

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:48:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548971.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_SRR1548971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548971.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:48:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,924,237
Mapped reads	3,921,914 / 43.95%
Unmapped reads	5,002,323 / 56.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	103,688 / 1.16%
Duplication rate	1.9%
Clipped reads	371,959 / 4.17%

2.2. ACGT Content

Number/percentage of A's	47,467,547 / 30.65%
Number/percentage of C's	29,702,969 / 19.18%
Number/percentage of T's	47,827,723 / 30.88%
Number/percentage of G's	29,888,278 / 19.3%
Number/percentage of N's	8,233 / 0.01%
GC Percentage	38.47%

2.3. Coverage

Mean	0.05
Standard Deviation	0.3665

2.4. Mapping Quality

Mean Mapping Quality	43.79
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2.5. Mismatches and indels

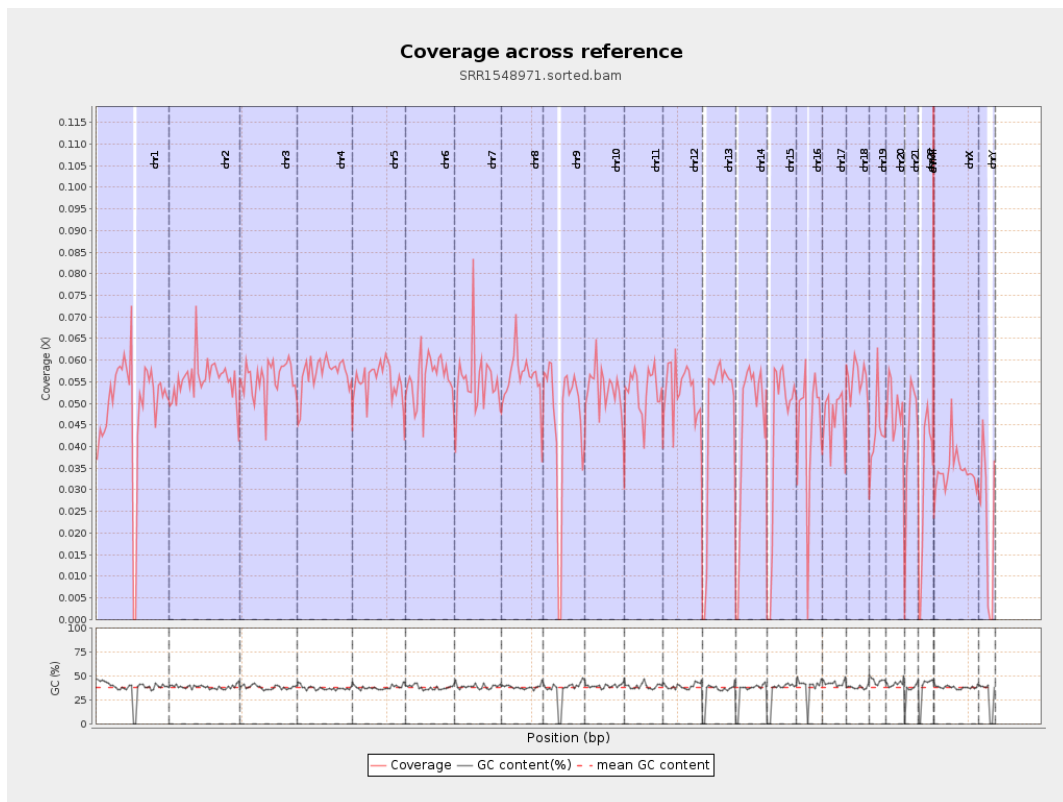
General error rate	0.32%
Mismatches	486,326
Insertions	6,620
Mapped reads with at least one insertion	0.17%
Deletions	16,946
Mapped reads with at least one deletion	0.43%
Homopolymer indels	44.61%

2.6. Chromosome stats

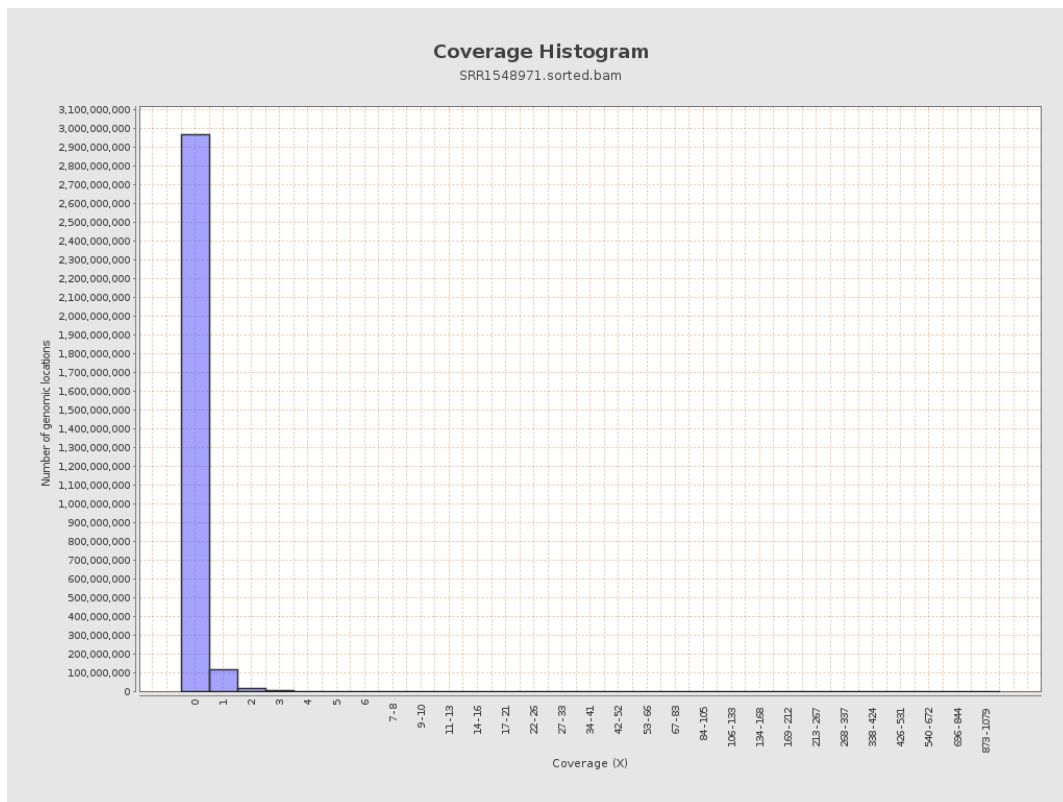
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12326174	0.0495	0.5919
chr2	243199373	13490032	0.0555	0.3395
chr3	198022430	11063833	0.0559	0.2708
chr4	191154276	10894568	0.057	0.2787
chr5	180915260	10001065	0.0553	0.2716
chr6	171115067	9553720	0.0558	0.302
chr7	159138663	8828770	0.0555	0.5233
chr8	146364022	8170136	0.0558	0.5986

chr9	141213431	6540892	0.0463	0.3086
chr10	135534747	7232435	0.0534	0.3098
chr11	135006516	7125042	0.0528	0.3417
chr12	133851895	7087983	0.053	0.2689
chr13	115169878	5345377	0.0464	0.2449
chr14	107349540	4794517	0.0447	0.2751
chr15	102531392	4441258	0.0433	0.2355
chr16	90354753	4039722	0.0447	0.251
chr17	81195210	3765111	0.0464	0.2563
chr18	78077248	4349810	0.0557	0.5225
chr19	59128983	2595782	0.0439	0.5542
chr20	63025520	3051290	0.0484	0.2547
chr21	48129895	2039694	0.0424	0.2554
chr22	51304566	1583567	0.0309	0.2307
chrMT	16571	3841	0.2318	0.5087
chrX	155270560	5324357	0.0343	0.2486
chrY	59373566	1267167	0.0213	0.2352

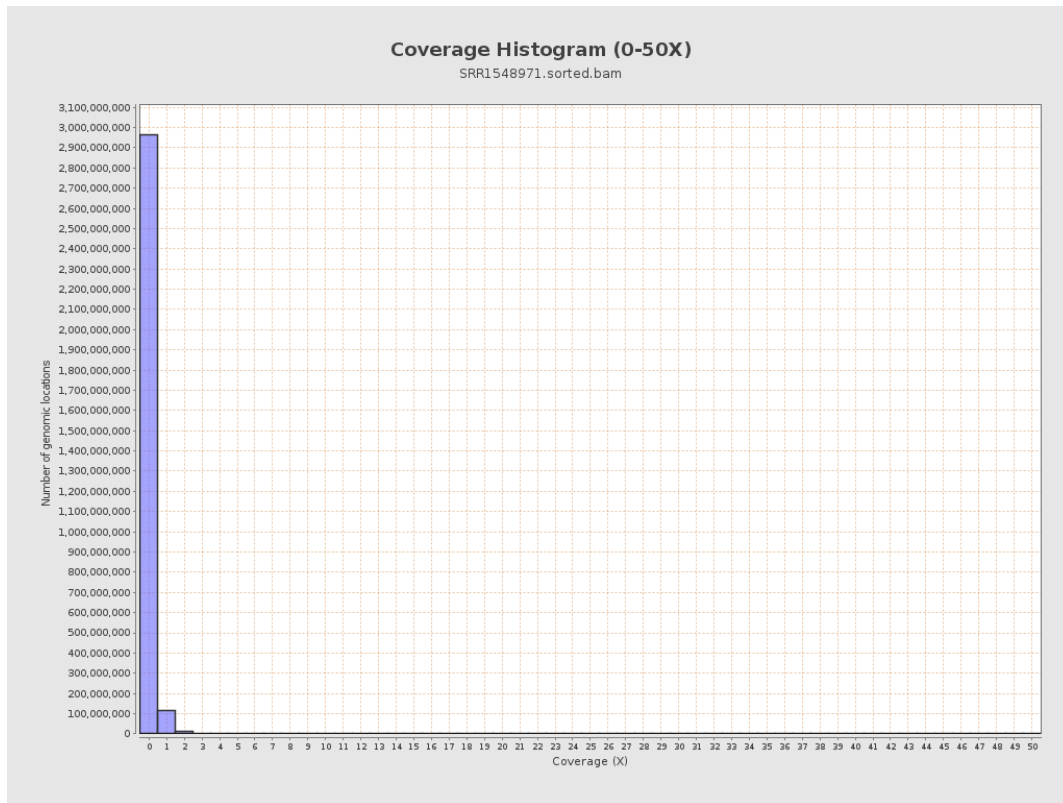
3. Results : Coverage across reference



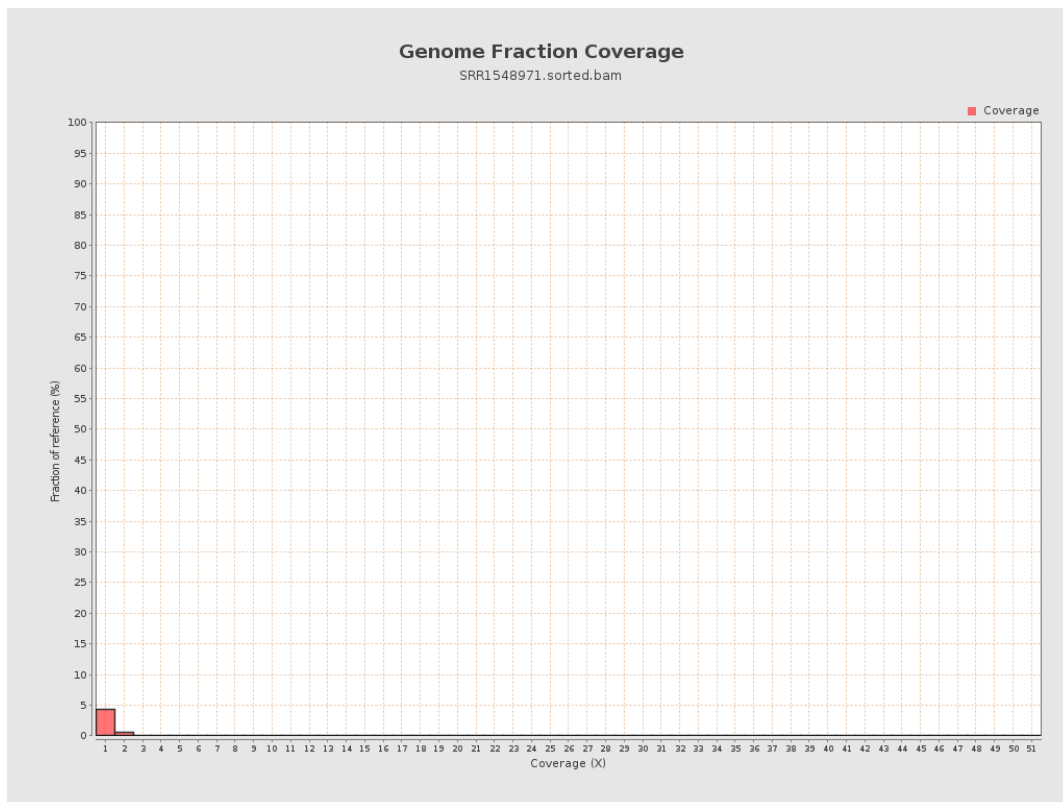
4. Results : Coverage Histogram



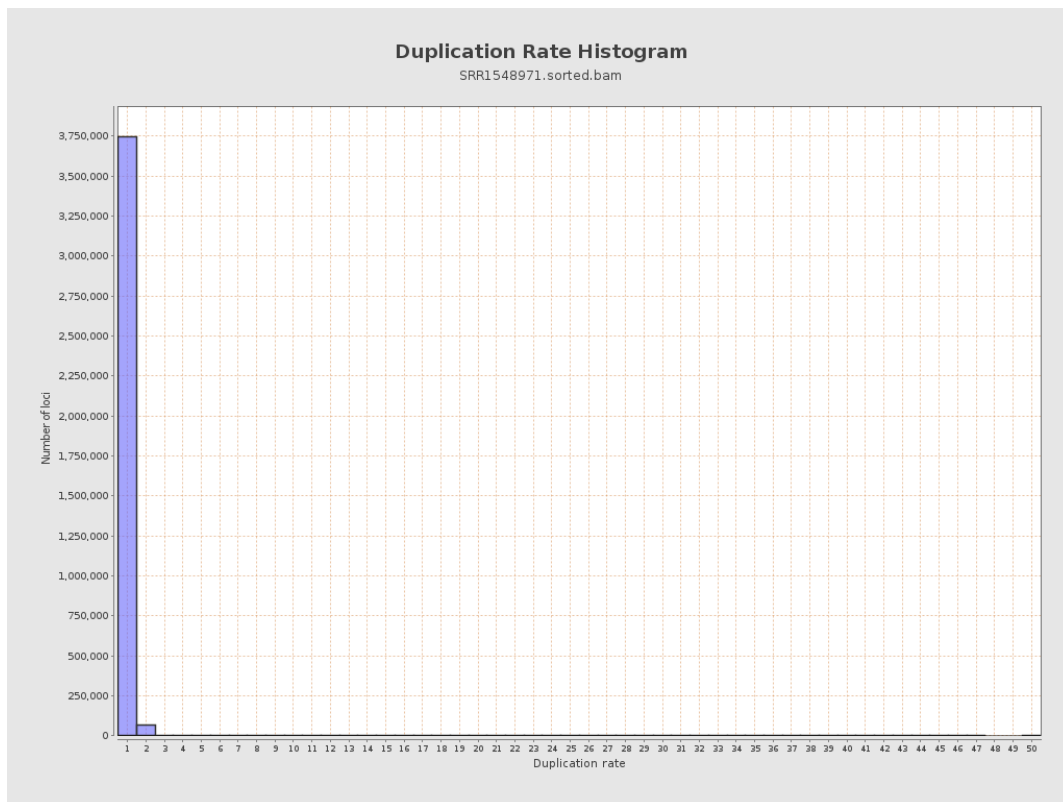
5. Results : Coverage Histogram (0-50X)



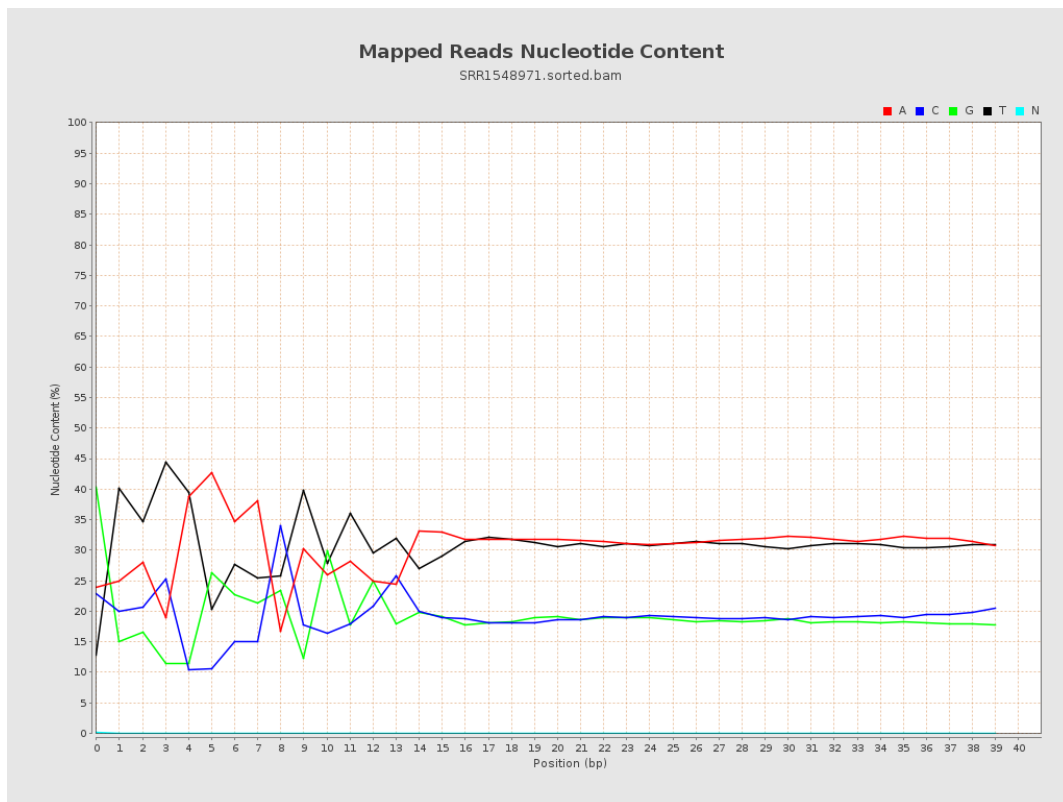
6. Results : Genome Fraction Coverage



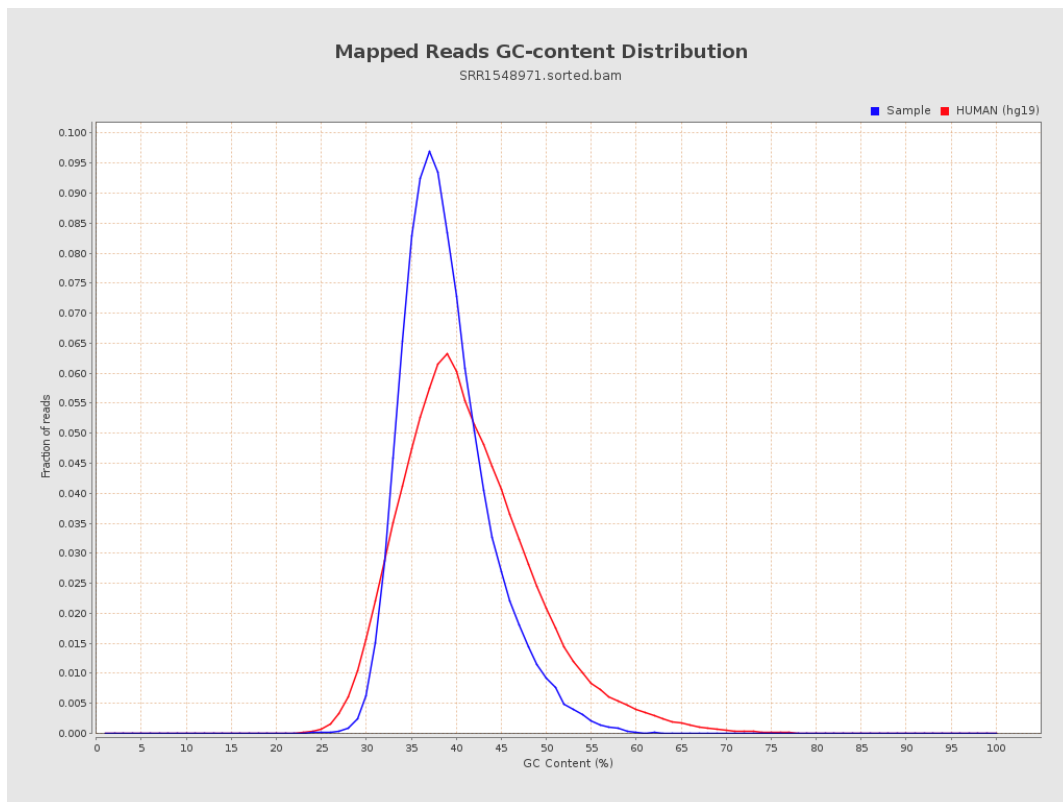
7. Results : Duplication Rate Histogram



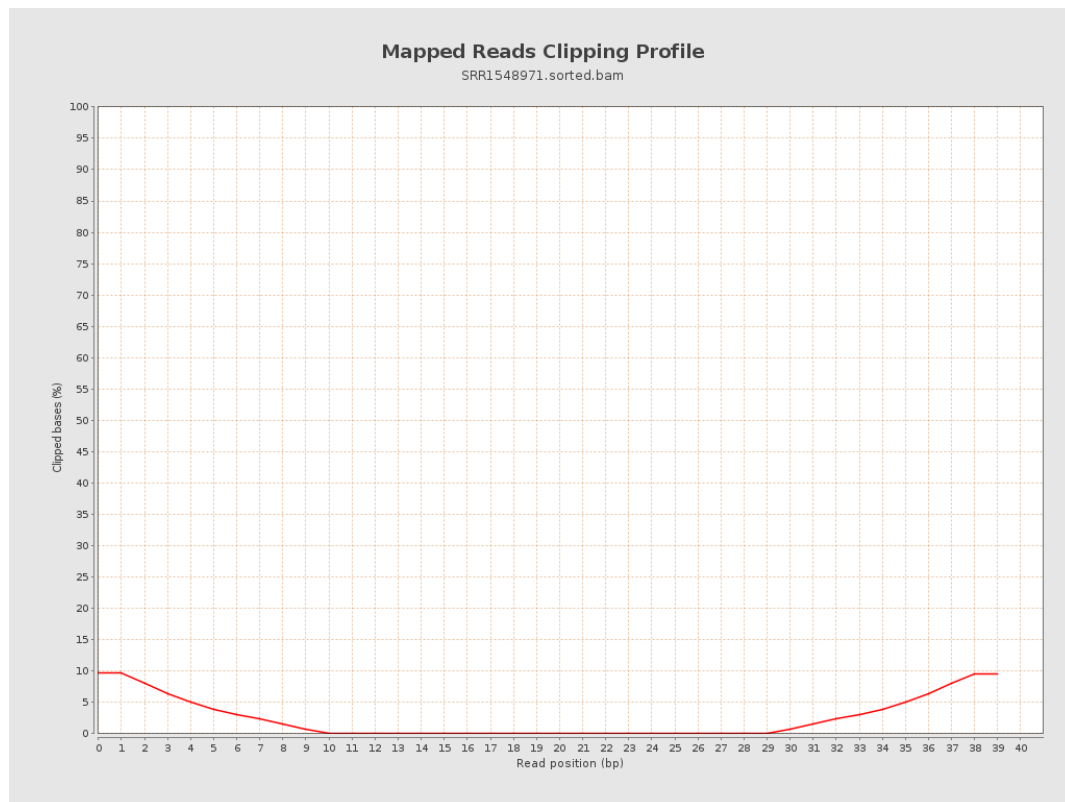
8. Results : Mapped Reads Nucleotide Content



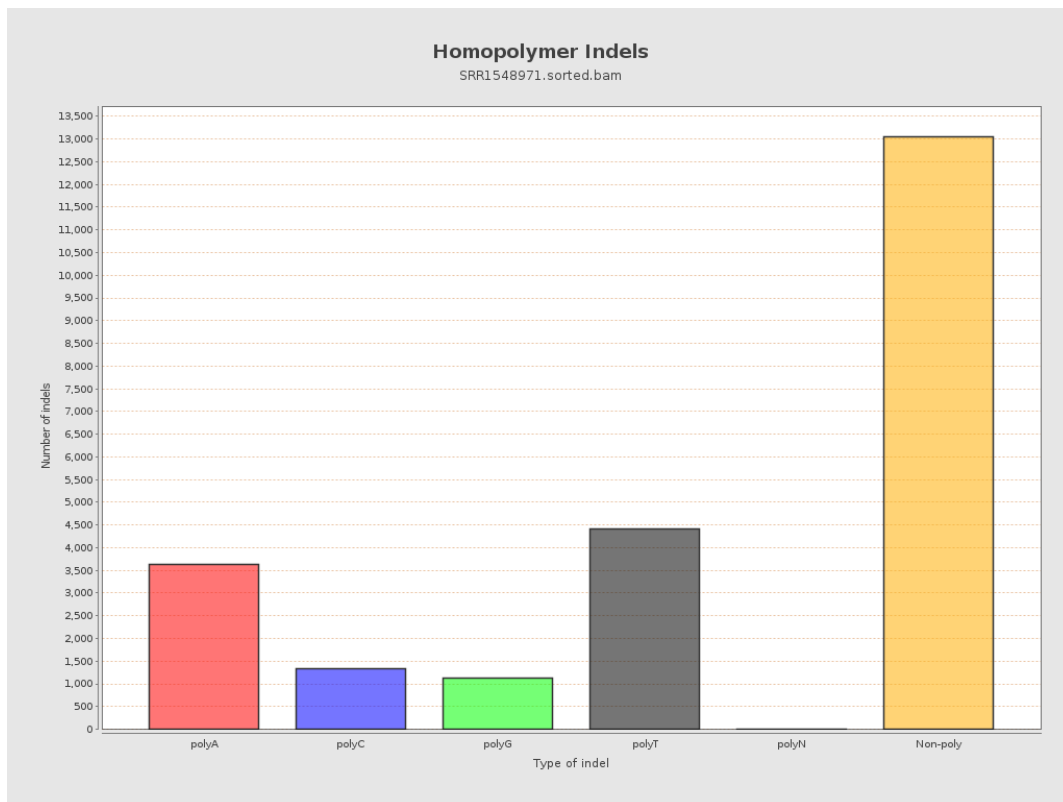
9. Results : Mapped Reads GC-content Distribution



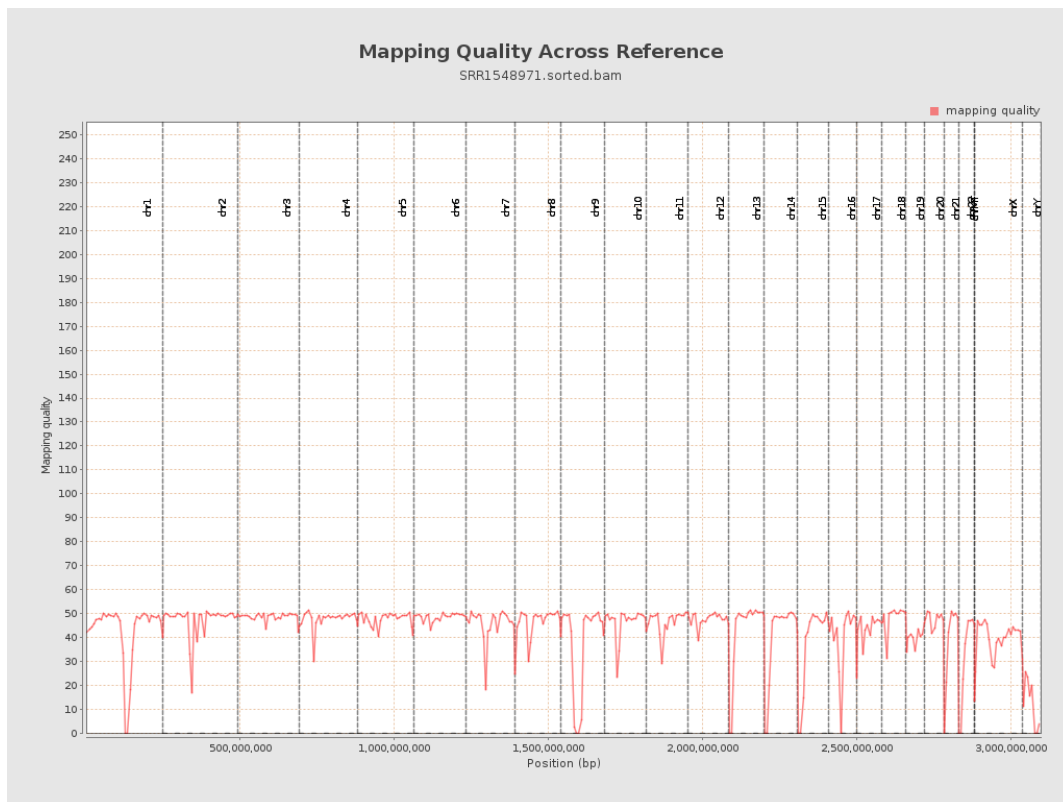
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

