Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:29:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068170.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_SRR6068170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068170.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:29:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,922,882
Mapped reads	1,653,972 / 86.02%
Unmapped reads	268,910 / 13.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,002 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	323,584 / 16.83%
Duplication rate	12.6%
Clipped reads	679,132 / 35.32%

2.2. ACGT Content

Number/percentage of A's	31,148,961 / 28.03%
Number/percentage of C's	19,774,656 / 17.8%
Number/percentage of T's	36,104,299 / 32.49%
Number/percentage of G's	23,959,235 / 21.56%
Number/percentage of N's	127,378 / 0.11%
GC Percentage	39.36%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.5201

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

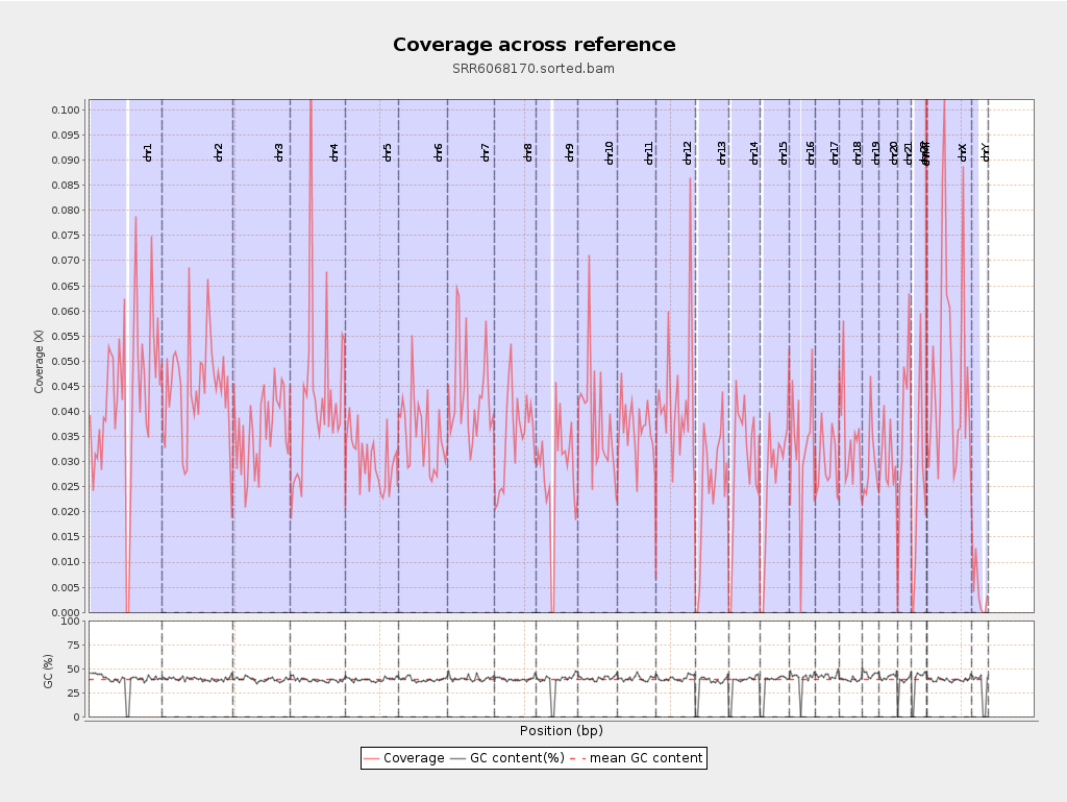
General error rate	0.9%
Mismatches	982,771
Insertions	8,050
Mapped reads with at least one insertion	0.48%
Deletions	30,173
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.08%

2.6. Chromosome stats

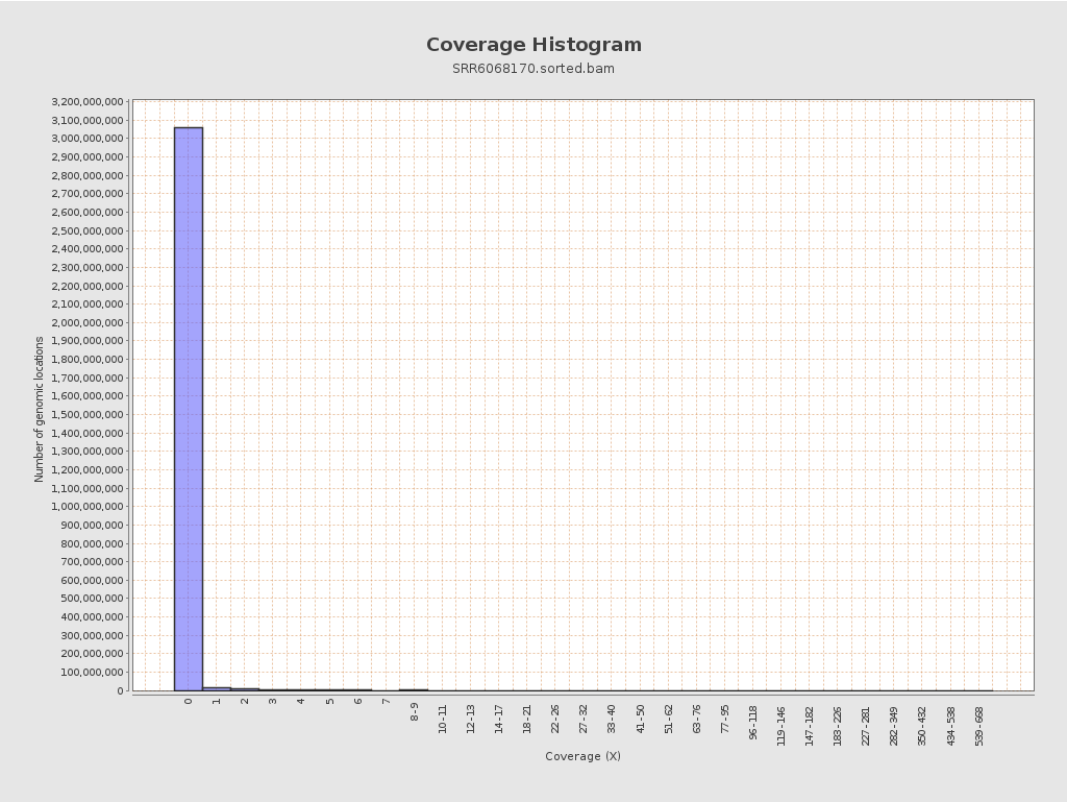
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10566148	0.0424	0.7261
chr2	243199373	10839557	0.0446	0.5516
chr3	198022430	7176365	0.0362	0.4514
chr4	191154276	8120339	0.0425	0.493
chr5	180915260	5495651	0.0304	0.4124
chr6	171115067	6097142	0.0356	0.4595
chr7	159138663	6932540	0.0436	0.5878

chr8	146364022	5133629	0.0351	0.541
chr9	141213431	3889288	0.0275	0.5022
chr10	135534747	5175332	0.0382	0.5615
chr11	135006516	4841780	0.0359	0.4995
chr12	133851895	5581257	0.0417	0.4923
chr13	115169878	2823717	0.0245	0.3751
chr14	107349540	3163606	0.0295	0.4191
chr15	102531392	2735136	0.0267	0.3789
chr16	90354753	2910468	0.0322	0.4332
chr17	81195210	2381334	0.0293	0.3976
chr18	78077248	2739395	0.0351	0.883
chr19	59128983	1756527	0.0297	0.5261
chr20	63025520	1906854	0.0303	0.4073
chr21	48129895	1796644	0.0373	0.4515
chr22	51304566	1194246	0.0233	0.3333
chrMT	16571	230550	13.9129	12.2495
chrX	155270560	7432181	0.0479	0.5461
chrY	59373566	247747	0.0042	0.1368

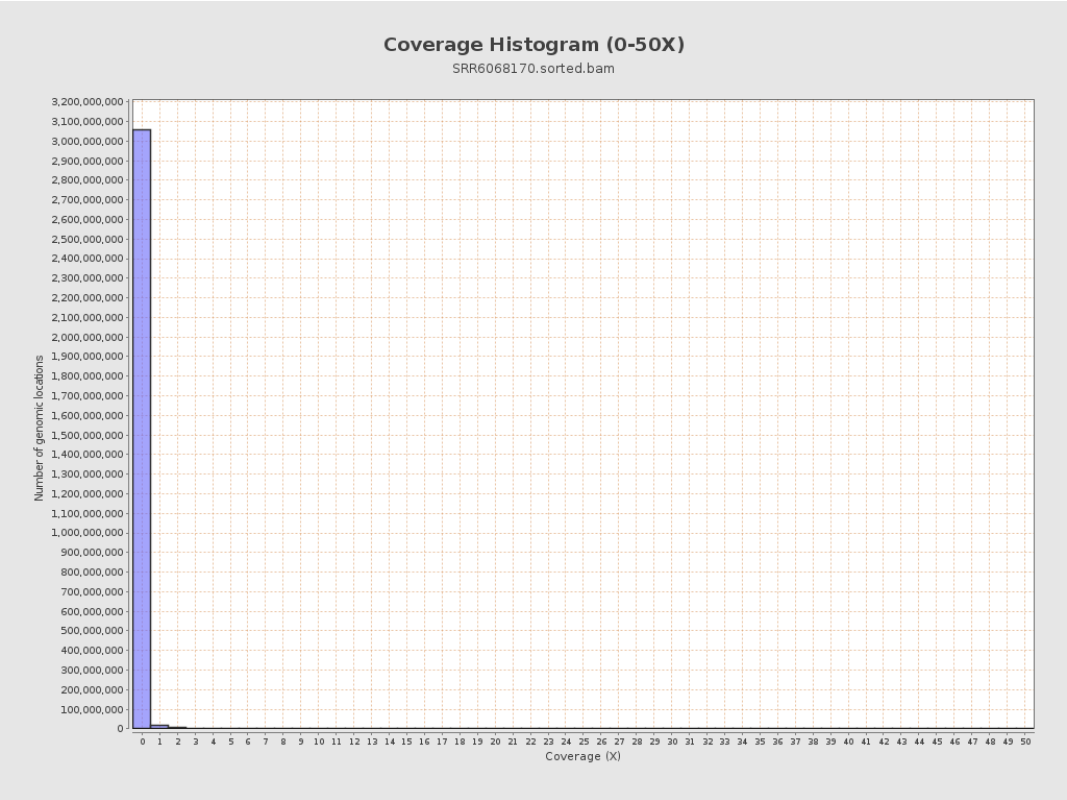
3. Results : Coverage across reference



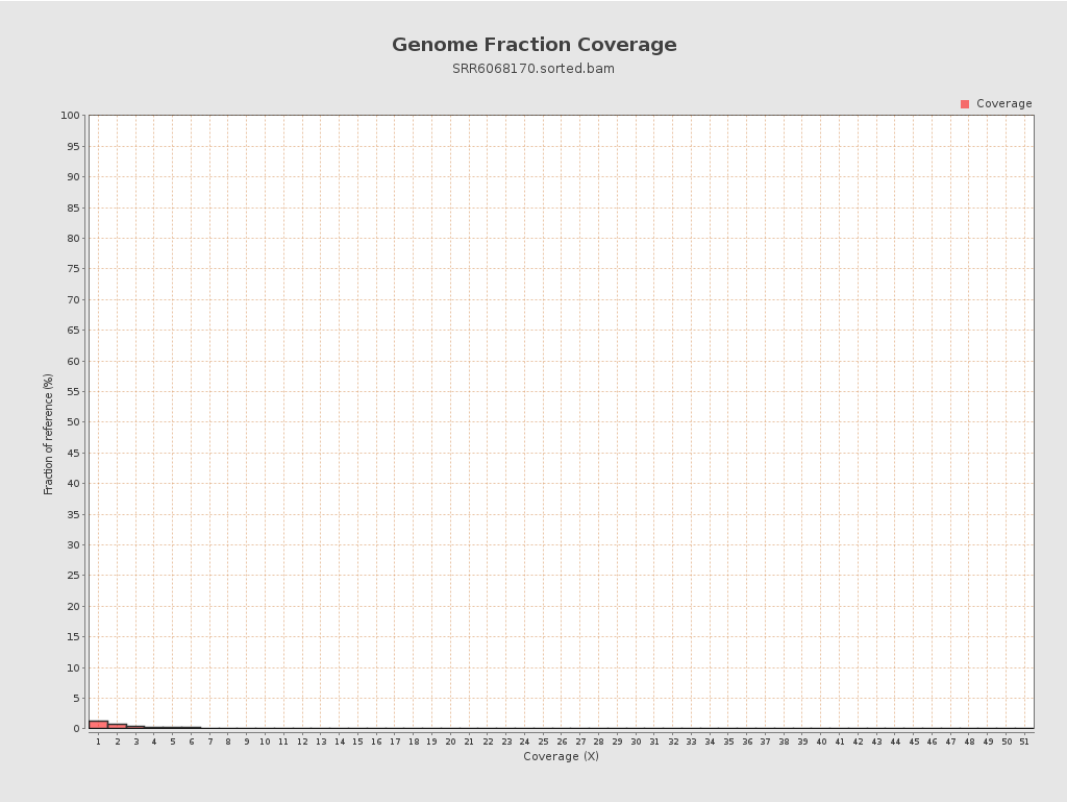
4. Results : Coverage Histogram



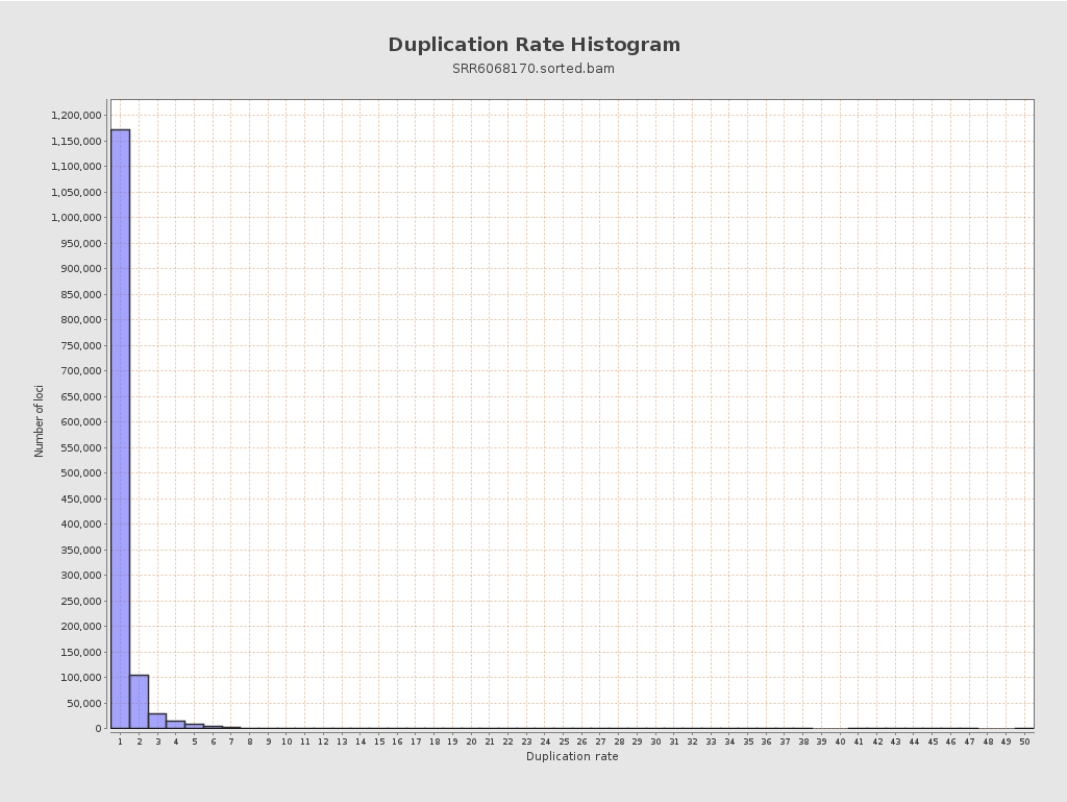
5. Results : Coverage Histogram (0-50X)



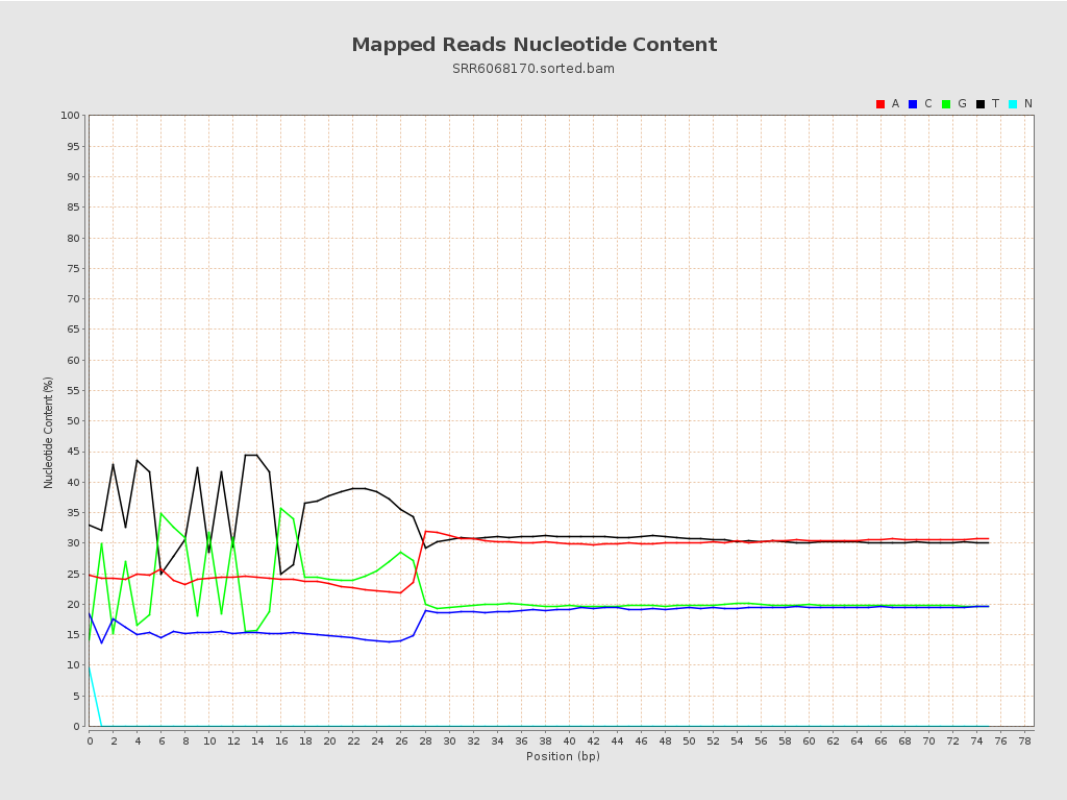
6. Results : Genome Fraction Coverage



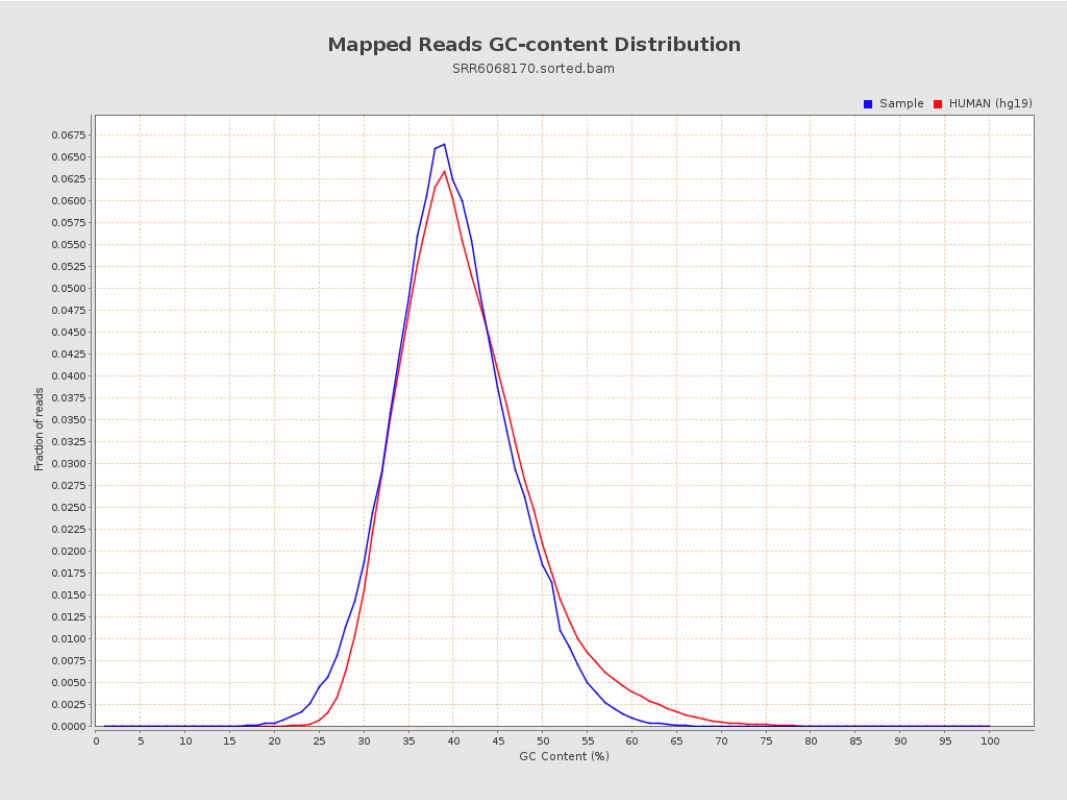
7. Results : Duplication Rate Histogram



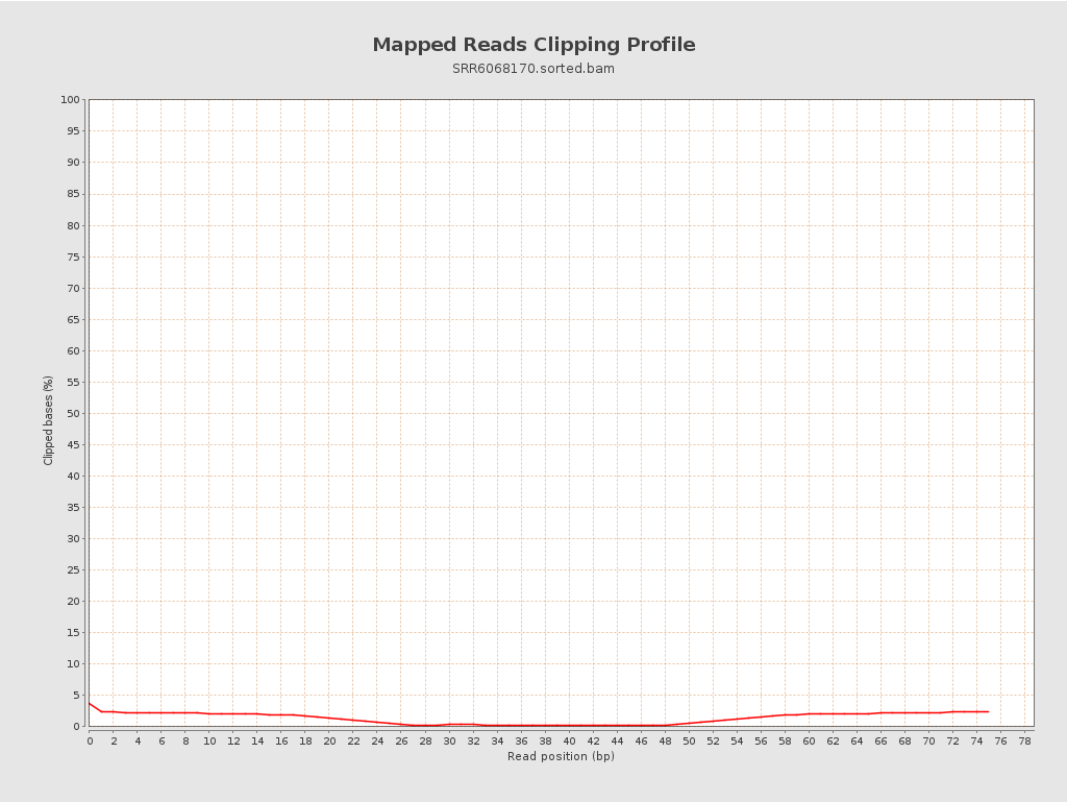
8. Results : Mapped Reads Nucleotide Content



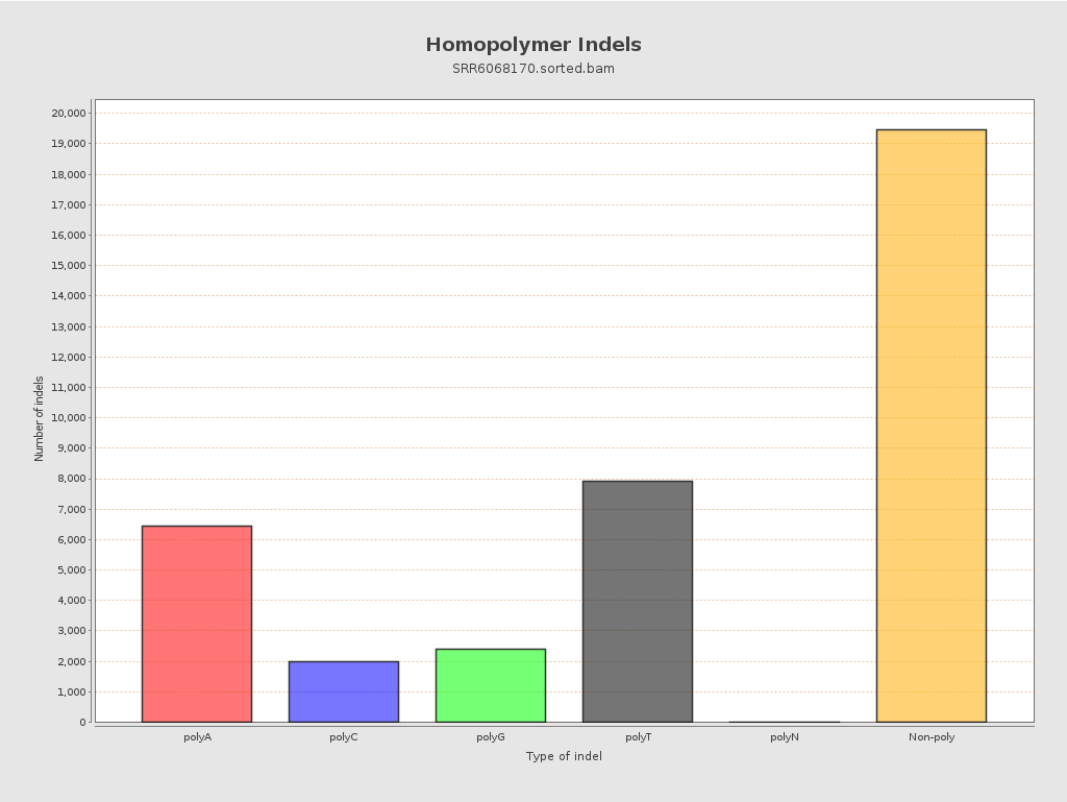
9. Results : Mapped Reads GC-content Distribution



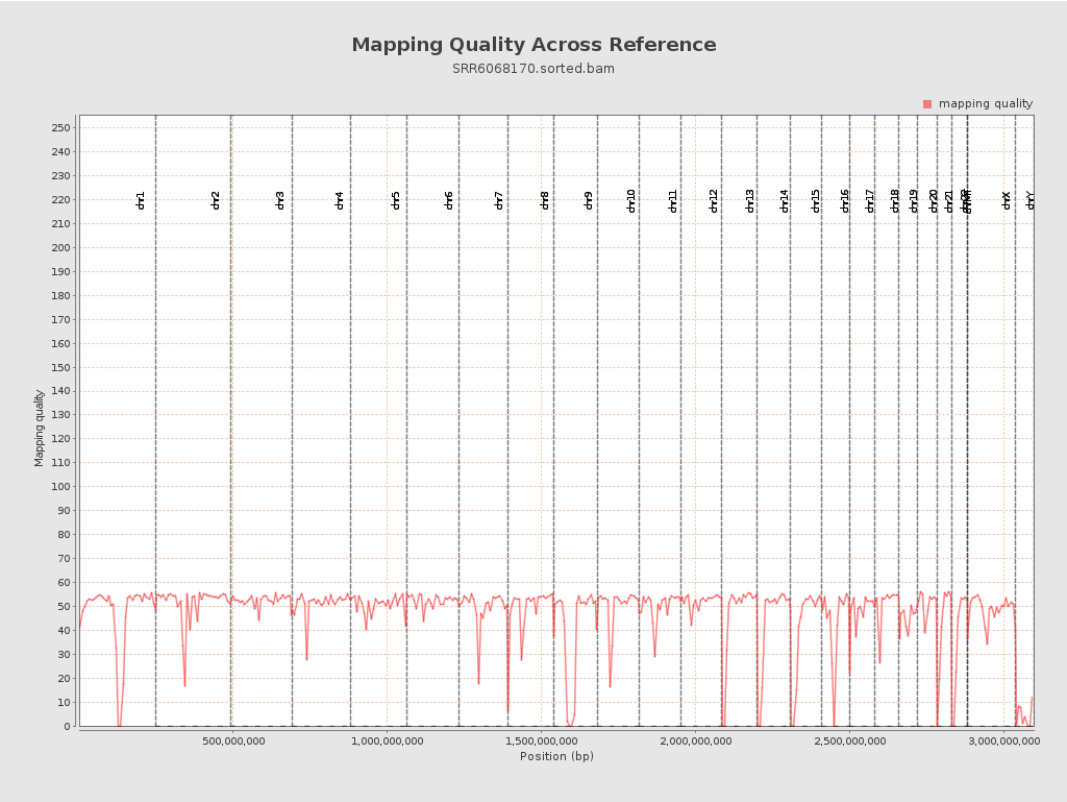
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram