Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:18:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068181.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_SRR6068181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:18:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,720,252
Mapped reads	4,467,680 / 94.65%
Unmapped reads	252,572 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,474 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	583,694 / 12.37%
Duplication rate	10.63%
Clipped reads	2,384,378 / 50.51%

2.2. ACGT Content

Number/percentage of A's	74,380,846 / 25.98%
Number/percentage of C's	51,504,019 / 17.99%
Number/percentage of T's	93,197,880 / 32.55%
Number/percentage of G's	67,183,929 / 23.47%
Number/percentage of N's	32,192 / 0.01%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0925

Standard Deviation	1.0306

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

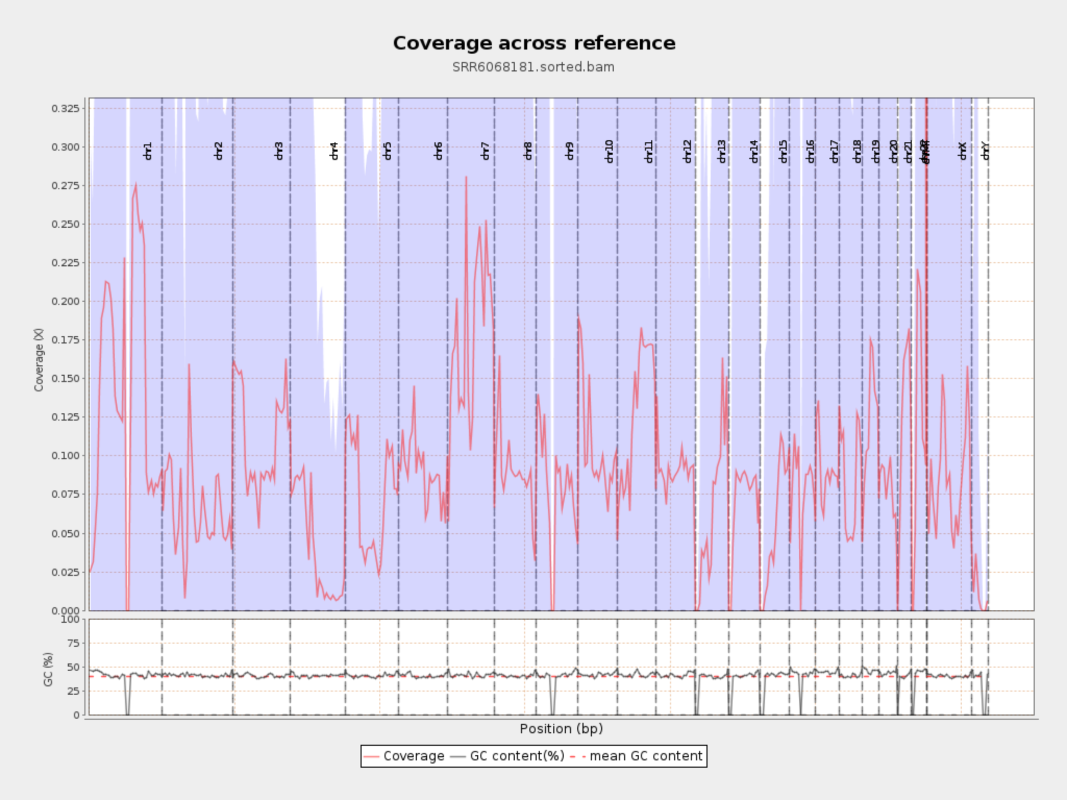
General error rate	0.58%
Mismatches	1,624,999
Insertions	17,733
Mapped reads with at least one insertion	0.39%
Deletions	69,023
Mapped reads with at least one deletion	1.53%
Homopolymer indels	44.26%

2.6. Chromosome stats

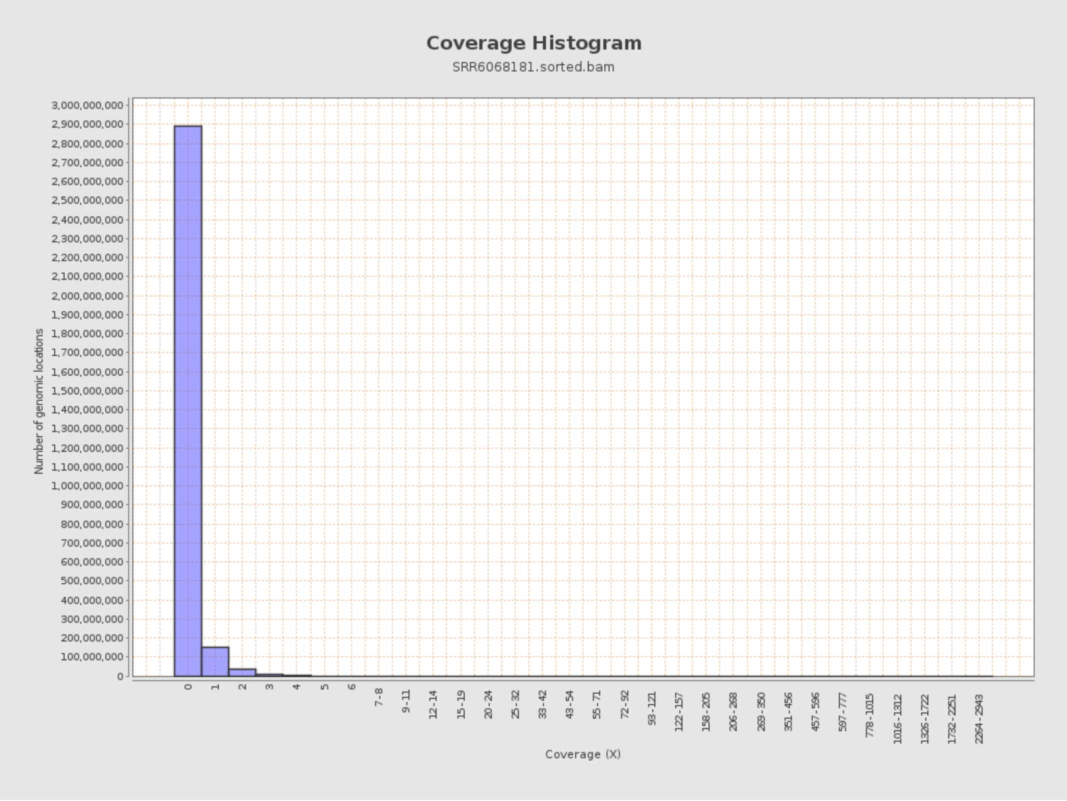
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34996548	0.1404	2.3278
chr2	243199373	15781934	0.0649	1.2429
chr3	198022430	21920405	0.1107	0.443
chr4	191154276	7539867	0.0394	0.311
chr5	180915260	13234356	0.0732	0.3654
chr6	171115067	15520480	0.0907	0.592
chr7	159138663	28790952	0.1809	2.06

chr8	146364022	13159723	0.0899	0.7033
chr9	141213431	11376170	0.0806	0.6996
chr10	135534747	14550988	0.1074	0.7614
chr11	135006516	17445853	0.1292	0.6665
chr12	133851895	12235894	0.0914	0.435
chr13	115169878	7578477	0.0658	0.3711
chr14	107349540	7488478	0.0698	0.4077
chr15	102531392	5546433	0.0541	0.3573
chr16	90354753	7099751	0.0786	0.427
chr17	81195210	7384041	0.0909	0.4469
chr18	78077248	6575119	0.0842	1.3585
chr19	59128983	7319837	0.1238	1.4837
chr20	63025520	5030027	0.0798	0.3947
chr21	48129895	5953390	0.1237	0.4928
chr22	51304566	5585722	0.1089	0.4416
chrMT	16571	249513	15.0572	8.4951
chrX	155270560	13459917	0.0867	0.4985
chrY	59373566	595882	0.01	0.3475

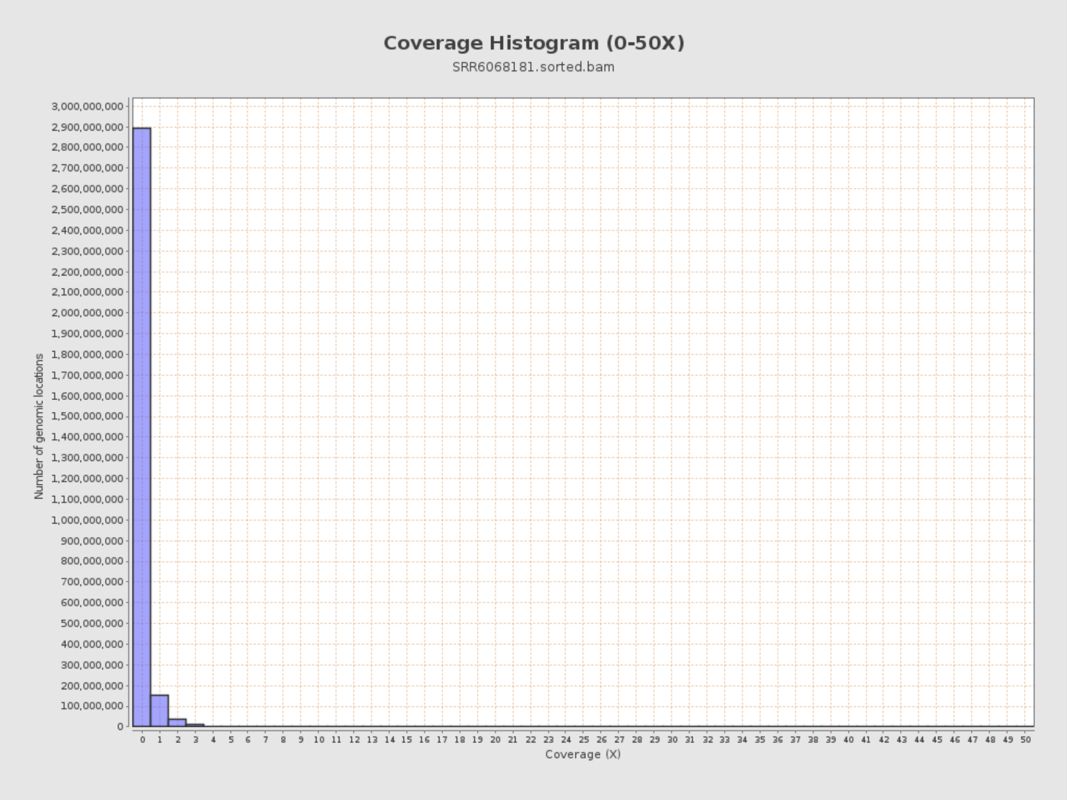
3. Results : Coverage across reference



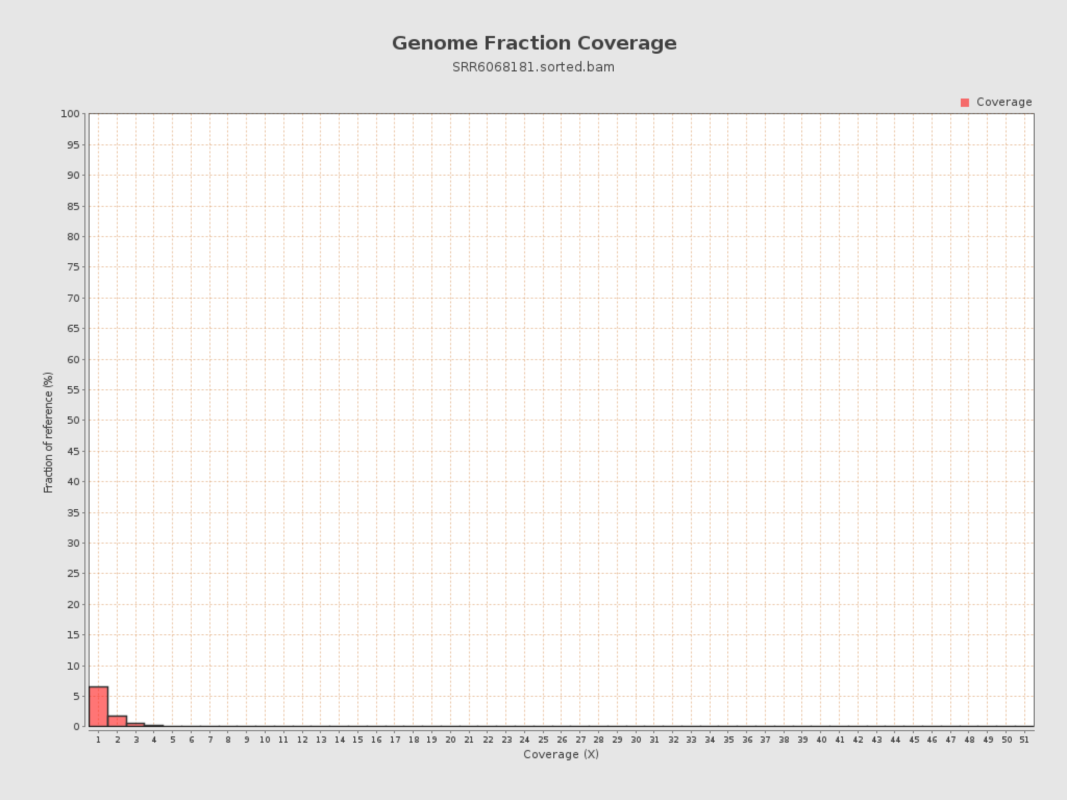
4. Results : Coverage Histogram



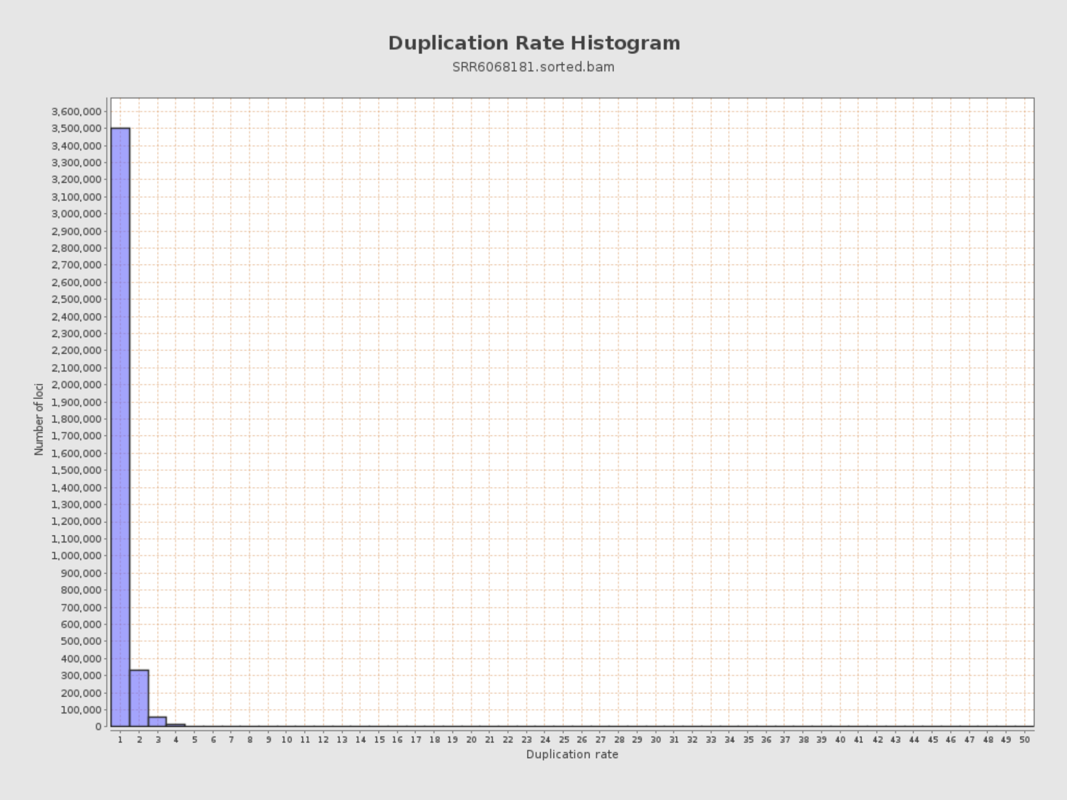
5. Results : Coverage Histogram (0-50X)



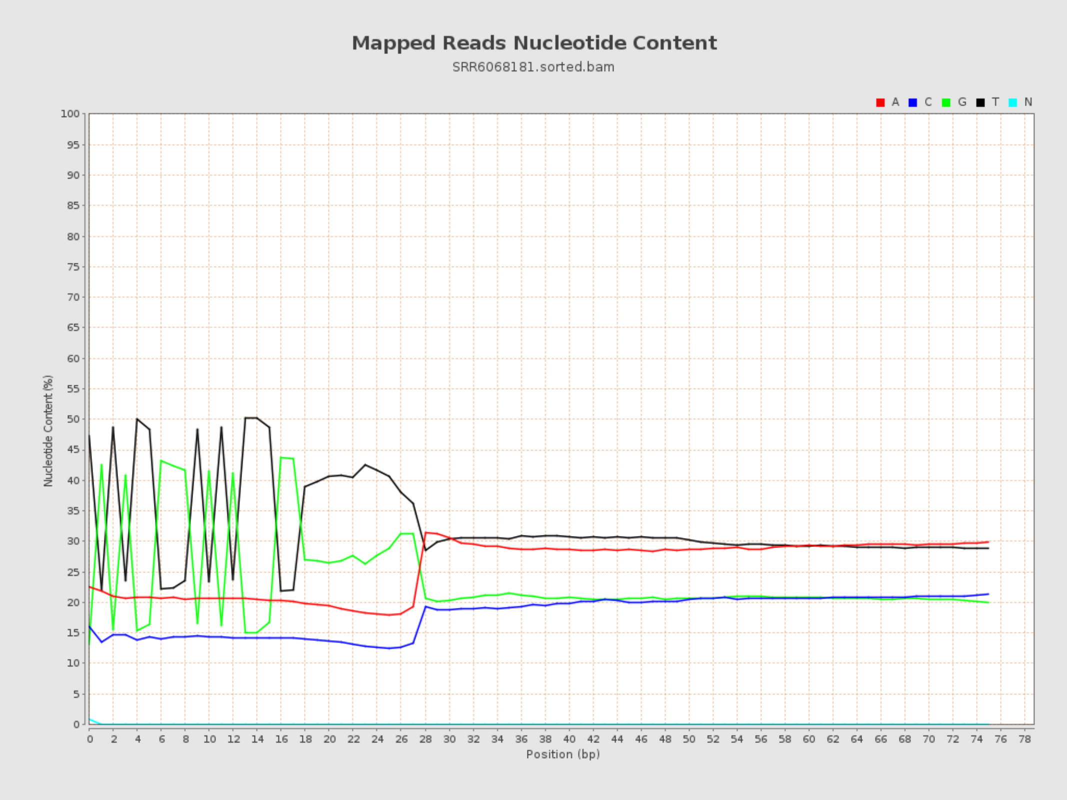
6. Results : Genome Fraction Coverage



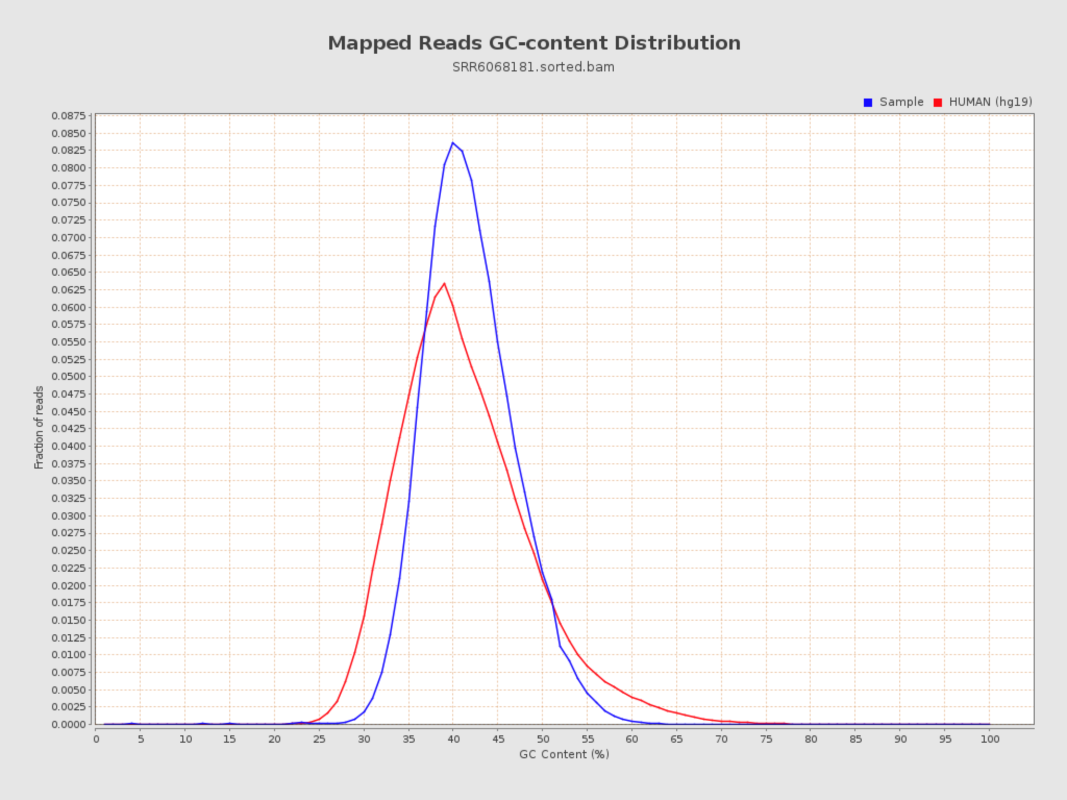
7. Results : Duplication Rate Histogram



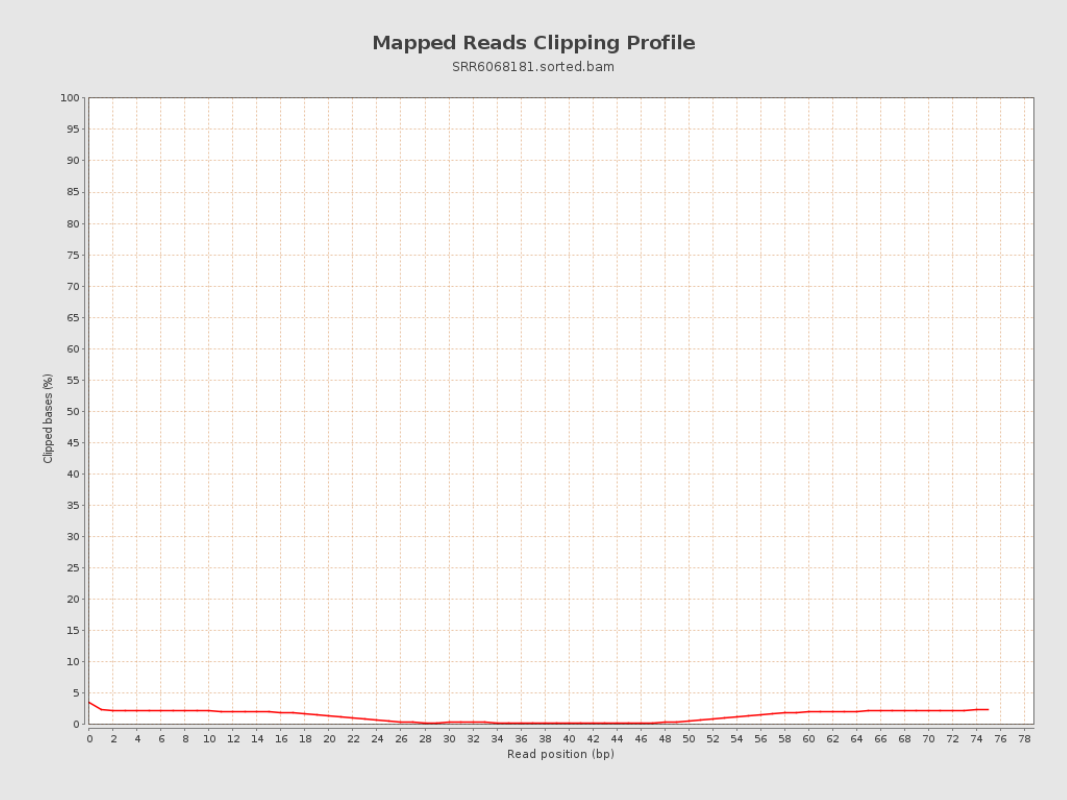
8. Results : Mapped Reads Nucleotide Content



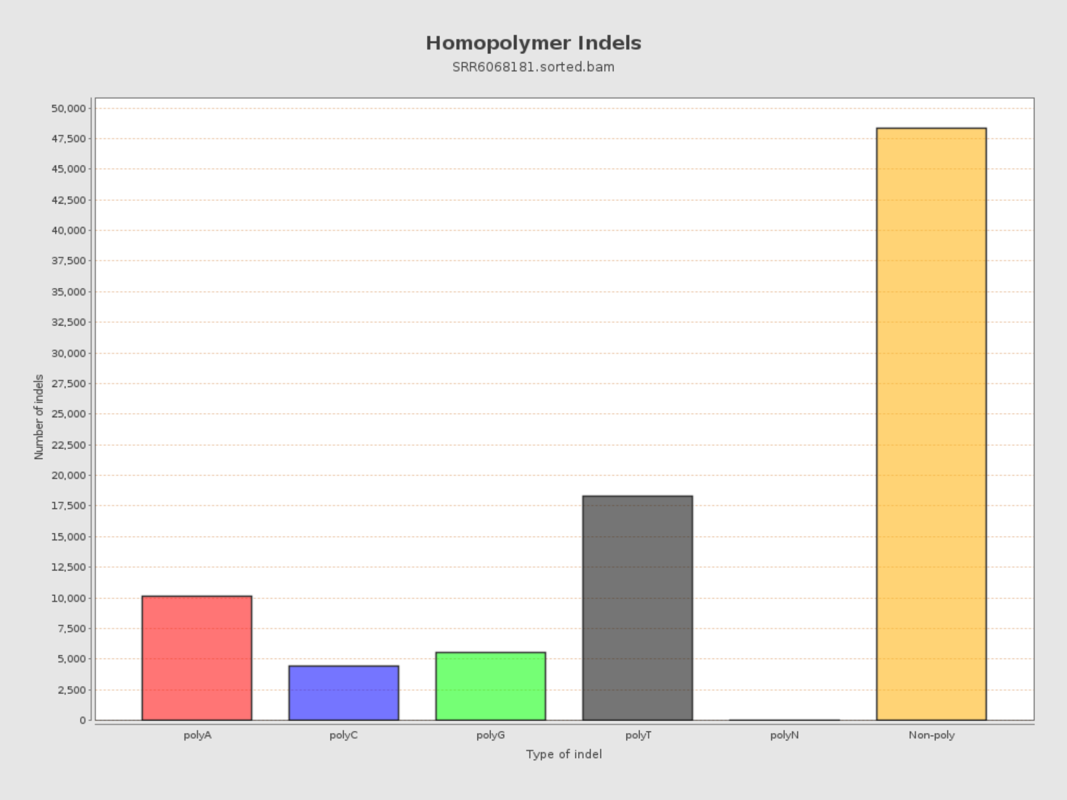
9. Results : Mapped Reads GC-content Distribution



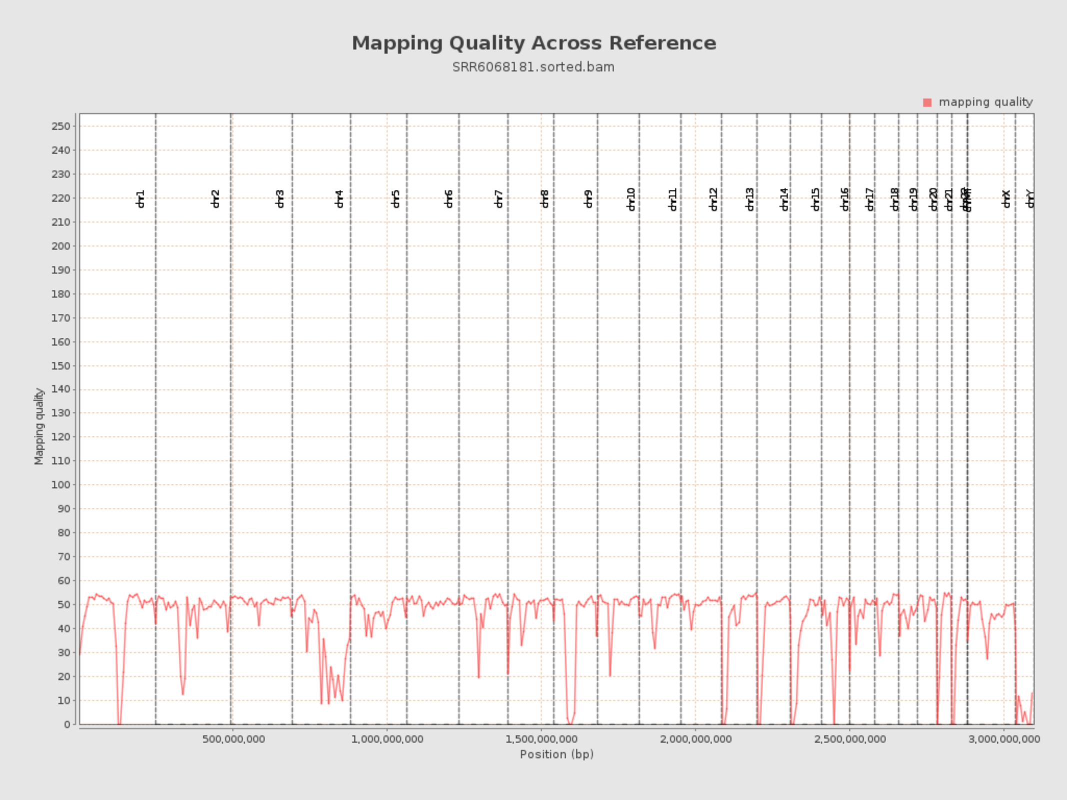
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram