Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:52:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524615.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_SRR10524615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:52:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,904,116
Mapped reads	1,778,382 / 93.4%
Unmapped reads	125,734 / 6.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,320 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	86,370 / 4.54%
Duplication rate	3.77%
Clipped reads	1,777,812 / 93.37%

2.2. ACGT Content

Number/percentage of A's	25,769,868 / 24.8%
Number/percentage of C's	19,281,622 / 18.56%
Number/percentage of T's	33,449,647 / 32.19%
Number/percentage of G's	25,396,637 / 24.44%
Number/percentage of N's	732 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.2916

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

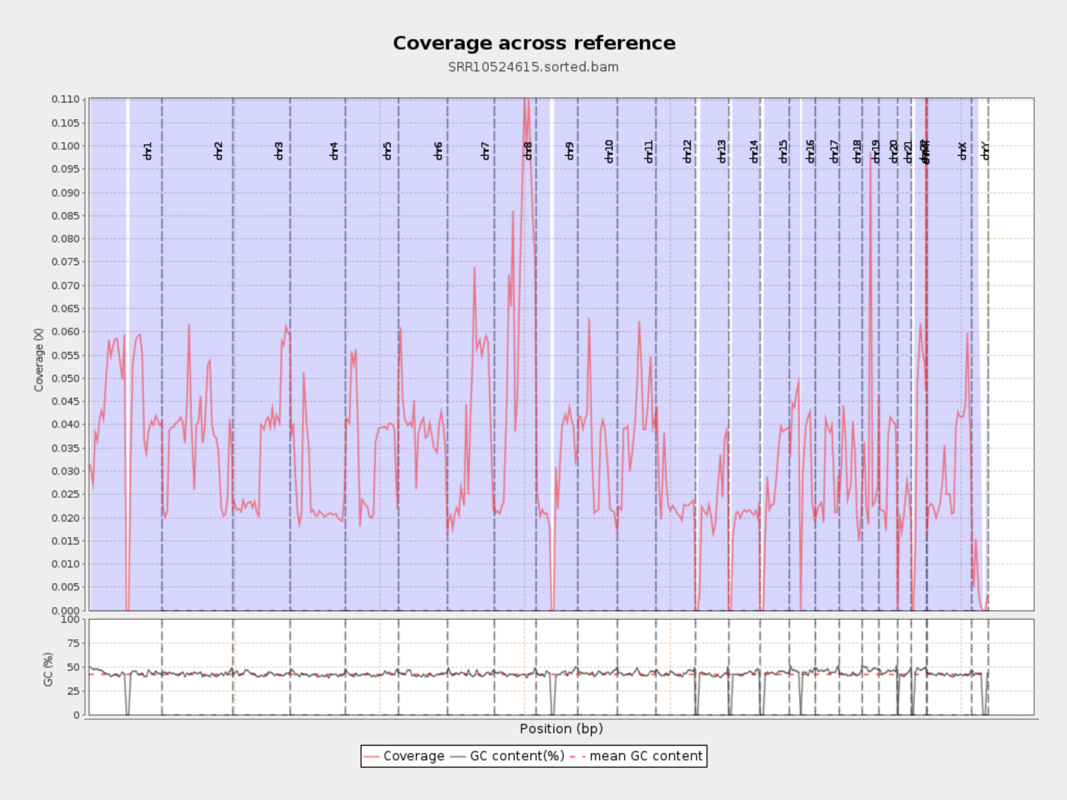
General error rate	0.48%
Mismatches	489,144
Insertions	6,474
Mapped reads with at least one insertion	0.36%
Deletions	19,906
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.43%

2.6. Chromosome stats

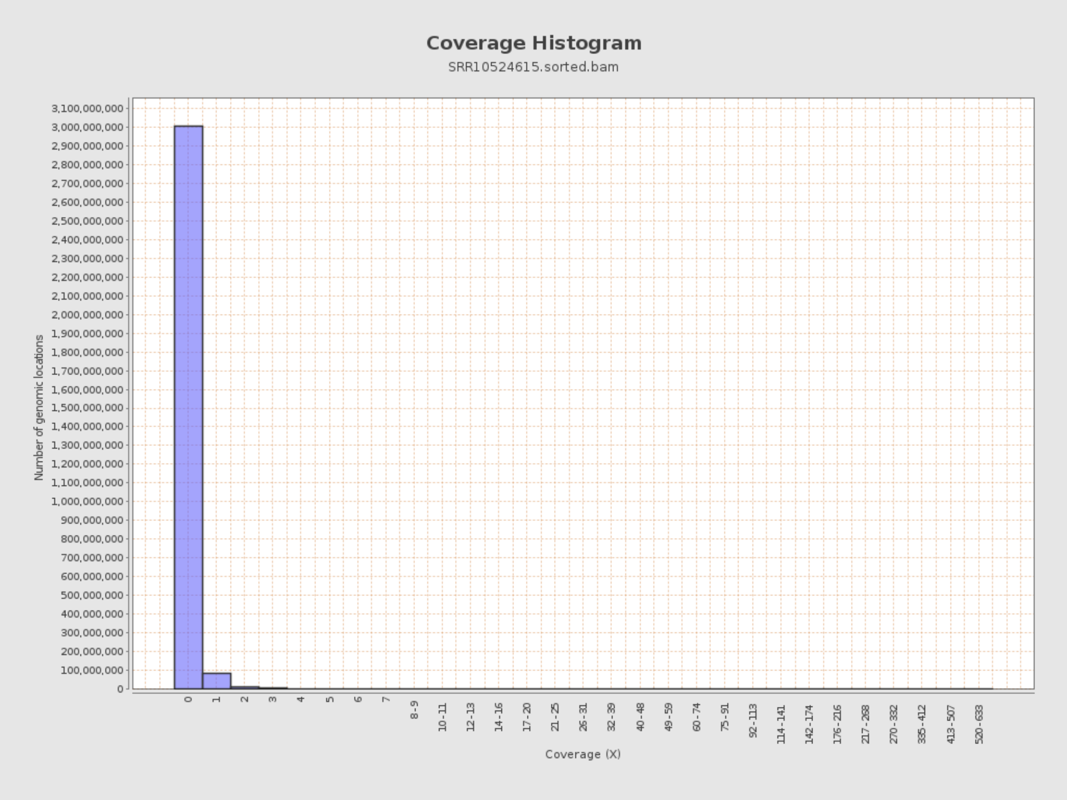
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10817051	0.0434	0.5265
chr2	243199373	8972158	0.0369	0.3301
chr3	198022430	6897436	0.0348	0.2105
chr4	191154276	4777696	0.025	0.2058
chr5	180915260	6370679	0.0352	0.2118
chr6	171115067	6826596	0.0399	0.2401
chr7	159138663	6256421	0.0393	0.3442

chr8	146364022	9222766	0.063	0.3954
chr9	141213431	3842141	0.0272	0.2604
chr10	135534747	4530106	0.0334	0.2972
chr11	135006516	5386227	0.0399	0.2918
chr12	133851895	3278673	0.0245	0.18
chr13	115169878	2430189	0.0211	0.1634
chr14	107349540	1934532	0.018	0.1549
chr15	102531392	2677999	0.0261	0.1954
chr16	90354753	3120930	0.0345	0.2214
chr17	81195210	2326696	0.0287	0.1996
chr18	78077248	2295450	0.0294	0.4103
chr19	59128983	2092839	0.0354	0.3606
chr20	63025520	1929216	0.0306	0.2008
chr21	48129895	953045	0.0198	0.1766
chr22	51304566	1893194	0.0369	0.2162
chrMT	16571	10850	0.6548	0.9874
chrX	155270560	4834756	0.0311	0.2263
chrY	59373566	254749	0.0043	0.1222

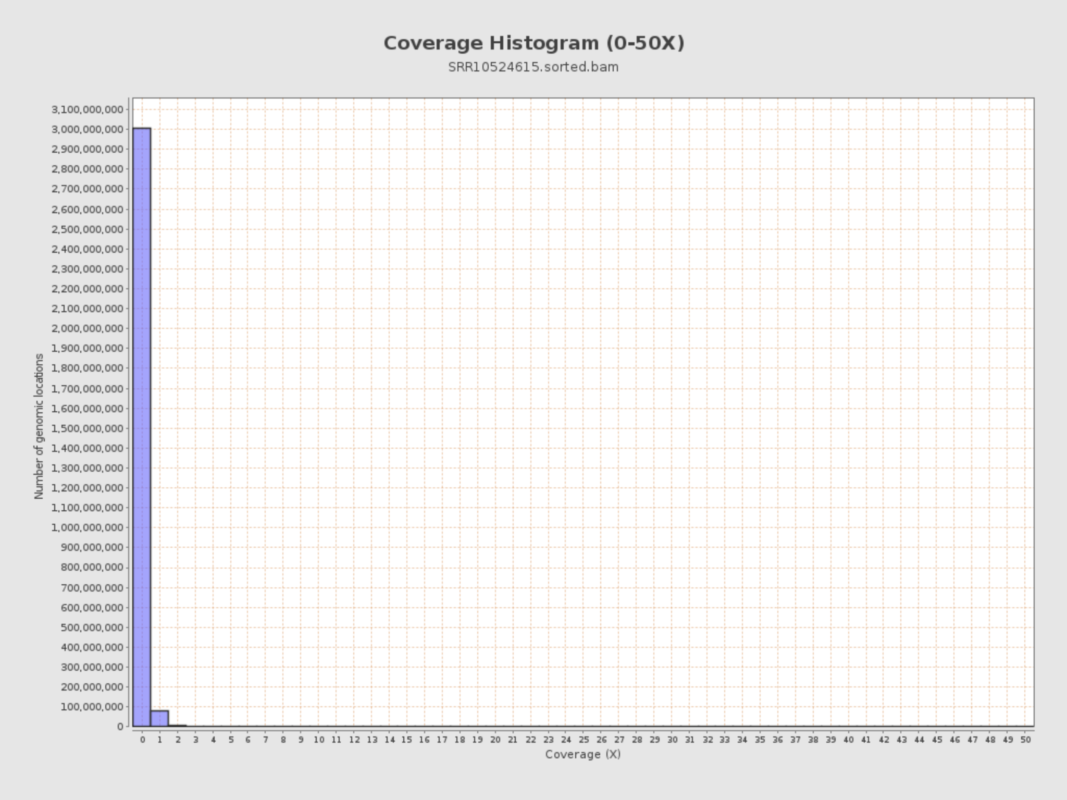
3. Results : Coverage across reference



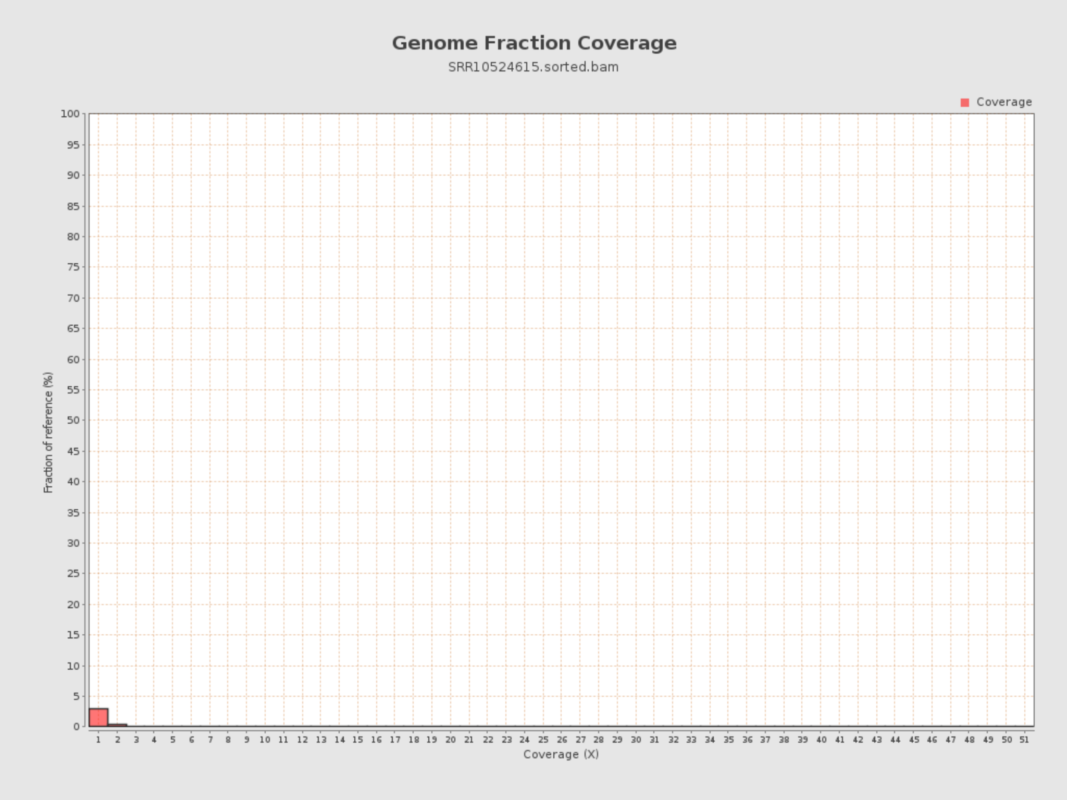
4. Results : Coverage Histogram



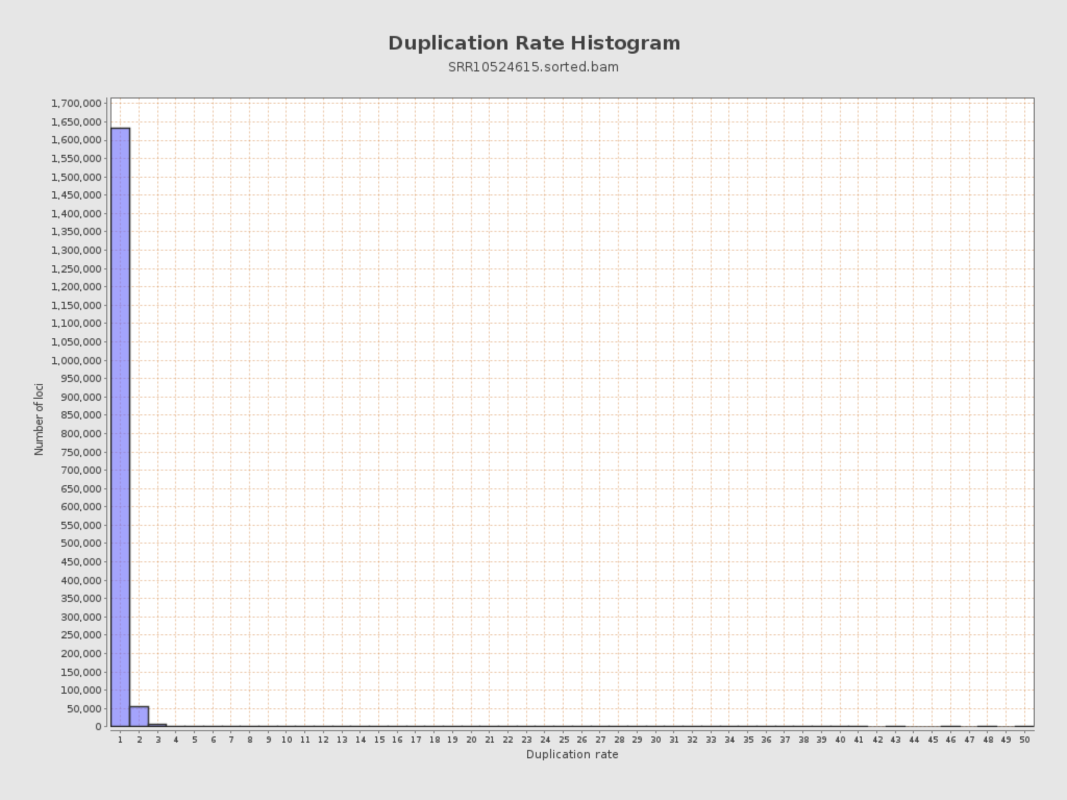
5. Results : Coverage Histogram (0-50X)



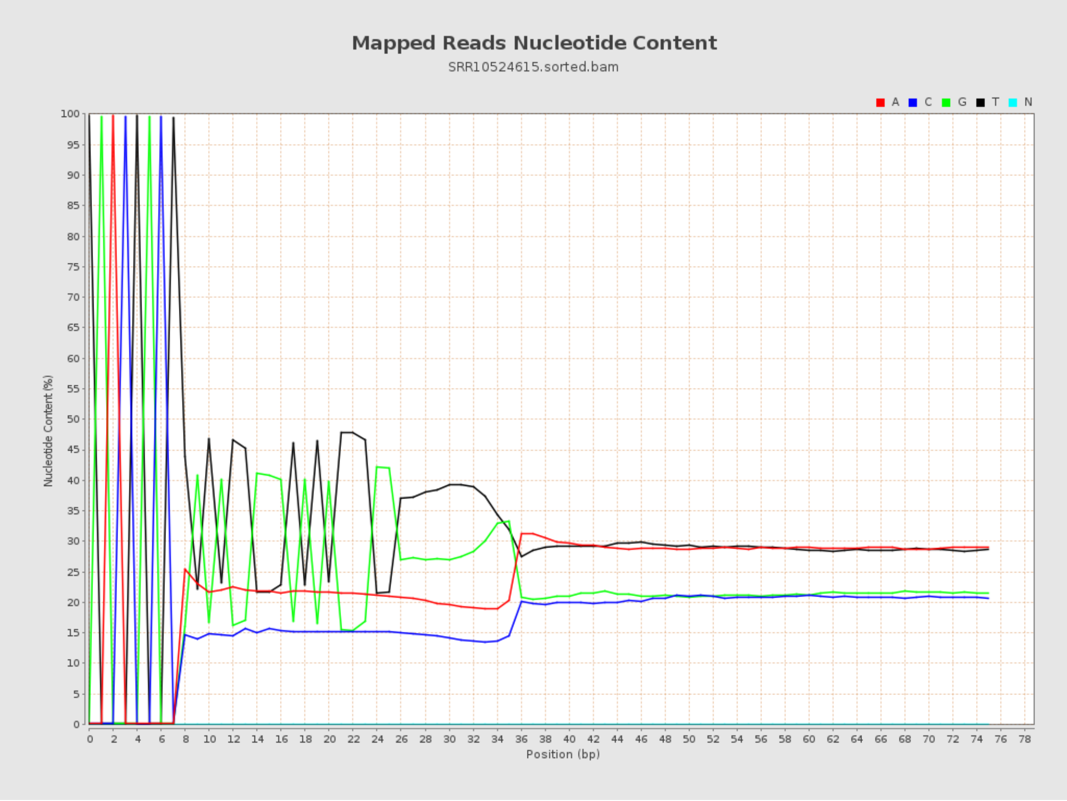
6. Results : Genome Fraction Coverage



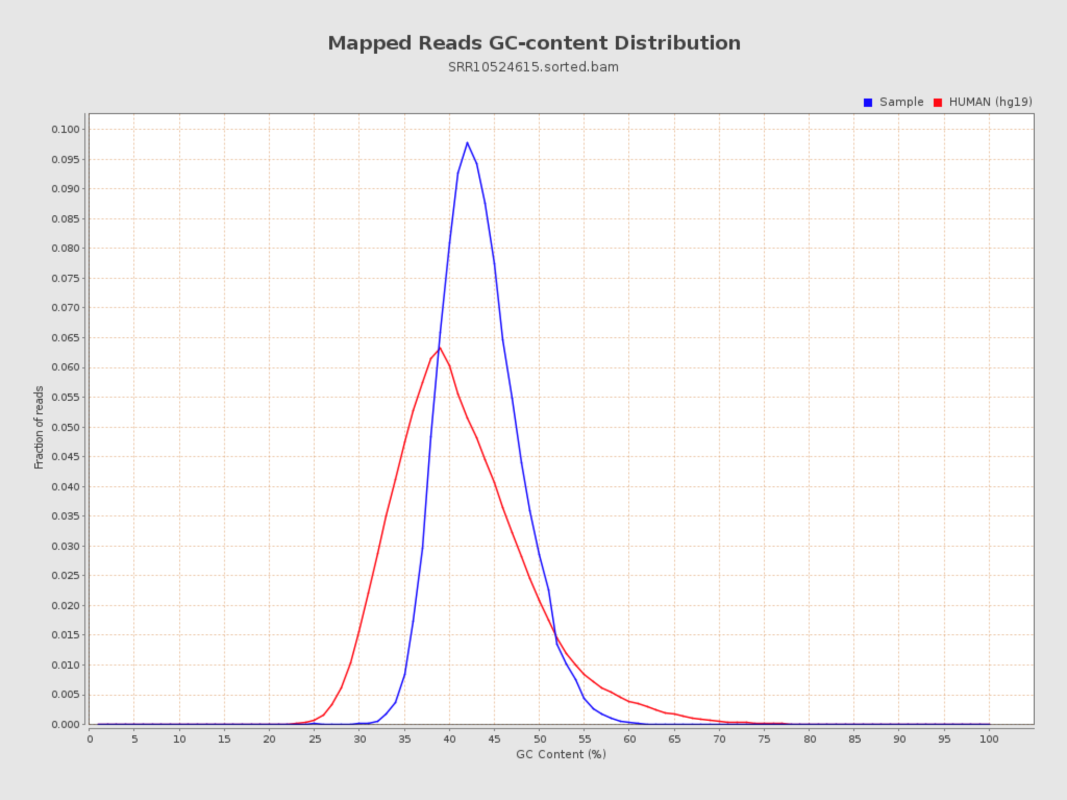
7. Results : Duplication Rate Histogram



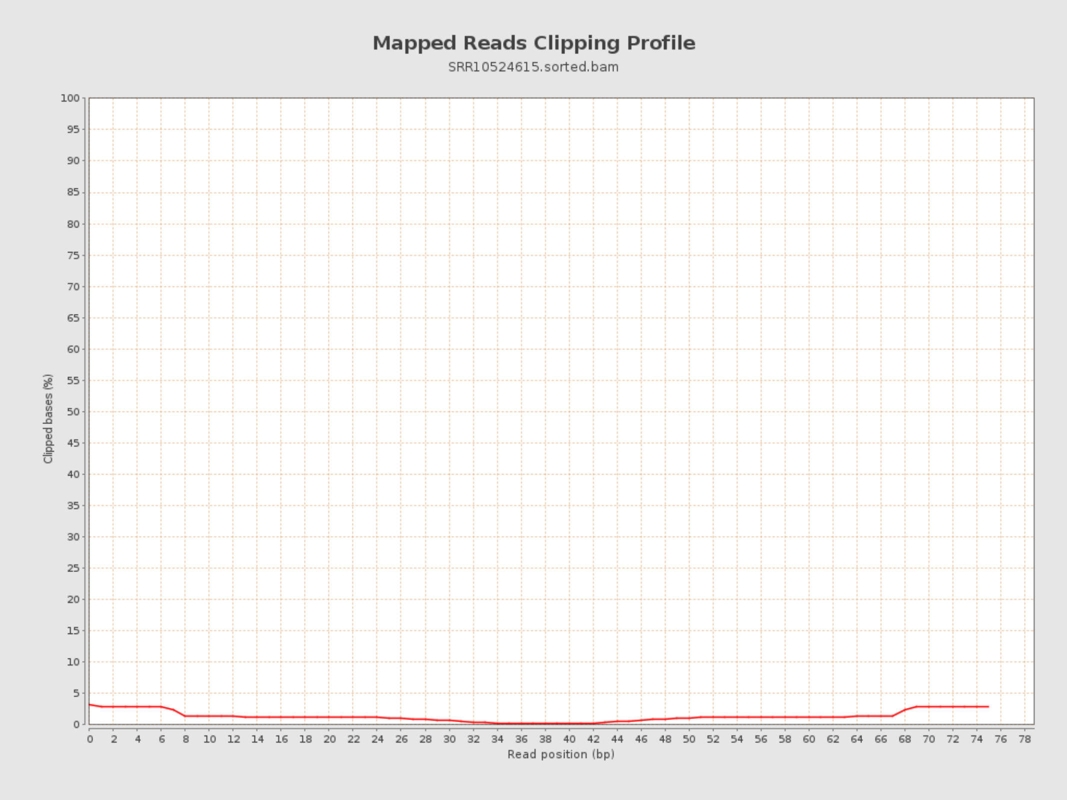
8. Results : Mapped Reads Nucleotide Content



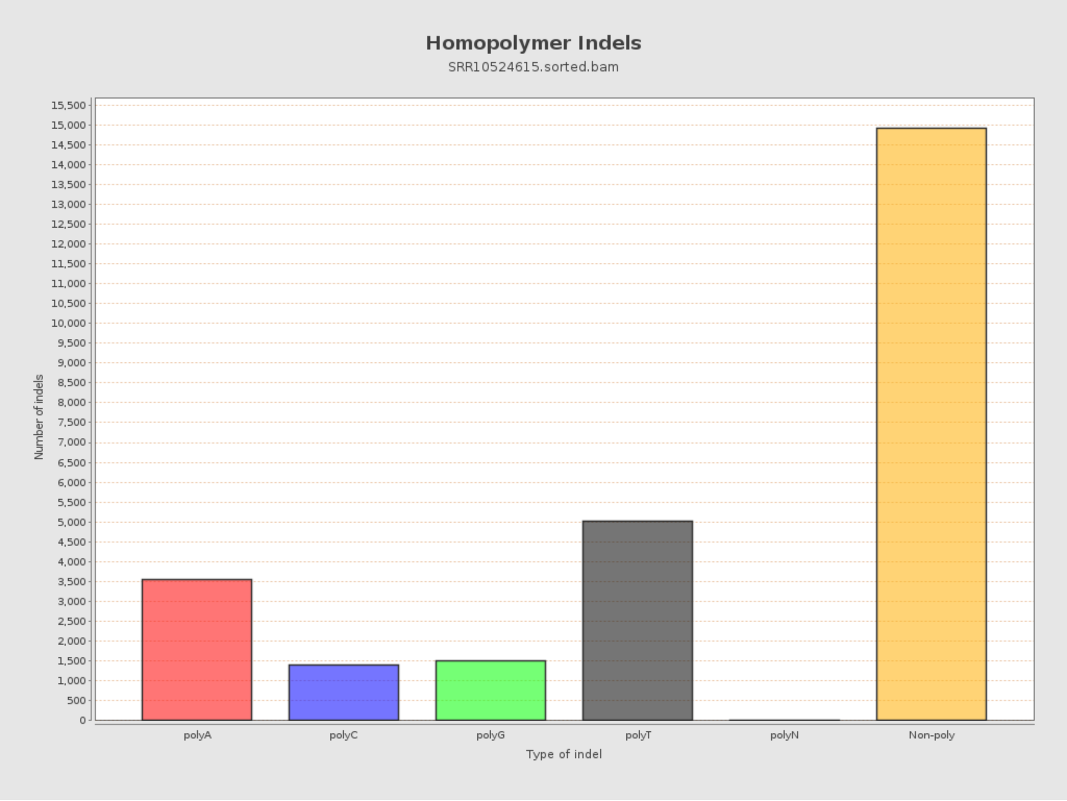
9. Results : Mapped Reads GC-content Distribution



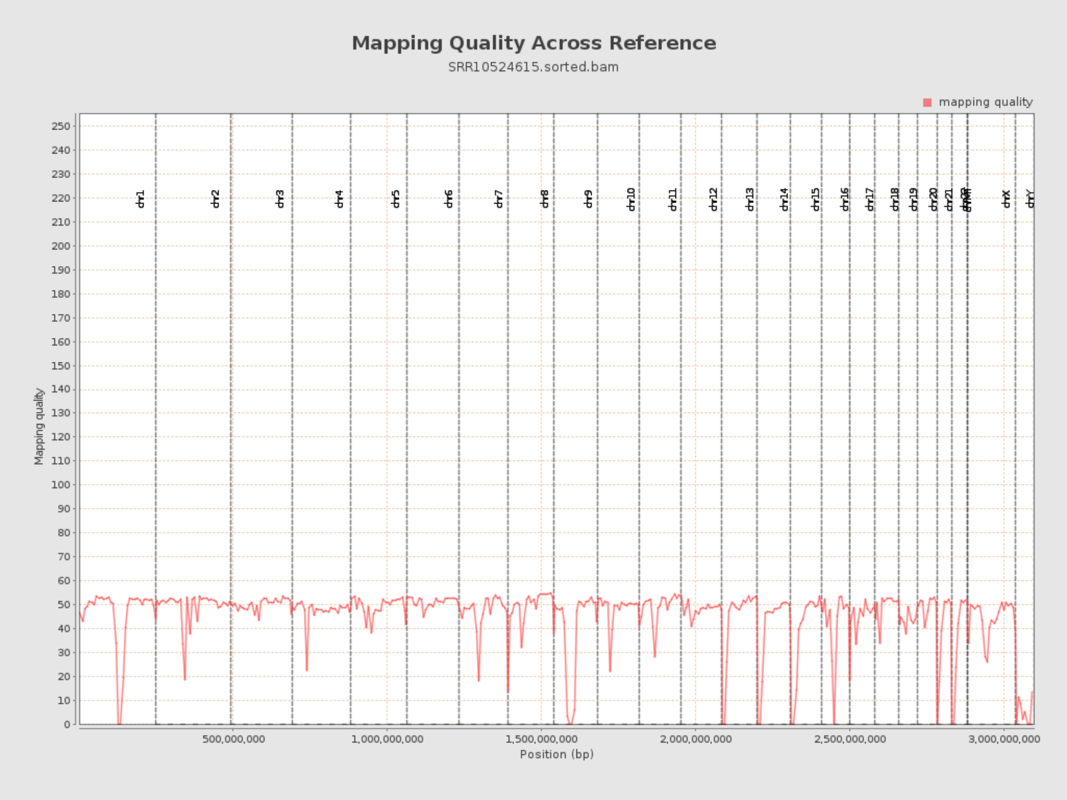
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram