Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:24:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068074.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_SRR6068074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:24:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,212,730
Mapped reads	3,957,417 / 93.94%
Unmapped reads	255,313 / 6.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,145 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	787,667 / 18.7%
Duplication rate	15.14%
Clipped reads	2,144,464 / 50.9%

2.2. ACGT Content

Number/percentage of A's	65,192,165 / 25.71%
Number/percentage of C's	46,033,214 / 18.16%
Number/percentage of T's	82,037,844 / 32.36%
Number/percentage of G's	60,252,588 / 23.76%
Number/percentage of N's	28,760 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0819

Standard Deviation	0.8605

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

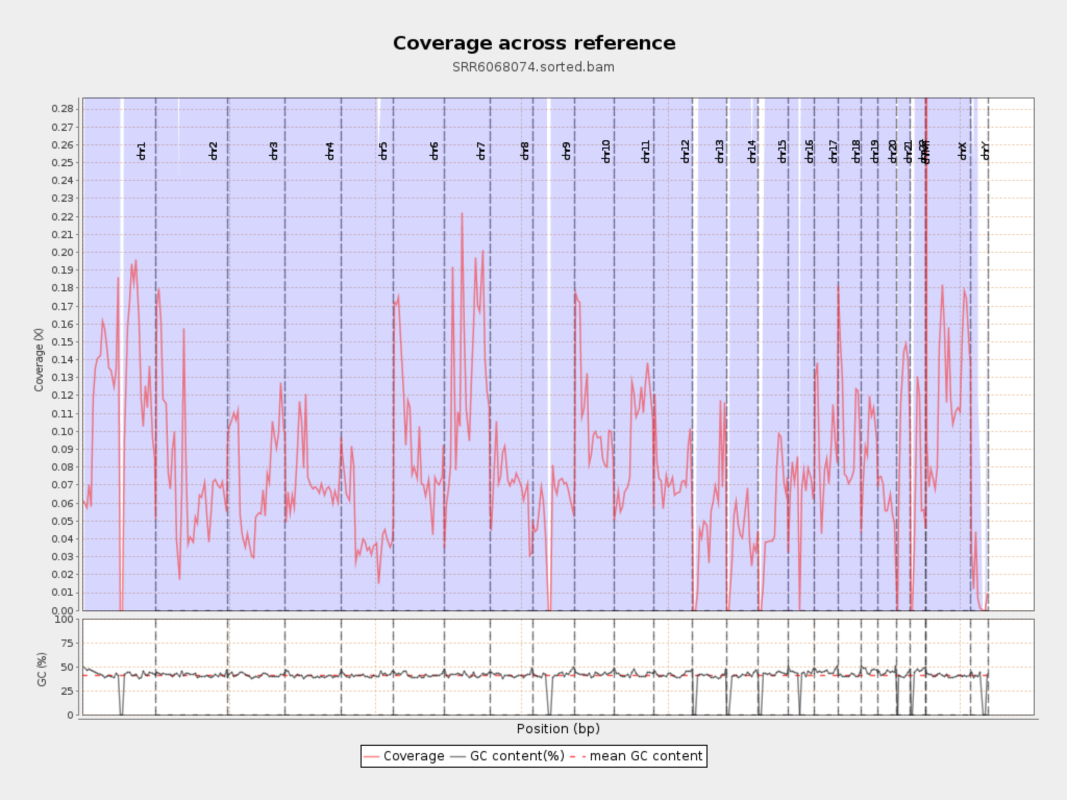
General error rate	0.55%
Mismatches	1,357,753
Insertions	16,698
Mapped reads with at least one insertion	0.42%
Deletions	54,114
Mapped reads with at least one deletion	1.35%
Homopolymer indels	44.35%

2.6. Chromosome stats

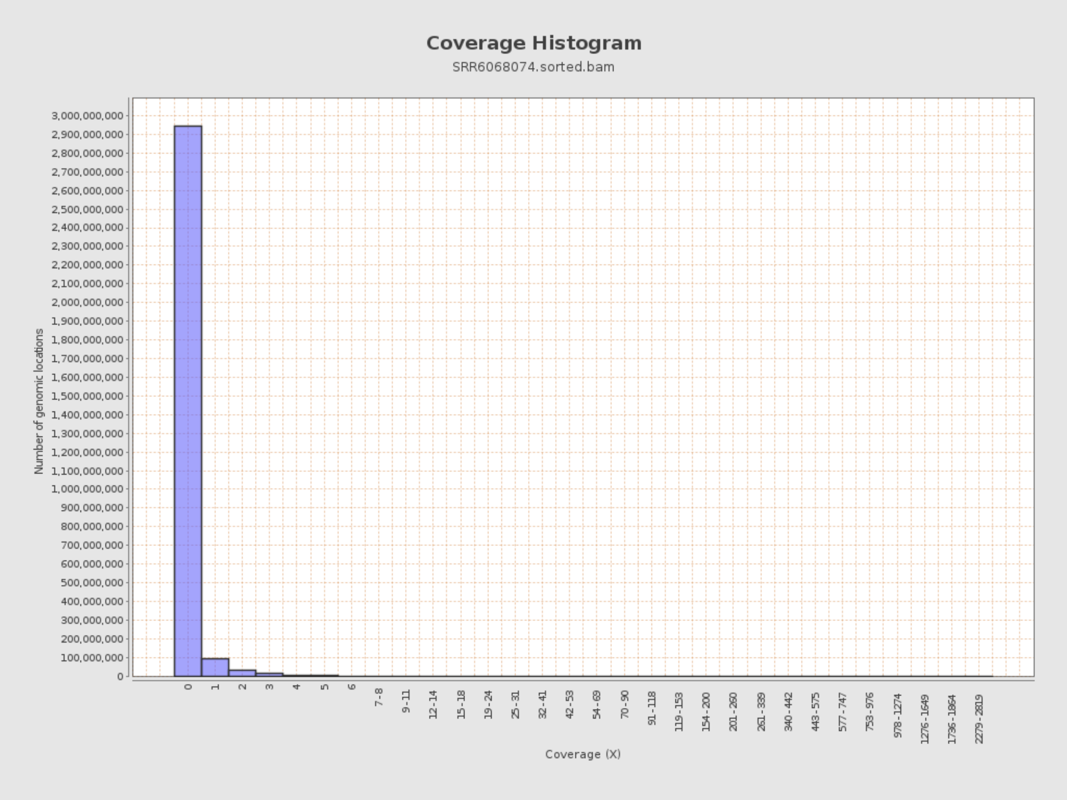
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30292885	0.1215	1.6124
chr2	243199373	18736763	0.077	1.4005
chr3	198022430	14796495	0.0747	0.4191
chr4	191154276	13992800	0.0732	0.4776
chr5	180915260	8329677	0.046	0.335
chr6	171115067	16284371	0.0952	0.6397
chr7	159138663	20840324	0.131	1.4169

chr8	146364022	10232836	0.0699	0.976
chr9	141213431	7903507	0.056	0.5951
chr10	135534747	14815595	0.1093	0.6702
chr11	135006516	12956958	0.096	0.5595
chr12	133851895	10151262	0.0758	0.4476
chr13	115169878	6143915	0.0533	0.3927
chr14	107349540	4152368	0.0387	0.3587
chr15	102531392	5030863	0.0491	0.3662
chr16	90354753	5866339	0.0649	0.427
chr17	81195210	7459725	0.0919	0.494
chr18	78077248	8074988	0.1034	1.1659
chr19	59128983	5589728	0.0945	1.0379
chr20	63025520	3799478	0.0603	0.4185
chr21	48129895	5178705	0.1076	0.5304
chr22	51304566	3159326	0.0616	0.3783
chrMT	16571	141647	8.5479	6.462
chrX	155270560	18969409	0.1222	0.6221
chrY	59373566	739661	0.0125	0.4458

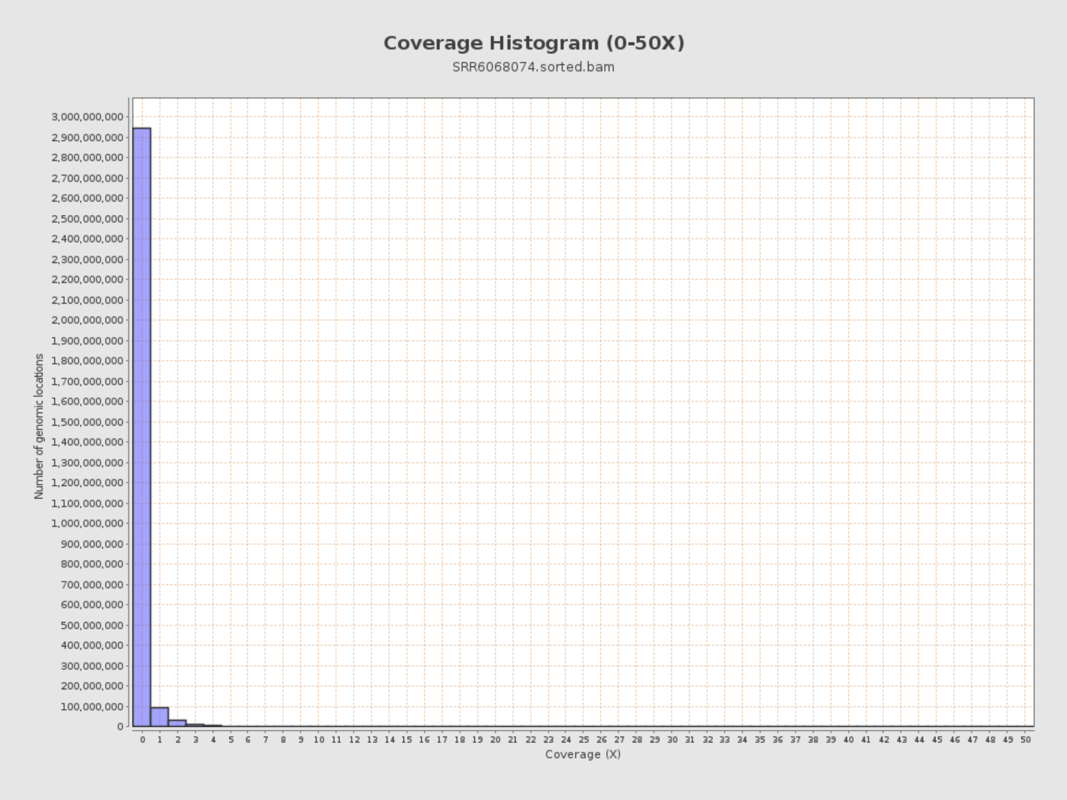
3. Results : Coverage across reference



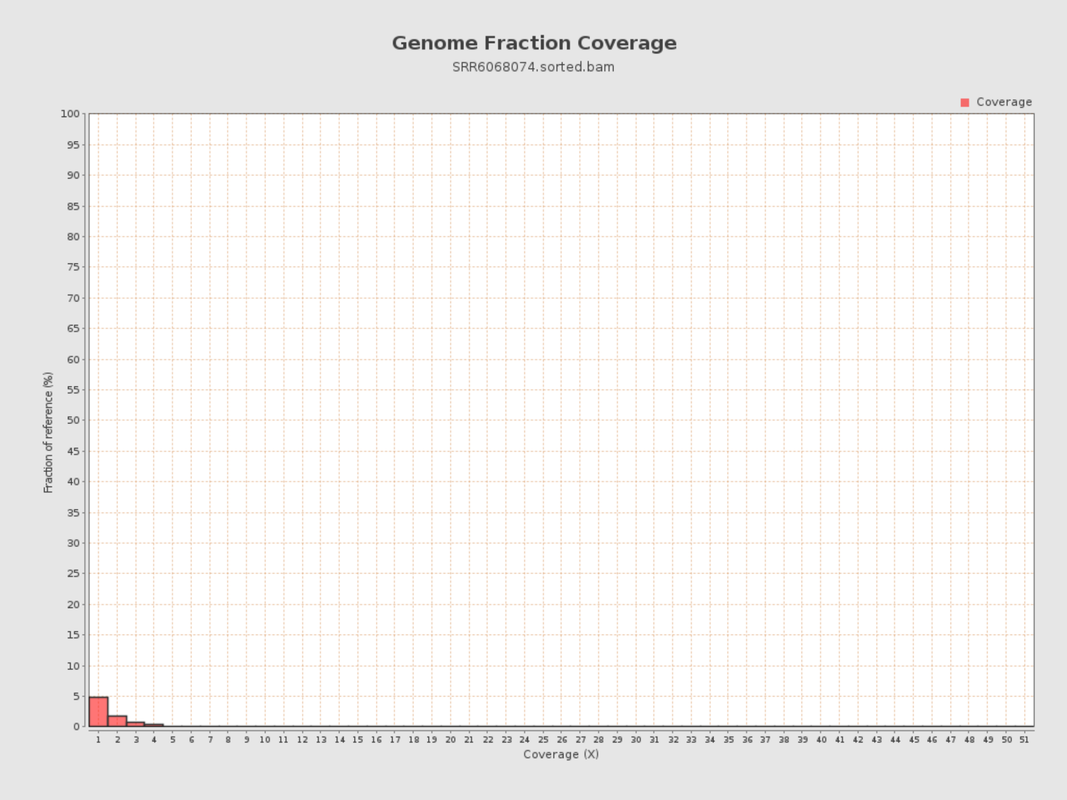
4. Results : Coverage Histogram



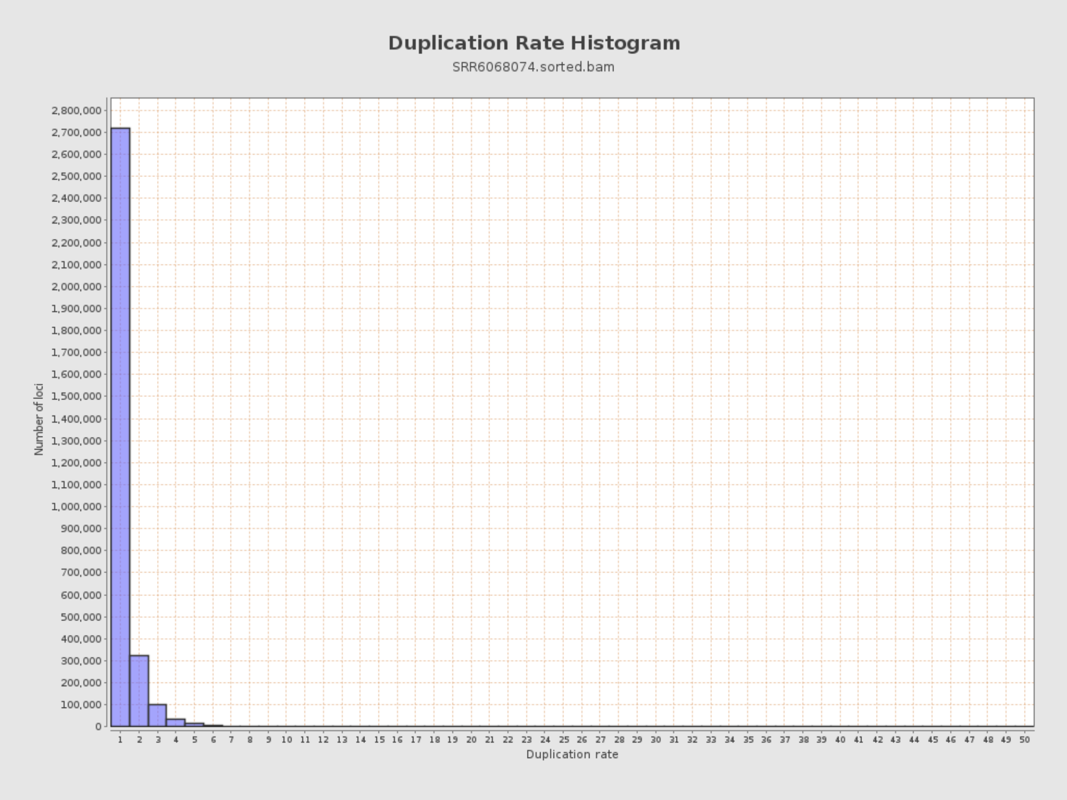
5. Results : Coverage Histogram (0-50X)



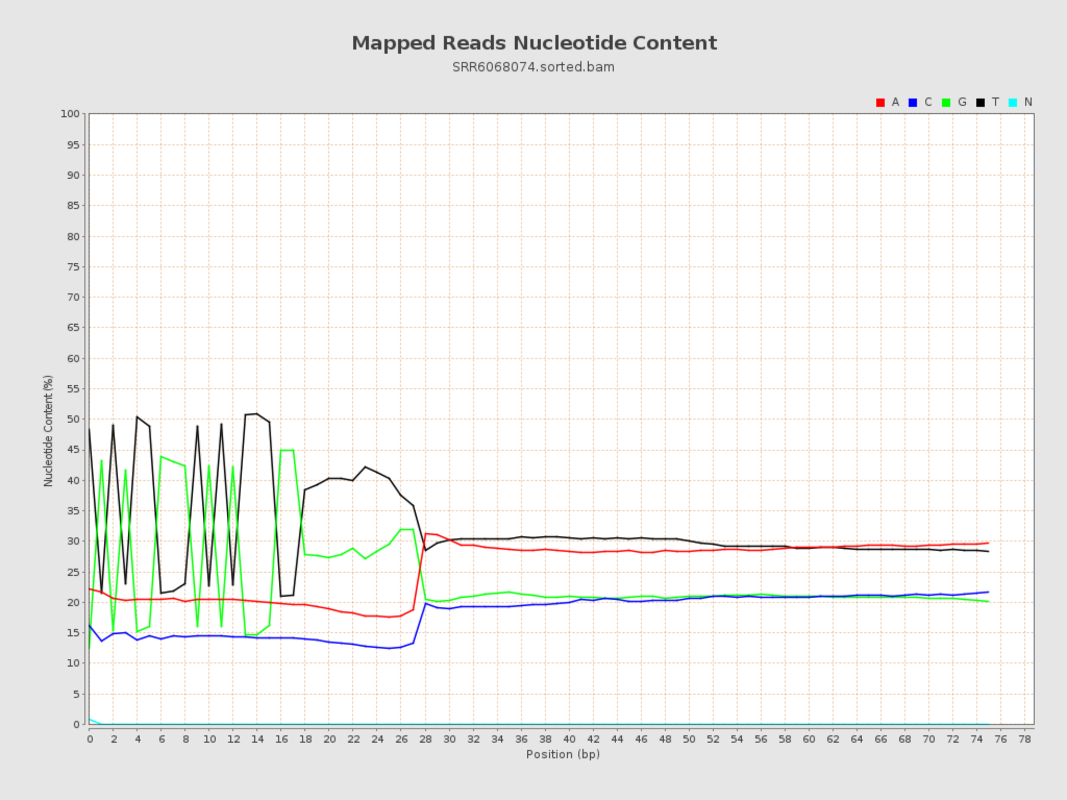
6. Results : Genome Fraction Coverage



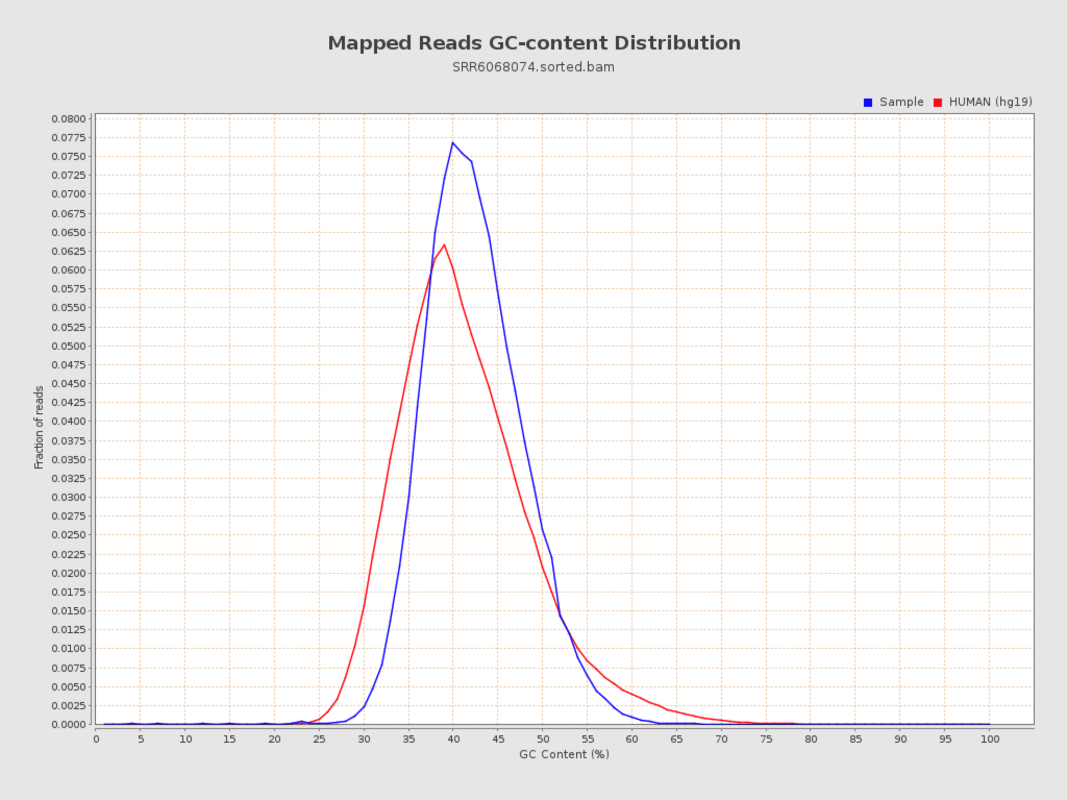
7. Results : Duplication Rate Histogram



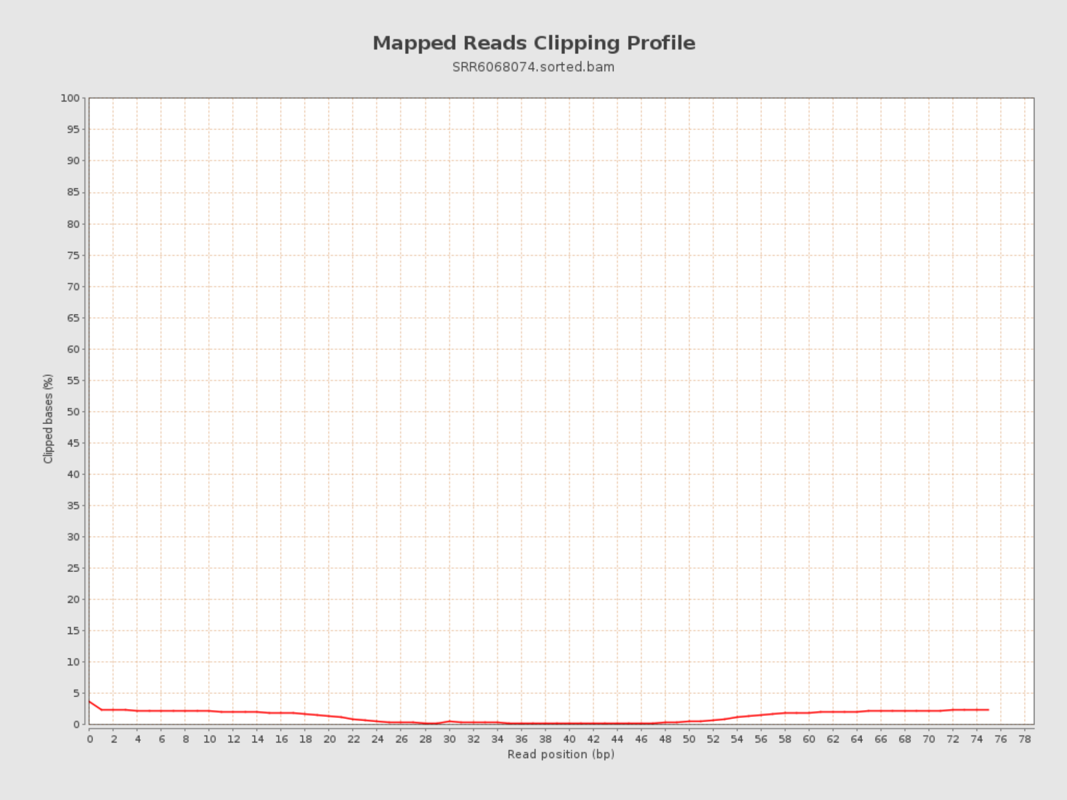
8. Results : Mapped Reads Nucleotide Content



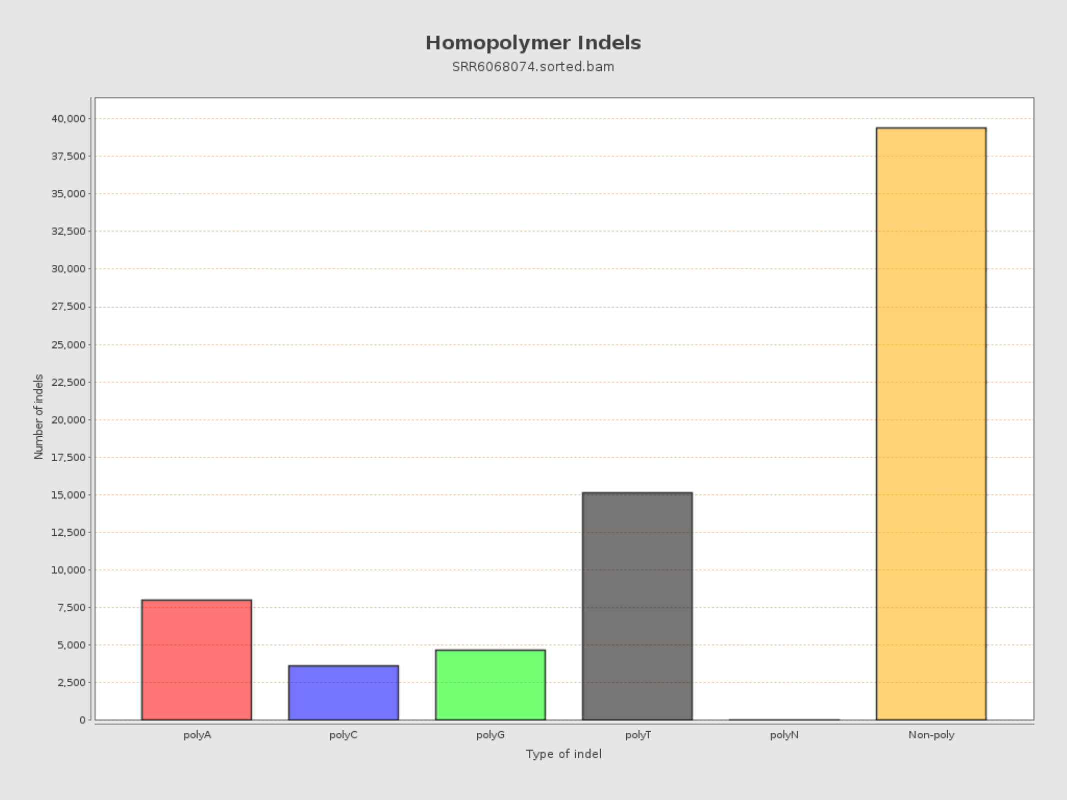
9. Results : Mapped Reads GC-content Distribution



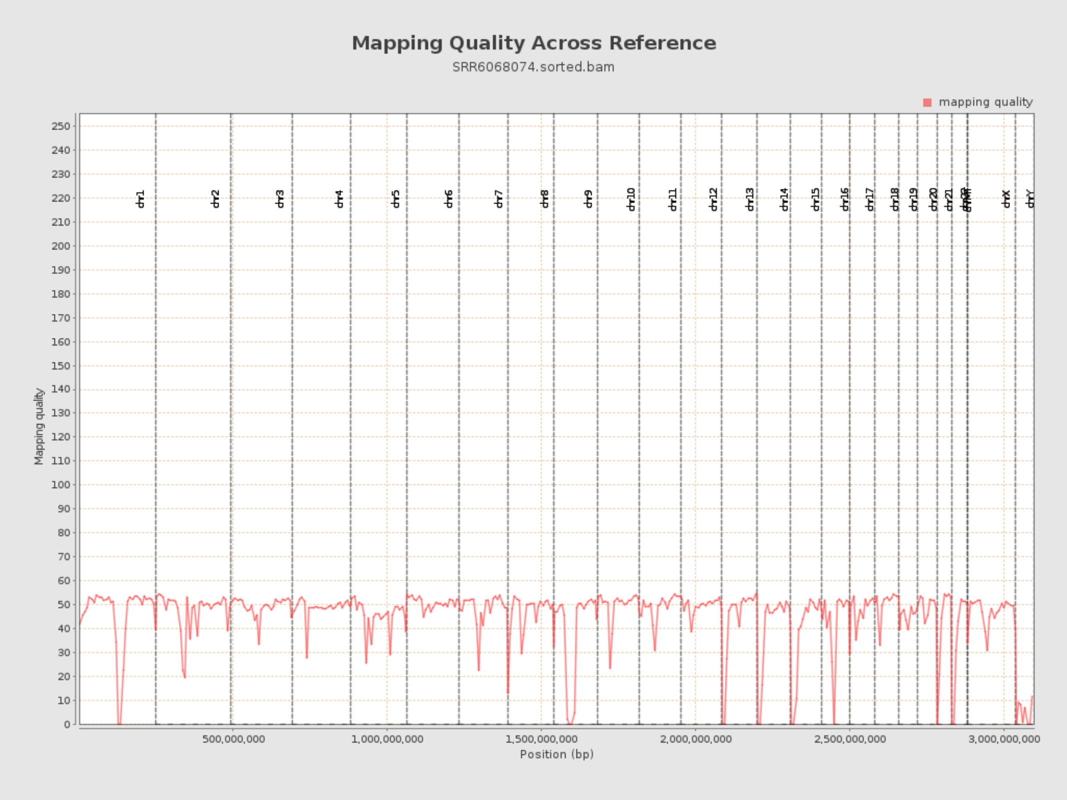
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram