Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:57:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004137.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_SRR6004137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:57:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,741,263
Mapped reads	1,548,965 / 88.96%
Unmapped reads	192,298 / 11.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,406 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	44,466 / 2.55%
Duplication rate	1.77%
Clipped reads	834,244 / 47.91%

2.2. ACGT Content

Number/percentage of A's	27,843,328 / 27.63%
Number/percentage of C's	18,642,841 / 18.5%
Number/percentage of T's	30,428,991 / 30.2%
Number/percentage of G's	23,830,149 / 23.65%
Number/percentage of N's	20,438 / 0.02%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3589

2.4. Mapping Quality

Mean Mapping Quality	41.95

2.5. Mismatches and indels

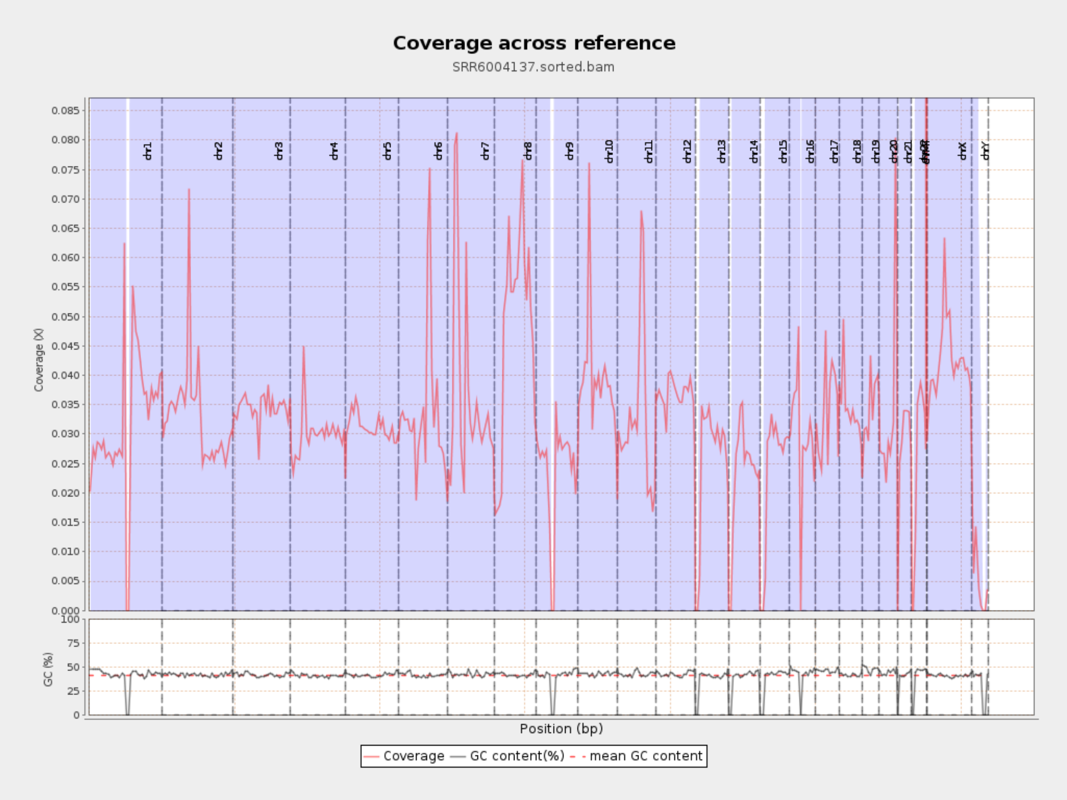
General error rate	0.91%
Mismatches	901,373
Insertions	9,249
Mapped reads with at least one insertion	0.59%
Deletions	28,966
Mapped reads with at least one deletion	1.85%
Homopolymer indels	43.61%

2.6. Chromosome stats

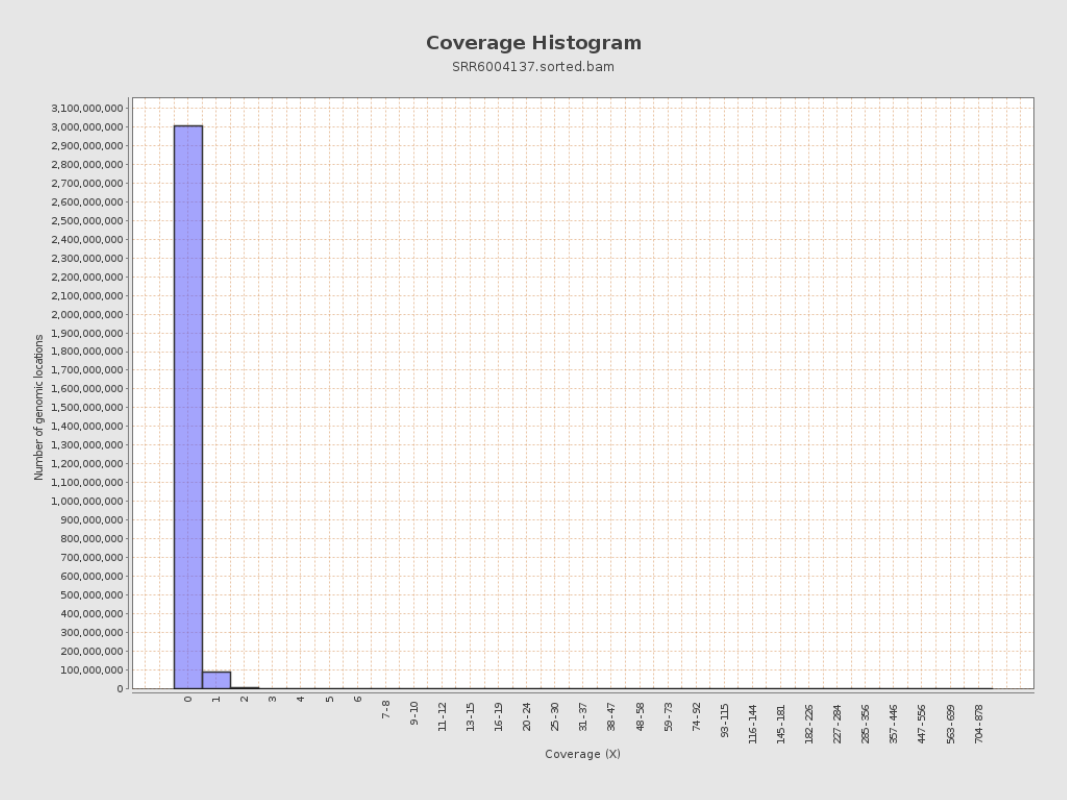
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7920860	0.0318	0.7407
chr2	243199373	8036451	0.033	0.4042
chr3	198022430	6808090	0.0344	0.2016
chr4	191154276	5708036	0.0299	0.1996
chr5	180915260	5656546	0.0313	0.1901
chr6	171115067	5784709	0.0338	0.2213
chr7	159138663	5943335	0.0373	0.4656

chr8	146364022	6998424	0.0478	0.3838
chr9	141213431	3342118	0.0237	0.3017
chr10	135534747	5389390	0.0398	0.3945
chr11	135006516	4440867	0.0329	0.2964
chr12	133851895	4934357	0.0369	0.2087
chr13	115169878	2938814	0.0255	0.1688
chr14	107349540	2457445	0.0229	0.1912
chr15	102531392	2414758	0.0236	0.1725
chr16	90354753	2668035	0.0295	0.2324
chr17	81195210	2781852	0.0343	0.2211
chr18	78077248	2714043	0.0348	0.6359
chr19	59128983	2041733	0.0345	0.5018
chr20	63025520	2229172	0.0354	0.2171
chr21	48129895	1333640	0.0277	0.1983
chr22	51304566	1265559	0.0247	0.1653
chrMT	16571	104936	6.3325	4.7789
chrX	155270560	6601079	0.0425	0.2568
chrY	59373566	299985	0.0051	0.1097

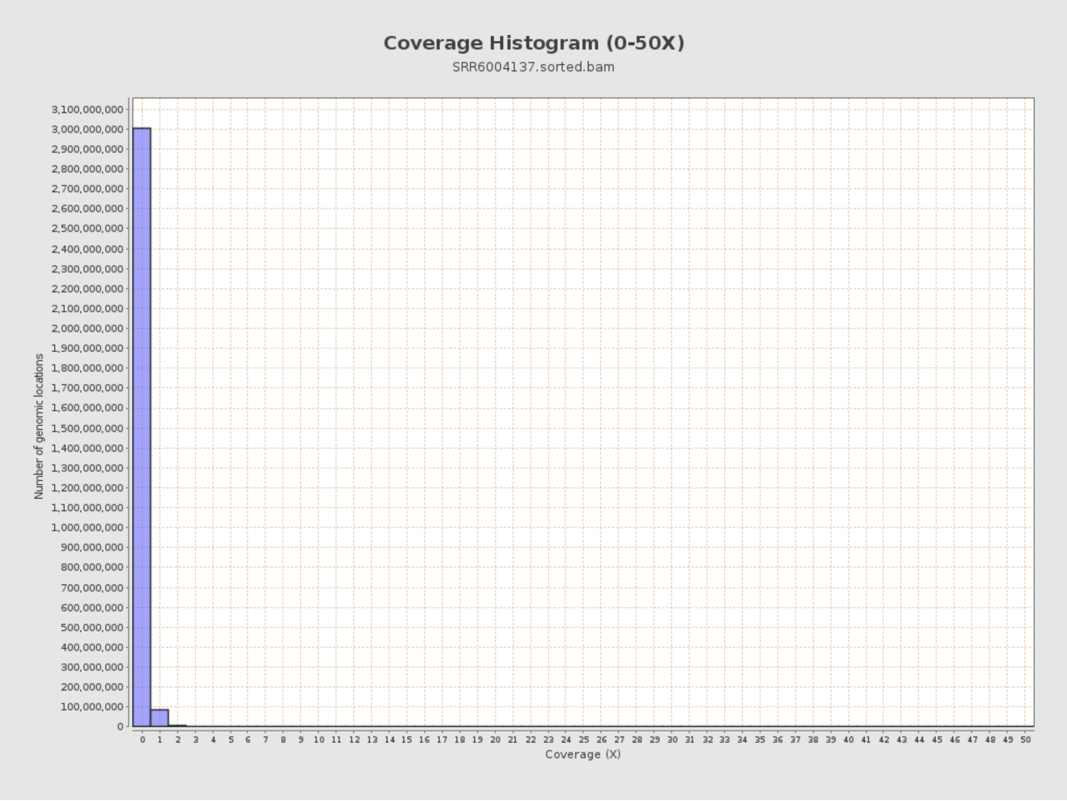
3. Results : Coverage across reference



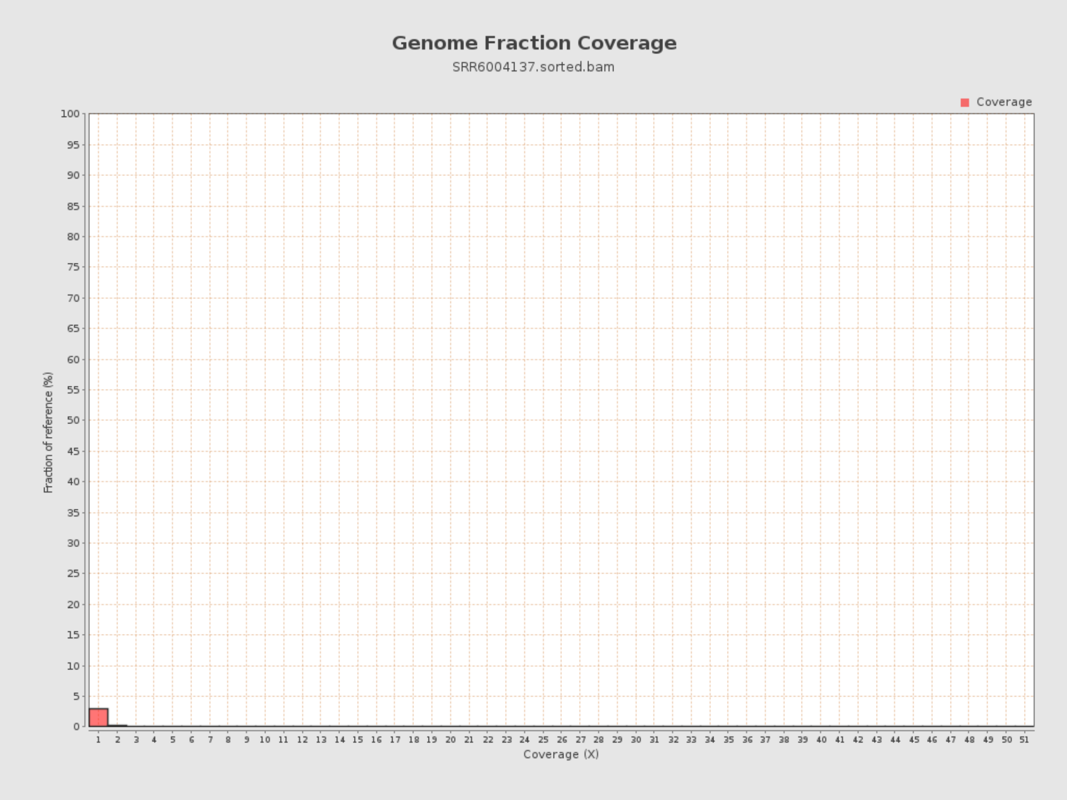
4. Results : Coverage Histogram



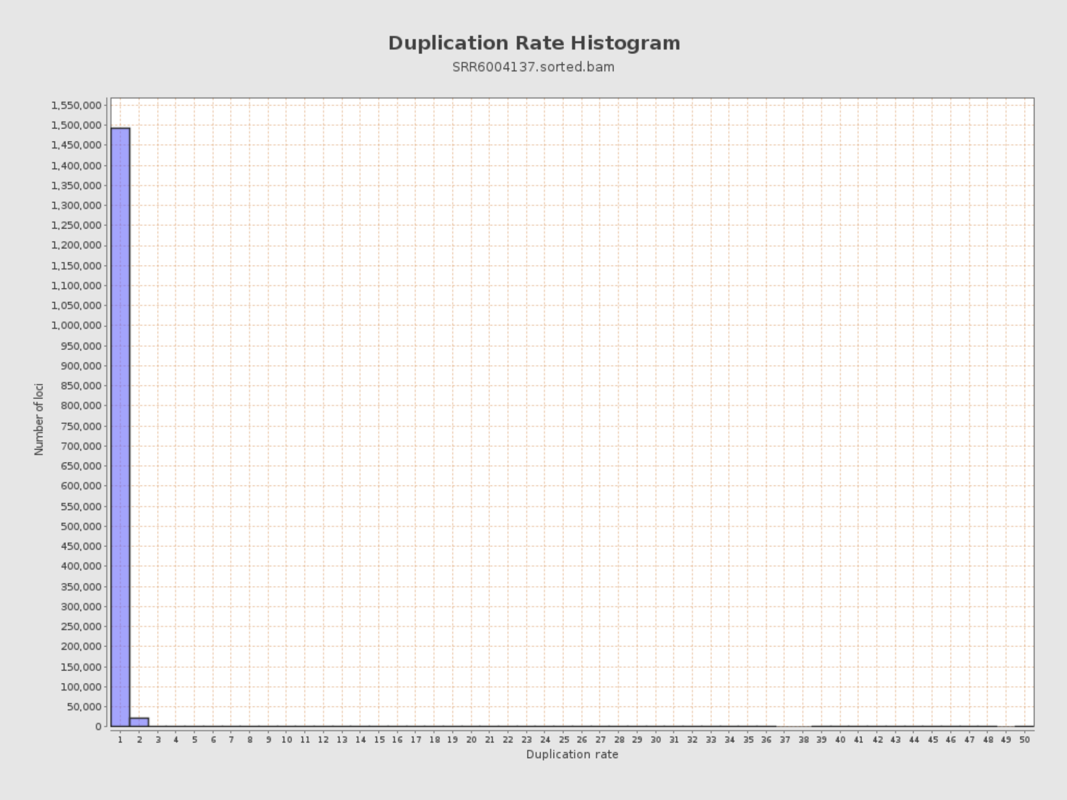
5. Results : Coverage Histogram (0-50X)



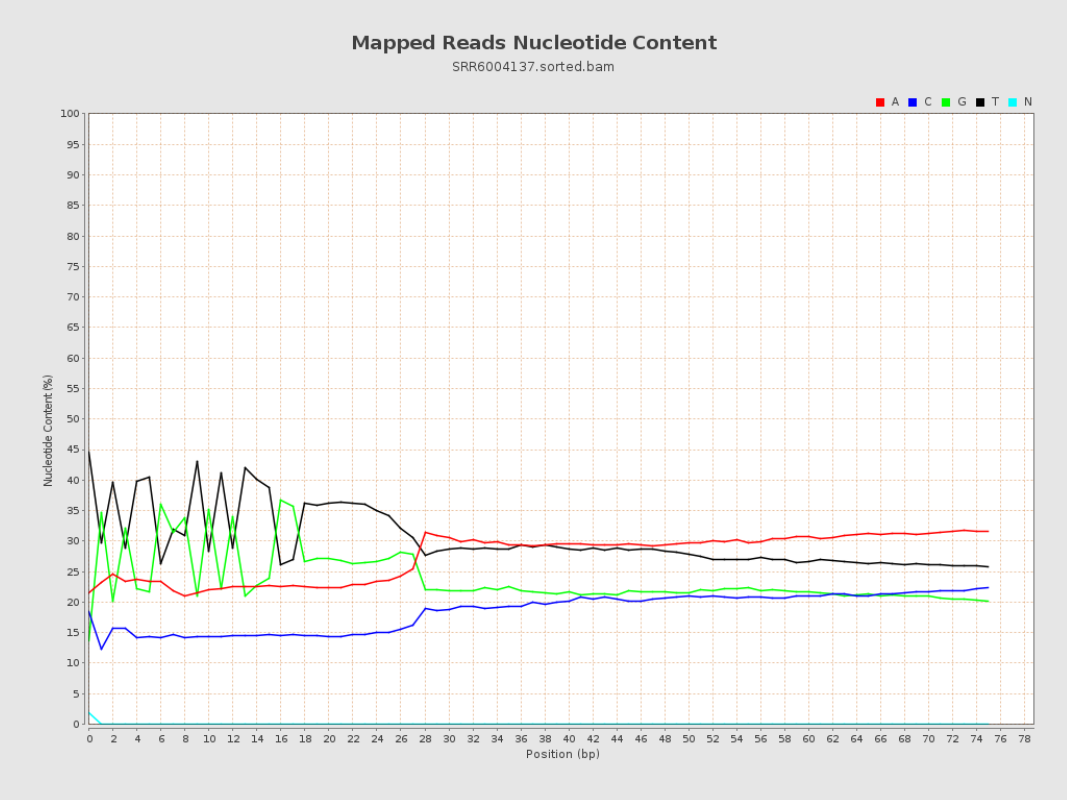
6. Results : Genome Fraction Coverage



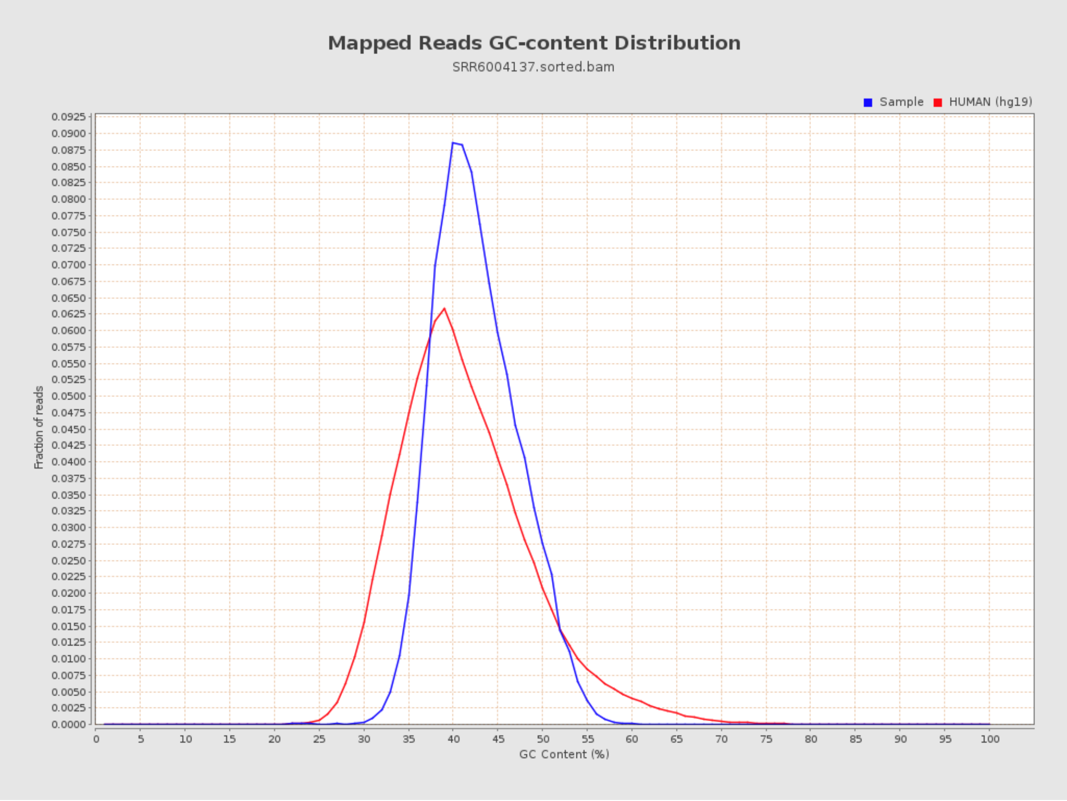
7. Results : Duplication Rate Histogram



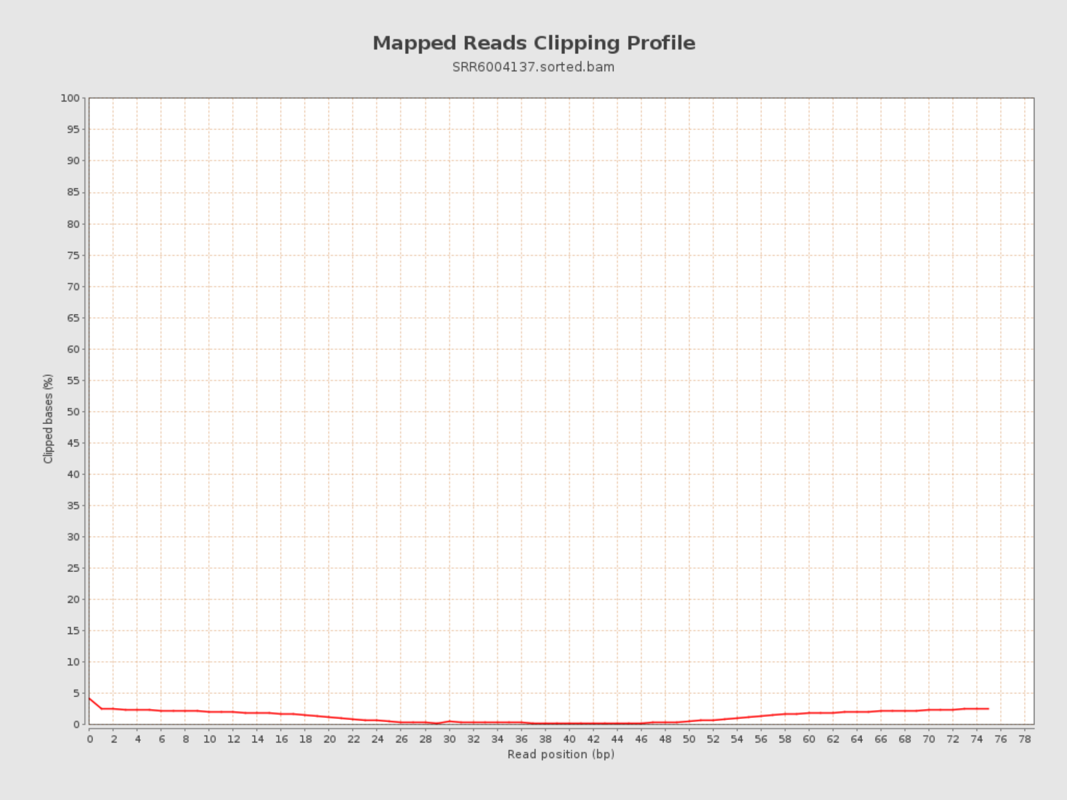
8. Results : Mapped Reads Nucleotide Content



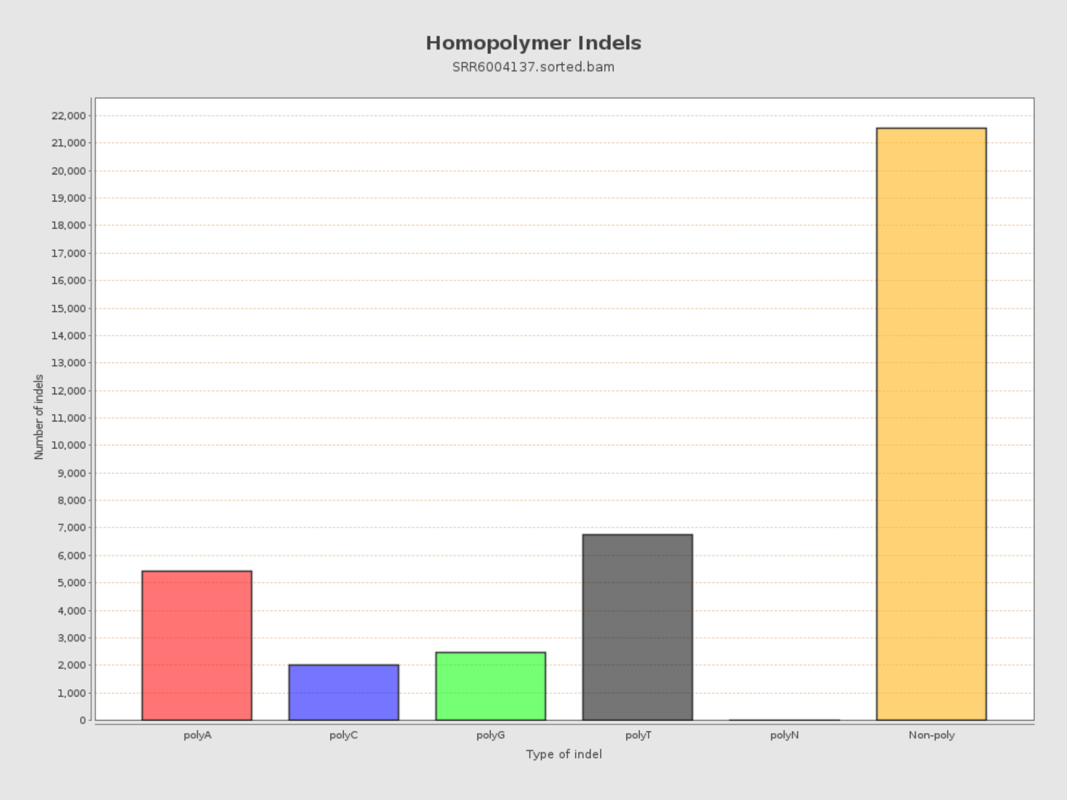
9. Results : Mapped Reads GC-content Distribution



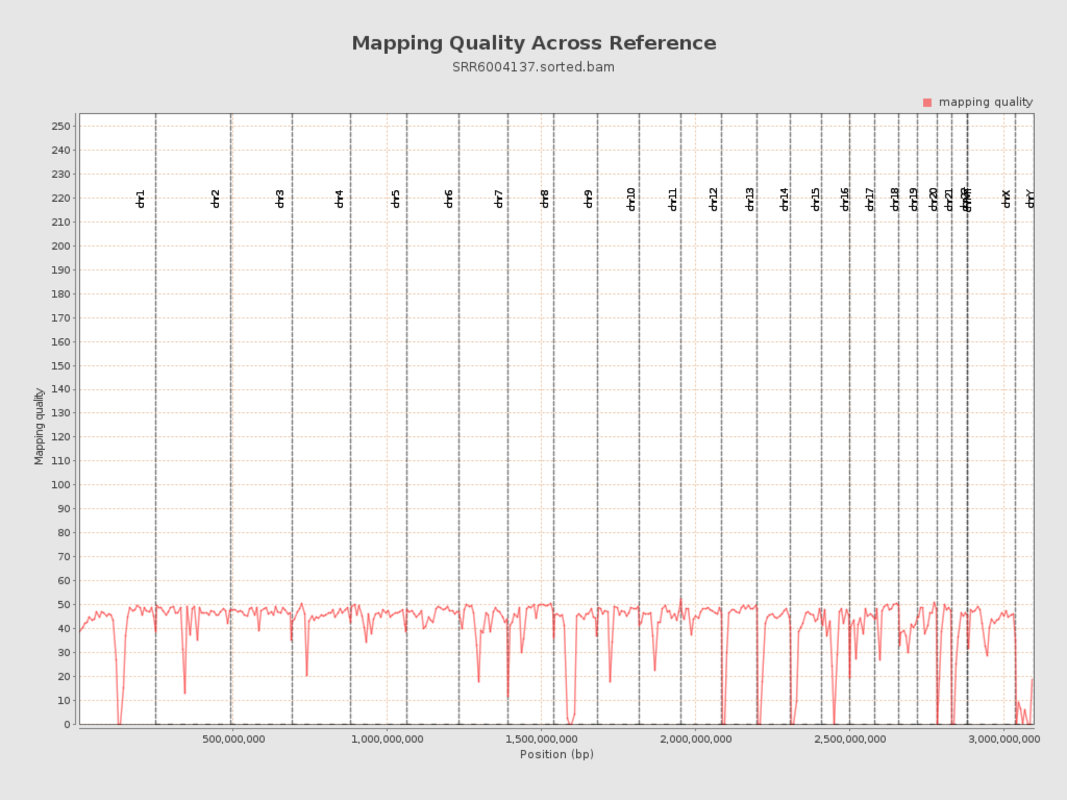
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram