Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:48:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004134.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_SRR6004134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:48:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,450,047
Mapped reads	1,314,350 / 90.64%
Unmapped reads	135,697 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,453 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	47,035 / 3.24%
Duplication rate	2.76%
Clipped reads	546,257 / 37.67%

2.2. ACGT Content

Number/percentage of A's	25,010,066 / 28.23%
Number/percentage of C's	16,159,127 / 18.24%
Number/percentage of T's	28,360,904 / 32.02%
Number/percentage of G's	19,046,842 / 21.5%
Number/percentage of N's	6,483 / 0.01%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2848

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

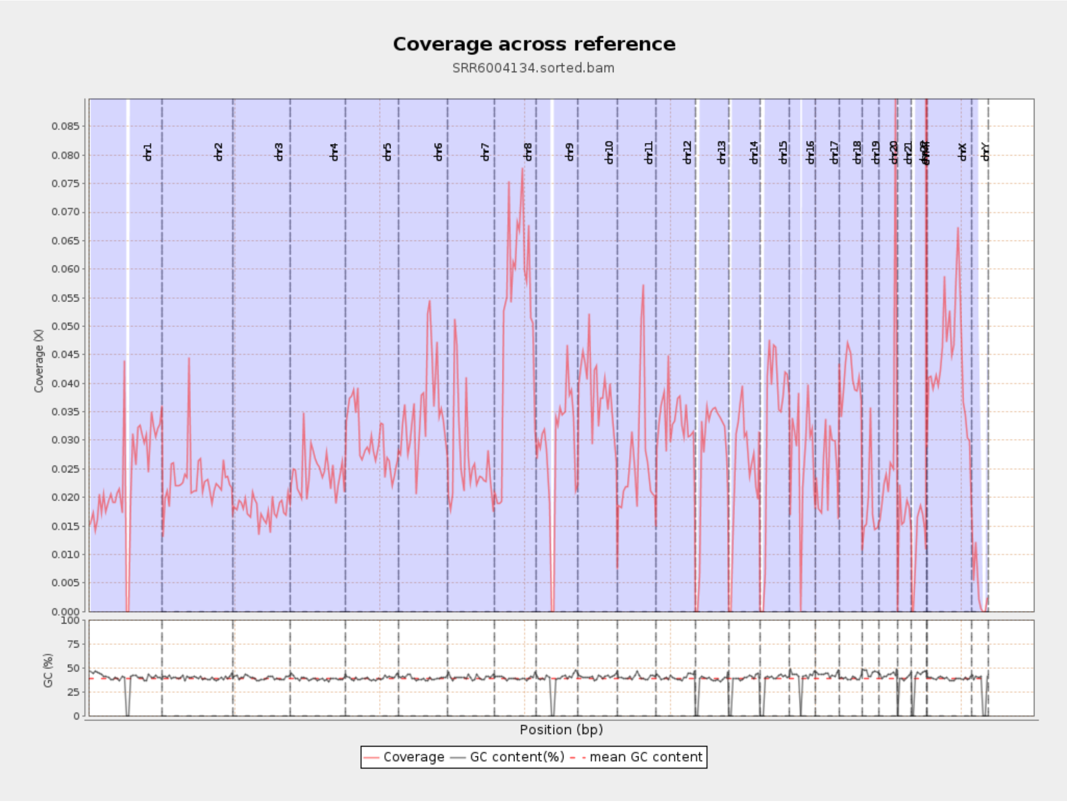
General error rate	0.91%
Mismatches	789,497
Insertions	7,001
Mapped reads with at least one insertion	0.53%
Deletions	25,387
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.3%

2.6. Chromosome stats

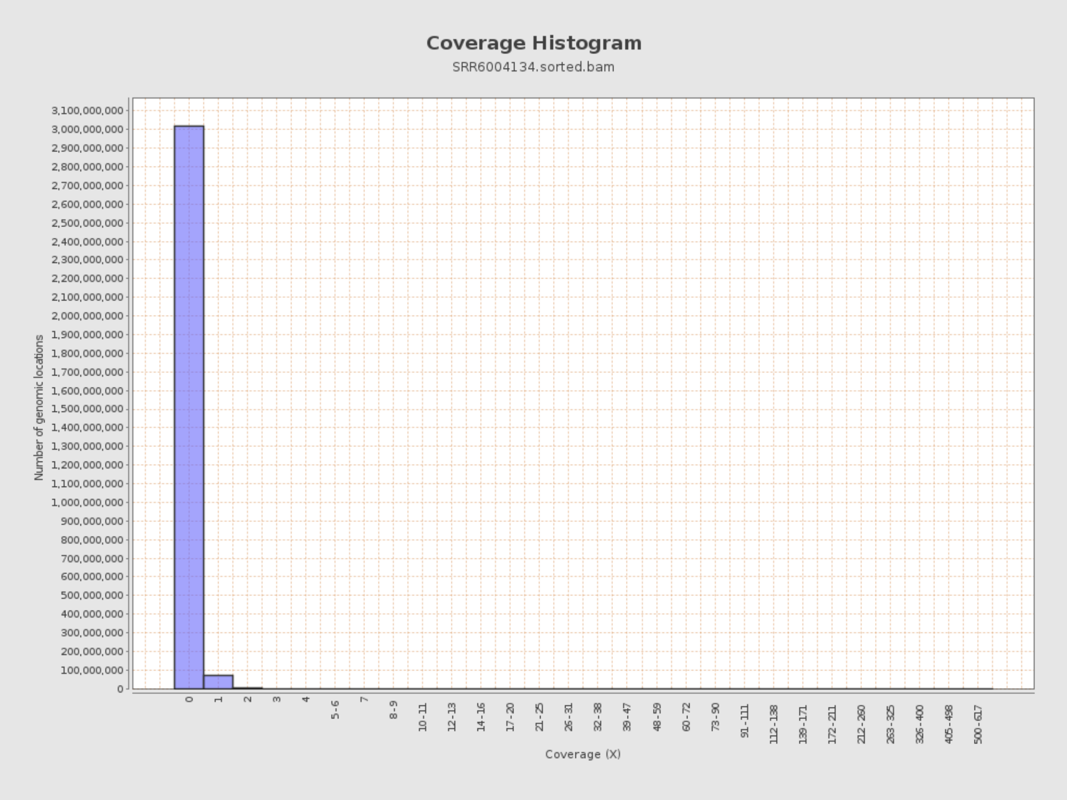
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5796764	0.0233	0.5407
chr2	243199373	5591682	0.023	0.2852
chr3	198022430	3542739	0.0179	0.1447
chr4	191154276	4655771	0.0244	0.1832
chr5	180915260	5410325	0.0299	0.1898
chr6	171115067	6030869	0.0352	0.2167
chr7	159138663	4283620	0.0269	0.2972

chr8	146364022	7472566	0.0511	0.4149
chr9	141213431	4071701	0.0288	0.2795
chr10	135534747	5266257	0.0389	0.2865
chr11	135006516	3610348	0.0267	0.2351
chr12	133851895	4480305	0.0335	0.204
chr13	115169878	3174731	0.0276	0.1834
chr14	107349540	2623699	0.0244	0.1806
chr15	102531392	3361934	0.0328	0.1969
chr16	90354753	2474834	0.0274	0.201
chr17	81195210	2024739	0.0249	0.1882
chr18	78077248	3182245	0.0408	0.4935
chr19	59128983	1086183	0.0184	0.3438
chr20	63025520	2006568	0.0318	0.1983
chr21	48129895	774741	0.0161	0.1587
chr22	51304566	600014	0.0117	0.1155
chrMT	16571	31612	1.9077	1.8293
chrX	155270560	6832132	0.044	0.2489
chrY	59373566	238572	0.004	0.1008

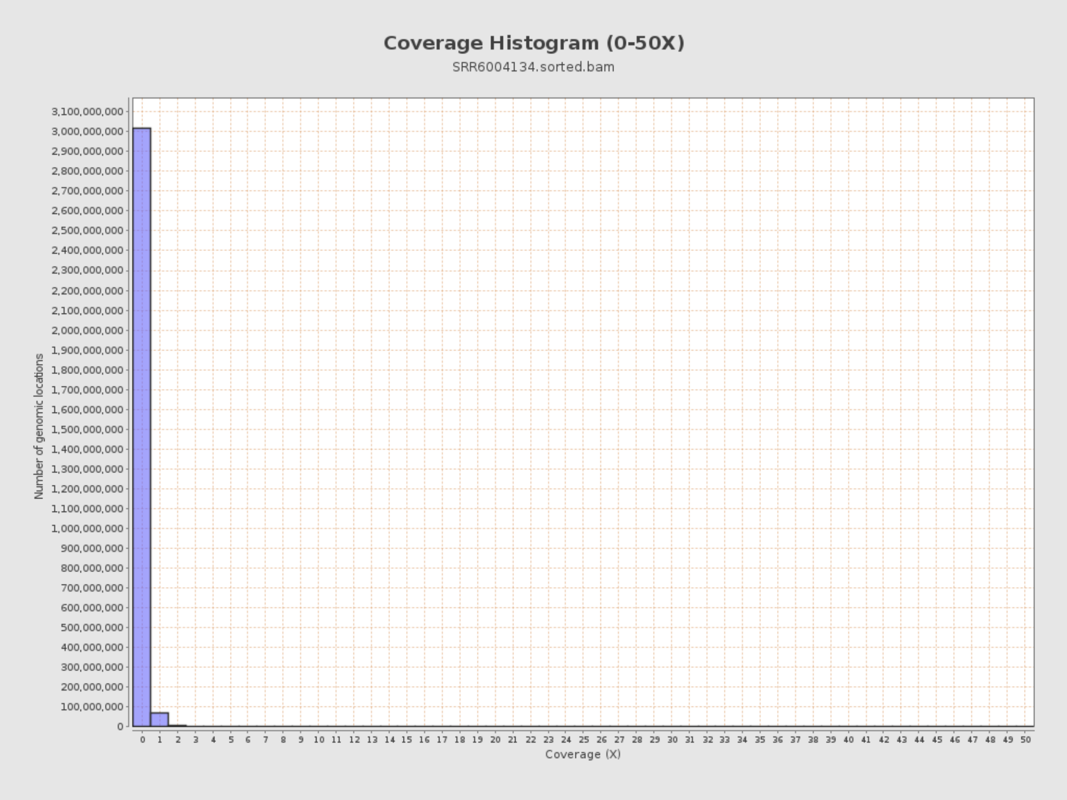
3. Results : Coverage across reference



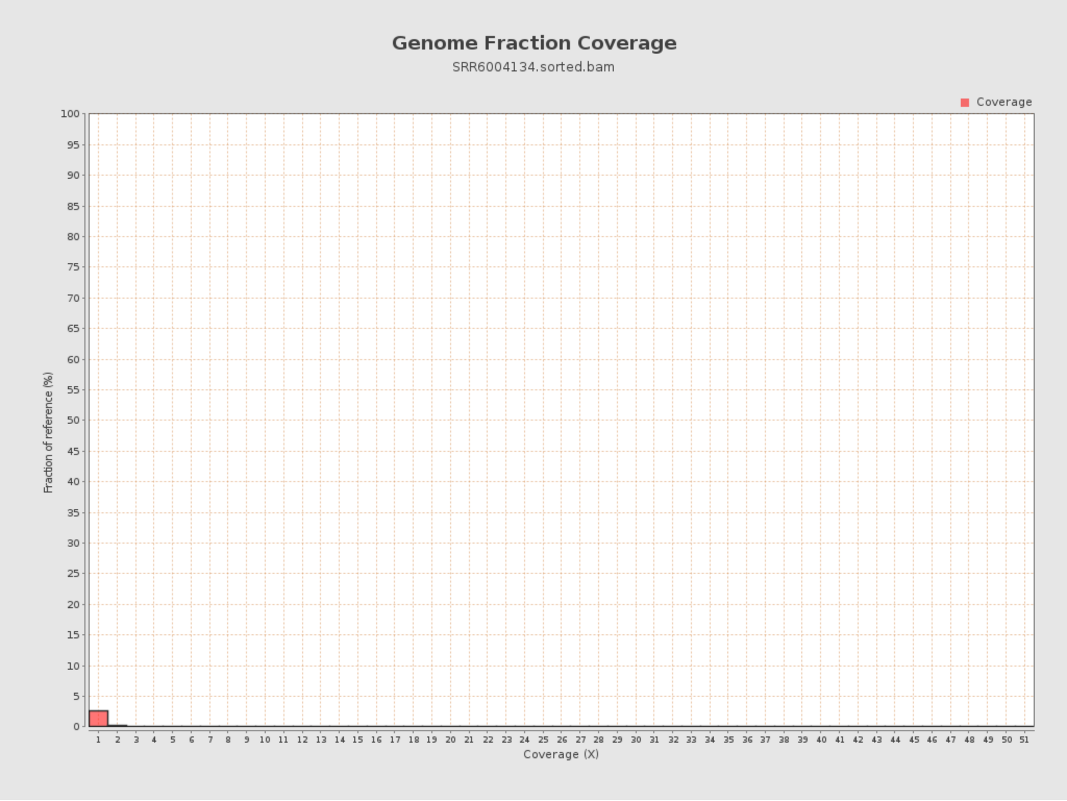
4. Results : Coverage Histogram



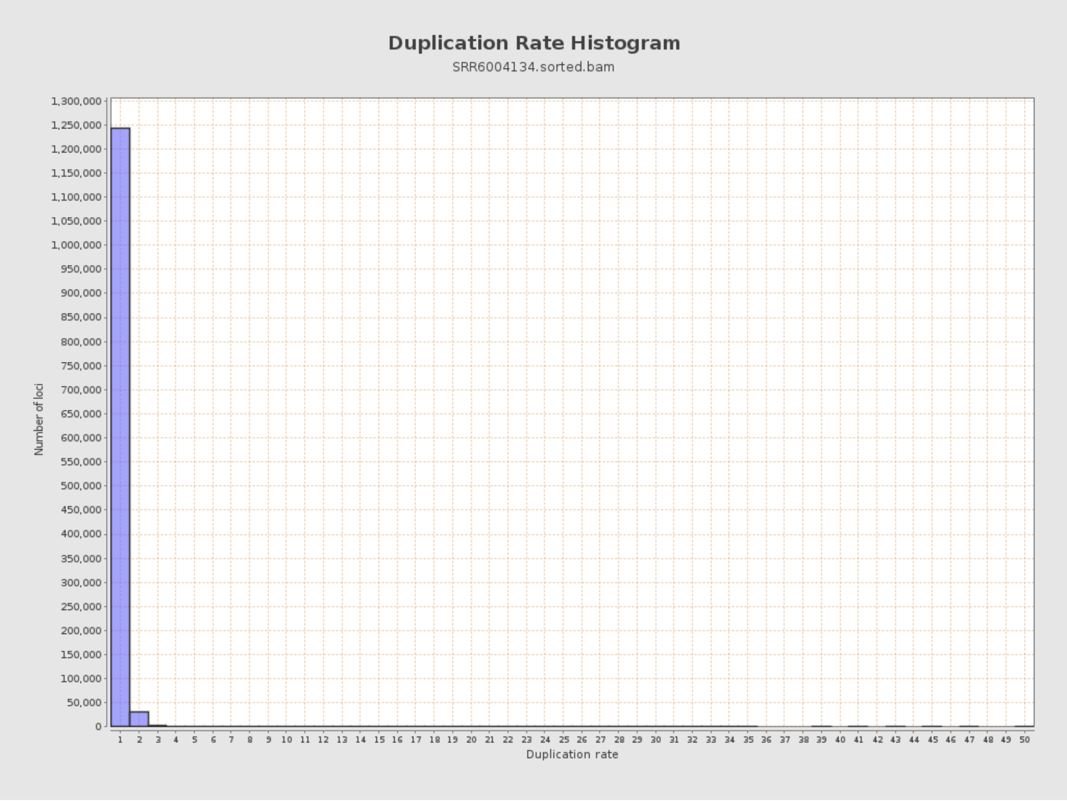
5. Results : Coverage Histogram (0-50X)



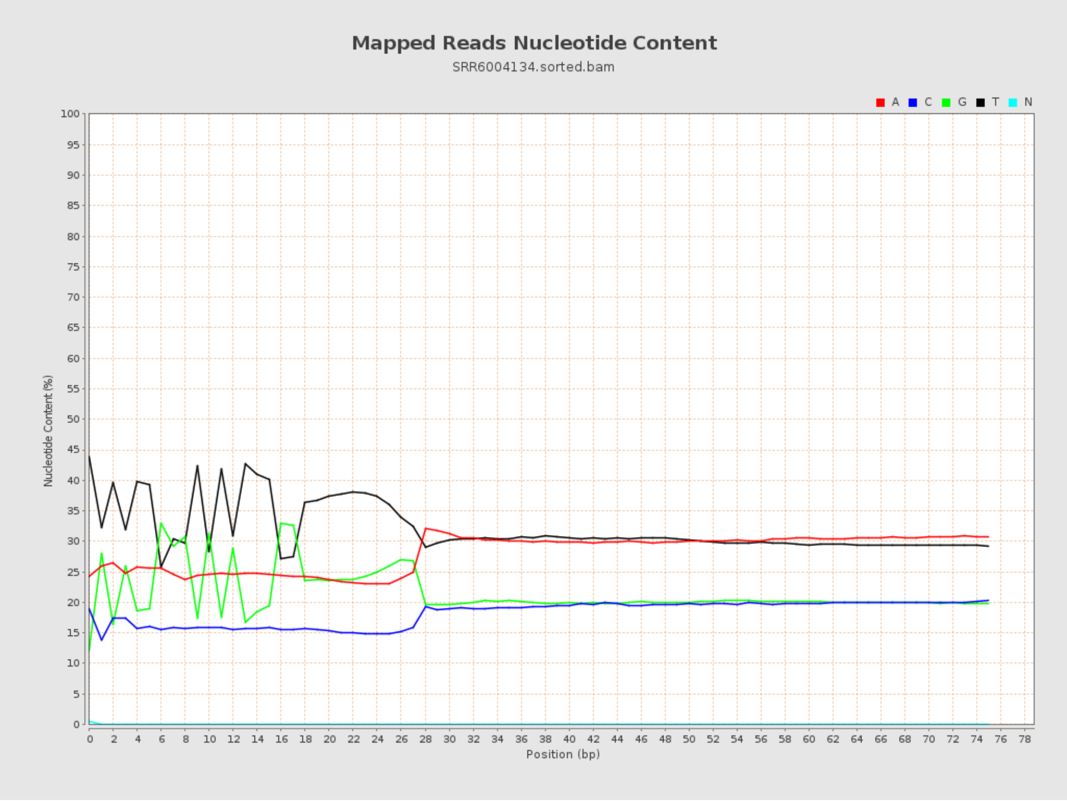
6. Results : Genome Fraction Coverage



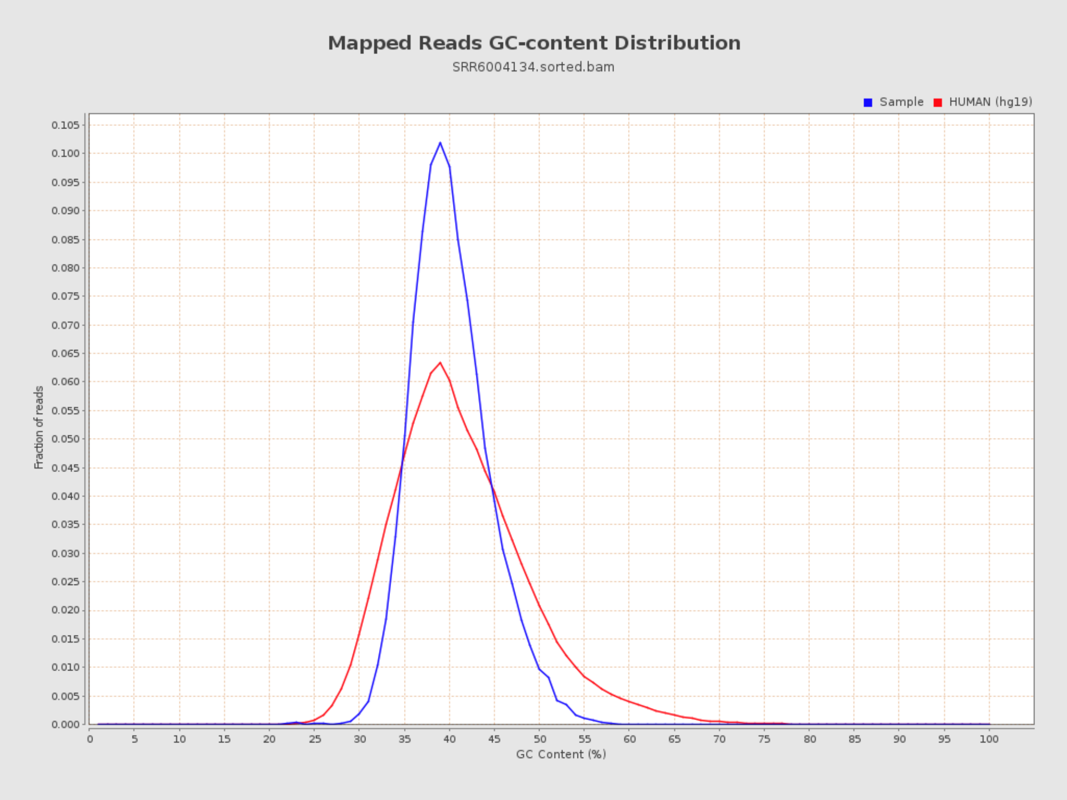
7. Results : Duplication Rate Histogram



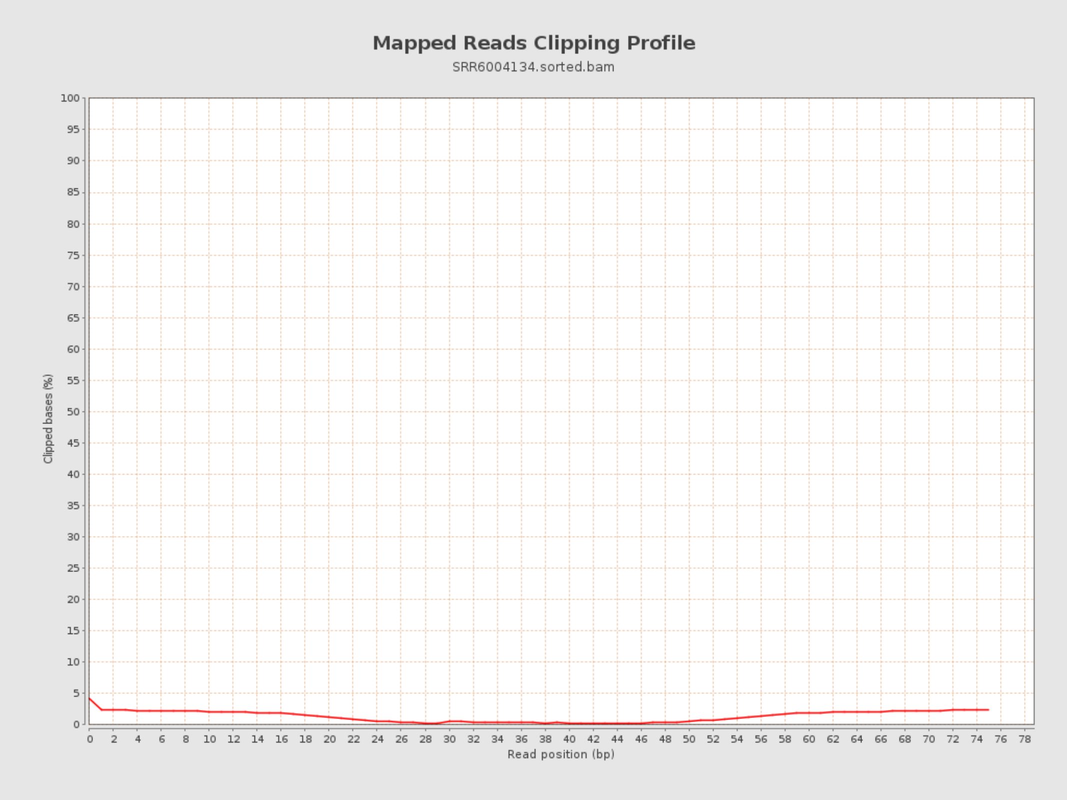
8. Results : Mapped Reads Nucleotide Content



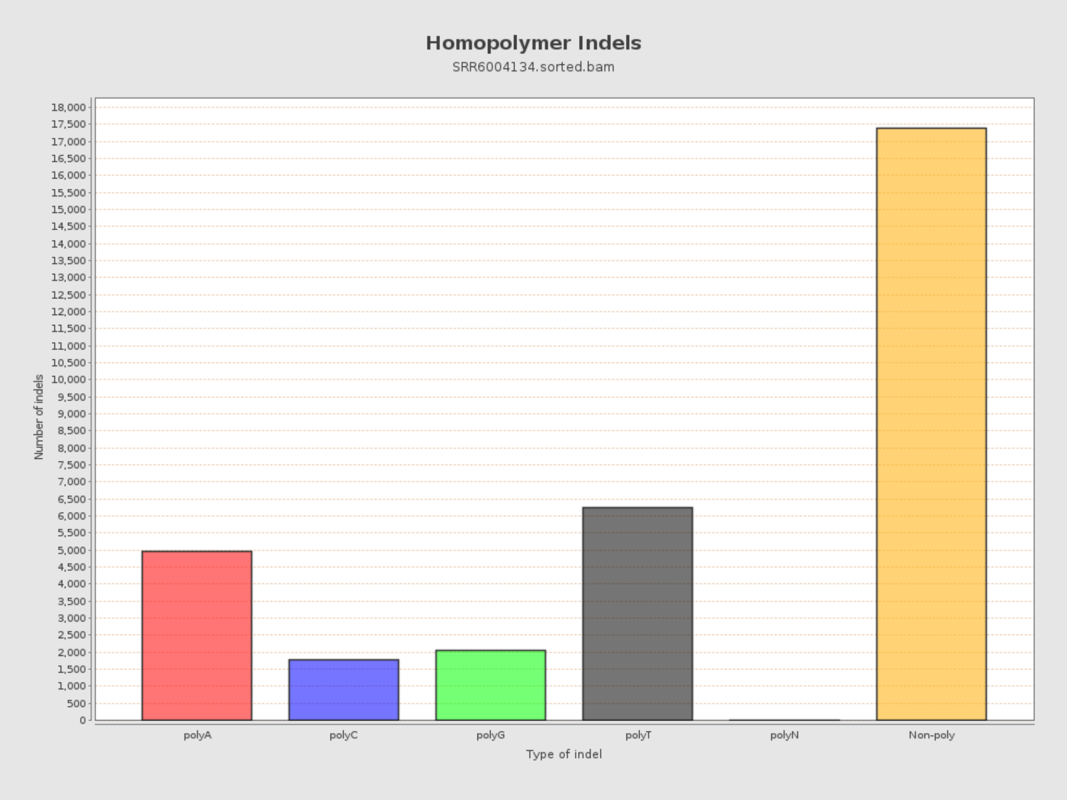
9. Results : Mapped Reads GC-content Distribution



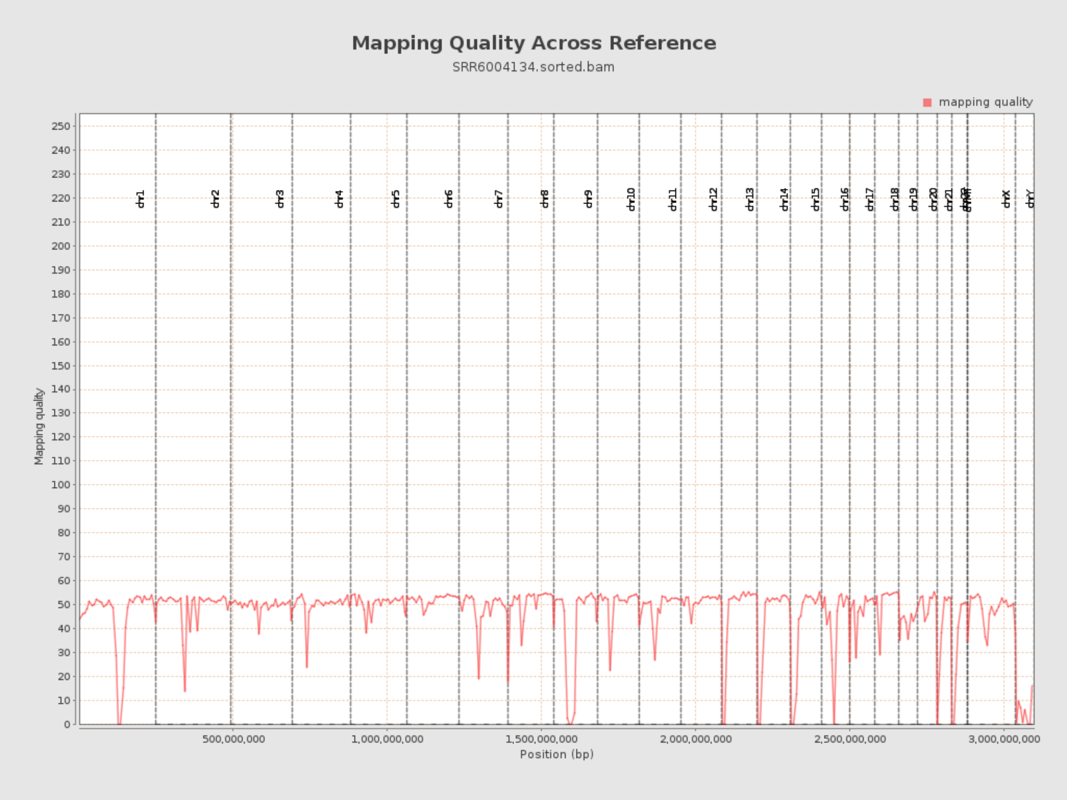
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram