Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:23:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004145.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_SRR6004145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:23:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,130,397
Mapped reads	3,535,259 / 85.59%
Unmapped reads	595,138 / 14.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,368 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	365,335 / 8.85%
Duplication rate	8.28%
Clipped reads	1,570,371 / 38.02%

2.2. ACGT Content

Number/percentage of A's	66,618,560 / 28.21%
Number/percentage of C's	41,822,736 / 17.71%
Number/percentage of T's	77,972,148 / 33.02%
Number/percentage of G's	49,717,456 / 21.05%
Number/percentage of N's	26,351 / 0.01%
GC Percentage	38.76%

2.3. Coverage

Mean	0.0763

Standard Deviation	0.6341

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

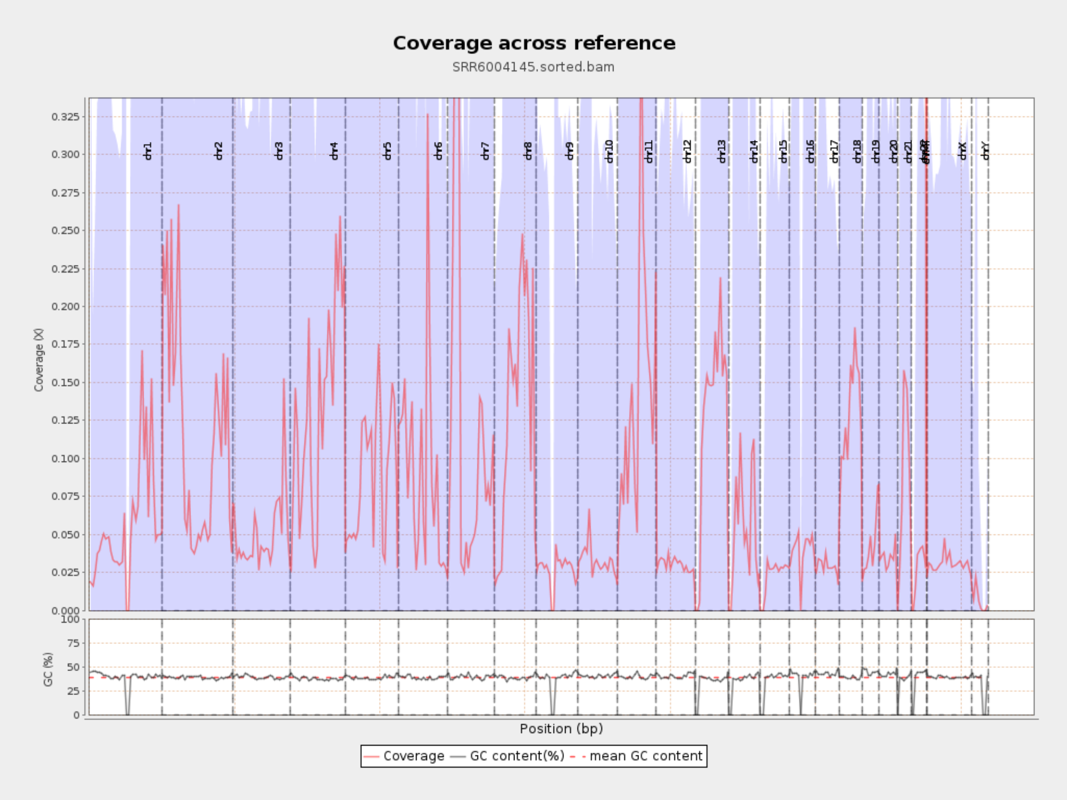
General error rate	0.92%
Mismatches	2,140,683
Insertions	19,455
Mapped reads with at least one insertion	0.55%
Deletions	63,938
Mapped reads with at least one deletion	1.79%
Homopolymer indels	48.44%

2.6. Chromosome stats

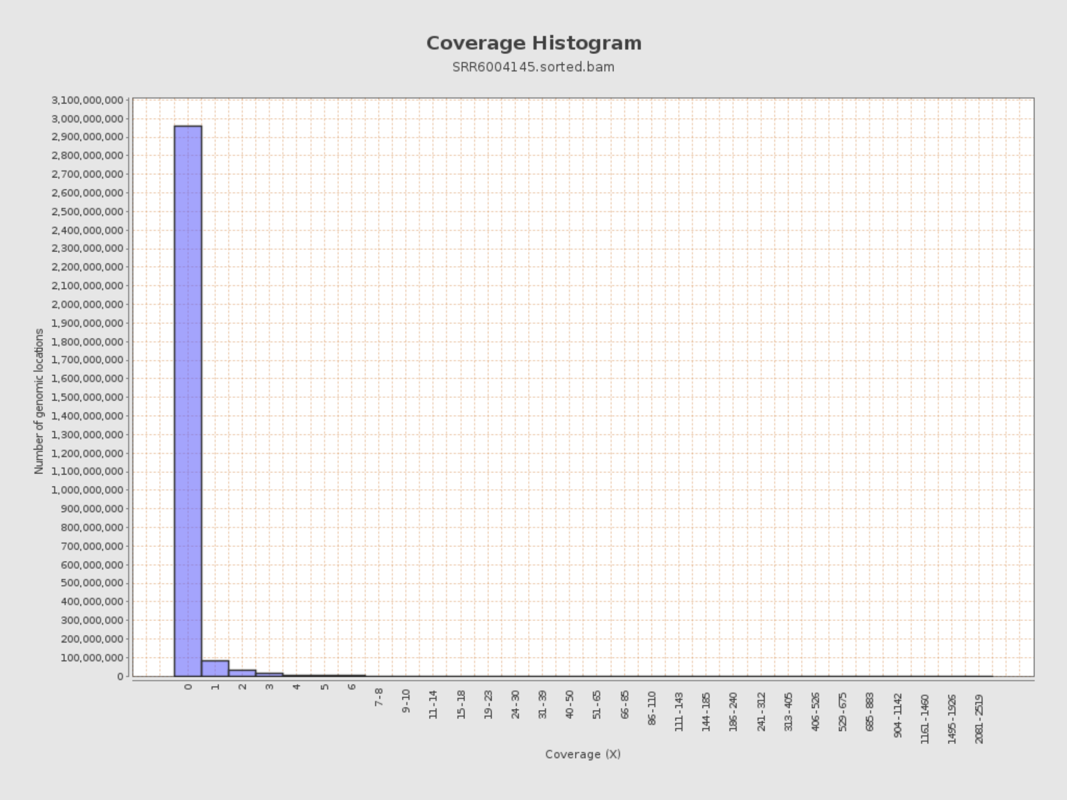
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14047966	0.0564	0.6576
chr2	243199373	28352099	0.1166	0.704
chr3	198022430	10174250	0.0514	0.3584
chr4	191154276	25635019	0.1341	0.5827
chr5	180915260	16125950	0.0891	0.466
chr6	171115067	15824430	0.0925	0.517
chr7	159138663	19684033	0.1237	0.6265

chr8	146364022	19542501	0.1335	1.5381
chr9	141213431	3768314	0.0267	0.3563
chr10	135534747	4526460	0.0334	0.4012
chr11	135006516	19579023	0.145	1.0963
chr12	133851895	4014280	0.03	0.2781
chr13	115169878	14673916	0.1274	0.5506
chr14	107349540	5854396	0.0545	0.3772
chr15	102531392	2387752	0.0233	0.2475
chr16	90354753	3565536	0.0395	0.3202
chr17	81195210	2322202	0.0286	0.4245
chr18	78077248	10332977	0.1323	0.8276
chr19	59128983	2510198	0.0425	0.4743
chr20	63025520	2205408	0.035	0.3049
chr21	48129895	4047823	0.0841	0.4777
chr22	51304566	1360342	0.0265	0.2477
chrMT	16571	574796	34.6869	21.3014
chrX	155270560	4783644	0.0308	0.3419
chrY	59373566	369715	0.0062	0.1634

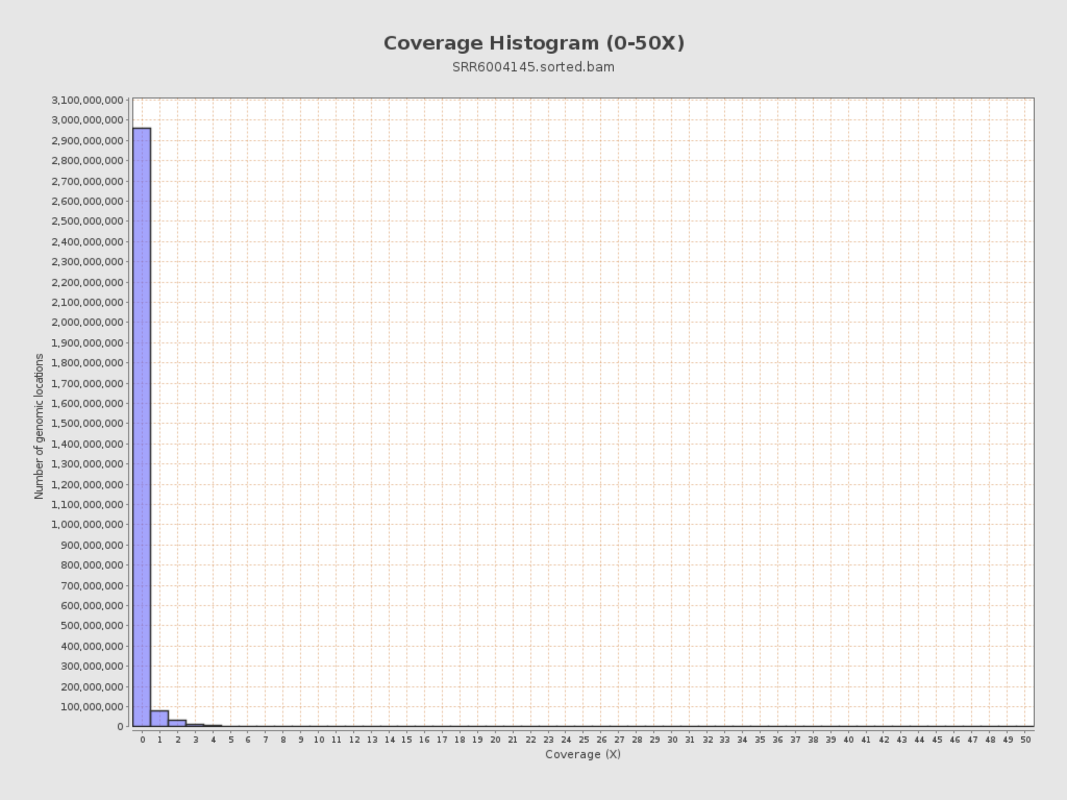
3. Results : Coverage across reference



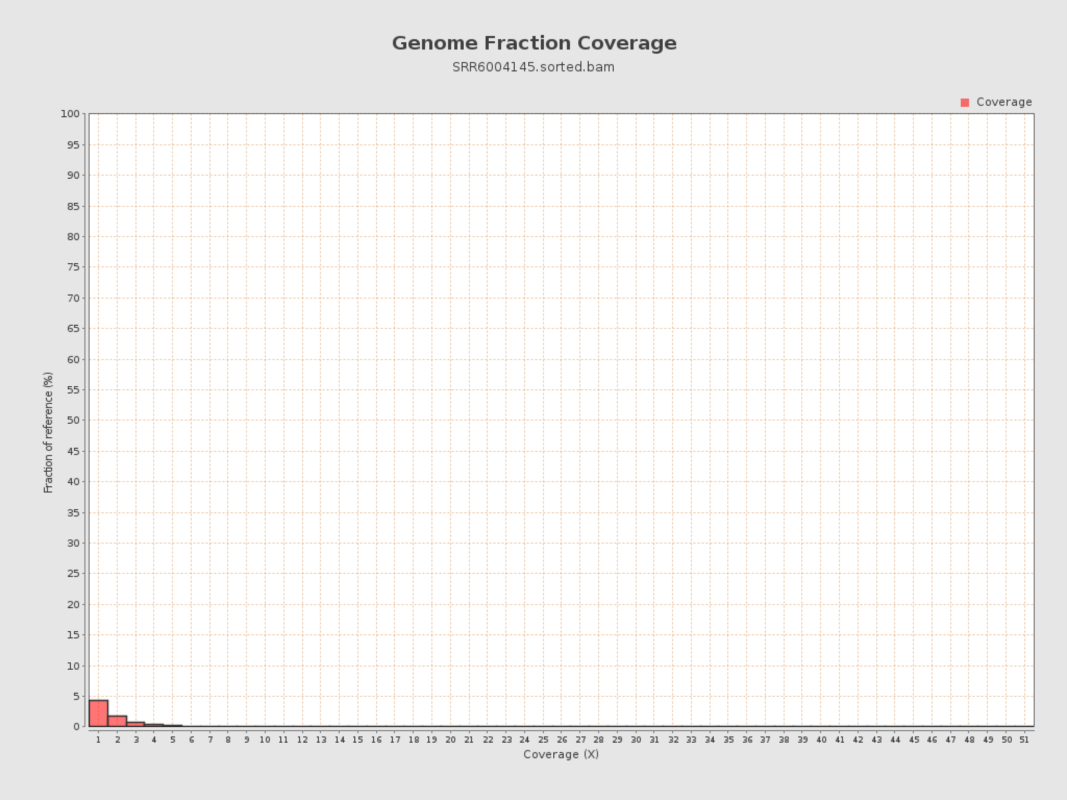
4. Results : Coverage Histogram



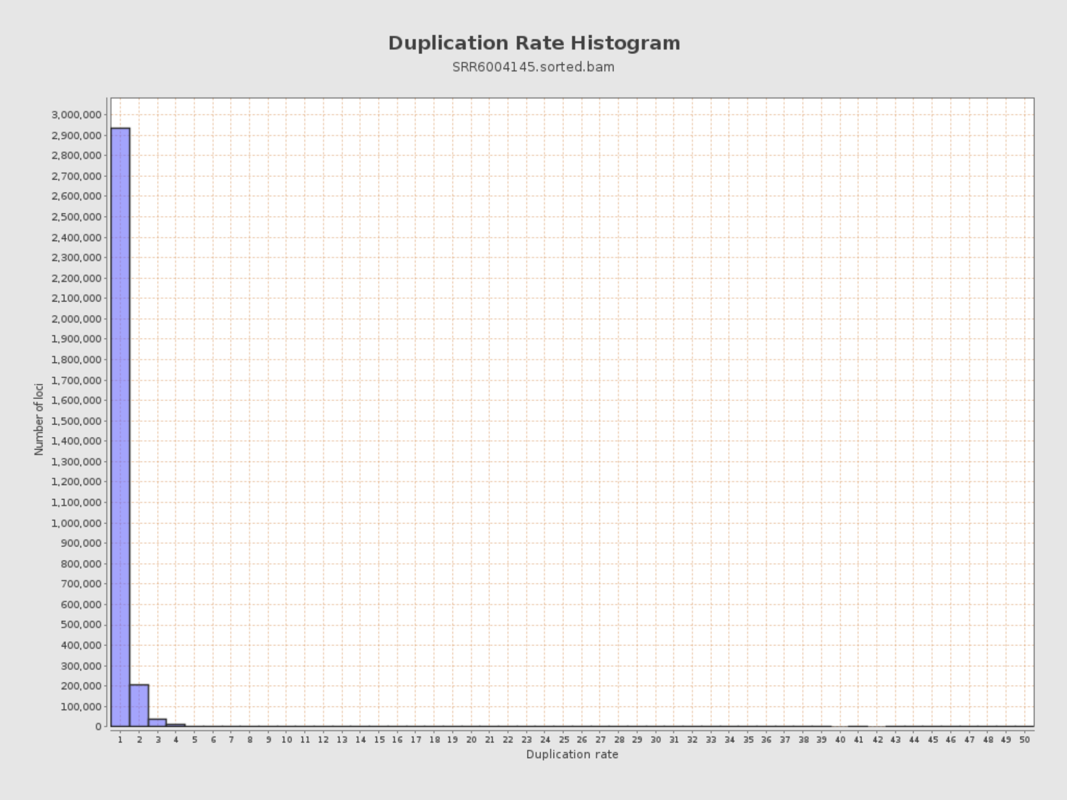
5. Results : Coverage Histogram (0-50X)



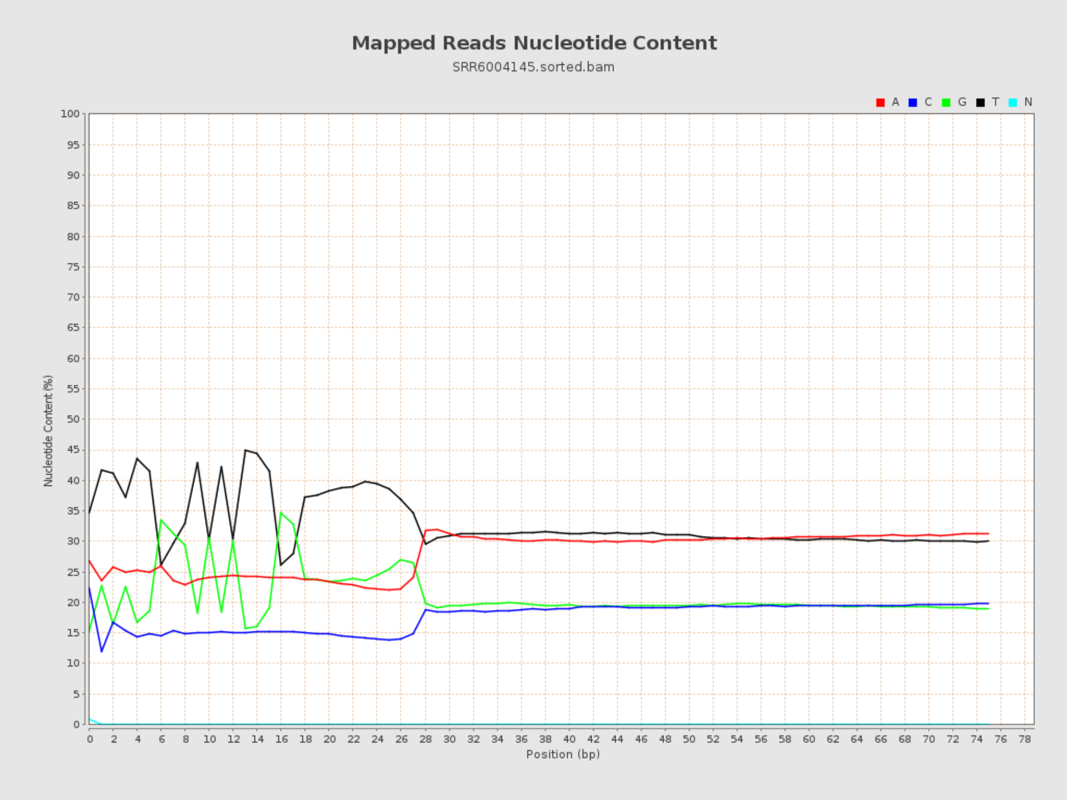
6. Results : Genome Fraction Coverage



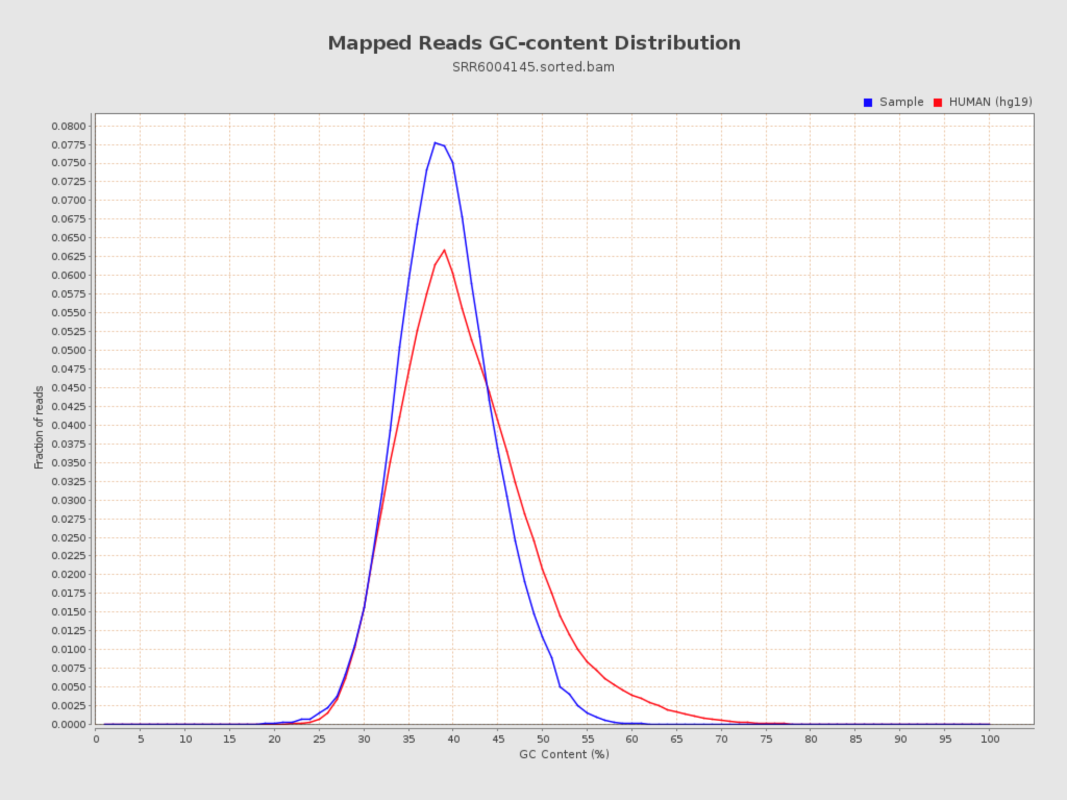
7. Results : Duplication Rate Histogram



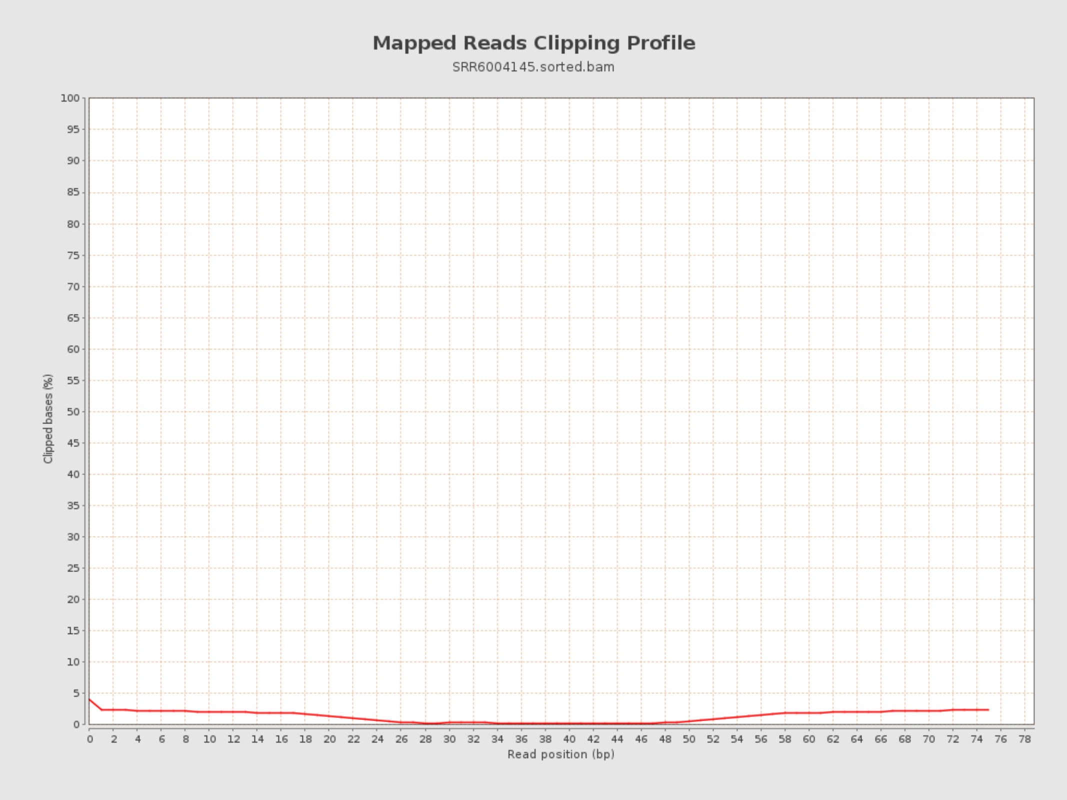
8. Results : Mapped Reads Nucleotide Content



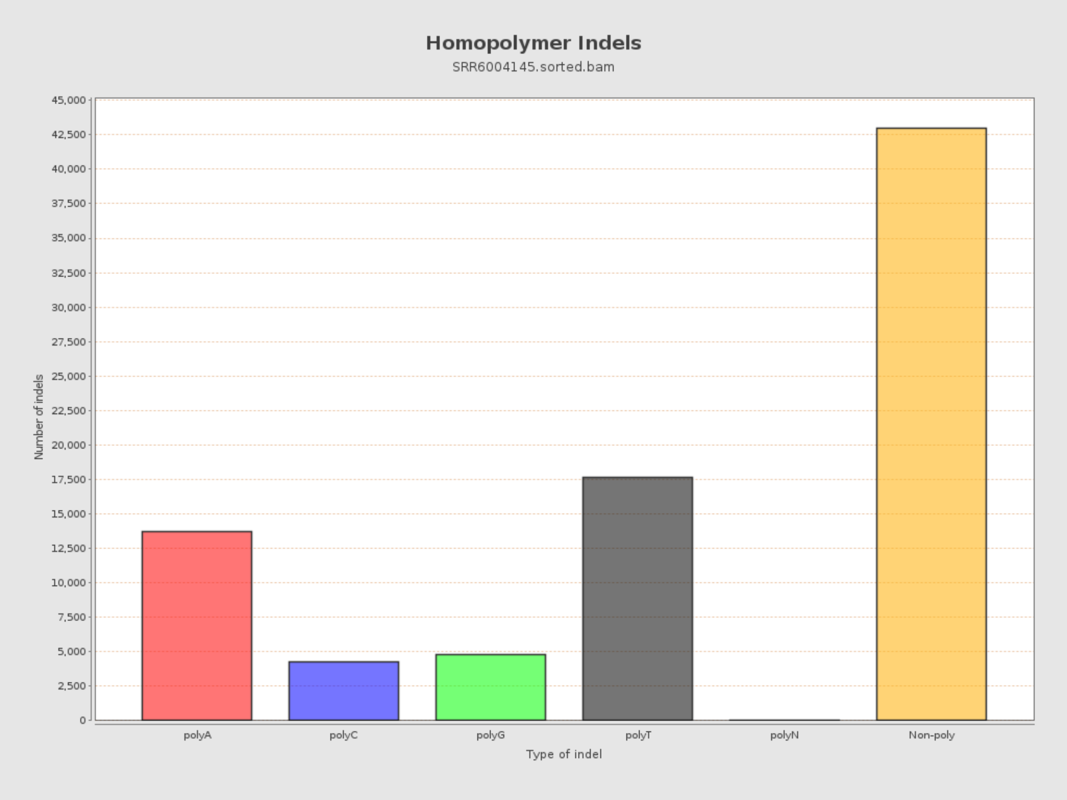
9. Results : Mapped Reads GC-content Distribution



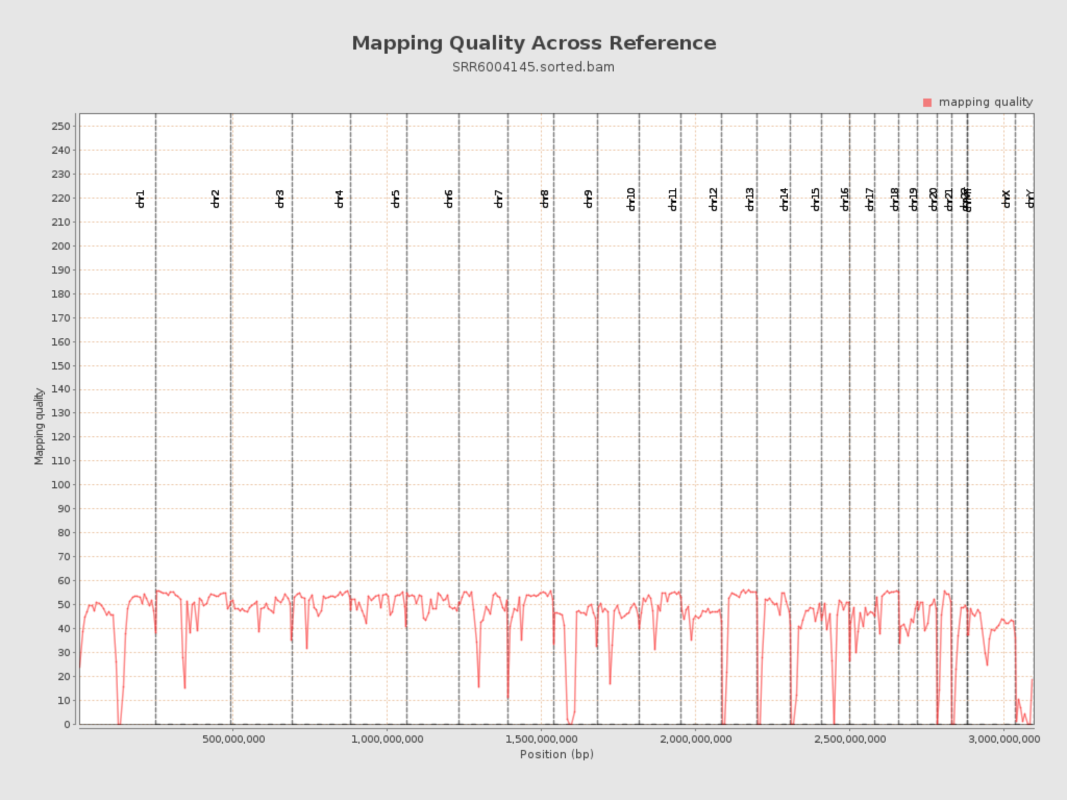
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram