Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:42:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080745.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_SRR3080745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:42:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,605,330
Mapped reads	5,415,092 / 81.98%
Unmapped reads	1,190,238 / 18.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,225 / 0.38%
Read min/max/mean length	30 / 66 / 66.13
Duplicated reads (estimated)	707,747 / 10.71%
Duplication rate	10.36%
Clipped reads	645,233 / 9.77%

2.2. ACGT Content

Number/percentage of A's	107,870,261 / 30.97%
Number/percentage of C's	69,606,243 / 19.98%
Number/percentage of T's	91,359,167 / 26.23%
Number/percentage of G's	78,713,350 / 22.6%
Number/percentage of N's	794,204 / 0.23%
GC Percentage	42.58%

2.3. Coverage

Mean	0.1126

Standard Deviation	0.718

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

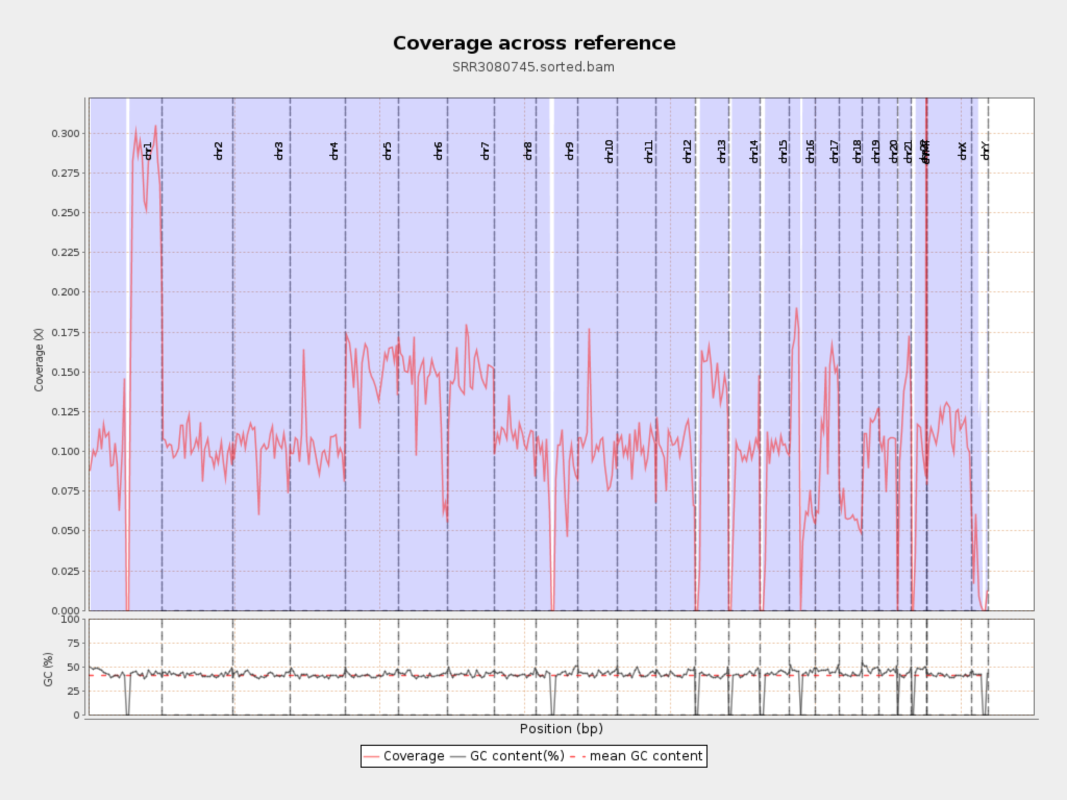
General error rate	1.04%
Mismatches	3,591,909
Insertions	24,329
Mapped reads with at least one insertion	0.45%
Deletions	59,946
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.35%

2.6. Chromosome stats

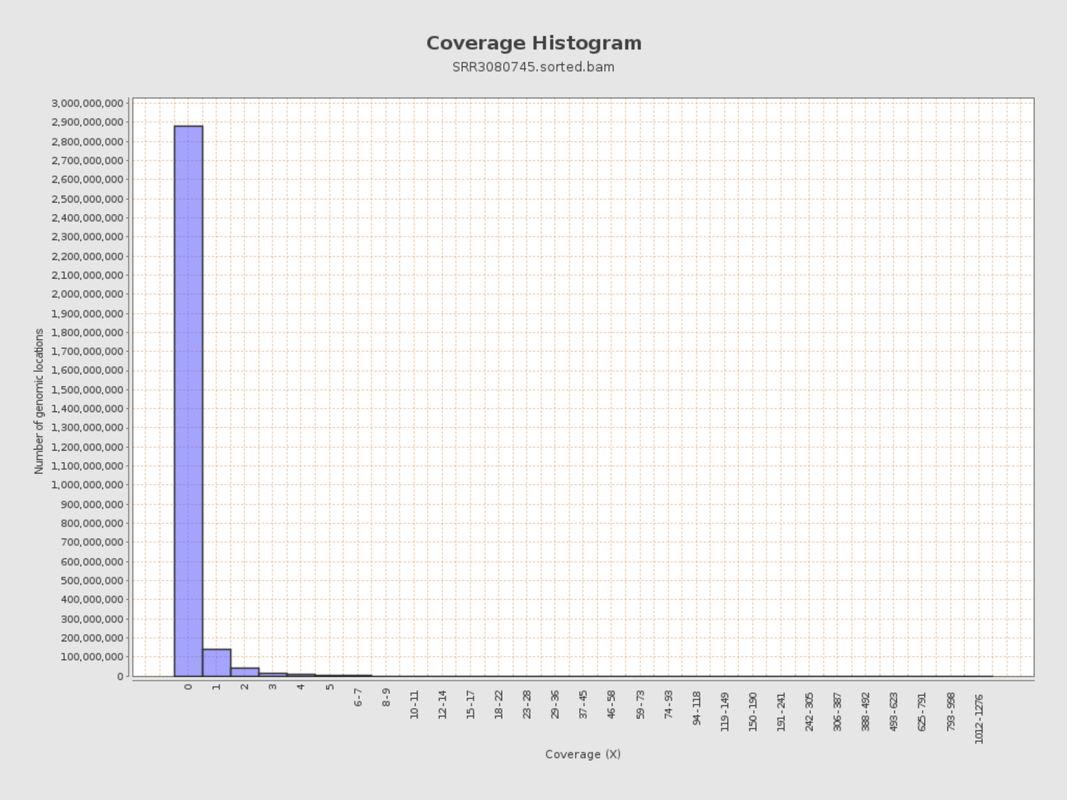
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42718193	0.1714	1.1189
chr2	243199373	24822530	0.1021	0.6418
chr3	198022430	20434690	0.1032	0.4944
chr4	191154276	19642003	0.1028	0.5626
chr5	180915260	27715468	0.1532	0.6047
chr6	171115067	23778687	0.139	0.7703
chr7	159138663	23794973	0.1495	1.0723

chr8	146364022	16056811	0.1097	0.9823
chr9	141213431	11463828	0.0812	0.5559
chr10	135534747	13988576	0.1032	0.7962
chr11	135006516	13931938	0.1032	0.6527
chr12	133851895	13722667	0.1025	0.4941
chr13	115169878	14252280	0.1238	0.5416
chr14	107349540	9037903	0.0842	0.517
chr15	102531392	8534153	0.0832	0.4448
chr16	90354753	8746028	0.0968	0.5386
chr17	81195210	9978327	0.1229	0.5728
chr18	78077248	4693860	0.0601	0.8751
chr19	59128983	6640914	0.1123	1.0284
chr20	63025520	6382587	0.1013	0.4998
chr21	48129895	5801360	0.1205	0.6123
chr22	51304566	3695712	0.072	0.4101
chrMT	16571	16052	0.9687	1.4938
chrX	155270560	17604320	0.1134	0.5439
chrY	59373566	1001131	0.0169	0.4865

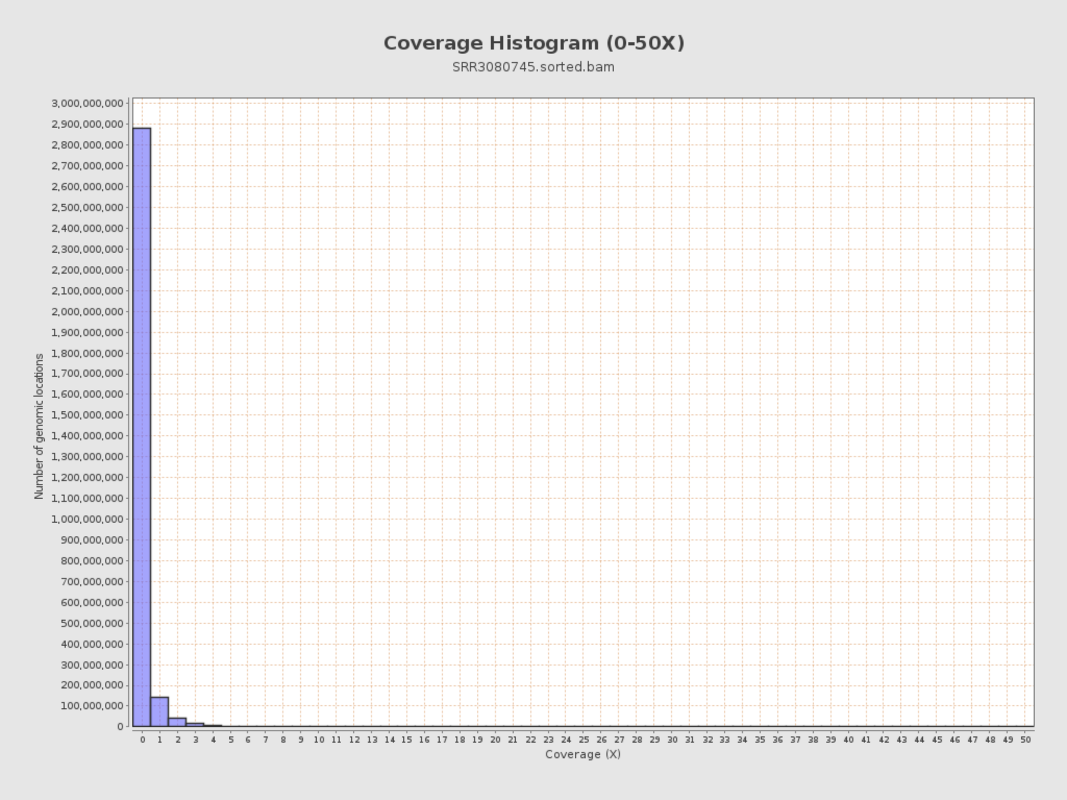
3. Results : Coverage across reference



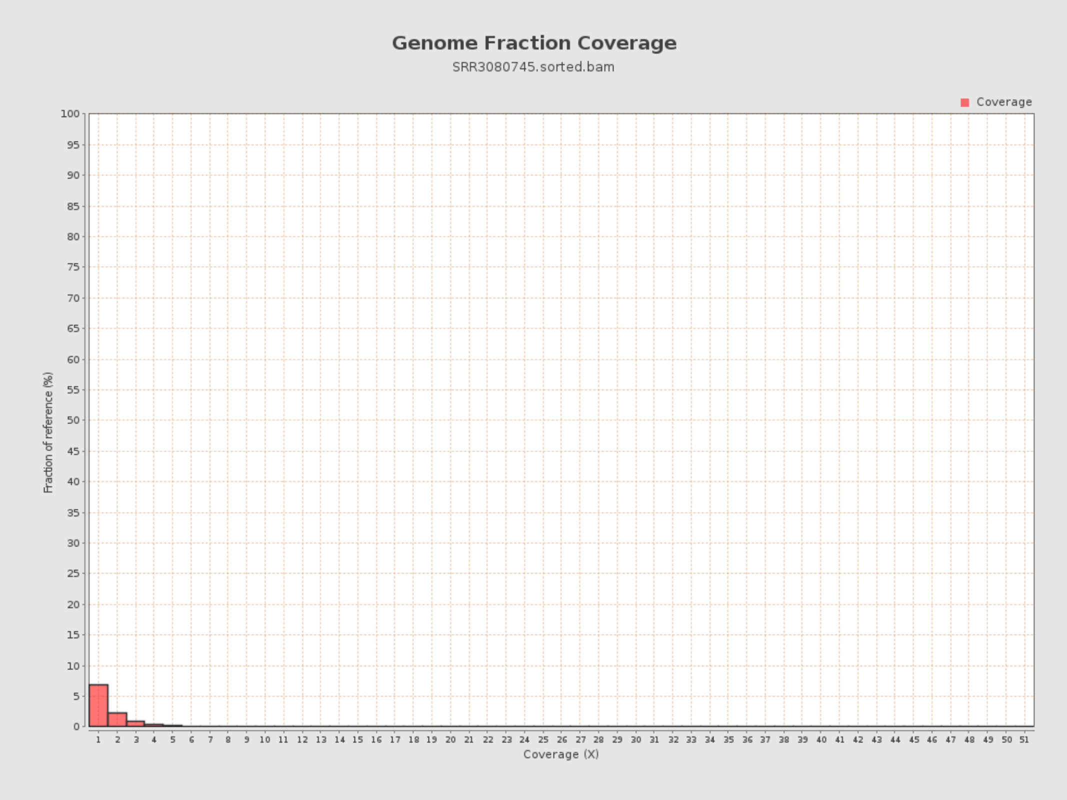
4. Results : Coverage Histogram



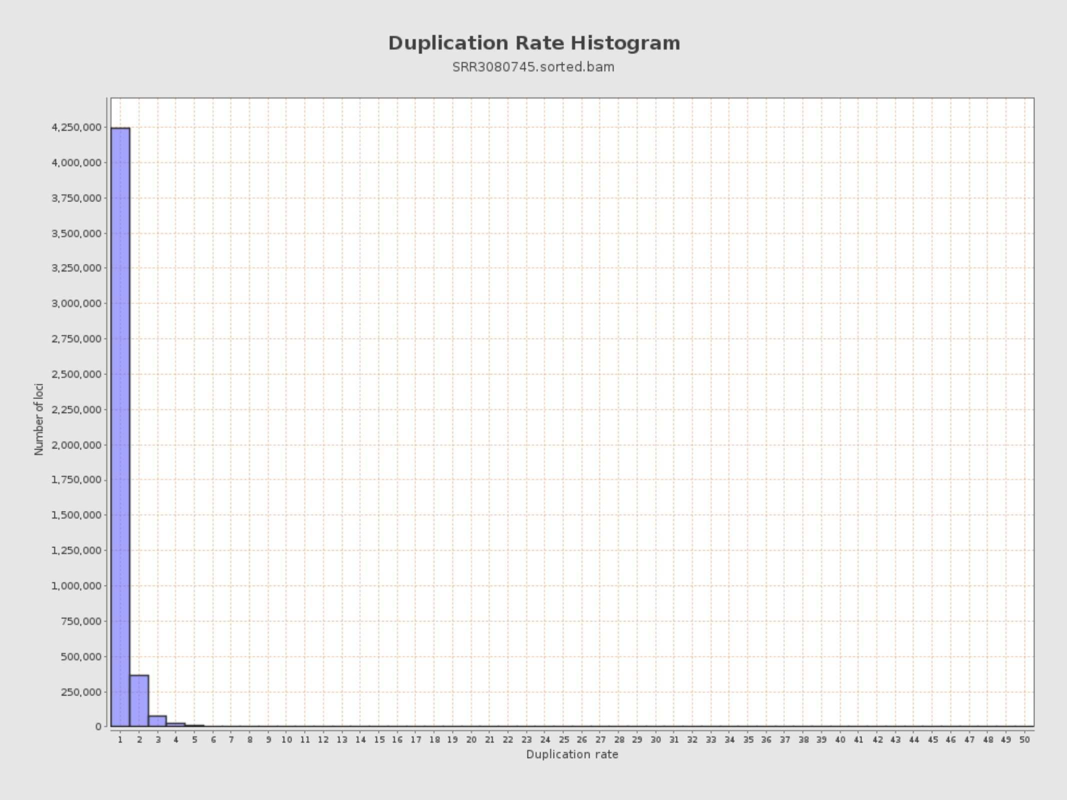
5. Results : Coverage Histogram (0-50X)



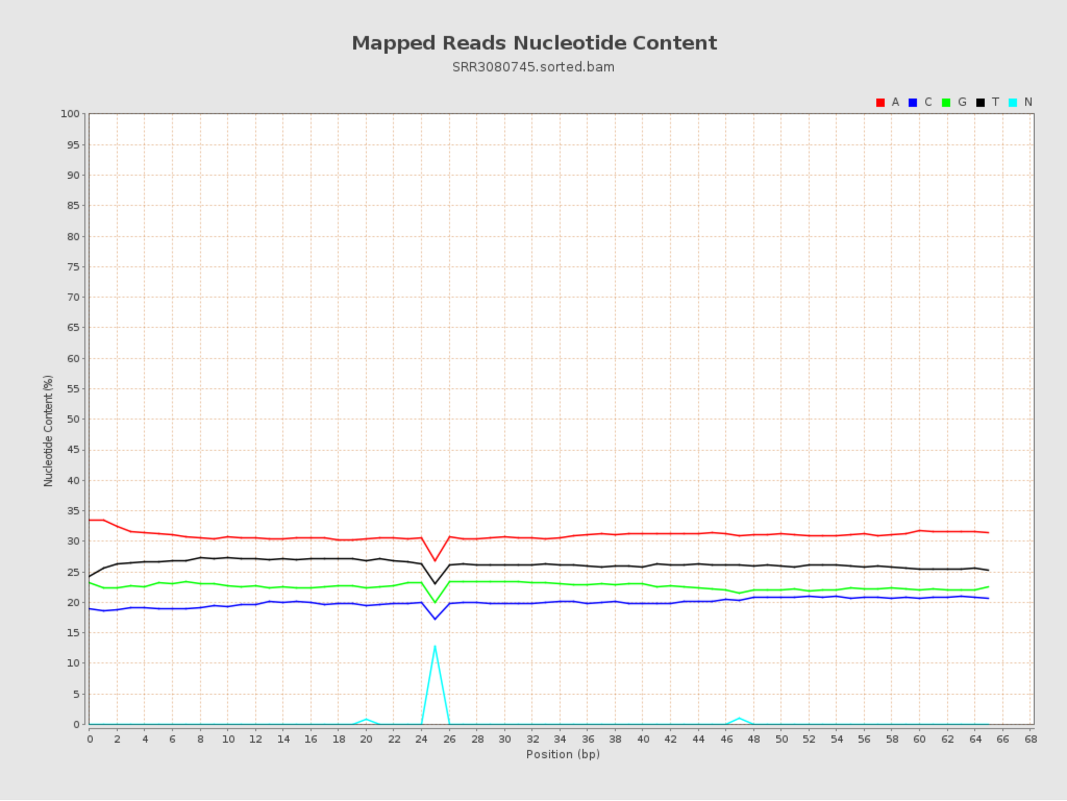
6. Results : Genome Fraction Coverage



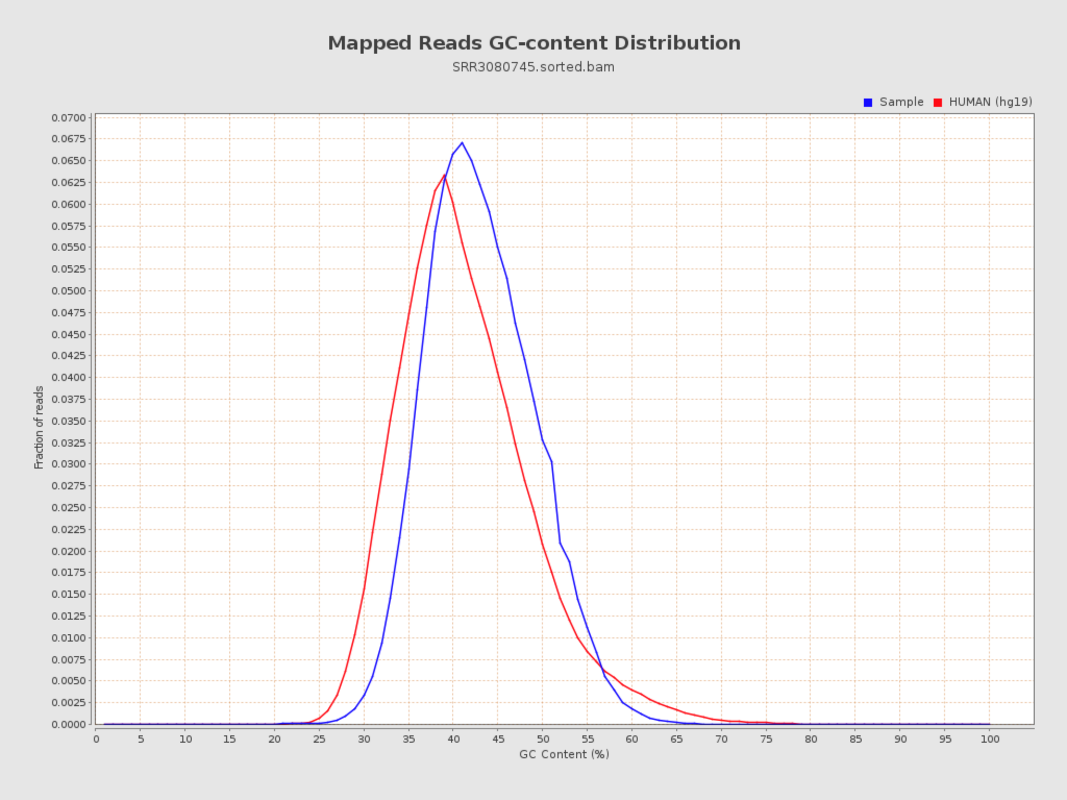
7. Results : Duplication Rate Histogram



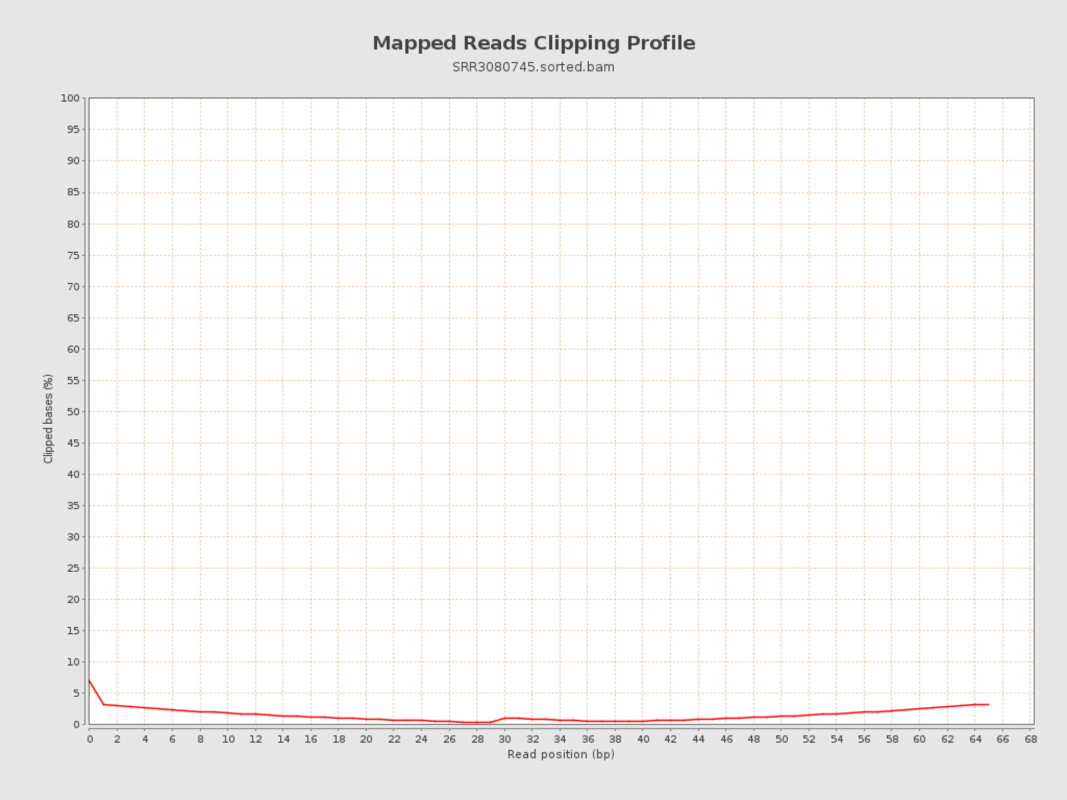
8. Results : Mapped Reads Nucleotide Content



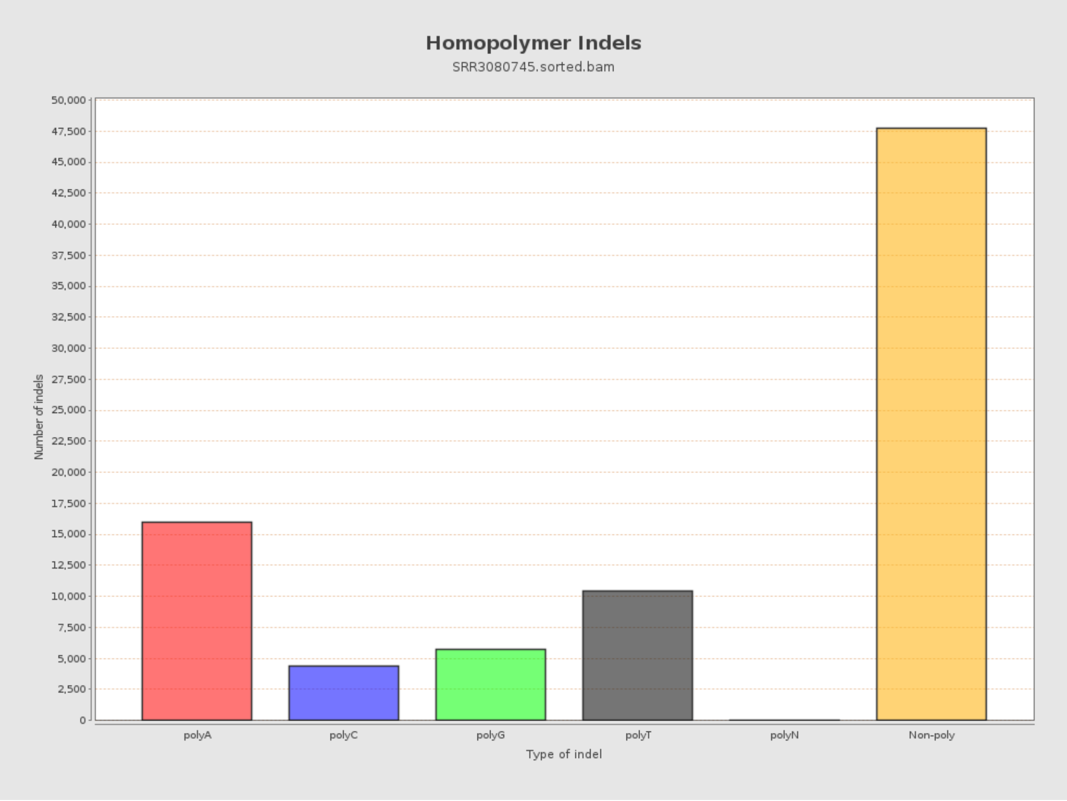
9. Results : Mapped Reads GC-content Distribution



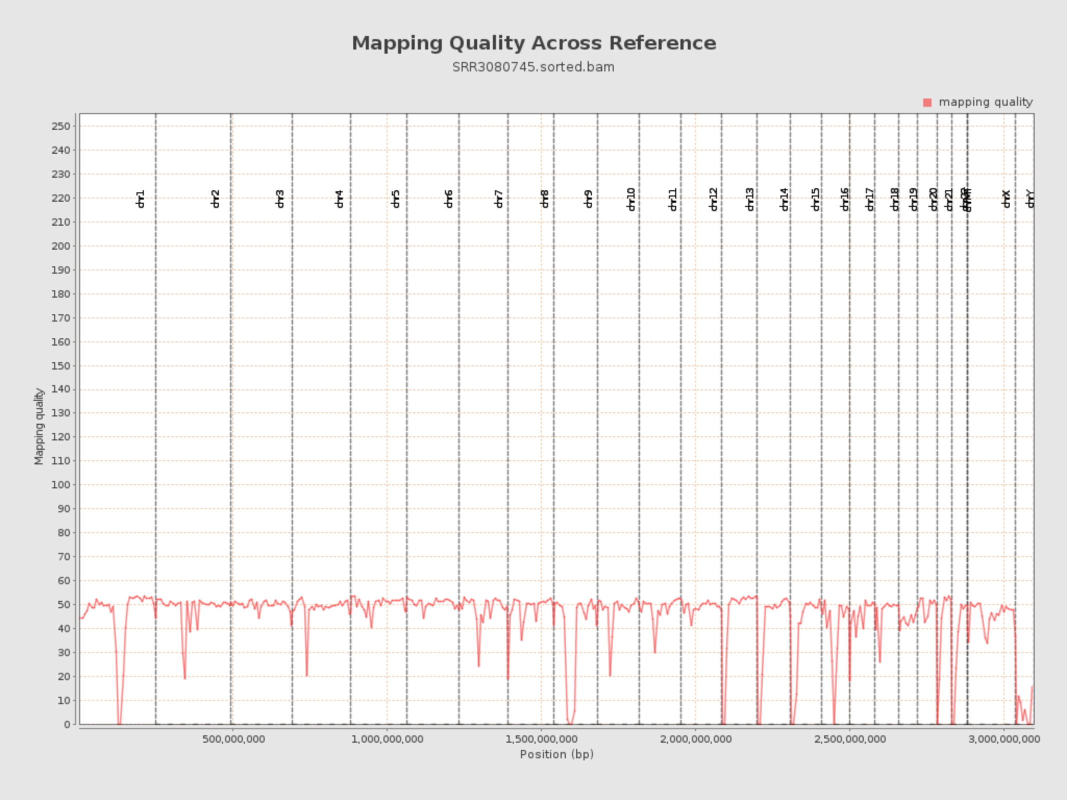
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram