Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:28:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013281.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_SRR6013281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:28:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,474,589
Mapped reads	2,246,998 / 90.8%
Unmapped reads	227,591 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,167 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	81,183 / 3.28%
Duplication rate	2.71%
Clipped reads	918,627 / 37.12%

2.2. ACGT Content

Number/percentage of A's	42,352,711 / 27.97%
Number/percentage of C's	27,810,420 / 18.37%
Number/percentage of T's	47,857,907 / 31.61%
Number/percentage of G's	33,378,094 / 22.05%
Number/percentage of N's	2,171 / 0%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.4268

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

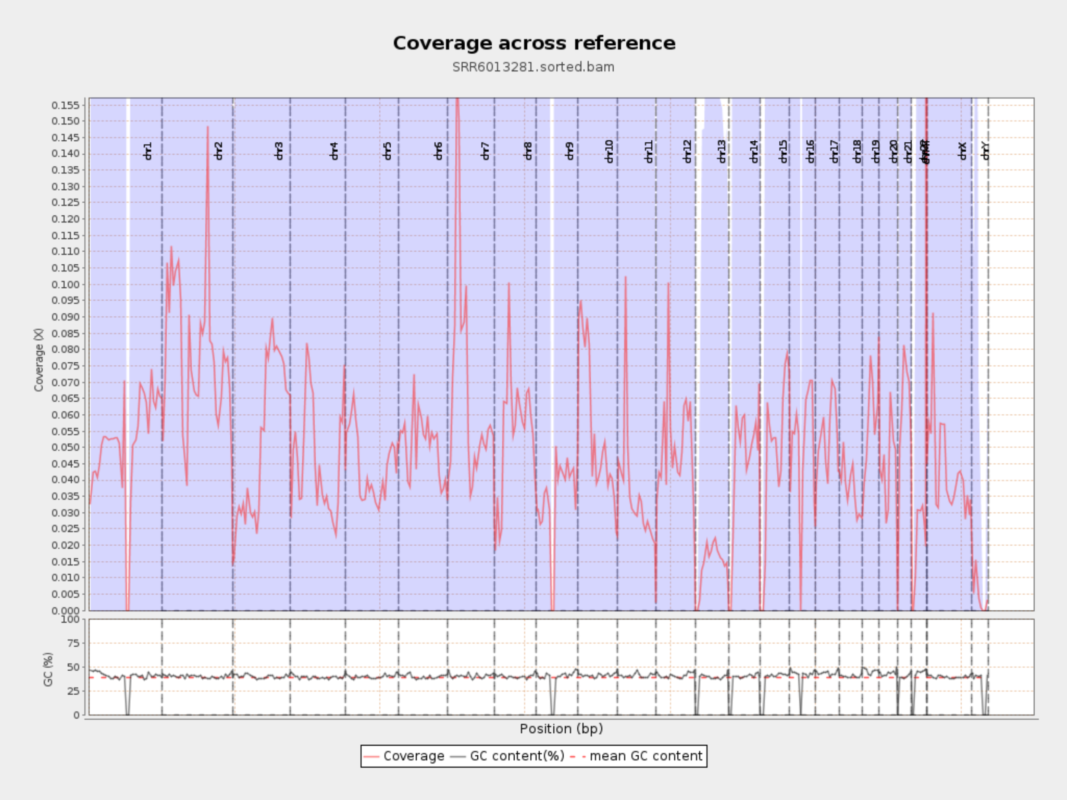
General error rate	0.7%
Mismatches	1,046,759
Insertions	10,586
Mapped reads with at least one insertion	0.47%
Deletions	40,237
Mapped reads with at least one deletion	1.77%
Homopolymer indels	47.12%

2.6. Chromosome stats

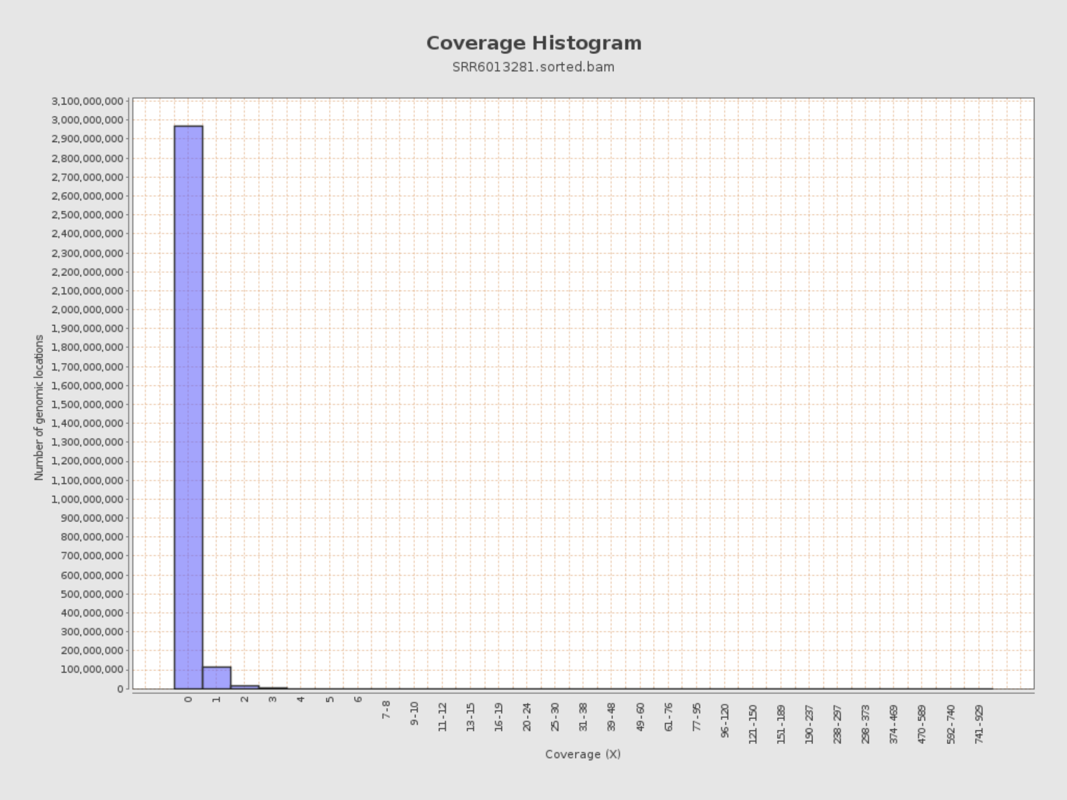
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12742518	0.0511	0.8073
chr2	243199373	19296196	0.0793	0.4654
chr3	198022430	10337386	0.0522	0.2579
chr4	191154276	8854996	0.0463	0.263
chr5	180915260	8005886	0.0443	0.2416
chr6	171115067	8673218	0.0507	0.3344
chr7	159138663	10864674	0.0683	0.8129

chr8	146364022	8031786	0.0549	0.49
chr9	141213431	4803976	0.034	0.3443
chr10	135534747	7750282	0.0572	0.3739
chr11	135006516	4862057	0.036	0.2673
chr12	133851895	6901291	0.0516	0.2612
chr13	115169878	1621334	0.0141	0.1339
chr14	107349540	4817281	0.0449	0.2573
chr15	102531392	4811853	0.0469	0.2671
chr16	90354753	4616100	0.0511	0.2721
chr17	81195210	4331288	0.0533	0.3071
chr18	78077248	2944736	0.0377	0.5895
chr19	59128983	3442022	0.0582	0.5501
chr20	63025520	2771711	0.044	0.2449
chr21	48129895	2857620	0.0594	0.2946
chr22	51304566	1041899	0.0203	0.1581
chrMT	16571	21806	1.3159	1.6263
chrX	155270560	6777988	0.0437	0.2669
chrY	59373566	290490	0.0049	0.1226

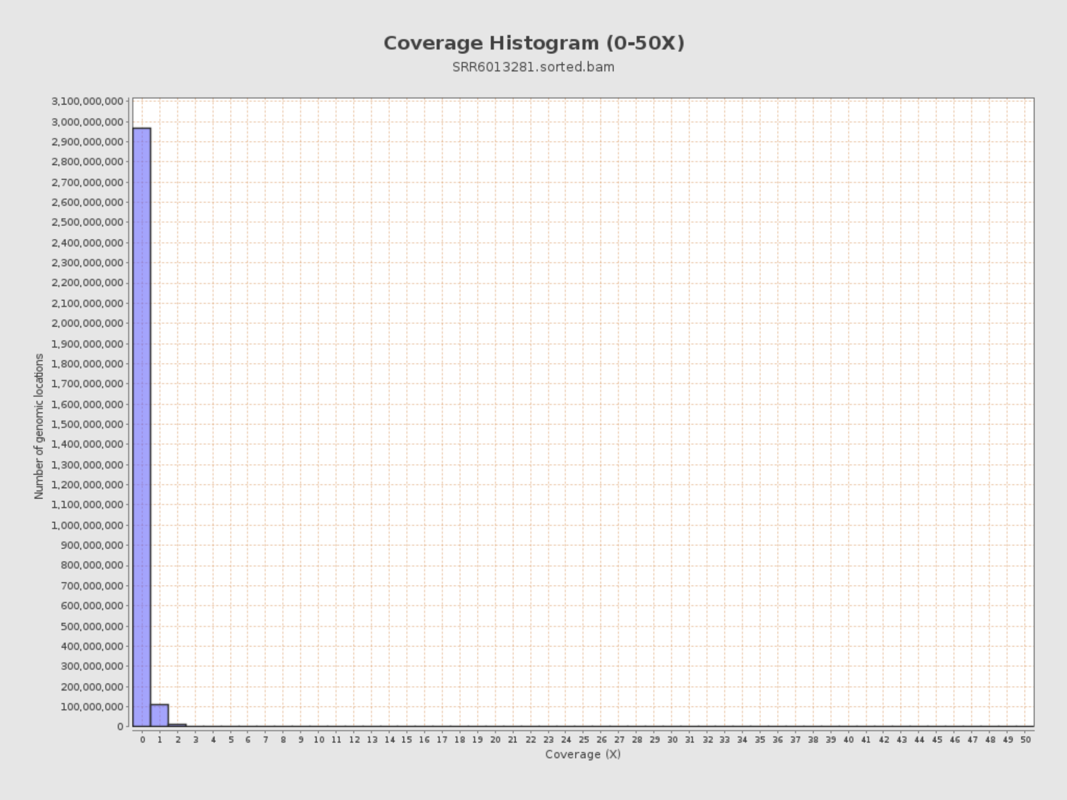
3. Results : Coverage across reference



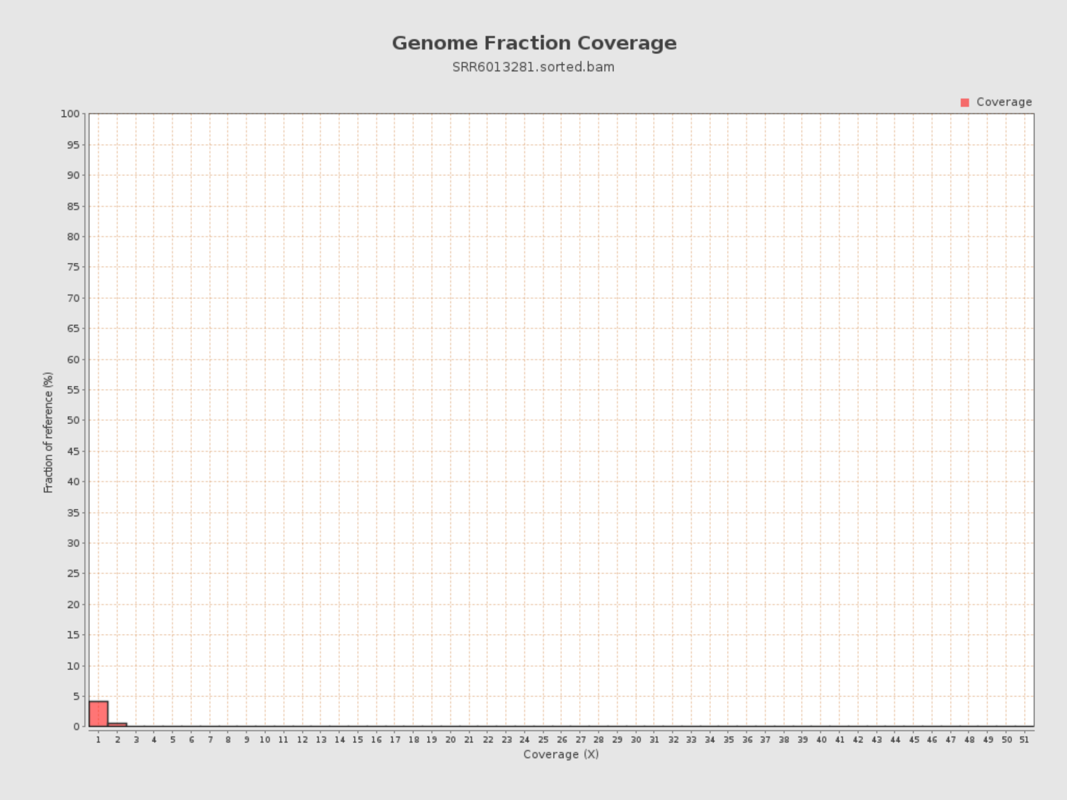
4. Results : Coverage Histogram



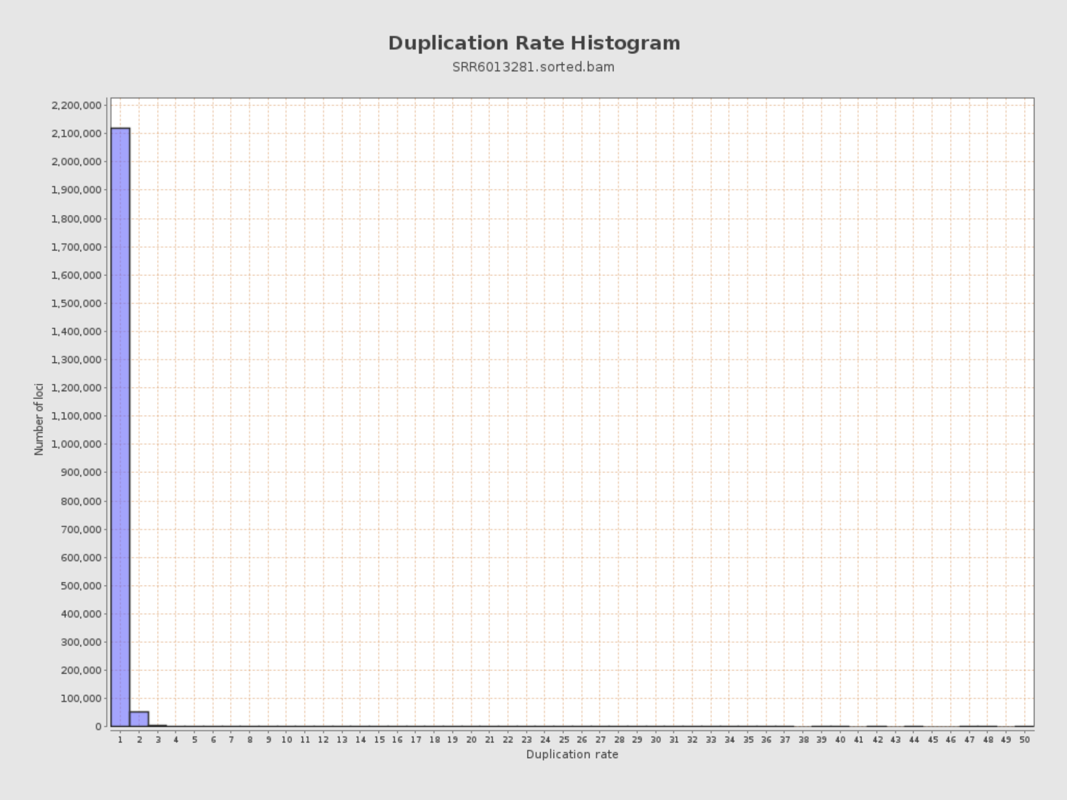
5. Results : Coverage Histogram (0-50X)



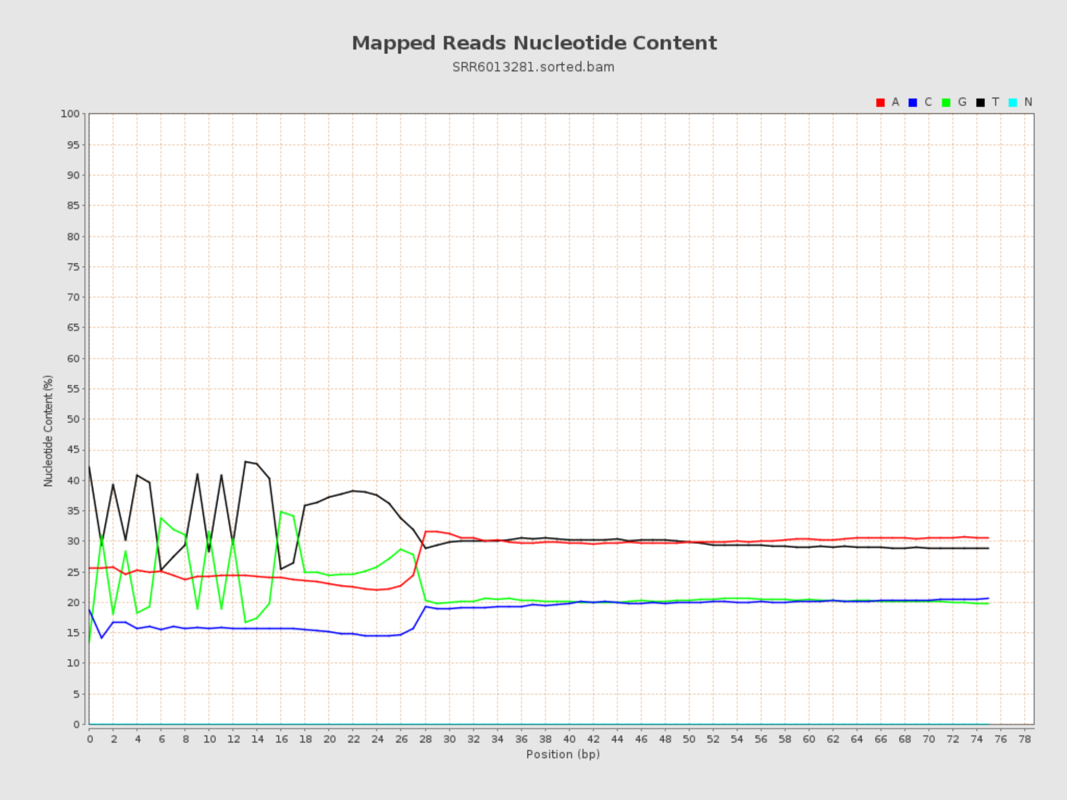
6. Results : Genome Fraction Coverage



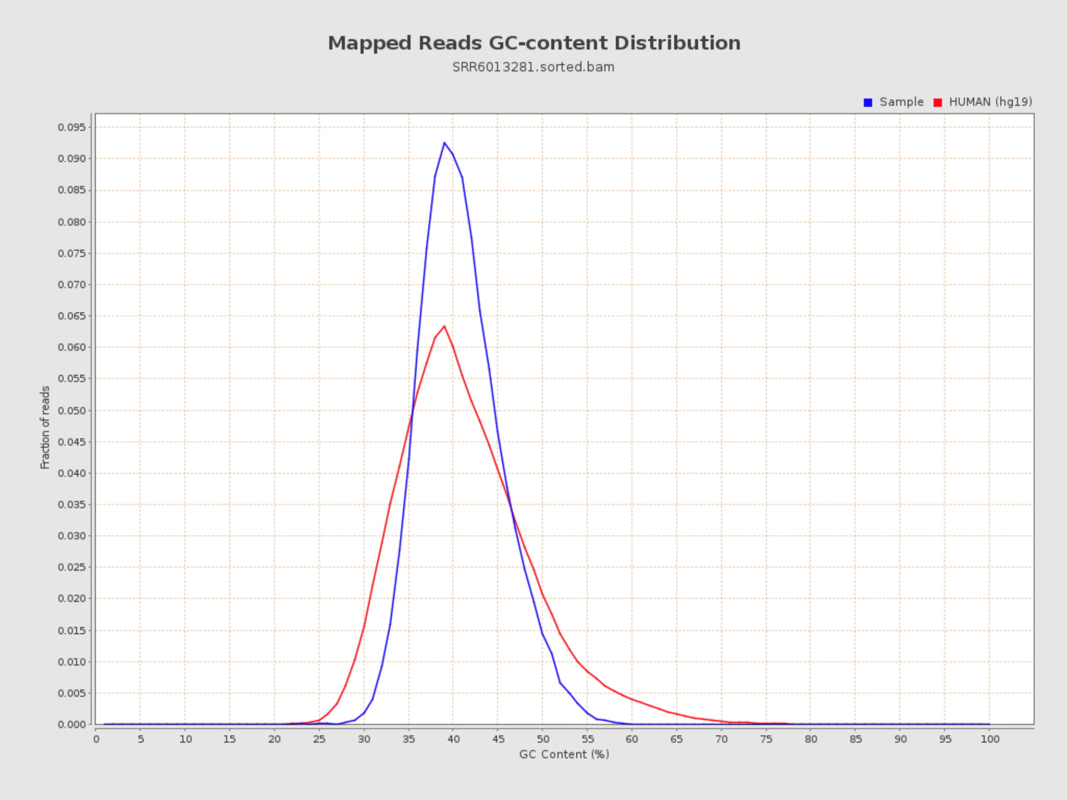
7. Results : Duplication Rate Histogram



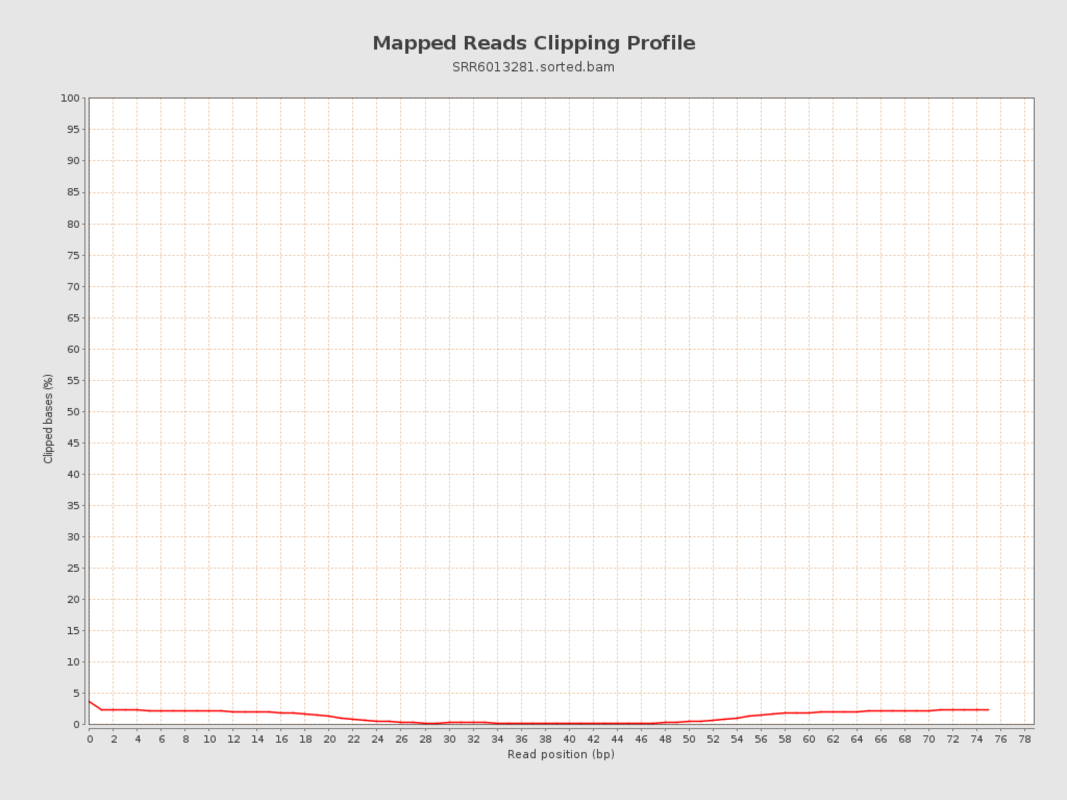
8. Results : Mapped Reads Nucleotide Content



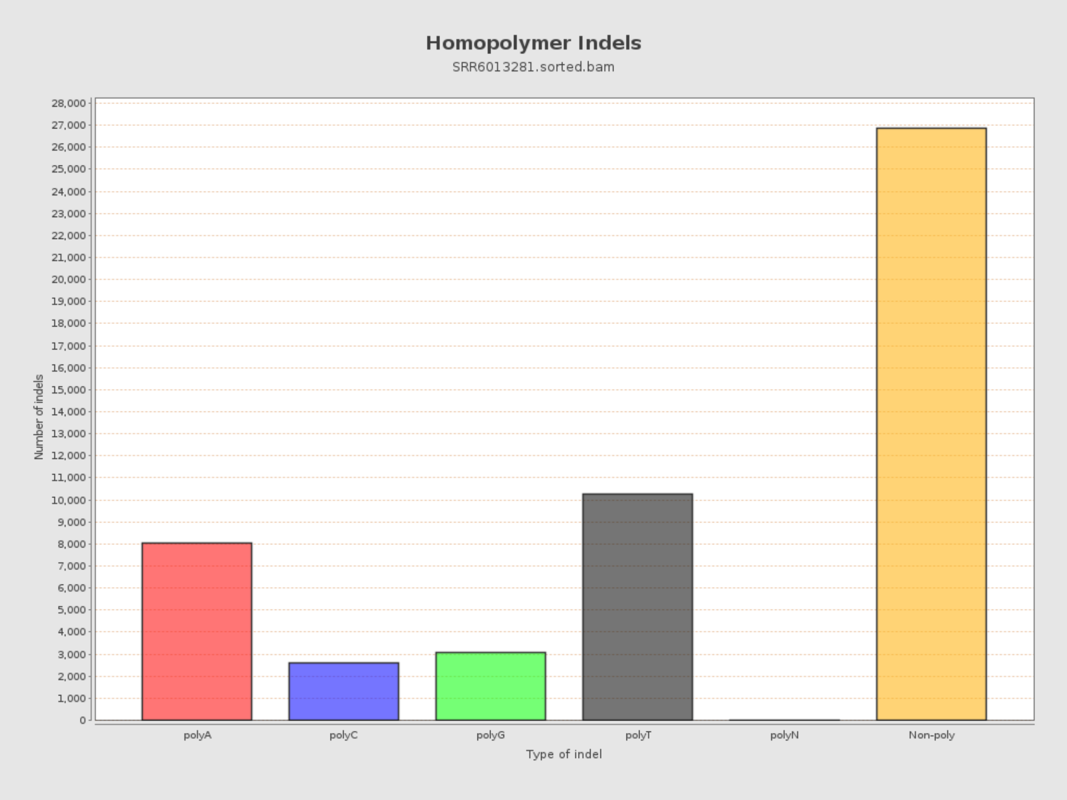
9. Results : Mapped Reads GC-content Distribution



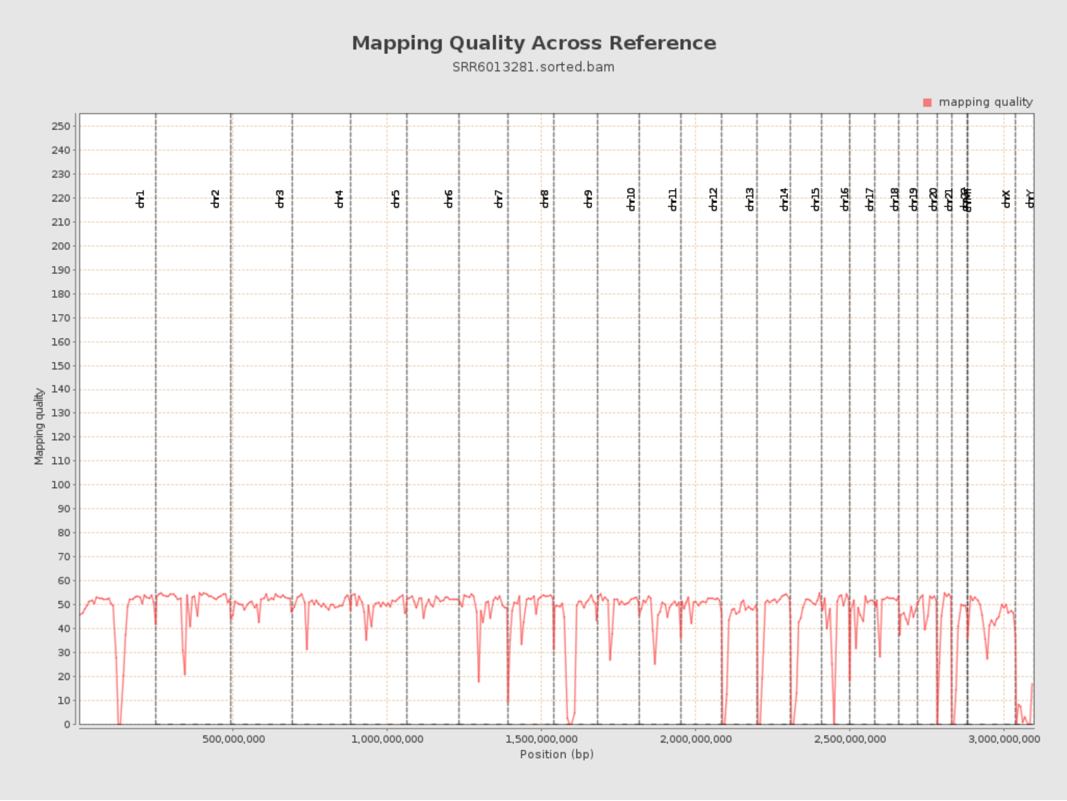
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram