

Table 3. Close correlation between genomic results obtained from clinically feasible and complex monocyte and T cell isolation methods

Correlation (r)	M1/M2	T1/T2
Patient 1	0.985	0.960
Patient 2	0.990	0.994
Patient 3	0.987	0.988
Patient 4	0.991	0.998
Patient 5	0.995	0.974
Control 1	0.994	0.990
Control 2	0.998	0.953
Control 3	0.998	0.995
Control 4	0.994	0.994
Control 5	0.993	0.994
MEAN	0.993	0.984
SD	0.004	0.016

There are no differentially expressed genes between M1/M2 or T1/T2 at the 1% false discovery rate. M1= monocytes isolated by rosette sep method step 1, T1= T lymphocytes isolated by rosette sep while M2 and T2 are the respective monocytes and T cells further purified by miltinyi columns. However, although the same genes are identified, a significantly higher number reached statistical significance in the more purified populations.