

Supplementary Materials for

Temporal evidence shows *Australopithecus sediba* is unlikely to be the ancestor of *Homo*

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The PDF file includes:

Fig. S1. Confirming our probability model results (Fig. 3) with simulations.

Fig. S2. Same analysis as in Fig. 3 but assuming hominin temporal durations of 2 Ma, A.L. 666-1 (2.33 Ma old) represents the oldest *Homo* fossil, or both.

Fig. S3. Uniform probability plots for 4- to 1-Ma-old hominin fossil horizons in South Africa and eastern Africa.

Fig. S4. Same analysis as in Fig. 3, but the probability of sampling a fossil horizon (i.e., FRP) from the last 25% of the ancestor's range is doubled.

Fig. S5. Schematic illustrating how proposing an ancestor-descendant relationship based on temporal evidence does not necessarily constrain the first-discovered fossil in each species to be in the "correct" order (i.e., where the ancestor's first-discovered fossil predates the descendant's).

Table S1. Previously proposed ancestor-descendant hominin species pairs ($n = 28$), and the year discovered and geological ages of the first-discovered specimen in each species.

References (26, 27)

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/5/5/eaav9038/DC1)

Data file S1 (.csv format). Hypothesized hominin ancestor–descendant species pairs.

Data file S2 (.csv format). Geological ages for first-discovered specimens of hominin species.

Data file S3 (.csv format). Four- to 1-Ma-old South African and eastern African hominin-bearing members and their geological ages.

Data file S4 (.pdf format). Dataset references.

Data file S5 (.R format). R code for analyses and creating figures.

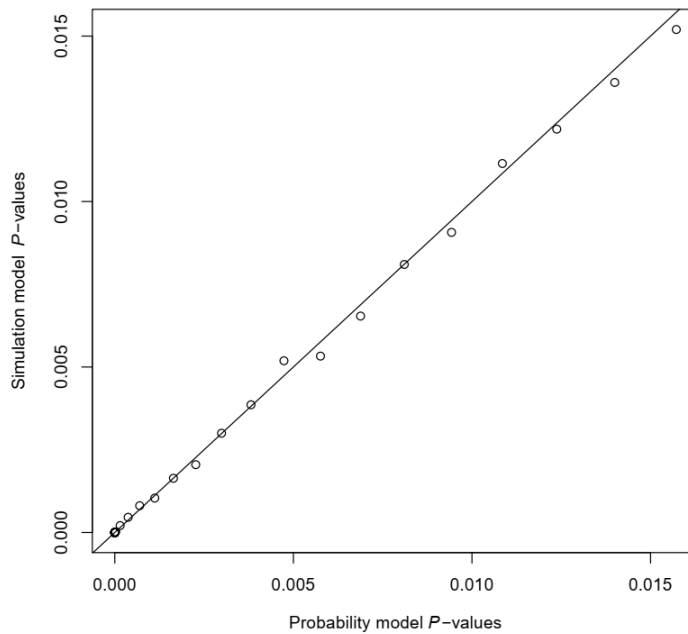


Fig. S1. Confirming our probability model results (Fig. 3) with simulations. Using time units of millions of years (Ma), we modeled the ancestor species as originating at time zero and going extinct at 0.97 (i.e., our assumed hominin temporal duration (6)). The descendant species is modeled as originating at 0.97 minus the amount of range overlap, and its extinction age is its origination age plus 0.97. Because we are only interested in the amount of time separating the ancestor's and descendant's fossil horizons, it does not matter exactly when these species originated or went extinct. Assuming the probability of sampling a fossil horizon is uniform throughout a species' temporal range, we randomly sampled one fossil horizon each from the ancestor's and descendant's temporal ranges and iterated this process 100,000 times. To calculate the P -value, we counted the proportion of times the ancestor's fossil horizon postdated the descendant's by at least 0.8 (i.e., the observed age difference between *A. sediba* and earliest *Homo*). Probability model P -values (x-axis) follow eq. 5c (see also Fig. 3). Different points represent different amounts of overlap, with larger P -values representing greater overlap.

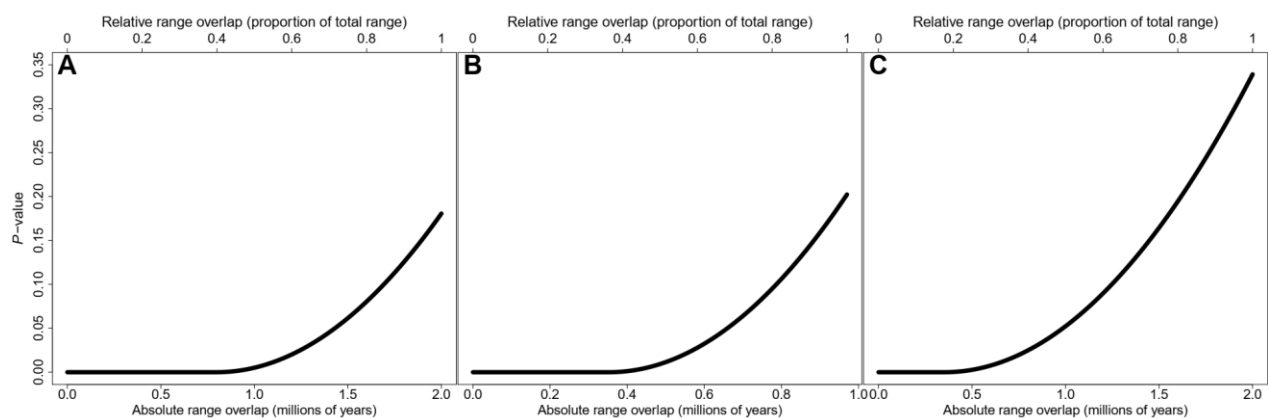


Fig. S2. Same analysis as in Fig. 3 but assuming (A) hominin temporal durations of 2 Ma, (b)

A.L. 666-1 (2.33 Ma old) represents the oldest *Homo* fossil, or (C) both.

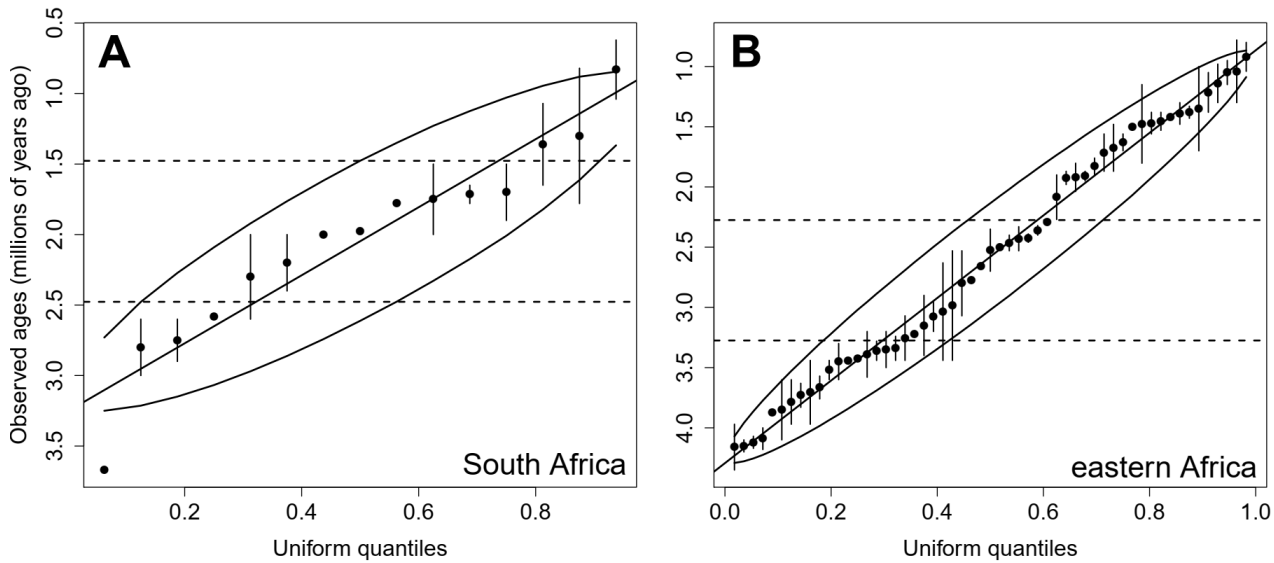


Fig. S3. Uniform probability plots for 4- to 1-Ma-old hominin fossil horizons in (A) South Africa ($n = 15$) and (B) eastern Africa ($n = 55$). Each point represents the age midpoint for one fossil horizon, which are defined as non-duplicated midpoint ages of hominin-bearing members (7, 8) (see Data File S3). The error bars represent the older and younger bracketing ages. The observed fossil horizon ages are plotted against standard uniform quantiles, and the linearity of this relationship (illustrated by the ordinary least squares [OLS] model) is used to assess the degree to which observed fossil horizons are uniformly and independently distributed through time. The 95% confidence bounds are calculated from 100,000 draws from a standard uniform distribution and are scaled to the observed data by multiplying and then adding the estimated OLS slope and intercept, respectively. The horizontal dashed lines represent ± 0.5 Ma surrounding the ages of (A) *Australopithecus sediba* (1.977 Ma old) and (B) the Ledi-Geraru *Homo* mandible (2-8-2.75 Ma old). Horizontal “stripes” of points within the dashed line region would indicate more fossil horizons preserved than expected during this time period and therefore a higher fossil recovery potential (FRP). We do not see this in (B), though there is some semblance of this in (A), but it is well within the expectations represented by the 95% confidence bound. This method assumes that hominin fossil horizons are an adequate proxy for FRP and that if FRP does differ among

horizons, the differences are randomly distributed through time within each region. Fossil horizon and age data can be found in Data File S3, and R code for creating these plots can be found in Data File S5. This method of testing the uniformity and independence of geological ages is from (7, 8).

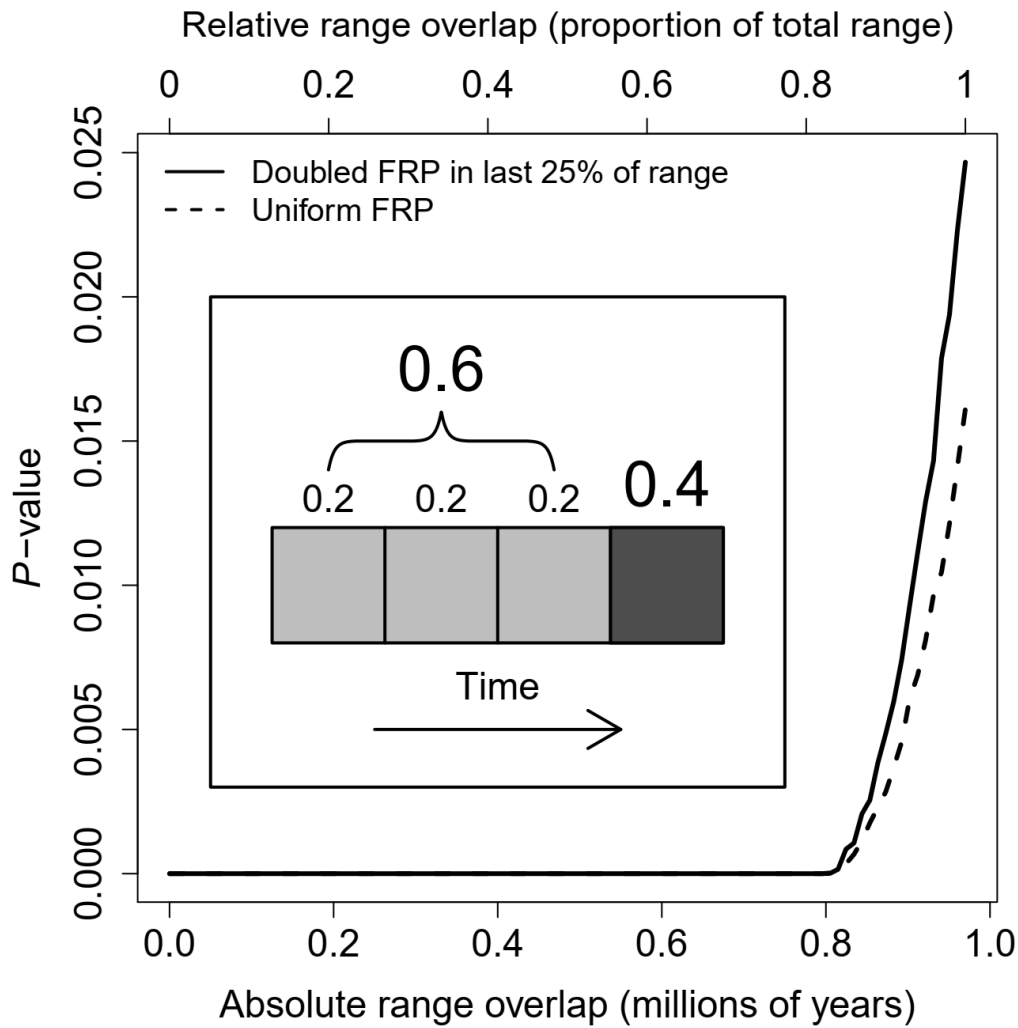


Fig. S4. Same analysis as in Fig. 3, but the probability of sampling a fossil horizon (i.e., FRP) from the last 25% of the ancestor's range is doubled. This analysis was done using simulations (see fig. S1 for how the simulations were conducted). The probability of sampling a horizon from the last 25% is twice as much as the probability of sampling a horizon from any of the other three quartiles, such that there is a 0.6 probability of sampling a horizon from the first 75% of the range and a 0.4 probability of sampling a horizon from the last 25% (inset). The dashed line represents results where the sampling probability in the ancestor's range is uniform through time (as in Fig. 3). For both curves, the probability of sampling a fossil horizon from the descendant's range is uniform through time.

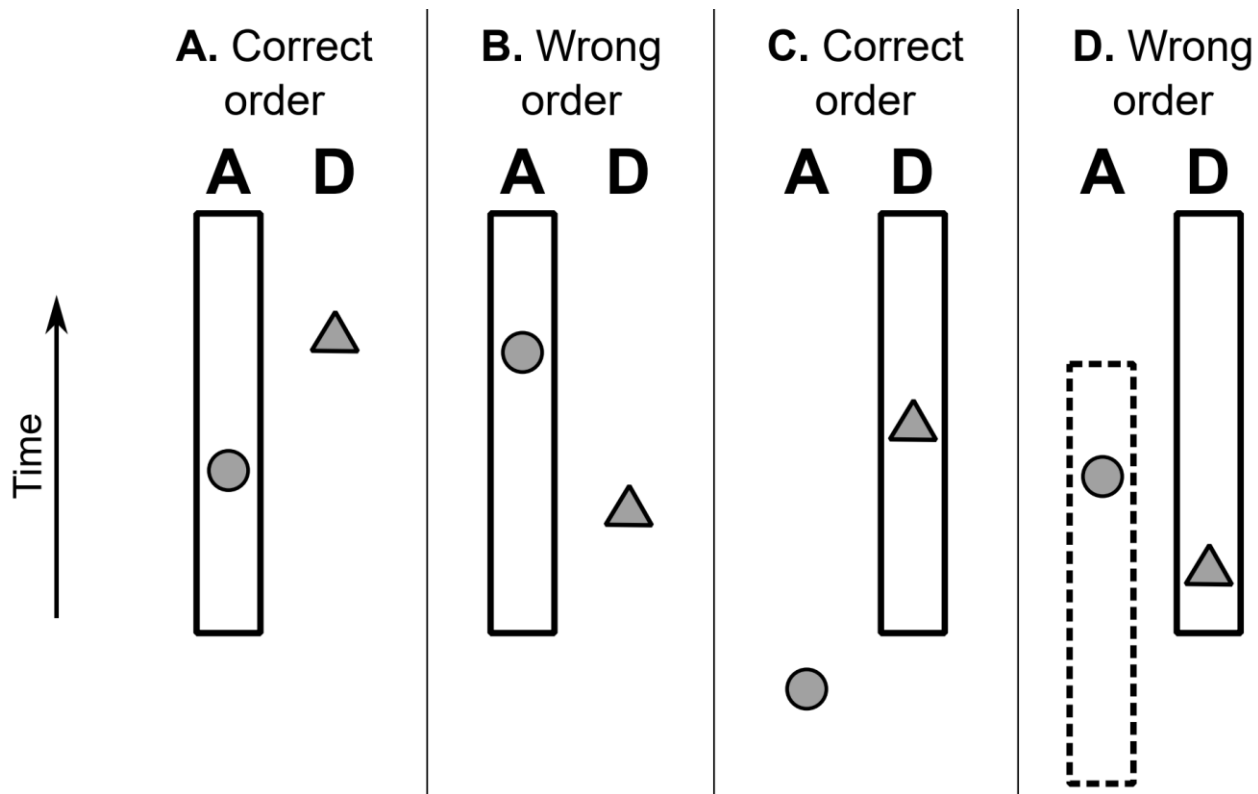


Fig. S5. Schematic illustrating how proposing an ancestor-descendant relationship based on temporal evidence does not necessarily constrain the first-discovered fossil in each species to be in the “correct” order (i.e., where the ancestor’s first-discovered fossil predates the descendant’s). “A” and “D” represent ancestral and descendant species, respectively, and their first-discovered fossils are represented by circles and triangles, respectively. Solid temporal ranges represent the species that was discovered first, such that its temporal range had multiple sampled fossil horizons when the second species was discovered. The second-discovered species is either represented by (A-C) a single point or (D) a dashed temporal range. If one subscribes to a strictly anagenetic or bifurcating cladogenetic view of hominin speciation, fossil horizons can never be recovered in the “wrong” order (i.e., where the ancestor’s fossil postdates the descendant’s) because there would be no temporal overlap between ancestors and descendants (Fig. 1). On the other hand, if one believes that hominin species can cladogenetically bud from each other such that their temporal ranges can overlap (Fig. 1), evolutionary relationships proposed based on temporal data require only that the descendant’s FAD postdates the ancestor’s FAD. (A) The newly discovered descendant fossil postdates the proposed ancestor’s FAD and

first-discovered fossil. Therefore, these first-discovered fossils were recovered in the correct order. **(B)** As before, the newly discovered descendant fossil postdates the ancestor's FAD, but this time the new descendant fossil predates the first-discovered fossil of the ancestor. Thus, these first-discovered fossils were recovered in the wrong order. The one empirical example of first-discovered hominin fossils being recovered in the wrong order follows this scenario (table S1). **(C, D)** depict similar scenarios but with the descendant species sampled first. **(C)** Because a newly discovered ancestor's fossil must predate the descendant's FAD (and therefore its entire known temporal range), this scenario will always lead to first-discovered fossils being found in the correct order. If the descendant species was discovered first, the only way first-discovered fossils can be found in the wrong order is if (1) **(D)** the ancestor-descendant relationship was proposed only after more of the ancestor's temporal range was discovered (represented by the dashed rectangle), or (2) one does not posit an evolutionary relationship based strictly on the ancestor's FAD predating the descendant's FAD, and recognizes that ancestors can exist contemporaneously with descendants, such that their first-discovered fossils can be recovered in the wrong order (as proposed with *A. sediba* and earliest *Homo* (1, 6)).

Table S1. Previously proposed ancestor-descendant hominin species pairs ($n = 28$), and the year discovered and geological ages of the first-discovered specimen in each species. Each fossil's geological age is represented by its older and younger bracketing ages. Bolded ancestor-descendant pairs represent those species whose temporal ranges overlap, as determined using the conservative first and last appearance dates from (26) [FAD of *Homo sapiens* is from (27)]. The asterisked ancestor-descendant pair indicates the only one whose first-discovered fossils were recovered in the wrong order. “s.l.” is *sensu lato*, and “s.s.” is *sensu stricto*. References can be found in Data files S1, S2, and S4.

Ancestor				Descendant			
Species	Year of discovery	Bracketing ages (millions of years ago)		Species	Year of discovery	Bracketing ages (millions of years ago)	
		Older	Younger			Older	Younger
<i>Ardipithecus kadabba</i>	1997	5.77	5.54	<i>Ardipithecus ramidus</i>	1993	4.40	4.40
<i>Ardipithecus ramidus</i>	1993	4.40	4.40	<i>Australopithecus anamensis</i>	1965	4.12	4.07
<i>Ardipithecus ramidus</i>	1993	4.40	4.40	Burtele foot	2009	3.47	3.20
<i>Australopithecus anamensis</i>	1965	4.12	4.07	<i>Australopithecus afarensis</i>	1939	3.83	3.63
<i>Australopithecus afarensis</i>	1939	3.83	3.63	<i>Paranthropus aethiopicus</i>	1967	2.60	2.60
<i>Paranthropus aethiopicus</i>	1967	2.60	2.60	<i>Paranthropus boisei</i>	1955	1.80	1.78
<i>Australopithecus afarensis</i>	1939	3.83	3.63	<i>Australopithecus garhi</i>	1990	2.50	2.50
<i>Australopithecus afarensis</i>	1939	3.83	3.63	Ledi-Geraru <i>Homo</i>	2013	2.80	2.75
<i>Australopithecus afarensis</i>	1939	3.83	3.63	<i>Homo habilis</i> s.s.	1959	2.04	1.80
<i>Kenyanthropus platyops</i>	1982	3.26	3.26	<i>Homo rudolfensis</i>	1971	1.56	1.38
Ledi-Geraru <i>Homo</i>	2013	2.80	2.75	<i>Homo habilis</i> s.s.	1959	2.04	1.80
<i>Australopithecus garhi</i>	1990	2.50	2.50	<i>Homo habilis</i> s.s.	1959	2.04	1.80

<i>Australopithecus afarensis</i>	1939	3.83	3.63	<i>Australopithecus africanus</i>	1924	3.03	2.58
<i>Australopithecus africanus</i>	1924	3.03	2.58	<i>Paranthropus robustus</i>	1938	1.90	1.90
<i>Australopithecus africanus</i>	1924	3.03	2.58	<i>Homo habilis s.s.</i>	1959	2.04	1.80
<i>Homo habilis s.s.</i>	1959	2.04	1.80	<i>Homo erectus s.l.</i>	1890	0.80	0.70
<i>Homo erectus s.l.*</i>	1890	0.80	0.70	<i>Homo antecessor*</i>	1994	0.90	0.80
<i>Homo erectus s.l.</i>	1890	0.80	0.70	<i>Homo heidelbergensis</i>	1907	0.61	0.61
<i>Homo erectus s.l.</i>	1890	0.80	0.70	<i>Homo rhodesiensis</i>	1921	0.30	0.30
<i>Homo antecessor</i>	1994	0.90	0.80	<i>Homo heidelbergensis</i>	1907	0.61	0.61
<i>Homo antecessor</i>	1994	0.90	0.80	<i>Homo rhodesiensis</i>	1921	0.30	0.30
<i>Homo erectus s.l.</i>	1890	0.80	0.70	<i>Homo sapiens</i>	1868	0.03	0.03
<i>Homo antecessor</i>	1994	0.90	0.80	<i>Homo neanderthalensis</i>	1856	0.04	0.04
<i>Homo antecessor</i>	1994	0.90	0.80	<i>Homo sapiens</i>	1868	0.03	0.03
<i>Homo heidelbergensis</i>	1907	0.61	0.61	<i>Homo neanderthalensis</i>	1856	0.04	0.04
<i>Homo heidelbergensis</i>	1907	0.61	0.61	<i>Homo sapiens</i>	1868	0.03	0.03
<i>Homo rhodesiensis</i>	1921	0.30	0.30	<i>Homo sapiens</i>	1868	0.03	0.03
<i>Homo erectus s.l.</i>	1890	0.80	0.70	<i>Homo floresiensis</i>	2003	0.02	0.02