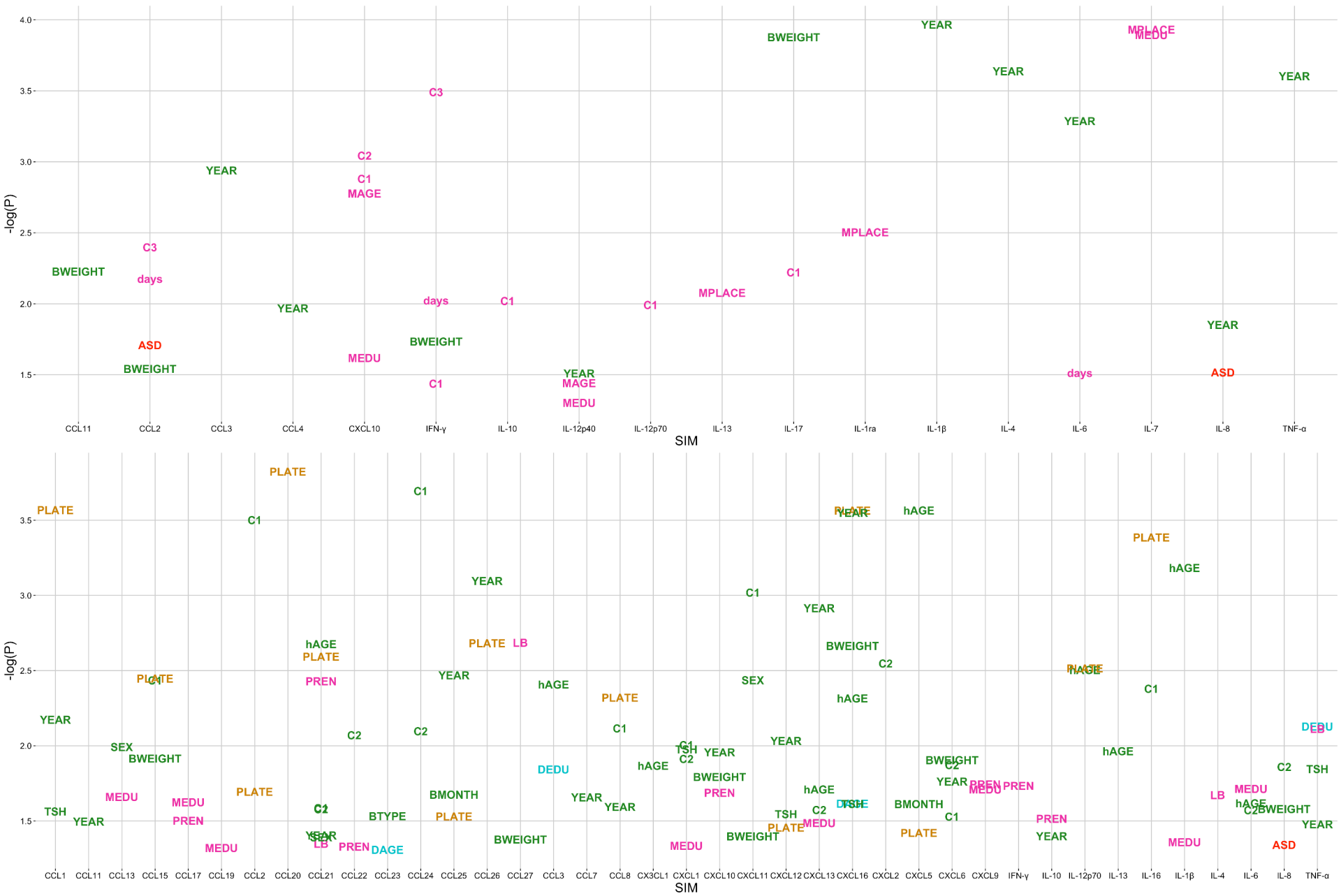
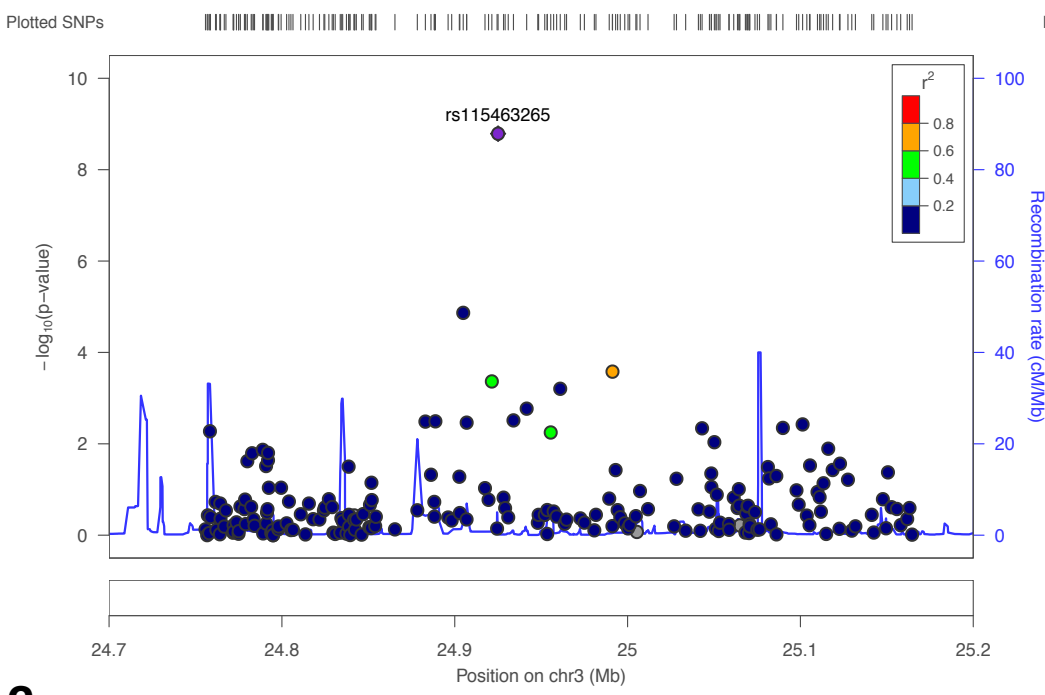
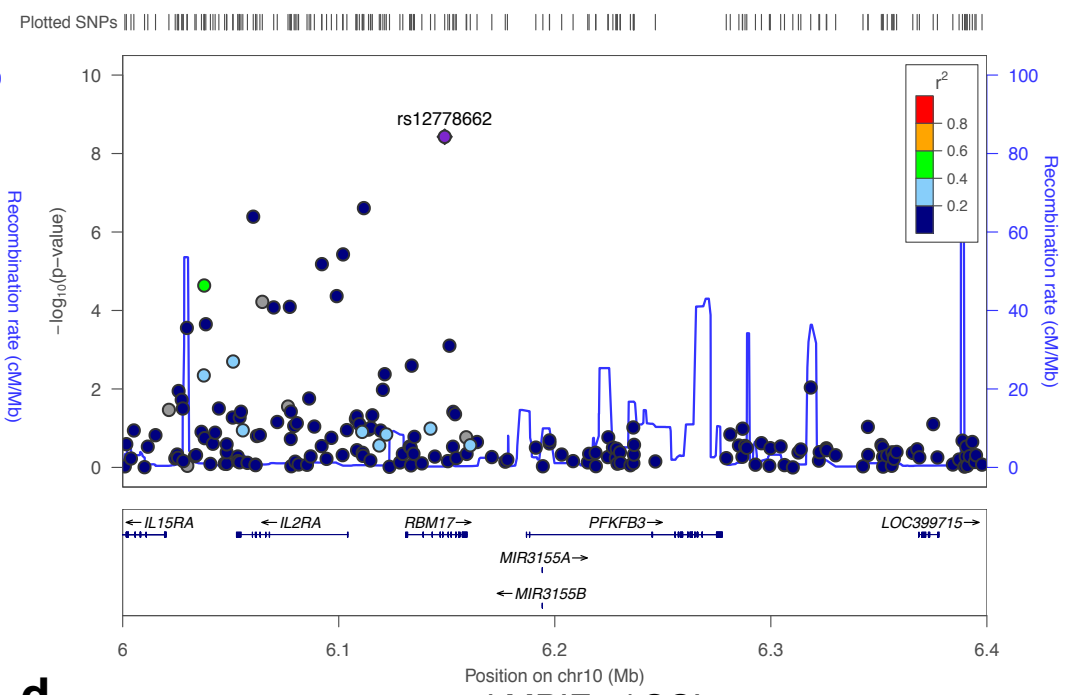

-log(P)
SIM
CCL11 CCL2 CCL3 CCL4 CXCL10 IFN-γ IL-10 IL-12p40 IL-12p70 IL-13 IL-17 IL-1ra IL-1β IL-4 IL-6 IL-7 IL-8 TNF-α
CCL1 CCL11 CCL13 CCL15 CCL17 CCL19 CCL2 CCL20 CCL21 CCL22 CCL23 CCL24 CCL25 CCL26 CCL27 CCL3 CCL7 CCL8 CX3CL1 CXCL1 CXCL10 CXCL11 CXCL12 CXCL13 CXCL16 CXCL2 CXCL5 CXCL6 CXCL9 IFN-γ IL-10 IL-12p70 IL-13 IL-16 IL-1β IL-4 IL-6 IL-8 TNF-α

Fig. S1 Significance levels of each confounding factor across the entire set of maternal and neonatal immune mediators. (**A**) The plot shows the significance level of covariates that reached P<0.1 in each of 22 maternal cytokine/chemokine models (**B**). The plot shows the significance level of covariates that reached P<0.1 in each of 42 neonatal cytokine/chemokine models. X-axis shows each SIM, Y-axis show –log(P-value). The covariates that come from neonates are shown in green, from mothers in pink, from fathers are in lightblue, ASD in red is significant for maternal CCL2 (*P*=0.019) and maternal/neonatal IL-8 (*P*=0.030 and *P*=0.045, respectively), PLATE, to control for potential technical differences related to the experiment, is in orange. Abbreviations: ASD: offspring affection status; BWEIGHT: neonatal birth weight; BMONTH: neonatal birth month; YEAR: neonatal birth year; BTYPE: neonatal birth type; SEX: neonatal gender; hAGE: hour after the birth at bloodspot time; TSH: neonatal TSH; PREN: maternal number of prenatal visits; LB: maternal live births; days: maternal gestational age at blood draw; MAGE: maternal age; MEDU: maternal education; DAGE: father age; DEDU: father education; PLATE: plate number; C1: principal component 1; C2: principal component 2; C3: principal component 3; Seven additional principal components used in each model are not shown.

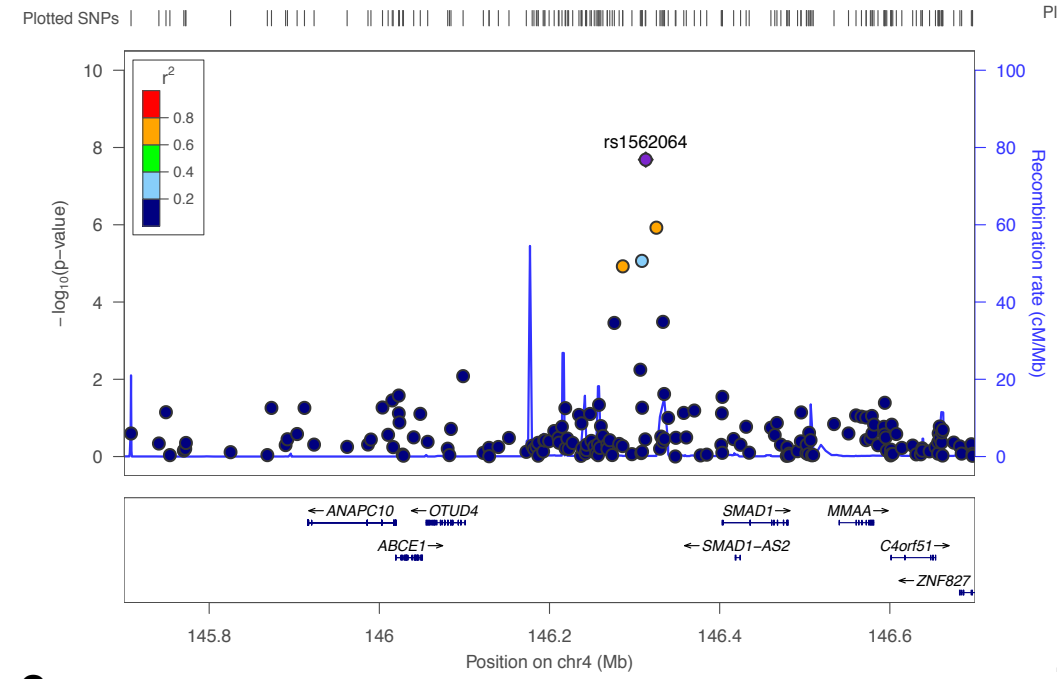
a


maternal eotaxin 1 / CCL11
Plotted SNPs
rs115463265
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
24.7
24.8
24.9
25
25.1
25.2
Position on chr3 (Mb)

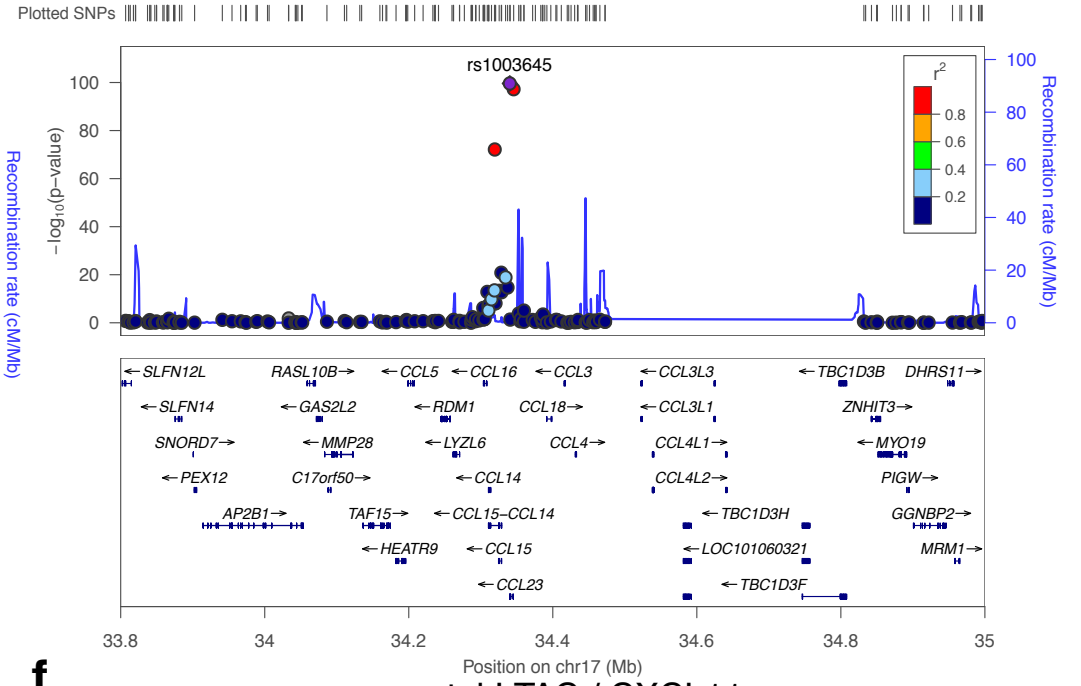
b


maternal sIL−2Ra
Plotted SNPs
rs12778662
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IL15RA
IL2RA
RBM17
PFKFB3
LOC399715
MIR3155A
MIR3155B
6
6.1
6.2
6.3
6.4
Position on chr10 (Mb)

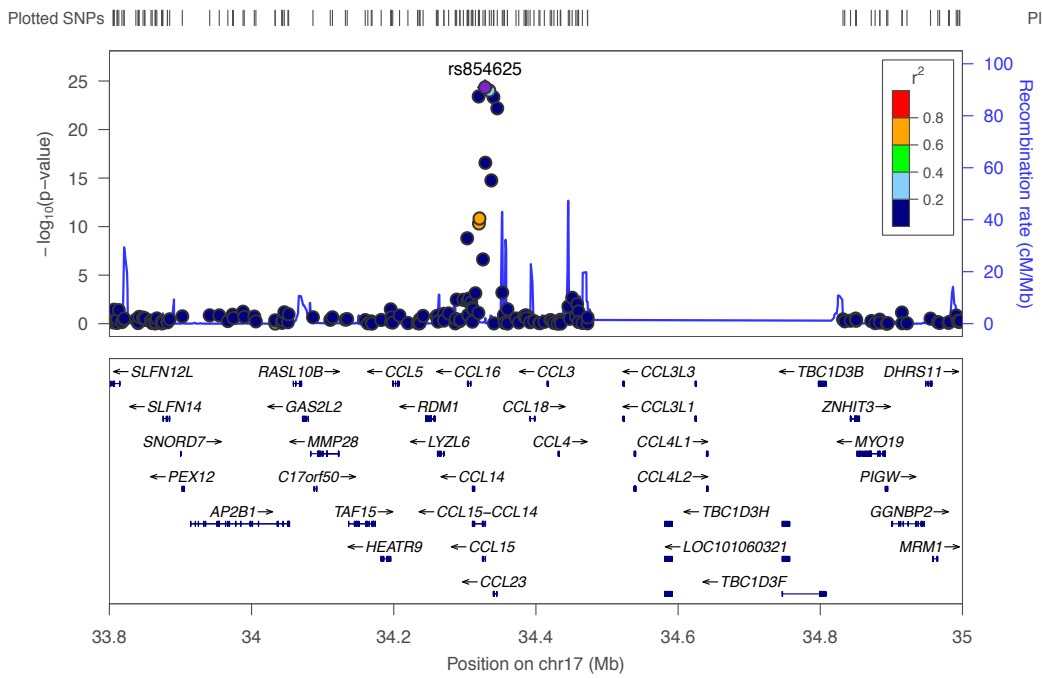
c


maternal IL1a
Plotted SNPs
rs1562064
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ANAPC10
OTUD4
SMAD1
MMAA
ABCE1
SMAD1−AS2
C4orf51
ZNF827
145.8
146
146.2
146.4
146.6
Position on chr4 (Mb)

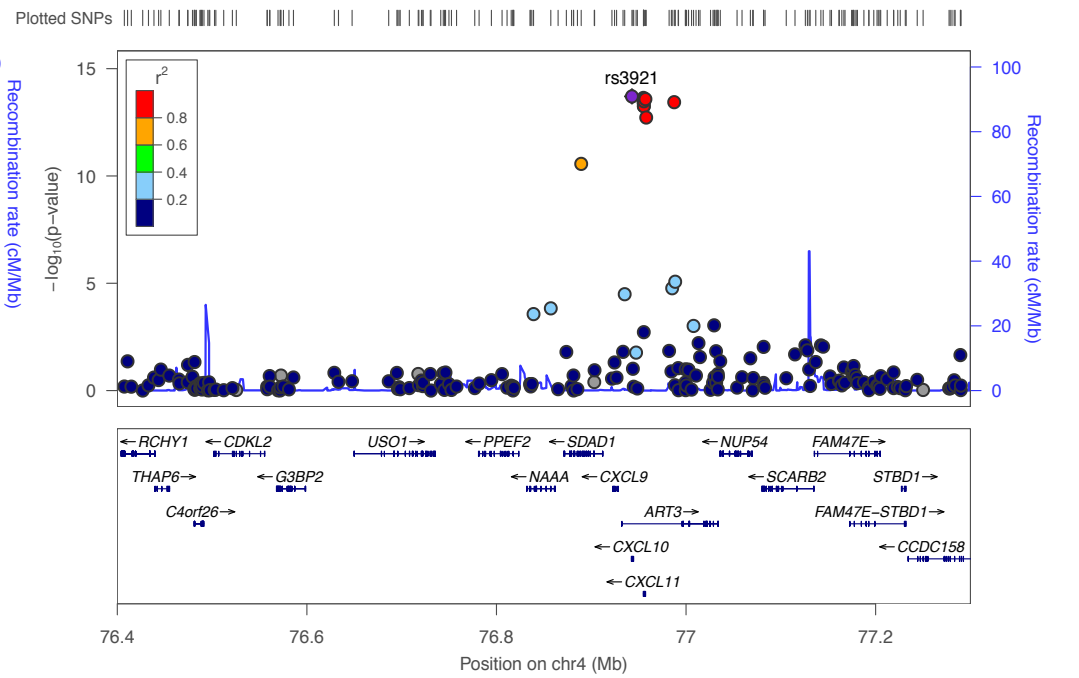
d

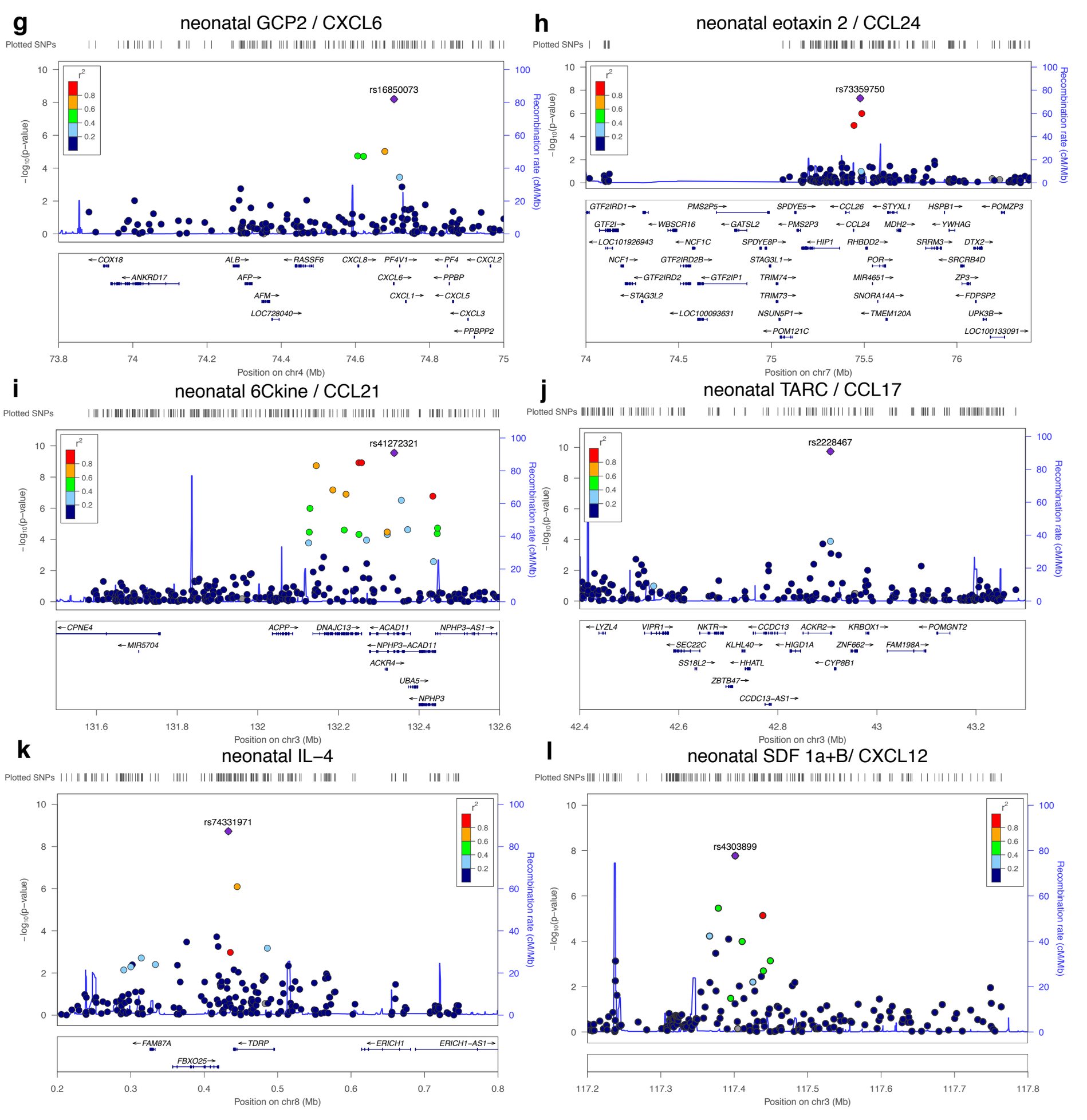

neonatal MPIF1 / CCL23
Plotted SNPs
rs1003645
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SLFN12L
RASL10B
CCL5
CCL16
CCL3
CCL3L3
TBC1D3B
DHRS11
SLFN14
GAS2L2
RDM1
CCL18
CCL3L1
ZNHIT3
SNORD7
MMP28
LYZL6
CCL4
CCL4L1
MYO19
PEX12
C17orf50
CCL14
CCL4L2
PIGW
AP2B1
TAF15
CCL15−CCL14
TBC1D3H
GGNBP2
HEATR9
CCL15
LOC101060321
MRM1
CCL23
TBC1D3F
33.8
34
34.2
34.4
34.6
34.8
35
Position on chr17 (Mb)

e


neonatal MIP1d / CCL15
Plotted SNPs
rs854625
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SLFN12L
RASL10B
CCL5
CCL16
CCL3
CCL3L3
TBC1D3B
DHRS11
SLFN14
GAS2L2
RDM1
CCL18
CCL3L1
ZNHIT3
SNORD7
MMP28
LYZL6
CCL4
CCL4L1
MYO19
PEX12
C17orf50
CCL14
CCL4L2
PIGW
AP2B1
TAF15
CCL15−CCL14
TBC1D3H
GGNBP2
HEATR9
CCL15
LOC101060321
MRM1
CCL23
TBC1D3F
33.8
34
34.2
34.4
34.6
34.8
35
Position on chr17 (Mb)

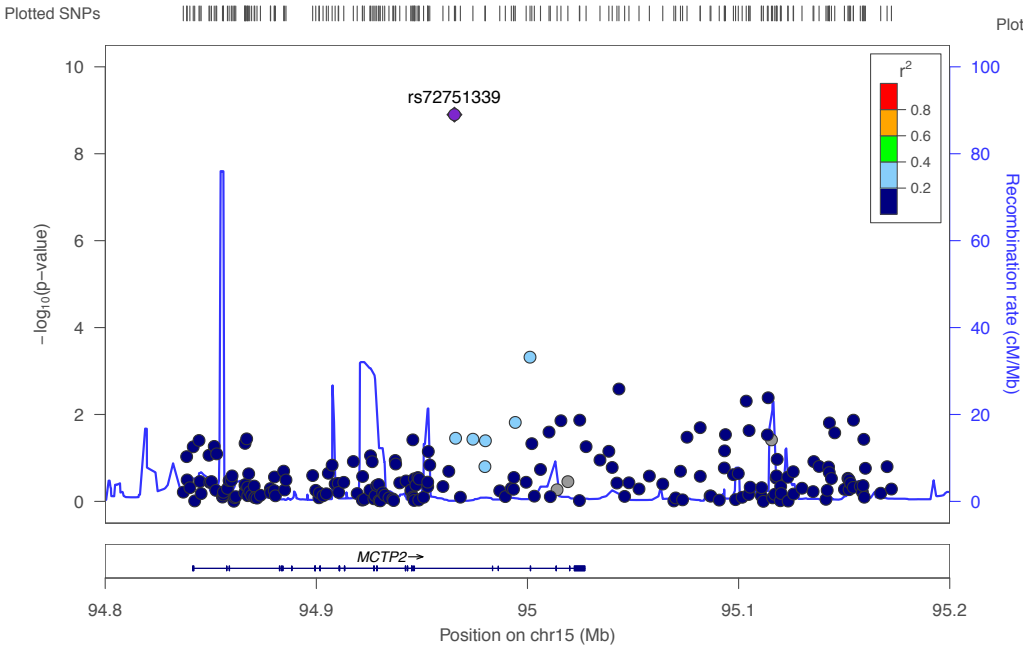
f


neonatal I TAC / CXCL11
Plotted SNPs
rs3921
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
RCHY1
CDKL2
USO1
PPEF2
SDAD1
NUP54
FAM47E
THAP6
G3BP2
NAAA
CXCL9
SCARB2
STBD1
C4orf26
ART3
FAM47E−STBD1
CXCL10
CCDC158
CXCL11
76.4
76.6
76.8
77
77.2
Position on chr4 (Mb)


g
neonatal GCP2 / CXCL6
Plotted SNPs
rs16850073
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
COX18
ANKRD17
ALB
AFP
AFM
LOC728040
RASSF6
CXCL8
PF4V1
CXCL6
CXCL1
PF4
PPBP
CXCL5
CXCL3
CXCL2
PPBPP2
Position on chr4 (Mb)
h
neonatal eotaxin 2 / CCL24
rs73359750
GTF2IRD1
PMS2P5
SPDYE5
CCL26
STYXL1
HSPB1
POMZP3
GTF2I
WBSCR16
GATSL2
PMS2P3
CCL24
MDH2
YWHAG
LOC101926943
NCF1C
SPDYE8P
HIP1
RHBDD2
SRRM3
DTX2
NCF1
GTF2IRD2B
STAG3L1
POR
SRCRB4D
GTF2IRD2
GTF2IP1
TRIM74
MIR4651
ZP3
STAG3L2
TRIM73
SNORA14A
FDPSP2
LOC100093631
NSUN5P1
TMEM120A
UPK3B
POM121C
LOC100133091
Position on chr7 (Mb)
i
neonatal 6Ckine / CCL21
rs41272321
CPNE4
MIR5704
ACPP
DNAJC13
ACAD11
NPHP3−AS1
NPHP3−ACAD11
ACKR4
UBA5
NPHP3
Position on chr3 (Mb)
j
neonatal TARC / CCL17
rs2228467
LYZL4
VIPR1
NKTR
CCDC13
ACKR2
KRBOX1
POMGNT2
SEC22C
KLHL40
HIGD1A
ZNF662
FAM198A
SS18L2
HHATL
CYP8B1
ZBTB47
CCDC13−AS1
Position on chr3 (Mb)
k
neonatal IL−4
rs74331971
FAM87A
TDRP
ERICH1
ERICH1−AS1
FBXO25
Position on chr8 (Mb)
l
neonatal SDF 1a+B/ CXCL12
rs4303899
Position on chr3 (Mb)

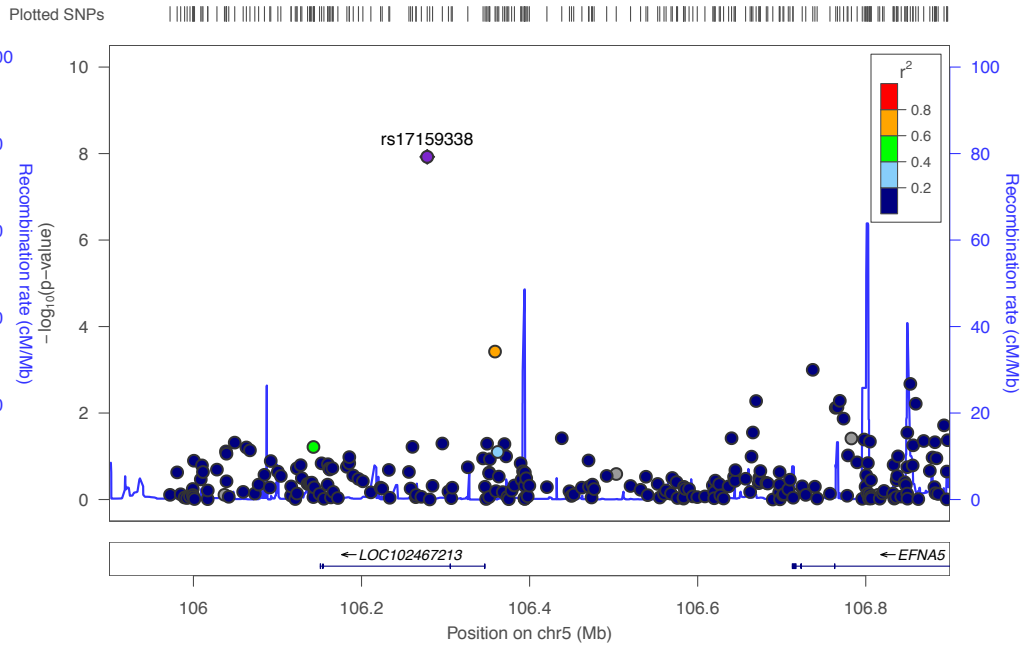
m

neonatal eotaxin 2 / CCL24



n

neonatal IL16



o

neonatal ENA−78 / CXCL5

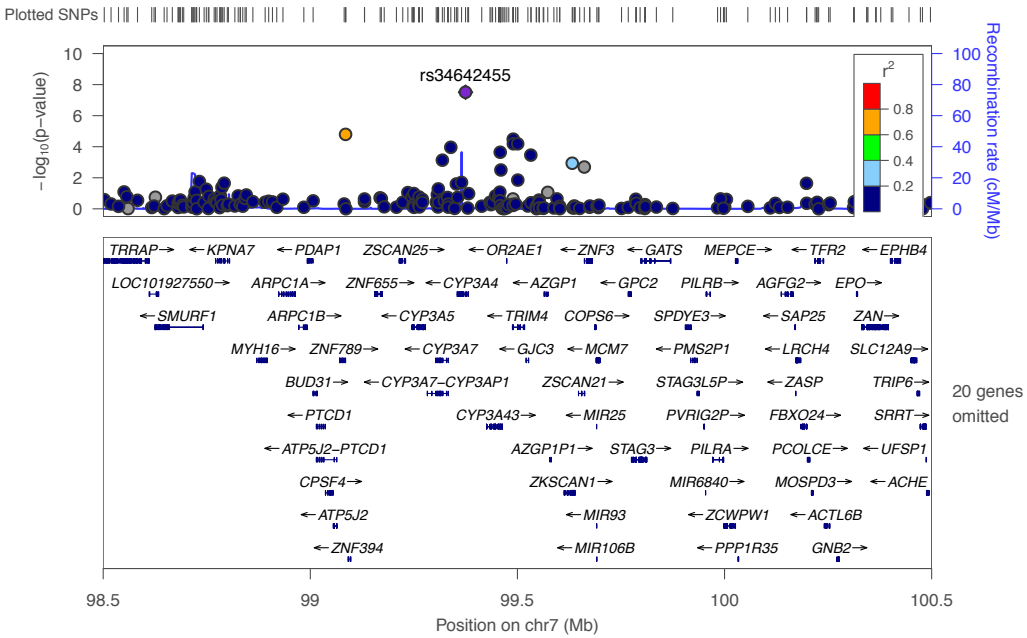


Fig. S2 Linkage disequilibrium regional genomic plots. Maternal genome-wide associated SNPs with maternal immune mediators (**A-C**); fetal genome-wide associated SNPs with neonatal immune mediators (**D-L**) and maternal genome-wide associated SNPs with neonatal immune mediators (**M-O**). The X-axis represents the genomic position; the Y-axis shows the negative logarithm of the observed association p-value for each tested SNP. Plotted with Locuzoom tool[42]

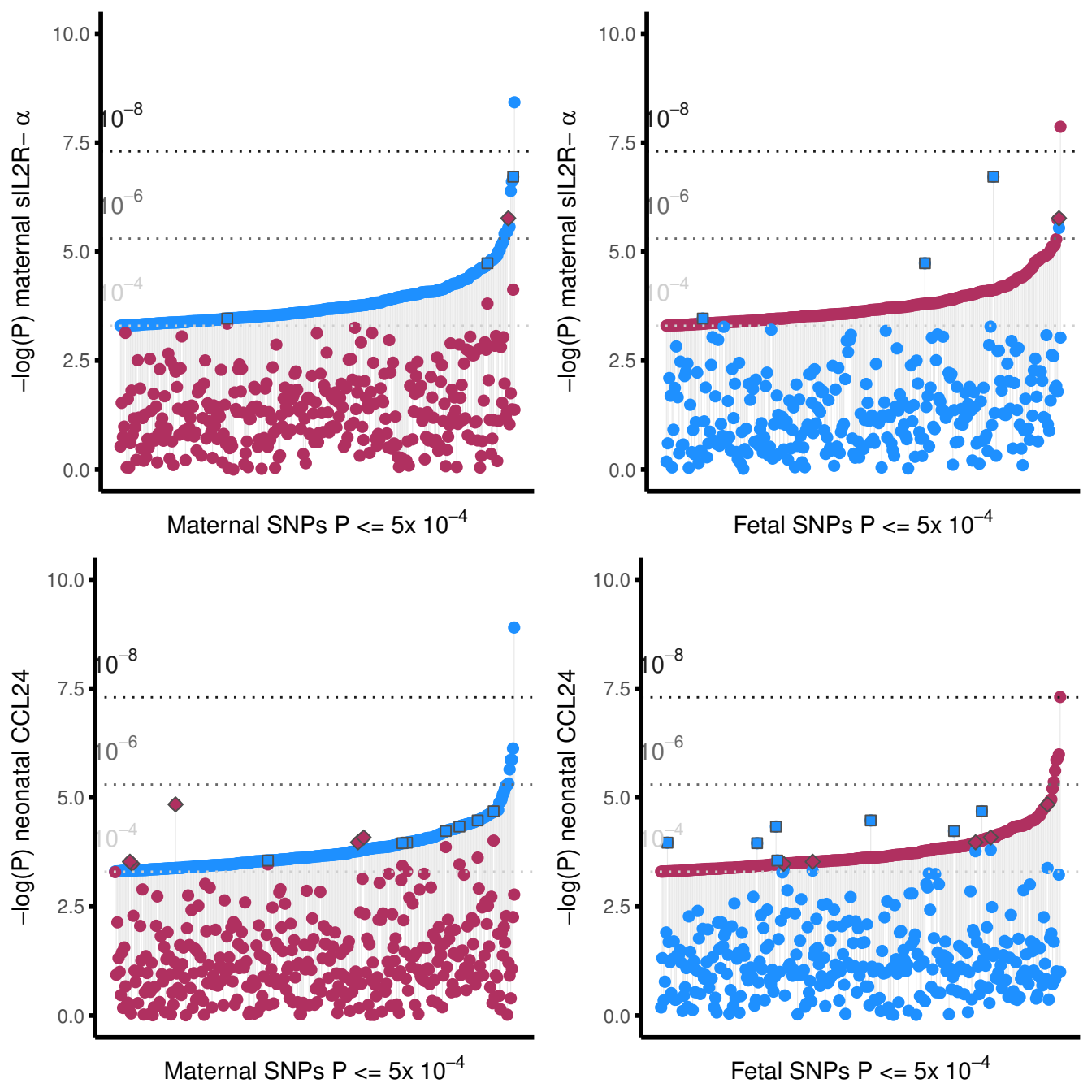

10.0
7.5
5.0
2.5
0.0
10^{-8}
10^{-6}
10^{-4}
−log(P) maternal sIL2R− α
Maternal SNPs P <= 5x 10^{-4}
Fetal SNPs P <= 5x 10^{-4}
−log(P) neonatal CCL24

Fig. S3 Maternal and fetal SNPs (*P* <= $5x10^{-4}$) from maternal sIL2R-a and neonatal CCL24 summary statistics. (**A**) Maternal ranked SNPs associated with maternal sIL2Ra and the corresponding fetal SNP association; (**B**) fetal ranked SNPs associated with maternal sIL2-Ra and the corresponding maternal SNP association; (**C**) maternal ranked SNPs associated with neonatal CCL24 and the corresponding fetal SNP association and (**D**) fetal ranked SNPs associated with neonatal CCL24 and the corresponding maternal SNP association. The X-axis represents the ranked SNPs based on the observed *P* <= $5x10^{-4}$ in one individual's genetics (maternal/fetal); the Y-axis shows the negative logarithm of the observed p-value for each tested SNP. The maternal SNPs and the fetal SNPs are shown in 'light blue' and 'purple', respectively. The SNPs that showed *P* <= $5x10^{-4}$ in both individuals are represented with a purple diamond when fetal-driven and with a light blue square when maternal-driven. No SNPs showed significant independent association with both individuals.