Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:25:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068123.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_SRR6068123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:25:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,416,228
Mapped reads	3,134,303 / 91.75%
Unmapped reads	281,925 / 8.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,118 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	889,877 / 26.05%
Duplication rate	20.49%
Clipped reads	2,060,613 / 60.32%

2.2. ACGT Content

Number/percentage of A's	49,436,688 / 25.59%
Number/percentage of C's	33,276,187 / 17.23%
Number/percentage of T's	64,407,936 / 33.34%
Number/percentage of G's	46,036,769 / 23.83%
Number/percentage of N's	20,516 / 0.01%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0624

Standard Deviation	0.5887

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

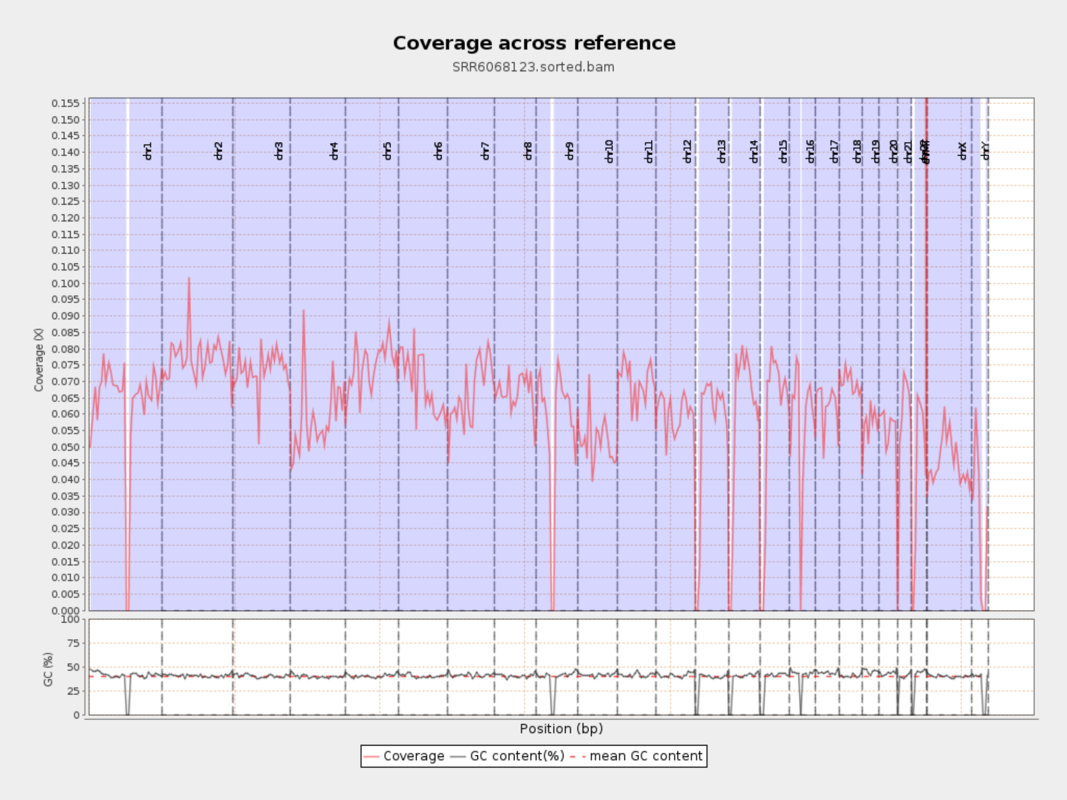
General error rate	0.65%
Mismatches	1,234,811
Insertions	12,737
Mapped reads with at least one insertion	0.4%
Deletions	52,323
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.43%

2.6. Chromosome stats

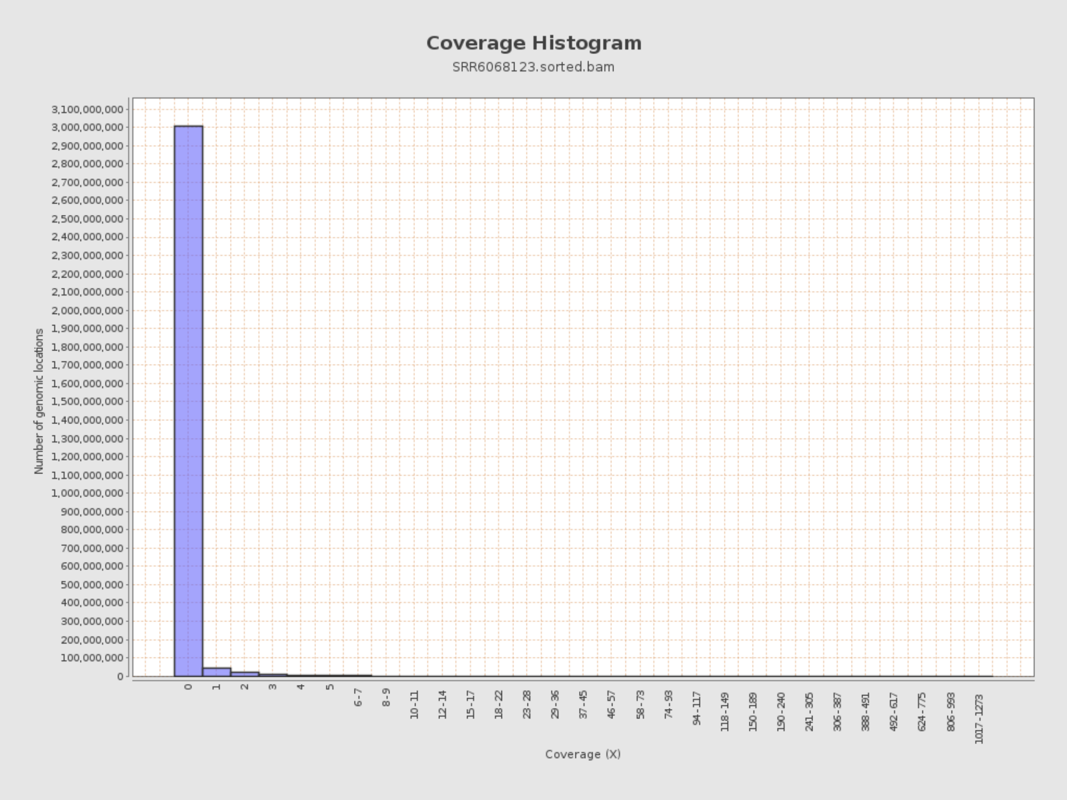
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15690072	0.0629	0.7185
chr2	243199373	18795117	0.0773	0.8421
chr3	198022430	14581672	0.0736	0.515
chr4	191154276	11159546	0.0584	0.4971
chr5	180915260	13592780	0.0751	0.5228
chr6	171115067	11793399	0.0689	0.5401
chr7	159138663	10640312	0.0669	0.625

chr8	146364022	9764368	0.0667	0.8101
chr9	141213431	7983830	0.0565	0.5196
chr10	135534747	6979688	0.0515	0.5065
chr11	135006516	9399032	0.0696	0.5881
chr12	133851895	8062343	0.0602	0.4702
chr13	115169878	6210461	0.0539	0.4469
chr14	107349540	6336149	0.059	0.4711
chr15	102531392	5858218	0.0571	0.4814
chr16	90354753	5203694	0.0576	0.4627
chr17	81195210	5060285	0.0623	0.4938
chr18	78077248	5441497	0.0697	0.8357
chr19	59128983	3375576	0.0571	0.5797
chr20	63025520	3518117	0.0558	0.4628
chr21	48129895	2737529	0.0569	0.4818
chr22	51304566	2087250	0.0407	0.3857
chrMT	16571	394163	23.7863	16.6828
chrX	155270560	7060438	0.0455	0.4263
chrY	59373566	1545253	0.026	0.3238

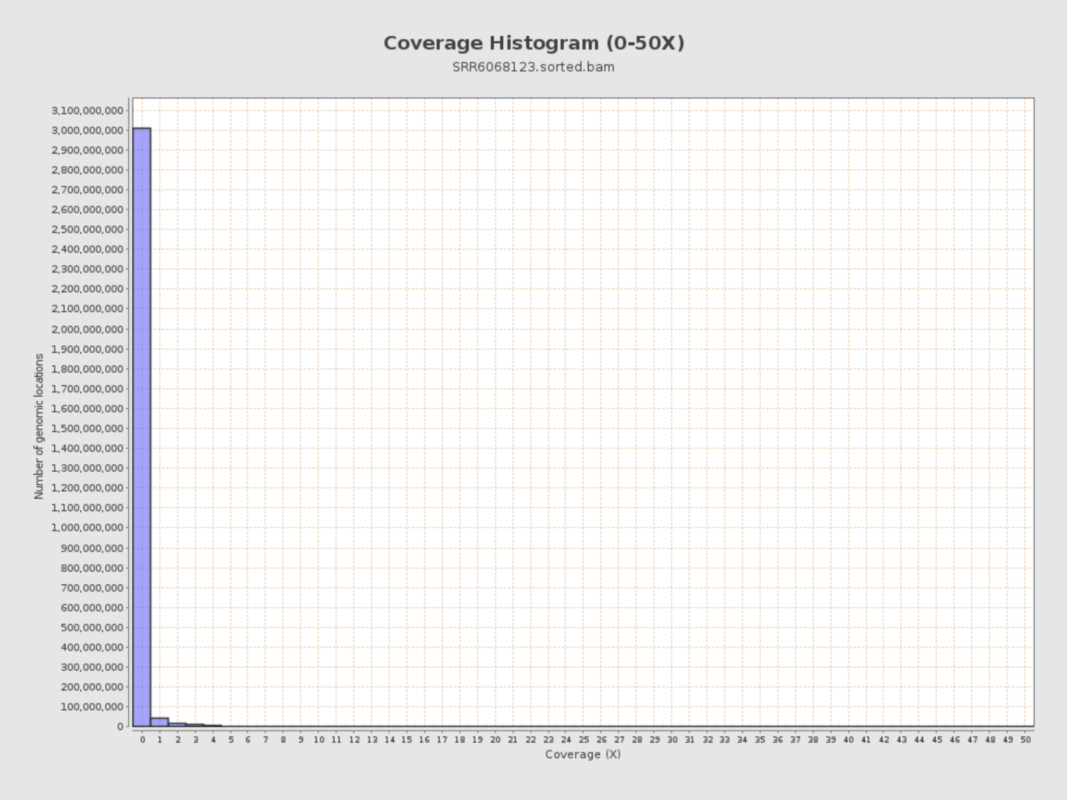
3. Results : Coverage across reference



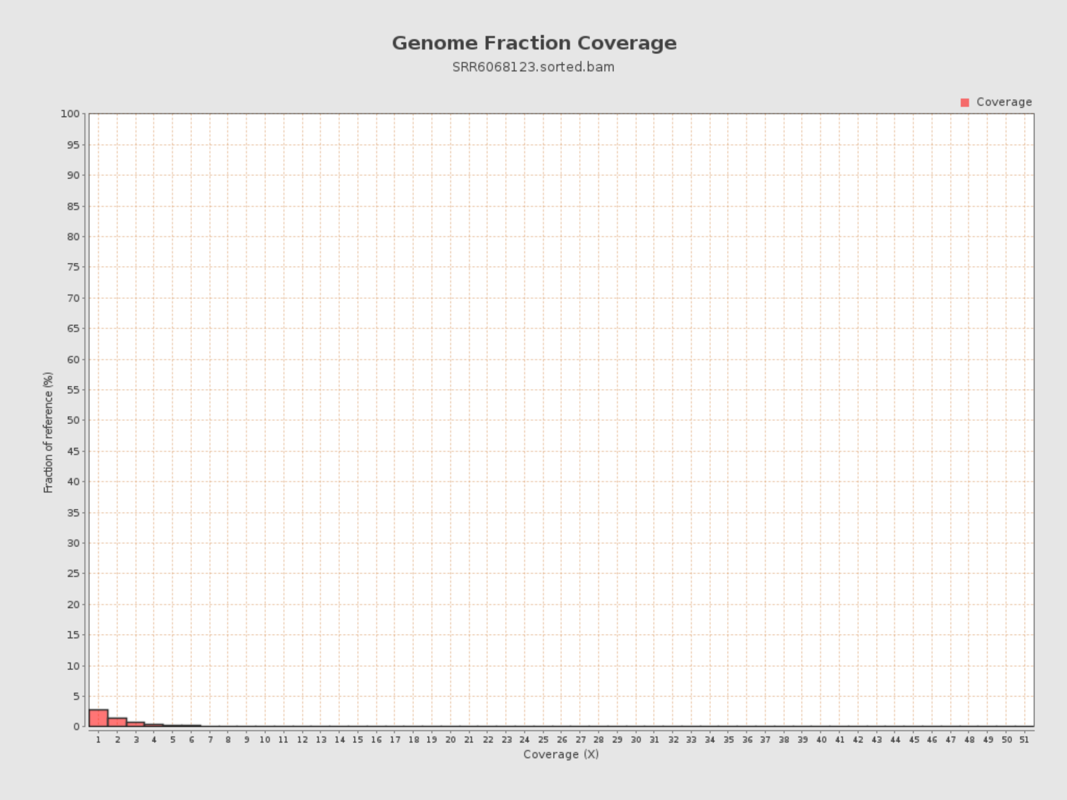
4. Results : Coverage Histogram



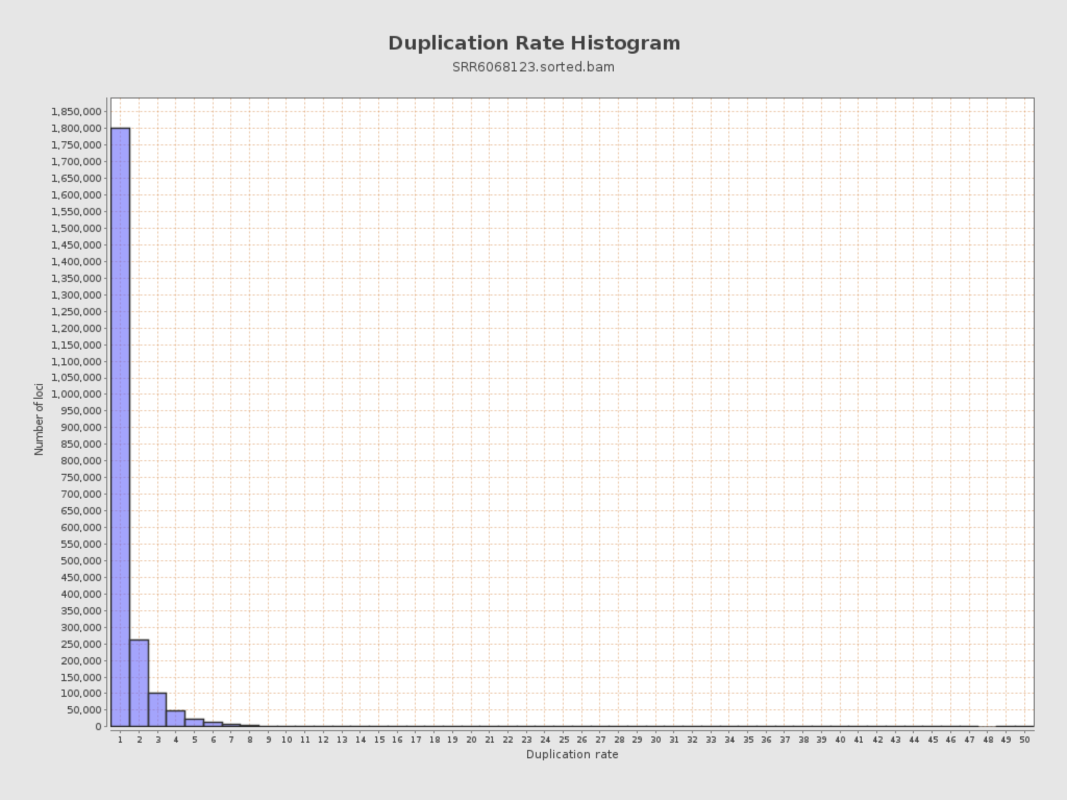
5. Results : Coverage Histogram (0-50X)



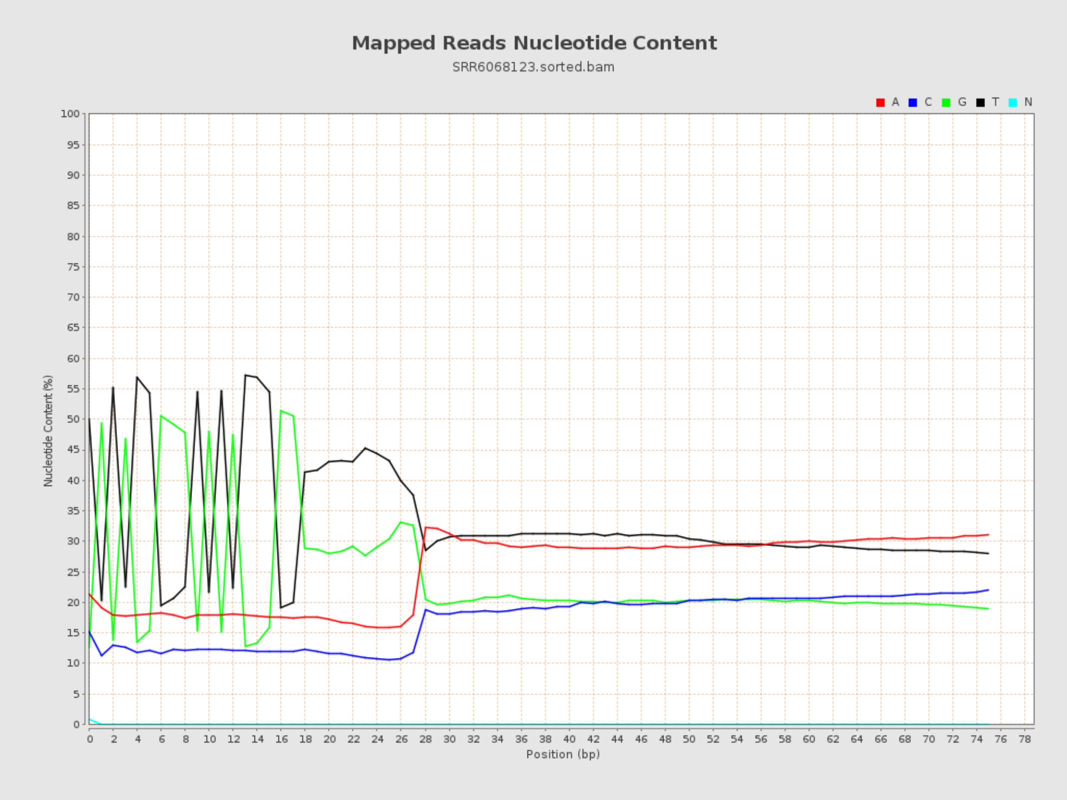
6. Results : Genome Fraction Coverage



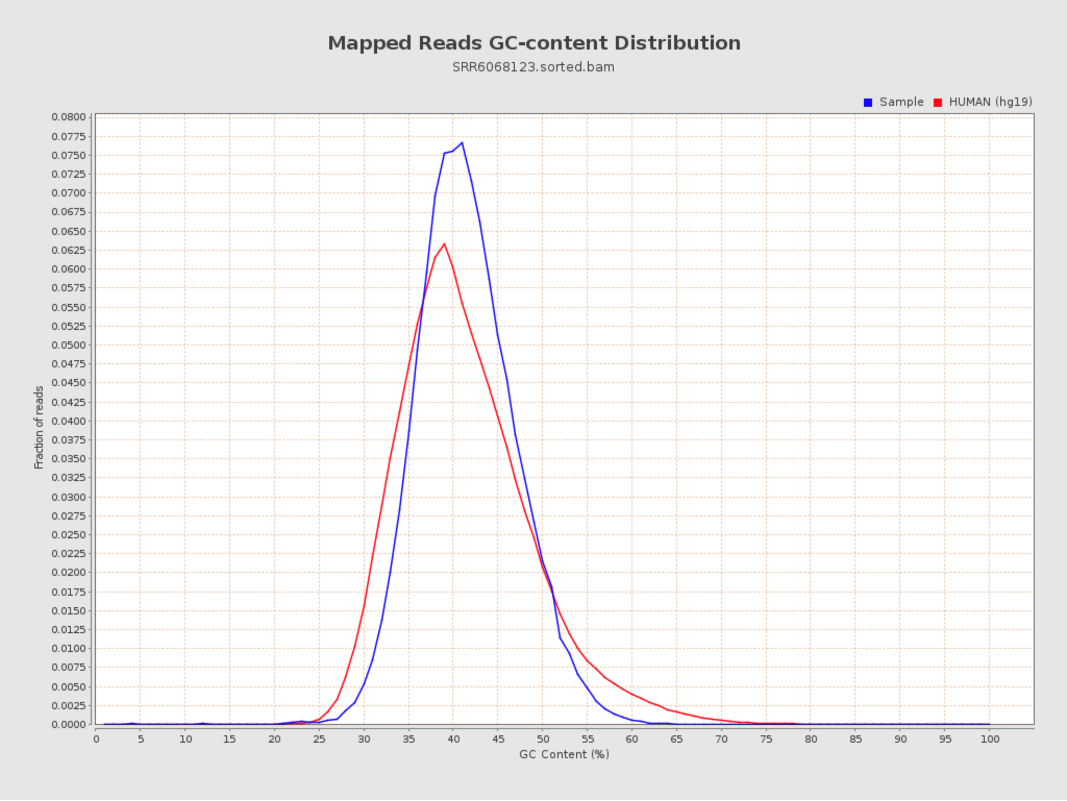
7. Results : Duplication Rate Histogram



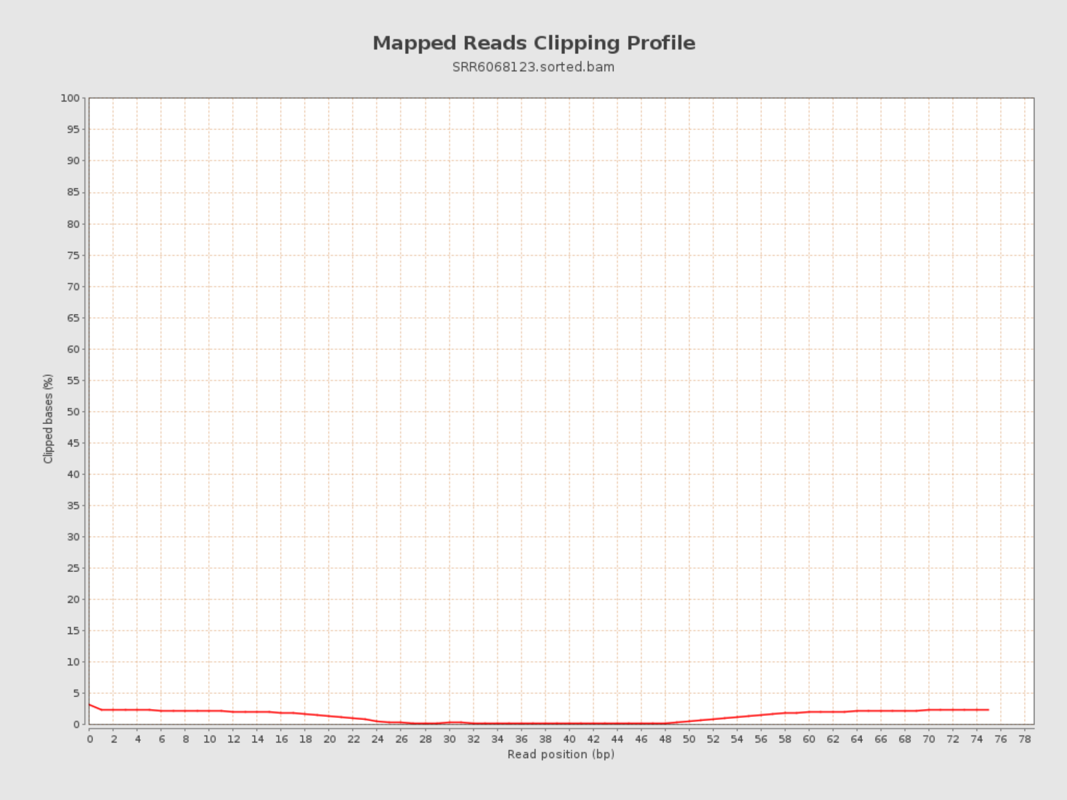
8. Results : Mapped Reads Nucleotide Content



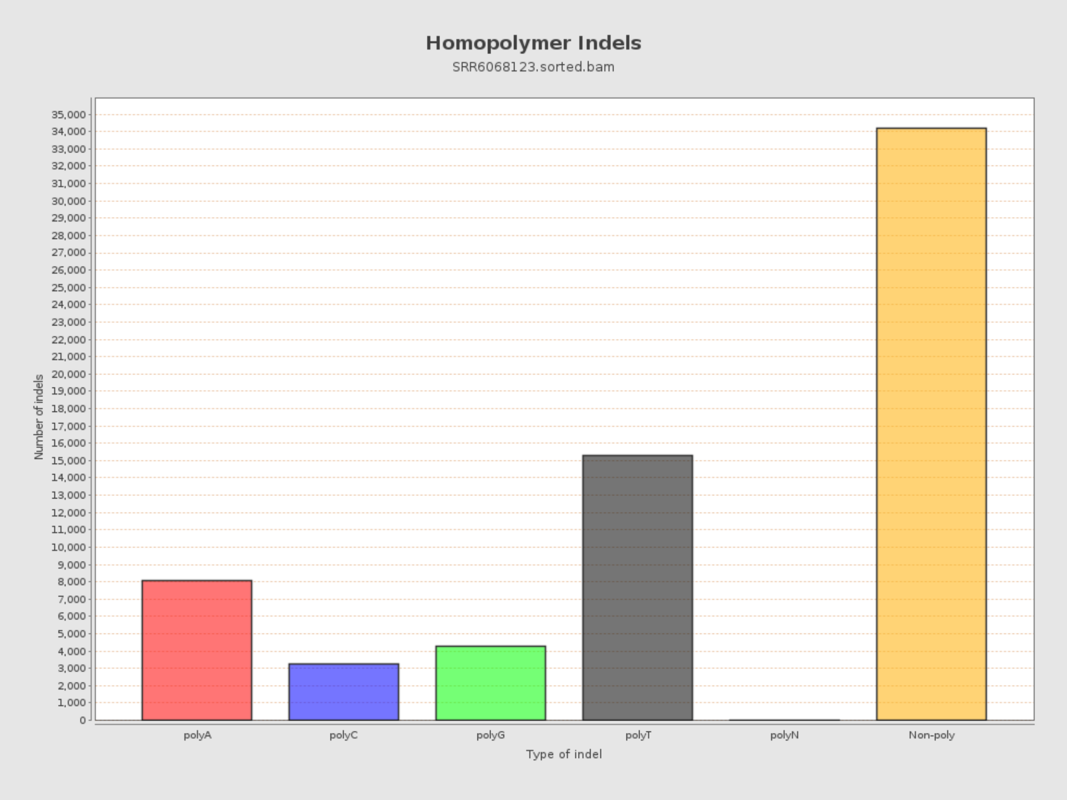
9. Results : Mapped Reads GC-content Distribution



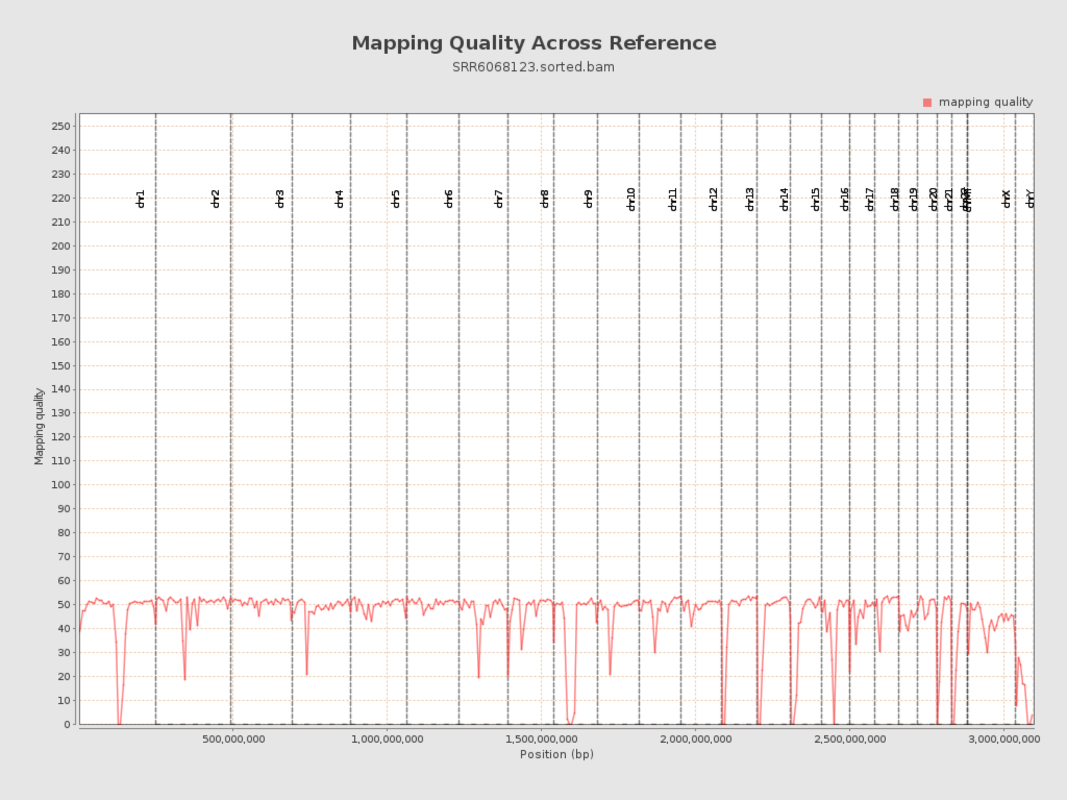
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram