



Figure S1. The representatives of PCA results from serum and HDL samples. PCA analysis was generated using the 1700-1500 cm^{-1} FTIR spectral range. PCA score plots of serum (A) and HDL (B). The blue and red represent the LP and HP groups, respectively. Score plots of serum and HDL exhibited no trend of discrimination for the LP and HP groups. HP – the elderly with a high percentage of pathogenic CD4^+ T cells; LP - the elderly with a low percentage of pathogenic CD4^+ T cells.

Table S1. Confusion matrix of classification model built by PLS-DA using exosome spectra in the 1700-1500 cm^{-1} region

Predictive Model	Flowcytometric Analysis	
	HP	LP
HP	11	9
LP	5	14

Abbreviations: HP – the elderly with a high percentage of pathogenic CD4^+ T cells; LP - the elderly with a low percentage of pathogenic CD4^+ T cells.

Table S2. Performance of classification model built by PLS-DA using exosome spectra in the 1700-1500 cm^{-1} region

Sample	Region (cm^{-1})	Algorithm	Performance				
			Acc (%)	Sens (%)	Spec (%)	PPV (%)	NPV (%)
Exosome	1700-1500	PLS-DA	64	69	61	55	74

Abbreviations: Acc - accuracy; Sens – sensitivity; Spec – specificity; PPV – positive predictive value; NPV – negative predictive value; PLS-DA – Partial Least Square Discriminant Analysis.