Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:33:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068142.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_SRR6068142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068142.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:33:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,597,138
Mapped reads	2,370,050 / 91.26%
Unmapped reads	227,088 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,557 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	965,909 / 37.19%
Duplication rate	23.72%
Clipped reads	1,549,787 / 59.67%

2.2. ACGT Content

Number/percentage of A's	36,856,816 / 25.13%
Number/percentage of C's	25,088,581 / 17.11%
Number/percentage of T's	49,419,624 / 33.7%
Number/percentage of G's	35,282,452 / 24.06%
Number/percentage of N's	14,949 / 0.01%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.7435

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

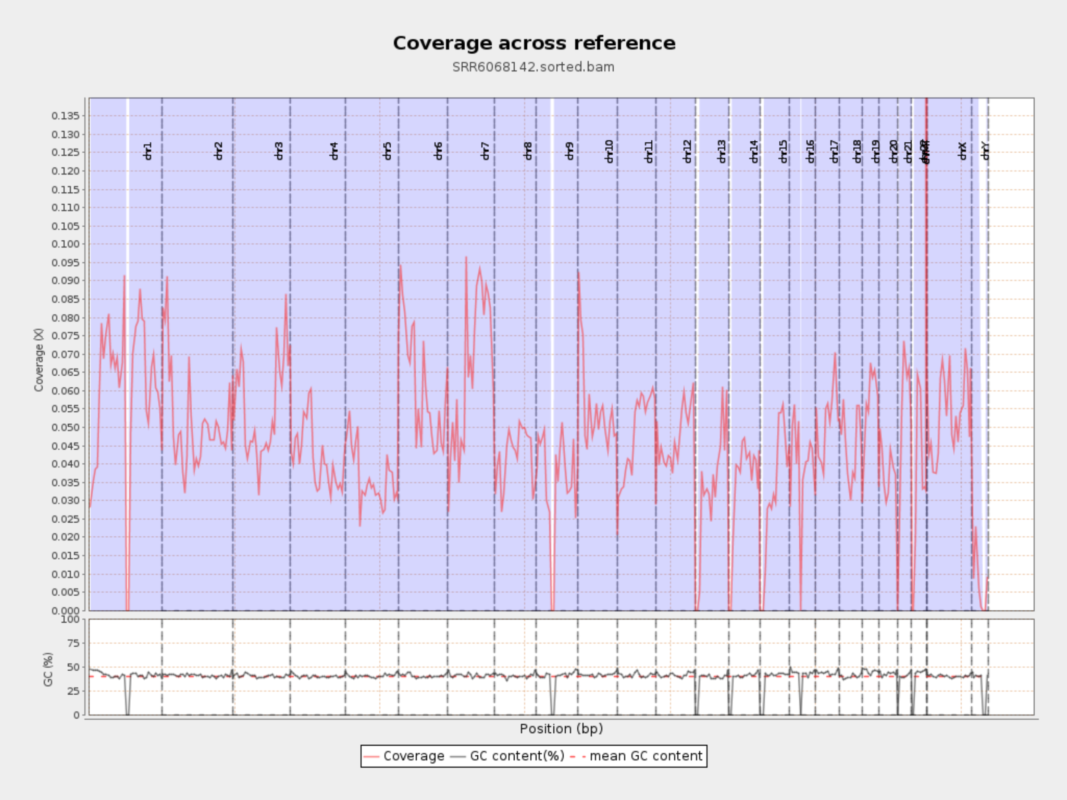
General error rate	0.67%
Mismatches	957,759
Insertions	9,637
Mapped reads with at least one insertion	0.4%
Deletions	40,558
Mapped reads with at least one deletion	1.69%
Homopolymer indels	47.19%

2.6. Chromosome stats

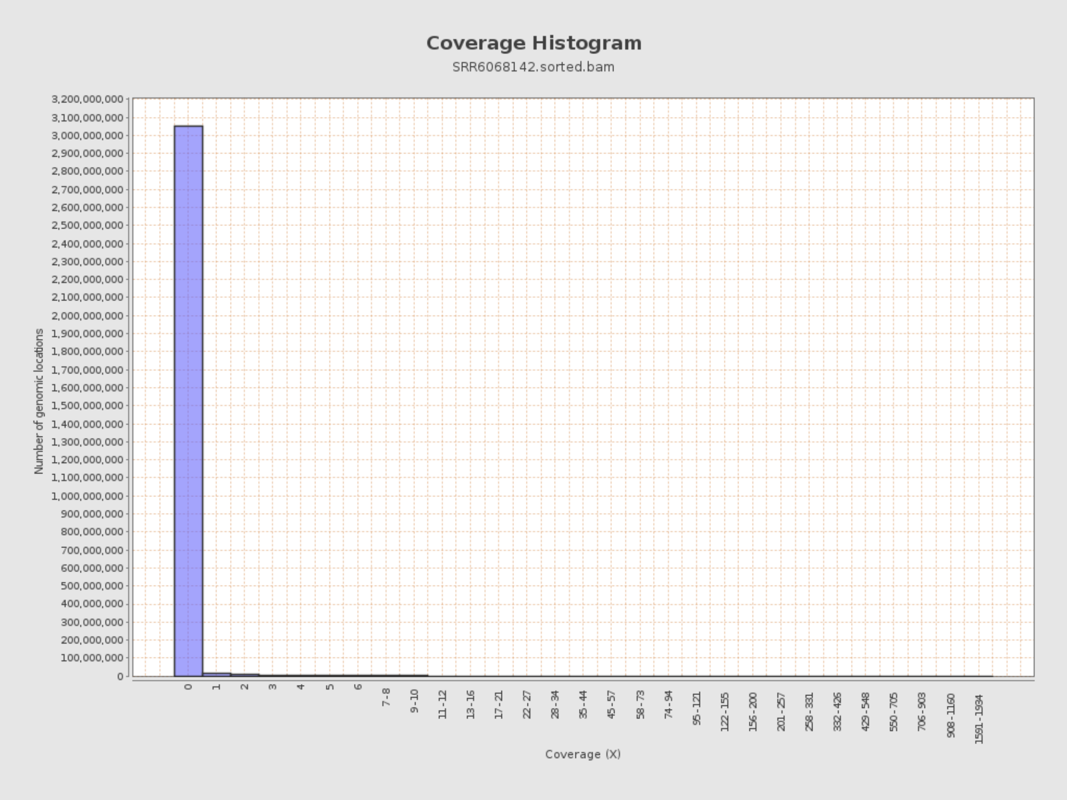
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15070520	0.0605	0.9665
chr2	243199373	12529300	0.0515	1.0658
chr3	198022430	10903484	0.0551	0.7292
chr4	191154276	7958006	0.0416	0.6472
chr5	180915260	6588881	0.0364	0.5288
chr6	171115067	10513916	0.0614	0.736
chr7	159138663	10598883	0.0666	0.9122

chr8	146364022	6194910	0.0423	0.8026
chr9	141213431	4946022	0.035	0.6215
chr10	135534747	7583305	0.056	0.675
chr11	135006516	6498891	0.0481	0.6647
chr12	133851895	6346640	0.0474	0.5971
chr13	115169878	3802220	0.033	0.5589
chr14	107349540	3653563	0.034	0.5162
chr15	102531392	3290887	0.0321	0.5601
chr16	90354753	3567716	0.0395	0.5735
chr17	81195210	4242568	0.0523	0.6085
chr18	78077248	3549016	0.0455	1.1358
chr19	59128983	3324572	0.0562	0.7903
chr20	63025520	2366183	0.0375	0.5621
chr21	48129895	2460890	0.0511	0.6471
chr22	51304566	1697279	0.0331	0.4858
chrMT	16571	192420	11.6119	13.3916
chrX	155270560	8361794	0.0539	0.6608
chrY	59373566	491582	0.0083	0.2372

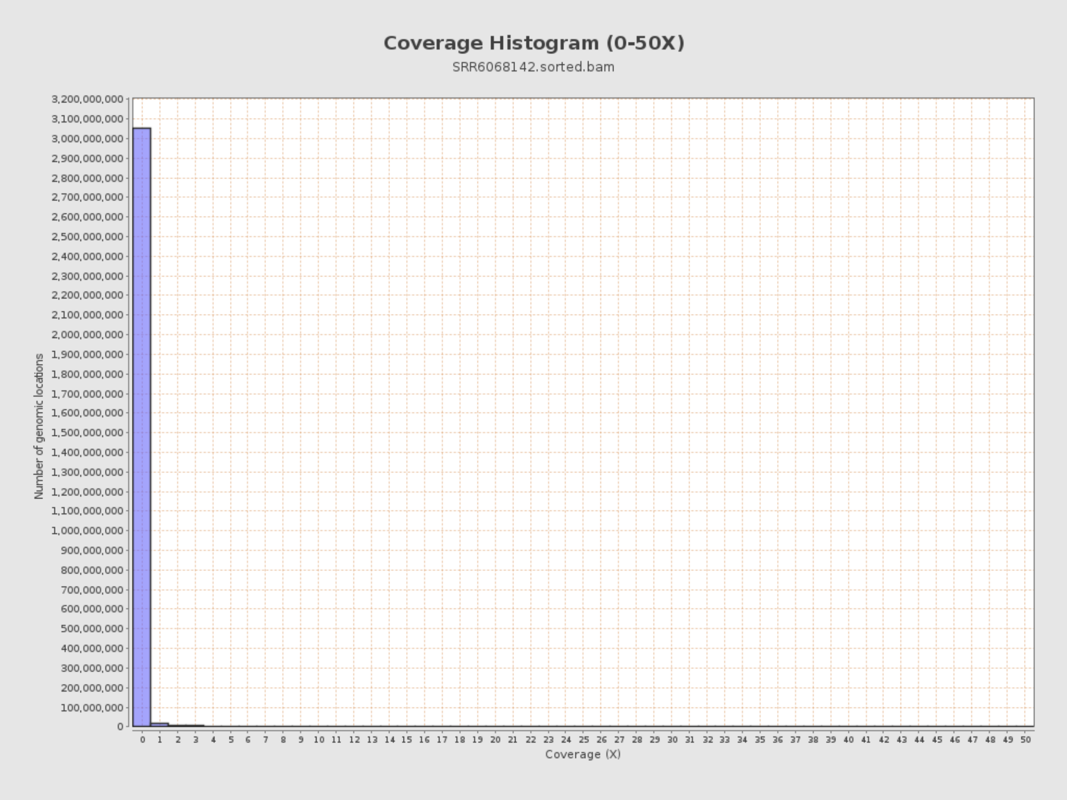
3. Results : Coverage across reference



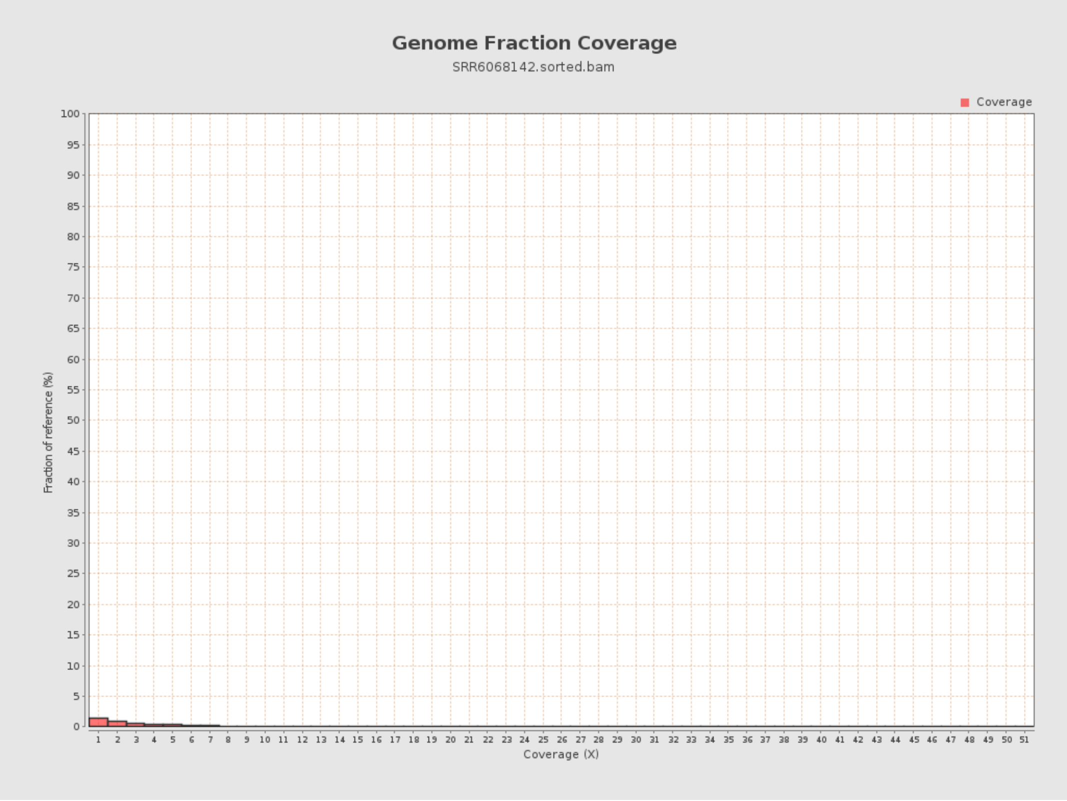
4. Results : Coverage Histogram



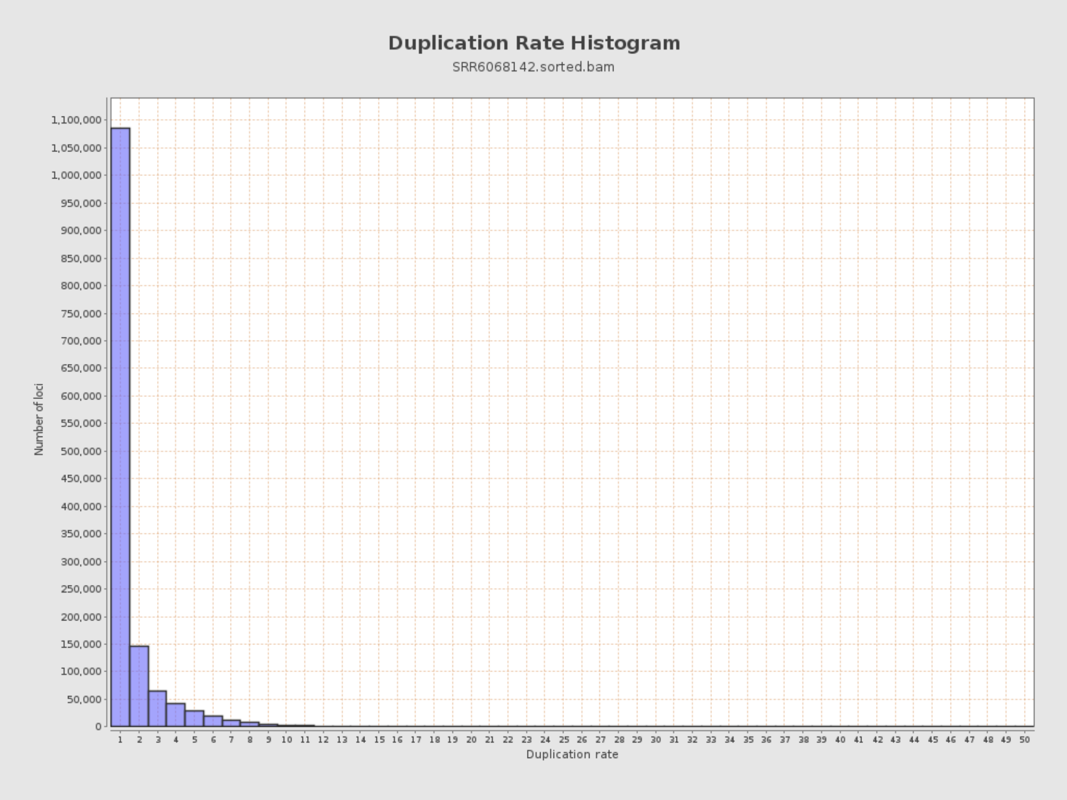
5. Results : Coverage Histogram (0-50X)



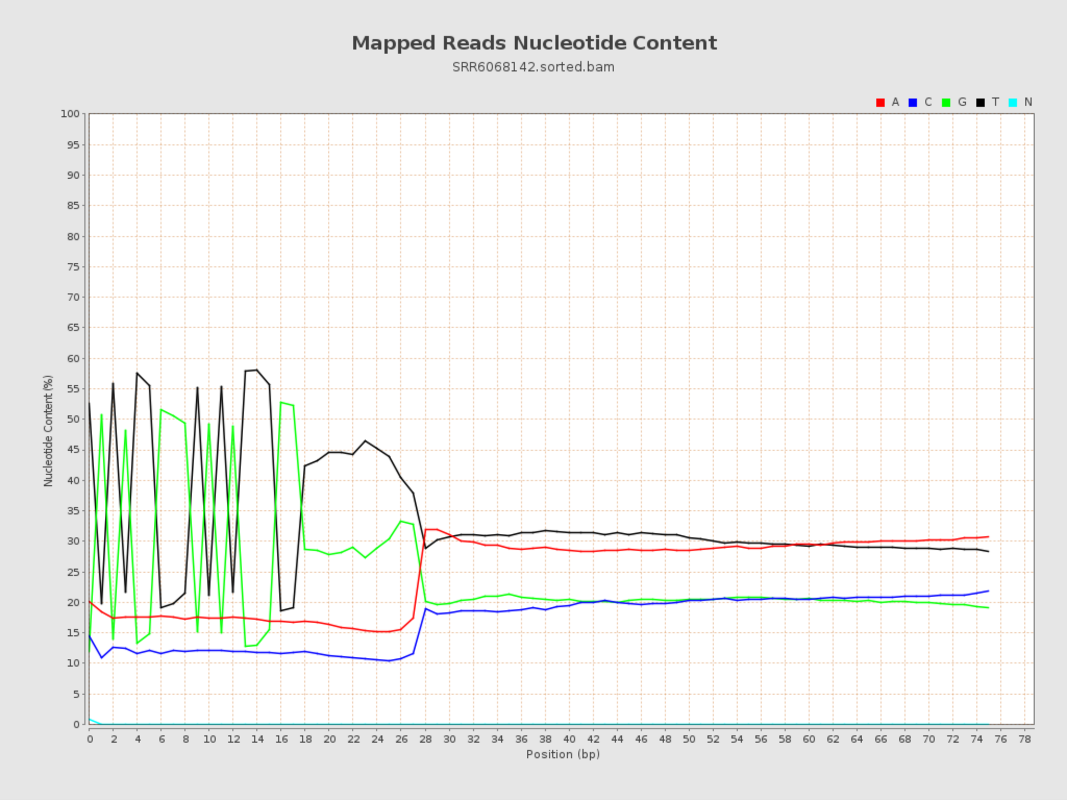
6. Results : Genome Fraction Coverage



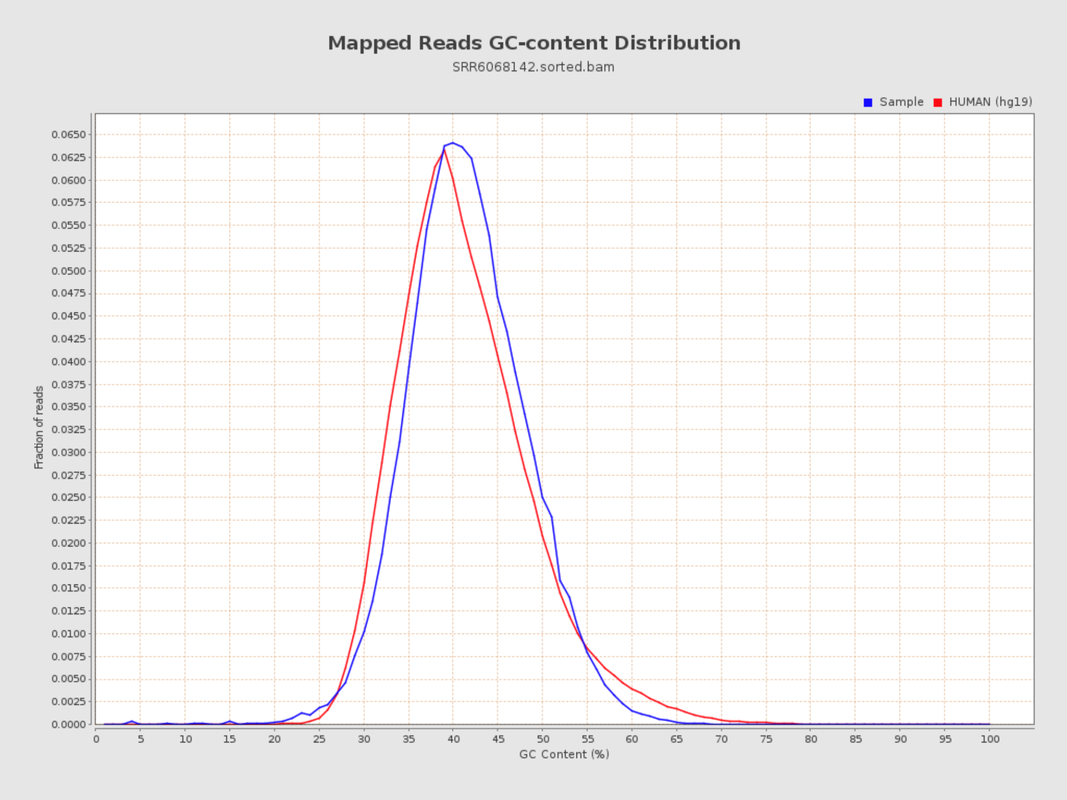
7. Results : Duplication Rate Histogram



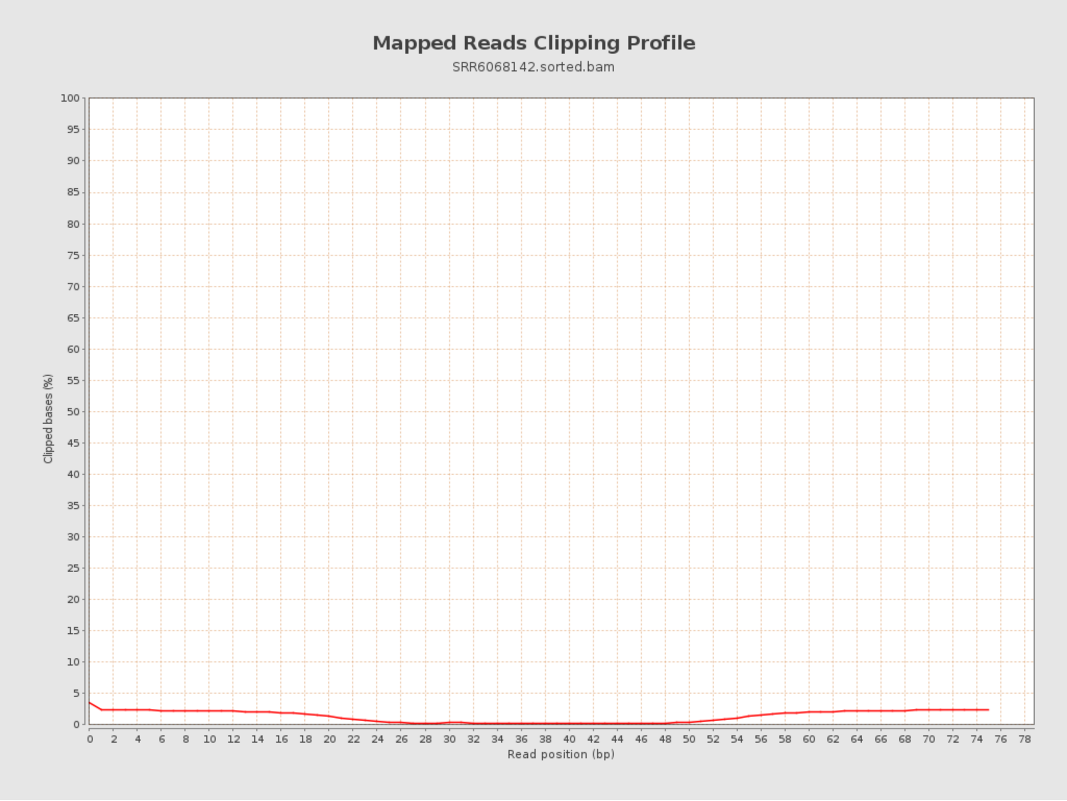
8. Results : Mapped Reads Nucleotide Content



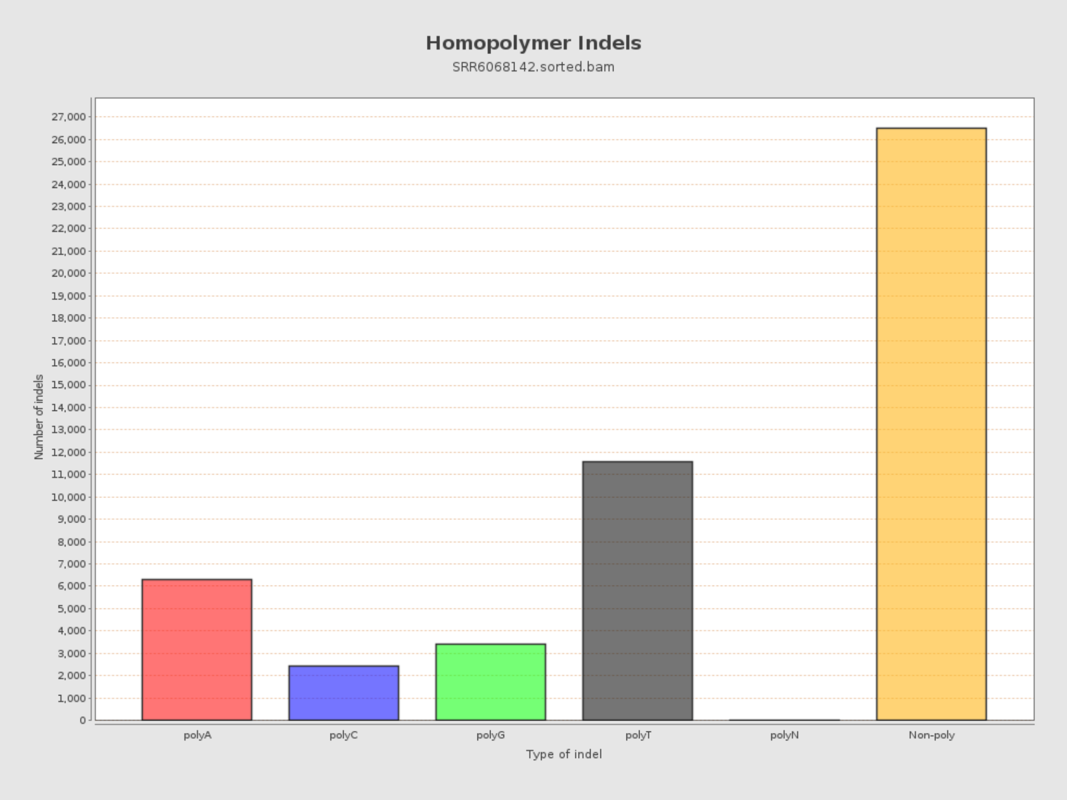
9. Results : Mapped Reads GC-content Distribution



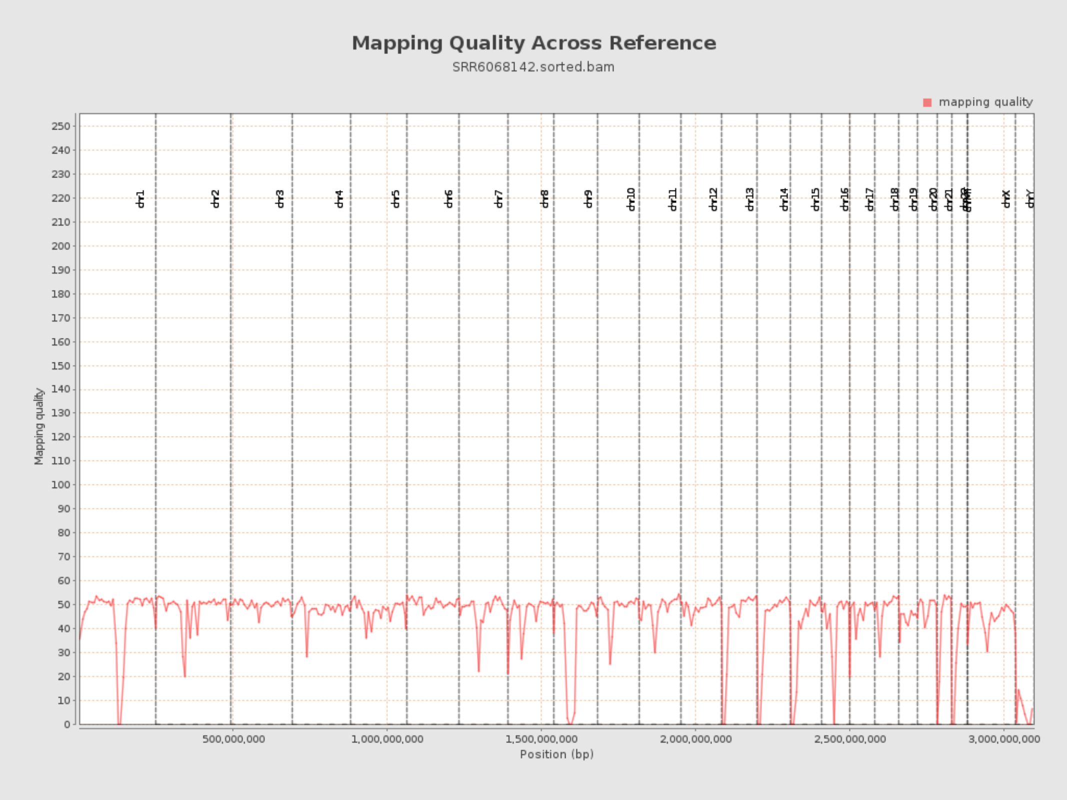
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram