Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:45:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068127.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_SRR6068127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:45:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,369,502
Mapped reads	4,119,217 / 94.27%
Unmapped reads	250,285 / 5.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,274 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	371,448 / 8.5%
Duplication rate	7.12%
Clipped reads	2,187,701 / 50.07%

2.2. ACGT Content

Number/percentage of A's	71,403,089 / 26.82%
Number/percentage of C's	48,036,033 / 18.04%
Number/percentage of T's	85,322,812 / 32.05%
Number/percentage of G's	61,465,318 / 23.08%
Number/percentage of N's	29,923 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.086

Standard Deviation	1.0676

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

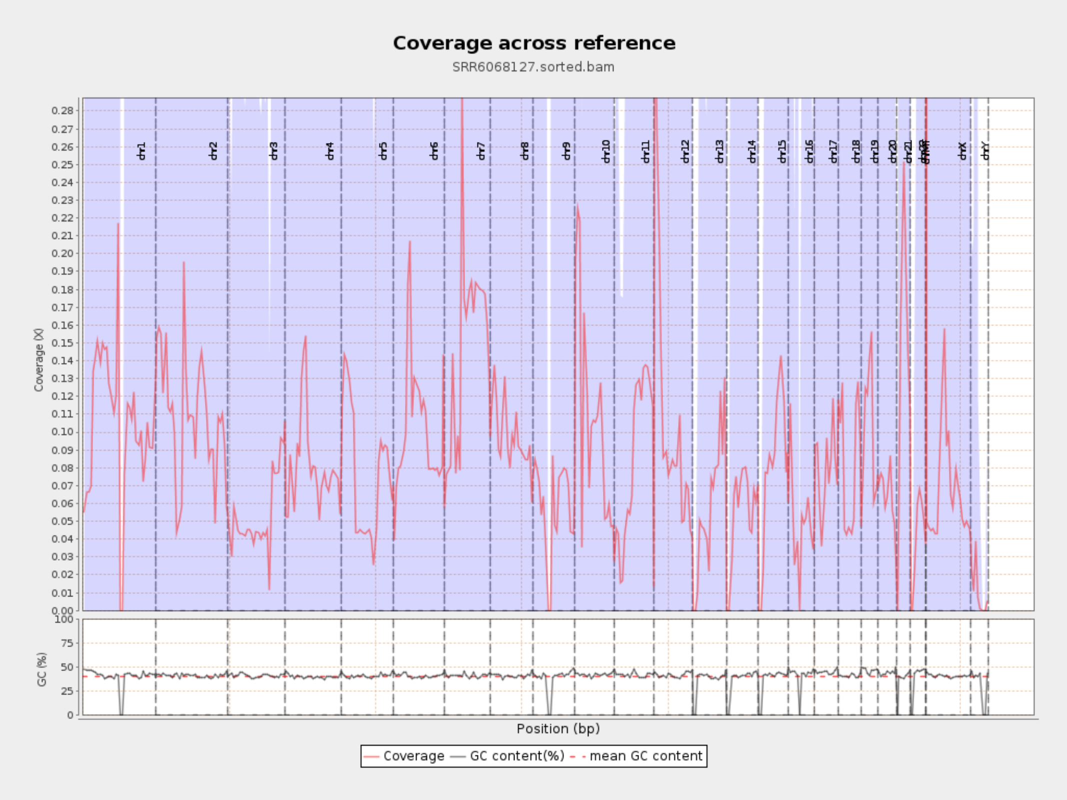
General error rate	0.6%
Mismatches	1,575,385
Insertions	17,805
Mapped reads with at least one insertion	0.43%
Deletions	64,579
Mapped reads with at least one deletion	1.55%
Homopolymer indels	44.38%

2.6. Chromosome stats

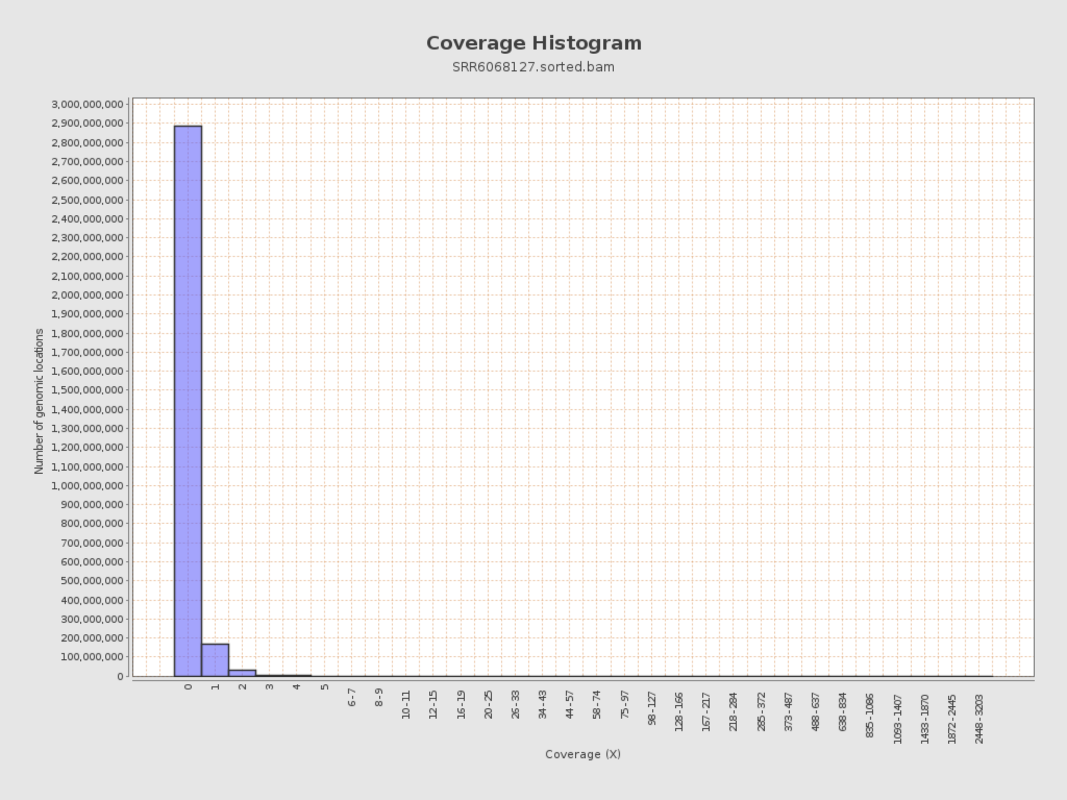
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26153673	0.1049	2.4618
chr2	243199373	26729897	0.1099	1.1271
chr3	198022430	10457641	0.0528	0.2848
chr4	191154276	15532193	0.0813	0.3765
chr5	180915260	13869585	0.0767	0.3513
chr6	171115067	17628222	0.103	0.5938
chr7	159138663	23408603	0.1471	2.2291

chr8	146364022	14286970	0.0976	1.2728
chr9	141213431	8184854	0.058	0.6788
chr10	135534747	14685663	0.1084	0.616
chr11	135006516	11528664	0.0854	0.4612
chr12	133851895	15227796	0.1138	0.4582
chr13	115169878	6827021	0.0593	0.3277
chr14	107349540	5858954	0.0546	0.3613
chr15	102531392	8137543	0.0794	0.39
chr16	90354753	4515055	0.05	0.3403
chr17	81195210	6505080	0.0801	0.3678
chr18	78077248	6356563	0.0814	1.2516
chr19	59128983	6143343	0.1039	1.4544
chr20	63025520	4096728	0.065	0.368
chr21	48129895	6753098	0.1403	0.4825
chr22	51304566	2097414	0.0409	0.2393
chrMT	16571	211586	12.7685	7.4888
chrX	155270560	10562199	0.068	0.4406
chrY	59373566	611312	0.0103	0.453

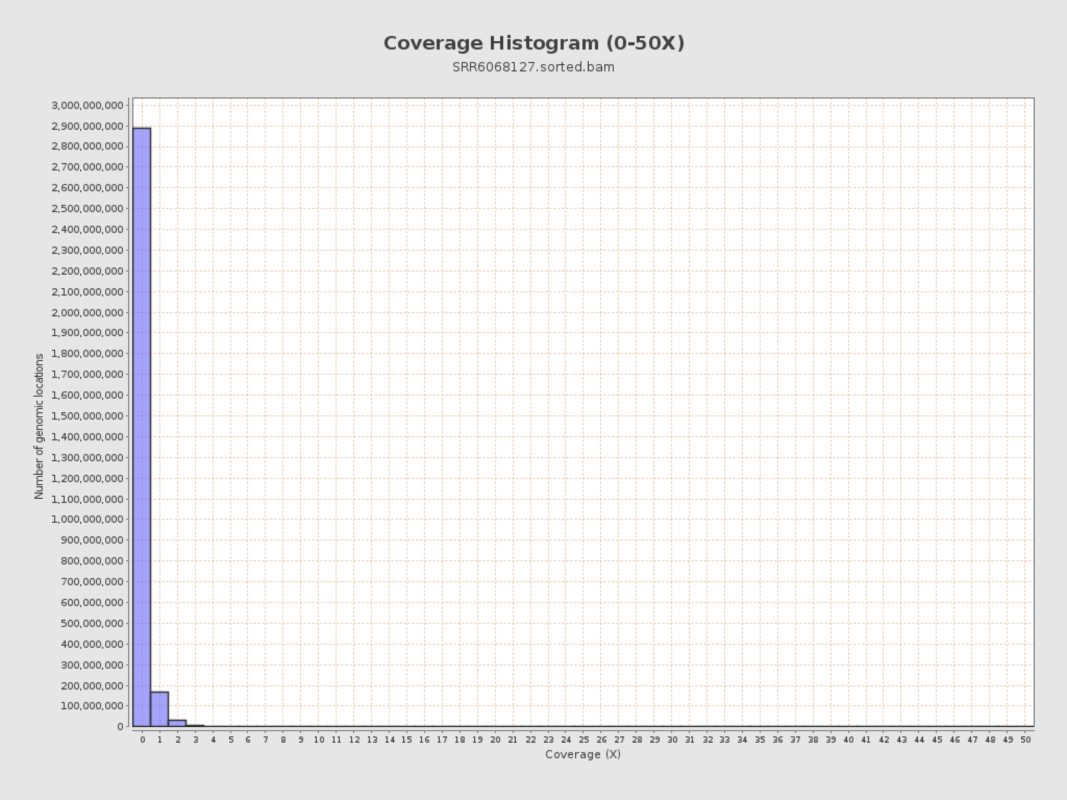
3. Results : Coverage across reference



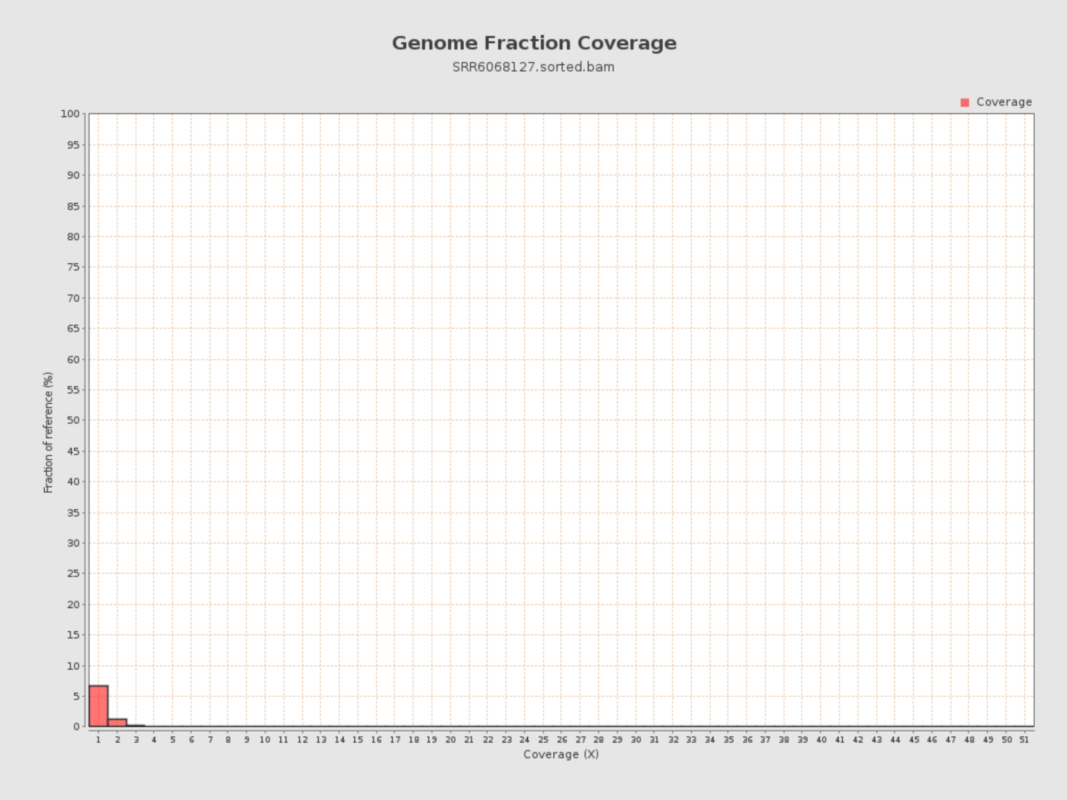
4. Results : Coverage Histogram



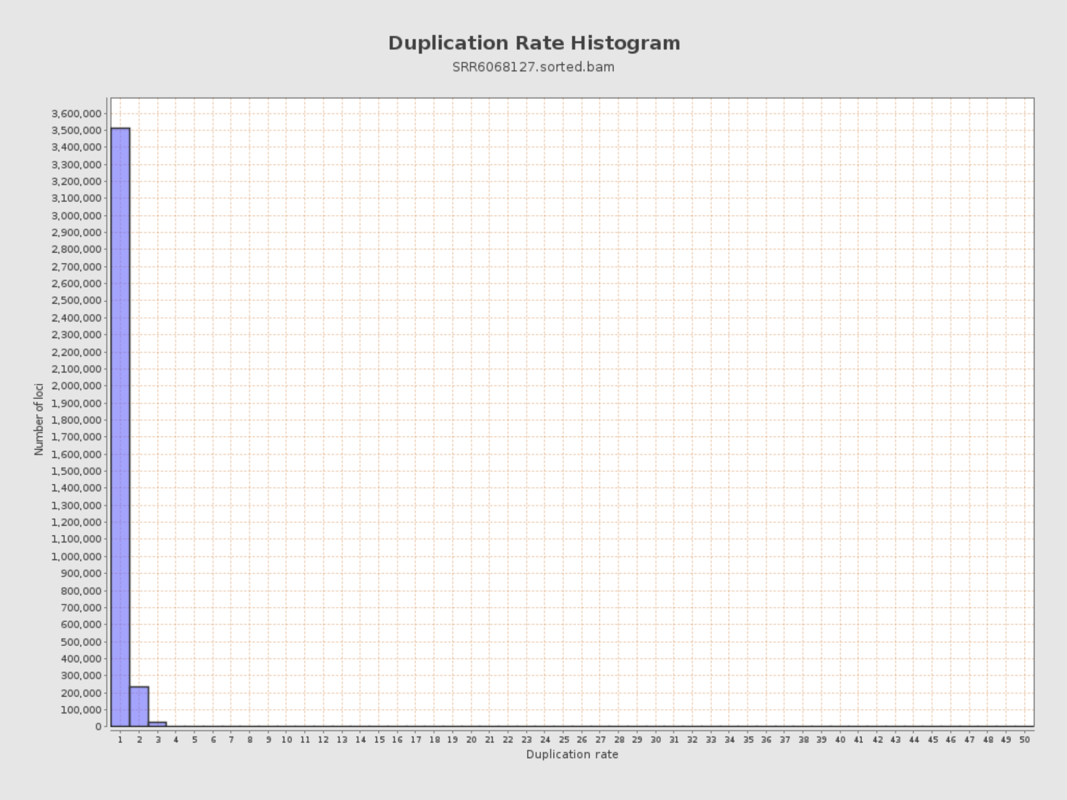
5. Results : Coverage Histogram (0-50X)



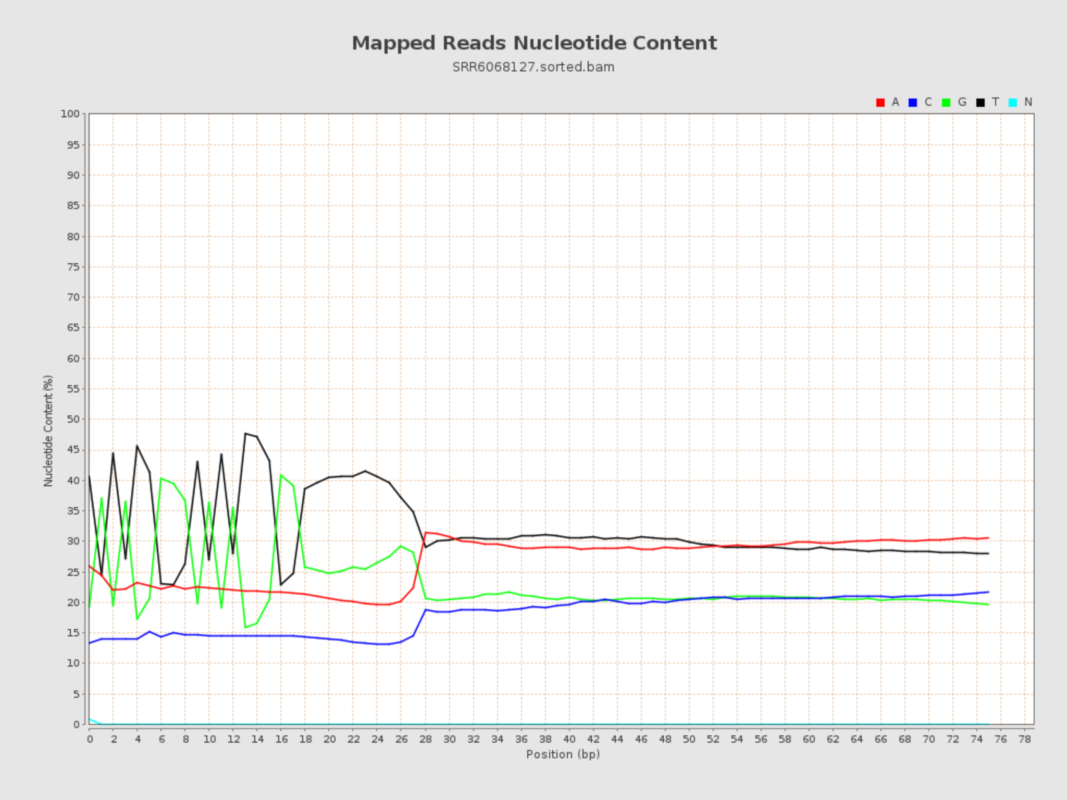
6. Results : Genome Fraction Coverage



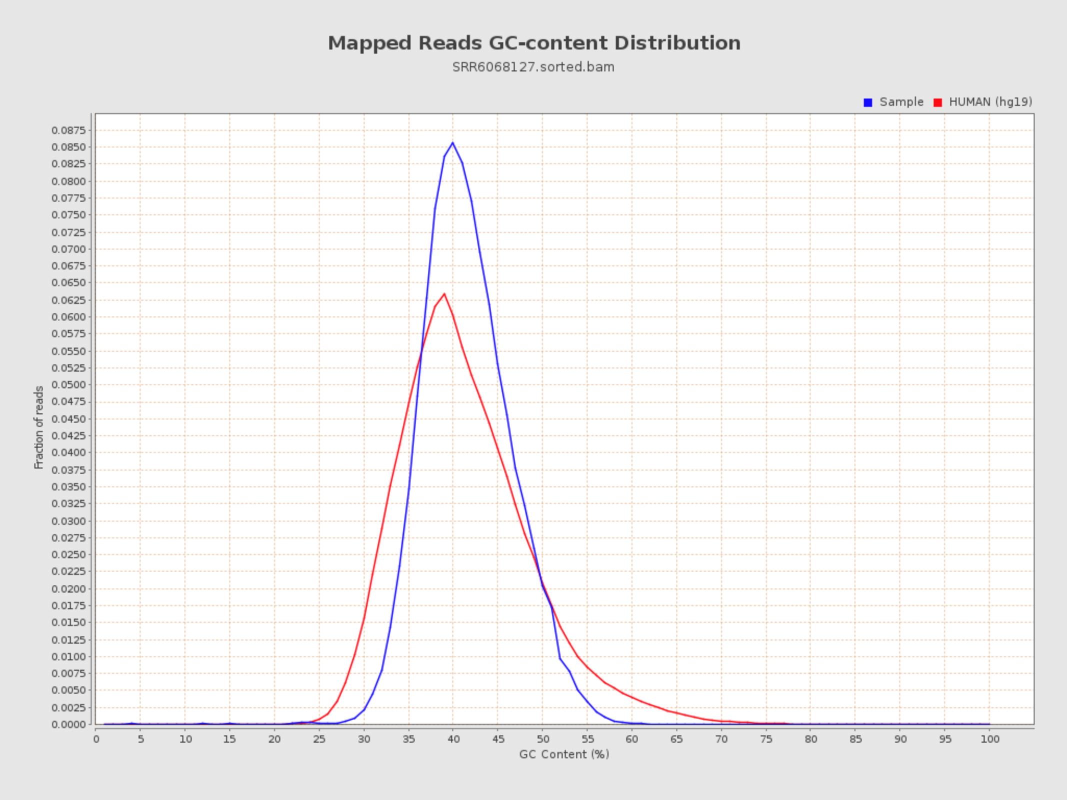
7. Results : Duplication Rate Histogram



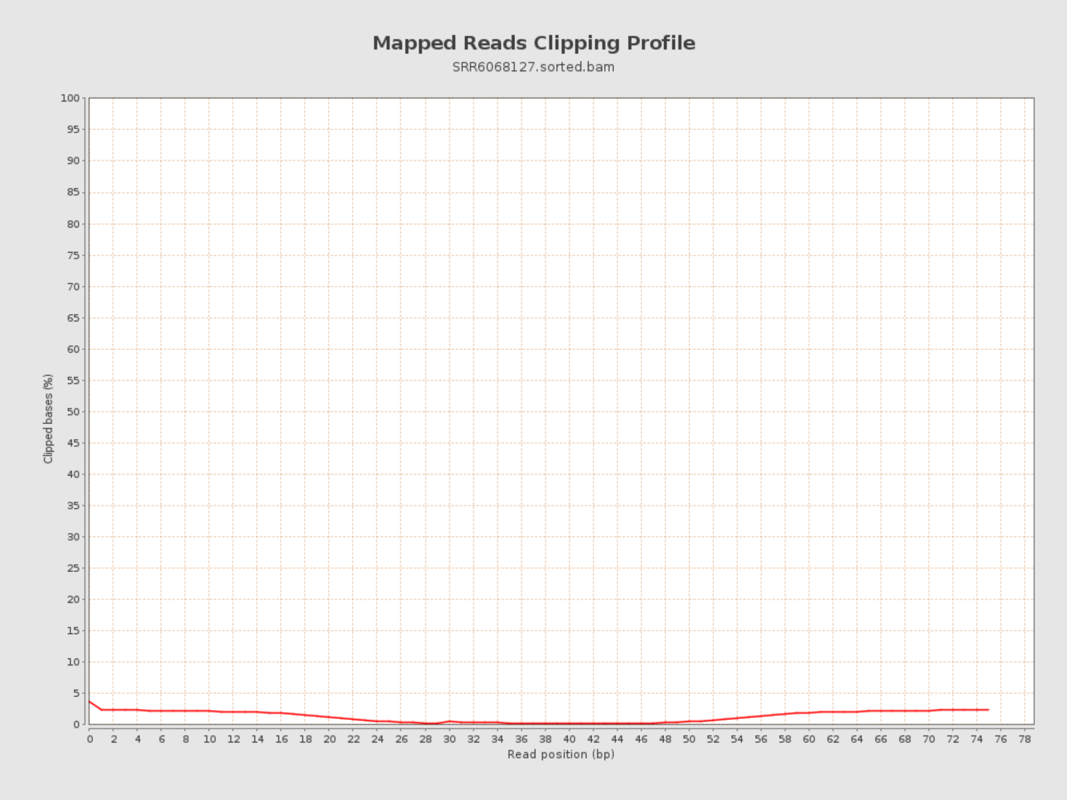
8. Results : Mapped Reads Nucleotide Content



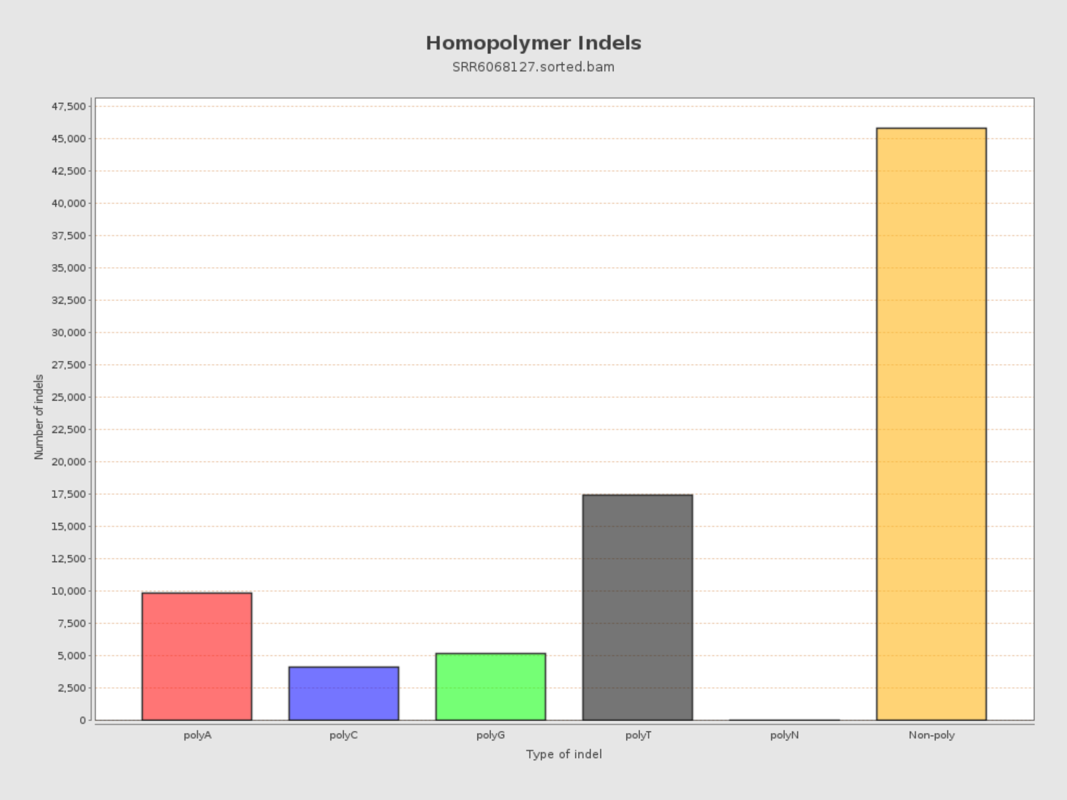
9. Results : Mapped Reads GC-content Distribution



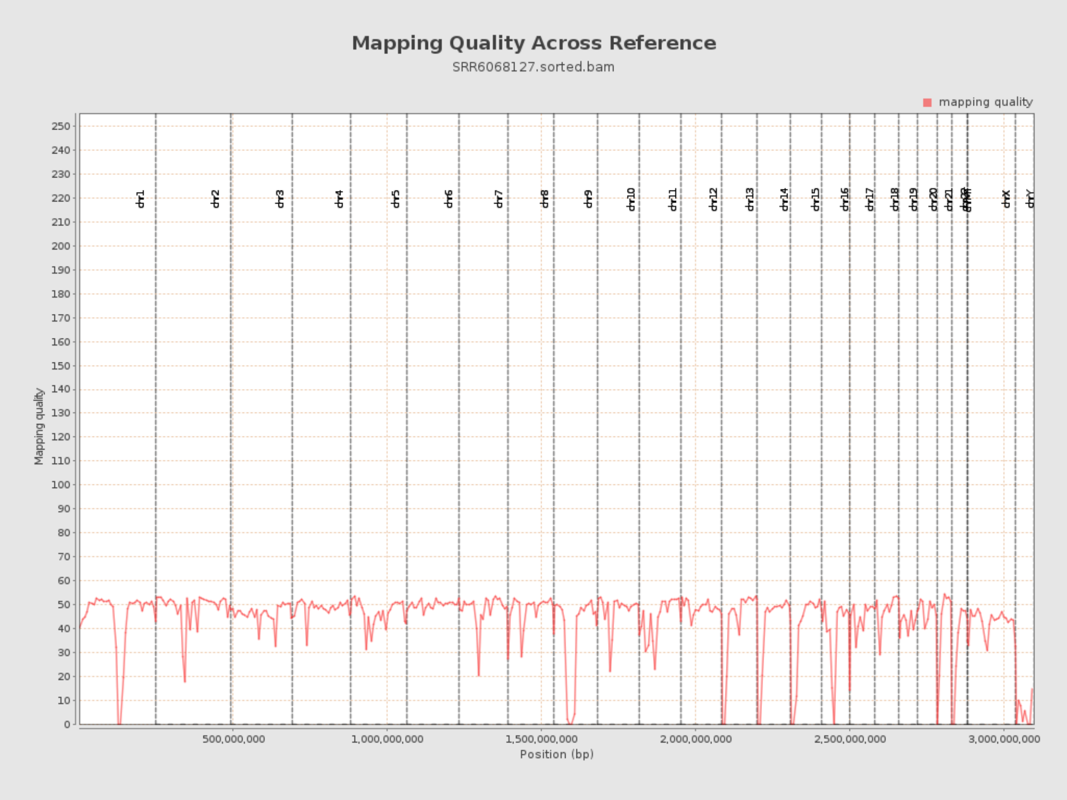
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram