Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:55:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013187.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_SRR6013187 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:55:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,942,938
Mapped reads	2,657,942 / 90.32%
Unmapped reads	284,996 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,615 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	185,106 / 6.29%
Duplication rate	4.87%
Clipped reads	1,221,635 / 41.51%

2.2. ACGT Content

Number/percentage of A's	48,080,747 / 27.3%
Number/percentage of C's	33,003,218 / 18.74%
Number/percentage of T's	54,916,268 / 31.18%
Number/percentage of G's	40,115,616 / 22.78%
Number/percentage of N's	20,536 / 0.01%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0569

Standard Deviation	0.6442

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

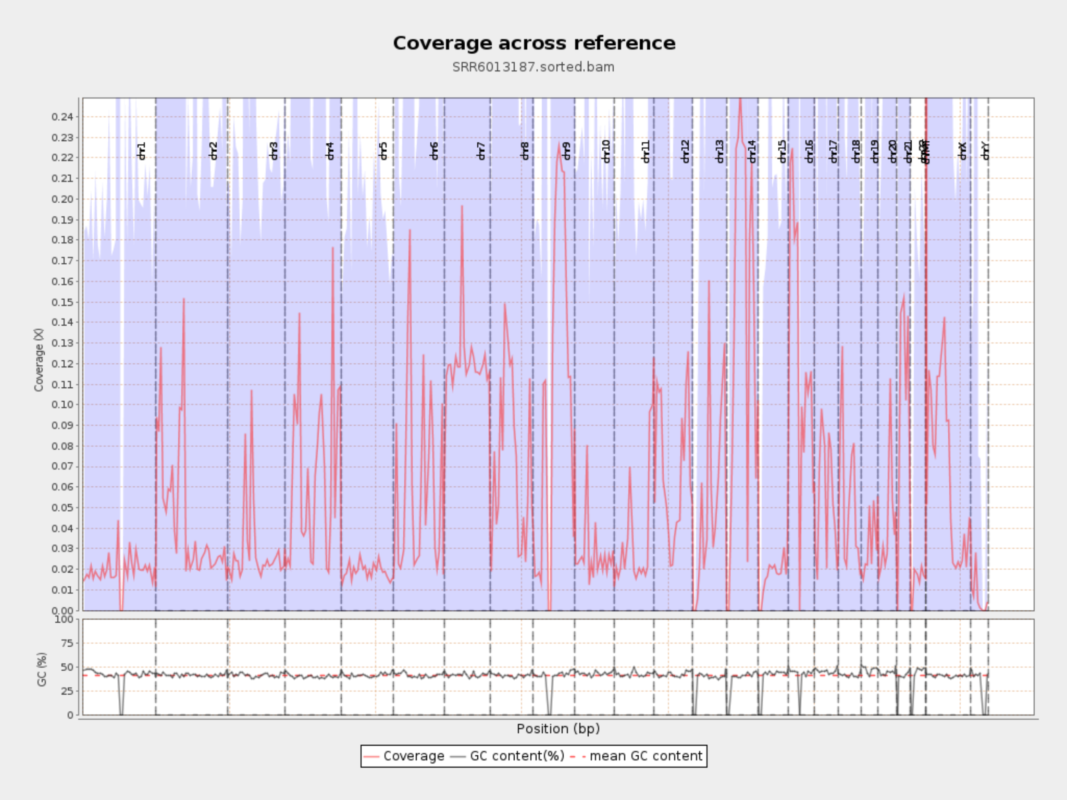
General error rate	0.79%
Mismatches	1,355,809
Insertions	13,389
Mapped reads with at least one insertion	0.5%
Deletions	46,333
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.94%

2.6. Chromosome stats

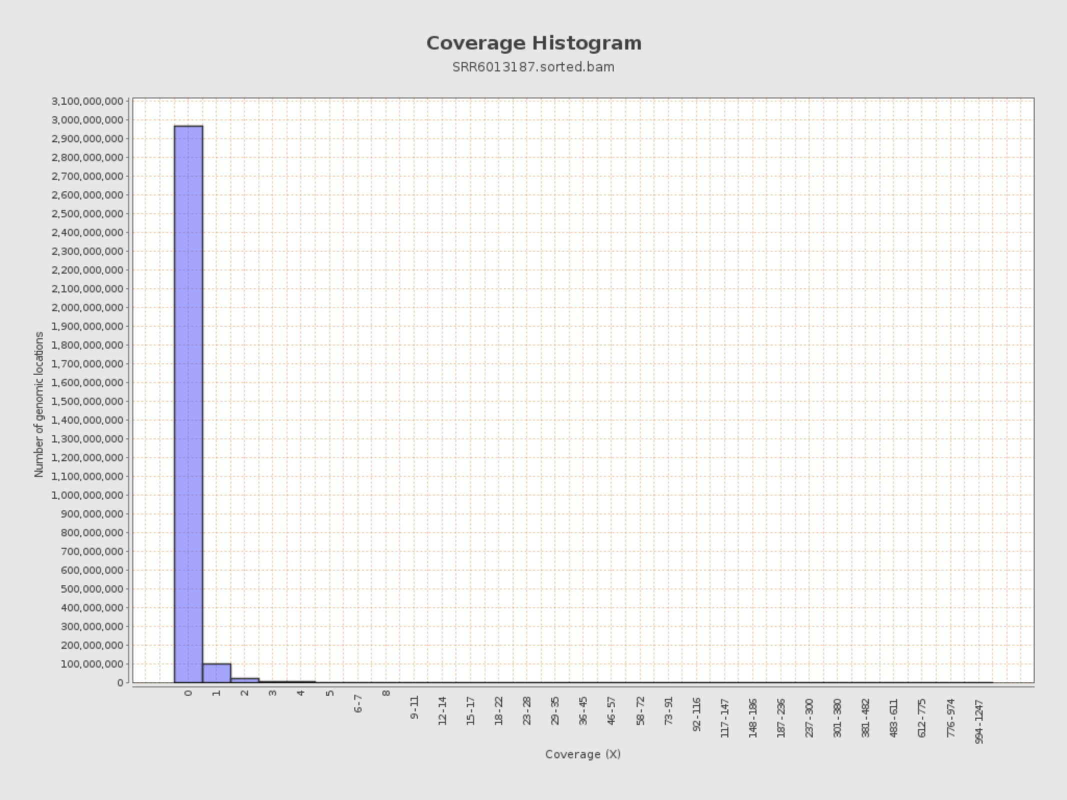
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4804878	0.0193	0.4829
chr2	243199373	11275222	0.0464	0.8261
chr3	198022430	5913439	0.0299	0.2256
chr4	191154276	12594936	0.0659	0.4336
chr5	180915260	3447818	0.0191	0.1886
chr6	171115067	10961729	0.0641	0.645
chr7	159138663	19240153	0.1209	1.4699

chr8	146364022	10843331	0.0741	0.6613
chr9	141213431	14845982	0.1051	0.7548
chr10	135534747	3643874	0.0269	0.5812
chr11	135006516	4667095	0.0346	0.4867
chr12	133851895	9119091	0.0681	0.3718
chr13	115169878	6598641	0.0573	0.312
chr14	107349540	15590544	0.1452	0.5888
chr15	102531392	1686328	0.0164	0.186
chr16	90354753	11050487	0.1223	0.558
chr17	81195210	4500784	0.0554	0.347
chr18	78077248	4318926	0.0553	1.4297
chr19	59128983	1848226	0.0313	0.7529
chr20	63025520	2603573	0.0413	0.3017
chr21	48129895	4792505	0.0996	0.5039
chr22	51304566	729357	0.0142	0.1517
chrMT	16571	83475	5.0374	3.4785
chrX	155270560	10662520	0.0687	0.5071
chrY	59373566	395594	0.0067	0.3127

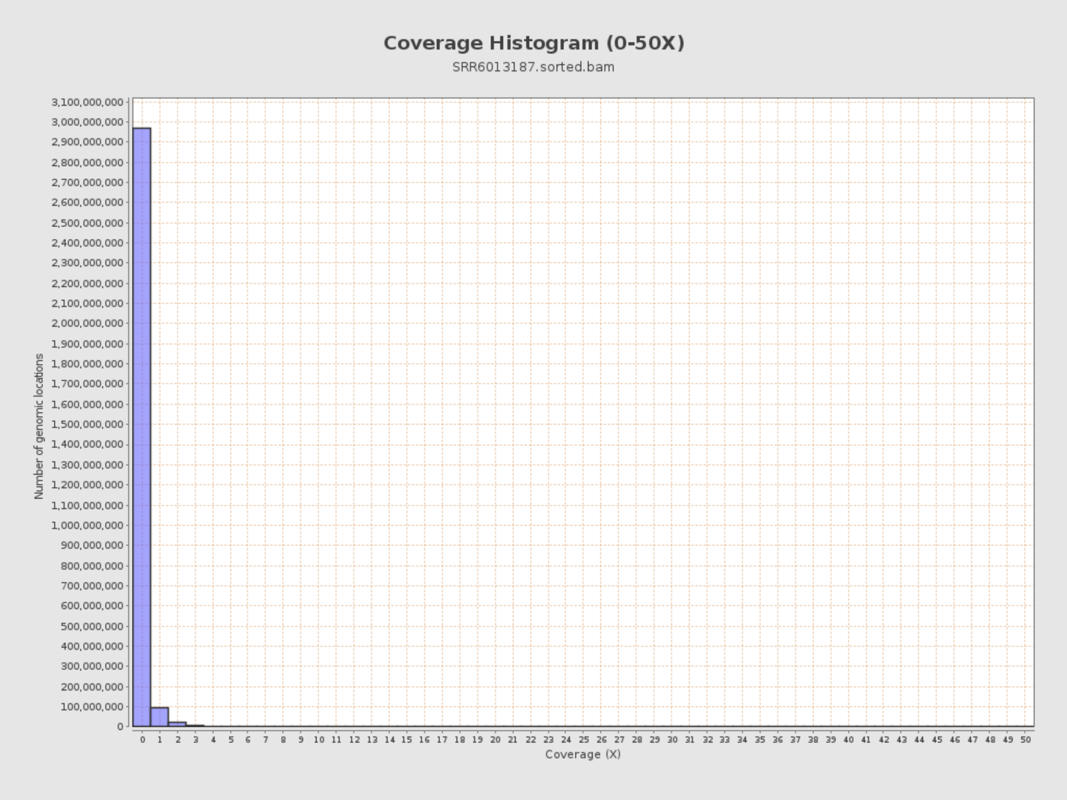
3. Results : Coverage across reference



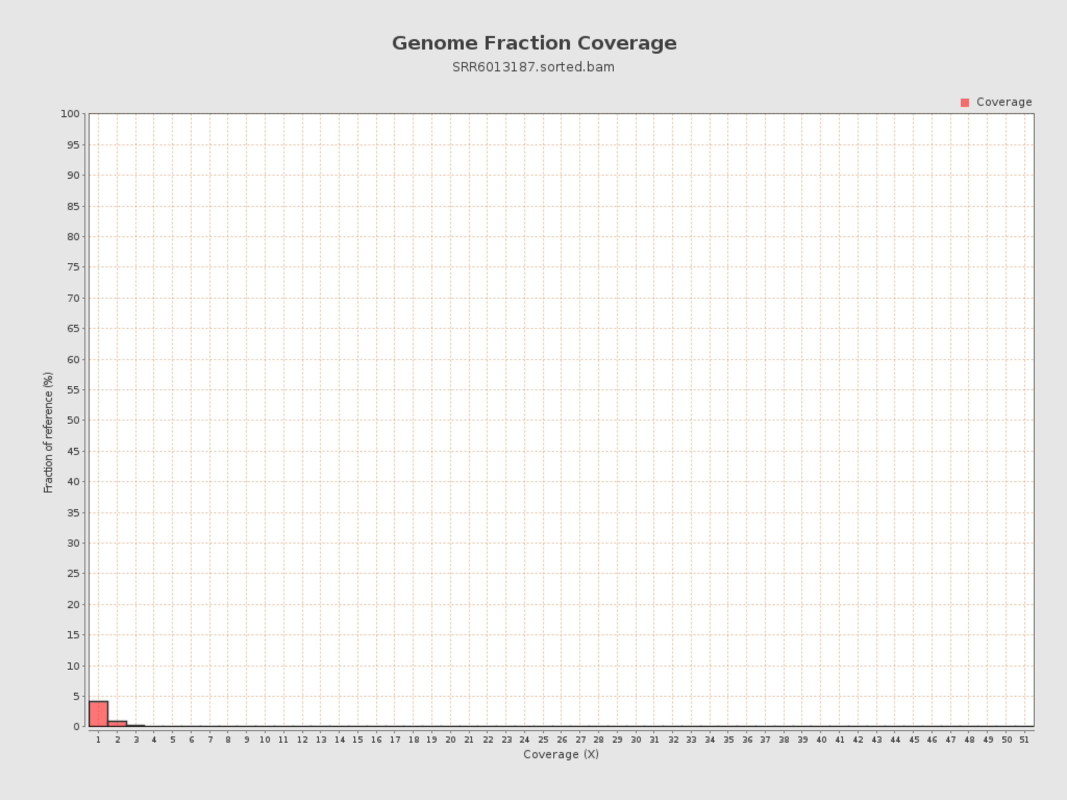
4. Results : Coverage Histogram



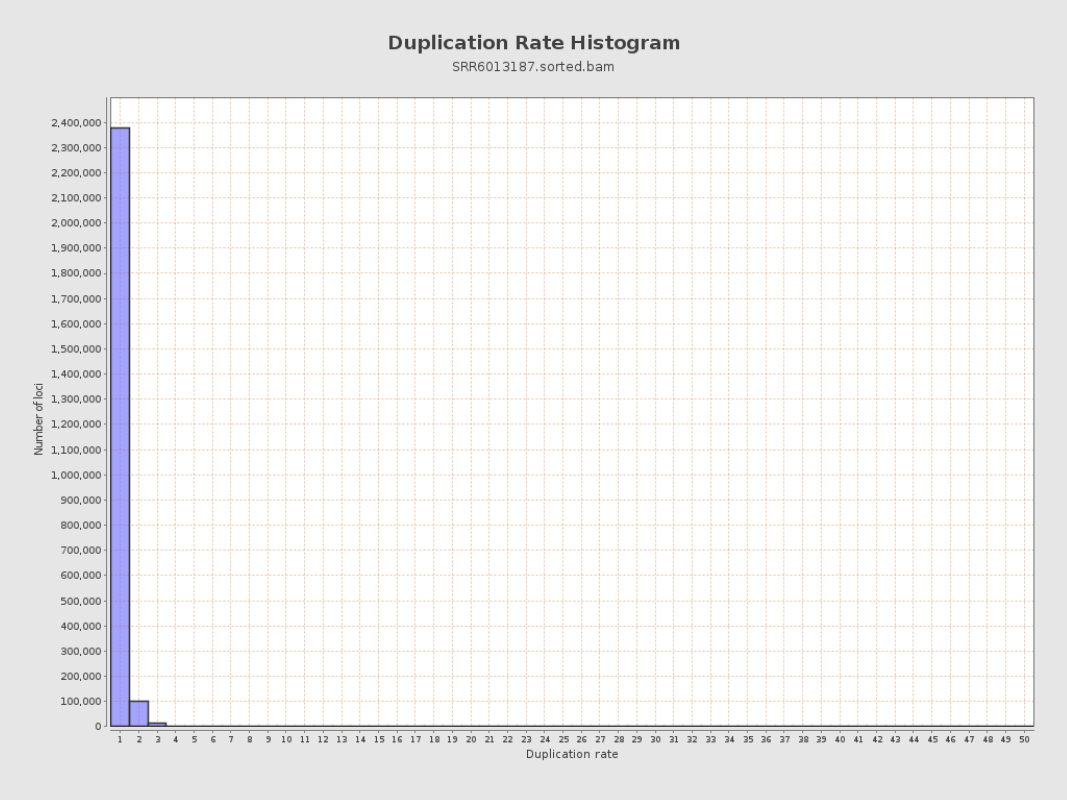
5. Results : Coverage Histogram (0-50X)



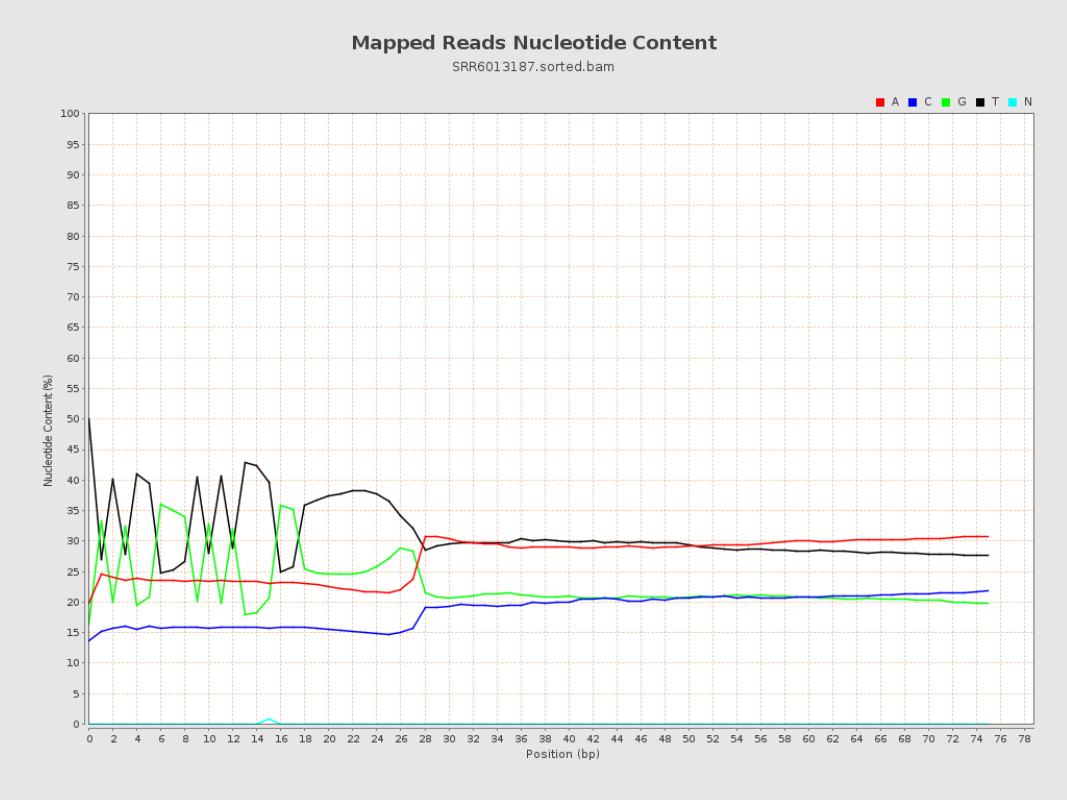
6. Results : Genome Fraction Coverage



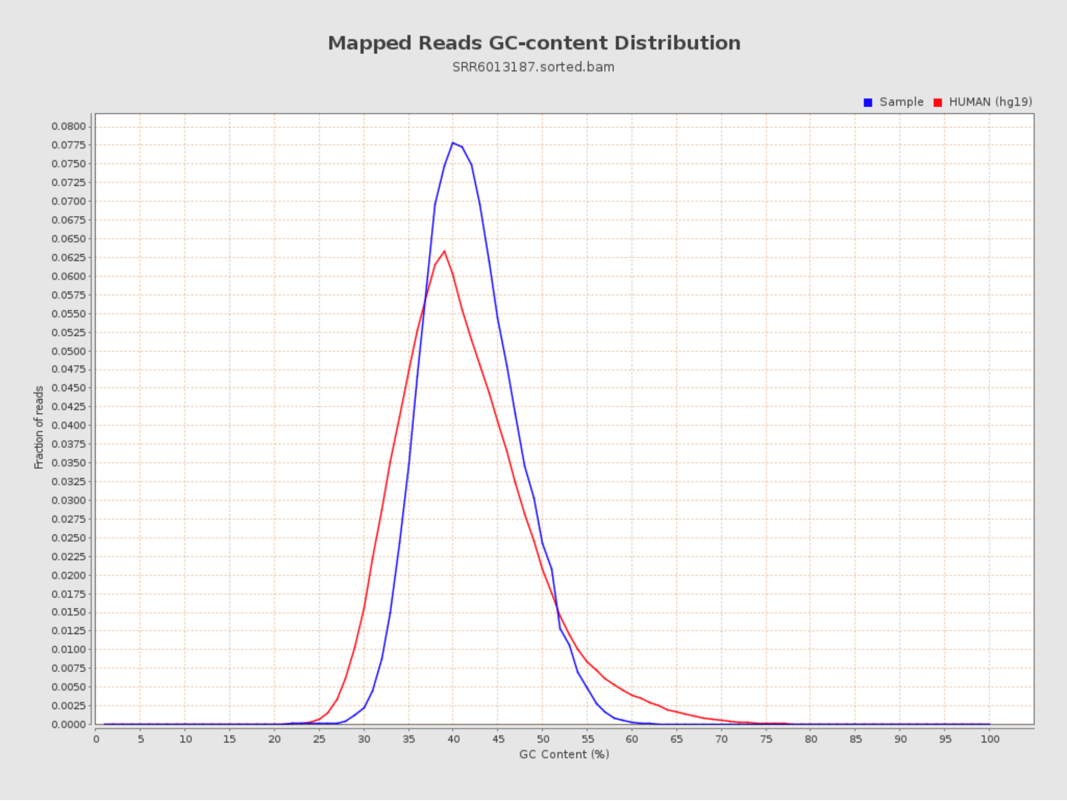
7. Results : Duplication Rate Histogram



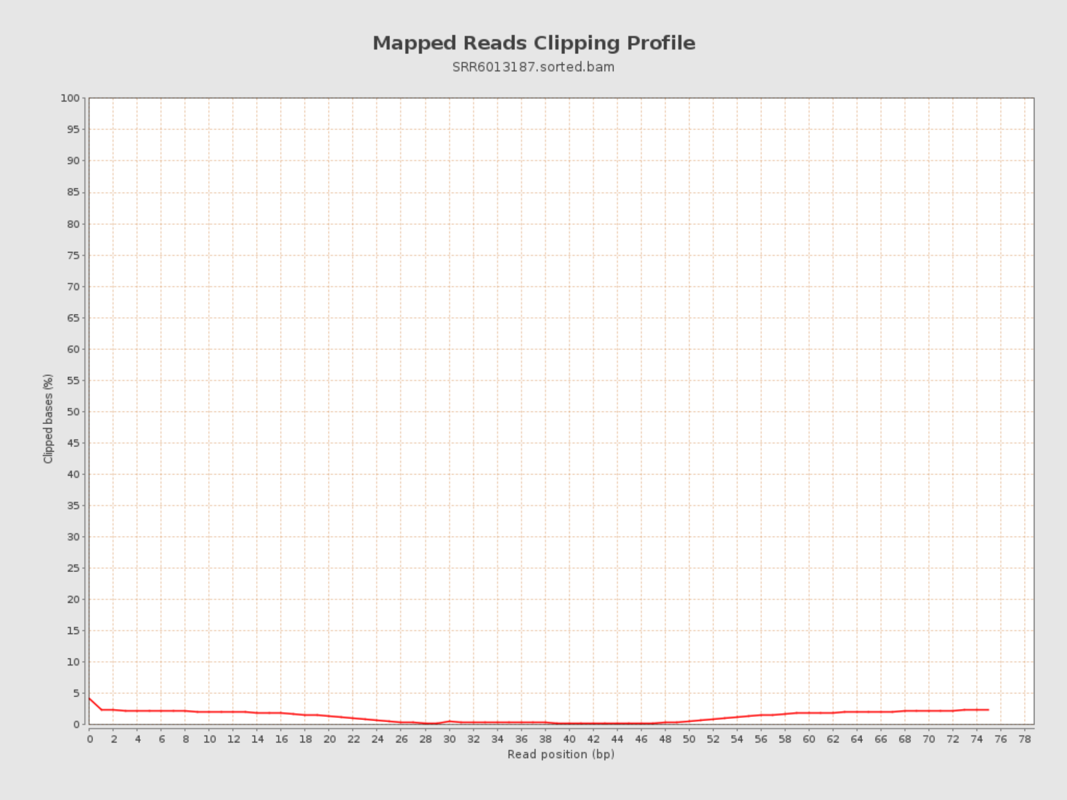
8. Results : Mapped Reads Nucleotide Content



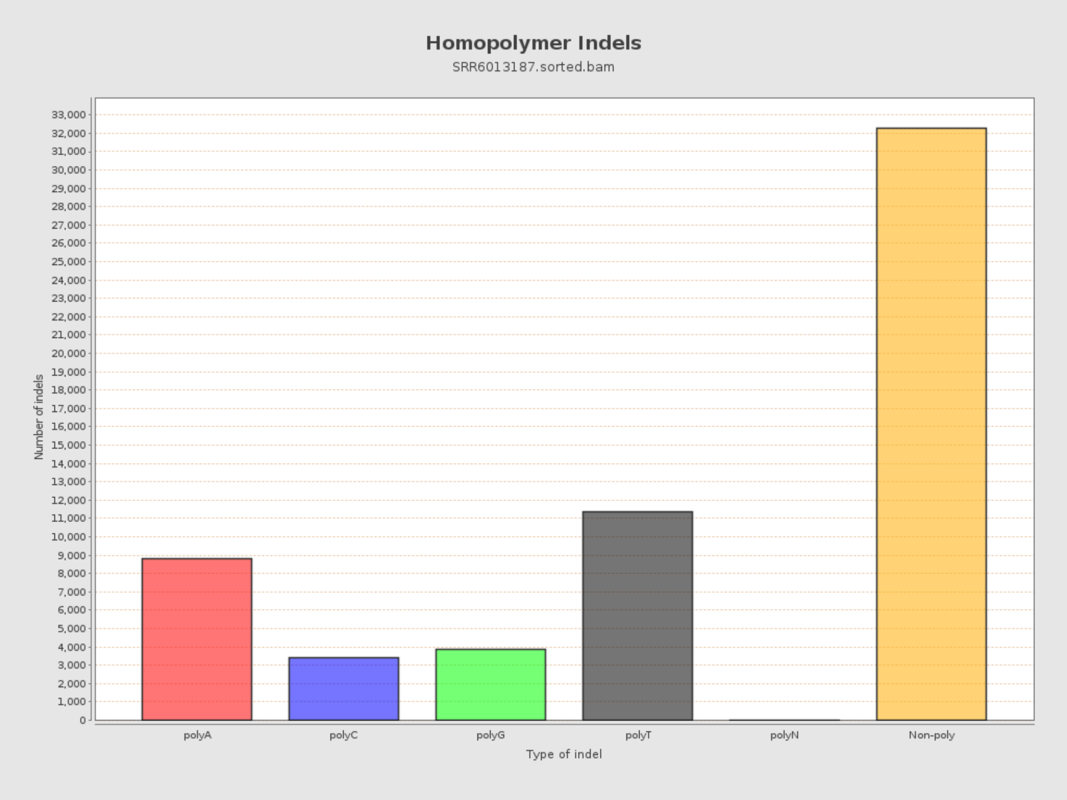
9. Results : Mapped Reads GC-content Distribution



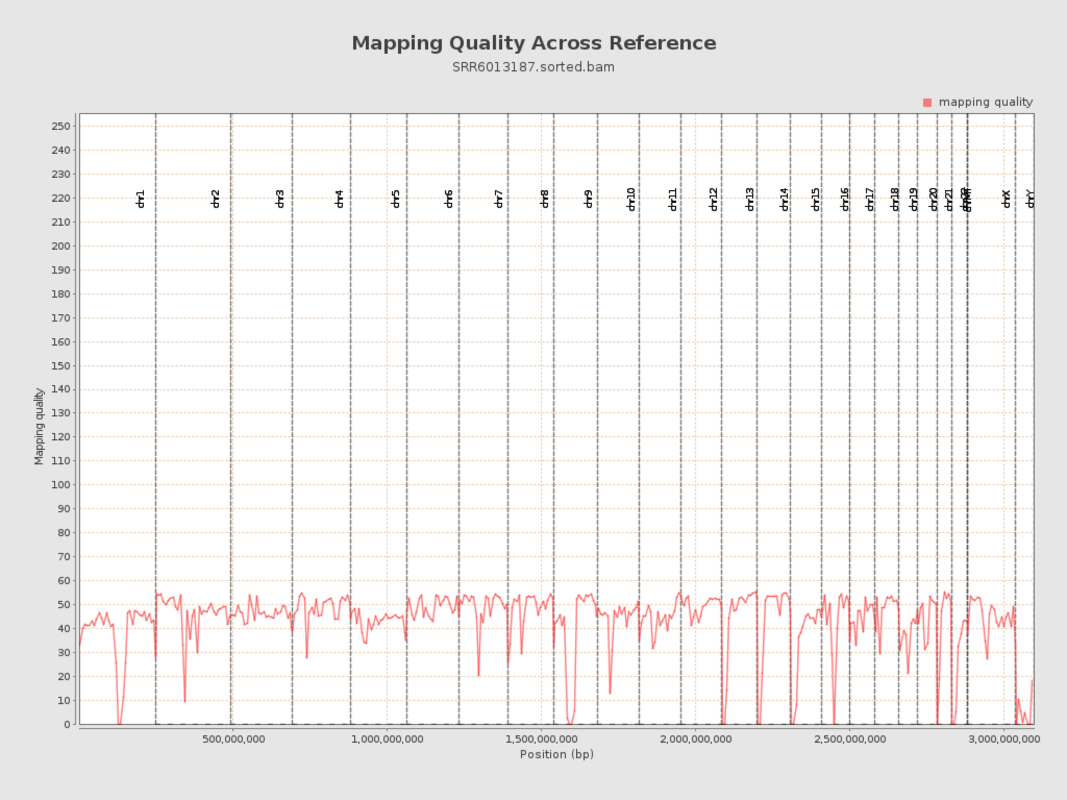
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram