S1 Table. Uniqueness analysis of capture and signal-enhancing probes.[a]

Probe #	Sequence,* 5'→3'	Number of potential target sequences in human genome:		
		perfect match	1 mismatch**	2 mismatches
CP1w	TTTCACTGT	95.014	N/A***	N/A
CP2w	GATTTCACTGT	3.999	N/A	N/A
CP3w	GAGATTTCACTGTAGCTA	1	2 (13,18)	3(1,18|17-18|17-18)
CP1m	TTTCTCTGT	114.261	N/A	N/A
CP2m	GATTTCTCTGT	4.686	N/A	N/A
CP3m	GAGATTTCTCTGTAGCTA	0	4 (1;18;1;1,18)	>7
P1	GCT AGA CCA AAA TCA CCT ATT TTT ACT GTG AGG TCT TCA TGA AGA AAT AT	1	0	0

[a] Numbers in parentheses indicate the position of mismatches in the sequences. The analysis of short capture sequences (9 nt and 11 nt) was performed determining the presence of this sequence from the human genome reference (hg19). For longer sequences (18 nt, 50 nt and 53 nt), we applied BLASTN via NCBI website. * The sequences are analyzed in absence of LNA modifications.

**"1 mismatch" indicates the number of compliments in the human genome if one base of the sequence is subsituted.

*** In the case of sequences with a high number of perfect matches, we did not check the amount of matches if 1 or more bases of the sequence were substituted.