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Supplemental Information

High Levels of Canonical Wnt Signaling Lead to Loss of Stemness and Increased Differentiation in Hematopoietic Stem Cells

Farbod Famili, Martijn H. Brugman, Erdogan Taskesen, Brigitta E.A. Naber, Riccardo Fodde, and Frank J.T. Staal

Supplementary Experimental Procedures

High levels of canonical Wnt signaling lead to loss of stemness and increased differentiation in hematopoietic stem cells.

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Supplemental Experimental procedures

Mouse bone marrow (BM) cells were isolated from femurs and tibiae, which were crushed in a mortar and filtered through 70 µm filters. The cells were stained using biotinylated lineage antibodies (MAC-1/CD11b, B220/CD45R, CD3e, CD4, NK1.1, Gr1, Ter119), Streptavidin PE, CD117 APC and Sca1 PECy7. LSK cells were isolated using a BD Aria II SORP cell sorter (Beckton-Dickinson) and were collected in Stemspan (Stem Cell Technologies), supplemented with mFlt3L (50 ng/ml), rmSCF (100 ng/ml) and rmTPO (10 ng/ml, all cytokines purchased from R&D sytems. The cells were incubated for 16 hr at 37°C and 5% CO₂. LSKs from Apc 15 Lox heterozygous mice with mildly elevated Wnt levels were shown to perform better in reconstitution experiments but are not integral part of the current study, as only subtle changes in gene expression were found.

Retroviral Production and Transduction

MSCV-Cre-IRES-GFP plasmid was kindly provided by H. Nakauchi (Institute of Medical Science, University of Tokyo, Japan) and viruses were generated with the Phoenix-packaging cell line. 40,000–70,000 sorted LSKs were stimulated overnight in serum-free medium (StemCell Technologies) supplemented with cytokines (100 ng/ml rmSCF, 10 ng/ml rmTPO, and 50 ng/ml rmFlt3L; from R&D) and transduced by spinoculation (800 x g, 2 hours, 32°C) with titrated amounts of virus with Retronectin (Takara Bio Inc.). Cells were cultured for 2 additional days. Subsequently, Cre-GFP expressing LSK cells were isolated using flow cytometic cell sorting and collected for RNA expression. For in vitro assays including apoptosis, proliferation and differentiation assays bulk of transduced and untransduced cells were used.

RNA amplification

RNA was isolated from the sorted transduced cells using Qiagen RNEasy micro columns (Qiagen, Hilden, Germany). RNA of more than 10,000 cells were then amplified using the Ovation RNA amplification system v2(Nugen Inc., San Carlos, CA, USA), processed using the Encore Biotin module (Nugen) and hybridized to Affymetrix mouse 430 2.0 Genechip arrays.

Data is available at the NCBI Gene Expression Omnibus (GEO), accession number GSE79495

Gene expression normalization. Gene expression data was measured in two batches. Raw data is normalized per batch with Robust Multi-Array Average (RMA), and batch correction is applied using Combat. Intensity values were mean centered per probe set. Gene symbols are mapped using MM9. As a result of the normalization, probe-intensity values follow a normal distribution for which intensities higher than 0 are up-regulated, and intensities lower than 0 are down-regulated. Principal component analysis and pairwise correlations across the 21 samples showed the expected results; wild-type and mutants, t1572, n1638, and Knock-Out samples are different from each other in the PCA-space and correlation map.

Gene expression analysis. Differential expressed genes for the APC samples are determined by using Limma, and genes are considered to be differential expressed between the two selected groups if mRNA levels differ with $P \leq 0.05$ after multiple test correction using Holm.

ChIP-Seq normalization. In this study we used massively parallel sequenced DNA-fragments bound by the transcription factors, TCF1, TCF7, and β -catenin. All the sequencing data is aligned using Burrows-Wheeler transformation (BWA), according MM9. We used several literature sources (Li et al., 2013a; Steinke et al., 2014; Zhang and Li, 2008; Zhang et al., 2000) (Wu et al., 2012).

ChIP-Seq analysis. Binding of transcription factors is determined by utilizing Hypergeometric Analysis of Tilling arrays (HATSEQ). A binding event was called when fragments are enriched based on default parameter settings, i.e., FWER significance level < 0.05, and a bandwidth (fragment size) of 300bp. We mapped the significantly detected binding sites to RefSeq genes in UCSC mm9 database (genome.ucsc.edu). A gene was designated as the target gene if the peak was present within 5000bp upstream of the transcription start site or inside of the gene.

For TCF1 (in mature CD8 T cells, accession number GSM1258235), we detected 591 significantly enriched regions (ranges between 104bp-1048bp, median: 233bp) by comparing it to control IgG using sorted postselect DP and CD4⁺8^{lo} thymocytes¹ (accession number GSM1258236). The detected regions could subsequently be mapped to 116 unique genes. For the two TCF1 experiments in murine thymocytes (GSM1285796 for TCF1-CAT and GSM1133644 for TCF1), we detected 732 (size ranges between 102bp-2632bp, median: 237bp), and 2600 (102bp-2632bp, median: 237bp) significant binding regions respectively after comparing to control TCF1-CAT-INPUT (GSM1285797) and TCF1-INPUT (GSM1133645) respectively. The detected regions could subsequently be mapped to respectively 131, and 653 unique genes (Table S2). The third analyzed ChIP-Seq data set was the binding of TCF7 (GSM773994). For TCF7 we detected 6395 significant binding regions (size ranges between 103bp-5840bp, median: 341bp) by comparing it to one control (input DNA of TCF7). These regions are subsequently mapped to 2015 genes (Table S2). The fourth public data set that we analyzed were three Beta-Catenin experiments, two with biotinylation and one based on FLAG-tag technology. As a background four different controls are used per experiment (2 with Beta-Catenin biotin without GSK and two GSK input samples). This resulted in respectively 990, 385, and 671 significant binding regions for Beta-Catenin-Biotin-rep1, Beta-Catenin-Biotin-rep2, and Beta-Catenin-Flag-rep1 and were mapped to 121, 49, and 79 genes (Table S2). Binding sites have median size of 336bp, 385bp, and 320bp.

To test the validity of the detected binding regions of each experiment, we expected an overrepresentation of WNT-associated genes. To test this, we overlaid the mapped genes with known WNT-associated genes (n=1136) from the Molecular Signature Database (MSigDB, v4.0), and detected that all seven ChIP-seq experiment showed a significant enrichment for binding in close vicinity of WNT-associated genes (P \leq 0.05, Table S1) based on the hypergeometric test. As an example, all seven experiments showed binding of in the transcriptional start site of *Axin2* (Figure S4A), whereas TCF1, and Beta-Catenin experiments showed also binding for *Lef1* (Figure S4A).

Pathway Analysis. Pathway analysis is performed by utilizing the Molecular Signature Database (MSigDB, v4.0) for the detection of enriched curated gene sets (C2), motif gene sets (C3), computational gene sets (C4), GO gene sets (C5), oncogenic signatures (C6), and immunologic signatures (C7). Gene sets and signatures are considered statistically significant when the P-value, derived from the hypergeometric test, is less or equal than 0.05 after correcting for multiple testing using Holm.

Mice

Mice were bred and maintained in the animal facilities of Leiden University Medical Center, in accordance with legal regulations in The Netherlands and with the approval of the Dutch animal ethical committee. C57Bl/6-CD45.1 (Ly5.1) and C57Bl/6-CD45.2 (Ly5.2) mice were obtained from the Jackson Laboratory. Mice

carrying targeted mutations on Apc were previously described (Fodde et al., 1994; Robanus-Maandag et al., 2010; Smits et al., 1999) and continuously backcrossed to C57BI/6 background.

Flow Cytometry

The following antibodies were obtained from BD Biosciences (San Diego, CA): anti CD11b-PE (M1/70), anti CD19-APC (ID3) and anti CD117 (2B6). For Lineage depletion these markers were used: CD3 (145-2C11), CD4 (L3T4), CD8 (53-6.7), CD11b (M1/70), Gr1 (RB6-8C5), B220 (Ra3-6B2), Ter119 (Ly76) and Nk1.1 (PK136) biotin and subsequently were stained with streptavidin eFluor 450 (48-4317) from eBioscience. The following antibodies were also purchased from eBiosiences: B220 PE-Cy7 (RA3-6B2), Gr1 eFluor 450 (RB6-8C5) and Sca1 PE-Cy7 (D7). Cells were stained in Fluorescenceactivated cell sorter (FACS) buffer (PBS, 2% bovine serum albumin, 0.1% sodium azide) for 30 min at 4 °C. Ultimately, Cells were washed and measured either on a Canto I, or an Aria (BD Biosciences). Data were analyzed using FlowJo software (Tree Star, Ashland, OR, USA).

Prolferation, apoptosis and differentiation assays

 5×10^4 sorted BM LSKs from APC WT and APC 15lox/15lox mice were transduced with titrated amount of CRE viruses in stemspan with FTS cytokines as previously described. For apoptosis assay harvested cells after 2 days (Day 0) or 5 days (Day 3) of culture, cells were stained with either 7AAD/AnnexinV (BD Bioscience), or PE-Active caspase-3 apoptosis kit (BD pharmingen) according to the manufacturer's instruction. For proliferation assay, cells were labelled with 5 uM Cell Proliferation Dye eFluor® 670 (eBioscience) at Day 0. Subsequently, cells were harvested at Day 3 and were assessed by flow cytometry for proliferation.

For differentiation assay 2×10^4 BM LSKs were used and transduced cells at Day 0 were transferred onto confluent monolayers of OP9 WT and cocultured for additional 14 days with AlphaMEM 10% FCS containing 50 ng/ml rmSCF, 10 ng/ml rmFlt3L and 10 ng/ml rmIL-7 (all cytokines from R&D). After 7 days cells were harvested and transferred onto new monolayer of OP9 cells, and half of the medium were replaced every 3-4 days. Finally, after 14 days of coculture cells were harvested and assessed by flow cytometry for B and myeloid lineage differentiation.

Supplemental Figure Legends

Suppl. Fig 1a: Validation of differential gene expression by Q-PCR. Sorted LSK cells were cultured and transduced with CRE-GFP as described in the supplemental experimental procedures. RNA was isolated and used for analysis by Q-PCR for the indicated Wnt target genes. **Suppl. Fig 1b:** Biological processes associated with clusters 1 and 2. For details see text

Suppl. Fig 2: High Wnt signaling is associated with differentiation into monocytes and B lymphocytes based on published gene sets.

Suppl. Fig 3: No differences in apoptosis and cell cycle in high Wnt signature when compared to published gene sets.

Suppl. Fig 4a: Tcf and beta catenin binding sites in the Lef1 and Axin2 promoters based on literature data mining of CHIP-Seq data

Suppl. Fig 4b: Differentially expressed genes from the gene expression profiles of heterozygote samples against 1572T,1638N, and full KO, and detected in A. 157 differential expressed genes with P<0.05 and B. the representation of 55 unique gene sets (see also Table S3)





Figure S2



Differentiation signatures as determined by Boiers (Cell Stem Cell 2013) and Chambers (Cell Stem Cell 2007).

Stem cell signature, such as proposed by Ivanova (Science 2002), Forsberg (PLoS One 2010), Chambers (Cell Stem Cell 2007) and de Graaf (PNAS 2010) and Ridell (Cell 2014) were mostly driven by only a few genes.

Figure S3





Figure S4

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Lef1

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Lef1

Distance to TSS: < 5kb



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Table S1		D <0.05	0
Gene-set		FBYSU.05	Genes ANXA1,APCDD1,CCR9,CD160,CDC23,GPR34,IL2RB,MYO5A,NTRK3.PDCD1.PLAGL1.PRSS23.PTP
All Curated gene sets		6.58E-06	RF,PVR,SH3BGRL2,SYTL2,TCF7,TULP3,XCL1,ZC3H12C
All Curated gene sets All Curated gene sets	LIU_PROSTATE_CANCER_DN	0.0002209	ANTXR1;CD93;CUU,DCLK1;FN1;FS1L1;IL18;LAMC1;PLA2G4C;FA114;1MEM163;1NS1 BEND5;CHST2;CUU;CRISPLD2;EPAS1;GPR155;ITGA2;PHLDA1;PLAGL1;PRSS23;RHOJ;ROBO1;TF
All Curated gene sets	ONDER_CDH1_TARGETS_2_DN	0.0002209	CP2L1, IMEM35, INS1, WIF1, ZCCHC14 ALDH1A3, CD83, CDK5R1, EPAS1, FGD6, FST, GJB5, IGSF3, IL18, ITGA2, KLF5, PTPRF, ROBO1, TFCP2L1
All Curated gene sets	DELYS_THYROID_CANCER_UP	0.0006965	ALDH1A3,ANXA1,CHST2,DPP4,ENTPD1,FN1,IGSF3,ITGA2,MED13,NRP2,NT5E,P4HA2,PRSS23,PT
All Curated gene sets	ST_WNT_BETA_CATENIN_PATHWAY	0.001009	APC,AXIN2,DKK2,FSTL1,NKD1,WIF1
All Curated gene sets	SANA_TNF_SIGNALING_DN	0.001009	ANTXR1,ANXA1,CLU,EPAS1,GIMAP6,NT5E,PHLDA1,RHOJ ABHD2 CLU DCLK1 FETUB GERA1 GPC4 MB21D2 MYO5A PPAP2A PRSS23 RASGRP1 RNE144B
All Curated gene sets	GOZGIT_ESR1_TARGETS_DN	0.001305	SDK1,SH3BGRL2,SHROOM3,SIPA1L2,SYTL2,THBD,THSD4
All Curated gene sets	CUI_TCF21_TARGETS_2_UP	0.001305	ANTXR1,APCDD1,ARSB,BMP4,BMPER,CLU,DCLK1,EMID1,FN1,GAS2L3,HUNK,KLF5,LYPD6B,NKD 1,NRP2
All Curated gene sets	GAVIN_PDE3B_TARGETS	0.001305	ENTPD1.IL18.LAMC1.NT5E.SYTL2
All Curated gene sets	NABA_MATRISOME	0.003449	ADAM22,ANXA1,BMP4,BMPER,CRISPLD2,ELFN1,EMID1,FN1,FREM2,FS1,FS1L1,GPC4,IL18,ISM1, KY,LAMC1,P4HA2,S100A5,SCUBE3,THSD4,WIF1,XCL1
All Curated gene sets	KEGG_WNT_SIGNALING_PATHWAY	0.00359	APC,AXIN2,CAMK2D,DKK2,LEF1,NFATC2,NKD1,TCF7,WIF1
All Curated gene sets	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN	0.005222	CAMK2D,DCLK1,DLC1,FAM63A,FN1,FSTL1,LAMC1,MB21D2,NT5E,PHLDA1,PRSS23,SIPA1L2
All Curated gene sets	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	0.005292	ADA,ALDH1A3,ANTXR1,ANXA1,CD14,FST,FSTL1,IL18,IL7R,KLF5,LAMC1,NT5E,PHLDA1,ZC3H12C
All Curated gene sets All Curated gene sets	SANSOM_WNT_PATHWAY_REQUIRE_MYC	0.007768	ABHD2,ALDH1A3,BACE1,BMP4,CLU,FST,NRP2,PHLDA1,TNFRSF19 AXIN2,LEF1,NKD1,TCF7,TNFRSF19,WIF1
All Curated gene sets	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP	0.008714	ADA,ANTXR1,ENTPD1,IRF4,NUDT4,OSBPL1A,PHLDA1,PVR,SH3BGRL2,SHROOM3,TULP3
All Curated gene sets	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS	0.008714	SULT1A1,TEK,TFCP2L1,THBD,TULP3,XCL1
All Curated gene sets	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP GAVIN_FOXP3_TARGETS_CLUSTER_P4	0.009692	ARHGAP28,ARSB,BMP4,BMPER,FST,GPC4,IL18,NT5E,TEK CCDC109B CD83 EPAS1 II 2RB LYPD6B PLAGL1 SH3BGRI 2
All Curated gene sets	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.01299	CCR2,CCR9,EDAR,IL17RB,IL18,IL2RB,IL7R,TNFRSF19,TNFRSF25,XCL1
All Curated gene sets	DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.01525	ABHD2,ALDH1A3,ANXA1,APCDD1,ATP13A4,BACE1,BDH1,BEND5,CAND2,CLU,EDAR,EPAS1,FAM 63A,FMN1,IL18,KLF5,LYPD6B,PRKAA2,PRSS23,SH3BGRL2,SMPD3,SNX31,SYTL2,TNFRSF19,TNS 1 TUBB3
All Curated gene sets	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1	0.01646	BMPER,CCDC101,CRISPLD2,DLC1,EFHD1,FREM2,GFRA1,ITGA2,MB21D2,MYO5A,PRSS23,SYTL2,
All Curated gene sets	SMID_BREAST_CANCER_NORMAL_LIKE_UP	0.01763	CCR2,CD3G,CLU,DPP4,GIMAP6,IL7R,LEF1,NT5E,SNCAIP,THBD,TNFRSF25,WIF1,XCL1
All Curated gene sets	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	0.01851	B4GALT5,CD14,CD93,CLU,EPAS1,PRSS23,THBD,TNS1 CCDC109B CD83 CD93 CLU DLC1 GIMAP6 II 7R RASGRP1 THBD TMEM35
All Curated gene sets	QI_PLASMACYTOMA_UP	0.02286	CARD11,CCR2,CD3G,CLU,DPP4,IL17RB,IL18,IL2RB,TUBB3,XCL1
All Curated gene sets	AMIT_EGF_RESPONSE_480_HELA	0.02337	ABHD2,DCLK1,FST,ITGA2,NUDT4,PTPRF,PVR,TUBB3 ADAM22,ANXA1,BMP4,ELFN1,FREM2,FST,FSTL1,GPC4,IL18,ISM1,KY,P4HA2,S100A5,SCUBE3,WI
All Curated gene sets		0.03018	F1,XCL1 BTI A CAMK2D CARD11 CCR2 CD14 CD160 CD3G CDC23 II 18 II 2RB II 7R IRF4 OSBPI 1A PDCD1
All Curated gene sets	REACTOME_IMMUNE_SYSTEM	0.03141	PVR,RAP1GAP2,RASGRP1,RNF14/B
All Curated gene sets	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP	0.03141	D
All Curated gene sets	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP	0.03313	ALDH1A3,ANXA1,BDH1,CLU,CRISPLD2,EDARADD,GPR155,NT5E,PPFIBP2,SULT1A1,TFCP2L1,TP D52L1,WIF1
All Curated gene sets	KIM_MYC_AMPLIFICATION_TARGETS_DN	0.03336	DCLK1,GAS2L3,IL17RB,KLF5,NFATC2,SHROOM3
All Curated gene sets	KEGG_BASAL_CELL_CARCINOMA	0.04862	APC,AXIN2,BMP4,LEF1,TCF7
All Curated gene sets All Curated gene sets	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN LINDGREN_BLADDER_CANCER_CLUSTER_2B	0.04862	ANTXR1,CD14,CLU,ENTPD1,EPAS1,GPR34,IL7R,TMEM163 CRISPI D2 FEHD1 ENTPD1 II 7R LEE1 MYO5A NRP2 TBC1D8 TCE7 THBD TNS1
All Curated gene sets	NUYTTEN EZH2 TARGETS UP	0.0488	ANXA1,AXIN2,B4GALT5,BACE1,CCDC109B,CD83,FGD6,FN1,GPR155,NT5E,P4HA2,PLAGL1,PRRG
All Queste discussion	SCHAEFFER PROSTATE DEVELOPMENT 48HR DN	0.0499	1,PTPRF,ROBO1,STX3,TCF7,THSD1,ZC3H12C
All Curated gene sets		0.0400	ANTXR1,CD83,CHDH,DKK2,GAS2L3,HUNK,LYPD6B,NRP2,P4HA2,PRTG,RHOJ,SIPA1L2
Computational gene sets	MODULE_46	2.83E-06	ANTXR1_CD83_CFDH_DKR2_GAS2L3,HUNK_LYPDbB_NRP2_P4HA2_PR1G,RHOJ,SIPA1L2 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTPD1,FN1,IL18,IL2RB,IL7R,P4HA2,PDC D1 XCI 1
Computational gene sets Computational gene sets	MODULE_46 MODULE_75	2.83E-06 2.83E-06	ANI XR1, CD83, CHDH, DKR2, GAS2L3, HUNK, LYPDBB, NRP2, PAHA2, PR1G, RHOUSIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, ENTPD1, FN1, IL 18, IL2RB, IL7R, P4HA2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL2RB, IL7R, P4HA2, PDCD1, TEK, VCL1
Computational gene sets Computational gene sets Computational gene sets Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART	2.83E-06 2.83E-06 0.000438	ANI,XR1,CD83,CHDH,UKK2,GAS2L3,HUNKLYPD9B,NRY2,PAHA2,PK1G,KHOJ,SHATL2 DAD,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTPD1,FN1,L18,IL2R8,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,FN1,IL18,IL2R8,IL7R,P4HA2,PDCD1,TEK, XCL1 AGTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17R8,IL2R8,ITGA2,NTRK3,PRRG1,PTPRF,R0B01,SHROOM3,STX3,SYT2,TEX,THBD1
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART	2.83E-06 2.83E-06 0.000438	ANI, XR1, CD83, CHD1, UKZ, GASZL3, HUNK, LYPDBB, NR2, ZHARZ, PKTG, KHOJ, SIPATLZ DAD, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DP44, FN1, IL18, IL128, IL17R, P4HA2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DP44, FN1, IL18, IL28, IL17R, P4HA2, PDCD1, TEK, XCL1 ACTIN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHROOM3, STX3, SYT12, TEK, THBD, T NFRSF25 ACTIN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK5R1, DCLK
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE	2.83E-06 2.83E-06 0.000438 0.0006684	ANI XR1 (2083) CHDI LKK2 (GAS2L3, HUNK LYPDB, NKP2/PAH2/PK1G, KHOU, SIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, ENTPD1, FN1, LI18, IL2RB, IL7R, P4HA2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL2RB, IL7R, P4HA2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ILTGA2, NTRK3, PRRG1, PTPRF, ROBO1, SHROOM3, STX3, SYTL2, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ILTGA2, NTRK3, PRRG1, PTPRF, ROBO1, SHROOM3, STX3, SYTL2, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCK5R1, DCLK 1, ENTPD1, GPC4, GPR114, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PLA2G4C, PPAP2A, PRRG1, PTPRF, P VR, RNF144B, ROB01, SHROOM3, SLC7A4, STX3, SYTL2, TBC10B, TEK, THBD, THRSF25 BACTN2, APC, BACE1, CACNA1B, CACNA1B, CARD11, CCR2, CCR9, CD149, CD149, CD83, DCLK4, ENTPD
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698	ANI,XR1,CD83,CHDI,UKK2,GAS,ZL3,HUNK,LYP,DBB,NKP2,PAHA2,PK1G,KHOJ,SIPATL2 DAD,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTI,IL18,IL2RB,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTI,IL18,IL2RB,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYTL2,TEK,THBD XCTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,CDK5R1,DCLK 1,ENTPD1,GPC4,GPR114,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PLA264C,PPAP2A,PRRG1,PTPRF,P VR,RNF144B,ROB01,SHROOM3,SLC7A4,STX3,SYTL2,TEK109,TEK THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRG1,PTPRF,P VR,RNF144B,ROB01,SHROOM3,SLC7A4,STX3,SYTL2,TEK,THBD,TNFRSF25
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722	ANI XR1 CD83 CHD1 LKR2 GAS2L3 HUNK LYPDB5 NR7-2 PAH22 PATG; HG1KH03, SIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, ENTPD1, FN1, L18, IL2RB, IL7R, P4HA2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, ENTI, IL18, IL2RB, IL7R, P4HA2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHR00M3, STX3, SYT1, ZTEK, THBD T, NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, CDK5R1, DCLK 1, ENTPD1, GPC4, GPR14, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PLA264C, PPAP2A, PRRG1, PTPRF, P VR, RNF144B, ROB01, SHR00M3, SLC7A4, STX3, SYTL2, TBC10B, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD 1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PPAR24, PRRG1, PTPRF, ROB01, SHR00M3, STX3, SYT L2, TEK, THBB, INFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD 1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHR00M3, STX3, SYT L2, TEK, THBB, INFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD 1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, PVR, RNF144B, ROB01, SHR00M3, STX3, SYT L2, TEK, THBB, INFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR144, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRG1, PTPRF, PVR, RNF144B, ROB01, SHR00M3, S LC7A4, STX3, SYTL2, TEK, THBD, TNFRSF25
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247	ANI,XR1,CD83,CHDI,UKK2,GXS,L3,HUNKLYPDBB,NKP2,PAHA2,PK1G,KHOJ,SIPATL2 DAD,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,ENTPD1,FN1,LI18,IL2RB,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,FN1,IL18,IL2RB,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYTL2,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF, PURA 2,RNF144B,ROB01,SHROOM3,SLC7A4,STX3,SYTL2,TEK,TBD10,TKEXFP25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRG1,PTPRF,P080,SHROOM3,STX3,SYT 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRG1,PTPRF,P080,SHROOM3,STX3,SYT 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRAC1,PTPRF,P016,0CB3,DCLK1,ENTPD1,GPC 4,GPR14,IL7CR8,IL2RB,ICGA2,NTRK3,PRAC1,PTPRF,P016,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,IL7CR8,IL2RB,ICGA2,NTRK3,PRAC1,PTPRF,P016,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,IL7CR8,IL2RB,ICGA2,NTRK3,PRAC1,PTPRF,P016,0CB3,DCLK1,ENTPD1,GPC 4,GPR14,IL7CR8,IL2RB,ICGA2,NTRK3,PRAC1,PTPRF,P02A,PRKAA2,PTPRF,RASGRP1,TEK,TNF 5925,TDR54,IL7CR8,IL2RB,ICGA2,NTRK3,NUDT4,PPAP2A,PRKAA2,PTPRF,RASGRP1,TEK,TNF 5925,TDR54,IL7CR8,IL7CR
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247 0.01613	ANI,XR1,CD83,CHDI,DKR2,GXS213,HUNKLYPD9B,NR2,ZPAH2,PHTG,HKH0,SIPATL2 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTP01,FN1,LI18,ILZRB,IL7R,PH4A2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,FN1,IL18,ILZRB,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYTL2,TEK,THBD,T NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRA2A,TRK3,PA2AC,PPA2A,PRRG1,PTPRF,P VR,RNF144B,ROB01,SHROM3,SLC7A4,STX3,SYTL2,TEK,D10,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1 ,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYT L2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1 ,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYT L2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1 ,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYT L2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR114,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRA2A,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYT L2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD14,PAPA2A,PRR42,PTPRF,RASGRP1,TEK,TNF R5725,TPO52L1,XCL1 AHSG,ANXA1,CCR2,CCR9,CCR3,CCR4,ST2,STTP1,TEK,TNF R5725,TPO52L1,XCL1
All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO)	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247 0.01613 0.01613	ANI XR1 CD83 CHDI LKR2 GAS2L3 HUNK LYPDBB, NR2 2PAH22 PATG3 (HG, HOUS) SIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DP4, ENTPD1, FN1, IL 81, ILZRB, IL7R, P4HA2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DP4, FN1, IL18, ILZRB, IL7R, P4HA2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHR0OM3, STX3, SYT12, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHR0OM3, STX3, SYT12, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR14, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PLA264C, PPAP2A, PRRG1, PTPRF, P VR, RNF144B, ROB01, SHR00M3, SLC7A4, STX3, SYTL2, TEK1B0, TNFRFF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD 1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PPAP2A, PRRG1, PTPRF, ROB01, SHR00M3, STX3, SYTL 2, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD 1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PPAP2A, PRRG1, PTPRF, ROB01, SHR00M3, STX3, SYTL 2, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD 1, GPC 4, HUNK, IL2RB, ILTRA, IL2RB, ITGA2, NTRK3, PRAG1, PTPRF, PVR, NF144B, ROB01, SHR00M3, STX3, SYTL 2, TEK, THBD, TNFRSF25 ANX31, AXI12, CCR2, CCR9, CO14, CD160, CD30, CD83, CDK5R1, DLC1, EDARADD, EPA51, FGD6, GPR 34, HUNK, IL2RB, ILTRA, KCNIP2, MED13, NTRK3, NUDT4, PPAP2A, PRKAA2, PTPRF, PASGRP1, TEK, TNF RS25, TPO52, IXCL1 AHS6, ANX41, CCR2, CCR9, CH372, ENTP01, ITGA2, PG1YRP2, SHR00M3, THBD, XCL1 CD14, CD160, CD36, GFRA1, GPR114, IL2RB, ILTR, MED13, NR22, PG1YRP2, PTRF, PVR, ROB01, TEK, TNFRS25
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY RESPONSE_EARLY HALLMARK_INFLAMMATORY RESPONSE	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.001722 0.0067247 0.01613 0.00613 0.006397	ANI,XR1,CD83,CHDI,UKK2,GK32L3,HUNKLYPDBB,NKP2/PAH2/PHC3/PHC3/HC14/HC3/HC3/HC3/HC3/HC3/HC3/HC3/HC3/HC3/HC3
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets Hallmark gene sets	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_COAGULATION HALLMARK_COAGULATION	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.001722 0.001613 0.006397 0.006397 0.006397	ANI,XR1,CD83,CHDI,UKK2,GK32L3,HUNKLYPUDB,NKP2,PAHA2,PK1G,KH0J,SIPATL2 DAD,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTI,IL18,IL2RB,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,ENTI,IL18,IL2RB,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHROOM3,STX3,SYTL2,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRG1,PTPRF,ROB01,SHROOM3,STX3,SYTL2,TEK,THBD 1,GPC4,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PPR24,PRRG1,PTPRF, PV R,RNF144B,ROB01,SHROOM3,SLC7A4,STX3,SYTL2,TEK,TBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PPR24,PRRG1,PTPRF, PVR,R0B01,SHROOM3,STX3,SYT L27EK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,P0E0,T68,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,P0E0,160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,PVR,R0B01,SHRO0M3,STX3,SYT L27EK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR144,GPR34,IL37RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,PVR,RNF144B,R0B01,SHRO0M3,STX3,SYT L27EK,THBD,TNFRSF25 ACTN2,APC,GACCF2,CCR9,CO14,QD160,CD36,CD83,DCLK61,IEDA7ADD,EPA51,FGD6,GPR 34,HUNK,IL2RB,IL7R,KCNIP2,MED13,NTRK3,NUDT4,PPAP2A,PRKAA2,PTPRF,RASGRP1,TEK,TNF RSF25,TPD52L1,XCL1 AN5G,ANXA1,CCR2,CCR9,CGH32,ENTP2,IEDA7,JRED13,NRP2,PGLYRP2,PTPRF,PVR,R0B01,TEK, TNFRSF25 ASHC2,UL1,FAM53,GFRA1,IL37RB,PRS23,RASGRP1,THSD4,TPD52L1 CD14,CHS12,IL18,IL2RB,ITGA2,PRS23,RASGRP1,THA2B ANXA1,ALU,DIPP4,FN1,ITGA2,PRS23,THBD
All Curated gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets Hallmark gene sets Hallmark gene sets	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY_RESPONSE_EARLY HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_INFLAMMATORY_RESPO	2.835-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.001722 0.001722 0.0017247 0.01613 0.006397 0.006397 0.006397	ANI,XR1,Cb83,CHD1,UKK2,GK32L3,HUNKLYPUBB,NKP2,PAHA2,PK1G,KH0J,SIPATL2 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,EN1,IL18,IL2RB,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DPP4,EN1,IL18,IL2RB,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROBO1,SHROOM3,STX3,SYTL2,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRG1,PTRF,ROBO1,SHROOM3,STX3,SYTL2,TEK,THBD, 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRC1,PTPRF,P VR,RNF144B,ROBO1,SHROOM3,SLC7A4,STX3,SYTL2,TEK,TBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRC1,PTPRF,ROBO1,SHROOM3,STX3,SYTL 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRAP2A,PRRC1,PTPRF,ROBO1,SHROOM3,STX3,SYTL 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRG1,PTRF,FVR,RNF144B,ROBO1,SHROOM3,STX3,SYTL 2,TEK,THBD,TNFRSF25 ACTN2,APC,GACCF2,CCR9,CO14,CD160,CD36,CD83,CDK5R1,DLC1,EDARADD,EPA51,FOD6,GPR 34,HUNK,IL2RB,IL7R,KCNIP2,MED13,NTRK3,NUDT4,PPAP2A,PRKAA2,PTPRF,RASGRP1,TEK,TNF RSF25,TPD521,XCL1 AHSG,ANXA1,CCR2,CCR9,CCH3C,ENTP2,IRED13,NRP2,PGLYRP2,PTPRF,PVR,R0B01,TEK, TNFRSF25 ACTN2,APC,BACB,ICR4,INTR8,PRSS23,RASGRP1,THSD4,TPD52L1 CD14,CO150,CD33,GFRA1,IG7R4,PRSS23,RASGRP1,THSD4,TPD52L1 CD14,C0152,IL2RB,IL7R,VPR,RASGRP1,RNF144B ANXA1,CLIP4,IN41,I1,CR2,PRSS23,THBD CD83,IL2RB,IRF4,MT5E,PHLDA1,PLAGL1,PPAP2A,SH3BGRL2 AXIN2,LEF1,NK01,TCC7
All Curateb gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_UNT_SIGNALING	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247 0.01613 0.004103 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397	ANI, XR1, CD83, CHD1, UKR2, GSX, SHUNK, LYPUBB, NK2, ZHTPD1, FN1, LT8, IL278, IL778, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL278, IL778, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL278, IL778, PH4A2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCL14, ENTPD1, GPC 4, GPR34, IL178, IL278, IL762, ILT78, IL278, IL778, IL278, IL778, IL278, IL278, IL1778, IL278, I
All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_INFLAMMATORY_INFLAMMATORY_INFLAMMATORY HALLMARK_INFLAMMATORY_INFLAMMATORY_INFLAMMATORY_INFLAMMATORY HALLMARK_INFLAMMATORY_INFLAMMATOR	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.0017247 0.01613 0.004103 0.004103 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397	ANI,XR1,Cb83,CHDLKR2,GS3,SHUNKLYPUBB,NR2,ZPATG,YNL,LTR1,LTR3,LZRB,ILTZ ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,ENTPD1,FN1,LT8,ILZRB,ILTR,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,FN1,IL18,ILZRB,ILTR,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLX1,ENTPD1,GPC 4,GPR34,IL17RB,ILZRB,ITGA2,NTRK3,PRRG1,PTPRF,ROBO1,SHROOM3,STX3,SYT2,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLX1,ENTPD1,GPC 4,GPR34,IL17RB,ILZRB,ITGA2,NTRK3,PRRG1,PTPRF,ROBO1,SHROOM3,STX3,SYT2,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLX1,ENTPD1,GPC4,GPR14,IL17RB,IL2RB,ITGA2,NTRK3,PAR2A,PRC1,PTPRF,PVR,RN61,PTPRF,P ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLX1,ENTPD1 4,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,R060,SHROOM3,STX3,SYT1, 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLX1,ENTPD1,GPC 4,GPR114,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,PVR,RN6144B,ROB01,SHROOM3,STX3,SYT1, 2,TEK,THBD,TNFRSF25 ANXA1,AXIN2,CCR2,CCR9,CD14,CD160,CD36,CD83,CDK5R1,DLC1,EDARADD,EPAS1,FGD6,GPR 34,HUNK,IL2RB,ILTR,KCNIP2,MED13,NTRK3,NUD14,PPAPAA,PRKAA2,PTPRF,RASGRP1,TEK,TNF RSF25,TPD52L1,XCL1 AHSG,ANXA1,CCR2,CCR9,CH4,CD160,CD36,CD83,CDK5R1,DLC1,EDARADD,EPAS1,FGD6,GPR 34,HUNK,IL2RB,ILTR,KCNIP2,MED13,NTRK3,NUD14,PPAPAA,PTRKAA2,PTPRF,PVR,R0B01,SHROOM3,S LC74A,STX3,STL3,TEK,THBD,TNFRSF25 ANXA1,AXIN2,CCR2,CCR9,CHST2,ENTPD1,ITGA2,PGLYRP2,SHROOM3,THBD,XCL1 CD14,CO150,CC33,GFRA1,GFRA1,IL17RB,PRSS23,RASGRP1,THSD4,TD52L1 CD14,CH572,IL18,ILZRB,ILTR,PK,RASGRP1,SHE144B ANXA1(LUDP4,FN1,TG2,PRSS23,TABD CD83,IL2RB,IRFA,MTSE,PHLDA1,PLAGL1,PPAPA,SHSBGRL2 AXIN2,LEF1,NK10,TCF7 ACTN2,CCR2,CD109,CD3,GPP4,EDARADD,IL17RB,RASGRP1,THBD,XCL1,XKRX ADA,AXIN2,CCR2,CD109,GDP4,ENAADD,IL17RB,RASGRP1,THBD,XCL1,XKRX ADA,AXIN2,CCR2,CD109,CD3,GPP4,EDAADD,IL17RB,IL7R,PCCD1,PTPRF,TUBB3
All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_OCAGULATION HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_OCAGULATION HALLMARK_COMPLEMENT GSE20136_EX_VIV_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VIV_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_DD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_DD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_NAIVE_DD4_TCELL_UP GSE20136_EX_VTCM_VS_DOC205_CONVERSION_VS_D02_TCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_EX_VTCM_VS_D02 GSE20136_E	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.0017247 0.01613 0.004103 0.004103 0.006397 0.01633 0.006397 0.01634 0.001054 0.001054 0.001054	ANI, XR1, LDB3, CHDL, KK2, GAS, L3, HUNK, LYP, DBB, NR-2, PAH2, PHTG, FNH, LHB, ILZB, ILTZ ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, ILHB, ILZB, ILTZ, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DP4, FN1, ILHB, ILZB, ILTZ, PH4A2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, ILZRB, ITGA2, NTRK3, PRRG1, PTPRF, ROBO1, SHROOM3, STX3, SYT12, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, ILZRB, ITGA2, NTRK3, PRAPA, TRST, STX1, STT2, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, ILZRB, ITGA2, NTRK3, PPAP2A, PRRG1, PTPRF, PVR, RNG01, STX3, SYT1, Z ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, ILZRB, ITGA2, NTRK3, PPAP2A, PRRG1, PTPRF, PVR, RN601, SHRO0M3, STX3, SYT1, Z TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, ILZRB, ITGA2, NTRK3, PRAP2A, PRRG1, PTPRF, PVR, RN601, SHRO0M3, STX3, SYT 2, TEK, THBD, TNFRSF25 ANXA1, XXN2, CCR2, CCR9, CD14, CD160, CD30, CD83, CDK5R1, DLC1, EDARADD, EPAS1, FGD6, GPR 34, HUNK, IL2RB, ILTR, KCMIP2, MED13, NTRK3, NUD14, PPAP2A, PTRKA2, PTPRF, RASGRP1, TEK, TNF RSF25, TPO52, I, XCL1 AHSG, ANXA1, CCR2, CCR9, CHST2, ENTPD1, ITGA2, PGLYRP2, SHRO0M3, THBD, XCL1 CD14, CD160, CD36, GFRA1, GPR14, IL2RB, IL7R, MCB13, NTRC3, PL2, PGLYRP2, SHRO0M3, THBD, XCL1 CD14, CHST2, IL, SILL, RCMIP2, MEASGRP1, TNFL4B ANXA1, CLU, DP4, FN1, ICTA2, PRS523, RASGRP1, TNFL4B ANXA1, CLU, DP4, FN1, ITGA2, PRS523, RASGRP1, THSD4, TPD52, 1 CD14, CHST2, IL18, IL7R, PK, RASGRP1, RNF144B ANXA1, CCR2, CD169, EDAS1, GPR4, ILANAP, RASGRP1, THSD4, TPD52, 1 CD3, IL2RB, IRR4, NTSE, PHLDA1, PLAG1, PPAP2A, SH3BGRL2 AXWA1, CCR2, CD109, EDAS1, GPP4, EMARDD, IL17RB, IL7R, PACSGRP1, THBD, XCL1, XKRX ADA,
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All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE PLASMA_MEMBRANE MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_INFLAMMATORY_RESPONSE_EARLY HALLMARK_INFLAMMATORY_RESPONSE HALLMARK_CESTROGEN_RESPONSE_EARLY HALLMARK_IL2_STAT5_SIGNALING HALLMARK_URT_STATO_SIGNALING HALLMARK_URT_SIGNALING	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.001722 0.001613 0.006397 0.006397 0.006397 0.006397 0.006397 0.006394 0.001634 0.001634 0.001634 0.001634 0.003344 0.003344 0.003344 0.003344 0.003344 0.003344	ANI,XR1,CD83,CHDI,UKK2,GK32L3,HUNKLYPUDB,NKP2/PAH2/PHTG,IKH0J,SHPAT2 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,PP4,ENTPD1,FN1,LI18,ILZ78,IL7R,P4HA2,PDC D1,XCL1 ADA,CCR2,CCR9,CD14,CD3G,CD83,CDK5R1,CLU,DP4,FN1,IL18,ILZ78,IL7R,P4HA2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROBO1,SHROOM3,STX3,SYT2,TEK,THBD,T NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROBO1,SHROOM3,STX3,SYT2,TEK,THBD,T NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRG1,PTPRF,PK R,RNF144B,ROBO1,SHROM3,SLC7A4,STX3,SYT12,TEK,TBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD14,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRC1,D17RF,ROBO1,SHROOM3,STX3,SYT 1,2TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD140,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRF,ROBO1,SHROOM3,STX3,SYT 1,2TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2,CCR9,CD140,CD160,CD83,DCLK1,ENTPD 1,GPC4,GPR34,IL17RB,IL2RB,ITGA2,NTRK3,PPAP2A,PRRF,N2RF,RASGRP1,TEK,TNF RSF25,TPD52L1,XCL1 AHSG,ANXA1,CCR2,CCR9,CD14,CD160,CD3G,CD83,CDK5R1,DLC1,EDARADD,EPAS1,FGD6,GPR 34,HUNK,IL2RB,IL7R,KCNIP2,MED13,NTRK3,NUD14,PPAP2A,PRKAA2,PTPRF,RASGRP1,TEK,TNF RSF25,TPD52L1,XCL1 AHSG,ANXA1,CCR2,CCR9,CHS72,ENTP1,ITGA2,PGLYRP2,SHRO0M3,THBD,XCL1 CD14,CD152,IL161,IL2RB,IL7R,VER,ASGRP1,TNF144B ANXA1,CUL,DP4,FN1,TIGA2,PRS523,THBD CCR2,CD83,GERA1,GPRA1,GPR34,IL17RB,RASGRP1,THED,XCL1,YKRX ADAAXN2,CCCC1098,CD36,DP4,EMASGRP1,RNF144B ANXA1,CUL,DP4,FN1,TGA2,PRS523,THBD CCR2,CD83,ICRE1,RF4,NT5E,PHARAD,IL17RB,RASGRP1,THED,XCL1,XKRX ADAAXN2,CCCC1098,CD36,DP4,EMARAD,IL17RB,IL7R,IL7R,IL7R,PD2,C11,XKRX ADAAXN2,CCCC1098,CD36,DP4,EMARAD,IL17RB,IL7R,IL7R,IL7R,IL7R,IL7R,PP2A2,SH3BGRL2 AXIN2,CCCC1098,CD36,DP4,EMARAD,IL47RB,IL7R,IL77,INFR5252,CCH14 ANS6,ANXA1,CCD2,CH170,IL77,
All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_COAGULATION HALLMARK_COAGULATION HALLMARK_COAGULATION HALLMARK_COAGULATION HALLMARK_COAGULATION HALLMARK_COAGULATION HALLMARK_COMPLEMENT GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE3096E_VIVO_VS_DEC205_CONVERSION_NAIVE_CD8_TCELL GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD8_TCELL GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD8_TCELL GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD8_TCELL GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD8_TCELL_DN GSE10326_CONV_VS_TREG_LN_DN	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.0017247 0.01613 0.004103 0.006397 0.006397 0.006397 0.006397 0.001654 0.001054 0.001054 0.001054 0.001054 0.001054 0.003344 0.003340 0.004039 0.003340 0.003403 0.004039 0.00340 0.003344 0.003403 0.004089 0.004089 0.00340 0.00055 0.000055 0.000155 0.0000000000	AN1XR1/Cb83/CH01LKR2/GRS2L3;HUNKLYPUbB,NR2/2H4R2/PHC3/HC15/HOJ/SIPATL2 ADA/CCR2/CCR9,CD14/CD3G,CD83,CDK5R1,CLU/DP4,ENTP01,FN1,L18,IL2RB,IL7R,PH4A2,PDC D1,XCL1 ADA/CCR2/CCR9,CD14/CD3G,CD83,CDK5R1,CLU/DP4,FN1,IL18,IL2RB,IL7R,PH4A2,PDCD1,TEK, XCL1 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11/CCR2/CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17R8,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHR0OM3,STX3,SYT12,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2/CCR9,CD14/CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17R8,IL2RB,ITGA2,NTRK3,PRRG1,PTPRF,ROB01,SHR0OM3,STX3,SYT12,TEK,THBD, NFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2/CCR9,CD14/CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR34,IL17R8,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,R0B01,SHR0OM3,STX3,SYT 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2/CCR9,CD160,CD83,DCLK1,ENTPD1 4,GPC4,GPR34,IL17R8,IL2RB,ITGA2,NTRK3,PPA2A,PRRG1,PTPRF,R0B01,SHR0OM3,STX3,SYT 2,TEK,THBD,TNFRSF25 ACTN2,APC,BACE1,CACNA1B,CACNA1D,CARD11,CCR2/CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,GPC4,GPC4,LCRA1B,CACNA1D,CARD11,CCR2/CCR9,CD160,CD83,DCLK1,ENTPD1,GPC 4,GPR14,CGR2,CCR9,CO14,CD160,CD3G,CD83,CDK5R1,DLC1,EDARADD,EPA51,FGD6,GPR 34,HUNK,IL2RB,IL7R,KCNIP2,MED13,NTRK3,NUDT4,PPAP2A,PRKA42,PTPRF,RASGRP1,TEK,TNF RSF25,TPO52L1,XCL1 AHS6,ANXA1,CCR2/CCR9,CCR3,CCR4,CTR2,PSHROM3,THBD,XCL1 CD14,CD160,CD3G,GFRA1,GPR14,IL2RB,IL7R,MED13,NRP2,PGLYRP2,PTPRF,PVR,R0B01,TEK, TNFRSF25 ADA3,L2R1,L17RB,IL7R,PVR,RASGRP1,RNF144B ANXA1,CUL0,DP4,FN1,TGA2,PRS23,3THBD CD33,L2R2B,IL7R,KCNIP2,AE3,STHBD CD33,L2R2B,IL7R,HD4,FN14,GPR34,IL17RB,RASGRP1,THBD,XCL1,XKRX ADA,ANN2,CCCC109B,CD30,DP4,ED1,RASD17,RNF144B ANXA1,CCDC109B,CD30,DP4,ED1,RASD17,RLF1,TRB,PA2SGRP1,THBD,XCL1,XKRX ADA,ANN2,CCDC109B,CD30,DP4,ED4,ED4,AD4,L17RB,IL7R,PA2ASGRP1,THBD,XCL1,XKRX ADA,ANN2,CCDC109B,CD30,DP4,ED4,ADAD1,ITRB,IL7R,PA2ASGRP1,THBD,XCL1,XKRX ADA,ANN2,CCDC109B,CD30,DP4,ED4,EDARADD,IL17RB,IL7R,PAPA2A,PTPRF,SVTL2,CDHHC23 ANXA1,CCDC109B,CD30,DP4,ED4,RADD1,IL7RB,IL7R,PAPA2A,PTPRF,SVTL2,CDHHC23 ANXA1,CCDC109B,CD30,DP4,ED4,ED4,ED4,L17RB,IL7R,PAPA2A,PTPRF,TUBB3
All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures Immunologic signatures	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_ESTROGEN_RESPONSE HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_BETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENIN_SIGNALING HALLMARK_UNT_DETA_CATENINS_ SIGNAL_TRANS_UNT_SIGNALING HALLMARK_UNT_DETA_CATENINS_ SIGNAL_TRANS_UNT_SIGNALING HALLMARK_UNT_DETA_CATENINS_ SIGNAL_TRANS_COMPLEX_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALLNG SIGNAL_TRANS_COMPLEX_UNT_SIGNALING HALLMARK_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING SIGNAL_TRANS_COMPLEX_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING SIGNAL_SIGNALING_NON_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_UNT_SIGNALING HALMARK_COMPLEX_UNT_SIGNALING HALMARK_UNT_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SIGNAL_SIGNALING SI	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247 0.01613 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397 0.001054 0.001054 0.003345 0.003344 0.003344 0.003345 0.003345 0.003344 0.003345 0.00335 0.0035 0.00335 0.00335 0.00335 0.00335 0.00335 0.0055 0.00550 0.005500000000	Ani XR1 CD83 CHD1 LKR2 GAS2L3 HUNK LYPDBB, NR2 ZPATA2, PK1G, HU, SIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL2R8, IL7R, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL2R8, IL7R, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDK5R1, CLU, DPP4, FN1, IL18, IL2R8, IL7R, PH4A2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17R8, IL2R8, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHROOM3, STX3, SYTL2, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17R8, IL2R8, ITGA2, NTRK3, PRR21, PTRF, PK3, PLA2G4C, PPAP2A, PRRG1, PTPRF, PK 7, RNF144B, ROB01, SHROOM3, SLC7A4, STX3, SYTL2, TBC1D8, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1 1, GPC4, GPR34, IL17R8, IL2R8, ITGA2, NTRK3, PPR24, PRRG1, PTPRF, ROB01, SHROOM3, STX3, SYTL2, ZTEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17R8, IL2R8, ITGA2, NTRK3, PPR61, PTPRF, PVR, RNF144B, ROB01, SHROOM3, STX3, SYTL2, ZTEK, THBD, TNFRSF25 ANXA1, AXIN2, CCR2, CCR9, CD14, CD160, CD30, CD83, CDK5R1, DL C1, EDARADD, EPAS1, FGD6, GPR 34, HUNK, IL2R8, ILTR8, NLE2R8, ITGA2, NTRK3, NUD14, PPA2A, PRKAA2, PTPRF, RASGRP1, TEK, TNF SF25, TPD521, XCL1 AD4, CD160, CD33, GFRA1, GPR114, IL2R8, ILTGA2, RECR4, SHR51, PD2, SHROOM3, STB3, SYTL2, TEK, TNF SF25, TPD521, XCL1 CD14, CD160, CD33, GFRA1, GPR114, IL2R8, ILTGA2, RECR4, SHR51, SHR52, SCL1 CD14, CD160, CD33, GFRA1, GPR114, IL2R8, ILTGA2, RECR4, SHR51, SHR52, SCL1 CD14, CD160, CD33, GFRA1, GPR114, IL2R8, ILTRA, PH2A2, SHB3GRL2 AXX1, CCCC, CO10, DP4, FM1, TGA2, PRSS23, RASGRP1, THED, XCL1, XKRX ADA, AXIN2, CCR2, CO13, CDR14, GPR34, ILTRA, RASGRP1, THED, XCL1, XKRX ADA, AXIN2, CCCC, C0100, RCD30, GPR4, GMAP6, ILTR, ILF7, PL77, TNR58, F25, ZCCHC14 ANX61, CCDC100, RCD30, G
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All Curateo gene sets Computational gene sets Computational gene sets Gene ontology (GO) Gene ontology (GO) Hallmark gene sets Hallmark gene sets Immunologic signatures Immunologic signatures Immunologic signatures Immunologi signatures	MODULE_46 MODULE_75 PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE_PART MEMBRANE PLASMA_MEMBRANE PLASMA_MEMBRANE MEMBRANE_PART SIGNAL_TRANSDUCTION RESPONSE_TO_EXTERNAL_STIMULUS RECEPTOR_ACTIVITY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_ESTROGEN_RESPONSE_EARLY HALLMARK_ESTROGEN_RESPONSE HALLMARK_COMPLEMENT GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_DN GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_DN GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_DN GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_DN GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_DN GSE20362_CTRL_VS_DILLS_LISA_LOA_TCELL_UP GSE20362_CTRL_VS_DILLS_LISA_CD4_TCELL_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_CTRL_VS_DCONV_THYMUS_UP GSE20362_MEMORY_CD4_TCELL_VS_DCELL_UP TGTTLVSFOX04_01	2.83E-06 2.83E-06 0.000438 0.0006684 0.0007698 0.001722 0.007247 0.01613 0.01613 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397 0.006397 0.00154 0.001054 0.001054 0.003344 0.00359 0.01559 0.01559 0.01654 0.01559 0.01634 0.036486 0.036449 0.036419 0.01634 0.01559 0.01634 0.01634 0.01559 0.01634 0.01634 0.01634 0.01634 0.01559 0.01634 0.01634 0.01634 0.01634 0.01559 0.01634 0.01634 0.01634 0.01634 0.01559 0.01634 0.01634 0.01634 0.01634 0.01559 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01634 0.01559 0.01559 0.016345 0.016440 0.016440	AN LARY LOB3 CHDILLARZ, GASZL3 HUNKLYPUDB, NH2 ZHANZ, PKTGJ, KHOJ, SIPATL2 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDKSR1, CLU, DPP4, FN1, IL18, IL2RB, IL7R, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDKSR1, CLU, DPP4, FN1, IL18, IL2RB, IL7R, PH4A2, PDC D1, XCL1 ADA, CCR2, CCR9, CD14, CD3G, CD83, CDKSR1, CLU, DPP4, FN1, IL18, IL2RB, IL7R, PH4A2, PDCD1, TEK, XCL1 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRRG1, PTPRF, ROB01, SHROOM3, STX3, SYTL2, TEK, THBD, T NFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD140, CD180, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PRA2, PRRG1, PTPRF, PK, RNF144B, ROB01, SHROOM3, SLC7A4, STX3, SYTL2, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD14, CD160, CD83, DCLK1, ENTPD1, GPC4, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PPR24, PRRG1, PTPRF, PKR, RNF144B, ROB01, SHROOM3, SLC7A4, STX3, SYTL2, TEK, THBD, TNFRSF25 ACTN2, APC, BACE1, CACNA1B, CACNA1D, CARD11, CCR2, CCR9, CD160, CD83, DCLK1, ENTPD1, GPC 4, GPR114, GPR34, IL17RB, IL2RB, ITGA2, NTRK3, PPR32, PRRG1, PTPRF, PKR, RNF144B, ROB01, SHROOM3, STX3, SYTL2, IEK, THBD, TNFRSF25 ANXA1, AXIN2, CCR2, CCR9, CD14, CD160, CD30, CD83, CDKSR1, DL C1, EDARADD, EPAS1, FGD6, GPR 34, HUNK, IL2RB, IL7R, KNLIP2, MED13, NTRK3, NUD14, PAPA2A, PRKAA2, PTPRF, RASGRP1, TEK, TNF SF25, TPD521, X/CL1 ASG, ANXA1, CCR2, CCR9, CH312, ENTPD1, ITGA2, PGLYRP2, SHROOM3, THBD, X/CL1 ACTN2, CCR2, CD16, GPR14, GPR114, IL2RB, IL7R, ME1013, NRP2, PGLYRP2, SHROOM3, THBD, X/CL1 CD14, CD160, CD36, GFRA1, GPR114, IL2RB, IL7R, ME103, NRP2, PGLYRP2, SHROOM3, THBD, X/CL1 ASG, ANXA1, CCR2, CCR9, CH512, ENTPD1, ITGA2, PGLYRP2, SHROOM3, THBD, X/CL1 ASG, ANXA1, CCR2, CCR9, GH512, ENTPD1, ITGA2, PGLYRP2, SHROOM3, THBD, X/CL1 ASG, ANXA1, CCR2, CC163, GFRA1, IL17RB, PRSS23, RASGRP1, THED, X/CL1, XKRX ADAAXN2, CCCC109B, CD33, GFRA1, GPR114, GPR34, IL17RB, RASGRP1, THED, X/CL12, Z/DH4C23 ANXA1, CCR
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Table S2				
Experiment	Study	Significantly detected binding regions	Mapped to genes within 5Kb from TSS	P-value, Significance with WNT-associated genesets from MsigDB
TCF1	GSE52070	591	116	0.033
TCE1(n-2)	GSE46662	732 in Sample 1	131	0.050
10FT (II-2)	G3L40002	2600 in Sample 2	653	9.395E-04
TCF7	GSE31221	6395	2015	0.017
		990 in Sample 1	121	2.273E-04
Beta-Catenin (n=3)	GSE43565	385 in Sample 2	49	9.564E-04
		671 in Sample 3	79	0.004

Table S3			
Gene-set	Pathway	P _{BY} <0.05	Genes
WNT gene sets	WNT_BOIERS_2013_LYMPHOID	0.01053	CCR9,LEF1,TCF7
All Curated gene sets		0.0001483	APC,AXIN2,DKK2,FSTL1,NKD1,WIF1 ALDH1A3,BACE1,BMP4,CLU,EBF1,FST,NRP2,PHLDA1,TNFR
All Curated gene sets	RIGGI_EWING_SARCOMA_PROGENITOR_DN	0.0006029	SF19
All Curated gene sets	SANSOM_WN1_PATHWAY_REQUIRE_MYC	0.001274	AXIN2,LEF1,NKD1,TCF7,TNFRSF19,WIF1 BEND5.CHST2.CLU.EPAS1.ITGA2.NDNF.PHLDA1.PRSS23.R
All Curated gene sets	LIU_PROSTATE_CANCER_DN	0.001855	OBO1,TFCP2L1,WIF1,ZCCHC14
All Curated gene sets	MATSUDA_NATURAL_KILLER_DIFFERENTIATION	0.001855	ANXA1,APCDD1,CCR9,CD160,EBF1,NTRK3,PDCD1,PRSS23 ,SH3BGRL2,TCF7,TULP3,ZC3H12C
All Curated gene sets	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN	0.001979	DCLK1,EBF1,FAM63A,FSTL1,IL17RD,MB21D2,NT5E,PHLDA1 ,PRSS23,SIPA1L2
All Curated gene sets	KUMAR_TARGETS_OF_MLL_AF9_FUSION	0.001979	ANXA1,CCR9,CD83,EBF1,EXTL3,GPC4,IL7R,IRF4,LEF1,TCF7 ,TNFRSF19
All Curated gene sets	CUI_TCF21_TARGETS_2_UP	0.003067	ANTXR1,APCDD1,ARSB,BMP4,CLU,DCLK1,HUNK,KLF5,LYP D6B,NKD1,NRP2
All Curated gene sets	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	0.003672	ADA,ALDH1A3,ANTXR1,ANXA1,FST,FSTL1,IL7R,KLF5,NT5E, PHLDA1,ZC3H12C
All Curated gene sets	DODD_NASOPHARYNGEAL_CARCINOMA_UP	0.003672	ALDH1A3,ANXA1,APCDD1,ATP13A4,BACE1,BDH1,BEND5,C LU,EBF1,EDAR,EPAS1,FAM63A,KLF5,LYPD6B,PRKAA2,PRS S23,SH3BGRL2,TNFRSF19,TUBB3,UST,WWC1
All Curated gene sets	DELYS_THYROID_CANCER_UP	0.003672	ALDH1A3,ANXA1,CHST2,DPP4,IGSF3,ITGA2,MED13,NRP2,N T5E,PRSS23,STX3
All Curated gene sets	ONDER_CDH1_TARGETS_2_DN	0.004116	ALDH1A3,CD83,EPAS1,FST,IGSF3,ITGA2,KLF5,ROBO1,TFC P2L1,THBD,WWC1
All Curated gene sets	SANA_TNF_SIGNALING_DN	0.004116	ANTXR1,ANXA1,CLU,EPAS1,NT5E,PHLDA1
All Curated gene sets	KEGG_WNT_SIGNALING_PATHWAY	0.004871	APC,AXIN2,DKK2,LEF1,NKD1,TCF7,WIF1
All Curated gene sets		0.003932	ANXA1.ARHGAP28.BACE1.DKK2.DPP4.EBF1.EPAS1.MED13.
All Curated gene sets	CUI_TCF21_TARGETS_2_DN	0.006368	NT5E,PPAP2A,SH3BGRL2,SHROOM3,SNCAIP,THBD
All Curated gene sets	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS	0.01287	AXIN2,CHST2,EFHD1,EXTL3,FAM63A,GPC4,KIF5C,LEF1,PD
All Curated gene sets	GAUSSMANN MUL AF4 FUSION TARGETS F UP	0 0141	ARHGAP28 ARSB BMP4 EST GPC4 II 17RD NT5E
All Curated gone sets		0.01970	ANTXR1,ANXA1,CHST2,FST,FSTL1,IL7R,NT5E,PHLDA1,RAI1
All ourated gene sets		0.01073	
All Curated gene sets	GOZGIT_ESR1_TARGETS_DN	0.03962	P1,SH3BGRL2,SHROOM3,SIPA1L2,THBD
All Curated gene sets	ENK_UV_RESPONSE_EPIDERMIS_DN	0.04184	ANXA1,APC,CD83,ITGA2,PHLDA1,PPAP2A,PRSS23,RAI14,R OBO1,THBD
All Curated gene sets	WNT_SIGNALING	0.04194	APC,LEF1,NKD1,TCF7,WIF1
All Curated gene sets	PID_PST_PATHWAY SENESE HDAC1 AND HDAC2 TARGETS UP	0.04605	APC, DKK2, NKD I, WIF I DCI K1 DKK2 EXTL3 II 7R NRIP3 PHI DA1 WWC1
All Curated gene sets	KIM MYC AMPLIFICATION TARGETS DN	0.04605	DCLK1,IL17RB,IL17RD,KLF5,SHROOM3
Motif gene sets	TTGTTT_V\$F0X04_01	3.15E-05	ANXA1,APC,AXIN2,BDH1,BMP4,CCDC109B,CD83,EBF1,EDA R,EXTL3,FAM63A,FST,FSTL1,IL7R,IRF4,ITGA2,KCNIP2,KLF5, NKD1,NRP2,NTRK3,RNF214,ROBO1,SNCAIP,TNFRSF19,XK RX,ZCCHC14
Motif gene sets	CTTTGA_V\$LEF1_Q2	0.0003071	ATP13A4,BACE1,CD160,CPB1,FAM63A,FST,GPC4,KY,LEF1, MB21D2,MED13,NKD1,NRP2,ROBO1,SLC22A23,SNCAIP,TC F7,TNFRSF19,XKRX
Motif gene sets	CAGGTG_V\$E12_Q6	0.001973	ACTN2,AXIN2,BACE1,BMP4,CD83,CPB1,EBF1,EDAR,EPAS1, EXTL3,FST,IGSF3,ITGA2,KCNIP2,LEF1,LYPD6B,MB21D2,NRI P3,NRP2,NTRK3,SH3BGRL2,SNCAIP,TCF7,UNC45B,UST,W
Motif gene sets	V\$TCF4_Q5	0.005048	FAM63A,FST,GPC4,KY,NKD1,NRP2,TCF7,TNFRSF19
Motif gene sets	TGGAAA V\$NFAT Q4 01	0.006748	ANTXR1,BMP4,DCLK1,DKK2,EBF1,EFHD1,FST,FSTL1,IGSF3, IL17RB,IL7R,IRF4,ITGA2,KCNIP2,KLF5,MED13,SH3BGRL2,S
		0.04400	NCAIP,TMEM163,TNFRSF19,XKRX ARHGAP28,BACE1,CHST2,EDAR,MED13,RNF214,UST,ZCC
Motif gene sets	TATTATA,MIR-374	0.01408	HC14 AHSG AXIN2 DCI K1 KYT FF1 MB21D2 MFD13 NRP2 NTRK3
Motif gene sets	TGCCAAR_V\$NF1_Q6	0.01468	RAI14,ROBO1,XKRX AXIN2 BMP4 EST ESTI 1 IRE4 KY NTRK3 ROBO1 SNCAIP TC
Motif gene sets	RTAAACA_V\$FREAC2_01	0.02911	F7,TNFRSF19,UNC45B,UST
Oncogenic signatures	CAMP_UP.V1_DN	5.78E-06	ANXA1,BACE1,CCR9,CD160,CD83,CHS12,FS1L1,IL7R,T0BB 3.ZCCHC14
Oncogenic signatures	AKT UP.V1 DN	0.04519	AXIN2,EDARADD,TNFRSF19,TULP3,WIF1,ZC3H12C
Immunologic signature	GSE24142_EARLY_THYMIC_PROGENITOR_VS_DN2_THYMOCYTE_DN	0.001121	ADA,AXIN2,CCDC109B,DPP4,EDARADD,IL17RB,IL7R,PDCD 1,TUBB3
Immunologic signature	GSE20366_EX_VIVO_VS_DEC205_CONVERSION_NAIVE_CD4_TCELL_UP	0.007534	ACTN2,CD160,EPAS1,GPR114,IL17RB,RASGRP1,THBD,XKR x
Immunologic signature	GSE10325_LUPUS_CD4_TCELL_VS_LUPUS_BCELL_UP	0.01556	ANXA1,CCDC109B,DPP4,IL7R,LEF1,TCF7,ZCCHC14
Immunologic signature	GSE14350_IL2RB_KO_VS_WT_TREG_DN	0.01556	CCDC109B,CD160,CD83,KY,NT5E,PDCD1,ZC3H12C
Immunologic signature	GSE24142_EARLY_THYMIC_PROGENITOR_VS_DN3_THYMOCYTE_DN	0.01556	
Immunologic signature	GSE24142_EARLY_THYMIC_PROGENITOR_VS_DN2_THYMOCYTE_ADULT_DN GSE26495 NAIVE VS PD1HIGH CD8 TCELL UP	0.01556	BDH1.BEND5.EDAR.EFHD1.LEF1.NT5E.PPAP2A
Immunologic signature	GSE26495_NAIVE_VS_PD1LOW_CD8_TCELL_UP	0.01556	BDH1,BEND5,EDAR,EFHD1,LEF1,NT5E,PPAP2A
Immunologic signature	GSE30962_PRIMARY_VS_SECONDARY_CHRONIC_LCMV_INF_CD8_TCELL_DN	0.01556	AHSG,ANXA1,EPAS1,GPR114,PRKAA2,RASGRP1,TMEM163
Immunologic signature Immunologic signature	GSE3982_BCELL_VS_CENT_MEMORY_CD4_TCELL_DN GSE7460_TCONV_VS_TREG_LN_DN	0.01556 0.01556	DPP4,IL7R,ITGA2,NDNF,PHLDA1,PRKAA2,TCF7 CD83,DPP4,IRF4,NT5E,PPAP2A,SH3BGRL2,ZC3H12C
Immunologic signature	GSE7460_TCONV_VS_TREG_THYMUS_DN	0.01556	CCDC109B,CD83,IGSF3,KIF5C,NRP2,PPAP2A,SH3BGRL2
Hollmork contracts		0.01000	
Hallmark gene sets	HALLWARK_WINI_BETA_CATENIN_SIGNALING HALLMARK COAGULATION	0.002609	ANINZ, LEFT, NKDT, TOF7 ANXA1.CLU, DPP4, ITGA2, PRSS23, THBD
Hallmark gene sets	HALLMARK_IL2_STAT5_SIGNALING	0.007102	CD83,IRF4,NT5E,PHLDA1,PPAP2A,SH3BGRL2
Hallmark gene sets	HALLMARK_KRAS_SIGNALING_DN	0.007102	CHST2,CPB1,EDAR,EFHD1,PDCD1,TFCP2L1
Hallmark gene sets	HALLMARK COMPLEMENT	0.04111	ACTN2,CLU,DPP4,KCNIP2,RASGRP1