

**Supplementary Table 1: The association between HIV disease markers and time to RLE resolution<sup>†</sup>.**

Analysis set	Parameter	Unadjusted Results			Adjusted Results <sup>1,2</sup>		
		Hazard Ratio (95% CI)	P-value	*	Hazard Ratio (95% CI)	P-Value	*
RNA only	HIV RNA copies (Log10) at RLE	0.74 (0.6,0.9)	<.001	*	0.76 (0.6,0.9)	0.002	*
	HIV RNA copies > 100,000 at RLE	0.29 (0.1,0.7)	0.004	*	0.31 (0.1,0.7)	0.005	*
	HIV RNA copies (Log10)(time-varying)	0.84 (0.7,1.0)	0.03	*	0.85 (0.7,1.0)	0.04	*
	HIV RNA, copies > 100K (time-varying)	0.58 (0.3,1.0)	0.06		0.61 (0.3,1.1)	0.10	
CD4 only	CD4 pct at RLE	1.02 (1.0,1.0)	<.001	*	1.02 (1.0,1.0)	<.001	*
	CD4 pct < 25 at RLE	0.63 (0.5,0.8)	0.002	*	0.66 (0.5,0.9)	0.01	*
	CD4 pct (time-varying)	1.02 (1.0,1.0)	0.001	*	1.02 (1.0,1.0)	0.003	*
	CD4 pct < 25 (time-varying)	0.62 (0.5,0.8)	0.002	*	0.64 (0.5,0.9)	0.005	*

<sup>†</sup> These two sets of analyses were performed on derived datasets with RNA viral load and CD4 data, respectively

<sup>1</sup> Each row represents a separate time to event multivariate regression analysis. Results adjust for the final core models, which were developed with p < 0.20 to include and p < 0.15 to remain.

<sup>2</sup> The core model for each analysis included Black race and CDC stage C.