Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:47:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525097.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_SRR10525097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,894,250
Mapped reads	2,671,781 / 92.31%
Unmapped reads	222,469 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,253 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	140,195 / 4.84%
Duplication rate	3.79%
Clipped reads	2,678,815 / 92.56%

2.2. ACGT Content

Number/percentage of A's	36,719,949 / 23.64%
Number/percentage of C's	31,595,594 / 20.34%
Number/percentage of T's	50,092,181 / 32.25%
Number/percentage of G's	36,928,813 / 23.77%
Number/percentage of N's	3,038 / 0%
GC Percentage	44.11%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.4368

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

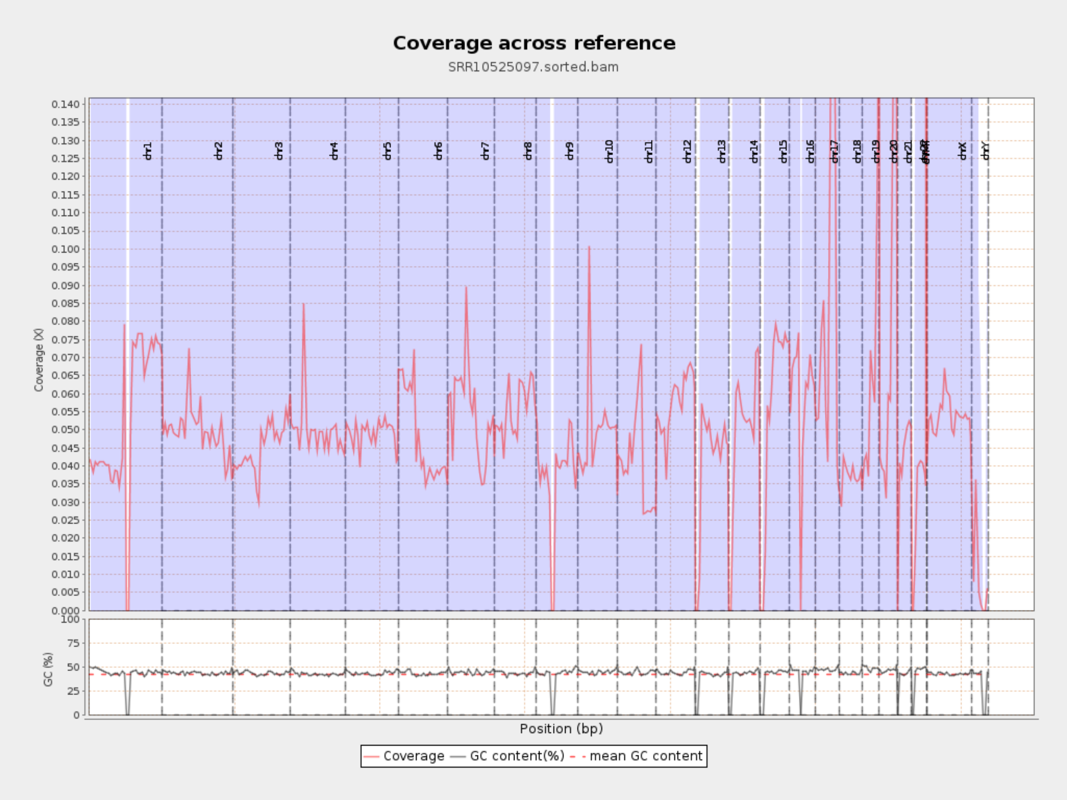
General error rate	0.51%
Mismatches	777,828
Insertions	9,806
Mapped reads with at least one insertion	0.37%
Deletions	29,971
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.76%

2.6. Chromosome stats

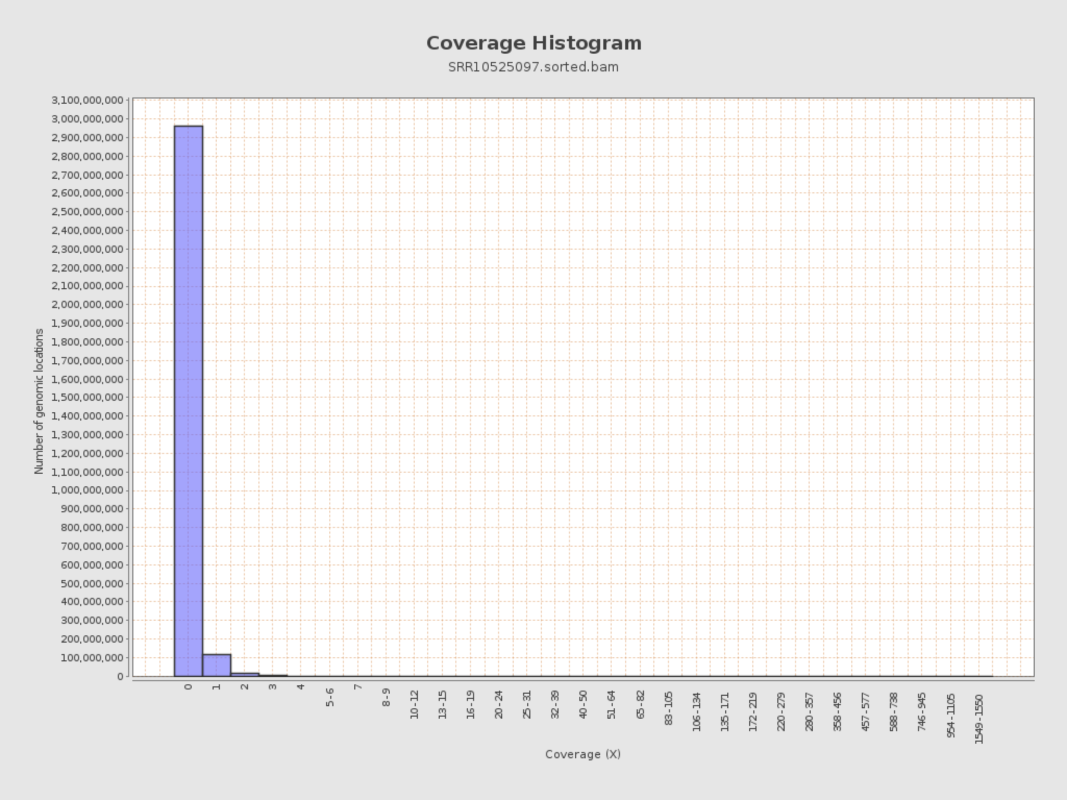
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13063831	0.0524	0.7275
chr2	243199373	12129817	0.0499	0.6714
chr3	198022430	8903251	0.045	0.2473
chr4	191154276	9501479	0.0497	0.3159
chr5	180915260	8864654	0.049	0.2517
chr6	171115067	8248047	0.0482	0.317
chr7	159138663	8795782	0.0553	0.5665

chr8	146364022	8155705	0.0557	0.5638
chr9	141213431	5122659	0.0363	0.2855
chr10	135534747	6780536	0.05	0.4542
chr11	135006516	5564243	0.0412	0.3167
chr12	133851895	7704256	0.0576	0.2745
chr13	115169878	4680241	0.0406	0.2313
chr14	107349540	5203293	0.0485	0.2601
chr15	102531392	5718667	0.0558	0.2738
chr16	90354753	5338933	0.0591	0.302
chr17	81195210	6823501	0.084	0.3557
chr18	78077248	2893925	0.0371	0.5312
chr19	59128983	3999523	0.0676	0.5497
chr20	63025520	5130006	0.0814	0.3458
chr21	48129895	2004518	0.0416	0.2949
chr22	51304566	1434887	0.028	0.1925
chrMT	16571	428858	25.88	14.6564
chrX	155270560	8348831	0.0538	0.2936
chrY	59373566	548503	0.0092	0.344

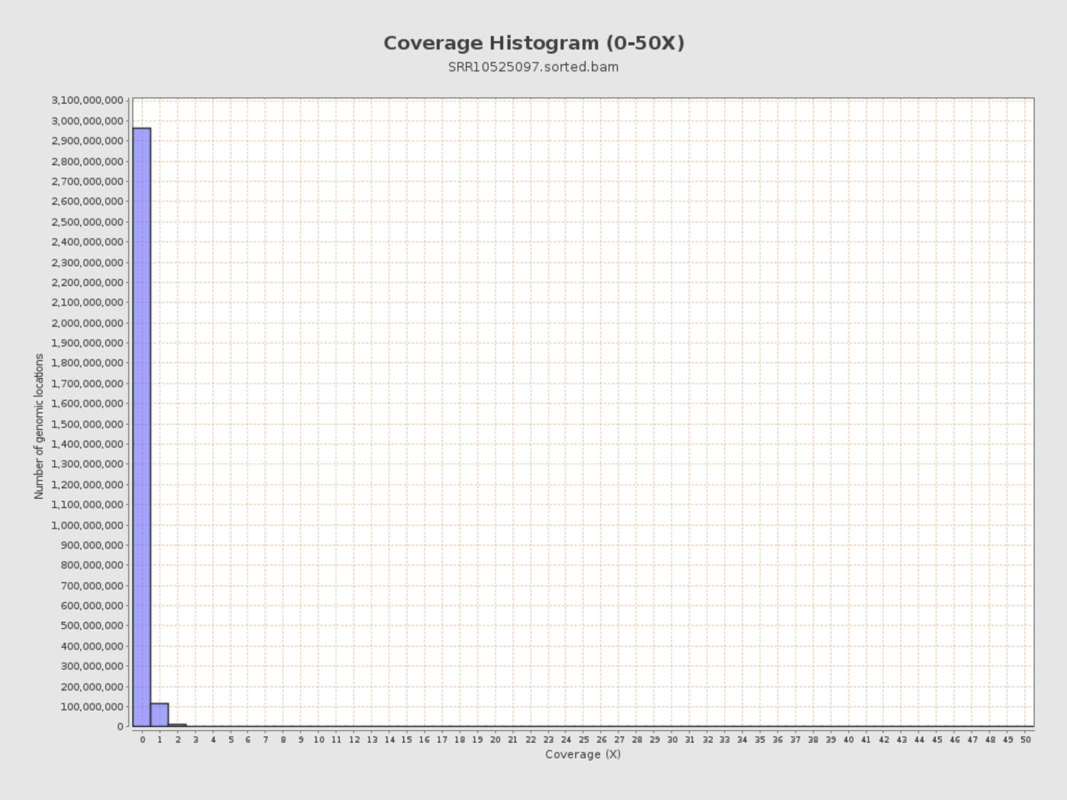
3. Results : Coverage across reference



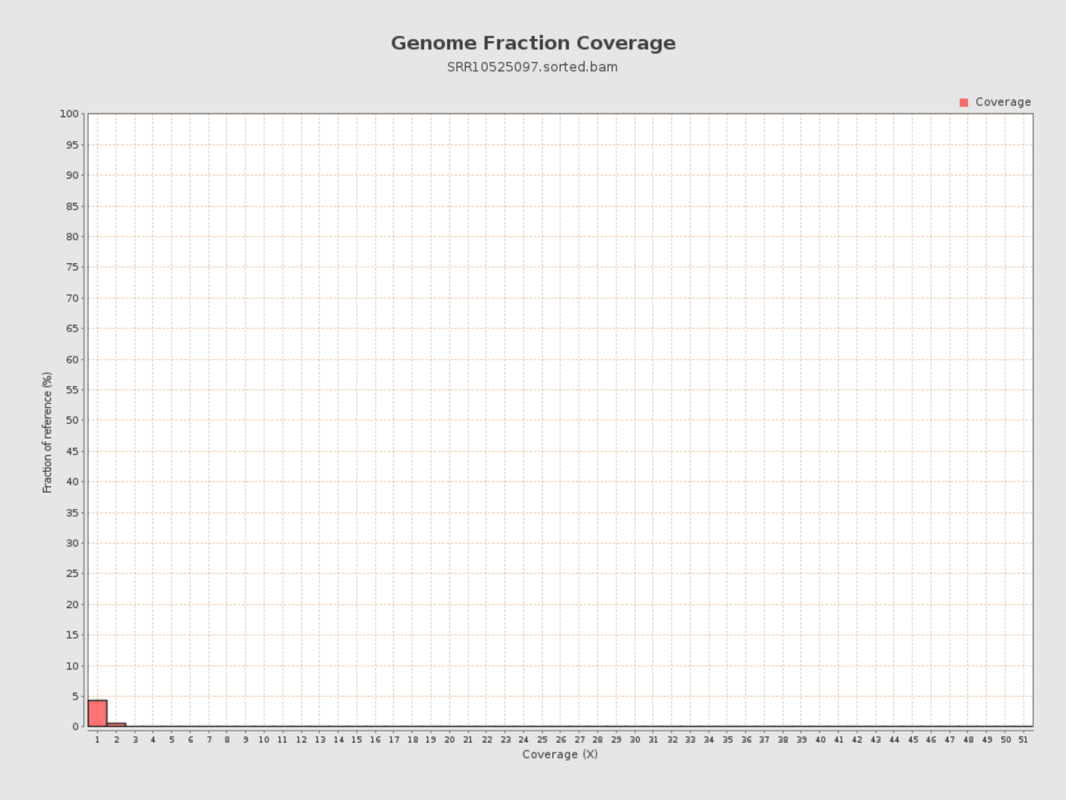
4. Results : Coverage Histogram



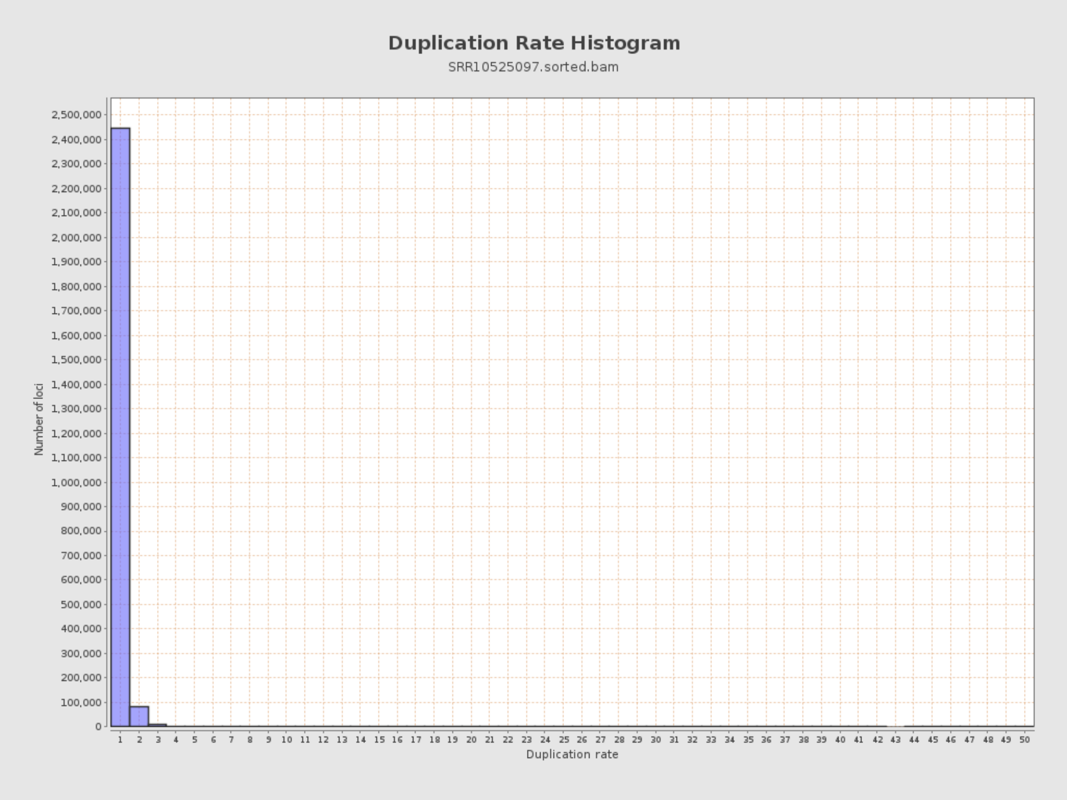
5. Results : Coverage Histogram (0-50X)



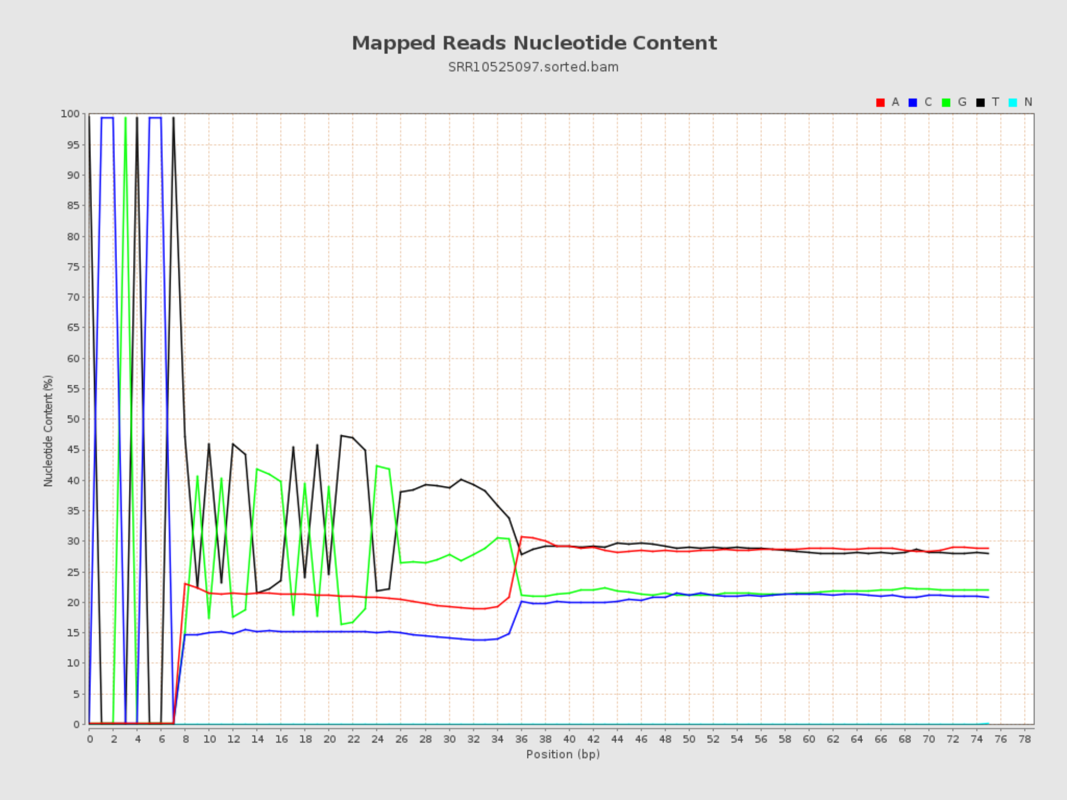
6. Results : Genome Fraction Coverage



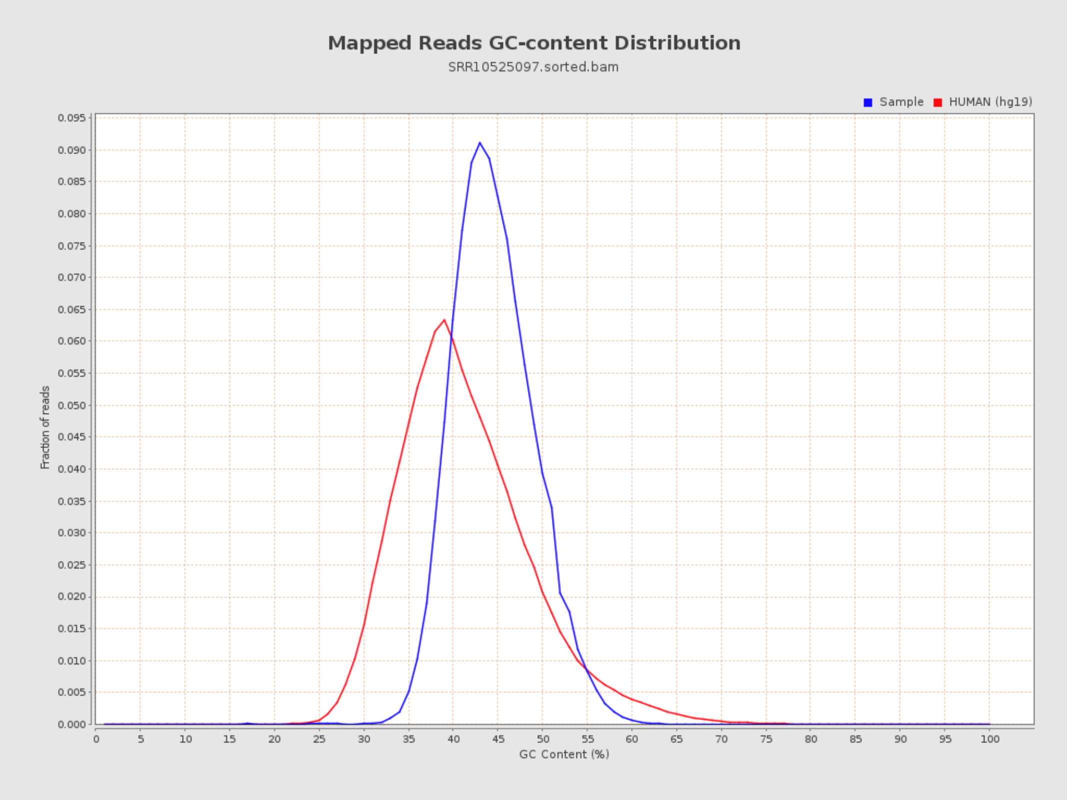
7. Results : Duplication Rate Histogram



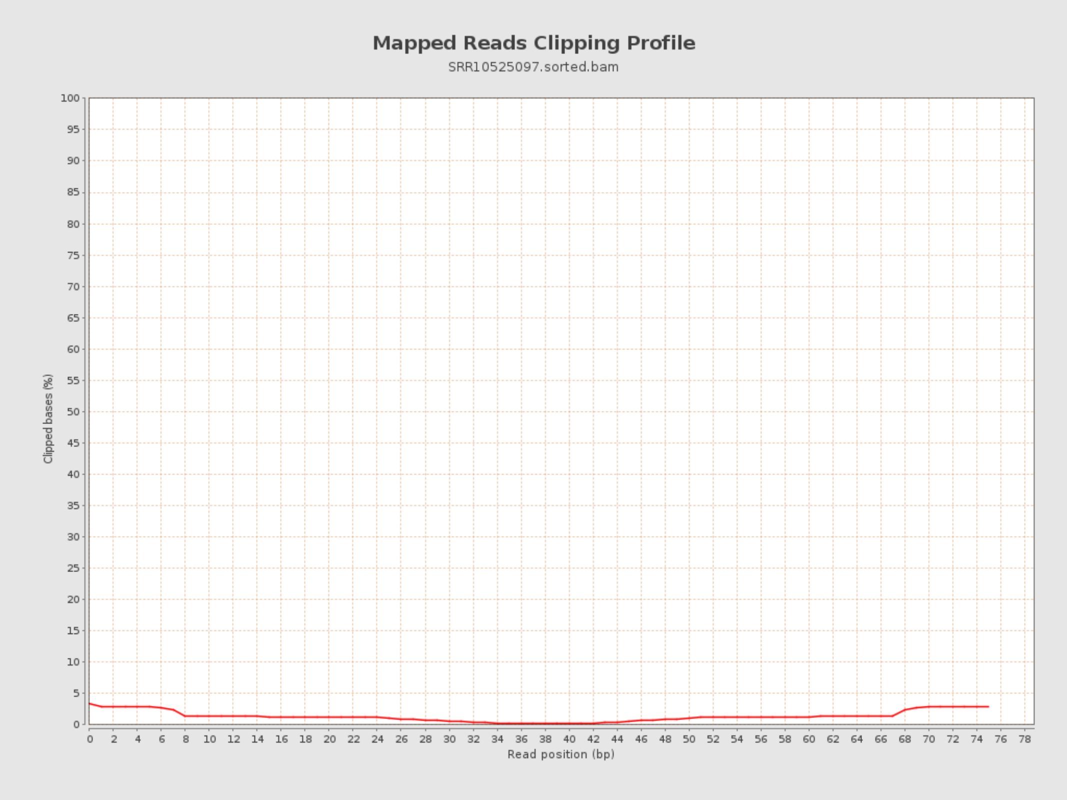
8. Results : Mapped Reads Nucleotide Content



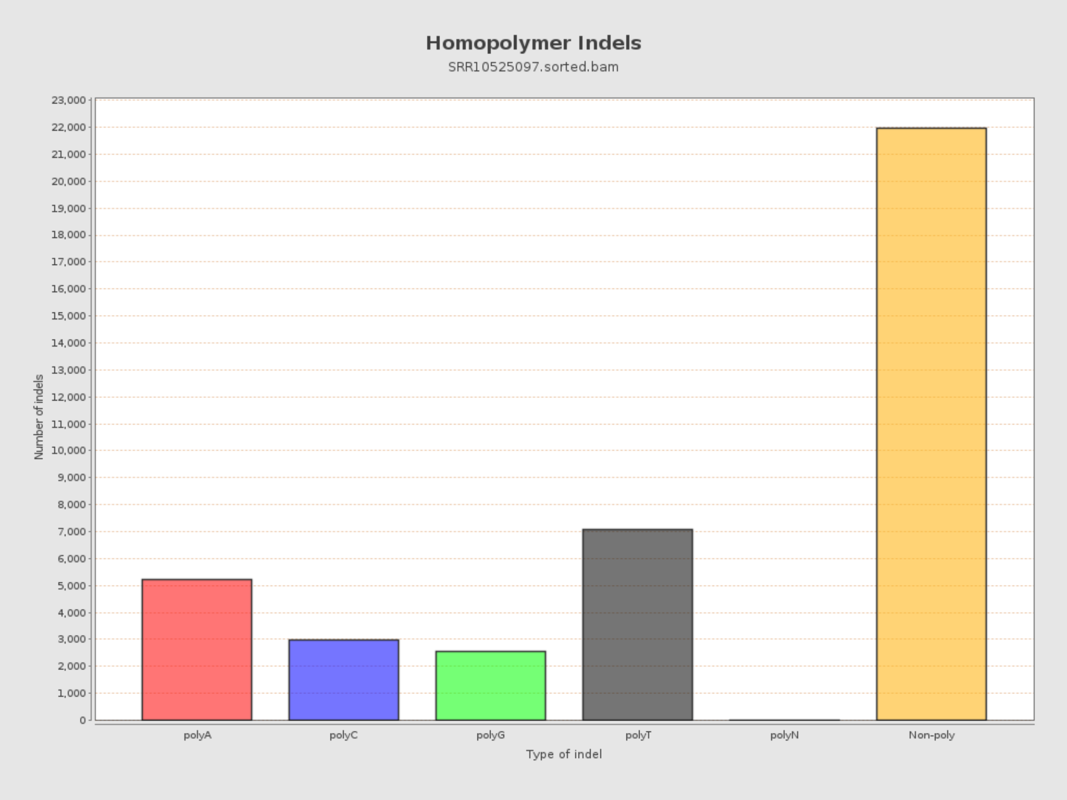
9. Results : Mapped Reads GC-content Distribution



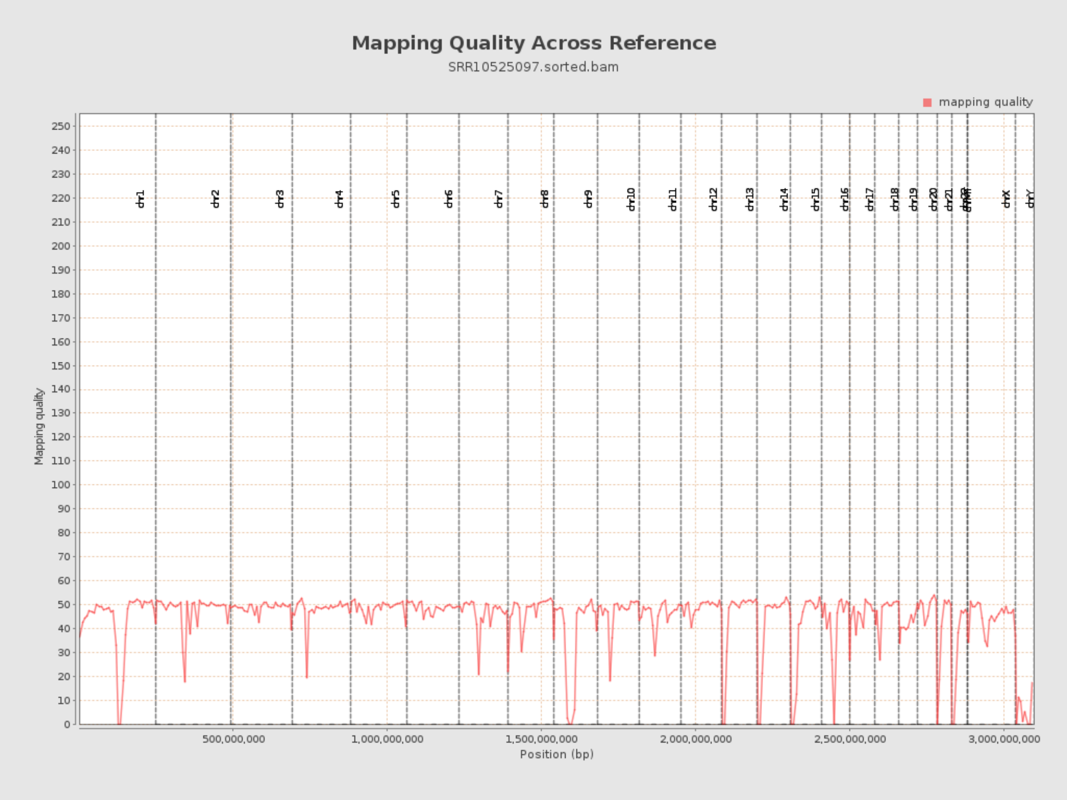
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram