

Additional file 2 – ATF 4.7 interface and HLA-C*03:03:01, 03:04:01:01 assignment.

Sequence reads are aligned to exon 1, 2, 3, 4 and 7. The only difference between HLA-C*03:03:01 and C*03:04:01:01 is located at the end of exon 2. The inability to call this genotype with the older ATF version was automatically solved by ATF 4.7. The blue bar indicate the variation (nt756 R=A+G) at the last position of exon 2.

The screenshot displays the ATF 4.7 interface with a sequence alignment view. The top toolbar includes options for DNA (HLA v1), Edit, Type (Genotyping), and various display settings like Dots, Unaligned, and Sort. The main window shows a genomic map with exons and introns, and a detailed alignment of sequence reads. A blue bar highlights a variation at position 756 (R=A+G) at the end of exon 2. A pop-up window for 'Sample 26' is visible, showing sequence navigation controls and variant calling options.

Sample	Sequence	Allele 1	Allele 2	MM	N-C	Differences
Sample 01	...AGTGAGTGACCCCGGCCCGGGGCGCAGG	C*03:03:01	C*03:04:01:01	0	0	
Sample 05	CCGAGTGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCC	C*03:03:01	C*03:04:01:02	0	0	3'UTR
Sample 07	CCGAGTGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCC	C*03:03:01	C*03:03:01	1	1	
Sample 11	CCGAGTGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCC	C*03:03:01	C*03:03:01	1	1	
Sample 15	>> gC.E2.F1.84-2	C*03:03:01	C*03:04:02	1	1	
Sample 18	CCGAGTGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCC	C*03:03:01	C*03:04:03	1	1	
Sample 20	<< gC.E2.R1.77-3	C*03:03:01	C*03:04:04	1	1	
Sample 21		C*03:03:01	C*03:04:05	1	1	
Sample 23		C*03:03:01	C*03:04:07	1	1	
Sample 24		C*03:03:01	C*03:04:08	1	1	
Sample 25		C*03:03:01	C*03:04:09	1	1	
Sample 26* gC		C*03:03:01	C*03:04:10	1	1	
		C*03:03:01	C*03:04:11	1	1	
		C*03:03:01	C*03:04:12	1	1	
		C*03:03:01	C*03:04:13	1	1	
		C*03:03:01	C*03:04:14	1	1	
		C*03:03:01	C*03:04:15	1	1	
		C*03:03:01	C*03:04:16	1	1	