Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:18:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081221.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_SRR3081221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:18:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,271,479
Mapped reads	1,980,747 / 87.2%
Unmapped reads	290,732 / 12.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,413 / 1.16%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	95,183 / 4.19%
Duplication rate	4.06%
Clipped reads	1,057,038 / 46.54%

2.2. ACGT Content

Number/percentage of A's	36,774,203 / 28.51%
Number/percentage of C's	25,068,609 / 19.43%
Number/percentage of T's	39,356,142 / 30.51%
Number/percentage of G's	27,780,457 / 21.54%
Number/percentage of N's	7,966 / 0.01%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3046

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

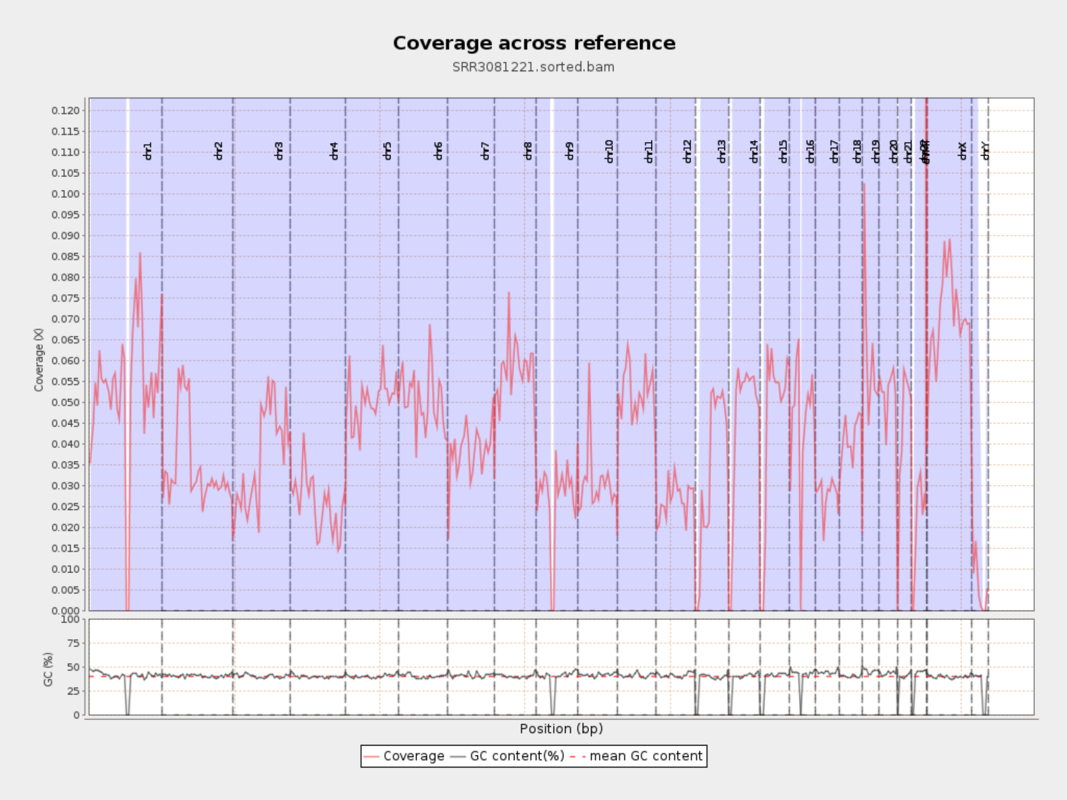
General error rate	0.92%
Mismatches	1,163,346
Insertions	9,683
Mapped reads with at least one insertion	0.48%
Deletions	29,578
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.84%

2.6. Chromosome stats

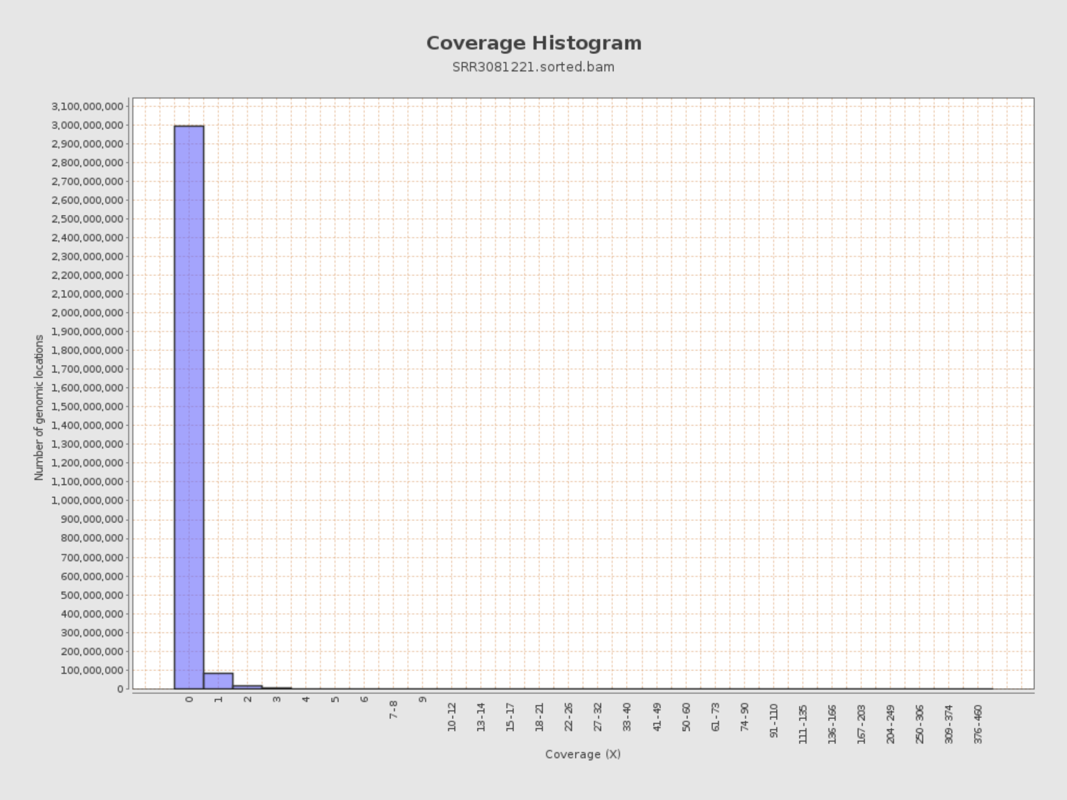
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13225960	0.0531	0.4547
chr2	243199373	8488501	0.0349	0.3462
chr3	198022430	7302246	0.0369	0.2336
chr4	191154276	4890475	0.0256	0.2029
chr5	180915260	9136866	0.0505	0.2718
chr6	171115067	8703845	0.0509	0.2983
chr7	159138663	6106371	0.0384	0.3108

chr8	146364022	8450093	0.0577	0.382
chr9	141213431	3757485	0.0266	0.2464
chr10	135534747	4134947	0.0305	0.3111
chr11	135006516	7033275	0.0521	0.3416
chr12	133851895	3533259	0.0264	0.1976
chr13	115169878	3913864	0.034	0.2252
chr14	107349540	4849555	0.0452	0.2641
chr15	102531392	4655103	0.0454	0.2635
chr16	90354753	4125417	0.0457	0.2681
chr17	81195210	2238704	0.0276	0.2146
chr18	78077248	3240899	0.0415	0.3775
chr19	59128983	3545416	0.06	0.3797
chr20	63025520	3227898	0.0512	0.276
chr21	48129895	2083736	0.0433	0.2609
chr22	51304566	1033420	0.0201	0.1688
chrMT	16571	85743	5.1743	4.2969
chrX	155270560	10897375	0.0702	0.3378
chrY	59373566	375291	0.0063	0.1283

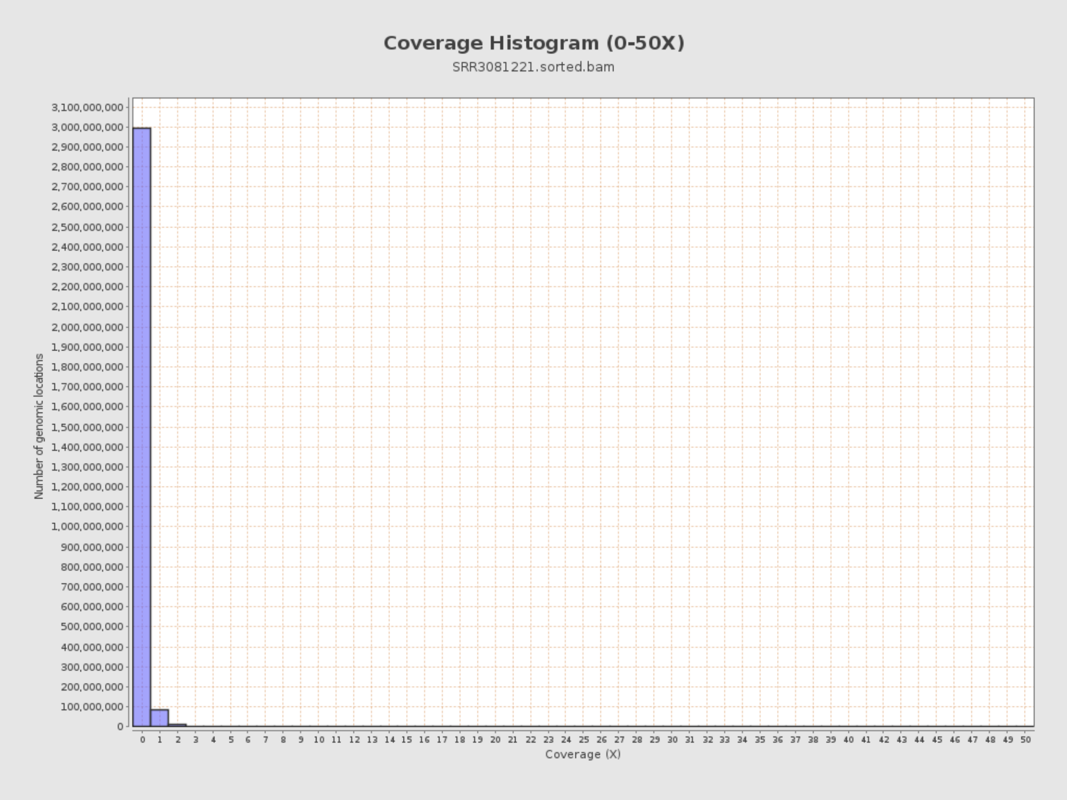
3. Results : Coverage across reference



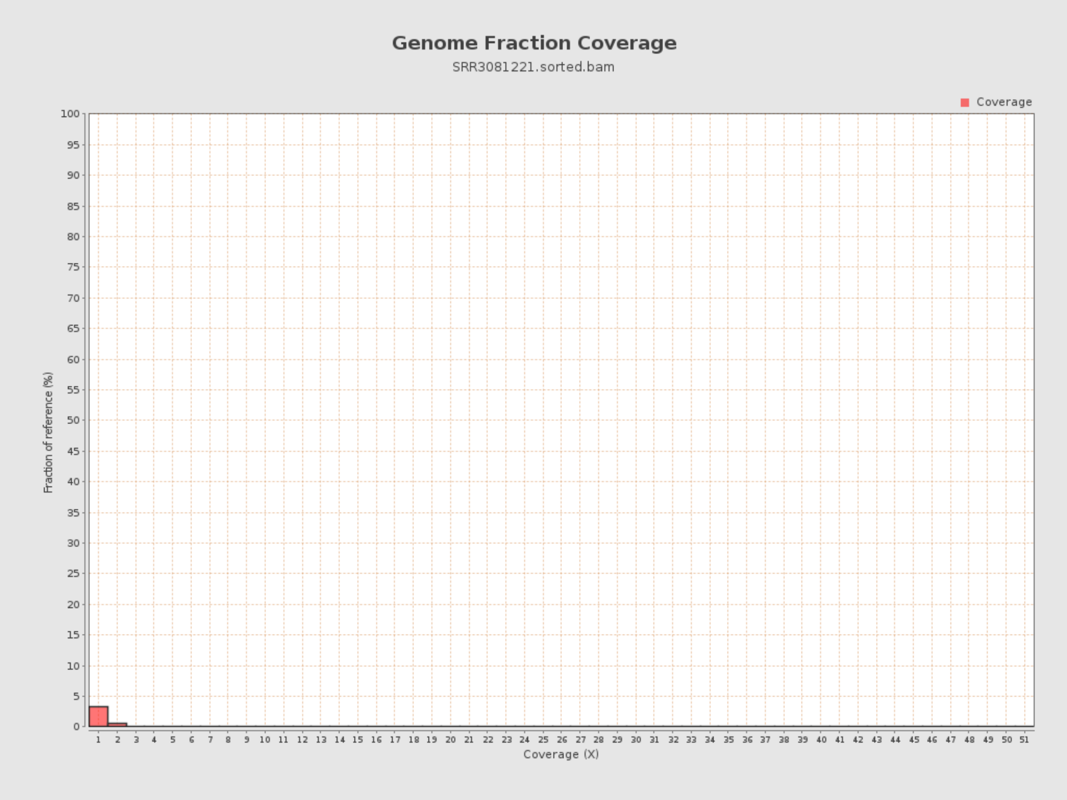
4. Results : Coverage Histogram



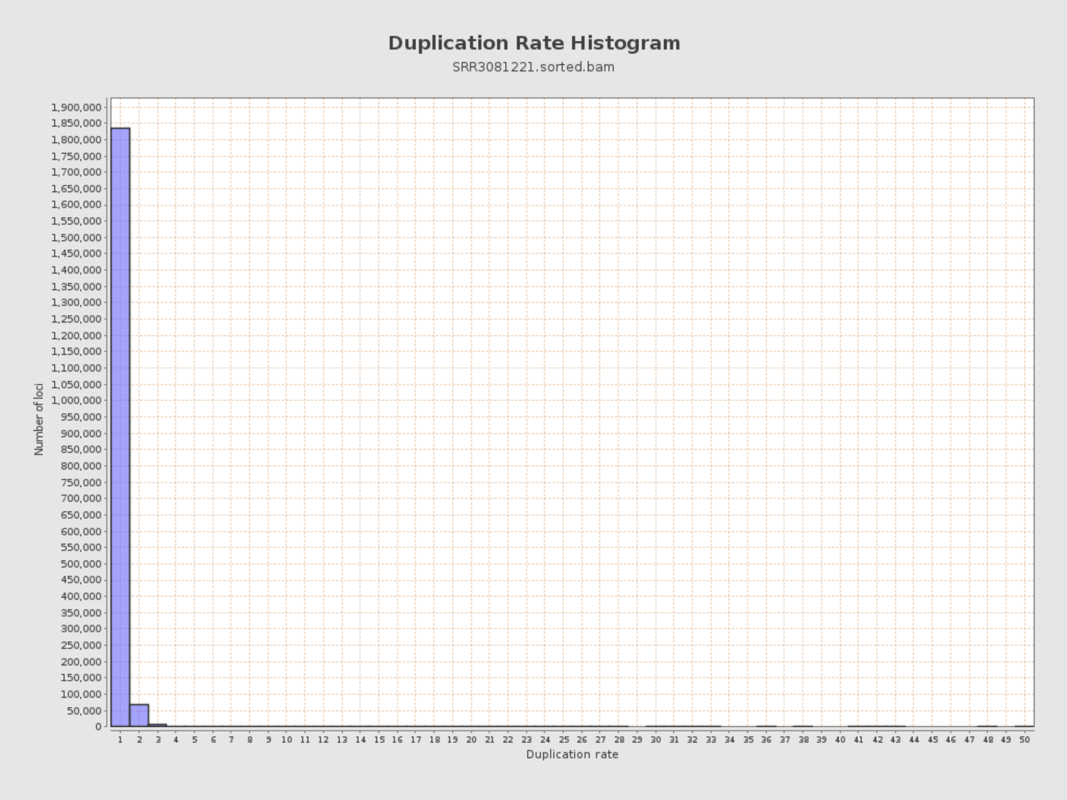
5. Results : Coverage Histogram (0-50X)



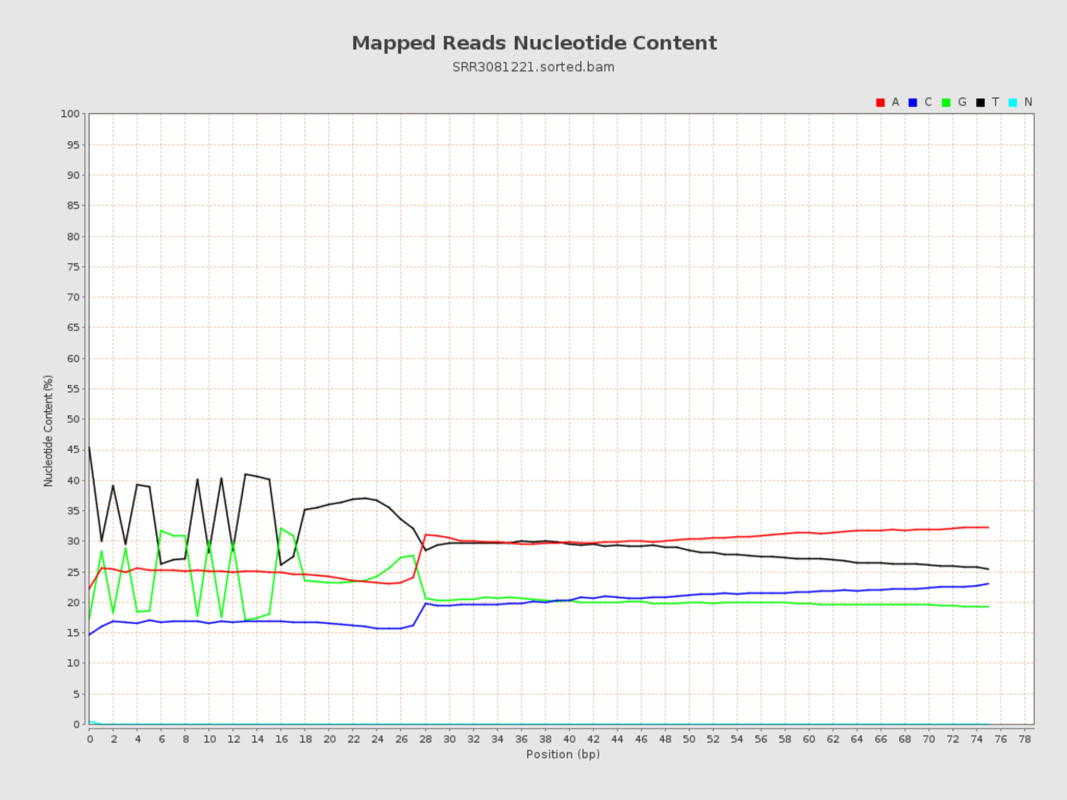
6. Results : Genome Fraction Coverage



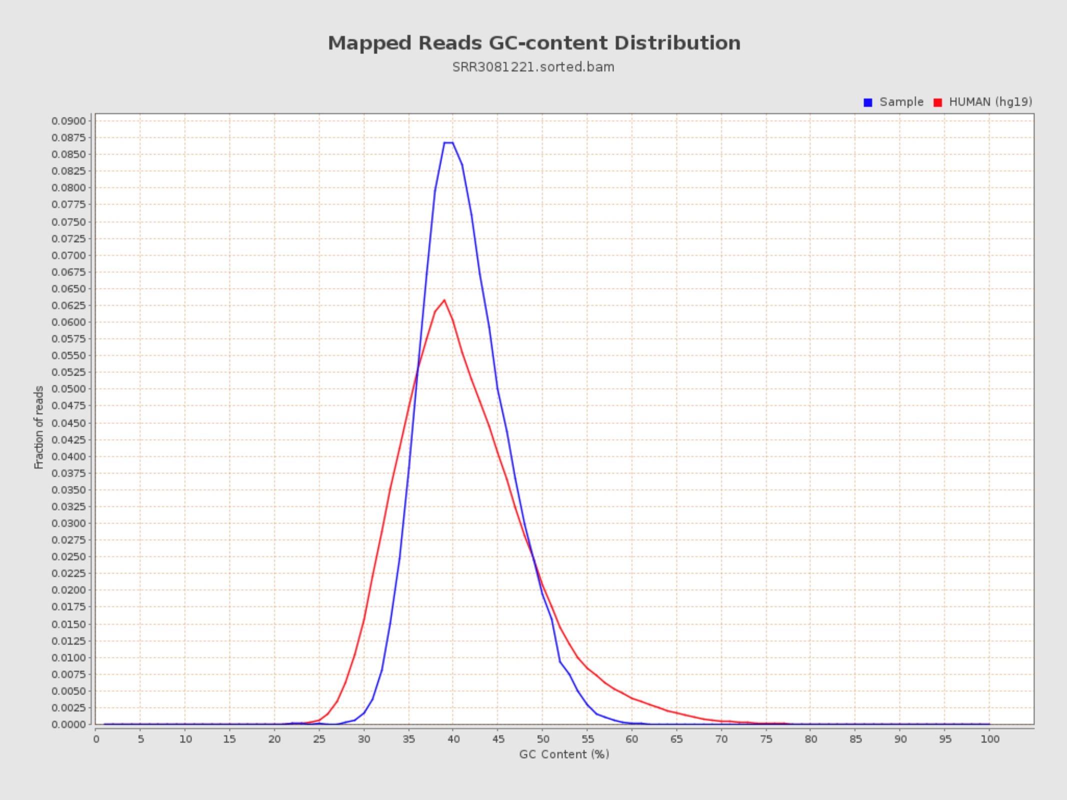
7. Results : Duplication Rate Histogram



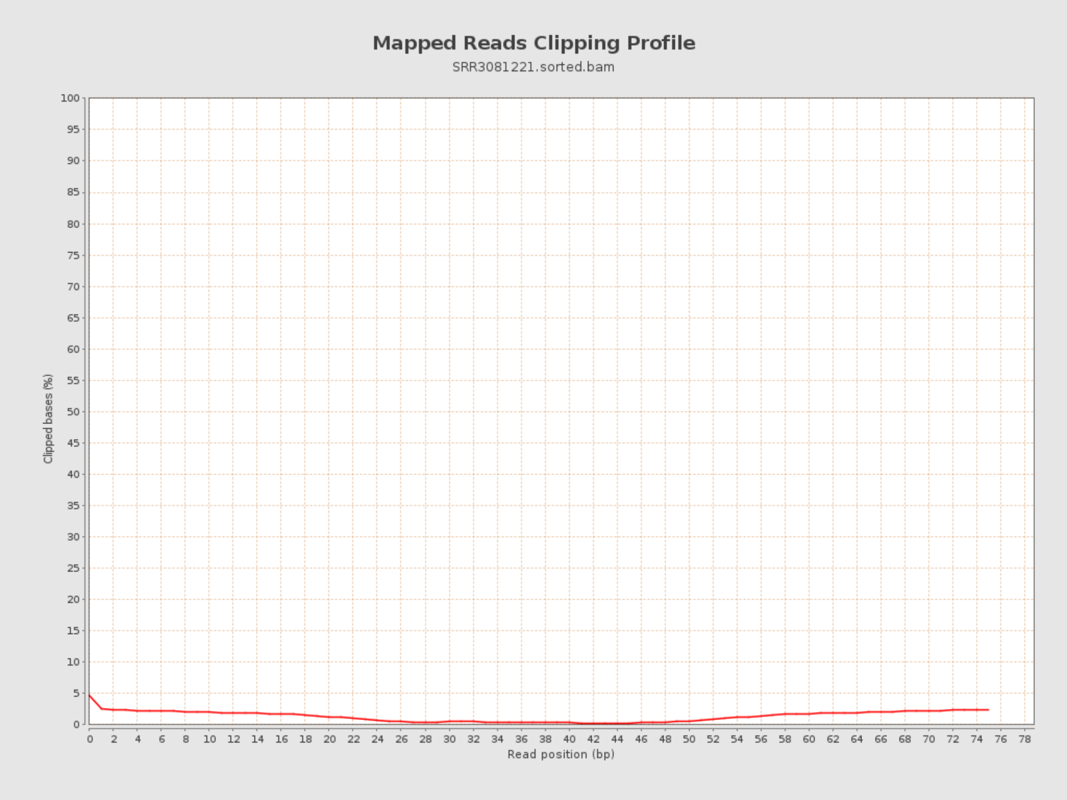
8. Results : Mapped Reads Nucleotide Content



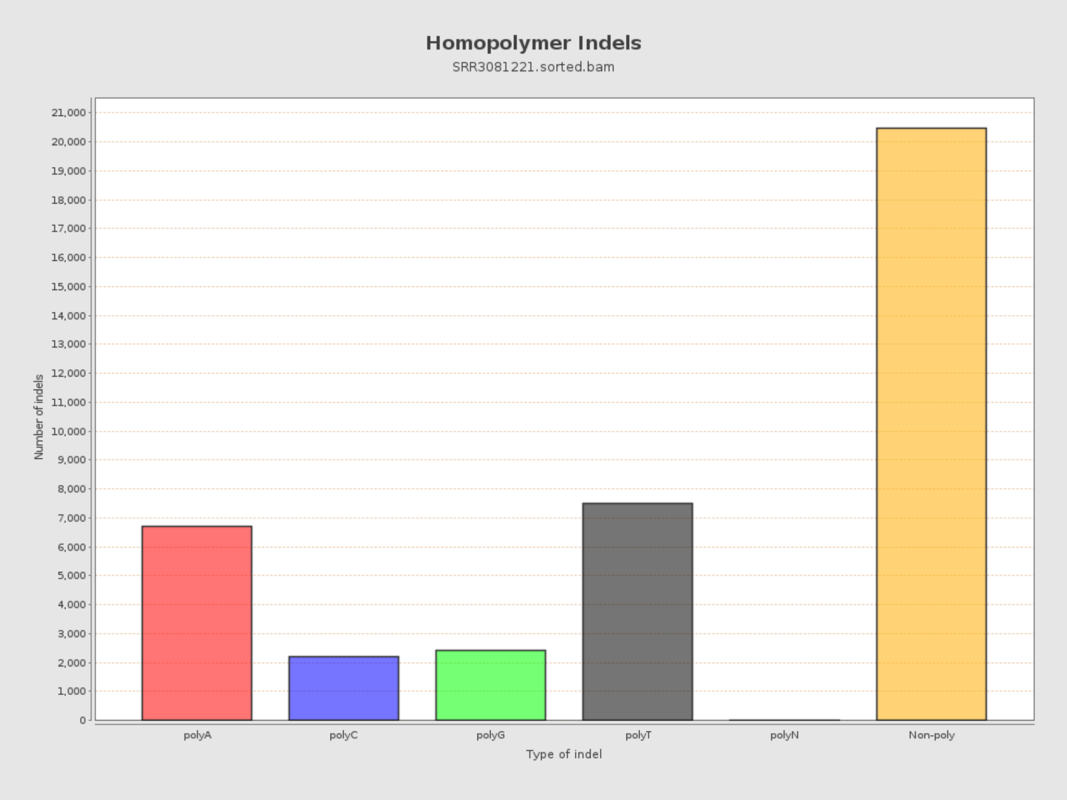
9. Results : Mapped Reads GC-content Distribution



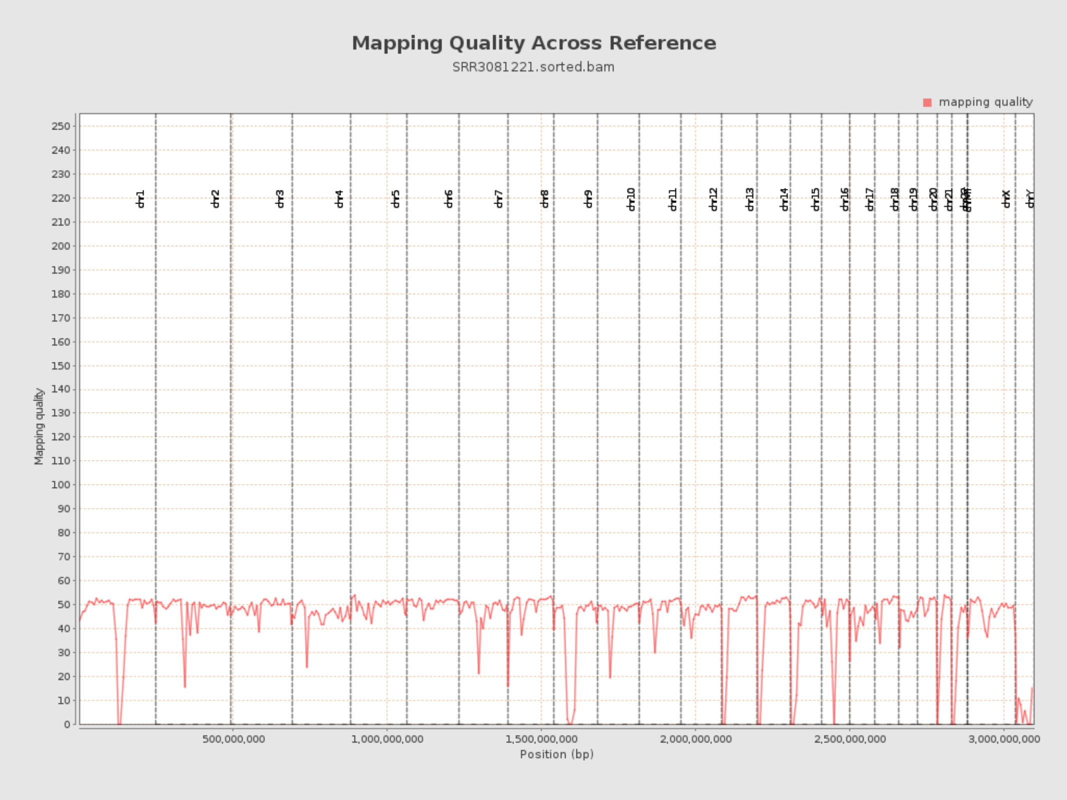
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram