Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:55:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524915.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_SRR10524915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524915.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:55:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,305,796
Mapped reads	2,095,369 / 90.87%
Unmapped reads	210,427 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,121 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	122,821 / 5.33%
Duplication rate	4.48%
Clipped reads	2,095,362 / 90.87%

2.2. ACGT Content

Number/percentage of A's	28,904,503 / 23.79%
Number/percentage of C's	23,619,127 / 19.44%
Number/percentage of T's	40,298,513 / 33.17%
Number/percentage of G's	28,671,854 / 23.6%
Number/percentage of N's	1,012 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3532

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

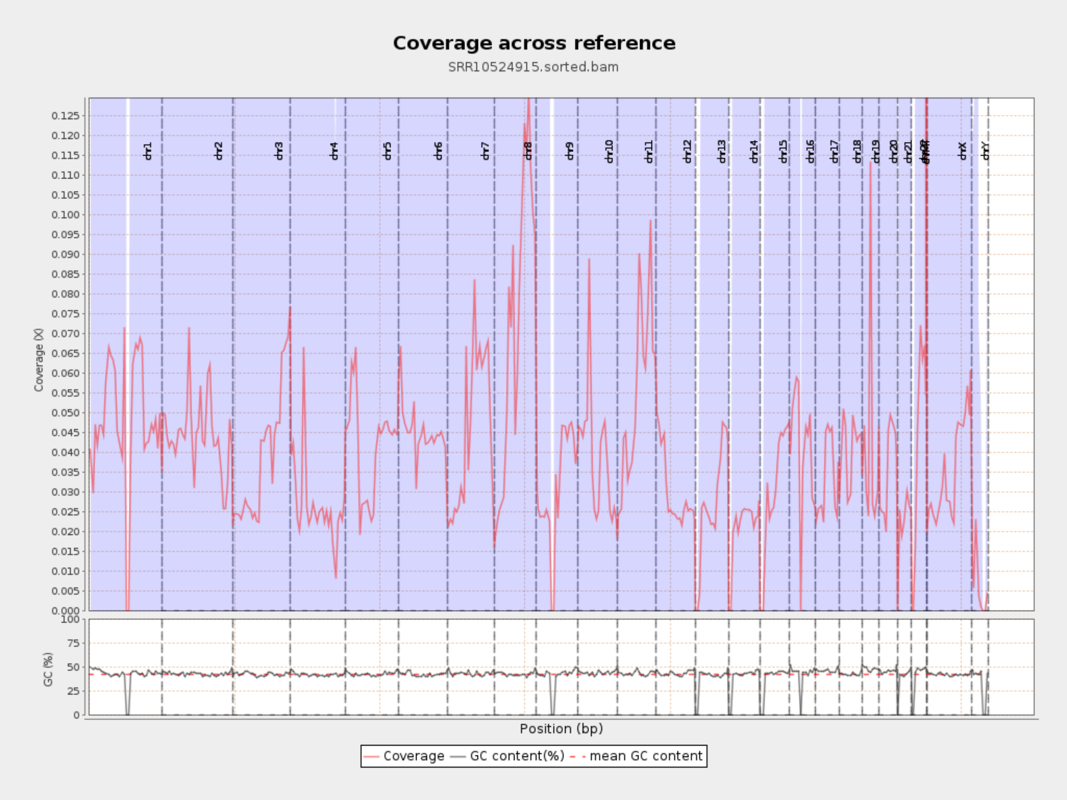
General error rate	0.52%
Mismatches	619,639
Insertions	8,727
Mapped reads with at least one insertion	0.41%
Deletions	23,518
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.32%

2.6. Chromosome stats

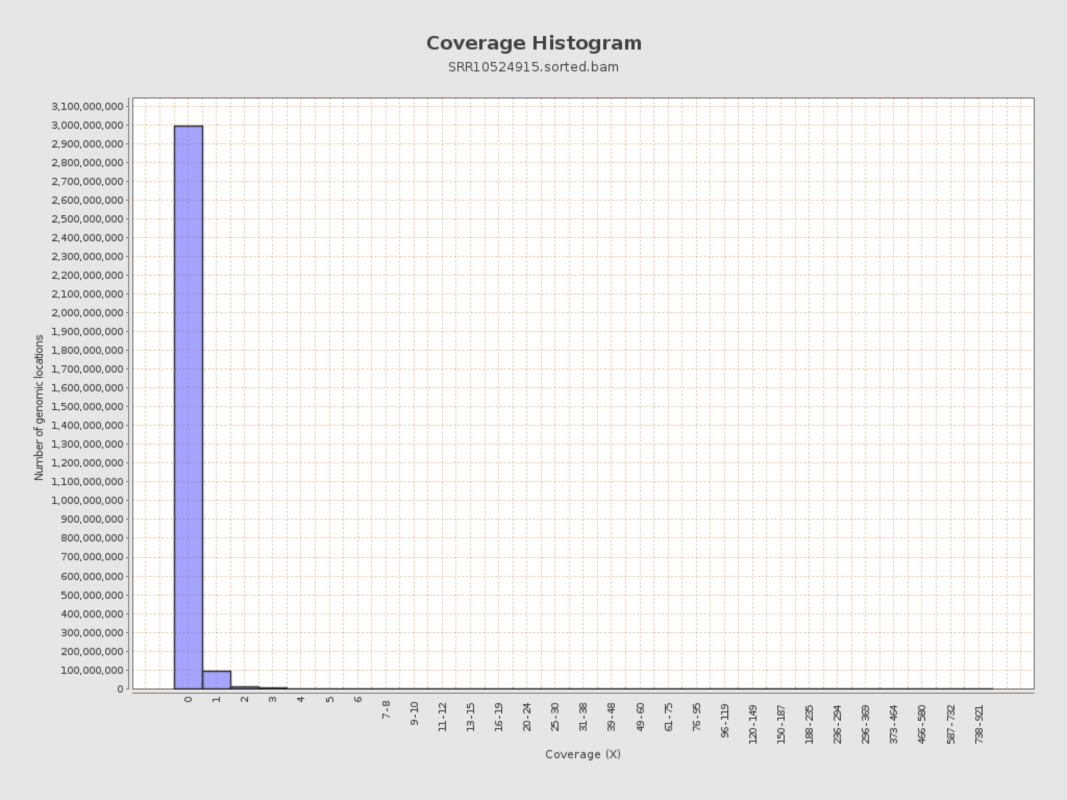
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11949228	0.0479	0.6886
chr2	243199373	10845603	0.0446	0.4088
chr3	198022430	7612378	0.0384	0.2275
chr4	191154276	5065704	0.0265	0.2382
chr5	180915260	7520810	0.0416	0.2326
chr6	171115067	7741154	0.0452	0.2664
chr7	159138663	7361712	0.0463	0.4482

chr8	146364022	10652070	0.0728	0.4366
chr9	141213431	4328541	0.0307	0.2725
chr10	135534747	5283298	0.039	0.4041
chr11	135006516	7447244	0.0552	0.3233
chr12	133851895	4001208	0.0299	0.2016
chr13	115169878	3039744	0.0264	0.1847
chr14	107349540	2202014	0.0205	0.175
chr15	102531392	3059992	0.0298	0.1971
chr16	90354753	3726827	0.0412	0.2514
chr17	81195210	2706896	0.0333	0.2155
chr18	78077248	3235976	0.0414	0.4744
chr19	59128983	2480578	0.042	0.4862
chr20	63025520	2256006	0.0358	0.225
chr21	48129895	1076129	0.0224	0.21
chr22	51304566	2148168	0.0419	0.236
chrMT	16571	38288	2.3105	2.0693
chrX	155270560	5413295	0.0349	0.2395
chrY	59373566	341415	0.0058	0.2013

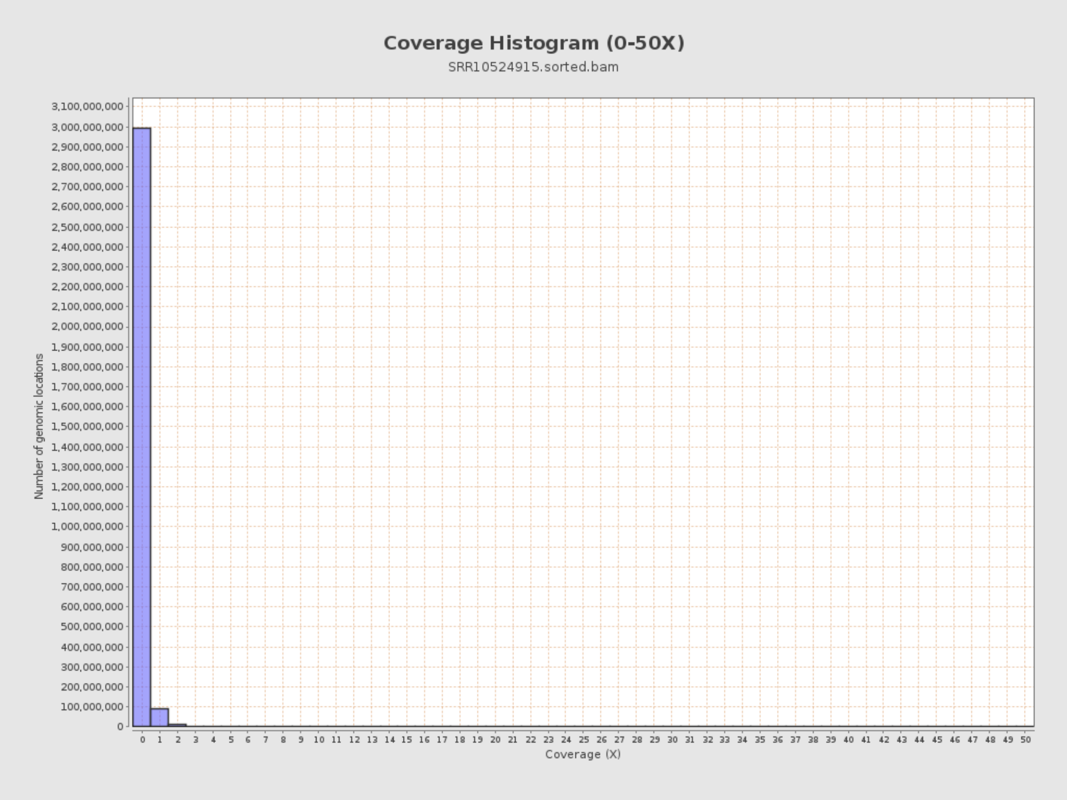
3. Results : Coverage across reference



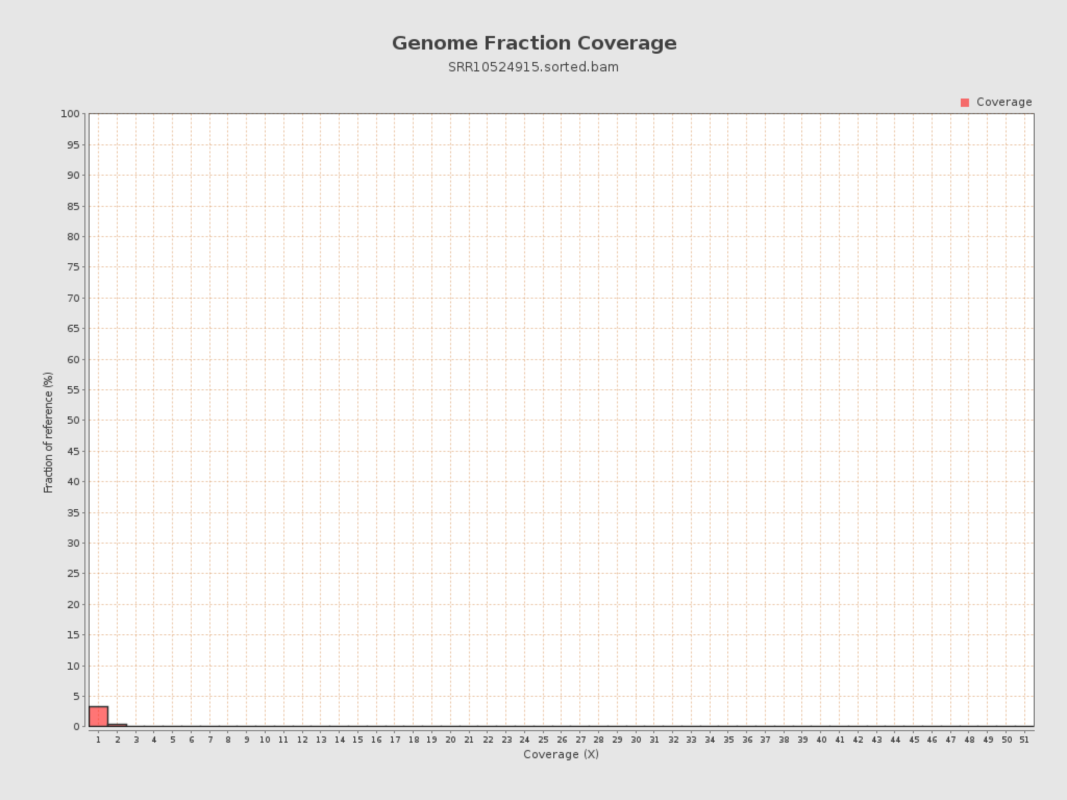
4. Results : Coverage Histogram



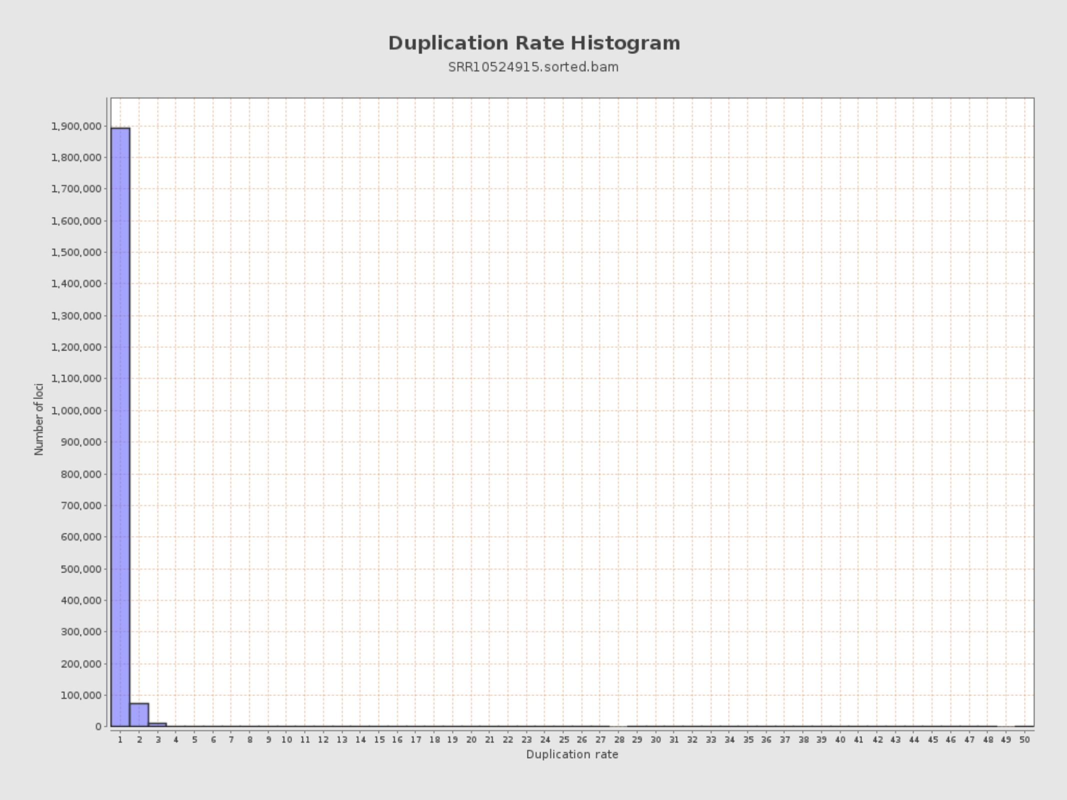
5. Results : Coverage Histogram (0-50X)



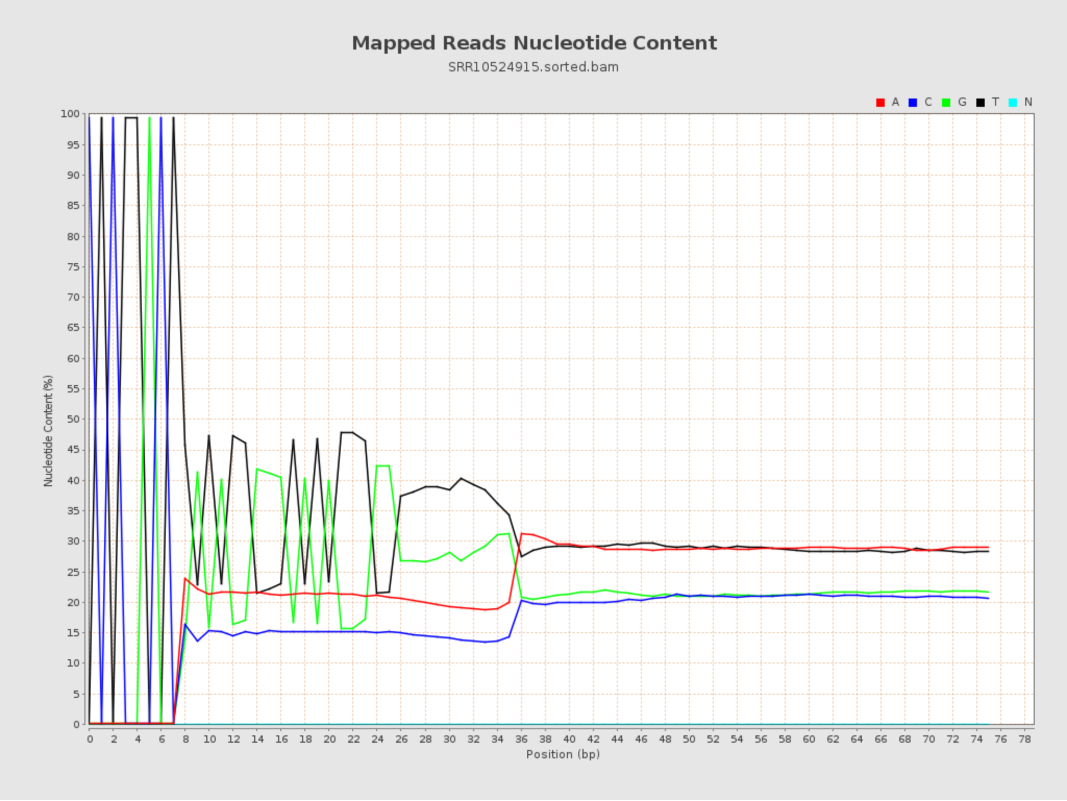
6. Results : Genome Fraction Coverage



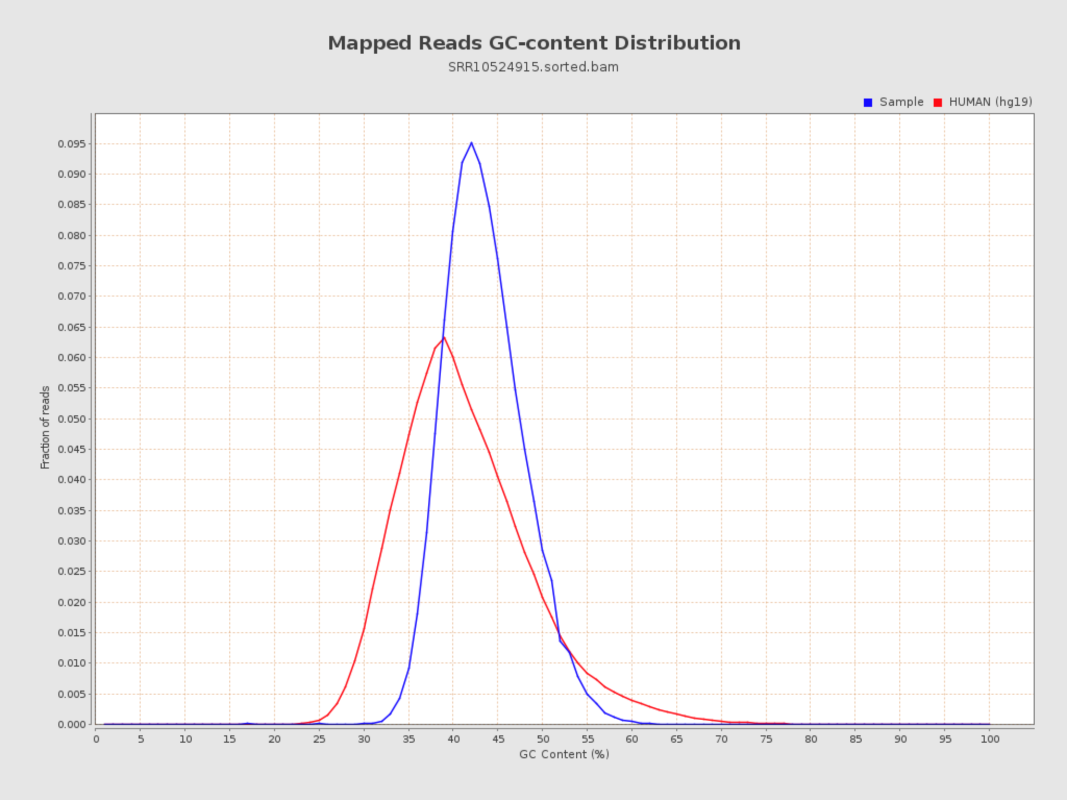
7. Results : Duplication Rate Histogram



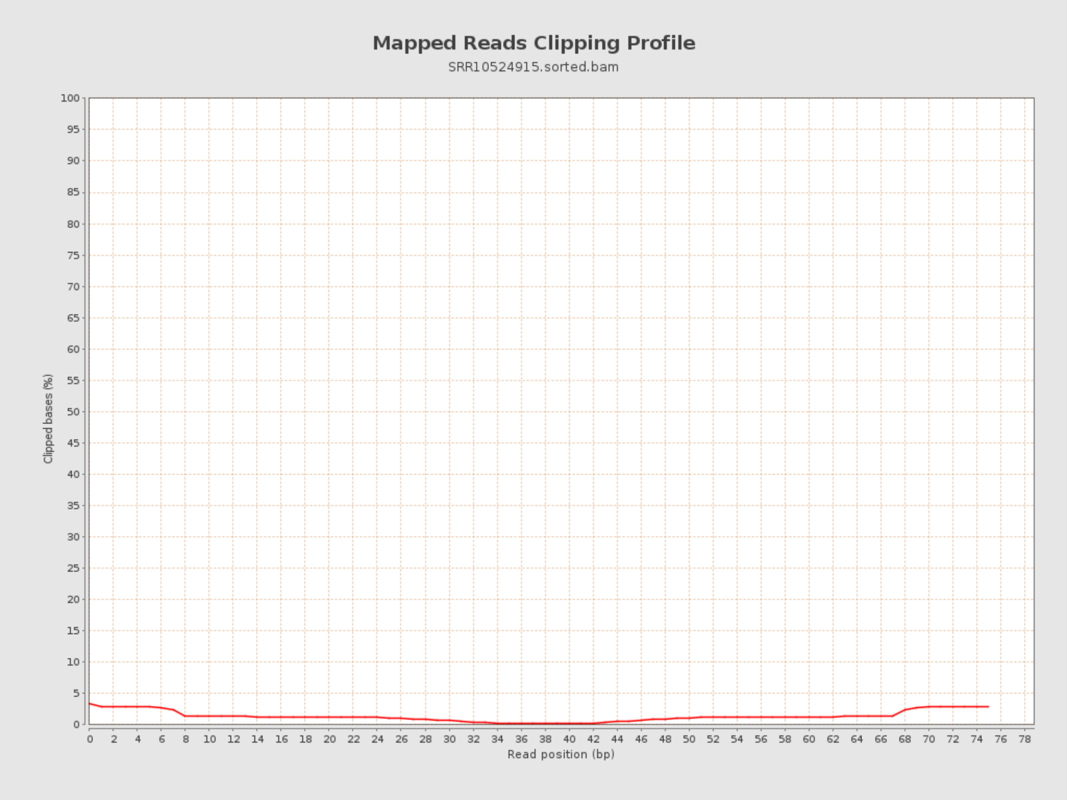
8. Results : Mapped Reads Nucleotide Content



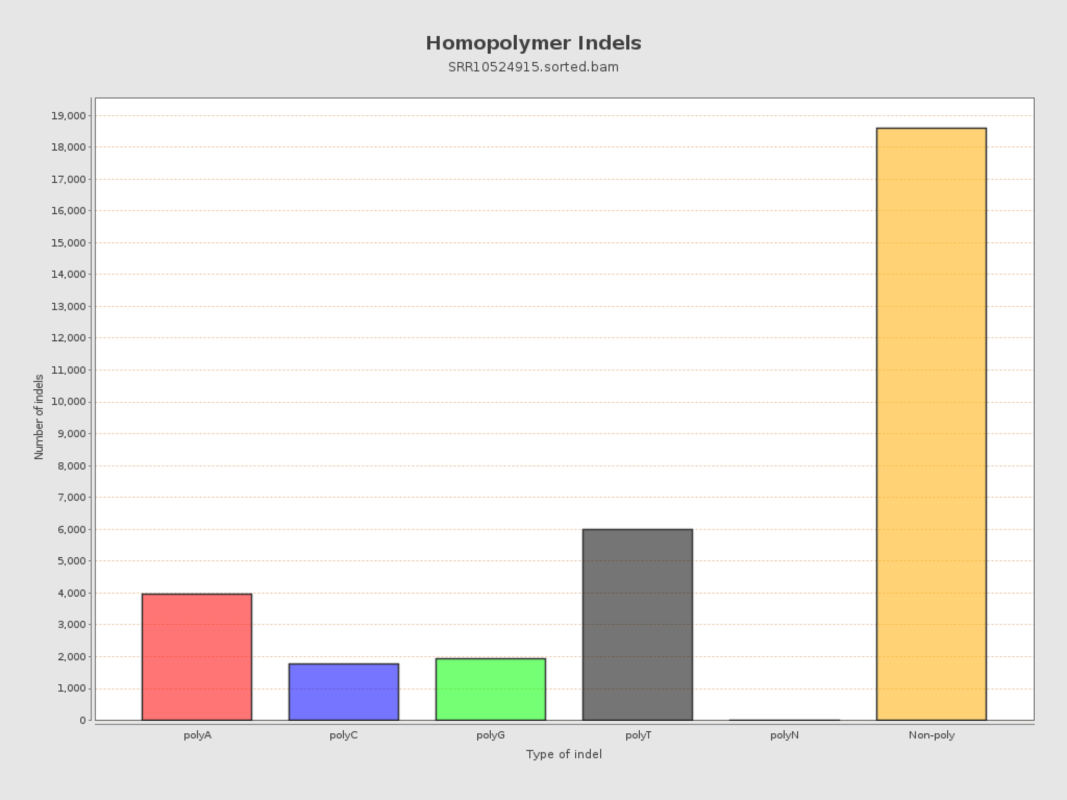
9. Results : Mapped Reads GC-content Distribution



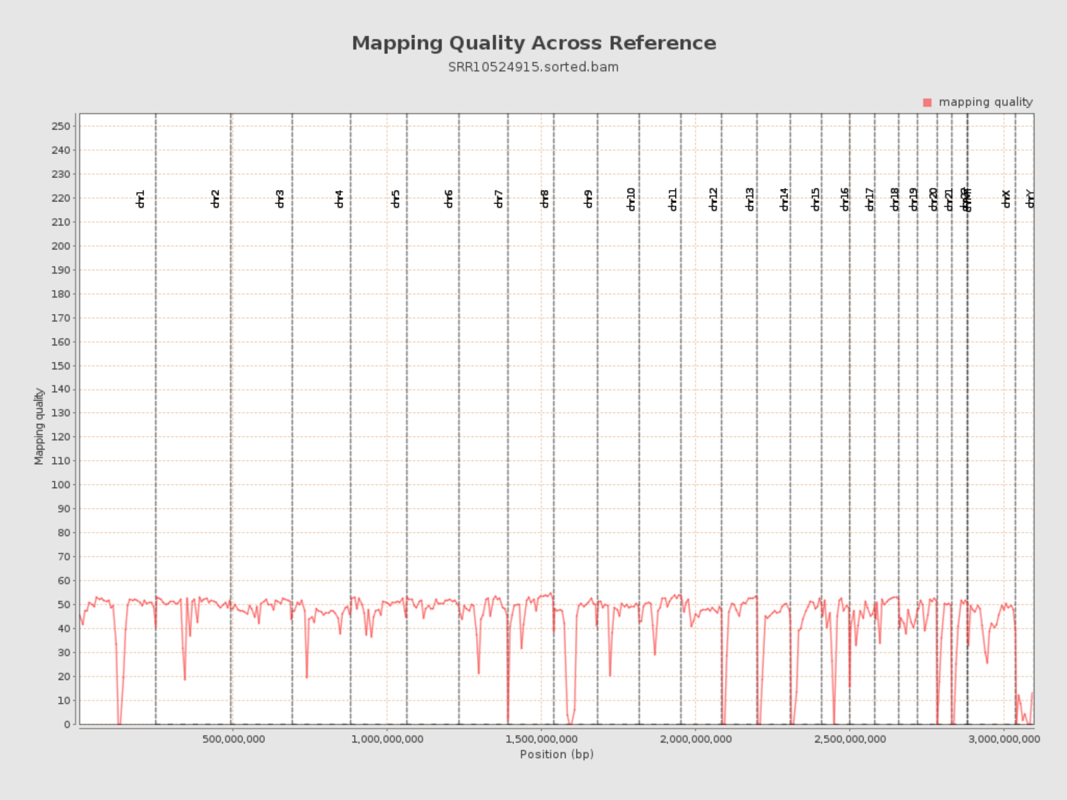
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram