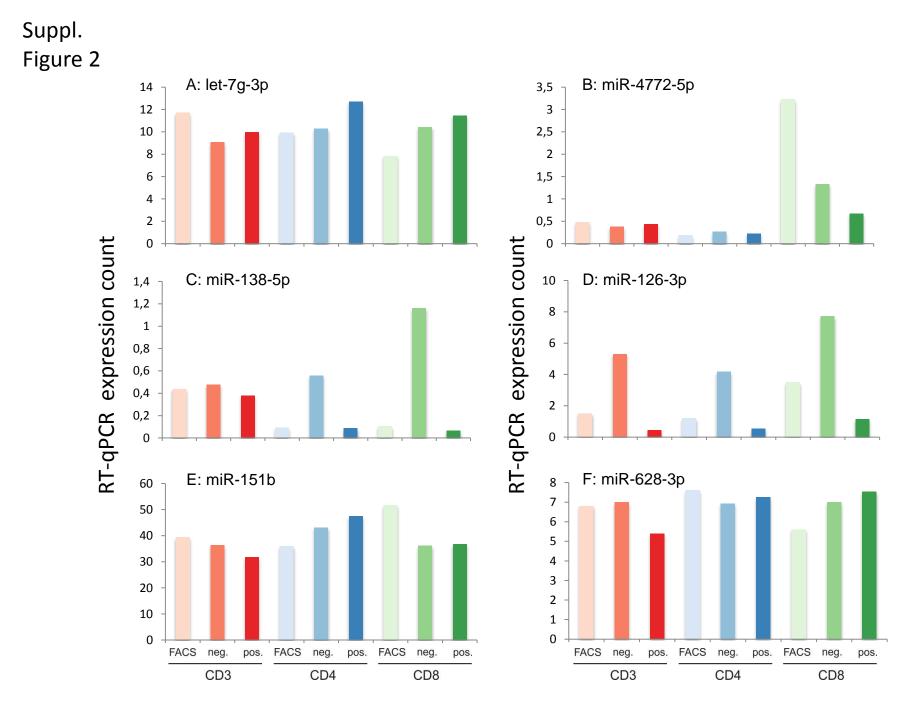
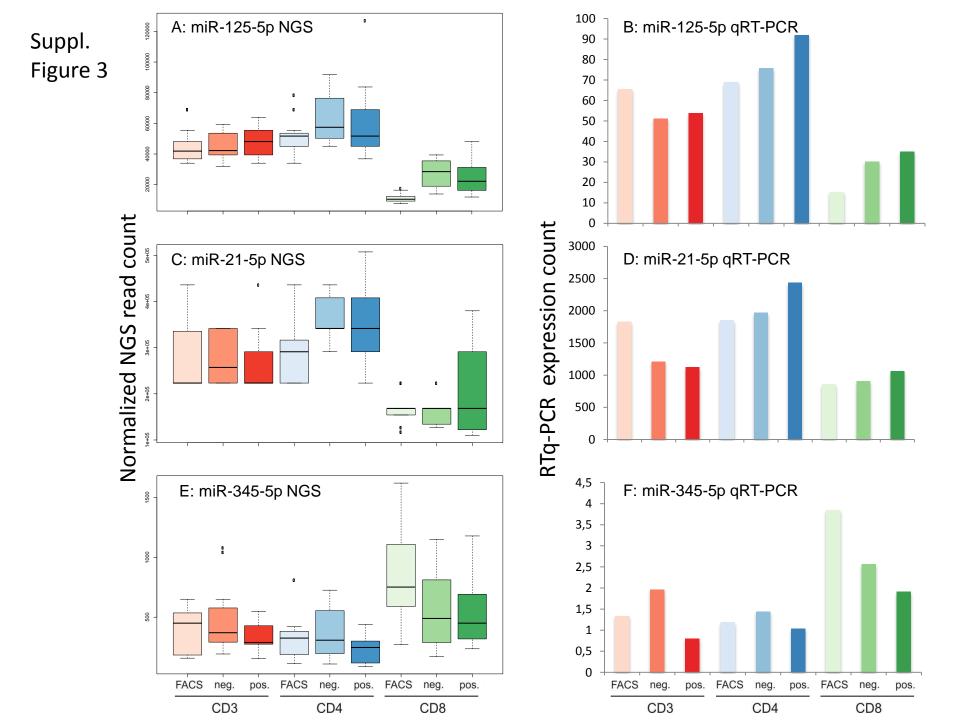


Suppl. Figure 1





## Supp. Figure 4

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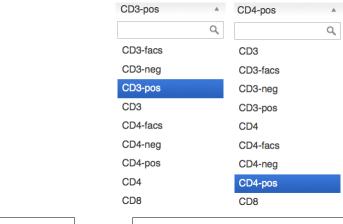
2

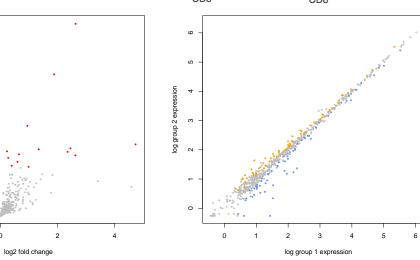
0

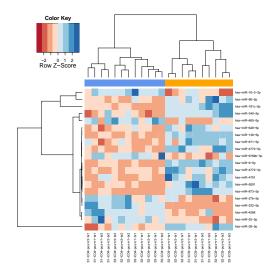
-2

0

-log10 p-value







Show	10	\$ entries

now 10 ; entries									Searc	Search:	
miRNA \$	median group 1 🛛 🗘	median group 2 🗘	stdv group 1 🛛 🗘	stdv group 2 🗘	fold change \$	In fold change $\diamond$	Wilcoxon Mann Whitney Test raw ⇔	Wilcoxon Mann Whitney Test adjusted $\diamond$	t-Test raw p-Value 🗘	t-Test adjusted p-Value -	
							p-Value	p-Value			
hsa-miR-138-5p	154.14	17.1	18.04	14.4	9.01	2.2	3.0929e-06	0.00055981	1.8179e-12	1.3161e-09	
hsa-miR-9-5p	79.81	19.72	13.65	11.43	4.05	1.4	8.6938e-05	0.0057221	2.3123e-09	8.3704e-07	
hsa-miR-181c-5p	9620.76	5091.8	1776.84	1001.06	1.89	0.64	8.4561e-05	0.0057221	3.1327e-06	0.00075604	
hsa-miR-222-5p	9.04	45.01	2.89	23.43	0.2	-1.6	3.0929e-06	0.00055981	1.5159e-05	0.0027437	
hsa-miR-873-5p	28.16	0.56	14.39	1.37	49.89	3.91	8.6938e-05	0.0057221	4.2382e-05	0.0061368	
hsa-miR-5091	19.12	3.72	8.28	1.85	5.14	1.64	8.6938e-05	0.0057221	7.2616e-05	0.0075886	
hsa-miR-27b-5p	34.94	74.14	15.31	16.62	0.47	-0.75	0.00060002	0.020686	7.3371e-05	0.0075886	
hsa-miR-4791	20.33	7.28	6.38	3.49	2.79	1.03	3.7115e-05	0.0044785	8.4523e-05	0.0076494	
hsa-miR-28-5p	13942.03	11446.19	1004.01	1023.73	1.22	0.2	0.0006897	0.022698	0.00011462	0.0085152	
hsa-miR-4772-3p	95.02	15.57	32.85	7.72	6.1	1.81	0.0001141	0.0068841	0.00011761	0.0085152	
Search miRNA	Search median group 1	Search median group 2	Search stdv group 1	Search stdv group 2	Search fold change	Search In fold change	Search Wilcoxon Mann W	Search Wilcoxon Mann W	Search t-Test raw p-Value	Search t-Test adjusted p-1	

isolation of	isolation technique	donor 1		donor 2		donor 3		mean	sd	mean (including technical	sd (including technical
		time point 1	time point 2	time point 1	time point 2	time point 1	time point 2	mean	su	replicates)	replicates)
	FACS_1	90.5	96.4	99.4	99.3	99.3	99.6	97.4	3.3	98.0	2.5
	FACS_2	98.6	95.8	98.9	99.1	99.3	99.3	98.5	1.2		
	negative_1	83.8	90.0	96.3	96.5	97.5	97	93.5	5.0	94.0	4.4
	negative_2	89.6	89.6	97.4	95.9	97.9	97	94.6	3.6		
	positive_1*	93.3	90.1	93.1	85.1	75.2	87.1	87.3	6.2	88.1	5.1
	positive_2*	86.1	95.0	89.2	88.1	91.1	84.2	89.0	3.5		
CD4 <sup>+</sup> cells	FACS_1	99.7	95.8	99.3	98.2	99.9	99.7	98.8	1.4	98.6	1.7
	FACS_2	99.5	94.5	99.0	97.8	99.9	99.8	98.4	1.9		
	negative_1	96.2	94.1	94.5	93.9	92.4	95.2	94.4	1.2	94.2	1.3
	negative_2	96.4	92.6	94.1	93.0	92.8	94.9	94.0	1.4		
	positive_1	99.8	94.6	99.9	99.9	100.0	99.9	99.0	2.0	99.0	2.0
	positive_2	99.9	94.2	99.8	99.9	99.9	99.9	98.9	2.1		
CD8 <sup>+</sup> cells	FACS_1	97.4	91.3	99.1	98.2	99.6	98.7	97.4	2.8	97.2	3.3
	FACS_2	98.8	88.7	98.8	97.8	99.4	98.6	97.0	3.7		
	negative_1	83.4	87.4	87.0	85.9	75.7	82.2	83.6	4.0	83.5	4.2
	negative_2	81.9	87.4	86.7	86.7	74.9	82.9	83.4	4.3		
	positive_1	98.4	96.1	99.8	99.4	99.4	98.8	98.7	1.2	98.3	1.4
	positive_2	98.6	95.0	n.d.	99.3	99.3	97.7	98.0	1.6		

Suppl. Table 1: Purity of different samples analyzed by flow cytometry.