

FASTQ FORMAT

Instrument	pipeline ver. (OBF ^{※1} name)	ASCII characters		Quality score		DDBJ Read Annotation Pipeline convert to fastq-sanger
		Range	Offset	Type	Range	
Illumina	Solexa pipeline earlier (fastq-solexa)	59-126	64	Solexa	-5 to 62	Not available
	Illumina 1.3+ (fastq-illumina)	64-126	64	PHRED	0 to 62	available
LS454	all ver. (fastq-sanger)	33-126	33	PHRED	0 to 93	—
ABI SOLID	all ver. (fastq-sanger)	33-126	33	PHRED	0 to 93	—
HELICOS	all ver. (fastq-sanger)	33-126	33	PHRED	0 to 93	—

※1 Open Bioinformatics Foundation(OBF, <http://www.open-bio.org/>)

see also: http://en.wikipedia.org/wiki/FASTQ_format

: Cock PJ *et al.* Nucleic Acids Res. 2010 Apr;38(6):1767-71. Epub 2009 Dec 16.

The DDBJ Read Annotation Pipeline uses only fastq-sanger.
The pipeline automatically converts fastq-illumina to fastq-sanger.