Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:51:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068948.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_SRR6068948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:51:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,431,235
Mapped reads	1,991,245 / 81.9%
Unmapped reads	439,990 / 18.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,064 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	77,954 / 3.21%
Duplication rate	2.85%
Clipped reads	1,039,957 / 42.77%

2.2. ACGT Content

Number/percentage of A's	34,334,141 / 26.65%
Number/percentage of C's	21,936,385 / 17.03%
Number/percentage of T's	42,944,109 / 33.33%
Number/percentage of G's	29,322,541 / 22.76%
Number/percentage of N's	309,326 / 0.24%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.3977

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

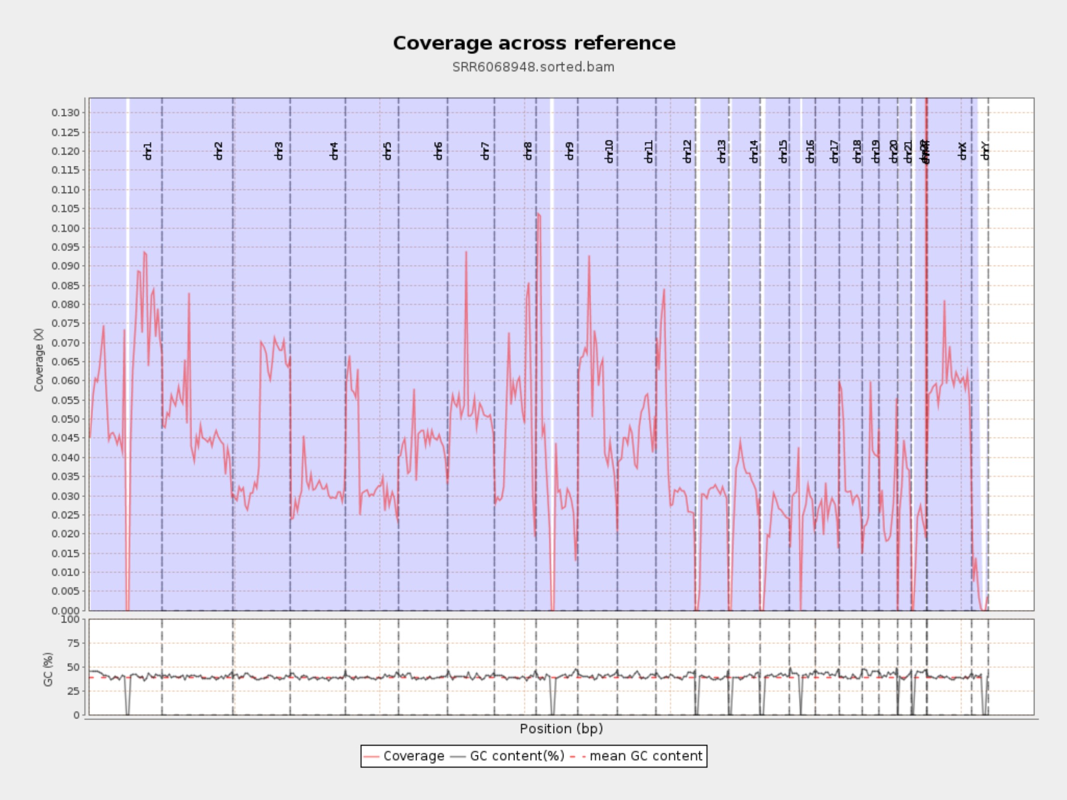
General error rate	0.96%
Mismatches	1,215,704
Insertions	11,435
Mapped reads with at least one insertion	0.57%
Deletions	34,865
Mapped reads with at least one deletion	1.73%
Homopolymer indels	48.48%

2.6. Chromosome stats

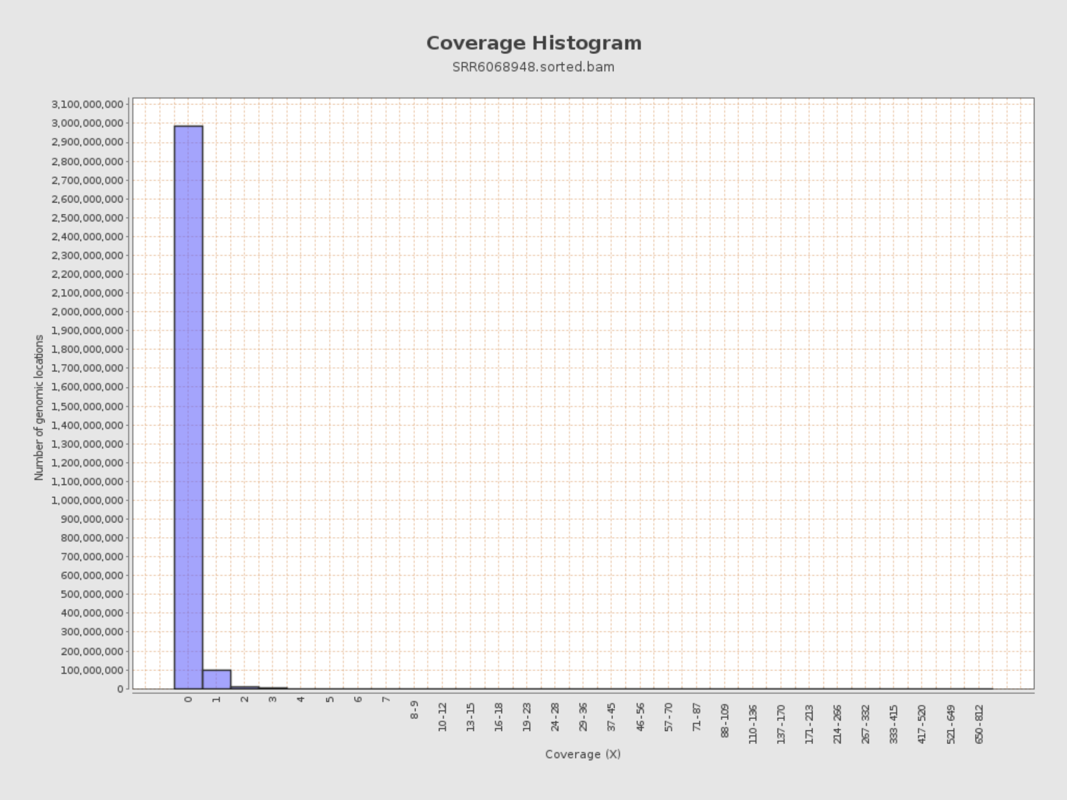
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15185712	0.0609	0.7369
chr2	243199373	11781200	0.0484	0.3972
chr3	198022430	9810668	0.0495	0.2568
chr4	191154276	5958299	0.0312	0.2112
chr5	180915260	6821108	0.0377	0.2178
chr6	171115067	7463001	0.0436	0.2929
chr7	159138663	8542460	0.0537	0.6809

chr8	146364022	7314001	0.05	0.5029
chr9	141213431	5127135	0.0363	0.386
chr10	135534747	7844224	0.0579	0.4685
chr11	135006516	6177513	0.0458	0.3614
chr12	133851895	5450648	0.0407	0.2335
chr13	115169878	2956495	0.0257	0.1764
chr14	107349540	3214112	0.0299	0.2238
chr15	102531392	2088719	0.0204	0.1582
chr16	90354753	2408465	0.0267	0.2136
chr17	81195210	2103180	0.0259	0.2069
chr18	78077248	2787523	0.0357	0.5885
chr19	59128983	2089209	0.0353	0.4663
chr20	63025520	1696202	0.0269	0.1994
chr21	48129895	1472407	0.0306	0.2155
chr22	51304566	870510	0.017	0.1433
chrMT	16571	185528	11.1959	7.5644
chrX	155270560	9242479	0.0595	0.3153
chrY	59373566	312884	0.0053	0.1093

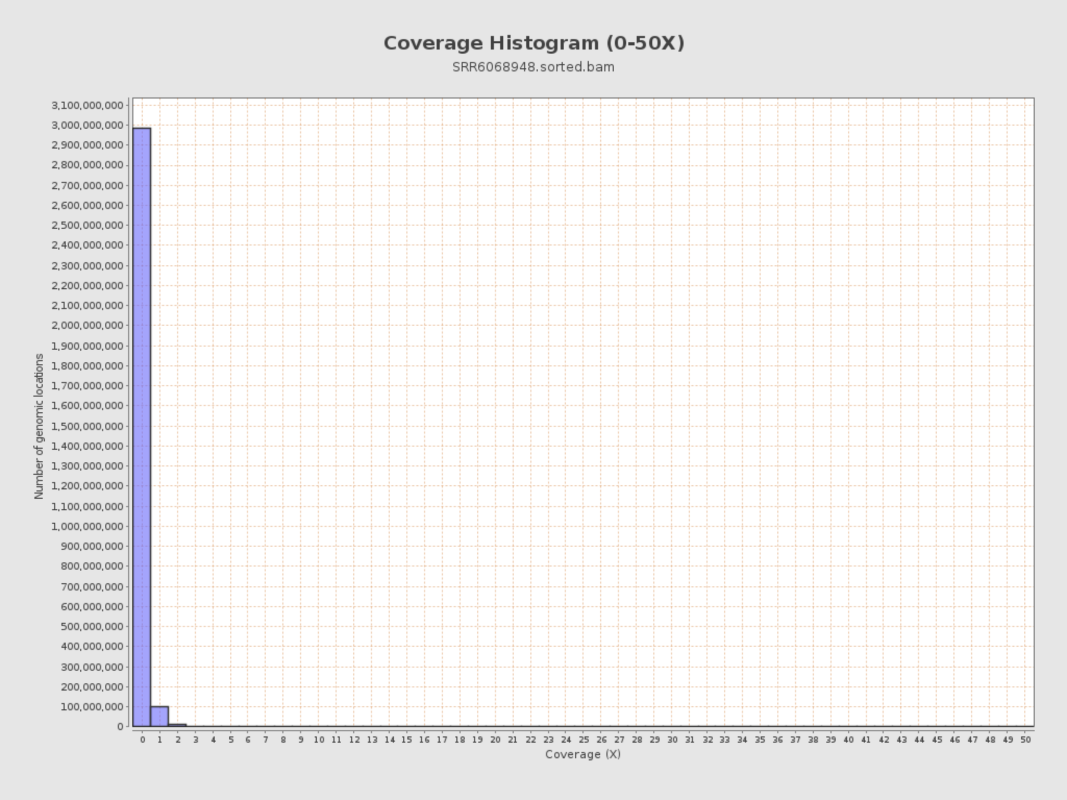
3. Results : Coverage across reference



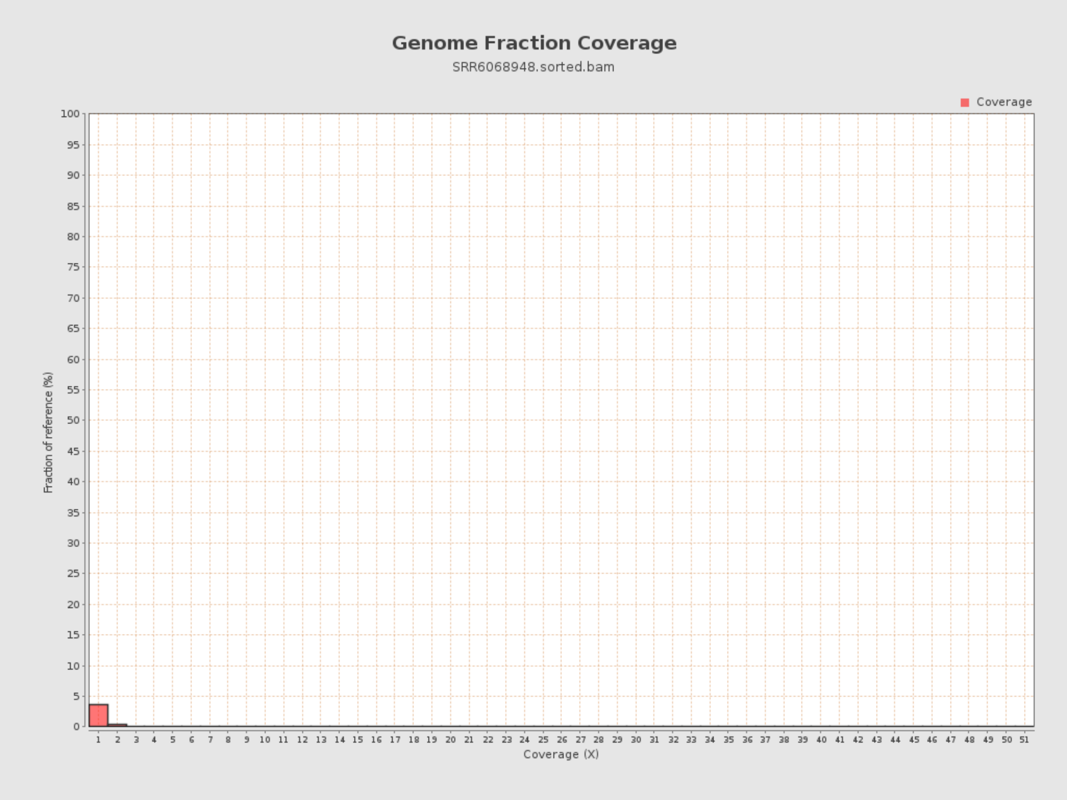
4. Results : Coverage Histogram



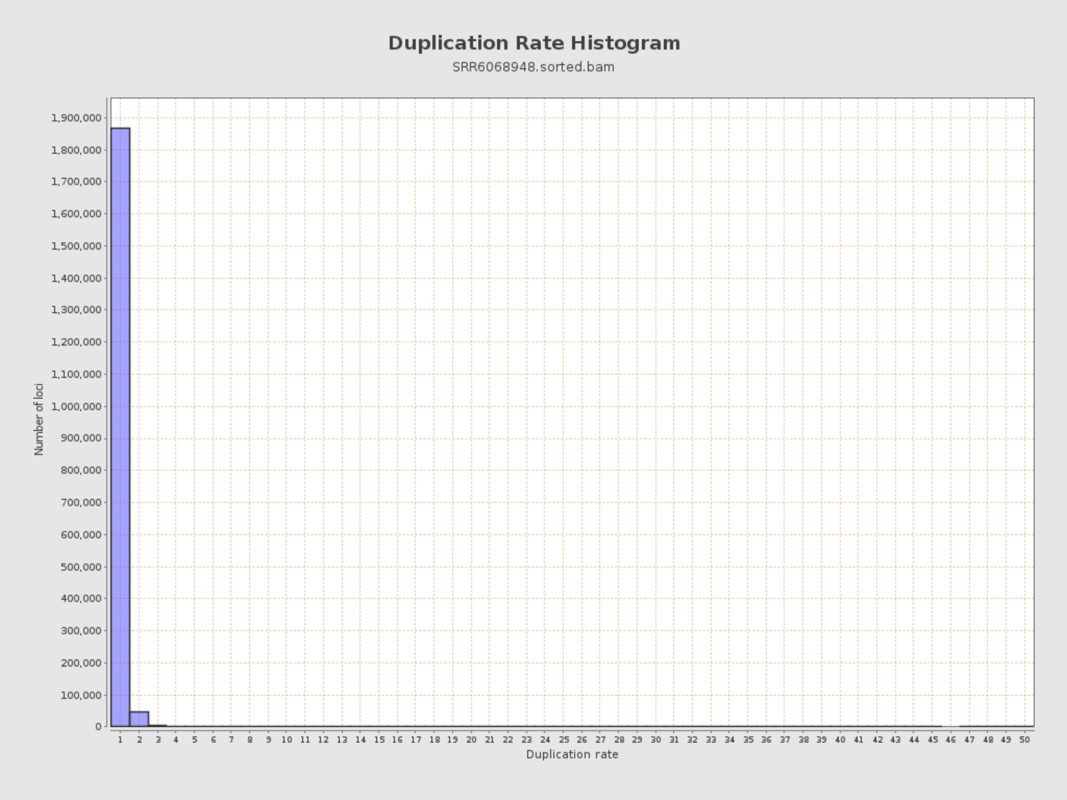
5. Results : Coverage Histogram (0-50X)



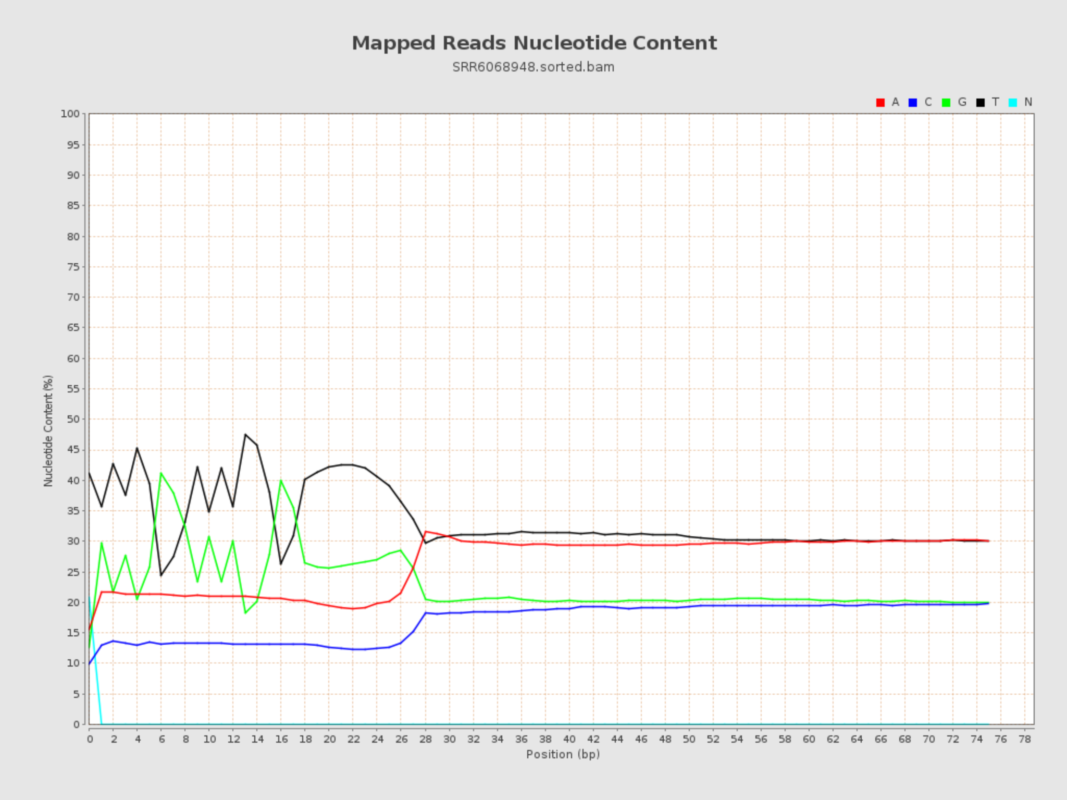
6. Results : Genome Fraction Coverage



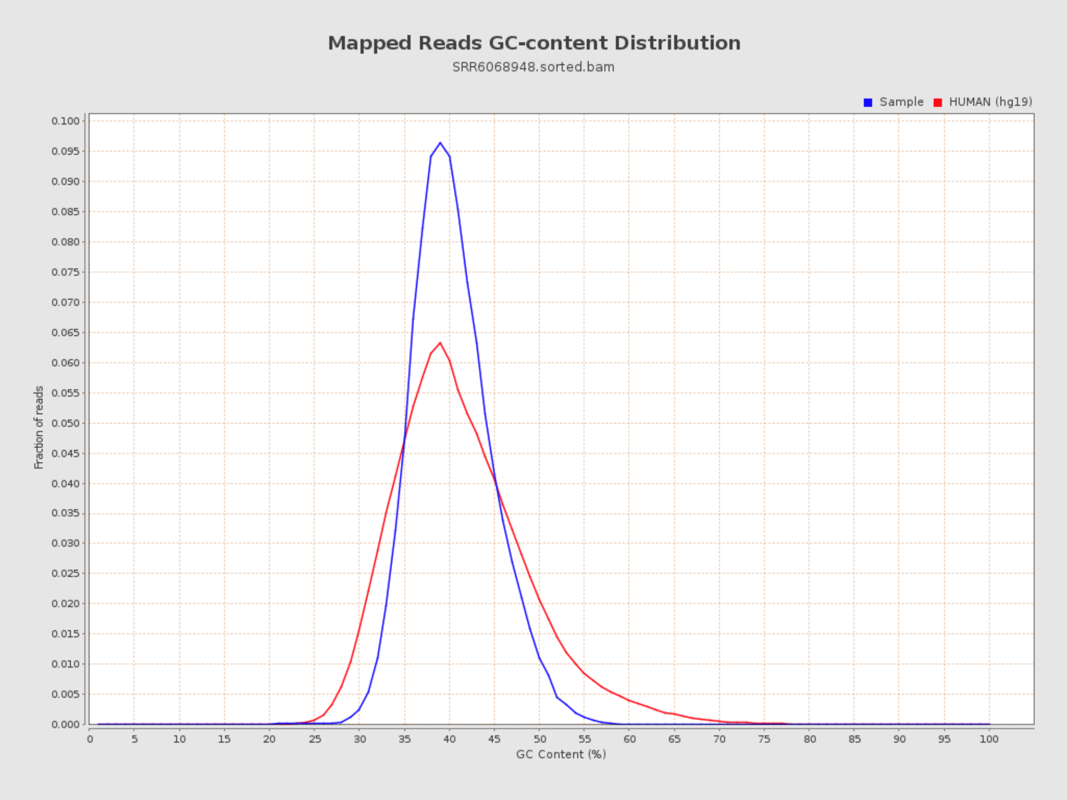
7. Results : Duplication Rate Histogram



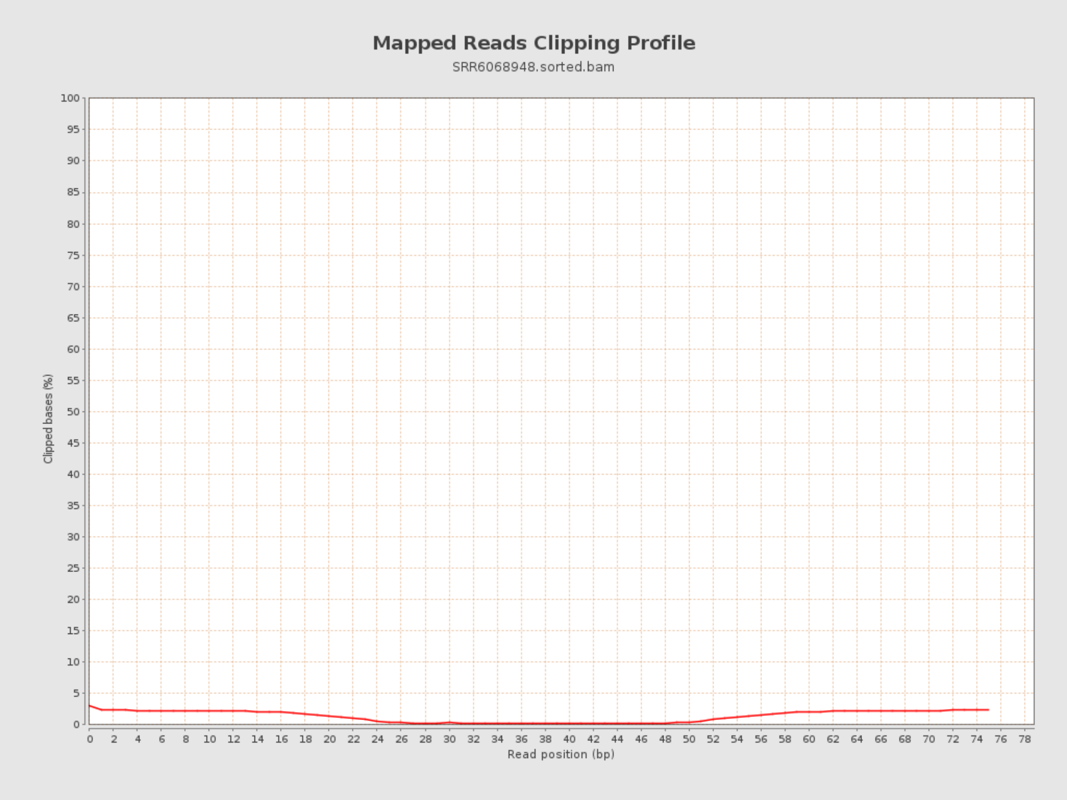
8. Results : Mapped Reads Nucleotide Content



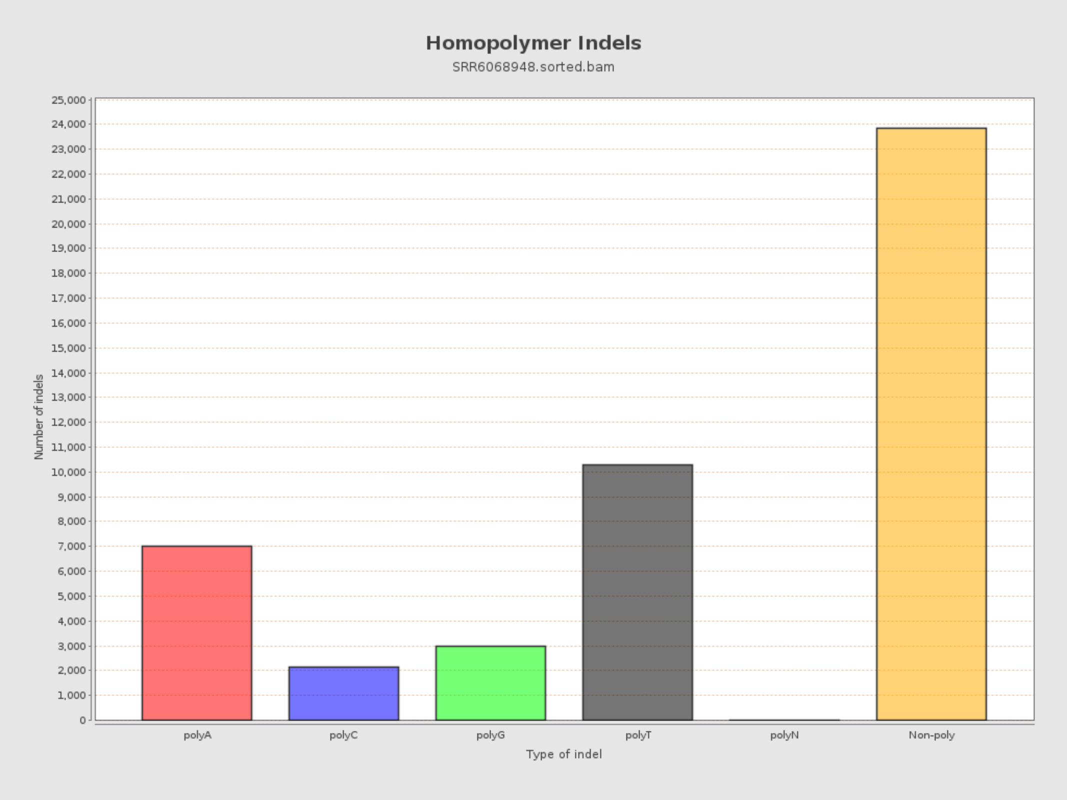
9. Results : Mapped Reads GC-content Distribution



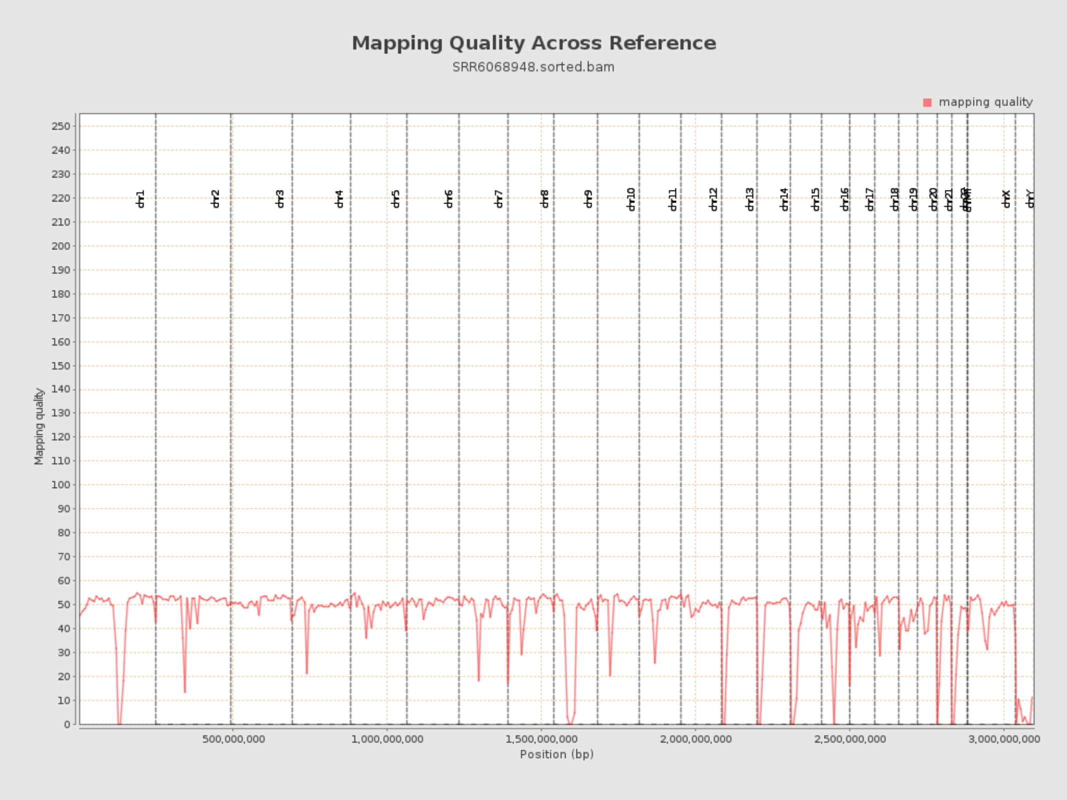
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram