Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:58:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068099.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_SRR6068099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:58:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,607,834
Mapped reads	2,368,810 / 90.83%
Unmapped reads	239,024 / 9.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,745 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	107,655 / 4.13%
Duplication rate	3.32%
Clipped reads	1,080,343 / 41.43%

2.2. ACGT Content

Number/percentage of A's	43,752,643 / 27.75%
Number/percentage of C's	29,170,225 / 18.5%
Number/percentage of T's	49,612,173 / 31.47%
Number/percentage of G's	35,113,154 / 22.27%
Number/percentage of N's	3,317 / 0%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.5084

2.4. Mapping Quality

Mean Mapping Quality	42.11

2.5. Mismatches and indels

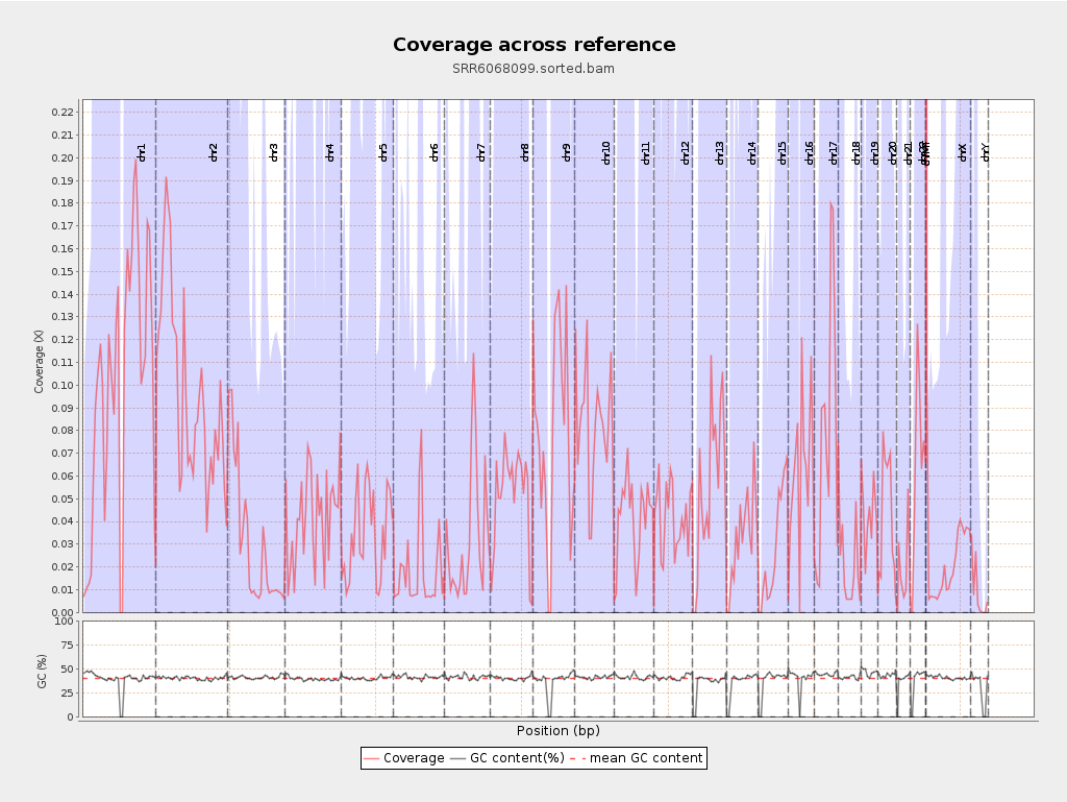
General error rate	0.81%
Mismatches	1,261,923
Insertions	12,370
Mapped reads with at least one insertion	0.52%
Deletions	44,010
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.85%

2.6. Chromosome stats

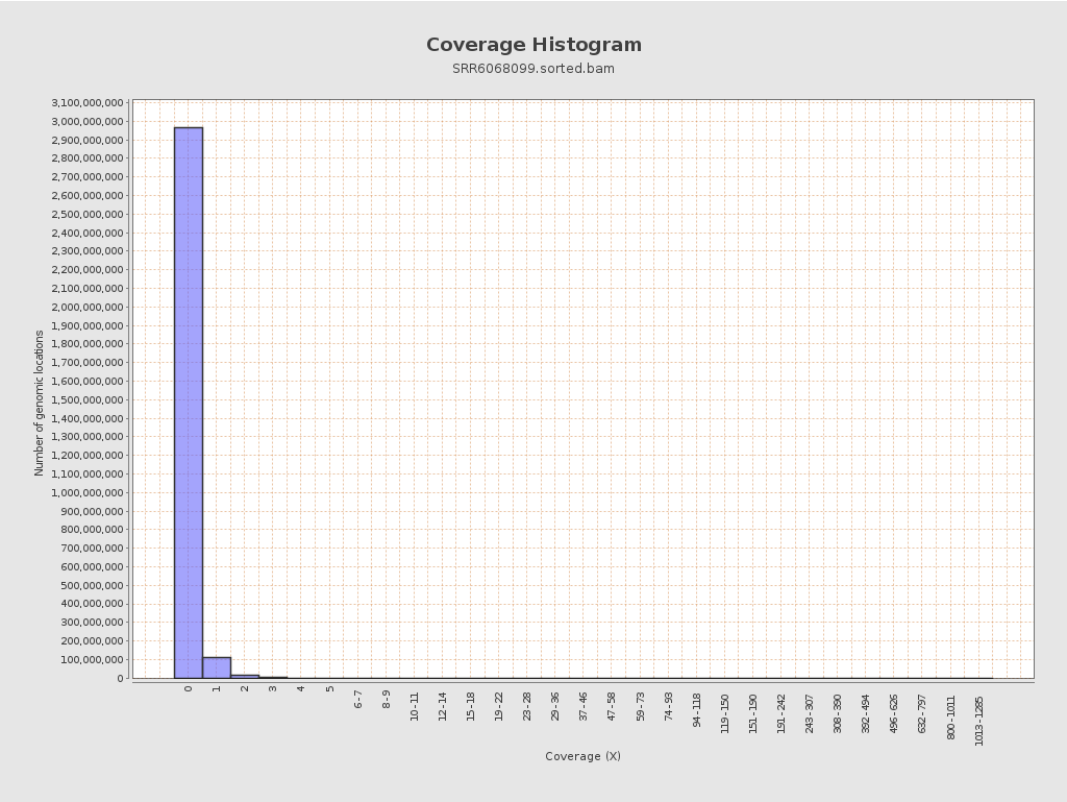
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24362683	0.0977	1.1564
chr2	243199373	23567715	0.0969	0.6217
chr3	198022430	6076775	0.0307	0.229
chr4	191154276	7961408	0.0416	0.2533
chr5	180915260	6319286	0.0349	0.2211
chr6	171115067	3151176	0.0184	0.1764
chr7	159138663	5351474	0.0336	0.2606

chr8	146364022	7446181	0.0509	0.4639
chr9	141213431	10954117	0.0776	0.5295
chr10	135534747	11073103	0.0817	0.6975
chr11	135006516	5704411	0.0423	0.3231
chr12	133851895	5661033	0.0423	0.2597
chr13	115169878	6506567	0.0565	0.2758
chr14	107349540	3587608	0.0334	0.2643
chr15	102531392	2851584	0.0278	0.1984
chr16	90354753	5524951	0.0611	0.3674
chr17	81195210	6431354	0.0792	0.3392
chr18	78077248	1633272	0.0209	0.7711
chr19	59128983	2400476	0.0406	0.9359
chr20	63025520	2779798	0.0441	0.2598
chr21	48129895	944760	0.0196	0.2001
chr22	51304566	3278358	0.0639	0.2946
chrMT	16571	61481	3.7102	2.9961
chrX	155270560	3586487	0.0231	0.2145
chrY	59373566	508834	0.0086	0.2814

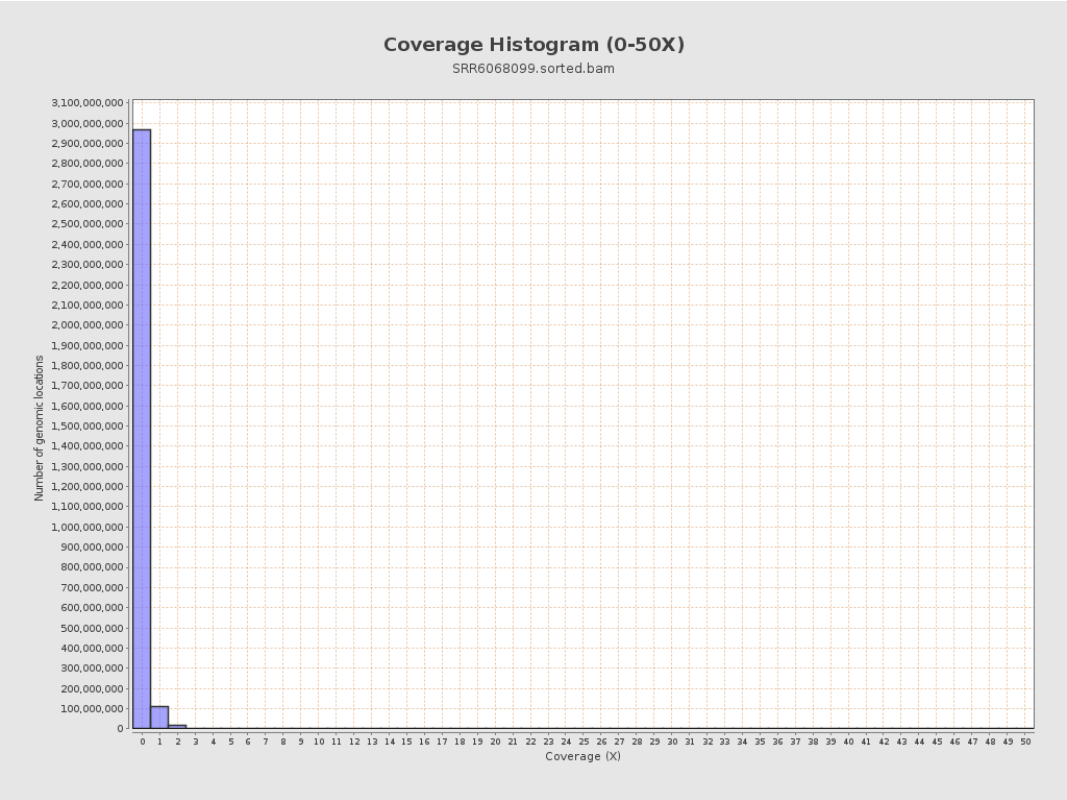
3. Results : Coverage across reference



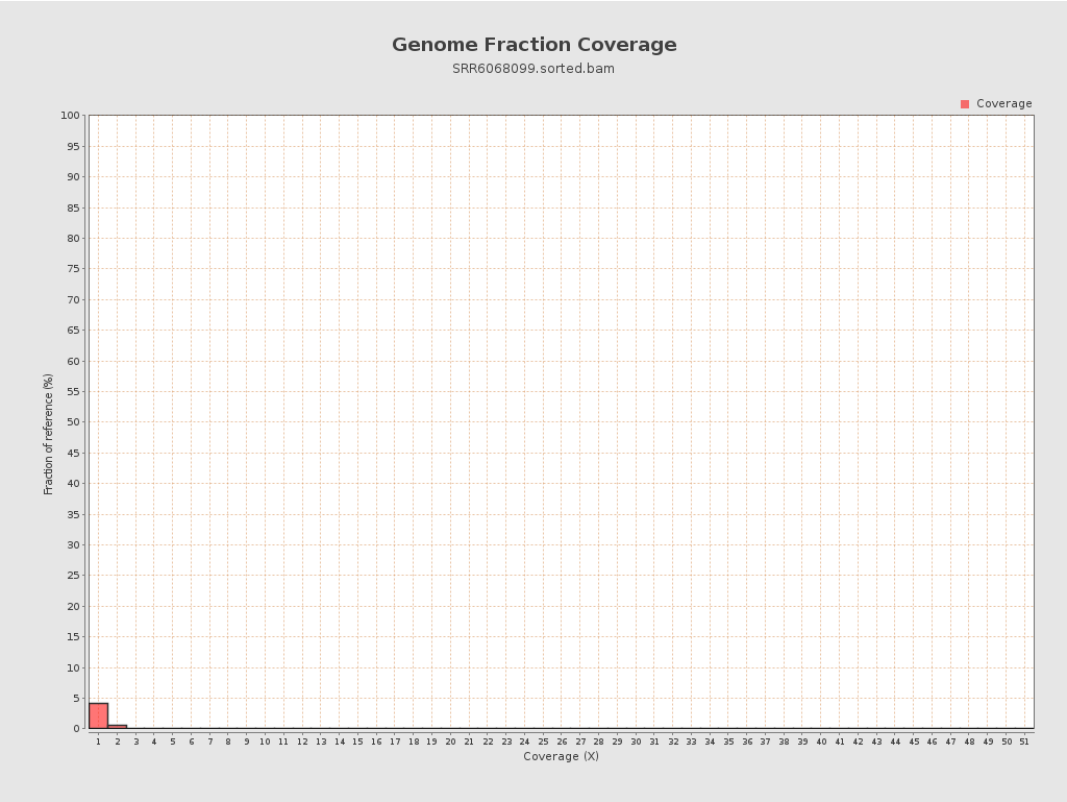
4. Results : Coverage Histogram



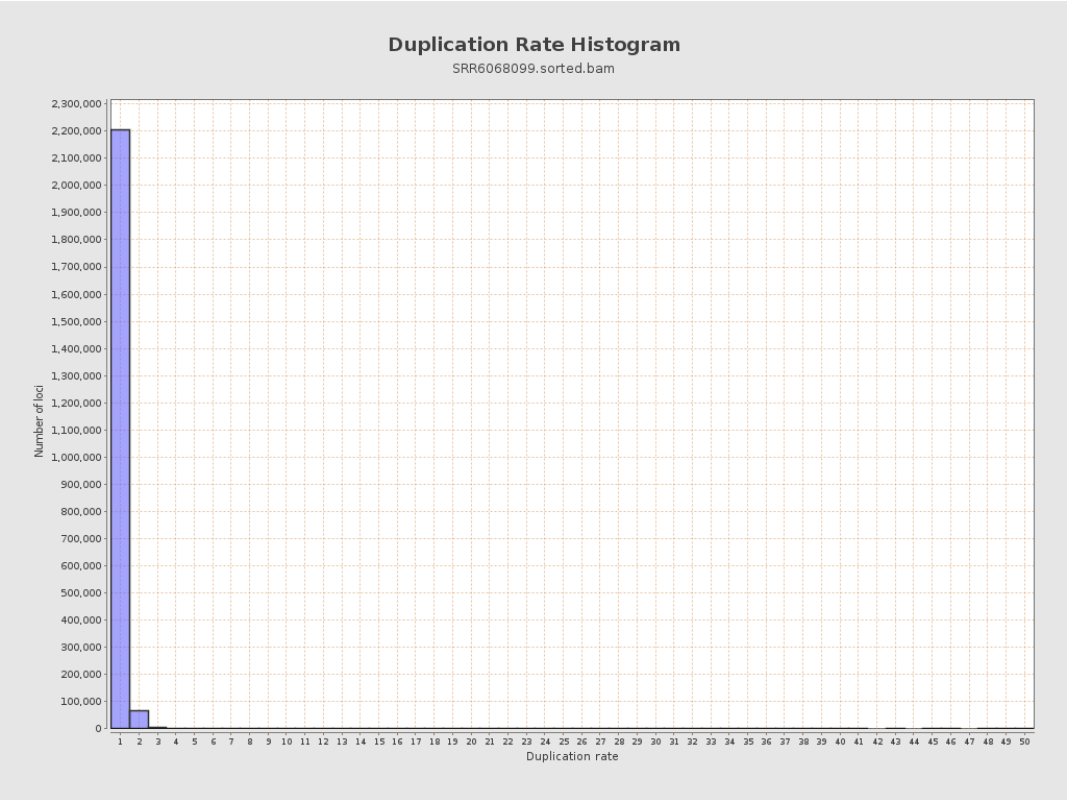
5. Results : Coverage Histogram (0-50X)



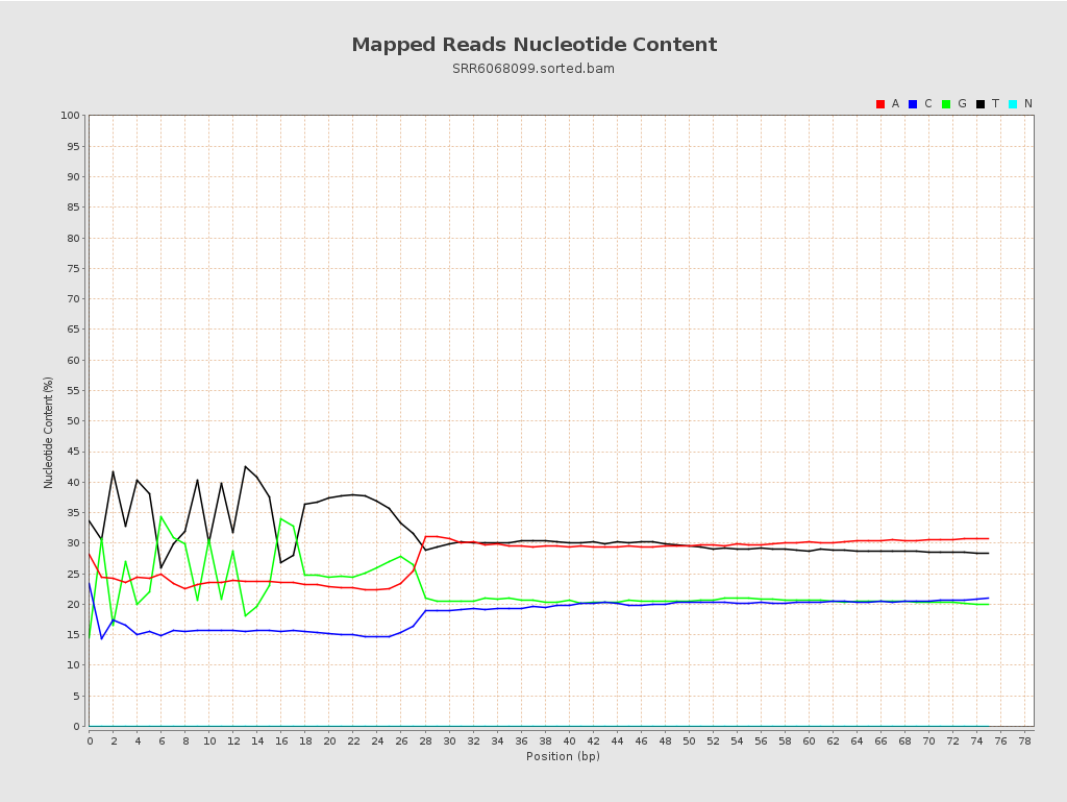
6. Results : Genome Fraction Coverage



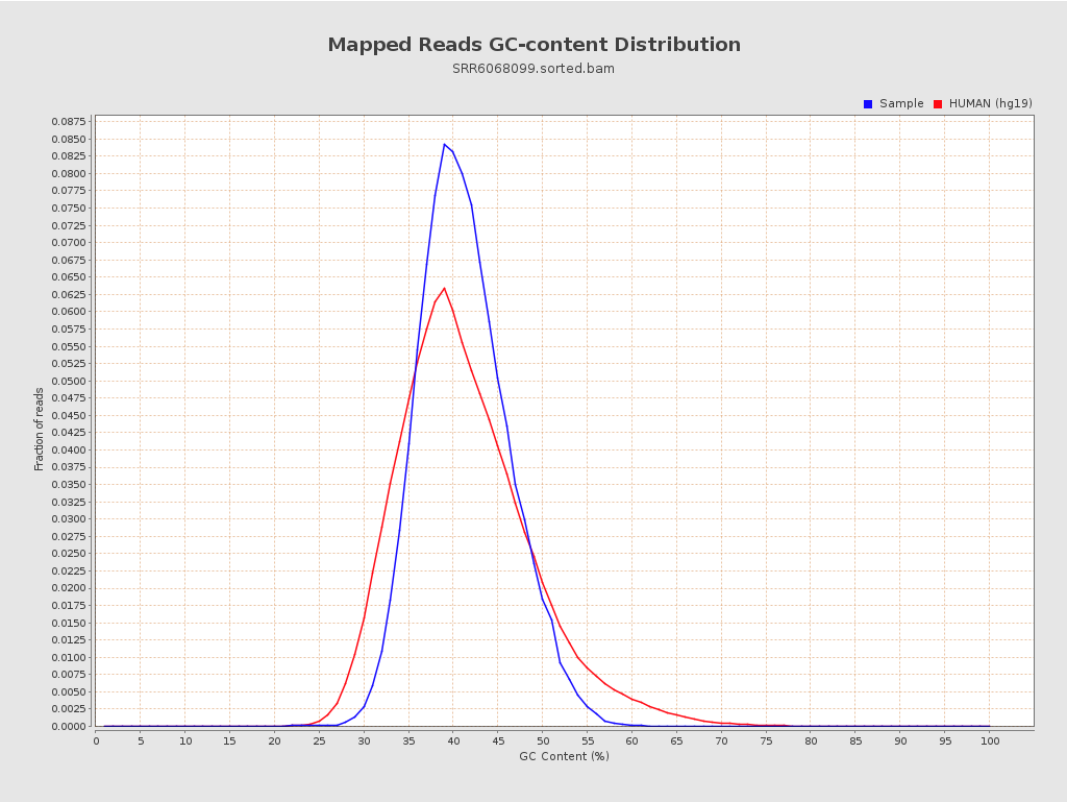
7. Results : Duplication Rate Histogram



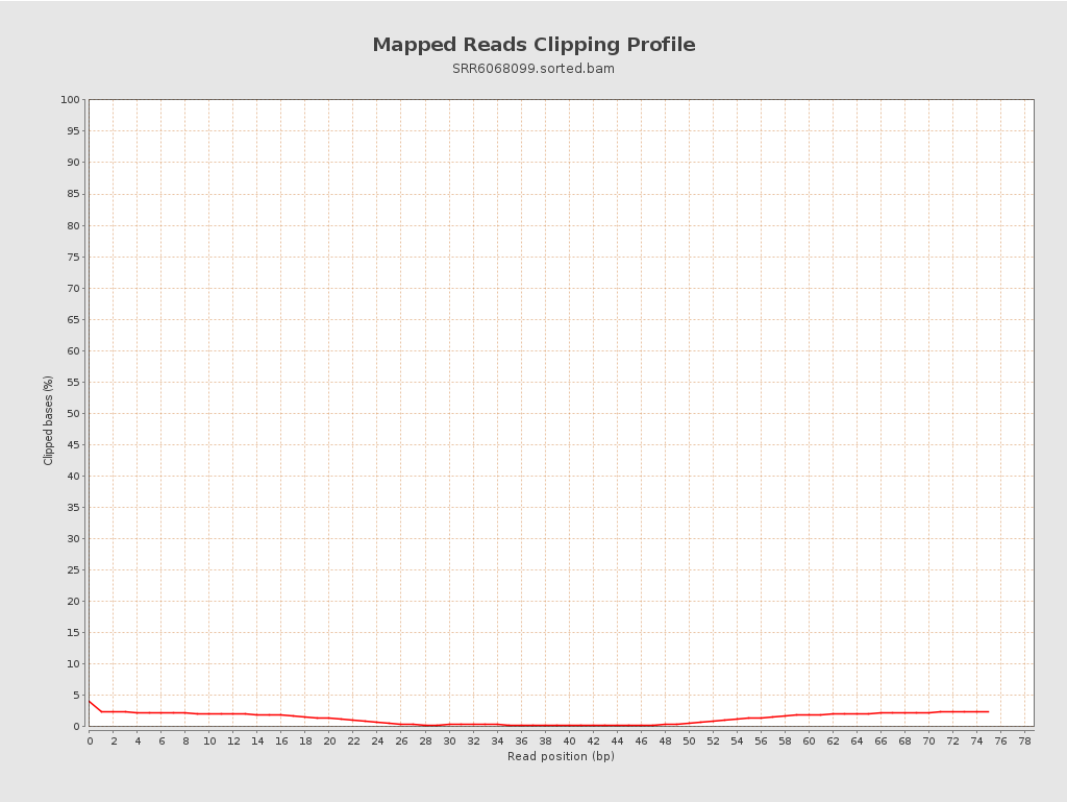
8. Results : Mapped Reads Nucleotide Content



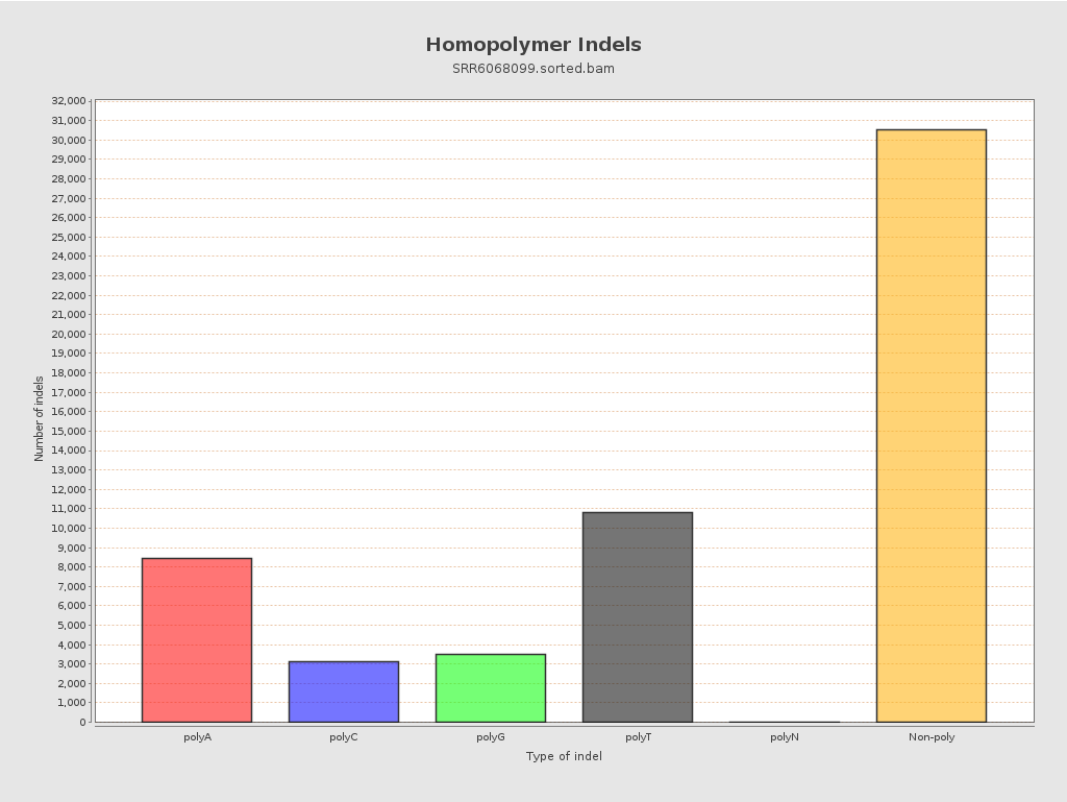
9. Results : Mapped Reads GC-content Distribution



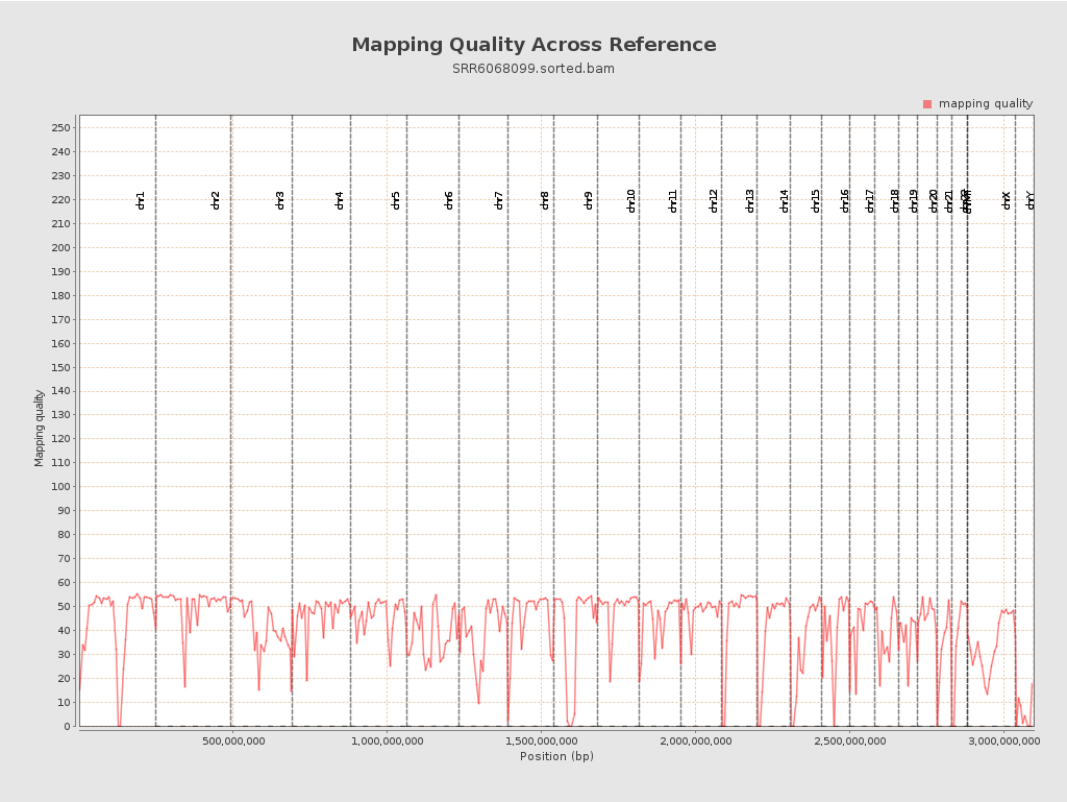
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram