Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524402.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_SRR10524402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524402.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:09:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,863,851
Mapped reads	5,397,196 / 92.04%
Unmapped reads	466,655 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,796 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	431,894 / 7.37%
Duplication rate	5.81%
Clipped reads	5,399,649 / 92.08%

2.2. ACGT Content

Number/percentage of A's	79,547,218 / 25.1%
Number/percentage of C's	61,866,838 / 19.52%
Number/percentage of T's	103,923,549 / 32.79%
Number/percentage of G's	71,551,681 / 22.58%
Number/percentage of N's	42,568 / 0.01%
GC Percentage	42.1%

2.3. Coverage

Mean	0.1024

Standard Deviation	0.9216

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

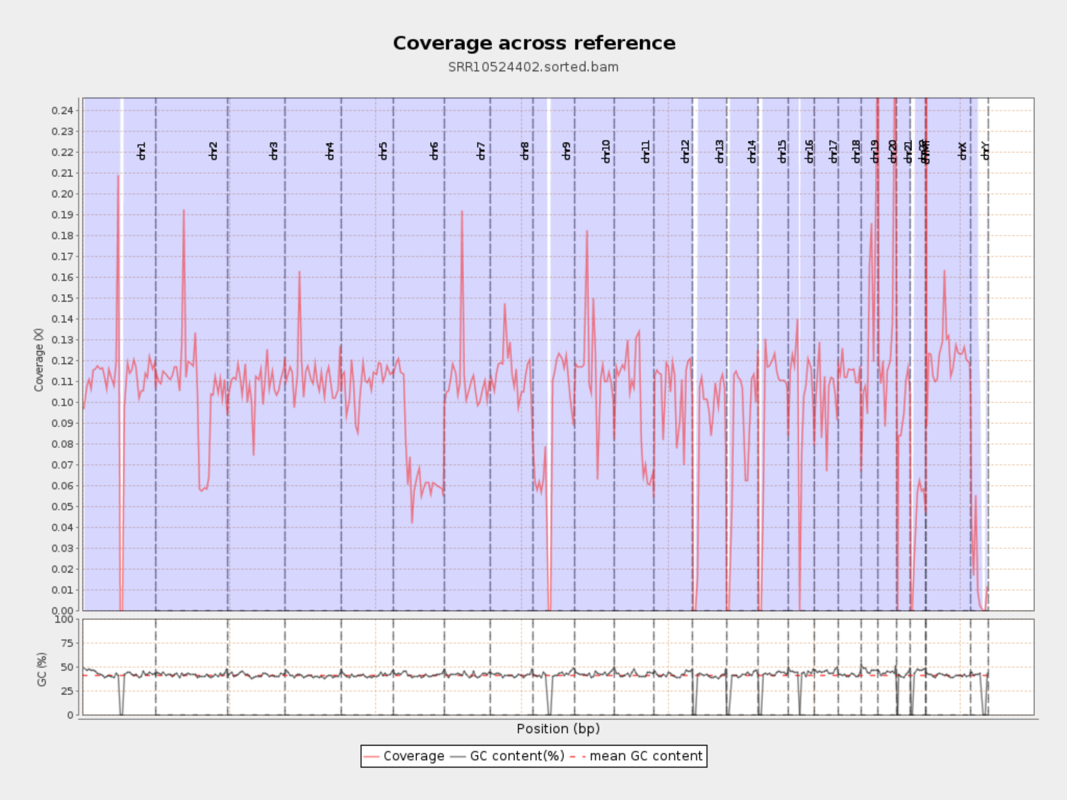
General error rate	0.5%
Mismatches	1,557,525
Insertions	21,277
Mapped reads with at least one insertion	0.39%
Deletions	57,898
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.63%

2.6. Chromosome stats

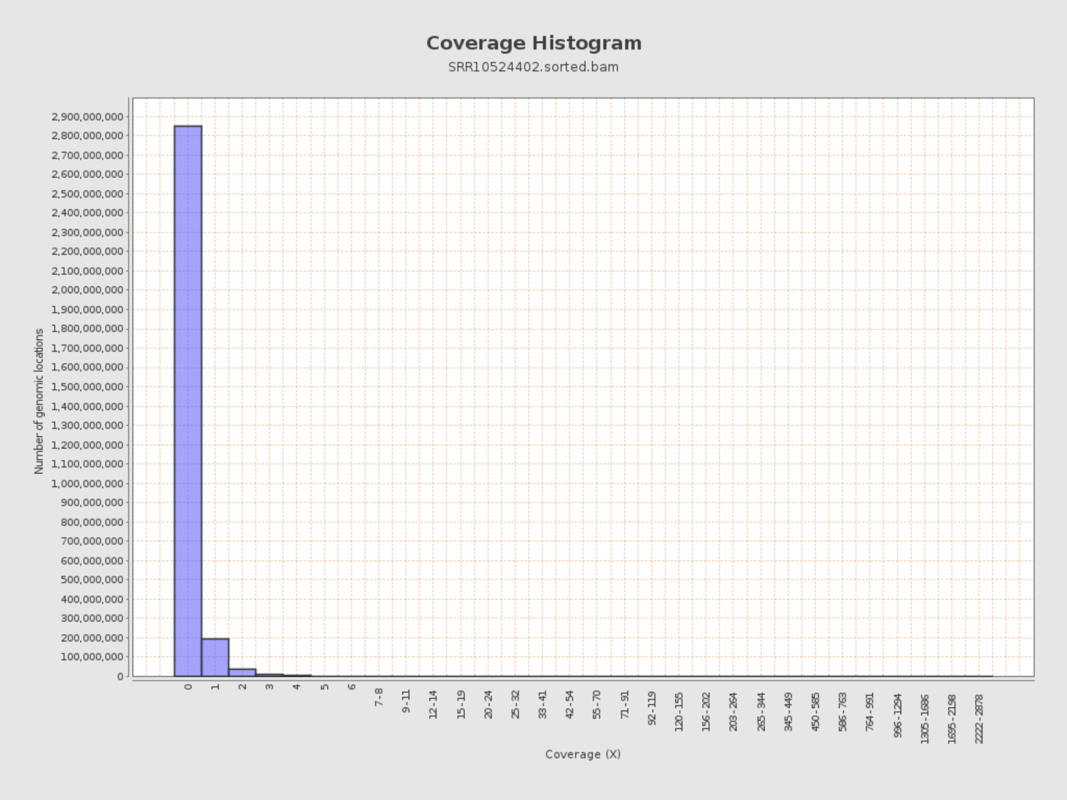
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26984281	0.1083	2.2349
chr2	243199373	25896685	0.1065	0.9832
chr3	198022430	21459003	0.1084	0.4094
chr4	191154276	21634897	0.1132	0.5227
chr5	180915260	19796470	0.1094	0.4146
chr6	171115067	12468502	0.0729	0.4159
chr7	159138663	17699712	0.1112	1.3657

chr8	146364022	16756699	0.1145	0.7496
chr9	141213431	11870901	0.0841	0.6191
chr10	135534747	15796227	0.1165	0.7458
chr11	135006516	13401407	0.0993	0.6719
chr12	133851895	14281935	0.1067	0.4396
chr13	115169878	9827234	0.0853	0.3633
chr14	107349540	8992286	0.0838	0.4057
chr15	102531392	9721153	0.0948	0.3901
chr16	90354753	9080385	0.1005	0.4521
chr17	81195210	8372037	0.1031	0.5083
chr18	78077248	8961300	0.1148	1.231
chr19	59128983	8730695	0.1477	1.3569
chr20	63025520	8787758	0.1394	0.5068
chr21	48129895	4294223	0.0892	0.4745
chr22	51304566	2112548	0.0412	0.2498
chrMT	16571	194709	11.75	7.5774
chrX	155270560	18948047	0.122	0.5605
chrY	59373566	954484	0.0161	0.3933

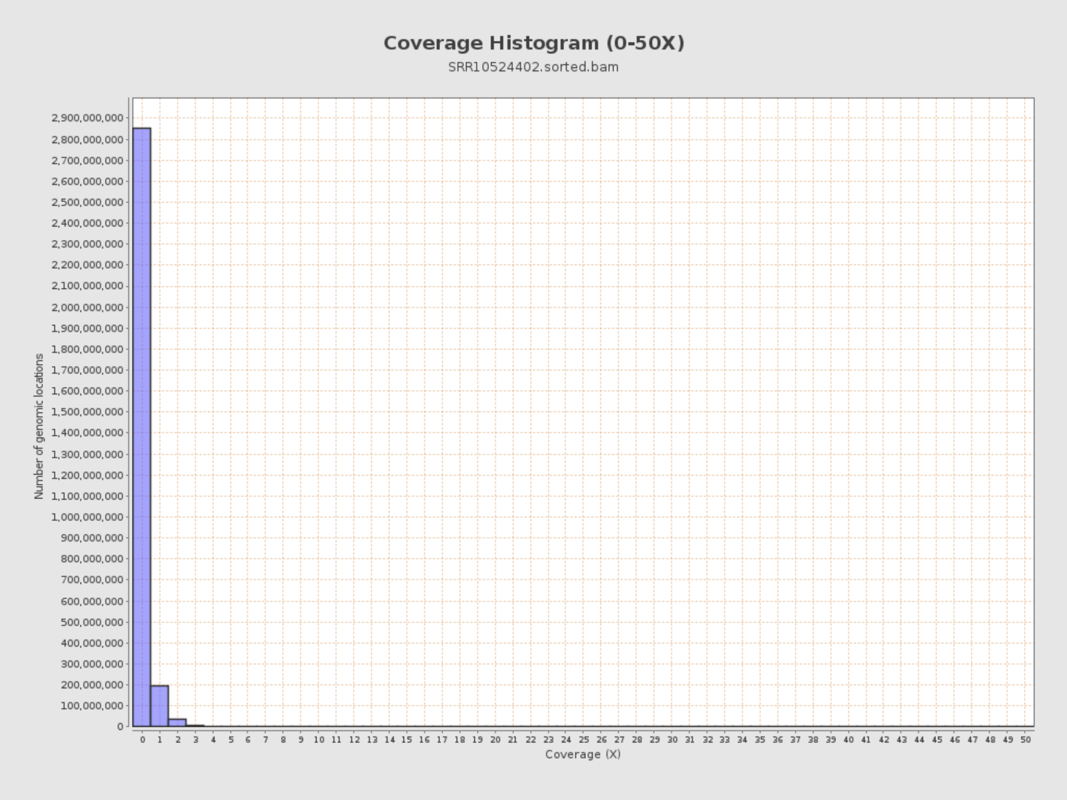
3. Results : Coverage across reference



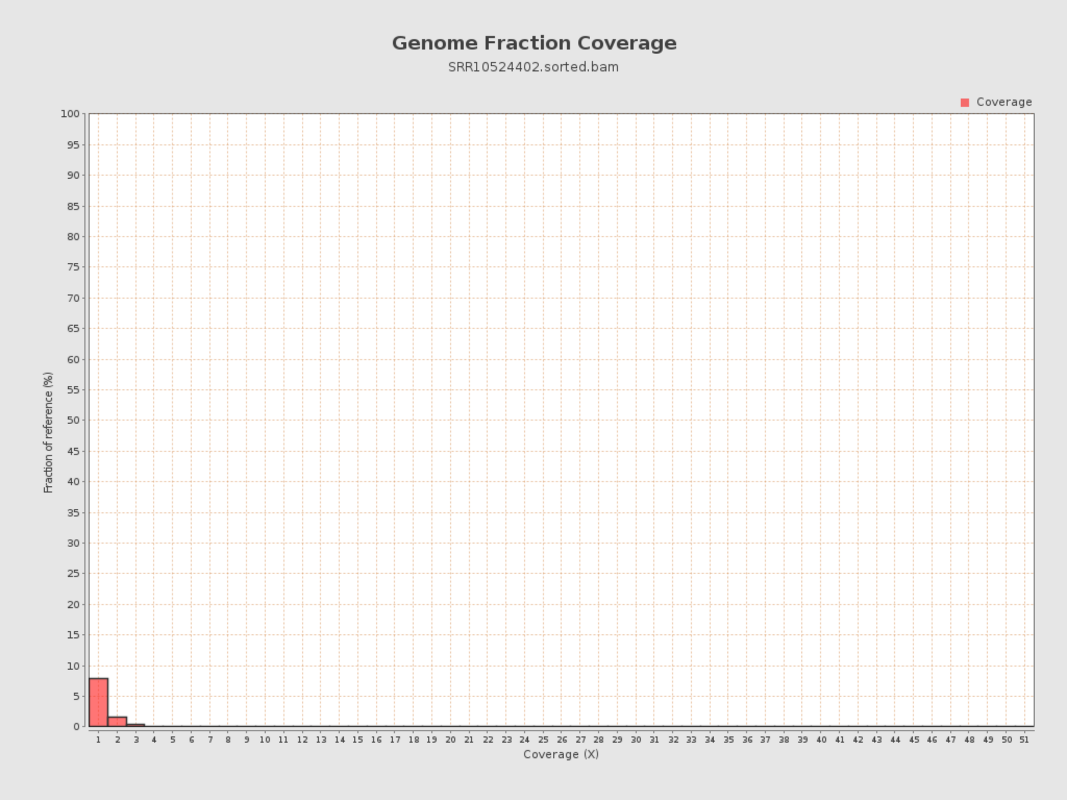
4. Results : Coverage Histogram



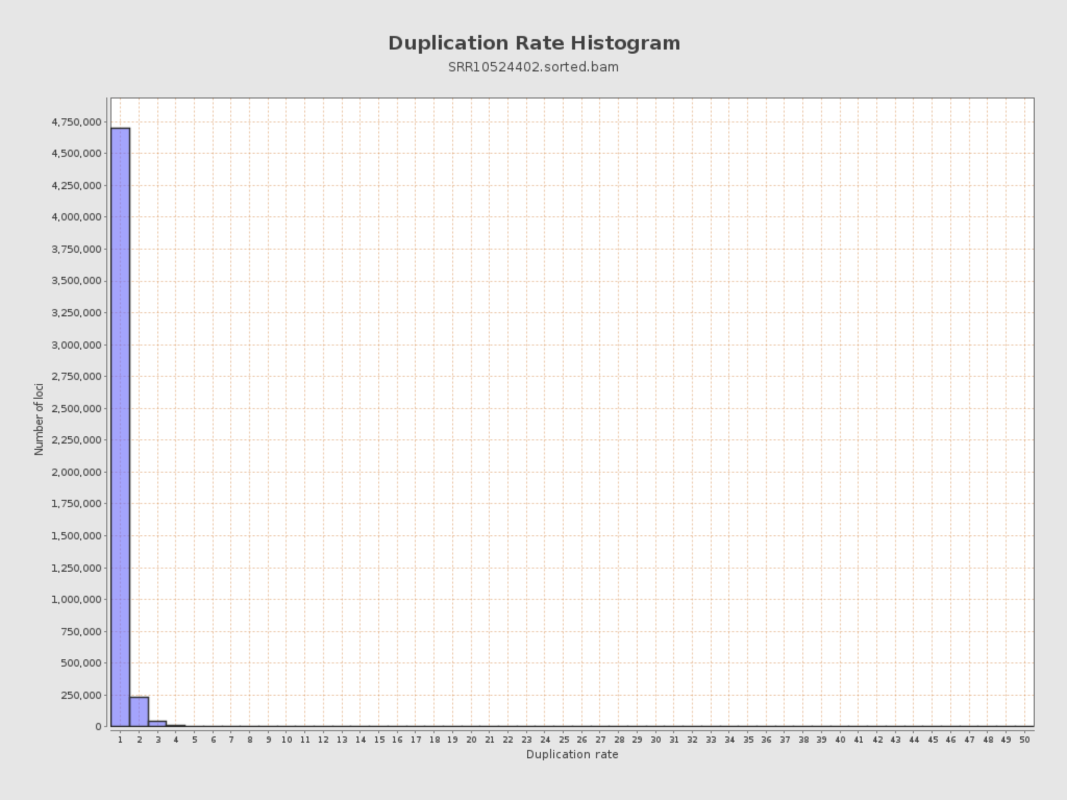
5. Results : Coverage Histogram (0-50X)



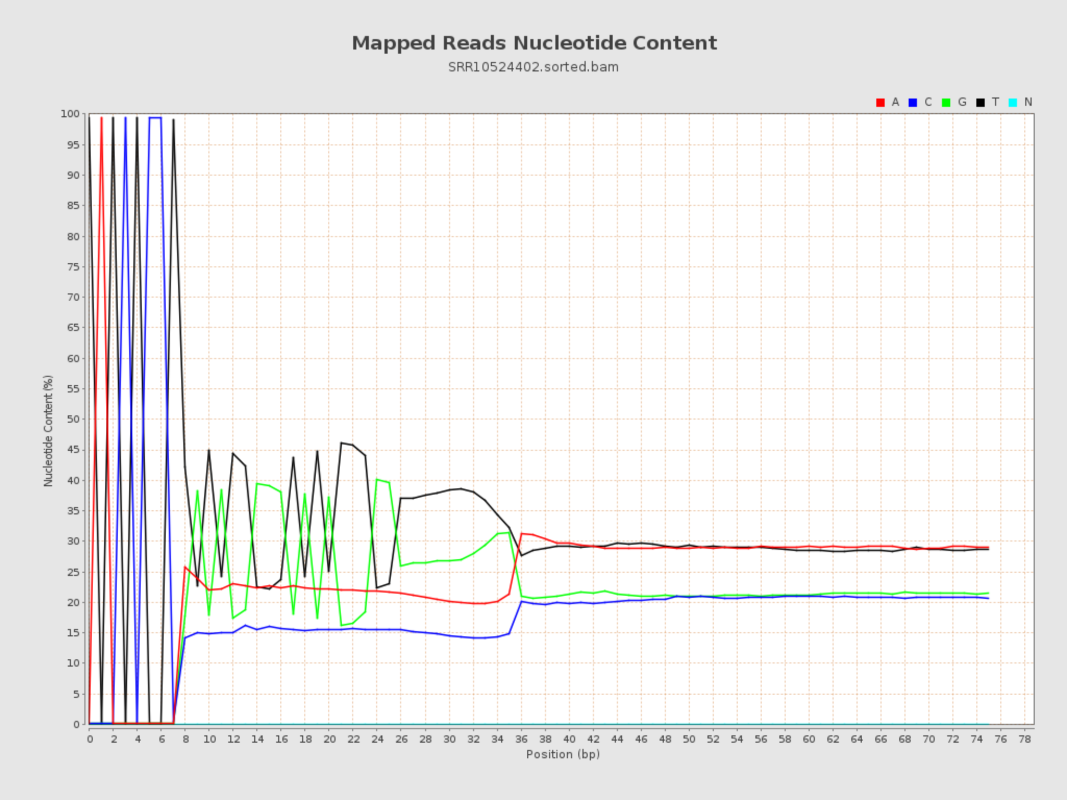
6. Results : Genome Fraction Coverage



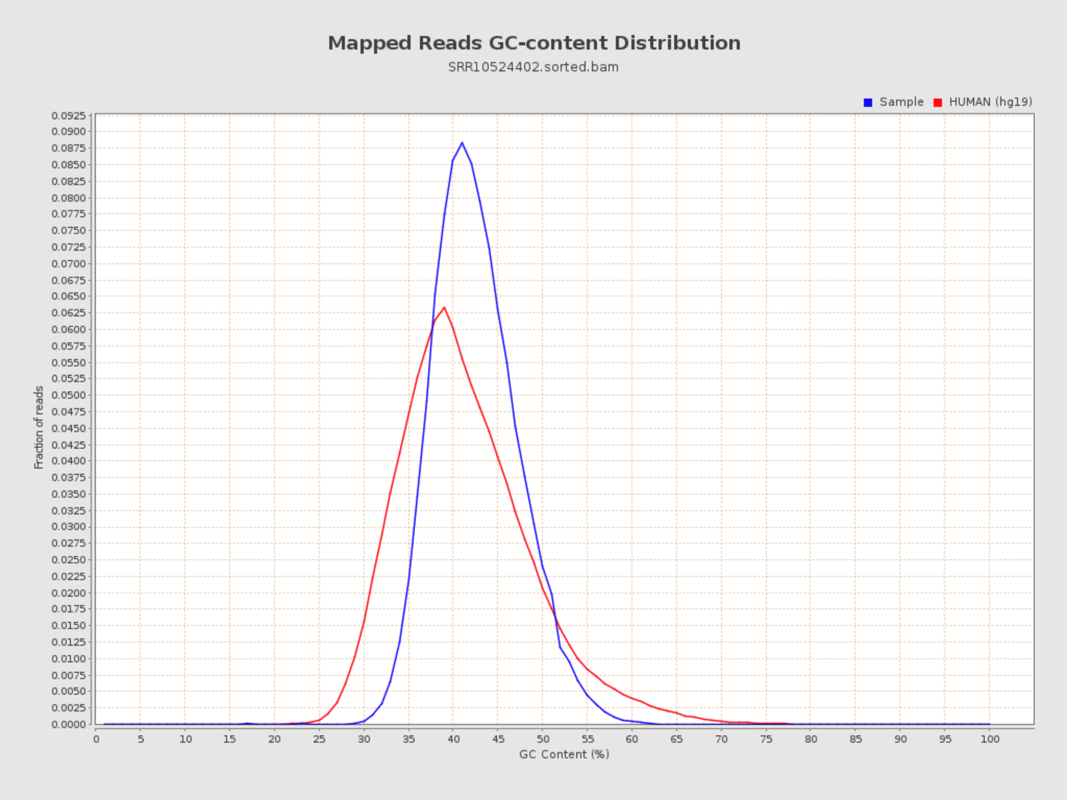
7. Results : Duplication Rate Histogram



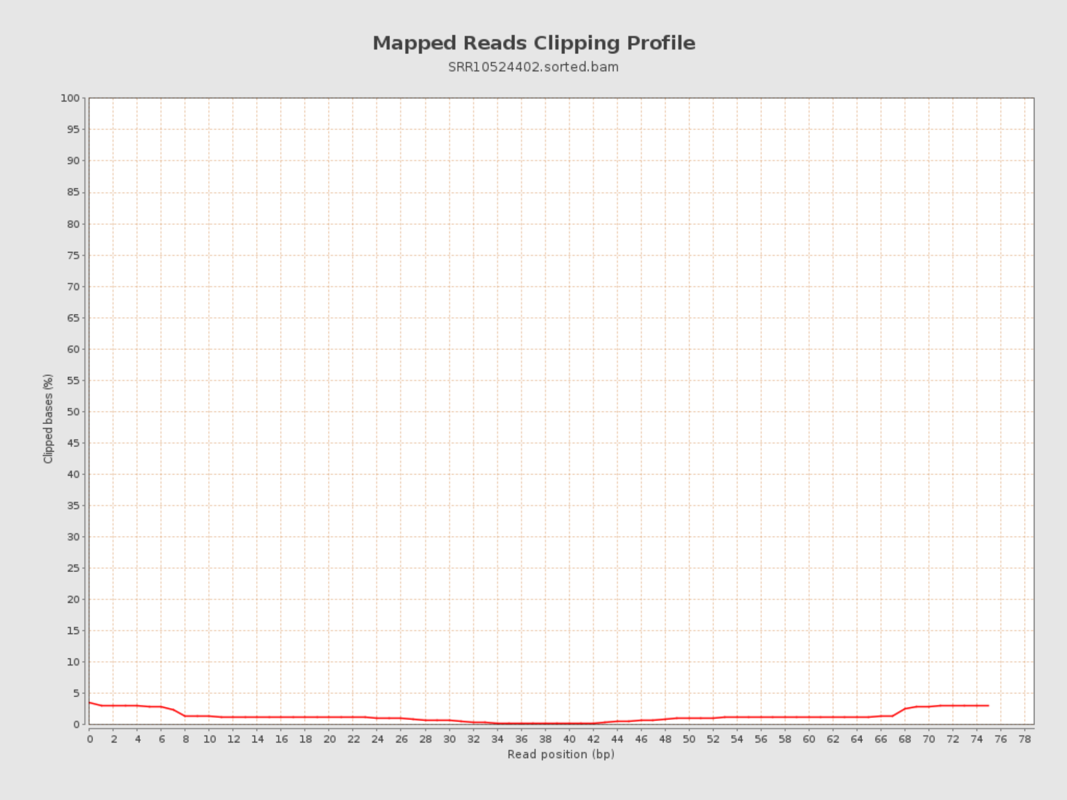
8. Results : Mapped Reads Nucleotide Content



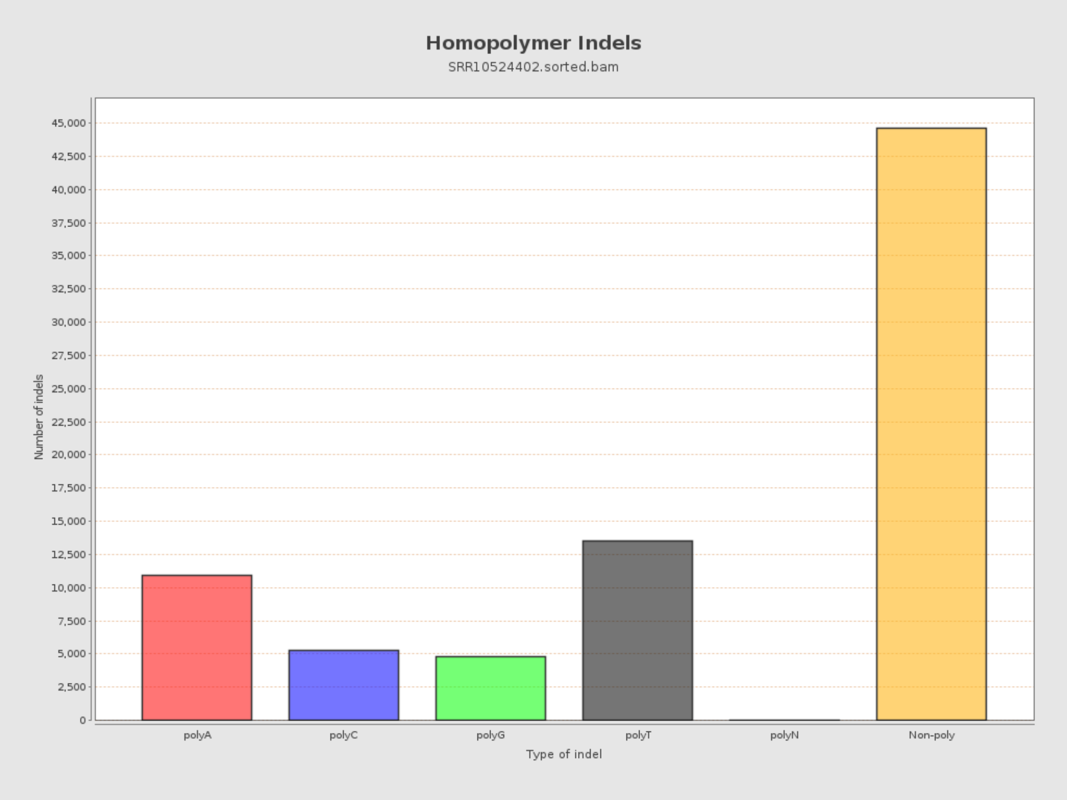
9. Results : Mapped Reads GC-content Distribution



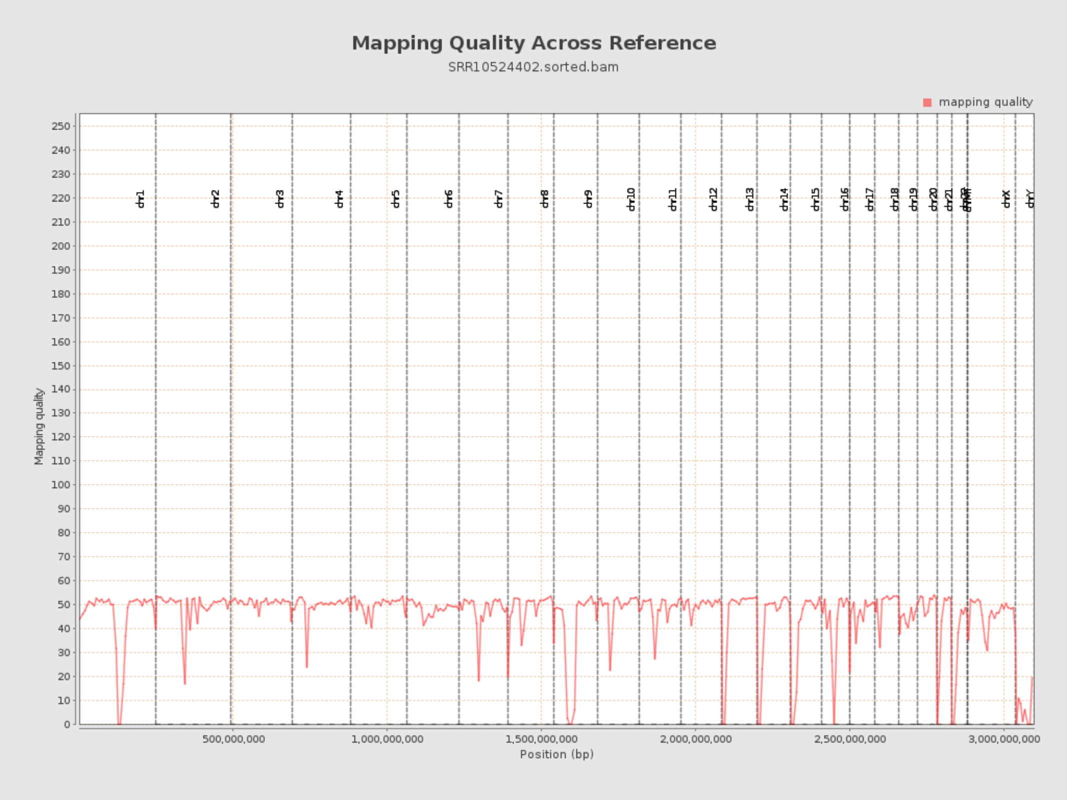
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram