Supplementary data

Long-term film mulching with manure amendment drives trade-offs between spring maize nutrient uptake and topsoil carbon stability on the Loess Plateau

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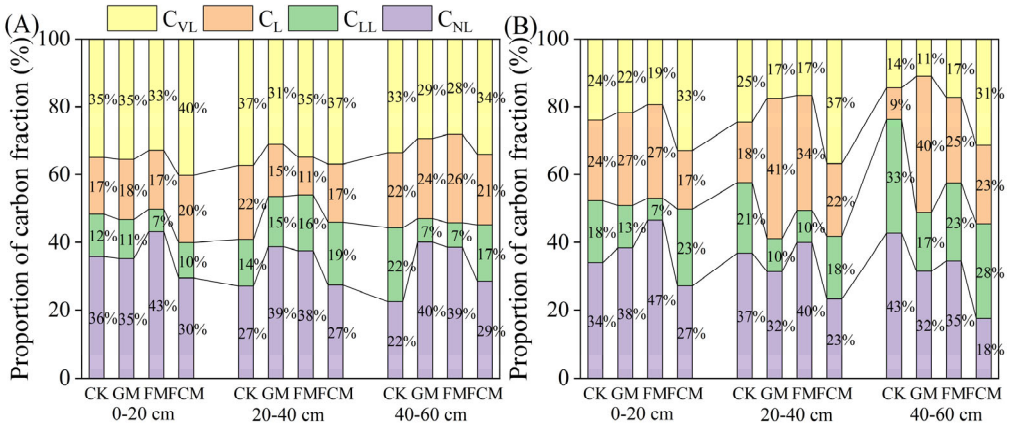


Figure S1. The proportion of C fractions based on gradient oxidation under different treatments in 2019 (A) and 2020 (B). Error bars are standard errors of means (n = 3). Different lowercase letters denote significant differences among treatments at $P < 0.05$. CK, GM, FM and FCM represent no mulching, gravel mulching, film mulching and film mulching with amendment, respectively. C_{VL}: very labile carbon; C_L: labile carbon; C_{LL}: less labile carbon; C_{NL}: non-labile carbon.

Table S1. The lability index (LI), carbon management index (CPI) and carbon management index (CMI) under different treatments in 2019 and 2020.

Treat-ment	Soil layers	2019			2020		
		LI	CPI	CMI	LI	CPI	CMI
CK	0-20 cm	1.00b	1.42ab	142b	1.38b	1.00b	138b
GM		1.04b	1.38ab	143b	1.33b	0.97b	128b
FM		0.95b	1.33b	126b	1.20b	0.88b	106c
FCM		1.32a	1.64a	216a	1.70a	1.37a	232a
CK	20-40 cm	1.00a	1.56a	156ab	1.29b	1.00a	129b
GM		0.94a	1.34a	124c	1.45b	0.87b	126b
FM		0.97a	1.39a	134bc	1.28b	0.91ab	115b
FCM		1.20a	1.45a	169a	1.95a	1.03a	201a
CK	40-60 cm	1.00a	1.50a	150a	0.95c	1.00a	95c
GM		0.95a	1.41a	133a	1.31b	0.97a	126b
FM		0.94a	1.37a	129a	1.25b	0.93a	117bc
FCM		1.02a	1.42a	144a	1.83a	1.01a	184a

Different lowercase letters in each column denote significant differences among treatments at $P < 0.05$.

Table S2. Pearson correlations among SOC parameters and microbial enzyme activities in the topsoil (n = 24).

	SOC	WSC	HWC	POXC	POC	C_{VL}	C_L	C_{LL}	C_{NL}	AP	PP	CMI
SOC	1											
WSC	0.25	1										
HWC	0.675**	0.305	1									
POXC	0.930**	0.294	0.616**	1								
POC	0.929**	0.271	0.631**	0.878**	1							
C_{VL}	0.804**	0.575**	0.541**	0.849**	0.783**	1						
C_L	0.39	-0.295	0.482*	0.406*	0.456*	0.067	1					
C_{LL}	0.771**	-0.101	0.227	0.655**	0.675**	0.393	0.262	1				
C_{NL}	0.239	-0.199	0.354	0.08	0.13	-0.012	-0.063	0.108	1			
AP	0.872**	0.411*	0.668**	0.918**	0.877**	0.929**	0.432*	0.452*	-0.033	1		
PP	0.768**	-0.171	0.339	0.603**	0.640**	0.337	0.203	0.917**	0.495*	0.379	1	
CMI	0.930**	0.354	0.627**	0.946**	0.919**	0.920**	0.371	0.610**	0.039	0.969**	0.547**	1

** Correlation is significant at the 0.01 level (2-tailed). * Correlation is significant at the 0.05 level (2-tailed).

R code S1. Random forest analysis of R codes and results

```
library(randomForest)> library(rfPermute)> library(A3)> set.seed(1234)> data
<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Plant.N
 ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,ntree
=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scale =
 TRUE), check.names = FALSE)#****> importance_mod
%IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
POXC 30.1600429   0.00990099     6830.4711         0.02970297
HWC  29.0764227   0.01980198     8662.7014         0.06930693
SOC  28.1201570   0.00990099     9793.1434         0.00990099
POC  21.1305227   0.00990099     6423.8785         0.11881188
CMI  19.7839985   0.00990099     5238.7640         0.11881188
CLL  17.4333336   0.06930693     3338.8449         0.63366337
AP   14.6231287   0.06930693     3107.1219         0.60396040
CVL  14.5693380   0.06930693     3038.0105         0.70297030
CNL   6.5610272   0.16831683     2106.1511         0.91089109
PP    2.4999950   0.37623762     1791.2018         0.97029703
CL   -0.1158372   0.40594059     1054.9349         1.00000000
WSC  -3.5739119   0.75247525      719.6423         1.00000000
library(randomForest)> library(rfPermute)> library(A3)>  set.seed(1234)> dat
a<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Plant.
P ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,ntre
e=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scale
= TRUE), check.names = FALSE)#****> importance_mod
%IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
CMI  33.358723   0.00990099     386.17951         0.00990099
AP   23.799180   0.00990099     217.57770         0.04950495
POC  21.988362   0.01980198     182.32196         0.25742574
POXC 20.024981   0.03960396     227.14733         0.05940594
SOC  19.523019   0.01980198     201.69015         0.02970297
CVL  15.211619   0.03960396     141.46591         0.25742574
CL   11.979885   0.07920792      62.76972         0.95049505
CNL  10.201613   0.06930693      45.17512         1.00000000
HWC   6.493221   0.18811881      80.03204         0.88118812
PP    4.440786   0.26732673      32.05749         1.00000000
CLL   2.022395   0.40594059      31.26809         1.00000000
WSC   1.500221   0.27722772      30.26955         1.00000000
library(randomForest)> library(rfPermute)> library(A3)> set.seed(1234)> data
<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Plant.K
 ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,ntree
=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scale =
 TRUE), check.names = FALSE)#****> importance_mod
```

```
%IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
CMI    26.0149779   0.01980198     3688.2686         0.02970297
HWC    23.5941030   0.00990099     3773.9895         0.07920792
AP     21.6800988   0.03960396     2813.4921         0.09900990
POC    20.5719310   0.03960396     2460.3551         0.20792079
SOC    20.1943525   0.00990099     2741.0728         0.04950495
CVL    19.9027244   0.03960396     2591.0300         0.18811881
POXC   19.4536034   0.02970297     2753.8263         0.06930693
CL      0.3843987   0.34653465     1097.1529         0.92079208
CLL    -0.4193923   0.51485149      369.2714         1.00000000
WSC    -6.9135397   0.84158416      533.9000         1.00000000
CNL    -8.6969809   0.94059406      465.7492         1.00000000
PP    -11.9299290   0.99009901      627.3033         1.00000000
 > library(randomForest)> library(rfPermute)> library(A3)> set.seed(1234)> d
ata<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Grai
n.N ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,nt
ree=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scal
e = TRUE), check.names = FALSE)#****> importance_mod
%IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
POXC 30.454063   0.00990099     3751.7298         0.01980198
SOC  27.742779   0.00990099     4379.4467         0.02970297
HWC  23.857332   0.01980198     3836.6341         0.11881188
CVL  23.032013   0.00990099     2965.0238         0.10891089
POC  19.887697   0.03960396     2660.7797         0.28712871
AP   19.319500   0.03960396     2343.9695         0.17821782
CMI  19.146593   0.04950495     2367.2362         0.17821782
CLL  16.968196   0.06930693     1569.9289         0.76237624
CNL   7.112647   0.19801980     1418.1462         0.87128713
WSC   3.665275   0.32673267      796.0848         1.00000000
CL    3.201369   0.28712871      687.4383         1.00000000
PP   -2.755247   0.59405941      505.4981         1.00000000>
library(randomForest)> library(rfPermute)> library(A3)> set.seed(1234)> data
<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Grain.P
 ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,ntree
=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scale =
 TRUE), check.names = FALSE)#****> importance_mod
%IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
CMI  28.7857342   0.00990099     229.62170         0.00990099
POC  24.4818038   0.01980198     170.77495         0.07920792
AP   19.2079791   0.02970297     150.27479         0.05940594
POXC 18.7636988   0.04950495     160.24838         0.04950495
CVL  16.0092444   0.04950495     133.68505         0.11881188
SOC  15.4450755   0.05940594      98.19812         0.22772277
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HWC  11.8670624   0.14851485     113.09785         0.38613861
CNL   9.9384934   0.10891089      35.31636         0.99009901
CL    6.7340087   0.16831683      43.23748         0.99009901
CLL   2.6009954   0.42574257      19.37047         1.00000000
WSC   1.0555445   0.36633663      15.92653         1.00000000
PP    0.7743315   0.50495050      24.61587         1.00000000
library(randomForest)> library(rfPermute)> library(A3)> > set.seed(1234)> da
ta<-read.csv("C:/Users/setzhang/Desktop/2.csv")> rf_model <- rfPermute(Grain.
K ~SOC+WSC+HWC+POXC+POC+CVL+CL+CLL+CNL+AP+PP+CMI,data,importance = TRUE,ntre
e=5000)> #读取显著性> importance_mod<- data.frame(importance(rf_model , scale
= TRUE), check.names = FALSE)#****> importance_mod
 %IncMSE %IncMSE.pval IncNodePurity IncNodePurity.pval
CVL  29.936065   0.00990099     111.91112         0.00990099
AP   27.049820   0.00990099     106.25407         0.00990099
POXC 25.535838   0.01980198      95.58715         0.02970297
SOC  24.874478   0.01980198      82.24939         0.04950495
POC  19.266885   0.01980198      60.42382         0.33663366
CMI  17.937045   0.03960396      50.97771         0.33663366
HWC  11.397563   0.10891089      35.38536         0.83168317
WSC   7.066782   0.21782178      35.33607         0.94059406
CLL   5.986360   0.27722772      14.31563         1.00000000
CL    5.409241   0.20792079      20.92500         0.99009901
PP    2.560785   0.26732673      16.29947         1.00000000
CNL  -3.092815   0.58415842      16.50835         1.00000000
```