Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:19:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525234.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_SRR10525234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:19:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	434,311
Mapped reads	411,629 / 94.78%
Unmapped reads	22,682 / 5.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,650 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	6,254 / 1.44%
Duplication rate	1.15%
Clipped reads	412,637 / 95.01%

2.2. ACGT Content

Number/percentage of A's	7,039,179 / 27.06%
Number/percentage of C's	5,100,141 / 19.61%
Number/percentage of T's	7,579,427 / 29.14%
Number/percentage of G's	6,292,417 / 24.19%
Number/percentage of N's	678 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.112

2.4. Mapping Quality

Mean Mapping Quality	46.93

2.5. Mismatches and indels

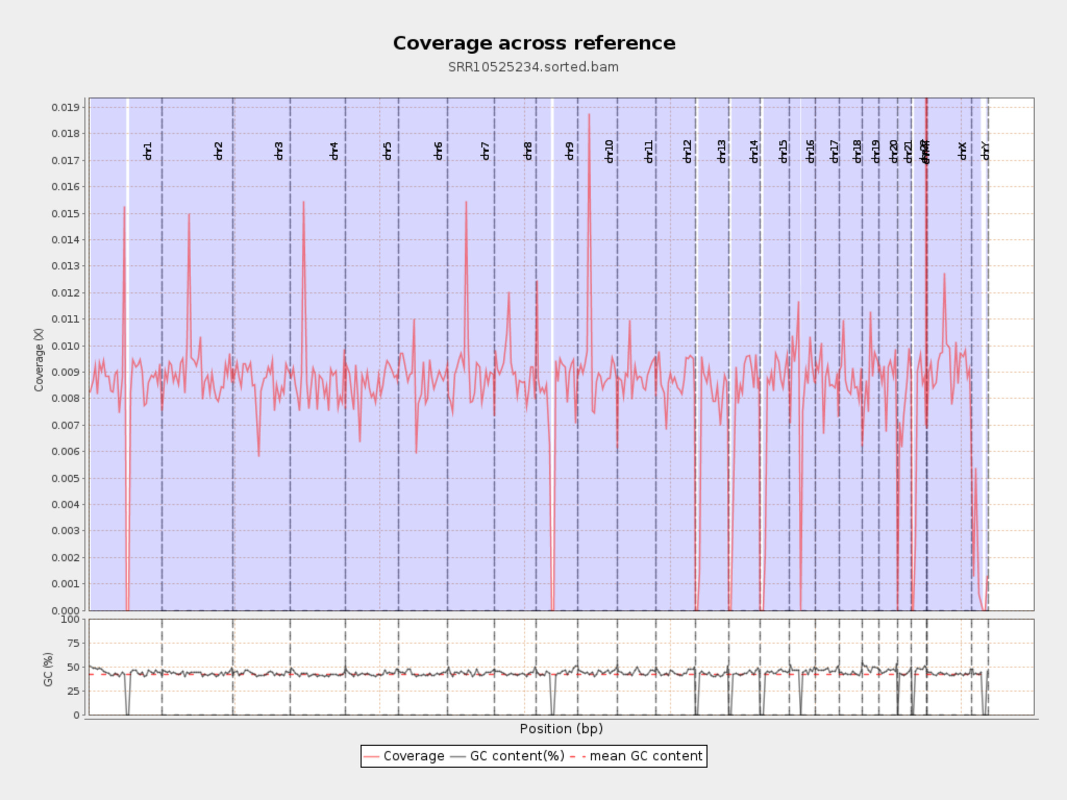
General error rate	0.5%
Mismatches	126,440
Insertions	1,600
Mapped reads with at least one insertion	0.39%
Deletions	5,601
Mapped reads with at least one deletion	1.35%
Homopolymer indels	43.56%

2.6. Chromosome stats

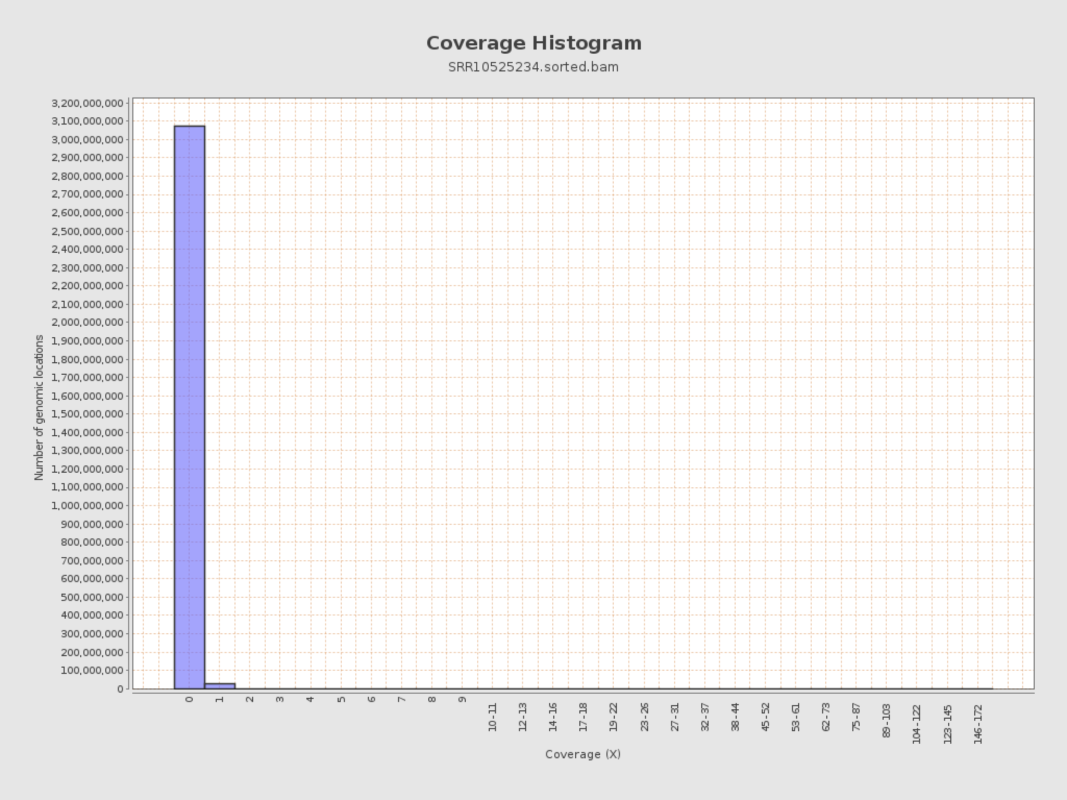
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2096916	0.0084	0.1708
chr2	243199373	2214799	0.0091	0.1168
chr3	198022430	1704621	0.0086	0.0956
chr4	191154276	1675297	0.0088	0.1006
chr5	180915260	1546264	0.0085	0.0951
chr6	171115067	1504515	0.0088	0.0995
chr7	159138663	1439506	0.009	0.1405

chr8	146364022	1329772	0.0091	0.1091
chr9	141213431	1083379	0.0077	0.1003
chr10	135534747	1271598	0.0094	0.1201
chr11	135006516	1197120	0.0089	0.1047
chr12	133851895	1174435	0.0088	0.0963
chr13	115169878	811979	0.0071	0.086
chr14	107349540	794650	0.0074	0.0904
chr15	102531392	734508	0.0072	0.087
chr16	90354753	772713	0.0086	0.0984
chr17	81195210	704690	0.0087	0.0975
chr18	78077248	691024	0.0089	0.1528
chr19	59128983	525524	0.0089	0.1353
chr20	63025520	553132	0.0088	0.0971
chr21	48129895	347620	0.0072	0.0907
chr22	51304566	312701	0.0061	0.0804
chrMT	16571	4954	0.299	0.5961
chrX	155270560	1443302	0.0093	0.1017
chrY	59373566	86108	0.0015	0.0572

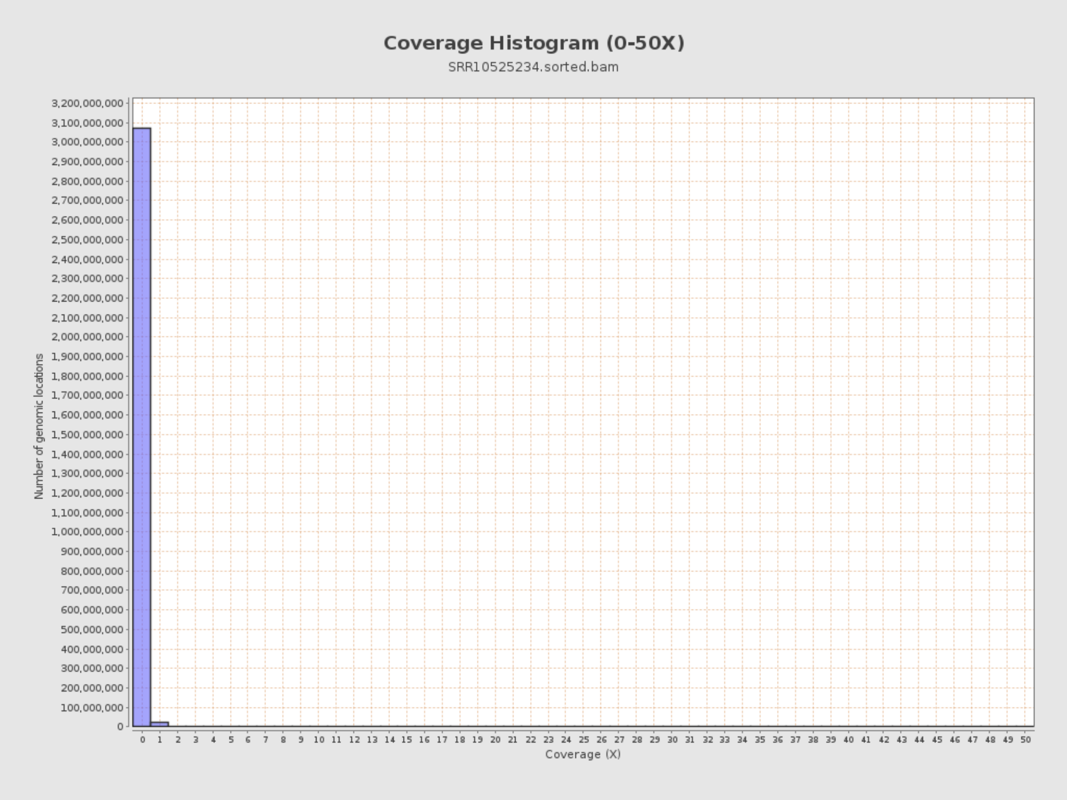
3. Results : Coverage across reference



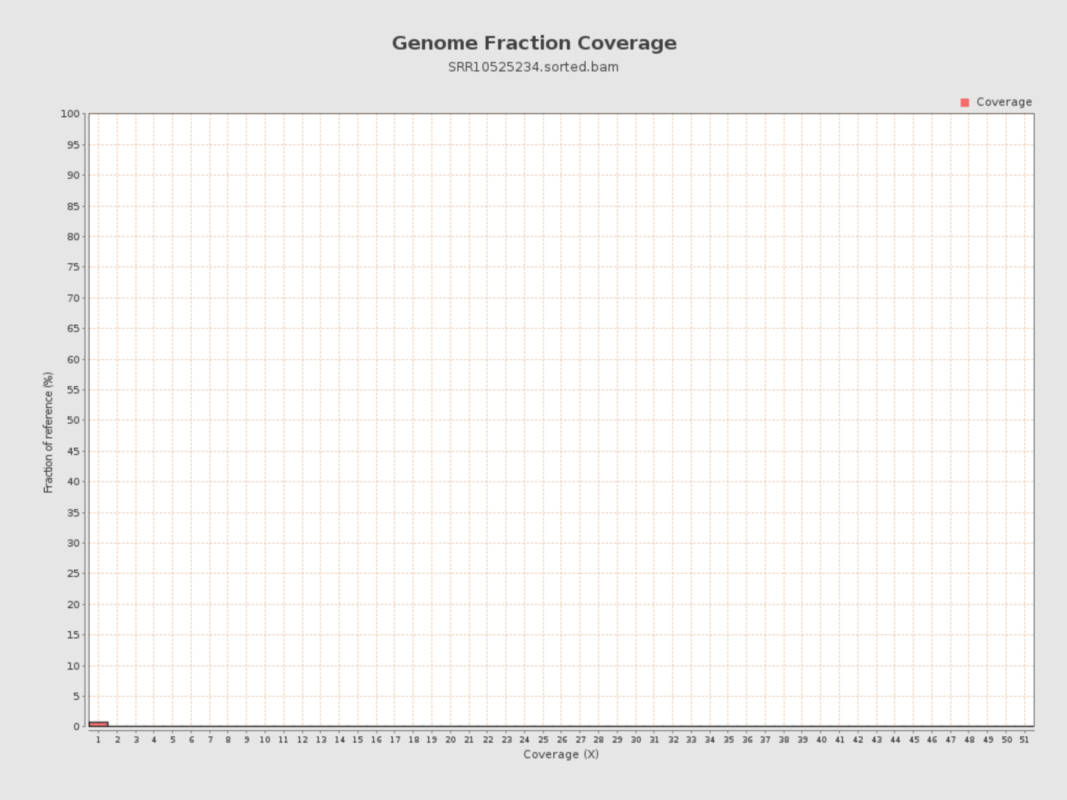
4. Results : Coverage Histogram



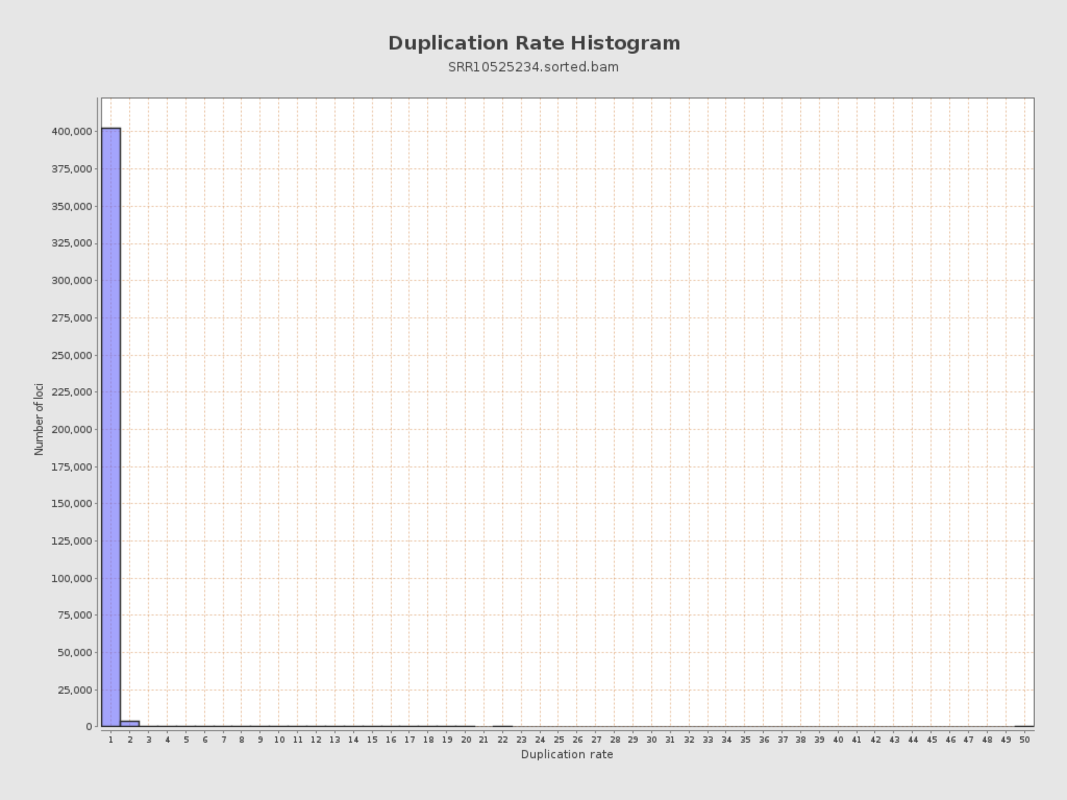
5. Results : Coverage Histogram (0-50X)



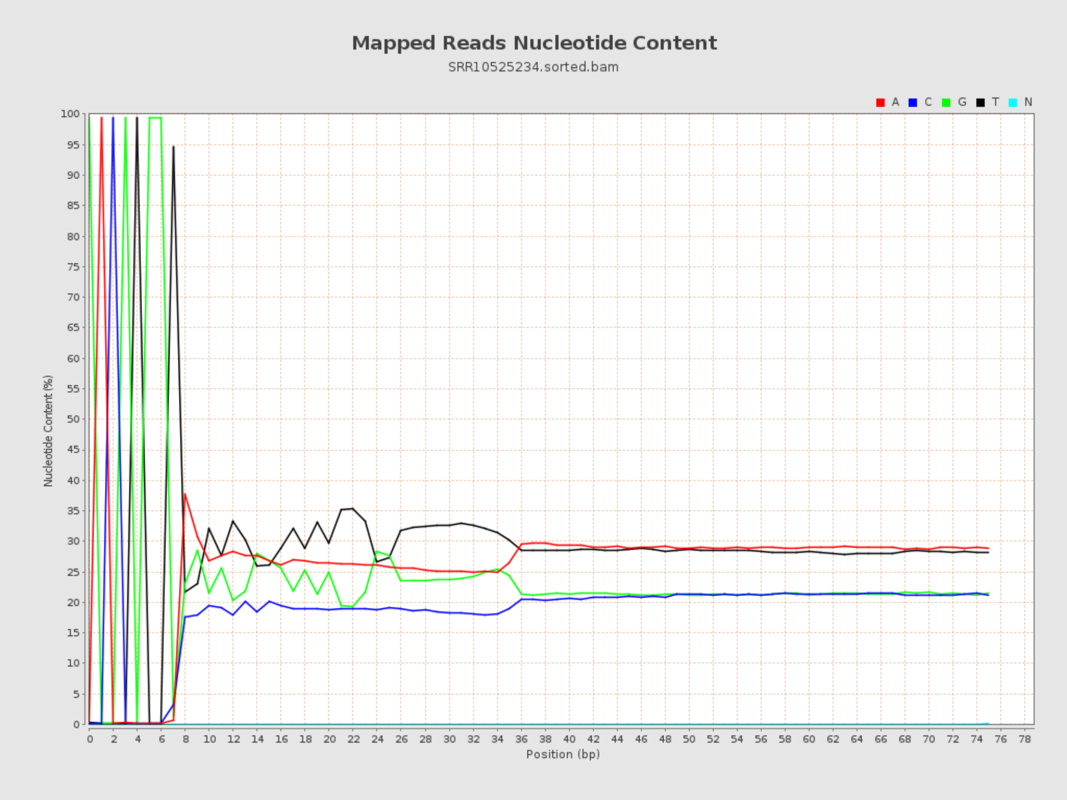
6. Results : Genome Fraction Coverage



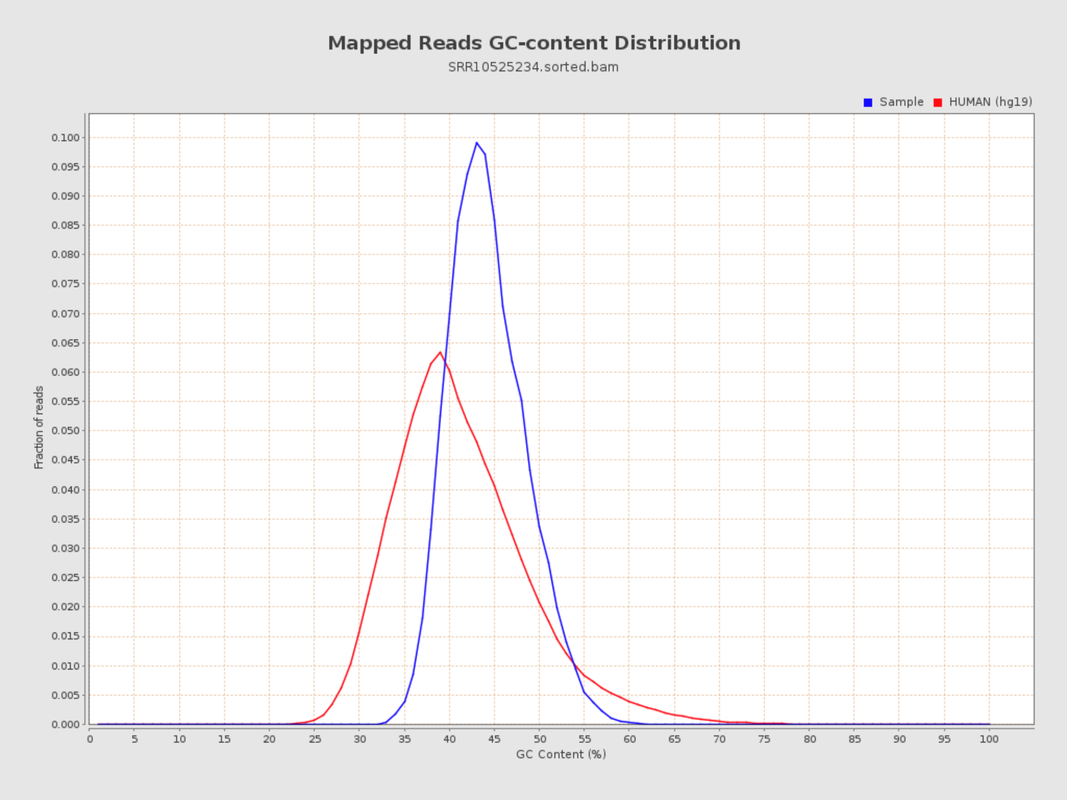
7. Results : Duplication Rate Histogram



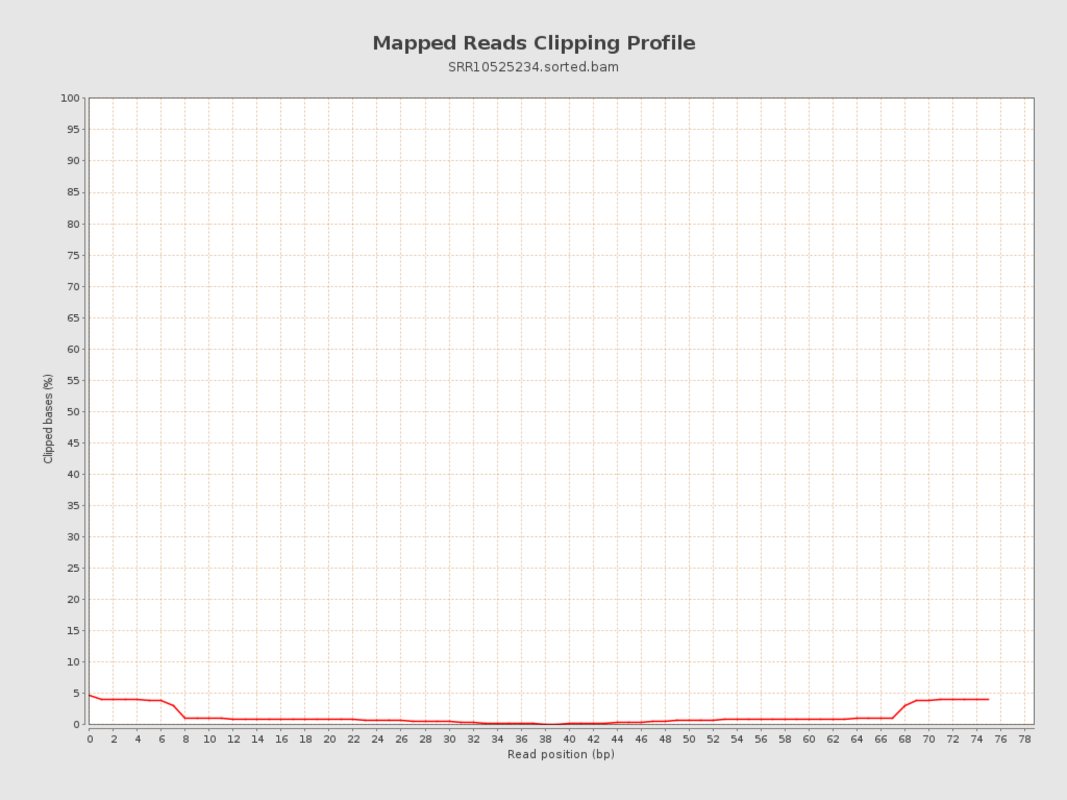
8. Results : Mapped Reads Nucleotide Content



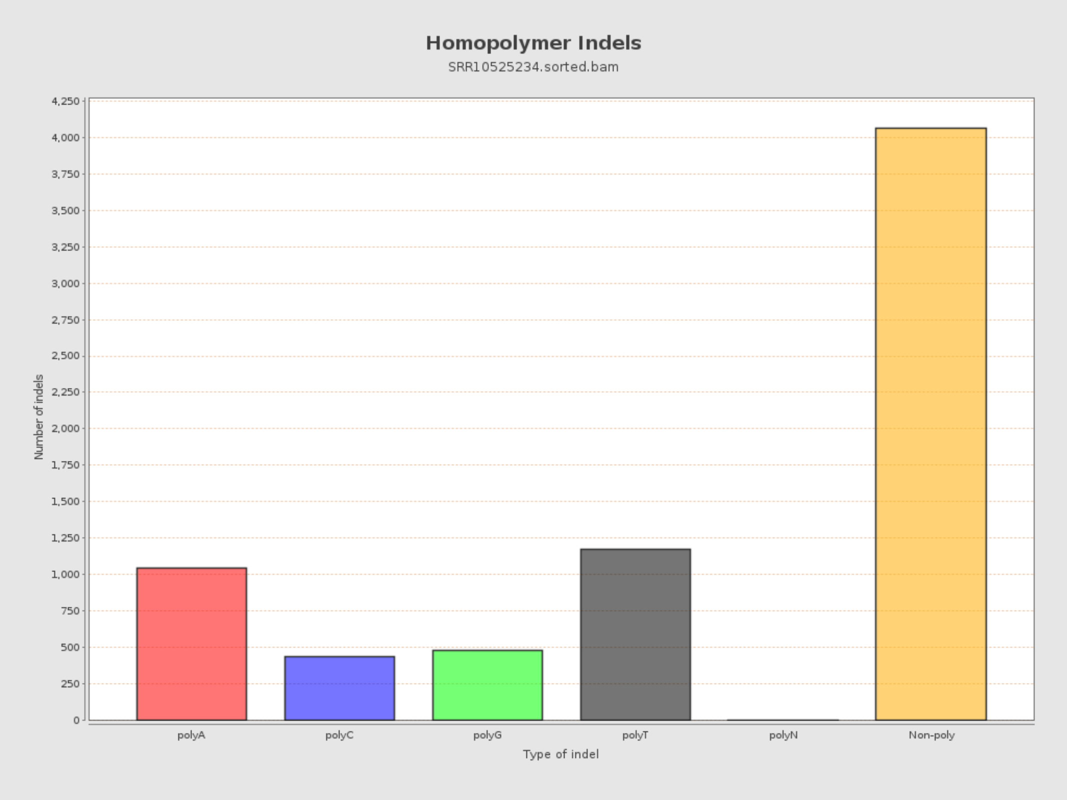
9. Results : Mapped Reads GC-content Distribution



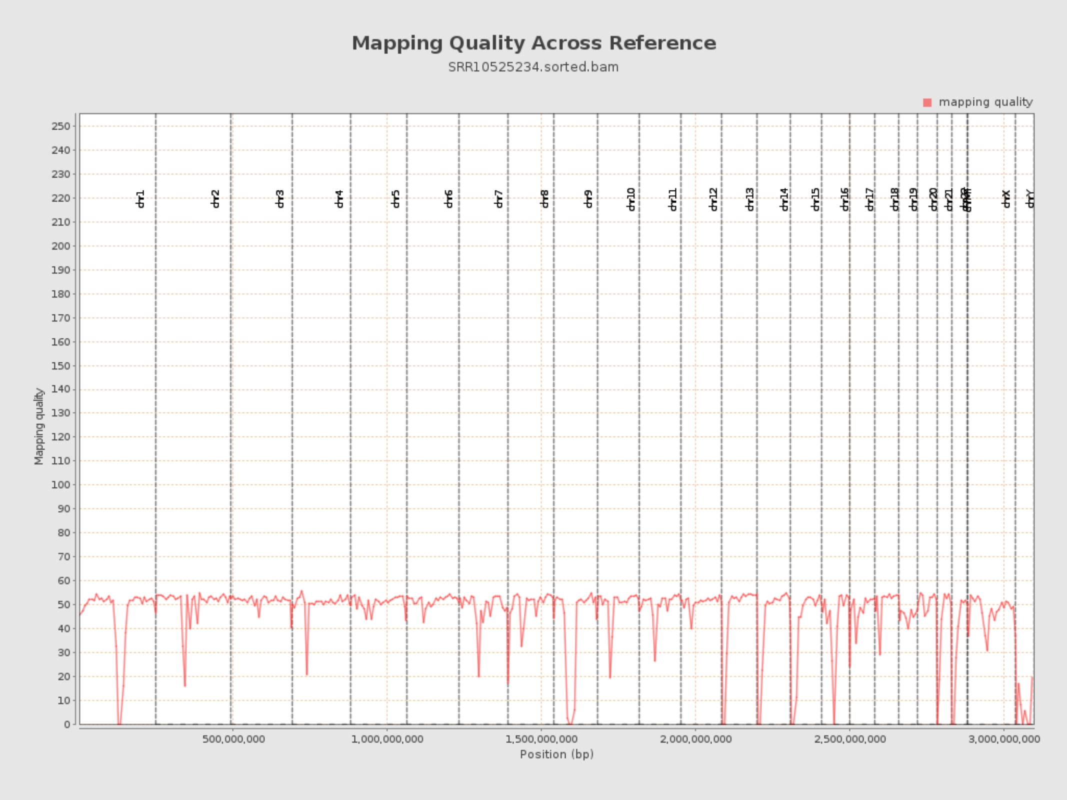
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram