

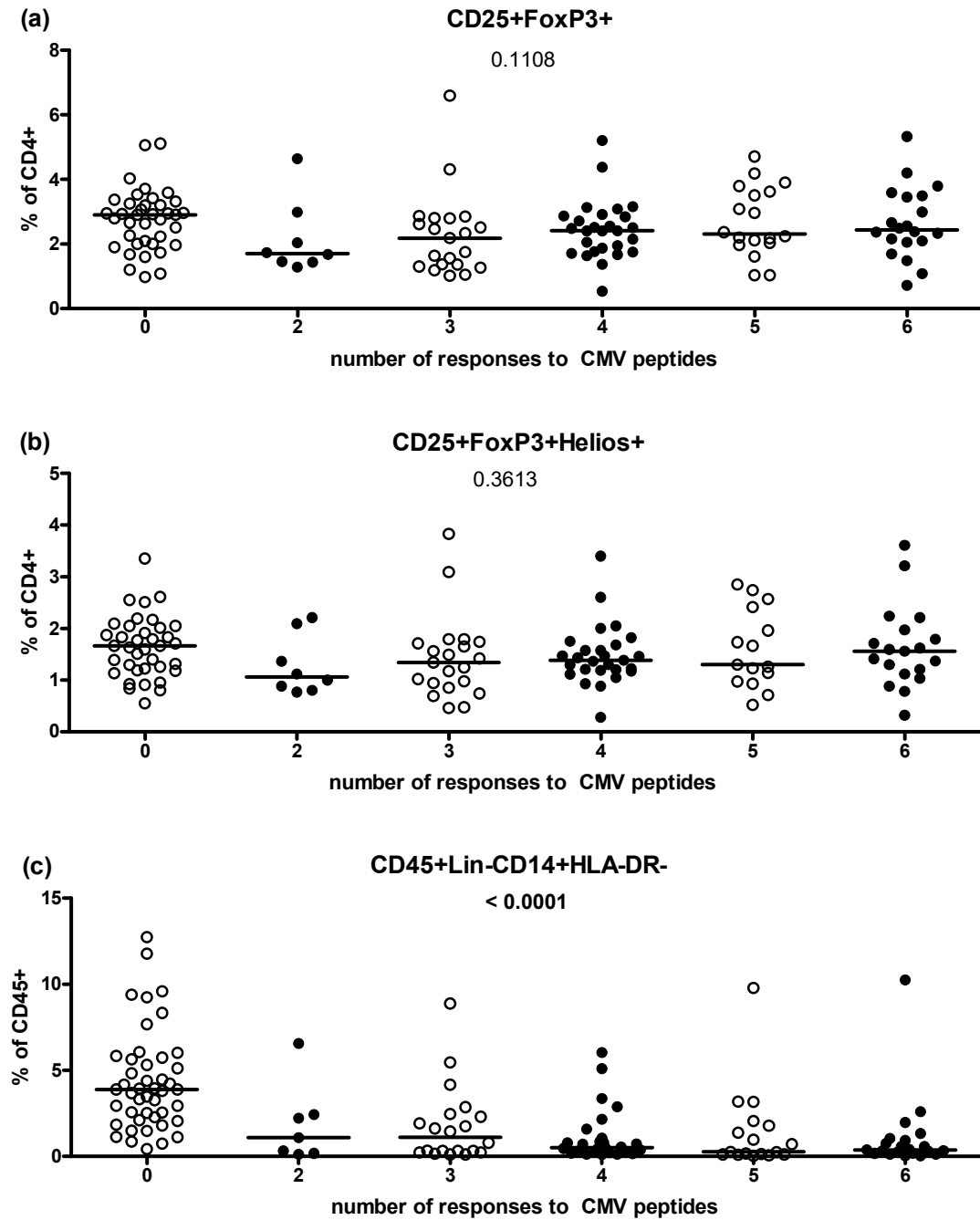
**Table S1.** Characteristics of the study participants; 81 twin pairs, MZ (Monozygotic), DZ (same-sex Dizygotic).

	All	Concordant CMV Seronegative		Concordant CMV Seropositive		CMV Discordant	
		MZ	DZ	MZ	DZ	MZ	DZ
Pairs	81	8	8	23	21	11	10
Gender <sup>1</sup>	124/38	7F/1M	7F/1M	16F/7M	17F/4M	8F/3M	7F/3M
Median age in years	48	44.5	47	48	49	44	58
Age range	41–77	42–47	44–72	41–70	41–77	41–59	43–73

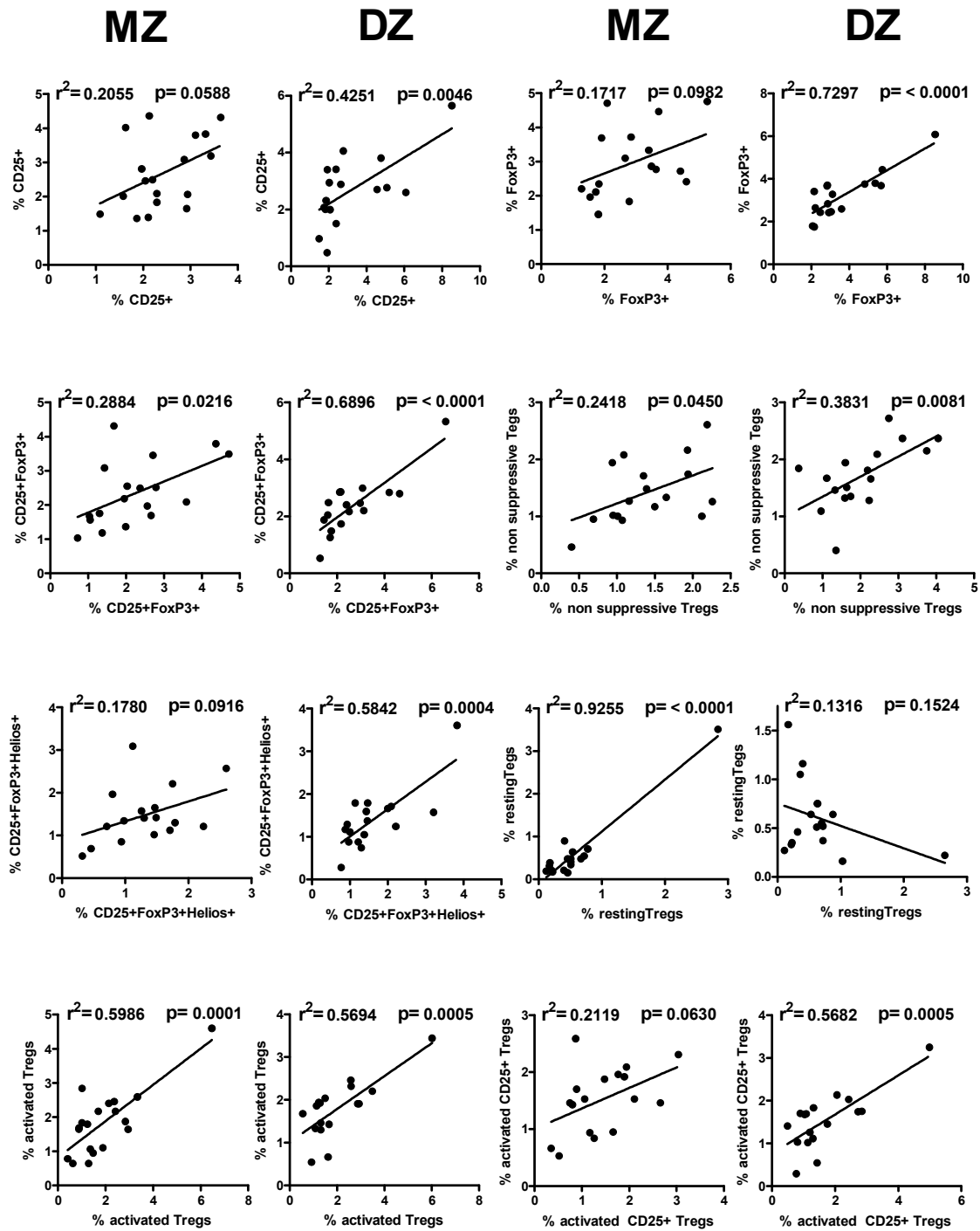
<sup>1</sup> F = female, M = male.**Table S2.** Impact of CMV-serostatus, age and gender on immune phenotypes.

Immune Subset	CMV- <sup>1</sup>	CMV+ <sup>1</sup>	≤48 <sup>2</sup>	>48 <sup>2</sup>	Female	Male
CD25+	2.9%	2.5% *	2.7%	2.4%	2.5%	3.0%
FoxP3+	3.6%	3.1%	3.1%	3.7% *	3.1%	3.6%
CD25+FoxP3+	2.9%	2.4%	2.4%	2.7% *	2.5%	2.5%
Non suppressive Tregs	1.9%	1.6%	1.7%	1.7%	1.7%	1.5%
CD25+FoxP3+Helios+	1.7%	1.4%	1.3%	1.7% **	1.4%	1.7%
resting Tregs	0.5%	0.5%	0.5%	0.5%	0.5%	0.4%
activated Tregs	2.1%	1.8%	1.8%	1.9%	1.8%	2.0%
activated CD25+ Tregs	1.7%	1.5%	1.5%	1.7%	1.5%	1.8%
FoxP3-Helios+	2.1%	2.0%	2.0%	2.0%	2.0%	2.3%
FoxP3+Helios+	2.0%	1.7%	1.6%	2.1% **	1.7%	2.0%
FoxP3+Helios-	1.8%	1.5% *	1.6%	1.7%	1.6%	1.5%
CD45RA+CD45RO-	41.0%	37.8%	38.4%	38.4%	38.2%	38.8%
CD45RA+CD45RO-FoxP3+Helios+	0.05%	0.05%	0.04%	0.07% ***	0.05%	0.05%
CD45RA-CD45RO+FoxP3+Helios+	1.5%	1.4%	1.4%	1.6%	1.4%	1.8%
CD8+FoxP3+	0.5%	0.4%	0.5%	0.6%	0.5%	0.4%
CD8+Helios+	21.5%	17.0%	18.4%	16.4%	18.9%	12.7%
CD14+	14.9%	12.1%	12.2%	12.4%	12.2%	12.4%
Lin-	32.1%	26.8% *	27.4%	28.9%	28.0%	30.0%
Lin-CD14-	16.0%	14.4%	14.2%	16.1%	14.5%	15.4%
Lin-CD14-CD15+	0.07%	0.06%	0.05%	0.06%	0.06%	0.07%
Lin-CD14-CD15+CD11b+	0.06%	0.05%	0.06%	0.05%	0.05%	0.06%
Lin-CD16-CD14+	14.1%	10.8%	11.2%	11.5%	11.3%	11.5%
Lin-CD16-CD14+HLA-DR+	11.0%	9.4%	9.7%	9.9%	9.9%	9.9%
Lin-CD16+CD14+	0.9%	0.8%	0.6%	0.9% *	0.9%	0.6%
Lin-CD16+CD14+HLA-DR+	0.8%	0.8%	0.6%	0.9% *	0.8%	0.6%
Lin-CD16+CD14low	9.9%	8.7%	7.9%	11.8% *	9.0%	8.8%
Lin-CD16+CD14lowHLA-DR+	1.5%	1.6%	1.1%	2.0% **	1.5%	1.5%
Lin-CD16-CD14-	5.3%	4.9%	5.4%	4.5%	4.7%	5.8% *
Lin-CD14+HLA-DR-	1.4%	0.5% **	0.8%	0.9%	0.8%	0.4%
Lin-CD14+HLA-DR+	11.7%	10.0%	10.3%	10.9%	10.4%	11.0%
Lin-CD14-HLA-DR-	3.9%	3.5%	3.4%	3.9%	3.7%	3.1%
Lin-CD14-HLA-DR+	12.3%	11.0%	10.5%	12.2%	10.9%	12.6% *

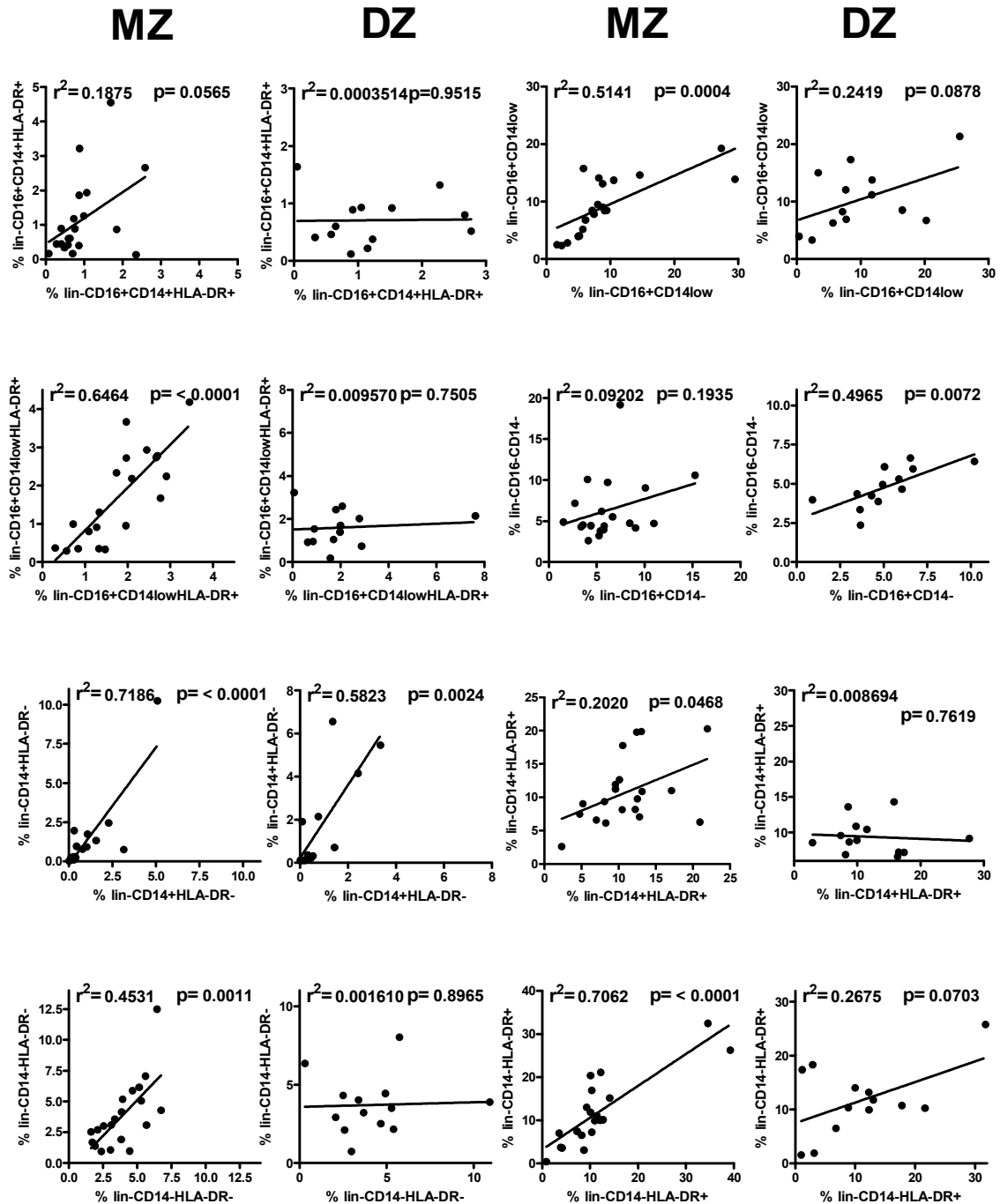
<sup>1</sup> CMV- = CMV-seronegative, CMV+ = CMV-seropositive. <sup>2</sup> 48 years is the median, median frequencies displayed. Mann Whitney *p* values with \* *p* ≤ 0.05, \*\* *p* < 0.01, \*\*\* *p* < 0.001.



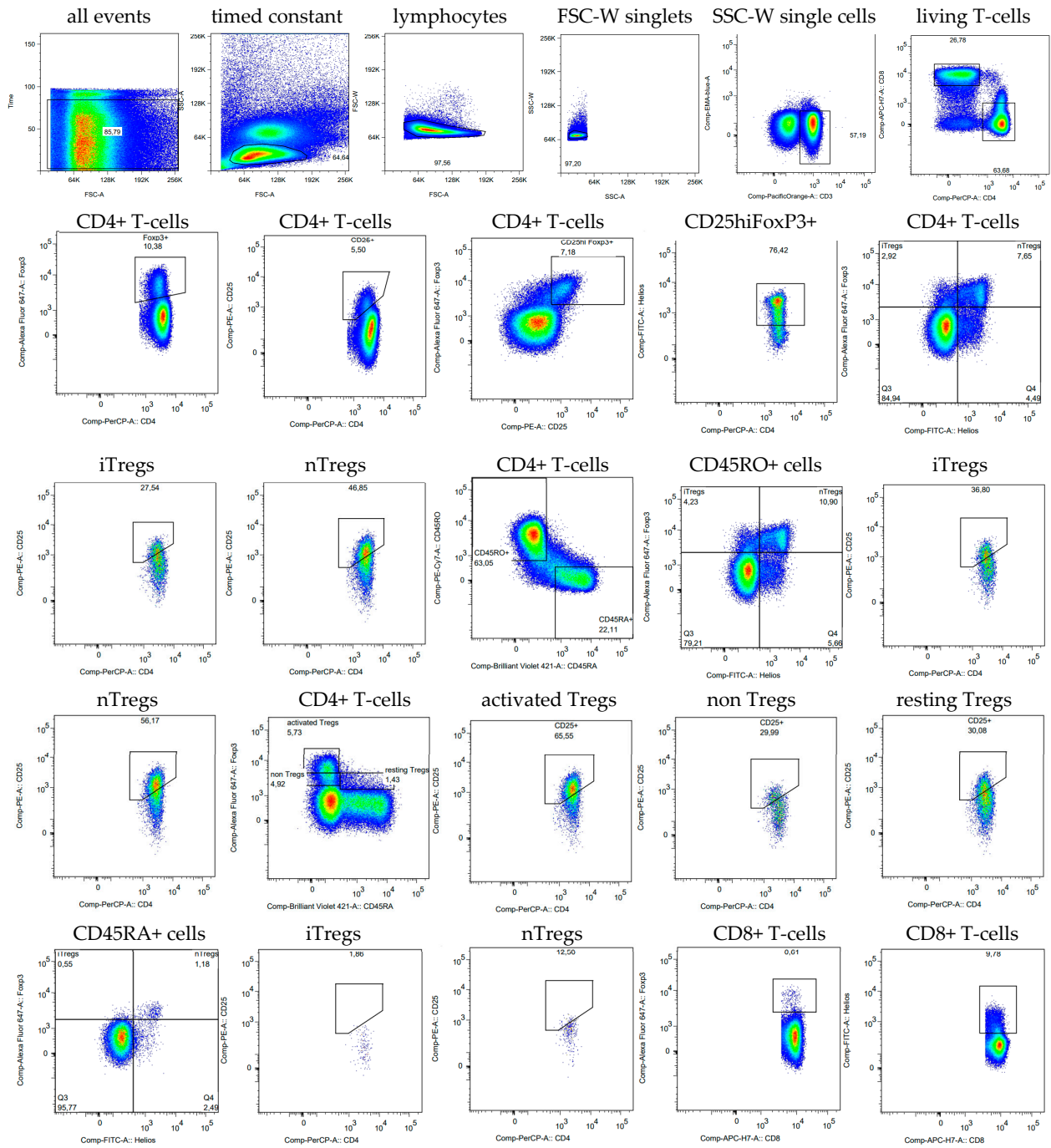
**Figure S1.** Frequencies of CD25+FoxP3+ (a), CD25+FoxP3+Helios+ (b) and CD14+HLA-DR- (c) suppressor cells within CMV-seronegative and CMV-seropositive twins grouped according to the number reactivities to the 6 CMV peptides investigated (IE-1, p150, CM2, p65, gB-1, gB-2). Borderline responses were considered negative. *P* values are shown for Kruskal-Wallis test and horizontal bars represent the medians.



**Figure S2.** Correlation analysis for differentiation status of Tregs within CMV-seropositive twin pairs. Scatter plots are shown for CMV-seropositive concordant monozygotic (MZ) and dizygotic (DZ) pairs. Each symbol represents one twin pair.



**Figure S3.** Correlation analysis for differentiation status of monocytes and MDSCs between CMV-seropositive co-twins. Scatter plots are shown for CMV-seropositive concordant monozygotic (MZ) and dizygotic (DZ) pairs. Each symbol represents one pair.



**Figure S4.** Treg panel gating strategy. Starting with all measured events various Treg phenotypes have been gated with the parental population named above each plot, here for a control sample.