

Supplementary Information for: A strategy to assess spillover risk of bat SARS-related coronaviruses in Southeast Asia

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Supplementary Table 1. A compiled list of bat SARSr-CoV hosts in Southeast Asia, their elevation limits, and the suitability of selected IUCN habitat types. An **X** indicates that a habitat is considered suitable for a species. Gray cell shading indicates habitats not included in a global map of terrestrial habitat types^{1,2}. Elevation and suitability data were sourced from the IUCN Red List³.

Species	Family	Reference	Elevation limits (m)		Suitable habitat types*																			
			Upper	Lower	1.4	1.5	1.6	1.9	3.4	3.5	3.7	3.8	4.4	6.0	7.1	7.2	8.2	14.1	14.2	14.3	14.4	14.5	14.6	15.8
<i>Aselliscus stoliczkanus</i>	Hipposideridae	4	NA	NA											X									
<i>Chaerephon plicatus</i>	Molossidae	5	950	0		X	X								X	X			X		X			X
<i>Hipposideros armiger</i>	Hipposideridae	6	2031	100				X							X	X								
<i>H. galeritus</i>	Hipposideridae	7	1100	0		X	X							X	X	X								
<i>H. gentilis**</i>	Hipposideridae	6	1900	0			X	X							X	X								
<i>H. larvatus</i>	Hipposideridae	7	2000	0			X	X							X	X								
<i>H. pratti</i>	Hipposideridae	6	2000	100											X									
<i>Nyctalus leisleri</i>	Vespertilionidae	8	2400	0	X							X		X					X					
<i>Rhinolophus acuminatus</i>	Rhinolophidae	9	1676	60			X								X									
<i>R. affinis</i>	Rhinolophidae	10	2000	290		X	X	X							X						X			
<i>R. creaghi</i>	Rhinolophidae	7	1500	0			X								X									
<i>R. ferrumequinum</i>	Rhinolophidae	7	3000	0	X							X	X		X	X			X					
<i>R. hipposideros</i>	Rhinolophidae	11	2000	0	X				X	X	X	X	X		X	X						X		
<i>R. luctus</i>	Rhinolophidae	12	1600	0		X	X	X							X	X								
<i>R. macrotis</i>	Rhinolophidae	4	1692	200		X	X	X							X	X								
<i>R. malayanus</i>	Rhinolophidae	13	1400	0			X								X			X		X	X			
<i>R. marshalli</i>	Rhinolophidae	14	1480	0			X								X					X	X		X	
<i>R. pearsonii</i>	Rhinolophidae	4	3077	123	X		X	X							X	X								
<i>R. pusillus</i>	Rhinolophidae	4	1370	200		X	X								X	X								
<i>R. rex</i>	Rhinolophidae	15	NA	NA			X								X									
<i>R. shameli</i>	Rhinolophidae	16	NA	NA		X	X								X									
<i>R. siamensis</i>	Rhinolophidae	12	NA	NA			X								X									
<i>R. sinicus</i>	Rhinolophidae	7	2769	500	X	X	X								X	X								
<i>R. steno</i>	Rhinolophidae	17	1700	0		X												X		X			X	
<i>R. thomasi</i>	Rhinolophidae	6	1100	400											X					X	X			
<i>Tadarida teniotis</i>	Molossidae	18	3100	0					X			X	X	X	X	X	X					X		

*Habitat type names: 1.4. Forest -- Temperate; 1.5. Forest -- Subtropical/tropical dry; 1.6. Forest -- Subtropical/tropical moist lowland; 1.9. Forest -- Subtropical/tropical moist montane; 3.4. Shrubland -- Temperate; 3.5. Shrubland -- Subtropical/tropical dry; 3.7. Shrubland -- Subtropical/tropical high altitude; 3.8. Shrubland -- Mediterranean-type shrubby vegetation; 4.4. Grassland -- Temperate; 6.0. Rocky areas (e.g. inland cliffs, mountain peaks); 7.1. Caves and Subterranean Habitats (non-aquatic) -- Caves; 7.2. Caves and Subterranean Habitats (non-aquatic) -- Other subterranean habitat; 8.2. Desert -- Temperate; 14.1. Arable Land; 14.2. Pastureland; 14.3. Plantations; 14.4. Rural Gardens; 14.5. Urban Areas; 14.6. Subtropical/Tropical Heavily Degraded Former Forest; 15.8. Seasonally Flooded Agricultural Land

***H. gentilis* was listed as *H. pomona* in Latinne et al. 2020, but *H. gentilis* was used for our analyses due to recent taxonomic revisions; see Methods.

Supplementary Table 2. Validation of species area of habitat (AOH) using cleaned occurrence records from the Global Biodiversity Information Facility (GBIF). Species are listed in order of decreasing percent of occurrence points within a 5 km radius of the species' AOH.

Species	Number of cleaned GBIF occurrence points	Number (%) of points within 5 km of AOH
<i>Rhinolophus luctus</i>	69	63 (91)
<i>R. creaghi</i>	41	37 (90)
<i>R. malayanus</i>	52	45 (87)
<i>R. shameli</i>	42	35 (83)
<i>Hipposideros galeritus</i>	80	64 (80)
<i>R. pusillus</i>	76	60 (79)
<i>H. larvatus</i>	139	109 (78)
<i>R. siamensis</i>	9	7 (78)
<i>R. affinis</i>	189	144 (76)
<i>R. pearsonii</i>	95	72 (76)
<i>Chaerephon plicatus</i>	69	52 (75)
<i>R. marshalli</i>	18	12 (67)
<i>H. gentilis</i>	29	18 (62)
<i>R. thomasi</i>	41	23 (56)
<i>Aselliscus stoliczkanus</i>	67	36 (54)
<i>R. ferrumequinum</i>	2	1 (50)
<i>H. armiger</i>	261	124 (48)
<i>R. acuminatus</i>	51	20 (40)
<i>R. macrotis</i>	35	13 (37)
<i>H. pratti</i>	6	2 (33)
<i>R. stheno</i>	54	15 (28)
<i>R. rex</i>	24	4 (17)
<i>R. sinicus</i>	14	2 (14)
<i>Tadarida teniotis</i>	5	0 (0)
<i>Nyctalus leisleri</i>	1	0 (0)
<i>R. hipposideros</i>	0	NA

Supplementary Table 3. Prevalence of human-bat contact within countries in Southeast Asia. Studies were identified via a systematic literature search (see Methods in main text).

Country	Study population	Description of bat contact	Prevalence of bat contact (number reporting contact/total population)	Timeframe of contact with bat	Reference
China	People living in areas near bat populations	Bats in house	12.7% (201/1585)	Previous 12 months	19
		Cooked or handled bats	0.6% (9/1585)		
Indonesia	People (mostly men) living in/near a forest conservation area	Expelling	10.7% (16/150)	Not reported	20
		Hold/capture/hunt	46.0% (69/150)		
		Cutting	13.3% (20/150)		
		Cooking	13.3% (20/150)		
		Eating	16.7% (25/150)		
		Selling	3.3% (5/150)		
Thailand	People living in areas with high bat density	Found live bat(s) in house, community, or tourist location	20.4% (128/626)	Previous 6 months	21
		Consumed bat meat	15.3% (96/626)		
		Cleaned bat guano from house or the community	12.5% (78/626)		
		Found dead bat(s) in house	10.4% (65/626)		
		Bat guano mining/collecting	7.3% (46/626)		
		Cleaned bat carcasses from house or the community	7.2% (45/626)		
		Other activities (e.g. hunted bats, exposed to bat urine)	6.5% (41/626)		
		Used bat guano	4.0% (25/626)		
		Bitten by a bat	2.6% (16/626)		
	Adult guano miners, bat	Inside bat cave or roost area	57.5% (61/106)	Exposed > 5	22

	hunters, game wardens, residents/personnel at temples with large bat roosts	Direct bat contact (unspecified)	27.4% (29/106)	times/year	
		Bat consumption	10.4% (11/106)		
		Bat scratch	5.7% (6/106)		
		Bat bite	1.9% (2/106)		
	People living in areas where bat roosts are present	Various (hunting bats, eating bats, collecting bat guano, cleaning bat feces, finding bat carcasses in houses and communities)	46.6% (142/305)	Previous 6 months	²³
Vietnam	People living in farming communities involved in raising, slaughtering, or processing wildlife or livestock	Maintained bat roosts to produce guano for fertilizer	1.2% (3/245)	Previous 12 months	²⁴

Supplementary Table 4. Human viral seroprevalence among individuals reporting contact with bats. Studies were identified via a systematic literature search (see Methods in main text).

Country	Pathogen	Description of bat contact	Seroprevalence (number positive/total tested)	Specificity	Reference
Australia	Hendra virus (then named equine morbillivirus)	“Prolonged, significant contact” in the context of being a flying fox carer	0% (0/128)	Not reported	²⁵
Cambodia	Nipah virus	Hunting bats	0% (0/4)	Not evaluated	²⁶
		Palm-juice collection and selling	0% (0/15)		
Cameroon	Nipah virus	Hunting bats	3.0% (3/99)	An assay that was previously validated as having a specificity of 94–100% was further refined	²⁷
		Butchering bats	4.1% (7/171)		
		General contact with bats (including hunting, butchering, and receiving bite or scratch)	3.1% (7/227)		
China	SARSr-CoV	General contact with bats	0.5% (1/199)	Not reported	¹⁹
	HKU10-CoV	General contact with bats	0.5% (1/199)		
	HKU9-CoV	General contact with bats	0% (0/199)		
	MERS-CoV	General contact with bats	0% (0/199)		
Lao PDR	SARS-CoV-2	Bat guano collectors	25% (3/12)	Not reported	²⁸ and pers. comm. with author A. Black
Malaysia	Tioman virus	Consumed fruit partially eaten by bats	6.3% (2/32)	Reported to be “highly specific”	²⁹
	Nipah virus	Physical contact (unspecified)	0% (0/15)	Not reported	³⁰
		Consumed fruit partially eaten by bats	0% (0/29)		
Republic of Congo	Ebola virus	General exposure to bats	14% (7/50)	Not reported, but authors used a “double immunofluorescence” protocol due to its higher specificity than regular immunofluorescence assays	³¹
		Consumption of bats	0% (0/23)		

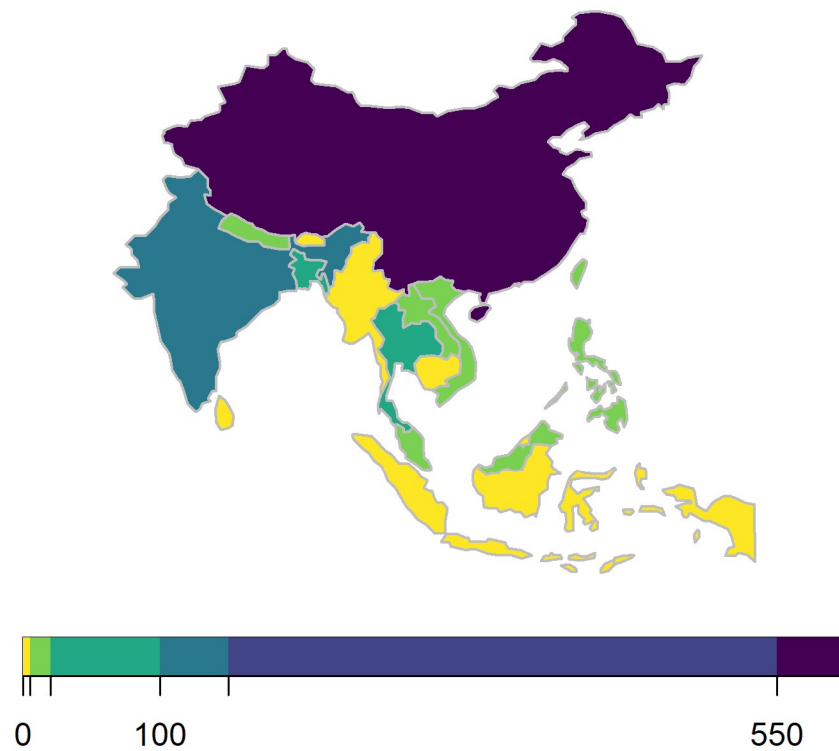
Supplementary Table 5. Duration of SARS-CoV immunoglobulin G (IgG) antibody detection among patients who recovered from SARS.

Time post-disease onset (as originally reported)	Time post-disease onset in months (used for curve fitting)	% (number positive/total tested) with detectable IgG	Reference
0-7 days	0.25	11.8 (2/17)	32
8-14 days	0.5	38.5 (10/26)	32
15-20 days	0.75	77.3 (17/22)	32
21-30 days	1	91.7 (33/36)	32
1 month	1	100 (36/36)	33
1 month	1	100 (17/17)	34
1 month	1	100 (37/37)	35
31-60 days	2	93.1 (67/72)	32
61-90 days	3	94.3 (33/35)	32
3 months	3	100 (19/19)	36
4 months	4	100 (36/36)	33
4 months	4	100 (41/41)	35
91-120 days	4	100 (11/11)	32
5 months	5	100 (13/13)	37
7 months	7	100 (41/41)	33
7 months	7	100 (44/44)	35
121-210 days	7	100 (23/23)	32
10 months	10	100 (37/37)	33
10 months	10	100 (37/37)	35
12 months	12	94.7 (18/19)	36
1 year	12	100 (17/17)	34
211-365 days	12	93.9 (46/49)	32
16 months	16	100 (32/32)	33
16 months	16	100 (32/32)	35
18 months	18	84.2 (16/19)	36
20 months	20	82.4 (14/17)	37
24 months	24	88.2 (30/34)	33
24 months	24	84.2 (16/19)	36

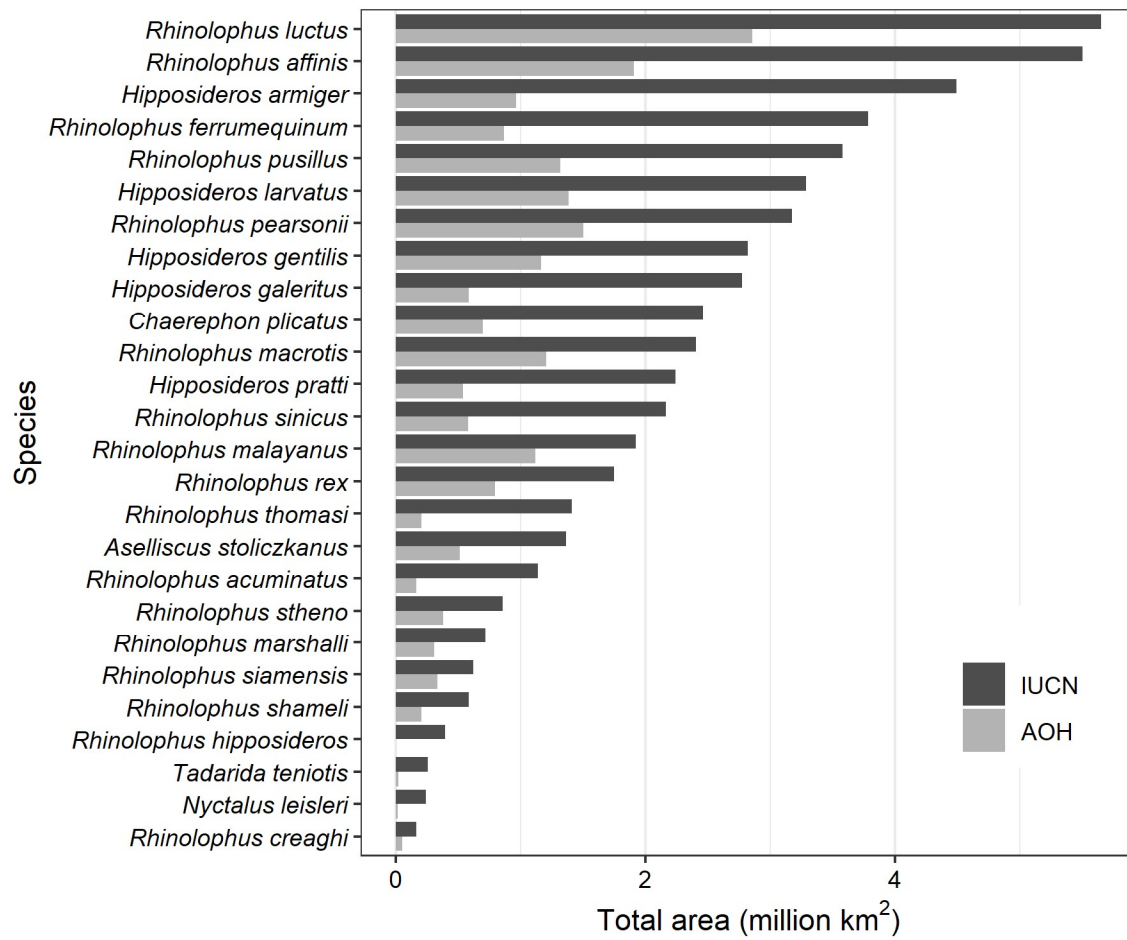
24 months	24	88.6 (31/35)	35
366-763 days	24	89.6 (86/96)	32
30 months	30	80.6 (29/36)	35
35 months	35	84.6 (11/13)	37
36 months	36	74.2 (23/31)	35
36 months	36	42.1 (8/19)	36
764-1265 days	36	53.6 (15/28)	32
72 months	72	8.9 (2/23)	38

Supplementary Figure 1. Bat coronavirus research effort, as measured by publication count, in Southeast Asia. In the figure legend, tick marks from left to right indicate 0, 5, 20, 100, 150, 550, and 600 publications.

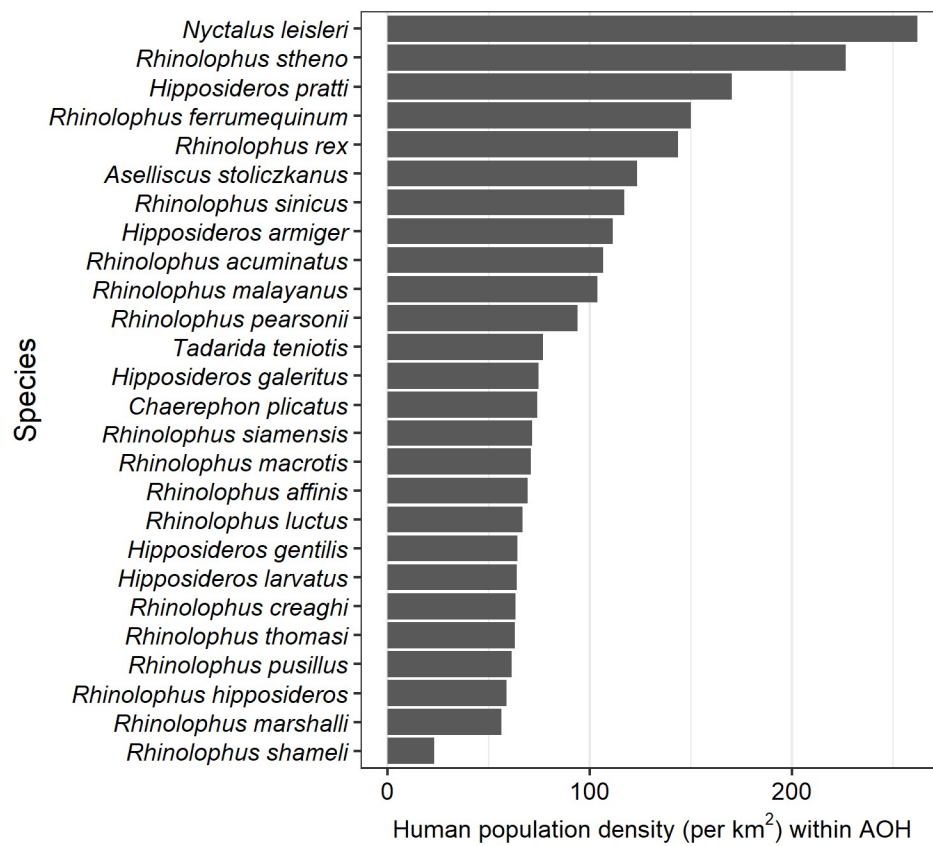
**Research Effort (PubMed):
(Bat OR Bats OR Chiroptera) AND Coronaviruses**



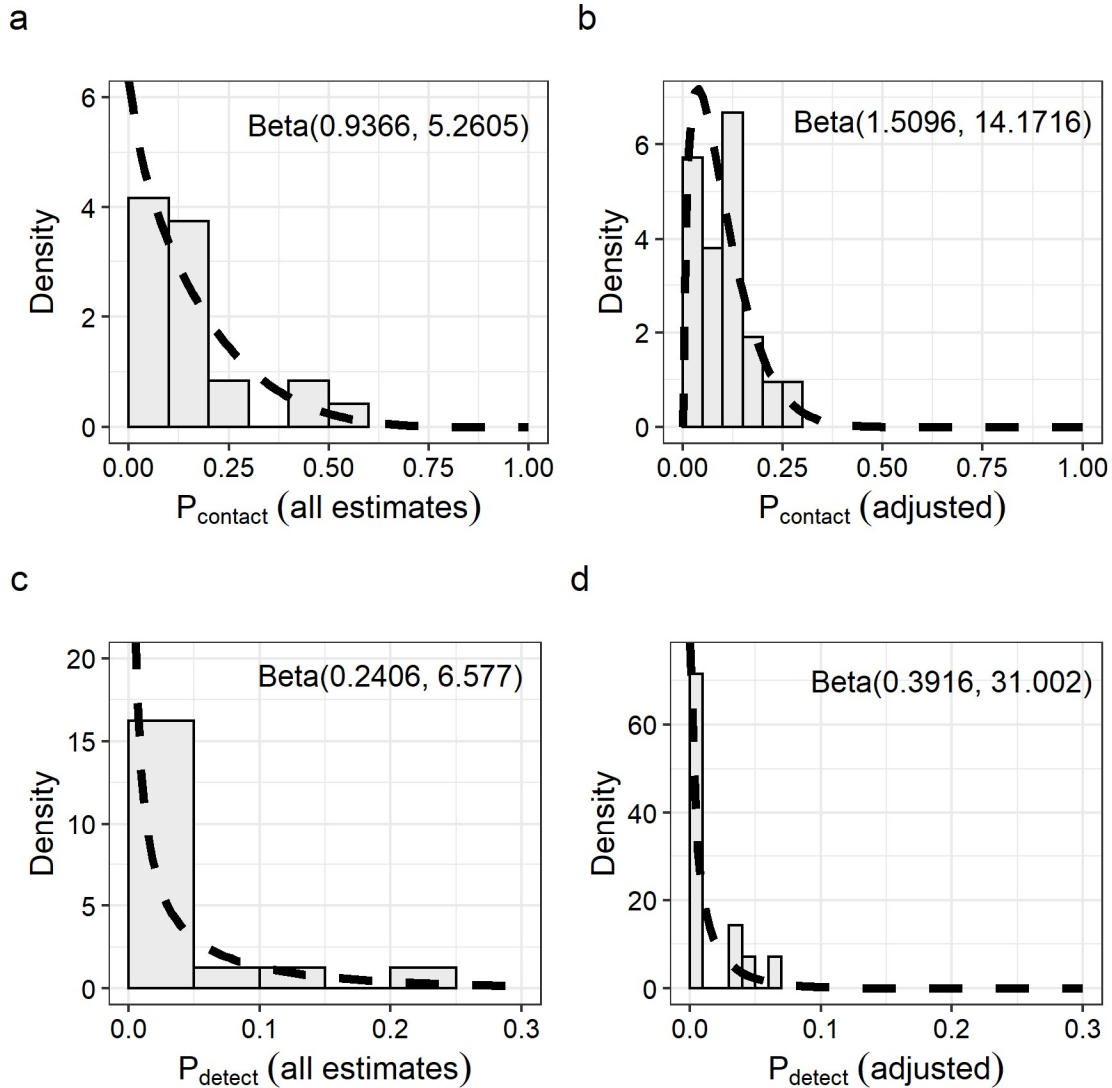
Supplementary Figure 2. Comparison of original IUCN species range sizes to AOH sizes, for Southeast Asia. Species are ordered by decreasing IUCN area.



Supplementary Figure 3. Human population density per km² within the AOH of each SARS-CoV bat host species.



Supplementary Figure 4. Fitted beta distributions for P_{contact} (the probability that a human comes into contact with a bat) and P_{detect} (the probability that a human-bat contact leads to a serologically detectable human infection). Panels **a** and **c** show the original distributions for the parameters. Panel **b** shows the re-fit P_{contact} distribution after excluding the three highest estimates of human-bat contact gathered from a literature search. Panel **d** shows the re-fit P_{detect} distribution after excluding the two highest estimates of seroprevalence gathered from a literature search. The R package `fitdistrplus` v1.1-3³⁹ was used to determine the shape parameters of the distributions.



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