Fig 1

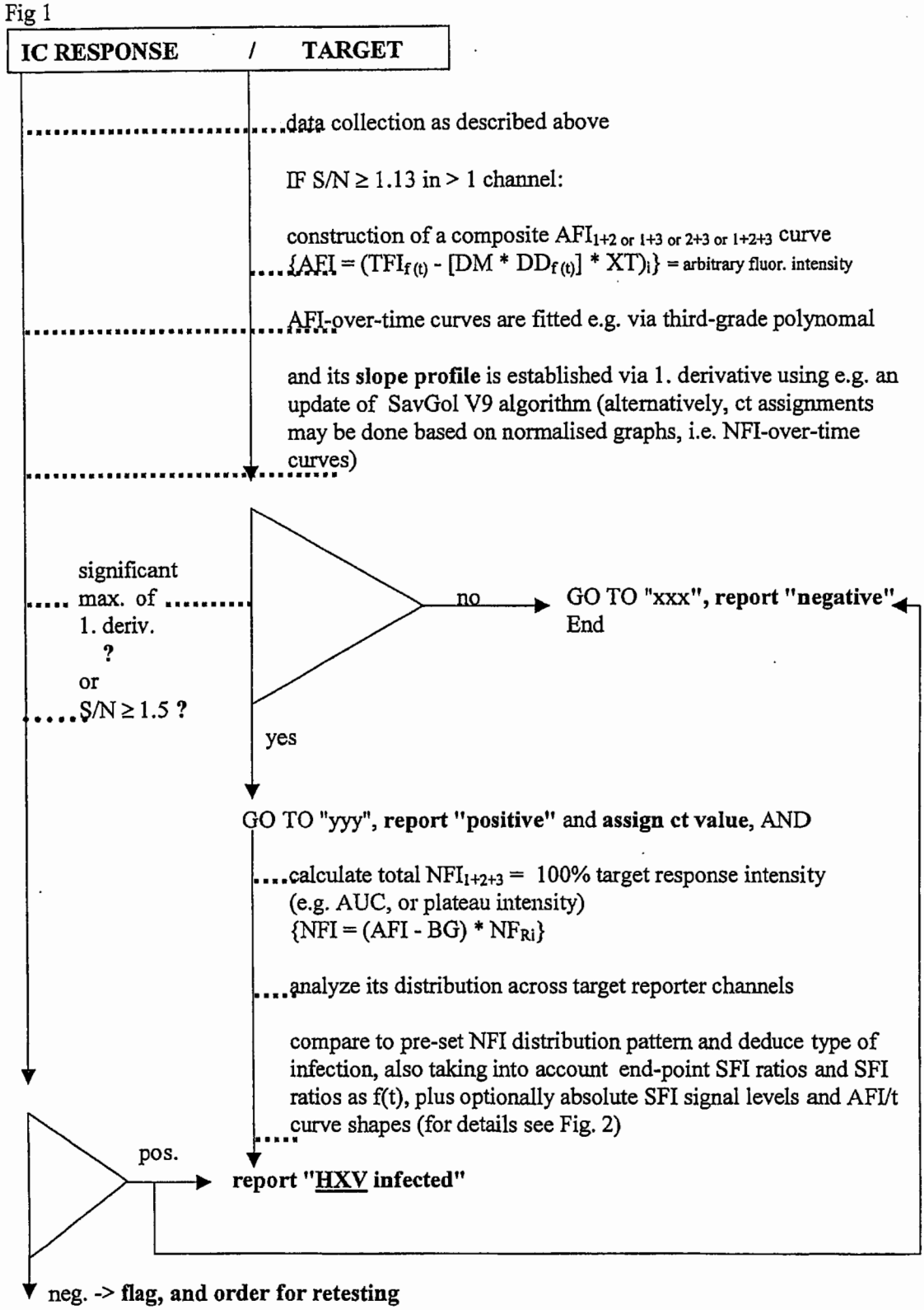

IC RESPONSE / TARGET
data collection as described above
IF S/N ≥ 1.13 in > 1 channel:
construction of a composite AFI1+2 or 1+3 or 2+3 or 1+2+3 curve
{AFI = (TFIf(t) - [DM * DDf(t)] * XT)i} = arbitrary fluor. intensity
AFI-over-time curves are fitted e.g. via third-grade polynomal
and its slope profile is established via 1. derivative using e.g. an update of SavGol V9 algorithm (alternatively, ct assignments may be done based on normalised graphs, i.e. NFI-over-time curves)
significant max. of 1. deriv. ? or S/N ≥ 1.5 ?
no
GO TO "xxx", report "negative"
End
yes
GO TO "yyy", report "positive" and assign ct value, AND
calculate total NFI1+2+3 = 100% target response intensity (e.g. AUC, or plateau intensity)
{NFI = (AFI - BG) * NFRi}
analyze its distribution across target reporter channels
compare to pre-set NFI distribution pattern and deduce type of infection, also taking into account end-point SFI ratios and SFI ratios as f(t), plus optionally absolute SFI signal levels and AFI/t curve shapes (for details see Fig. 2)
pos.
report "HXV infected"
neg. -> flag, and order for retesting

Fig. 2: Deconvolution scheme for signal distribution analysis according to the present invention for an assay with the primary result "positive"

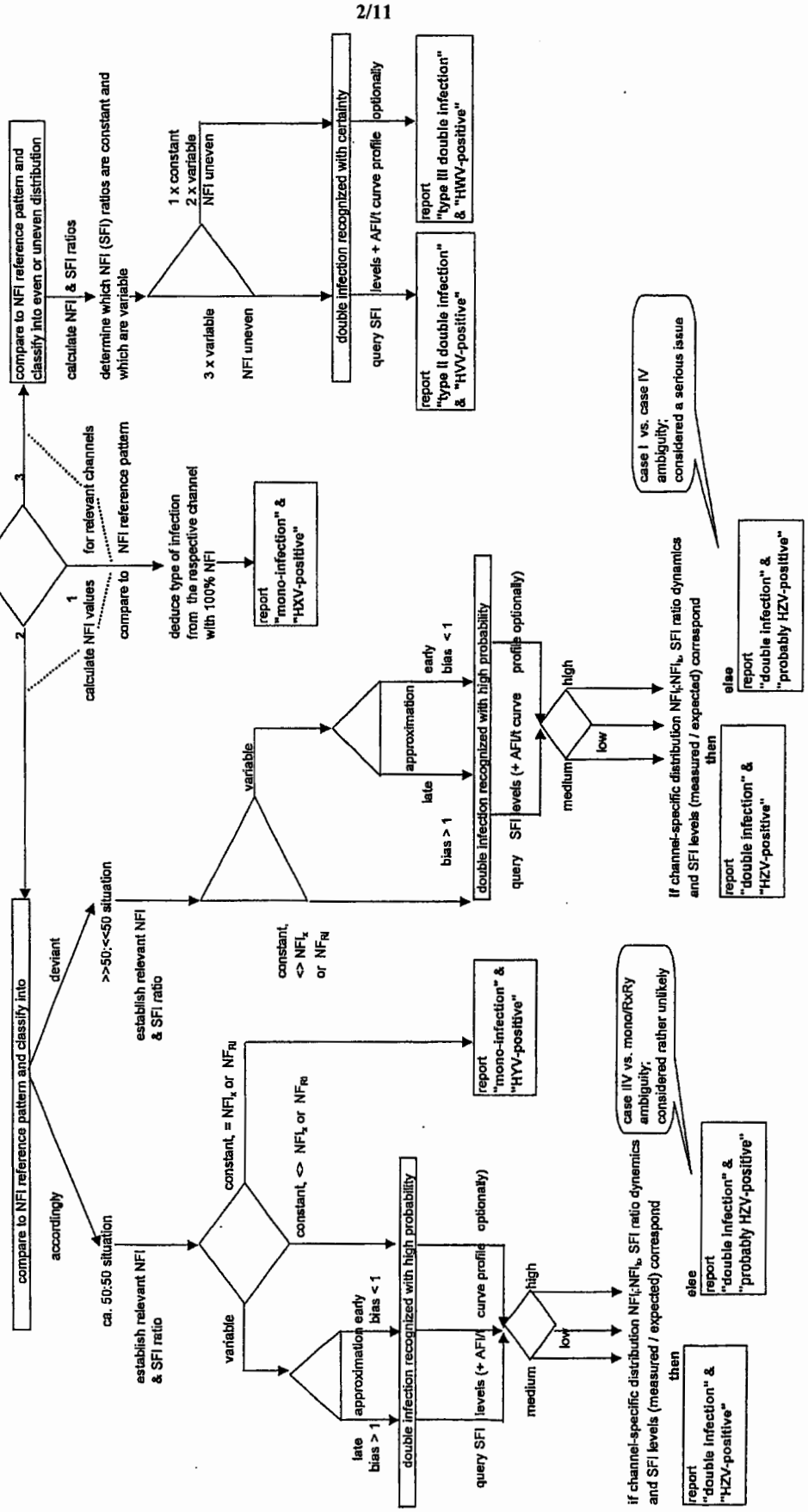
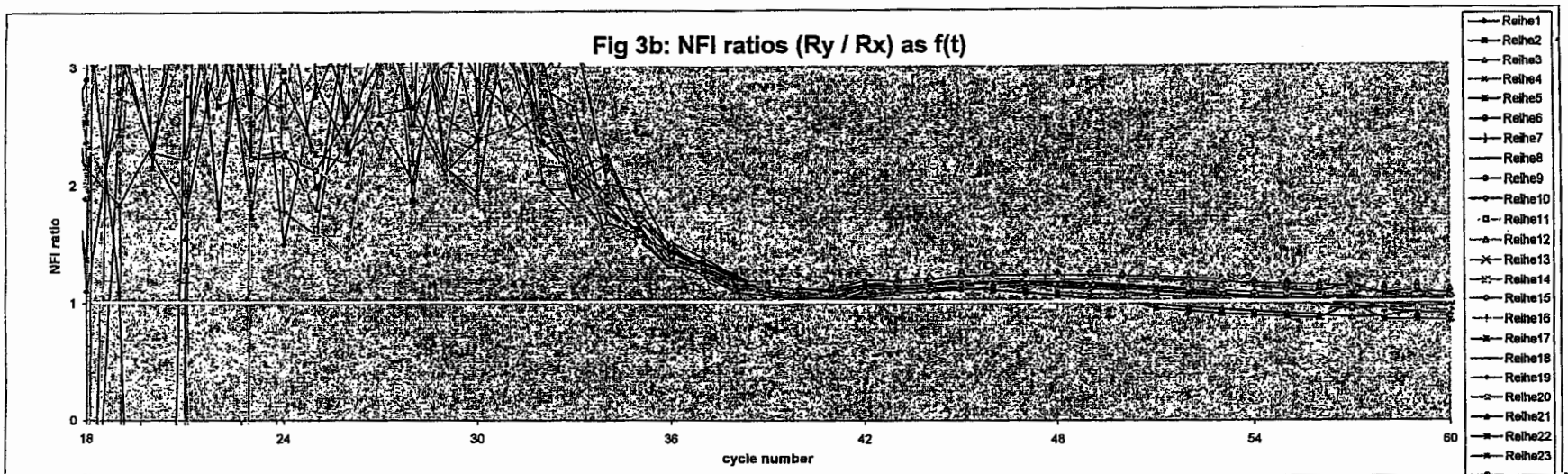


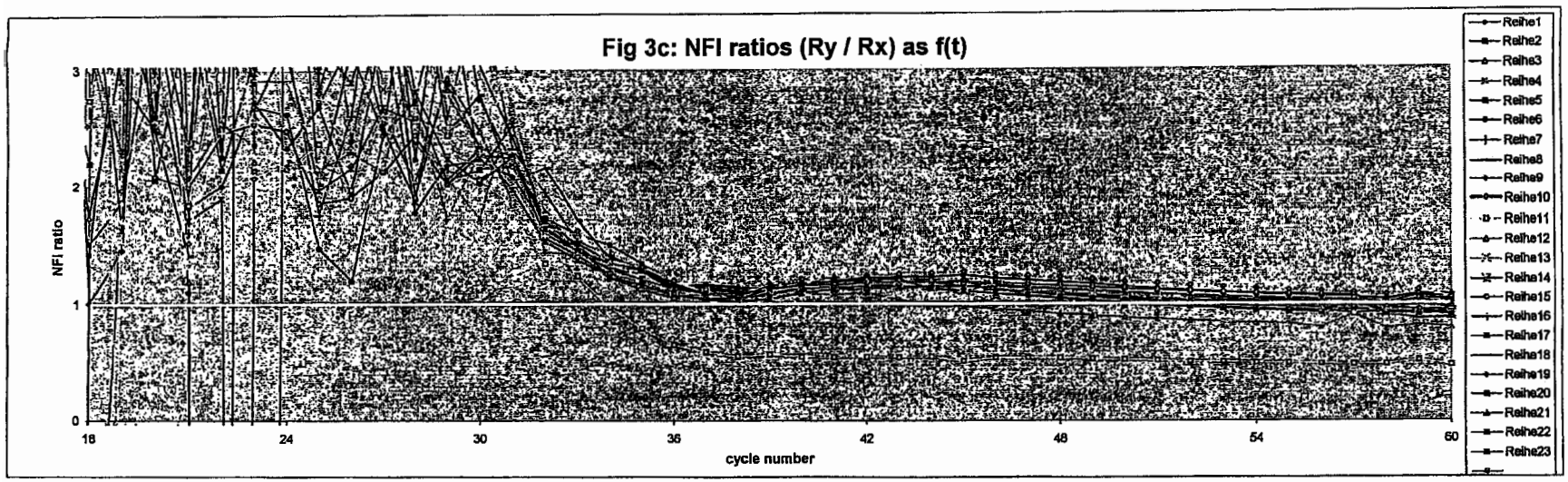
Fig 3a: NFI ratios (Ry / Rx) as f(t)

Rx =	FAM	Ry =	JA274	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI => AFI) for reaction #	=	min	[cycles]	max	NFI ratio(55-60) / trace	
				25	HBV	extracted	831	1	41	-	60	1,12	constant
Normalization factor =		11,40		25	HBV	extracted	554	2	40	-	60	0,91	constant
=>				25	HBV	extracted	528	3	41	-	60	1,08	constant
Ry/NF: Rx = 50 : 50 distribution of NFI				25	HBV	extracted	674	4	41	-	60	1,20	constant
to be expected in case of coupled				25	HBV	extracted	506	5	40	-	60	1,00	constant
signal generation				25	HBV	extracted	794	6	40	-	60	1,10	constant
=>		NFI ratio = 1,0		25	HBV	extracted	230	7	43	-	60	0,91	constant
else:	85 : 15		5,67	25	HBV	extracted	527	8	40	-	60	1,04	constant
	80 : 20		4,00	25	HBV	extracted	406	9	39	-	60	1,15	constant
	75 : 25		3,00	25	HBV	extracted	552	10	40	-	60	1,10	constant
	70 : 30		2,33	25	HBV	extracted	474	11	40	-	60	0,95	constant
	65 : 35		1,86	25	HBV	extracted	602	12	40	-	60	1,16	constant
	60 : 40		1,50	25	HBV	extracted	772	13	40	-	60	1,04	constant
	55 : 45		1,22	25	HBV	extracted	451	14	41	-	60	0,98	constant
	53 : 47		1,13	25	HBV	extracted	589	15	40	-	60	0,94	constant
	47 : 53		0,89	25	HBV	extracted	463	16	40	-	60	0,95	constant
	45 : 55		0,82	25	HBV	extracted	610	17	40	-	60	1,00	constant
	40 : 60		0,67	25	HBV	extracted	593	18	41	-	60	1,01	constant
	35 : 65		0,54	25	HBV	extracted	501	19	42	-	60	0,92	constant
	30 : 70		0,43	25	HBV	extracted	525	20	41	-	60	0,93	constant
	25 : 75		0,33	25	HBV	extracted	732	21	40	-	60	1,07	constant
	20 : 80		0,25	25	HBV	extracted	663	22	40	-	60	1,03	constant
	15 : 85		0,18	25	HBV	extracted	541	23	43	-	60	1,22	constant
				25	HBV	extracted	839	24	40	-	60	1,12	constant



Rx =	FAM	Ry =	JA274
Normalization factor =		11,40	
=>			
Ry/NF: Rx = 50 : 50 distribution of NFI to be expected in case of coupled signal generation			
=>		NFI ratio = 1,0	
else:	85 : 15	5,67	
	80 : 20	4,00	
	75 : 25	3,00	
	70 : 30	2,33	
	65 : 35	1,86	
	60 : 40	1,50	
	55 : 45	1,22	
	53 : 47	1,13	
	47 : 53	0,89	
	45 : 55	0,82	
	40 : 60	0,67	
	35 : 65	0,54	
	30 : 70	0,43	
	25 : 75	0,33	
	20 : 80	0,25	
	15 : 85	0,18	

[cp/ml]	analyte nucleic acid		SFI (Ry)	valid range (SFI -> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace	
100	HBV	extracted	759	1		38	-	60	1,00	constant
100	HBV	extracted	786	2		38	-	60	1,00	constant
100	HBV	extracted	606	3		39	-	60	0,90	constant
100	HBV	extracted	645	4		38	-	60	1,05	constant
100	HBV	extracted	711	5		39	-	60	1,03	constant
100	HBV	extracted	714	6		38	-	60	0,99	constant
100	HBV	extracted	598	7		38	-	60	1,04	constant
100	HBV	extracted	664	8		37	-	60	1,03	constant
100	HBV	extracted	631	9		38	-	60	1,01	constant
100	HBV	extracted	606	10		38	-	60	1,09	constant
100	HBV	extracted	704	11		38	-	60	1,11	constant
100	HBV	extracted	641	12		38	-	60	1,16	bordeerline
100	HBV	extracted	839	13		38	-	60	1,04	constant
100	HBV	extracted	687	14		38	-	60	0,93	constant
100	HBV	extracted	734	15		39	-	60	1,01	constant
100	HBV	extracted	749	16		38	-	60	0,99	constant
100	HBV	extracted	916	17		38	-	60	0,98	constant
100	HBV	extracted	753	18		38	-	60	1,11	constant
100	HBV	extracted	855	19		38	-	60	0,99	constant
100	HBV	extracted	780	20		38	-	60	1,04	constant
100	HBV	extracted	748	21		39	-	60	0,99	constant
100	HBV	extracted	762	22		39	-	60	0,89	constant
100	HBV	extracted	706	23		38	-	60	1,02	constant
100	HBV	extracted	757	24		38	-	60	1,09	constant



Rx =	FAM	Ry =	JA274

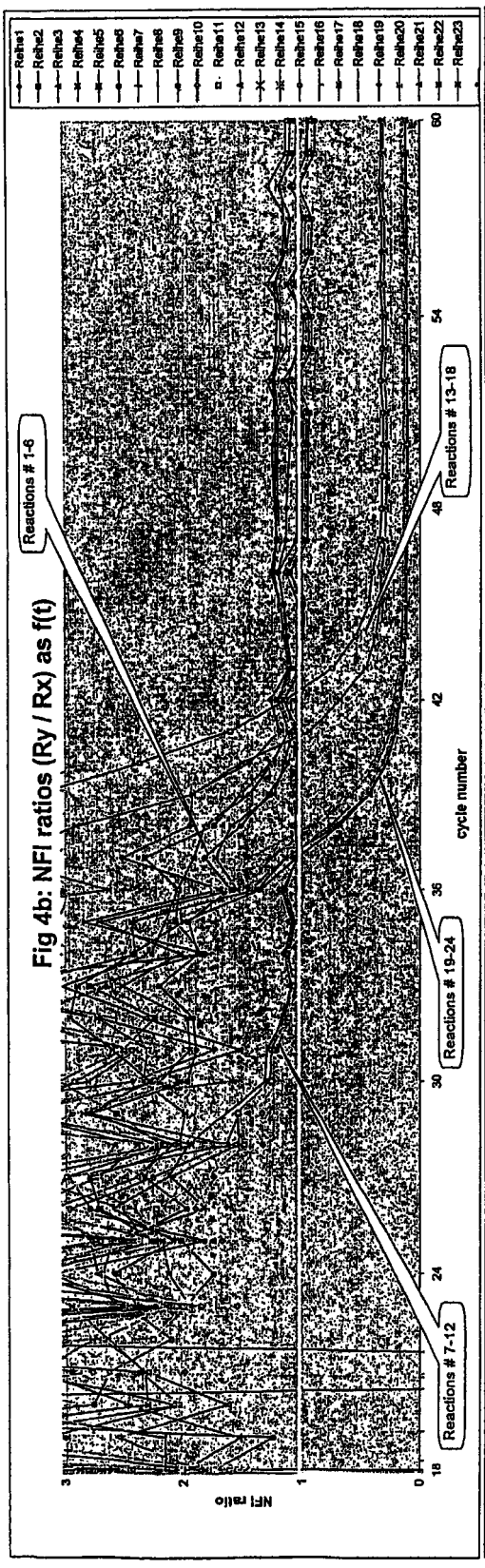
Normalization factor =	11,40
=>	
Ry/NF : Rx = 60 : 50 distribution of NFI to be expected in case of coupled signal generation	
=>	NFI ratio = 1,0

else:	85 : 15	5,67
	80 : 20	4,00
	75 : 25	3,00
	70 : 30	2,33
	65 : 35	1,86
	60 : 40	1,50
	55 : 45	1,22
	53 : 47	1,13
	47 : 53	0,89
	45 : 55	0,82
	40 : 60	0,67
	35 : 65	0,54
	30 : 70	0,43
	25 : 75	0,33
	20 : 80	0,25
	15 : 85	0,18

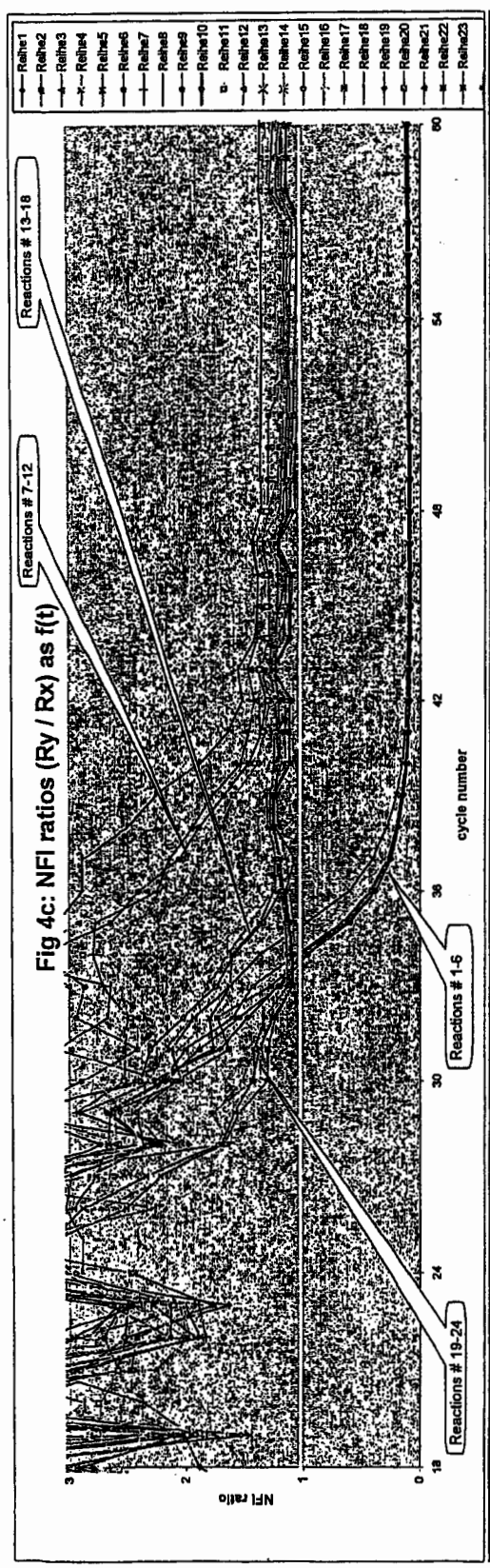
[cp/ml]	analyte nucleic acid		SFI (Ry)	valid range (SFI -> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace	
500	HBV	extracted	786	1		36	-	60	0,98	constant
500	HBV	extracted	918	2		36	-	60	1,01	constant
500	HBV	extracted	937	3		36	-	60	1,03	constant
500	HBV	extracted	782	4		36	-	60	0,97	constant
500	HBV	extracted	731	5		36	-	60	0,96	constant
500	HBV	extracted	823	6		36	-	60	0,98	constant
500	HBV	extracted	690	7		36	-	60	0,99	constant
500	HBV	extracted	648	8		36	-	60	1,00	constant
500	HBV	extracted	672	9		35	-	60	1,06	constant
500	HBV	extracted	616	10		35	-	60	1,10	constant
500	HBV	extracted	148	11		36	-	60	0,49	var. / m-
500	HBV	extracted	661	12		35	-	60	1,02	constant
500	HBV	extracted	860	13		36	-	60	0,95	constant
500	HBV	extracted	1005	14		35	-	60	0,97	constant
500	HBV	extracted	903	15		35	-	60	1,01	constant
500	HBV	extracted	904	16		35	-	60	0,99	constant
500	HBV	extracted	856	17		35	-	60	0,98	constant
500	HBV	extracted	952	18		36	-	60	0,95	constant
500	HBV	extracted	767	19		36	-	60	0,93	constant
500	HBV	extracted	847	20		36	-	60	0,93	constant
500	HBV	extracted	698	21		35	-	60	0,82	constant
500	HBV	extracted	892	22		35	-	60	0,95	constant
500	HBV	extracted	855	23		36	-	60	0,93	constant
500	HBV	extracted	813	24		35	-	60	0,96	constant

Rx =	FAM	Ry =	JA274	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI --> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace
				5000	HBV extracted	741	1		32	-	60	1,04 constant
Normalization factor =		11,40		5000	HBV extracted	856	2		32	-	60	0,99 constant
=>				5000	HBV extracted	811	3		32	-	60	0,97 constant
Ry/NF : Rx = 50 : 50 distribution of NFI to be expected in case of coupled signal generation				5000	HBV extracted	748	4		32	-	60	1,02 constant
				5000	HBV extracted	802	5		32	-	60	0,99 constant
				5000	HBV extracted	894	6		32	-	60	0,99 constant
=>		NFI ratio = 1,0		5000	HBV extracted	670	7		32	-	60	1,02 constant
else:	85 : 15		5,67	5000	HBV extracted	735	8		32	-	60	1,01 constant
	80 : 20		4,00	5000	HBV extracted	765	9		32	-	60	1,02 constant
	75 : 25		3,00	5000	HBV extracted	637	10		32	-	60	0,99 constant
	70 : 30		2,33	5000	HBV extracted	763	11		31	-	60	1,03 constant
	65 : 35		1,86	5000	HBV extracted	701	12		31	-	60	1,03 constant
	60 : 40		1,50	5000	HBV extracted	934	13		32	-	60	0,96 constant
	55 : 45		1,22	5000	HBV extracted	845	14		32	-	60	0,99 constant
	53 : 47		1,13	5000	HBV extracted	859	15		32	-	60	0,94 constant
				5000	HBV extracted	813	16		32	-	60	0,94 constant
	47 : 53		0,89	5000	HBV extracted	962	17		32	-	60	0,96 constant
	45 : 55		0,82	5000	HBV extracted	827	18		32	-	60	0,99 constant
	40 : 60		0,67	5000	HBV extracted	910	19		32	-	60	1,01 constant
	35 : 65		0,54	5000	HBV extracted	670	20		31	-	60	0,97 constant
	30 : 70		0,43	5000	HBV extracted	845	21		32	-	60	0,93 constant
	25 : 75		0,33	5000	HBV extracted	967	22		32	-	60	0,93 constant
	20 : 80		0,25	5000	HBV extracted	847	23		32	-	60	0,96 constant
	15 : 85		0,18	5000	HBV extracted	902	24		32	-	60	0,96 constant

Rx =	FAM	Ry =	JA274	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI --> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace
				50/50	HBV/HCV	755	1		39	-	60	0,59 var. / m-
Normalization factor =		11,40		50/50	HBV/HCV	extracted	671	2	38	-	60	0,71 var. / m-
	=>			50/50	HBV/HCV	extracted	555	3	38	-	60	0,74 var. / m-
Ry/NF: Rx = 50 : 50 distribution of NFI				50/50	HBV/HCV	extracted	687	4	38	-	60	0,72 var. / m-
to be expected in case of coupled				50/50	HBV/HCV	extracted	704	5	39	-	60	0,71 var. / m-
signal generation				50/50	HBV/HCV	extracted	772	6	39	-	60	0,62 var. / m-
	=>		NFI ratio = 1,0	50/50	HBV/HCV	extracted	704	7	36	-	60	0,65 var. / m-
else:	85 : 15		5,67	50/50	HBV/HCV	extracted	700	8	36	-	60	0,62 var. / m-
	80 : 20		4,00	50/50	HBV/HCV	extracted	539	9	38	-	60	0,57 var. / m-
	75 : 25		3,00	50/50	HBV/HCV	extracted	537	10	37	-	60	0,55 var. / m-
	70 : 30		2,33	50/50	HBV/HCV	extracted	737	11	37	-	60	0,61 var. / m-
	65 : 35		1,86	50/50	HBV/HCV	extracted	625	12	33	-	60	0,64 var. / m-
	60 : 40		1,50	50/5000	HBV/HCV	extracted	353	13	34	-	60	0,43 var. / m+
	55 : 45		1,22	50/5000	HBV/HCV	extracted	717	14	32	-	60	0,50 var. / m+
	53 : 47		1,13	50/5000	HBV/HCV	extracted	639	15	31	-	60	0,50 var. / m+
				50/5000	HBV/HCV	extracted	711	16	32	-	60	0,50 var. / m+
	47 : 53		0,89	50/5000	HBV/HCV	extracted	424	17	34	-	60	0,37 var. / m+
	45 : 55		0,82	50/5000	HBV/HCV	extracted	492	18	34	-	60	0,39 var. / m+
	40 : 60		0,67	50/5000	HBV/HCV	extracted	588	19	26	-	60	0,49 var. / m+
	35 : 65		0,54	50/5000	HBV/HCV	extracted	495	20	32	-	60	0,41 var. / m+
	30 : 70		0,43	50/5000	HBV/HCV	extracted	425	21	34	-	60	0,39 var. / m+
	25 : 75		0,33	50/5000	HBV/HCV	extracted	187	22	33	-	60	0,46 var. / m+
	20 : 80		0,25	50/5000	HBV/HCV	extracted	607	23	26	-	60	0,51 var. / m+
	15 : 85		0,18	50/5000	HBV/HCV	extracted	667	24	26	-	60	0,52 var. / m+



Ry =	JA274	Rx =	FAM	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI --> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace
				25	HBV extracted	395		1	47	-	60	1,01 constant
Normalization factor =		12,00		25	HBV extracted	423		2	46	-	60	1,15 borderline
=>				25	HBV extracted	582		3	46	-	60	1,19 borderline
Ry/NF: Rx = 50 : 50 distribution of NFI				25	HBV extracted	448		4	46	-	60	1,10 constant
to be expected in case of coupled				25	HBV extracted	495		5	46	-	60	1,12 constant
signal generation				25	HBV extracted	605		6	46	-	60	0,99 constant
=>		NFI ratio = 1,0		10000	HBV extracted	882		7	39	-	60	1,00 constant
else:	85 : 15		5,67	10000	HBV extracted	843		8	39	-	60	0,97 constant
	80 : 20		4,00	10000	HBV extracted	772		9	39	-	60	0,94 constant
	75 : 25		3,00	10000	HBV extracted	743		10	38	-	60	0,97 constant
	70 : 30		2,33	10000	HBV extracted	971		11	38	-	60	0,98 constant
	65 : 35		1,86	10000	HBV extracted	868		12	39	-	60	0,99 constant
	60 : 40		1,50	1:1000/50	HIV-1-O/HCV extracted	74		13	47	-	60	0,43 offset
	55 : 45		1,22	1:1000/50	HIV-1-O/HCV extracted	84		14	47	-	60	0,47 offset
	53 : 47		1,13	1:1000/50	HIV-1-O/HCV extracted	98		15	48	-	60	0,33 offset
				1:1000/50	HIV-1-O/HCV extracted	84		16	48	-	60	0,23 var. / m-
	47 : 53		0,89	1:1000/50	HIV-1-O/HCV extracted	76		17	47	-	60	0,30 offset
	45 : 55		0,82	1:1000/50	HIV-1-O/HCV extracted	81		18	---	-	---	4,25 #WERT!
	40 : 60		0,67	1:1000/500	HIV-1-O/HCV extracted	88		19	46	-	60	0,14 var. / m+
	35 : 65		0,54	1:1000/500	HIV-1-O/HCV extracted	86		20	47	-	60	0,17 offset
	30 : 70		0,43	1:1000/500	HIV-1-O/HCV extracted	85		21	45	-	60	0,16 offset
	25 : 75		0,33	1:1000/500	HIV-1-O/HCV extracted	88		22	45	-	60	0,11 offset
	20 : 80		0,25	1:1000/500	HIV-1-O/HCV extracted	59		23	45	-	60	0,13 offset
	15 : 85		0,18	1:1000/500	HIV-1-O/HCV extracted	76		24	45	-	60	0,14 var. / m+



Ry =	JA274	Rx =	FAM	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI -> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace
Normalization factor =		12,00		1:1000/6000	HIV-1-O/HCV	extracted	*75*	1	43	-	60	0,10 var. / m+
		=>		1:1000/5000	HIV-1-O/HCV	extracted	*89*	2	43	-	60	0,11 var. / m+
				1:1000/5000	HIV-1-O/HCV	extracted	*108*	3	43	-	60	0,11 var. / m+
Ry/NF: Rx = 60 : 50 distribution of NFI				1:1000/5000	HIV-1-O/HCV	extracted	*88*	4	43	-	60	0,12 var. / m+
to be expected in case of coupled				1:1000/5000	HIV-1-O/HCV	extracted	*102*	5	43	-	60	0,12 var. / m+
signal generation				1:1000/5000	HIV-1-O/HCV	extracted	*102*	6	43	-	60	0,11 var. / m+
=>		NFI ratio = 1,0		50/1:1000	HBV/HIV-1-O	extracted	538	7	50	-	60	1,18 offset
else:	85 : 15		5,67	50/1:1000	HBV/HIV-1-O	extracted	492	8	47	-	60	1,35 offset
	80 : 20		4,00	50/1:1000	HBV/HIV-1-O	extracted	646	9	55	-	60	1,24 offset
	75 : 25		3,00	50/1:1000	HBV/HIV-1-O	extracted	602	10	54	-	60	1,16 offset
	70 : 30		2,33	50/1:1000	HBV/HIV-1-O	extracted	687	11	45	-	60	1,24 offset
	65 : 35		1,86	50/1:1000	HBV/HIV-1-O	extracted	657	12	46	-	60	1,28 offset
	60 : 40		1,50	500/1:1000	HBV/HIV-1-O	extracted	691	13	43	-	60	1,14 offset
	55 : 45		1,22	500/1:1000	HBV/HIV-1-O	extracted	814	14	43	-	60	1,15 offset
	53 : 47		1,13	500/1:1000	HBV/HIV-1-O	extracted	812	15	43	-	60	1,18 offset
				500/1:1000	HBV/HIV-1-O	extracted	860	16	43	-	60	1,26 offset
	47 : 53		0,89	500/1:1000	HBV/HIV-1-O	extracted	744	17	43	-	60	1,15 offset
	45 : 55		0,82	500/1:1000	HBV/HIV-1-O	extracted	741	18	43	-	60	1,18 offset
	40 : 60		0,67	5000/1:1000	HBV/HIV-1-O	extracted	847	19	38	-	60	1,14 offset
	35 : 65		0,54	5000/1:1000	HBV/HIV-1-O	extracted	843	20	39	-	60	1,12 constant
	30 : 70		0,43	5000/1:1000	HBV/HIV-1-O	extracted	745	21	39	-	60	1,07 constant
	25 : 75		0,33	5000/1:1000	HBV/HIV-1-O	extracted	896	22	39	-	60	1,09 constant
	20 : 80		0,25	5000/1:1000	HBV/HIV-1-O	extracted	744	23	39	-	60	1,07 constant
	15 : 85		0,18	5000/1:1000	HBV/HIV-1-O	extracted	859	24	39	-	60	1,11 constant

Ry =	JA274	Rx =	FAM	[cp/ml]	analyte nucleic acid	SFI (Ry)	valid range (SFI --> AFI) for reaction #	=	min	[cycles]	max	NFI ratio (55-60) / trace	
				200/60	HBV/HCV extracted	720	1		45	-	60	0,69	var. / m-
Normalization factor =		12,00		200/60	HBV/HCV extracted	654	2		45	-	60	0,71	var. / m-
	=>			200/60	HBV/HCV extracted	704	3		44	-	60	0,88	offset
Ry/NF: Rx = 50 : 50 distribution of NFI				200/60	HBV/HCV extracted	672	4		46	-	60	0,72	offset
to be expected in case of coupled				200/60	HBV/HCV extracted	646	5		44	-	60	0,78	offset
signal generation				200/60	HBV/HCV extracted	670	6		44	-	60	1,01	constant
	=>	NFI ratio = 1,0		200/2000	HBV/HCV extracted	670	7		44	-	60	0,54	var. / m+
else:	85 : 15		5,67	200/2000	HBV/HCV extracted	706	8		44	-	60	0,53	var. / m+
	80 : 20		4,00	200/2000	HBV/HCV extracted	609	9		43	-	60	0,54	var. / m+
	75 : 25		3,00	200/2000	HBV/HCV extracted	637	10		43	-	60	0,57	var. / m+
	70 : 30		2,33	200/2000	HBV/HCV extracted	787	11		44	-	60	0,56	var. / m+
	65 : 35		1,86	200/2000	HBV/HCV extracted	681	12		43	-	60	0,56	var. / m+
	60 : 40		1,50	1000/60	HBV/HCV extracted	768	13		43	-	60	0,69	var. / m-
	55 : 45		1,22	1000/60	HBV/HCV extracted	854	14		43	-	60	0,77	offset
	53 : 47		1,13	1000/60	HBV/HCV extracted	862	15		42	-	60	0,80	offset
				1000/60	HBV/HCV extracted	800	16		43	-	60	0,79	offset
	47 : 53		0,89	1000/60	HBV/HCV extracted	703	17		44	-	60	0,72	var. / m-
	45 : 55		0,82	1000/60	HBV/HCV extracted	799	18		43	-	60	0,71	var. / m-
	40 : 60		0,67	10000/60	HBV/HCV extracted	646	19		38	-	60	0,98	constant
	35 : 65		0,54	10000/60	HBV/HCV extracted	758	20		38	-	60	0,61	var. / m-
	30 : 70		0,43	10000/60	HBV/HCV extracted	735	21		39	-	60	0,95	constant
	25 : 75		0,33	10000/60	HBV/HCV extracted	716	22		38	-	60	0,61	var. / m-
	20 : 80		0,25	10000/60	HBV/HCV extracted	535	23		37	-	60	0,72	var. / m-
	15 : 85		0,18	10000/60	HBV/HCV extracted	771	24		38	-	60	0,64	var. / m-

Fig. 5: we consider a panel of potentially ambiguous samples

assignments:			AmpDet efficiency:
P1	HIV-1-M	R1 / R2;	high
P2	HIV-1-O	R1;	low
P3	HIV-2	R2;	low
P4	HCV	R3;	high
P5	HBV	R1 / R3;	high
P6	CMV	R2 / R3;	medium
IC (internal control)		R4	

Roughly similar titres are assumed for all infections considered here.



model data set 3:	NFI values				NFI distribution; NFI ratios			SFI intensities	NFI trace as f(t)			Diagnosis
	Ch1	Ch2	Ch3	total		Ch1	Ch2	Ch3	(or differences)	R1/R2	R1/R3	R2/R3	
S1 =?	31	30	38	99	S1	32,90	32,13	35,97		signal in all target-related channels			
	34	33	33	100	S2	34,67	34,17	31,17	high	constant	variable / bias <> 1 / early	variable / bias <> 1 / early	Co-infection HIV-1-M and HCV
	32	35	33	100	S3	34,50	34,17	31,33					
	33	32	35	100	S4	33,67	33,50	32,83					
	32	30	38	100	S5	34,50	33,50	32,00					
	30	33	37	100	S6	33,17	33,17	33,67					
S2 = ?	3	15	82	100	*mean values (arithmetic)*				low-medium			variable / late / bias > 1	Co-infection HIV-2 and HCV
	2	20	78	100	*according to reference; deviating*								
	1	24	75	100									
	0	27	73	100		Ch1	Ch2	Ch3					
	1	20	79	100	S1	4,24	5,93	7,01					
	3	21	76	100	S2	3,63	12,21	6,67					
S3 = ?	24	49	27	100	S3	6,22	9,18	5,98		signal in all target-related channels			
	21	49	30	100	S4	4,90	4,65	2,26	medium	variable / bias < 1 / late	variable / bias > 1 / late	variable / bias > 1 / late	Co-infection HIV-1-M and HAV
	28	46	26	100	S5	6,42	2,68	5,57					
	27	44	29	100	S6	5,95	3,51	9,41					
	25	48	27	100	*threefold standard deviation*								
	22	53	25	100									
S4 = ?	52	48	0	100									
	50	49	1	100		Ch1	Ch2	Ch3	high		variable / late / bias > 1		Co-infection HBV and HIV-1-O
	47	52	1	100	P1	48	51	0					
	50	48	2	100	P2	100	0	0					
	49	50	1	100	P3	0	100	0					
	50	50	0	100	P4	0	0	100					
S5 = ?	48	1	52	99	P5	50	0	50					
	48	2	50	100	P6	0	50	50	low		variable / late / bias > 1		Co-infection HIV-1-O and HCV
	45	0	55	100	*NFI reference pattern*								
	49	0	51	100									
	46	1	53	100									
	47	2	51	100		Ch1	Ch2	Ch3					
S6 = ?	40	0	60	100	P1	16,50	16,50	5,00					
	41	1	58	100	P2	16,50	5,00	16,50	high		variable / early / bias < 1		Co-infection HBV and HCV
	43	1	56	100	P3	5,00	16,50	16,50					
	37	2	61	100	P4	5,00	5,00	16,50					
	42	3	55	100	P5	16,50	5,00	16,50					
	38	0	62	100	P6	5,00	16,50	16,50					

10% / 20%-off-set bands pertinent to 100% & 50%-mean values, and factor 5 pertinent to 6% values i.e. accepted ranges for reference pattern

legend: - variable / constant pertains to the NFI ratio along the reaction coordinate
- early / late denotes the approximation of the final value in case of var. ratios