Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:44:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124792.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_SRR3124792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:44:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	708,372
Mapped reads	707,411 / 99.86%
Unmapped reads	961 / 0.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	324,912 / 45.87%
Read min/max/mean length	30 / 151 / 179.3
Duplicated reads (estimated)	1,027,205 / 145.01%
Duplication rate	9.42%
Clipped reads	674,597 / 95.23%

2.2. ACGT Content

Number/percentage of A's	31,754,106 / 30.09%
Number/percentage of C's	19,757,101 / 18.72%
Number/percentage of T's	33,694,258 / 31.93%
Number/percentage of G's	20,307,999 / 19.25%
Number/percentage of N's	0 / 0%
GC Percentage	37.97%

2.3. Coverage

Mean	0.0341

Standard Deviation	80.6448

2.4. Mapping Quality

Mean Mapping Quality	49.06

2.5. Mismatches and indels

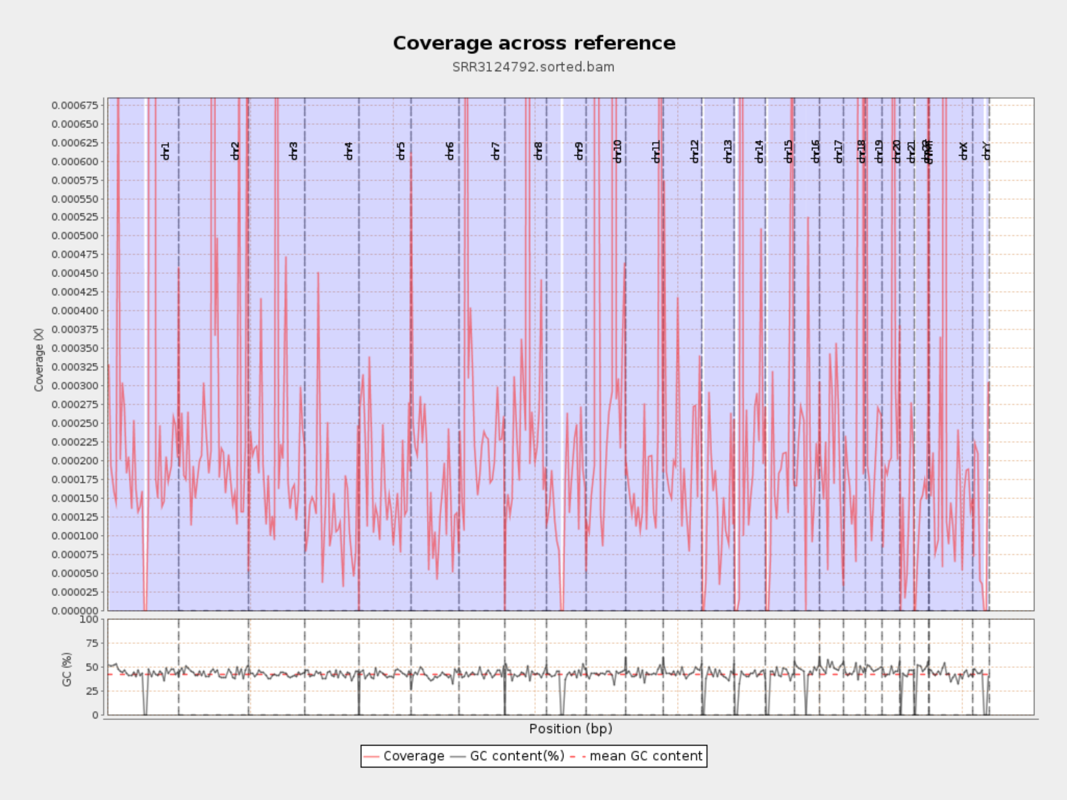
General error rate	0.73%
Mismatches	765,122
Insertions	4,411
Mapped reads with at least one insertion	0.62%
Deletions	25,111
Mapped reads with at least one deletion	3.52%
Homopolymer indels	53.93%

2.6. Chromosome stats

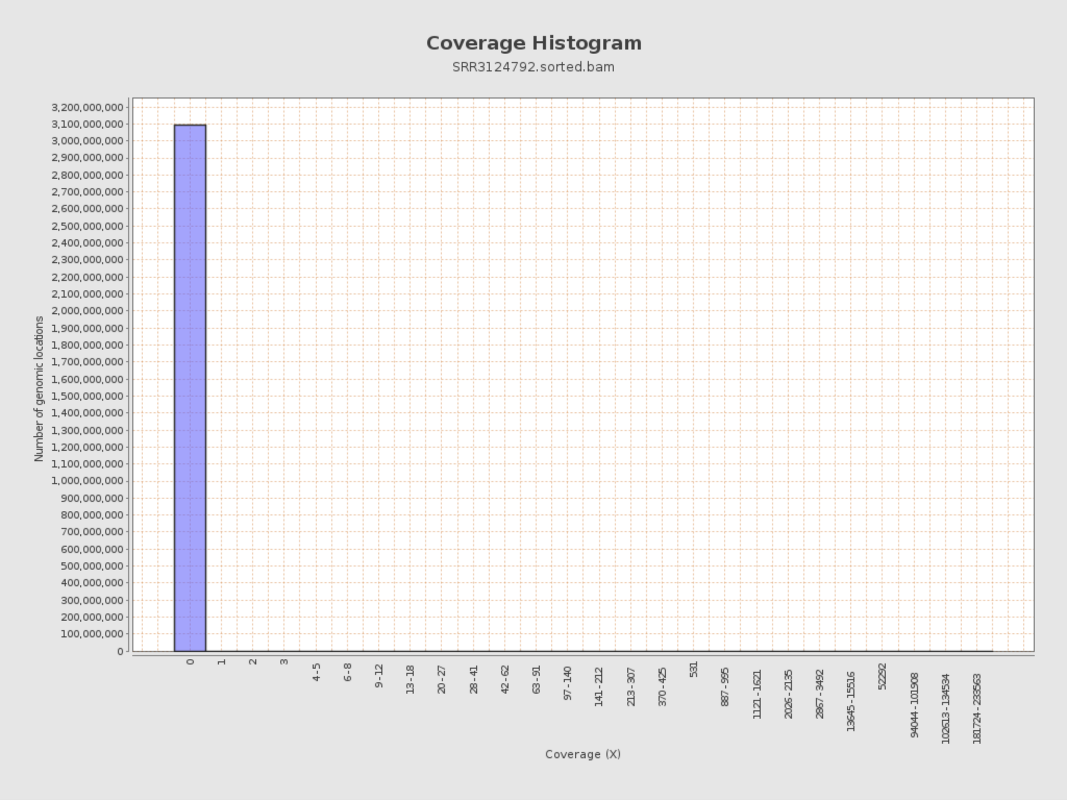
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	378836	0.0015	1.0337
chr2	243199373	82731	0.0003	0.1175
chr3	198022430	48629	0.0002	0.1065
chr4	191154276	26412	0.0001	0.0119
chr5	180915260	31411	0.0002	0.0134
chr6	171115067	30013	0.0002	0.0382
chr7	159138663	44478	0.0003	0.094

chr8	146364022	65472	0.0004	0.1612
chr9	141213431	20991	0.0001	0.0122
chr10	135534747	104478897	0.7709	385.4126
chr11	135006516	30907	0.0002	0.0593
chr12	133851895	30000	0.0002	0.0166
chr13	115169878	14970	0.0001	0.0128
chr14	107349540	32510	0.0003	0.1807
chr15	102531392	23491	0.0002	0.0421
chr16	90354753	18770	0.0002	0.0148
chr17	81195210	17406	0.0002	0.032
chr18	78077248	59663	0.0008	0.2961
chr19	59128983	21253	0.0004	0.0815
chr20	63025520	20713	0.0003	0.0588
chr21	48129895	5959	0.0001	0.0133
chr22	51304566	5863	0.0001	0.0107
chrMT	16571	347	0.0209	0.1432
chrX	155270560	42980	0.0003	0.1149
chrY	59373566	6672	0.0001	0.0109

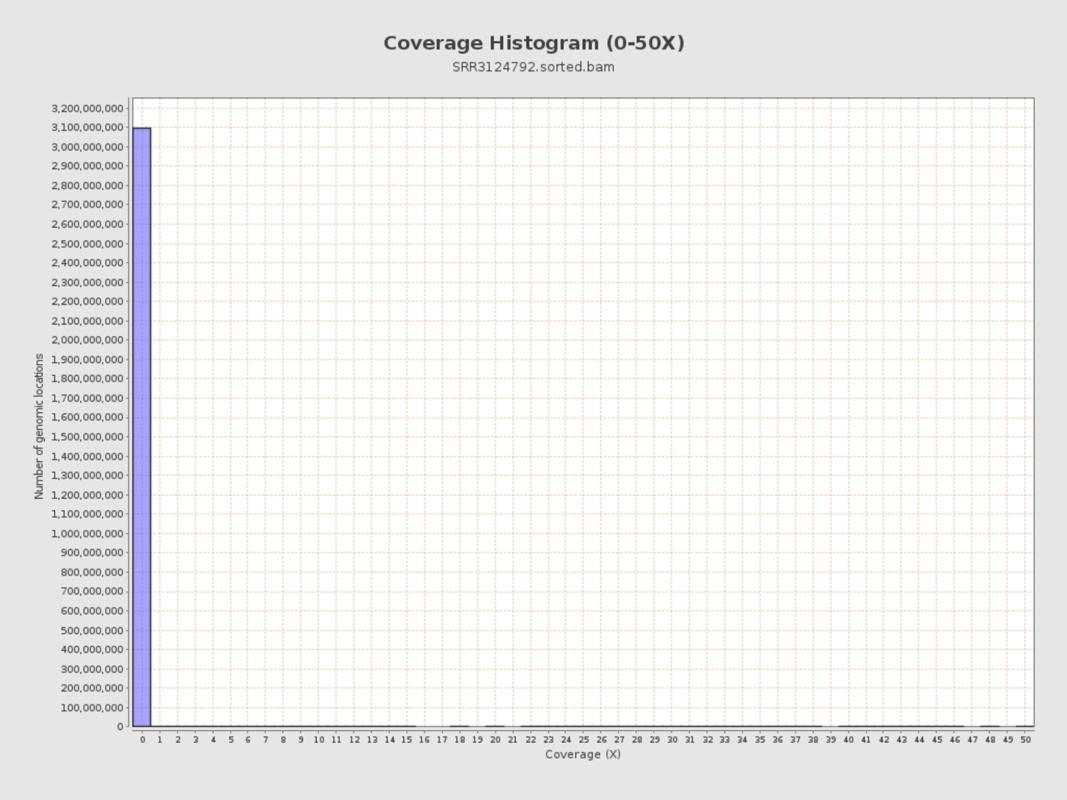
3. Results : Coverage across reference



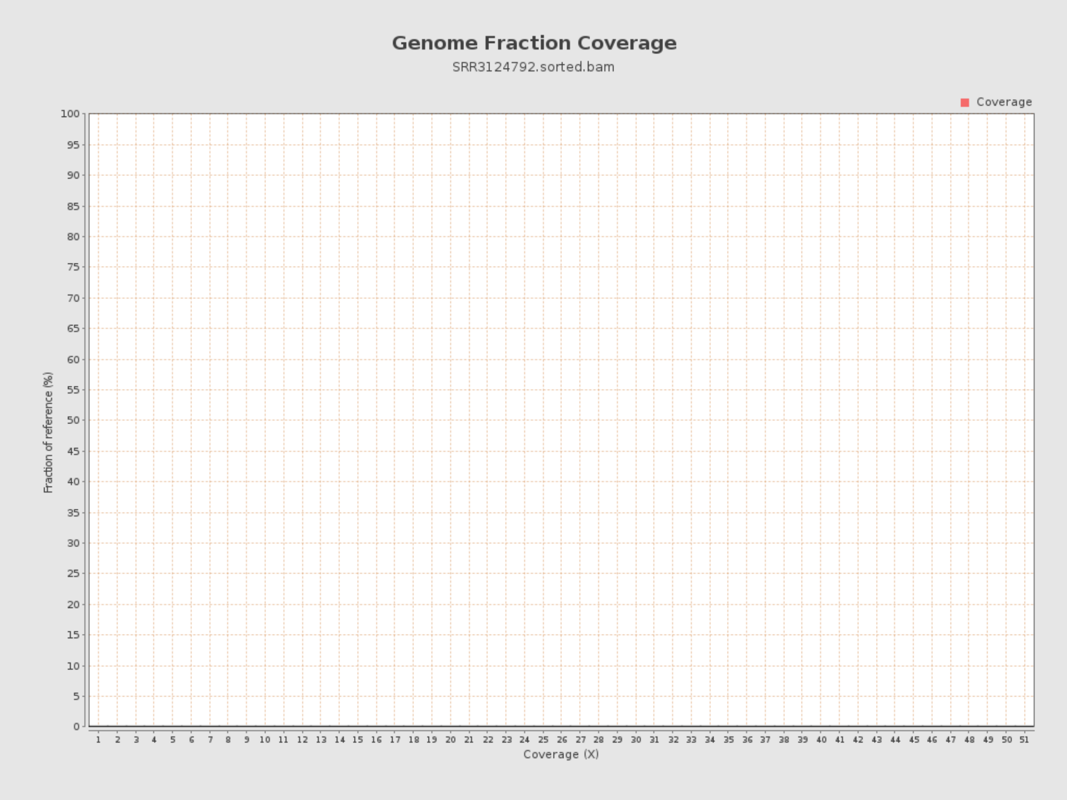
4. Results : Coverage Histogram



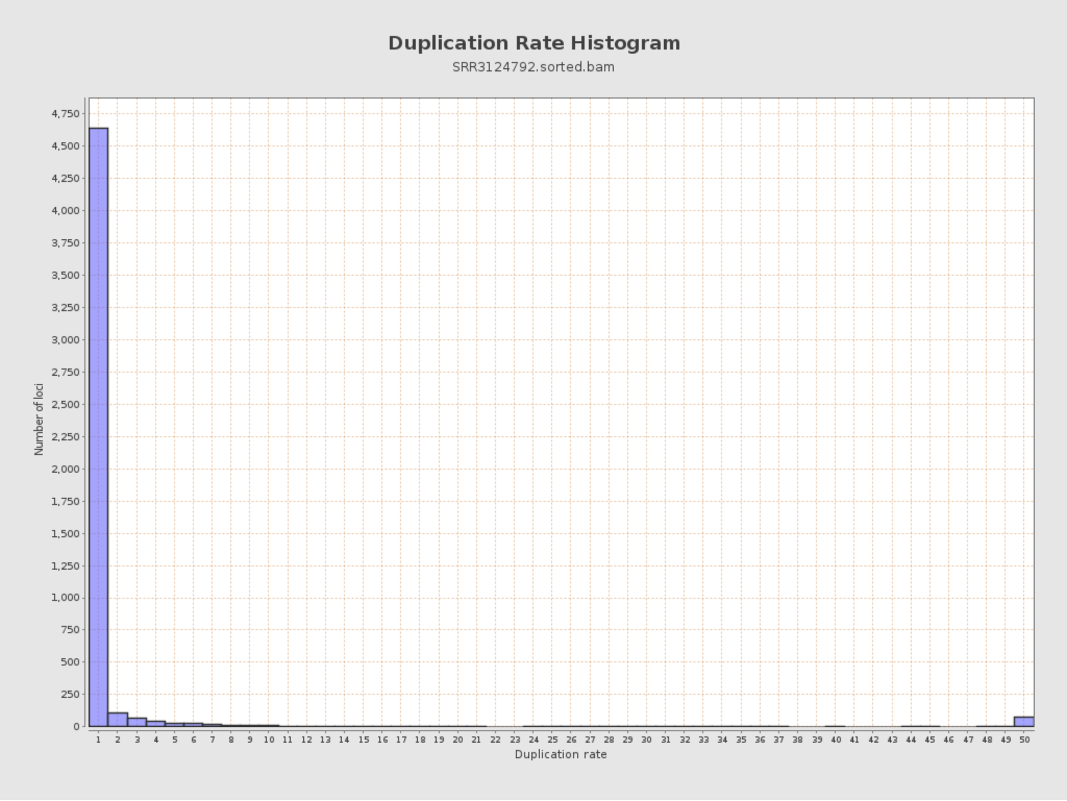
5. Results : Coverage Histogram (0-50X)



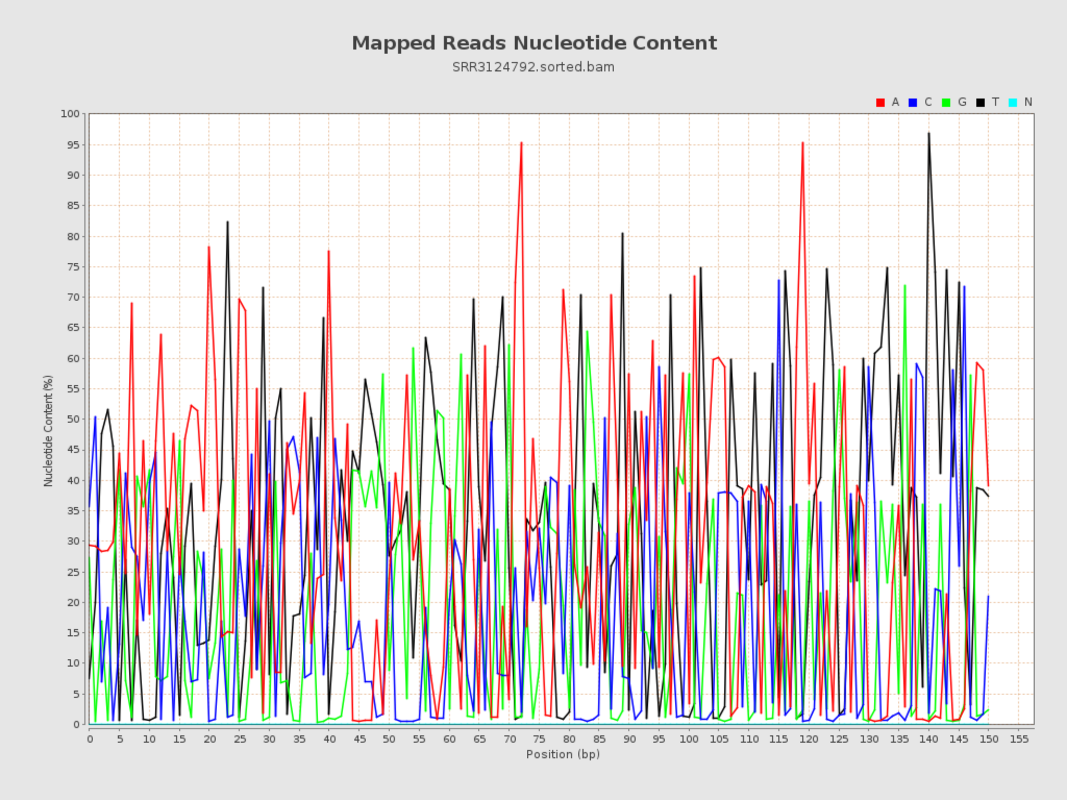
6. Results : Genome Fraction Coverage



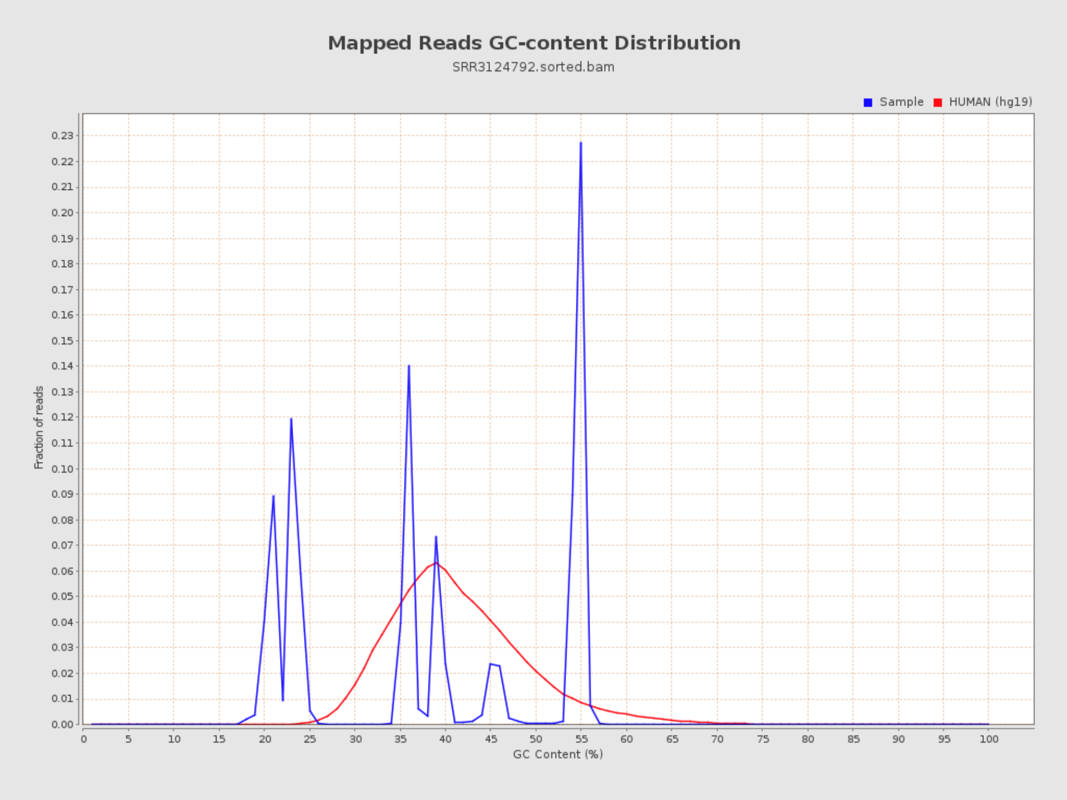
7. Results : Duplication Rate Histogram



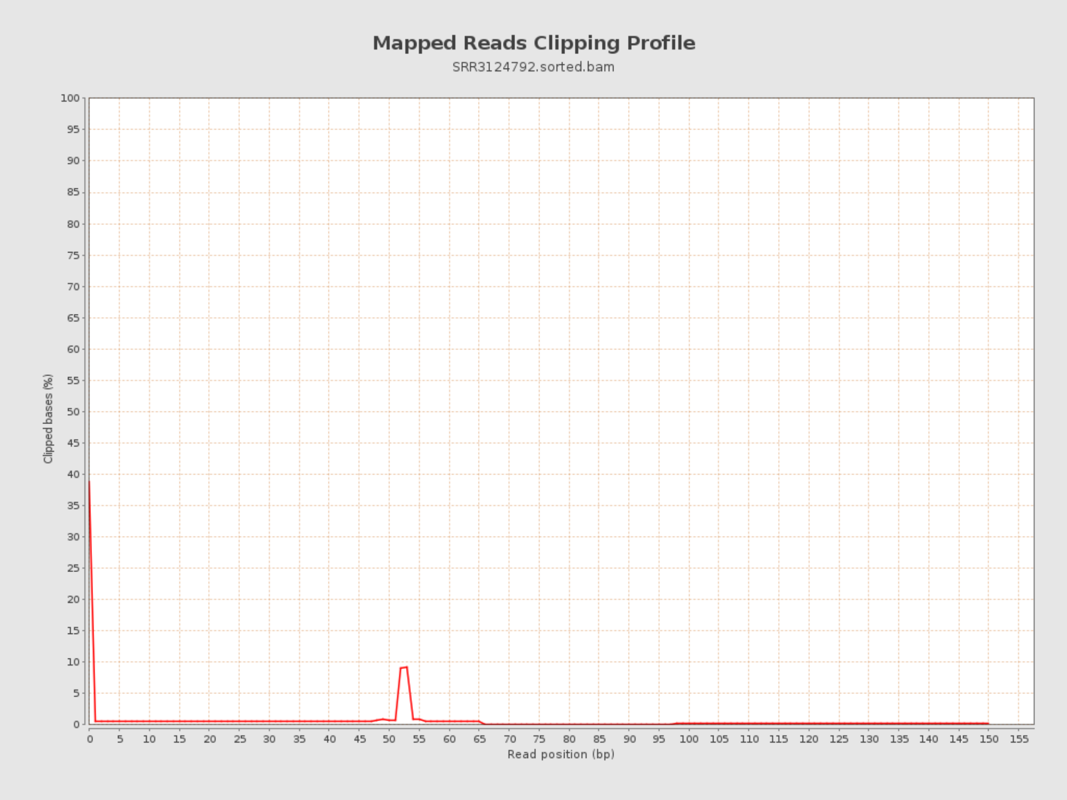
8. Results : Mapped Reads Nucleotide Content



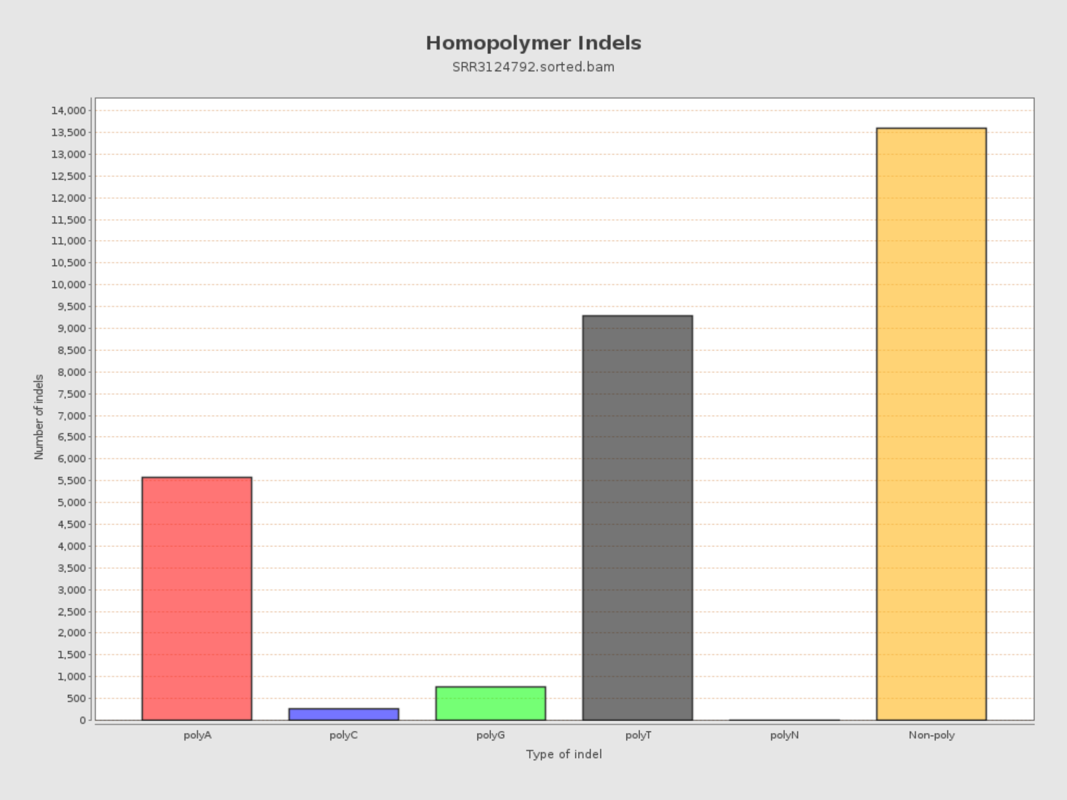
9. Results : Mapped Reads GC-content Distribution



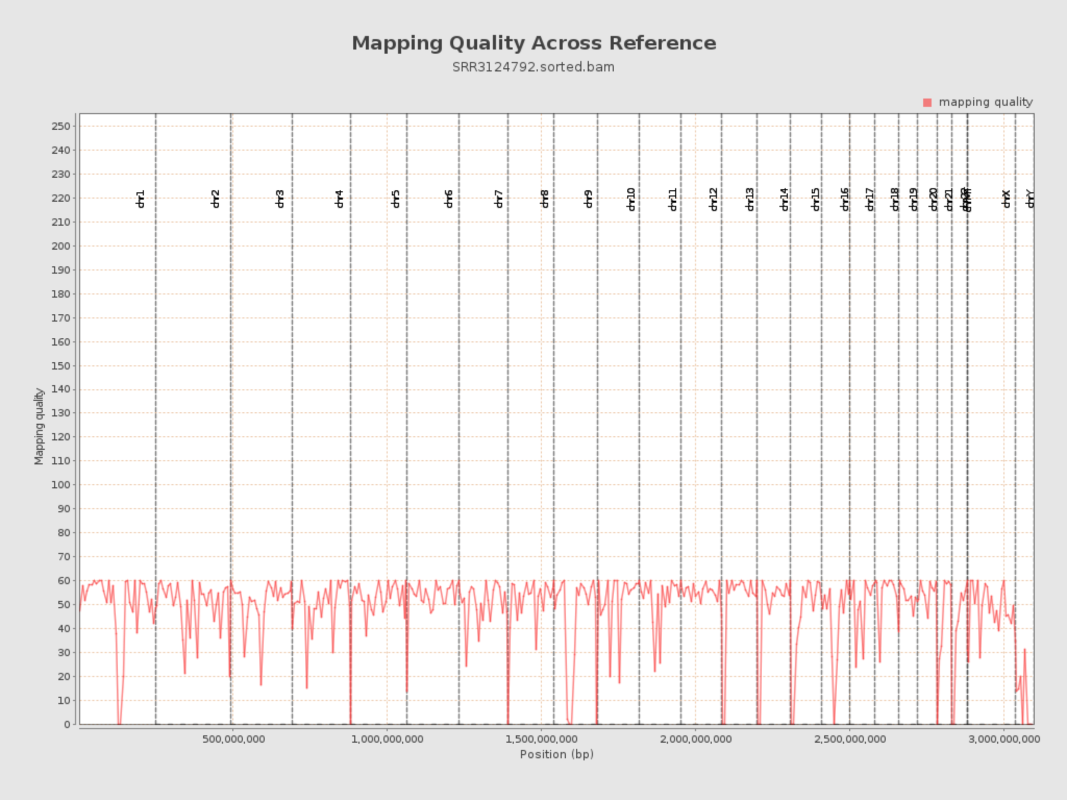
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram