

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:22:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548996.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_SRR1548996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548996.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:22:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,898,191
Mapped reads	6,844,605 / 86.66%
Unmapped reads	1,053,586 / 13.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	544,135 / 6.89%
Duplication rate	7.21%
Clipped reads	350,486 / 4.44%

2.2. ACGT Content

Number/percentage of A's	81,641,495 / 30.05%
Number/percentage of C's	53,961,573 / 19.86%
Number/percentage of T's	81,767,047 / 30.1%
Number/percentage of G's	54,290,309 / 19.98%
Number/percentage of N's	2,712 / 0%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0878
Standard Deviation	0.7331

2.4. Mapping Quality

Mean Mapping Quality	44.34
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2.5. Mismatches and indels

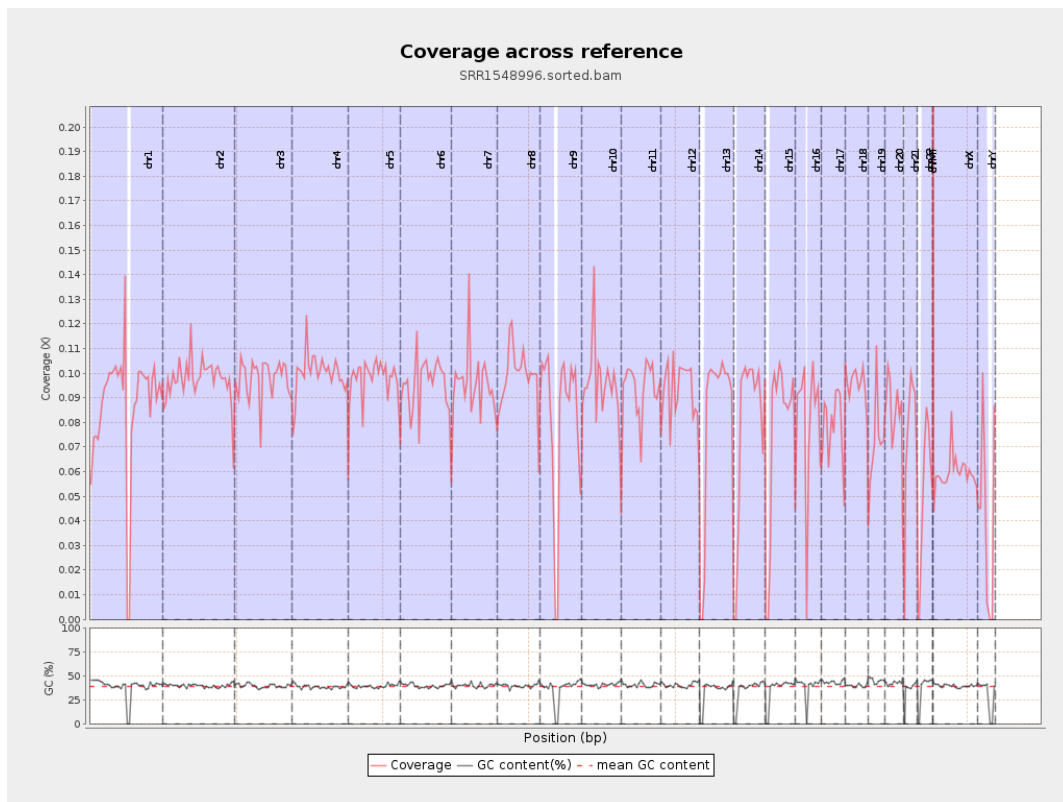
General error rate	0.3%
Mismatches	796,266
Insertions	8,159
Mapped reads with at least one insertion	0.12%
Deletions	23,017
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.51%

2.6. Chromosome stats

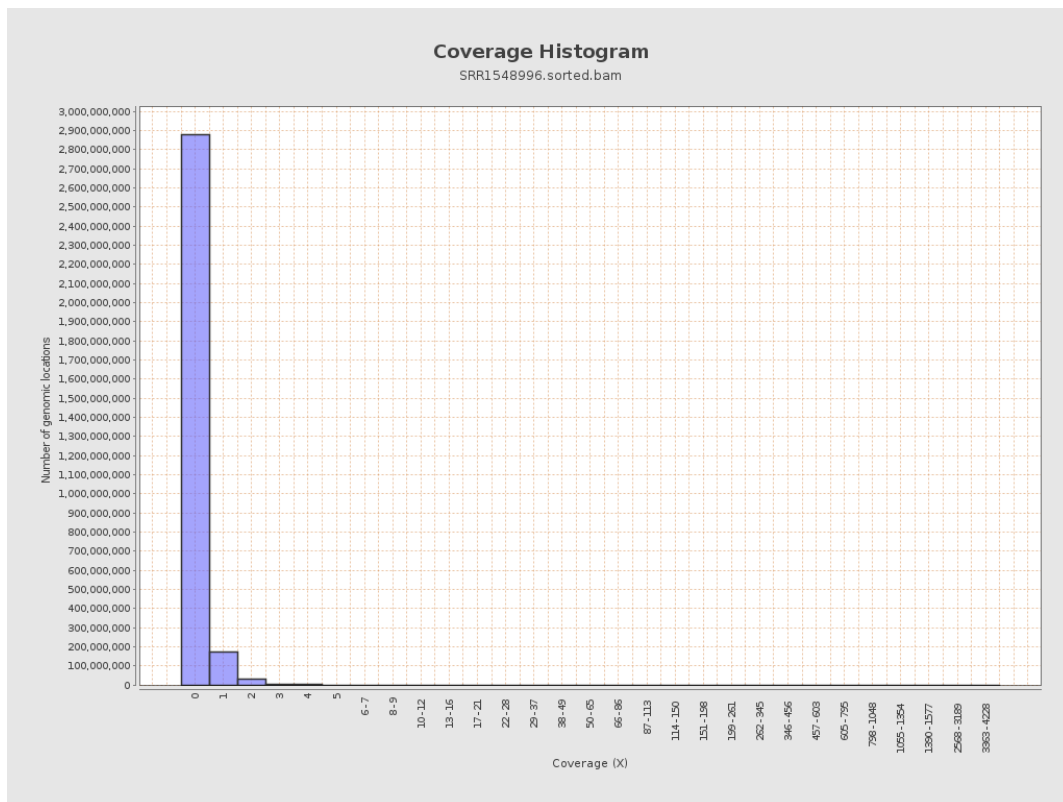
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21701324	0.0871	1.2012
chr2	243199373	23754906	0.0977	0.5231
chr3	198022430	19368302	0.0978	0.3728
chr4	191154276	19163734	0.1003	0.4152
chr5	180915260	17619244	0.0974	0.381
chr6	171115067	16428919	0.096	0.4417
chr7	159138663	15111670	0.095	0.7709
chr8	146364022	14468622	0.0989	2.1019

chr9	141213431	11566301	0.0819	0.4825
chr10	135534747	13011801	0.096	0.5746
chr11	135006516	12635553	0.0936	0.4775
chr12	133851895	12468821	0.0932	0.3851
chr13	115169878	9411690	0.0817	0.3381
chr14	107349540	8546020	0.0796	0.4151
chr15	102531392	7709763	0.0752	0.3252
chr16	90354753	7121727	0.0788	0.3809
chr17	81195210	6432705	0.0792	0.3742
chr18	78077248	7505579	0.0961	0.9602
chr19	59128983	4303678	0.0728	0.937
chr20	63025520	5361664	0.0851	0.37
chr21	48129895	3567380	0.0741	0.3932
chr22	51304566	2630226	0.0513	0.2943
chrMT	16571	6622	0.3996	0.7305
chrX	155270560	9242424	0.0595	0.3831
chrY	59373566	2554060	0.043	0.472

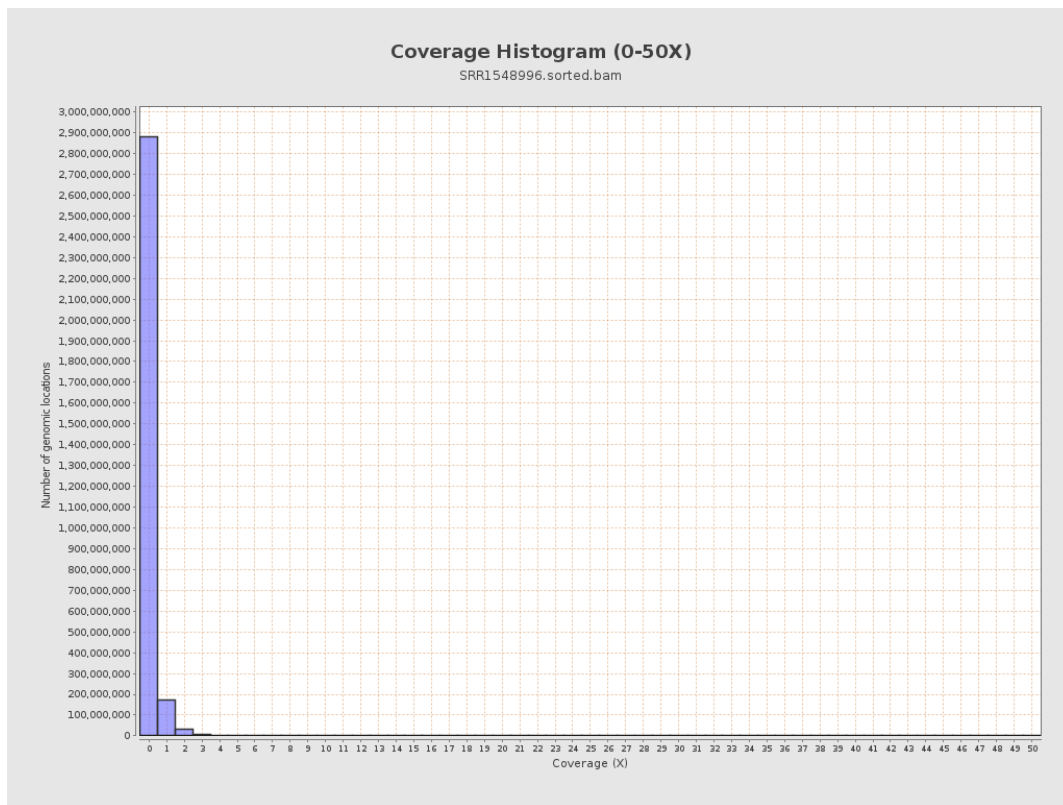
3. Results : Coverage across reference



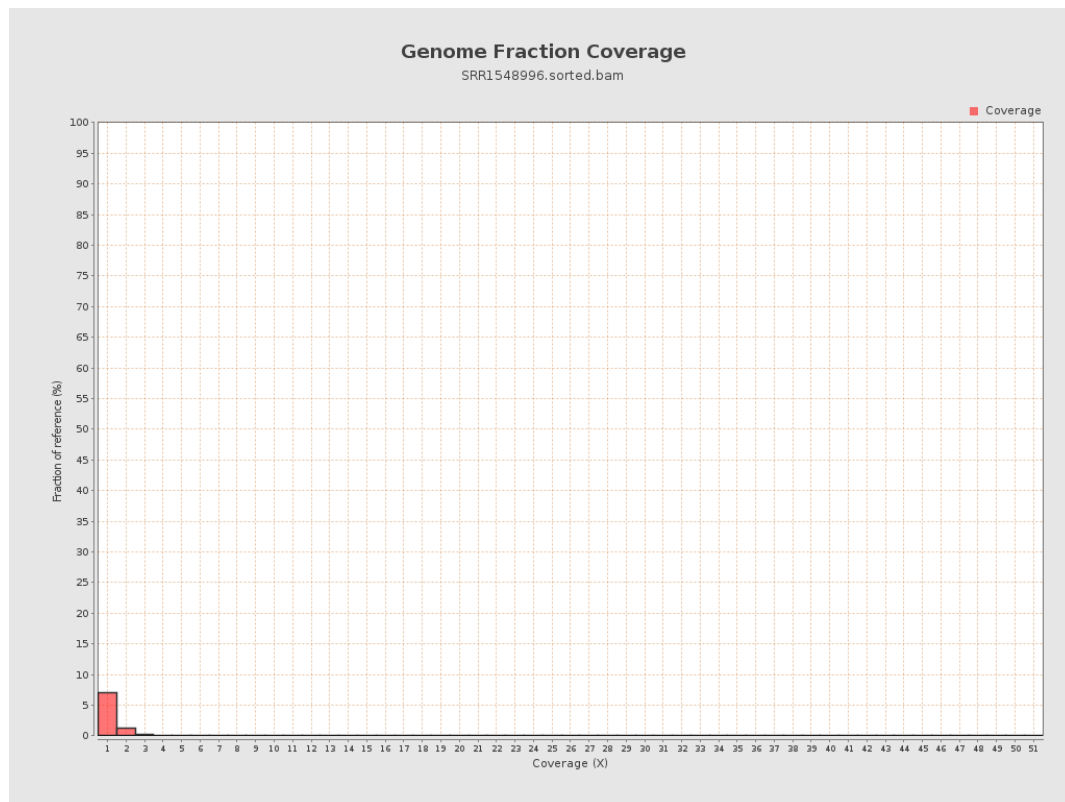
4. Results : Coverage Histogram



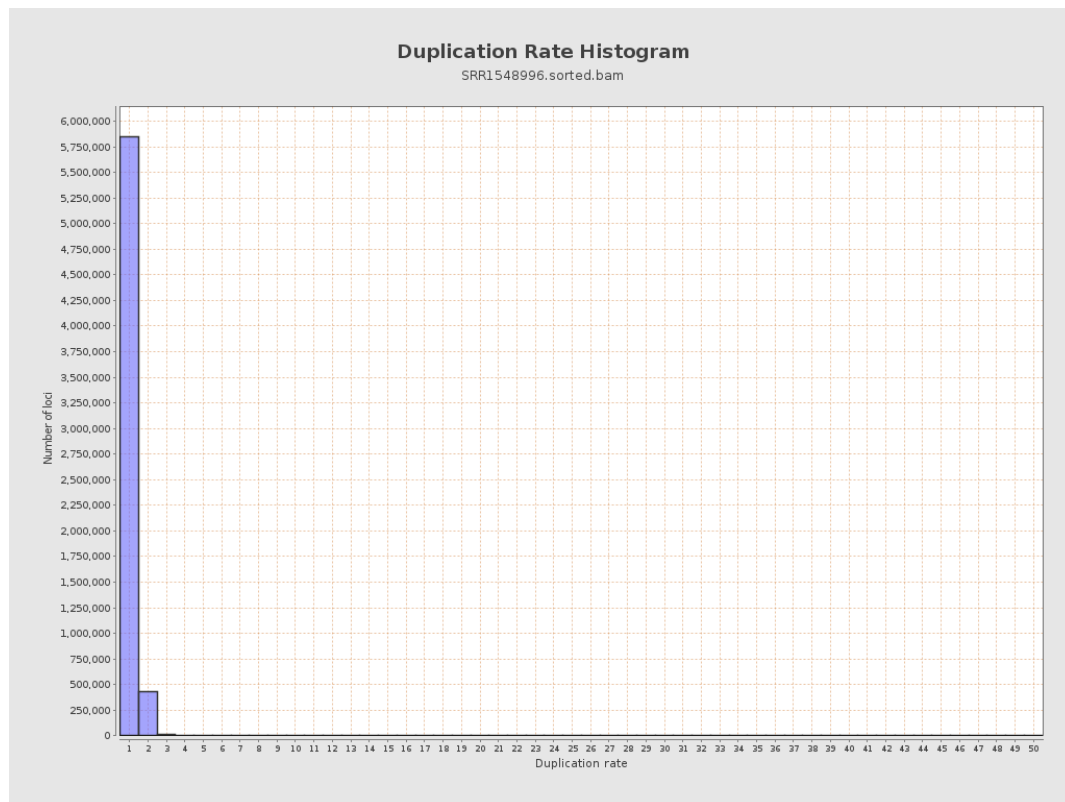
5. Results : Coverage Histogram (0-50X)



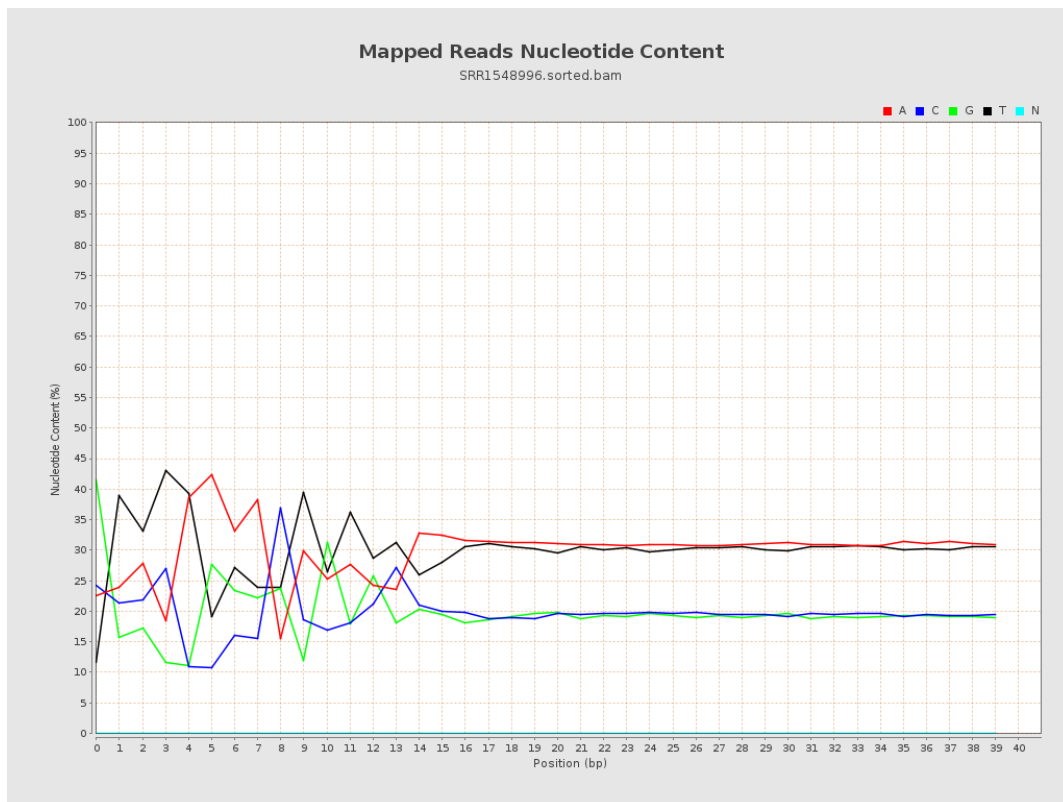
6. Results : Genome Fraction Coverage



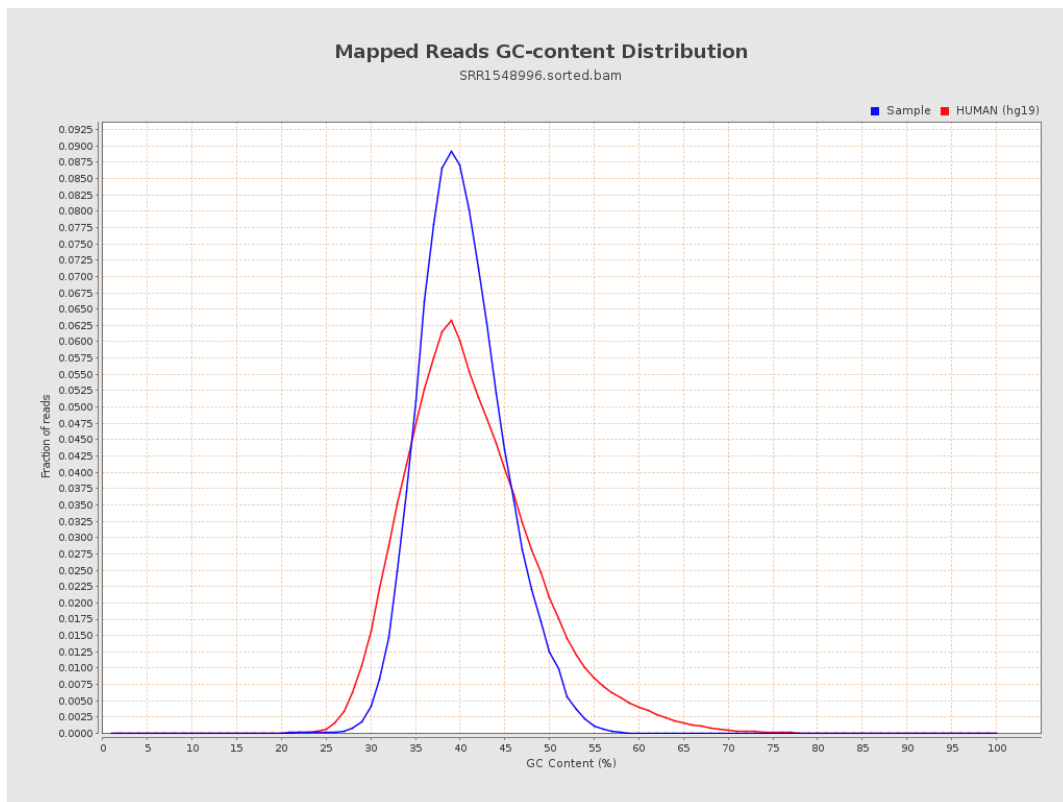
7. Results : Duplication Rate Histogram



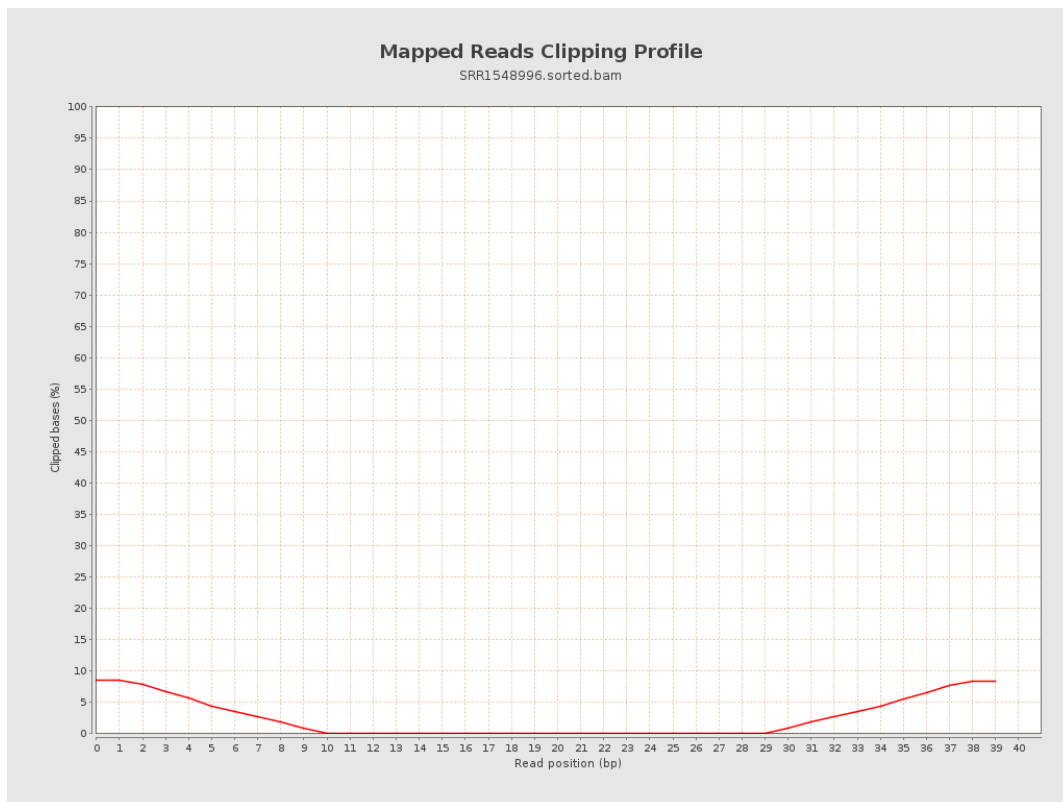
8. Results : Mapped Reads Nucleotide Content



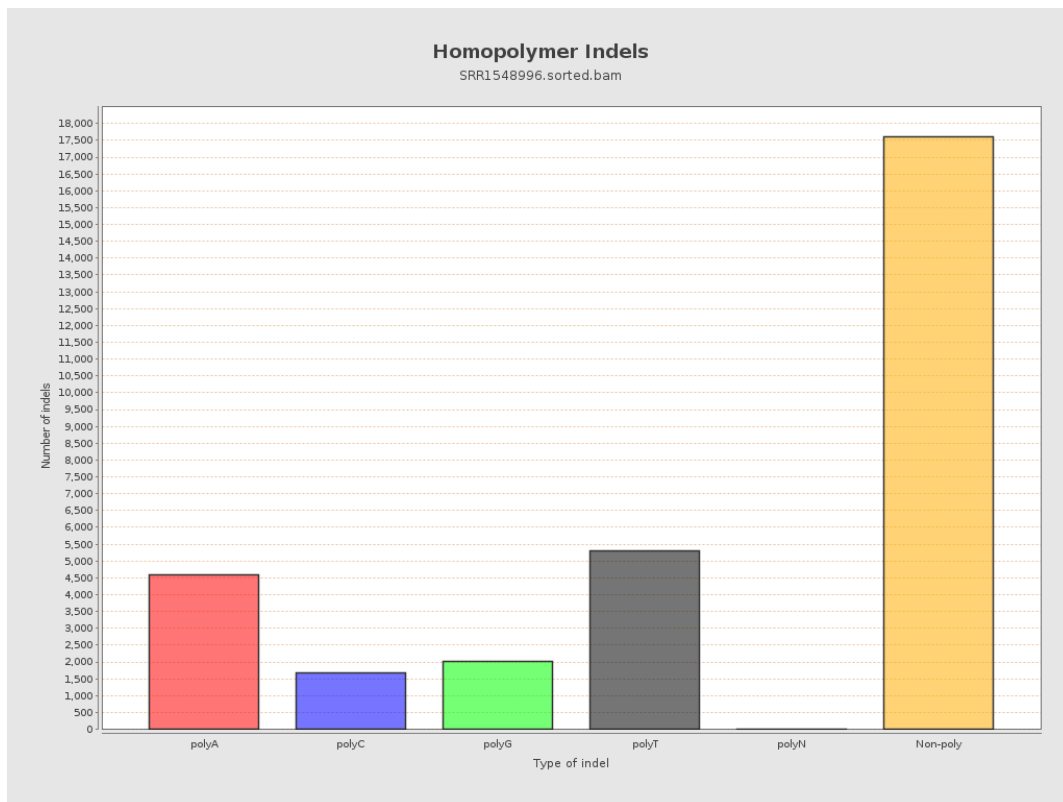
9. Results : Mapped Reads GC-content Distribution



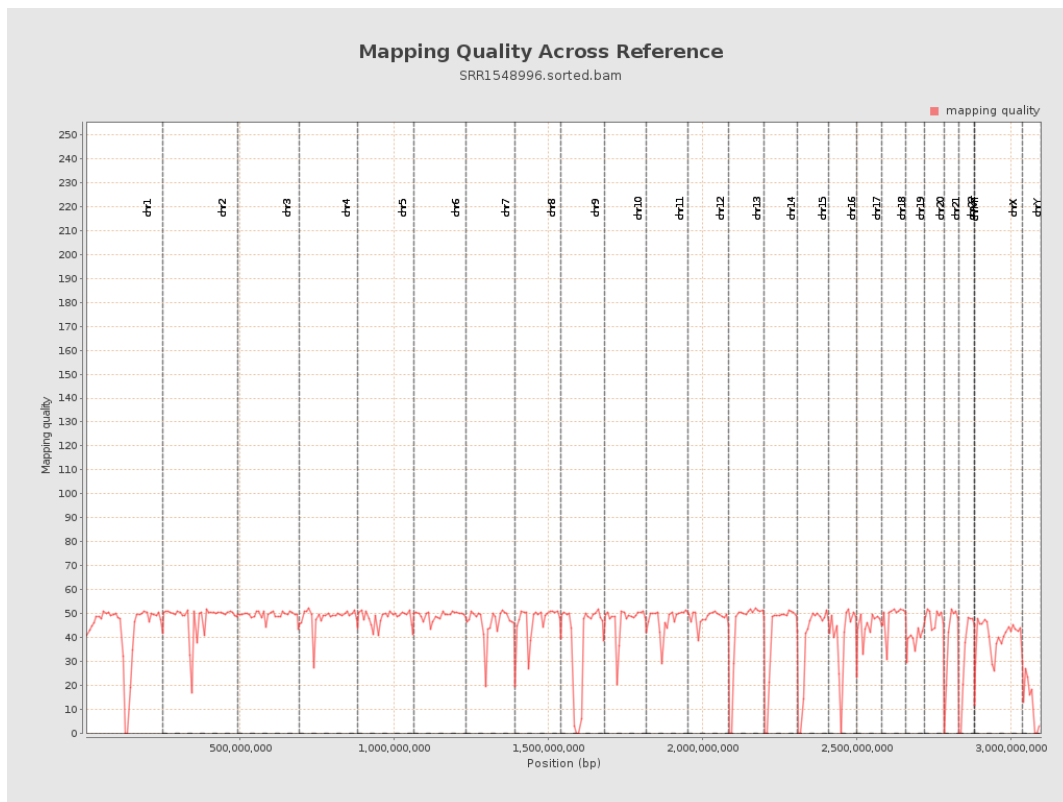
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

