Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:25:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819025.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_SRR1819025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:25:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,437
Mapped reads	1,491,652 / 97.72%
Unmapped reads	34,785 / 2.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,176 / 1.52%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	579,755 / 37.98%
Duplication rate	31.75%
Clipped reads	1,500,362 / 98.29%

2.2. ACGT Content

Number/percentage of A's	40,463,761 / 29.34%
Number/percentage of C's	28,496,402 / 20.66%
Number/percentage of T's	38,788,949 / 28.12%
Number/percentage of G's	30,162,337 / 21.87%
Number/percentage of N's	6,676 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.5512

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

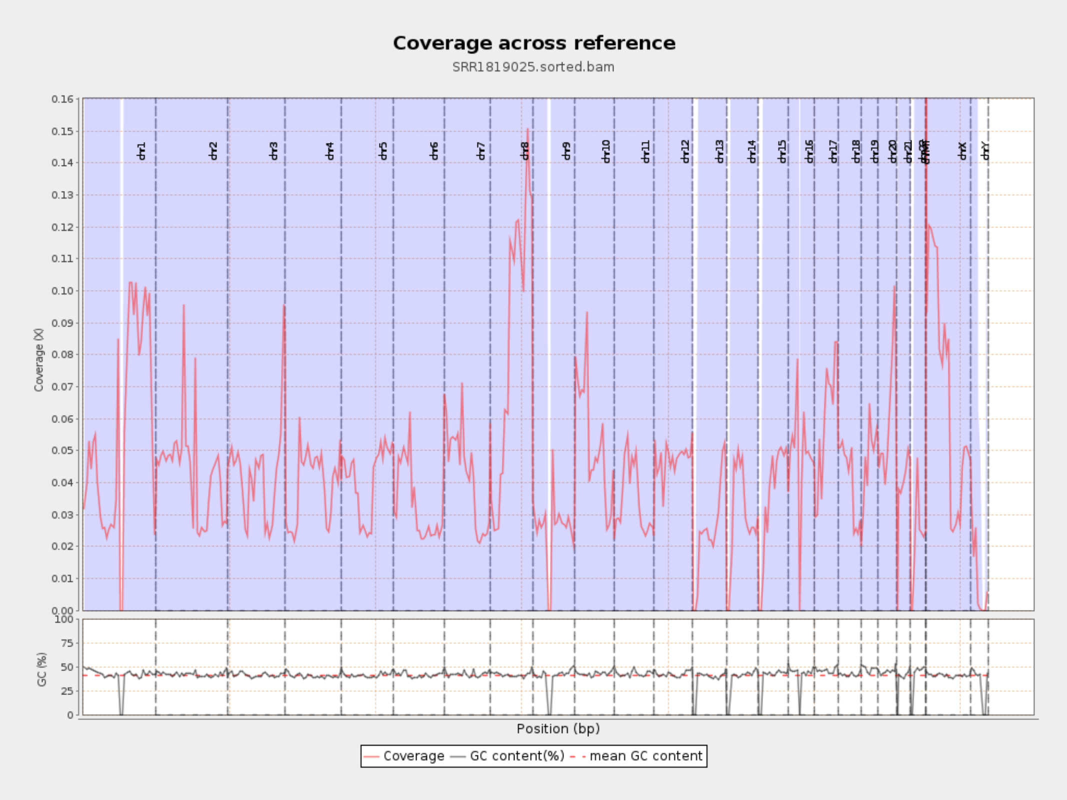
General error rate	0.66%
Mismatches	864,958
Insertions	22,128
Mapped reads with at least one insertion	1.43%
Deletions	48,123
Mapped reads with at least one deletion	3.13%
Homopolymer indels	40.56%

2.6. Chromosome stats

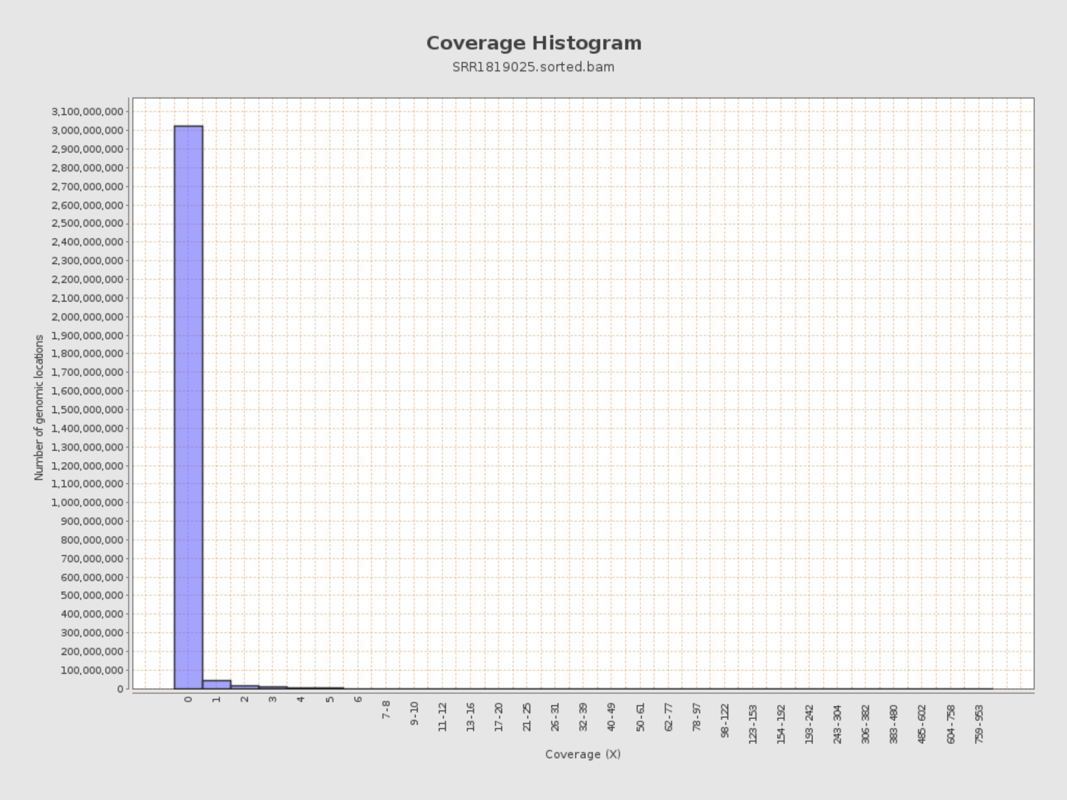
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13853840	0.0556	0.8858
chr2	243199373	10661136	0.0438	0.9037
chr3	198022430	8500113	0.0429	0.3494
chr4	191154276	7505046	0.0393	0.3777
chr5	180915260	7431953	0.0411	0.3524
chr6	171115067	5664141	0.0331	0.3513
chr7	159138663	6759567	0.0425	0.5908

chr8	146364022	12660751	0.0865	0.5546
chr9	141213431	3594589	0.0255	0.4364
chr10	135534747	7130578	0.0526	0.6465
chr11	135006516	4674347	0.0346	0.358
chr12	133851895	6340763	0.0474	0.3717
chr13	115169878	2922426	0.0254	0.2641
chr14	107349540	3195912	0.0298	0.304
chr15	102531392	3558514	0.0347	0.3139
chr16	90354753	4299754	0.0476	0.675
chr17	81195210	4793312	0.059	0.4544
chr18	78077248	3172206	0.0406	0.5641
chr19	59128983	2825756	0.0478	0.8006
chr20	63025520	3901923	0.0619	0.4516
chr21	48129895	1856099	0.0386	0.3511
chr22	51304566	1098951	0.0214	0.2652
chrMT	16571	103053	6.2189	5.664
chrX	155270560	10933150	0.0704	0.4971
chrY	59373566	571410	0.0096	0.5802

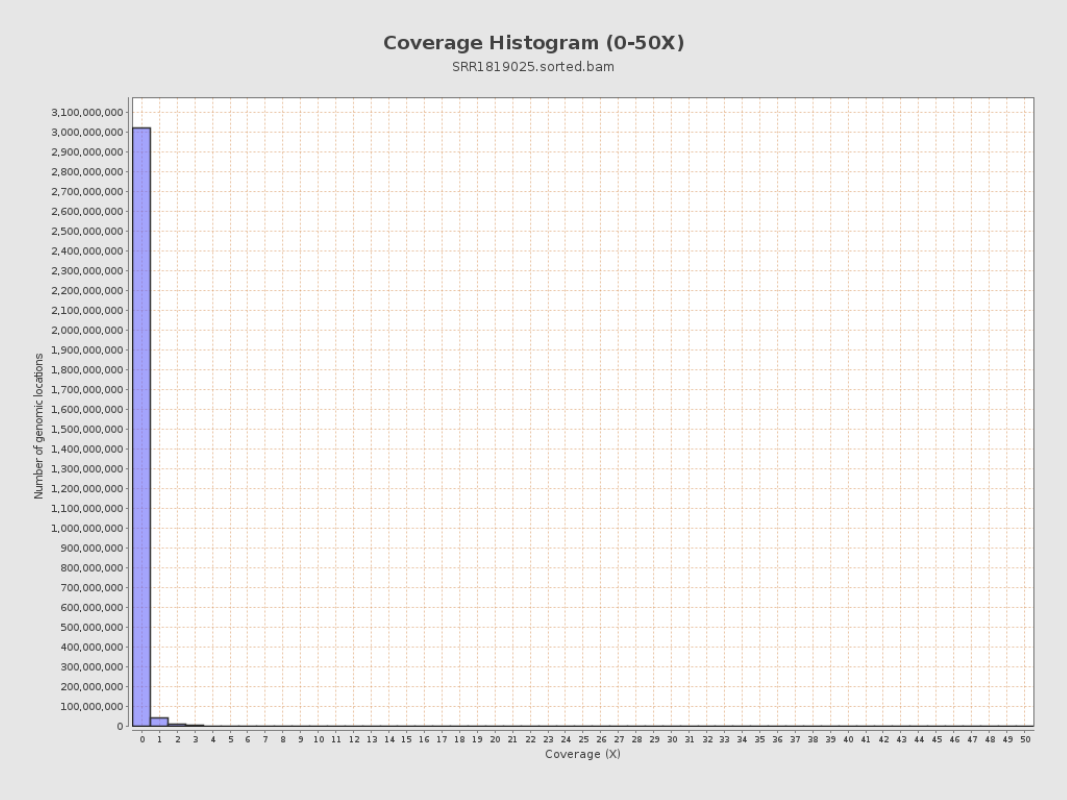
3. Results : Coverage across reference



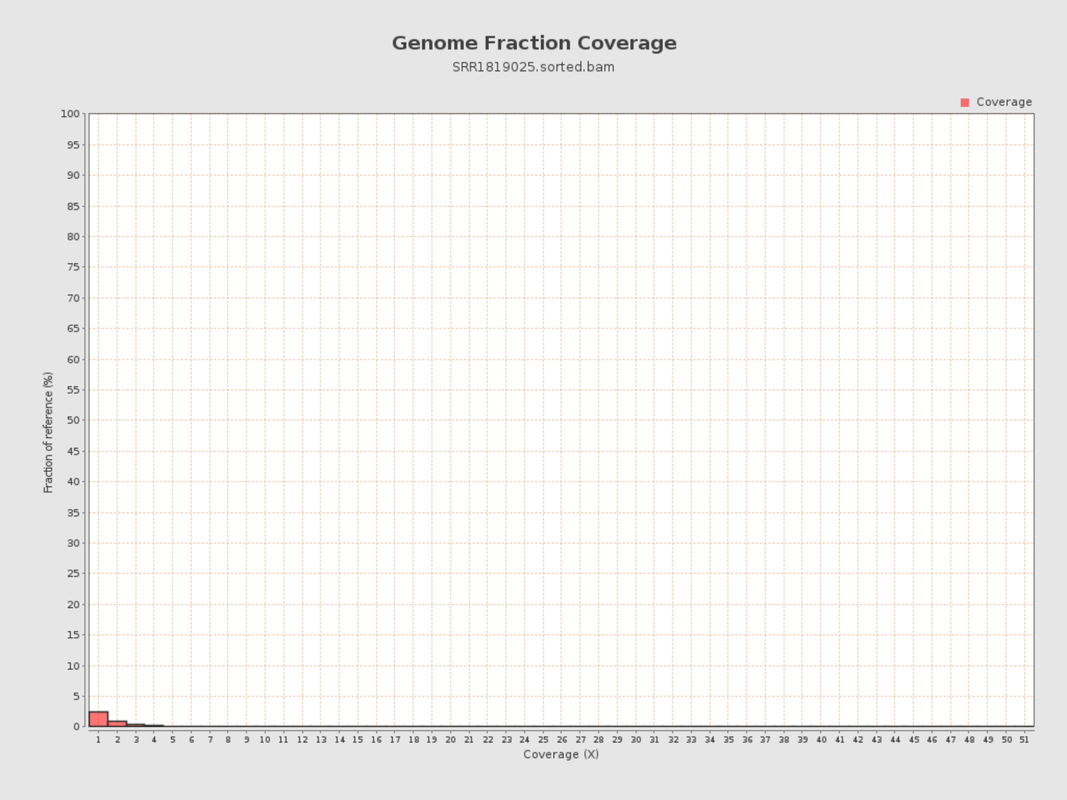
4. Results : Coverage Histogram



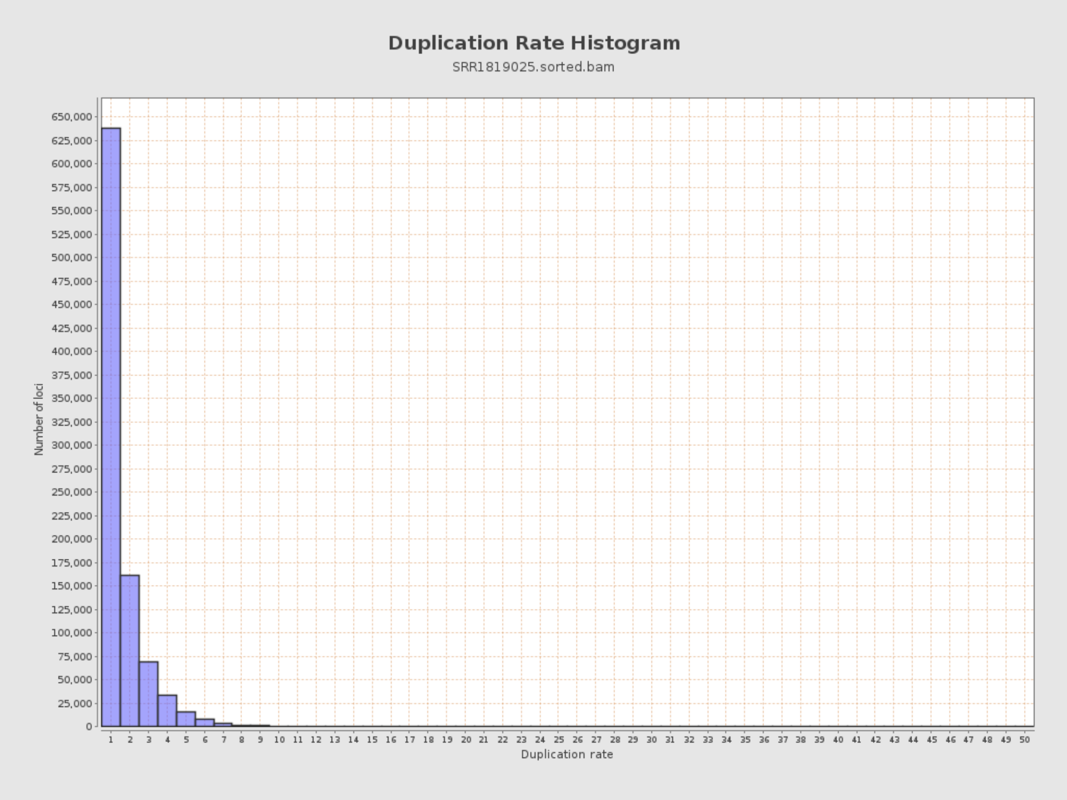
5. Results : Coverage Histogram (0-50X)



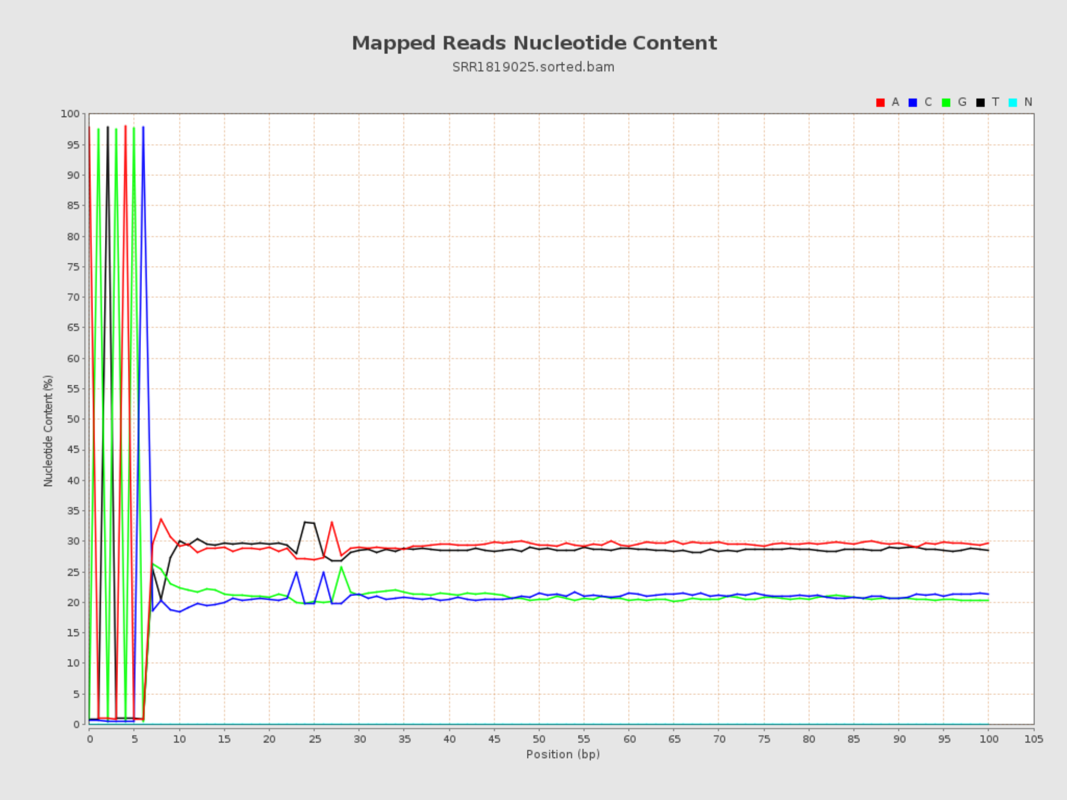
6. Results : Genome Fraction Coverage



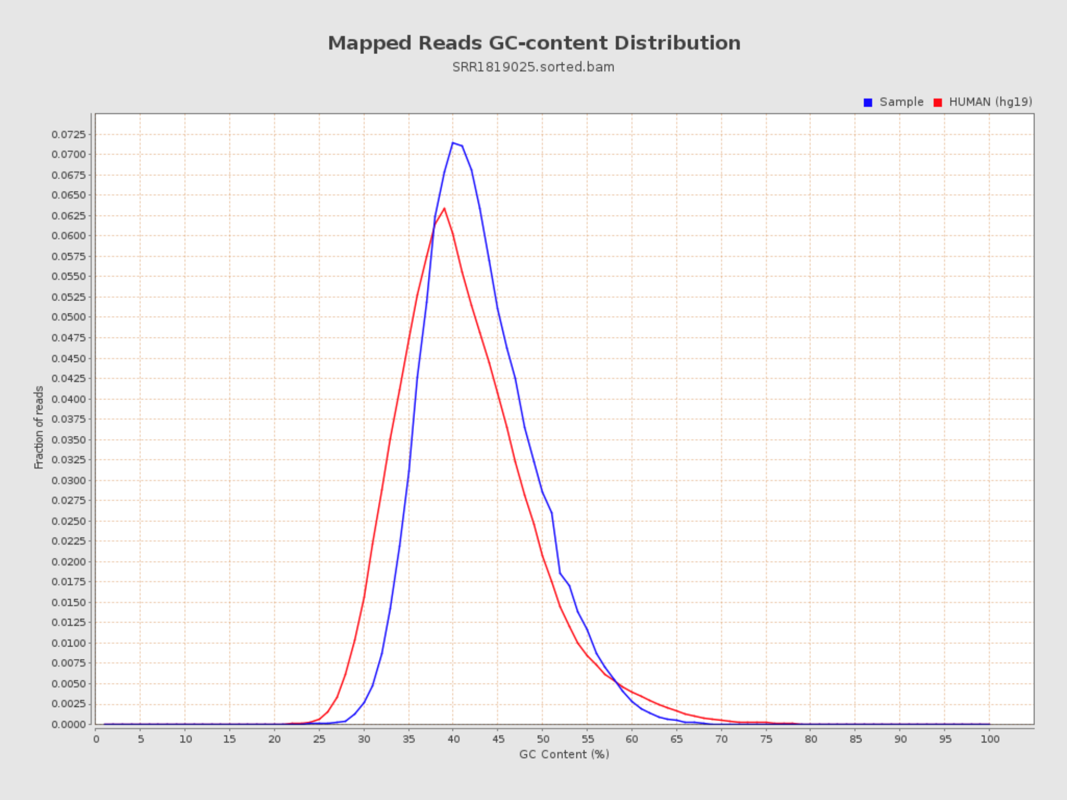
7. Results : Duplication Rate Histogram



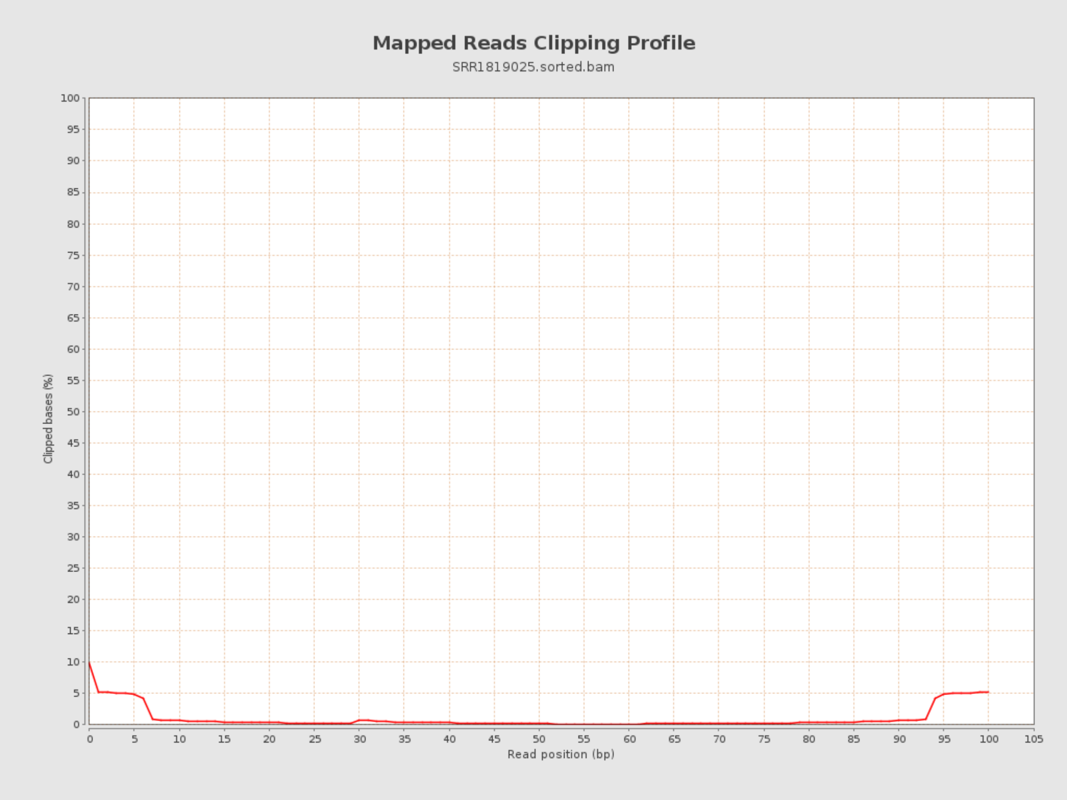
8. Results : Mapped Reads Nucleotide Content



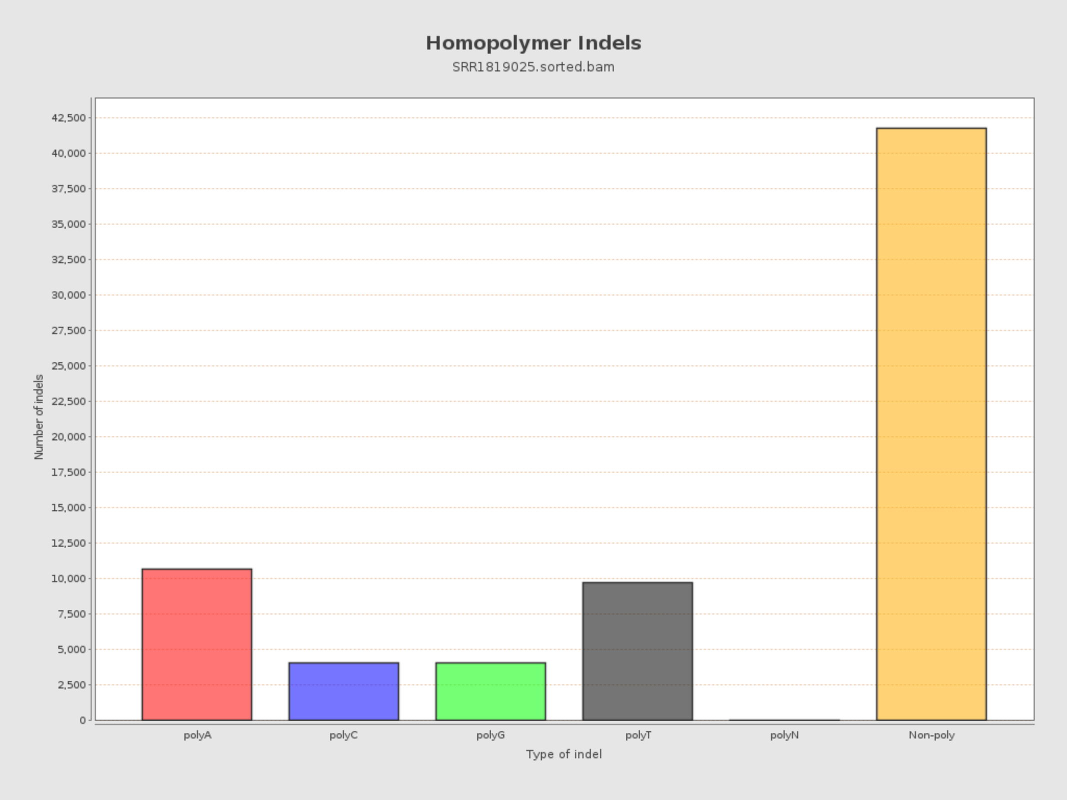
9. Results : Mapped Reads GC-content Distribution



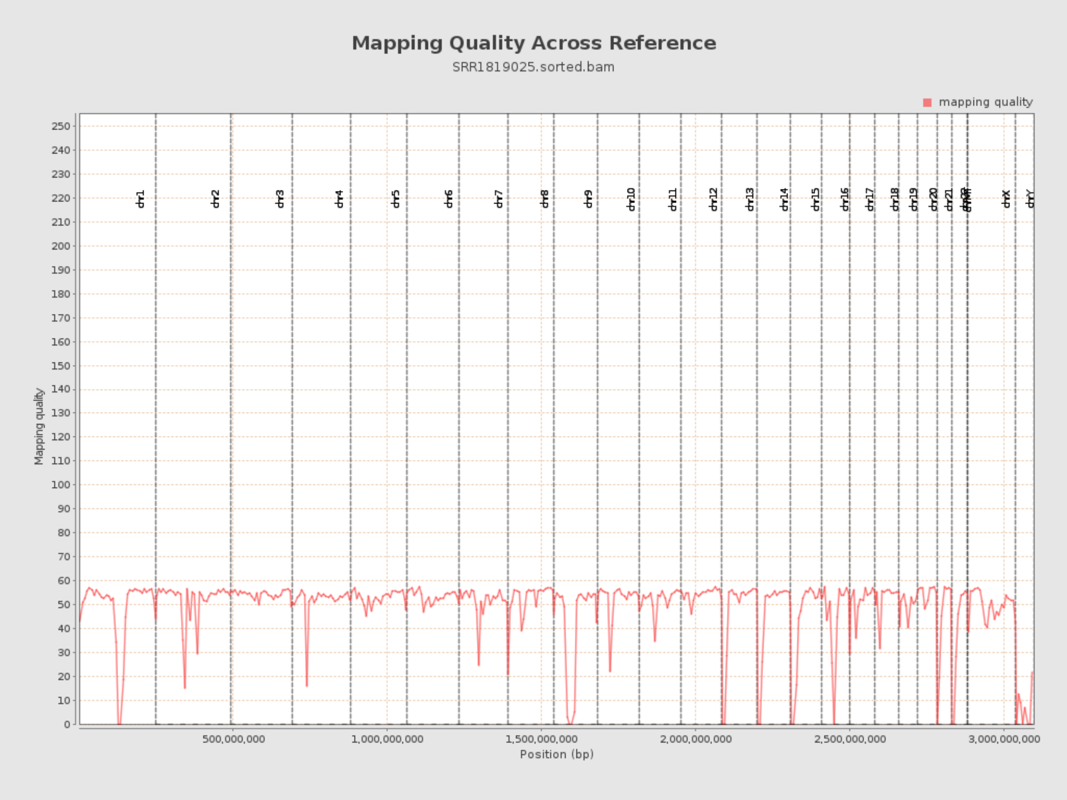
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram