Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:41:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525045.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_SRR10525045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:41:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	533,873
Mapped reads	489,901 / 91.76%
Unmapped reads	43,972 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,241 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	19,497 / 3.65%
Duplication rate	3.4%
Clipped reads	489,986 / 91.78%

2.2. ACGT Content

Number/percentage of A's	7,076,240 / 24.92%
Number/percentage of C's	5,419,801 / 19.08%
Number/percentage of T's	9,102,709 / 32.05%
Number/percentage of G's	6,798,933 / 23.94%
Number/percentage of N's	2,432 / 0.01%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1225

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

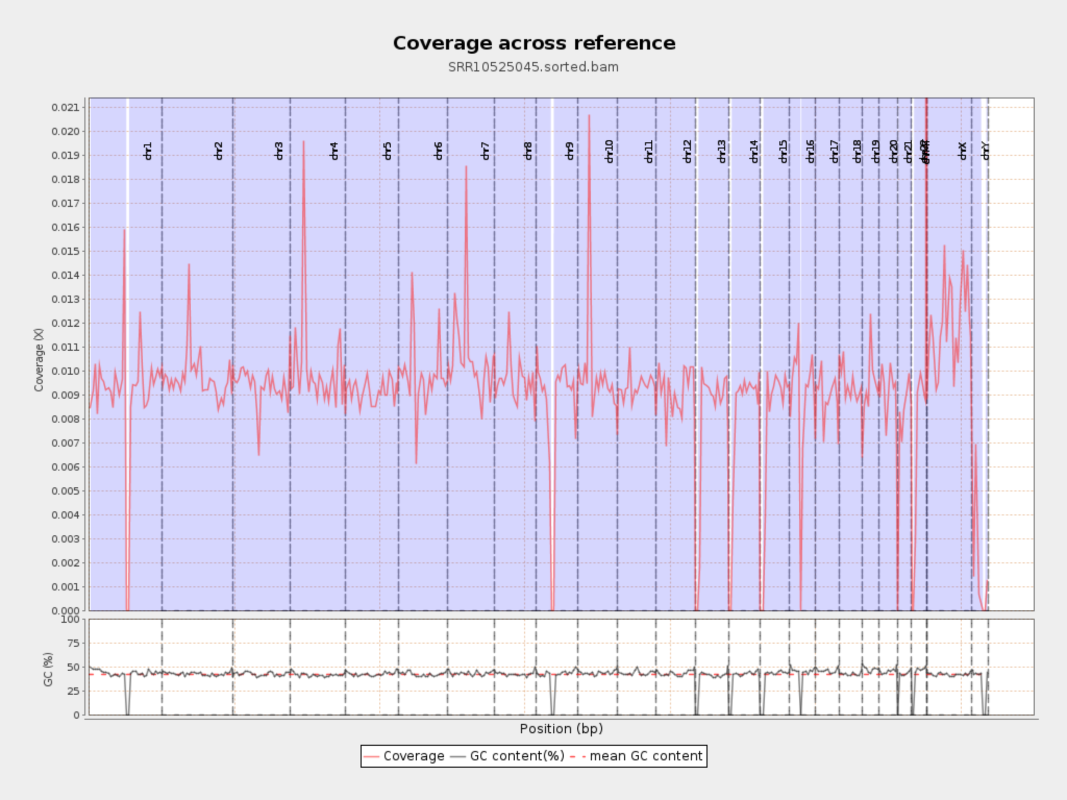
General error rate	0.5%
Mismatches	137,843
Insertions	2,011
Mapped reads with at least one insertion	0.41%
Deletions	5,584
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.99%

2.6. Chromosome stats

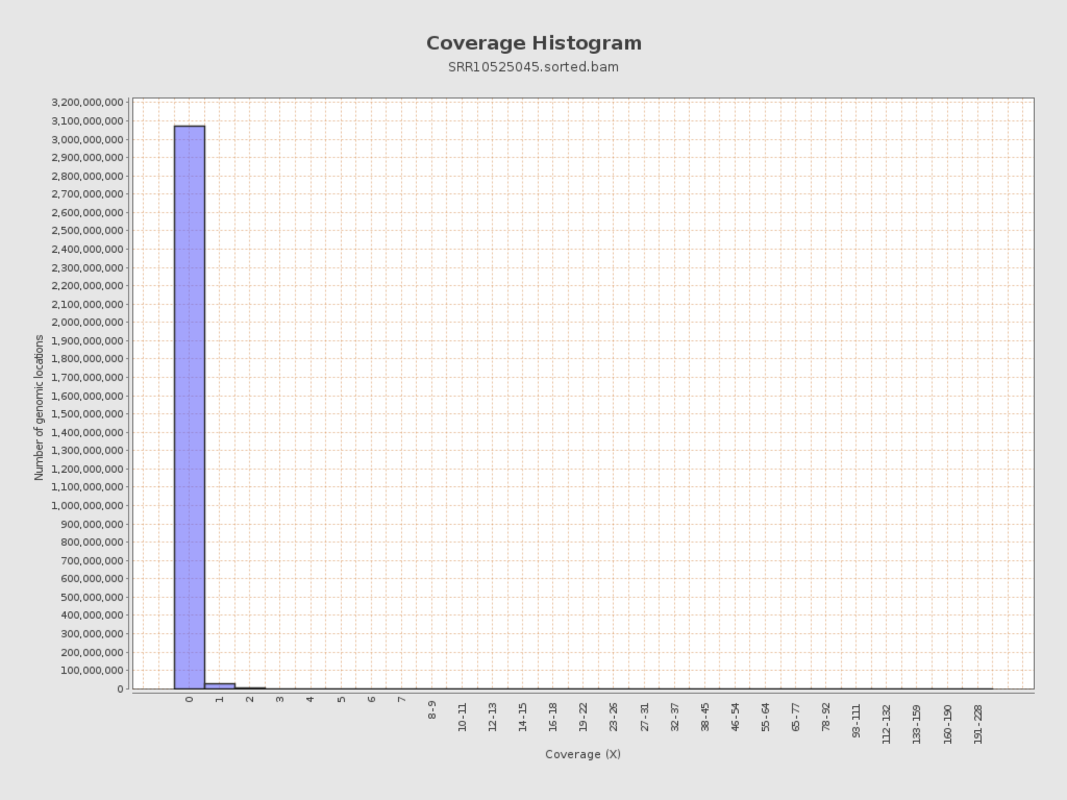
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2262410	0.0091	0.1877
chr2	243199373	2371515	0.0098	0.1353
chr3	198022430	1853407	0.0094	0.1022
chr4	191154276	1933484	0.0101	0.1141
chr5	180915260	1656708	0.0092	0.1015
chr6	171115067	1683414	0.0098	0.1093
chr7	159138663	1695864	0.0107	0.1523

chr8	146364022	1399498	0.0096	0.1321
chr9	141213431	1158988	0.0082	0.1049
chr10	135534747	1356496	0.01	0.1318
chr11	135006516	1261095	0.0093	0.1118
chr12	133851895	1226400	0.0092	0.1038
chr13	115169878	890791	0.0077	0.093
chr14	107349540	830464	0.0077	0.0942
chr15	102531392	778508	0.0076	0.0921
chr16	90354753	796825	0.0088	0.1022
chr17	81195210	722297	0.0089	0.1015
chr18	78077248	736791	0.0094	0.1449
chr19	59128983	559009	0.0095	0.1408
chr20	63025520	576203	0.0091	0.1023
chr21	48129895	373850	0.0078	0.0991
chr22	51304566	328421	0.0064	0.0849
chrMT	16571	1926	0.1162	0.3399
chrX	155270560	1848102	0.0119	0.1205
chrY	59373566	106723	0.0018	0.0735

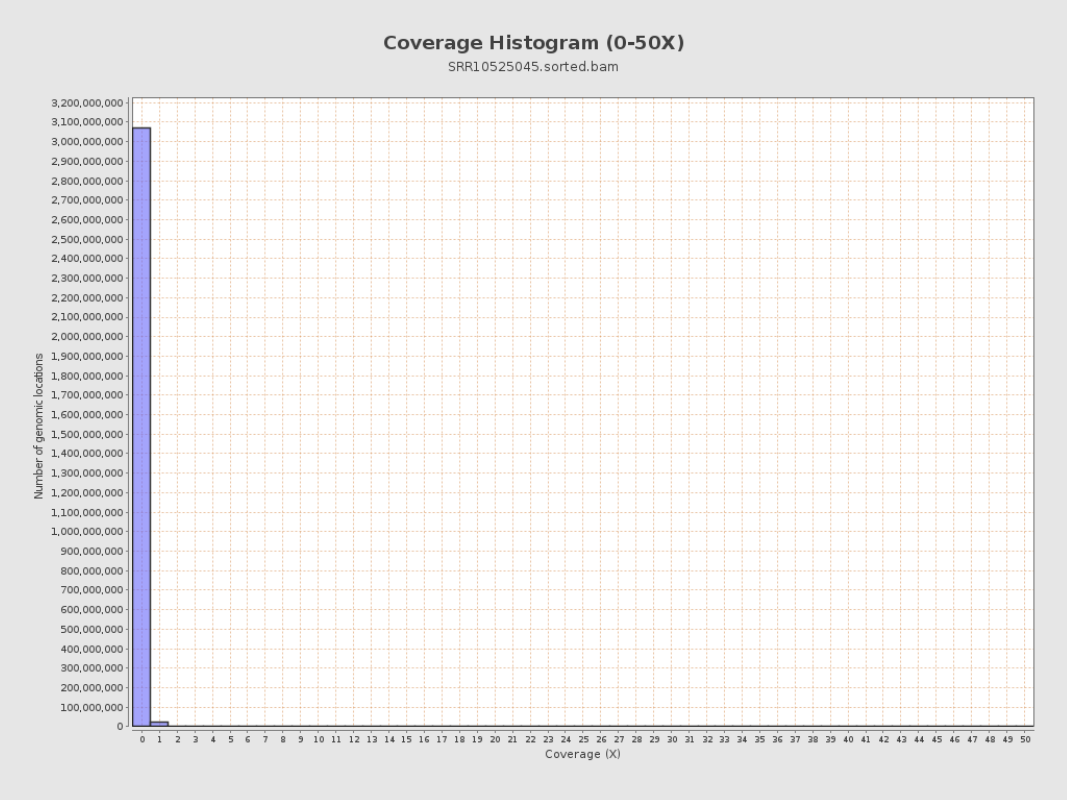
3. Results : Coverage across reference



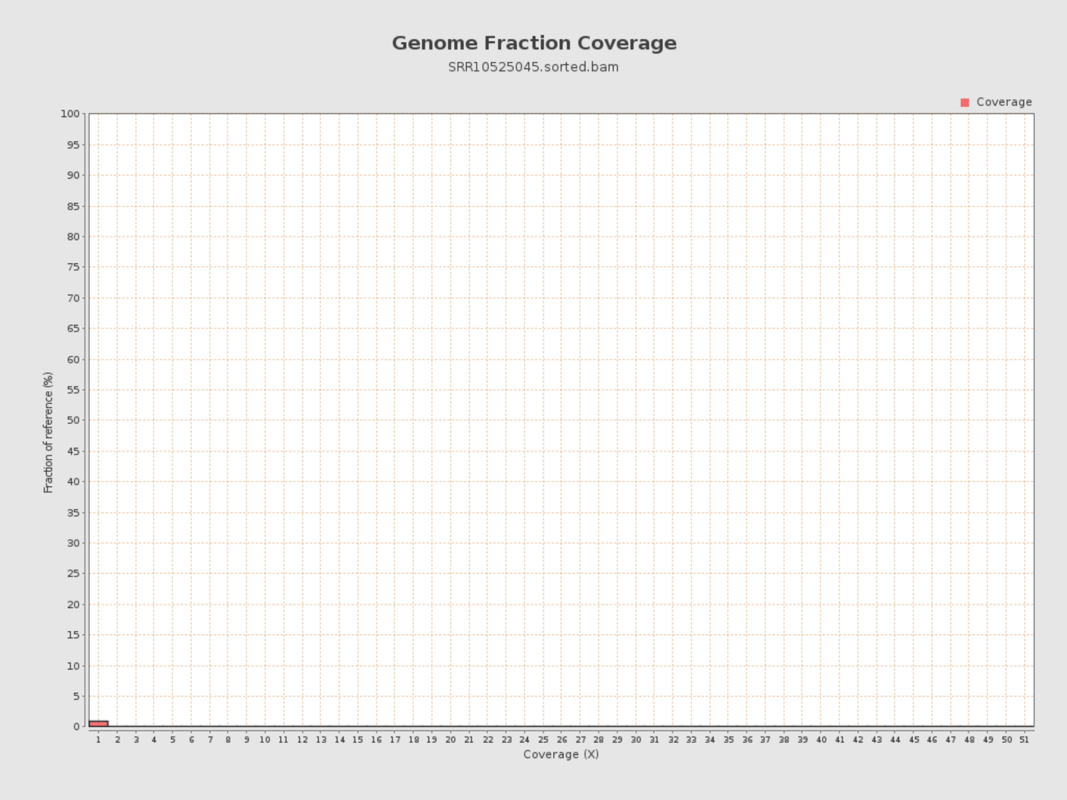
4. Results : Coverage Histogram



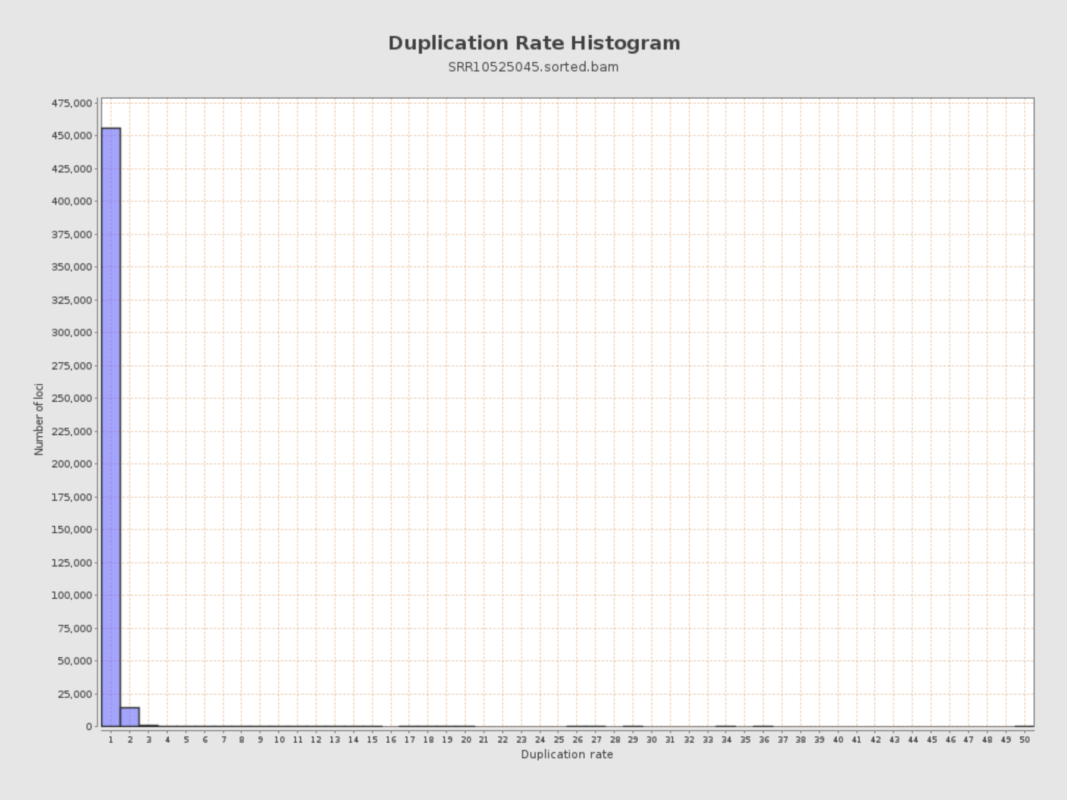
5. Results : Coverage Histogram (0-50X)



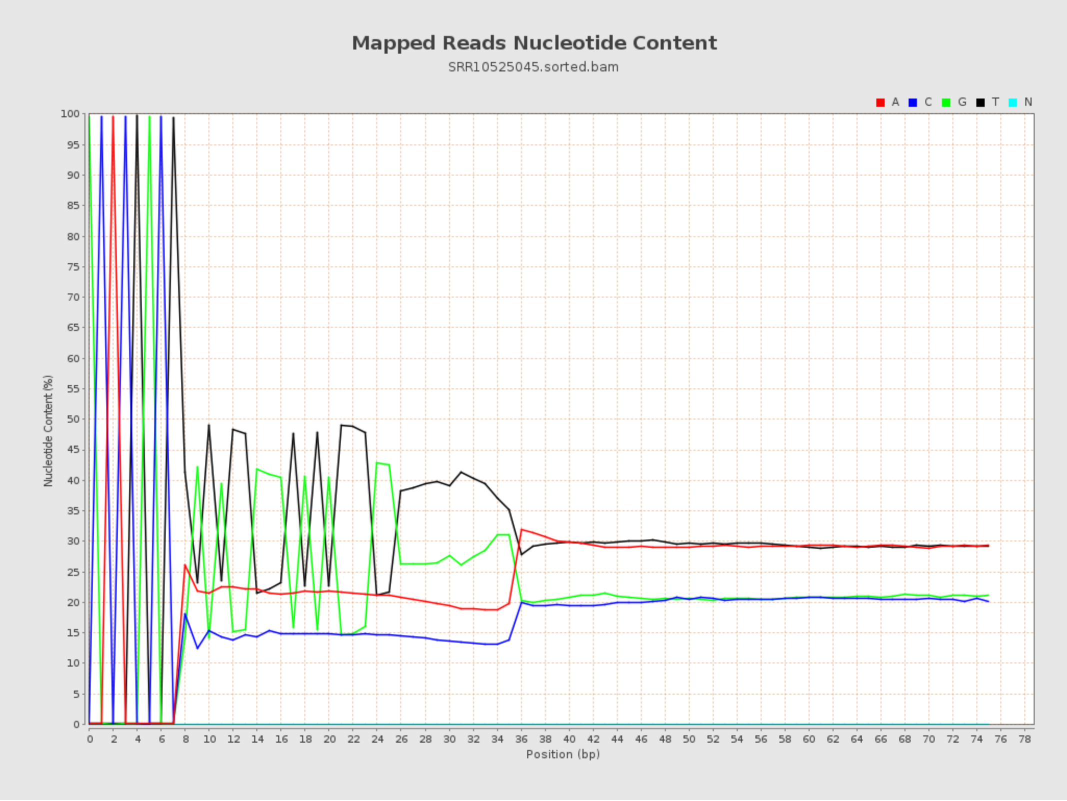
6. Results : Genome Fraction Coverage



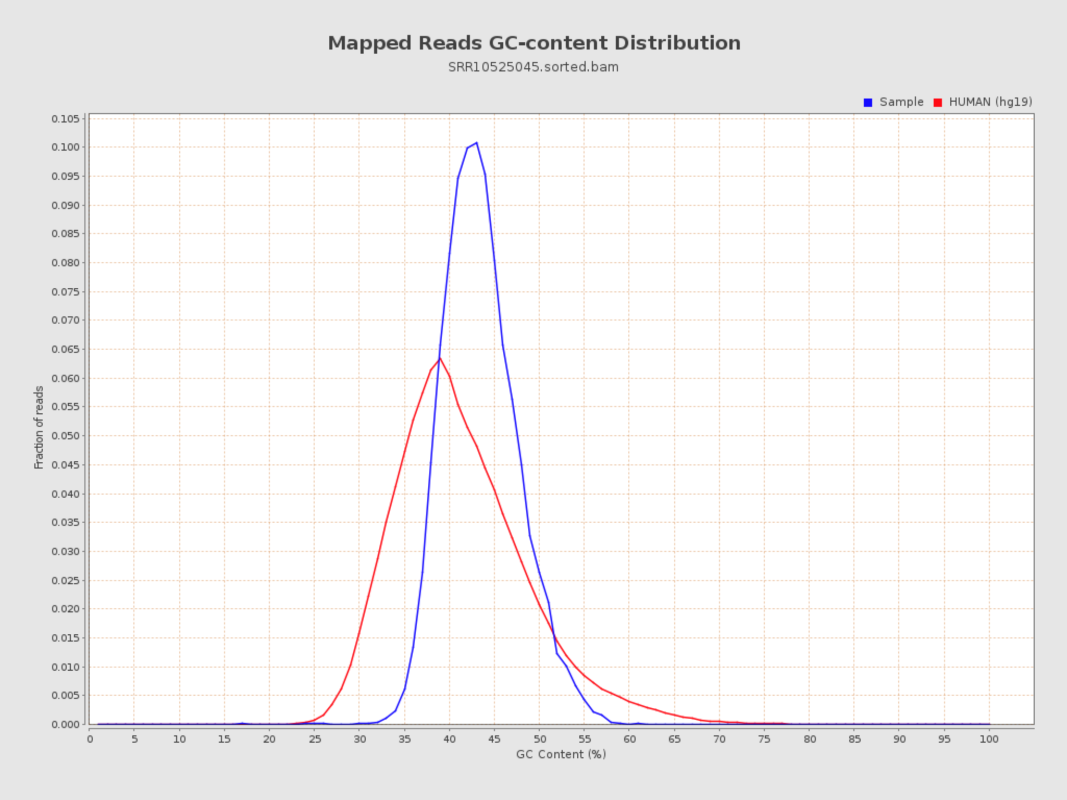
7. Results : Duplication Rate Histogram



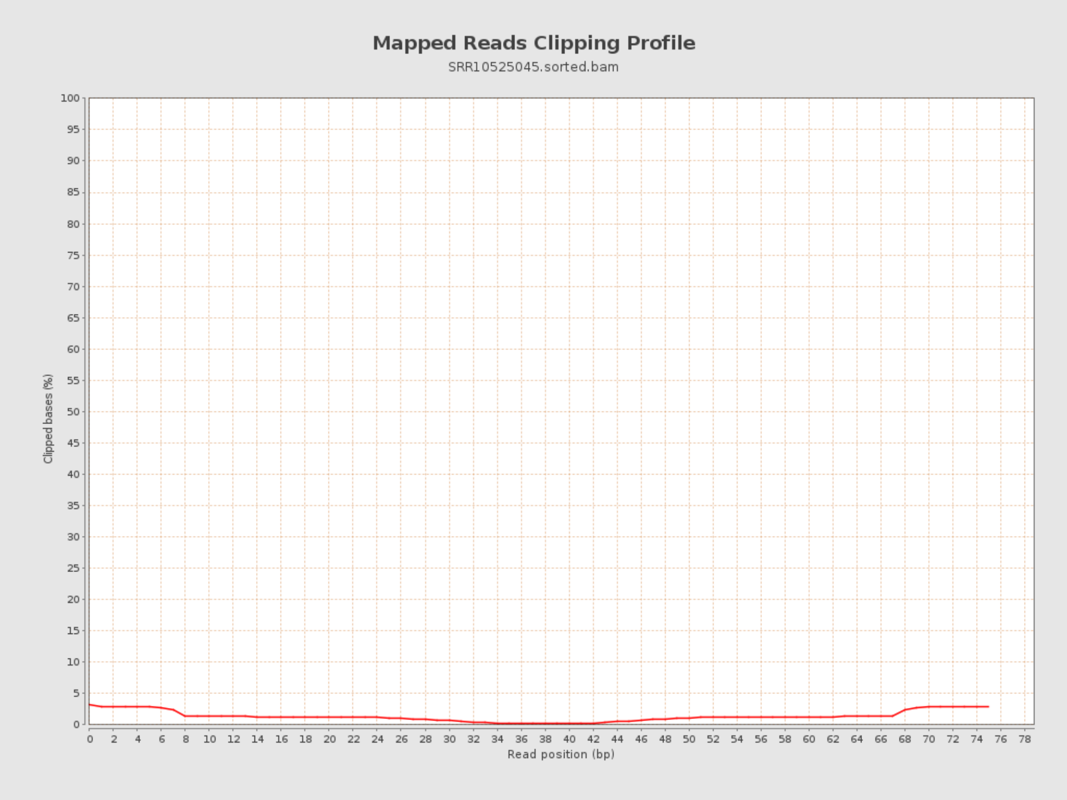
8. Results : Mapped Reads Nucleotide Content



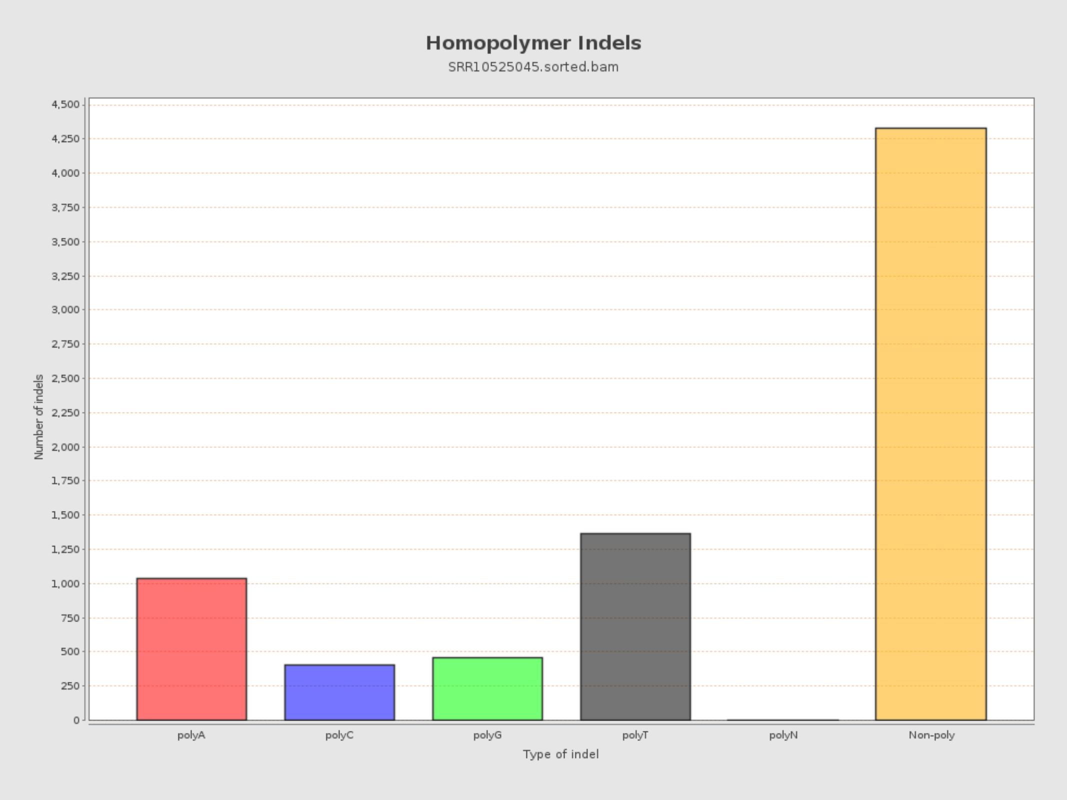
9. Results : Mapped Reads GC-content Distribution



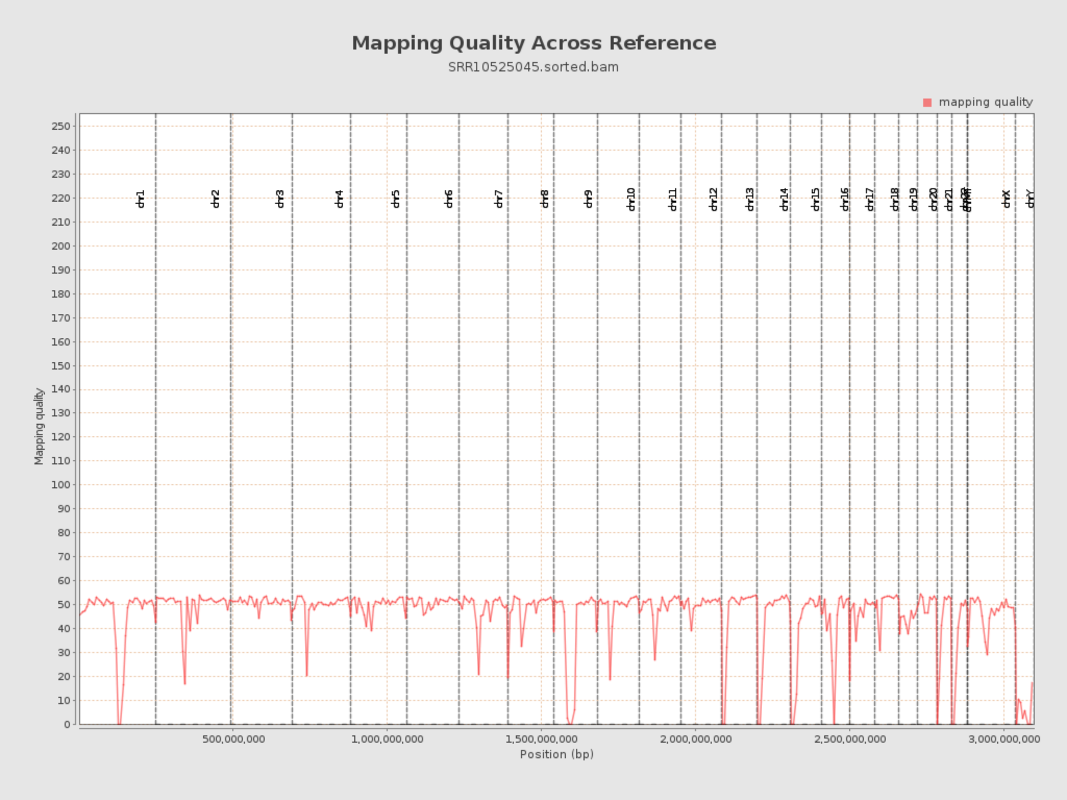
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram