

HCV Phylogeography of the General Population and High-Risk Groups in Cyprus Identifies the Island as a Global Sink for and Source of Infection

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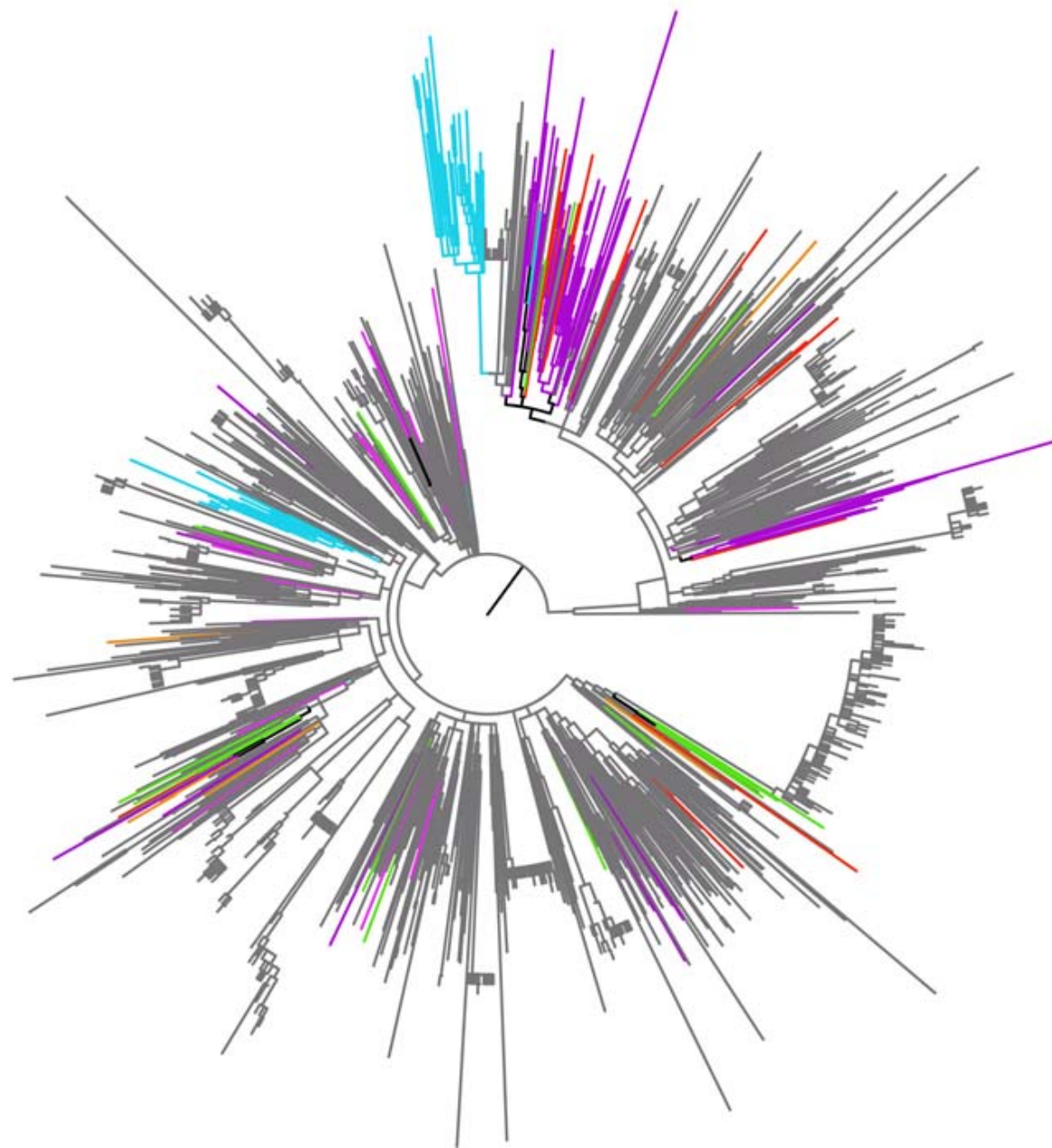
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Supplementary Figures and Tables

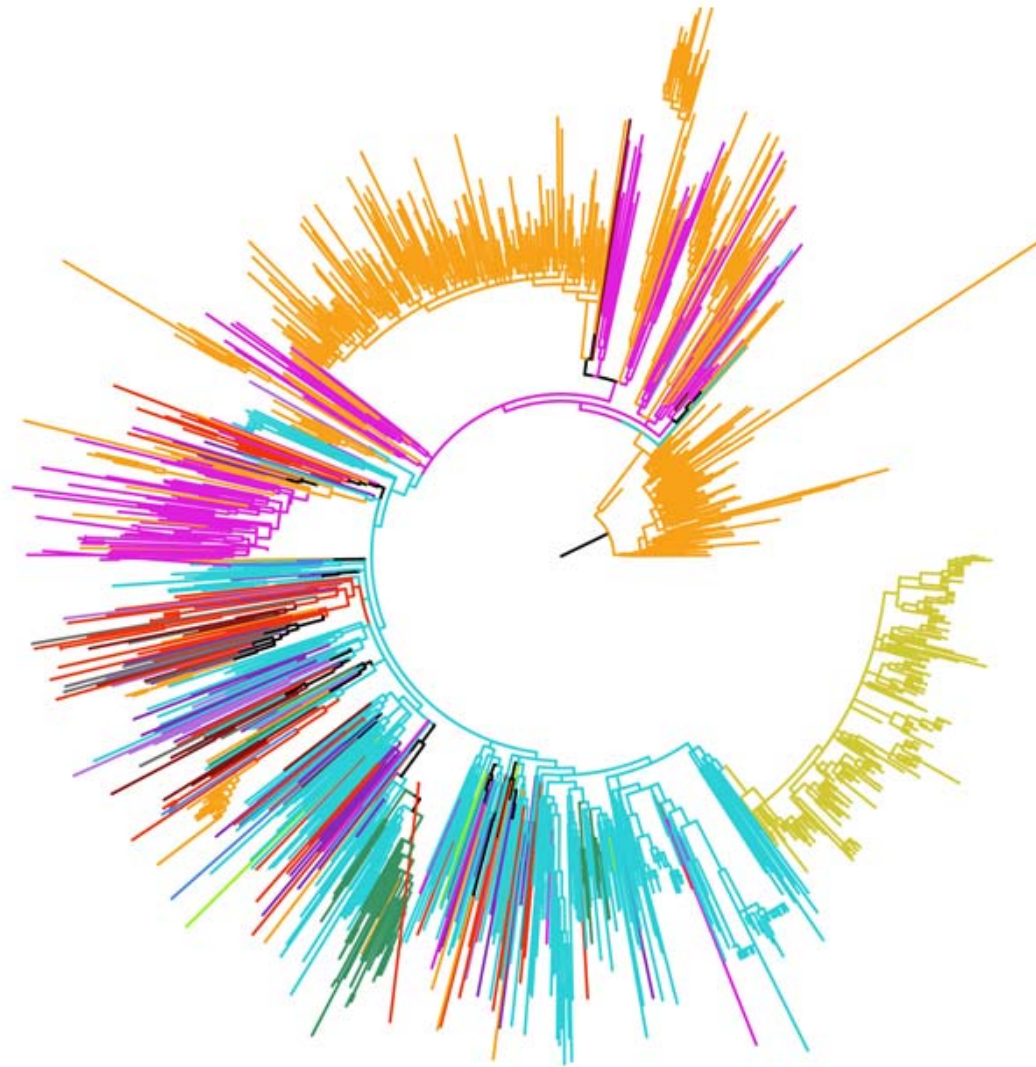
Supplementary Figure S1A

- China
- Cyprus
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- Japan
- Switzerland
- Thailand
- United States



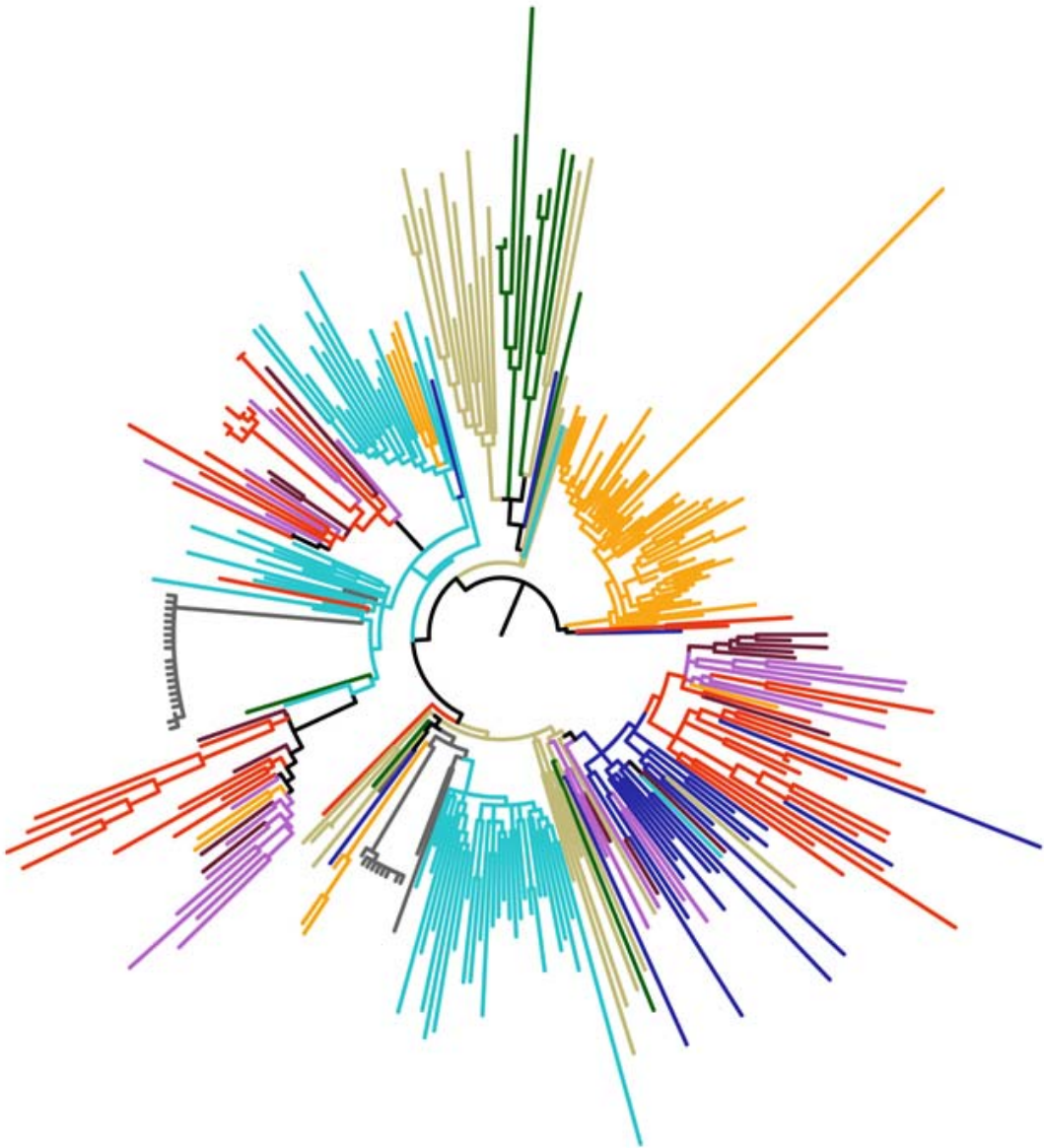
Supplementary Figure S1B

- Belarus
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- Ireland
- Japan
- Russian Federation
- Switzerland
- Tajikistan
- Thailand
- United States
- Uzbekistan



Supplementary Figure S1C

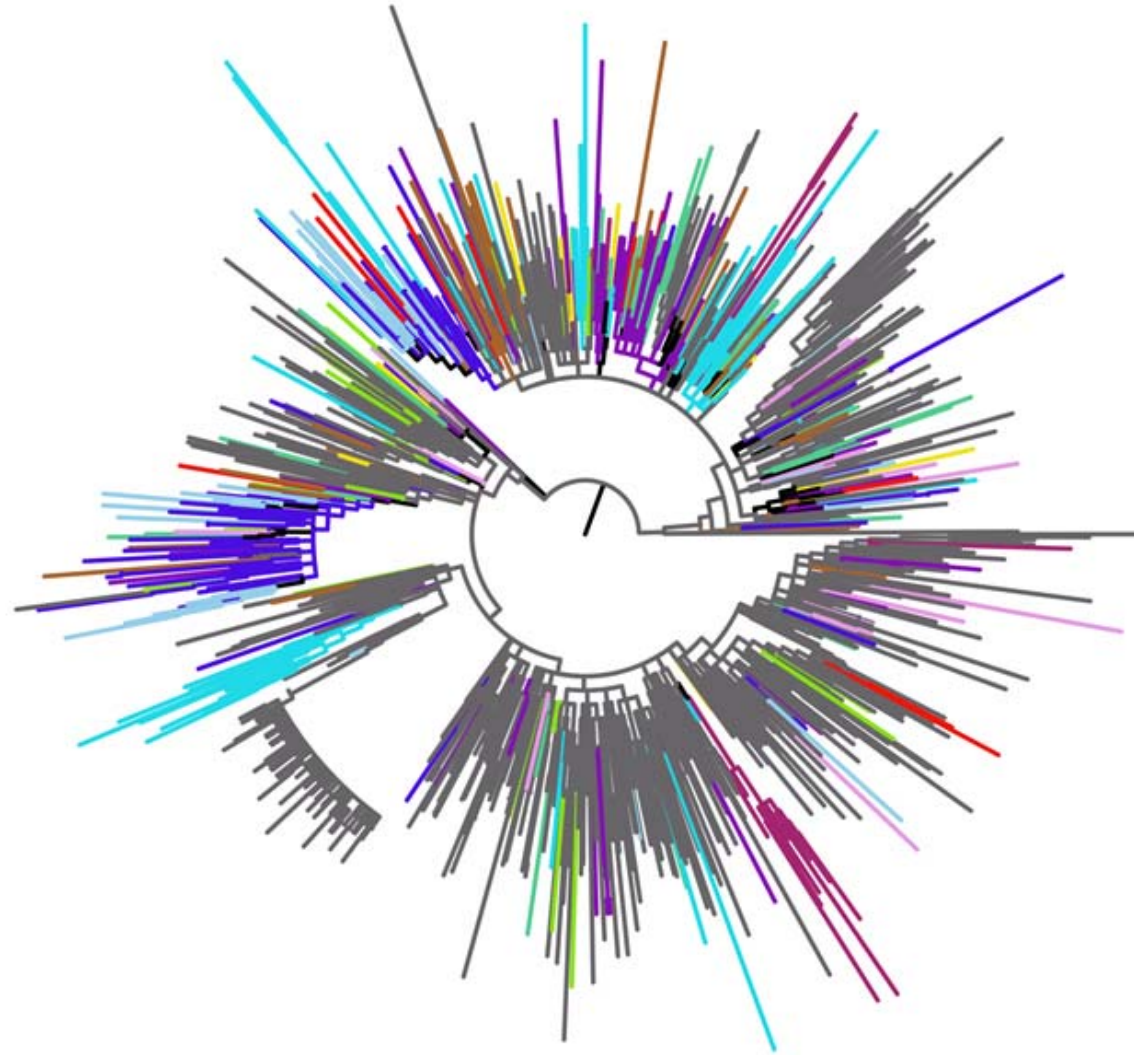
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Supplementary Figure S1. Phylogeographic trees of Core-E1. Maximum likelihood (ML), midpoint-rooted phylogeographic tree showing HCV viral clades in different colors by country. **(A)** Core-E1 subtype 1a, **(B)** Core-E1 subtype 1b, and **(C)** Core-E1 subtype 3a.

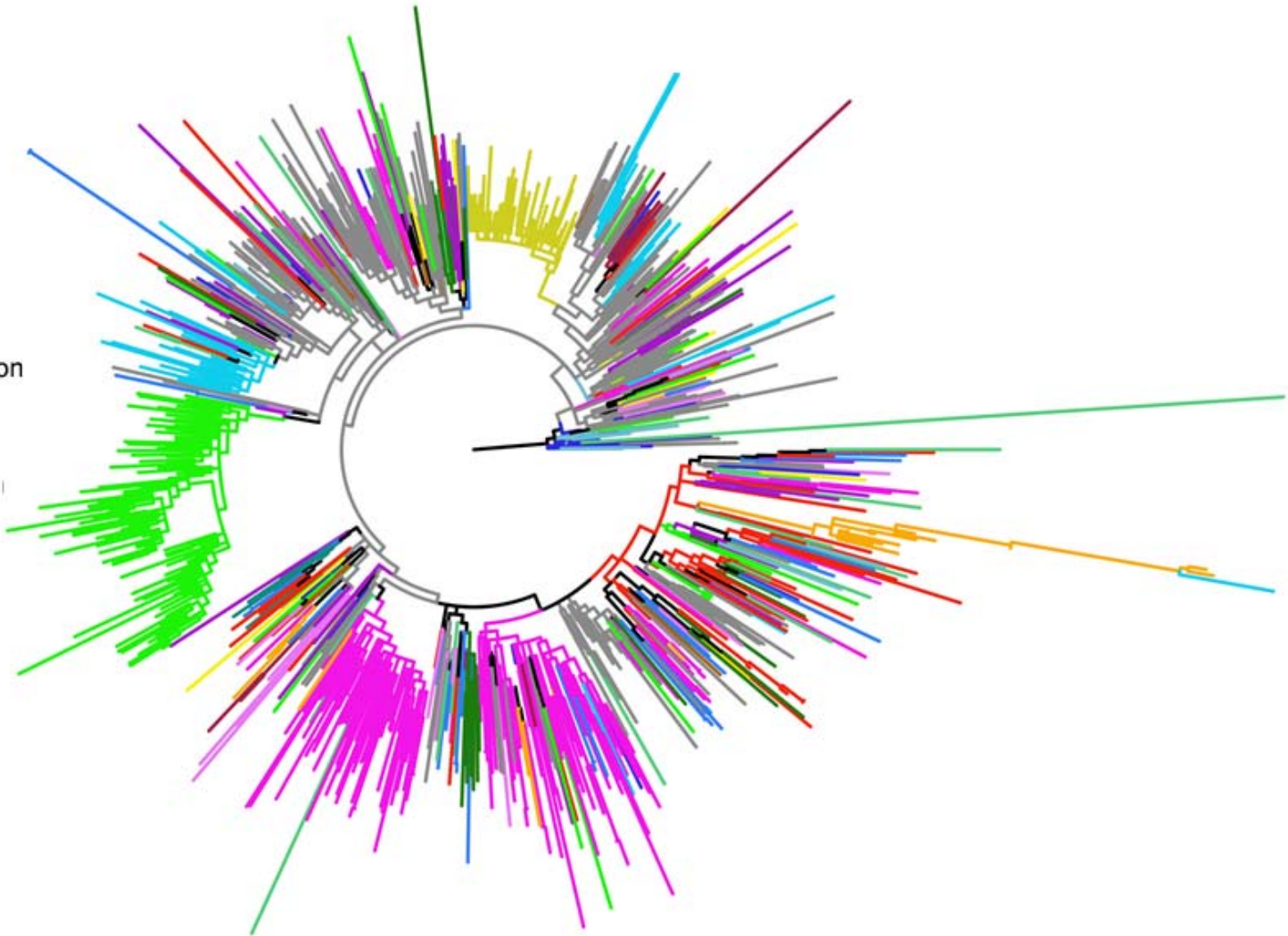
Supplementary Figure S2A

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- Cyprus
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- Greece
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- New Zealand
- Switzerland
- Thailand
- United Kingdom
- United States
- Vietnam

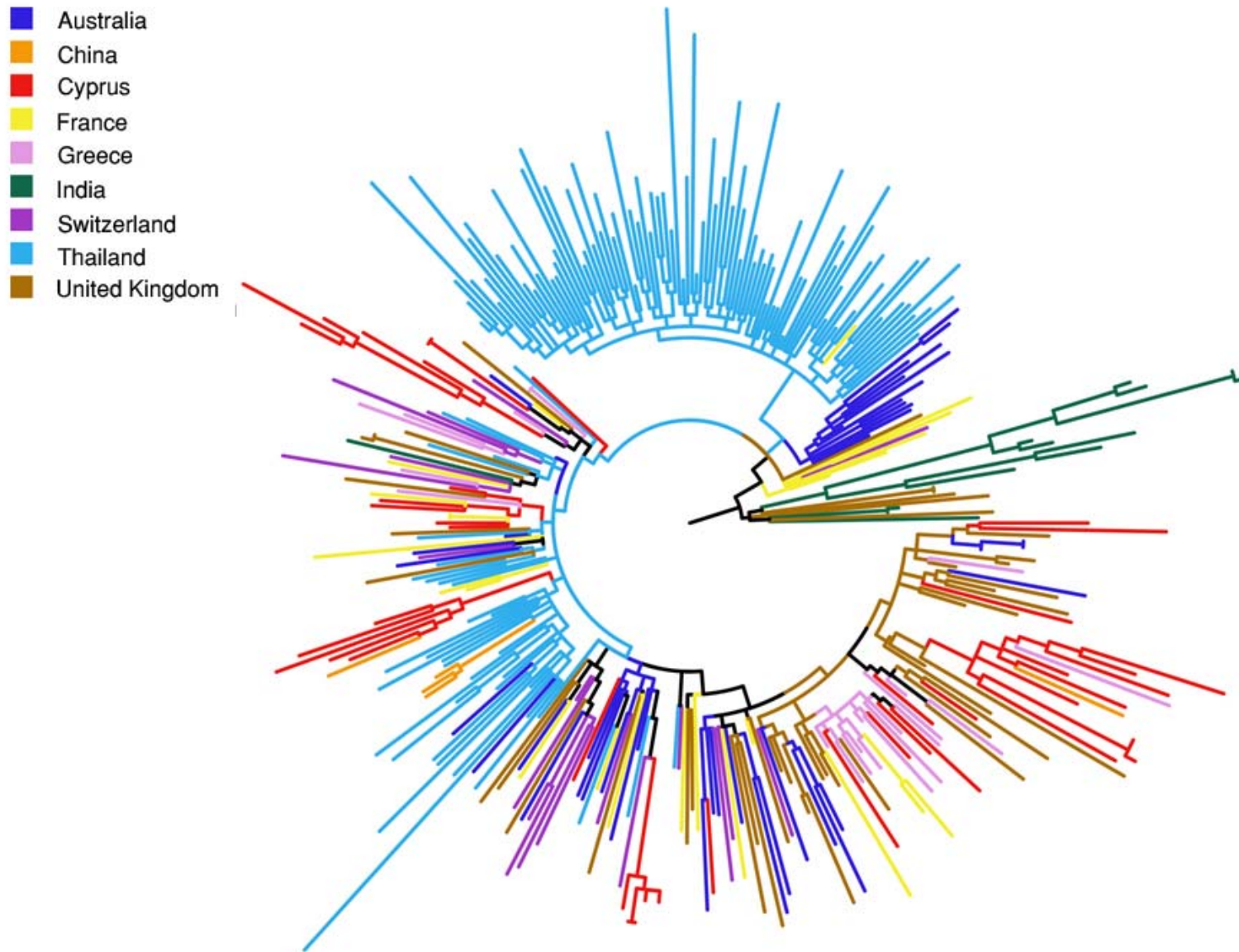


Supplementary Figure S2B

- Australia
- China
- Cyprus
- France
- Germany
- Greece
- Ireland
- Italy
- Japan
- Netherlands
- New Zealand
- Russian Federation
- Spain
- Switzerland
- Thailand
- United Kingdom
- United States
- Vietnam



Supplementary Figure S2C



Supplementary Figure S2. Phylogeographic trees of NS5B. Maximum likelihood (ML), midpoint-rooted phylogeographic tree showing HCV viral clades in different colors by country. **(A)** NS5B subtype 1a, **(B)** NS5B subtype 1b, and **(C)** NS5B subtype 3a.

Supplementary Table S1. Core-E1 Viral Mobility. Means of observed migration events across all bootstrap trees between different countries. Cells in bold indicate statistically significant pathways (compared to the null- hypothesis of panmixis) after Bonferroni correction for multiple comparisons. Core -E1 subtype **(A)** 1a, **(B)** 1b, and **(C)** 3a.

Supplementary Table S1a. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 1a encoding Core-E1 region

		Importing to						
		China	Cyprus	Germany	Japan	Switzerland	Thailand	USA
Exporting from	China (7)		0.017	0.010	0.000	0.120	0.017	0.000
	Cyprus (14)	0.000		0.051	0.000	0.098	0.015	0.081
	Germany (21)	0.015	0.015		0.005	0.042	0.005	0.125
	Japan (14)	0.000	0.000	0.005		0.000	0.000	0.000
	Switzerland (48)	0.015	1.895	1.419	0.034		0.377	2.4
	Thailand (55)	0.000	0.059	0.022	0.042	0.081		0.632
	US (1279)	3.850	6.662	12.017	12.777	13.748	4.909	

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. USA, United States of America. For each country, the number in parenthesis indicate the number of HCV subtype 1a sequences (encoding the CORE-E1 region) isolated from and used in the analysis.

Supplementary Table S1b. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 1b encoding the Core-E1 region

		Importing to											
		Belarus	China	Cyprus	Germany	Ireland	Japan	Russia	Switzerland	Tajikistan	Thailand	USA	Uzbekistan
Exporting from	Belarus (16)		0.081	0.252	0.000	0.000	0.042	0.012	0.032	0.034	0.000	0.360	0.279
	China (529)	0.208		0.975	0.044	0.000	5.51	0.262	0.770	0.659	0.091	2.306	0.397
	Cyprus (53)	0.985	0.760		0.071	0.000	0.282	0.223	1.189	0.951	0.017	0.380	0.826
	Germany (7)	0.000	0.000	0.000		0.000	0.000	0.000	0.002	0.005	0.000	0.000	0.000
	Ireland (192)	0.000	0.015	0.235	0.000		0.005	0.000	0.007	0.000	0.012	0.265	0.000
	Japan (122)	0.223	10.025	0.635	0.022	0.000		0.076	0.652	0.409	0.049	1.892	0.137
	Russia (7)	0.005	0.015	0.037	0.000	0.000	0.002		0.002	0.002	0.015	0.005	0.005
	Switzerland (40)	0.074	0.377	0.615	0.071	0.005	0.218	0.056		0.093	0.049	0.488	0.118
	Tajikistan (13)	0.039	0.100	0.059	0.015	0.000	0.032	0.005	0.044		0.002	0.034	0.056
	Thailand (39)	0.002	1.002	0.047	0.007	0.000	0.049	0.015	0.100	0.015		0.588	0.002
	US (274)	3.407	7.221	13.243	3.887	0.902	8.88	2.098	15.385	2.588	5.990		3.358
	Uzbekistan (12)	0.091	0.029	0.284	0.000	0.000	0.012	0.012	0.078	0.159	0.002	0.017	

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. USA, United States of America. For each country, the number in parenthesis indicate the number of HCV subtype 1b sequences (encoding the CORE-E1 region) isolated from and used in the analysis.

Supplementary Table S1c. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 3a encoding Core-E1 region

		Importing to								
		Belarus	China	Cyprus	India	Pakistan	Thailand	GB	USA	Uzbekistan
Exporting from	Belarus (16)		0.147	0.526	0.009	0.026	0.022	0.289	0.009	0.458
	China (70)	0.018		0.072	0.031	0.211	0.175	0.105	0.009	0.048
	Cyprus (44)	1.487	0.377		0.031	0.079	0.121	1.423	0.057	1.873
	India (24)	0.004	0.026	0.011		0.169	0.046	0.116	0.044	0.050
	Pakistan (28)	0.208	0.401	0.590	1.583		0.91	1.175	0.511	0.649
	Thailand (65)	0.107	1.632	1.379	0.919	0.941		0.787	1.728	0.417
	GB (22)	1.825	0.265	1.682	0.257	0.866	1.026		0.204	1.173
	US (43)	0.018	0.079	0.046	0.081	0.057	0.246	0.046		0.094
	Uzbekistan (25)	1.875	0.770	2.270	0.053	0.169	0.057	0.294	0.061	

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. GB, United Kingdom; USA, United States of America. For each country, the number in parenthesis indicate the number of HCV subtype 3a sequences (encoding the CORE-E1 region) isolated from and used in the analysis.

Supplementary Table S2. NS5B Viral Mobility. Means of observed migration events across all bootstrap trees between different countries. Cells in bold indicate statistically significant pathways (compared to the null- hypothesis of panmixis) after Bonferroni correction for multiple comparisons. NS5B subtype **(A)** 1a, **(B)** 1b, and **(C)** 3a.

Supplementary Table S2a. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 1a encoding NS5B region

		Importing to											
		Australia	Cyprus	France	Germany	Greece	Italy	New Zealand	Switzerland	Thailand	GB	USA	Vietnam
Exporting from	Australia (71)		0.557	0.183	0.863	0.437	0.733	7.173	2.343	1.087	2.013	1.683	0.027
	Cyprus (11)	0.017		0.000	0.000	0.003	0.007	0.03	0.017	0.017	0.000	0.020	0.007
	France (15)	0.160	0.003		0.057	0.090	0.027	0.000	0.043	0.050	0.010	0.107	0.000
	Germany (32)	0.140	0.010	0.007		0.037	0.030	0.027	0.087	0.043	0.043	0.233	0.013
	Greece (24)	0.027	0.020	0.043	0.110		0.037	0.01	0.043	0.010	0.057	0.043	0.000
	Italy (32)	0.230	0.043	0.127	0.213	0.203		0.063	0.643	0.147	0.397	0.283	0.040
	New Zealand (49)	3.470	0.430	0.037	0.110	0.117	0.200		0.370	0.837	0.613	0.443	0.003
	Switzerland (80)	0.923	0.873	0.687	1.337	1.367	2.947	0.317		0.873	1.233	2.213	0.323
	Thailand (70)	0.627	0.253	0.460	0.067	0.230	0.527	0.31	0.830		1.090	1.833	0.753
	GB (42)	0.297	0.150	0.137	0.103	0.210	0.177	0.200	0.797	0.370		0.673	0.053
	US (629)	14.58	3.627	6.060	16.93	11.843	9.033	9.643	23.293	17.22	13.157		3.613
Vietnam (21)	0.003	0.003	0.000	0.000	0.000	0.000	0.000	0.003	0.063	0.000	0.047		

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. GB, United Kingdom; and USA, United States of America. For each country, the number in parenthesis indicate the number of HCV subtype 1a sequences (encoding the NS5B region) isolated from and used in the analysis.

		Importing to																	
		AU	CN	CY	FR	DE	GR	IE	IT	JP	NL	NZ	RU	ES	CH	TH	GB	USA	VN
Importing from	AU (26)		0.006	0.086	0.039	0.208	0.064	0.000	0.161	0.094	0.006	0.908	0.139	0.05	0.153	0.183	0.008	0.422	0.000
	CN (23)	0.000		0.025	0.014	0.036	0.017	0.000	0.022	0.267	0.000	0.000	0.039	0.003	0.039	0.783	0.000	0.081	0.05
	CY (54)	0.575	0.05		0.150	0.569	0.383	0.006	1.408	0.742	0.114	0.558	1.078	1.600	0.65	0.189	0.144	0.661	0.036
	FR (12)	0.017	0.008	0.067		0.014	0.006	0.003	0.017	0.031	0.006	0.003	0.008	0.028	0.017	0.008	0.006	0.006	0.003
	DE (148)	0.053	0.019	0.336	0.058		0.142	0.003	0.289	0.131	0.003	0.017	0.128	0.092	0.456	0.144	0.025	0.711	0.014
	GR (22)	0.033	0.003	0.233	0.042	0.083		0.000	0.108	0.094	0.006	0.006	0.161	0.097	0.086	0.006	0.019	0.083	0.014
	IE (72)	0.011	0.011	0.028	0.008	0.000	0.028		0.022	0.264	0.000	0.000	0.025	0.028	0.081	0.019	0.000	0.742	0.061
	IT (30)	0.069	0.028	0.358	0.192	0.256	0.144	0.000		0.278	0.011	0.081	0.214	0.075	0.203	0.022	0.014	0.164	0.000
	JP (153)	1.825	2.753	1.714	0.35	1.131	0.783	0.831	2.056		0.033	0.083	1.725	1.061	1.306	0.842	0.183	4.031	0.444
	NL (6)	0.036	0.000	0.536	0.006	0.000	0.008	0.000	0.014	0.006		0.000	0.714	0.003	0.064	0.000	0.000	0.008	0.000
	NZ (13)	0.622	0.003	0.094	0.053	0.036	0.022	0.000	0.131	0.053	0.003		0.039	0.022	0.058	0.269	0.008	0.233	0.000
	RU (38)	0.061	0.036	0.744	0.075	0.253	0.322	0.003	0.336	0.164	0.178	0.058		0.122	0.506	0.039	0.022	0.208	0.011
	ES (33)	0.131	0.022	0.789	0.267	0.094	0.131	0.003	0.483	0.142	0.017	0.006	0.300		0.769	0.022	0.033	0.433	0.000
	CH (49)	0.142	0.028	0.411	0.233	0.556	0.192	0.014	0.311	0.233	0.022	0.067	0.253	0.528		0.064	0.083	0.464	0.014
	TH (48)	0.008	0.003	0.331	0.006	0.553	0.036	0.003	0.575	0.044	0.000	0.042	0.019	0.044	1.186		0.056	1.783	0.011
GB (7)	0.003	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000		0.000	0.000	
US (231)	7.569	0.767	10.011	4.358	9.111	7.572	1.053	6.961	11.381	0.744	2.328	7.831	8.081	13.317	5.408	3.500		1.728	
VN (12)	0.489	0.000	0.181	0.006	0.000	0.003	0.003	0.006	0.014	0.000	0.000	0.003	0.003	0.000	0.025	0.000	0.492		

Supplementary Table S2b. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 1b encoding NS5B region

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. AU, Australia; CN, China; CY, Cyprus; FR, France; DE, Germany; GR, Greece; IE, Ireland; IT, Italy; JP, Japan; NL, Netherlands; RU, Russian Federation; ES, Spain; CH, Switzerland; TH, Thailand; GB, United Kingdom; USA, United States of America and VN, Vietnam. For each country, the number in parenthesis indicate the number of HCV subtype 1b sequences (encoding the NS5B region) isolated from and used in the analysis.

Supplementary Table S2c. Mean of observed migration events across all bootstrap trees for each pathway for HCV subtype 3a encoding NS5B region

		Importing to								
		Australia	China	Cyprus	France	Greece	India	Switzerland	Thailand	GB
Exporting from	Australia (42)		0.081	1.103	1.175	0.431	0.314	0.722	1.283	1.253
	China (5)	0.000		0.000	0.000	0.000	0.000	0.003	0.003	0.006
	Cyprus (45)	0.475	1.831		0.972	1.197	0.222	0.478	0.328	0.650
	France (25)	0.458	0.008	0.325		0.167	0.053	0.350	0.222	0.497
	Greece (22)	0.275	0.003	2.383	0.986		0.006	0.192	0.042	1.214
	India (15)	0.008	0.000	0.008	0.019	0.006		0.022	0.039	0.119
	Switzerland (19)	0.647	0.017	0.325	0.514	0.642	0.119		0.325	0.608
	Thailand (130)	4.319	0.461	1.292	3.139	0.667	0.653	2.206		2.447
	GB (58)	5.083	0.053	2.756	2.661	2.425	0.867	1.636	0.842	

Note. Cells in bold indicate statistically significant pathways (compared to the null-hypothesis of panmixis) after Bonferroni correction for multiple comparisons. GB, United Kingdom. For each country, the number in parenthesis indicate the number of HCV subtype 3a sequences (encoding the NS5B region) isolated from and used in the analysis.