Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:45:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082501.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_SRR3082501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082501.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:45:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,683,751
Mapped reads	2,443,145 / 91.03%
Unmapped reads	240,606 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,446 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	103,461 / 3.86%
Duplication rate	3.18%
Clipped reads	991,414 / 36.94%

2.2. ACGT Content

Number/percentage of A's	47,312,637 / 28.45%
Number/percentage of C's	31,090,220 / 18.69%
Number/percentage of T's	52,227,400 / 31.4%
Number/percentage of G's	35,689,112 / 21.46%
Number/percentage of N's	3,562 / 0%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.4757

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

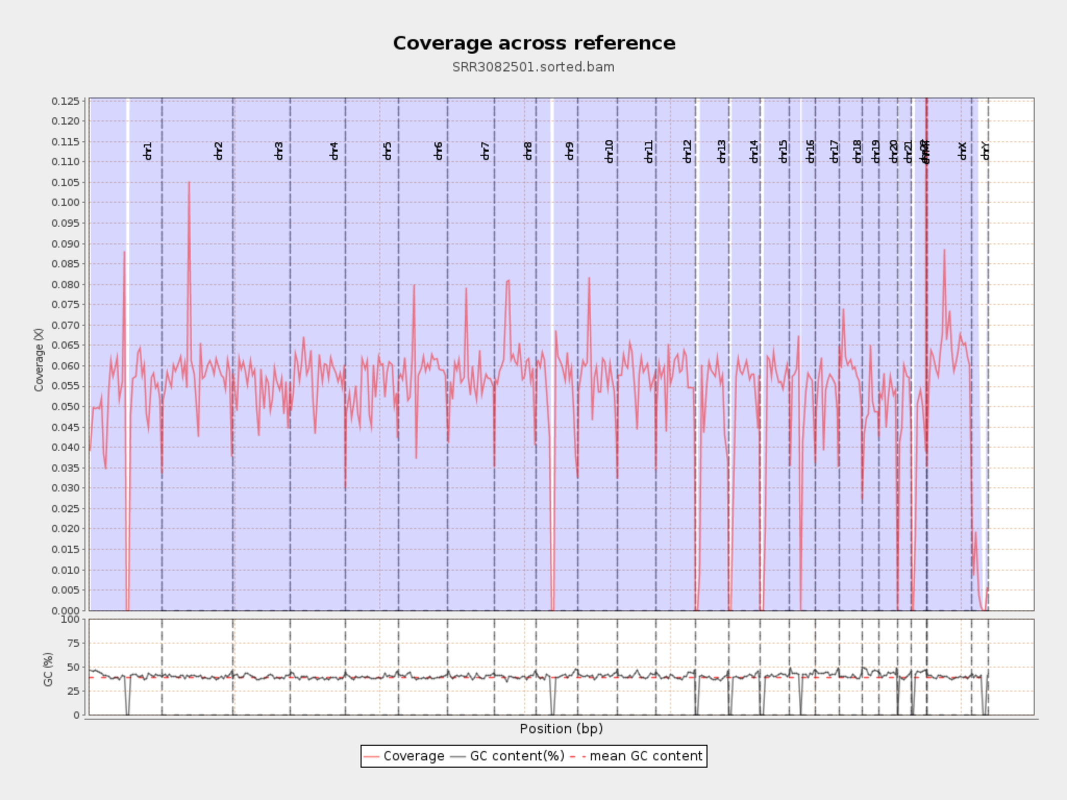
General error rate	0.86%
Mismatches	1,413,207
Insertions	13,436
Mapped reads with at least one insertion	0.55%
Deletions	43,657
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.4%

2.6. Chromosome stats

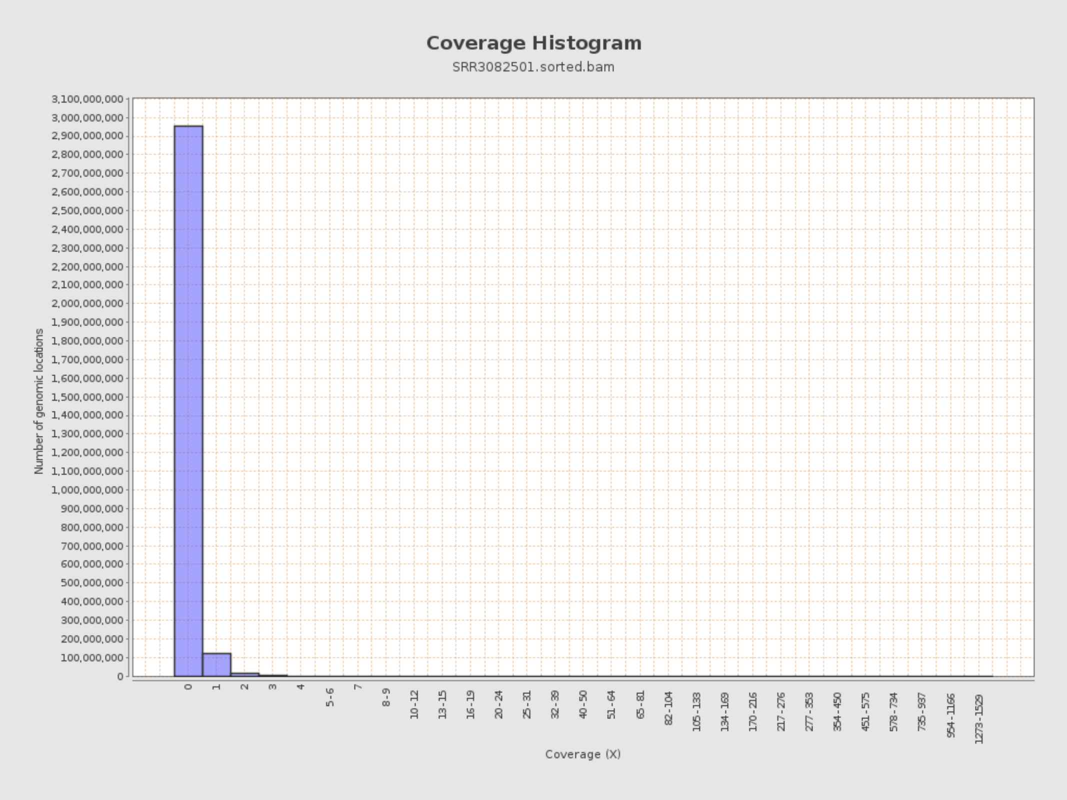
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12692977	0.0509	0.7783
chr2	243199373	14327657	0.0589	0.5569
chr3	198022430	10866475	0.0549	0.2649
chr4	191154276	11069375	0.0579	0.2879
chr5	180915260	9830803	0.0543	0.2655
chr6	171115067	10029479	0.0586	0.3652
chr7	159138663	9129245	0.0574	0.4375

chr8	146364022	8940593	0.0611	0.9653
chr9	141213431	7198372	0.051	0.4358
chr10	135534747	7853555	0.0579	0.4008
chr11	135006516	7789992	0.0577	0.5147
chr12	133851895	7699480	0.0575	0.2809
chr13	115169878	5192844	0.0451	0.2411
chr14	107349540	5088899	0.0474	0.27
chr15	102531392	4867894	0.0475	0.2579
chr16	90354753	4458556	0.0493	0.2792
chr17	81195210	4288560	0.0528	0.3347
chr18	78077248	4731545	0.0606	0.8946
chr19	59128983	2896932	0.049	0.538
chr20	63025520	3274079	0.0519	0.2712
chr21	48129895	2235883	0.0465	0.2646
chr22	51304566	1756450	0.0342	0.2077
chrMT	16571	9578	0.578	0.914
chrX	155270560	9790524	0.0631	0.3452
chrY	59373566	373685	0.0063	0.1378

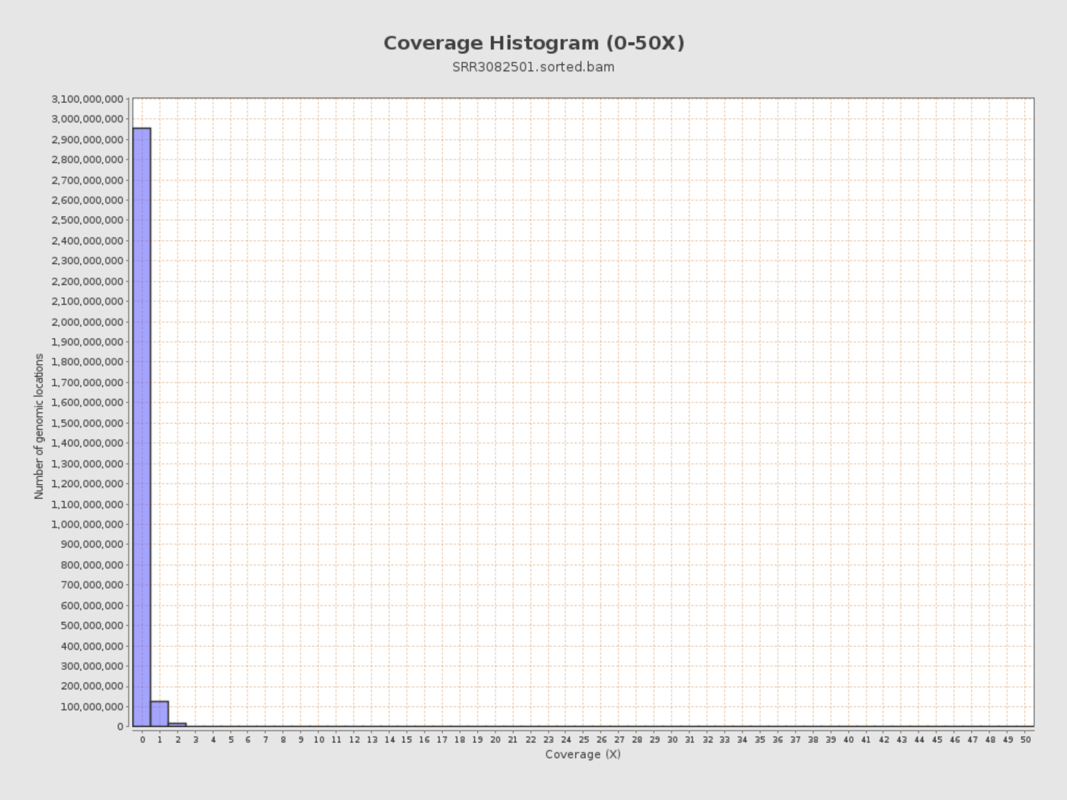
3. Results : Coverage across reference



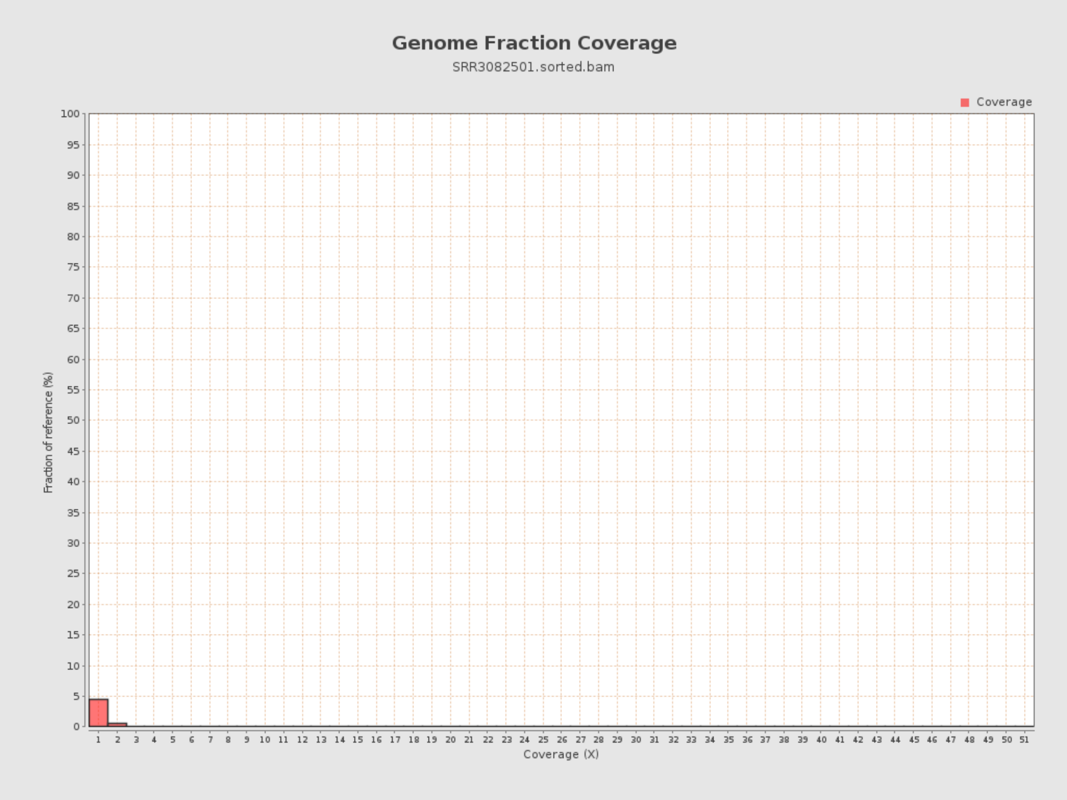
4. Results : Coverage Histogram



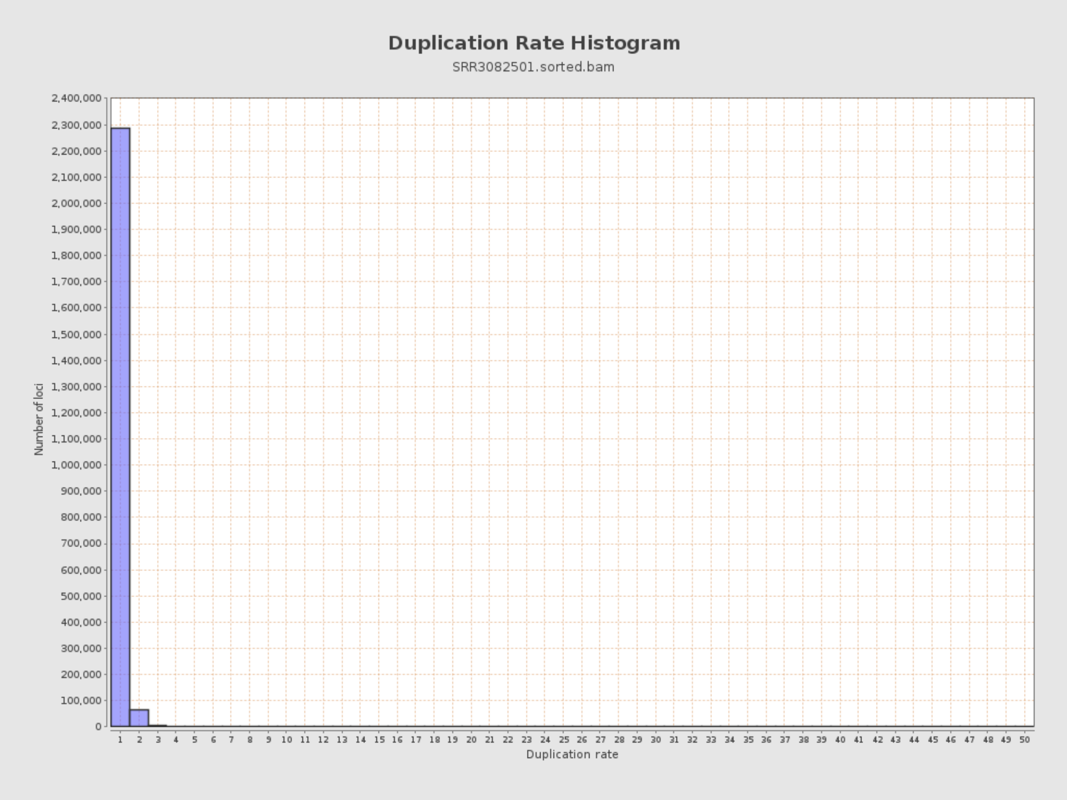
5. Results : Coverage Histogram (0-50X)



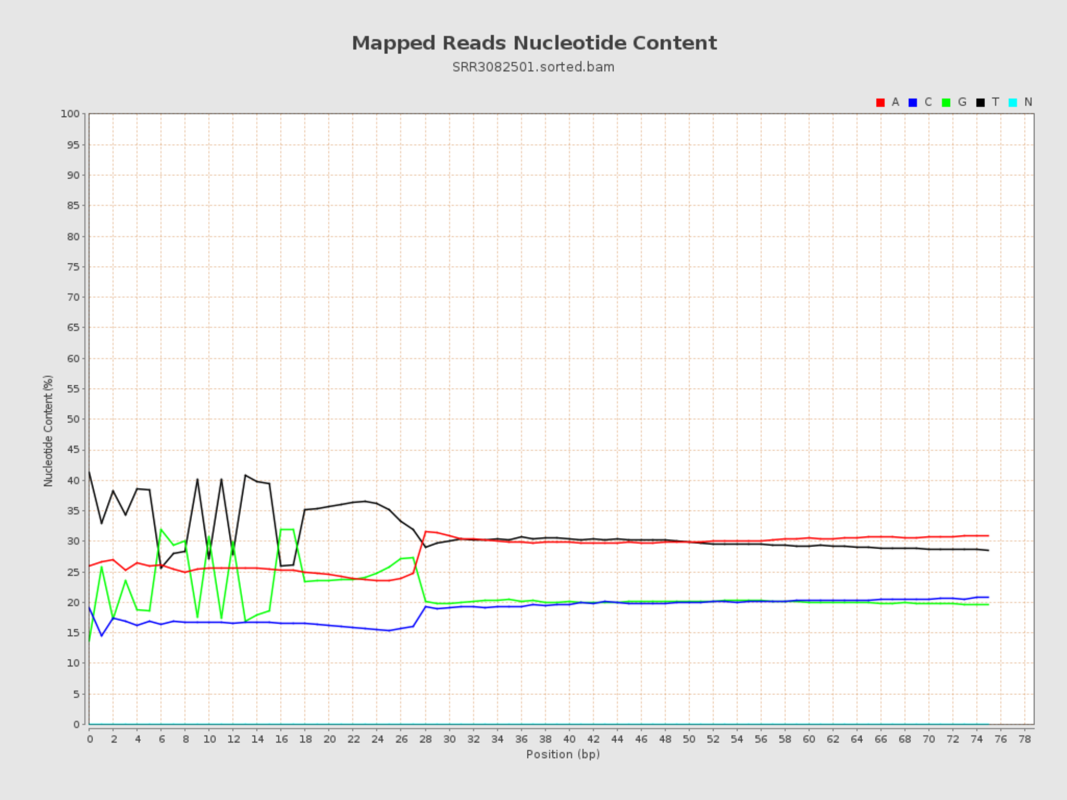
6. Results : Genome Fraction Coverage



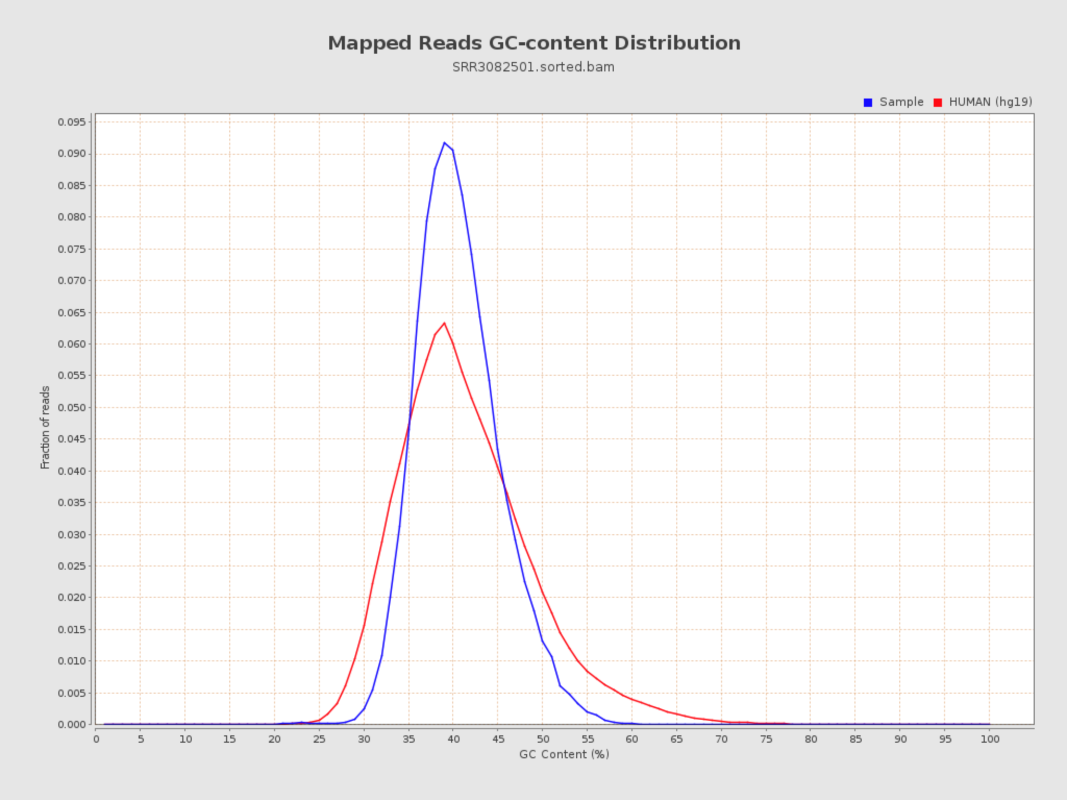
7. Results : Duplication Rate Histogram



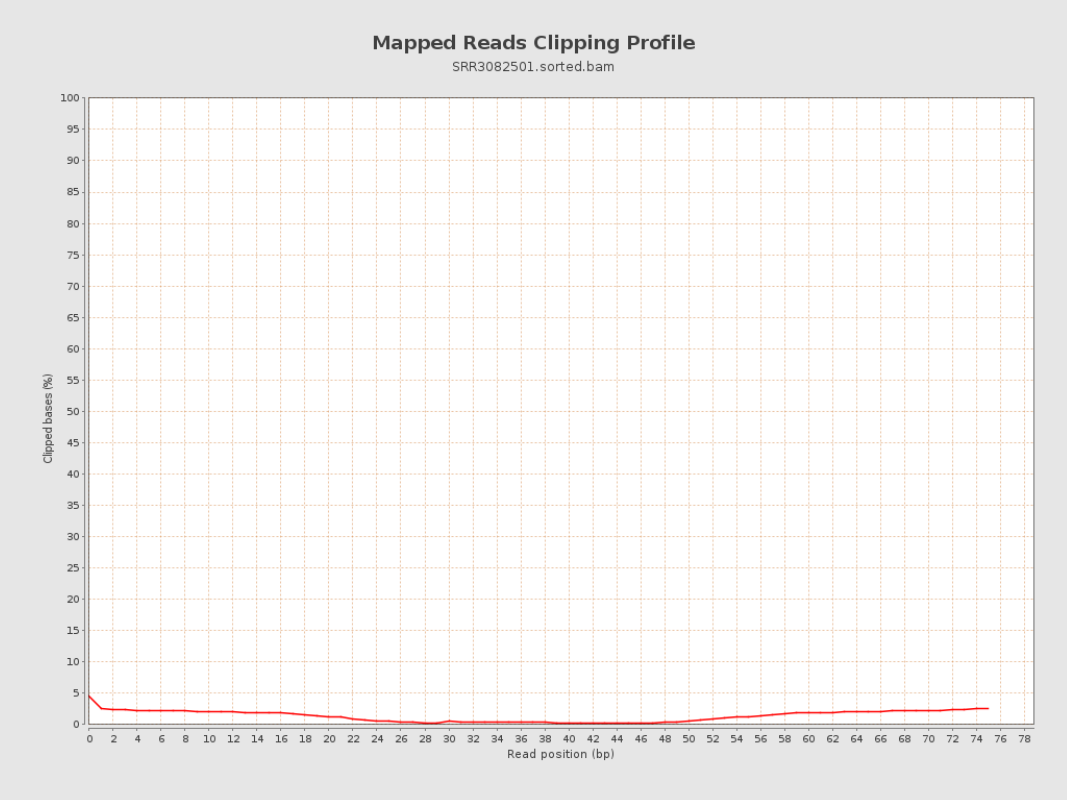
8. Results : Mapped Reads Nucleotide Content



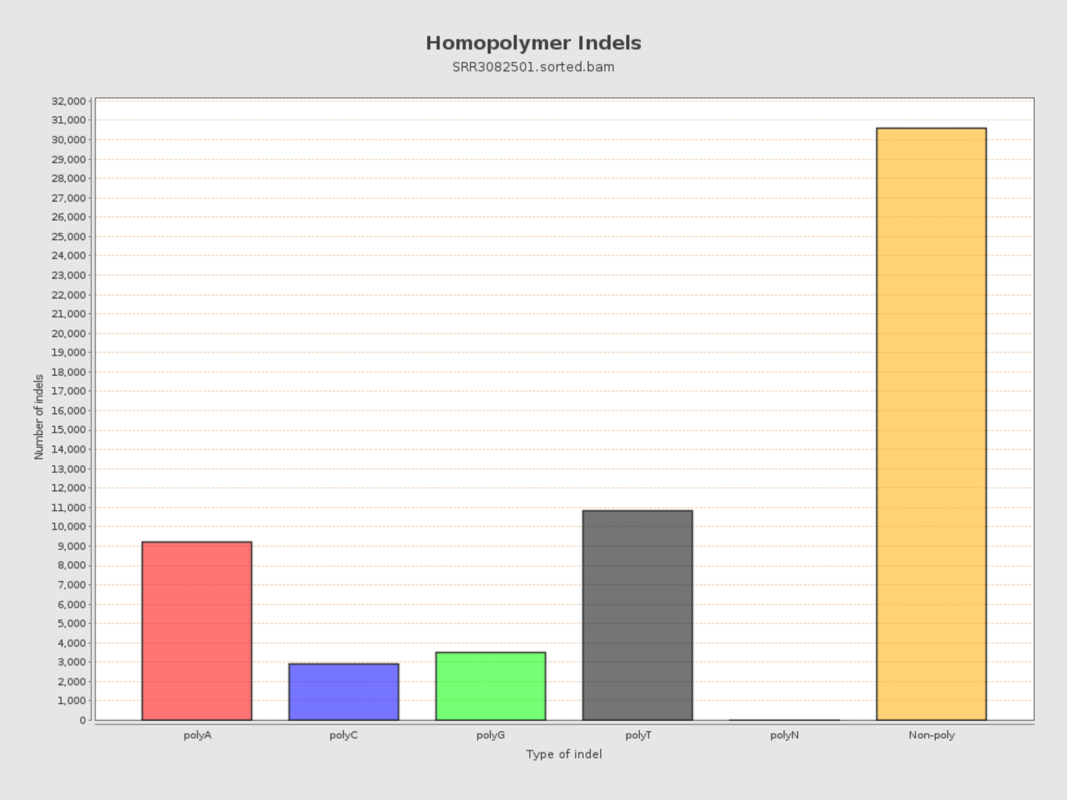
9. Results : Mapped Reads GC-content Distribution



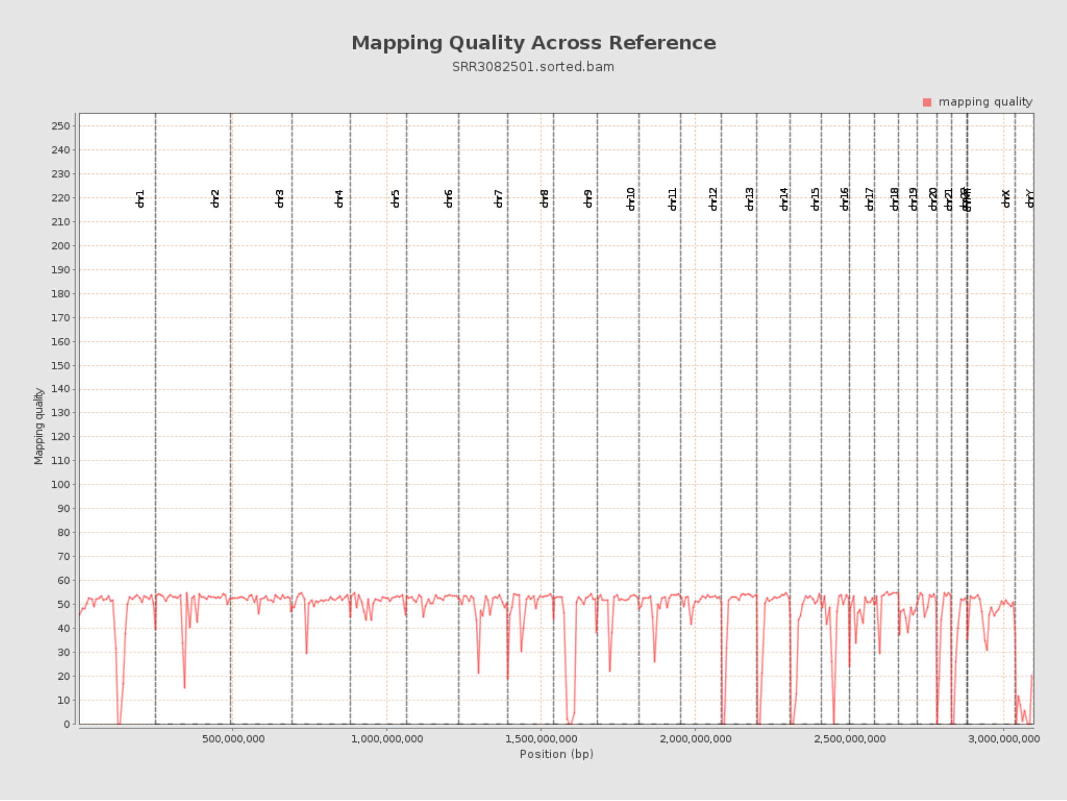
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram