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.

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IMGT/C 3.9.0.0 2012-07-12 *TEST V711721731741													
Base 756 (756) CSSAGWGARCCTGCGGAAMCTGCRCGGCYACTACAACYAGAGCRASGMCVGTGAGTGACCCCGGGCCGGGGGGGCGCAGG Start: 232 (232) 5'UTR 232													
cDNA 271, Exon 2 270 C U A 2 1 R Stop: 3199 (3199) 3'UTR 13													
	ple 01						ACCCCGGCCC	GGGGCGCAG		Allele 2	MM 0 N-C	Differences	
	ple 05		CCGAGT	GAGCCTGCGGAACCT	GCGCGGCTACTACAACCAG	AGCGAGGCC <mark>R</mark> ******	********	*******	* C*03:03:01	C*03:04:01:01	0		
Sam	ple 07								C*03:03:01	C*03:04:01:02	0	3'UTR	
Sam	ple 11		CCGAGT	GAGCCTGCGGAACCT	GCGCGGCTACTACAACCAG	AGCGAGGCC <mark>AGTGAGTG</mark>	ACCCCGGCCC	GGGGCGC+0	G C*03:03:01	C*03:03:01	1		
Sam	ple 15		>> gC.	E2.F1.84-2					C*03:03:01	C*03:04:02	1		
Sam	ple 18		CCGAGT	GAGCCTGCGGAACCT	GCGCGGCTACTACAACCAG	AGCGAGGCC <mark>GGTGAGTG</mark>	ACCCCGGCCC	GGGGCGCAG	G C*03:03:01	C*03:04:03	1		
Sam	ple 20		<< g0.	E2.R1.77-3					C*03:03:01	C*03:04:04	1		
Sam	ple 21							_	C*03:03:01	C*03:04:05	1		
Sam	ple 23			Sample 26					C*03:03:01	C*03:04:07	1		
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Sam	ple 25						· · · · ·		C*03:03:01	C*03:04:09	1		
	gA					G - +	-	-	C*03:03:01	C*03:04:10	1		
	gB			No Offset		BCS V Edit			C*03:03:01	C*03:04:11	1		
Sam	ple 26* gC			No Offset	▼ Master				C*03:03:01	C*03:04:12	1		
	DPB1								C*03:03:01	C*03:04:13	1		
	DQB1								C*03:03:01	C*03:04:14	1		
	DRB1								C*03:03:01	C*03:04:15	1		
	Generi	ic i							C*03:03:01	C*03:04:16	1		