

Appendix

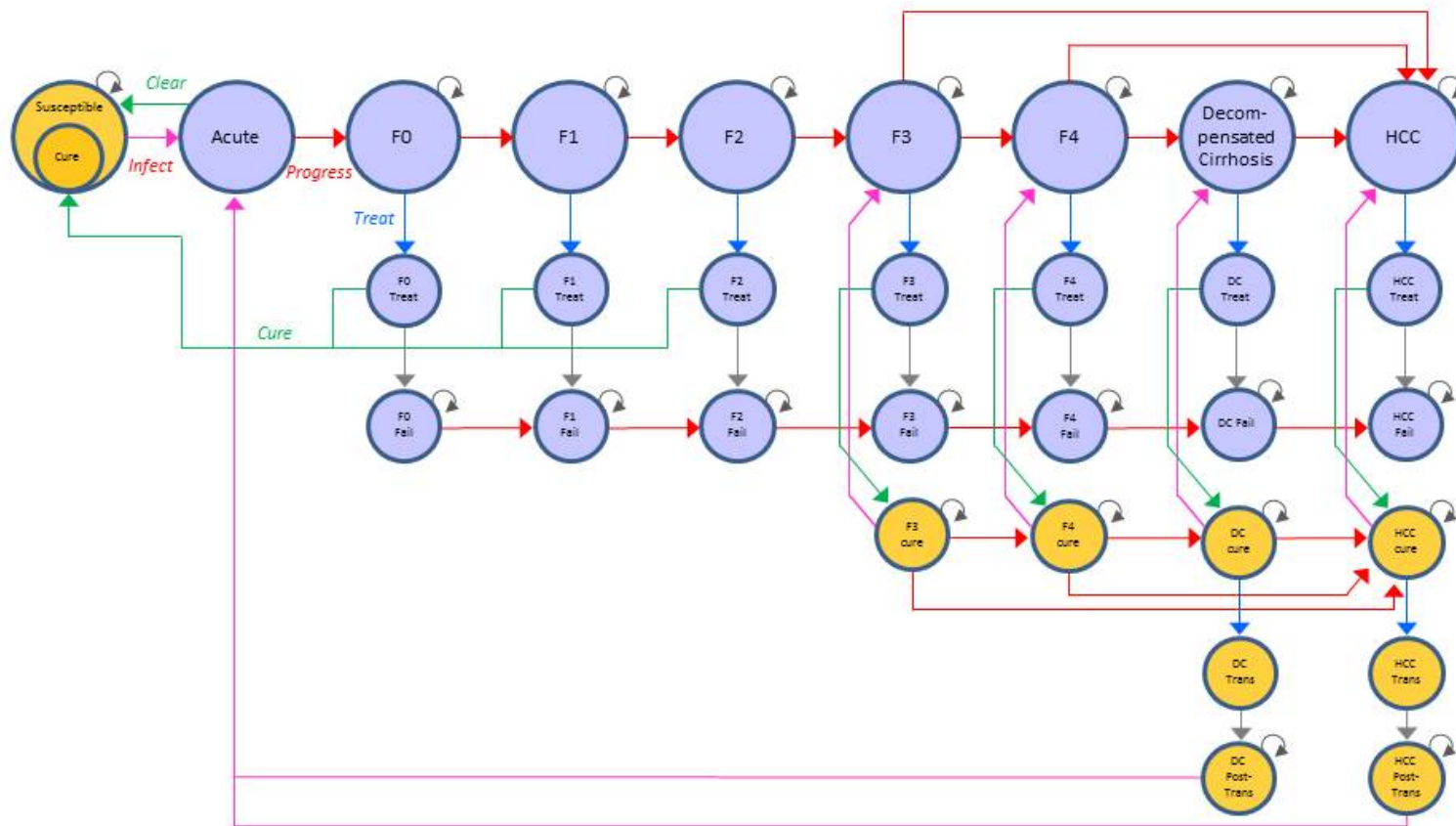
Conceptual Model

The hepatitis C virus (HCV) is a transmissible viral infection that is often asymptomatic in the early stages of the disease, but can progress to serious liver complications including cirrhosis and hepatocellular cancer over years or decades with grave consequences for health and medical costs. (1-3) A discrete time Markov model was developed in Excel to simulate the progression of an HCV-susceptible population through infection, acute, and then chronic HCV, as depicted in Exhibit A1 below. The population in each stage of disease was updated at each time step by cycling the model. The time step (or model cycle duration) was taken to be one year. The Metavir scoring system, designed to quantify the degree of liver fibrosis in patients with liver diseases such as HCV, was used to define disease severity for different stages of the model.(4) The Metavir scoring system is described in Table A1.

Table A1. Metavir Stage Descriptions (4)

Stage	Description
0	No fibrosis
1	Periportal fibrotic expansion
2	Periportal septae (septum)
3	Porto-central septae
4	Compensated cirrhosis

Exhibit A1. Hepatitis C Transmission Simulation Model Schematic



SOURCE Authors' analysis.

NOTES: All states have transitions to "dead." "Trans" = Transplant. Red Arrow = Progression; Blue Arrow = Treat; Green Arrow = Cure; Pink Arrow = Transmission. Blue shading of a shape indicates infectious/infected population. Yellow shading of a shape indicates uninfected and susceptible population.

Upon initial infection, patients enter an “acute” phase which they must leave after one model cycle. They may die, spontaneously clear the disease without treatment, or progress to “chronic” disease, consisting of seven stages of liver damage: Metavir scores F0-F4, decompensated cirrhosis (DC) and hepatocellular carcinoma (HCC). Patients may stay in any disease state except acute for more than one cycle.

Patients in stage F0 or higher may receive HCV treatment during the simulation; if not cured, treated patients may progress or die at the same rates as infected and untreated patients. If HCV is cured in stages F0-F2, patients are no longer infectious and liver damage is assumed to be reversed.(5, 6) These patients return to the susceptible population with healthy livers; if re-infected, they re-commence disease progression at the acute stage.

Patients cured of HCV in stages F3 and higher are no longer infectious, but may progress to additional liver damage more slowly than patients with uncured HCV.(7) They are susceptible for re-infection at the same rate as patients without liver damage, but if re-infected, re-enter the infected population with their existing level of liver damage. Patients with DC or HCC who are cured of HCV are no longer infectious and become eligible for liver transplants. The transplant stage lasts exactly one cycle, after which patients move to a post-transplant state. If these patients are re-infected, they re-enter the infected population with healthy livers at the acute stage. Consistent with current clinical practice, patients who are co-infected with HIV (all patients in the sexual exposure group, more details described below) are not eligible for liver transplants.(8, 9)

Populations Modeled

Three distinct subpopulations are modeled, defined by their HCV exposure route: healthcare (HC), injection drug use (PWID), and sexual (SX). The three exposure groups are modeled independently—an individual can belong to only one exposure group for the duration of the simulation. There is assumed to be no ongoing transmission in the HC exposure group, since effective screening of blood products for HCV was introduced in 1992. Because it is a closed cohort, the HC population shrinks over time, and is assumed to be aging and subject to increasing mortality rates over the course of a simulation. The PWID and SX exposure groups are assumed to have constant mortality rates and experience ongoing entry and exit such that their size remains constant over the simulation.

Within each exposure group, the three HCV genotypes most common in the US (genotypes 1, 2 and 3) are modeled.(10) This permits us to model HCV prevalence and transmission with greater nuance, and to account for the fact that different genotypes respond differently to treatment; (11) may progress at different rates; (12, 13) and involve different mortality risks.(14) Patients may only be infected with one genotype at a time, but once cured, a patient can be re-infected with any of the three genotypes.

Transmission Function

In the PWID and SX exposure groups, for each genotype, the rate at which individuals are infected is modeled dynamically as a function of the number in the exposure group who are currently infected with the given genotype. Individuals who are uninfected (susceptible) at the beginning of a year t are at risk of becoming HCV infected and the probability of becoming infected during year t (i.e., the annual incidence rate) is given by:

$$Pr(\text{infected}_{t+1}|\text{susceptible}_t) = K \times \frac{N_t^{\text{infected}}}{N_t^{\text{infected}} + N_t^{\text{susceptible}}} \quad (1)$$

where t is the year, N_t^{infected} is the number of people infected at the beginning of year t , and $N_t^{\text{susceptible}}$ is the number of people susceptible at the beginning of year t . The transmission model specified by equation (1) assumes that the incidence rate is proportional to the fraction of individuals in an exposure group who are infected. The proportionality constant K is calibrated to ensure that the incidence rate (the left side of equation 1) matches the empirical estimate of disease incidence rate at model start ($t=0$):

$$K = \frac{(\text{incidence rate})(N_{t_0}^{\text{infected}} + N_{t_0}^{\text{susceptible}})}{N_{t_0}^{\text{infected}}} \quad (2)$$

The incidence rates and proportionality constants K for each exposure group by genotype are reported in Table A2.

Table A2. Starting Annual Incidence Rates and Values of K

	Annual Incidence Rate	Calculated K
Healthcare Exposure		
Genotype 1	0	0
Genotype 2	0	0
Genotype 3	0	0
Injection Drug Use		
Genotype 1	0.016	0.039
Genotype 2	0.0036	0.039
Genotype 3	0.0027	0.039
Sexual Transmission		
Genotype 1	0.0065	0.040
Genotype 2	0.0014	0.040
Genotype 3	0.0011	0.040

SOURCE Williams et al. (2011) (15) and authors' calculations.

Treatment Scenarios

Four treatment scenarios are modeled, as described in the main article. They differ in terms of both which and how many patients are treated, and the treatments used. The Baseline scenario assumes that HCV treatment consists of the most effective regimen available prior to the introduction of direct-acting antivirals (DAA), which is pegylated interferon alpha plus ribavirin (PR). Regimens consisting of PR plus a first generation DAA such as telaprevir or boceprevir were also considered for the baseline scenario but ultimately rejected for several reasons: They have significantly worse side effect and adverse event profiles, cannot be used by large segments of the population due to potential interactions with many common drugs (statins, sulfonyleureas, benzodiazepines, etc.), and are unlikely to be cost-effective vs. PR in the US among patients with severe liver disease

such as those treated in the baseline scenario. In addition, both boceprevir and telaprevir have been withdrawn from the US market.

The other three scenarios assume that HCV treatment consists of the most effective regimen currently available. The Baseline and Treat Advanced scenarios are inspired by state Medicaid programs that limit access to newer treatments by requiring patients to meet clinical criteria — often requiring patients to undergo liver biopsy to establish that their liver disease severity has reached F3 or higher — to gain prior authorization. (16-20)

Regimen drugs, duration, efficacy and costs differ by infection genotype, as detailed in Table A3.

Table A3. Regimens, Duration and Efficacy for Four Treatment Scenarios Modeled

	Baseline			Treat Advanced			Treat All Diagnosed		Treat 5%		
Population treated	All diagnosed patients with F3 or greater			Same as Baseline			All diagnosed patients with F0 or greater		5% of patients with F0 or greater		
Drugs used	PR 48 weeks for GT1 PR 24 weeks for GT2/3			sofosbuvir + ledipasvir 12 wks for GT1 sofosbuvir + ribavirin 12 weeks for GT2 sofosbuvir + ribavirin 24 weeks for GT3			Same as Treat Advanced		Same as Treat Advanced		
<i>Regimen Cost</i>											
				Yr 1 (21-23)	Yrs 2-14 (21-23)	Yrs 15+ (21-23)					
Genotype 1	\$35,000(24)			\$100,000(25)	\$64,000	\$21,000	Same as Treat Advanced	Same as Treat Advanced			
Genotype 2	\$17,000(24)			\$100,000(25)	\$64,000	\$21,000					
Genotype 3	\$17,000(24)			\$200,000 (21, 22, 25)	\$128,000	\$42,000					
<i>Cure (SVR12) rates by disease stage</i>											
Genotype	F0-F2	F3	F4, DC, HCC	F0-F3		F4, DC, HCC		F0-F3	F4, DC, HCC	F0-F3	F4, DC, HCC
1	0.60 (26)	0.51 (26)	0.33 (26)	0.99 (27-29)		0.99 (27-29)		Same as Treat Advanced	Same as Treat Advanced		
2	0.76 (26)	0.61 (26)	0.57 (26)	0.97 (27-29)		0.91 (27-29)					
3	Same as GT2(26)			0.94 (27-29)		0.92 (27-29)					

The scenarios involve treating some fixed proportion of the prevalent population in *each* model cycle. The Treat All and Treat Advanced scenarios treat all prevalent patients who have been diagnosed with HCV in particular disease stages, which likely represents the maximum possible treatment group since only diagnosed patients can be treated. Current estimates of HCV diagnosis rates cluster around 50%.(30, 31) Once treated in the first model cycle, many of the currently diagnosed patients are cured and removed from the prevalent population, yet in subsequent model cycles, the same proportion of the remaining prevalent patients are treated. Thus, these aggressive treatment scenarios implicitly assume that prevalent patients continue to be diagnosed such that the diagnosis rate remains constant and the same proportion of prevalent patients is available for treatment.

The treatments used in the non-Baseline scenarios include drugs that are currently protected under patent, but that have seen stiff price competition from recent market entrants. To account for these pricing dynamics, the model reduces treatment costs by 46% (22) in years 2-14, to account for branded competition, and a further reduction of 33% in year 15, for a total reduction upon patent expiration of 79%, assumed to be the marginal cost of producing the drugs.(21)

Starting Populations

At model start, the size of the total infected population in the model across all disease stages is 2,700,000 people.(32) This includes 21,870 incident patients,(33) who are distributed across the three exposure groups according to estimates from Williams et al.,(15) and within each exposure group across three genotypes according to the prevalence of each genotype in the overall population, as estimated by Manos et al (2012).(10) These incident patients make up the populations in the acute phases at the start of the simulation. The remaining 2,678,130 non-incident infected population at model start are then distributed across exposure groups and genotypes following the same logic. These patients are then further distributed across disease stages as in Hagan (2014).(34-36) The distribution of the infected population by exposure group, genotype, and disease stage is given in Table A4.

Table A4. Size and distribution of model populations at start of simulation

		Healthcare Exposure	PWID	Sexual Exposure
Uninfected/Susceptible		74,415,696 (37)	777,354 (38)	461,600 (39)
Genotype 1	<i>Acute</i>	0	12,754	2,992
	<i>F0</i>	181,764	119,438	13,532
	<i>F1</i>	374,220	272,160	34,020
	<i>F2</i>	235,224	171,072	21,384
	<i>F3</i>	149,688	108,864	13,608
	<i>F4</i>	64,152	46,656	5,832
	<i>DC</i>	32,076	23,328	2,916
	<i>HCC</i>	32,076	23,328	2,916
Genotype 2	<i>Acute</i>	0	2,834	665
	<i>F0</i>	40,392	26,542	3,007
	<i>F1</i>	83,160	60,480	7,560
	<i>F2</i>	52,272	38,016	4,752
	<i>F3</i>	33,264	24,192	3,024
	<i>F4</i>	14,256	10,368	1,296
	<i>DC</i>	7,128	5,184	648
	<i>HCC</i>	7,128	5,184	648
Genotype 3	<i>Acute</i>	0	2,127	498
	<i>F0</i>	30,294	19,905	2,256
	<i>F1</i>	62,370	45,360	5,670
	<i>F2</i>	39,204	28,512	3,564
	<i>F3</i>	24,948	18,144	2,268
	<i>F4</i>	10,692	7,776	972
	<i>DC</i>	5,346	3,888	486
	<i>HCC</i>	5,346	3,888	486

SOURCE Authors' analysis and CDC (2014);(40) Manos (2012);(10) Williams (2011);(15) and Hagan (2014)(35)

Model Outputs

Each year, the model produces the number of people in every disease state. These disease-state populations are then multiplied by published estimates of annual per-person values for quality-adjusted life years (QALYs) in each disease state; each QALY is valued at \$150,000 to generate the total value of QALYs produced by a treatment scenario.(41) Other annual per-person estimates of economic measures including treatment costs and non-treatment medical expenditures are similarly applied to disease-state populations to generate population-wide estimates. These estimates are assumed to be constant over the duration of the simulation. Dollar values are discounted at 3% per year to produce present discounted values of future value streams.(42)

Patients who die within a cycle are assumed to transition out of the simulation following a uniform probability distribution with a mean of six months. Model outputs for such patients are calculated as half the values as for those who don't die during the cycle.

Model Parameters

Model parameters are taken from the published literature, with efforts made to find exposure group- and genotype-specific values wherever possible. The Healthcare exposure group was defined to be US residents born between 1945 and 1965, and contains the largest number of HCV-infected patients. It is modeled with a mortality rate that increases at 8% per year as the closed cohort ages over time.(43) Model parameters for the healthcare exposure cohort and their sources are provided in Table A5.

The PWID exposure group has the highest incidence rate, reflecting the greater transmission among this population. The PWID cohort also has the highest starting mortality rates for both the infected and uninfected populations.(44) Model parameters for the PWID cohort and their sources are provided in Table A6.

The Sexual exposure group is characterized by co-infection with HIV, which affects the progression of HCV (45), and in our analysis is principally composed of men who have sex with men. Model parameters for the Sexual exposure group and their sources are provided in Table A7.

Annual Mortality Rates

Disease stage-, exposure group-, and genotype-specific annual mortality rates were calculated as follows: the annual mortality rate for each exposure group was taken from the literature (37, 44, 46) and used for the background mortality rate for the uninfected population in that group. Since the healthcare exposure group is a closed cohort whose average age increases over the simulation, we assume that the background mortality rate grows at 8% per year in this group.(43) For the other two exposure groups, we assume a stable age distribution, or that the exiting of older individuals is offset by ongoing entry of younger individuals into these exposure groups, and assume a constant background mortality. While it is possible that improved treatments may lead to slight aging of these two exposure groups, those effects could be offset by younger ages at entry into the groups (e.g., younger age at initiation of drug use or sexual activity). Accordingly, in the absence of clear trends on the ages of initiation for these risk behaviors, we have opted for the simplest plausible assumption of a stable (stationary) age distribution in the PWID and sexual exposure groups over the time span of our forecasts.

To calculate the annual mortality rates for HCV-infected individuals with genotype 1 in stages acute-F2 in each exposure group, the group's background mortality rate was multiplied by 2.37, the ratio of the all-cause mortality rate of the HCV infected relative to the non-HCV infected based on the Third National Health and Nutrition Examination Survey.(47) To calculate the F3-F4 mortality rates for genotype 1 in each group, the F2 mortality rate was multiplied by 3.77, the ratio of mortality at fibrosis stages F3-F4 versus F2 from McCombs et al. (2014). (14) Annual mortality rate estimates for decompensated cirrhosis and hepatocellular carcinoma for genotype 1 in each exposure group were taken from Younossi et al. (2014).(48)

These genotype 1 mortality rate estimates were multiplied by 0.85 and 0.94 to create similar estimates for genotypes 2 and 3, respectively, based on the relative ratios for each genotype, from McCombs et al. (2014).(14)

Table A5. Model Parameters for the Healthcare Exposure Group, Genotypes 1-3 (citation numbers in parentheses)

	Genotype 1	Genotype 2	Genotype 3
Annual Mortality Rate			
Susceptible (Background)	0.006 (37)		
Acute, F0-F2	0.0142(47)	0.0121(14, 47)	0.0134(14, 47)
F3, F4	0.0536(14, 47)	0.0456(14, 47)	0.0504(14, 47)
DC	0.135(48-50)	0.1148(14, 48-50)	0.1269 (14, 48-50)
HCC	0.427(48, 51, 52)	0.363(14, 48, 51, 52)	0.4014 (14, 48, 51, 52)
Transplant ^a	0.165(53)		
Post-Transplant ^b	0.0226(14, 37)		
Annual Background Mortality Growth Rate	.08 (43)		
Annual Transition Probability			
Acute → Spontaneous Clearance	0.18 (54)		
F0 → F1	0.076 (36, 55, 56)		
F1 → F2	0.095 (36, 55, 56)		
F2 → F3	0.108 (36, 55, 56)		
F3 → F4	0.134 (36, 55, 56)		
F3 → HCC	0.008 (48, 57)	0.008 (48, 57)	0.0144 (12, 48, 57)
F4 → DC	0.039 (48, 49, 58)	0.0265 (12, 48, 58)	0.0507 (12, 48, 58)
F4 → HCC	0.025 (48, 49)	0.0138 (12, 48, 49)	0.045 (12, 48, 49)
DC → HCC	0.025 (48, 49)	0.0138 (12, 48, 49)	0.045 (12, 48, 49)
DC → Transplant	0.031 (59, 60)		
HCC → Transplant	0.103 (58, 59)		
F3 Cure → F4 Cure	0.0375 (7)		
F3 Cure → HCC Cure	0.0029 (7)		
F4 Cure → DC Cure	0.0109 (7)		
F4 Cure → HCC Cure	0.009 (7)		
DC Cure → HCC Cure	0.007 (7)		
QALY Weights			
Susceptible, Acute	0.86 (59, 61)		
F0-F1	0.84 (60, 61)		

	Genotype 1	Genotype 2	Genotype 3
F2, F3, F3 Cure		0.79,(60, 61)	
F4, F4 Cure		0.76 (59, 62)	
DC, DC Cure		0.69 (59, 62)	
DC Transplant^a		0.50 (59, 62)	
DC Post-Transplant^b		0.71 (9, 63)	
HCC, HCC Cure		0.67 (59, 62)	
HCC Transplant^a		0.5 (59, 62)	
HCC Post-Transplant^b		0.71 (9, 63)	
Annual Medical Expenditures			
Susceptible		\$6,894 (64)	
Acute, F0, F1, F2, F3		\$16,792 (65)	
F0 Fail, F1 Fail, F2 Fail, F3 Fail		\$10,915 (65, 66)	
F4		\$19,919 (65)	
F4 Fail		\$15,138 (65, 66)	
DC		\$55,649 (65)	
DC Fail		\$38,954 (65, 66)	
DC Transplant^a		\$160,040 (65)	
DC Post-Transplant^b		\$ 160,040 (65)	
HCC		\$123,405 (65)	
HCC Fail		\$86,384 (65, 66)	
HCC Transplant^a		\$160,040 (65)	
HCC Post-Transplant^b		\$160,040 (65)	

NOTE ^aYear of liver transplant; ^bAll subsequent years after liver transplant;

Table A6. Model Parameters for the PWID Exposure Group, Genotypes 1-3 (citation numbers in parentheses)

	Genotype 1	Genotype 2	Genotype 3
Annual Mortality Rate			
Susceptible	0.0264 (44)		
Acute, F0-F2	0.0626 (44, 47)	0.0532 (14, 44, 47)	0.0588 (14, 44, 47)
F3, F4	0.2359 (14, 44, 47)	0.2005 (14, 44, 47)	0.2217 (14, 44, 47)
DC	0.135 (48-50)	0.1148 (14, 48-50)	0.1269 (14, 48-50)
HCC	0.427 (48-50)	0.363 (14, 48-50)	0.4014 (14, 48-50)
Transplant ^a	0.1650 (53)		
Post-Transplant ^b	0.0995 (14, 44)		
Annual Transition Probability			
Acute → Spontaneous Clearance	0.18 (67)		
F0 → F1	0.116 (36, 68-73)		
F1 → F2	0.085 (36, 68-73)		
F2 → F3	0.085 (36, 68-73)		
F3 → F4	0.13 (36, 68-73)		
F3 → HCC	0.008 (48, 57)	0.008 (48, 57)	0.0144 (12, 48, 57)
F4 → DC	0.039 (48, 49, 58)	0.0265 (12, 48, 58)	0.0507 (12, 48, 58)
F4 → HCC	0.025 (48, 49, 58)	0.0138 (12, 48, 49)	0.045 (12, 48, 49)
DC → HCC	0.025 (48, 49, 58)	0.0138 (12, 48, 49)	0.045 (12, 48, 49)
DC → Transplant	0.031 (59, 60)		
HCC → Transplant	0.103 (58, 59)		
F3 Cure → F4 Cure	0.0364 (7)		
F3 Cure → HCC Cure	0.0029 (7)		
F4 Cure → DC Cure	0.0109 (7)		
F4 Cure → HCC Cure	0.009 (7)		
DC Cure → HCC Cure	0.007 (7)		
QALY Weights	Same as for healthcare exposure group. See Table A5 for values.		
Annual Medical Expenditures	Same across exposure groups and genotype. See Table A5 for values.		

NOTE ^aYear of liver transplant; ^bAll subsequent years after liver transplant

Table A7. Model Parameters for the Sexual Exposure Group, Genotypes 1-3 (citation numbers in parentheses)

	Genotype 1	Genotype 2	Genotype 3
Annual Mortality Rate			
Susceptible	0.0001 (46)		
Acute, F0-F2	0.0003 (46, 47)	0.0002 (14, 46, 47)	0.0003 (14, 46, 47)
F3, F4	0.001 (14, 46, 47)	0.0009 (14, 46, 47)	0.001 (14, 46, 47)
DC	0.135 (48-50)	0.1148 (14, 48-50)	0.1269 (14, 48-50)
HCC	0.427 (48-50)	0.363 (14, 48-50)	0.4014 (14, 48-50)
Transplant ^a	0.137 (74, 75)		
Post Transplant ^b	0.052 (74, 75)		
Annual Transition Probability			
Acute → Spontaneous Clearance	0.13 (76)		
F0 → F1	0.122 (45)		
F1 → F2	0.115 (45)		
F2 → F3	0.124 (45)		
F3 → F4	0.115 (45)		
F3 → HCC	0.016 (9, 48, 57, 77)	0.016 (9, 48, 57, 77)	0.0288 (12, 48, 57, 77)
F4 → DC	0.078 (9, 48, 49, 58, 78)	0.053 (12, 48, 49, 58, 78)	0.1014 (48, 49, 58, 78)
F4 → HCC	0.05 (9, 48, 49, 77)	0.0275 (12, 48, 49, 77)	0.09 (48, 49, 77)
DC → HCC	0.05 (9, 48, 49, 77)	0.0275 (12, 48, 49)	0.09 (48, 49)
DC → Transplant	0 (9)		
HCC → Transplant	0 (9)		
F3 Cure → F4 Cure	0.0322 (7)		
F3 Cure → HCC Cure	0.0058 (7)		
F4 Cure → DC Cure	0.0218 (7)		
F4 Cure → HCC Cure	0.018 (7)		
DC Cure → HCC Cure	0.014 (7)		
QALY Weights			
Susceptible, Acute	0.87 (8, 74)		
F0-F1	0.85 (8, 60, 74)		
F2, F3, F3 Cure	0.80 (8, 60, 74)		
F4, F4 Cure	0.68 (8, 74)		
DC, DC Cure	0.48 (8, 74)		
DC Transplant ^a	0.81 (8, 74)		
DC Post-Transplant ^b	0.81 (8, 74)		
HCC, HCC Cure	0.23 (8, 74)		
HCC Transplant ^a	0.81 (8, 74)		

	Genotype 1	Genotype 2	Genotype 3
HCC Post-Transplant^b	0.81 (8, 74)		
Medical Expenditures	Same across exposure groups and genotype. See Table A5 for values.		

NOTE ^aYear of liver transplant; ^bAll subsequent years after liver transplant

Sensitivity Analyses

We conducted sensitivity analyses along several dimensions, exploring the impact of changes in key variables on social value, total infected population after 50 years, and the time needed for the infected population to fall below 200,000, the threshold at which HCV would be considered a rare disease in the US.(79) These results are presented in Tables A8 and A9.

Table A8: Infected Population Results of Sensitivity Analyses on Key Model Parameters

	Model Outcome							
	Number Infected in Year 50				Years Until Rare Disease Status ⁷			
	Treat 5%	Baseline	Treat Advanced	Treat All Diagnosed	Treat 5%	Baseline	Treat Advanced	Treat All Diagnosed
Base Case Results	38,759	206,618	102,912	1,371	26	50+	36	7
Sensitivity Analyses	Treat 5%	Baseline	Treat Advanced	Treat All Diagnosed	Treat 5%	Baseline	Treat Advanced	Treat All Diagnosed
Increase starting infected population to 3.2 million	39,467	217,447	112,180	1,555	27	50+	38	N/C
QALYs valued at \$50K	N/C	N/C	N/C	N/C	N/C	50+	N/C	N/C
QALYs valued at \$100K	N/C	N/C	N/C	N/C	N/C	50+	N/C	N/C
QALYs valued at \$200K	N/C	N/C	N/C	N/C	N/C	50+	N/C	N/C
Allow retreatment in Baseline scenario ¹	N/C	191,736	N/C	N/C	N/C	48	N/C	N/C
Increase diagnosis rate ^{2,3}	N/C	N/C	N/C	N/C	N/C	50+	N/C	6
Reduce treatment rate ^{3,4}	N/C	210,945	119,626	1,772	N/C	50+	37	11
No branded discounts ⁵	N/C	N/C	N/C	N/C	N/C	50+	N/C	N/C
Reduce quality of life in F0-F1 ⁶	N/C	N/C	N/C	N/C	N/C	50+	N/C	N/C

Source: Authors' Analysis

NOTES:

¹Implemented by improving the cure rate for PR therapy by 10-20% and cost of PR therapy by 27-44% (80)

²Diagnosis rate among healthcare exposure group increased to 75% to account for recent introduction of recommendations for universal screening among baby boomers(81)

³Change implemented in all but Treat 5% scenario

⁴In each group receiving treatment, treatment applied to only 50% of those who are infected and diagnosed

⁵No drug discounts until year 15 when drug prices fall by 79% due to loss of patent protection (21-23)

⁶QALY weights are lower for F0-F2, per McEwan et al. (59)

⁷The US Rare Diseases Act of 2002 defines a rare disease as “any disease or condition that affects less than 200,000 people in the United States” (82)(85)(83)(83)⁸³⁸³

Abbreviations: N/C = no change from Base Case; QALY = Quality adjusted life year; F0-F2 = fibrosis scores F0-F2 on the Metavir scale.

Table A9: Social Value Results of Sensitivity Analyses on Key Model Parameters

	Social Value Net of Baseline (\$bil)					
	Treat 5%		Treat Advanced		Treat All Diagnosed	
	Lower Bound	Upper Bound	Lower Bound	Upper Bound	Lower Bound	Upper Bound
Base Case Results	347	349	126	131	1,188	1,222
	Treat 5%		Treat Advanced		Treat All Diagnosed	
Sensitivity Analyses	Lower Bound	Upper Bound	Lower Bound	Upper Bound	Lower Bound	Upper Bound
Increase starting infected population to 3.2 million	407	410	149	154	1,403	1,442
QALYs valued at \$50K	170	172	39	44	578	611
QALYs valued at \$100K	258	260	83	87	883	916
QALYs valued at \$200K	435	437	170	175	1,493	1,527
Allow retreatment in Baseline scenario ¹	321	323	101	105	1,162	1,196
Increase diagnosis rate ^{2,3}	333	334	143	147	1,247	1,281
Reduce treatment rate ^{3,4}	380	387	93	97	1,016	1,047
No branded discounts ⁵	382	384	156	161	1,242	1,276
Reduce quality of life in F0-F1 ⁶	374	377	130	134	1,266	1,300

Source: Authors' Analysis

NOTES:

¹Implemented by improving the cure rate for PR therapy by 10-20% and cost of PR therapy by 27-44% (80)

²Diagnosis rate among healthcare exposure group increased to 75% to account for recent introduction of recommendations for universal screening among baby boomers(81)

³Change implemented in all but Treat 5% scenario

⁴In each group receiving treatment, treatment applied to only 50% of those who are infected and diagnosed

⁵No drug discounts until year 15 when drug prices fall by 79% due to loss of patent protection (21-23)

⁶QALY weights are lower for F0-F2, per McEwan et al. (59)

Abbreviations: N/C = no change from Base Case; QALY = Quality adjusted life year; F0-F2 = fibrosis scores F0-F2 on the Metavir scale

Starting Infected Population

There is no consensus regarding the prevalence of HCV (detected + undetected) among the US population—widely cited estimates range from 2.7 million (32) to 3.2 million (1). We use the more conservative figure in the main analysis, but explore in a sensitivity analysis on how our results would change if the starting infected population were 3.2 million instead.

Value of a QALY

Estimates of the value of a quality-adjusted life-year (QALY) from the value of life literature vary widely.(41) The cost-effectiveness literature often cites values of \$50,000–100,000,(83) while labor economics, product safety, and workplace safety literature publish estimates that center around \$300,000 (in 2000 dollars).(84) Similar values are reported in studies that use out-of-pocket payment decisions by patients and prescribing decisions by physicians.(85) More recently, researchers have questioned the continued use of the \$50,000 figure, given its “murky origins” more than 20 years ago, lack of adjustment for inflation or economic growth, and suggest that values of \$100,000-\$150,000 are more appropriate.(86) We value QALYs at \$150,000 for the baseline analysis, and consider values ranging from \$50,000 to \$200,000 in sensitivity analyses.

Re-treatment

For model tractability, we assume that patients are treated at most once per infection. However, patients who fail initial treatment with PR have sometimes been re-treated (80), despite treatment guidelines that recommend against it due to the low probability of cure and significant side effects associated with PR treatments (4). To explore the impact that re-treatment of patients who fail initial PR treatment could have on model results, we conducted a sensitivity analysis in which the SVR rate and cost for PR therapy were increased under the assumption that 65% of patients who fail initial treatment are re-treated with 48 additional weeks of PR with a lower probability of attaining SVR than treatment naïve patients. SVR rates were increased by 10-20% and costs were increased by 27-44% (depending on genotype and fibrosis stage).(80)

Diagnosis and Treatment Rates

The maximum proportion of infected patients in any disease state that can be treated is limited by the rate of diagnosis among the population, as well as the available treatment capacity. To explore the impact that changes in each of these factors would have on our model results, we change the proportion of patients who receive treatment, as a fraction of those infected, in three of our four treatment scenarios: Baseline, Treat Advanced, and Treat All Diagnosed. The Treat 5% treatment scenario is assumed to simply treat 5% of all infected patients in each disease state; the 5% does not vary by diagnosis rate or treatment capacity. Current estimates of HCV diagnosis rates tend to cluster around 50%.(30, 31)

For the diagnosis rate sensitivity analysis, we assume that recent recommendations for universal screening among baby boomers (81) increases the diagnosis rate in our healthcare exposure group from 50% to 75% (it remains at 50% in the other two exposure groups). For the treatment rate sensitivity analysis, we assume that, among patients in a

disease state targeted for treatment, only 50% of those infected and diagnosed receive treatment in any period.(31)

QALY Decrement

For utility weights associated with a life-year spent in each model disease state, the main analysis follows Salomon et al. (60) and reduces the utility of the uninfected state by 2% for mild disease (Acute-F1) and by 6% for moderate disease (F2-F3). QALY weights for F4 and higher are taken from McEwan et al.(59) in the base analysis. In a sensitivity analysis, we employed QALY weights from McEwan for all disease states, which are lower than those from Salomon for mild to moderate disease.

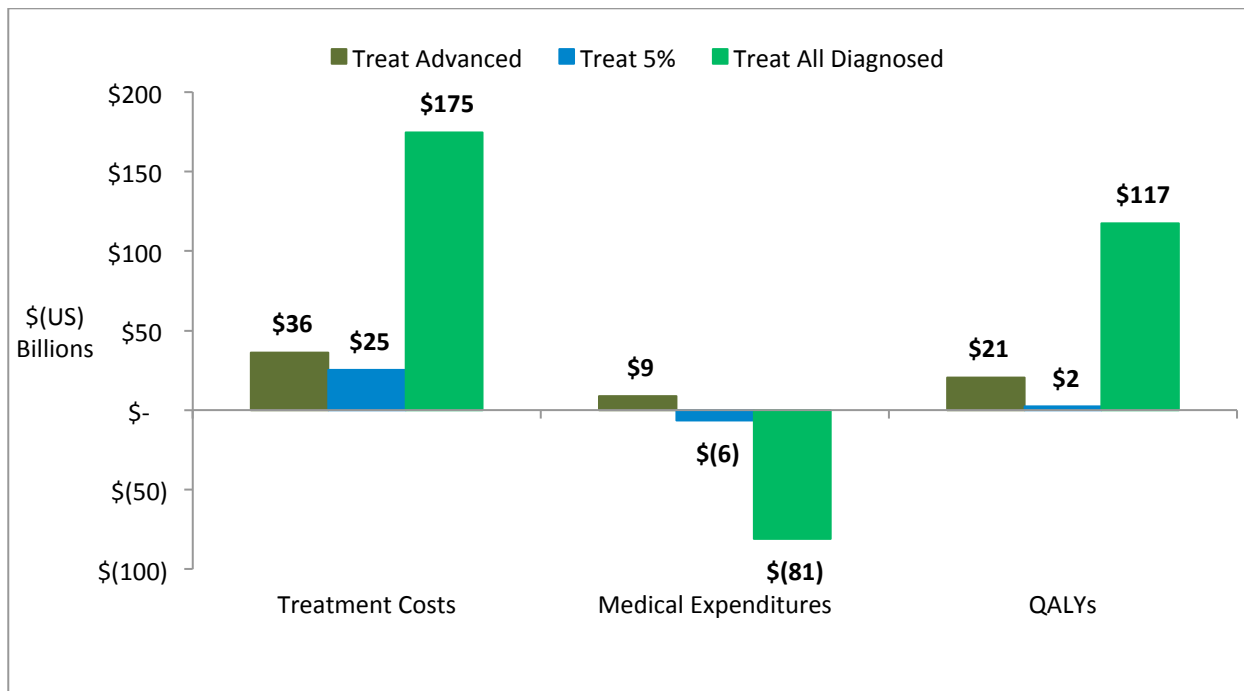
Price Discounts

The main analysis assumes that branded drugs used for treatment cost their full price in the first year, are discounted by 46% in years 2-14 due to entry from other branded competitors, and are discounted by 79% in years 15+ after loss of patent protection.(21-23) In this sensitivity analysis, we explore what happens if no branded entry occurs and treatments remain at their list price until patent expiration.

Time Horizon

The discounted cumulative results reported in Exhibit 3 in the manuscript are based on a 50-year time horizon; if a ten-year horizon is used instead, treatment costs, medical expenditures and value from QALYs all have the same general shape as in the 50-year case, but only the Treat All scenario has total benefits exceeding treatment costs after ten years. The ten year results are presented in Exhibit A2 below:

Exhibit A2. Discounted costs and benefits for alternative treatment strategies net of Baseline over a 10-year period



SOURCE Authors' analysis

NOTE "Baseline" treatment scenario treats all of the HCV infected and diagnosed population with advanced disease (F3 and higher) every period with old agents; "Treat Advanced" treats the same population as Baseline with new agents; "Treat 5%" treats 5% of the total HCV infected population (F0 and above) every period with new agents; "Treat All Diagnosed" treats all of the HCV infected and diagnosed population (F0 and above) every period with new agents. All model parameters are taken from the literature. QALYs are valued at \$150,000 each (41); discount rate = 3% (42).

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