Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:26:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068940.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_SRR6068940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:26:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,453,032
Mapped reads	2,909,492 / 84.26%
Unmapped reads	543,540 / 15.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,445 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	136,939 / 3.97%
Duplication rate	3.53%
Clipped reads	1,320,948 / 38.25%

2.2. ACGT Content

Number/percentage of A's	53,594,520 / 27.73%
Number/percentage of C's	33,496,372 / 17.33%
Number/percentage of T's	64,052,855 / 33.14%
Number/percentage of G's	41,632,751 / 21.54%
Number/percentage of N's	479,002 / 0.25%
GC Percentage	38.88%

2.3. Coverage

Mean	0.0625

Standard Deviation	0.5681

2.4. Mapping Quality

Mean Mapping Quality	47.29

2.5. Mismatches and indels

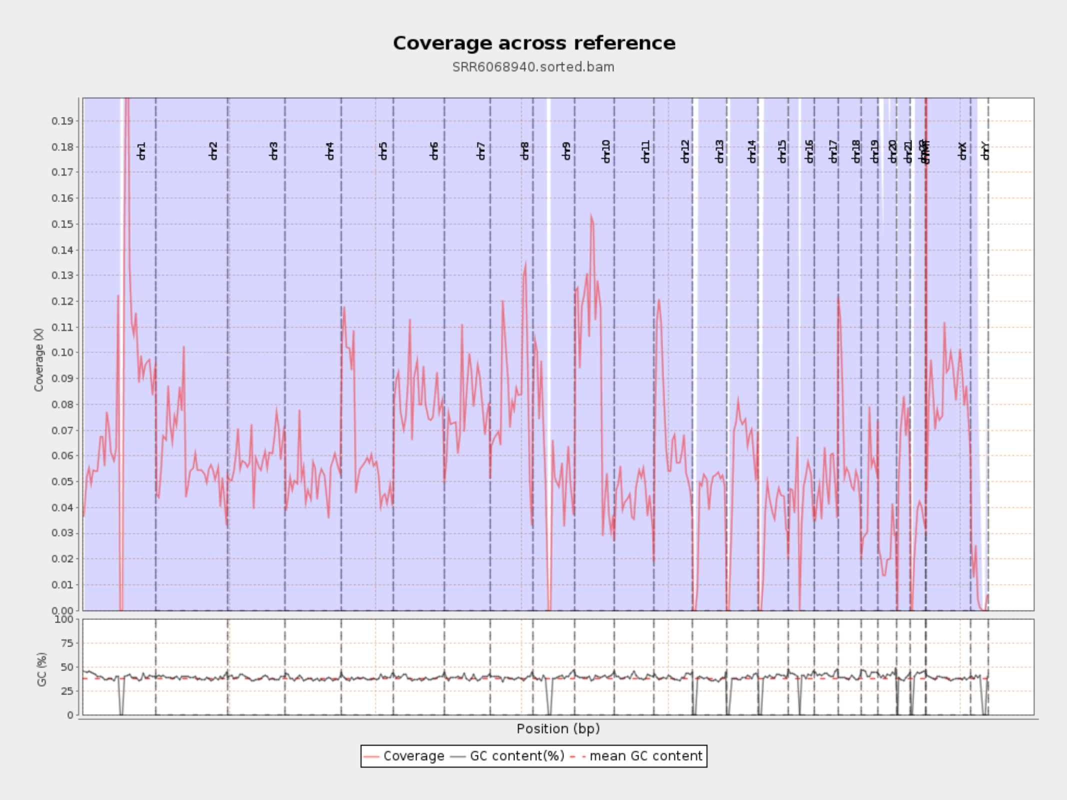
General error rate	1.04%
Mismatches	1,981,195
Insertions	17,303
Mapped reads with at least one insertion	0.59%
Deletions	52,982
Mapped reads with at least one deletion	1.8%
Homopolymer indels	48.33%

2.6. Chromosome stats

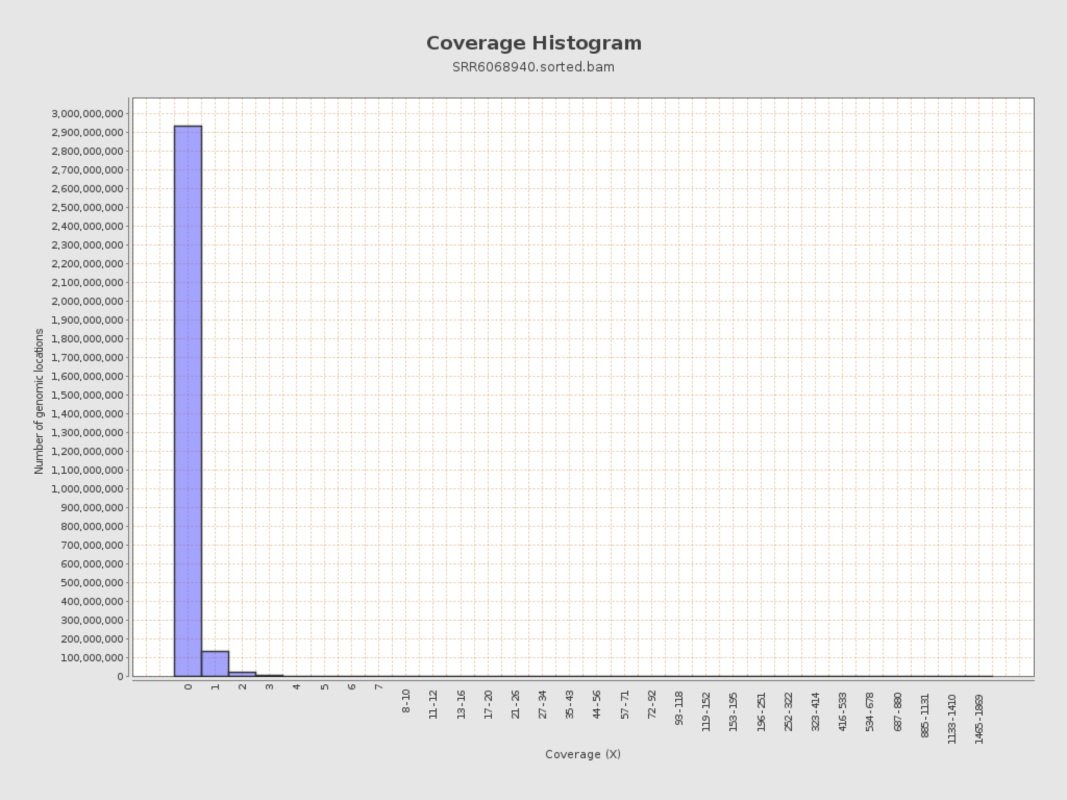
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20377824	0.0818	1.1045
chr2	243199373	14428130	0.0593	0.4855
chr3	198022430	11817866	0.0597	0.2858
chr4	191154276	9778759	0.0512	0.303
chr5	180915260	11762534	0.065	0.2982
chr6	171115067	14219557	0.0831	0.4394
chr7	159138663	12527460	0.0787	0.6941

chr8	146364022	12193014	0.0833	1.2312
chr9	141213431	7912682	0.056	0.4143
chr10	135534747	13032128	0.0962	0.5375
chr11	135006516	5994804	0.0444	0.3981
chr12	133851895	9362854	0.0699	0.3133
chr13	115169878	4767455	0.0414	0.2369
chr14	107349540	6215780	0.0579	0.3022
chr15	102531392	3409299	0.0333	0.2113
chr16	90354753	3839183	0.0425	0.2751
chr17	81195210	3915378	0.0482	0.2762
chr18	78077248	4988078	0.0639	0.8286
chr19	59128983	2807159	0.0475	0.639
chr20	63025520	1452426	0.023	0.2147
chr21	48129895	2986357	0.062	0.3134
chr22	51304566	1434298	0.028	0.197
chrMT	16571	373348	22.5302	11.3485
chrX	155270560	13232183	0.0852	0.3884
chrY	59373566	513921	0.0087	0.1868

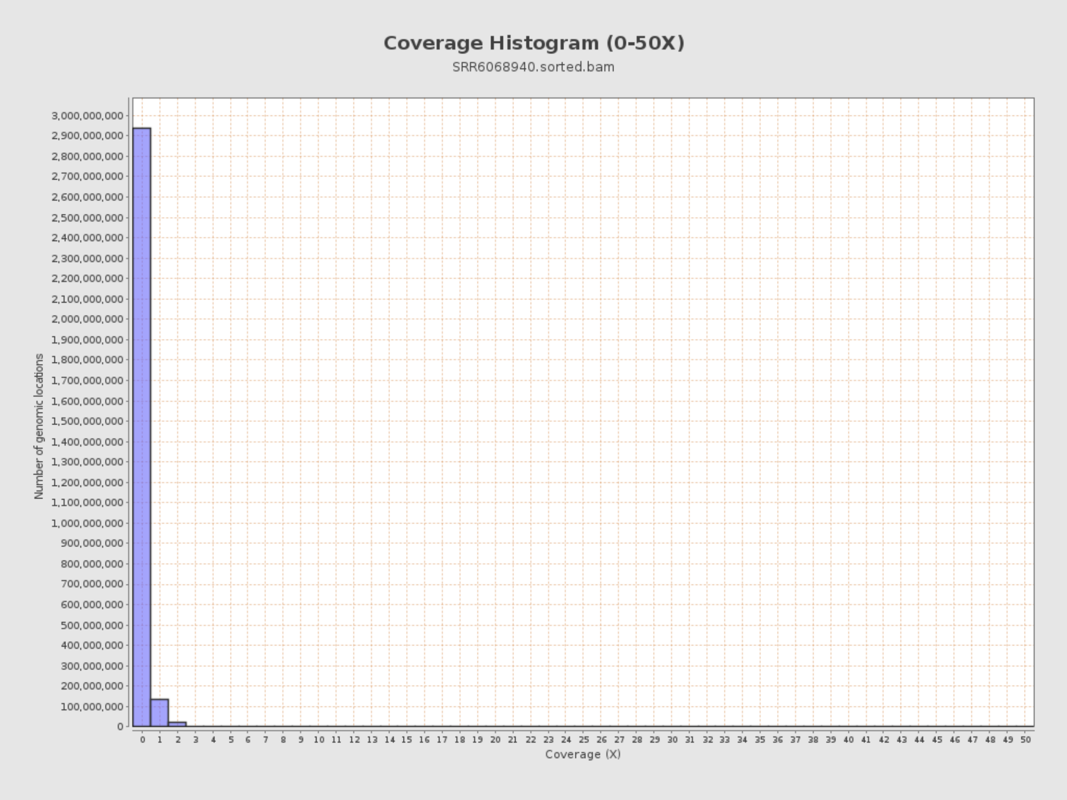
3. Results : Coverage across reference



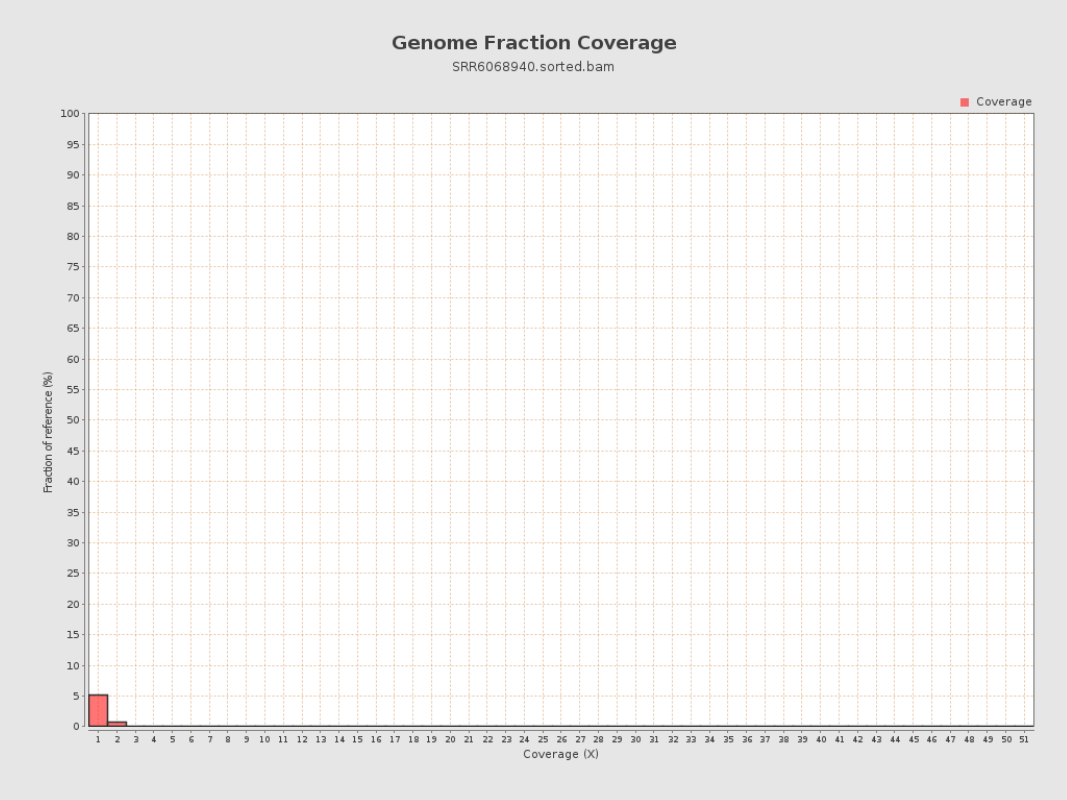
4. Results : Coverage Histogram



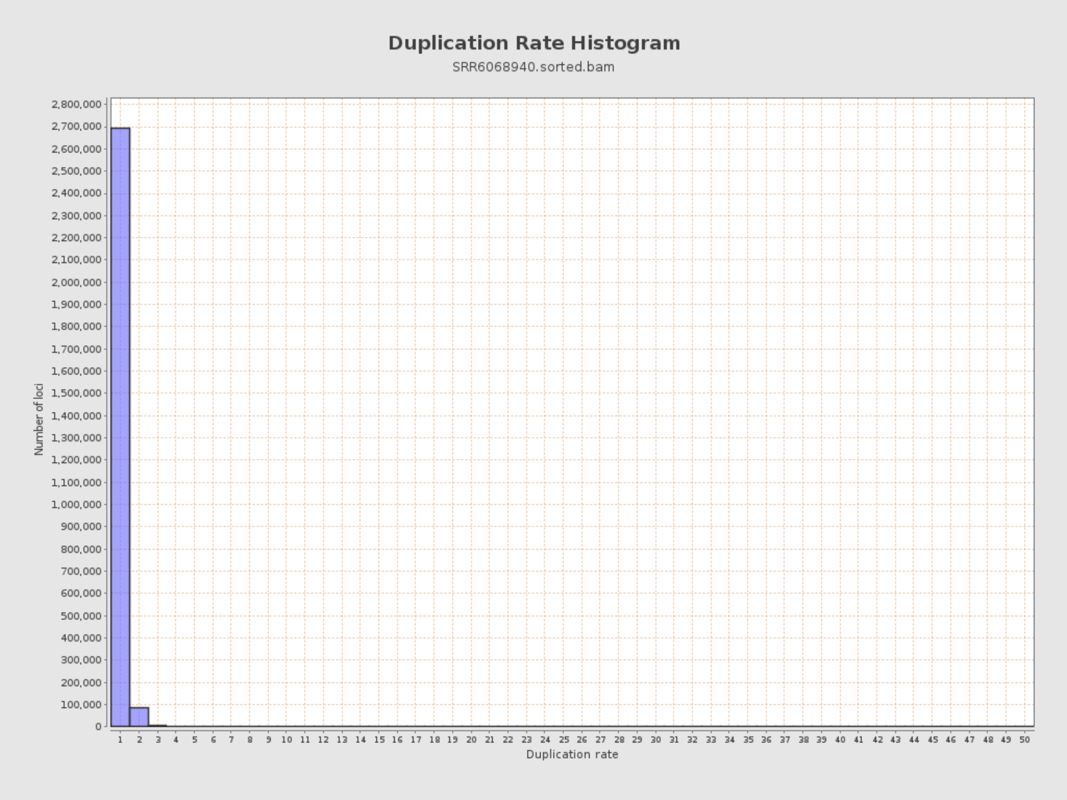
5. Results : Coverage Histogram (0-50X)



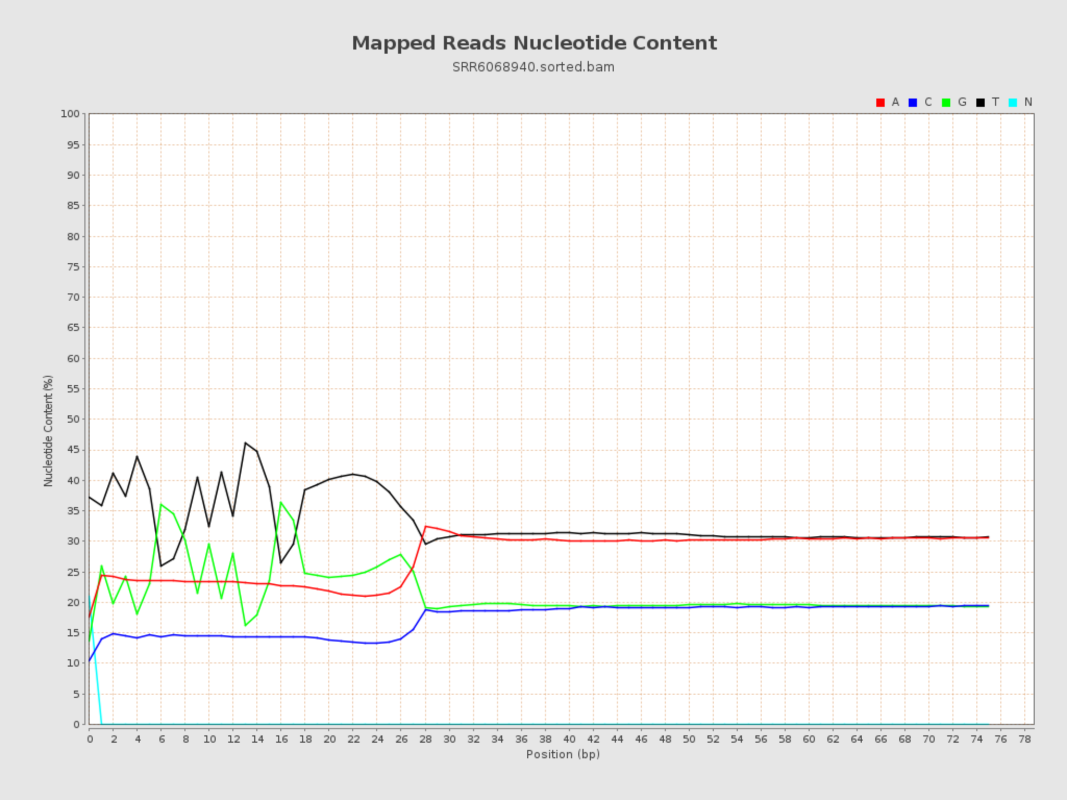
6. Results : Genome Fraction Coverage



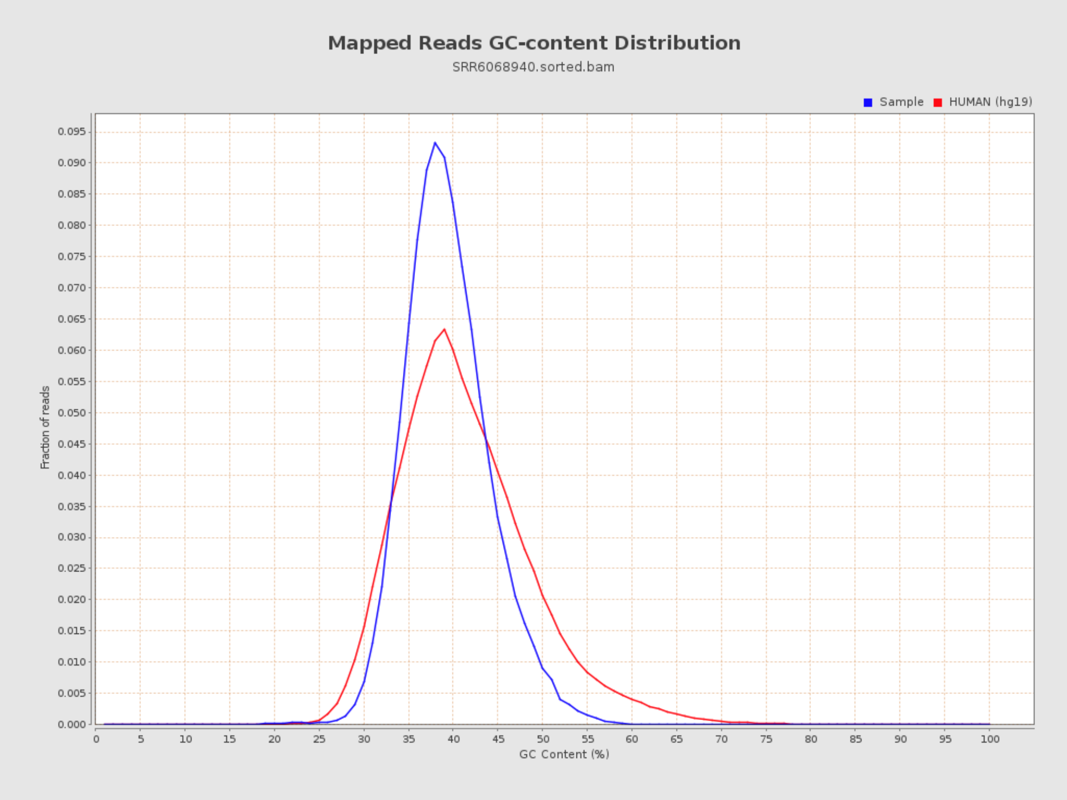
7. Results : Duplication Rate Histogram



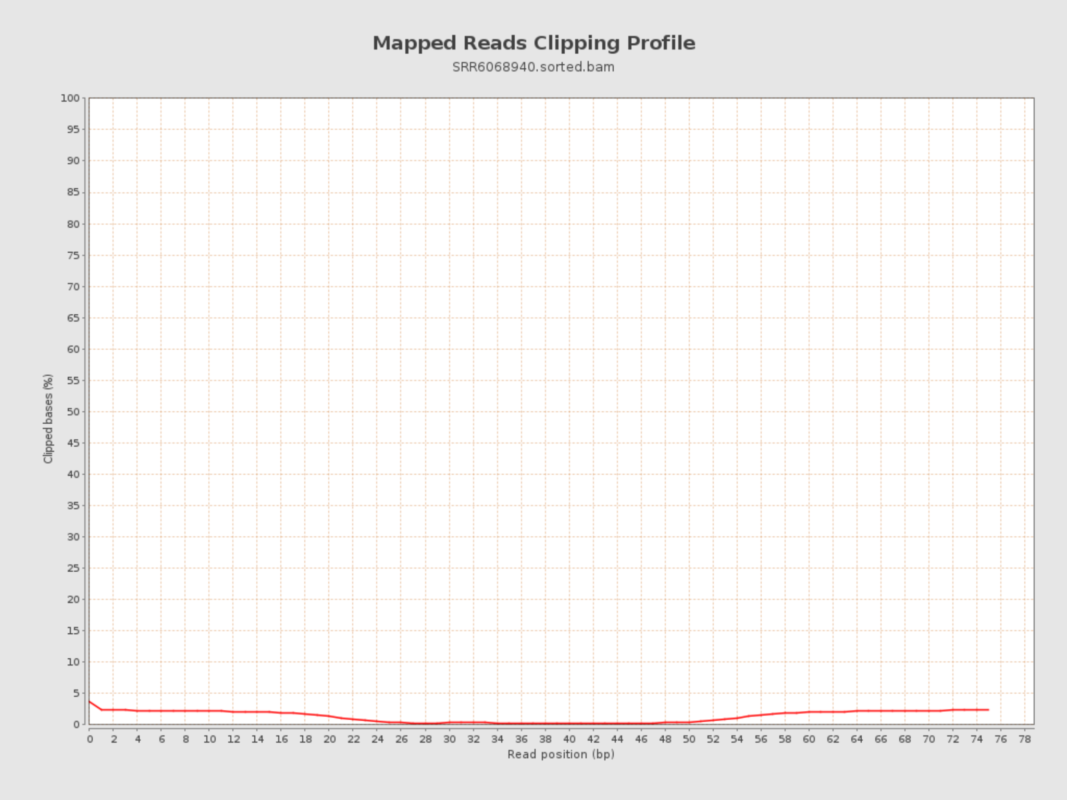
8. Results : Mapped Reads Nucleotide Content



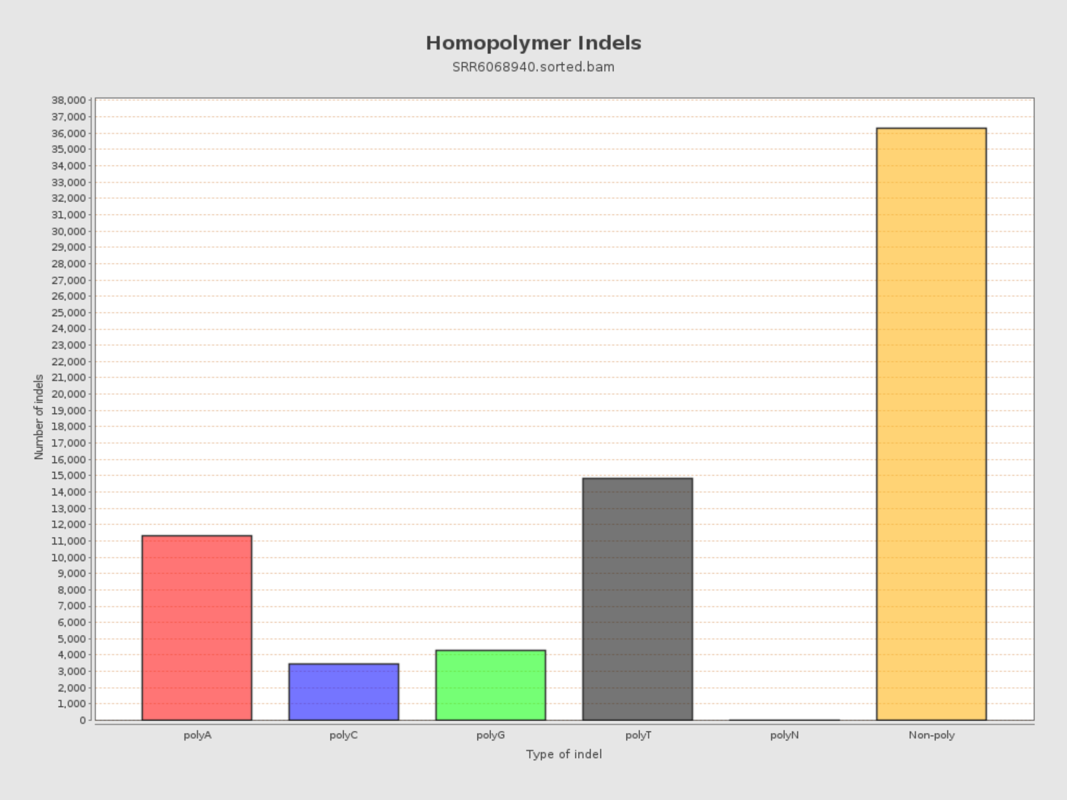
9. Results : Mapped Reads GC-content Distribution



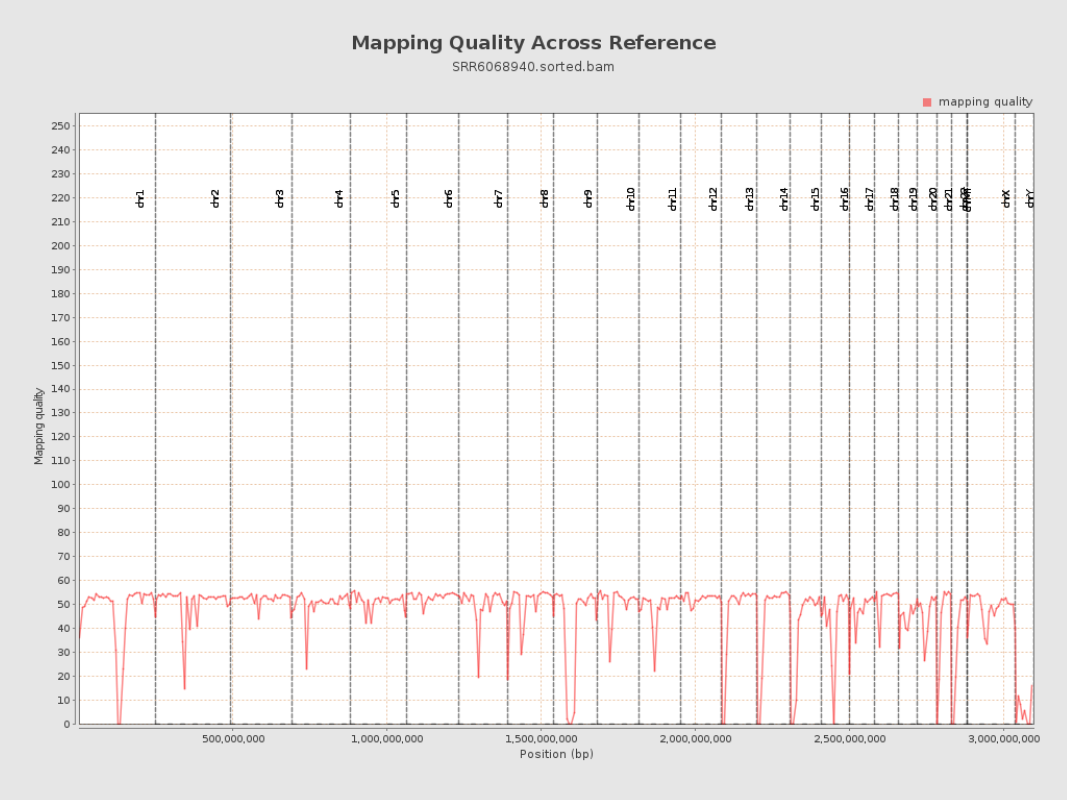
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram