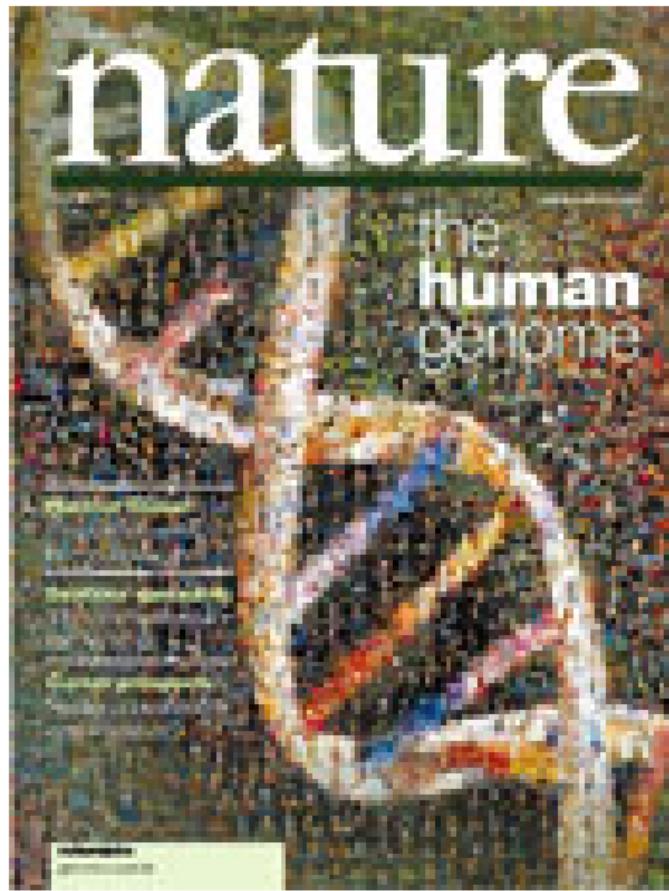


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the  
human  
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The mouse genome

A international consor-

tium reports

Genome annotation

Regulatory elements

Evolutionary tracks

Gene expression

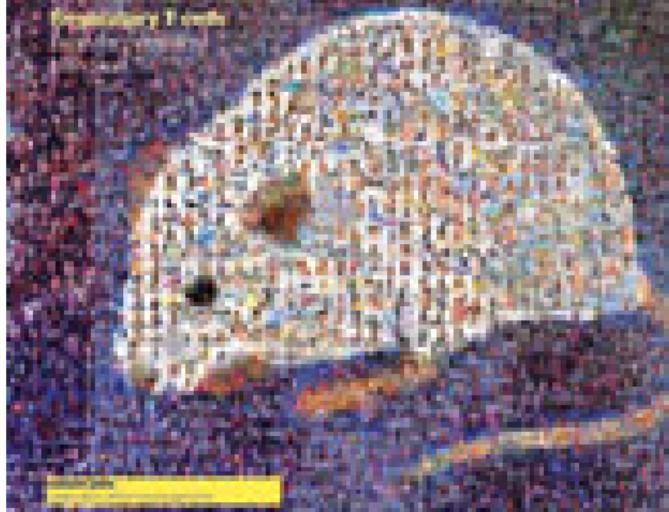
Genetic variation

Genotype arrays

Genotype data

Genotype tracks

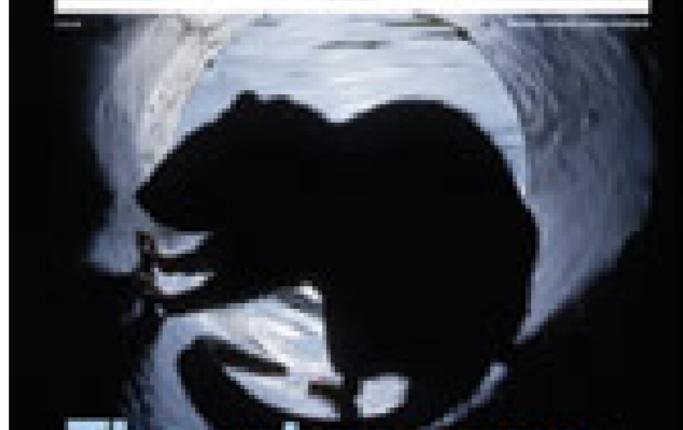
Genotype variation



10 April 2002

The international weekly journal of science

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## The rat genome

Insights into mammalian evolution

Superconductivity  
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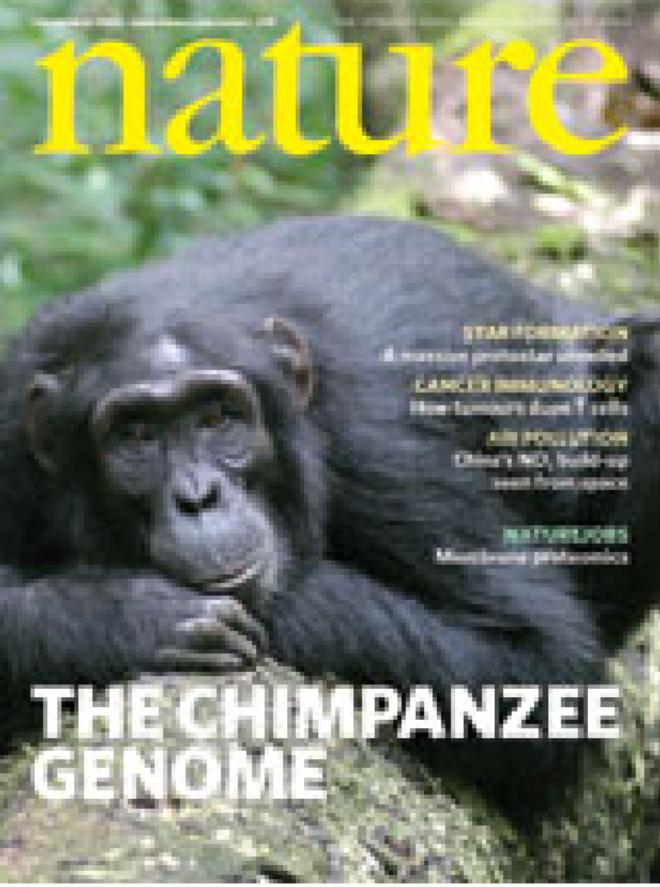
# The chicken genome

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Allele frequencies

Climate's CO<sub>2</sub> feedback  
and oxygen levels

IN PERSPECTIVE

Measuring phylogenetics

## THE CHIMPANZEE GENOME

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QUANTUM  
MEMORY  
Controlling  
single photons  
THE GENETICS  
OF MONKEYS  
A puzzle  
Balancing act  
IN PURSUIT  
OF PLEASURE  
Depression's  
role revisited

## THE DOG GENOME



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against competition  
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Drosophila and Linux  
BOOK REVIEWS FROM THE PRESS  
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polycomb-like genes in insect development

## HONEYBEE GENOME

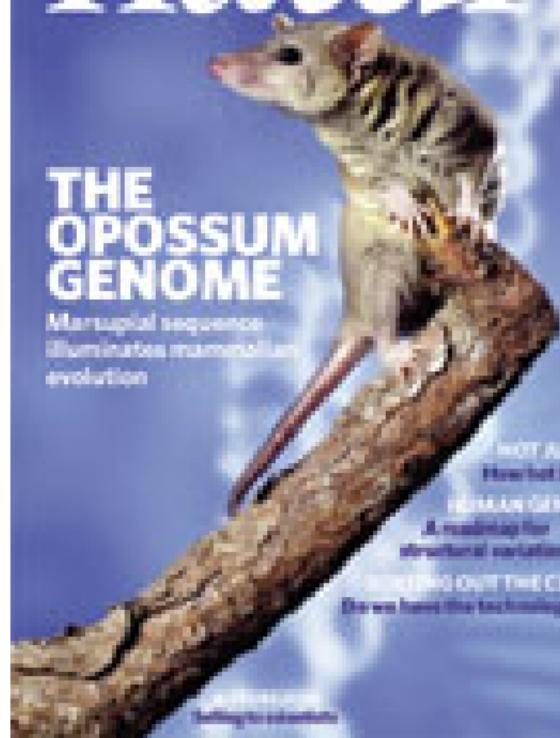
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Harvard Medical School

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## THE OPOSSUM GENOME

Mammal sequence  
illuminates mammalian  
evolution



WOLF JÜPTNER  
Peter Holt & Bill

UMAN GENOMICS  
A reading for  
structural variation

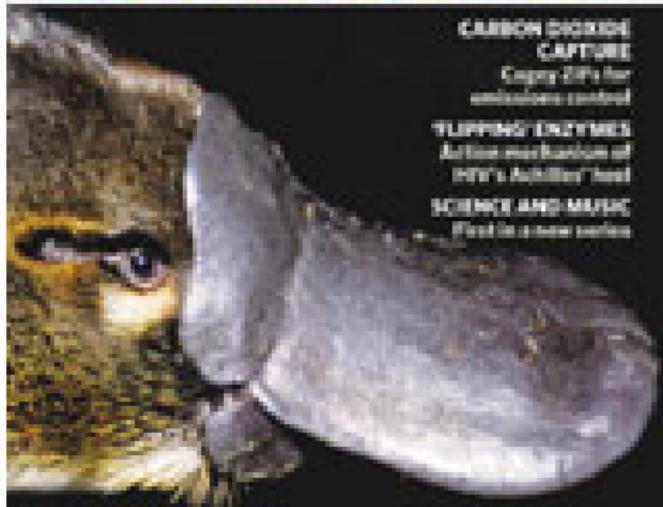
CHECK OUT THE CLIMATE  
Do we have the technology?

Biological Sciences

Volume 431 Number 7000 2004

The international weekly journal of science

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## CARBON DIOXIDE CAPTURE

Capturing CO<sub>2</sub> for  
industrial control

## FLIPPING ENYMES

Active mechanism of  
HIV's protease found

## SCIENCE AND MUSIC

From the music section

## THE PLATYPUS GENOME

Sequence analysis reveals clues  
to early mammalian evolution

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## STAR FORMATION

Where binary twins  
grow apart

## WEATHER

Modifying  
Clouds for gold  
in Beijing

## ROBOTIC LIMBS

Controlling by  
a thought

NATURE  
Reviews  
Physics  
with  
commentary

## THE AMPHioxus GENOME

The long awaited genome of the last  
common ancestor of the vertebrates



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## GIANT PANDA GENOME

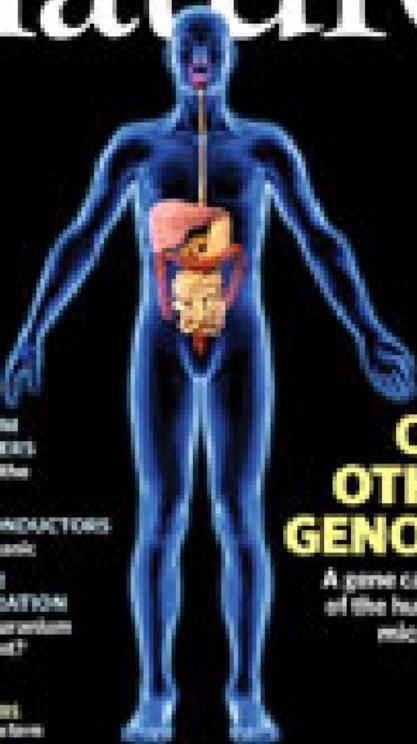
First generation sequencing  
reveals Jingjing's DNA sequence

1.5 MBD sequenced  
with a depth of about 10x

RNA-Seq analysis  
An atlas of gene expression

EVOLUTIONARY GENOMICS  
The panda is walking

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QUANTUM  
COMPUTERS  
Choosing the  
best bases

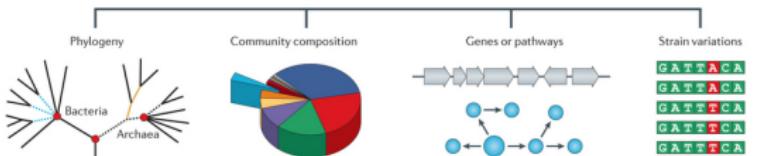
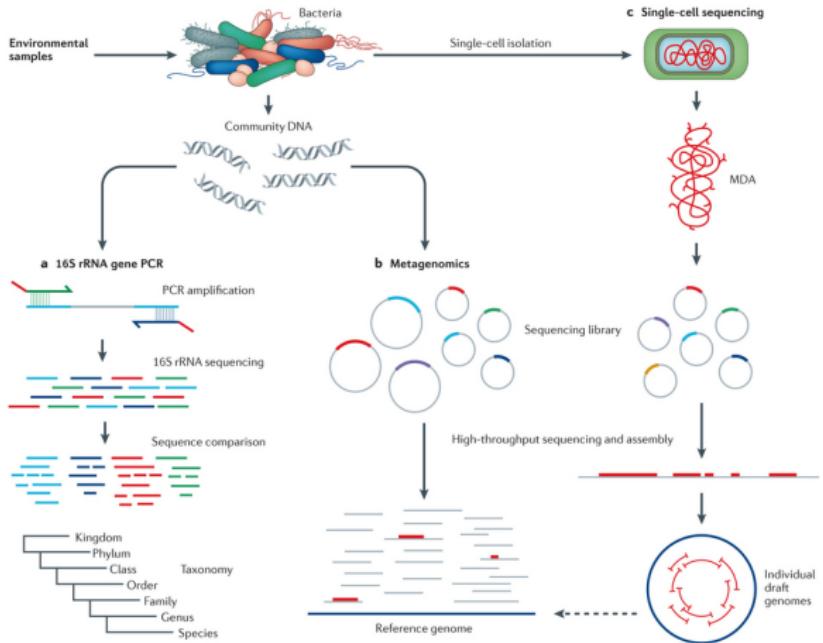
SUPERCONDUCTORS  
Going organic

NUCLEAR  
PROLIFERATION  
Has been unwise  
enrichment?

NATUREJOBS  
Down in the dirt

## OUR OTHER GENOME

A gene catalogue  
of the human gut  
microbiome



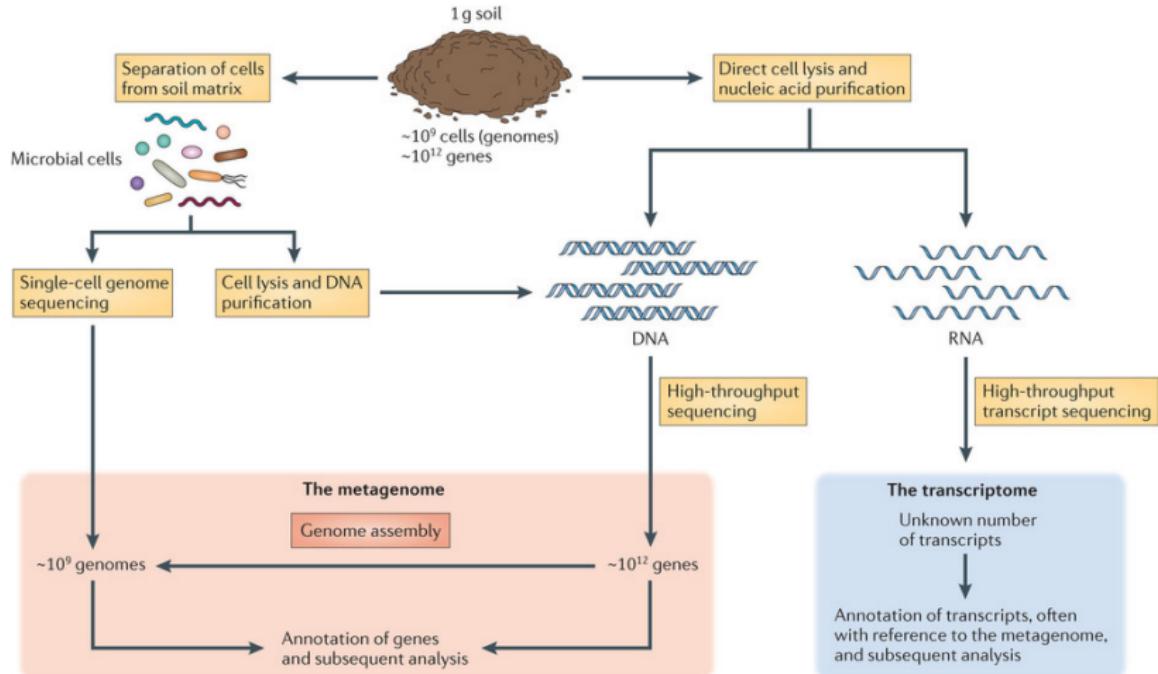


Table 1 | Summary of MCG platforms

Platform	Model	Processor	Memory	Reads	Writes	Error profile	Performance	Cost per TB
	(chip)	(chip)	(chip)	(chip)	(chip)	(chip)	(chip)	(chip)
<b>Sequencing by synthesis (SBS)</b>								
SQ5000	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
SQ5000	HiSeq	71.000						
SQ5000	HiSeq	50.000						
SQ5000	HiSeq	30.000						
SQ5000	HiSeq	20.000						
SQ5000	HiSeq	10.000						
SQ5000	HiSeq	5.000						
SQ5000	HiSeq	2.000						
SQ5000	HiSeq	1.000						
SQ5000	HiSeq	500						
SQ5000	HiSeq	200						
SQ5000	HiSeq	100						
SQ5000	HiSeq	50						
SQ5000	HiSeq	20						
SQ5000	HiSeq	10						
SQ5000	HiSeq	5						
SQ5000	HiSeq	2						
SQ5000	HiSeq	1						
SQ5000	HiSeq	0.5						
SQ5000	HiSeq	0.2						
SQ5000	HiSeq	0.1						
SQ5000	HiSeq	0.05						
SQ5000	HiSeq	0.02						
SQ5000	HiSeq	0.01						
SQ5000	HiSeq	0.005						
SQ5000	HiSeq	0.002						
SQ5000	HiSeq	0.001						
SQ5000	HiSeq	0.0005						
SQ5000	HiSeq	0.0002						
SQ5000	HiSeq	0.0001						
SQ5000	HiSeq	50000						
SQ5000	HiSeq	20000						
SQ5000	HiSeq	10000						
SQ5000	HiSeq	5000						
SQ5000	HiSeq	2000						
SQ5000	HiSeq	1000						
SQ5000	HiSeq	500						
SQ5000	HiSeq	200						
SQ5000	HiSeq	100						
SQ5000	HiSeq	50						
SQ5000	HiSeq	20						
SQ5000	HiSeq	10						
SQ5000	HiSeq	5						
SQ5000	HiSeq	2						
SQ5000	HiSeq	1						
SQ5000	HiSeq	0.5						
SQ5000	HiSeq	0.2						
SQ5000	HiSeq	0.1						
SQ5000	HiSeq	0.05						
SQ5000	HiSeq	0.02						
SQ5000	HiSeq	0.01						
SQ5000	HiSeq	0.005						
SQ5000	HiSeq	0.002						
SQ5000	HiSeq	0.001						
SQ5000	HiSeq	0.0005						
SQ5000	HiSeq	0.0002						
SQ5000	HiSeq	0.0001						
SQ5000	HiSeq	50000						
SQ5000	HiSeq	20000						
SQ5000	HiSeq	10000						
SQ5000	HiSeq	5000						
SQ5000	HiSeq	2000						
SQ5000	HiSeq	1000						
SQ5000	HiSeq	500						
SQ5000	HiSeq	200						
SQ5000	HiSeq	100						
SQ5000	HiSeq	50						
SQ5000	HiSeq	20						
SQ5000	HiSeq	10						
SQ5000	HiSeq	5						
SQ5000	HiSeq	2						
SQ5000	HiSeq	1						
SQ5000	HiSeq	0.5						
SQ5000	HiSeq	0.2						
SQ5000	HiSeq	0.1						
SQ5000	HiSeq	0.05						
SQ5000	HiSeq	0.02						
SQ5000	HiSeq	0.01						
SQ5000	HiSeq	0.005						
SQ5000	HiSeq	0.002						
SQ5000	HiSeq	0.001						
SQ5000	HiSeq	50000						
SQ5000	HiSeq	20000						
SQ5000	HiSeq	10000						
SQ5000	HiSeq	5000						
SQ5000	HiSeq	2000						
SQ5000	HiSeq	1000						
SQ5000	HiSeq	500						
SQ5000	HiSeq	200						
SQ5000	HiSeq	100						
SQ5000	HiSeq	50						
SQ5000	HiSeq	20						
SQ5000	HiSeq	10						
SQ5000	HiSeq	5						
SQ5000	HiSeq	2						
SQ5000	HiSeq	1						
SQ5000	HiSeq	0.5						
SQ5000	HiSeq	0.2						
SQ5000	HiSeq	0.1						
SQ5000	HiSeq	0.05						
SQ5000	HiSeq	0.02						
SQ5000	HiSeq	0.01						
SQ5000	HiSeq	0.005						
SQ5000	HiSeq	0.002						
SQ5000	HiSeq	0.001						
<b>Sequencing by synthesis (SBS) - CPT</b>								
BioXp 3200	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
BioXp 3200	HiSeq	71.000						
BioXp 3200	HiSeq	50.000						
BioXp 3200	HiSeq	30.000						
BioXp 3200	HiSeq	20.000						
BioXp 3200	HiSeq	10.000						
BioXp 3200	HiSeq	5.000						
BioXp 3200	HiSeq	2.000						
BioXp 3200	HiSeq	1.000						
BioXp 3200	HiSeq	500						
BioXp 3200	HiSeq	200						
BioXp 3200	HiSeq	100						
BioXp 3200	HiSeq	50						
BioXp 3200	HiSeq	20						
BioXp 3200	HiSeq	10						
BioXp 3200	HiSeq	5						
BioXp 3200	HiSeq	2						
BioXp 3200	HiSeq	1						
BioXp 3200	HiSeq	0.5						
BioXp 3200	HiSeq	0.2						
BioXp 3200	HiSeq	0.1						
BioXp 3200	HiSeq	0.05						
BioXp 3200	HiSeq	0.02						
BioXp 3200	HiSeq	0.01						
BioXp 3200	HiSeq	0.005						
BioXp 3200	HiSeq	0.002						
BioXp 3200	HiSeq	0.001						
<b>Sequencing by synthesis (SBS) - CPT - R</b>								
BioXp 3200	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
BioXp 3200	HiSeq	71.000						
BioXp 3200	HiSeq	50.000						
BioXp 3200	HiSeq	30.000						
BioXp 3200	HiSeq	20.000						
BioXp 3200	HiSeq	10.000						
BioXp 3200	HiSeq	5.000						
BioXp 3200	HiSeq	2.000						
BioXp 3200	HiSeq	1.000						
BioXp 3200	HiSeq	500						
BioXp 3200	HiSeq	200						
BioXp 3200	HiSeq	100						
BioXp 3200	HiSeq	50						
BioXp 3200	HiSeq	20						
BioXp 3200	HiSeq	10						
BioXp 3200	HiSeq	5						
BioXp 3200	HiSeq	2						
BioXp 3200	HiSeq	1						
BioXp 3200	HiSeq	0.5						
BioXp 3200	HiSeq	0.2						
BioXp 3200	HiSeq	0.1						
BioXp 3200	HiSeq	0.05						
BioXp 3200	HiSeq	0.02						
BioXp 3200	HiSeq	0.01						
<b>Sequencing by synthesis (SBS) - R</b>								
NewBlitz	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
NewBlitz	HiSeq	71.000						
NewBlitz	HiSeq	50.000						
NewBlitz	HiSeq	30.000						
NewBlitz	HiSeq	20.000						
NewBlitz	HiSeq	10.000						
NewBlitz	HiSeq	5.000						
NewBlitz	HiSeq	2.000						
NewBlitz	HiSeq	1.000						
NewBlitz	HiSeq	500						
NewBlitz	HiSeq	200						
NewBlitz	HiSeq	100						
NewBlitz	HiSeq	50						
NewBlitz	HiSeq	20						
NewBlitz	HiSeq	10						
NewBlitz	HiSeq	5						
NewBlitz	HiSeq	2						
NewBlitz	HiSeq	1						
NewBlitz	HiSeq	0.5						
NewBlitz	HiSeq	0.2						
NewBlitz	HiSeq	0.1						
NewBlitz	HiSeq	0.05						
NewBlitz	HiSeq	0.02						
NewBlitz	HiSeq	0.01						
<b>Sequencing by synthesis (SBS) - R - Long Read</b>								
HiSeq	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
HiSeq	HiSeq	71.000						
HiSeq	HiSeq	50.000						
HiSeq	HiSeq	30.000						
HiSeq	HiSeq	20.000						
HiSeq	HiSeq	10.000						
HiSeq	HiSeq	5.000						
HiSeq	HiSeq	2.000						
HiSeq	HiSeq	1.000						
HiSeq	HiSeq	500						
HiSeq	HiSeq	200						
HiSeq	HiSeq	100						
HiSeq	HiSeq	50						
HiSeq	HiSeq	20						
HiSeq	HiSeq	10						
HiSeq	HiSeq	5						
HiSeq	HiSeq	2						
HiSeq	HiSeq	1						
HiSeq	HiSeq	0.5						
HiSeq	HiSeq	0.2						
HiSeq	HiSeq	0.1						
HiSeq	HiSeq	0.05						
HiSeq	HiSeq	0.02						
HiSeq	HiSeq	0.01						
<b>Sequencing by synthesis (SBS) - R - Long Read - No illumina</b>								
NewBlitz	WGS	80 Gb		-1000P		4.0%	±12.5% M1000	\$47
NewBlitz	HiSeq	71.000						
NewBlitz	HiSeq	50.000						
NewBlitz	HiSeq	30.000						
NewBlitz	Hi							

Age, approximate; CI indicates confidence interval;  $\beta$ , logistic log base parameter;  $\alpha$ , intercept term;  $n$ , number of observations;  $R^2$ , likelihood ratio statistic;  $P$ , test of significance;  $p$ , not available;  $H_0$ , null hypothesis of no single and no synergistic effect;  $H_1$ , relative risk; \*Shows favorable trend; \*\*Shows unfavorable trend; \*\*\*Shows significant ( $<0.05$ ) association; Not available as this instrument could not be estimated or only available as an aggregated measure. In this procedure, hazard decreases linearly over time. This information is not available. \*Not available as a single instrument.

Platform	Read length (bp)	Throughput	Reads	Runtime	Error profile	Instrument cost (US\$)	Cost per Gb (US\$, approx.)
<b>Sequencing by ligation</b>							
SOLiD 5500 Wildfire	50 (SE)	80 Gb	~700 M*	6 d*	≤0.1%, AT bias <sup>#</sup>	NA <sup>†</sup>	\$130 <sup>#</sup>
	75 (SE)	120 Gb					
	50 (SE)*	160 Gb*					
SOLiD 5500 xl	50 (SE)	160 Gb	~1.4 B*	10 d*	≤0.1%, AT bias <sup>#</sup>	\$251,000 <sup>#</sup>	\$70 <sup>#</sup>
	75 (SE)	240 Gb					
	50 (SE)*	320 Gb*					
BGISEQ-500 FCS <sup>155</sup>	50–100 (SE/PE)*	8–40 Gb*	NA <sup>†</sup>	24 h*	≤0.1%, AT bias <sup>#</sup>	\$250 (REF. 155)	NA <sup>†</sup>
BGISEQ-500 FCL <sup>155</sup>	50–100 (SE/PE)*	40–200 Gb*	NA <sup>†</sup>	24 h*	≤0.1%, AT bias <sup>#</sup>	\$250,000 (REF. 155)	NA <sup>†</sup>

Platform	Read length (bp)	Throughput	Reads	Runtime	Error profile	Instrument cost (US\$)	Cost per Gb (US\$, approx.)
<b>Sequencing by synthesis: CRT</b>							
Illumina MiniSeq Mid output	150 (SE)*	2.1–2.4 Gb*	14–16 M*	17 h*	<1%, substitution <sup>#</sup>	\$50,000 (REF. 118)	\$200–300 (REF. 118)
Illumina MiniSeq High output	75 (SE)	1.6–1.8 Gb	22–25 M (SE)*	7 h	<1%, substitution <sup>#</sup>	\$50,000 (REF. 118)	\$200–300 (REF. 118)
	75 (PE)	3.3–3.7 Gb	44–50 M (PE)*	13 h			
	150 (PE)*	6.6–7.5 Gb*		24 h*			
Illumina MiSeq v2	36 (SE)	540–610 Mb	12–15 M (SE)	4 h	0.1%, substitution <sup>#</sup>	\$99,000 <sup>#</sup>	~\$1,000
	25 (PE)	750–850 Mb	24–30 M (PE)*	5.5 h			\$996
	150 (PE)	4.5–5.1 Gb		24 h			\$212
	250 (PE)*	7.5–8.5 Gb*		39 h*			\$142 <sup>#</sup>
Illumina MiSeq v3	75 (PE)	3.3–3.8 Gb	44–50 M (PE)*	21–56 h*	0.1%, substitution <sup>#</sup>	\$99,000 <sup>#</sup>	\$250
	300 (PE)*	13.2–15 Gb*					\$110 <sup>#</sup>
Illumina NextSeq 500/550 Mid output	75 (PE)	16–20 Gb	Up to 260 M (PE)*	15 h	<1%, substitution <sup>#</sup>	\$250 <sup>#</sup>	\$42
	150 (PE)*	32–40 Gb*		26 h*			\$40 <sup>#</sup>
Illumina NextSeq 500/550 High output	75 (SE)	25–30 Gb	400 M (SE)*	11 h	<1%, substitution <sup>#</sup>	\$250 <sup>#</sup>	\$43
	75 (PE)	50–60 Gb	800 M (PE)*	18 h			\$41
	150 (PE)*	100–120 Gb*		29 h*			\$33 <sup>#</sup>
Illumina HiSeq2500 v2 Rapid run	36 (SE)	9–11 Gb	300 M (SE)*	7 h	0.1%, substitution <sup>#</sup>	\$690 <sup>#</sup>	\$230
	50 (PE)	25–30 Gb	600 M (PE)*	16 h			\$90
	100 (PE)	50–60 Gb		27 h			\$52
	150 (PE)	75–90 Gb		40 h			\$45
	250 (PE)*	125–150 Gb*		60 h*			\$40 <sup>#</sup>
Illumina HiSeq2500 v3	36 (SE)	47–52 Gb	1.5 B (SE)	2 d	0.1%, substitution <sup>#</sup>	\$690 <sup>#</sup>	\$180
	50 (PE)	135–150 Gb	3 B (PE)*	5.5 d			\$78
	100 (PE)*	270–300 Gb		11 d*			\$45 <sup>#</sup>

Platform	Read length (bp)	Throughput	Reads	Runtime	Error profile	Instrument cost (US\$)	Cost per Gb (US\$, approx.)
Illumina HiSeq2500 v4	36 (SE)	64–72 Gb	2 B (SE)	29 h	0.1%, substitution <sup>g</sup>	\$690 <sup>f</sup>	\$150
	50 (PE)	180–200 Gb	4 B (PE)*	2.5 d			\$58
	100 (PE)	360–400 Gb		5 d			\$45
	125 (PE)*	450–500 Gb*		6 d*			\$30 <sup>f</sup>
Illumina HiSeq3000/4000	50 (SE)	105–125 Gb	2.5 B (SE)*	1–3.5 d*	0.1%, substitution <sup>g</sup>	\$740/\$900 (REF. 156)	\$50
	75 (PE)	325–375 Gb					\$31
	150 (PE)*	650–750 Gb*					\$22 (REF. 157)
Illumina HiSeq X	150 (PE)*	800–900 Gb per flow cell*	2.6–3 B (PE)*	<3 d*	0.1%, substitution <sup>g</sup>	\$1,000 <sup>g,s</sup>	\$7.0 <sup>f</sup>
Qiagen GeneReader	NA <sup>f</sup>	12 genes; 1,250 mutations <sup>22</sup>	NA <sup>f</sup>	Several days <sup>22</sup>	Similar to other SBS systems <sup>22</sup>	NA <sup>f</sup>	\$400–\$600 per panel <sup>22</sup>

Platform	Read length (bp)	Throughput	Reads	Runtime	Error profile	Instrument cost (US\$)	Cost per Gb (US\$, approx.)
<b>Sequencing by synthesis: SNA</b>							
454 GS Junior	Up to 600; 400 average (SE, PE)*	35 Mb*	-0.1 M*	10 h*	1%, indel <sup>b</sup>	NA <sup>b</sup>	\$40,000*
454 GS Junior+	Up to 1,000; 700 average (SE, PE)*	70 Mb*	-0.1 M*	18 h*	1%, indel <sup>b</sup>	\$108,000*	\$19,500*
454 GS FLX Titanium XLR70	Up to 600; 450 mode (SE, PE)*	450 Mb*	-1 M*	10 h*	1%, indel <sup>b</sup>	NA <sup>b</sup>	\$15,500*
454 GS FLX Titanium XL+	Up to 1,000; 700 mode (SE, PE)*	700 Mb*	-1 M*	23 h*	1%, indel <sup>b</sup>	\$450,000*	\$9,500*
Ion PGM 314	200 (SE)	30–50	400,000–550,000*	23 h	1%, indel <sup>b</sup>	\$49 <sup>c</sup>	\$25–3,500*
	400 (SE)	60–100 Mb*		3.7 h*			
Ion PGM 316	200 (SE)	300–500 Mb	2–3 M*	3 h	1%, indel <sup>b</sup>	\$49 <sup>c</sup>	\$700–1,000*
	400 (SE)*	600 Mb–1 Gb*		4.9 h*			
Ion PGM 318	200 (SE)	600 Mb–1 Gb	4–5.5 M*	4 h	1%, indel <sup>b</sup>	\$49 <sup>c</sup>	\$450–800*
	400 (SE)*	1–2 Gb*		7.3 h*			
Ion Proton	Up to 200 (SE)	Up to 10 Gb*	60–80 M*	2–4 h*	1%, indel <sup>b</sup>	\$224 <sup>c</sup>	\$80*
Ion S5 520	200 (SE)	600 Mb–1 Gb	3–5 M*	2.5 h	1%, indel <sup>b</sup>	\$65 (REF. 158)	\$2,400*
	400 (SE)*	1.2–2 Gb*		4 h*			\$1,200*
Ion S5 530	200 (SE)	3–4 Gb	15–20 M*	2.5 h	1%, indel <sup>b</sup>	\$65 (REF. 158)	\$950*
	400 (SE)*	6–8 Gb*		4 h*			\$475*
Ion S5 540	200 (SE)*	10–15 Gb*	60–80 M*	2.5 h*	1%, indel <sup>b</sup>	\$65 (REF. 158)	\$300*

Platform	Read length (bp)	Throughput	Reads	Runtime	Error profile	Instrument cost (US\$)	Cost per Gb (US\$, approx.)
<b>Single-molecule real-time long reads</b>							
Pacific BioSciences RS II	-20 Kb	500 Mb–1 Gb*	~55,000*	4 h*	13% single pass, ≤1% circular consensus read, indel <sup>b</sup>	\$695 <sup>b</sup>	\$1,000*
Pacific Biosciences Sequel	8–12 Kb <sup>69</sup>	3.5–7 Gb*	~350,000*	0.5–6 h*	NA <sup>i</sup>	\$350 (REF. 69)	NA <sup>i</sup>
Oxford Nanopore MK 1 MinION	Up to 200 Kb <sup>159</sup>	Up to 1.5 Gb <sup>159</sup>	>100,000 (REF. 159)	Up to 48 h <sup>160</sup>	~12%, indel <sup>159</sup>	\$1,000*	\$750*
Oxford Nanopore PromethION	NA <sup>i</sup>	Up to 4 Tb*	NA <sup>i</sup>	NA <sup>i</sup>	NA <sup>i</sup>	\$75*	NA <sup>i</sup>
<b>Synthetic long reads</b>							
Illumina Synthetic Long-Read	-100 Kb synthetic length*	See HiSeq 2500	See HiSeq 2500	See HiSeq 2500	See HiSeq 2500 (possible barcoding and partitioning errors)	No additional instrument required	~\$1,000*
10X Genomics	Up to 100 Kb synthetic length*	See HiSeq 2500	See HiSeq 2500	See HiSeq 2500	See HiSeq 2500 (possible barcoding and partitioning errors)	\$75 (REFS 72, 161)	See HiSeq 2500 +\$500 per sample <sup>161</sup>