

Figure S1. Percentages of $\gamma\delta$ T cells positive for V δ 1, V δ 2, V δ 3 and V γ 9 according to gestation age.

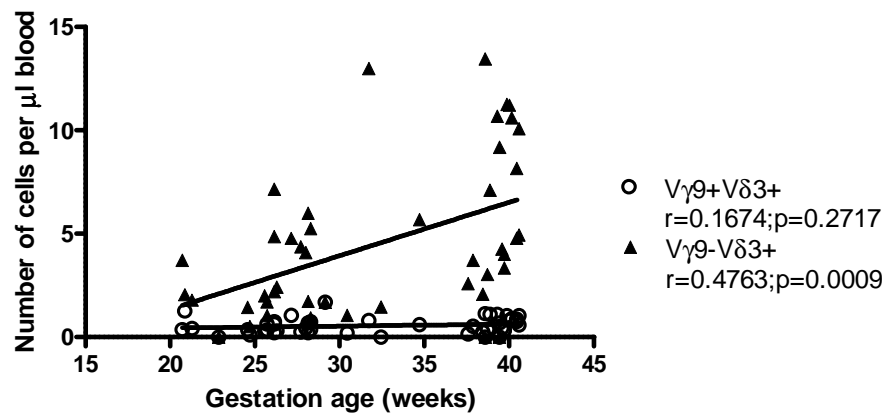
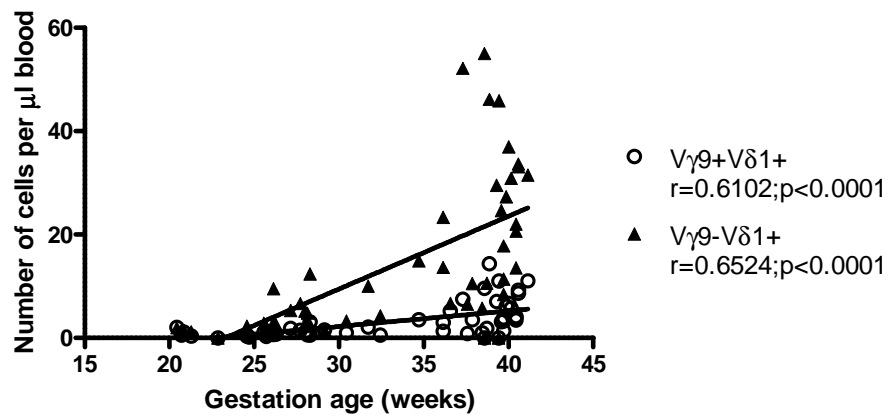
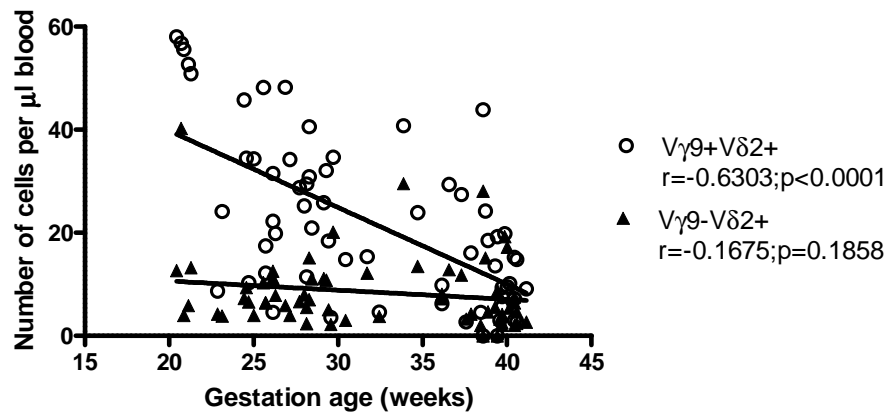


Figure S2. Absolute number counts of $\gamma\delta$ T cell subsets according to gestation age.

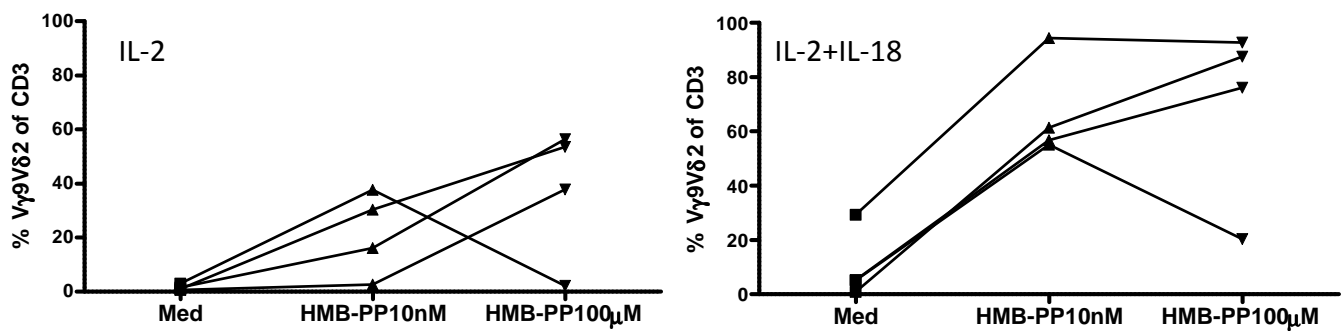


Figure S3. Incubation with 100 μ M HMB-PP in the presence of IL-2+IL-18 results in the highest expansion of fetal V γ 9V δ 2 T cells. Fetal PBMC (<30 weeks of gestation) were cultured for 10 days with HMB-PP (10 nM or 100 μ M) in the presence of IL-2 (left panel) or in the presence of IL-2+IL-18 (right panel). Each line represents data obtained from one fetal sample.

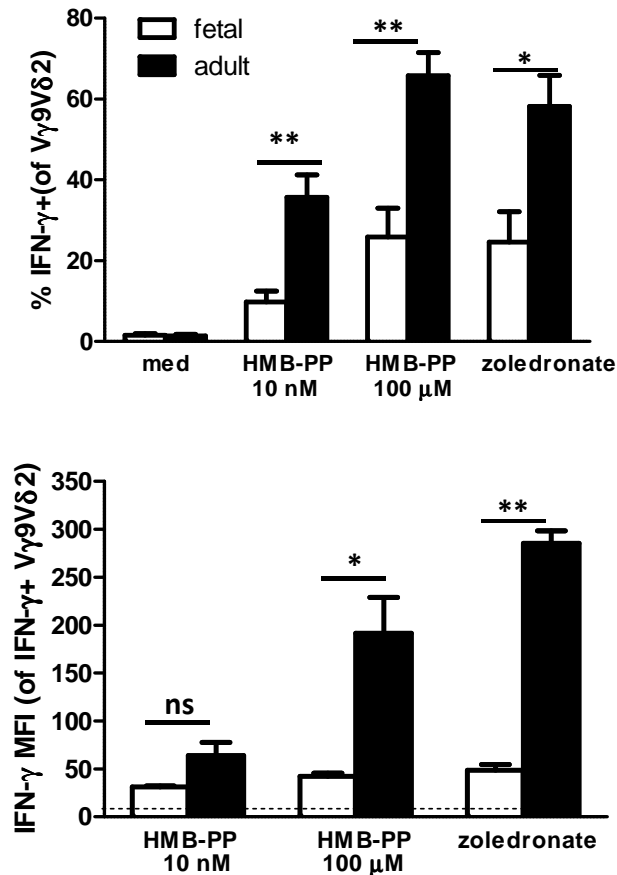


Figure S4. HMB-PP and zoledronate can induce IFN- γ production in fetal V γ 9V δ 2 T cells but significantly less than in adult V γ 9V δ 2 T cells. Fetal (<30 weeks of gestation) and adult PBMC were stimulated for 3 days with HMB-PP and zoledronate in the presence of IL-2. Top panel: percentage of V γ 9V δ 2 T cells positive for IFN- γ (fetal: n=5, adult: n=6); bottom panel: MFI of IFN- γ from the IFN- γ positive V γ 9V δ 2 T cells (fetal and adult: n=3). The total MFI for IFN- γ in the medium control was around 8, as indicated by the dashed line. Gate was put on CD3+ γ δ +V γ 9+V δ 2+ cells; IFN- γ induction was only observed in the V γ 9V δ 2 T cell subset. Mean values with SEM are shown.

Table S1A. Primer sequences used for spectratyping and sequencing
5'-3'

Cδ	GTAGAATTCCTCACCAG-ACAAG
Vδ1	CTGTCAACTTCAAGAAA-GCAGCGAAATC
Vδ2	ATACCGAGAAAAG GACATCTATG
Vδ3	GTACCGGATAAGGCCAGATTA
Cγ	CAAGAA GACAAAGGTATGTTCCAG
Vγ2	GCAAGCACAAAGGAASAAC TTGAG
Vγ3	GTACTATGACGTCTCCACCG
Vγ4	ATGACTCCTACACCTCCAGC
Vγ5/3	CCCAGGAGGTGGAGCTGGAT
Vγ9	ATCAACGCTGGCAGTCC
Run-off reaction (spectratyping):	
Cδ-FAM	ACGGATGGTTTGGTATGAG GCTGA
Cγ-FAM	AATAGTGGGCTTGGGGAAAC

Table S1B. Primer sequences used to quantify gene expression within sorted fetal blood Vγ9Vδ2 and αβ T cells
5'-3'

GZMA-F	ATT-CTT-GGG-GCT-CAC-TCA-ATA-AC
GZMA-R	GGG-TCA-TAG-CAT-GGA-TAG-GGA-AA
GZMB-F	CCC-TGG-GAA-AAC-ACT-CAC-ACA
GZMB-R	GCA-CAA-CTC-AAT-GGT-ACT-GTC-G
GZMH-F	CTG-GCT-GGG-GTT-ATG-TCT-CAA
GZMH-R	GGC-TAC-GTC-CTT-ACA-CAC-GAG
GZMK-F	GGG-GCT-TAT-ATG-ACT-CAT-GTG-TG
GZMK-R	GTG-GAT-CAA-TCA-GAA-CAC-CTC-C
GZMM-F	ACA-CCC-GCA-TGT-GTA-ACA-ACA
GZMM-R	GGA-GGC-TTG-AAG-ATG-TCA-GTG
IFNG-F	TCG-GTA-ACT-GAC-TTG-AAT-GTC-CA
IFNG-R	TCG-CTT-CCC-TGT-TTT-AGC-TGC
IL2-F	AAC-TCC-TGT-CTT-GCA-TTG-CAC
IL2-R	GCT-CCA-GTT-GTA-GCT-GTG-TTT
TNFA-F	CCT-CTC-TCT-AAT-CAG-CCC-TCT-G
TNFA-R	GAG-GAC-CTG-GGA-GTA-GAT-GAG
IL4-F	CCA-ACT-GCT-TCC-CCC-TCT-G
IL4-R	TCT-GTT-ACG-GTC-AAC-TCG-GTG
IL17A-F	AGA-TTA-CTA-CAA-CCG-ATC-CAC-CT
IL17A-R	GGG-GAC-AGA-GTT-CAT-GTG-GTA
Tbet-F	TTG-AGG-TGA-ACG-ACG-GAG-AG
Tbet-R	CCA-AGG-AAT-TGA-CAG-TTG-GGT
eomes-F	GTG-CCC-ACG-TCT-ACC-TGT-G
eomes-R	CCT-GCC-CTG-TTT-CGT-AAT-GAT
Runx3-F	AGC-ACC-ACA-AGC-CAC-TTC-AG
Runx3-R	GGG-AAG-GAG-CGG-TCA-AAC-TG
PLZF-F	GAA-GCG-GTT-CCT-GGA-TAG-TTT-G
PLZF-R	CAC-CGC-ACT-GAT-CAC-AGA-CAA
IL18RAP-F	CTG-GAT-TGA-AAT-AGT-GCT-GCT-GTA-C
IL18RAP-R	TGC-ATA-GGA-TAC-GAA-AGC-ATC-AAA
NKp30-F	TGG-ATT-CTA-TGC-TGT-CAG-CTT-TCT
NKp30-R	GGT-CAG-ACA-TTT-GCC-CTG-GTA
perforin-F	GAC-TGC-CTG-ACT-GTC-GAG-G
perforin-R	TCC-CGG-TAG-GTT-TGG-TGG-AA
CCR5-F	TTC-TGG-GCT-CCC-TAC-AAC-ATT
CCR5-R	TTG-GTC-CAA-CCT-GTT-AGA-GCT-A
CXCR3-F	CCA-CCT-AGC-TGT-AGC-AGA-CAC
CXCR3-R	AGG-GCT-CCT-GCG-TAG-AAG-TT
CCR7-F	TGA-GGT-CAC-GGA-CGA-TTA-CAT
CCR7-R	GTA-GGC-CCA-CGA-AAC-AAA-TGA-T
cyclophilin-F	TGC-TGG-ACC-CAA-CAC-AAA-TG
cyclophilin-R	TGC-CAT-CCA-ACC-ACT-CAG-TCT
actin-F	CCC-AGC-CAT-GTA-CGT-TGC-TA
actin-R	TCA-CCG-GAG-TCC-ATC-ACG-AT

(Table S2, continued)

Panel	Row	Date	Sequence	Panel	Row	Date	Sequence	Panel	Row	Date	Sequence		
GD-006 29w0d	10	1/16	tgt gcc ttg tgg gag gtg C A L W E V	c P	10	1/16	atg tgc a L C	c P	10	1/16	atg tgc a L C		
	11	1/16	tgt gcc ttg tgg ga C A L W E V			11	1/16			g D	11	1/16	atg tgc a L C
	11	1/16	tgt gcc ttg tgg gag C A L W E			11	1/16			g V	11	1/16	atg tgc a L C
	12	1/16	tgt gcc ttg tgg gag gtg C A L W E V			11	1/16			g V	11	1/16	atg tgc a L C
	12	1/16	tgt gcc ttg tgg gag gtg C A L W E V			12	1/18			gtc aat V N	12	1/18	atg tgc a L C
	13	1/16	tgt gcc ttg tgg gag C A L W E			13	3/18			gg R	13	3/18	atg tgc a L C
	13	1/16	tgt gcc ttg tgg gag C A L W E			14	5/18			cac H	14	5/18	atg tgc a L C
	14	6/16	tgt gcc ttg tgg gag gtg C A L W E V			14	1/18			t at M	14	1/18	atg tgc a L C
	14	1/16	tgt gcc ttg tgg gag gtg C A L W E V			14	1/18			cc P	14	1/18	atg tgc a L C
	14	1/16	tgt gc C A			14	1/18			ga E	14	1/18	atg tgc a L C
15	1/16	tgt gcc ttg tgg gag C A L W E	16	1/18	gt cga tat tcc tat acc acg G R Y S Y T T	16	1/18	atg tgc a L C					
GD-012 30w3d	9	1/18	tgt gcc ttg tgg C A L W	c P	9	1/18	atg tgc a L C	c P	9	1/18	atg tgc a L C		
	10	1/18	tgt gcc ttg tgg gag gtg C A L W E V			10	1/18			g D	10	1/18	atg tgc a L C
	10	1/18	tgt gcc ttg tgg g C A L W			10	1/18			g V	10	1/18	atg tgc a L C
	10	1/18	tgt gcc ttg tgg C A L W			10	1/18			gtc aat V N	10	1/18	atg tgc a L C
	11	1/18	tgt gcc ttg tgg gag gtg C A L W E V			11	1/18			gg R	11	1/18	atg tgc a L C
	13	3/18	tgt gcc ttg tgg gag C A L W E			13	3/18			gg R	13	3/18	atg tgc a L C
	14	5/18	tgt gcc ttg tgg gag gtg C A L W E V			14	5/18			cac H	14	5/18	atg tgc a L C
	14	1/18	tgt gcc ttg tgg gag gtg C A L W E V			14	1/18			t at M	14	1/18	atg tgc a L C
	14	1/18	tgt gcc ttg tgg gag gtg C A L W E V			14	1/18			cc P	14	1/18	atg tgc a L C
	14	1/18	tgt gcc ttg tgg C A L W			14	1/18			ga E	14	1/18	atg tgc a L C
16	1/18	tgt gcc ttg tgg gag g C A L W E	16	1/18	gt cga tat tcc tat acc acg G R Y S Y T T	16	1/18	atg tgc a L C					

Grey shading indicates the highly enriched public/invariant CDR3y9 CALWEVQELGKKIKVF sequence.

Table S3
Sequencing data of the CDR3y9 of sorted V γ 9V δ 2 $\gamma\delta$ T cells and nonV γ 9V δ 2 $\gamma\delta$ T cells from peripheral blood
of three different fetuses before 30 weeks of gestation

	CDR3g9 length (aa)	Freq.	3'V-REGION	P3'V	N-REGION	P5'J	5'J-REGION	JUNCTION (aa)	J-GENE
GD-018 V γ 9V δ 2	9	1/10	tgtgccttgaggaggt		cc		ggttcaagatatt	CALWEVRFKIF	TRGJP1
	11	1/10	tgtgccttgaggag				ttggc caaaaaatcaaggtatt	CALWELGKKIKVF	TRGJP
	12	1/10	tgtgccttgaggaggtg		aa		gaattataagaactctt	CALWEVKNYKKLF	TRGJ1
	13	1/10	tgtgccttgaggag		aag		gagttggc caaaaaatcaaggtatt	CALWEKELGKKIKVF	TRGJP
	13	1/10	tgtgccttgaggag				aagagttggc caaaaaatcaaggtatt	CALWEEELGKKIKVF	TRGJP
	14	5/10	tgtgccttgaggaggtg				caagagttggc caaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP
	out of frame		tgtgccttgaggag		gggggaagtgggc		aaaaaatcaaggtatt	CALWEGGKLGKKSRY	TRGJP
GD-018 nonV γ 9V δ 2	9	1/13	tgtgccttgaggag		ag		tataagaactctt	CALWEEYKFLF	TRGJ1
	10	1/13	tgtgccttgagg				aattataagaactctt	CALWNYKKLF	TRGJ1
	10	1/13	tgtgccttgaggaggtg				tattataagaactctt	CALWEVYKFLF	TRGJ1 or TRGJ2
	14	1/13	tgtgccttgaggaggtg		agg		gagttggc caaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP
	14	1/13	tgtgccttgaggaggtg		agg		gagttggc caaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP
	14	1/13	tgtgccttgaggaggtg		agggagttggccaag		aaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP
	14	1/13	tgtgccttgagg		cga		ggccaagagttggc caaaaaatcaaggtatt	CALWARQELGKKIKVF	TRGJP
	14	1/13	tgtgccttgagg		cga		ggccaagagttggc caaaaaatcaaggtatt	CALWARQELGKKIKVF	TRGJP
	14	1/13	tgtgccttgagg		cga		ggccaagagttggc caaaaaatcaaggtatt	CALWARQELGKKIKVF	TRGJP
	14	1/13	tgtgccttgagg		aatcaagt		agagttggc caaaaaatcaaggtatt	CALWENQVELGKKIKVF	TRGJP
	15	2/13	tgtgccttgaggag		caagagttggcca		aaaaaatcaaggtatt	CALQELGKKNQGI	TRGJP
		out of frame		tgtgccttgaggag			taccactggtggttcaagatatt	CALWEYHVLVQDI	TRGJP1
GD-019 V γ 9V δ 2	11	2/8	tgtgccttgaggaggt		ctc		ttattataagaactctt	CALWEVSYYKFLF	TRGJ1
	12	1/8	tgtgccttgaggag			t	ataccactggtggttcaagatatt	CALWEYTTGWFKIF	TRGJP1
	13	1/8	tgtgccttgaggag				caagagttggc caaaaaatcaaggtatt	CALWEQELGKKIKVF	TRGJP
	14	2/8	tgtgccttgaggaggtg				caagagttggc caaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP
	14	1/8	tgtgccttgaggaggtg	c	g		agagttggc caaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP
	15	1/8	tgtgccttgaggag		ccagga		caagagttggc caaaaaatcaaggtatt	CALWEPQELGKKIKVF	TRGJP
GD-019 nonV γ 9V δ 2	9	1/8	tgtgccttgaggag		cctgg		ataagaactctt	CALWDLDKLFLF	TRGJ1 or TRGJ2
	10	1/8	tgtgccttgaggaggt		aa		attataagaactctt	CALWEVNYKFLF	TRGJ1 or TRGJ2
	16	1/8	tgtgccttgaggaggt		tgggccc		caagagttggc caaaaaatcaaggtatt	CALWEVGPQELGKKIKVF	TRGJP
	out of frame		tgtgccttgaggag		g		agtagtattggtatcaagacgtt	CALWEGVIGSRR	TRGJP2
	out of frame		tgtgccttgaggaggtg	c	gatgcaa		tattataagaactctt	CALWEVRCNIIRNS	TRGJ1
	out of frame		tgtgccttgaggaggtg		cgcaacctc	at	ataccactggtggttcaagatatt	CALWEAQPHIPLVGSRY	TRGJP1
out of frame		tgtgccttgaggag		acgcccacttc		aattataagaactctt	CALWETPKLSIIIRNS	TRGJ1	
out of frame		tgtgccttgaggaggtg		g		agtagtattggtatcaagacgtt	CALWEGVIGSRR	TRGJP2	
GD-023 V γ 9V δ 2	11	1/7	tgtgccttgaggag				ttggc caaaaaatcaaggtatt	CALWELGKKIKVF	TRGJP
	13	1/7	tgtgccttgaggaggtg				gagttggc caaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP
	13	1/7	tgtgccttgaggaggt				agagttggc caaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP
	13	1/7	tgtgccttgaggag				caagagttggc caaaaaatcaaggtatt	CALWEQELGKKIKVF	TRGJP
	14	1/7	tgtgccttgaggaggtg		atcgg		gtggc caaaaaatcaaggtatt	CALWEVIGLGGKIKVF	TRGJP
	14	2/7	tgtgccttgaggaggtg				caagagttggc caaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP
	out of frame		tgtgccttgaggag		caagagttggcca		aaaaaatcaaggtatt	CALWEQELGKKNQGI	TRGJP
GD-023 nonV γ 9V δ 2	11	1/10	tgtgccttgaggaggtg		agg		tattataagaactctt	CALWEVRYKFLF	TRGJ2
	11	1/10	tgtgcct				ggccaagagttggc caaaaaatcaaggtatt	CAWQELGKKIKVF	TRGJP
	12	2/10	tgtgccttgaggaggtg		agaggc		tattataagaactctt	CALWEVRYKFLF	TRGJ1
	12	2/10	tgtgccttgaggaggtg	ca			tagtgattggtatcaagacgtt	CALWEVHSDWIKTF	TRGJP2
	15	2/10	tgtgccttgaggag		ccatt		gcaagagttggc caaaaaatcaaggtatt	CALWEPLQELGKKIKVF	TRGJP
	16	2/10	tgtgccttgaggaggtg	ca	gacggaga		agttggc caaaaaatcaaggtatt	CALWEVQTEKLGKIKVF	TRGJP
	out of frame		tgtgccttgaggag		tg		aagagttggc caaaaaatcaaggtatt	CALWE*RVGQKNQGI	TRGJP
	out of frame		tgtgccttgaggaggtg		acca		aagaactctt	CALWEVTKETL	TRGJ1 or TRGJ2
	out of frame		tgtgccttgaggaggtg		acca		aagaactctt	CALWEVTKETL	TRGJ1 or TRGJ2
	out of frame		tgtgccttgaggaggtg		acca		aagaactctt	CALWEVTKETL	TRGJ1 or TRGJ2
	out of frame		tgtgccttgaggaggtg		acca		aagaactctt	CALWEVTKETL	TRGJ1 or TRGJ2

Grey shading: public/invariant CDR3y9 sequence CALWEVQELGKKIKVF

Table S4
Sequencing data of the CDR3_{γ9} of three different fetuses (< 30 weeks gestation) before (ex-vivo) and after
HMB-PP-induced proliferation

	CDR3 length (aa)	Freq.	3'V-REGION	P3'V	N-REGION	P5'J	5'-J-REGION	JUNCTION (aa)	J-GENE	
GD-002 Ex-vivo	9	1/18	tggtccttgaggagg		ggatg		gaaactctt	CALWEVGVKLF	TRGJ1	
	10	2/18	tggtccttg		ctgtg		cactggttggtcaagatatt	CALRVGTGWFKIF	TRGJP1	
	11	1/18	tggtccttg				agagttggccaaaaaatcaaggtatt	CAL*ELGKKIKVF	TRGJP	
	12	1/18	tggtccttgagg		ccttca		aattataagaactctt	CALWEPSNYKKLF	TRGJ2	
	12	1/18	tggtccttg		caagagtgggcag		aaaaatcaaggtatt	CALWQELGRKIKVF	TRGJP	
	13	1/18	tggtccttgagg				aagagtggccaaaaaatcaaggtatt	CALWEEELGKKIKVF	TRGJP	
	13	1/18	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWQELGKKIKVF	TRGJP	
	13	1/18	tggtccttgagg	c			agttggccaaaaaatcaaggtatt	CALWEVQLGKKIKVF	TRGJP	
	13	1/18	tggtccttgagg				gagttggccaaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP	
	14	1/18	tggtccttgagg	c	gg		gagttggccaaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP	
	14	5/18	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	14	1/18	tggtccttgagg	ca	ag		atacactggttcaagatatt	CALWEVDTTGWFKIF	TRGJP1	
	15	1/18	tggtccttgagg		ga		gcaagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	GD-002 After HMB-PP- induced proliferation	10	1/11	tggtccttgagg		cgcg		attataagaactctt	CALWERDYKLF	TRGJ1
		11	1/11	tggtccttgagg				aattataagaactctt	CALWEVNYKKLF	TRGJ2
13		1/11	tggtccttgagg		t		gagttggccaaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP	
14		4/11	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
14		1/11	tggtccttgagg		t		caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
14		1/11	tggtccttgagg	ca	ggg		gtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
15		1/11	tggtccttgagg	ca	tac		agagttggccaaaaaatcaaggtatt	CALWEVHTELGKKIKVF	TRGJP	
15		1/11	tggtccttgagg	c			ggcaagagtggccaaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP	
15		1/11	tggtccttgagg		cccccc		caagagtggccaaaaaatcaaggtatt	CALWEPPQELGKKIKVF	TRGJP	
GD-011 Ex-vivo	9	1/9	tggtccttg		ag		gaattataagaactctt	CALRNYKKLF	TRGJ2	
	10	1/9	tggtccttgagg		ctcg		attataagaactctt	CALWEPDYKLF	TRGJ1	
	11	1/9	tggtccttg		g		aagagtggccaaaaaatcaaggtatt	CALWELGKKIKVF	TRGJP	
	13	1/9	tggtccttgagg				agagttggccaaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP	
	13	1/9	tggtccttgagg		ca		caagagtggccaaaaaatcaaggtatt	CALWAQELGKKIKVF	TRGJP	
	14	3/9	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	15	1/9	tggtccttgagg	ca	ggg		agagttggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
out of frame		tggtccttgagg		agggtc		aagaactctt	CALWEGSRNS	TRGJ1 or TRGJ2		
out of frame		tggtccttgagg		tc		aagaactctt	CALWDQETL	TRGJ1 or TRGJ2		
out of frame		tggtccttgagg	ca	agag		actctt	CALWEVQETL	TRGJ1 or TRGJ2		
GD-011 After HMB-PP- induced proliferation	12	1/11	tggtccttgagg		gt		gagttggccaaaaaatcaaggtatt	CALWVQELGKKIKVF	TRGJP	
	12	1/11	tggtccttgagg		a		aagagtggccaaaaaatcaaggtatt	CALWVQELGKKIKVF	TRGJP	
	12	1/11	tggtccttgagg				agttggccaaaaaatcaaggtatt	CALWEEELGKKIKVF	TRGJP	
	13	1/11	tggtccttgagg				aagagtggccaaaaaatcaaggtatt	CALWEEELGKKIKVF	TRGJP	
	14	4/11	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	14	1/11	tggtccttgagg	ca	g		gagttggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	14	1/11	tggtccttgagg		at		caagagtggccaaaaaatcaaggtatt	CALWEDQELGKKIKVF	TRGJP	
14	1/11	tggtccttgagg		a		aagagtggccaaaaaatcaaggtatt	CALWEVKELGKKIKVF	TRGJP		
GD-013 Ex-vivo	11	1/12	tggtccttgagg				laccactggttcaagatatt	CALWDTTGWFKIF	TRGJP1	
	11	1/12	tggtccttgagg	ca	ggga		tataagaactctt	CALWEVQYKLF	TRGJ1	
	11	1/12	tggtccttgagg	c			attataagaactctt	CALWEVHYKKLF	TRGJ1	
	12	1/12	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWQELGKKIKVF	TRGJP	
	13	1/12	tggtccttgagg				gagttggccaaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP	
	14	6/12	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	14	1/12	tggtccttgagg	c	cc		gagttggccaaaaaatcaaggtatt	CALWEVPELGGKIKVF	TRGJP	
	out of frame		tggtccttgagg		agtggc		tcaaggtatt	CAL*VGQKSQGI	TRGJP	
GD-013 After HMB-PP- induced proliferation	13	1/11	tggtccttgagg	c			agttggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	13	1/11	tggtccttgagg				gagttggccaaaaaatcaaggtatt	CALWEVELGKKIKVF	TRGJP	
	14	6/11	tggtccttgagg				caagagtggccaaaaaatcaaggtatt	CALWEVQELGKKIKVF	TRGJP	
	14	2/11	tggtccttgagg	c	g		agagttggccaaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP	
	14	1/11	tggtccttgagg	c	gg		gagttggccaaaaaatcaaggtatt	CALWEVRELGKKIKVF	TRGJP	

Grey shading: public/invariant CDR3_{γ9} sequence CALWEVQELGKKIKVF

Table S5. Percentages of activation (HLA-DR) and differentiation (CD27, CD28, CD45RO) markers, NKR (CD94, NKG2A, NKG2C, CD158, NKG2D, CD161 and KLRG1), granule-associated molecules (perforin, granzyme A, granzyme B, granzyme K and granulysin), chemokine receptors (CCR5, CCR6, CCR7, CCR9 and CX3CR1), transcription factors (T-bet and eomes) and cytokines (IFN- γ , IL-2, TNF- α after 4h stimulation with PMA/ionomycin) on fetal blood $\gamma\delta$ and $\alpha\beta$ T cells at mid-gestation.

Marker	$\gamma\delta$ T cells - mean \pm SD (min-max)	$\alpha\beta$ T cells - mean \pm SD (min-max)	p value ($\gamma\delta$ vs $\alpha\beta$), n
HLA-DR	1.28 \pm 0.82 (0.47-3.00)	0.45 \pm 0.26 (0.18-1.04)	p=0.031, n=9
CD27-CD28-	0.58 \pm 0.47 (0.00-1.22)	0.80 \pm 0.90 (0.04-2.05)	p>0.05, n=5
CD45RO	32.13 \pm 12.37 (18.04-55.60)	9.04 \pm 4.96 (5.00-19.68)	p<0.001, n=11
Ki-67	15.02 \pm 4.02 (8.40-22.03)	11.83 \pm 4.96 (4.70-21.00)	p=0.042, n=12
CD94	9.22 \pm 5.39 (3.07-19.11)	0.29 \pm 0.17 (0.10-0.56)	p<0.01, n=7
NKG2A	18.03 \pm 17.70(5.00-63.45)	3.44 \pm 5.86 (0.21-18.20)	p<0.01, n=10
NKG2C	2.23 \pm 2.19 (0.14-7.64)	0.24 \pm 0.10 (0.12-0.44)	p =0.016, n=10
CD158a	6.14 \pm 5.39 (1.55-16.70)	0.64 \pm 0.60 (0.09-1.85)	p<0.01, n=11
CD158b	6.24 \pm 5.93 (1.28-17.40)	0.90 \pm 0.68 (0.19-2.24)	p=0.013, n=11
NKG2D	50.29 \pm 19.80 (15-83.32)	25.08 \pm 14.18 (3.00-46.15)	p<0.001, n=10
CD161	67.24 \pm 9.55 (57.14-84.05)	8.48 \pm 3.16 (3.01-12.26)	p<0.001, n=6
KLRG1	49.77 \pm 15.41 (25.53-67.34)	27.85 \pm 14.29 (4.31-47.23)	p<0.001, n=8
perforin	1.64 \pm 0.86 (0.40-2.54)	0.70 \pm 0.77 (0.15-2.34)	p=0.029, n=7
Granzyme A	47.75 \pm 21.35 (11.73-94.15)	2.61 \pm 3.67 (0.44-14.25)	p<0.001, n=19
Granzyme B	1.54 \pm 0.90 (0.60-3.49)	1.50 \pm 2.01 (0.18-6.70)	p>0.05, n=11
Granzyme K	45.35 \pm 10.50 (29.97-61.61)	1.71 \pm 1.62 (0.39-4.03)	p<0.001, n=6
Granulysin	1.17 \pm 0.76 (0.10-2.56)	1.07 \pm 1.12 (0.13-4.00)	p>0.05, n=11
CCR5	19.62 \pm 8.15 (10.48-28.44)	1.06 \pm 0.89 (0.38-2.52)	p<0.01, n=5
CCR6	12.40 \pm 5.03 (6.44-18.51)	2.87 \pm 0.59 (2.26-3.63)	p=0.023, n=4
CCR7	66.65 \pm 4.13 (60.79-70.47)	94.39 \pm 2.48 (91.04-96.32)	p<0.01, n=4
CCR9	4.36 \pm 1.70 (2.25-6.40)	0.90 \pm 0.62 (0.34-1.77)	P<0.01, n=4
CX3CR1	4.45 \pm 2.46 (1.62-6.08)	0.78 \pm 0.45 (0.35-1.25)	P> 0.05, n=3
T-bet	42.44 \pm 10.72 (23.00-61.27)	3.73 \pm 4.65 (0.41-12.00)	p<0.001, n=12
Eomes	45.35 \pm 3.23 (41.87-51.86)	6.97 \pm 5.04 (0.48-17.20)	p<0.001, n=12
IFN- γ	26.45 \pm 5.44 (17.54-32.42)	1.58 \pm 2.01 (0.34-7.11)	p<0.001, n=10
IL-2	7.39 \pm 1.52 (5.19-9.50)	32.66 \pm 7.27 (20.61-40.35)	p<0.001, n=7
TNF- α	5.66 \pm 4.12 (0.10-11.83)	2.85 \pm 1.65 (1.18-5.78)	p=0.051, n=6
IL-4	Not detected	Not detected	
IL-17	Not detected	Not detected	

Table S6. Gene expression analysis (microarray) of sorted fetal blood V γ 9V δ 2 T cells and $\alpha\beta$ T cells (<30 weeks of gestation).

Symbol	Illumina ID	M	p	
Chemokines, cytokines and receptors				
IL18RAP	ILMN_1721762	2.47	0.0000001	
CCL5 (RANTES)	ILMN_1773352	1.84	0.0000001	
CXCR4	ILMN_1801584	1.22	0.0000439	
CXCR3	ILMN_1797975	0.86	0.0000299	
CD84 (SLAMF5)	ILMN_1698367	0.69	0.0005255	
CCR4	ILMN_2086143	0.62	0.0003042	
TGFB β 3	ILMN_1784287	0.81	0.0000155	
EBI2	ILMN_1798706	0.71	0.0005299	
IFNG	ILMN_2207291	0.42	0.0007387	
NK: receptors, signaling and granule-associated molecules				
GMP-17 (NKG7)	ILMN_1682993	2.74	0.0000005	
GZMK	ILMN_1710734	2.32	0.0000001	
S1PR5	ILMN_2073184	2.00	0.0000237	
KLRB1, CD161	ILMN_2079655	1.79	<0.0000001	
PRF1	ILMN_1740633	1.51	0.0009307	
PIK3AP1	ILMN_1652787	1.40	0.0000061	
CST7 (cystatin F)	ILMN_1679826	1.36	0.0000823	
STX11	ILMN_1720771	1.25	0.0000149	
ELF4 (MEF)	ILMN_1652082	1.22	0.0000025	
PILRB	ILMN_1768754	1.15	0.0003007	
PLCG2	ILMN_1815719	1.12	0.0000023	
NCR3 (NKp30)	ILMN_2044471	1.00	0.0000441	
HCST (DAP10)	ILMN_1699931	0.94	0.0000913	
PIK3R1 (p85; GRB1)	ILMN_2398235	0.94	0.0003928	
PIK3CG	ILMN_1770433	0.86	0.0006724	
TYROBP (DAP12)	ILMN_1778977	0.84	0.0008443	
FCRL3	ILMN_1797428	0.84	0.0000429	
GZMA	ILMN_1779324	0.79	0.0006917	
FNBP1	ILMN_1797342	0.76	0.0001454	
TXNIP (VDUP1)	ILMN_1697448	0.69	0.0000386	
KLRG1	ILMN_2124920	0.67	0.0003379	
CD247 (CD3zeta)	ILMN_2377669	0.54	0.0001315	
FCRL3	ILMN_1699599	0.51	0.0004603	
GAB3	ILMN_1805979	0.45	0.0002846	
RAC2	ILMN_1709795	0.45	0.000586	
JAKMIP1 (Marlin 1)	ILMN_1784141	0.40	0.0007327	
Transcription factors				
PLZF (ZBTB16)	ILMN_1750496	2.12	<0.0000001	
BHLHB2 (STRA13)	ILMN_1768534	1.84	0.0000018	
NR4A2 (NURR1)	ILMN_2339955	1.36	0.0000025	
BHLHA38 (TWIST1)	ILMN_1672908	1.32	0.0010628	
MAF	ILMN_1719543	1.29	0.0000022	
NR4A3	ILMN_1807298	1.29	0.0002119	
FOSL2	ILMN_1725175	1.25	0.0000022	
MYBL1	ILMN_3241046	1.18	0.0007205	
FOXP4	ILMN_1773809	1.15	0.0001531	
LITAF	ILMN_1713934	0.92	0.0002150	
KLF4	ILMN_2137789	0.92	0.0000836	
JUNB	ILMN_2086077	0.86	0.0001723	
DDX3X (C/EBP delta)	ILMN_1794392	0.84	0.0000454	
BZW1	ILMN_1793846	0.81	0.0000529	
HNRNPUL1	ILMN_3257430	0.81	0.0004457	
RUNX3	ILMN_1787461	0.79	0.0000287	
EGR1	ILMN_1762899	0.76	0.0006082	
KLF10	ILMN_1659122	0.74	0.0000611	
MAFF	ILMN_1680139	0.74	0.0004494	
REL	ILMN_2124064	0.74	0.0003637	
NFIL3	ILMN_1707312	0.64	0.0008908	
KLF2	ILMN_1735930	0.62	0.0007467	
KLF11	ILMN_1751656	0.62	0.0003109	
MYC	ILMN_1680618	0.60	0.0000732	
CDK9	ILMN_1747556	0.58	0.0002243	
HHEX	ILMN_1762712	0.56	0.0002216	
BZW1	ILMN_1704760	0.49	0.0009906	
MLL3	ILMN_2295183	0.47	0.0009164	
SERTAD2	ILMN_1651347	0.45	0.0005114	
Adhesion				
ITGAM (CD11b)	ILMN_1685009	1.15	0.0000027	
CD97	ILMN_1676718	0.45	0.0002600	
AMICA1 (JAML)	ILMN_1778723	0.45	0.0004771	

Lists of increased expressed genes in fetal blood V γ 9V δ 2 T cells compared to fetal blood $\alpha\beta$ T cells (same fetuses) related to 'chemokines, cytokines and their receptors', 'NK cells', 'transcription factors' and 'adhesion molecules'. M (log₂ fold change V γ 9V δ 2/ $\alpha\beta$) reflects the differential expression of a gene. N= 4 fetuses.

■ : gene is also enriched in adult blood V γ 9V δ 2 T cells compared to adult $\alpha\beta$ T cells; based on Pont *et al* (1) comparing four sorted adult blood V γ 9+ T cell samples (NCBI GEO data set under accession number GSE27291) with six sorted adult blood $\alpha\beta$ T cell samples (GSE15659 and GSE8059).

Table S7. Gene expression data of 16 genes from sorted V γ 9V δ 2 T cells compared to the expression within sorted $\alpha\beta$ T cells derived from the same fetuses, as determined by real-time PCR.

Gene	Fetus			
	GD-018	GD-019	GD-020	GD-023
PLZF	5.28	4.65	2.89	3.04
Foxp1	-2.83	-4.49	-2.88	-4.54
T-bet	2.25	11.83	8.13	14.46
Eomes	3.23	2.07	6.10	7.50
Runx3	2.53	0.70	2.59	1.35
IFN- γ	3.76	-2.10	2.56	2.31
IL-2	2.78	-0.34	-4.79	-1.33
TNF- α	0.05	-0.20	-0.18	-0.43
IL18RAP	2.56	10.21	3.98	6.71
NKp30	0.36	2.98	2.69	2.97
perforin	2.83	1.03	2.38	-0.03
granzyme K	4.23	5.53	3.87	3.69
granzyme A	2.38	1.58	2.11	-0.64
CCR5	13.06	7.92	7.08	10.82
CXCR3	2.62	5.19	3.28	1.98
CCR7	-1.11	-2.67	-0.12	-2.48
IL-4	not detected			
IL-13	not detected			
IL-17	not detected			

Data are expressed as log₂ of fold change V γ 9V δ 2/ $\alpha\beta$ for each individual fetus.

Table S8. Gene expression data of selected genes from sorted V γ 9V δ 2 T cells compared to the expression within sorted nonV γ 9V δ 2 $\gamma\delta$ T cells derived from the same fetuses, as determined by real-time PCR.

Gene	Fetus			
	GD-018	GD-019	GD-020	GD-023
T-bet	4.97	1.44	5.64	3.32
Eomes	13.27	5.10	8.43	1.50
IL18RAP	3.86	1.87	-0.31	2.24
perforin	6.46	3.42	1.19	-0.02
granzyme K	1.96	0.89	0.27	2.23
granzyme A	3.95	2.04	1.99	0.84
CCR5	-0.6	8.33	2.04	11.01
CXCR3	1.37	1.16	1.15	1.36

Data are expressed as log₂ of fold change V γ 9V δ 2/nonV γ 9V δ 2 for each individual fetus.

Table S9. Comparison between gene expression enriched in adult (Pont *et al.*, (1)) and fetal (this study) V γ 9V δ 2 T cells

Pont et al: cytokine/receptor	This study	Pont et al: NK cytotoxicity	This study
CCL3		CASP3	
CCL5, RANTES		FASLG	
CCR2		FCGR3A	
CCR5		FCGR3B	
CSF1		GZMB	
CXCL11		IFNG	
CXCL9		KLRC1, NKG2A	
CXCR3		KLRC2, NKG2C	
CXCR6		KLRD1, CD94	
FASL G		KLRK1, NKG2D	
IFNG		PIK3R3	
IL12RB2		PLCG2	
IL15	M=0.40;p=0.005	PRF1	
IL18R1	M=0.40;p=0.021	SHC4	
IL23R		TYROBP, DAP12	
IL2RA		ULBP2	
IL2RB	M=0.71;p=0.002	NKG7	
IL4			
IL9R		Pont et al: Th1	This study
LIF		AUTS2	
TNFRSF11A		CCL3	
TNFRSF12A		CCL3L1	
TNFRSF1B		CCL5, RANTES	
TNFSF14	M=0.45;p=0.019	CD38	
TNFSF4		CXCL9	
TNFSF9		CCR5	
		CXCR3	
Pont et al: Jak/STAT	This study	DNAJC6	
IFNG		GOS2	
IL12RB2		GNLY	
IL15	M=0.40;p=0.005	GZMB	
IL23R		GZMH	
IL2RA		GZMK	
IL2RB		IFNG	
IL4		IL12RB2	
IL9R		IL18RAP	
LIF		IL18R1	M=0.40;p=0.021
PIK3R3		IRF8	
SOCS1		LRP8	
STAT4	M=0.51; p=0.008	PLAUR	
		PRF1	
		TNFRSF1B	

Tables are based on enriched genes in adult V γ 9V δ 2 T cells vs adult $\alpha\beta$ T cells by Pont *et al.* (1)

- :also enriched expression in fetal V γ 9V δ 2 T cells vs fetal $\alpha\beta$ T cells (as analyzed by microarray analysis and/or real-time PCR)
- :indication of enriched expression by microarray analysis (but not meeting the criteria of M>0.4 and p<0.001)

References Appendix

1. Pont F, Familiades, J., Dejean, S., Fruchon, S., Cendron, D. *et al.* (2012) The gene expression profile of phosphoantigen-specific human gammadelta T lymphocytes is a blend of alphabeta T-cell and NK-cell signatures. *Eur. J. Immunol* 42(1):228-240.