Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:54:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068129.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_SRR6068129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:54:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,357,347
Mapped reads	3,086,609 / 91.94%
Unmapped reads	270,738 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,485 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,151,029 / 34.28%
Duplication rate	23.42%
Clipped reads	2,085,811 / 62.13%

2.2. ACGT Content

Number/percentage of A's	47,891,066 / 25.35%
Number/percentage of C's	32,985,265 / 17.46%
Number/percentage of T's	62,612,564 / 33.15%
Number/percentage of G's	45,394,850 / 24.03%
Number/percentage of N's	19,230 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.6858

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

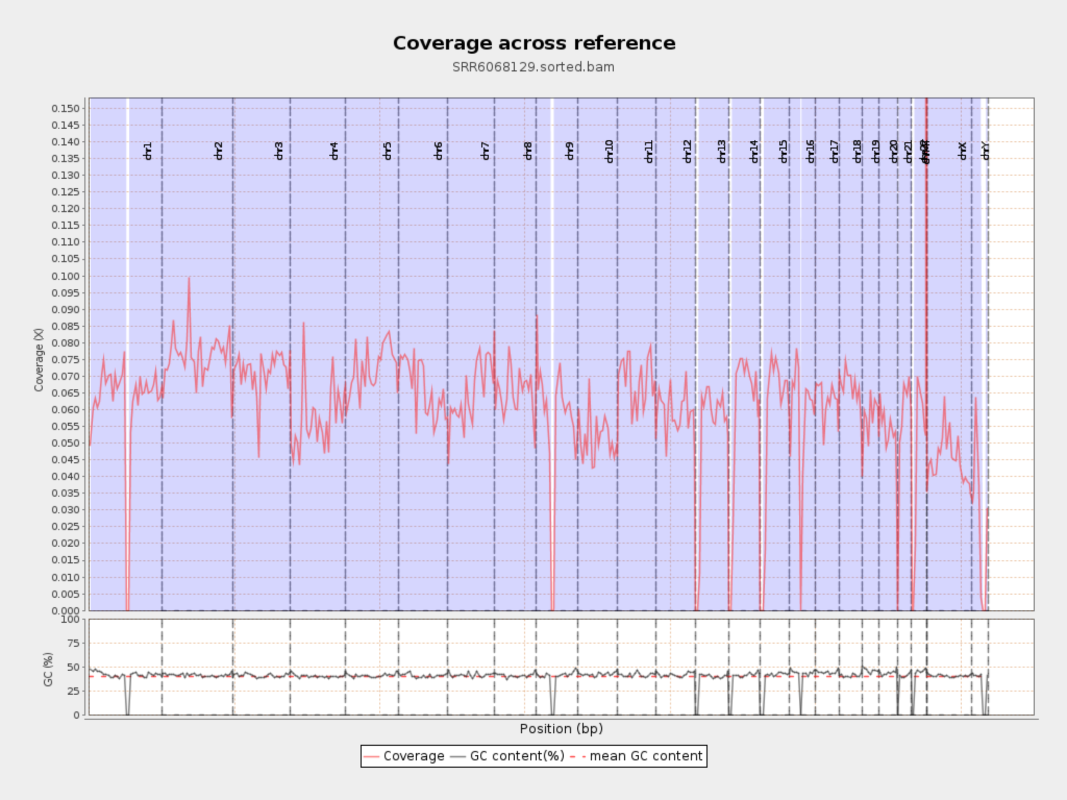
General error rate	0.65%
Mismatches	1,199,057
Insertions	12,308
Mapped reads with at least one insertion	0.4%
Deletions	50,638
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.84%

2.6. Chromosome stats

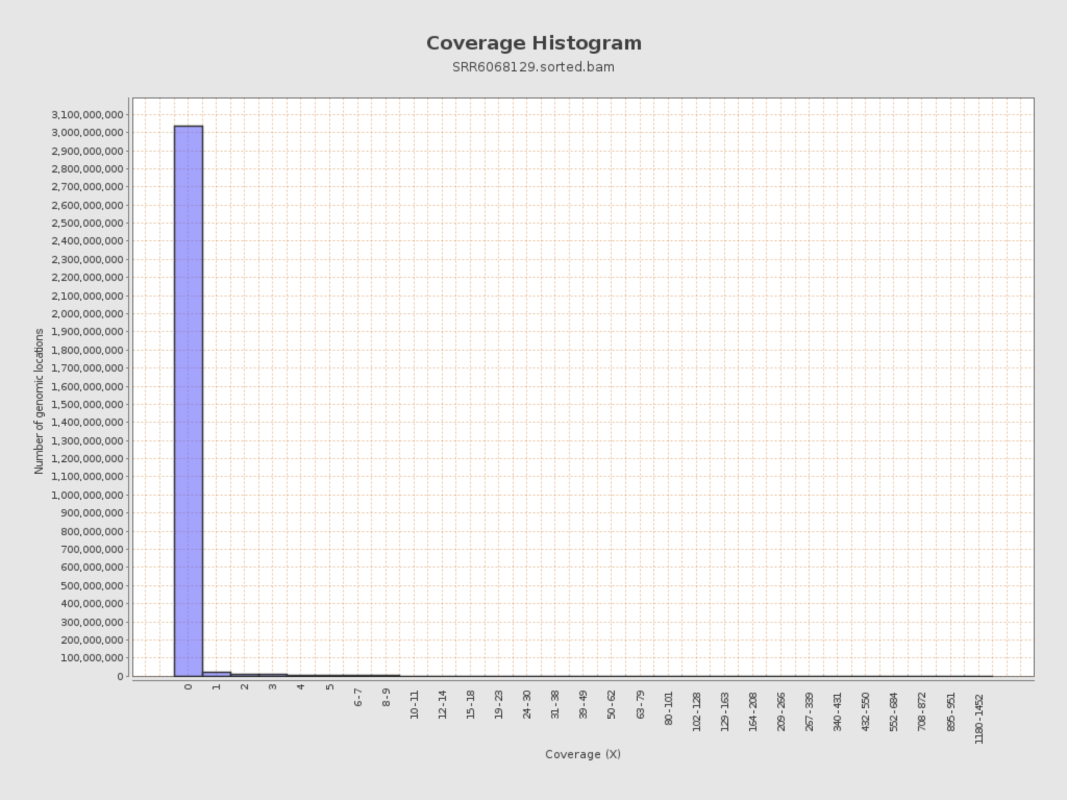
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15386599	0.0617	0.7679
chr2	243199373	18603732	0.0765	0.977
chr3	198022430	14068590	0.071	0.6398
chr4	191154276	10893266	0.057	0.5964
chr5	180915260	13119970	0.0725	0.6436
chr6	171115067	11366518	0.0664	0.6697
chr7	159138663	10324508	0.0649	0.7203

chr8	146364022	9532756	0.0651	0.8276
chr9	141213431	7762542	0.055	0.6024
chr10	135534747	6970961	0.0514	0.6081
chr11	135006516	9227817	0.0684	0.729
chr12	133851895	7987632	0.0597	0.5841
chr13	115169878	5870022	0.051	0.5478
chr14	107349540	6206052	0.0578	0.5837
chr15	102531392	5664621	0.0552	0.5768
chr16	90354753	5229513	0.0579	0.5792
chr17	81195210	5082617	0.0626	0.6254
chr18	78077248	5239508	0.0671	0.9947
chr19	59128983	3417583	0.0578	0.6733
chr20	63025520	3407520	0.0541	0.5607
chr21	48129895	2672511	0.0555	0.5705
chr22	51304566	2193659	0.0428	0.4791
chrMT	16571	239351	14.444	12.9172
chrX	155270560	7028455	0.0453	0.5118
chrY	59373566	1496592	0.0252	0.3819

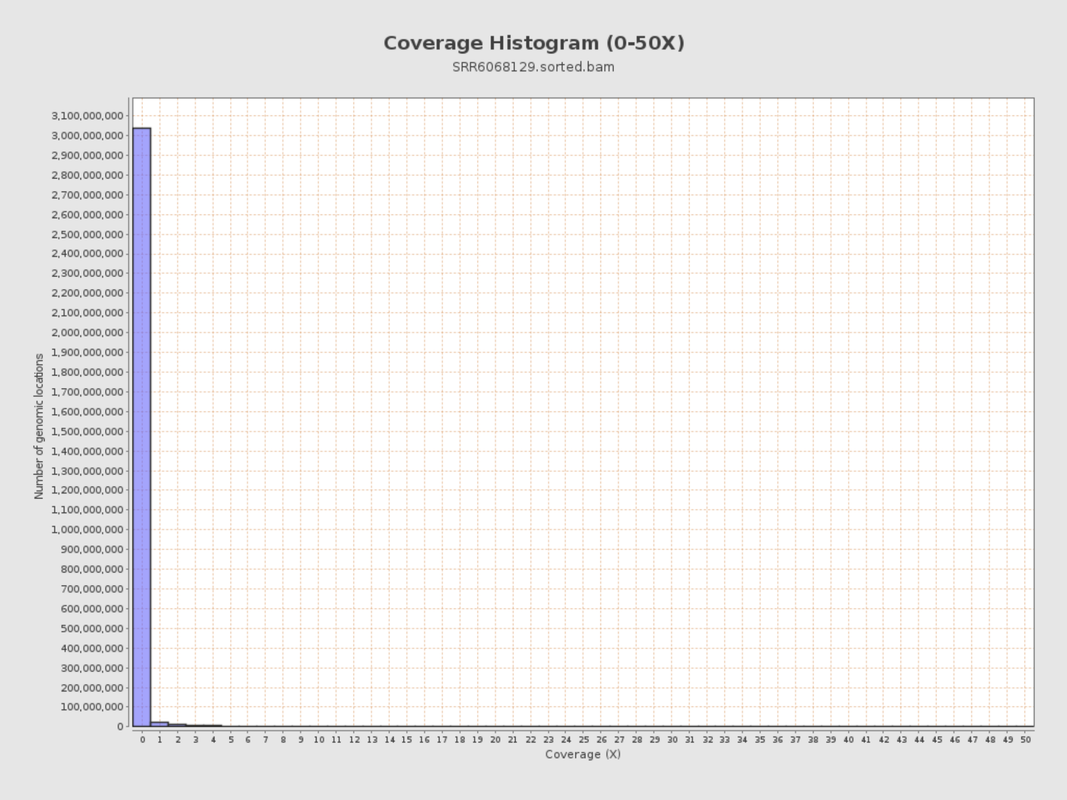
3. Results : Coverage across reference



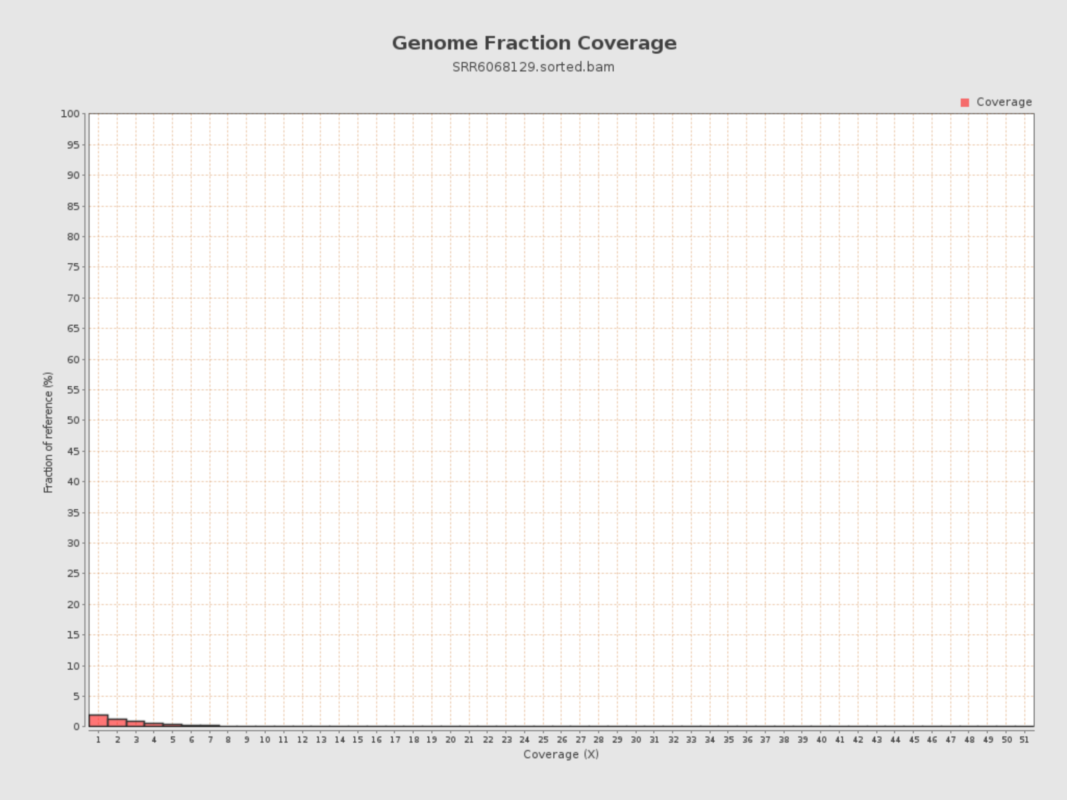
4. Results : Coverage Histogram



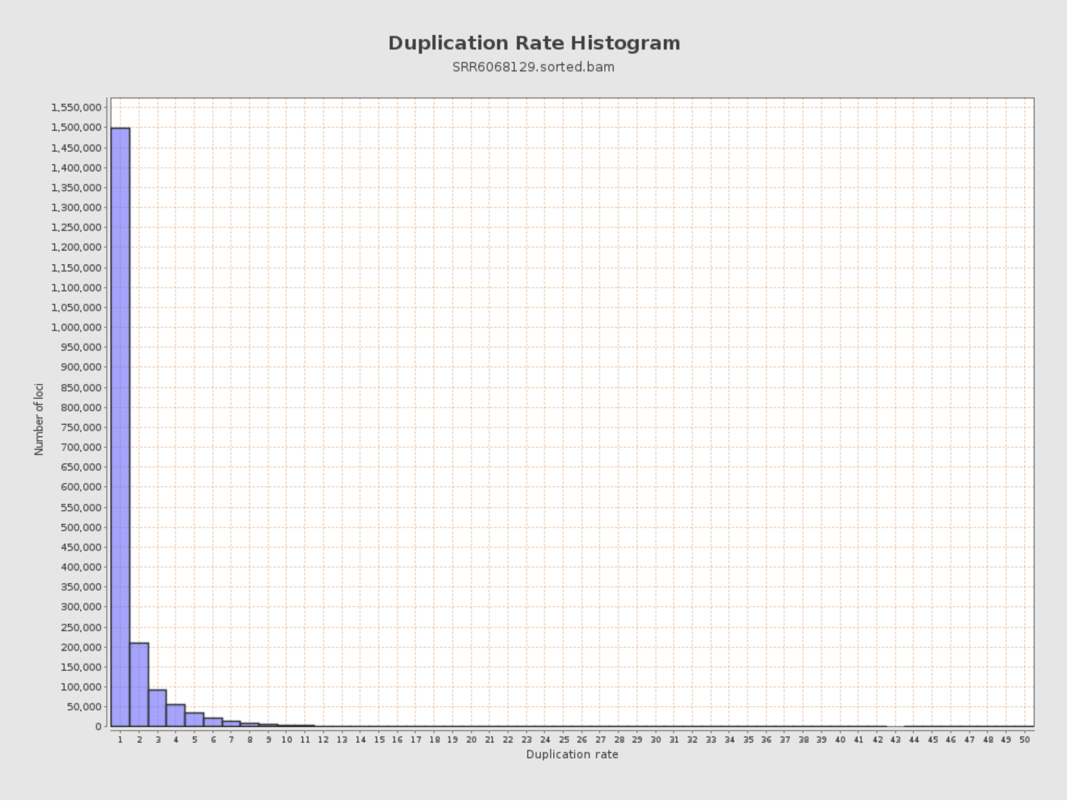
5. Results : Coverage Histogram (0-50X)



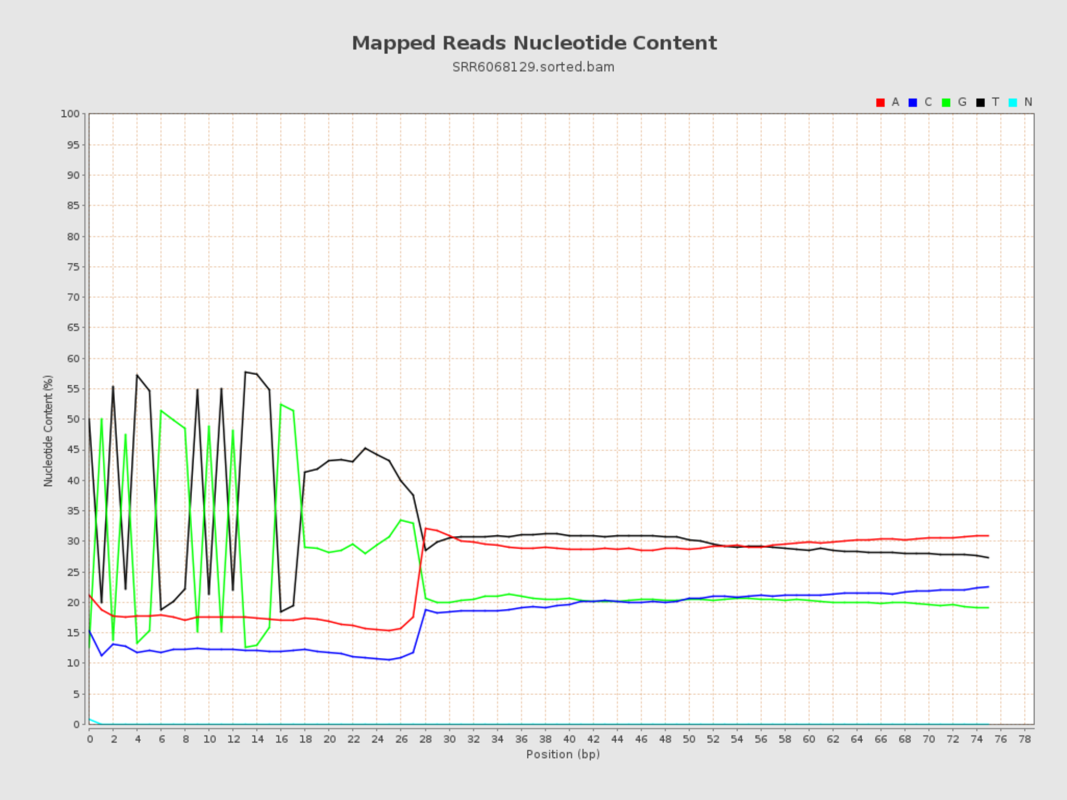
6. Results : Genome Fraction Coverage



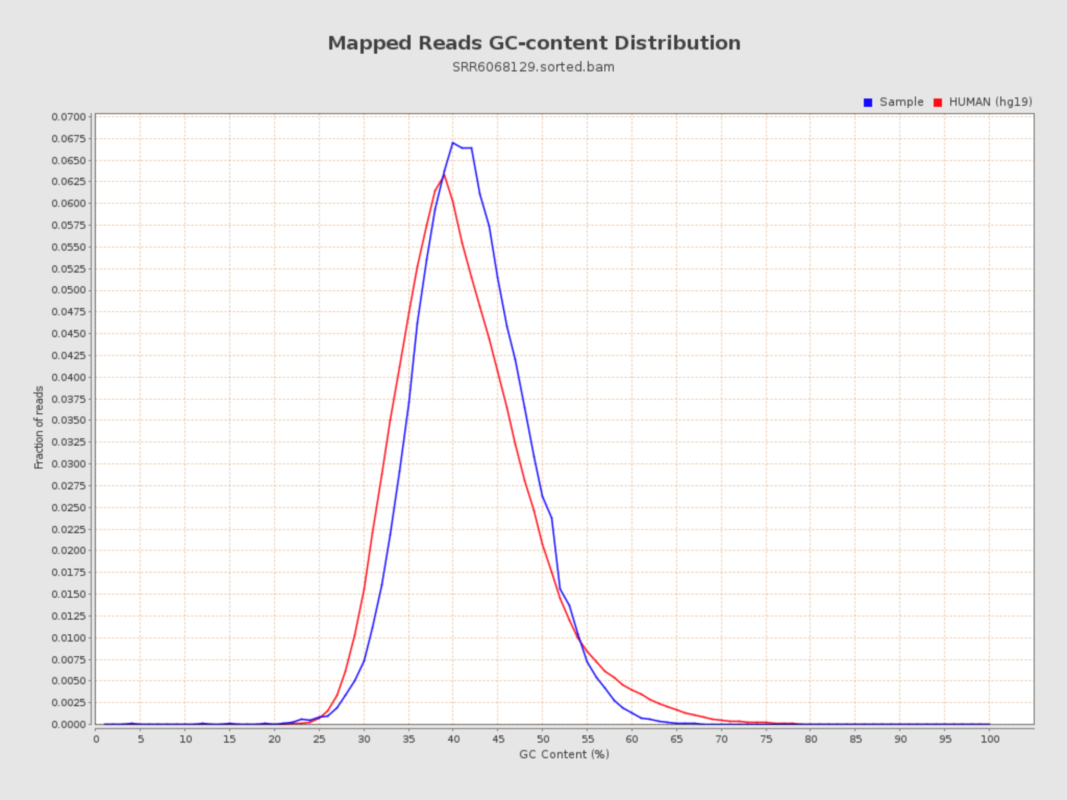
7. Results : Duplication Rate Histogram



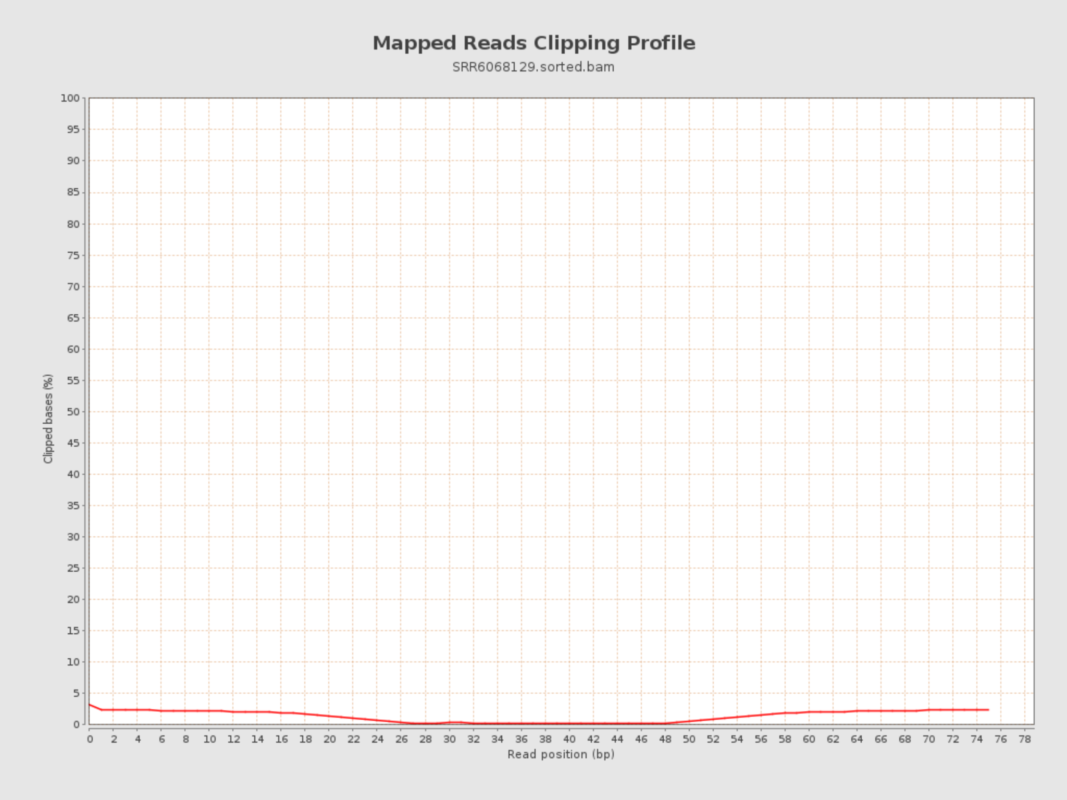
8. Results : Mapped Reads Nucleotide Content



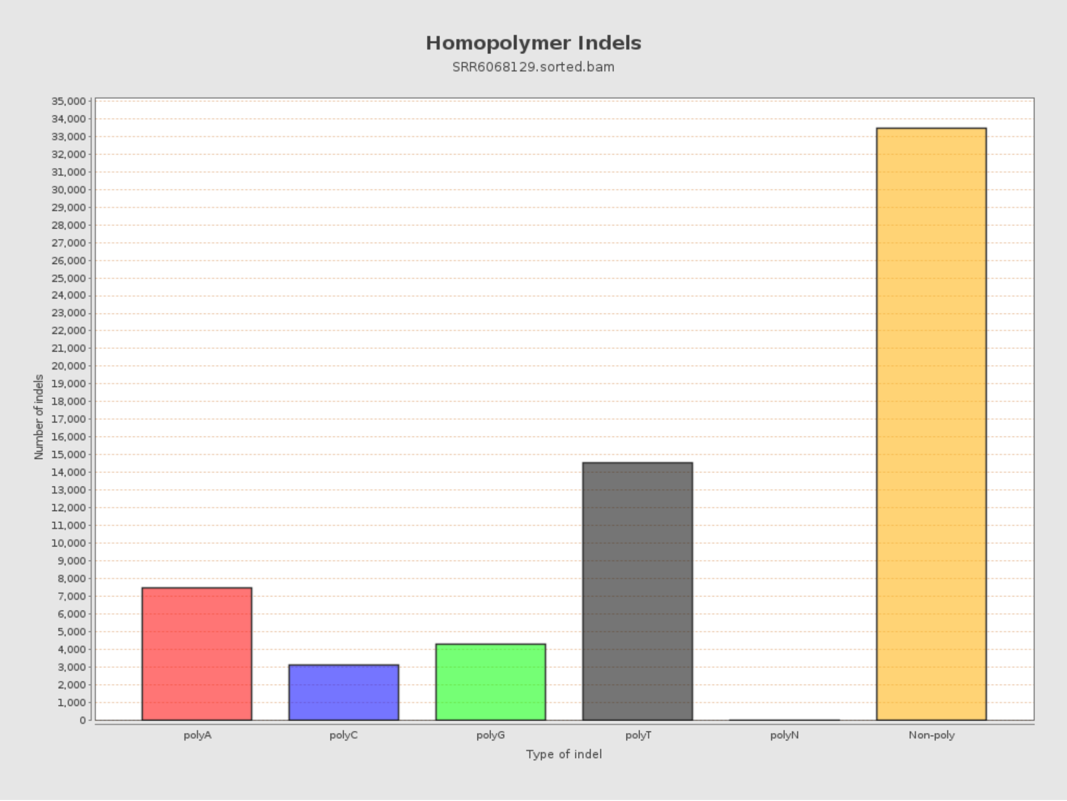
9. Results : Mapped Reads GC-content Distribution



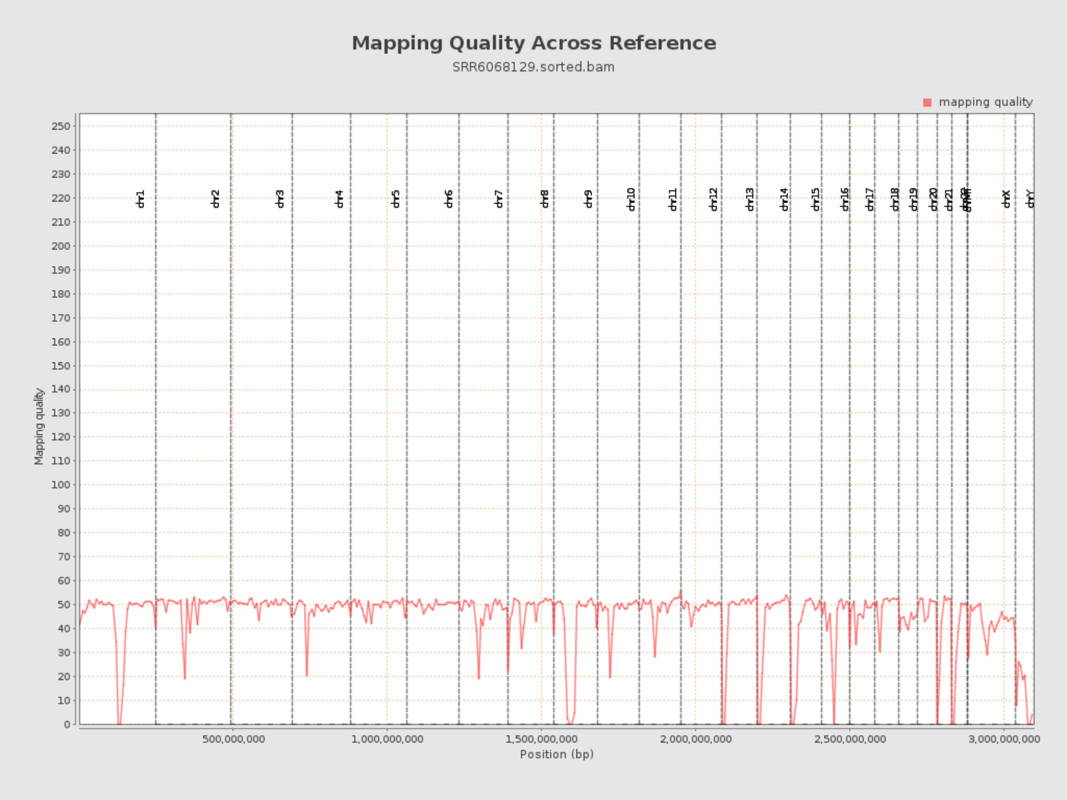
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram