Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:15:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068087.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_SRR6068087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:15:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,475,890
Mapped reads	4,199,435 / 93.82%
Unmapped reads	276,455 / 6.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,911 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	775,886 / 17.33%
Duplication rate	14.67%
Clipped reads	2,247,043 / 50.2%

2.2. ACGT Content

Number/percentage of A's	70,339,702 / 26.11%
Number/percentage of C's	47,675,830 / 17.7%
Number/percentage of T's	88,982,980 / 33.03%
Number/percentage of G's	62,344,771 / 23.14%
Number/percentage of N's	30,808 / 0.01%
GC Percentage	40.84%

2.3. Coverage

Mean	0.087

Standard Deviation	1.0522

2.4. Mapping Quality

Mean Mapping Quality	40.99

2.5. Mismatches and indels

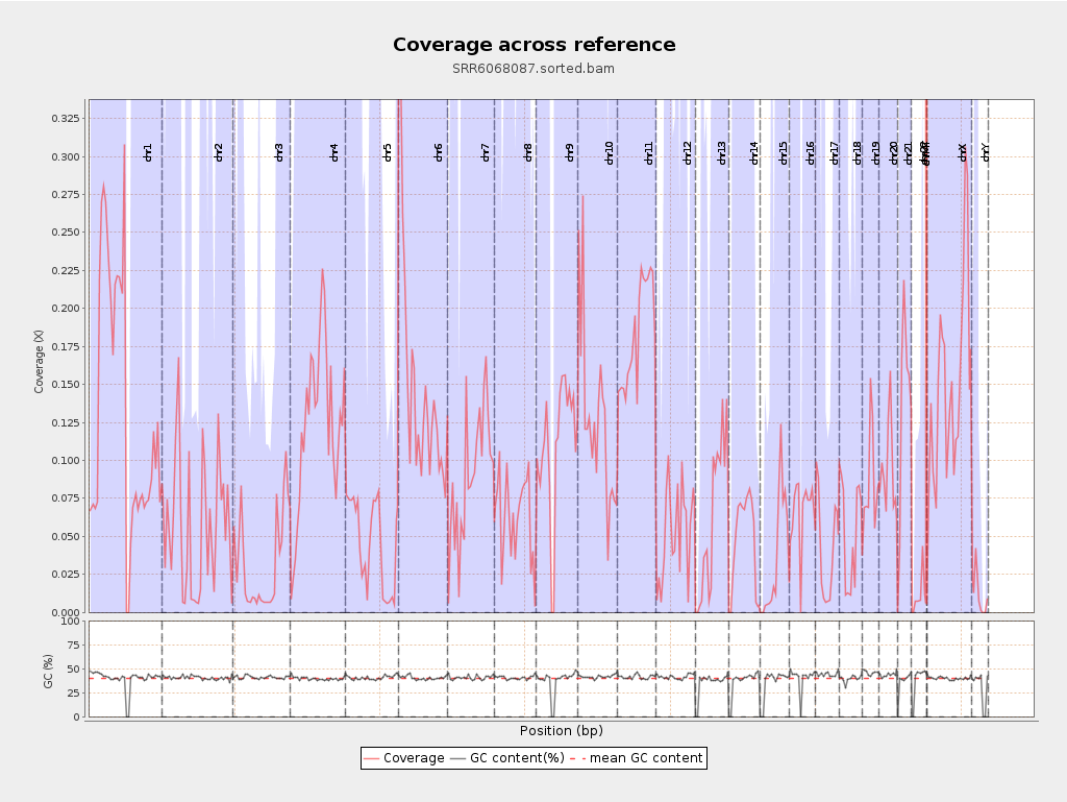
General error rate	0.55%
Mismatches	1,456,988
Insertions	18,152
Mapped reads with at least one insertion	0.43%
Deletions	58,104
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.85%

2.6. Chromosome stats

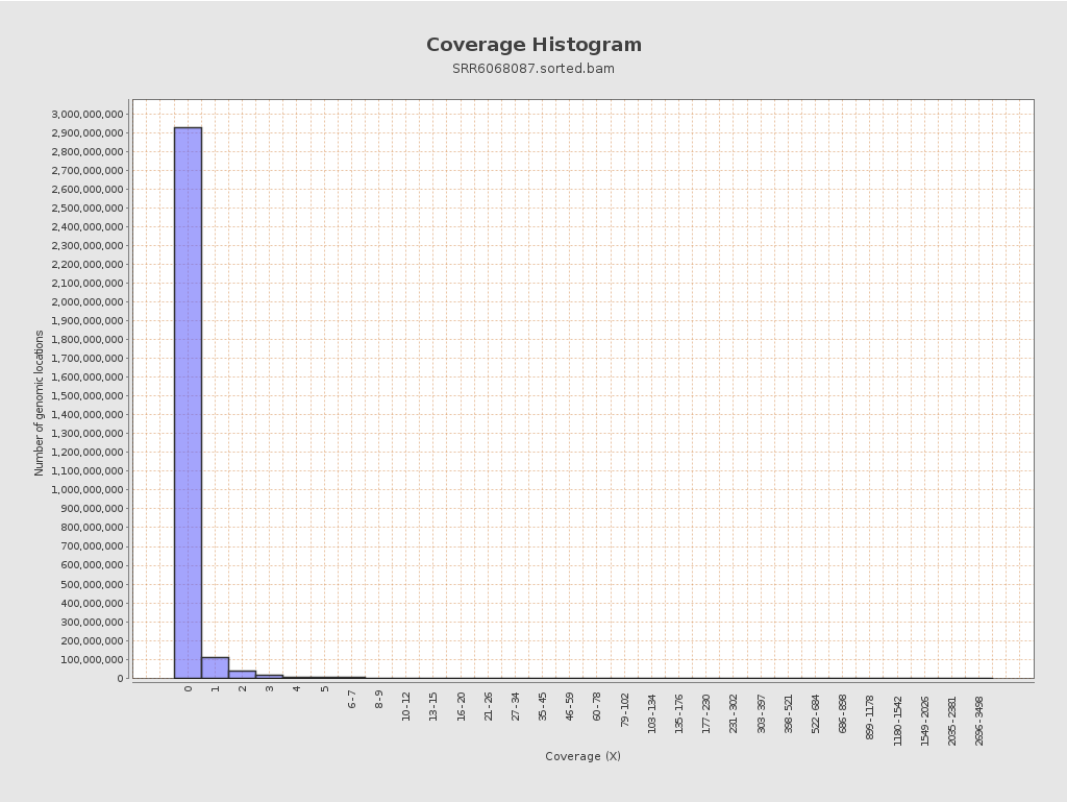
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	32846686	0.1318	2.3481
chr2	243199373	13540152	0.0557	1.6807
chr3	198022430	6443501	0.0325	0.2827
chr4	191154276	23590663	0.1234	0.6009
chr5	180915260	8176053	0.0452	0.3358
chr6	171115067	25333835	0.1481	0.735
chr7	159138663	14505620	0.0912	1.1555

chr8	146364022	9148143	0.0625	0.8906
chr9	141213431	15416480	0.1092	0.8192
chr10	135534747	17317959	0.1278	0.7478
chr11	135006516	24485667	0.1814	1.0639
chr12	133851895	7179709	0.0536	0.4339
chr13	115169878	7060818	0.0613	0.423
chr14	107349540	5122221	0.0477	0.4329
chr15	102531392	3719357	0.0363	0.3372
chr16	90354753	6040704	0.0669	0.466
chr17	81195210	3291963	0.0405	0.4573
chr18	78077248	4056201	0.052	1.3437
chr19	59128983	5154014	0.0872	1.3611
chr20	63025520	5940379	0.0943	0.5031
chr21	48129895	6433217	0.1337	0.5961
chr22	51304566	615679	0.012	0.1516
chrMT	16571	503721	30.3977	19.2189
chrX	155270560	22883652	0.1474	0.703
chrY	59373566	668151	0.0113	0.4657

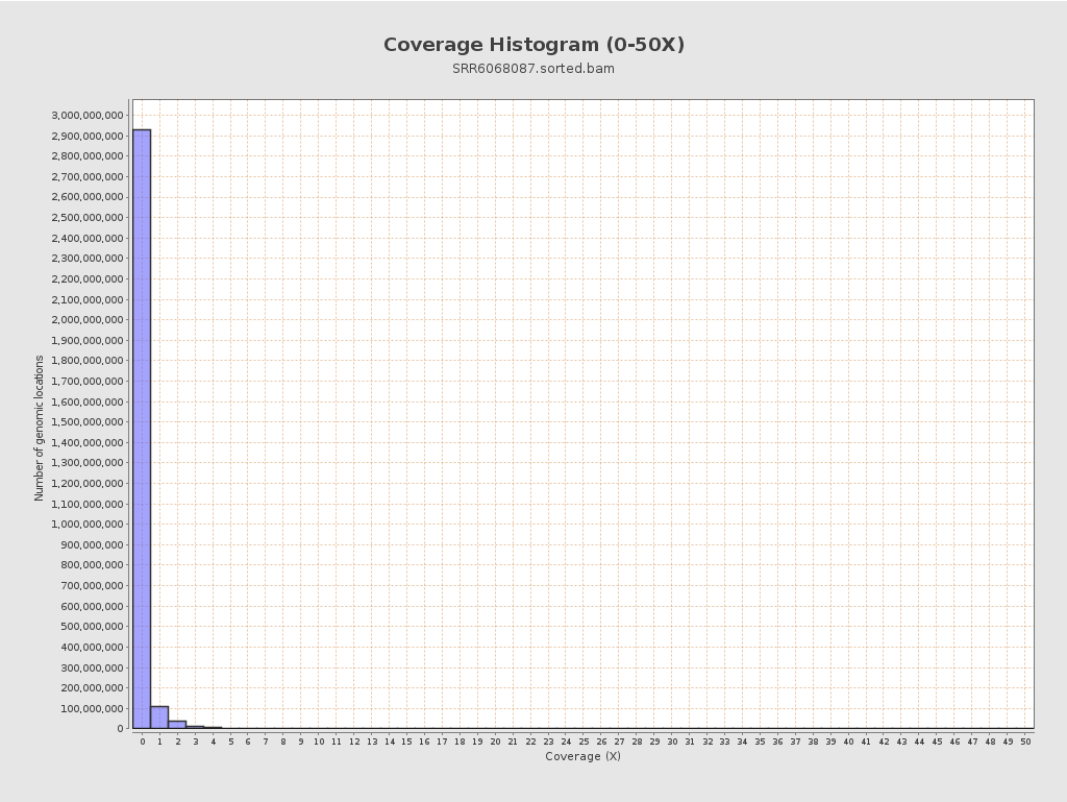
3. Results : Coverage across reference



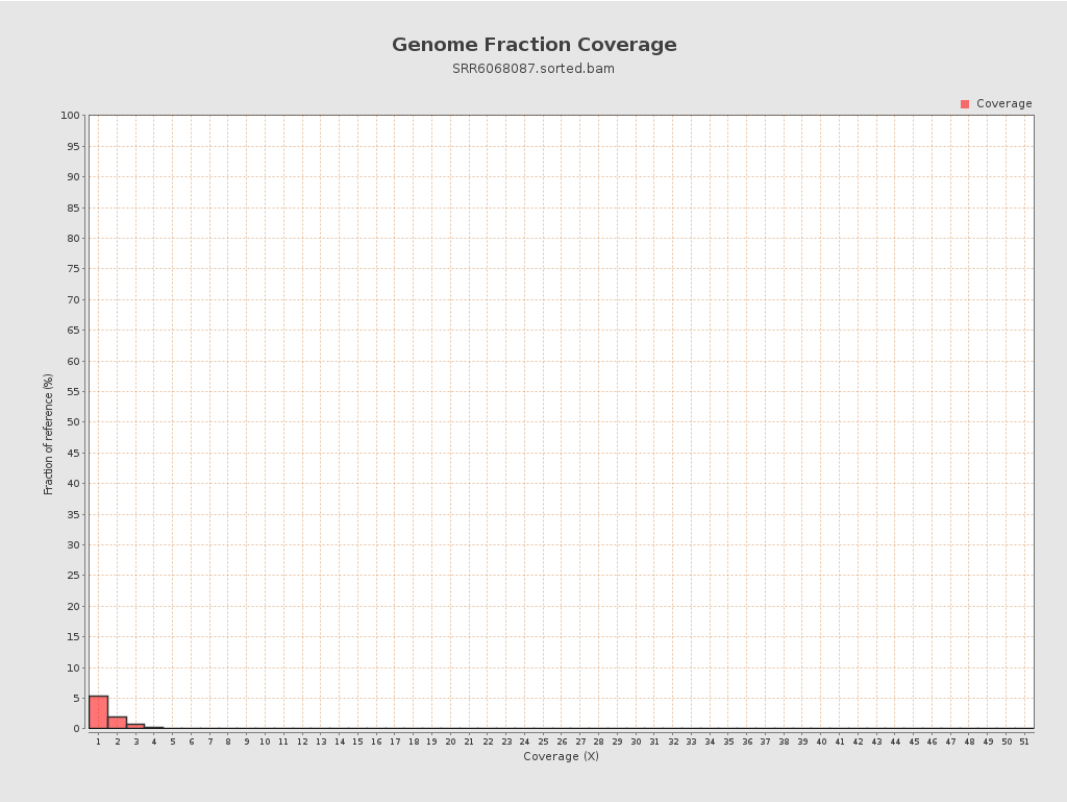
4. Results : Coverage Histogram



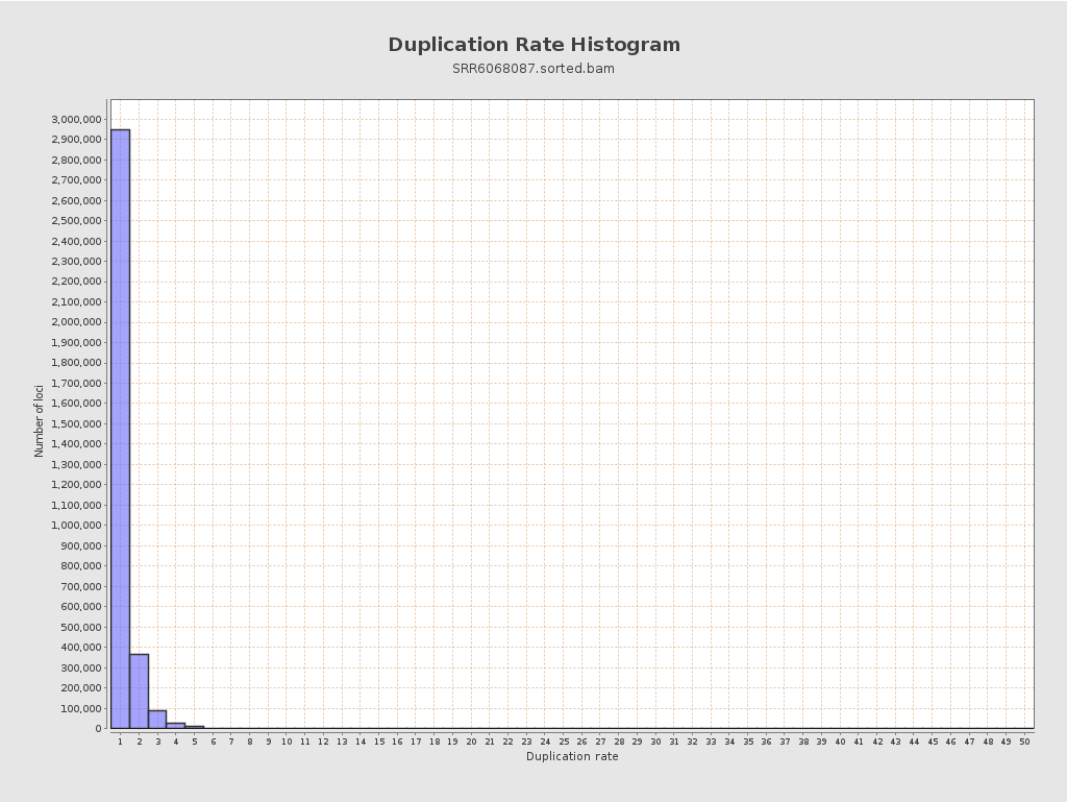
5. Results : Coverage Histogram (0-50X)



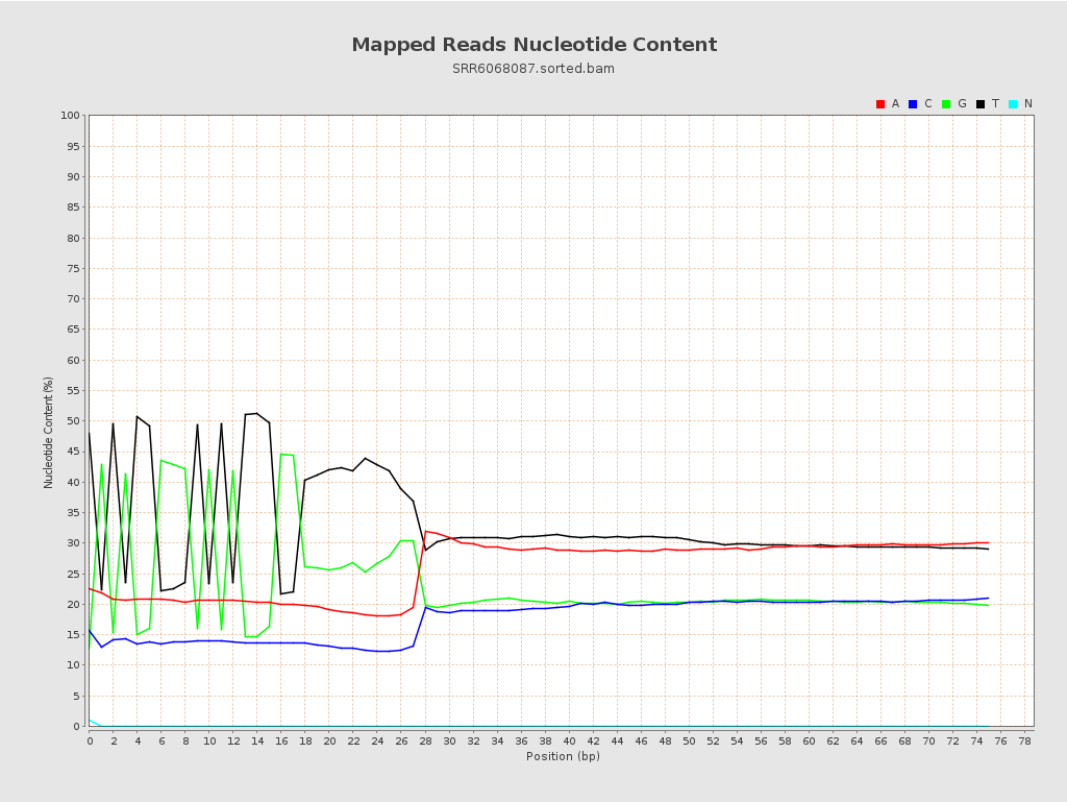
6. Results : Genome Fraction Coverage



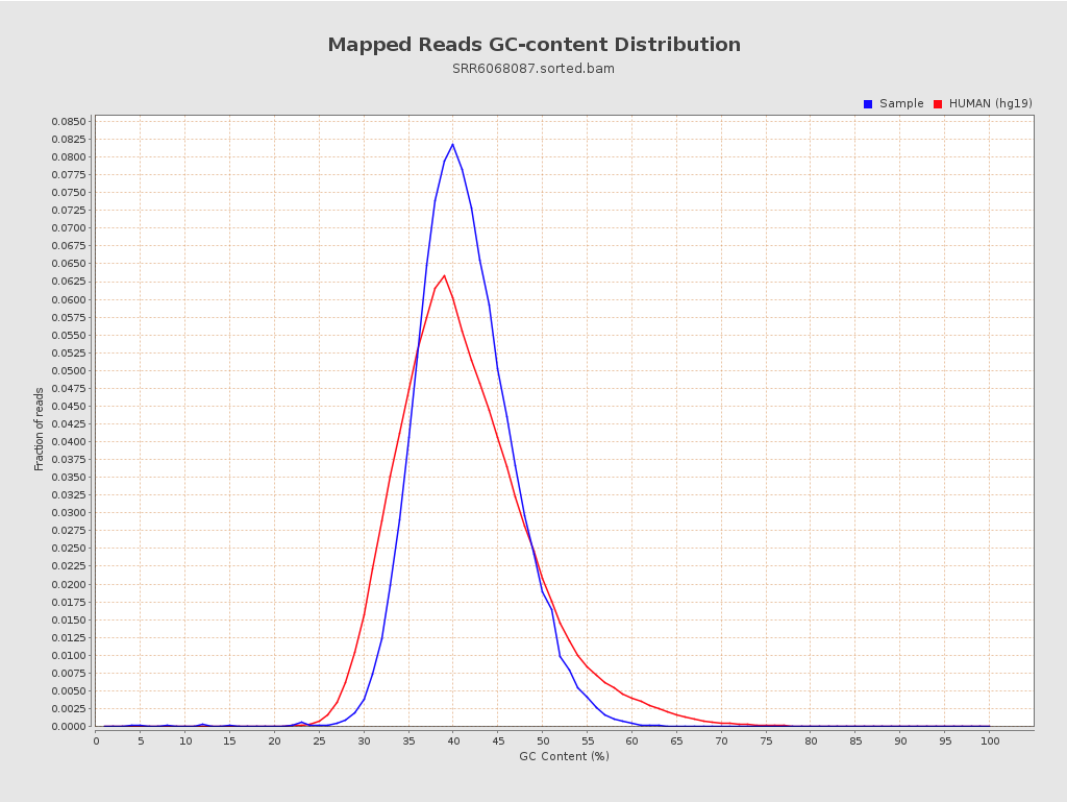
7. Results : Duplication Rate Histogram



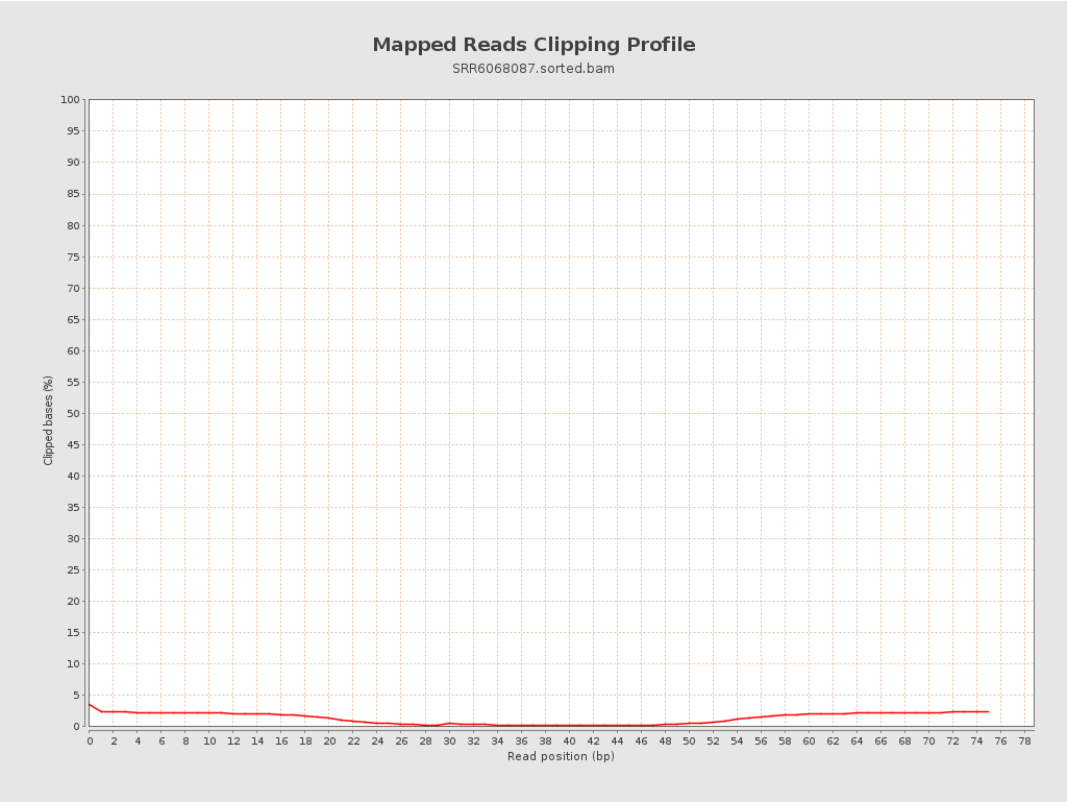
8. Results : Mapped Reads Nucleotide Content



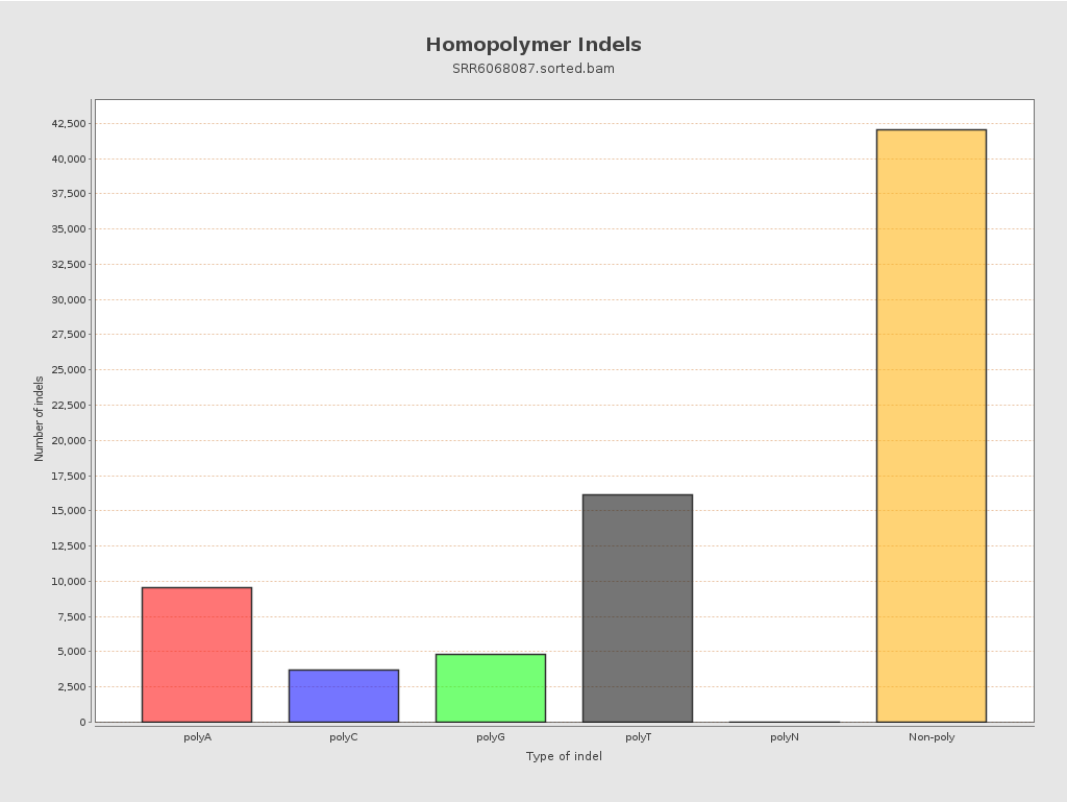
9. Results : Mapped Reads GC-content Distribution



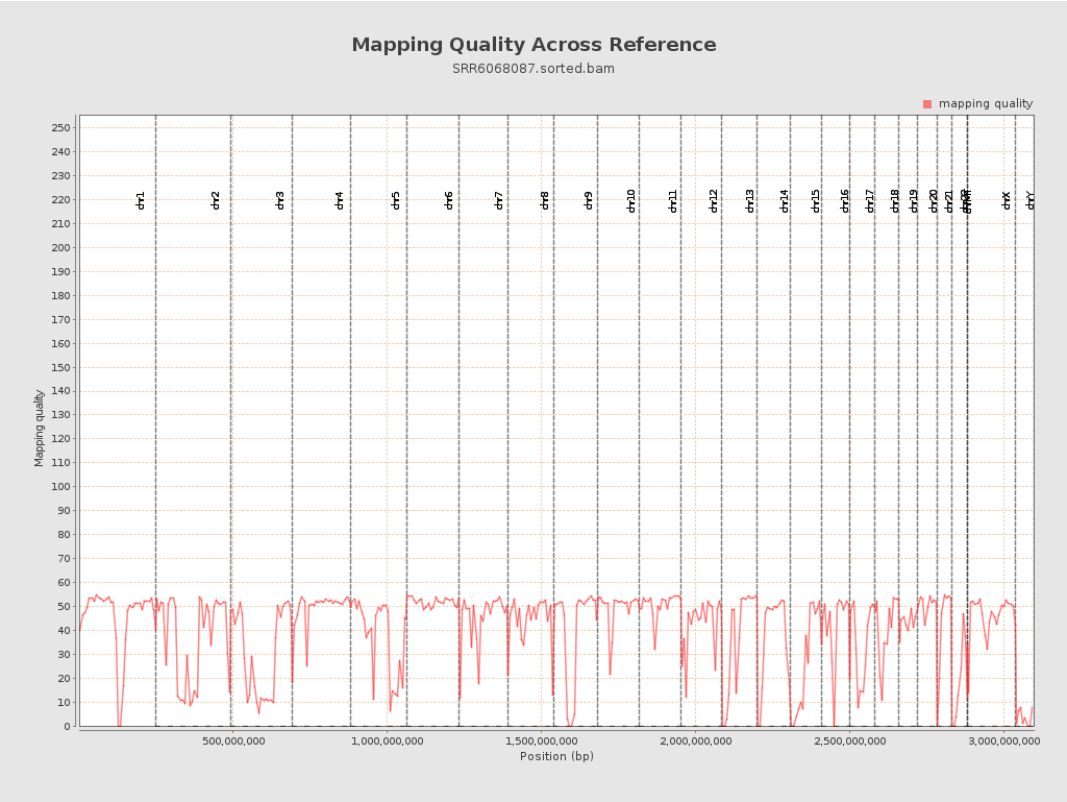
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram