Identification and Validation of a Mitochondria Calcium Uptake-Related Gene Signature for

Predicting Prognosis in COAD

Jianjun Zhu^{1#}, Wentao Zhang^{2#}, Jingjia Chang², Jin Wu³, Hao Wu², Xintong Zhang², Zhigao Ou²,

Ting Tang², Li Li², Ming Liu^{2*}, Yongfan Xin^{4*}

¹Department of Cell Biology and Medical Genetics, Shanxi Medical University, Department of Hepatological Surgery, First Hospital of Shanxi Medical University, Taiyuan, Shanxi, China. ²Department of Cell Biology and Medical Genetics, Shanxi Medical University, Taiyuan, Shanxi, China.

³Department of Molecular & Cellular Biology, Roswell Park Comprehensive Cancer Center, Elm and Carlton Streets, Buffalo, NY 14263, USA.

⁴Department of oncology and vascular intervention, First Hospital of Shanxi Medical University, Taiyuan, Shanxi, China.

#Jianjun Zhu and Wentao Zhang contributed equally to the work.

Corresponding authors: Yongfan Xin, E-mail:15541190713@163.com; Department of oncology and vascular intervention, First Hospital of Shanxi Medical University, Taiyuan, Shanxi, China. Ming Liu, E-mail: <u>lium0421@163.com</u>; Department of Cell Biology and Medical Genetics, Shanxi Medical University, Taiyuan, Shanxi, China.

Supplementary figure legend

Figure S1 The mRNA expressions of MCU complex members in colon cancer (GSE39582). *P < 0.05; **P < 0.01.

Figure S2 The relationships between the mRNA expression of MCU complex members and clinicopathological characteristics

Figure S3 The prognostic value of individual MCU complex members in COAD patients (GEPIA). A, OS. B, RFS

Figure S4 Genetic variations of the mutation of MCU complex members (cBioPortal), and Gene-gene interaction network, protein-protein interaction network and correlation analysis of the MCU complex members in colon cancer. **A**, Overview the genetic variations analyses of MCU complex members. **B**, Correlation analysis between the mRNA expression of MCU complex members and tumor mutational burden (TMB) of COAD patients. C, Co-mutation analysis between the MCU complex members and high-frequency genes in COAD. D, Protein-protein interaction network analysis through String database. E, Correlation analysis of the MCU complex members. F, Gene-gene interaction network analysis of MCU complex members. Through GeneMANIA.

Figure S5 The relationships between the mRNA expression of MCU complex members and immune cell infiltration.

Figure S6 The relationships between the mRNA expression of MCU complex members and immune checkpoint and immunotherapy. **a**, The expression of PD1, PDL-L1 and CTLA4 in the low-expression and high-expression groups based on the median expressions of each MCU complex members in COAD, respectively. **b**, The distribution of responder and non-responder to anti CTLA-4/PD-1 immunotherapy in the low-expression and high-expression groups based on the median expression of each MCU complex members in COAD, respectively.

Figure S7 Correlation analysis between the expression of MCU complex members and immune checkpoint molecules.

Figure S8 The relationships between risk scores and clinicopathological characteristics of COAD patients from training set.

Figure S9 Validation of the risk signature in the validation datasets (GSE29623 and GSE39582). **A**, Heatmap of mRNA expression of MCU complex members in low-risk and high-risk group. **B**, The mRNA expression of cMCU complex members in low-risk and high-risk group. **C**, K-M survival between low-risk and high-risk group. **D**, ROC curve and AUC at 1, 3, and 5 years for the risk score. **P < 0.01; ***P < 0.001.

Figure S10 Functional enrichment analysis of MCU and its co-expression genes. Gene Ontology (GO) analysis.

Figure S11 The associations between risk scores and immune cell infiltration. **A**, The abundance of 22 immune infiltrates between the low-risk and high-risk group. **B**, The relationship between risk score and the estimate score.C, The relationship between risk score and the expression of macrophages marker genes.

Figure S12 The associations between risk scores and immune cell infiltration.

Supplementary Table

Gene	Full name	Function of the encoded protein	Also known as
symbol			
MCU	mitochondrial calcium	This gene encodes a calcium transporter that	HsMCU;
	uniporter	localizes to the mitochondrial inner membrane. The	C10orf42;
		encoded protein interacts with mitochondrial	CCDC109A
		calcium uptake 1.	
MCUb	mitochondrial calcium	Predicted to enable calcium channel inhibitor	CCDC109B
	uniporter dominant	activity. Predicted to be involved in calcium import	
	negative subunit beta	into the mitochondrion and mitochondrial calcium	
		ion homeostasis. Located in mitochondrion and	
		nucleoplasm. Is integral component of mitochondrial	
		inner membrane. Part of uniplex complex	
MCUR1	mitochondrial calcium	Involved in calcium import into the mitochondrion	FMP32;
	uniporter regulator 1	and positive regulation of mitochondrial calcium ion	C6orf79;
		concentration. Is integral component of	CCDC90A
		mitochondrial inner membrane	
SMDT1	single-pass membrane	This gene encodes a core regulatory component of a	DDDD; EMRE;
	protein with aspartate	calcium channel in the mitochondrial inner	C22orf32
	rich tail 1	membrane	
MICU1	mitochondrial calcium	This gene encodes an essential regulator of	CALC; EFHA3;
	uptake 1	mitochondrial Ca2+ uptake under basal conditions.	MPXPS;
		The encoded protein interacts with the mitochondrial	CBARA1; ara
		calcium uniporter, a mitochondrial inner membrane	CALC
		Ca2+ channel, and is essential in preventing	
		mitochondrial Ca2+ overload, which can cause	
		excessive production of reactive oxygen species and	
		cell stress.	
MICU2	mitochondrial calcium	Enables protein heterodimerization activity.	EFHA1;
	uptake 2	Involved in calcium import into the mitochondrion	1110008L20Rik
		and negative regulation of mitochondrial calcium	
		ion concentration. Located in mitochondrial inner	
		membrane and mitochondrial intermembrane space.	
		Part of uniplex complex	
MICU3	mitochondrial calcium	Predicted to enable calcium ion binding activity.	EFHA2
	uptake family member	Predicted to be involved in calcium import into the	
	3	mitochondrion and mitochondrial calcium ion	
		homeostasis. Predicted to be located in	
		mitochondrial inner membrane. Predicted to be part	
		of uniplex complex	

Supplementary Table 1 Detail information of MCU complex members.







P value

*

ns ns

ns

0.191 0.14 *** **

0.125 **

0.113

0.041 ns

0.029 ns

0.026 0.011 0.006

ns

-0.01 ns

-0.02 ns

-0.02 -0.02 -0.04 ns ns ns -0.05 ns

-0.06 ns

-0.07 ns

-0.08 ns

-0.08 -0.09 -0.1 ns

-0.11 *

-0.11 *

-0.11 -0.12 -0.12 -0.13

-0.16 *** -0.17 ***

-0.19 ***

-0.2 *** ***

ns

*

* * * **

В

CCL14 WNT5B FES FRMD4A EIF4A1 HK3 SLC15A3 CRYBB1 C5AR2 CNR2 CCL23 CCL23 CNR1 CCD300LB FZD2 BEIF1 NME8 CD4 FPR1 FRAT2 GPP27 GPR27 MS4A2 NPL HNMT CCL26 FPR2 BASP1 FAM198B IGSF6 AIF1 VNN1 HRH1

		r	P value
	HLA-DQB3	0.122	*
	HLA-DPA2	0.103	*
	HLA-DRB9	0.024	ns
	HLA-DPA3	-0.05	ns
	HLA-DQB2	-0.05	ns
	HLA-DPB1	-0.06	ns
=	HLA-DRB6	-0.08	ns
00	HLA-DQB1	-0.08	ns
age	HLA-DQA2	-0.09	ns
hq	HLA-DRB5	-0.09	ns
cro	HLA-DRB1	-0.1	*
Ĕ	HLA-DPA1	-0.11	*
M1	CD68	-0.11	*
_	HLA-DPB2	-0.11	*
	HLA-DQA1	-0.11	*
	CD80	-0.17	***
	NOS2	-0.17	***
	HLA-DRA	-0.17	***
	CD86	-0.17	***
		r	P value
-	VEGFA	0.194	***
S	DLG4	0.171	***
age	CLEC10A	-0.05	ns
h	MAF	-0.08	ns
cro	CD163	-0.1	*
ma	MRC1	-0.11	*
121	CD200R1	-0.13	**
2	MSR1	-0.16	**

		r	r value
	DUSP2	0.056	ns
	KNTC1	-0.03	nc
	CCDZ	0.00	110
	LUR/	-0.03	ns
	PSAT1	-0.03	ns
	IARS	-0.05	ns
	PRC1	-0.13	ns
	COLE	0.12	
	UCL5	-0.13	ns
	CCL20	-0.15	**
	ETS1	-0.15	**
-	CCIA	-0.16	**
5	CELL	0.17	
41	SELL	-0.17	***
Â	EXO1	-0.17	***
P	AIM2	-0.18	***
Ē	NILIES	0.10	
S	NUFZ	-0.19	***
÷	CCNB1	-0.19	***
4	ITK	-0.2	***
	BRIP1	-0.22	***
	TDATI	0.22	1.11
	TRALL	-0.23	***
	SAMSN1	-0.26	***
	KIF11	-0.28	***
	DIDCO	0.20	
	DIRCO	-0.29	***
	RTKN2	-0.3	***
	RGS1	-0.31	***
	ESCOR	-0.20	
	13002	0.58	- **
	EXOC6	-0.43	***
		r	P value
	ELMO2	0.331	***
	000	0.201	
	ATULA	0.301	
	A IHL1	0.23	***
	STX4	0.217	***
	TRADD	0.083	ns
	COLIAN	0.04	0.0
	COL4A1	0.04	ns
	IFITM2	0.022	ns
	VIM	-0.02	ns
	ITCP2	0.02	nc
_	11002	-0.02	113
8	BZW2	-0.03	ns
÷	NDUFB9	-0.04	ns
4	I SP1	-0.04	ns
5	CEVNI2	0.05	00
Š	SEANS	-0.05	115
Ĕ	GLIPR1	-0.08	ns
E	EVN	-0.00	nc
ě	1 1 1 1	-0.03	110
m	SIRPG	-0.11	*
tralme	SIRPG	-0.11	*
entralme	SIRPG CYLD	-0.11	*
Central me	SIRPG CYLD XRCC6	-0.11 -0.16 -0.18	*
Central me	SIRPG CYLD XRCC6 AOP3	-0.11 -0.16 -0.18 -0.21	***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2	-0.11 -0.16 -0.18 -0.21	***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2	-0.11 -0.16 -0.18 -0.21 -0.22	**** *** *** ***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK	-0.13 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23	**** *** *** *** ***
Centralme	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24	* * * * * * * * * * * * * * * * * * *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1	-0.13 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26	* * * * * * * * * * * * * * * * * * *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1	-0.13 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26	***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28	* * * * * * * * * * * * * * * * * * *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29	* * * * * * * * * * * * * * * * * * *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31	**************************************
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42	113 * * * * * * * * * * * * *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42	113 * * *** * ****
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r	**** **** **** *** *** *** *** *** ***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34	-0.13 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315	**** **** **** **** **** **** **** **** ****
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REPS1	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167	* * *** *** *** *** *** *** *** *** ***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REPS1 TAL1	-0.03 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098	**** **** **** **** **** **** **** **** ****
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 IIGB1 SMAD4 KLF5 ABHD3 II.34 REPS1 TAL1 CASO1	-0.03 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.023	* * *** * *** *** *** *** *** *** *** *
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REPS1 TAL1 CASQ1 CTAL1	-0.03 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.07	* * *** *** *** *** *** *** *** *** ***
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 II.34 REP51 TAL1 CASQ1 EZH2	-0.13 -0.14 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.07 0.008	**************************************
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REP51 TAL1 CASQ1 EZH2 EXH2 PTCS1	-0.03 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.07 0.008 -0	**************************************
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REPS1 TAL1 CASQ1 EZH2 PTGS1 NEFL	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.07 0.008 -0.07	**************************************
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 II34 REPS1 TAL1 CASQ1 ZAL1 CASQ1 ZAL2 PTGS1 NEFL PTGS1 NEFL	-0.03 -0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.07 0.008 -0.01 -0.01	**************************************
Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 GB1 SMAD4 KLF5 ABHD3 II.34 REP51 TAL1 CASQ1 EZH2 PTGS1 NEFL DOCK9	-0.11 -0.16 -0.18 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.167 0.098 0.077 0.098 0.077 0.008 -0.07	**************************************
ell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 TGB1 TGB1 TGB1 TGB1 TGB1 TGB1 TGB1 TGB	-0.11 -0.11 -0.12 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.27 -0.315 -0.098 -0.07 -0.012 -0.02 -0.02	**************************************
T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 TGB1 TGB1 II34 REP51 ABHD3 II34 REP51 ABHD3 II34 REP51 CASQ1 EZH2 PTGS1 CASQ1 EZH2 PTGS1 NGFL DOCK9 USP9Y ATM	-0.11 -0.11 -0.16 -0.18 -0.21 -0.23 -0.24 -0.29 -0.24 -0.28 -0.29 -0.31 -0.42 r 0.015 -0.42 r 0.015 0.067 -0.098 0.07 -0.02 -0.02	**** **** **** **** **** **** **** **** ****
14 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 IG61 SMAD4 KLF5 ABHD3 II.34 REP51 TAL1 CASQ1 EZH2 PTGS1 NEFL PTGS1 NEFL DOCK9 USP9Y ATM	-0.31 -0.11 -0.16 -0.18 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.057 0.098 0.167 0.098 0.167 0.009 -0.01 -0.02 -0.02 -0.02	**************************************
CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 ITGB1 ITGB1 ITGB1 II34 REP51 TAL1 CASQ1 EZH2 DCK9 USP9Y ATM DARS CD300E	-0.31 -0.11 -0.16 -0.18 -0.22 -0.23 -0.24 -0.29 -0.29 -0.29 -0.29 -0.31 -0.42 r 0.315 -0.42 r 0.098 0.07 0.098 0.07 -0.01 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02	**************************************
ry CD4T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 TGB1 SMAD4 KLF5 ABHD3 II.34 REPS1 TAL1 EZH2 PTGS1 EZH2 PTGS1 NEFL DOCK9 USP9Y ATM DARS CD300E	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.28 -0.29 -0.31 -0.42 r 0.055 0.167 r 0.098 0.07 -0.01 -0.02 -0.01 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.01 -0.02 -0.02 -0.01 -0.02 -0.02 -0.01 -0.02 -0.02 -0.03 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.23 -0.24 -0.24 -0.22 -0.23 -0.24 -0.24 -0.22 -0.23 -0.24 -0.24 -0.25 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.29 -0.24 -0.29 -0.09 -0.	113 * ****
nory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 IL34 REPS1 TAL1 CASQ1 EZH2 PTGS1 NEFL DOCK9 VISPBY ATM DARS CD300E SCG2	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.28 -0.29 -0.28 -0.29 -0.315 0.167 -0.42 r 0.315 0.06 -0.09 -0.01 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.23 -0.24 -0.24 -0.26 -0.28 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.23 -0.24 -0.29 -0.24 -0.29 -0.23 -0.24 -0.29 -0.24 -0.29 -0.23 -0.24 -0.29 -0.23 -0.24 -0.29 -0.315 -0.42 -0.	113 4 4 4 4 4 4 4 4 4 4 4 4 4
emory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REPS1 TAL1 EZH2 PTGS1 CASQ1 EZH2 DOCK9 USP9Y ATM DARS CD300E SCG2 SIGLEC14	-0.31 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.28 -0.28 -0.28 -0.28 -0.29 -0.31 -0.42 r 0.315 0.067 -0.01 -0.02 -0.23 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.29 -0.21 -0.22 -0.29 -0.24 -0.29 -0.29 -0.29 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.21 -0.29 -0.20 -0.20 -0.29 -0.21 -0.29 -0.01 -0.02 -0.0	113 * ****
memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 IT	-0.31 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.315 0.467 -0.42 r 0.315 0.667 -0.02 -0.02 -0.01 -0.02 -0.23 -0.24 -0.22 -0.23 -0.24 -0.22 -0.23 -0.24 -0.22 -0.23 -0.24 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.23 -0.24 -0.22 -0.22 -0.315 -0.42 -0	113 - - - - - - - - - - - - -
tor memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 IL34 REP51 TAL1 EZH2 PTGS1 EZH2 PTGS1 CASQ1 EZH2 DOCK9 USP9Y ATM DARS CD3006 SCG2 SIGLEC14 SIGLEC6 SIGDEC14	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.057 -0.01 -0.42 r 0.057 -0.02 -0.01 -0.21 -0.22 -0.23 -0.24 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.26 -0.28 -0.24 -0.28 -0.24 -0.28 -0.24 -0.28 -0.29 -0.24 -0.28 -0.24 -0.28 -0.24 -0.28 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.016 -0.00 -0.02 -	113 * * *** *** *** *** *** ***
ector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 IT	-0.11 -0.11 -0.16 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.28 -0.29 -0.28 -0.29 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.21 -0.28 -0.21 -0.28 -0.28 -0.21 -0.28 -0.28 -0.29 -0.21 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.28 -0.29 -0.28 -0.29 -0.28 -0.29 -0.28 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.29 -0.09	113 214 214 214 214 214 214 214 214
Effector memory CD4 T cell	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 KLF5 ABHD3 II34 REP51 CASQ1 EZH2 PTGS1 DOCK9 USP9Y SIGLEC14 SIGLEC6 SDPR WIPF1	-0.11 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.26 -0.28 -0.29 -0.27 -0.28 -0.29 -0.28 -0.29 -0.28 -0.29 -0.21 -0.20 -0.21 -0.20 -0.21 -0.20 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.22 -0.22 -0.22 -0.22 -0.22 -0.22 -0.22 -0.22 -0.24 -0.21 -0.22 -0.24 -0.26 -0.21 -0.22 -0.22 -0.24 -0.26 -0.26 -0.28 -0.21 -0.22 -0.22 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.24 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.28 -0.29 -0.24 -0.29 -0.24 -0.28 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.28 -0.29 -0.24 -0.29 -0.29 -0.24 -0.29 -0.09 -0.01 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.04 -0.02 -0.02 -0.04 -0.02 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.09 -0.04 -0.04 -0.09 -0.04 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.05 -0.04 -0.04 -0.05 -0.04	113 * * * * * * * * * * * * *
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 II34 REPS1 TAL1 CASQ1 EZH2 PTGS1 NEFL DOCK9 USPBY ATM DARS CD300E SIGLEC14 SIGLEC14 WIPF1 PDGFRL	-0.11 -0.11 -0.16 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.077 0.088 -00 -0.01 -0.02 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.24 -0.26 -0.28 -0.29 -0.29 -0.29 -0.31 -0.24 -0.29 -0.31 -0.24 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.02	113 * *** *** *** *** *** *** **
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 GB1 GB1 SMAD4 KLF5 ABHD3 II34 REP51 TAL1 CASQ1 EZH2 PTGS1 CASQ1 EZH2 PTGS1 CASQ1 EZH2 DCCK9 USP9Y USP9Y SIGLEC14 SIGLEC6 SDPR VIPF1 PDGFRL TIPIN	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.315 0.067 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.03 -0.04 -0.02 -0.03 -0.04 -0.02 -0.03 -0.04 -0.02 -0.02 -0.23 -0.24 -0.26 -0.26 -0.26 -0.28 -0.29 -0.22 -0.23 -0.24 -0.26 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.09 -0.09 -0.09 -0.09 -0.09 -0.09 -0.02 -0.0	113 2 2 2 2 2 2 2 2 2 2 2 2 2
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 TGB1 TGB1 TGB1 TGB1 TGB1 TGB1 TGB1	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.21 -0.24 -0.26 -0.28 -0.29 -0.21 -0.22 -0.22 -0.22 -0.22 -0.21 -0.22 -0.22 -0.21 -0.21 -0.22 -0.22 -0.22 -0.22 -0.22 -0.22 -0.22 -0.24 -0.26 -0.21 -0.22 -0.24 -0.26 -0.22 -0.24 -0.26 -0.22 -0.22 -0.24 -0.26 -0.22 -0.24 -0.26 -0.24 -0.26 -0.22 -0.22 -0.24 -0.26 -0.22 -0.22 -0.24 -0.26 -0.22 -0.24 -0.26 -0.28 -0.29 -0.24 -0.29 -0.20 -0.24 -0.29 -0.20 -0.20 -0.20 -0.20 -0.20 -0.20 -0.20 -0.20 -0.20 -0.20 -0.02	113 * ******
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 GB1 GB1 KLF5 ABHD3 II34 REP51 TAL1 CASQ1 EZH2 PTGS1 CASQ1 EZH2 PTGS1 CASQ1 EZH2 DCCK9 USP9Y USP9Y USP9Y SIGLEC14 SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCRB	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 r 0.05 r 0.07 -0.02 -0.02 -0.03 -0.04 -0.09 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.03 -0.04 -0.02 -0.03 -0.04 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.05 -0.25 -0.0	115 4 4 4 4 4 4 4 4 4 4 4 4 4
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 CD63 BMI1 ITGB1 ITGB1 TGB1 TGB1 TGB1 TGB1 CASQ1 EZH2 DOCK9 USPBY ATM DARS SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCRB GDE1	-0.11 -0.16 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.29 -0.29 -0.29 -0.42 -0.29 -0.42 -0.42 -0.42 -0.42 -0.42 -0.44 -0.44 -0.45 -0.09 -0.01 -0.02 -0.24 -0.04 -0.04 -0.04 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.04	113 211 211 211 211 211 211 211
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 GB1 SMAD4 KLF5 ABHD3 II.34 REP51 ABHD3 II.34 REP51 CASQ1 EZH2 PTGS1 CASQ1 EZH2 PTGS1 DCCK9 USP9Y ATM DARS CD300E SIGLEC14 SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCRB GDE1 TFFC	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 -0.09 -0.01 -0.09 -0.01 -0.02 -0.02 -0.02 -0.02 -0.03 -0.04 -0.09 -0.02 -0.02 -0.02 -0.03 -0.04 -0.09 -0.02	113 * * * * * * * * * * * * *
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 ITGB1 CASQ1 EZH2 DOCK9 USPBY ATM DARS SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCRB GDE1 TFEC TPK1	-0.11 -0.16 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.29 -0.29 -0.29 -0.42 -0.42 -0.42 -0.42 -0.42 -0.42 -0.42 -0.42 -0.42 -0.42 -0.44 -0.45	113 214 214 214 214 214 214 214 214
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 GB1 II34 KLF5 ABHD3 II34 REP51 ABHD3 II34 REP51 CASQ1 EZH2 PTG51 DCK9 USP9Y ATM DARS CD300E SIGLEC14 SIGLEC6 SIGLEC6 SIGPRL TIPIN UQCR8 GDE1 TFEC TPK1	-0.11 -0.16 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.21 -0.20 -0.21 -0.22 -0.23 -0.21 -0.22 -0.23 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.29 -0.21 -0.22 -0.23 -0.29 -0.21 -0.20 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.29 -0.21 -0.22 -0.29 -0.21 -0.29 -0.21 -0.29 -0.20 -0.29 -0.20 -0.29 -0.20 -0.29 -0.20 -0.29 -0.20 -0.29 -0.20 -0.20 -0.20 -0.02 -0.03 -0.04 -0.01 -0.02	115 2 2 2 2 2 2 2 2 2 2 2 2 2
Effector memory CD4.1 cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABHD3 II.34 REPS1 II.34 REPS1 II.34 REPS1 II.34 REPS1 II.34 REPS1 II.34 REPS1 II.34 REPS1 CASQ1 EZH2 DOCK9 VICS1 SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCRB GDE1 TFEC TPK1 ZCCB1	-0.11 -0.16 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.29 -0.29 -0.29 -0.42 r 0.315 -0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 0.5 0.167 7 0.098 0.07 0.002 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.02 -0.01 -0.02 -0.02 -0.02 -0.02 -0.14 -0.06 -0.07 -0.02 -0.02 -0.14 -0.16 -0.16 -0.07 -0.02 -0.02 -0.14 -0.16 -0.16 -0.07 -0.02 -0.02 -0.03 -0.07 -0.01 -0.02 -0.02 -0.02 -0.02 -0.14 -0.16 -0.16 -0.16 -0.17 -0.12 -0.12 -0.14 -0.12 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2 -0.2-0.2 -0.2	115 3 4 4 4 4 4 4 4 4 4 4 4 4 4
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 KLF5 ABH03 II34 REP51 TAL1 CASQ1 EZH2 PTGS1 DOCK9 USP9Y ATM DARS CD300E SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCR8 GDE1 TFEC TPK1 ZCR81	-0.11 -0.11 -0.16 -0.21 -0.22 -0.23 -0.24 -0.29 -0.24 -0.29 -0.29 -0.31 -0.42 r -0.29 -0.31 -0.42 r -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.21 -0.20 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.21 -0.22 -0.23 -0.21 -0.21 -0.22 -0.23 -0.24 -0.21 -0.22 -0.23 -0.24 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.23 -0.29 -0.21 -0.22 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.22 -0.22 -0.22 -0.23 -0.24 -0.29 -0.21 -0.22 -0.29 -0.21 -0.22 -0.29 -0.21 -0.22 -0.29 -0.21 -0.22 -0.29 -0.21 -0.22 -0.29 -0.22 -0	113 2 2 2 2 2 2 2 2 2 2 2 2 2
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXAZP2 AHNAK CD63 BMI1 ITGB1 SMAD4 KLF5 ABH03 II34 REPS1 TAL1 CAS21 PTGS1 DOCK9 USSP9Y ATM DARS SIGLEC14 SIGLEC14 SIGLEC14 DOCR8 DDEFR TIPIN UQCR8 GDE1 TFEC TPK1 ZCR81 EXOSC9	-0.11 -0.16 -0.11 -0.21 -0.22 -0.23 -0.24 -0.26 -0.29 -0.29 -0.29 -0.42 r 0.315 -0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 r 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.41 0.41 0.41 0.41 0.41 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.4200.42 0.420000000000000	115 2 2 2 2 2 2 2 2 2 2 2 2 2
Effector memory CD4 T cell Central me	SIRPG CYLD XRCC6 AQP3 ANXA2P2 AHNAK CD63 BMI1 ITGB1 KLF5 ABH03 II34 REPS1 CASQ1 EZH2 PTGS1 NEFL DOCK9 USP9Y SIGLEC14 SIGLEC6 SDPR WIPF1 PDGFRL TIPIN UQCR8 GDE1 TFEC TPK1 ZCRB1 VEFL DOCK9 VSOC8	-0.11 -0.16 -0.11 -0.22 -0.23 -0.24 -0.24 -0.26 -0.28 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.29 -0.31 -0.42 -0.098 -0.07 -0.02 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.24 -0.29 -0.25 -0.29 -0.21 -0.22 -0.22 -0.23 -0.24 -0.29 -0.02	113 2 2 2 2 2 2 2 2 2 2 2 2 2

	r	P value
CHST12	0.335	***
CDK5R1	0.327	***
RAF1	0.27	***
SYNM	0.168	***
CEBPA	0.166	***
TYRO3	0.107	*
CD83	0.097	*
IRRC32	0.076	ns
MC5R	0.058	ns
B3GAT1	0.048	ns
DPP4	0.042	ns
CSF1R	######	ns
NCR2	-0.01	ns
NCAM1	-0.01	ns
CECR1	-0.01	ns
BCL6	-0.01	ns
PDCD1	-0.01	ns
MICA	-0.02	ns
SIGLECA	-0.02	ns
PDCD6	-0.03	ns
SIGLEC7	-0.05	ns
CLEC10A	-0.05	ns
NRP1	-0.1	*
CLIC3	-0.11	*
PRDX1	-0.13	**
CD84	-0.13	**
GPR18	-0.13	**
CD200	-0.14	**
PDCD11G2	-0.15	**
CLECAA	-0.19	***
EGE2	-0.19	***
IGMN	-0.2	***
RAFT1F	-0.25	***
IVNS1ARP	-0.3	***
CTSS	-0.38	***
0.00	r	P value
L1CAM	0.297	***
LRP1	0.218	***
PTGIR	0.189	***
PRSS23	0.124	*
STAB1	0.118	#
FOXP3	0.051	ns
CD72	0.032	ns
MARCO	-0.01	ns
LRRC42	-0.11	*
PELO	-0.11	*
MRC1	-0.11	*
CLEC5A	-0.14	**
MS4A6A	-0.16	**
ITGA4	-0.17	***
PLEK	-0.17	***
MMP12	-0.18	***
ST8SIA4	-0.19	***
MNDA	-0.2	***
LIPA	-0.29	***

T follicular helper cell

T cells regulator

	r	P value
IGF2	0.228	***
TRAF1	0.228	***
RYR1	0.203	***
DUSP14	0.169	***
CD151	0.141	**
MAN1B1	0.134	**
LTC4S	0.125	**
P2RX5	0.075	ns
DAB1	0.063	ns
SELP	0.05	ns
SELE	0.048	ns
GFPT2	0.038	ns
COL5A3	0.03	ns
METRNL	0.022	ns
DLEU7	0.016	ns
IL12A	0.015	ns
STAC	0.015	ns
GREM2	0.013	ns
F12	-0	ns
ADAM8	-0.01	ns
CD7	-0.01	ns
COL4A4	-0.02	ns
BST1 TNERSE1A	-0.02	ns
GPR25	-0.02	ns
HAVCR1	-0.03	ns
ICAM3	-0.03	ns
CD70	-0.04	ns
HTR2B	-0.04	ns
HSDIIBI	-0.05	ns
SIT1	-0.05	ns
SKAP1	-0.06	ns
CFHR3	-0.06	ns
RGS16	-0.06	ns
TBX21	-0.06	ns
CHRM3	-0.06	ns
CALD1	-0.08	ns
GAB3	-0.08	ns
SIGLEC10	-0.09	ns
FCGR2C	-0.09	ns
TEP2	-0.09	ns +
RCSD1	-0.1	*
CD68	-0.11	*
CD52	-0.11	*
GATM	-0.11	*
DOC2B	-0.11	*
MMD	-0.11	*
ENC1	-0.13	**
CD53	-0.14	**
FBXO30	-0.14	**
TLR8	-0.15	**
CLEC74	-0.15	***
FAM134B	-0.18	***
TIGIT	-0.18	***
B3GALNT1	-0.19	***
CD96	-0.22	***
TRAFEIDS	-0.23	***
CD47	-0.24	***
SH3KBP1	-0.25	***
EMP1	-0.26	***
SAV1	-0.27	***
SLC35B3	-0.27	***
AHCY12	-0.27	***
MDH1	-0.34	***
ALCAM	-0.35	***
BBS12	-0.36	***

Type 1 T helper cell

Type 2 T helper cell

Type 17 T helper cell

	r	P value
GATA3	0.067	ns
ASB2	0.049	ns
CSRP2	0.036	ns
NRP2	-0.01	ns
DLCI	-0.04	ns
TMPRSS3	-0.00	ns
RBMS3	-0.07	ns
CENPF	-0.08	ns
LAMP3	-0.1	*
IL26	-0.11	*
OSBPL1A	-0.12	*
PHLDA1	-0.13	**
CDC25C	-0.13	**
DAPK1	-0.15	**
HELLS	-0.16	***
CXCR6	-0.17	***
PLA2G4A	-0.17	***
CDC7	-0.17	***
GSTA4	-0.21	***
DUSP6	-0.22	***
CNIAI1	-0.20	***
DNAIC12	-0.27	***
EVI5	-0.31	***
RNF125	-0.32	***
DHFR	-0.33	***
RAB27B	-0.48	***
40001	r 0.210	P value
ABCBI	0.219	***
TNIP2	0.14	**
CD40	0.102	*
IL17F	0.057	ns
C2CD4B	0.051	ns
IL17RC	0.046	ns
ILDR1	0.032	ns
IL17RA	0.026	ns
ULIZA	#####	ns
CCDC65	-0.01	ns
IL17C	-0.04	ns
PTGDR2	-0.05	ns
ADAMTS1	-0.05	ns
IL23A	-0.09	ns
CAMTA1	-0.09	ns
ANK1	-0.12	*
SH2D6	-0.13	**
ABCAL	-0.13	**
B3GALT2	-0.10	***
CEACAM3	-0.23	***
IFT80	-0.25	***
CA2	-0.26	***
LONRF3	-0.27	***
ANKRD22	-0.3	***
	0.5	
	0.5	
	0	
	-0.5	
0.01 <p≤0< td=""><td>.05</td><td>*</td></p≤0<>	.05	*
0.001 <p≤< td=""><td>0.01</td><td>**</td></p≤<>	0.01	**
P>0.05		ns