Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:46:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525024.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_SRR10525024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,830,261
Mapped reads	3,509,575 / 91.63%
Unmapped reads	320,686 / 8.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,524 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	252,454 / 6.59%
Duplication rate	5.3%
Clipped reads	3,513,772 / 91.74%

2.2. ACGT Content

Number/percentage of A's	52,859,994 / 25.76%
Number/percentage of C's	36,723,268 / 17.89%
Number/percentage of T's	64,058,491 / 31.21%
Number/percentage of G's	51,574,029 / 25.13%
Number/percentage of N's	2,025 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0663

Standard Deviation	0.544

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

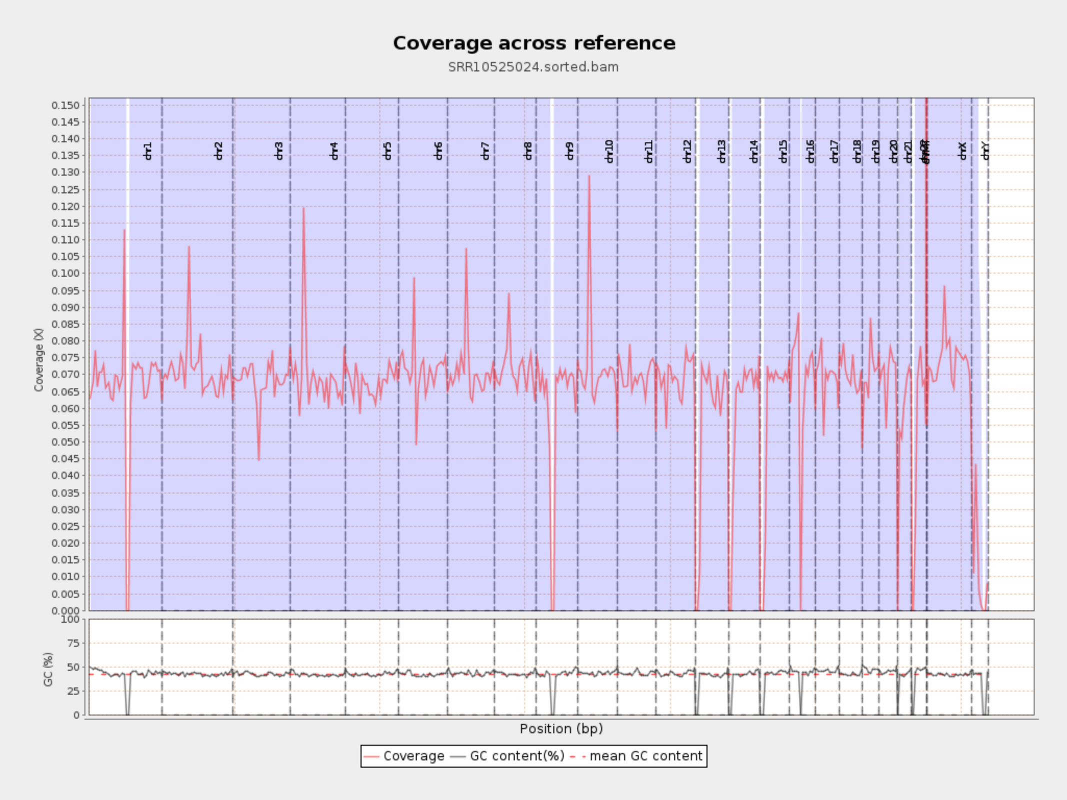
General error rate	0.5%
Mismatches	997,257
Insertions	13,437
Mapped reads with at least one insertion	0.38%
Deletions	39,842
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.53%

2.6. Chromosome stats

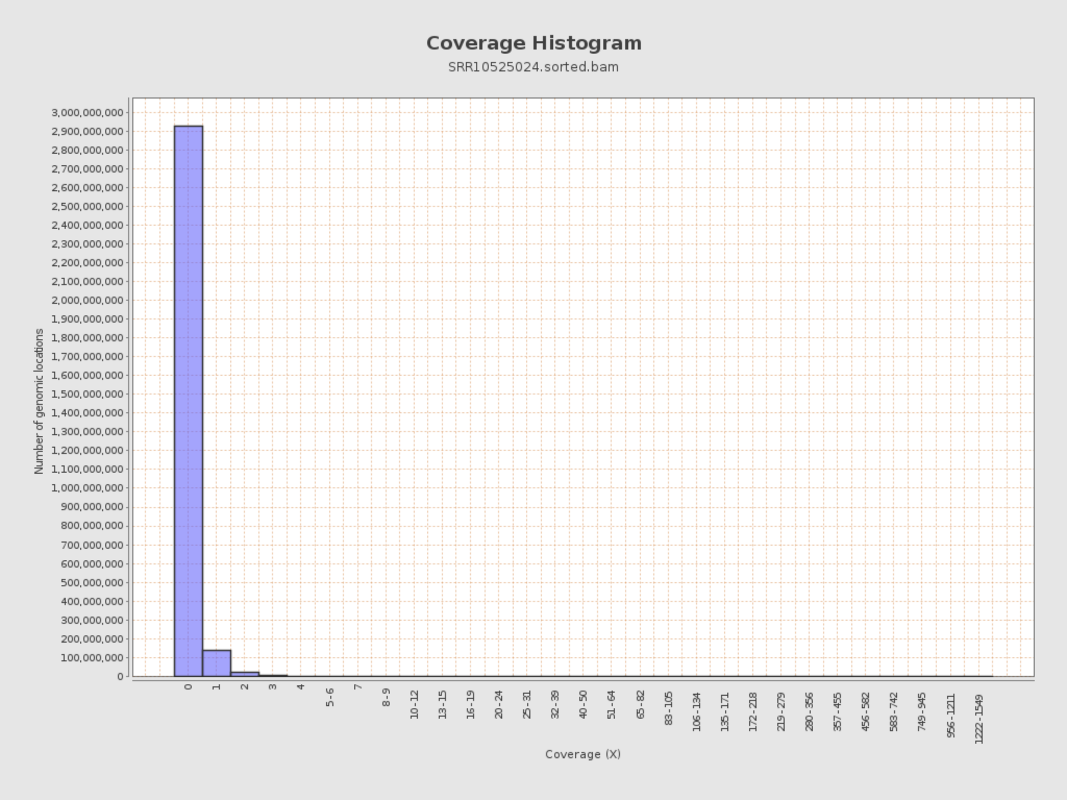
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16470488	0.0661	1.1058
chr2	243199373	17387200	0.0715	0.6145
chr3	198022430	13474327	0.068	0.3176
chr4	191154276	13275412	0.0694	0.4213
chr5	180915260	12230128	0.0676	0.3157
chr6	171115067	12199577	0.0713	0.4533
chr7	159138663	11323497	0.0712	0.6353

chr8	146364022	10467746	0.0715	0.5983
chr9	141213431	8455890	0.0599	0.4355
chr10	135534747	9803629	0.0723	0.6042
chr11	135006516	9390333	0.0696	0.4801
chr12	133851895	9277022	0.0693	0.3279
chr13	115169878	6435440	0.0559	0.2846
chr14	107349540	6130044	0.0571	0.3063
chr15	102531392	5758496	0.0562	0.2972
chr16	90354753	6074433	0.0672	0.3494
chr17	81195210	5613374	0.0691	0.3834
chr18	78077248	5524332	0.0708	0.7901
chr19	59128983	4196256	0.071	0.6631
chr20	63025520	4407079	0.0699	0.3316
chr21	48129895	2713535	0.0564	0.3655
chr22	51304566	2489268	0.0485	0.2612
chrMT	16571	27088	1.6347	1.6435
chrX	155270560	11470035	0.0739	0.3861
chrY	59373566	690034	0.0116	0.3569

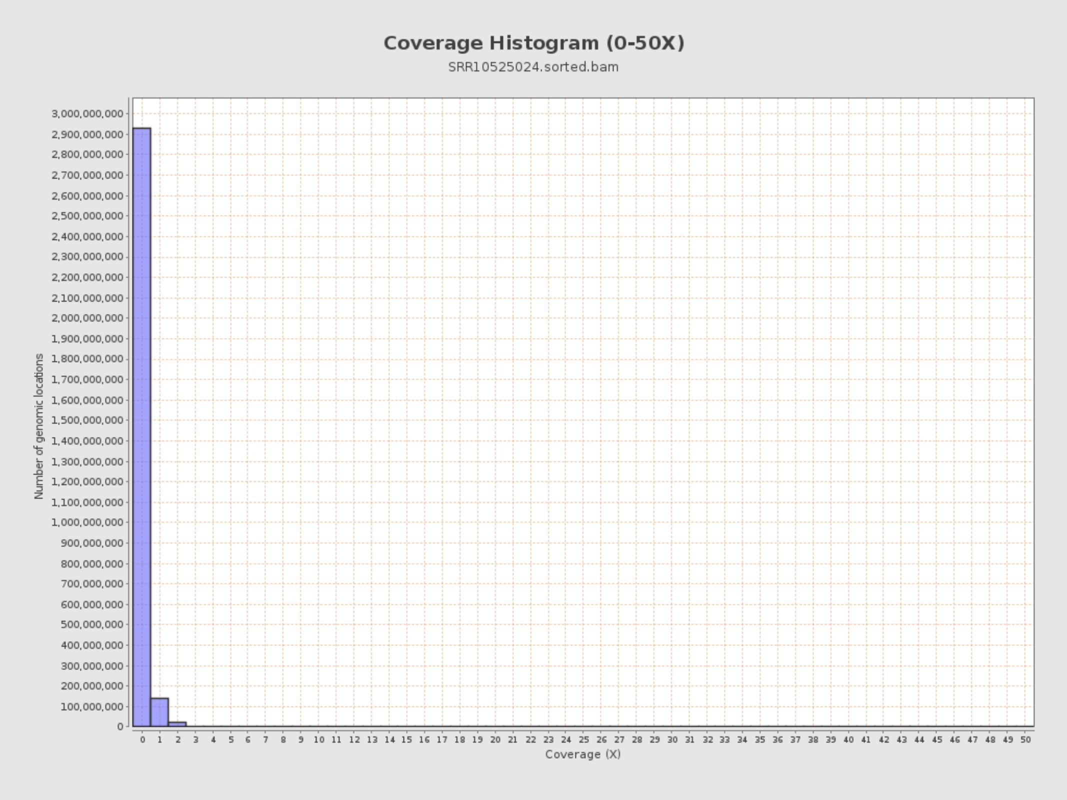
3. Results : Coverage across reference



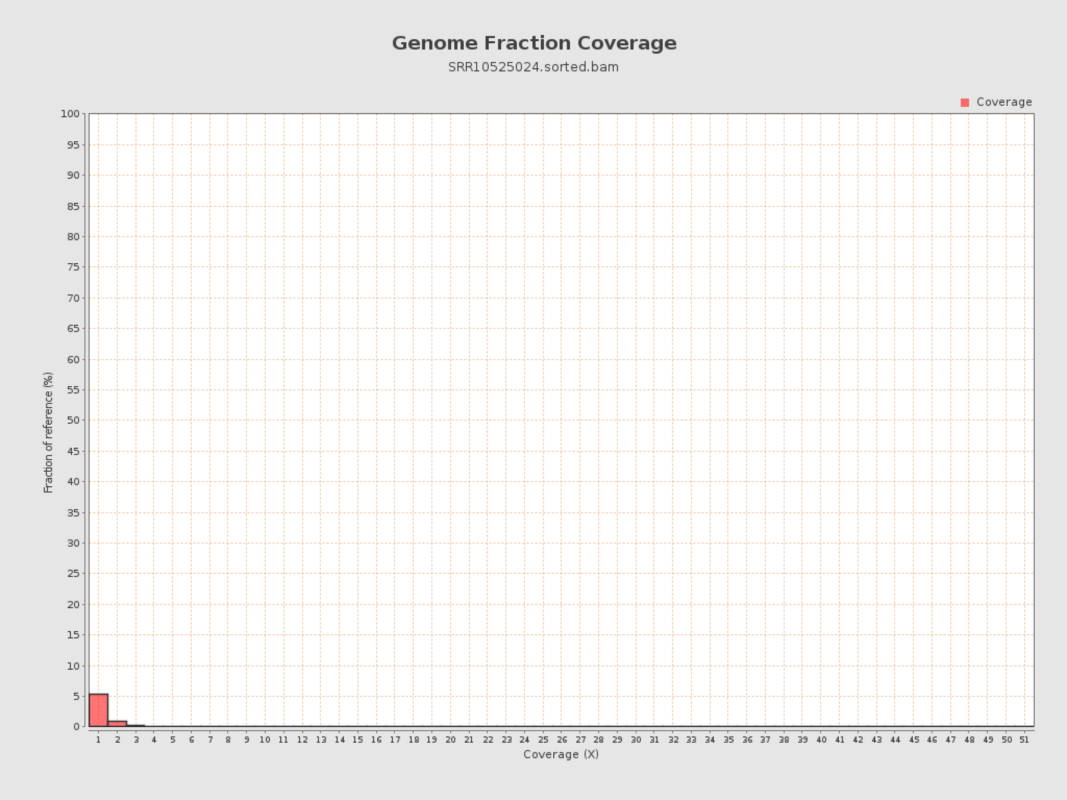
4. Results : Coverage Histogram



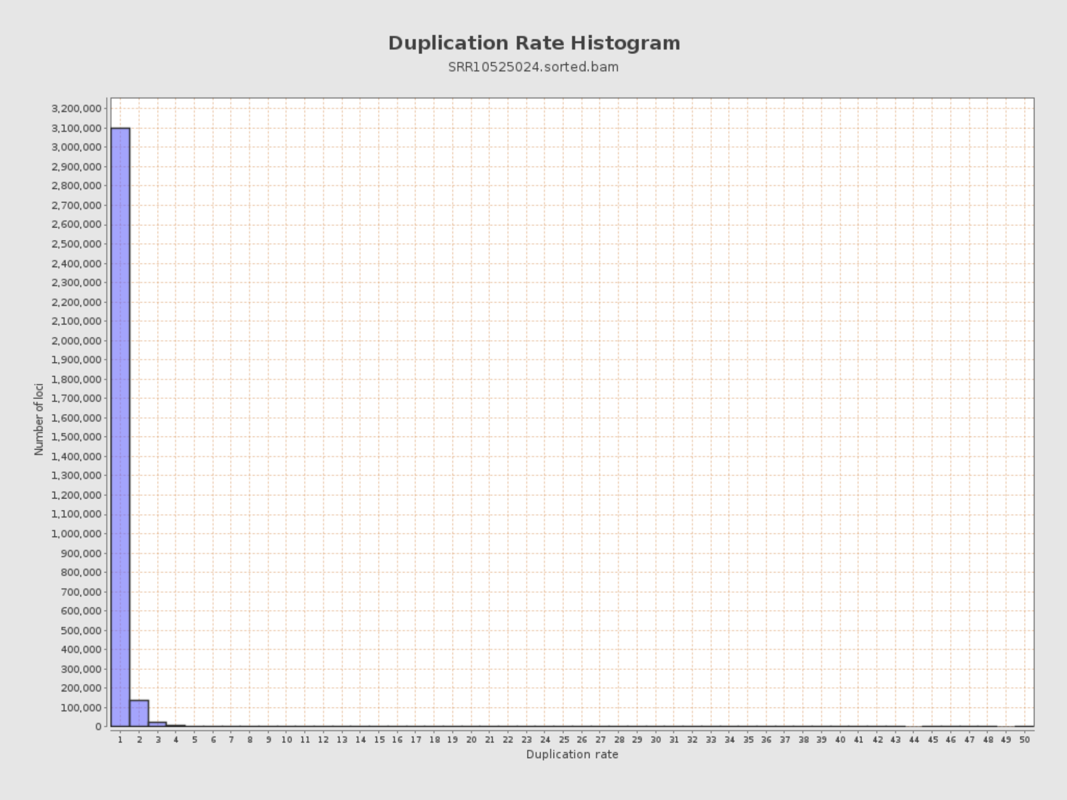
5. Results : Coverage Histogram (0-50X)



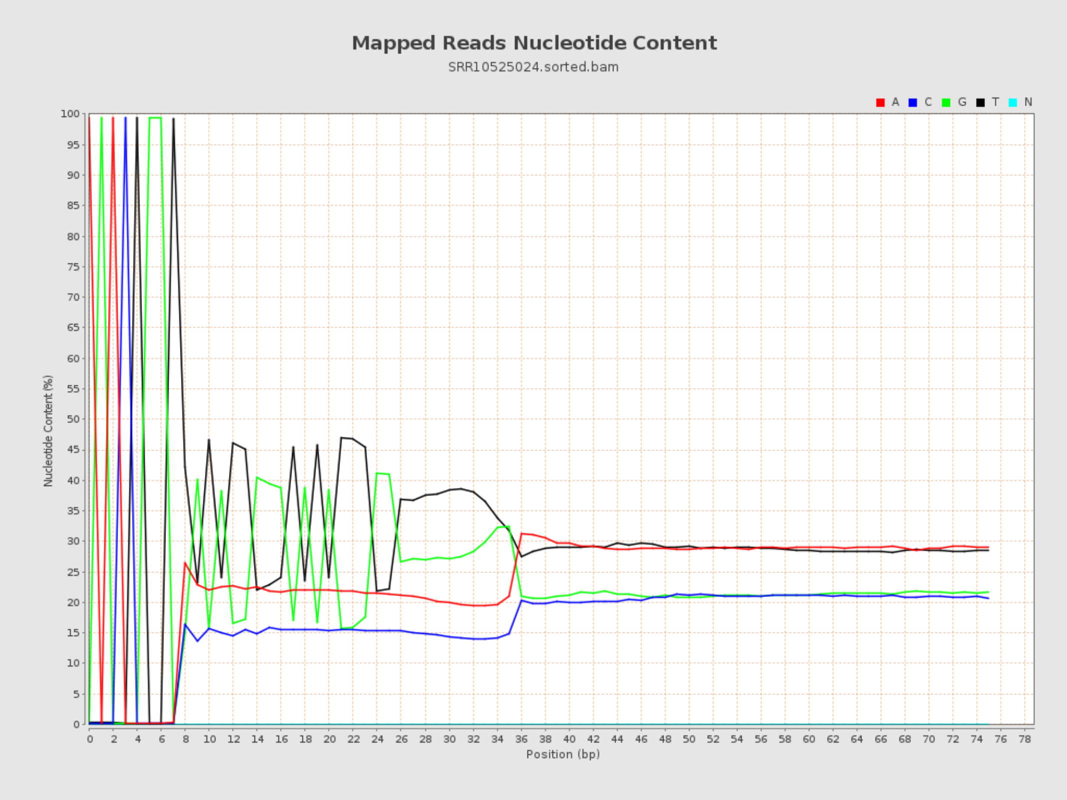
6. Results : Genome Fraction Coverage



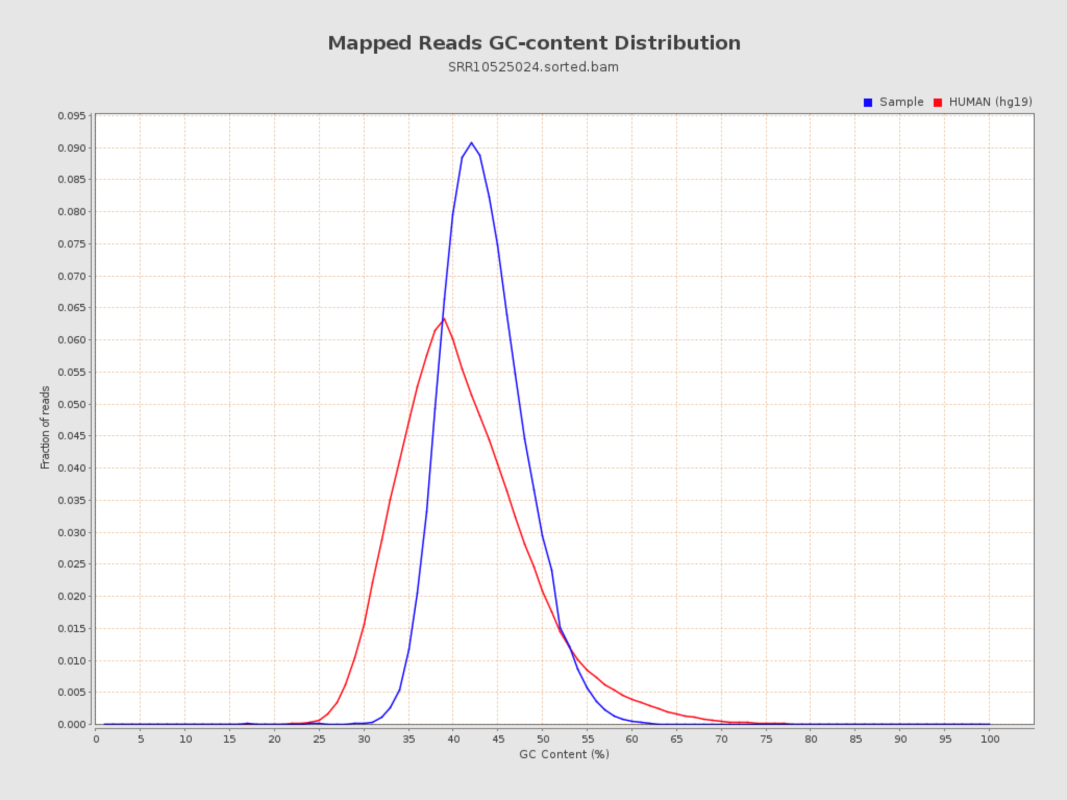
7. Results : Duplication Rate Histogram



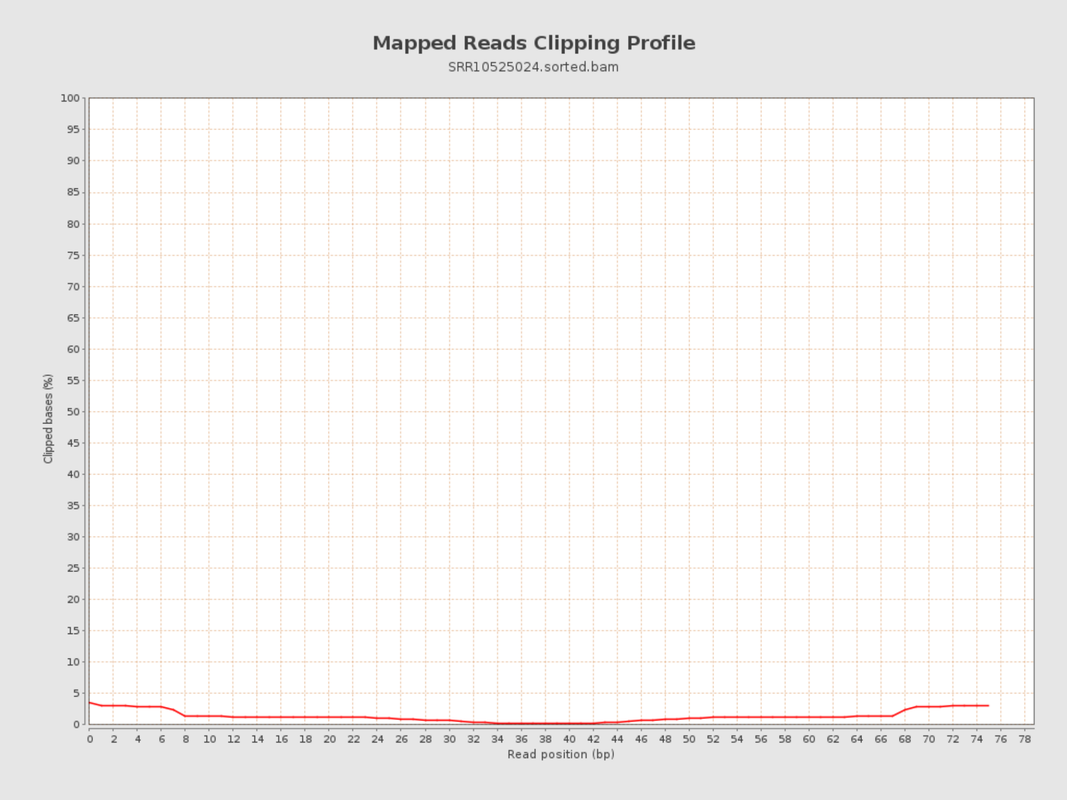
8. Results : Mapped Reads Nucleotide Content



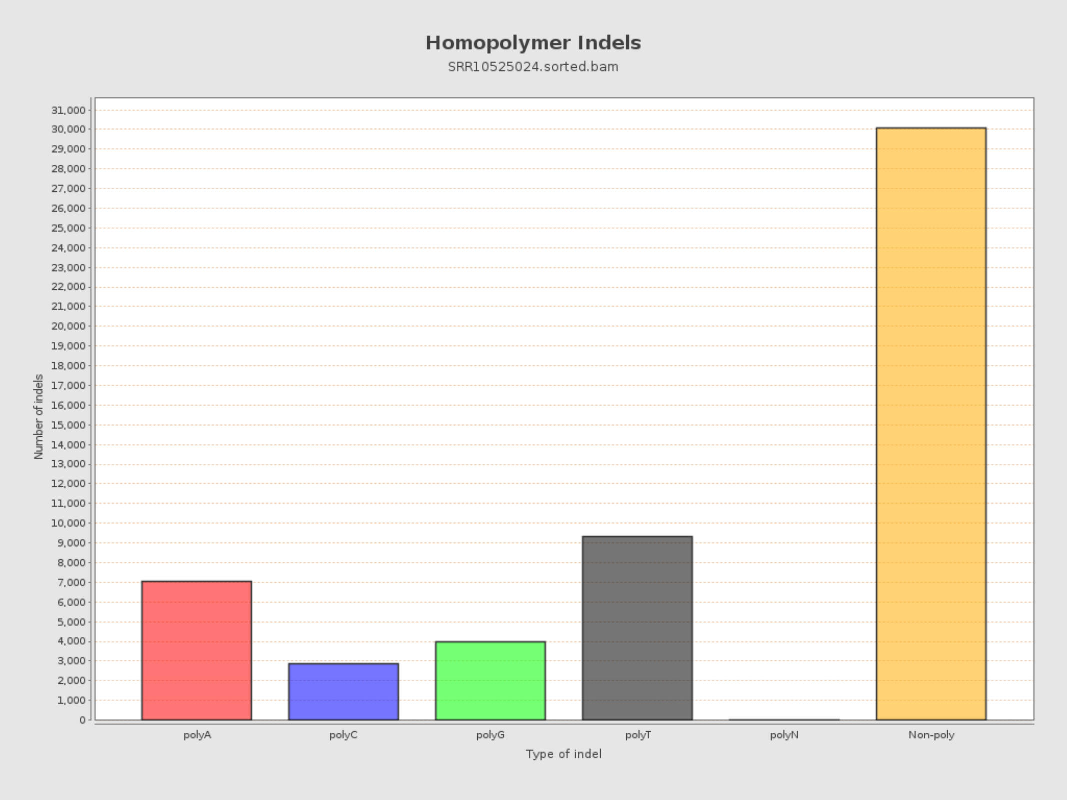
9. Results : Mapped Reads GC-content Distribution



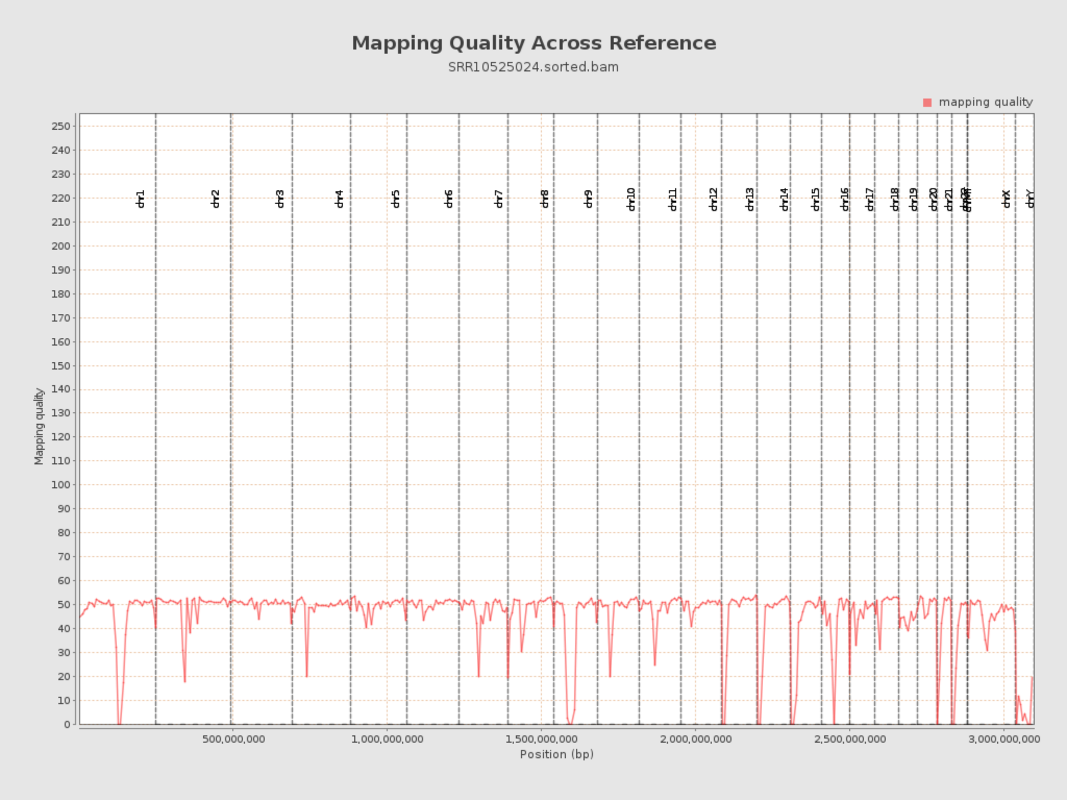
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram