Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:32:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525194.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_SRR10525194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:32:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	443,520
Mapped reads	407,035 / 91.77%
Unmapped reads	36,485 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,214 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	5,495 / 1.24%
Duplication rate	0.99%
Clipped reads	406,398 / 91.63%

2.2. ACGT Content

Number/percentage of A's	6,960,261 / 27.83%
Number/percentage of C's	4,953,559 / 19.81%
Number/percentage of T's	7,258,119 / 29.02%
Number/percentage of G's	5,834,683 / 23.33%
Number/percentage of N's	576 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.1117

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

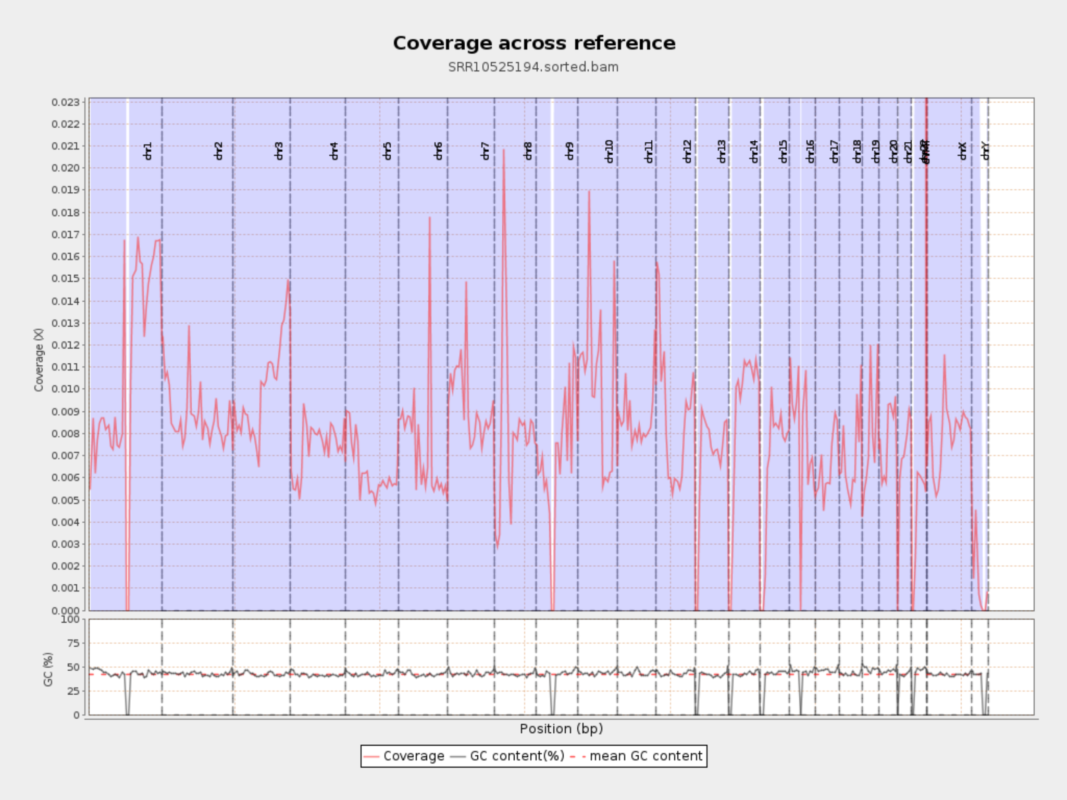
General error rate	0.51%
Mismatches	123,470
Insertions	2,296
Mapped reads with at least one insertion	0.56%
Deletions	5,456
Mapped reads with at least one deletion	1.33%
Homopolymer indels	43.12%

2.6. Chromosome stats

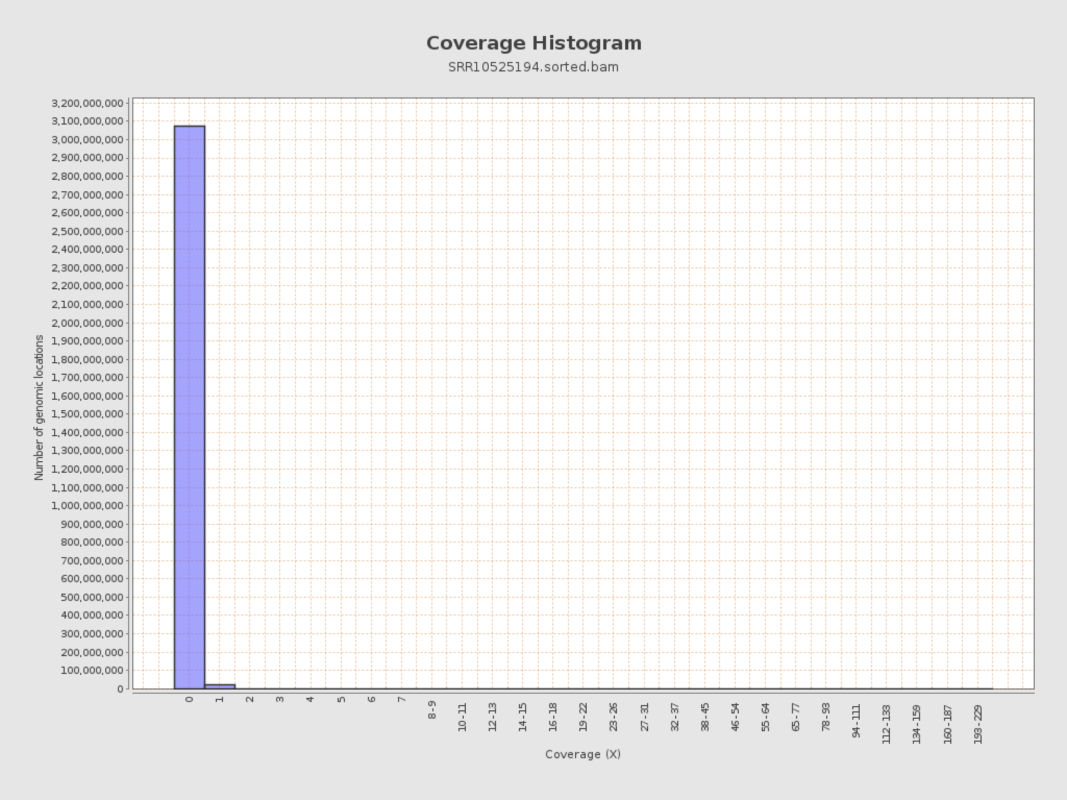
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2694476	0.0108	0.1977
chr2	243199373	2151459	0.0088	0.1159
chr3	198022430	1983432	0.01	0.1022
chr4	191154276	1409681	0.0074	0.0893
chr5	180915260	1139449	0.0063	0.0811
chr6	171115067	1274657	0.0074	0.0914
chr7	159138663	1495839	0.0094	0.1387

chr8	146364022	1170112	0.008	0.1
chr9	141213431	961378	0.0068	0.0912
chr10	135534747	1413365	0.0104	0.1238
chr11	135006516	1169225	0.0087	0.1016
chr12	133851895	1164347	0.0087	0.0957
chr13	115169878	784179	0.0068	0.0843
chr14	107349540	947654	0.0088	0.0964
chr15	102531392	663002	0.0065	0.082
chr16	90354753	699732	0.0077	0.0935
chr17	81195210	529594	0.0065	0.0838
chr18	78077248	541688	0.0069	0.132
chr19	59128983	468203	0.0079	0.1383
chr20	63025520	489612	0.0078	0.0908
chr21	48129895	327479	0.0068	0.0863
chr22	51304566	214013	0.0042	0.0658
chrMT	16571	4502	0.2717	0.5302
chrX	155270560	1243140	0.008	0.0945
chrY	59373566	75780	0.0013	0.0529

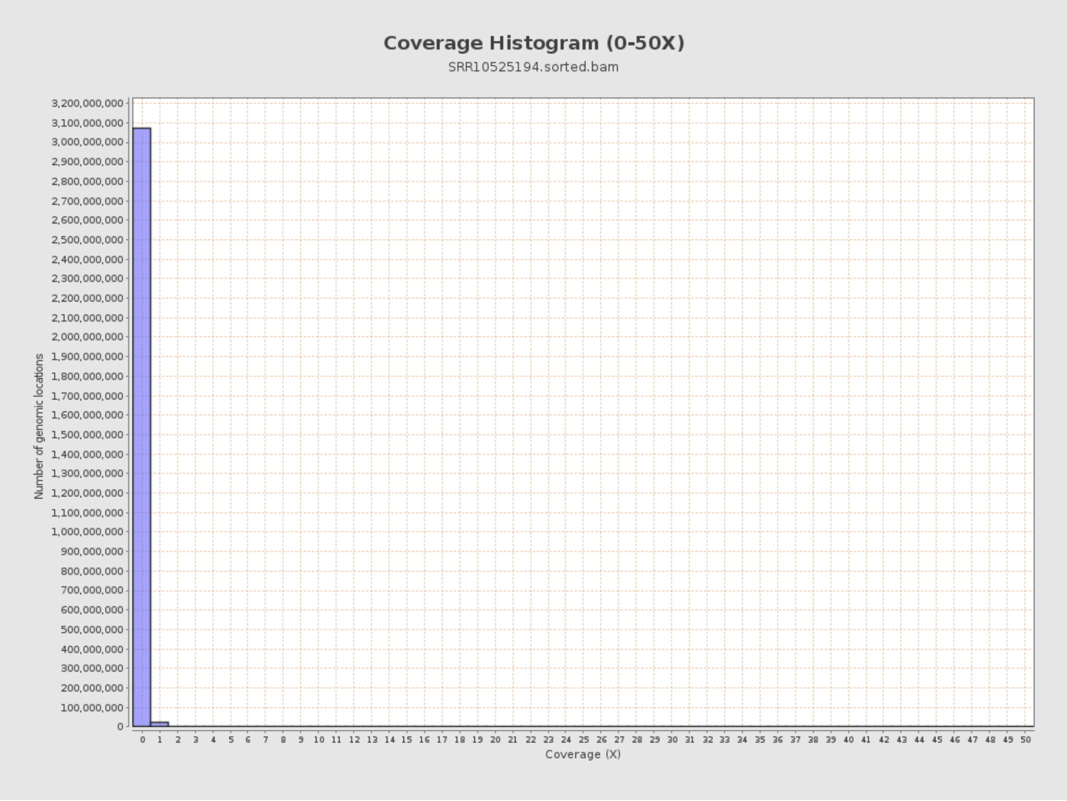
3. Results : Coverage across reference



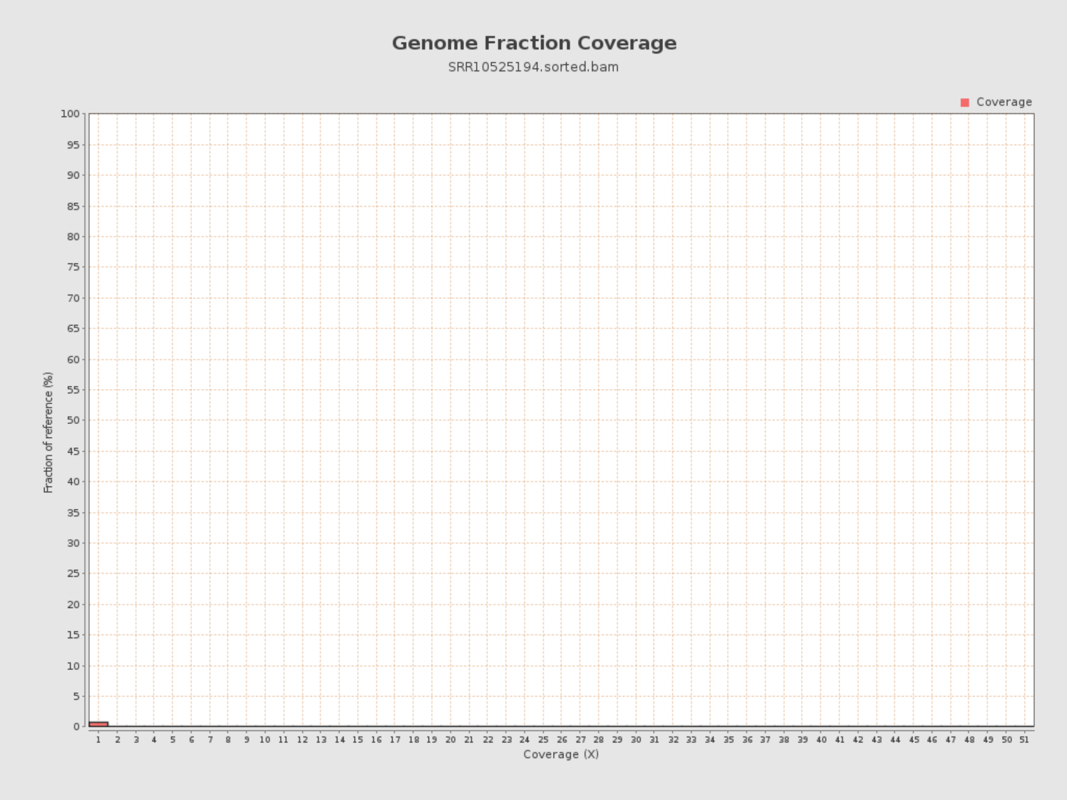
4. Results : Coverage Histogram



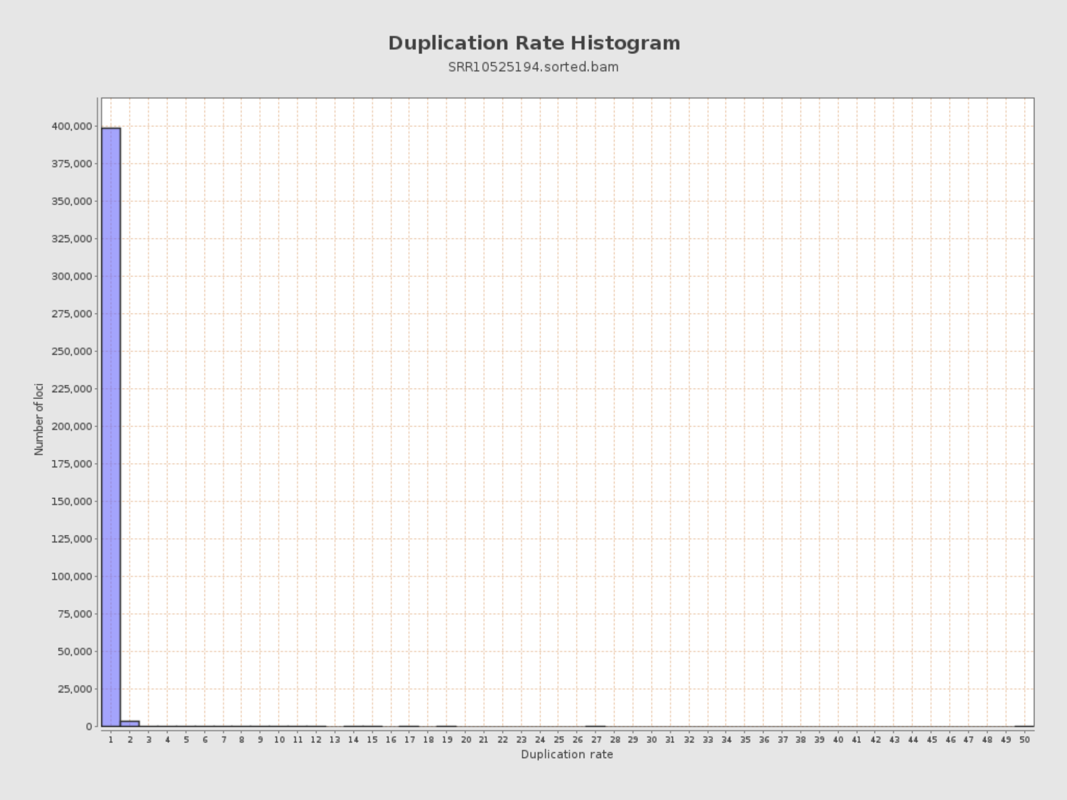
5. Results : Coverage Histogram (0-50X)



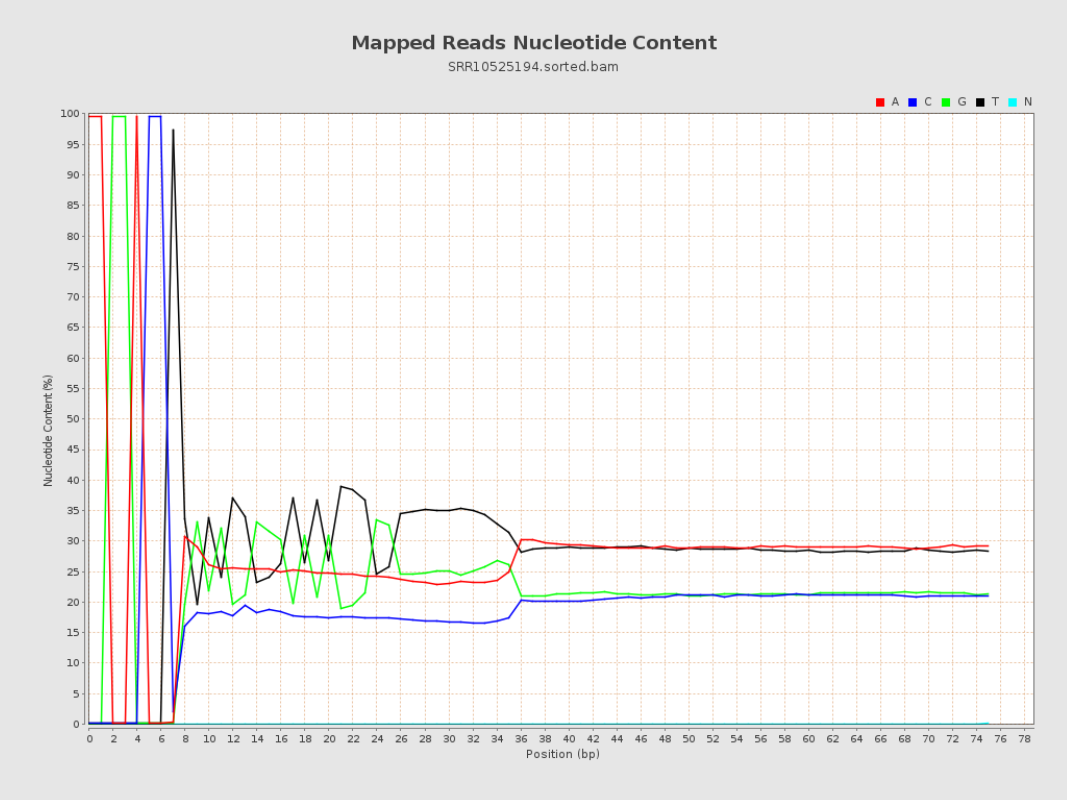
6. Results : Genome Fraction Coverage



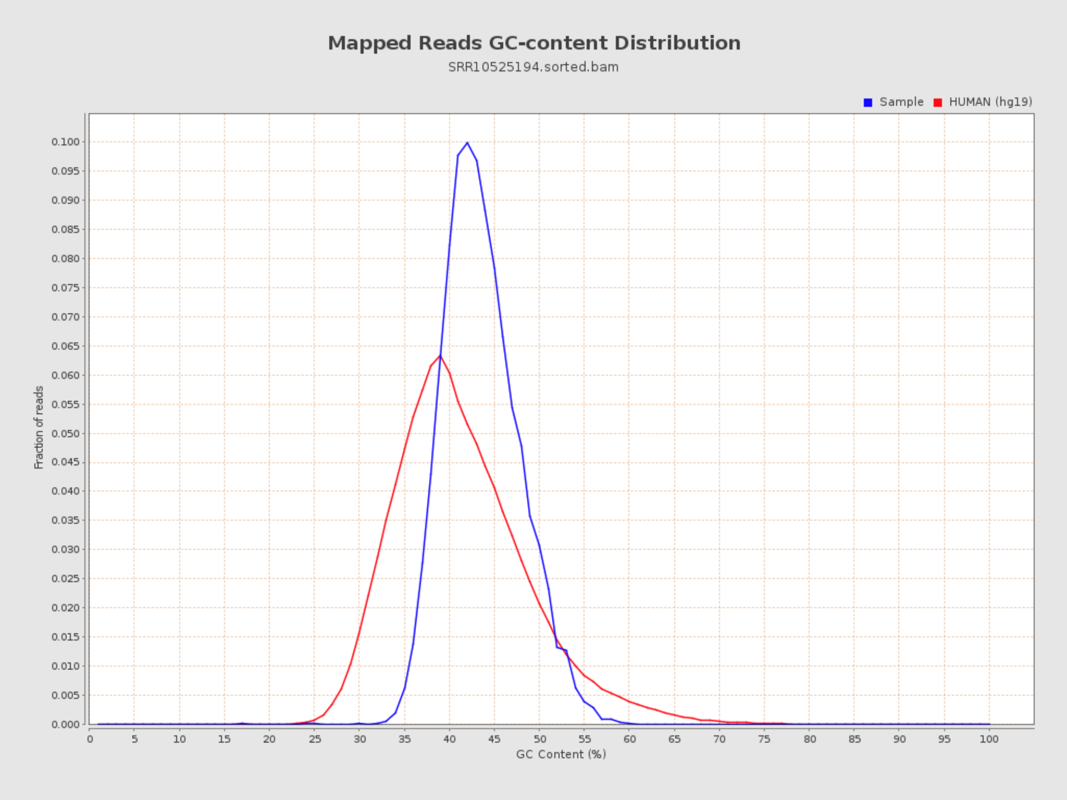
7. Results : Duplication Rate Histogram



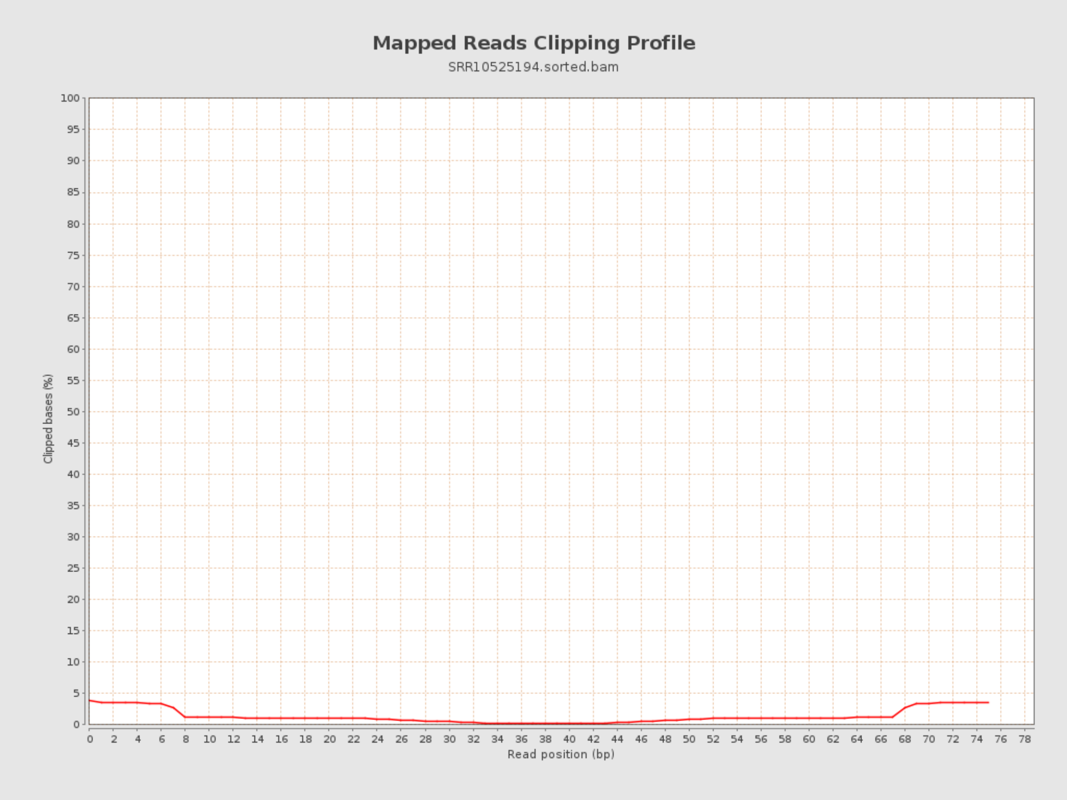
8. Results : Mapped Reads Nucleotide Content



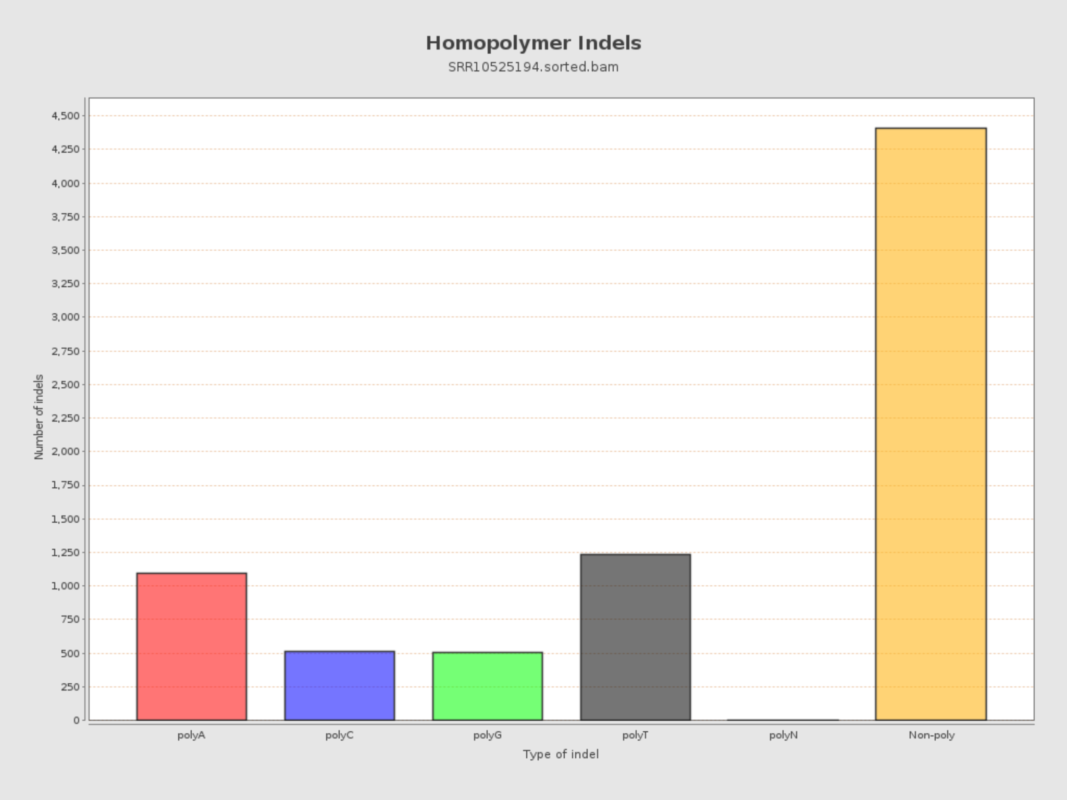
9. Results : Mapped Reads GC-content Distribution



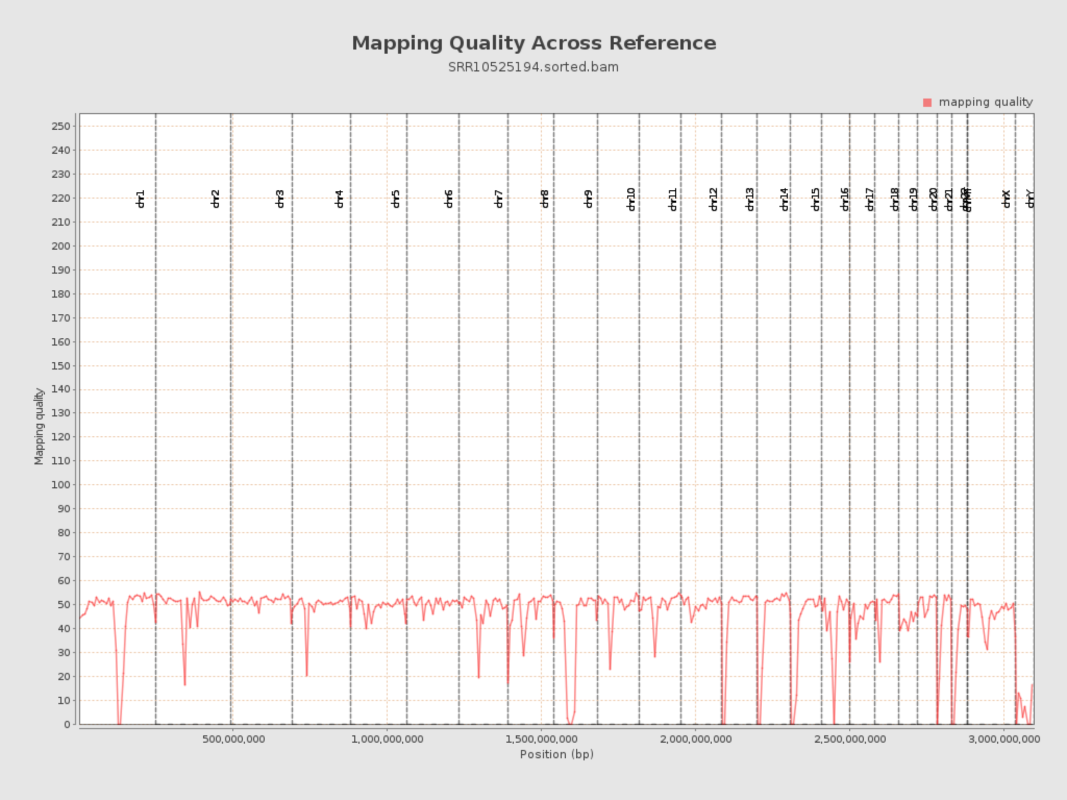
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram