

id	weight combination	half-live $T_{SCM1}$ [years]	half-live $T_{SCM2}$ [years]	$T_{SCM2}/T_{SCM}$	f
DW01	0.15*YF+0.35*T	0.02	23.87	0.25	0.000
	0.20*YF+0.30*T	0.02	18.67	0.25	0.000
	0.25*YF+0.25*T	0.02	13.92	0.25	0.001
	0.30*YF+0.20*T	0.02	14.15	0.26	0.001
	0.35*YF+0.15*T	0.02	11.20	0.25	0.001
	<b>median</b>	<b>0.02</b>	<b>14.15</b>	<b>0.25</b>	<b>0.001</b>
DW04	0.15*YF+0.35*T	0.18	5.49	0.35	0.017
	0.20*YF+0.30*T	0.18	4.26	0.33	0.021
	0.25*YF+0.25*T	0.14	4.59	0.58	0.041
	0.30*YF+0.20*T	0.14	7.93	0.58	0.023
	0.35*YF+0.15*T	1.84	7.88	0.51	0.196
	<b>median</b>	<b>0.18</b>	<b>5.49</b>	<b>0.51</b>	<b>0.023</b>
DW10	0.15*YF+0.35*T	1.29	14.45	0.52	0.087
	0.20*YF+0.30*T	0.23	6.92	0.44	0.026
	0.25*YF+0.25*T	0.69	9.09	0.51	0.075
	0.30*YF+0.20*T	0.15	7.84	0.52	0.020
	0.35*YF+0.15*T	0.50	6.27	0.53	0.083
	<b>median</b>	<b>0.50</b>	<b>7.84</b>	<b>0.52</b>	<b>0.075</b>
DW11	0.15*YF+0.35*T	0.38	13.43	0.82	0.116
	0.20*YF+0.30*T	2.31	11.20	0.83	0.500
	0.25*YF+0.25*T	0.90	8.39	0.25	0.001
	0.30*YF+0.20*T	0.91	9.36	0.26	0.001
	0.35*YF+0.15*T	0.78	9.87	0.25	0.001
	<b>median</b>	<b>0.90</b>	<b>9.87</b>	<b>0.82</b>	<b>0.307</b>

**S3 Table. Impact of relative weighting of telomere length and YFV data.**

Parameter estimates (and medians) estimated using the explicit heterogeneity model for the five weighting strategies in S1 Fig. The table shows half-life estimates for the  $T_{SCM1}$  and  $T_{SCM2}$  populations respectively, the relative size of the  $T_{SCM2}$  subpopulation ( $T_{SCM2}/T_{SCM}$ ), and the fraction of cells generated from each clonal burst that enter the long-lived  $T_{SCM2}$  subpopulation ( $f$ ). Different rows (for a given individual) correspond to different weighting strategies, where the weights applied to the yellow fever virus (YF) and telomere length (T) datasets are indicated in the second column “weight combination”, and the weight applied to the labelling dataset was in all cases 0.5.