

Supplementary Table 3. Upregulated genes in TIL^{hi} /DI^{hi} group

#	Gene Symbol	Description	Biological Process (GO)
1	ACTR3	actin related protein 3	GO:0016344 meiotic chromosome movement towards spindle pole;GO:0034314 Arp2/3 complex-mediated actin nucleation;GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis
2	ADGRE5	adhesion G protein-coupled receptor E5	GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response;GO:0007189 adenylate cyclase-activating G protein-coupled receptor signaling pathway
3	AEN	apoptosis enhancing nuclease	GO:0000738 DNA catabolic process, exonucleolytic;GO:0045071 negative regulation of viral genome replication;GO:0042771 intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
4	AIF1	allograft inflammatory factor 1	GO:0014739 positive regulation of muscle hyperplasia;GO:0071672 negative regulation of smooth muscle cell chemotaxis;GO:0071673 positive regulation of smooth muscle cell chemotaxis
5	ANXA5	annexin A5	GO:0002576 platelet degranulation;GO:0070588 calcium ion transmembrane transport;GO:0007596 blood coagulation
6	APOL1	apolipoprotein L1	GO:0051838 cytolysis by host of symbiont cells;GO:0051801 cytolysis in other organism involved in symbiotic interaction;GO:0051873 killing by host of symbiont cells
7	APOL2	apolipoprotein L2	GO:0006953 acute-phase response;GO:0060135 maternal process involved in female pregnancy;GO:0008203 cholesterol metabolic process
8	ARHGAP30	Rho GTPase activating protein 30	GO:0043547 positive regulation of GTPase activity;GO:0051056 regulation of small GTPase mediated signal transduction;GO:0043087 regulation of GTPase activity
9	ARPC5L	actin related protein 2/3 complex subunit 5 like	GO:0034314 Arp2/3 complex-mediated actin nucleation;GO:0045010 actin nucleation;GO:0030838 positive regulation of actin filament polymerization
10	ASPM	assembly factor for spindle microtubules	GO:0045769 negative regulation of asymmetric cell division;GO:0021873 forebrain neuroblast division;GO:0051661 maintenance of centrosome location

11	BST2	bone marrow stromal cell antigen 2	GO:0002737 negative regulation of plasmacytoid dendritic cell cytokine production;GO:0002736 regulation of plasmacytoid dendritic cell cytokine production;GO:1901253 negative regulation of intracellular transport of viral material
12	C12orf57	chromosome 12 open reading frame 57	GO:0021540 corpus callosum morphogenesis;GO:0021952 central nervous system projection neuron axonogenesis;GO:0021678 third ventricle development
13	C1QC	complement C1q C chain	GO:0045650 negative regulation of macrophage differentiation;GO:0030853 negative regulation of granulocyte differentiation;GO:0030852 regulation of granulocyte differentiation
14	CCR1	C-C motif chemokine receptor 1	GO:0090026 positive regulation of monocyte chemotaxis;GO:0045672 positive regulation of osteoclast differentiation;GO:0071677 positive regulation of mononuclear cell migration
15	CD3D	CD3d molecule	GO:0045059 positive thymic T cell selection;GO:0045061 thymic T cell selection;GO:0043368 positive T cell selection
16	CD52	CD52 molecule	GO:0007204 positive regulation of cytosolic calcium ion concentration;GO:0045730 respiratory burst;GO:0051480 regulation of cytosolic calcium ion concentration
17	CD53	CD53 molecule	GO:1901741 positive regulation of myoblast fusion;GO:1901739 regulation of myoblast fusion;GO:0060143 positive regulation of syncytium formation by plasma membrane fusion
18	CDK9	cyclin dependent kinase 9	GO:1903839 positive regulation of mRNA 3'-UTR binding;GO:2001168 positive regulation of histone H2B ubiquitination;GO:1903837 regulation of mRNA 3'-UTR binding
19	CHD3	chromodomain helicase DNA binding protein 3	GO:0032508 DNA duplex unwinding;GO:0043044 ATP-dependent chromatin remodeling;GO:0007098 centrosome cycle
20	CKAP2L	cytoskeleton associated protein 2 like	
21	CKAP4	cytoskeleton associated protein 4	GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response;GO:0042119 neutrophil activation

22	CMTM3	CKLF like MARVEL transmembrane domain containing 3	GO:0050861 positive regulation of B cell receptor signaling pathway;GO:0050855 regulation of B cell receptor signaling pathway;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway
23	CRK	CRK proto-oncogene, adaptor protein	GO:0035685 helper T cell diapedesis;GO:0035684 helper T cell extravasation;GO:1990859 cellular response to endothelin
24	CSF2RB	colony stimulating factor 2 receptor subunit beta	GO:0038043 interleukin-5-mediated signaling pathway;GO:0038156 interleukin-3-mediated signaling pathway;GO:0036016 cellular response to interleukin-3
25	CTSB	cathepsin B	GO:0046697 decidualization;GO:0046718 viral entry into host cell;GO:0002224 toll-like receptor signaling pathway
26	CXCR6	C-X-C motif chemokine receptor 6	GO:0070098 chemokine-mediated signaling pathway;GO:0007204 positive regulation of cytosolic calcium ion concentration;GO:0019079 viral genome replication
27	CYBB	cytochrome b-245 beta chain	GO:1904845 cellular response to L-glutamine;GO:1904044 response to aldosterone;GO:1904844 response to L-glutamine
28	DDB2	damage specific DNA binding protein 2	GO:0035518 histone H2A monoubiquitination;GO:0006295 nucleotide-excision repair, DNA incision, 3'-to lesion;GO:0000717 nucleotide-excision repair, DNA duplex unwinding
29	DDX3Y	DEAD-box helicase 3 Y-linked	GO:0007276 gamete generation;GO:0019953 sexual reproduction;GO:0048609 multicellular organismal reproductive process
30	DOCK10	dedicator of cytokinesis 10	GO:0002315 marginal zone B cell differentiation;GO:0002313 mature B cell differentiation involved in immune response;GO:0002335 mature B cell differentiation
31	EIF1AY	eukaryotic translation initiation factor 1A Y-linked	GO:0006413 translational initiation;GO:0006412 translation;GO:0043043 peptide biosynthetic process
32	EMC6	ER membrane protein complex subunit 6	GO:0000045 autophagosome assembly;GO:1905037 autophagosome organization;GO:0016236 macroautophagy

33	FAM107B	family with sequence similarity 107 member B	
34	FCGR2A	Fc fragment of IgG receptor IIa	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0038094 Fc-gamma receptor signaling pathway
35	FCGR2B	Fc fragment of IgG receptor IIb	GO:0001814 negative regulation of antibody-dependent cellular cytotoxicity;GO:0001797 negative regulation of type IIa hypersensitivity;GO:0002893 negative regulation of type II hypersensitivity
36	FLI1	Fli-1 proto-oncogene, ETS transcription factor	GO:0035855 megakaryocyte development;GO:0098751 bone cell development;GO:0030219 megakaryocyte differentiation
37	FLT3	fms related receptor tyrosine kinase 3	GO:0002328 pro-B cell differentiation;GO:0002318 myeloid progenitor cell differentiation;GO:0043552 positive regulation of phosphatidylinositol 3-kinase activity
38	FZD2	frizzled class receptor 2	GO:0090179 planar cell polarity pathway involved in neural tube closure;GO:0090178 regulation of establishment of planar polarity involved in neural tube closure;GO:0090177 establishment of planar polarity involved in neural tube closure
39	GBP1	guanylate binding protein 1	GO:1900041 negative regulation of interleukin-2 secretion;GO:0050860 negative regulation of T cell receptor signaling pathway;GO:0050858 negative regulation of antigen receptor-mediated signaling pathway
40	GMFG	glia maturation factor gamma	GO:0034316 negative regulation of Arp2/3 complex-mediated actin nucleation;GO:0051126 negative regulation of actin nucleation;GO:0034315 regulation of Arp2/3 complex-mediated actin nucleation
41	GPR34	G protein-coupled receptor 34	GO:0035589 G protein-coupled purinergic nucleotide receptor signaling pathway;GO:0035590 purinergic nucleotide receptor signaling pathway;GO:0035588 G protein-coupled purinergic receptor signaling pathway
42	GZMA	granzyme A	GO:0032078 negative regulation of endodeoxyribonuclease activity;GO:0032076 negative regulation of deoxyribonuclease activity;GO:0032071 regulation of endodeoxyribonuclease activity

43	HAPLN3	hyaluronan and proteoglycan link protein 3	GO:0001501 skeletal system development;GO:0007417 central nervous system development;GO:0007155 cell adhesion
44	HOXB6	homeobox B6	GO:0048704 embryonic skeletal system morphogenesis;GO:0034101 erythrocyte homeostasis;GO:0048706 embryonic skeletal system development
45	HSPA7	heat shock protein family A (Hsp70) member 7 (pseudogene)	GO:0051085 chaperone cofactor-dependent protein refolding;GO:0051084 'de novo' posttranslational protein folding;GO:0042026 protein refolding
46	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0006958 complement activation, classical pathway
47	IGHV4-31	immunoglobulin heavy variable 4-31	GO:0006958 complement activation, classical pathway;GO:0050853 B cell receptor signaling pathway;GO:0002455 humoral immune response mediated by circulating immunoglobulin
48	IGKV2-24	immunoglobulin kappa variable 2-24	GO:0002377 immunoglobulin production;GO:0002440 production of molecular mediator of immune response;GO:0002250 adaptive immune response
49	IGLV1-44	immunoglobulin lambda variable 1-44	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0006958 complement activation, classical pathway
50	IL2RB	interleukin 2 receptor subunit beta	GO:0038110 interleukin-2-mediated signaling pathway;GO:0035723 interleukin-15-mediated signaling pathway;GO:0071352 cellular response to interleukin-2
51	ISG20	interferon stimulated exonuclease gene 20	GO:0000738 DNA catabolic process, exonucleolytic;GO:0045071 negative regulation of viral genome replication;GO:1903901 negative regulation of viral life cycle
52	ITGA1	integrin subunit alpha 1	GO:0032516 positive regulation of phosphoprotein phosphatase activity;GO:0042311 vasodilation;GO:0042059 negative regulation of epidermal growth factor receptor signaling pathway

53	KDM5D	lysine demethylase 5D	GO:0034721 histone H3-K4 demethylation, trimethyl-H3-K4-specific;GO:0034720 histone H3-K4 demethylation;GO:0060765 regulation of androgen receptor signaling pathway
54	LAPTM5	lysosomal protein transmembrane 5	GO:1990830 cellular response to leukemia inhibitory factor;GO:1990823 response to leukemia inhibitory factor;GO:0071345 cellular response to cytokine stimulus
55	LCP1	lymphocyte cytosolic protein 1	GO:0071803 positive regulation of podosome assembly;GO:0044319 wound healing, spreading of cells;GO:0035722 interleukin-12-mediated signaling pathway
56	LCP2	lymphocyte cytosolic protein 2	GO:0038095 Fc-epsilon receptor signaling pathway;GO:0050852 T cell receptor signaling pathway;GO:0038093 Fc receptor signaling pathway
57	LEPROTL1	leptin receptor overlapping transcript like 1	GO:2000009 negative regulation of protein localization to cell surface;GO:0032511 late endosome to vacuole transport via multivesicular body sorting pathway;GO:2000008 regulation of protein localization to cell surface
58	LRRC73	leucine rich repeat containing 73	
59	MAP7D1	MAP7 domain containing 1	GO:0000226 microtubule cytoskeleton organization;GO:0007017 microtubule-based process;GO:0007010 cytoskeleton organization
60	MMP9	matrix metalloproteinase 9	GO:2000697 negative regulation of epithelial cell differentiation involved in kidney development;GO:2001268 negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway;GO:0051549 positive regulation of keratinocyte migration
61	MRPS21	mitochondrial ribosomal protein S21	GO:0070126 mitochondrial translational termination;GO:0070125 mitochondrial translational elongation;GO:0006415 translational termination
62	MS4A6A	membrane spanning 4-domains A6A	
63	MSANTD3	Myb/SANT DNA binding domain containing 3	

64	MYL6	myosin light chain 6	GO:0030049 muscle filament sliding;GO:0033275 actin-myosin filament sliding;GO:0070252 actin-mediated cell contraction
65	NCALD	neurocalcin delta	GO:0003073 regulation of systemic arterial blood pressure;GO:0008217 regulation of blood pressure;GO:0019722 calcium-mediated signaling
66	NINJ1	ninjurin 1	GO:1990384 hyaloid vascular plexus regression;GO:0001954 positive regulation of cell-matrix adhesion;GO:0060033 anatomical structure regression
67	NMI	N-myc and STAT interactor	GO:0045355 negative regulation of interferon-alpha biosynthetic process;GO:0045358 negative regulation of interferon-beta biosynthetic process;GO:1902524 positive regulation of protein K48-linked ubiquitination
68	P2RY13	purinergic receptor P2Y13	GO:0035589 G protein-coupled purinergic nucleotide receptor signaling pathway;GO:0007194 negative regulation of adenylate cyclase activity;GO:0035590 purinergic nucleotide receptor signaling pathway
69	PAFAH1B1	platelet activating factor acetylhydrolase 1b regulatory subunit 1	GO:0021819 layer formation in cerebral cortex;GO:0021540 corpus callosum morphogenesis;GO:0021801 cerebral cortex radial glia guided migration
70	PARP8	poly(ADP-ribose) polymerase family member 8	GO:0070213 protein auto-ADP-ribosylation;GO:0006471 protein ADP-ribosylation;GO:0030968 endoplasmic reticulum unfolded protein response
71	PFN1	profilin 1	GO:0051497 negative regulation of stress fiber assembly;GO:1900029 positive regulation of ruffle assembly;GO:0001843 neural tube closure
72	PHPT1	phosphohistidine phosphatase 1	GO:0050860 negative regulation of T cell receptor signaling pathway;GO:2000984 negative regulation of ATP citrate synthase activity;GO:0035774 positive regulation of insulin secretion involved in cellular response to glucose stimulus
73	PIGC	phosphatidylinositol glycan anchor biosynthesis class C	GO:0016254 preassembly of GPI anchor in ER membrane;GO:0006506 GPI anchor biosynthetic process;GO:0006505 GPI anchor metabolic process
74	PLS3	plastin 3	GO:0051639 actin filament network formation;GO:0051017 actin filament bundle assembly;GO:0061572 actin filament bundle organization

75	PSMB6	proteasome 20S subunit beta 6	GO:0002223 stimulatory C-type lectin receptor signaling pathway;GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;GO:0002220 innate immune response activating cell surface receptor signaling pathway
76	PTPRC	protein tyrosine phosphatase receptor type C	GO:0048304 positive regulation of isotype switching to IgG isotypes;GO:0048302 regulation of isotype switching to IgG isotypes;GO:1905451 positive regulation of Fc-gamma receptor signaling pathway involved in phagocytosis
77	RAC2	Rac family small GTPase 2	GO:0090023 positive regulation of neutrophil chemotaxis;GO:0060753 regulation of mast cell chemotaxis;GO:1903955 positive regulation of protein targeting to mitochondrion
78	RAP1B	RAP1B, member of RAS oncogene family	GO:2000301 negative regulation of synaptic vesicle exocytosis;GO:1902804 negative regulation of synaptic vesicle transport;GO:0045955 negative regulation of calcium ion-dependent exocytosis
79	RASGRP1	RAS guanyl releasing protein 1	GO:0033089 positive regulation of T cell differentiation in thymus;GO:0032825 positive regulation of natural killer cell differentiation;GO:1902715 positive regulation of interferon-gamma secretion
80	RBMXL1	RBMX like 1	GO:0048026 positive regulation of mRNA splicing, via spliceosome;GO:0050685 positive regulation of mRNA processing;GO:0033120 positive regulation of RNA splicing
81	RNASEK	ribonuclease K	GO:0090502 RNA phosphodiester bond hydrolysis, endonucleolytic;GO:0090501 RNA phosphodiester bond hydrolysis;GO:0090305 nucleic acid phosphodiester bond hydrolysis
82	RNASEK-C17orf49	RNASEK-C17orf49 readthrough	
83	RORA	RAR related orphan receptor A	GO:0021702 cerebellar Purkinje cell differentiation;GO:0072539 T-helper 17 cell differentiation;GO:0021694 cerebellar Purkinje cell layer formation
84	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	GO:0050869 negative regulation of B cell activation;GO:0050732 negative regulation of peptidyl-tyrosine phosphorylation;GO:0002820 negative regulation of adaptive immune response

85	SGK1	serum/glucocorticoid regulated kinase 1	GO:0070294 renal sodium ion absorption;GO:0003096 renal sodium ion transport;GO:0060453 regulation of gastric acid secretion
86	SKA1	spindle and kinetochore associated complex subunit 1	GO:0031110 regulation of microtubule polymerization or depolymerization;GO:0031109 microtubule polymerization or depolymerization;GO:0070507 regulation of microtubule cytoskeleton organization
87	SLC15A3	solute carrier family 15 member 3	GO:0035672 oligopeptide transmembrane transport;GO:0006857 oligopeptide transport;GO:1902600 proton transmembrane transport
88	SLC2A3	solute carrier family 2 member 3	GO:0019852 L-ascorbic acid metabolic process;GO:0043312 neutrophil degranulation;GO:1904659 glucose transmembrane transport
89	SSU72	SSU72 homolog, RNA polymerase II CTD phosphatase	GO:0070940 dephosphorylation of RNA polymerase II C-terminal domain;GO:0006369 termination of RNA polymerase II transcription;GO:0006378 mRNA polyadenylation
90	TARP	TCR gamma alternate reading frame protein	
91	TCIRG1	T cell immune regulator 1, ATPase H ⁺ transporting V0 subunit a3	GO:0097188 dentin mineralization;GO:0090383 phagosome acidification;GO:0035711 T-helper 1 cell activation
92	TMEM45A	transmembrane protein 45A	
93	TMSB10	thymosin beta 10	GO:0042989 sequestering of actin monomers;GO:0030837 negative regulation of actin filament polymerization;GO:0032272 negative regulation of protein polymerization
94	TNFRSF10A	TNF receptor superfamily member 10a	GO:0036462 TRAIL-activated apoptotic signaling pathway;GO:0007250 activation of NF-kappaB-inducing kinase activity;GO:1902042 negative regulation of extrinsic apoptotic signaling pathway via death domain receptors
95	TPM3	tropomyosin 3	GO:0030049 muscle filament sliding;GO:0033275 actin-myosin filament sliding;GO:0070252 actin-mediated cell contraction

96	NCOR2	nuclear receptor corepressor 2	GO:1903799 negative regulation of production of miRNAs involved in gene silencing by miRNA;GO:0060766 negative regulation of androgen receptor signaling pathway;GO:0060965 negative regulation of gene silencing by miRNA
97	TRAJ17	T cell receptor alpha joining 17	
98	TRAV20	T cell receptor alpha variable 20	GO:0002250 adaptive immune response;GO:0006955 immune response;GO:0002376 immune system process
99	TRBC1	T cell receptor beta constant 1	GO:0006958 complement activation, classical pathway;GO:0050853 B cell receptor signaling pathway;GO:0050852 T cell receptor signaling pathway
100	TRBV19	T cell receptor beta variable 19	GO:0002250 adaptive immune response;GO:0006955 immune response;GO:0007166 cell surface receptor signaling pathway
101	TRBV7-2	T cell receptor beta variable 7-2	GO:0002250 adaptive immune response;GO:0006955 immune response;GO:0007166 cell surface receptor signaling pathway
102	TRDV2	T cell receptor delta variable 2	GO:0002377 immunoglobulin production;GO:0002440 production of molecular mediator of immune response;GO:0002250 adaptive immune response
103	EIPR1	EARP complex and GARP complex interacting protein 1	GO:1905281 positive regulation of retrograde transport, endosome to Golgi;GO:2001137 positive regulation of endocytic recycling;GO:1905279 regulation of retrograde transport, endosome to Golgi
104	TXLNGY	taxilin gamma pseudogene, Y-linked	
105	VAMP8	vesicle associated membrane protein 8	GO:1903595 positive regulation of histamine secretion by mast cell;GO:1903593 regulation of histamine secretion by mast cell;GO:0043308 eosinophil degranulation
106	RAB6D	RAB6D, member RAS oncogene family	GO:0006891 intra-Golgi vesicle-mediated transport;GO:0006890 retrograde vesicle-mediated transport, Golgi to ER;GO:0042147 retrograde transport, endosome to Golgi
107	ZC3H12C	zinc finger CCCH-type containing 12C	GO:0090305 nucleic acid phosphodiester bond hydrolysis;GO:0090304 nucleic acid metabolic

			process;GO:0006139 nucleobase-containing compound metabolic process
108	ZNF618	zinc finger protein 618	