Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:28:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548962.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_SRR1548962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:28:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,482,376
Mapped reads	7,424,678 / 87.53%
Unmapped reads	1,057,698 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	390,213 / 4.6%
Duplication rate	2.9%
Clipped reads	706,366 / 8.33%

2.2. ACGT Content

Number/percentage of A's	82,025,430 / 27.99%
Number/percentage of C's	63,526,054 / 21.68%
Number/percentage of T's	83,704,748 / 28.56%
Number/percentage of G's	63,777,615 / 21.76%
Number/percentage of N's	382 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0947
Standard Deviation	1.1361

2.4. Mapping Quality

Mean Mapping Quality	34.29

2.5. Mismatches and indels

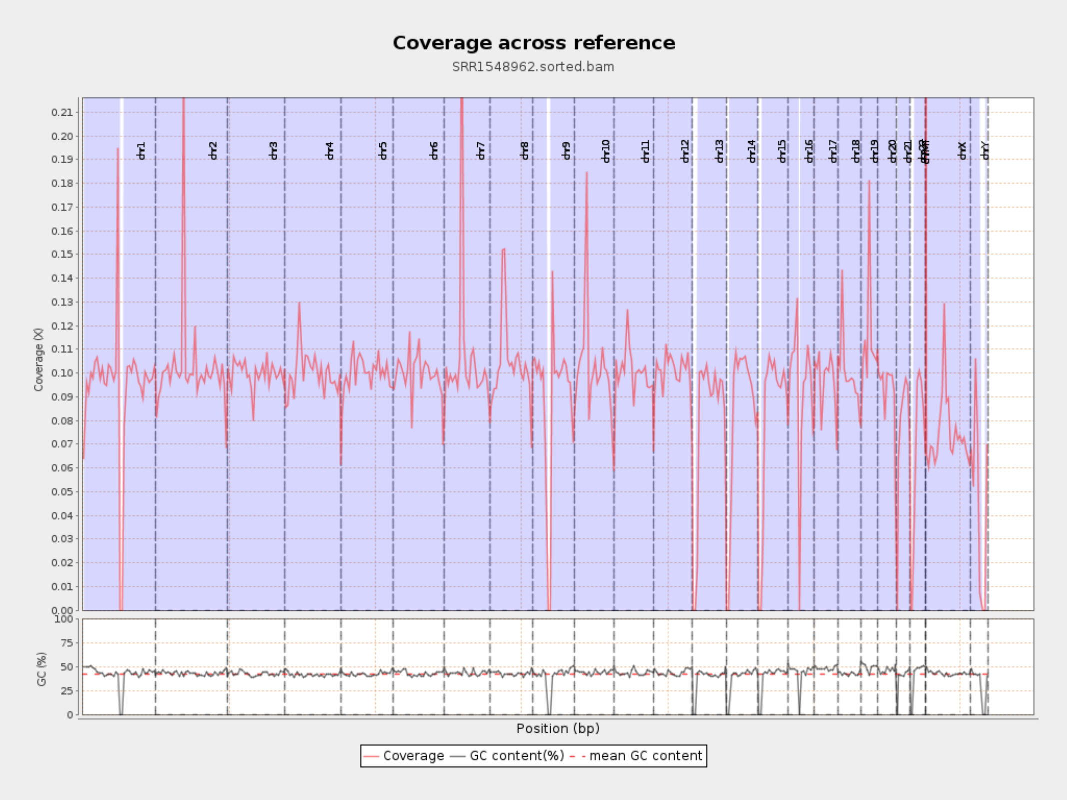
General error rate	0.35%
Mismatches	1,018,877
Insertions	11,147
Mapped reads with at least one insertion	0.15%
Deletions	23,147
Mapped reads with at least one deletion	0.31%
Homopolymer indels	37.34%

2.6. Chromosome stats

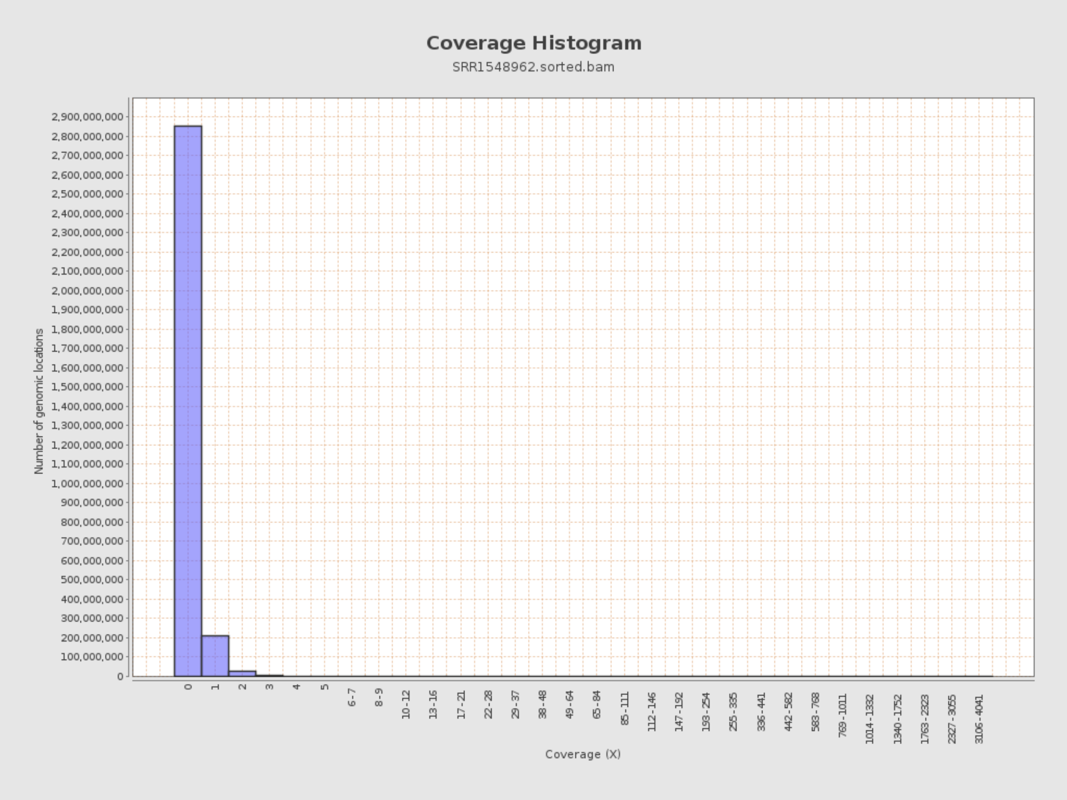
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23533012	0.0944	2.1255
chr2	243199373	25029858	0.1029	1.081
chr3	198022430	19766145	0.0998	0.3789
chr4	191154276	19185749	0.1004	0.429
chr5	180915260	18070575	0.0999	0.4133
chr6	171115067	17066718	0.0997	0.4259
chr7	159138663	17120547	0.1076	1.9129
chr8	146364022	15252559	0.1042	2.0709

chr9	141213431	12545030	0.0888	1.144
chr10	135534747	13936029	0.1028	0.8298
chr11	135006516	13552271	0.1004	0.7676
chr12	133851895	13560251	0.1013	0.4548
chr13	115169878	9148618	0.0794	0.3184
chr14	107349540	8973372	0.0836	0.6311
chr15	102531392	8172631	0.0797	0.3472
chr16	90354753	8211654	0.0909	0.5284
chr17	81195210	7966260	0.0981	0.4181
chr18	78077248	7882919	0.101	2.2103
chr19	59128983	6817338	0.1153	2.1288
chr20	63025520	5892769	0.0935	0.4192
chr21	48129895	3680794	0.0765	0.5672
chr22	51304566	3337350	0.065	0.5085
chrMT	16571	9390	0.5667	1.013
chrX	155270560	11606009	0.0747	0.6145
chrY	59373566	2745824	0.0462	0.4158

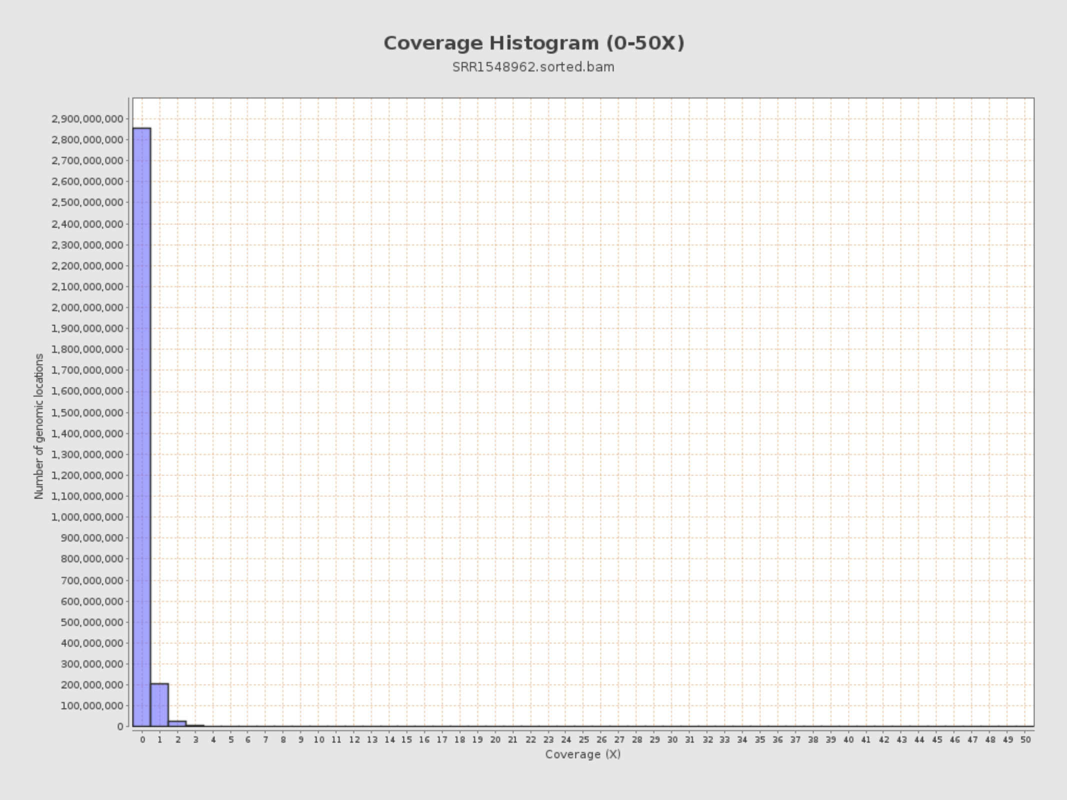
3. Results : Coverage across reference



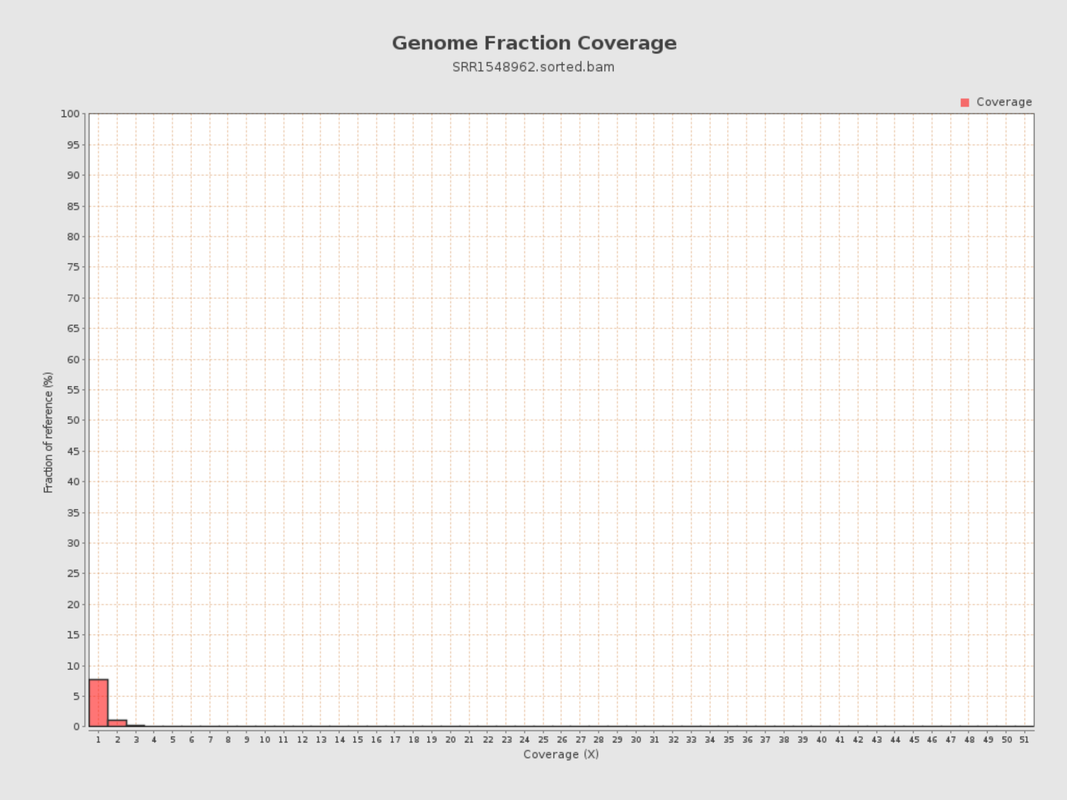
4. Results : Coverage Histogram



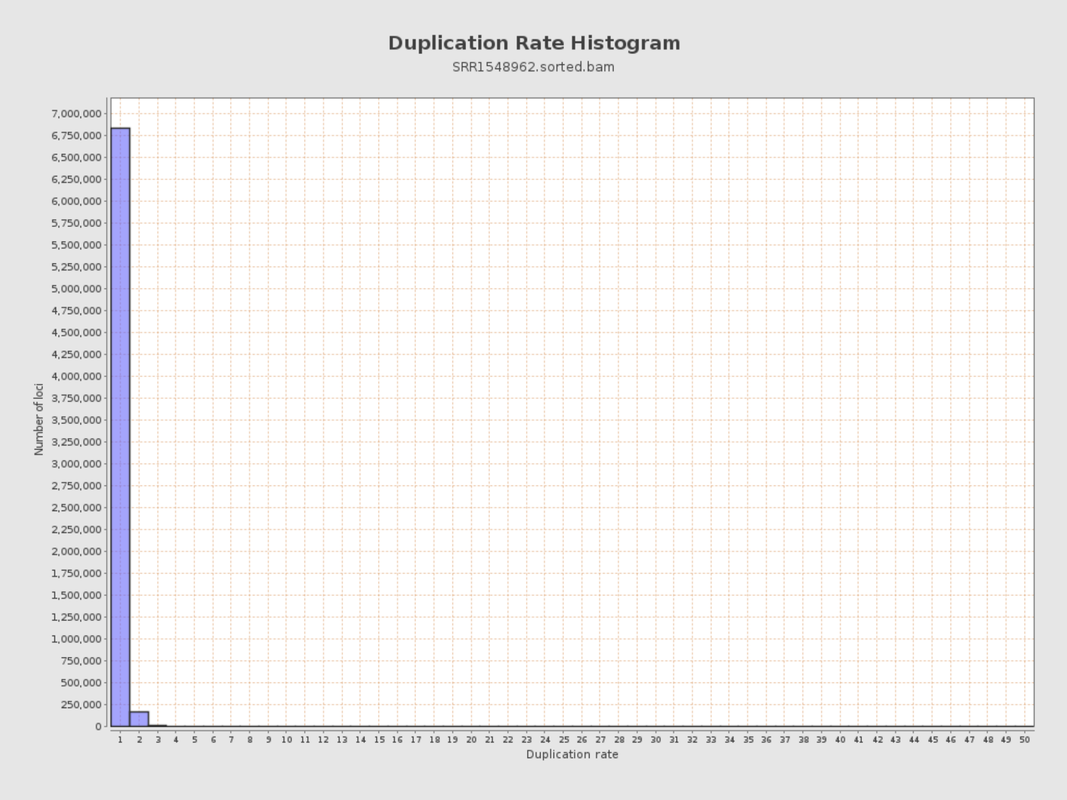
5. Results : Coverage Histogram (0-50X)



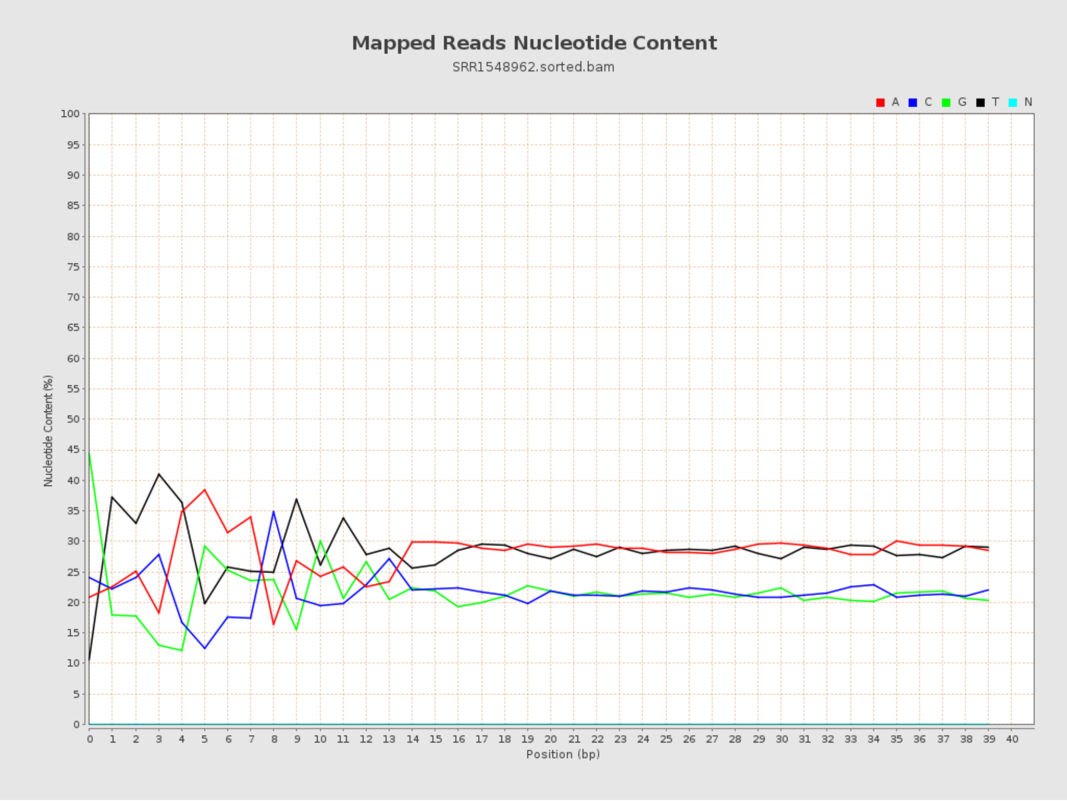
6. Results : Genome Fraction Coverage



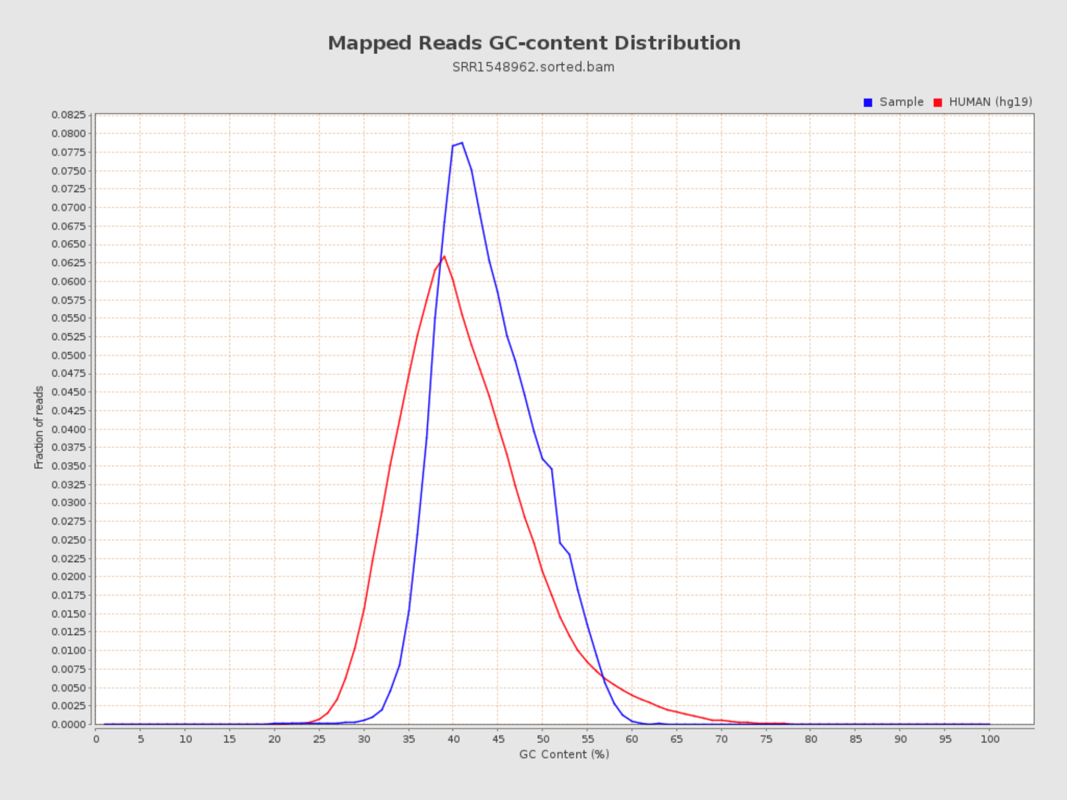
7. Results : Duplication Rate Histogram



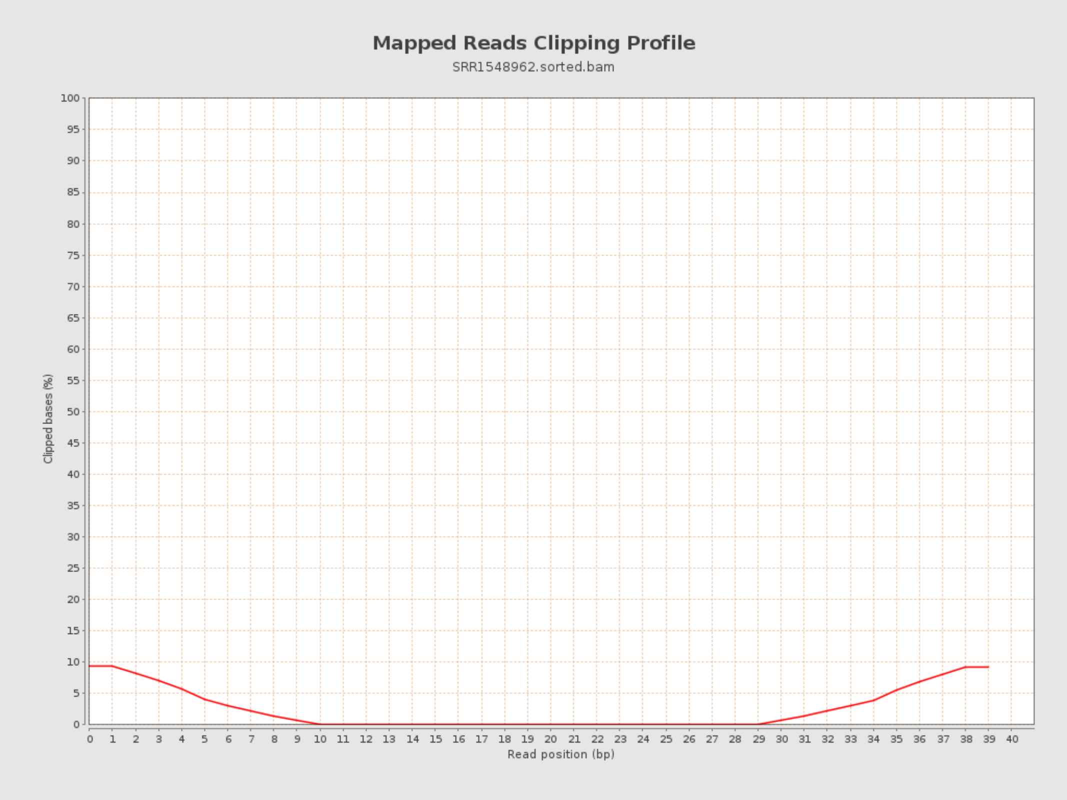
8. Results : Mapped Reads Nucleotide Content



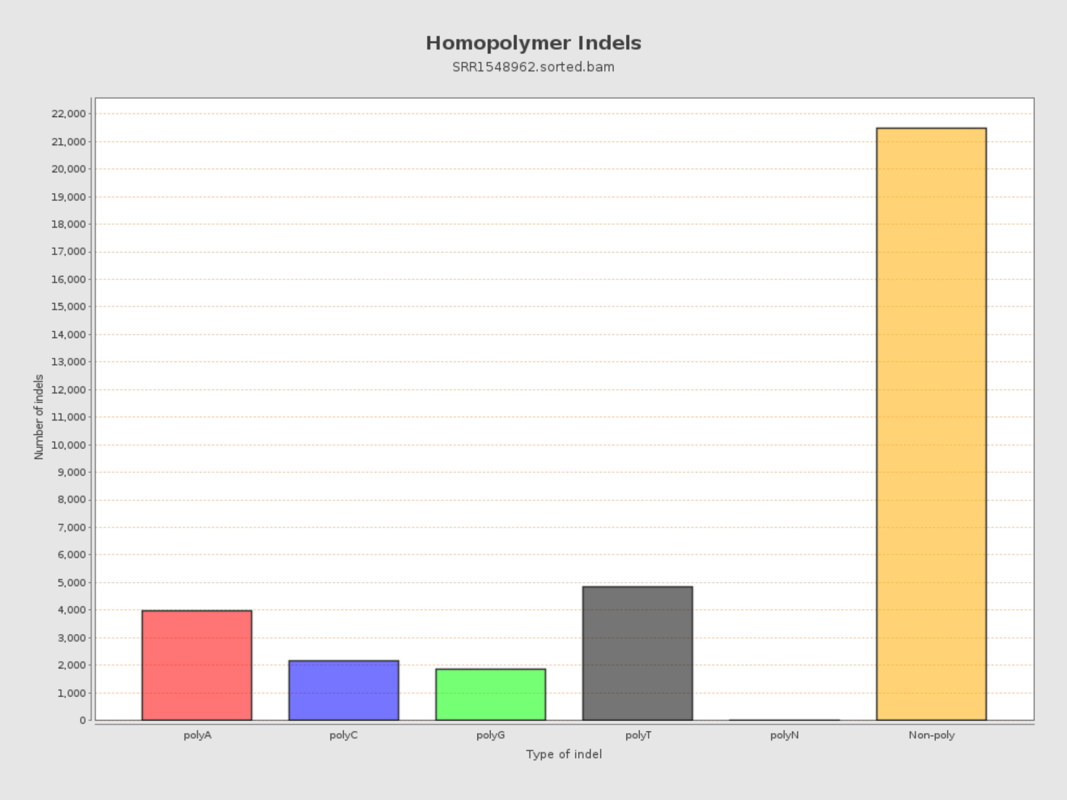
9. Results : Mapped Reads GC-content Distribution



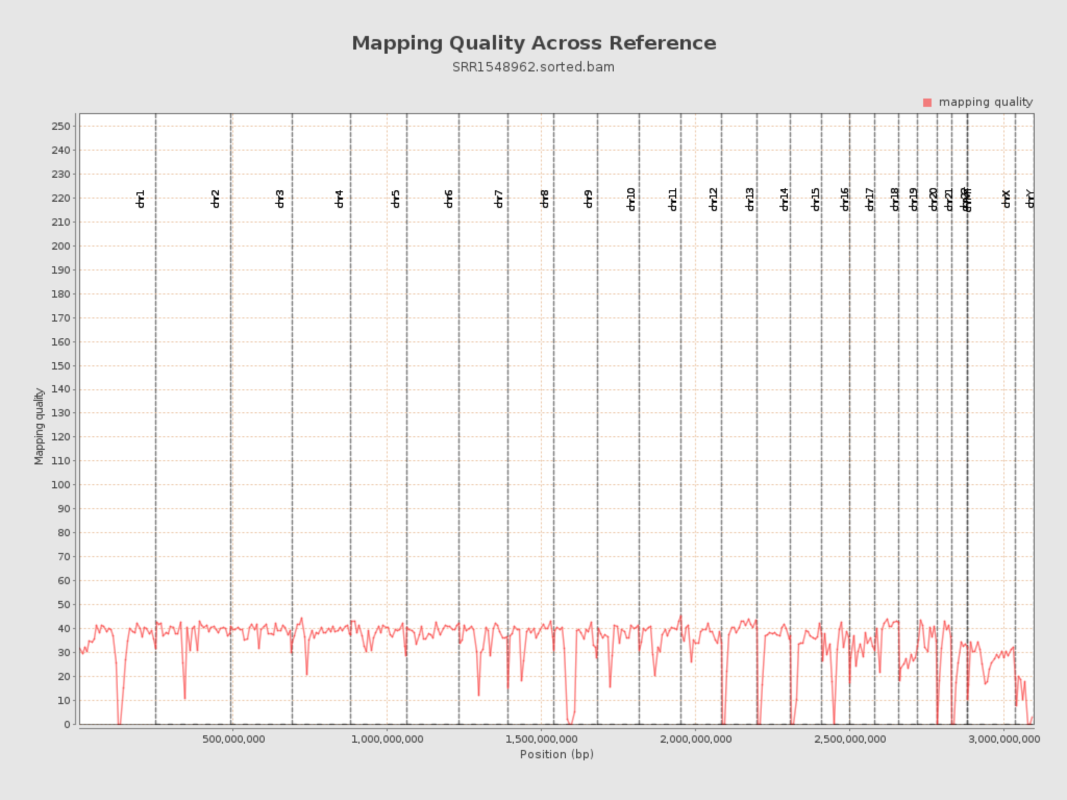
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram