Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:13:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524436.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_SRR10524436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524436.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	616,912
Mapped reads	569,082 / 92.25%
Unmapped reads	47,830 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,812 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,831 / 2.4%
Duplication rate	2.01%
Clipped reads	570,428 / 92.47%

2.2. ACGT Content

Number/percentage of A's	8,235,624 / 24.83%
Number/percentage of C's	6,401,809 / 19.3%
Number/percentage of T's	10,503,704 / 31.67%
Number/percentage of G's	8,025,963 / 24.2%
Number/percentage of N's	3,278 / 0.01%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1366

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

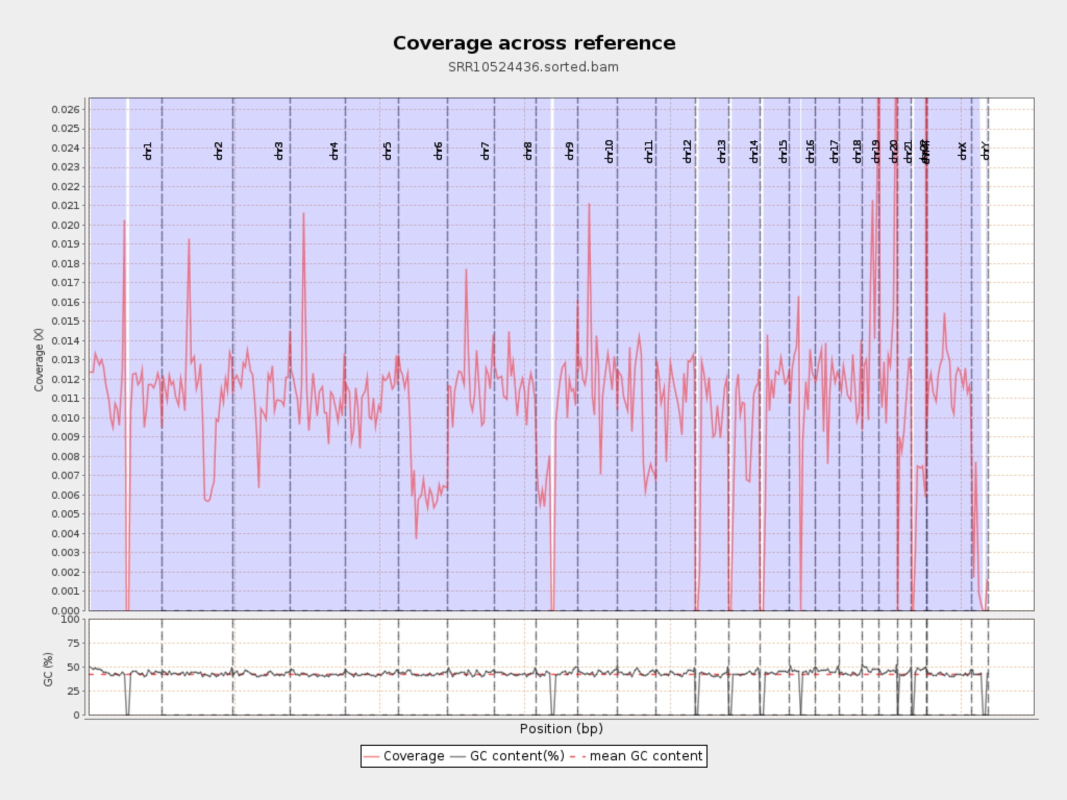
General error rate	0.51%
Mismatches	165,116
Insertions	2,408
Mapped reads with at least one insertion	0.42%
Deletions	5,365
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.6%

2.6. Chromosome stats

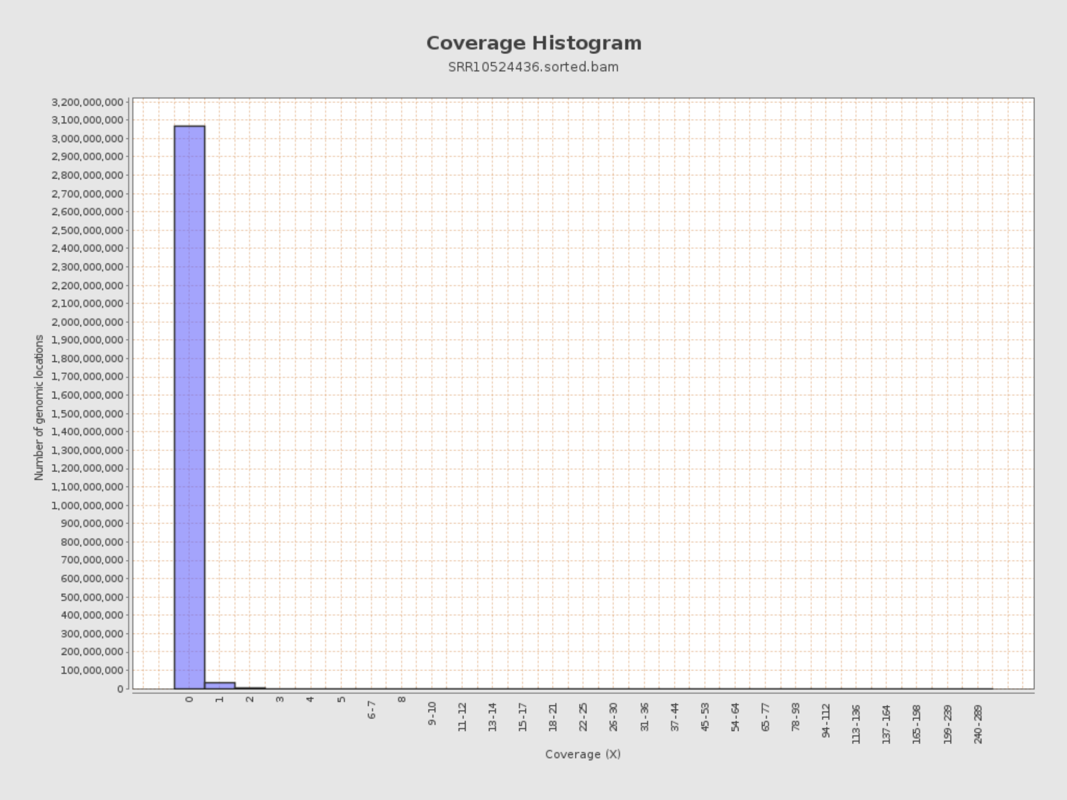
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2778816	0.0111	0.239
chr2	243199373	2688241	0.0111	0.1651
chr3	198022430	2248295	0.0114	0.1117
chr4	191154276	2164558	0.0113	0.1222
chr5	180915260	1990188	0.011	0.11
chr6	171115067	1283743	0.0075	0.0929
chr7	159138663	1902016	0.012	0.1534

chr8	146364022	1721018	0.0118	0.1239
chr9	141213431	1199663	0.0085	0.105
chr10	135534747	1689541	0.0125	0.143
chr11	135006516	1396121	0.0103	0.1174
chr12	133851895	1537920	0.0115	0.1134
chr13	115169878	1048391	0.0091	0.0997
chr14	107349540	921014	0.0086	0.098
chr15	102531392	1018325	0.0099	0.1045
chr16	90354753	1024624	0.0113	0.114
chr17	81195210	957155	0.0118	0.1174
chr18	78077248	910015	0.0117	0.1569
chr19	59128983	990246	0.0167	0.1798
chr20	63025520	978801	0.0155	0.1345
chr21	48129895	454866	0.0095	0.1097
chr22	51304566	257168	0.005	0.0751
chrMT	16571	21792	1.3151	1.4119
chrX	155270560	1876025	0.0121	0.1185
chrY	59373566	120880	0.002	0.0761

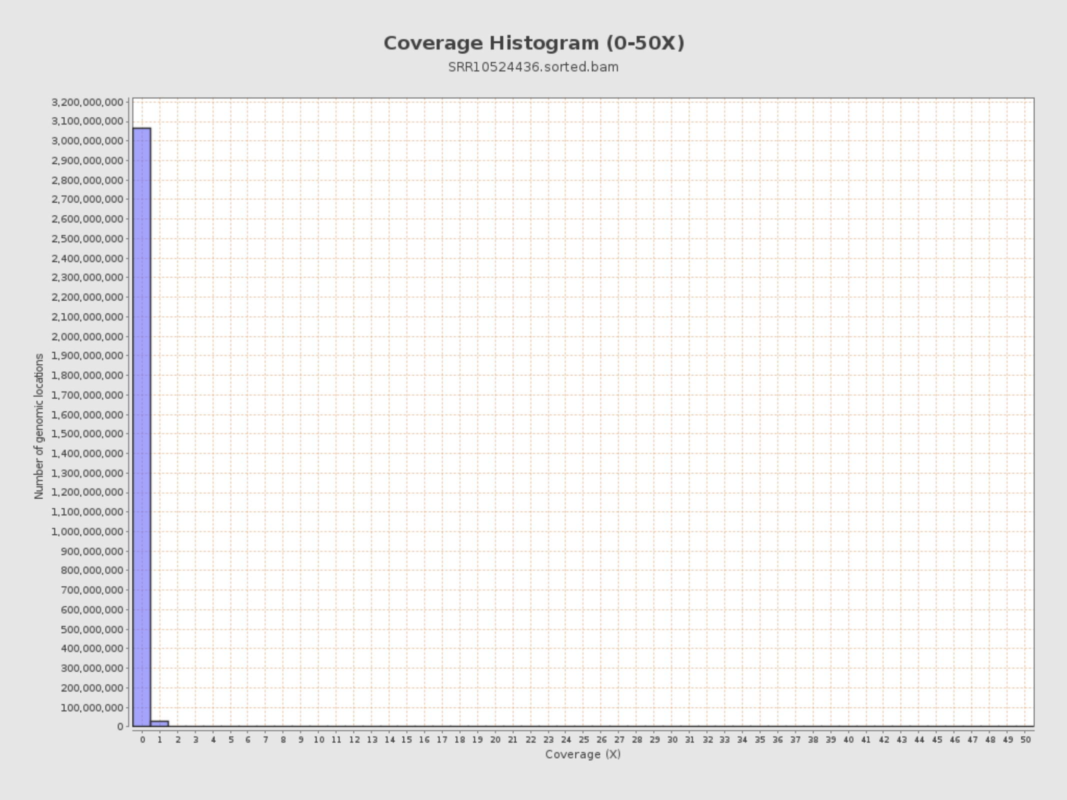
3. Results : Coverage across reference



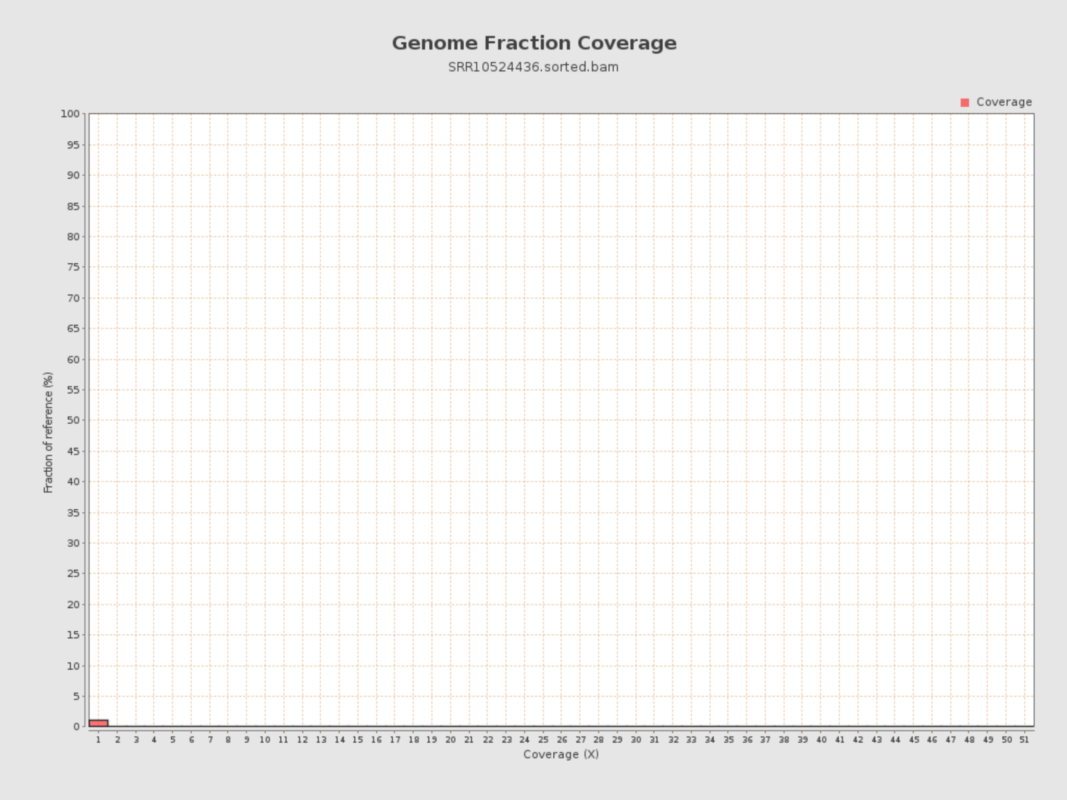
4. Results : Coverage Histogram



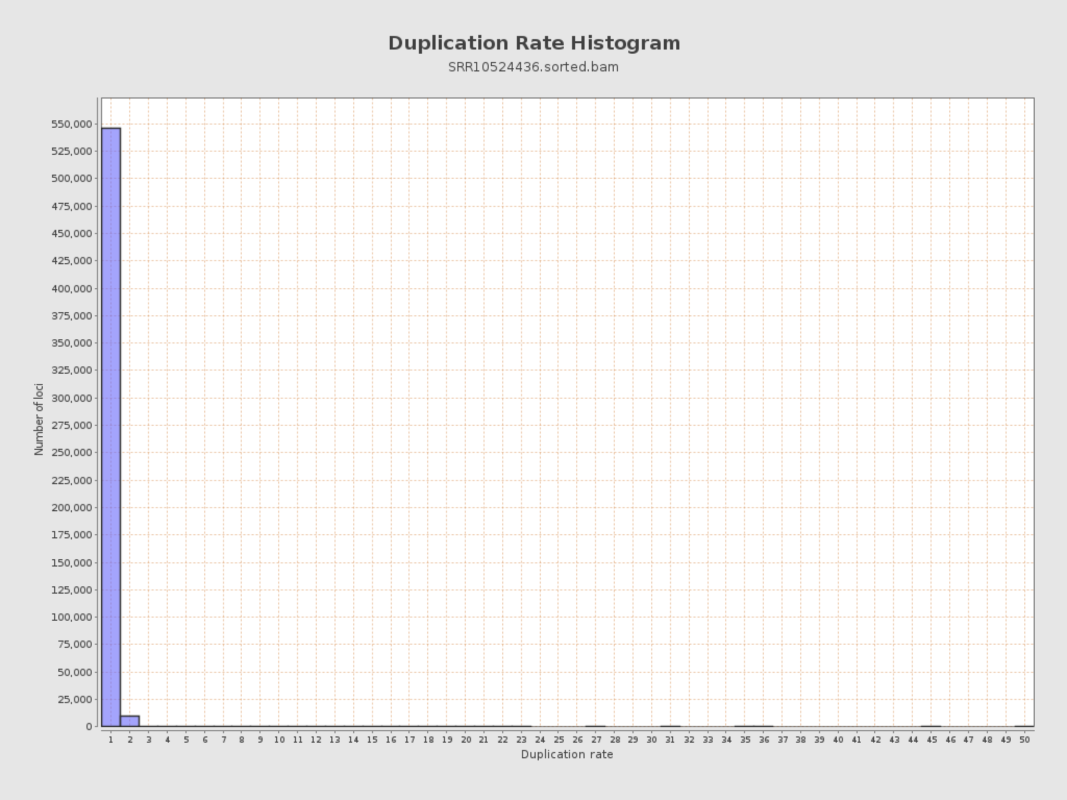
5. Results : Coverage Histogram (0-50X)



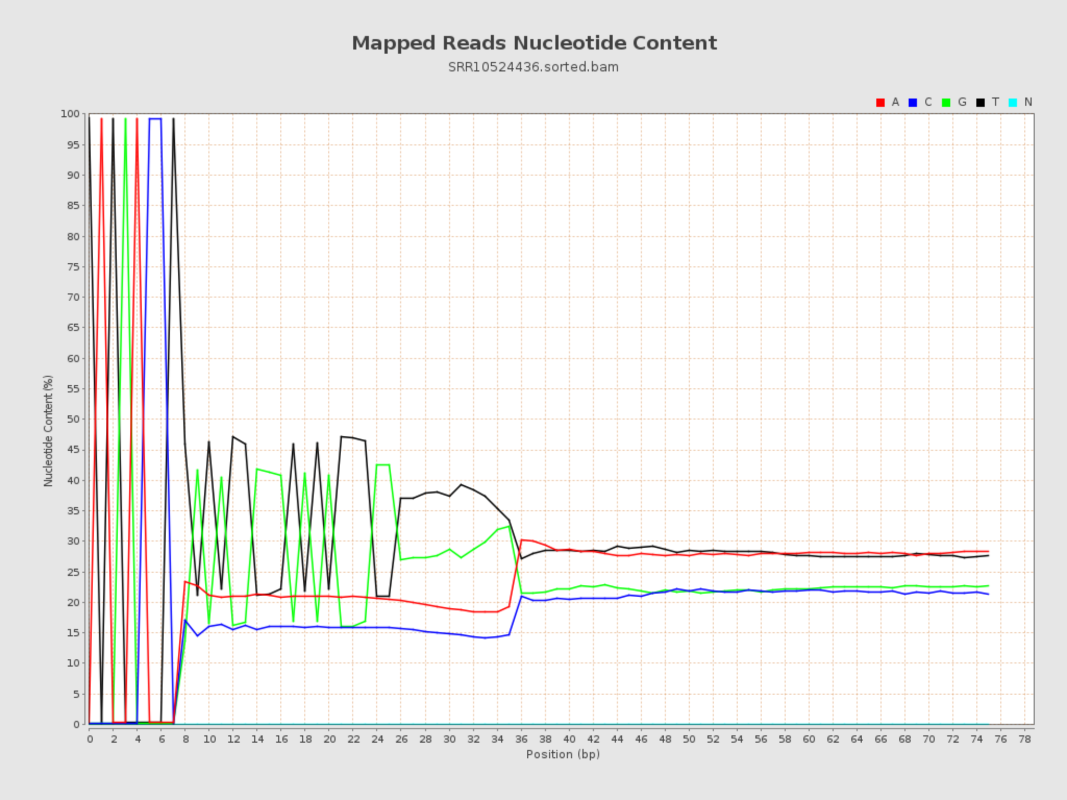
6. Results : Genome Fraction Coverage



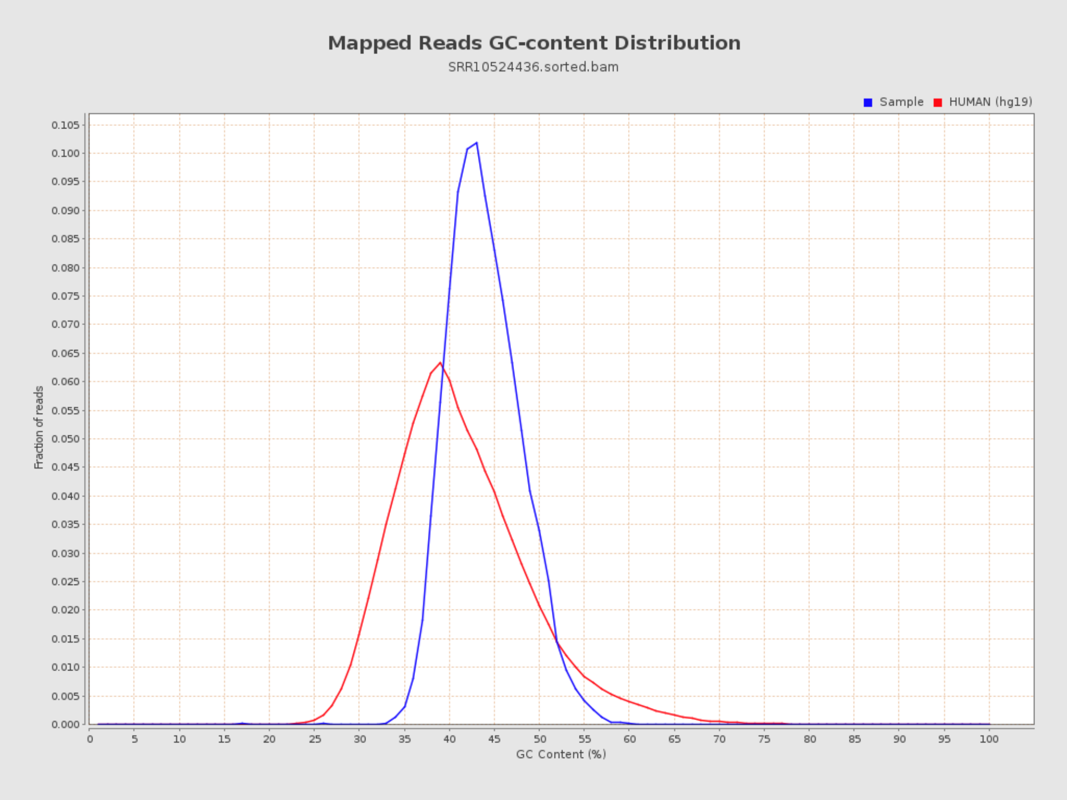
7. Results : Duplication Rate Histogram



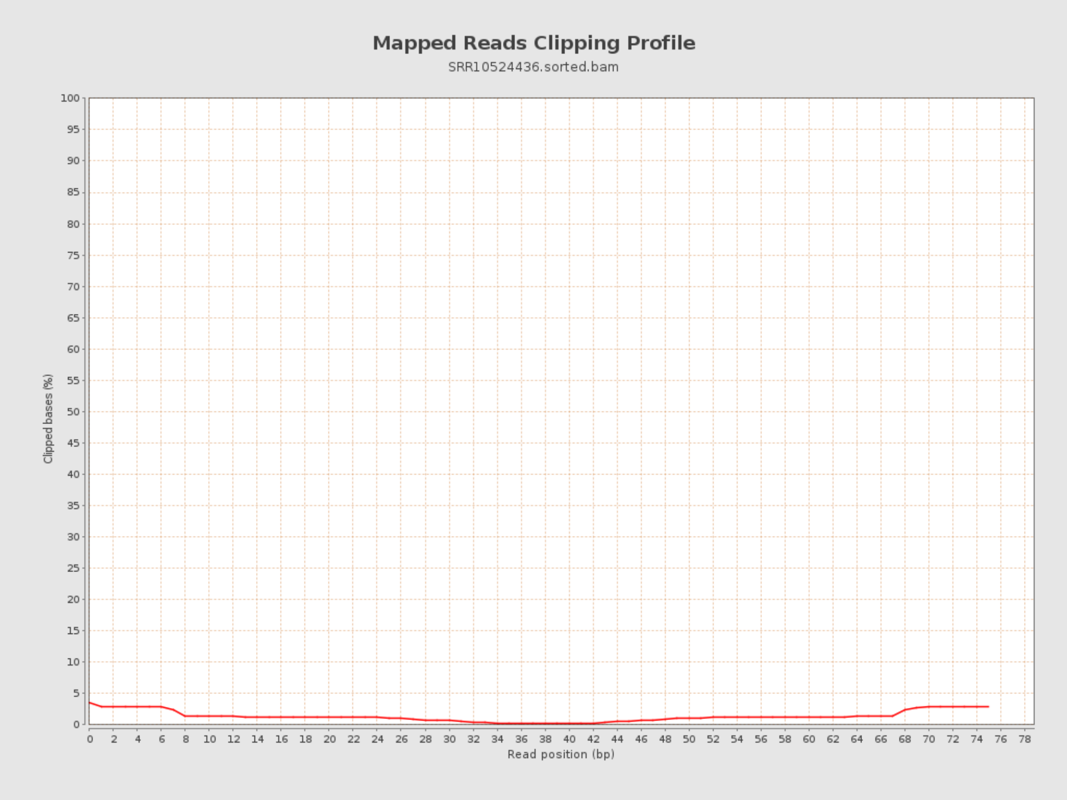
8. Results : Mapped Reads Nucleotide Content



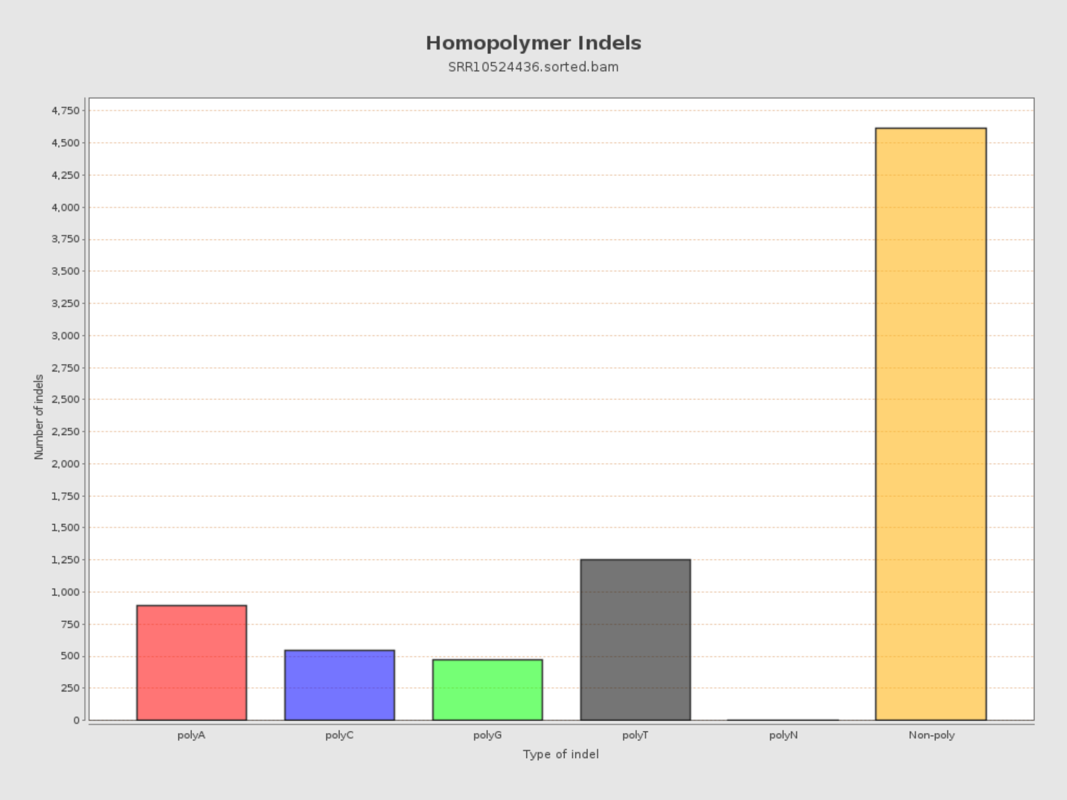
9. Results : Mapped Reads GC-content Distribution



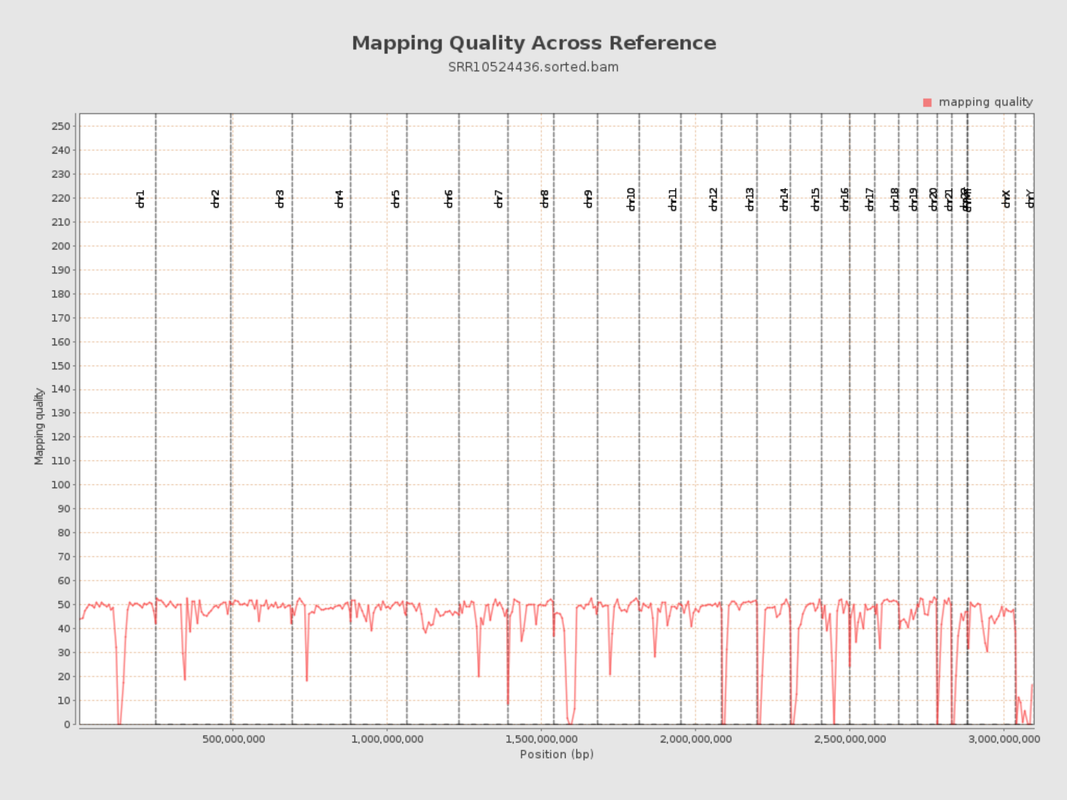
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram