Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:17:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068104.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_SRR6068104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:17:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,533,327
Mapped reads	5,271,730 / 95.27%
Unmapped reads	261,597 / 4.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,965 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	914,231 / 16.52%
Duplication rate	14.19%
Clipped reads	2,634,951 / 47.62%

2.2. ACGT Content

Number/percentage of A's	91,447,348 / 26.76%
Number/percentage of C's	60,236,213 / 17.63%
Number/percentage of T's	112,832,479 / 33.02%
Number/percentage of G's	77,122,132 / 22.57%
Number/percentage of N's	39,247 / 0.01%
GC Percentage	40.2%

2.3. Coverage

Mean	0.1104

Standard Deviation	1.0537

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

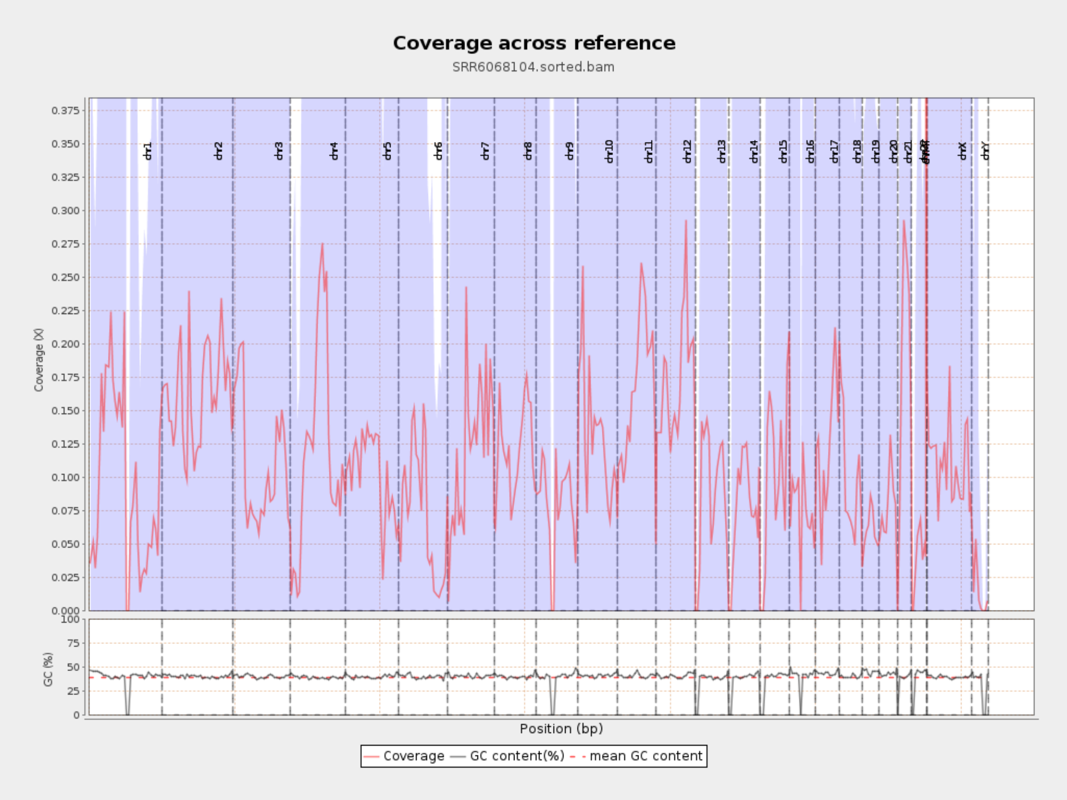
General error rate	0.56%
Mismatches	1,885,536
Insertions	22,333
Mapped reads with at least one insertion	0.42%
Deletions	88,444
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.38%

2.6. Chromosome stats

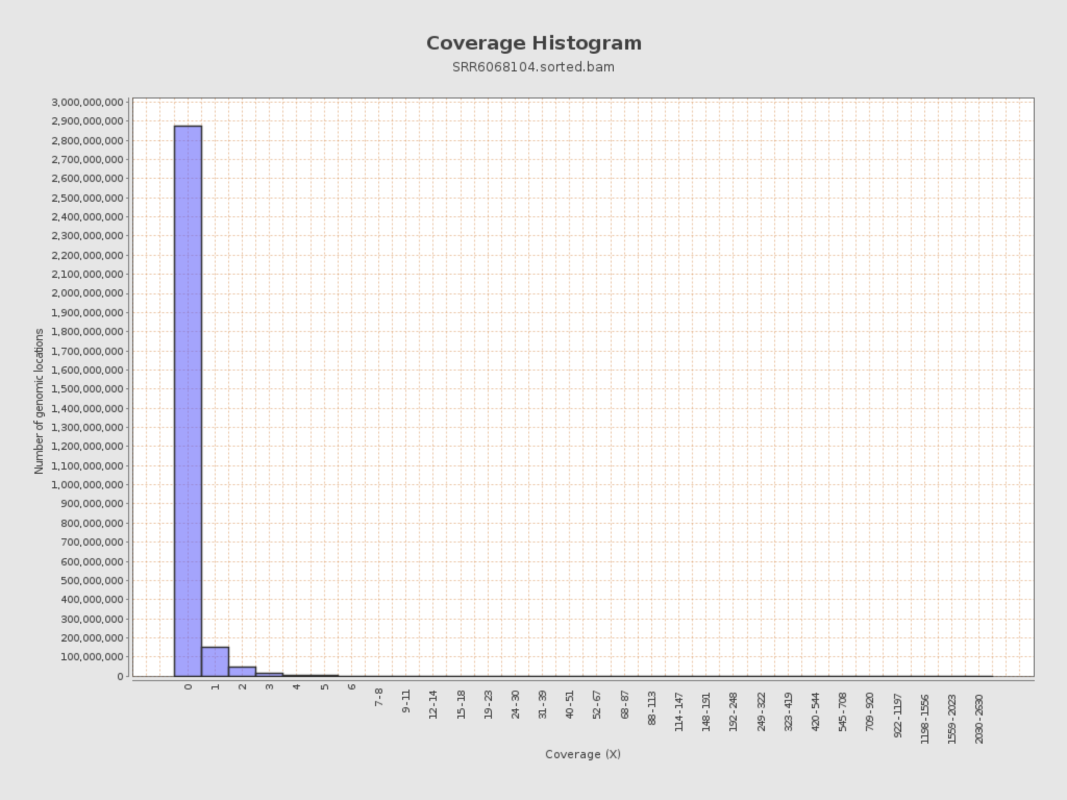
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23474593	0.0942	2.1125
chr2	243199373	39403776	0.162	1.4551
chr3	198022430	21921761	0.1107	0.4763
chr4	191154276	22696137	0.1187	0.5576
chr5	180915260	18599996	0.1028	0.4675
chr6	171115067	12216686	0.0714	0.5436
chr7	159138663	19502907	0.1226	1.5602

chr8	146364022	17615292	0.1204	1.2506
chr9	141213431	11124906	0.0788	0.8918
chr10	135534747	18041007	0.1331	0.9594
chr11	135006516	22845525	0.1692	0.8541
chr12	133851895	23238623	0.1736	0.6486
chr13	115169878	9968842	0.0866	0.4606
chr14	107349540	8149537	0.0759	0.4958
chr15	102531392	10360270	0.101	0.4921
chr16	90354753	6716054	0.0743	0.4974
chr17	81195210	10032362	0.1236	0.5639
chr18	78077248	7828998	0.1003	1.6884
chr19	59128983	3624619	0.0613	1.4481
chr20	63025520	4918705	0.078	0.4793
chr21	48129895	8972641	0.1864	0.6677
chr22	51304566	1939444	0.0378	0.265
chrMT	16571	451705	27.2588	16.1134
chrX	155270560	17290953	0.1114	0.601
chrY	59373566	897214	0.0151	0.5886

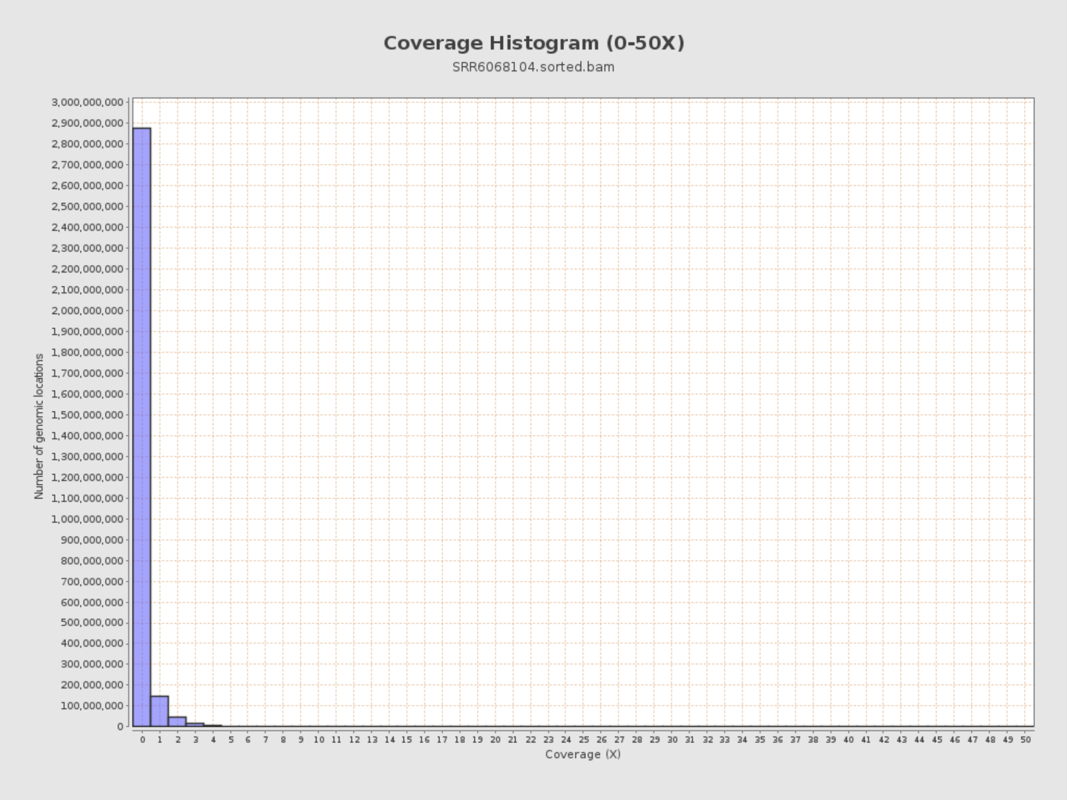
3. Results : Coverage across reference



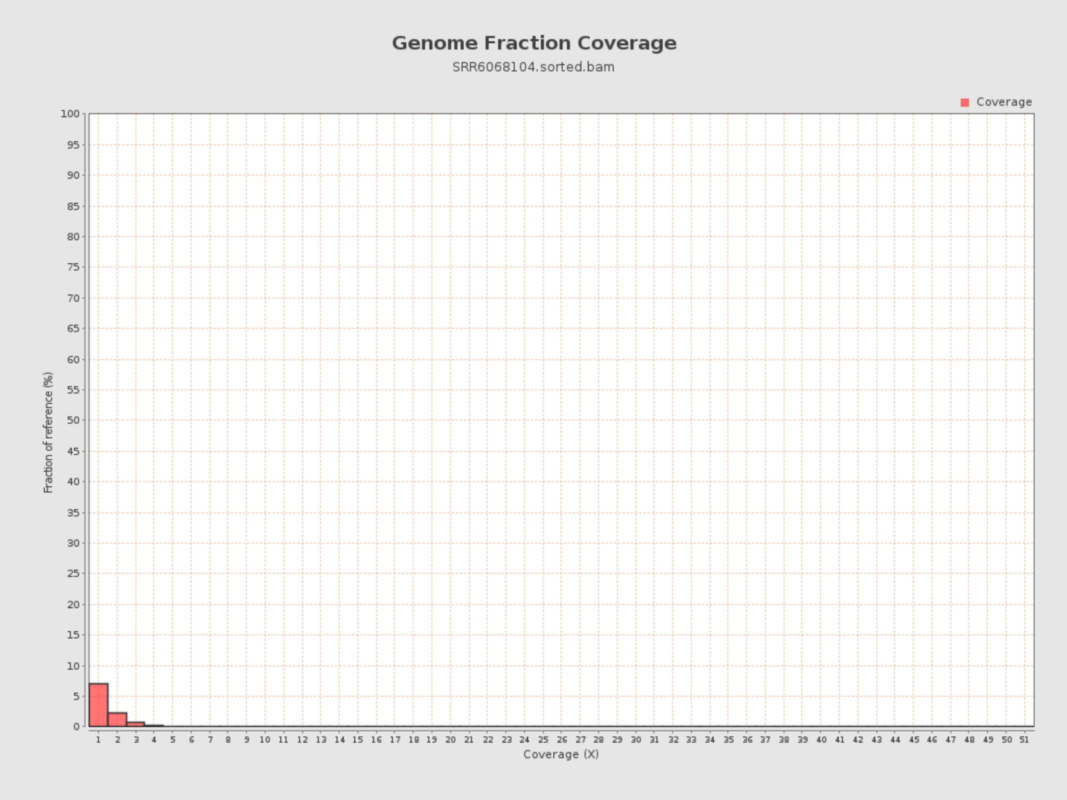
4. Results : Coverage Histogram



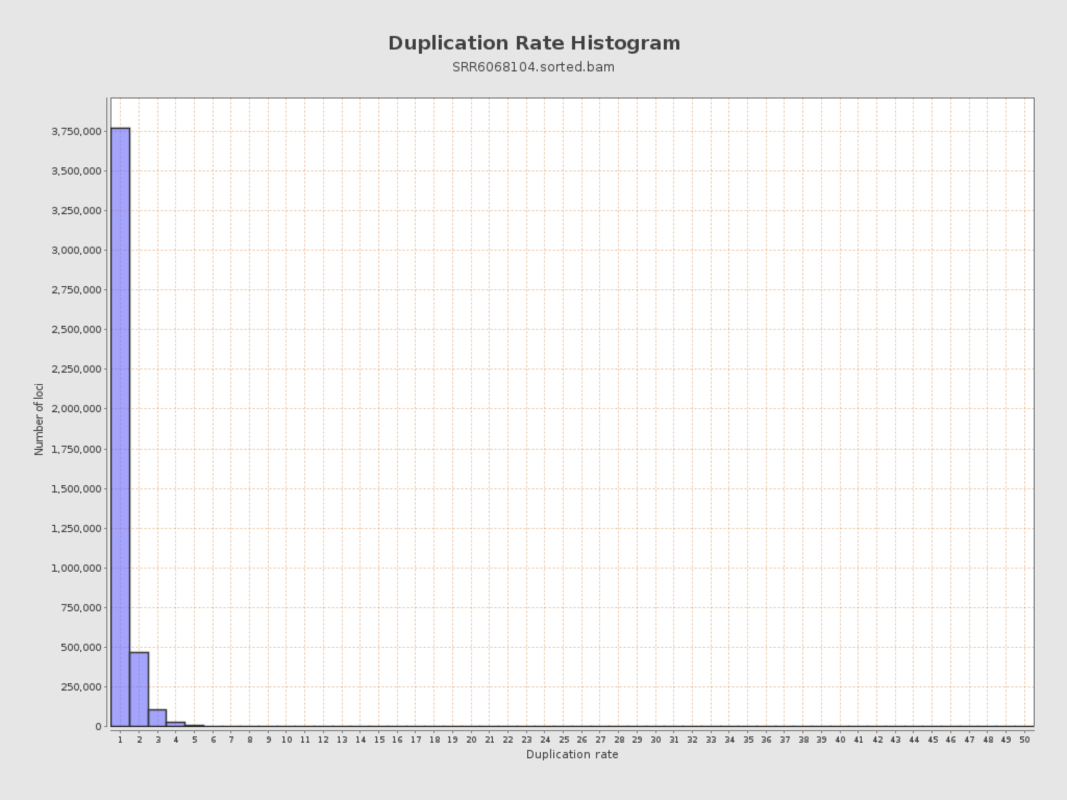
5. Results : Coverage Histogram (0-50X)



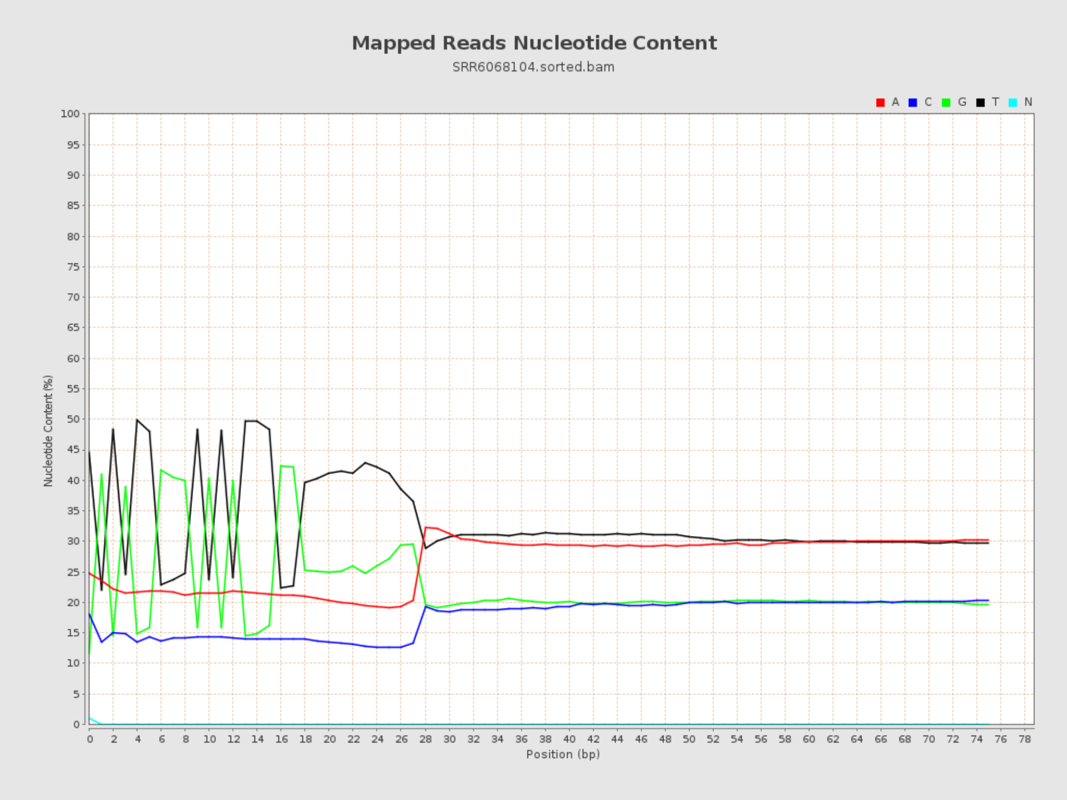
6. Results : Genome Fraction Coverage



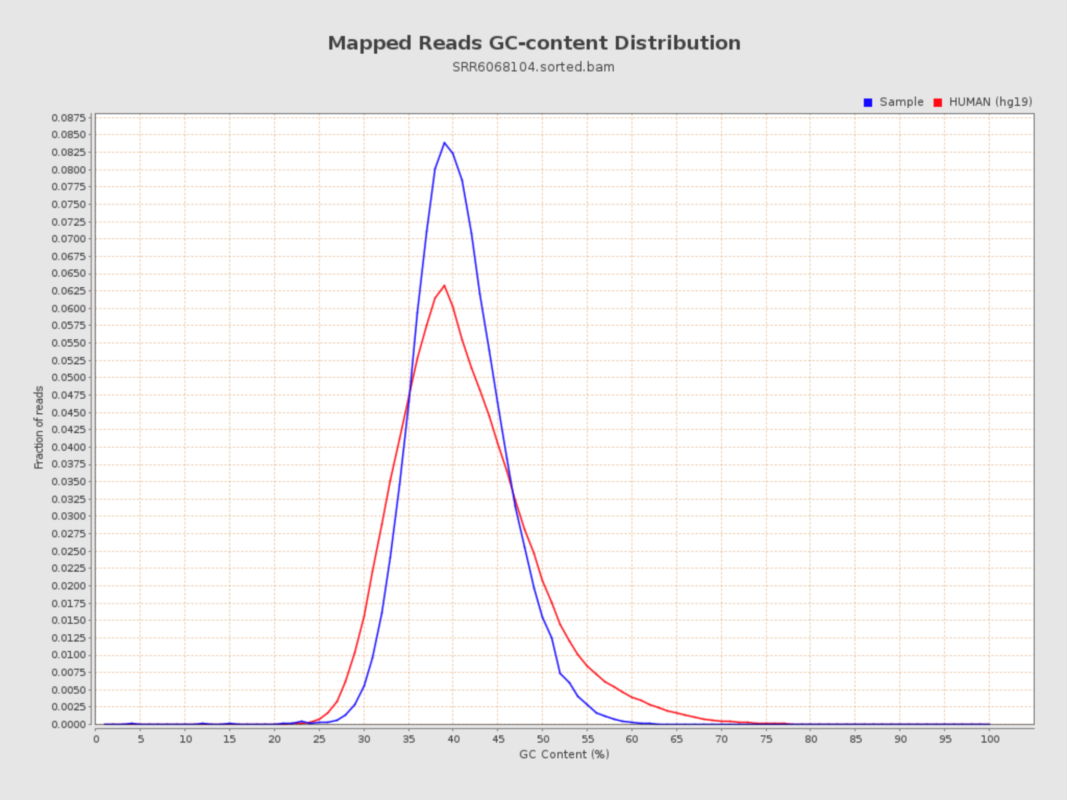
7. Results : Duplication Rate Histogram



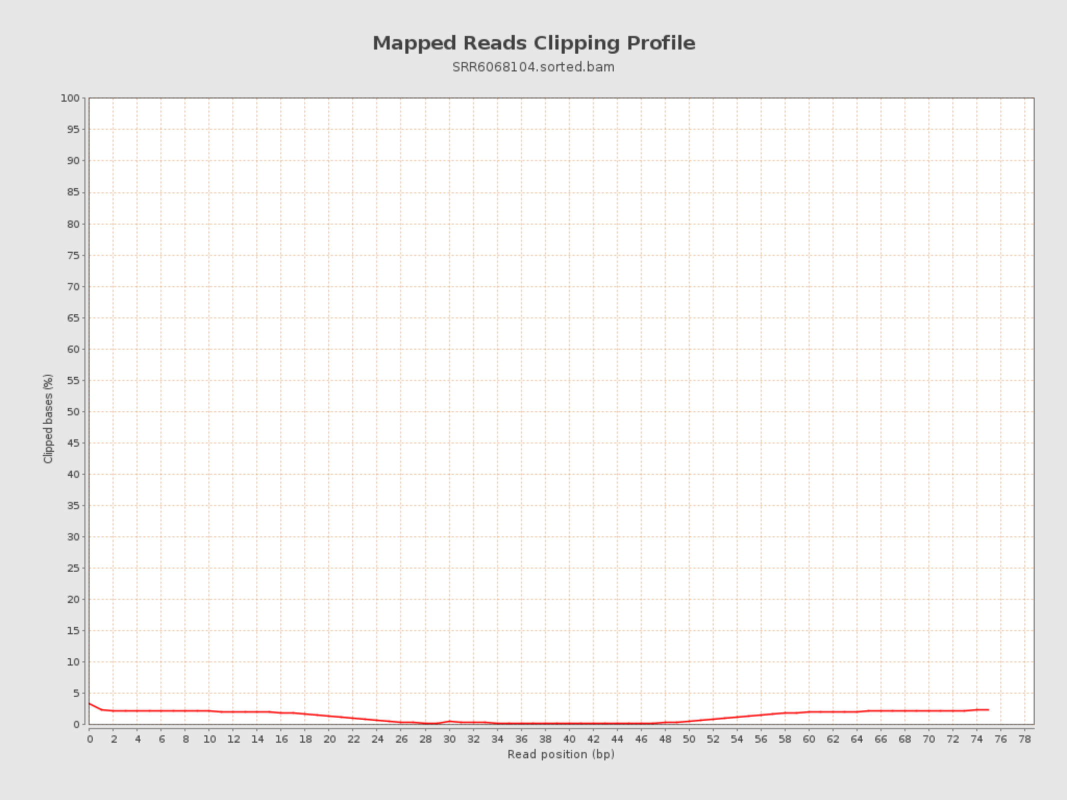
8. Results : Mapped Reads Nucleotide Content



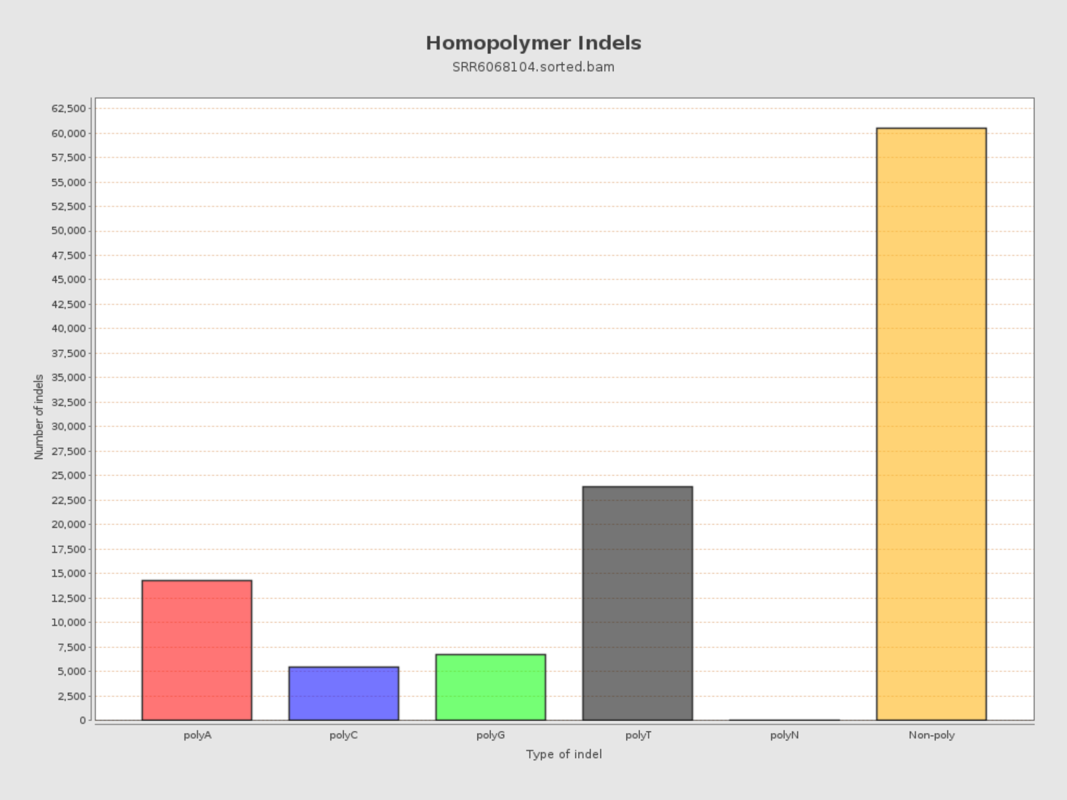
9. Results : Mapped Reads GC-content Distribution



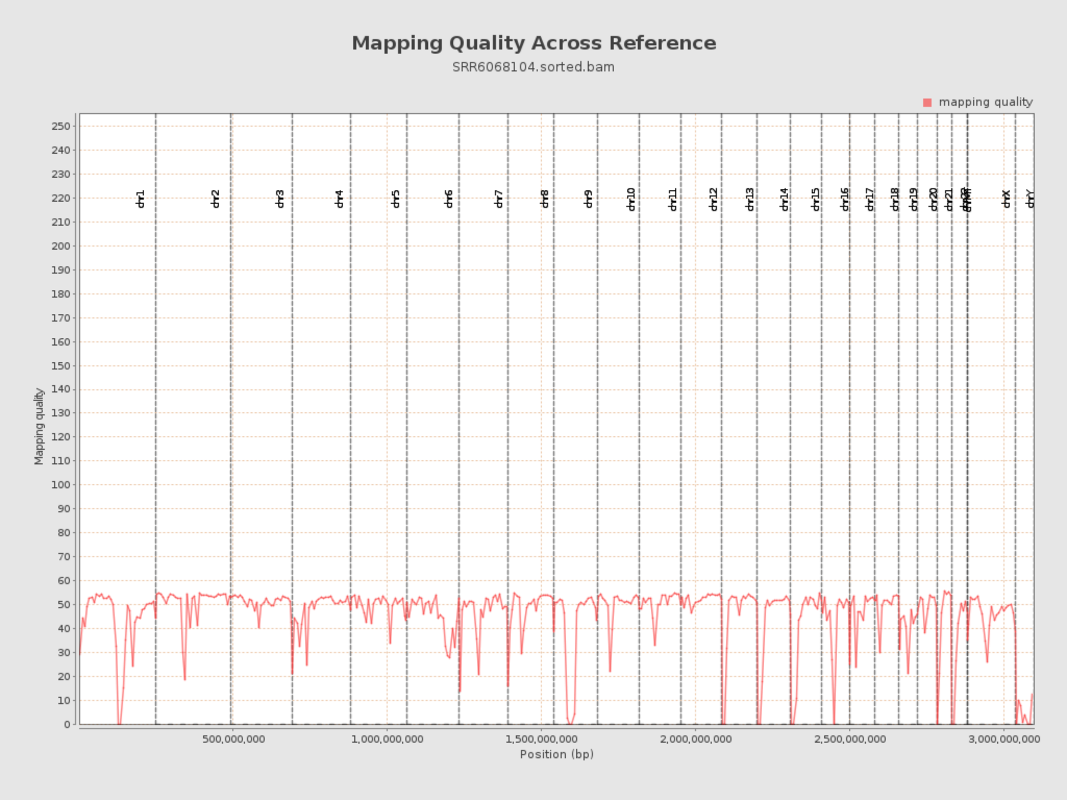
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram