

Supplementary Table 1. *Mapping quality controls* . Columns are: 'participant', the anonymized participant identifier; 'timepoint', the time point at the blood draw; 'input_nb', the total number of deep-sequencing fragments; 'input_len', the total length in nucleotides of the paired-ended fragment; 'map_unique', the number of uniquely mapped fragments (mapped to a unique genetic locus); 'map_unique_pct', the percentage of; 'map_len', the average length of maps in nucleotides; 'map_multiple', the number of fragments that did not uniquely map but mapped to at most ten loci; 'map_multiple_pct', the percentage of; 'pct_good', the percentage of fragments that mapped to at most ten loci (= map_unique_pct + map_multiple_pct); 'map_multiple_too_many_pct', the percentage of fragments that mapped to more than ten loci (unspecific mapping); 'too_short_pct', the percentage of fragments whose mapping length was too short (<30 nucleotides; fortuitous but short sub-sequence match); 'other_pct', the percentage of unmapped fragments for other reasons than specificity or length.

partici pant	time point	input_nb	input_len	map_unique	map_uniq		map_multiple	map_multi	pct_good	map_m ultiple_t		
					ue_pct	map_len				oo_ma	too_sh	other_
				map_unique		le		ple_pct		nypct	ort_pct	pct
PS001	t0	68,258,976	202.00	50,678,148	74.24%	194.17	17,519,769	25.67%	99.91%	0.06%	0.02%	0.01%
PS001	t2	67,036,371	202.00	47,120,085	70.29%	194.38	19,845,403	29.60%	99.89%	0.08%	0.01%	0.01%
PS001	t3	56,545,905	202.00	42,288,868	74.79%	191.10	14,204,692	25.12%	99.91%	0.07%	0.01%	0.02%
PS004	t0	68,662,689	202.00	43,273,618	63.02%	193.74	25,345,455	36.91%	99.93%	0.04%	0.01%	0.01%
PS004	t2	73,734,927	202.00	55,041,393	74.65%	192.07	18,606,512	25.23%	99.88%	0.10%	0.01%	0.01%
PS004	t3	82,472,489	202.00	56,331,797	68.30%	193.22	26,067,562	31.61%	99.91%	0.07%	0.01%	0.01%