Dear Prof. Vermeesch,

Thank you for your suggestion! We agree that we should mention the effect of negative inheritance/age upfront. Therefore, we have made the following changes to our manuscript:

For the abstract, we changed the first sentence as "…, while retaining the advantages of linear inversion for surfaces with inheritance and age much greater than zero." We also added a sentence in line 13-14: "For surfaces with very low inheritance or age, it is important to apply a constrained inversion to obtain the correct result distributions."

For the "Conclusion" section, we added "For surfaces with low inheritance or age, as demonstrated with the Beida River sample site and the simulated profiles, unconstrained inversion could lead to incorrect distributions for inversion results. Therefore, the linear regression we proposed here requires applying the nonnegative constraint on such depth profile data." in line 410-412.

We appreciate the time and effort you and reviewers put into our manuscript. We hope our revision meets your expectations.

Yiran Wang

Track-changes for the supplement (previous revision):

Combined linear regression and Monte Carlo approach to modelling exposure age depth profiles

Supporting information

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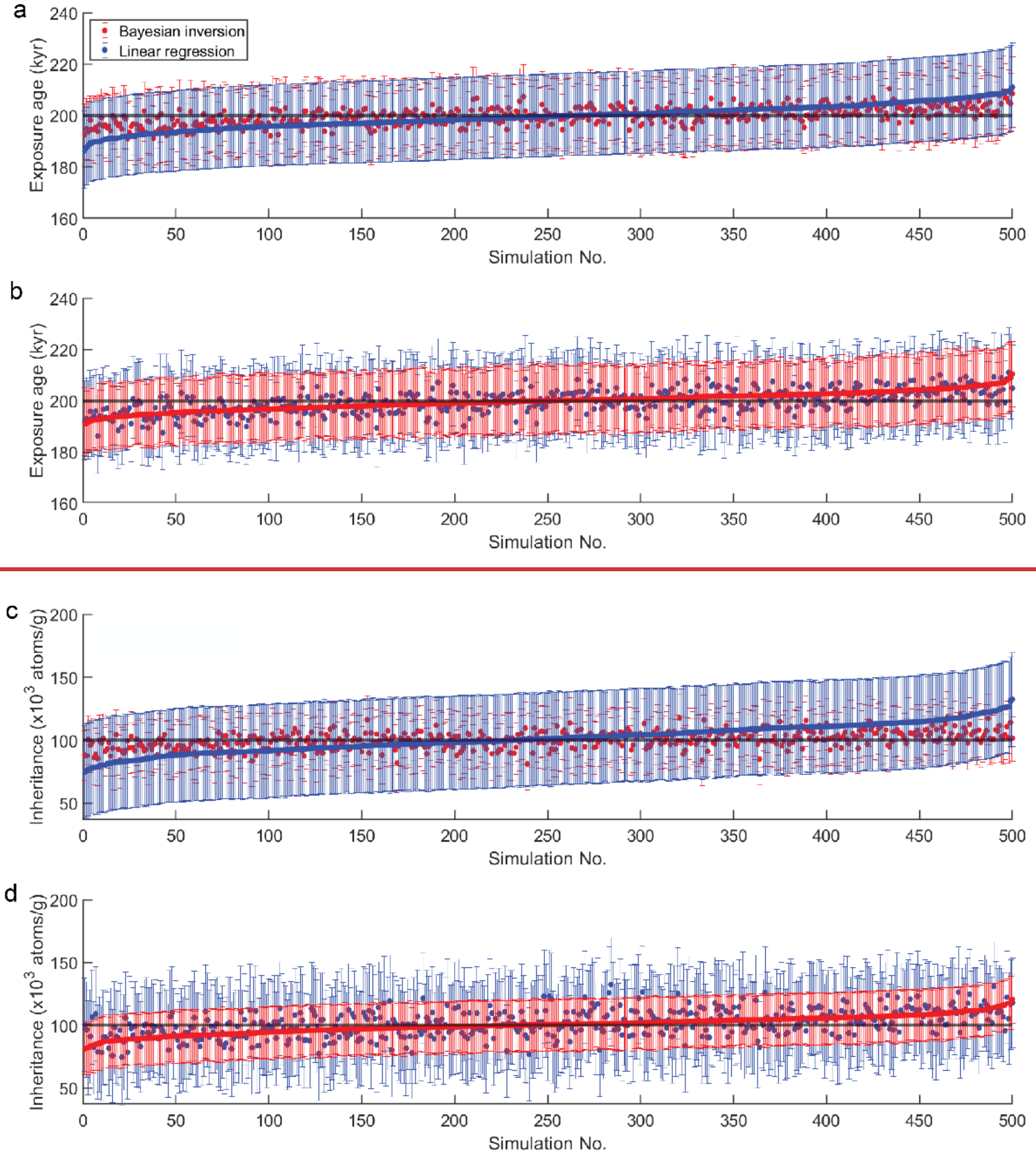
1. Simulated ~~TCN~~CN depth profiles

Our simulation process is conducted with following steps:

1. For each scenario, we first produce an ideal depth profile based on given exposure age, inheritance, production rate, attenuation, density, etc.
2. Next, we produce a suite of simulated depth profiles with each sample deviated from the true value based on an imposed error distribution which defined as “deviation of sample concentration. In addition, an independent analytical uncertainty is also assigned for each sample. The mean of the sample depth is the same as the true value; but an uncertainty is assigned for each sample depth. The remaining parameters (density, production rate, attenuation) are the same as the ideal profile, with no imposed uncertainty.
3. For each profile within the suite, we estimate the exposure age and inheritance based on the samples generated in step 2, using both least-squares linear regression and forward modeling (Bayesian Monte Carlo) approaches.
4. From the analysis suite we compare the resulting distributions of the estimated age and inheritance using both methods with the true value and with each other.

1.1 Deviation of sample concentrations



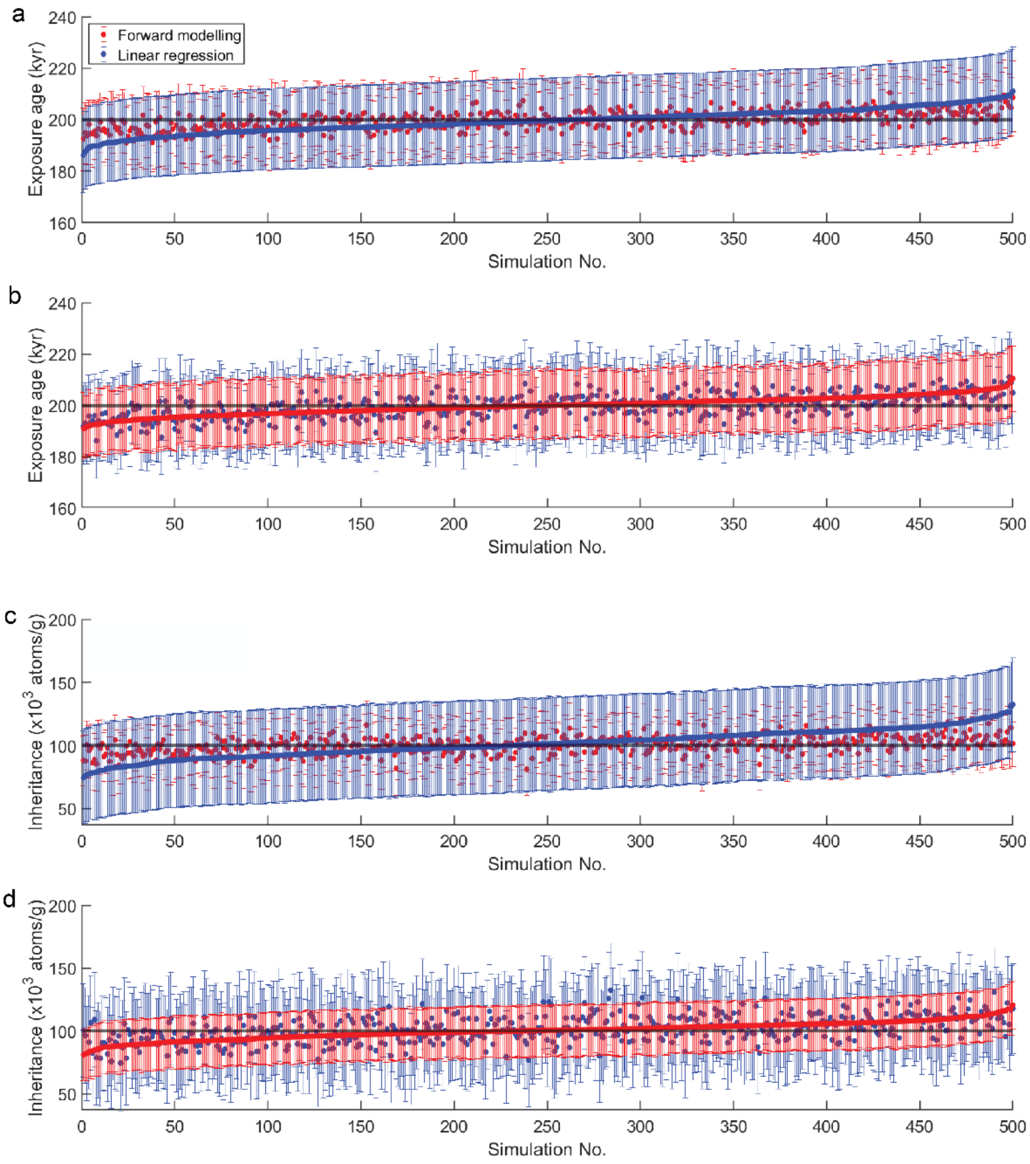
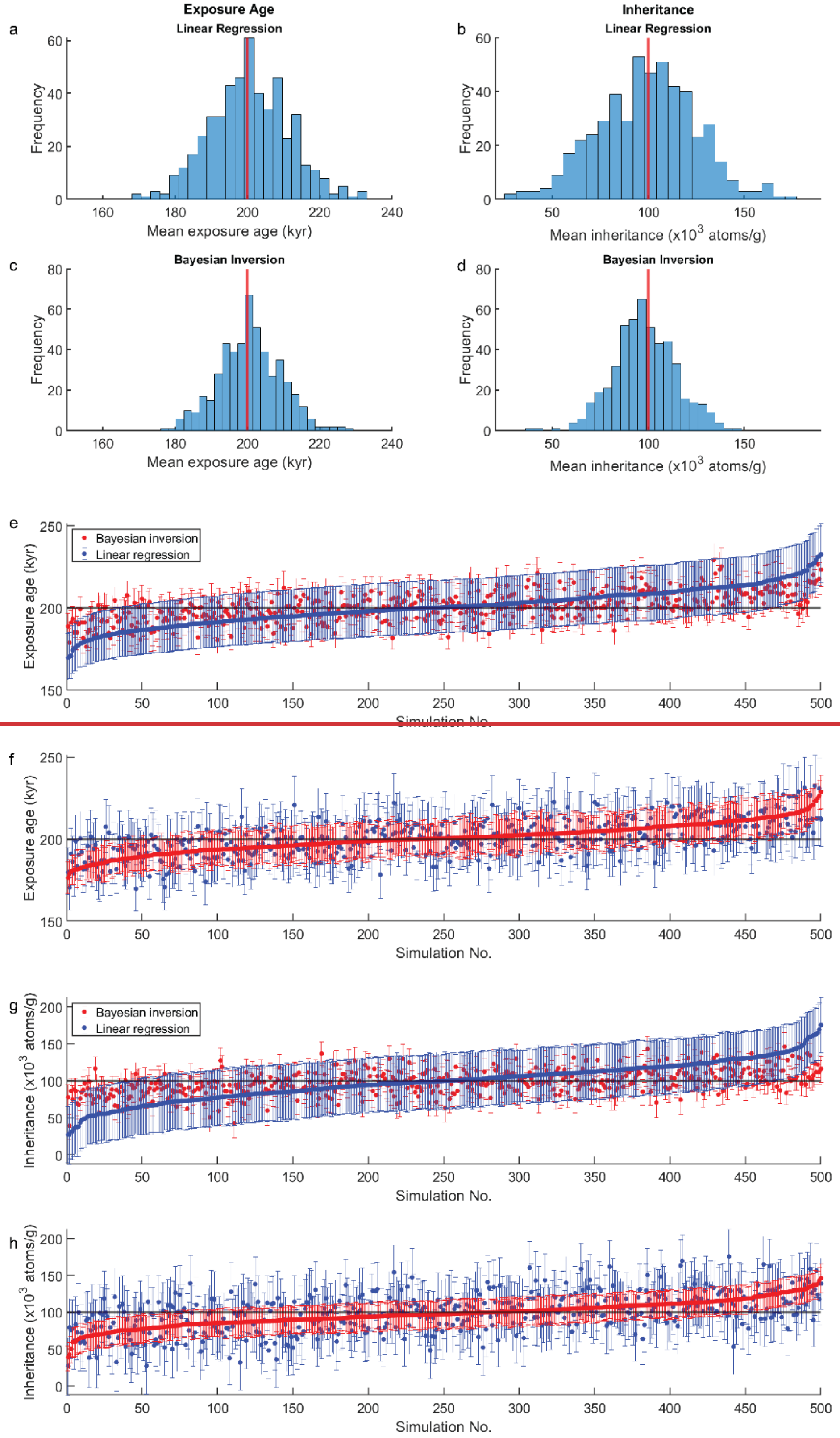


Figure S1 Distributions of age (a and b) and inheritance (c and d) estimation results for 500 simulated ~~TCN~~CN profiles with 2% imposed deviation of sample concentration. a. Distribution of exposure age, sorted by mean age estimated from linear regression (eq. 4). b. Distribution of exposure age, sorted mean age estimated using a ~~Bayesian~~forward approach. c. Distribution of inheritance, sorted by mean inheritance estimated from linear regression (eq. 4). d. Distribution of inheritance, sorted by mean inheritance estimated using a ~~Bayesian~~forward approach.


Exposure Age
Inheritance
a
Linear Regression
b
Linear Regression
Frequency
Mean exposure age (kyr)
Mean inheritance (x10^3 atoms/g)
c
Bayesian Inversion
d
Bayesian Inversion
160
180
200
220
240
50
100
150
0
20
40
60
80
e
Bayesian inversion
Linear regression
Exposure age (kyr)
250
200
150
Simulation No.
0
50
100
150
200
250
300
350
400
450
500
f
g
Inheritance (x10^3 atoms/g)
h

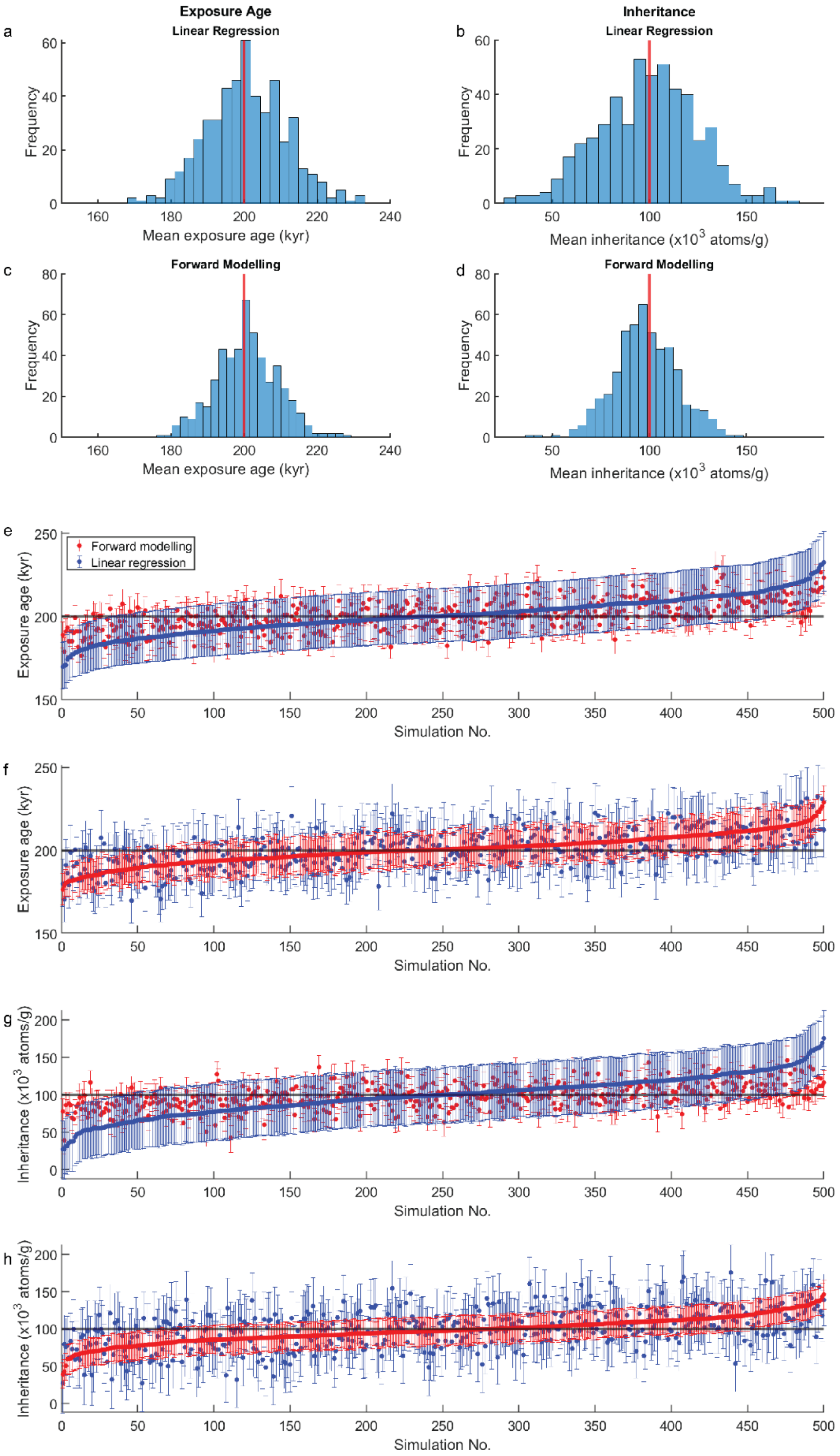
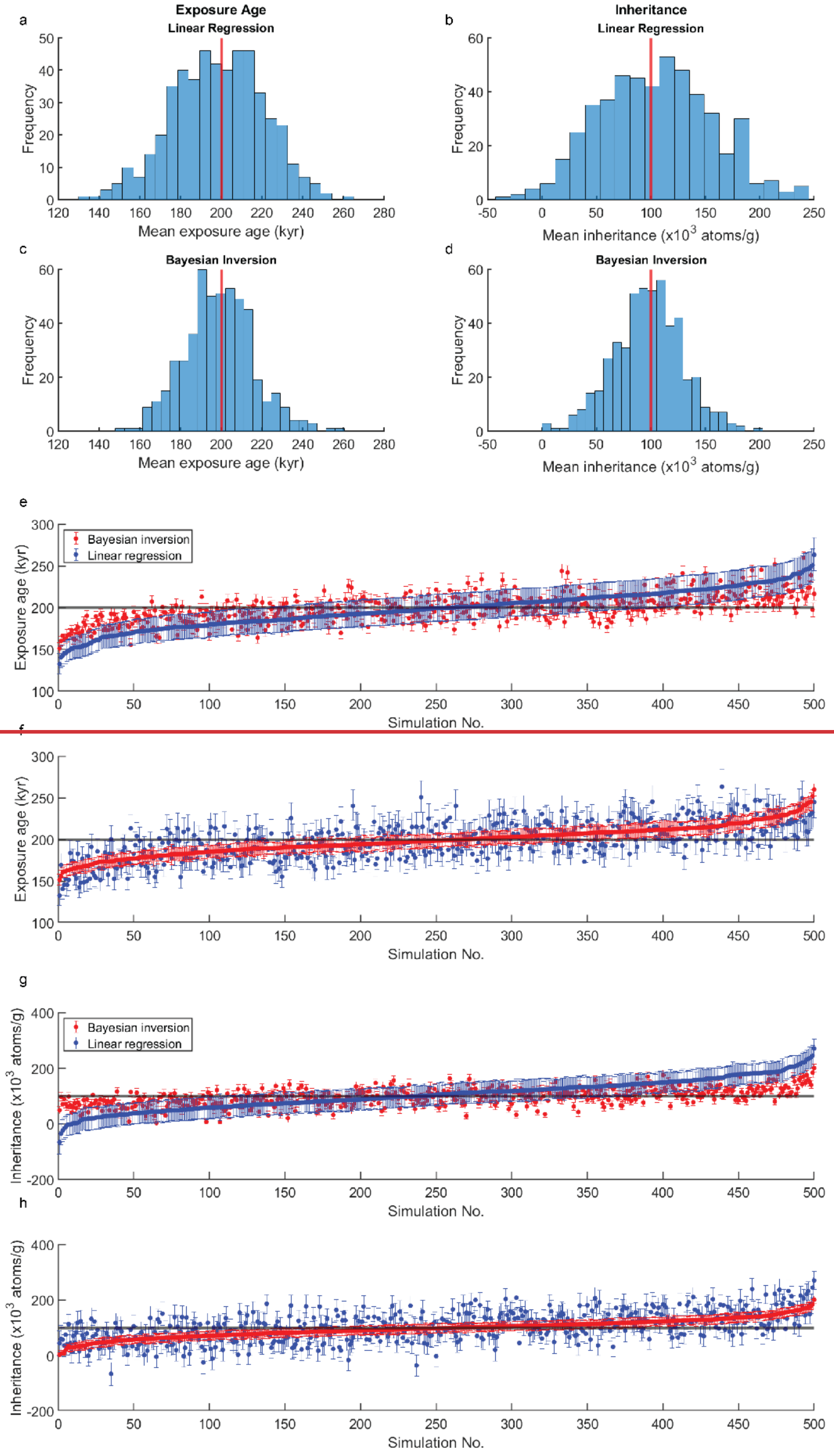


Figure S2 Distribution of age (a, b, e, f) and inheritance (c, d, g, h) estimation results for 500 simulated ~~TCN~~CN profiles with 5% imposed deviation of sample concentration. a. and b. Histogram of the mean exposure age estimated from linear

regression and a ~~Bayesian~~forward approach. c. and d. Histogram of mean inheritance estimated from linear regression a ~~Bayesian~~forward approach. e. Distribution of exposure age, sorted by mean age estimated from linear regression (eq. 4). f. Distribution of exposure age, sorted mean age estimated using a ~~Bayesian~~forward approach. g. Distribution of inheritance, sorted by mean inheritance estimated from linear regression (eq. 4). h. Distribution of inheritance, sorted by mean inheritance estimated using a ~~Bayesian~~forward approach.


a
Exposure Age
Linear Regression
Frequency
Mean exposure age (kyr)
b
Inheritance
Linear Regression
Frequency
Mean inheritance (x10^3 atoms/g)
c
Bayesian Inversion
Frequency
Mean exposure age (kyr)
d
Bayesian Inversion
Frequency
Mean inheritance (x10^3 atoms/g)
e
Bayesian inversion
Linear regression
Exposure age (kyr)
Simulation No.
f
Exposure age (kyr)
Simulation No.
g
Bayesian inversion
Linear regression
Inheritance (x10^3 atoms/g)
Simulation No.
h
Inheritance (x10^3 atoms/g)
Simulation No.

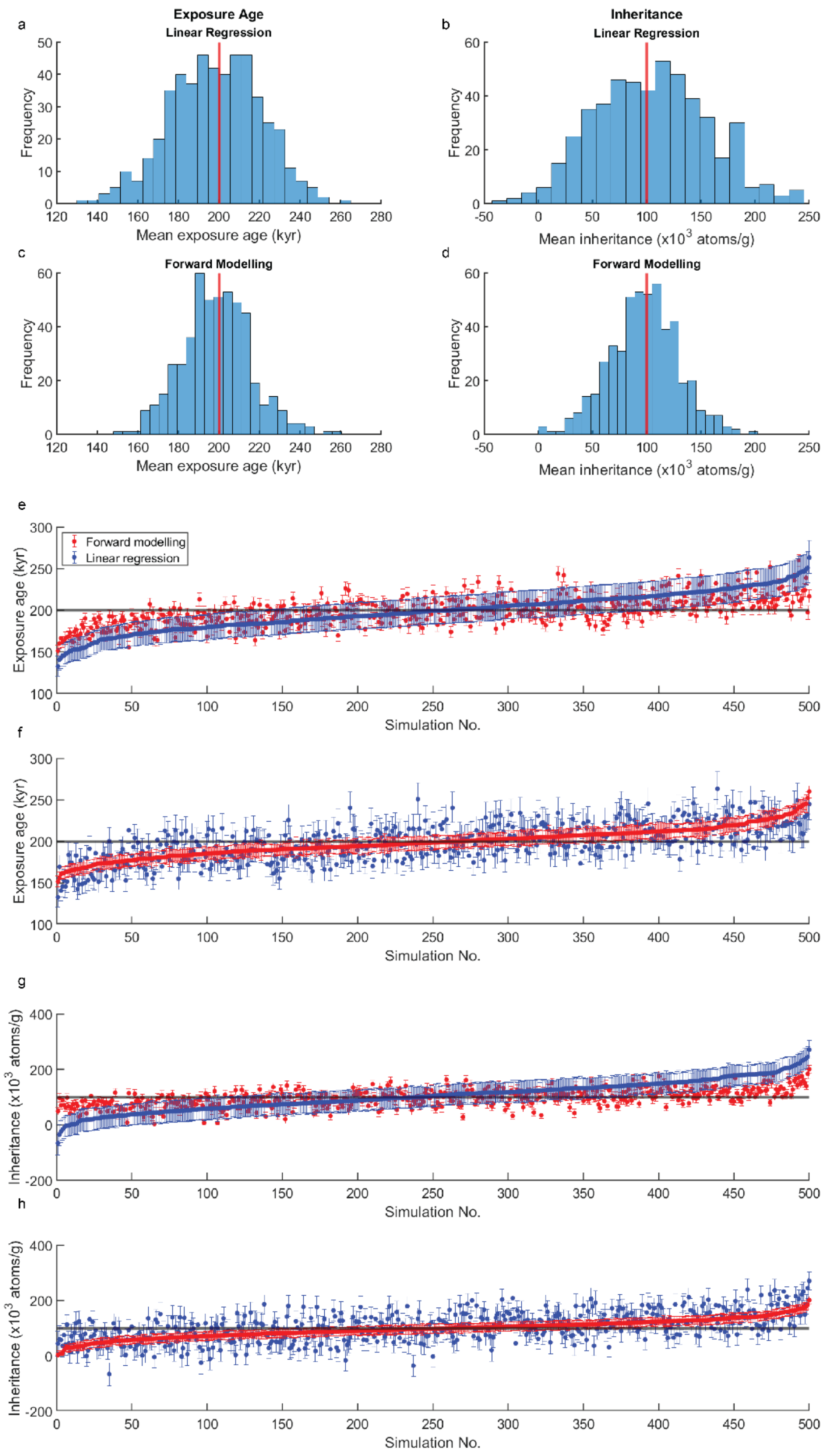
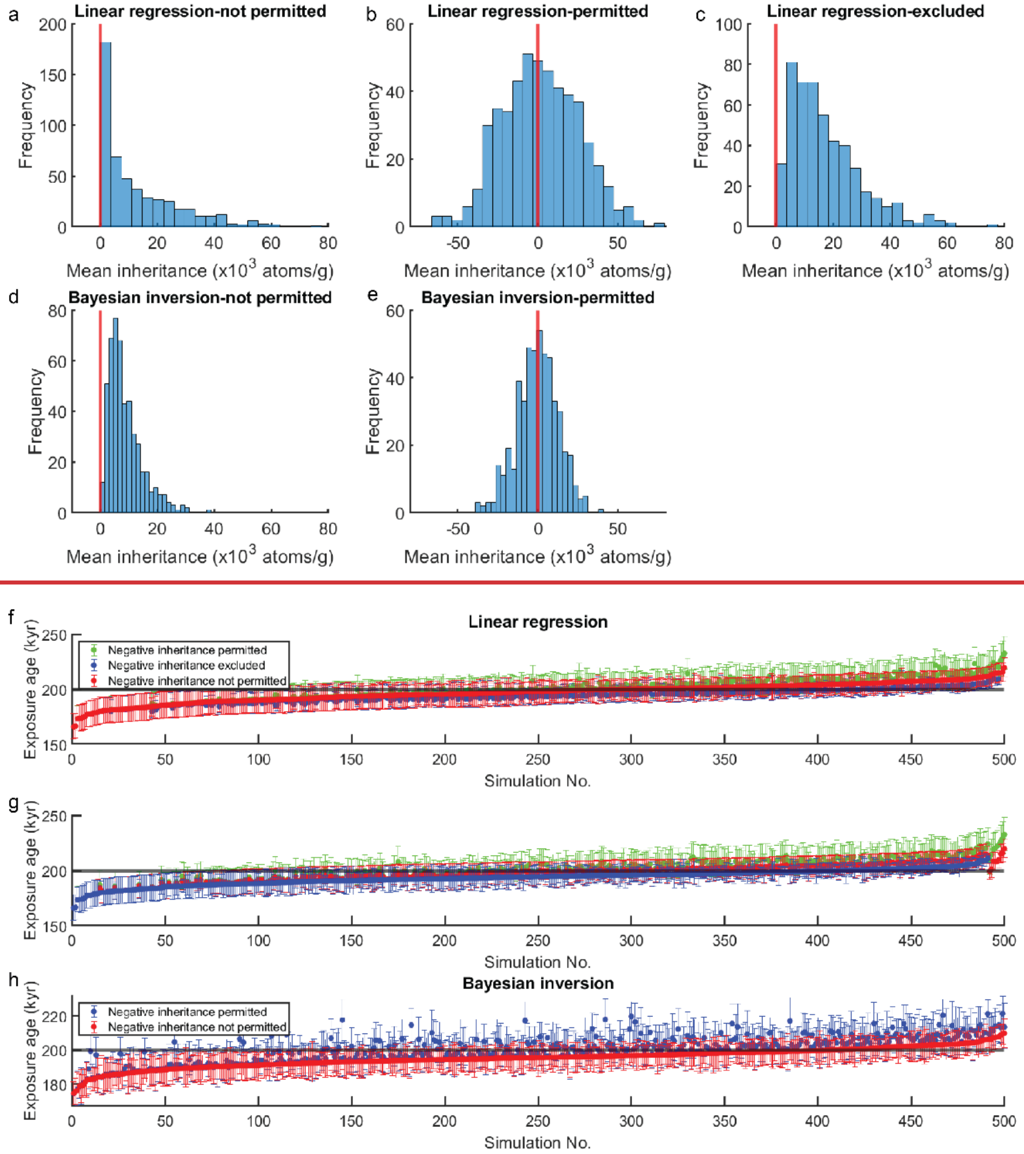


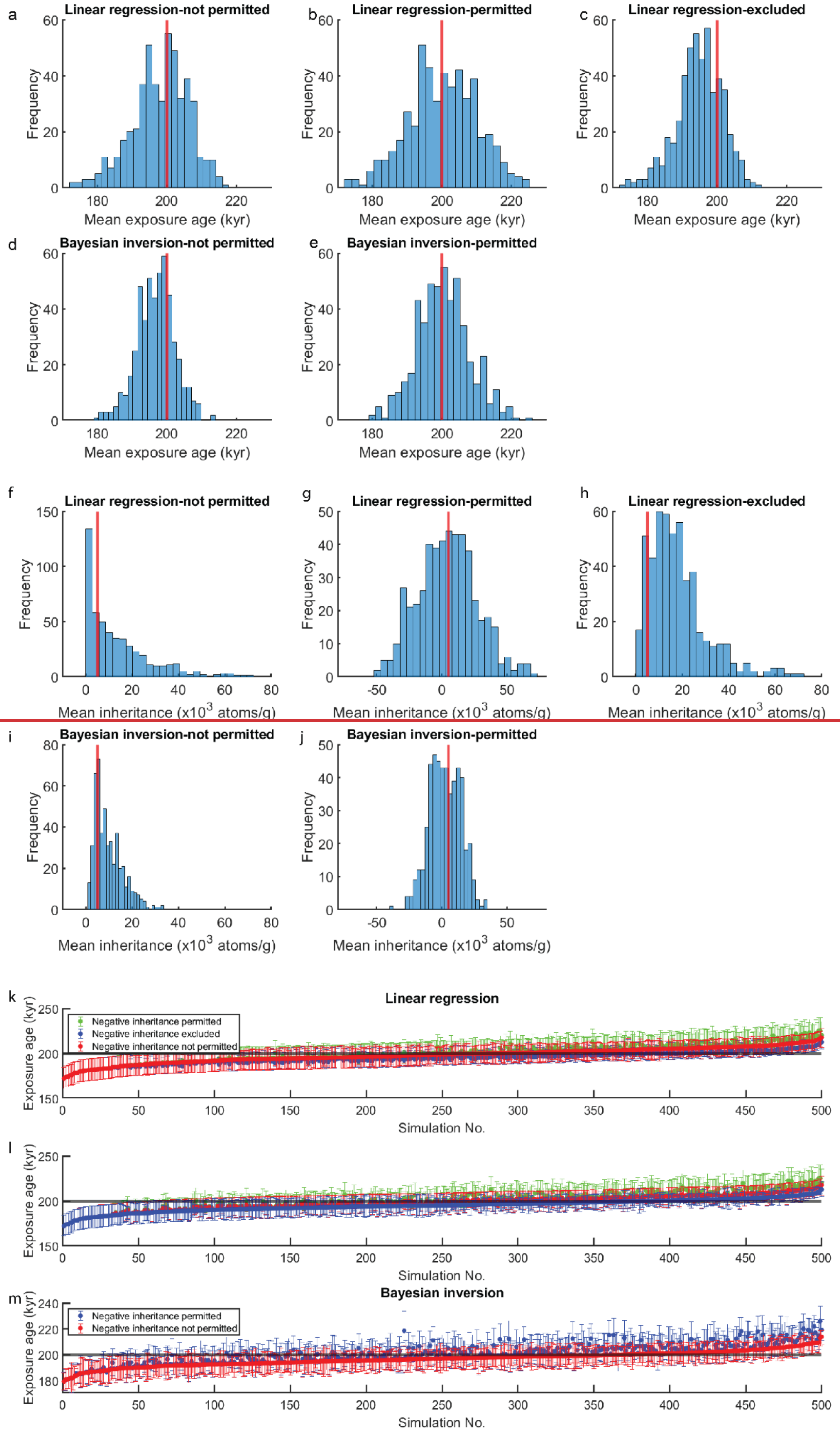
Figure S3 Distribution of age (a, b, e, f) and inheritance (c, d, g, h) estimation results for 500 simulated ~~TCN~~CN profiles with 10% imposed deviation of sample concentration. a. and b. Histogram of the mean exposure age estimated from linear

regression and a ~~Bayesian~~forward approach. c. and d. Histogram of mean inheritance estimated from linear regression a ~~Bayesian~~forward approach. e. Distribution of exposure age, sorted by mean age estimated from linear regression (eq. 4). f. Distribution of exposure age, sorted mean age estimated using a ~~Bayesian~~forward approach. g. Distribution of inheritance, sorted by mean inheritance estimated from linear regression (eq. 4). h. Distribution of inheritance, sorted by mean inheritance estimated using a ~~Bayesian~~forward approach.

1.2 ~~Low inheritance~~Denudation depth

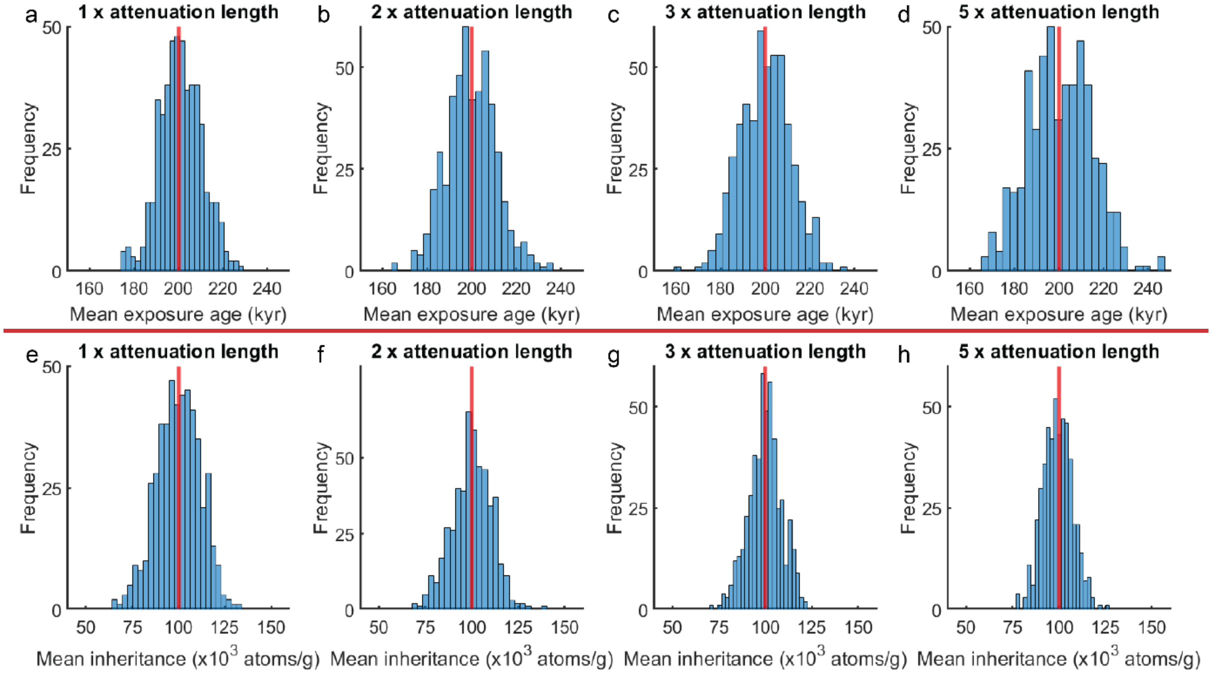


~~Figure S4 Distribution of estimation results for 500 simulated zero inheritance TCN profiles with 5% imposed deviation of sample concentration. a-e. Histogram of the mean inheritance estimated from linear regression and a Bayesian approach under different inversion schemes: not permitting negative inheritance during inversion (a and d), permit negative inheritance during inversion (b and e), excluding negative inheritance results after inversion (c, linear inversion only). f. Distribution of exposure age estimated from linear regression, sorted from mean age estimated by not permitting negative inheritance during inversion. g. Distribution of exposure age estimated from linear regression, sorted from mean age estimated by excluding negative inheritance after inversion. h. Distribution of exposure age estimated from a Bayesian approach, sorted from mean age estimated by not permitting negative inheritance during inversion.~~


a
Linear regression-not permitted
b
Linear regression-permitted
c
Linear regression-excluded
d
Bayesian inversion-not permitted
e
Bayesian inversion-permitted
Frequency
Mean exposure age (kyr)
180
200
220
0
20
40
60
f
Linear regression-not permitted
g
Linear regression-permitted
h
Linear regression-excluded
i
Bayesian inversion-not permitted
j
Bayesian inversion-permitted
Mean inheritance (x10^3 atoms/g)
-50
0
50
80
150
100
k
Linear regression
Negative inheritance permitted
Negative inheritance excluded
Negative inheritance not permitted
Exposure age (kyr)
Simulation No.
250
150
300
350
400
450
500
l
m
Bayesian inversion
240
Negative inheritance permitted
Negative inheritance not permitted

~~**Figure S5 Distribution of estimation results for 500 simulated low inheritance (5000 atoms/g) TCN profiles with 5% imposed deviation of sample concentration. a-e. Histogram of the mean exposure age estimated from linear regression and a Bayesian approach under different inversion schemes: not permitting negative inheritance during inversion (a and d), permit negative inheritance during inversion (b and e), excluding negative inheritance results after inversion (c, linear inversion only). f-j. Histogram of the mean inheritance estimated from linear regression and a Bayesian approach under different inversion schemes: not permitting negative inheritance during inversion (f and i), permit negative inheritance during inversion (g and j), excluding negative inheritance results after inversion (h, linear inversion only). k. Distribution of exposure age estimated from linear regression, sorted from mean age estimated by not permitting negative inheritance during inversion. l. Distribution of exposure age estimated from linear regression, sorted from mean age estimated by excluding negative inheritance after inversion. m. Distribution of exposure age estimated from a Bayesian approach, sorted from mean age estimated by not permitting negative inheritance during inversion.**~~

~~1.3 Denudation depth~~



~~Figure S6 Distribution of mean exposure age (a-d) and inheritance (e-h) estimated from a Bayesian approach for 500 simulated (5000 atoms/g) TCN~~

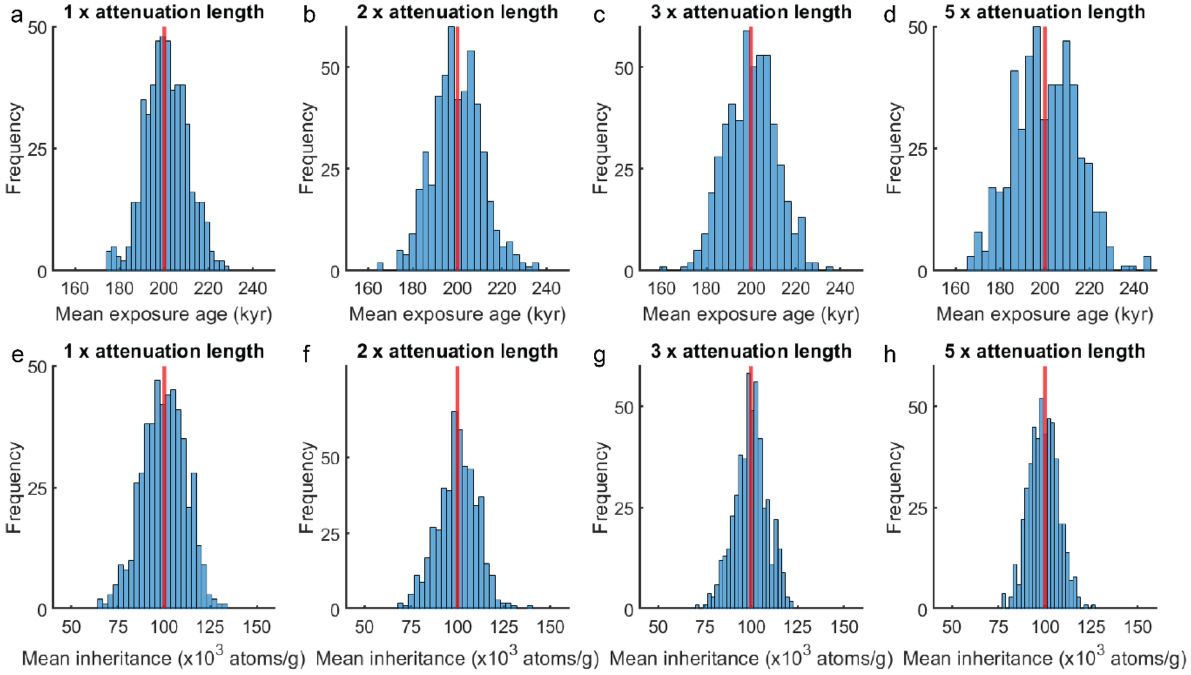
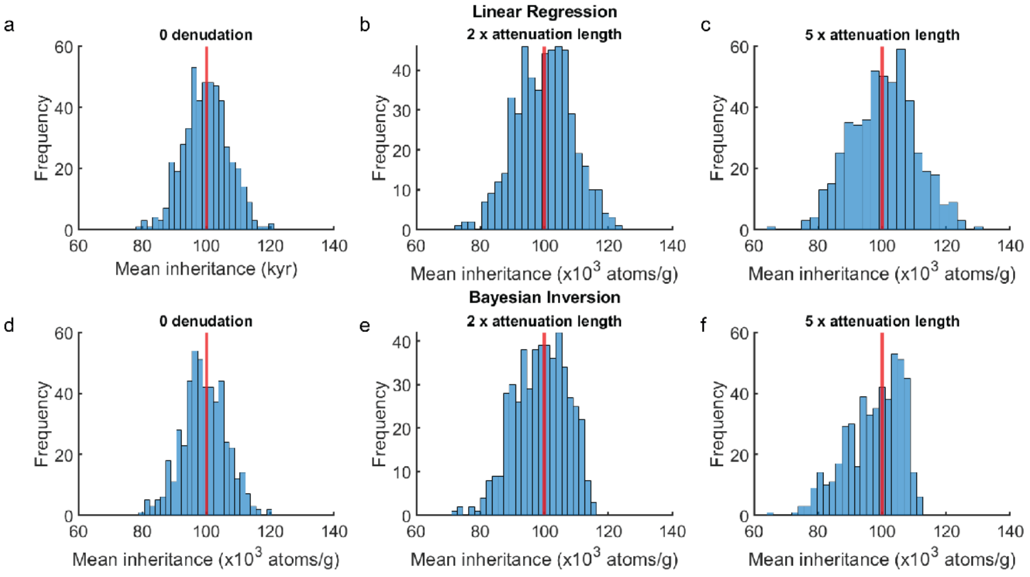
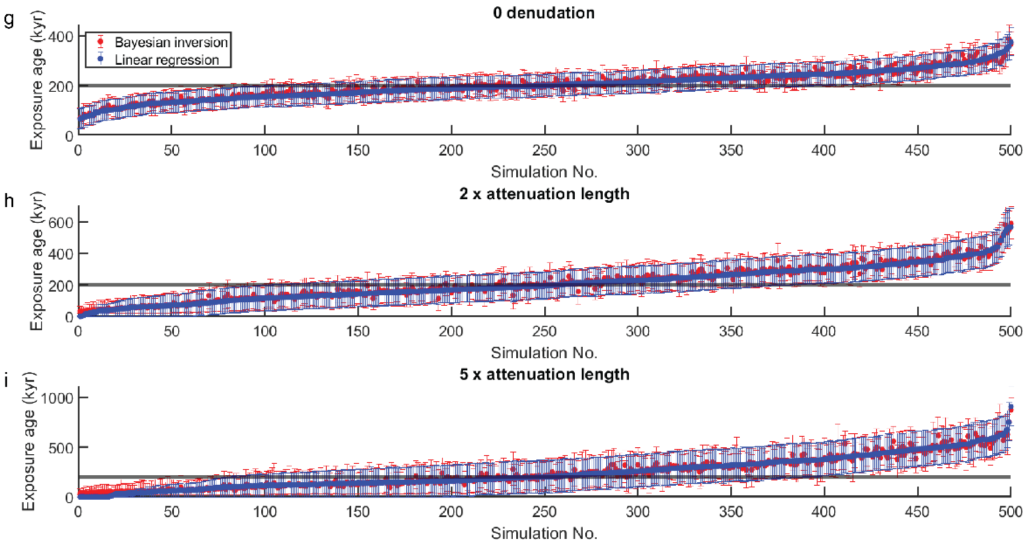


Figure S4 Distribution of mean exposure age (a-d) and inheritance (e-h) estimated from a forward approach for 500 simulated (5000 atoms/g) CN profiles with 5% imposed deviation of sample concentration and with total denudation equals to 1 (a and e), 2 (b and f), 3 (c and g) and 5-times (d and h) attenuation length of spallation. Red vertical line annotates the true age and true inheritance.

1.~~4~~3 Deep sample profile





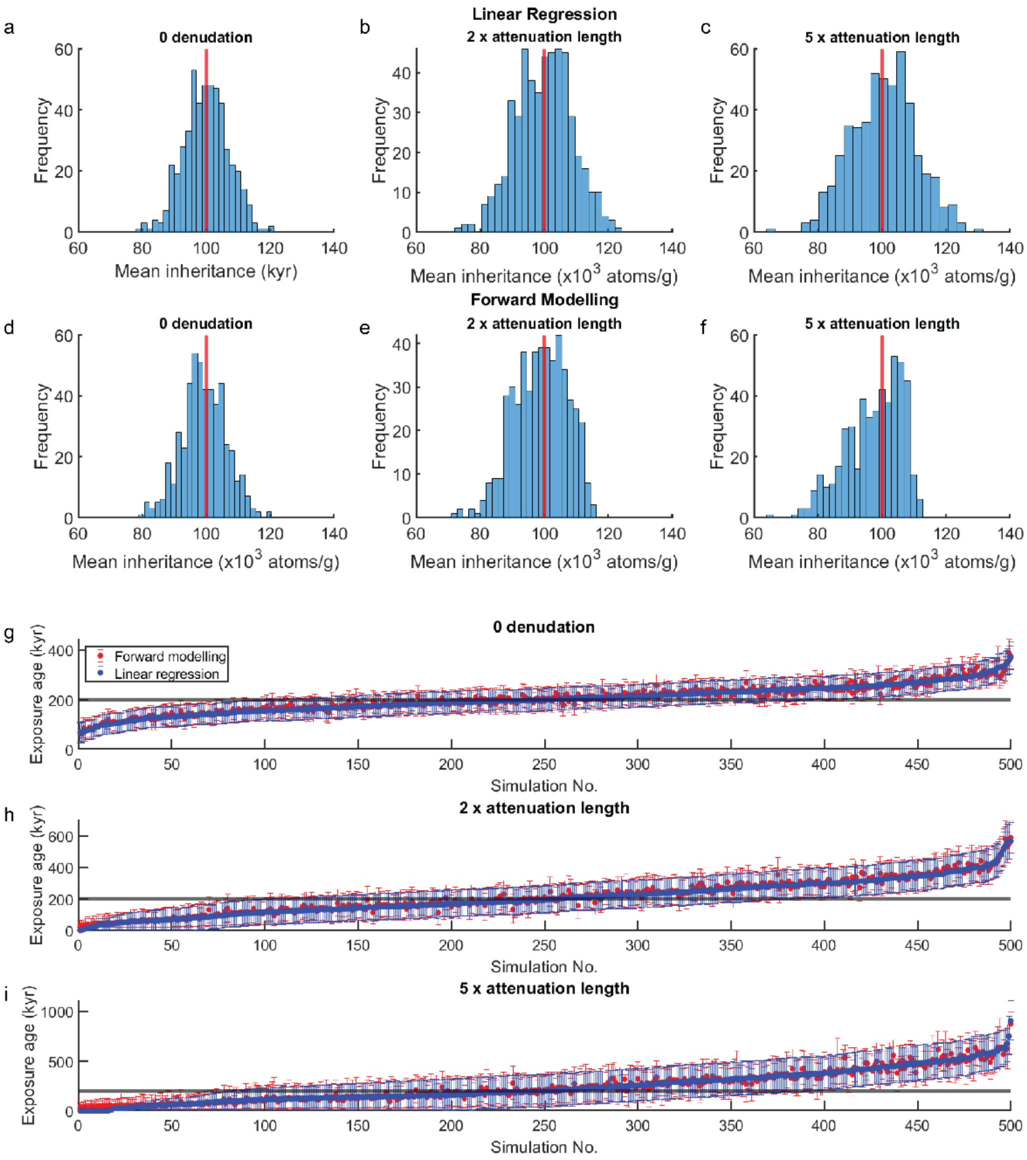
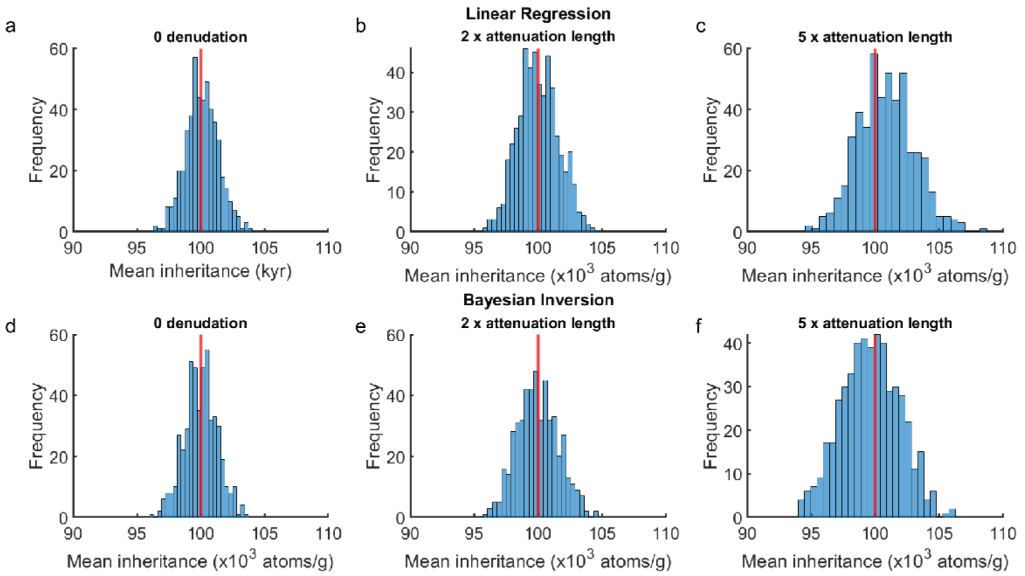
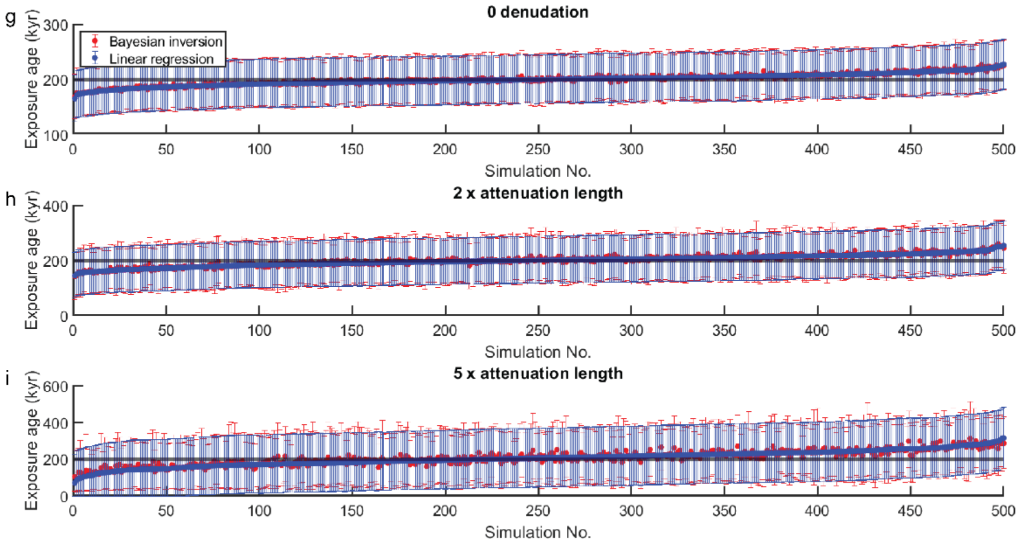


Figure ~~S7~~S5 Distribution of estimation results from linear regression and a ~~Bayesian~~forward approach for 500 simulated ~~TCN~~CN deep (3-5 m) profiles with denudations equal to 0 (a, d, g), 2 (b, e, h), and 5-times (c, f, i) attenuation length, and with 5% imposed deviation of sample concentration. 500 groups of inversion results. a-f. Histograms of the mean inheritance estimated from linear regression (a-c) and a ~~Bayesian~~forward approach (d-f). g-h. Distribution of exposure age, sorted by mean age estimated from linear regression.


Linear Regression
a
0 denudation
Frequency
Mean inheritance (kyr)
b
2 x attenuation length
Frequency
Mean inheritance (x10^3 atoms/g)
c
5 x attenuation length
Frequency
Mean inheritance (x10^3 atoms/g)
Bayesian Inversion
d
0 denudation
Frequency
Mean inheritance (x10^3 atoms/g)
e
2 x attenuation length
Frequency
Mean inheritance (x10^3 atoms/g)
f
5 x attenuation length
Frequency
Mean inheritance (x10^3 atoms/g)
90
95
100
105
110
0
10
20
30
40
60


g
0 denudation
Bayesian inversion
Linear regression
Exposure age (kyr)
Simulation No.
h
2 x attenuation length
Exposure age (kyr)
Simulation No.
i
5 x attenuation length
Exposure age (kyr)
Simulation No.
0
50
100
150
200
250
300
350
400
450
500
600

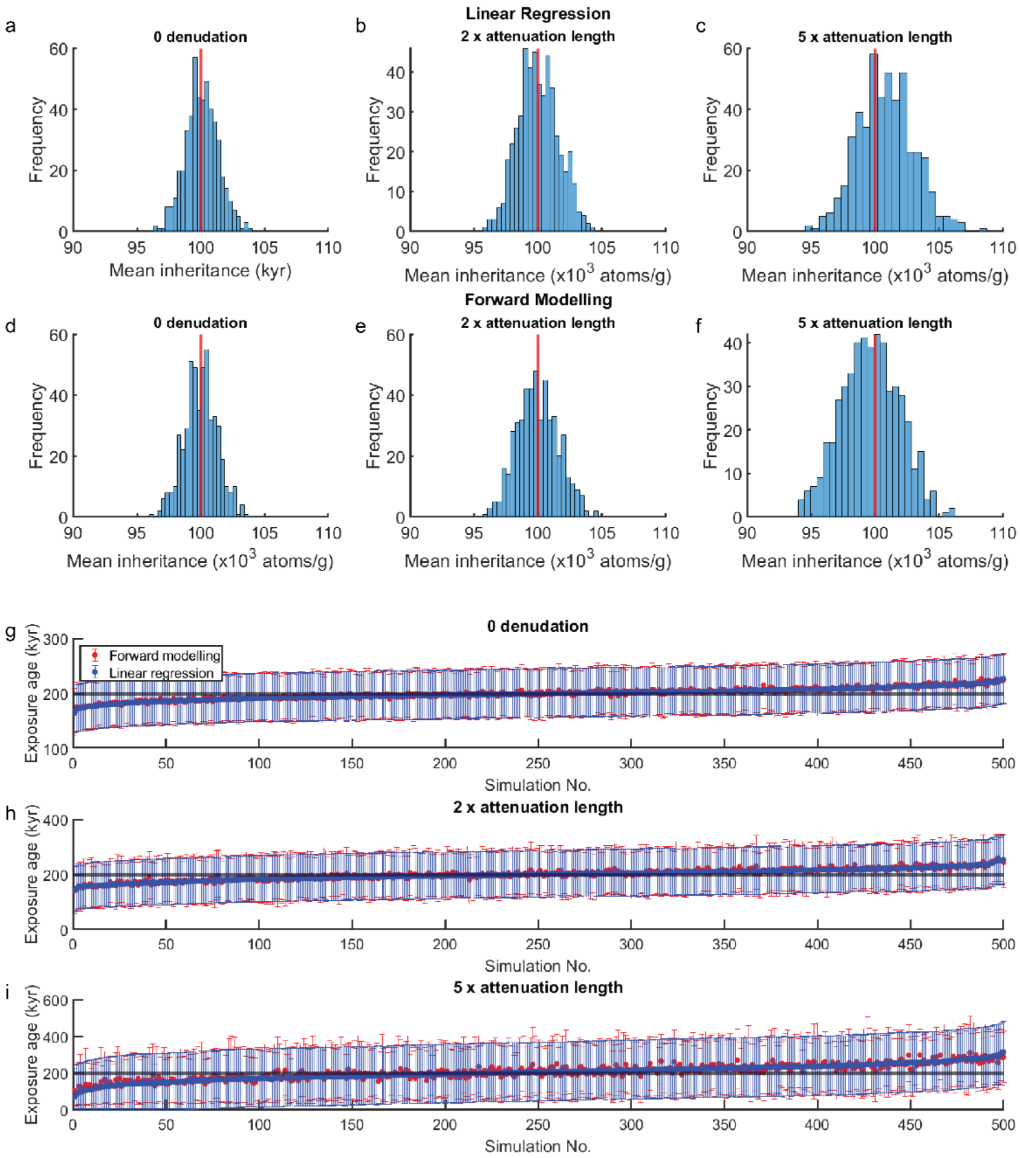


Figure ~~S8~~S6 Distribution of estimation results from linear regression and a ~~Bayesian~~forward approach for 500 simulated ~~TCN~~CN deep (3-5 m) profiles with denudations equal to 0 (a, d, g), 2 (b, e, h), and 5-times (c, f, i) attenuation length, and with 1% imposed deviation of sample concentration. 500 groups of inversion results. a-f. Histograms of the mean inheritance estimated from linear regression (a-c) and a ~~Bayesian~~forward approach (d-f). g-h. Distribution of exposure age, sorted by mean age estimated from linear regression.

2. Case Examples

Table S1 ^{10}Be concentration and the production rate at each sample depth for the two sample sites.

Beida River Terrace (Wang et al., 2020)			Lees Ferry Terrace (Hidy et al, 2010)		
Sample ID	^{10}Be Concentration; C_1[1] (10^5 atoms/g)	P_{zn} (atoms/(g×yr))	Sample ID	^{10}Be Concentration (10^5 atoms/g)	P_{zn} (atoms/(g×yr))
BT2-2-20	14.33 ± 0.39	13.82 ± 0.91	GC-04-LF-404.30s	5.69±0.17	6.35 ± 0.48
BT2-2-45	9.84 ± 0.36	9.94 ± 0.65	GC-04-LF-404.60s	4.07±0.11	4.09 ± 0.48
BT2-2-75	5.68 ± 0.23	6.69 ± 0.44	GC-04-LF-404.100s	2.92±0.09	2.27 ± 0.39
BT2-2-110	4.09 ± 0.21	4.22 ± 0.28	GC-04-LF-404.140s	2.03±0.06	1.26 ± 0.29
BT2-2-150	2.96 ± 0.11	2.84 ± 0.19	GC-04-LF-404.180s	1.57±0.05	0.7 ± 0.2
BT2-2-180	2.63 ± 0.08	1.68 ± 0.11	GC-04-LF-404.220s	1.34±0.04	0.39 ± 0.13

[1] C1 is the concentration prior to the onset of loess accumulation, following the approach introduced by Hetzel et al., (2004).

Table S2 Values for parameters used in exposure age calculation.

Parameter	Values (Wang et al., 2020)	Values (Hidy et a., 2010)
Surface production rate (nucleon-negative muon-fast muon) (atom/(g×yr))	23.4, 0.~~031~~0958, 0.~~036~~0413 [1]	9.51, 0.~~145~~ 0596, 0.~~115~~0314 [2]
Density (g/cm^3)	2.2	2.2-2.5 (uniform distribution)
Attenuation (nucleon- negative muon-fast muon) (g/cm^2)	167, ~~1500, 4320~~873, 2125 [1]	160±5, ~~1500, 4320~~1070, 2434 [2]
Eroded thickness (cm)	40±10 (normal distribution)	0-30 (uniform distribution)

[1] The production rate for nucleon is calculated based on the “LSD” scaling scheme (Lifton et al., 2014), the production rates and attenuation length for negative and fast muons are ~~calculated based on the scaling scheme~~approximated from ~~Braucher et al., 2011~~the site-specific muon production rate at depth using model 1B from Balco, 2017.

[2] 5-term approximation for muogenic production is applied in the original paper, here we use a 2-term exponential approximation calculated using model 1B from Balco, 2017.