

**Table S1** Age-related changes to biomarkers of monocyte activation

	Effect of Age		Effect of sex
	Coefficient	P value <sup>1</sup>	P value <sup>2</sup>
<i>Monocytes (%)</i>			
Classical (CD14 <sup>++</sup> CD16 <sup>-</sup> )	-0.11	<b>&lt;0.001</b>	NS
Intermediate (CD14 <sup>++</sup> CD16 <sup>+</sup> )	0.06	<b>&lt;0.001</b>	<b>&lt;0.001</b>
Non-classical (CD14 <sup>+</sup> CD16 <sup>++</sup> )	0.05	<b>0.035</b>	<b>0.003</b>
Total CD16 <sup>+</sup>	0.12	<b>&lt;0.001</b>	NS
<i>Soluble factors</i>			
CXCL10	1.29	<b>&lt;0.001</b>	<b>&lt;0.001</b>
sCD14	2.18	NS	NS
sCD163	4.49	<b>0.012</b>	<b>&lt;0.001</b>
Neopterin	0.05	<b>&lt;0.001</b>	NS
LPS	0.12	NS	<b>&lt;0.001</b>

<sup>1</sup> P value <0.05 indicates the parameter changes significantly with age (ie. slope of the regression was significantly different to zero).

<sup>2</sup> P value indicates whether sex significantly contributed to age-related changes.

**Table S2:** Difference in age between HIV+ individuals and controls for any given level of monocyte activation marker.

	<i>n</i>	Estimated difference (Years) <sup>#</sup>	
		HIV+ Viremic	HIV+ VS
<b><i>Monocytes (%)</i></b>			
Classical (CD14 <sup>++</sup> CD16 <sup>-</sup> )	264	-10.7 (-15.4, -6.1)	-2.9 (-6.9, 1.2)
Intermediate (CD14 <sup>++</sup> CD16 <sup>+</sup> )	264	-11.3 (-16.1, -6.5)	-3.7 (-7.7, 0.3)
Non-classical (CD14 <sup>+</sup> CD16 <sup>++</sup> )	264	-9.7 (-14.4, -5.1)	-2.4 (-6.6, 1.7)
Total CD16 <sup>+</sup>	264	-10.6 (-15.2, 5.9)	-2.7 (-6.8, 1.3)
<b><i>Soluble factors</i></b>			
CXCL10	204	-12.0 (-18.9, -4.9) <sup>1</sup>	- 4.0 (-9.1, 1.1) <sup>1</sup>
sCD163	246	-11.6 (-17.0, -6.3)	-2.5 (-6.6, 1.7)
Neopterin	251	-12.9 (-18.4, -7.4) <sup>1</sup>	-1.8 (-6.1, 2.5) <sup>1</sup>

# As determined by regression analysis, where the value of the coefficient estimates the difference in age between HIV+ individuals and controls for any given level of parameter. Median and 95% confidence intervals shown.

<sup>1</sup> Where the slope was significantly different to HIV- individuals, an interaction term was introduced. The resulting equation was solved for the median marker level of the entire cohort, and the coefficient for that value shown.