Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:29:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068090.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_SRR6068090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:29:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,739,484
Mapped reads	2,586,038 / 69.15%
Unmapped reads	1,153,446 / 30.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,673 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	974,735 / 26.07%
Duplication rate	20.54%
Clipped reads	1,520,915 / 40.67%

2.2. ACGT Content

Number/percentage of A's	41,140,487 / 25.31%
Number/percentage of C's	28,980,498 / 17.83%
Number/percentage of T's	53,618,879 / 32.99%
Number/percentage of G's	38,786,492 / 23.86%
Number/percentage of N's	17,255 / 0.01%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.7995

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

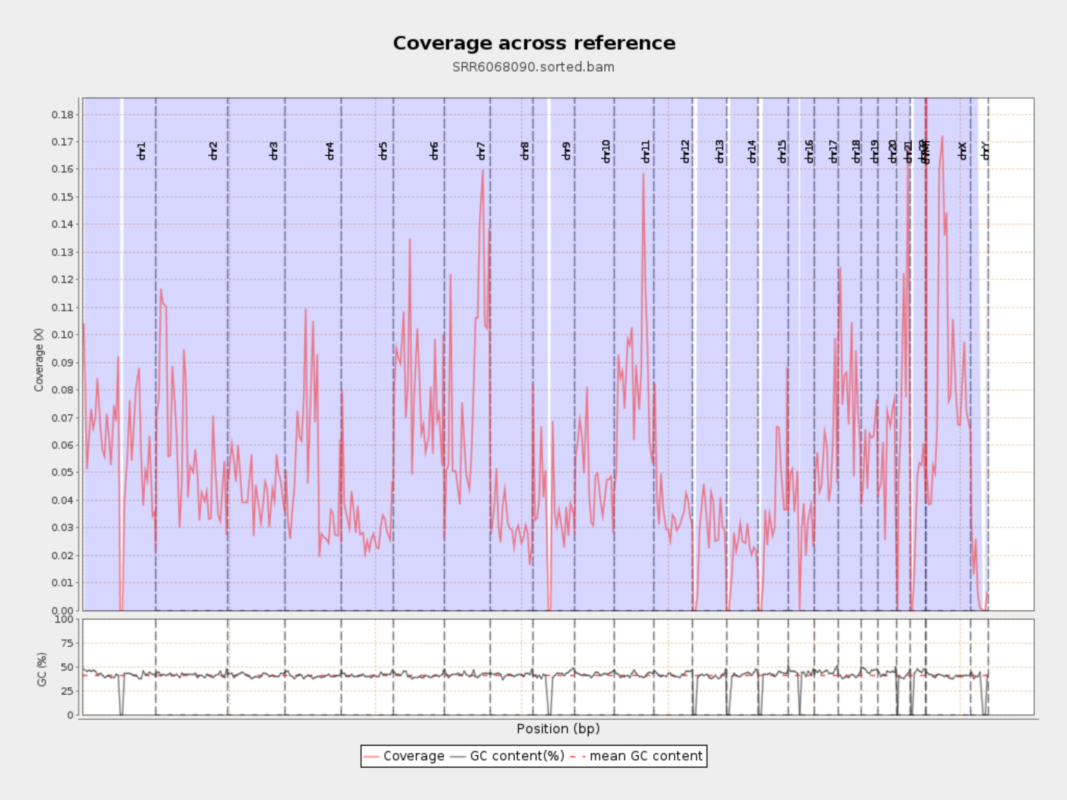
General error rate	0.61%
Mismatches	975,506
Insertions	10,825
Mapped reads with at least one insertion	0.41%
Deletions	44,701
Mapped reads with at least one deletion	1.71%
Homopolymer indels	44.93%

2.6. Chromosome stats

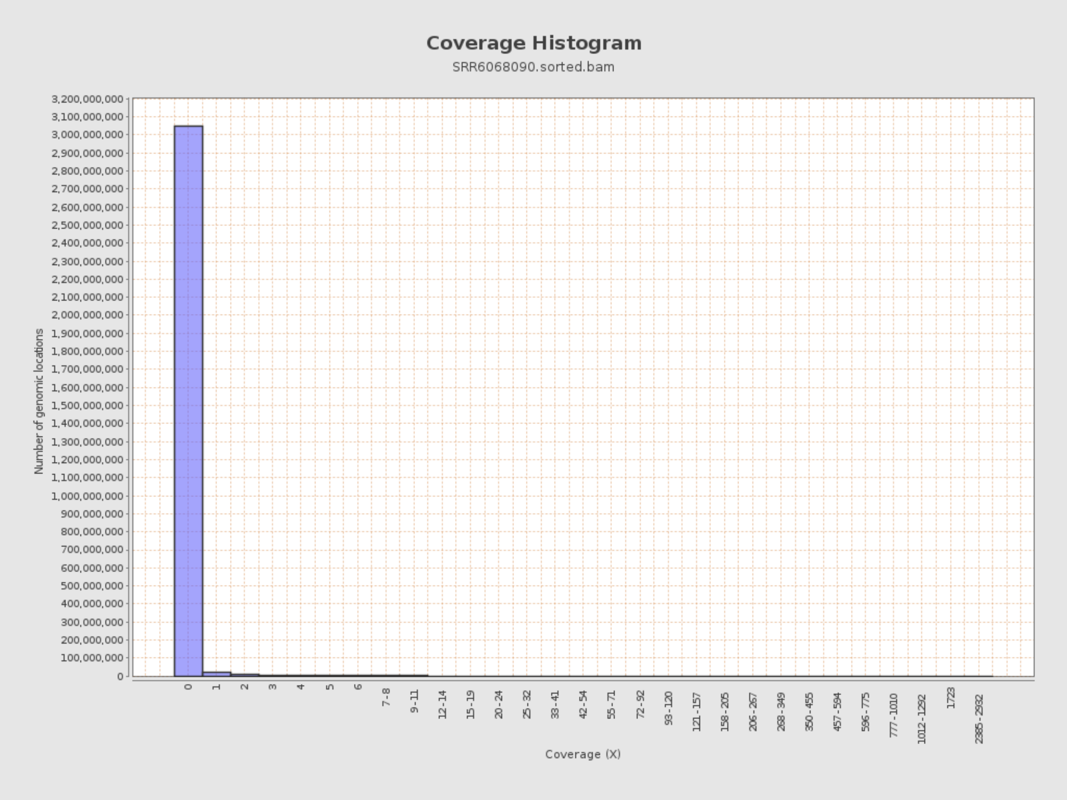
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14749640	0.0592	1.0043
chr2	243199373	14332835	0.0589	1.4759
chr3	198022430	8865338	0.0448	0.5902
chr4	191154276	9749903	0.051	0.5991
chr5	180915260	5931577	0.0328	0.501
chr6	171115067	13658741	0.0798	0.8827
chr7	159138663	12724368	0.08	0.83

chr8	146364022	4466528	0.0305	0.6245
chr9	141213431	4962656	0.0351	0.5566
chr10	135534747	6608222	0.0488	0.6629
chr11	135006516	11634701	0.0862	0.8552
chr12	133851895	4980110	0.0372	0.5471
chr13	115169878	3212203	0.0279	0.4871
chr14	107349540	2246379	0.0209	0.4001
chr15	102531392	3518299	0.0343	0.5107
chr16	90354753	3048124	0.0337	0.5218
chr17	81195210	4563201	0.0562	0.6628
chr18	78077248	6505929	0.0833	1.2856
chr19	59128983	3468165	0.0587	0.815
chr20	63025520	3621194	0.0575	0.6471
chr21	48129895	3990682	0.0829	0.7626
chr22	51304566	1858986	0.0362	0.5232
chrMT	16571	113722	6.8627	8.5772
chrX	155270560	13240694	0.0853	0.7863
chrY	59373566	569720	0.0096	0.2801

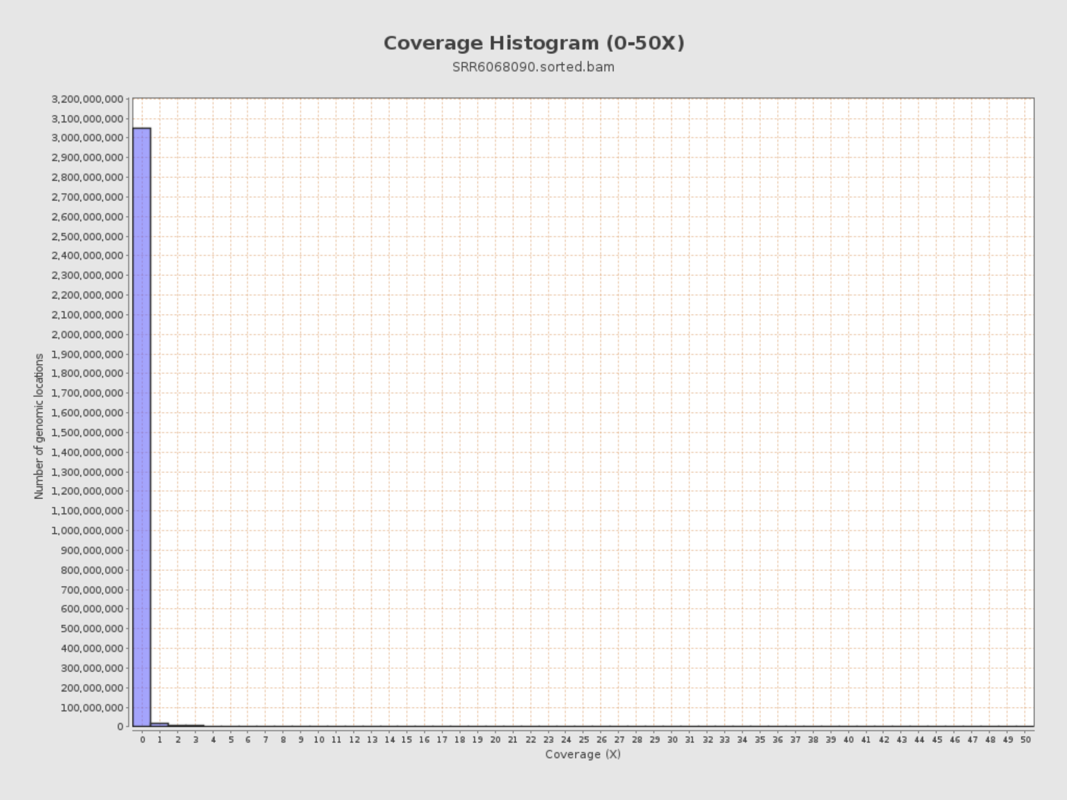
3. Results : Coverage across reference



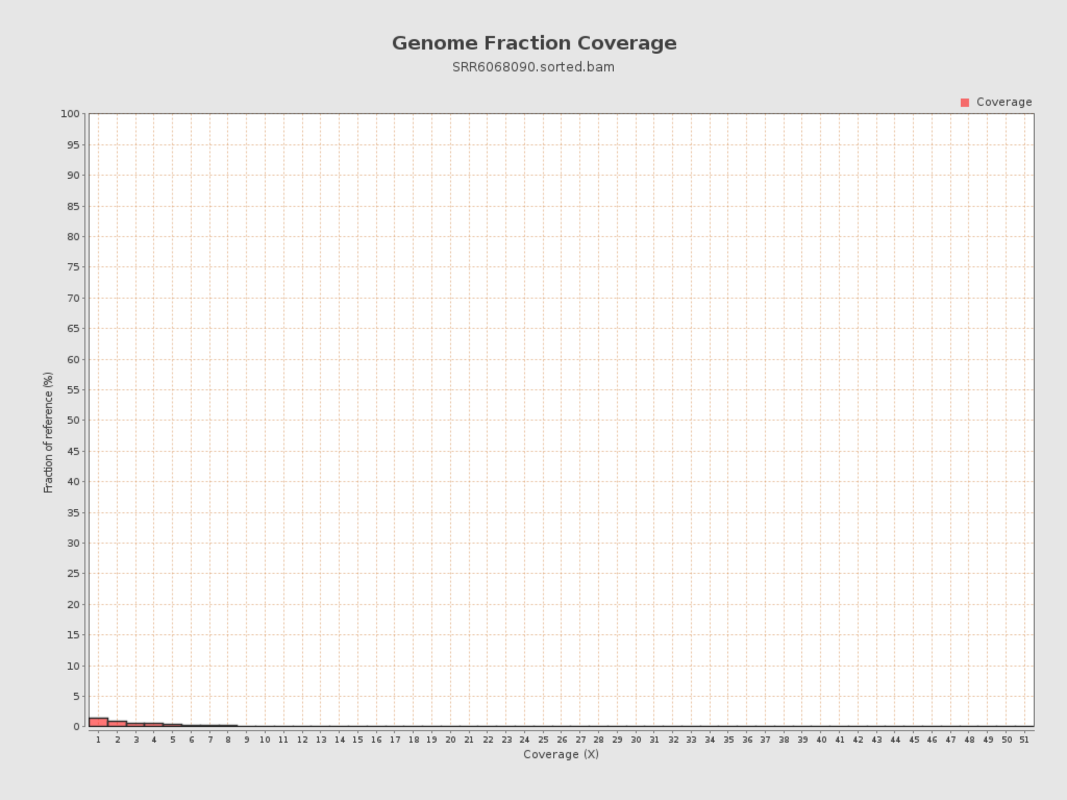
4. Results : Coverage Histogram



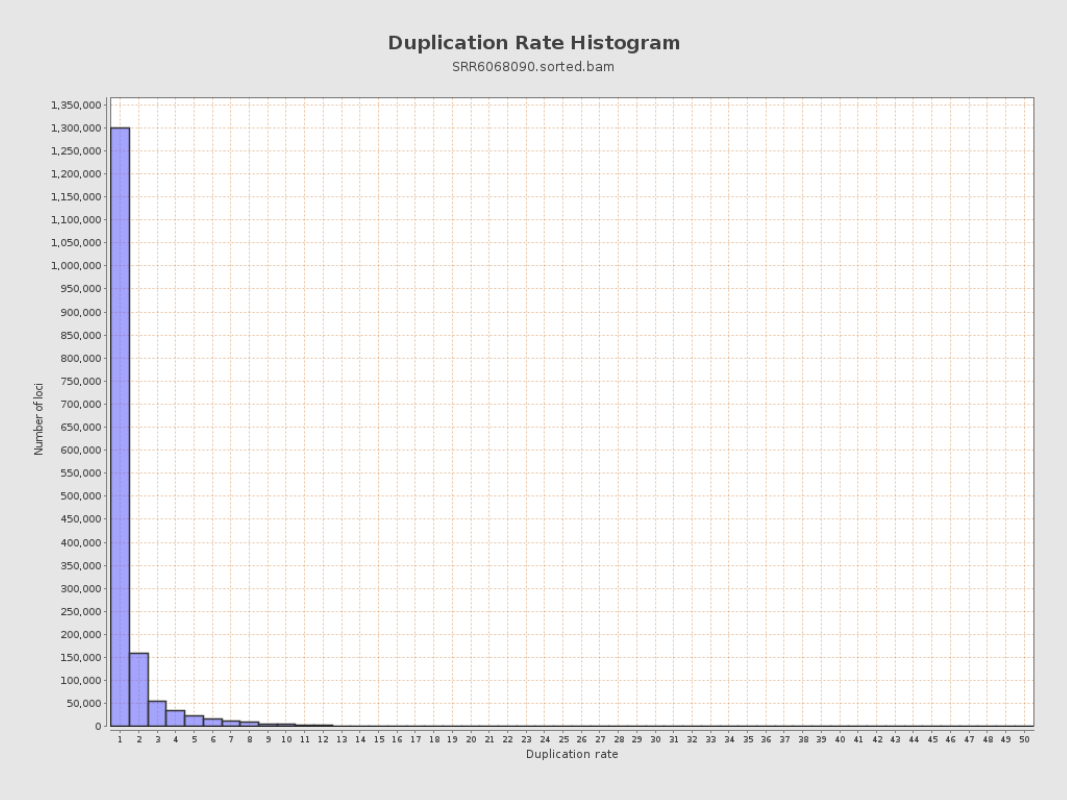
5. Results : Coverage Histogram (0-50X)



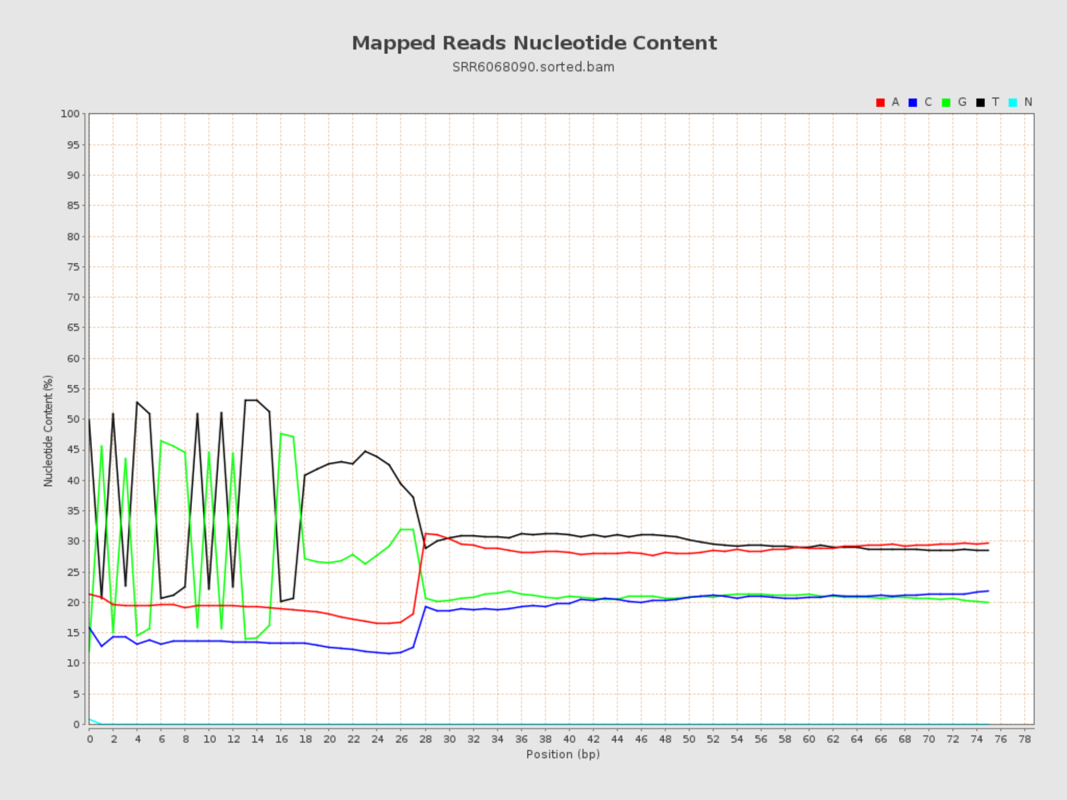
6. Results : Genome Fraction Coverage



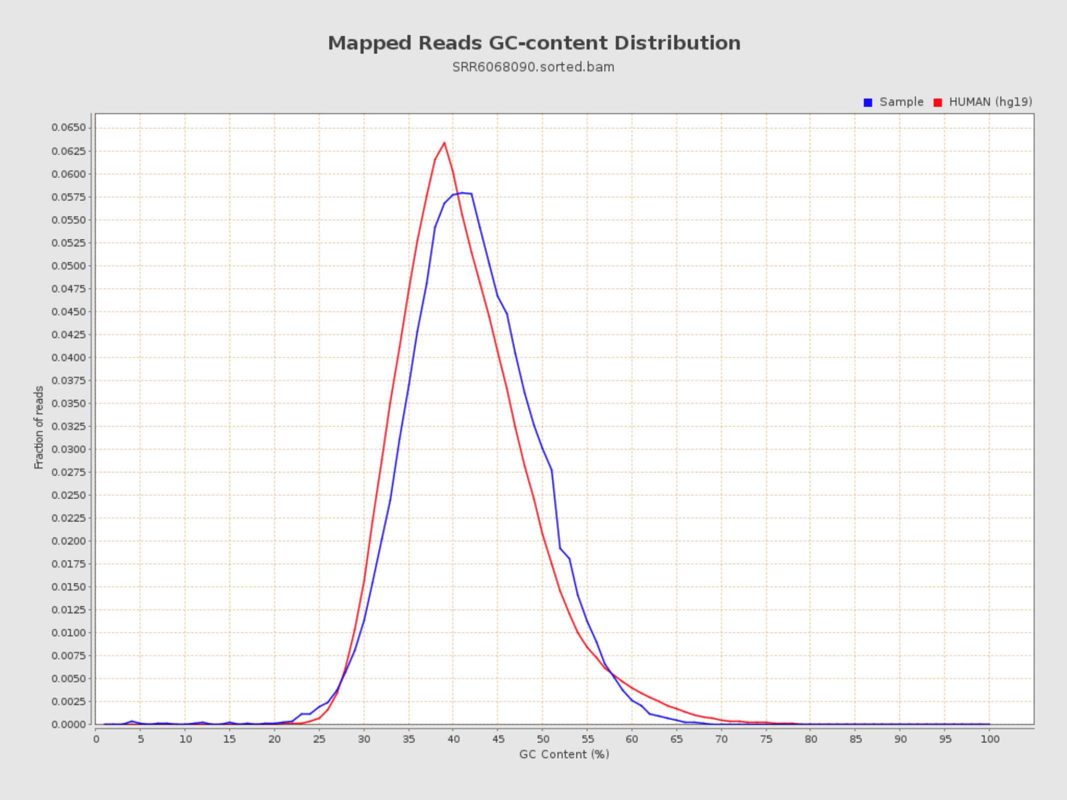
7. Results : Duplication Rate Histogram



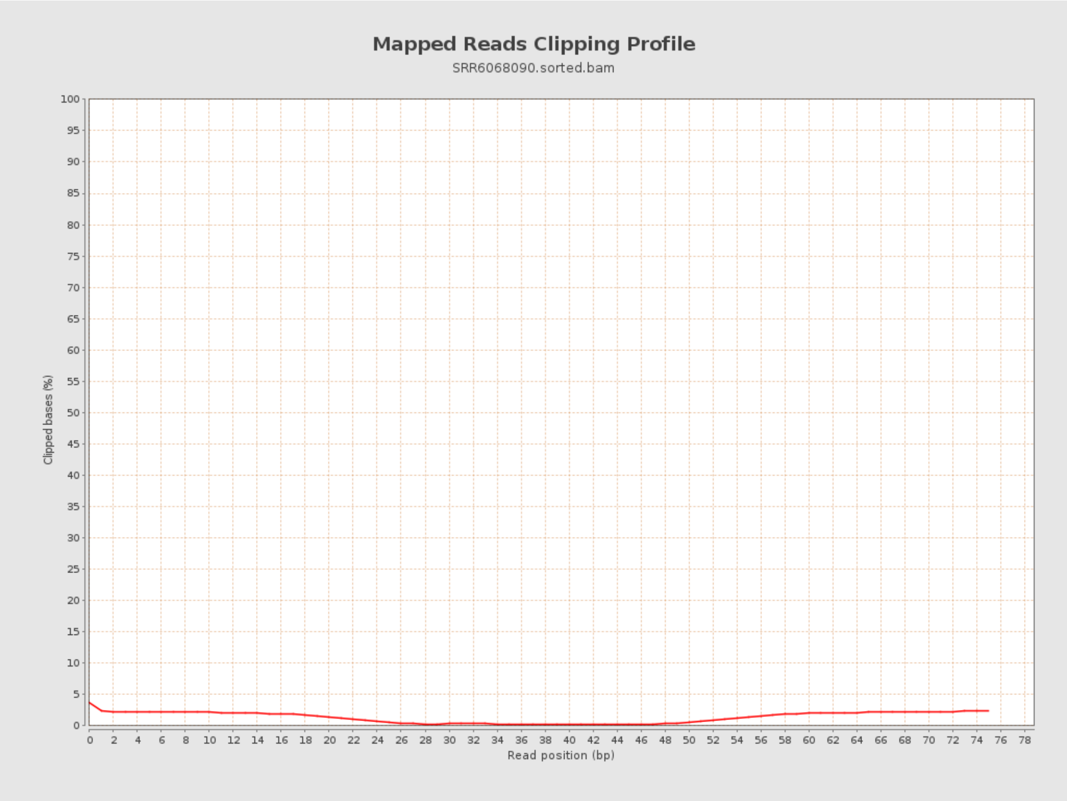
8. Results : Mapped Reads Nucleotide Content



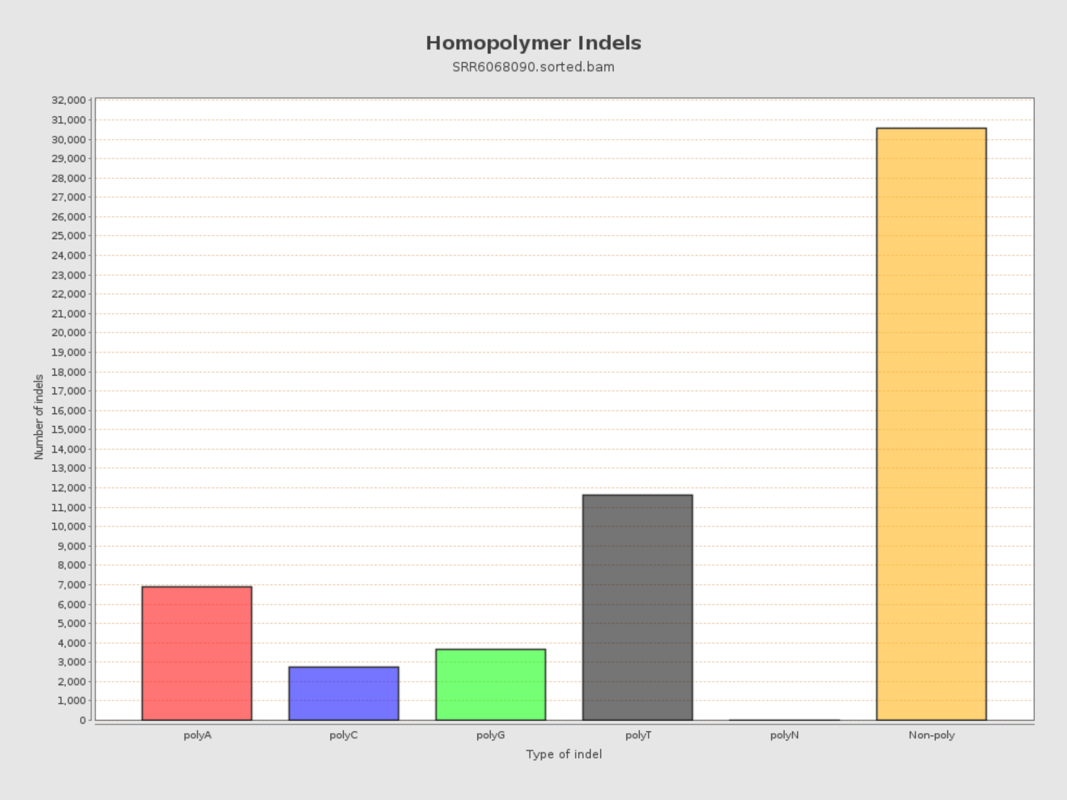
9. Results : Mapped Reads GC-content Distribution



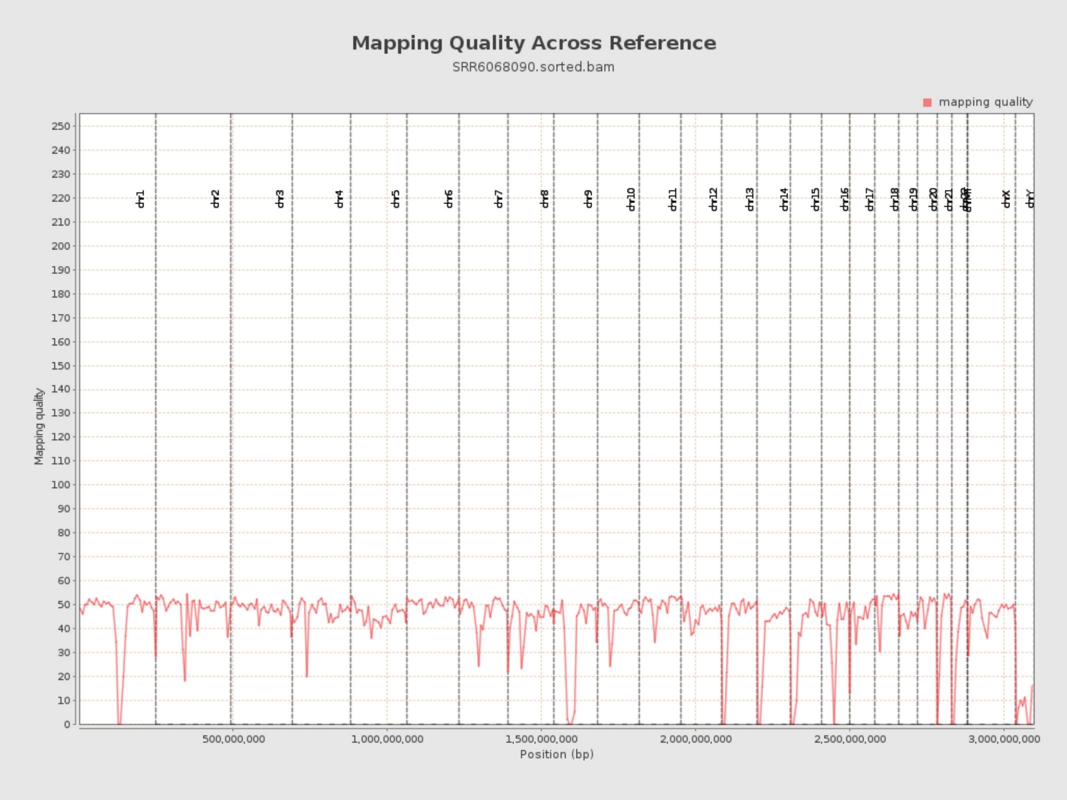
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram