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Reporting Summary

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For all statistical	analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a Confirmed	, which regards, table regards, main text, or Methods Section.
☐ ☐ The exa	act sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
A state	ment on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
The star	tistical test(s) used AND whether they are one- or two-sided nmon tests should be described solely by name; describe more complex techniques in the Methods section.
A descri	ption of all covariates tested
A descri	ption of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
A full de	scription of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) iation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
For null	hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted lues as exact values whenever suitable.
For Baye	sian analysis, information on the choice of priors and Markov chain Monte Carlo settings
	archical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
Estimate	is of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
	Our web collection on statistics for biologists contains articles on many of the points above.
Software ar	nd code
Policy information	about availability of computer code
Data collection	No software was used
Data analysis	No software was used
or manuscripts utilizin eviewers. We strongly	g custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.
Data	
All manuscripts m - Accession code - A description of	about <u>availability of data</u> ust include a <u>data availability statement</u> . This statement should provide the following information, where applicable: s, unique identifiers, or web links for publicly available datasets any restrictions on data availability sets or third party data, please ensure that the statement adheres to our <u>policy</u>

The obtained metagenomic profiles have been uploaded into the NCBI SRA database and are accessible via the accession number: PRJNA574851.

Field-spe	ecific reporting
	one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.
∠ Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences
For a reference copy of	the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>
Life scien	acos study dosign
LITE SCIEI	nces study design
All studies must di	sclose on these points even when the disclosure is negative.
Sample size	Research on non-human primates is inherently difficult, so only the 5 transgenic A53T monkeys (Niu et al.2015) generated in our previous study were assigned as A53T group. Correspondingly, we selected 5 normal monkeys that the age and weight are similar to A53T transgenic monkeys as the control group.
Data exclusions	In our study, no data were excluded from the analyses.
Replication	There are 5 monkeys in the A53T group and the control group. Because transgenic animals are very rare, it is difficult to repeat the experiment. But the investigator were blinded during data collection and analysis, so the reliability of data anlysis is guaranteed.
Randomization	5 transgenic A53T monkeys (Niu et al.2015) generated in our previous study were assigned as A53T group and 5 normal monkeys that the age and weight are similar to A53T transgenic monkeys as the control group.
Blinding	The investigator were blinded to group allocation during data collection and analysis.
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Reportin	g for specific materials, systems and methods
system or method list	on from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, ed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response. Derimental systems Methods
n/a Involved in th	e study n/a Involved in the study
Antibodies	ChIP-seq
Eukaryotic	_ low eyemeny
	ogy and archaeology MRI-based neuroimaging
	earch participants
Clinical data	
Dual use re	search of concern
Animals and	other organisms
Policy information a	bout studies involving animals; ARRIVE guidelines recommended for reporting animal research
Laboratory anima	
Wild animals	The study did not involve wild animals.
Field-collected sar	nples All of the animals were individually caged. The animal room was set on a 12 hours light: 12 hours darkness cycle. The temperature
	and the humidity of the animal room were kept at 18 °C to 26 °C and 40% to 70%, respectively. The animals were fed twice per day with commercial monkey chow (LabDiet, Harlan Laboratories, Inc., USA). Fresh fruits and vegetables (including apples, bananas, pears, onions, cabbage) were supplemented once per day. Stool was collected on the morning of the same date, and the samples were immediately stored in the -80°C refrigerator until testing.
Ethics oversight	All procedures were approved by the Institutional Animal Care and Use Committee of Kunming University of Science and Technology, and were performed in accordance with the Guide for the Care and Use of Laboratory Animals (8th edition).
lote that full informati	on on the approval of the study protocol must also be provided in the manuscript.