

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:33:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708588.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1708588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708588.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:33:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,941,668
Mapped reads	3,793,835 / 96.25%
Unmapped reads	147,833 / 3.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	35,863 / 0.91%
Duplication rate	0.95%
Clipped reads	49,847 / 1.26%

2.2. ACGT Content

Number/percentage of A's	58,637,368 / 30.99%
Number/percentage of C's	35,857,977 / 18.95%
Number/percentage of T's	58,355,160 / 30.84%
Number/percentage of G's	36,365,582 / 19.22%
Number/percentage of N's	6,614 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.2561
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2.4. Mapping Quality

Mean Mapping Quality	46.74
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2.5. Mismatches and indels

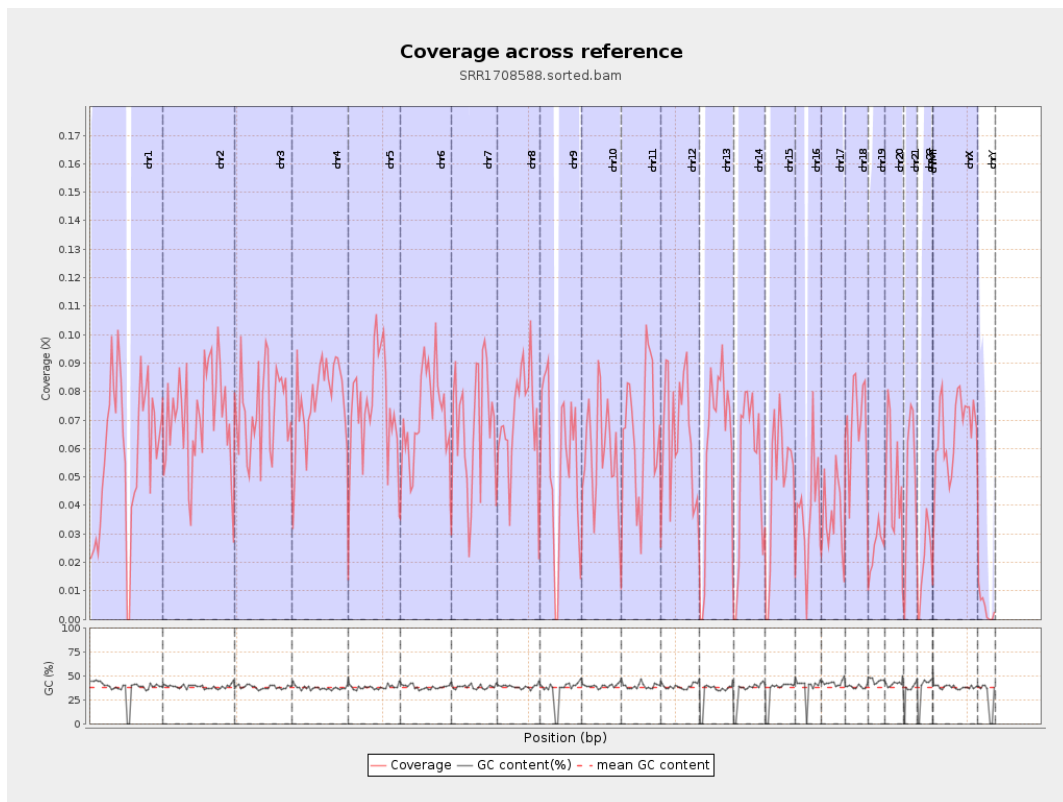
General error rate	0.15%
Mismatches	271,668
Insertions	11,895
Mapped reads with at least one insertion	0.31%
Deletions	9,650
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.58%

2.6. Chromosome stats

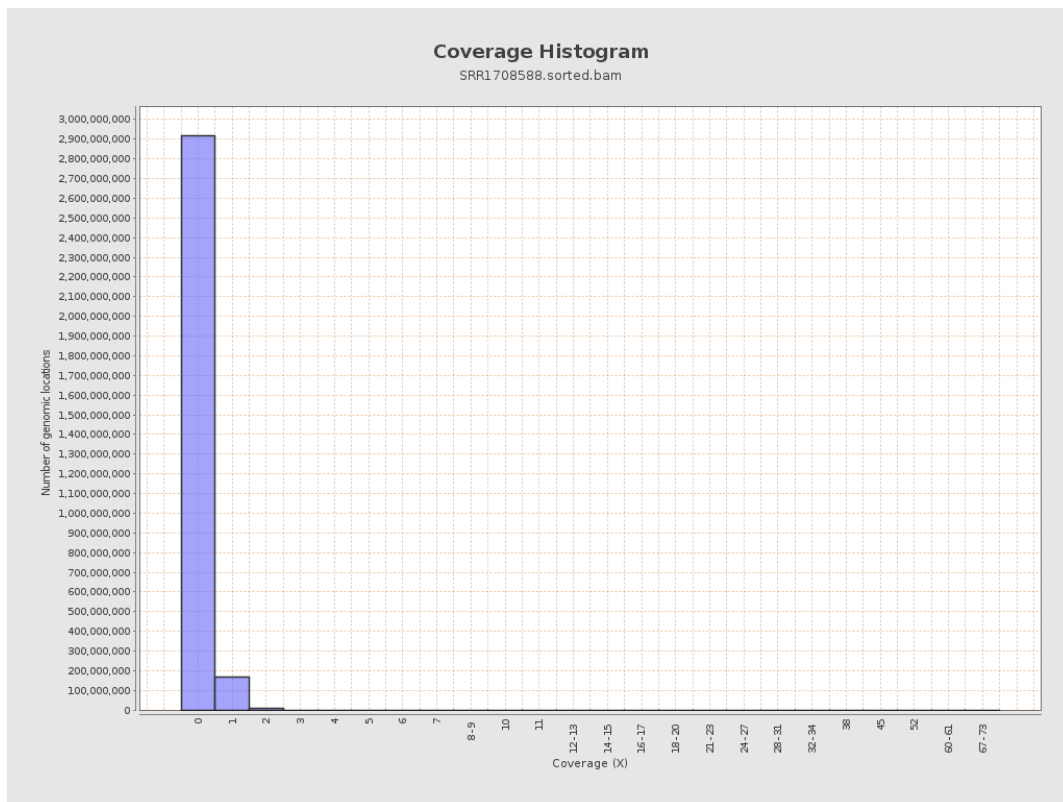
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14518507	0.0582	0.2531
chr2	243199373	17279266	0.071	0.2809
chr3	198022430	14572358	0.0736	0.2794
chr4	191154276	14791600	0.0774	0.2857
chr5	180915260	13381854	0.074	0.2797
chr6	171115067	12283227	0.0718	0.2756
chr7	159138663	10685867	0.0671	0.2674

chr8	146364022	10319181	0.0705	0.2734
chr9	141213431	7866945	0.0557	0.2442
chr10	135534747	7984712	0.0589	0.2497
chr11	135006516	8908953	0.066	0.2658
chr12	133851895	8642381	0.0646	0.2618
chr13	115169878	7139197	0.062	0.257
chr14	107349540	5671579	0.0528	0.2373
chr15	102531392	4917871	0.048	0.2268
chr16	90354753	3356024	0.0371	0.1983
chr17	81195210	2999802	0.0369	0.1985
chr18	78077248	5418954	0.0694	0.2712
chr19	59128983	1512449	0.0256	0.1637
chr20	63025520	3104661	0.0493	0.2293
chr21	48129895	2291419	0.0476	0.2265
chr22	51304566	1057839	0.0206	0.1479
chrMT	16571	332	0.02	0.1468
chrX	155270560	10291503	0.0663	0.2648
chrY	59373566	242700	0.0041	0.0664

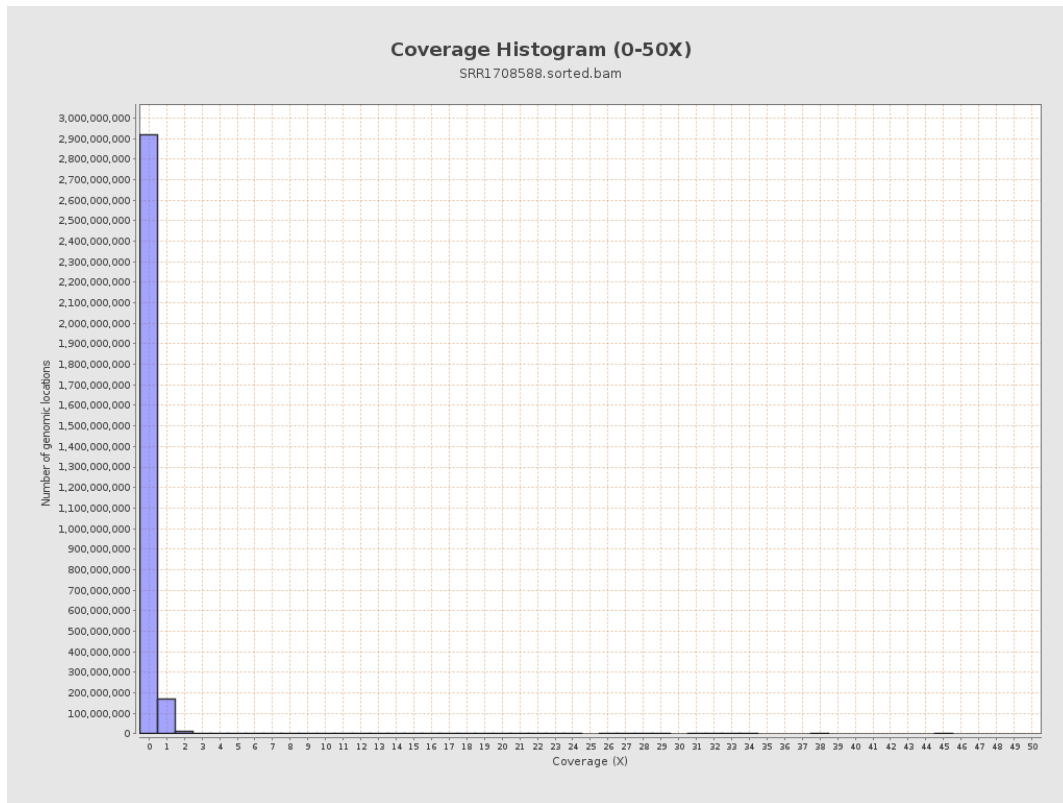
3. Results : Coverage across reference



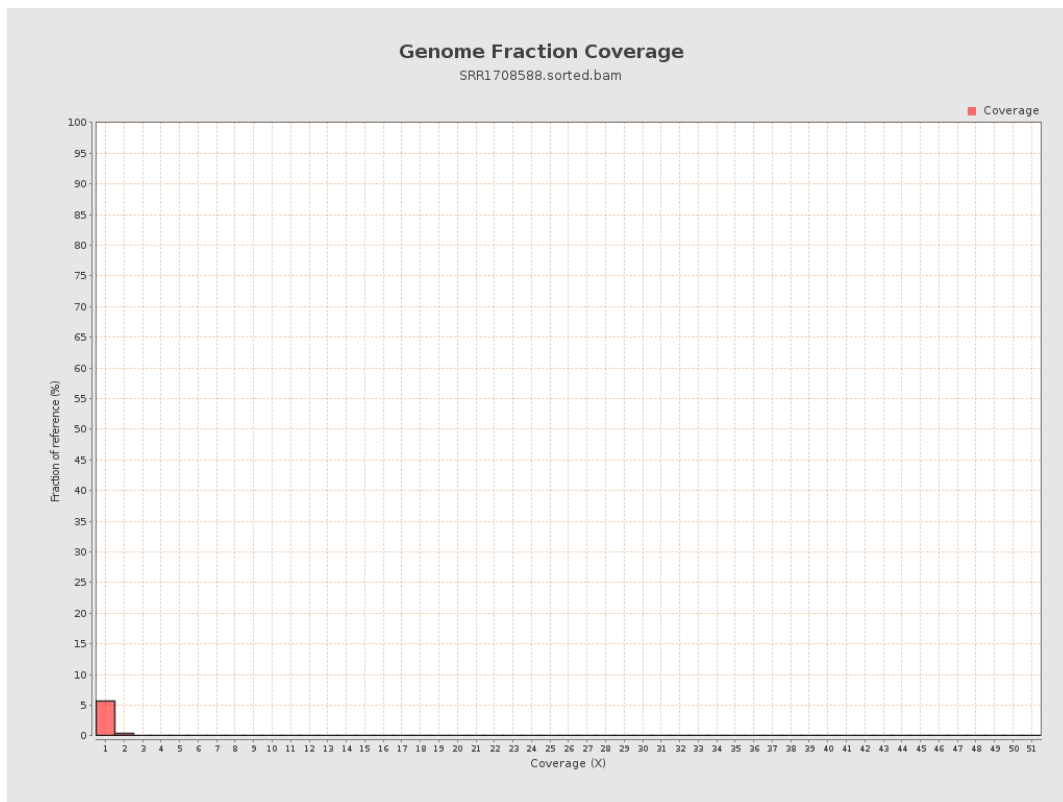
4. Results : Coverage Histogram



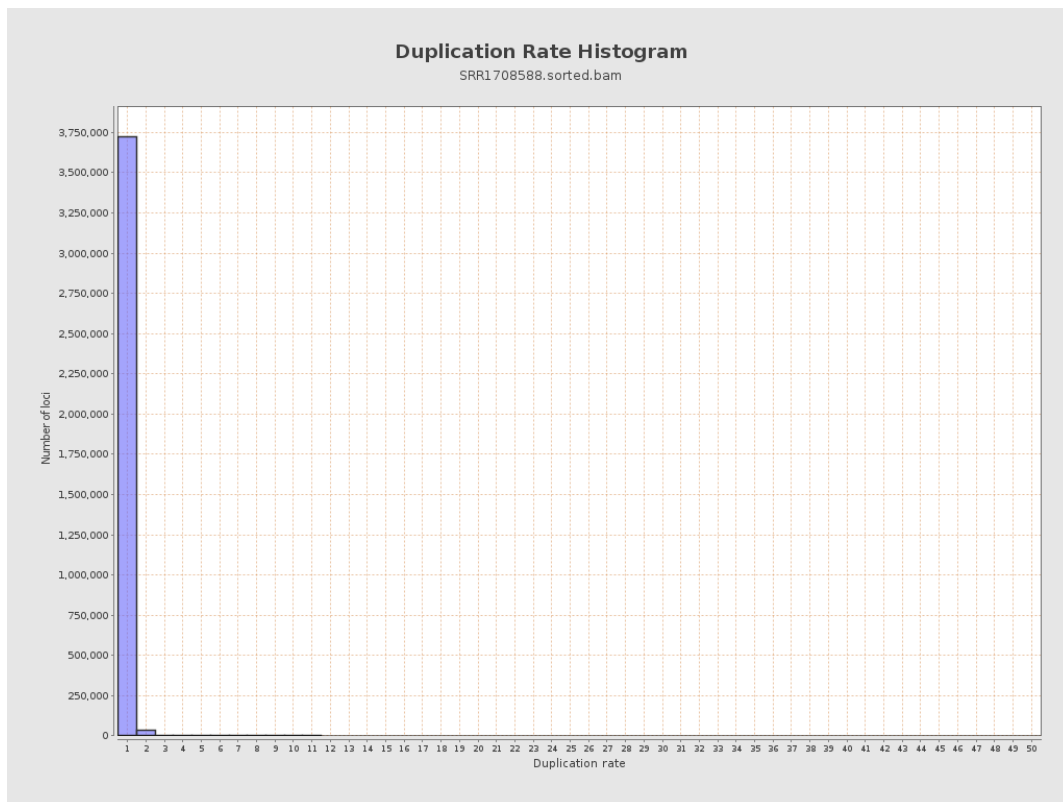
5. Results : Coverage Histogram (0-50X)



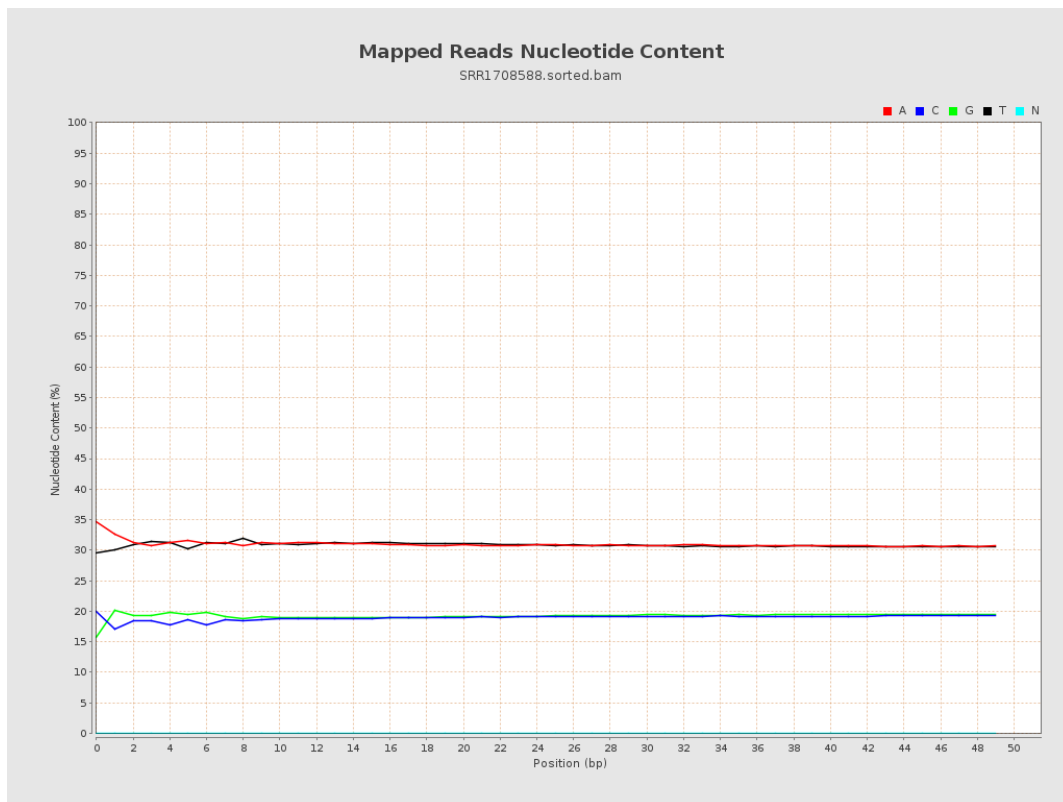
6. Results : Genome Fraction Coverage



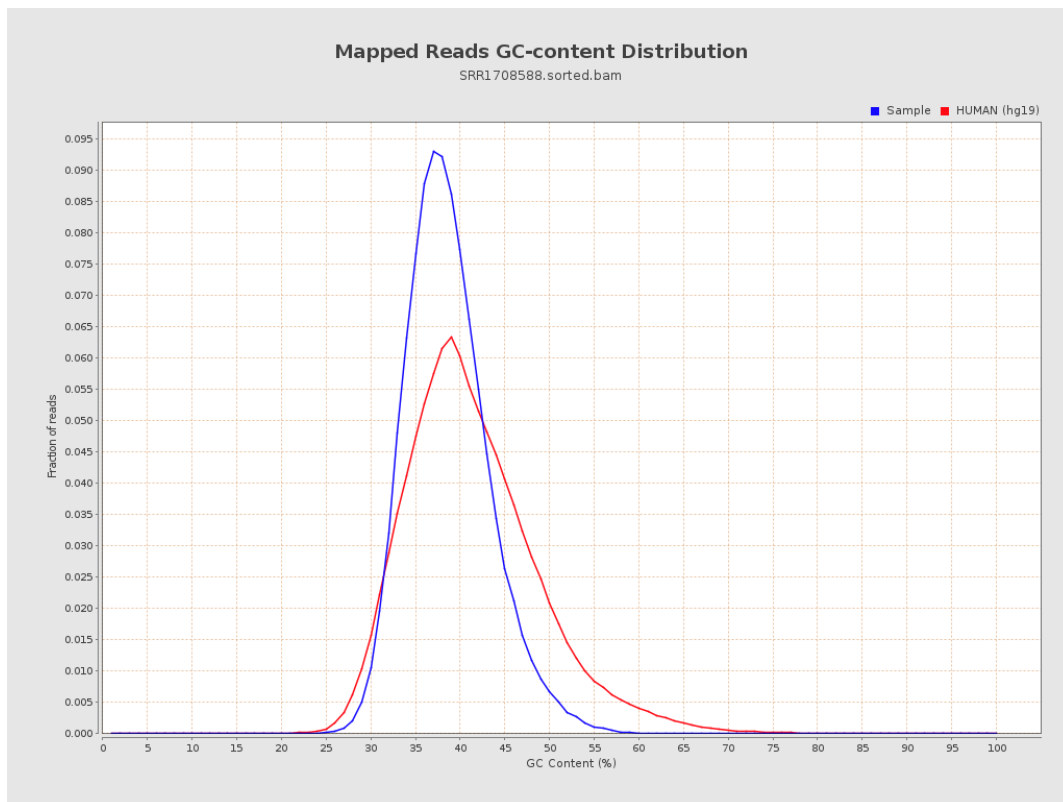
7. Results : Duplication Rate Histogram



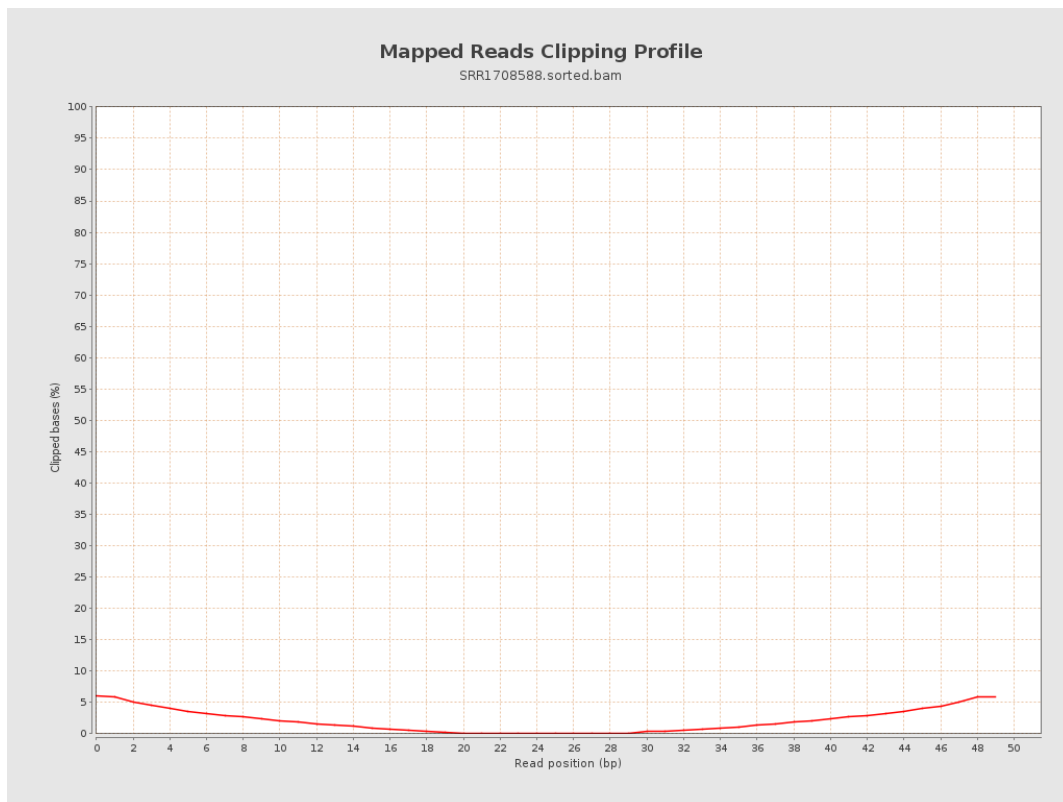
8. Results : Mapped Reads Nucleotide Content



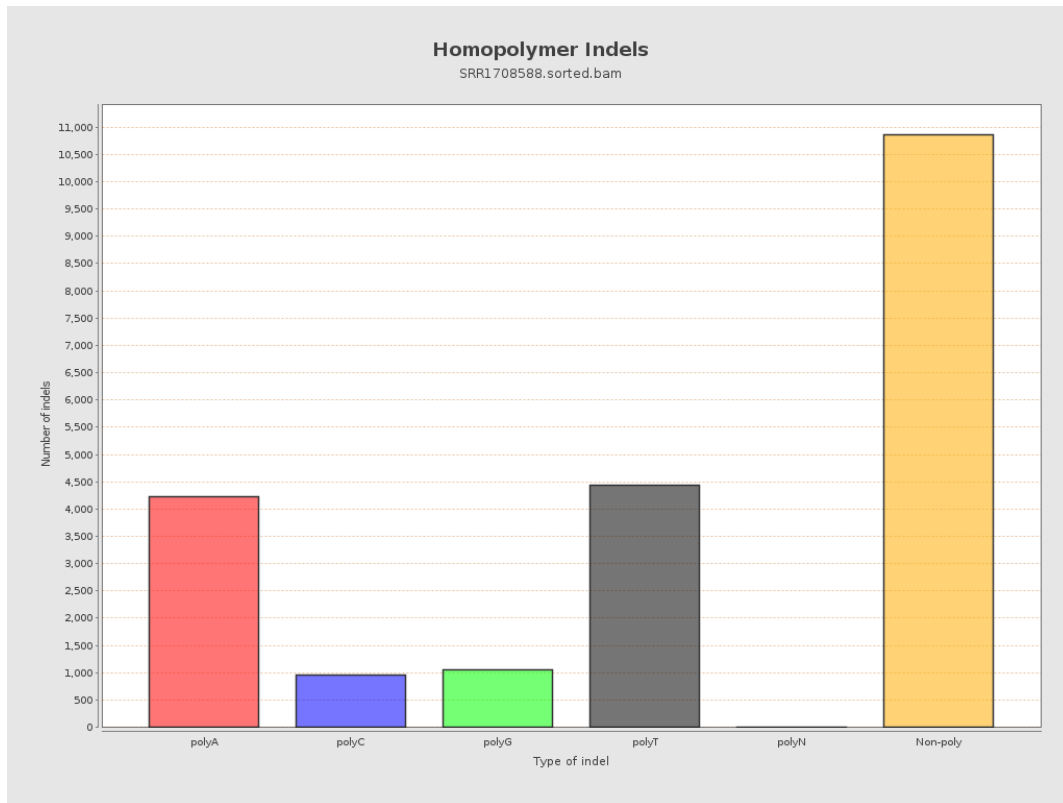
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

