

Table S1: Limit of Detection (LoD) for HCV Genotypes 1, 2, 3, and 4 by cobas 6800/8800 HCV and cobas 4800 HCV

		Detection of HCV	
		cobas 6800/8800 HCV	cobas 4800 HCV
Genotype 1	Nominal Titer (IU/mL) ^a	Nominal Titer (\log_{10} IU/mL)	% (#)
	1000	3.00	100 (40)
	100	2.00	100 (40)
	50	1.70	100 (40)
	25	1.40	100 (40)
	15	1.18	100 (40)
	10	1.00	97.5 (39)
	5	0.70	90 (36)
LoD by Probit [95% CI]		75 (30)	77.5 (31)
		8.2 [6.7, 14.4]	11.7 [8.9, 21.5]
Genotype 2	737	2.87	100 (40)
	74	1.87	100 (40)
	37	1.57	100 (40)
	18	1.26	100 (40)
	11	1.05	100 (40)
	7	0.87	97.5 (39)
	4	0.57	92.5 (37)
	LoD by Probit [95% CI]		95 (38)
		6.3 [4.9, 12.0]	87.5 (35)
		82.5 (33)	57.5 (23)
Genotype 3	585	2.77	100 (40)
	59	1.76	100 (40)
	29	1.46	100 (40)
	15	1.16	100 (40)
	9	0.94	100 (40)
	6	0.77	100 (40)
	3	0.46	90 (36)
	LoD by Probit [95% CI]		80 (32)
		6.1 [4.6, 11.1]	80 (32)
Genotype 4	558	2.75	100 (40)
	56	1.75	100 (40)
	28	1.45	100 (40)
	14	1.14	97.5 (39)
	8	0.92	94.9 (37/39) ^b
	6	0.75	87.5 (35)
	3	0.45	64.1 (25/39) ^b
	LoD by Probit [95% CI]		42.5 (17)
		13.7 [10.5, 21.6]	75 (30)
		64.1 (25/39) ^b	57.5 (23)
		42.5 (17)	20.0 (8)
		18.4 [14.2, 27.6]	

^a for GT2, 3, and 4, the values for the expected concentrations of each panel member were assigned using a linearization method on the mean observed titers from Abbott

^b Only 39 replicates for Genotype 4, at both 1.14 and 0.75 \log_{10} IU

Table S2: Observed HCV RNA concentration for genotypes 1-4 by cobas 6800/8800 HCV and cobas 4800 HCV

		Observed HCV RNA Concentration (\log_{10} IU/mL) ^a								
		cobas 6800/8800 HCV			cobas 4800 HCV					
Genotype 1	Nominal Titer (IU/mL) ^b	Nominal Titer (\log_{10} IU/mL)	Mean	SD [%CV]	Accuracy ^c	Linearity ^d	Mean	SD [%CV]	Accuracy ^c	Linearity ^d
	1000	3.00	3.04	0.07 [2.17]	0.04	-0.15	2.92	0.08 [2.79]	-0.08	-0.11
	100	2.00	2.15	0.08 [3.84]	0.15	-0.04	2.01	0.10 [5.03]	0.01	-0.02
	50	1.70	1.92	0.11 [5.64]	0.22	0.03	1.67	0.18 [10.52]	-0.03	-0.06
	25	1.40	1.65	0.18 [10.80]	0.26	0.07	1.46	0.14 [9.72]	0.06	0.03
	15	1.18	1.46	0.15 [10.06]	0.29	0.1	1.37	0.11 [8.13]	0.19	0.16
	10	1.00								
	5	0.70								
Genotype 2	737	2.87	3.05	0.12 [3.86]	0.19	-0.09	2.87	0.12 [4.05]	0	-0.05
	74	1.87	2.13	0.10 [4.50]	0.26	-0.02	1.91	0.13 [6.77]	0.04	-0.01
	37	1.57	1.90	0.08 [4.31]	0.33	0.05	1.57	0.14 [11.52]	0	-0.05
	18	1.26	1.61	0.16 [10.13]	0.34	0.06	1.42	0.15 [10.29]	0.16	0.11
	11	1.05								
	7	0.87								
	4	0.57								
Genotype 3	585	2.77	2.97	0.06 [2.16]	0.21	-0.04	2.97	0.10 [3.68]	0.21	-0.04
	59	1.76	2.02	0.08 [4.07]	0.26	0.01	2.02	0.14 [8.00]	0.26	0.01
	29	1.46	1.75	0.14 [8.04]	0.29	0.04	1.75	0.14 [9.30]	0.29	0.04
	15	1.16								
	9	0.94								
	6	0.77								
Genotype 4	3	0.46								
	558	2.75	2.74	0.07 [2.64]	0	-0.07	2.52	0.09 [3.71]	-0.23	-0.08
	56	1.75	1.83	0.11 [6.08]	0.08	0.01	1.61	0.15 [9.56]	-0.13	0.01
	28	1.45	1.57	0.16 [10.16]	0.13	0.06	1.38	0.12 [8.41]	-0.06	0.08
	14	1.14								
	8	0.92								
	6	0.75								
	3	0.45								

^a Calculated for all measurements from samples with nominal concentrations above LoD/LLoQ (i.e., above $1.18 \log_{10}$ IU)

^b for GT2, 3, and 4, the values for the expected concentrations of each panel member were assigned using a linearization method on the mean observed titers from

^c Accuracy = Observed Mean (\log_{10} IU/mL) – Nominal Concentration (\log_{10} IU/mL)

^d Linearity = Observed Mean (\log_{10} IU/mL) – Linearized (\log_{10} IU/mL)

SD = standard deviation; CV = coefficient of variation

Table S3: Limit of Detection (LoD) and Observed HCV RNA concentration for genotypes 1, 2, 3, and 4 by CAP/CTM v.2

		Observed HCV RNA Concentration (\log_{10} IU/mL) ^a					
	Nominal Titer (IU/mL) ^b	Nominal Titer (\log_{10} IU/mL)	% Detection of HCV (# of n=40 replicates)	Mean	SD [CV%]	Accuracy ^c	Linearity ^d
Genotype 1	1000	3.00	100 (40)	3.13	0.06 [1.90]	0.13	0.04
	100	2.00	100 (40)	2.10	0.13 [6.23]	0.1	0.02
	50	1.70	100 (40)	1.69	0.19 [11.36]	-0.01	-0.09
	25	1.40	100 (40)	1.47	0.13 [9.19]	0.07	-0.02
	15	1.18	92.5 (37)	1.32	0.12 [8.90]	0.14	0.06
	10	1.00	87.5 (35)				
	5	0.70	50 (20)				
	LoD by Probit [95% CI]		14.4 [12.0, 19.0]				
Genotype 2	737	2.87	100 (40)	3.15	0.06 [2.05]	0.28	0.03
	74	1.87	100 (40)	2.11	0.14 [6.50]	0.25	-0.01
	37	1.57	100 (40)	1.81	0.20 [10.85]	0.24	-0.01
	18	1.26	100 (40)	1.51	0.20 [13.32]	0.24	-0.01
	11	1.05	100 (40)				
	7	0.87	92.5 (37)				
	4	0.57	62.5 (25)				
	LoD by Probit [95% CI]		7.6 [6.2, 11.5]				
Genotype 3	585	2.77	100 (40)	3.04	0.05 [1.75]	0.27	0.01
	59	1.76	100 (40)	2.05	0.11 [5.52]	0.28	0.03
	29	1.46	100 (40)	1.68	0.16 [9.57]	0.22	-0.04
	15	1.16	100 (40)				
	9	0.94	97.5 (39)				
	6	0.77	100 (40)				
	3	0.46	80 (32)				
	LoD by Probit [95% CI]		5.0 [3.8, 9.0]				
Genotype 4	558	2.75	100 (40)	2.95	0.06 [2.02]	0.21	0.05
	56	1.75	100 (40)	1.90	0.23 [11.93]	0.15	-0.01
	28	1.45	100 (40)	1.55	0.18 [11.31]	0.11	-0.05
	14	1.14	90 (36)				
	8	0.92	70 (28)				
	6	0.75	57.5 (23)				
	3	0.45	52.5 (21)				
	LoD by Probit [95% CI]		19.5 [14.5, 32.6]				

^a Calculated for all measurements from samples with nominal concentrations above LoD/LLoQ (i.e., above 1.18 \log_{10} IU)

^b for GT2, 3, and 4, the values for the expected concentrations of each panel member were assigned using a linearization method on the mean observed titers from Abbott m2000 HCV, and rounded to the nearest IU

^c Accuracy = Observed Mean (\log_{10} IU/mL) – Nominal Concentration (\log_{10} IU/mL)

^d Linearity = Observed Mean (\log_{10} IU/mL) – Linearized (\log_{10} IU/mL)

SD = standard deviation; CV = coefficient of variation

Table S4: Limit of Detection (LoD) and Observed HCV RNA concentration for genotype 1 by HPS/CTM v2

Observed HCV RNA Concentration (\log_{10} IU/mL) ^a						
Nominal Titer (IU/mL)	Nominal Titer (\log_{10} IU/mL)	% Detection of HCV (# of n=40 replicates)	Mean	SD [CV%]	Accuracy ^b	Linearity ^c
1000	3.00	100 (40)	3.03	0.06 [2.12]	0.03	-0.06
100	2.00	100 (40)	2.10	0.10 [4.97]	0.1	0.01
50	1.70	100 (40)	1.79	0.11 [5.94]	0.09	0
25	1.40	100 (40)	1.54	0.12 [7.54]	0.15	0.05
15	1.18	100 (40)				
10	1.00	100 (40)				
5	0.70	90 (36)				
LoD by Probit [95% CI]		6.81 [0.26, 14.59]				

^a Calculated for all measurements from samples with nominal concentrations above LoD/LLoQ (i.e., above 1.18 \log_{10} IU)

^b Accuracy = Observed Mean (\log_{10} IU/mL) – Nominal Concentration (\log_{10} IU/mL)

^c Linearity = Observed Mean (\log_{10} IU/mL) – Linearized (\log_{10} IU/mL)

SD = standard deviation; CV = coefficient of variation

**Table S5. Distribution of sample results across cobas 6800/8800 HCV versus CAP/CTM HCV v2
(log₁₀ IU/mL)**

cobas 6800/8800 HCV	CAP/CTM v2				Total
	Target not detected	< 15 IU/mL	15 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target not detected	45	1	0	0	46
< 15 IU/mL	2	2	1	0	5
15 to 1E+08 IU/mL	1	8	185	0	194
> 1E+08 IU/mL	0	0	0	0	0
Total	48	11	186	0	245

Note: The lower limit of quantitation (LLOQ) of both cobas 6800/8800 HCV and CAP/CTM v2

is 15 IU/mL. The common linear range of both assays is 15 to 1E+08 IU/mL.

CAP/CTM v2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; HCV= hepatitis C virus

**Table S6. Distribution of sample results across cobas 6800/8800 HCV versus HPS/CTM v2
(\log_{10} IU/mL)**

cobas 6800/8800 HCV	HPS/CTM v2				Total
	Target not detected	< 25 IU/mL	25 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target not detected	42	4	0	0	46
< 25 IU/mL	1	6	1	0	8
25 to 1E+08 IU/mL	1	12	177	0	190
> 1E+08 IU/mL	0	0	0	0	0
Total	44	22	178	0	244

Note: The lower limit of quantitation (LLOQ) of cobas 6800/8800 HCV is 15 IU/mL and for

HPS/CTM v2 it is 25 IU/mL. The common linear range of both assays is 25 to 1E+08 IU/mL.

HCV= hepatitis C virus; HPS/CTM v2 = COBAS® TaqMan® HCV Test, version 2 for use with the

High Pure System

**Table S7. Distribution of sample results across cobas 6800/8800 HCV versus cobas 4800 HCV
(\log_{10} IU/mL)**

cobas 4800 HCV	cobas 6800/8800 HCV				Total
	Target not detected	< 15 IU/mL	15 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target not detected	38	1	2	0	41
< 15 IU/mL	3	0	6	0	9
15 to 1E+08 IU/mL	1	2	174	0	177
> 1E+08 IU/mL	0	0	0	0	0
Total	42	3	182	0	227

Note: The lower limit of quantitation (LLOQ) for both cobas 4800 HCV and cobas 6800/8800

HCV is 15 IU/mL. The common linear range of both assays is 15 to 1E+08 IU/mL.

HCV = hepatitis C virus

Table S8. Distribution of sample results across cobas 4800 HCV versus CAP/CTM v2 (\log_{10} IU/mL)

cobas 4800 HCV	CAP/CTM v2				Total
	Target not detected	< 15 IU/mL	15 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target not detected	41	1	0	0	42
< 15 IU/mL	3	2	4	0	9
15 to 1E+08 IU/mL	1	6	170	0	177
> 1E+08 IU/mL	0	0	0	0	0
Total	45	9	174	0	228

Note: The lower limit of quantitation (LLOQ) for both cobas 4800 HCV and CAP/CTM v2 is 15 IU/mL. The common linear range of both assays is 15 to 1E+08 IU/mL.

CAP/CTM v2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; HCV= hepatitis C virus

Table S9. Distribution of sample results across cobas 4800 HCV versus HCV HPS v2 (\log_{10} IU/mL)

cobas 4800 HCV	HPS/CTMv2				Total
	Target Not Detected	< 25 IU/mL	25 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target Not Detected	39	3	0	0	42
< 25 IU/mL	1	14	4	0	19
25 to 1E+08 IU/mL	0	4	162	0	166
> 1E+08 IU/mL	0	0	0	0	0
Total	40	21	166	0	227

Note: The lower limit of quantitation (LLOQ) cobas 4800 HCV is 15 IU/mL and for HCV HPS v2

it is 25 IU/mL. The common linear range of both assays is 25 to 1E+08 IU/mL.

HCV= hepatitis C virus; HPS/CTM v2 = COBAS® TaqMan® HCV Test, version 2 for use with the High Pure System.

Table S10. Distribution of sample results across HPS/CTM v2 versus CAP/CTM v2 (\log_{10} IU/mL)

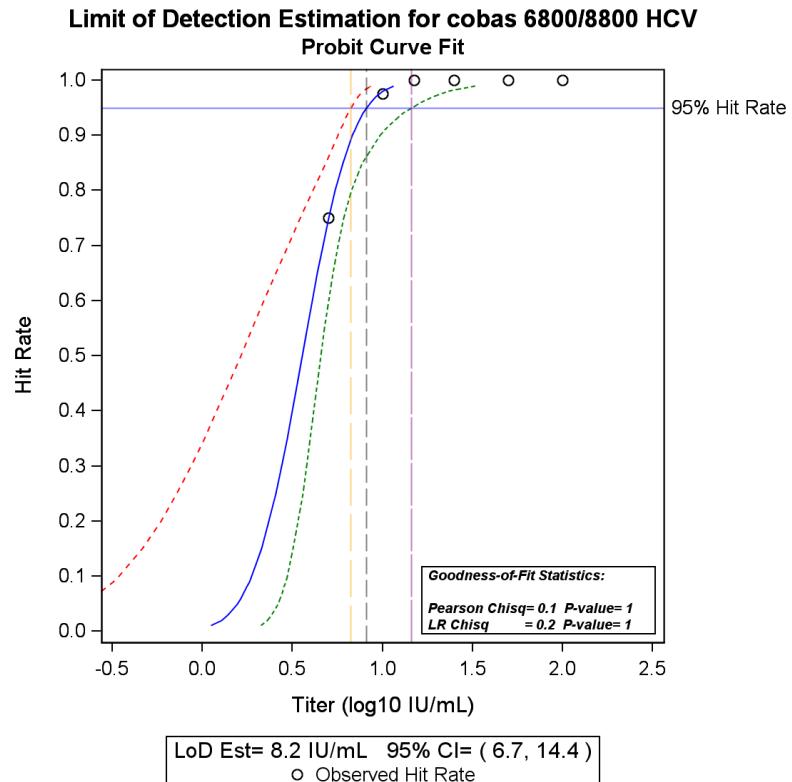
HPS/CTM v2	CAP/CTM v2				Total
	Target Not Detected	< 25 IU/mL	25 to 1E+08 IU/mL	> 1E+08 IU/mL	
Target Not Detected	44	0	0	0	44
< 25 IU/mL	5	12	6	0	23
25 to 1E+08 IU/mL	0	6	172	0	178
> 1E+08 IU/mL	0	0	0	0	0
Total	49	18	178	0	245

Note: The lower limit of quantitation (LLOQ) of HPS/CTM v2 is 25 IU/mL and for CAP/CTM v2

it is 15 IU/mL. Hence, the common linear range of both assays is 25 to 1E+08 IU/mL.

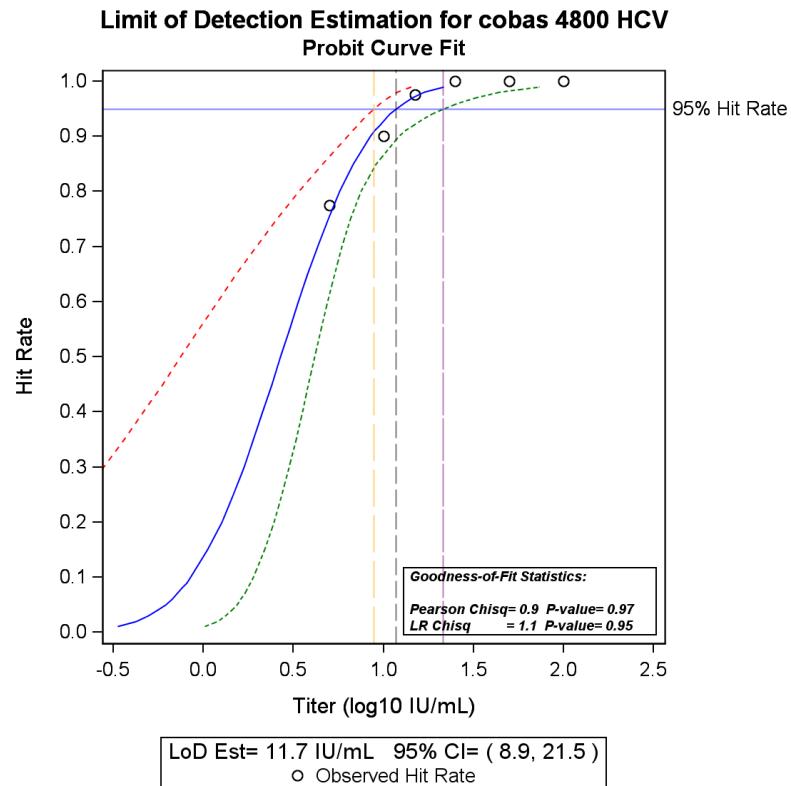
CAP/CTM v2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; HCV = hepatitis C virus; HPS/CTM v2 = COBAS® TaqMan® HCV Test, version 2 for use with the High Pure System.

Figure S1. Limit of detection for cobas 6800/8800 HCV for genotype 1



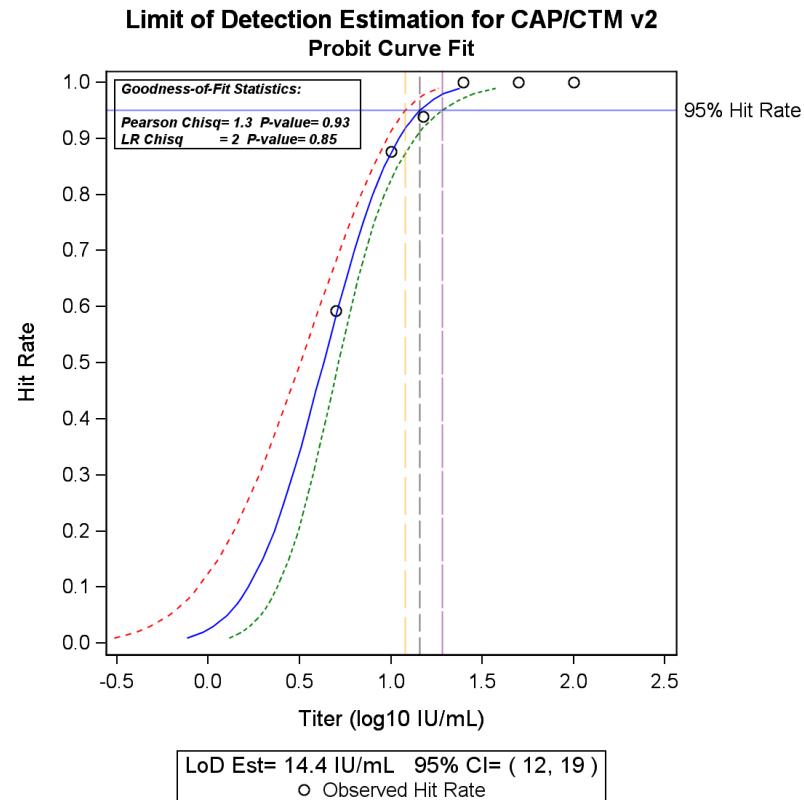
CI = confidence interval; HCV= hepatitis C virus; LOD = limit of detection

Figure S2. Limit of detection for cobas 4800 HCV for genotype 1



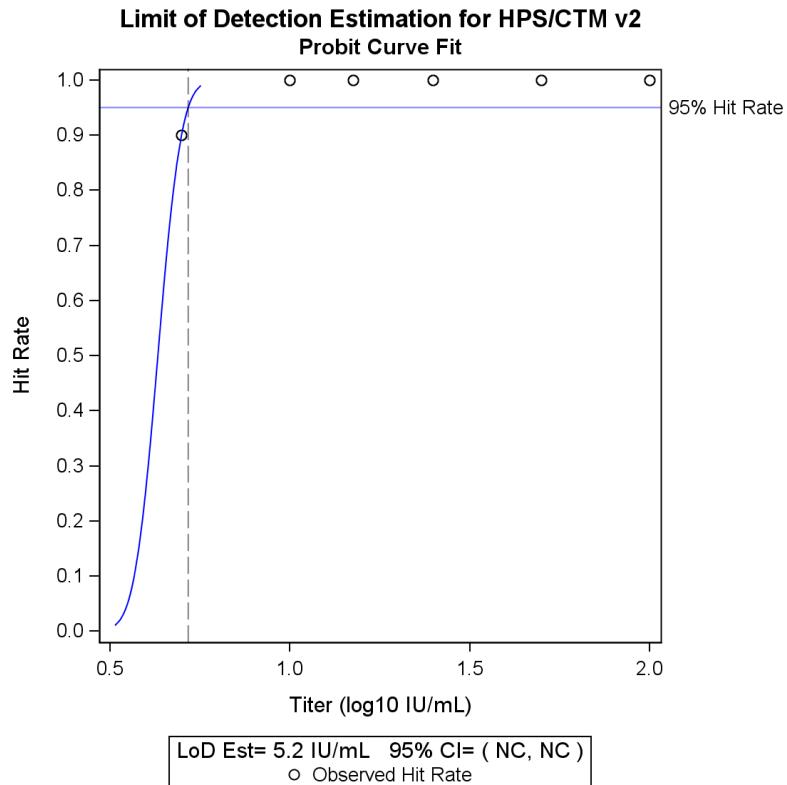
CI = confidence interval; HCV= hepatitis C virus; LOD = limit of detection

Figure S3. Limit of detection estimation for CAP/CTM v2 for genotype 1



CAP/CTMv2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; CI = confidence interval; HCV= hepatitis C virus; LOD = limit of detection

Figure S4. Limit of detection estimation for HPS/CTM v2 for genotype 1



CI = confidence interval; HCV= hepatitis C virus; HPS/CTMv2 = COBAS[®] TaqMan[®] HCV Test, version 2 for use with the High Pure System; LOD = limit of detection

Figure S5a. Deming regression plot for cobas 4800 HCV versus CAP/CTM v2 (n=170)

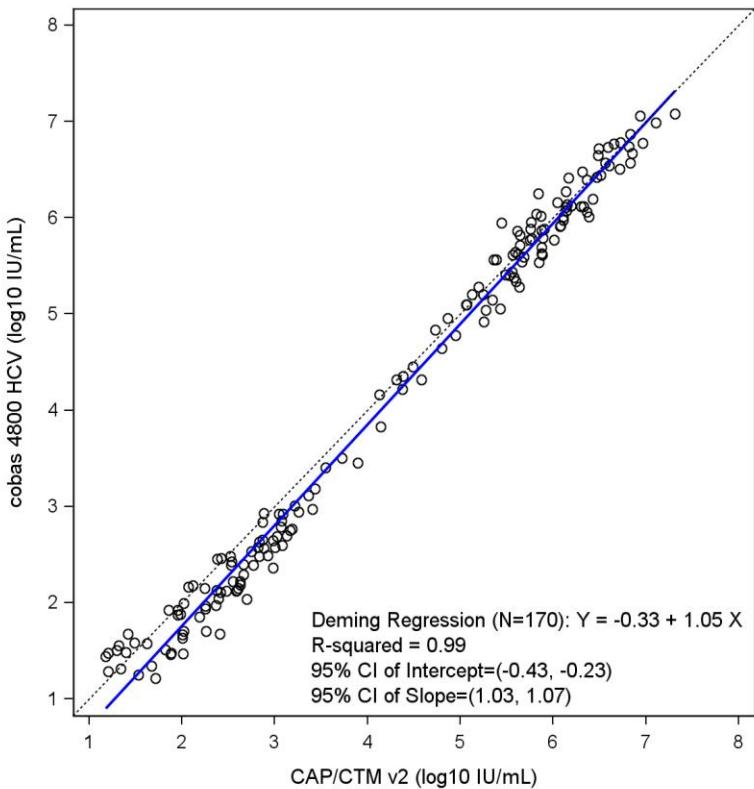
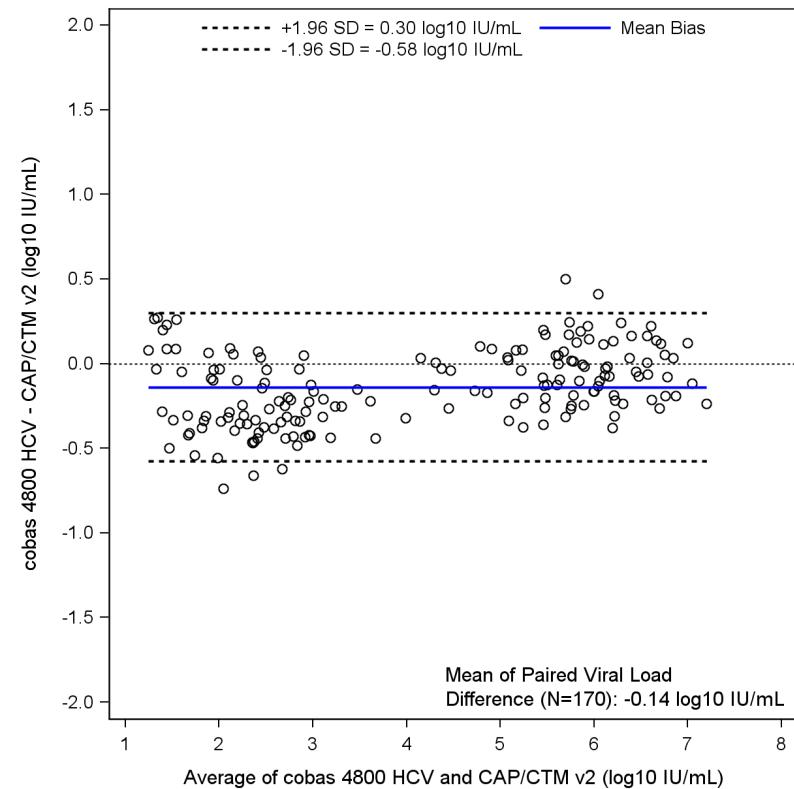


Figure S5b. Bland Altman plot for cobas 4800 HCV versus CAP/CTM v2 (n=170)



CAP/CTMv2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; CI = confidence interval; HCV= hepatitis C virus

Figure S6a. Deming regression plot for cobas 4800 HCV versus HPS/CTM v2 (n=162)

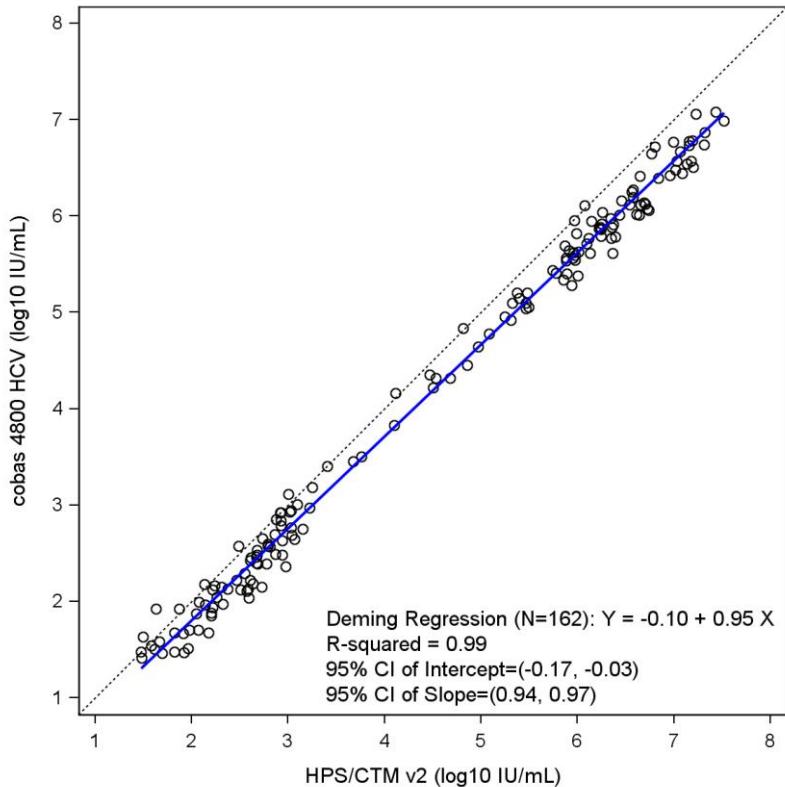
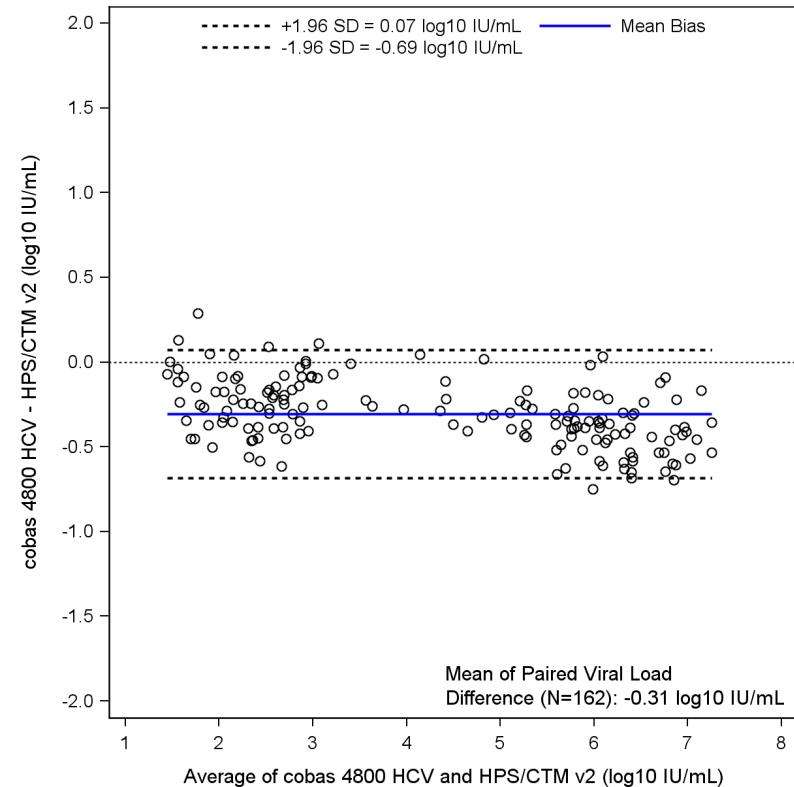


Figure S6b. Bland Altman plot for cobas 4800 HCV versus HPS/CTM v2 (n=162)



CI = confidence interval; HCV= hepatitis C virus; HPS/CTMv2 = COBAS® TaqMan® HCV Test, version 2 for use with the High Pure System

Figure S7a. Deming regression plot for HPS/CTM v2 versus CAP/CTM v2 (n=172)

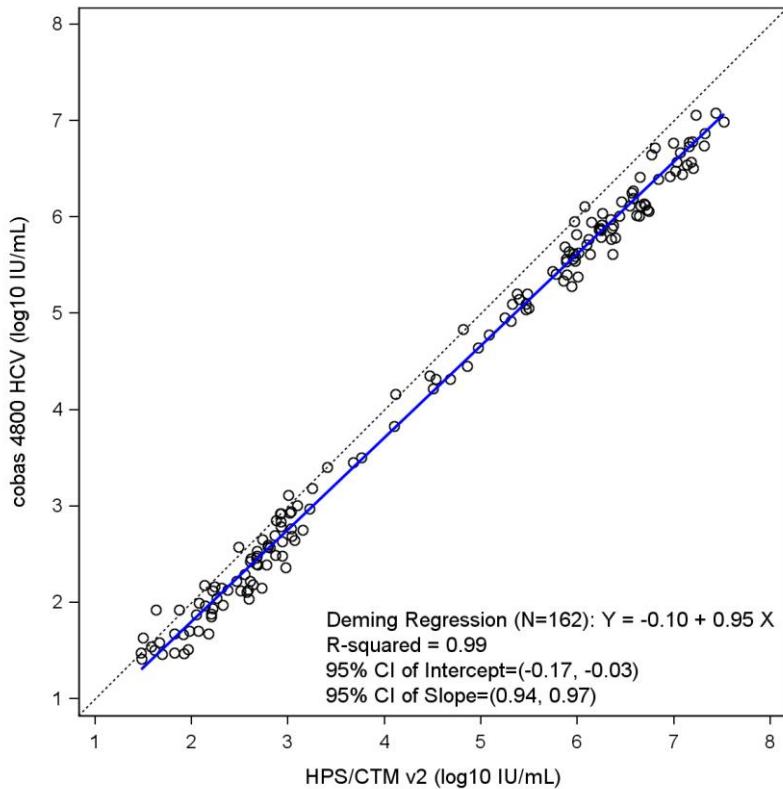
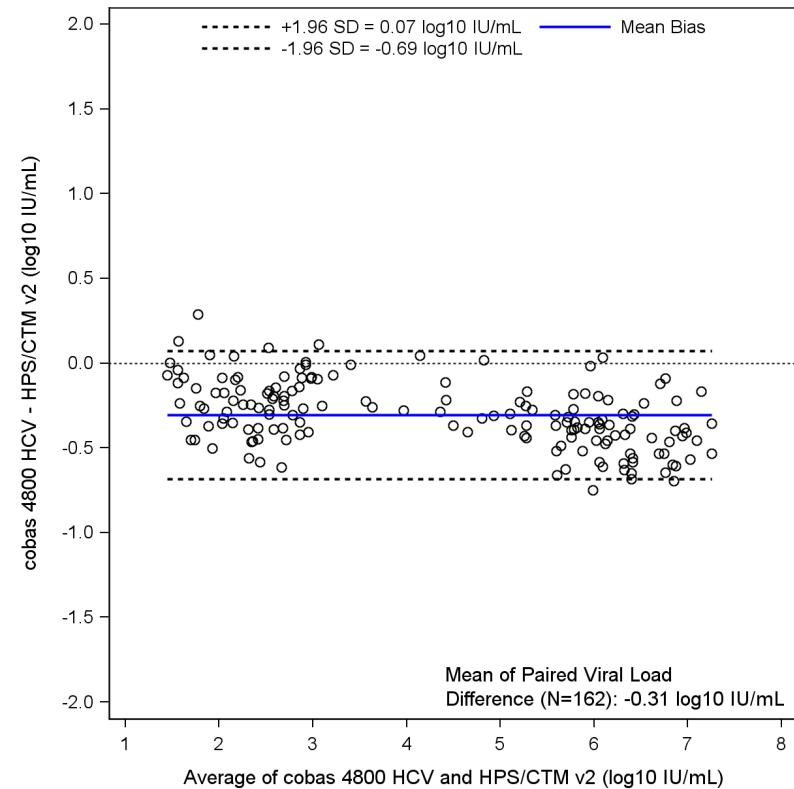


Figure S7b. Bland Altman plot for HPS/CTM v2 versus CAP/CTM v2 (n=172)



CAP/CTMv2 = COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, version 2.0; CI = confidence interval; HCV= hepatitis C virus; HPS/CTMv2 = COBAS® TaqMan® HCV Test, version 2 for use with the High Pure System