPS26, RPS27, RPS28, RPL6, RPL31,	403	188		
37	GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	22	5.140187	1.11E-16	RPL35A, RPL17, RPL36A, ZFP622, RPL15, RPL35, RPL23A, RPL24, RPL38, RPL39, RPL28, RPL31, RPL6, RPL	403	91		
38	GOTERM_CC_DIRECT	GO:0030529~intracellular ribonucleoprotein complex	33	7.71028	1.35E-13	RPL17, RPL15, RPL38, RPL39, RPS2, RPS3, RPS28, RPL6, RPL31, RPLP0, RPL9, RPL8, RPL3, RPL11, RPS20,	403	320		
39	GOTERM_CC_DIRECT	GO:0022627~cytosolic small ribosomal subunit	15	3.504673	2.08E-12	RPSA, RPS15A, RPS9, RPS6, RPS4X, RPS2, RPS3, RPS26, RPS27, RPS28, RPS16, RPS13, RPS20, RPS23, RPS2	403	53		
97	KEGG_PATHWAY	mmu03010:Ribosome	37	8.64486	9.50E-26	RPL17, RPL36A, RPL15, RPL35, RPS15A, RPL38, RPS2, RPL39, RPS3, RPS26, RPS27, RPS28, RPL6, RPL31,	205	145		
98	KEGG_PATHWAY	mmu05168:Herpes simplex infection	19	4.439252	9.19E-06	GLTSCR2, RNASEL, H2-M3, SOCS3, PML, TNFSF14, TNFRSF14, CCL5, H2-Q6, H2-Q7, DDX58, H2-OA, JUN, IR	205	208		
99	KEGG_PATHWAY	mmu04612:Antigen processing and presentation	12	2.803738	9.40E-06	CTSL, KLRC2, H2-OA, H2-M3, H2-OB, IFNG, H2-T22, H2-T23, H2-Q6, H2-Q7, B2M, TAPBP	205	82		
100	KEGG_PATHWAY	mmu04940:Type I diabetes mellitus	10	2.336449	3.27E-05	CPE, H2-OA, H2-M3, H2-OB, IFNG, H2-T22, H2-T23, GZMB, H2-Q6, H2-Q7	205	62		
101	KEGG_PATHWAY	mmu05332:Graft-versus-host disease	9	2.102804	5.89E-05	H2-OA, H2-M3, H2-OB, IFNG, H2-T22, H2-T23, GZMB, H2-Q6, H2-Q7	205	52		
102	KEGG_PATHWAY	mmu05330:Allograft rejection	9	2.102804	1.02E-04	H2-OA, H2-M3, H2-OB, IFNG, H2-T22, H2-T23, GZMB, H2-Q6, H2-Q7	205	56		
54	KEGG_PATHWAY	mmu03010:Ribosome	10	3.831418	7.88E-04	RPL30, RPL19, RPS17, RPL21, RPL27A, RPL26, RPL36, RPLP2, FAU, RPL10A	132	145	7691	4.018286
55	**KEGG_PATHWAY**	**mmu04630:Jak-STAT signaling pathway**	**10**	**3.831418**	**7.88E-04**	**IL12RB2, IRF9, IL2RB, STAT4, IL12RB1, IL10RA, PIK3CD, STAT1, IFNGR1, STAT2**	**132**	**145**	**7691**	**4.018286**
56	KEGG_PATHWAY	mmu05162:Measles	9	3.448276	0.002171	IRF9, PRKCQ, IL2RB, IFIH1, PIK3CD, OAS3, STAT1, IFNGR1, STAT2	132	136	7691	3.855782
57	KEGG_PATHWAY	mmu05168:Herpes simplex infection	11	4.214559	0.002822	IRF9, FOS, IFIH1, SRSF5, SP100, GTF2I, OAS3, STAT1, DAXX, IFNGR1, STAT2	132	208	7691	3.08133
58	KEGG_PATHWAY	mmu04380:Osteoclast differentiation	8	3.065134	0.005586	IRF9, FOS, PLCG2, PIK3CD, STAT1, JUNB, IFNGR1, STAT2	132	126	7691	3.699375
59	KEGG_PATHWAY	mmu04380:Osteoclast differentiation	8	3.065134	0.005586	IRF9, FOS, PLCG2, PIK3CD, STAT1, JUNB, IFNGR1, STAT2	132	126	7691	3.699375
60	KEGG_PATHWAY	mmu05321:Inflammatory bowel disease (IBD)	5	1.915709	0.01778	IL12RB2, STAT4, IL12RB1, STAT1, IFNGR1	132	59	7691	4.937725
61	KEGG_PATHWAY	mmu05321:Inflammatory bowel disease (IBD)	5	1.915709	0.01778	IL12RB2, STAT4, IL12RB1, STAT1, IFNGR1	132	59	7691	4.937725