Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:52:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524962.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_SRR10524962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:52:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	551,812
Mapped reads	511,725 / 92.74%
Unmapped reads	40,087 / 7.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,286 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	8,565 / 1.55%
Duplication rate	1.2%
Clipped reads	512,642 / 92.9%

2.2. ACGT Content

Number/percentage of A's	7,730,177 / 25.84%
Number/percentage of C's	5,306,981 / 17.74%
Number/percentage of T's	9,274,334 / 31%
Number/percentage of G's	7,602,667 / 25.41%
Number/percentage of N's	367 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1207

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

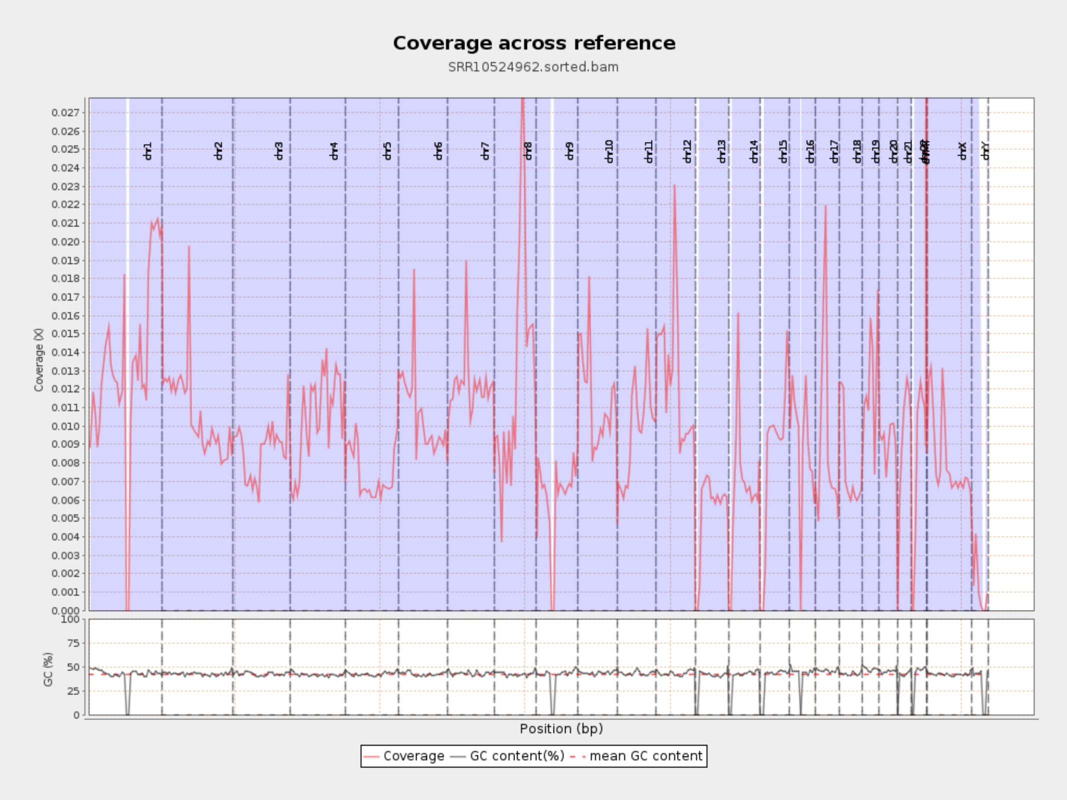
General error rate	0.49%
Mismatches	143,304
Insertions	1,614
Mapped reads with at least one insertion	0.31%
Deletions	5,760
Mapped reads with at least one deletion	1.12%
Homopolymer indels	45.59%

2.6. Chromosome stats

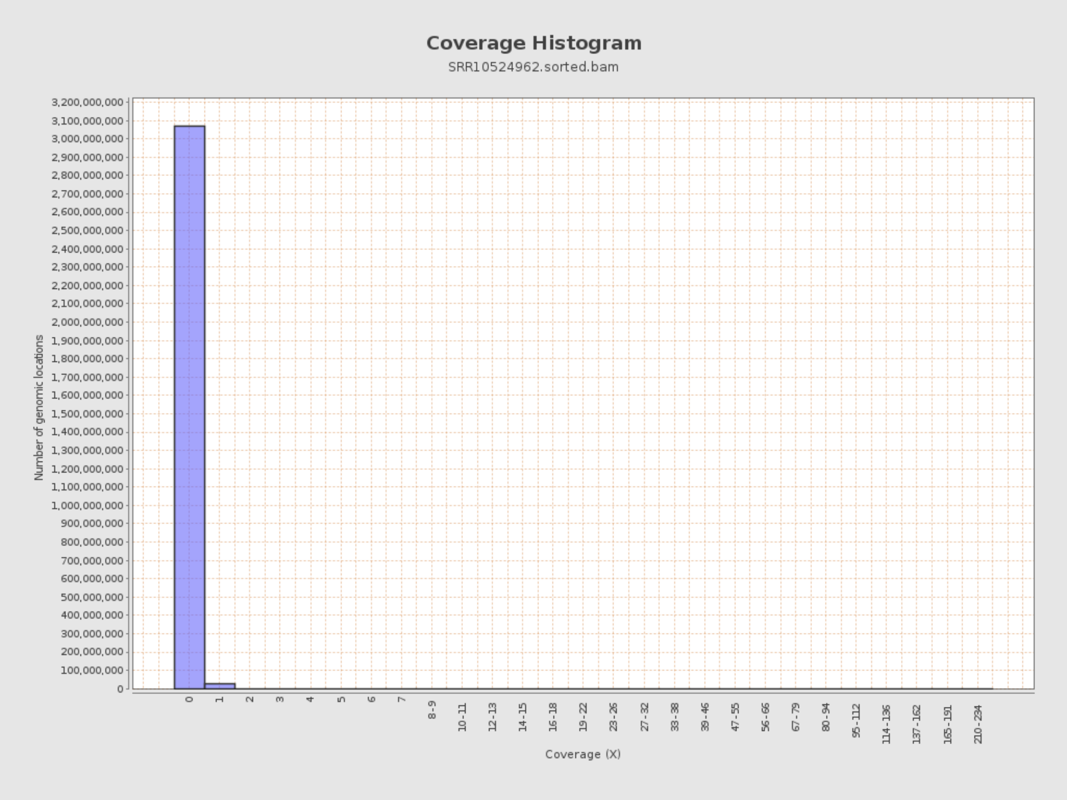
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3299783	0.0132	0.1961
chr2	243199373	2599552	0.0107	0.1315
chr3	198022430	1723081	0.0087	0.0959
chr4	191154276	2003165	0.0105	0.1075
chr5	180915260	1344514	0.0074	0.0892
chr6	171115067	1824773	0.0107	0.1239
chr7	159138663	1953542	0.0123	0.1558

chr8	146364022	1886454	0.0129	0.1297
chr9	141213431	869717	0.0062	0.095
chr10	135534747	1553330	0.0115	0.1233
chr11	135006516	1304348	0.0097	0.1175
chr12	133851895	1679671	0.0125	0.1151
chr13	115169878	614351	0.0053	0.0752
chr14	107349540	702843	0.0065	0.0847
chr15	102531392	862265	0.0084	0.0964
chr16	90354753	798637	0.0088	0.0985
chr17	81195210	769119	0.0095	0.1154
chr18	78077248	608998	0.0078	0.1286
chr19	59128983	733790	0.0124	0.1345
chr20	63025520	572893	0.0091	0.0982
chr21	48129895	439291	0.0091	0.1005
chr22	51304566	401850	0.0078	0.0911
chrMT	16571	2453	0.148	0.368
chrX	155270560	1299182	0.0084	0.0997
chrY	59373566	76902	0.0013	0.0428

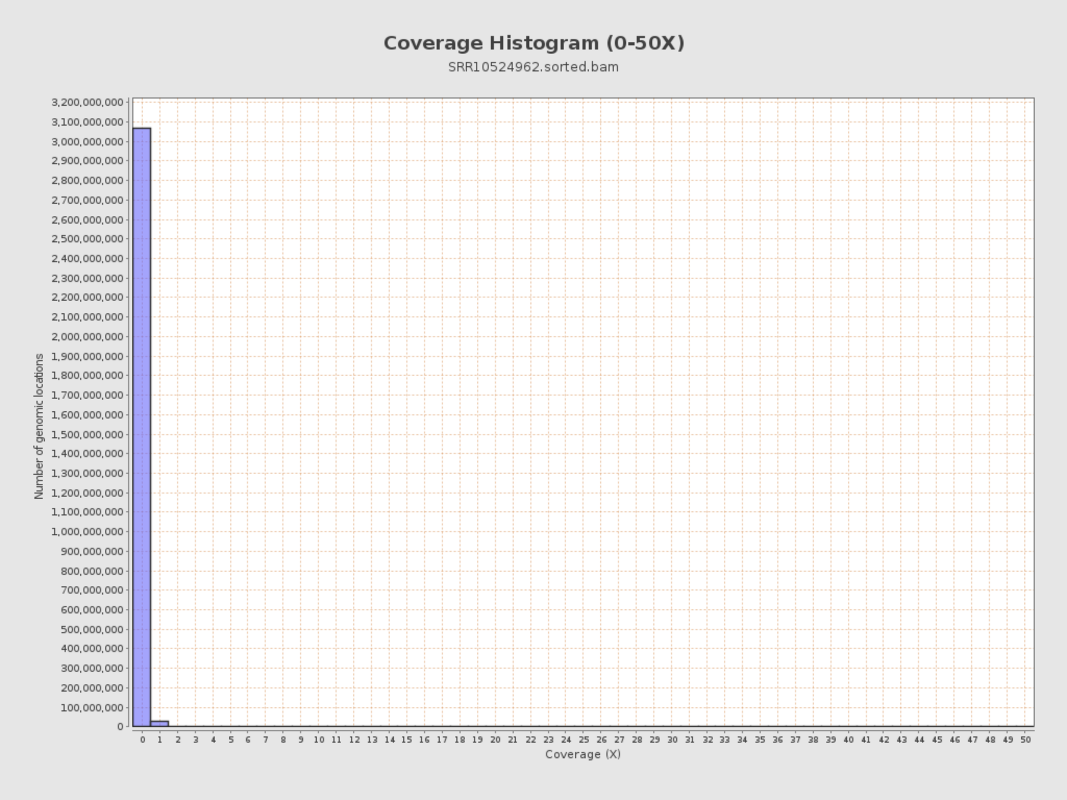
3. Results : Coverage across reference



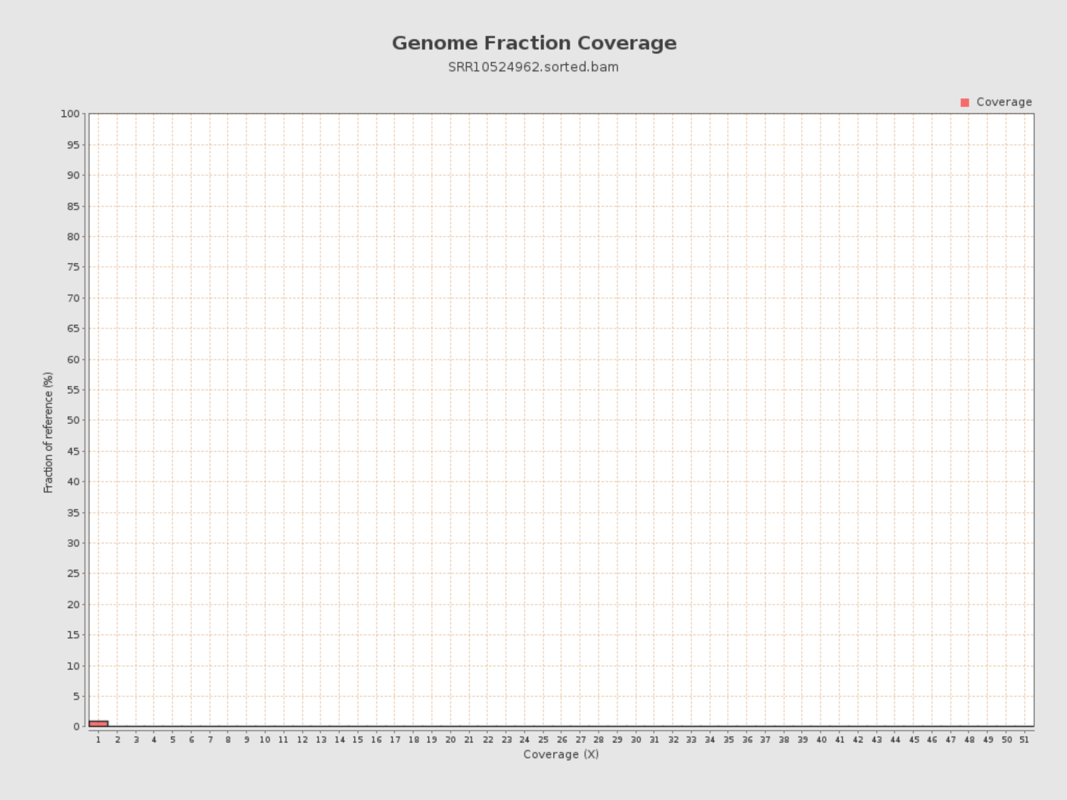
4. Results : Coverage Histogram



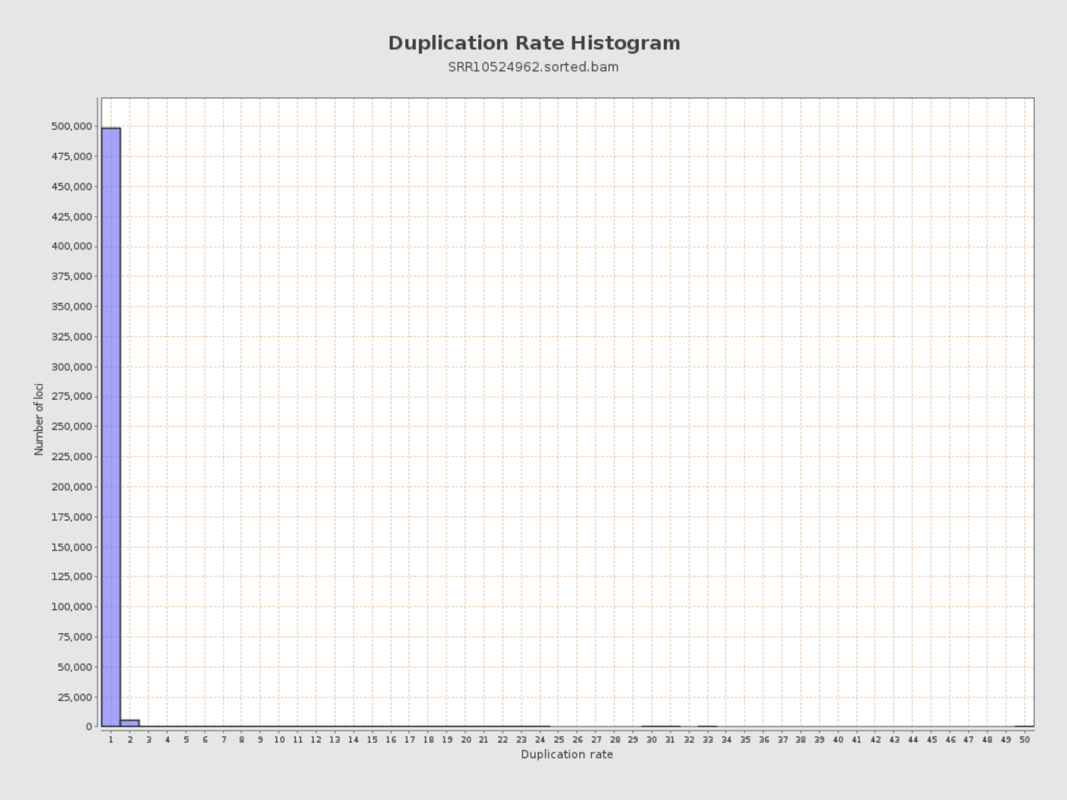
5. Results : Coverage Histogram (0-50X)



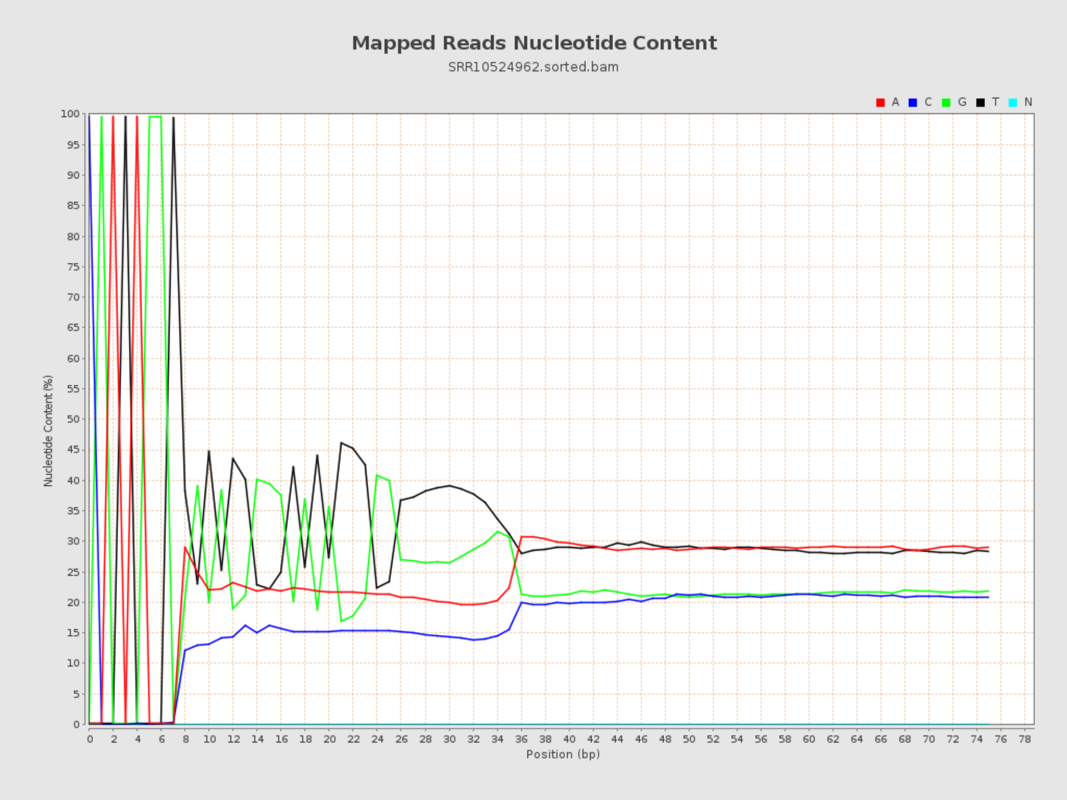
6. Results : Genome Fraction Coverage



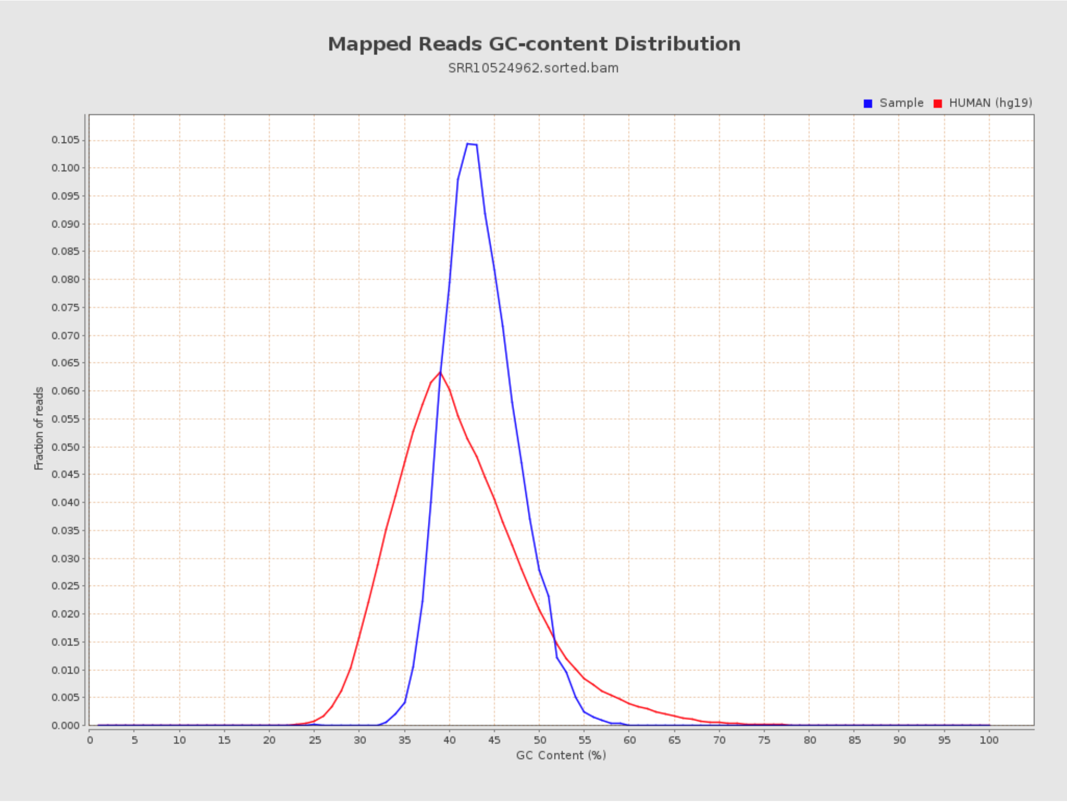
7. Results : Duplication Rate Histogram



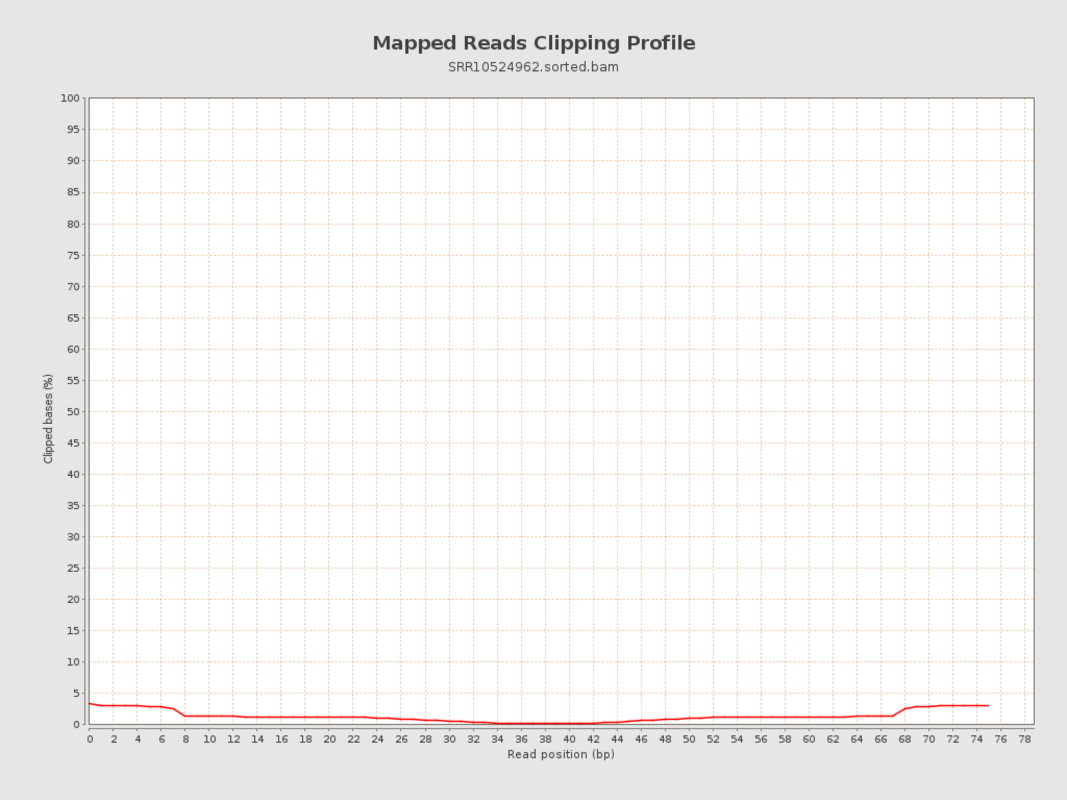
8. Results : Mapped Reads Nucleotide Content



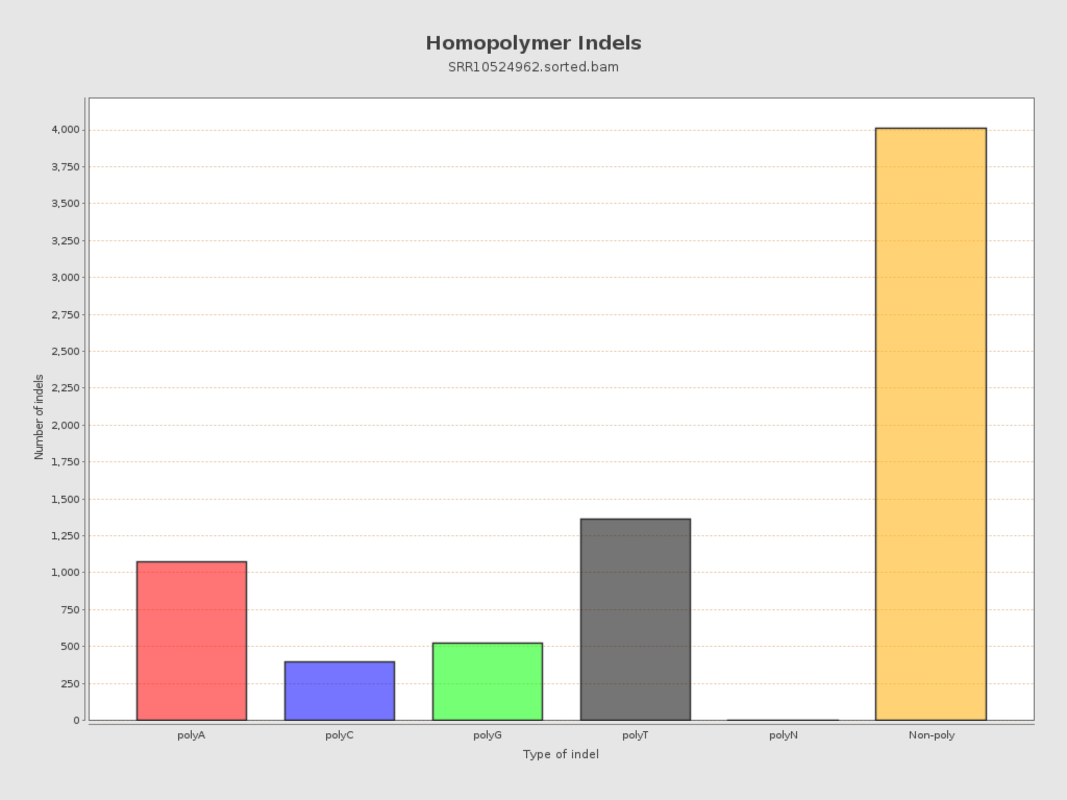
9. Results : Mapped Reads GC-content Distribution



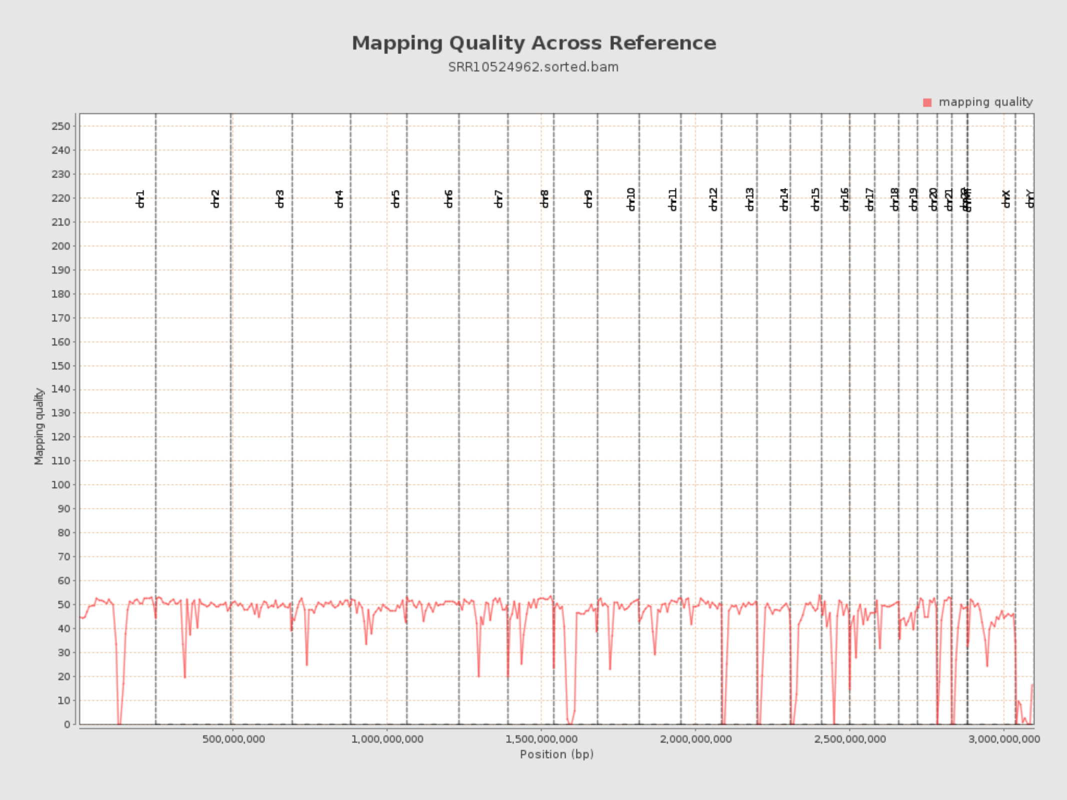
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram