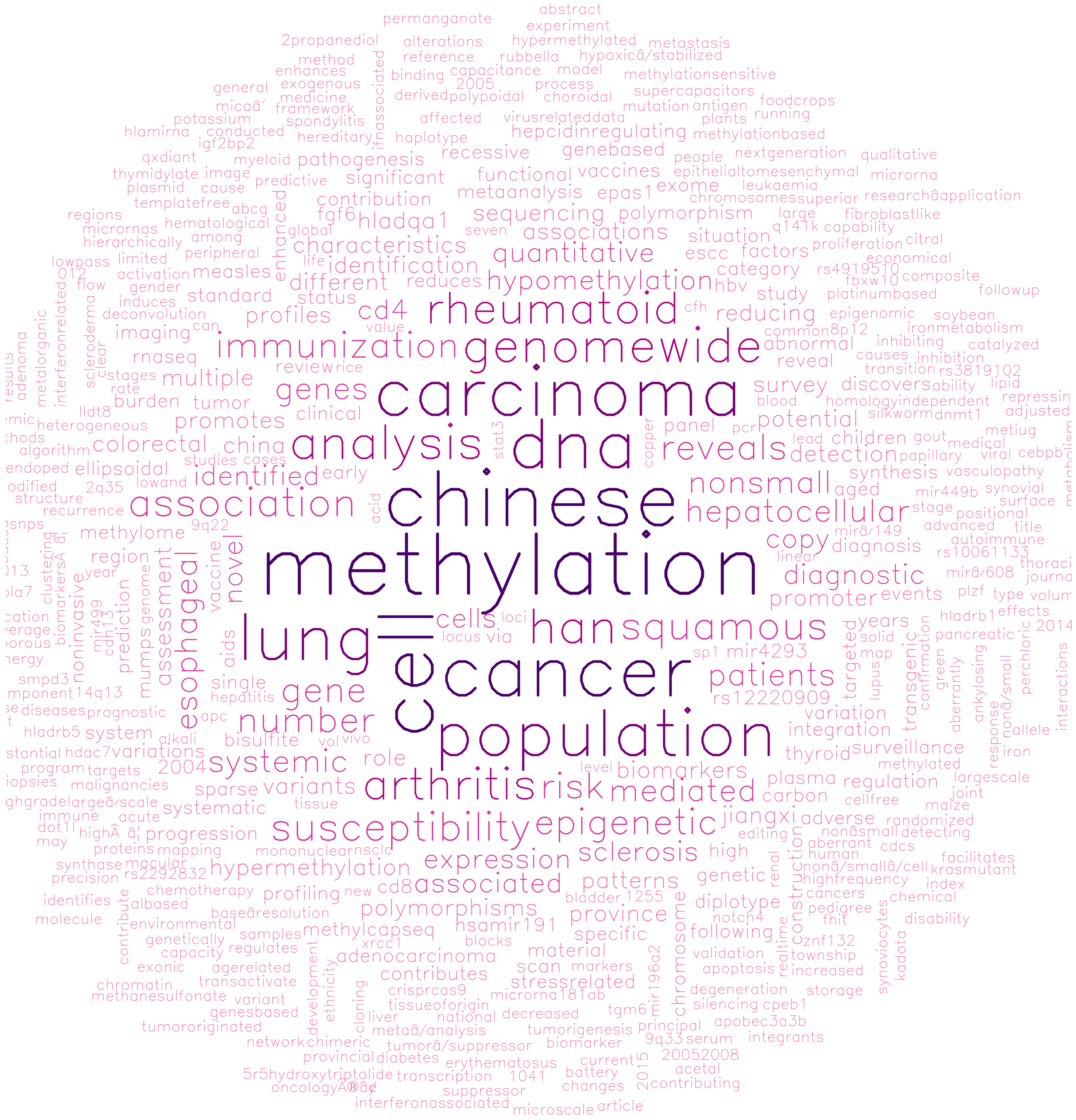
methylation
chinese
cancer
carcinoma
dna
cell
population
lung
genomewide
rheumatoid
analysis
immunization
arthritis
risk
susceptibility
epigenetic
han
squamous
association
hepatocellular
nonsmall
reveals
patients
gene
number
genes
systemic
mediated
expression
associated
hypermethylation
esophageal
diagnostic
hypomethylation
quantitative
cells
sequencing
polymorphism
associations
characteristics
identification
different
cd4
identified
colorectal
china
promotes
multiple
profiles
sclerosis
patterns
polymorphisms
province
hsamir191
methylcapseq
adenocarcinoma
specific
variants
biomarkers
plasma
regulation
surveillance
integration
variation
thyroid
promoter
events
diagnosis
copy
detection
potential
children
survey
discovers
reducing
study
category
factors
situation
escc
hbv
synthesis
aged
panel
pathogenesis
significant
contribution
hladqa1
fgf6
functional
vaccines
metaanalysis
epas1
exome
recessive
genebased
hepcidinregulating
measles
standard
status
reduces
imaging
rnaseq
burden
tumor
clinical
review
rice
value
ellipsoidal
methylome
region
assessment
vaccine
novel
aids
single
hepatitis
bisulfite
role
systematic
progression
mapping
profiling
cd8
jiangxi
adverse
genetic
diplotype
following
chromosome
construction
material
scan
markers
stressrelated
contributes
crisprcas9
microrna181ab
tissueoforigin
decreased
tumorigenesis
principal
biomarker
permanganate
abstract
experiment
2propanediol
alterations
hypermethylated
metastasis
method
reference
rubbella
hypoxicâ/stabilized
enhances
binding
capacitance
model
methylationsensitive
general
exogenous
2005
process
supercapacitors
medicine
derived
polypoidal
choroidal
micaâ´
framework
mutation
antigen
foodcrops
potassium
spondylitis
affected
virusrelateddata
plants
running
hlamirna
conducted
hereditary
haplotype
methylationbased
igf2bp2
ifnassociated
qxdiant
myeloid
people
nextgeneration
qualitative
thymidylate
image
predictive
epithelialtomesenchymal
microrna
plasmid
cause
leukaemia
templatefree
abcg
chromosomes
superior
researchâapplication
regions
enhanced
global
large
fibroblastlike
micrornas
hematological
seven
q141k
capability
hierarchically
among
proliferation
citral
lowpass
limited
peripheral
life
economical
012
activation
rs4919510
fbxw10
composite
flow
gender
platinumbased
followup
induces
cfh
epigenomic
soybean
deconvolution
can
common8p12
ironmetabolism
interferonrelated
metalorganic
adenoma
results
scleroderma
clear
inhibiting
catalyzed
abnormal
causes
inhibition
reveal
transition
rs3819102
stages
rate
ability
lipid
homologyindependent
repressin
lldt8
blood
silkworm
dnmt1
adjusted
heterogeneous
pcr
metiug
algorithm
stat3
copper
lead
gout
medical
studies
cases
papillary
viral
cebpb
endoped
early
vasculopathy
odified
lowand
2q35
mir449b
synovial
structure
surface
recurrence
acid
stage
psnps
9q22
advanced
title
mirâ/149
autoimmune
clustering
markersÂ â
linear
rs10061133
year
thoraci
mirâ/608
journa
la7
biomarker
noninvasive
prediction
genome
mumps
plzf
type
volum
cation
loci
hladrb1
effects
erage
mir499
cdh13
locus
via
solid
2014
orous
pancreatic
ergy
sp1
mir4293
map
lupus
smpd3
targeted
transgenic
confirmation
green
aberrantly
ankylosing
response
nonâ/small
perchloric
interactions
mponent
14q13
rs12220909
diseases
prognostic
apc
allele
hladrb5
system
alkali
vol
vivo
iron
stantial
hdac7
variations
years
program
targets
2004
level
methylated
iopsies
malignancies
largescale
joint
highgrade
largeâ/scale
sparse
tissue
carbon
cellfree
maize
immune
acute
randomized
dot1l
highÂ â
editing
nonâsmall
detecting
may
proteins
mononuclearnscle
aberrant
human
cdcs
synthase
macular
renal
facilitates
precision
rs2292832
nonâ/smallâ/cell
krasmutant
highfrequency
index
chemotherapy
new
bladder
1255
cancers
chemical
identifies
albased
pedigree
contribute
baseâresolution
notch4
fhit
disability
molecule
environmental
realtime
samples
znf132
genetically
xrcc1
blocks
township
regulates
development
capacity
validation
exonic
agerelated
ethnicity
apoptosis
increased
chromatin
transactivate
mir196a2
degeneration
storage
synoviocytes
kadota
methanesulfonate
variant
cloning
silencing
cpeb1
genesbased
liver
national
tgm6
tumororiginated
metaâ/analysis
apobec3a3b
network
chimeric
tumorâ/suppressor
9q33
serum
integrants
provincial
diabetes
erythematosus
current
20052008
5r5hydroxytriptolide
transcription
1041
battery
2015
acetal
oncologyÂ®â¢
suppressor
changes
2contributing
interferonassociated
microscale
article
metabolism