Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:50:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524480.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_SRR10524480 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524480.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:50:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524480.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,297,172
Mapped reads	1,183,486 / 91.24%
Unmapped reads	113,686 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,642 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	47,773 / 3.68%
Duplication rate	3.14%
Clipped reads	1,182,952 / 91.19%

2.2. ACGT Content

Number/percentage of A's	17,212,906 / 25.25%
Number/percentage of C's	12,455,421 / 18.27%
Number/percentage of T's	22,085,313 / 32.4%
Number/percentage of G's	16,419,517 / 24.08%
Number/percentage of N's	1,419 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.022

Standard Deviation	0.2195

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

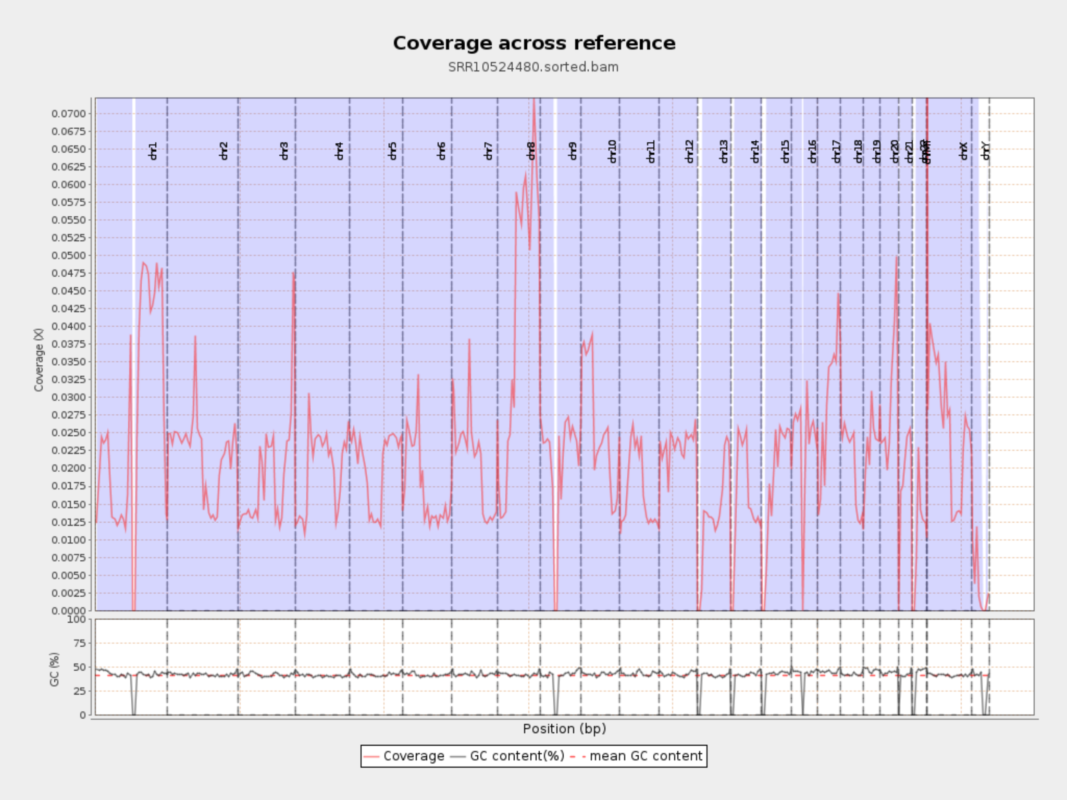
General error rate	0.49%
Mismatches	324,676
Insertions	4,806
Mapped reads with at least one insertion	0.4%
Deletions	12,526
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.76%

2.6. Chromosome stats

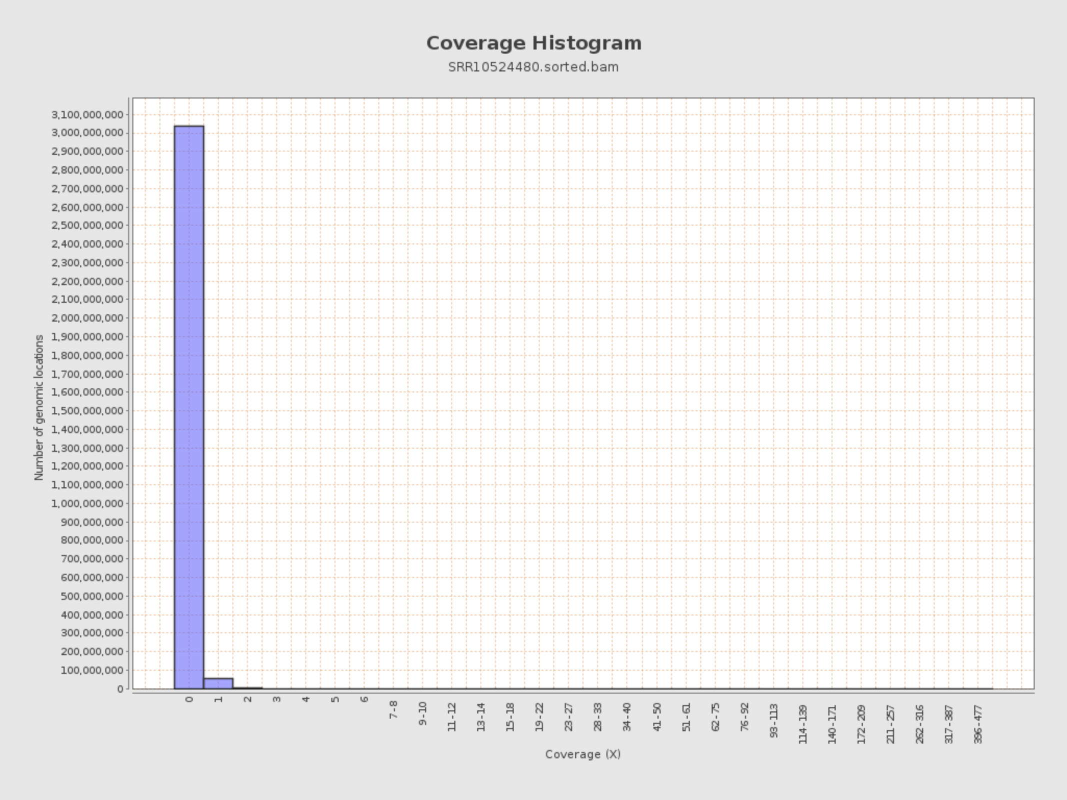
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6671818	0.0268	0.3765
chr2	243199373	5380017	0.0221	0.2504
chr3	198022430	3755162	0.019	0.1512
chr4	191154276	3832140	0.02	0.171
chr5	180915260	3711150	0.0205	0.1568
chr6	171115067	2993566	0.0175	0.1777
chr7	159138663	3388690	0.0213	0.2775

chr8	146364022	6253474	0.0427	0.2525
chr9	141213431	2947313	0.0209	0.1975
chr10	135534747	3574549	0.0264	0.2197
chr11	135006516	2308624	0.0171	0.2168
chr12	133851895	3123417	0.0233	0.1672
chr13	115169878	1549556	0.0135	0.1287
chr14	107349540	1658564	0.0155	0.1381
chr15	102531392	1840143	0.0179	0.1545
chr16	90354753	2110633	0.0234	0.176
chr17	81195210	2379852	0.0293	0.1927
chr18	78077248	1611328	0.0206	0.307
chr19	59128983	1401219	0.0237	0.276
chr20	63025520	1908955	0.0303	0.1934
chr21	48129895	931416	0.0194	0.1592
chr22	51304566	559422	0.0109	0.1133
chrMT	16571	4727	0.2853	0.5541
chrX	155270560	4090361	0.0263	0.1926
chrY	59373566	209881	0.0035	0.1004

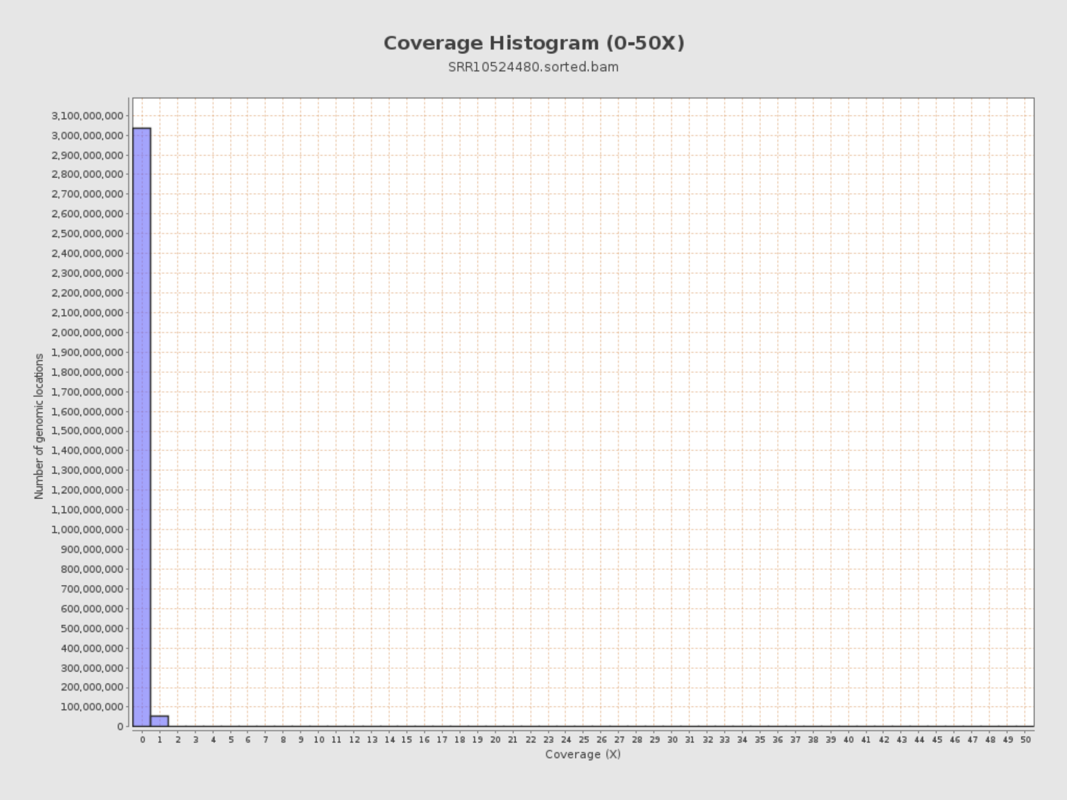
3. Results : Coverage across reference



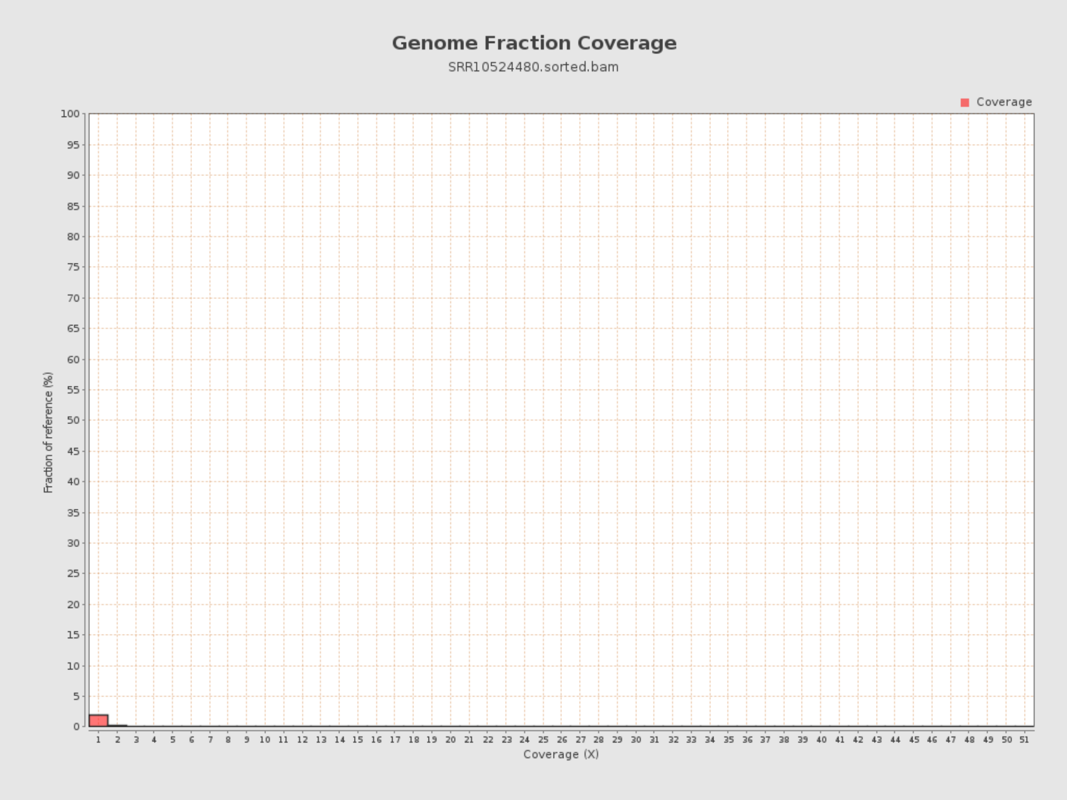
4. Results : Coverage Histogram



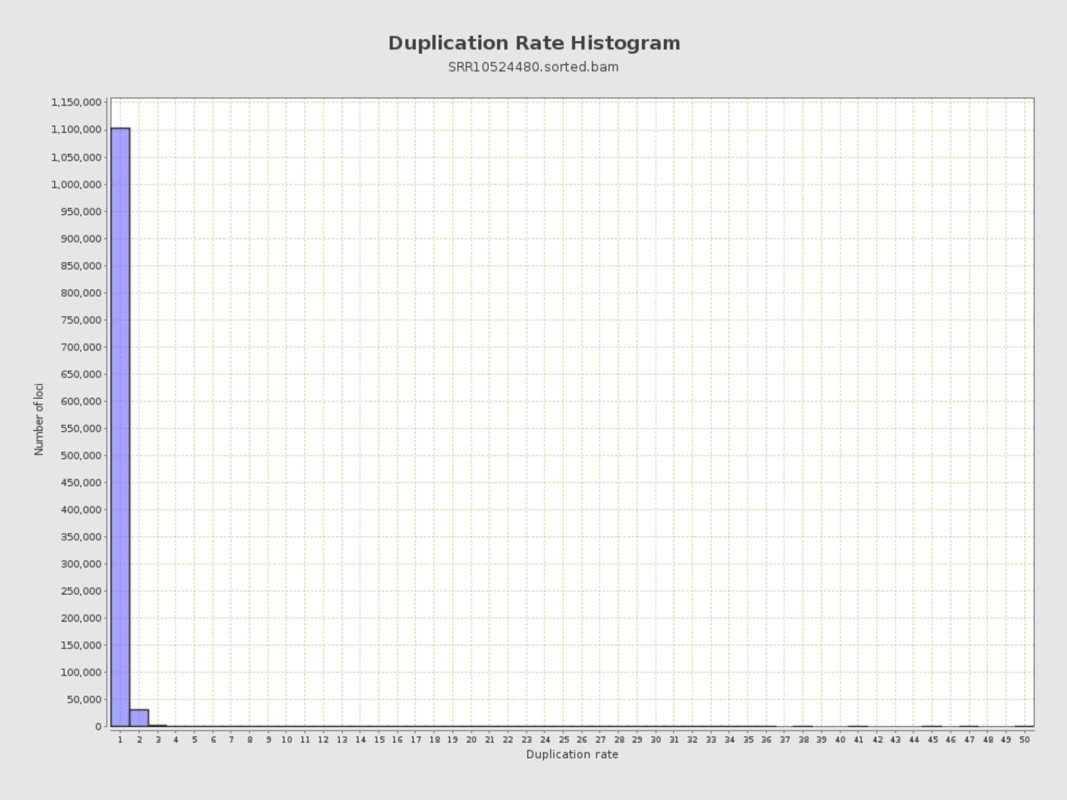
5. Results : Coverage Histogram (0-50X)



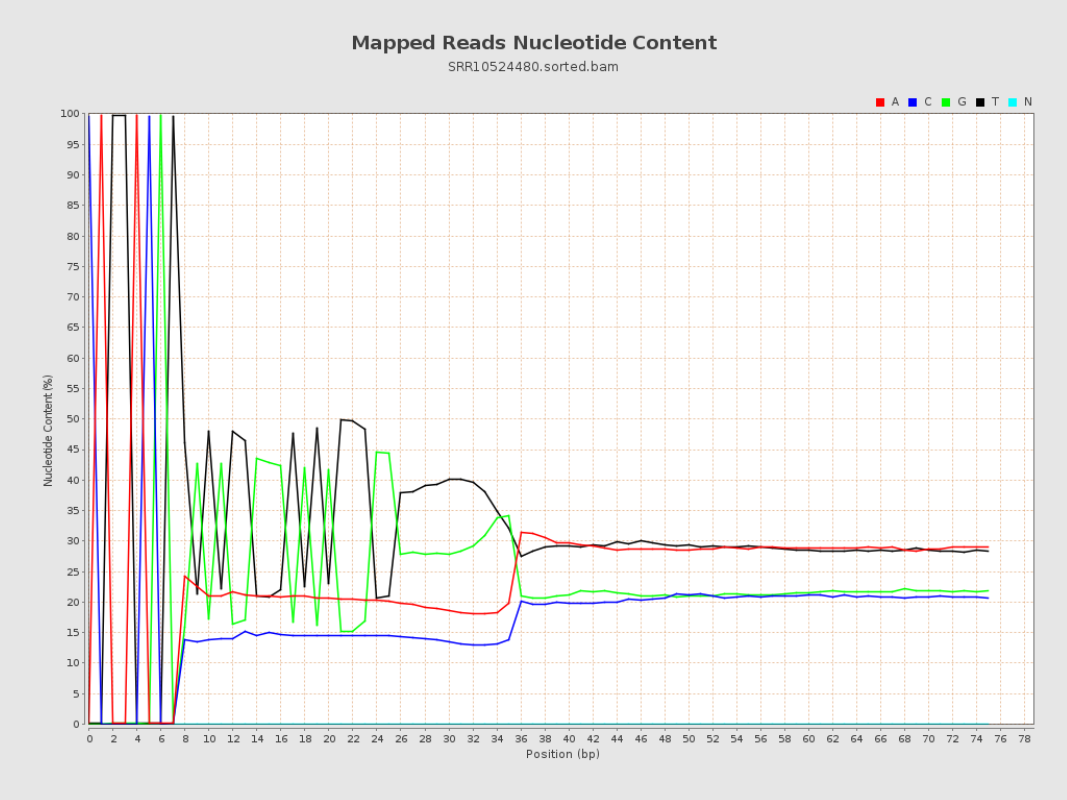
6. Results : Genome Fraction Coverage



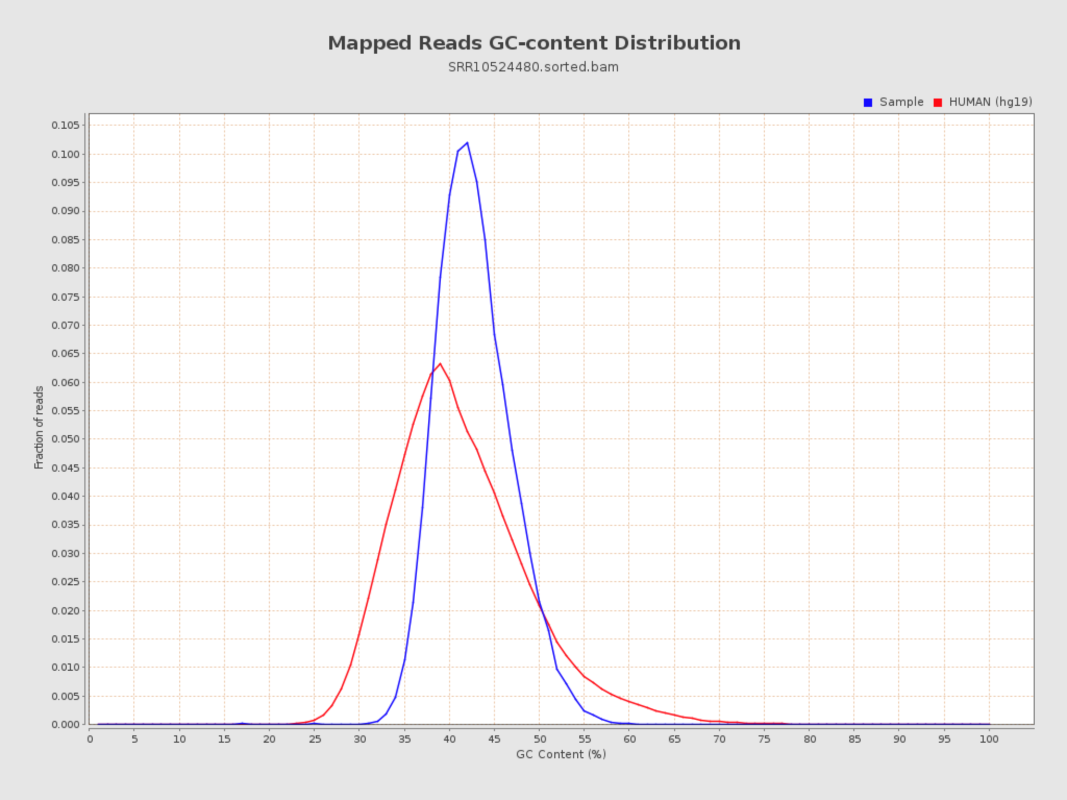
7. Results : Duplication Rate Histogram



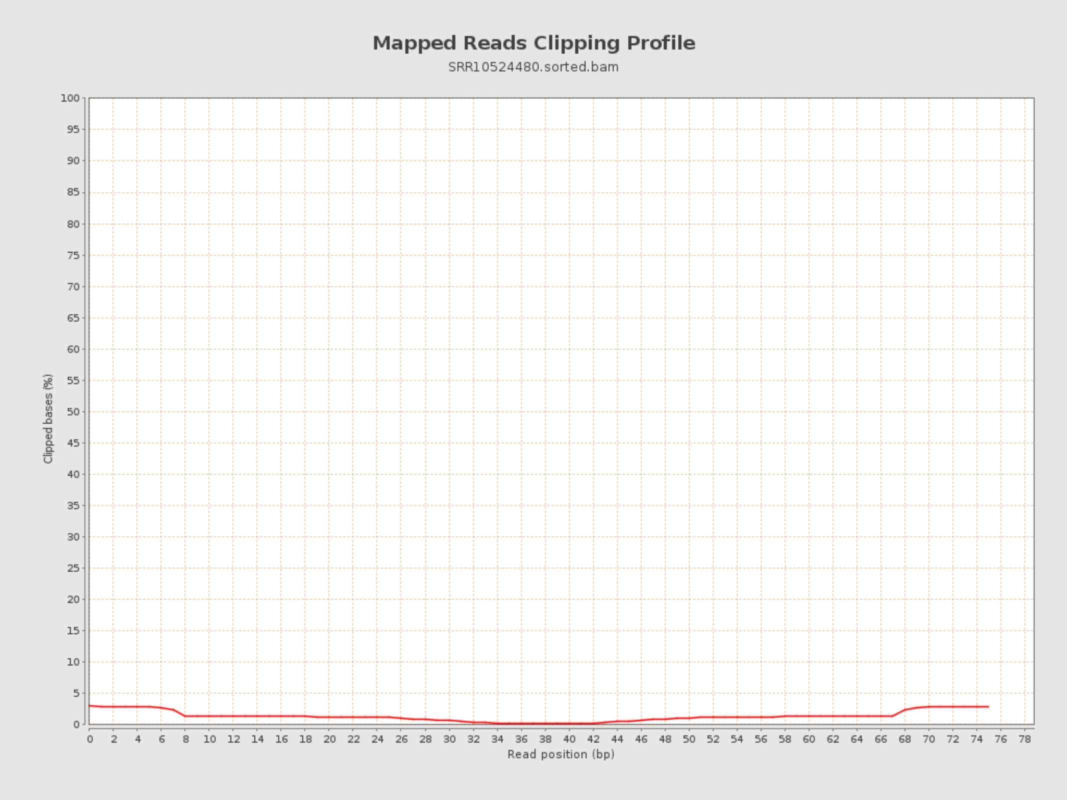
8. Results : Mapped Reads Nucleotide Content



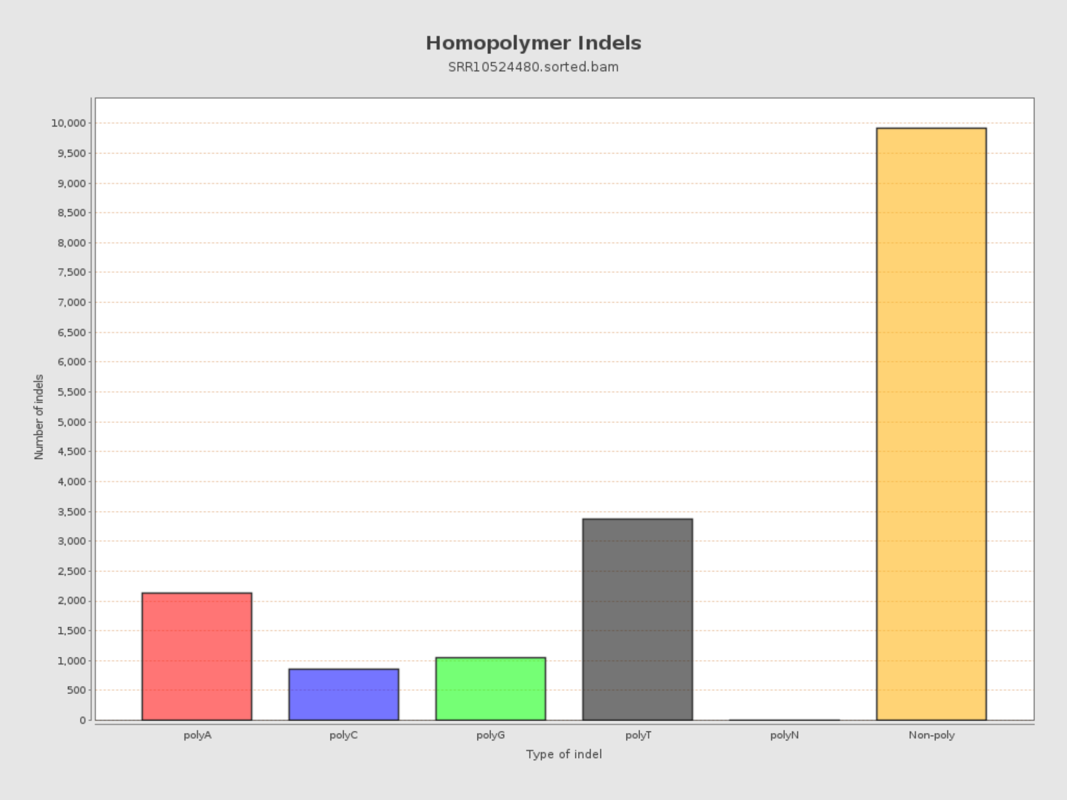
9. Results : Mapped Reads GC-content Distribution



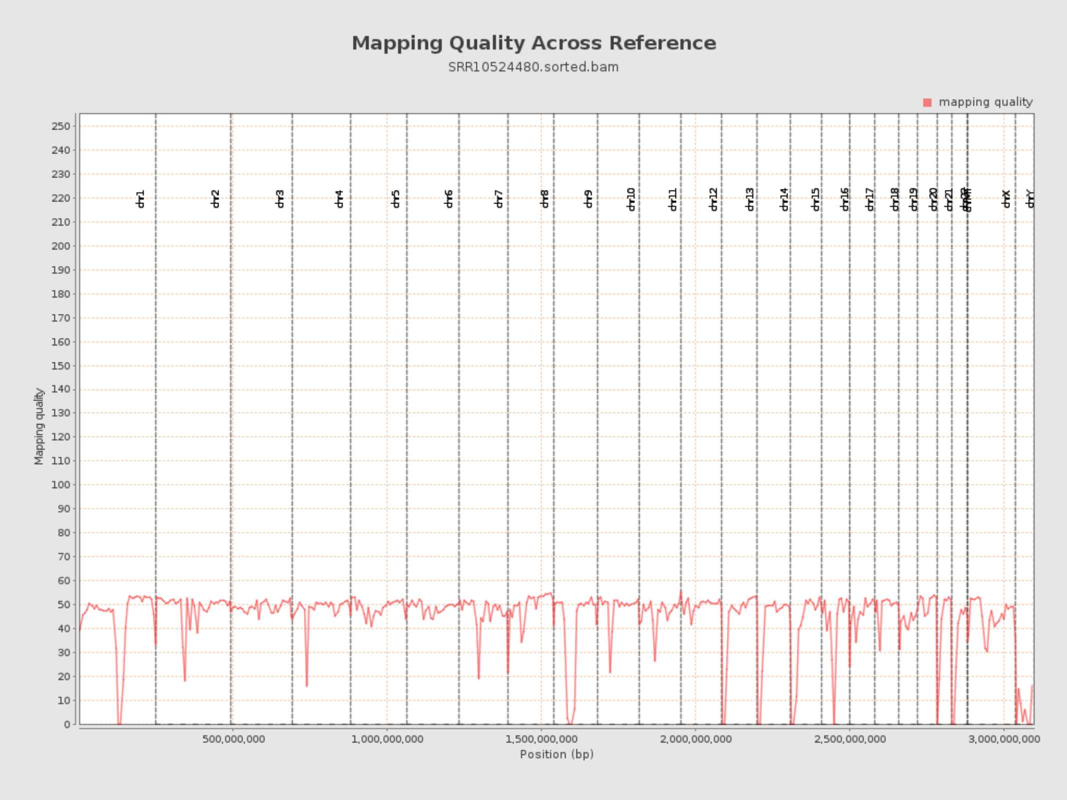
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram