Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004154.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_SRR6004154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:59:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,756,030
Mapped reads	2,410,507 / 87.46%
Unmapped reads	345,523 / 12.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,578 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	121,295 / 4.4%
Duplication rate	4.3%
Clipped reads	1,102,198 / 39.99%

2.2. ACGT Content

Number/percentage of A's	44,346,481 / 27.69%
Number/percentage of C's	29,689,731 / 18.54%
Number/percentage of T's	50,634,110 / 31.61%
Number/percentage of G's	35,464,324 / 22.14%
Number/percentage of N's	26,979 / 0.02%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.3722

2.4. Mapping Quality

Mean Mapping Quality	42.55

2.5. Mismatches and indels

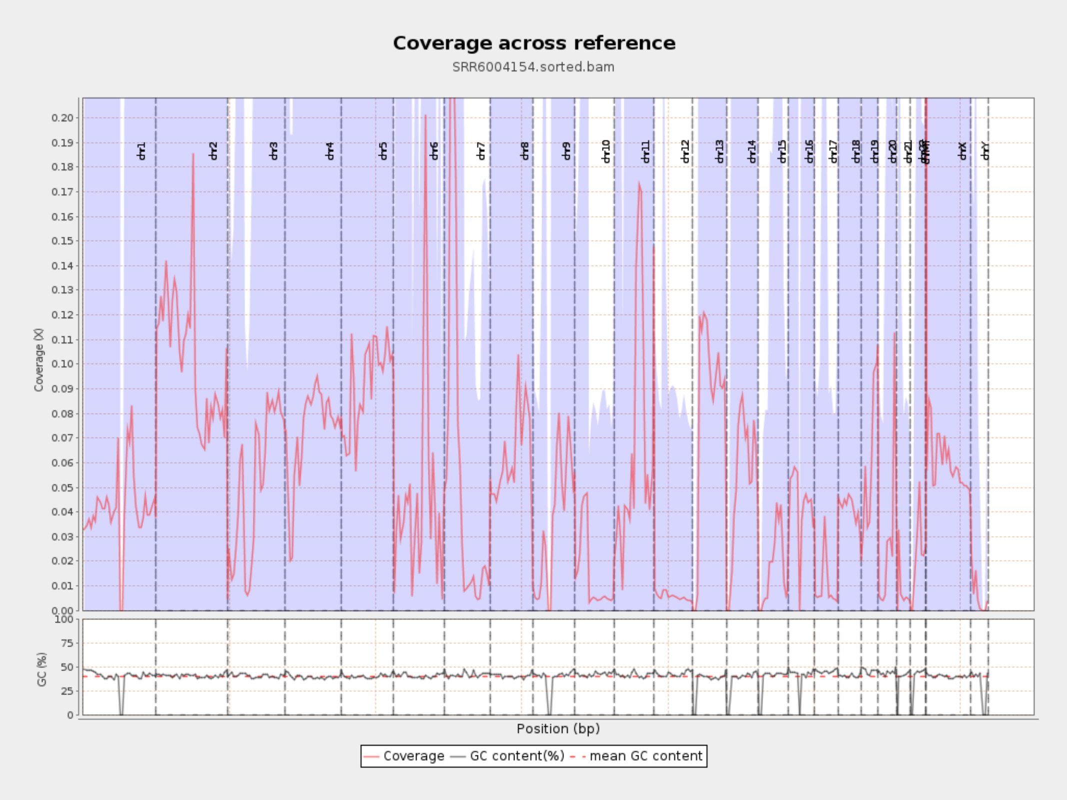
General error rate	0.9%
Mismatches	1,418,289
Insertions	10,833
Mapped reads with at least one insertion	0.45%
Deletions	44,357
Mapped reads with at least one deletion	1.82%
Homopolymer indels	45.6%

2.6. Chromosome stats

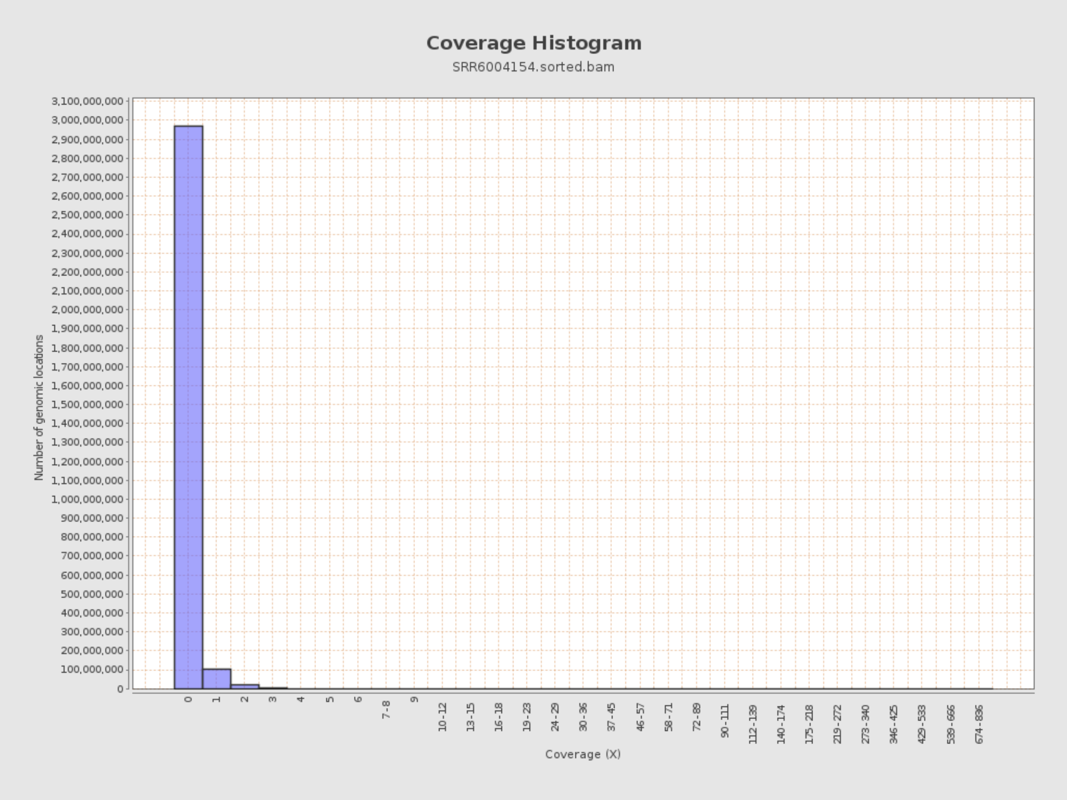
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10439257	0.0419	0.7436
chr2	243199373	24886155	0.1023	0.4387
chr3	198022430	10139732	0.0512	0.27
chr4	191154276	13847330	0.0724	0.322
chr5	180915260	16698505	0.0923	0.3614
chr6	171115067	7701969	0.045	0.299
chr7	159138663	8776315	0.0551	0.315

chr8	146364022	9311597	0.0636	0.4188
chr9	141213431	5173119	0.0366	0.2821
chr10	135534747	1868178	0.0138	0.2626
chr11	135006516	8866191	0.0657	0.3573
chr12	133851895	760475	0.0057	0.1009
chr13	115169878	9648380	0.0838	0.3443
chr14	107349540	5773654	0.0538	0.2801
chr15	102531392	1731348	0.0169	0.152
chr16	90354753	3804943	0.0421	0.2609
chr17	81195210	805117	0.0099	0.1397
chr18	78077248	3268396	0.0419	0.4432
chr19	59128983	3516562	0.0595	0.5634
chr20	63025520	1864760	0.0296	0.2146
chr21	48129895	435282	0.009	0.1308
chr22	51304566	1154164	0.0225	0.176
chrMT	16571	74023	4.467	3.6053
chrX	155270560	9337642	0.0601	0.3126
chrY	59373566	353682	0.006	0.1182

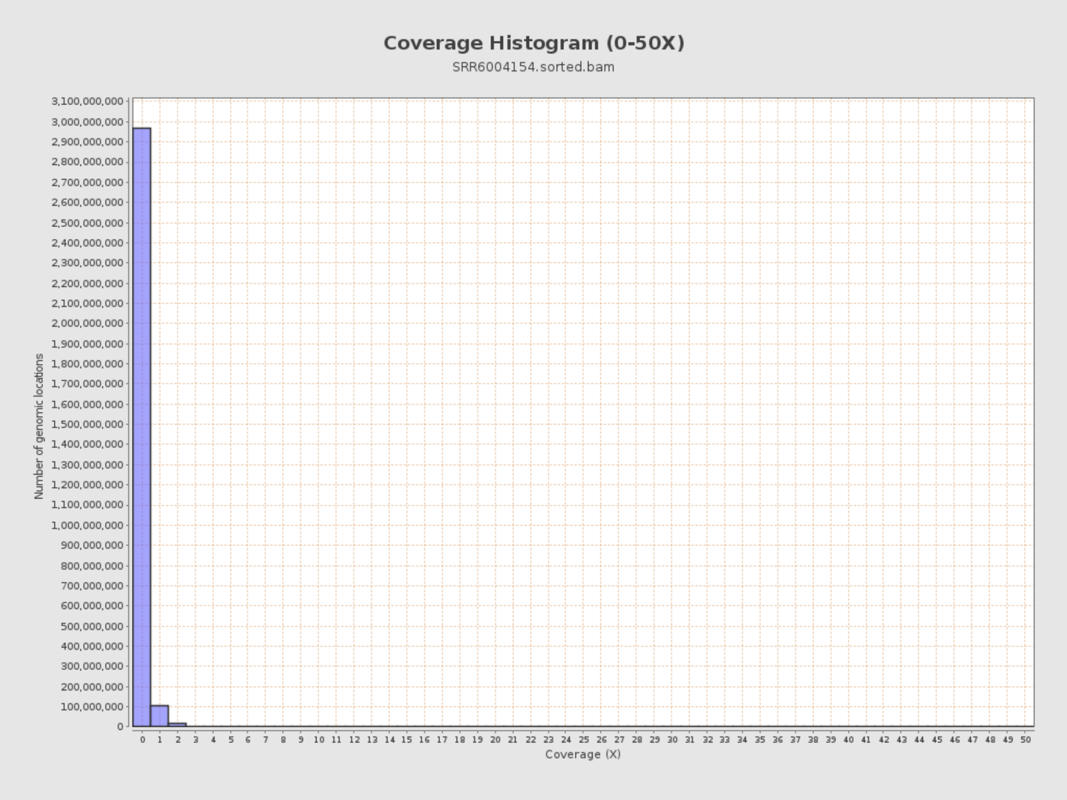
3. Results : Coverage across reference



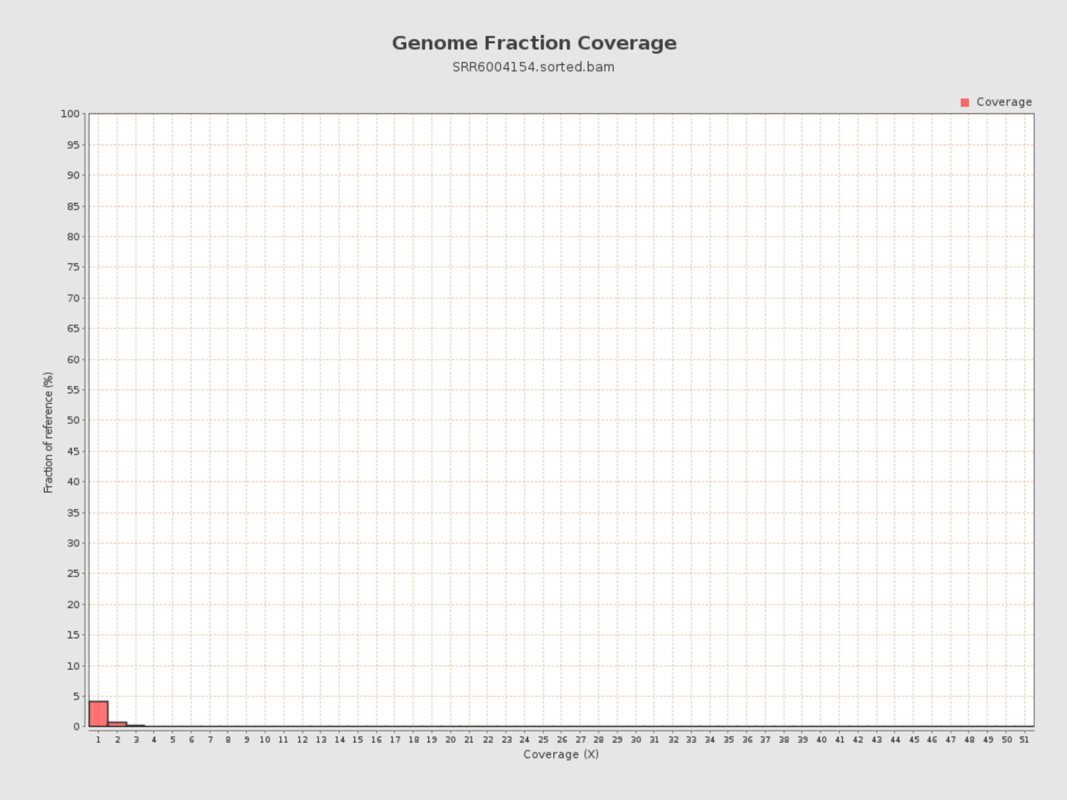
4. Results : Coverage Histogram



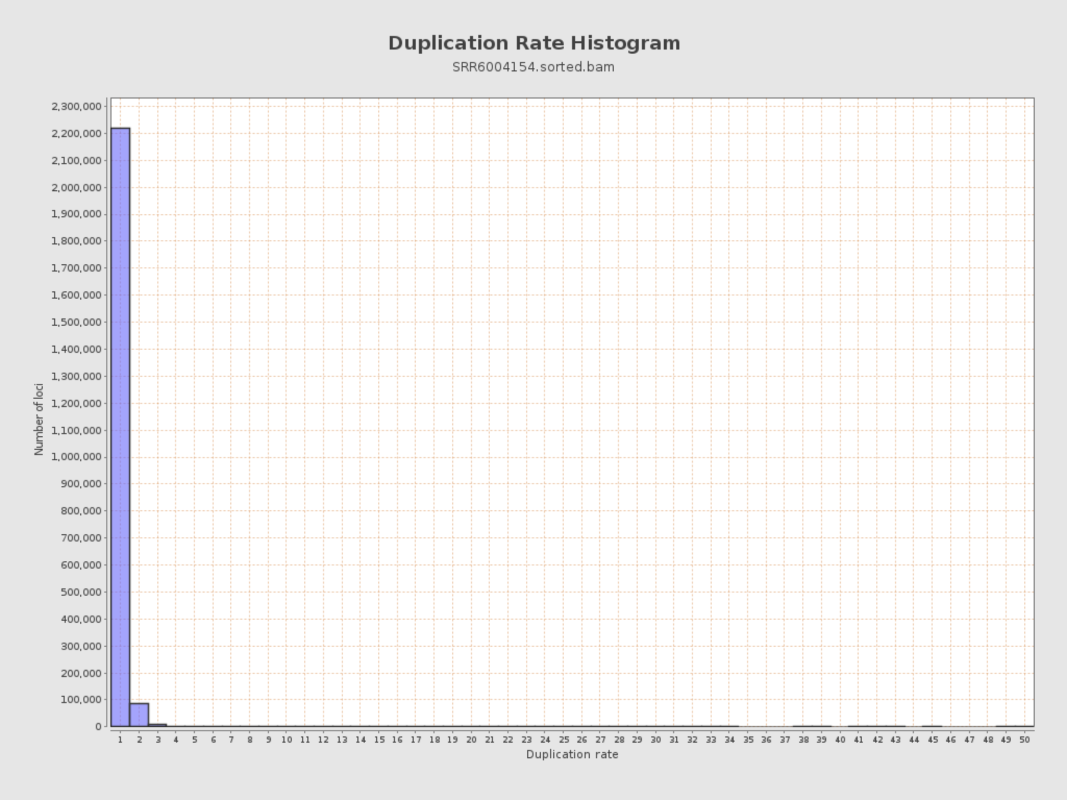
5. Results : Coverage Histogram (0-50X)



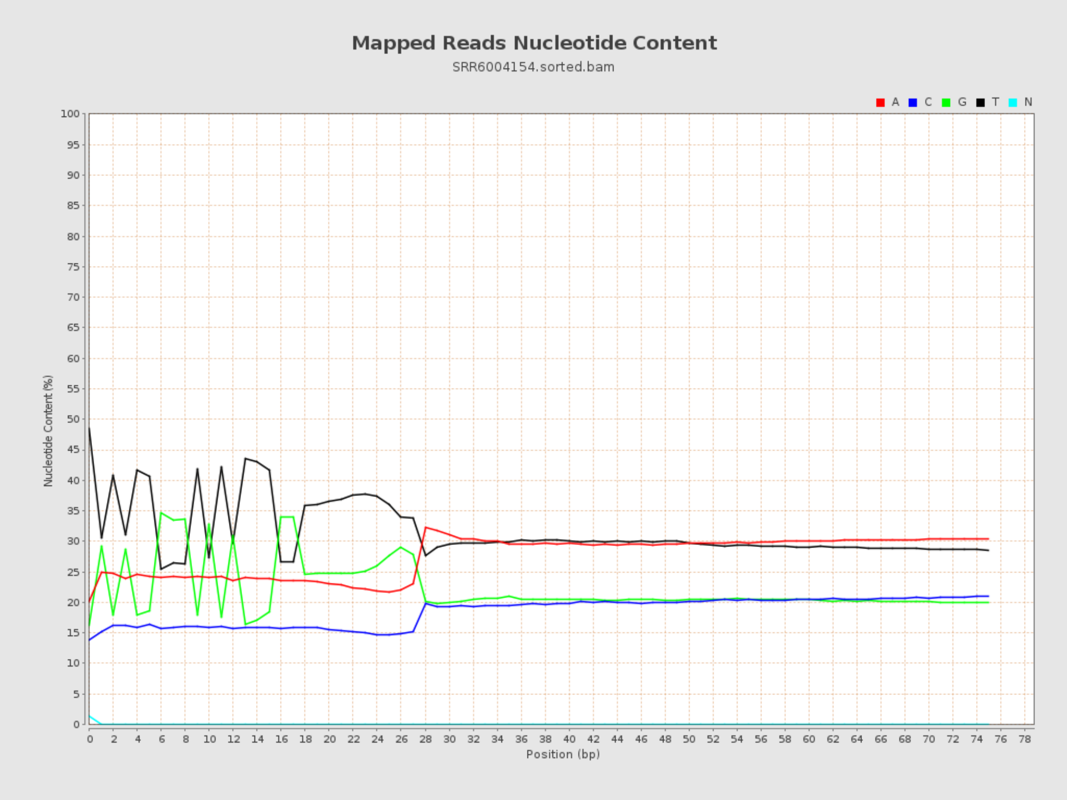
6. Results : Genome Fraction Coverage



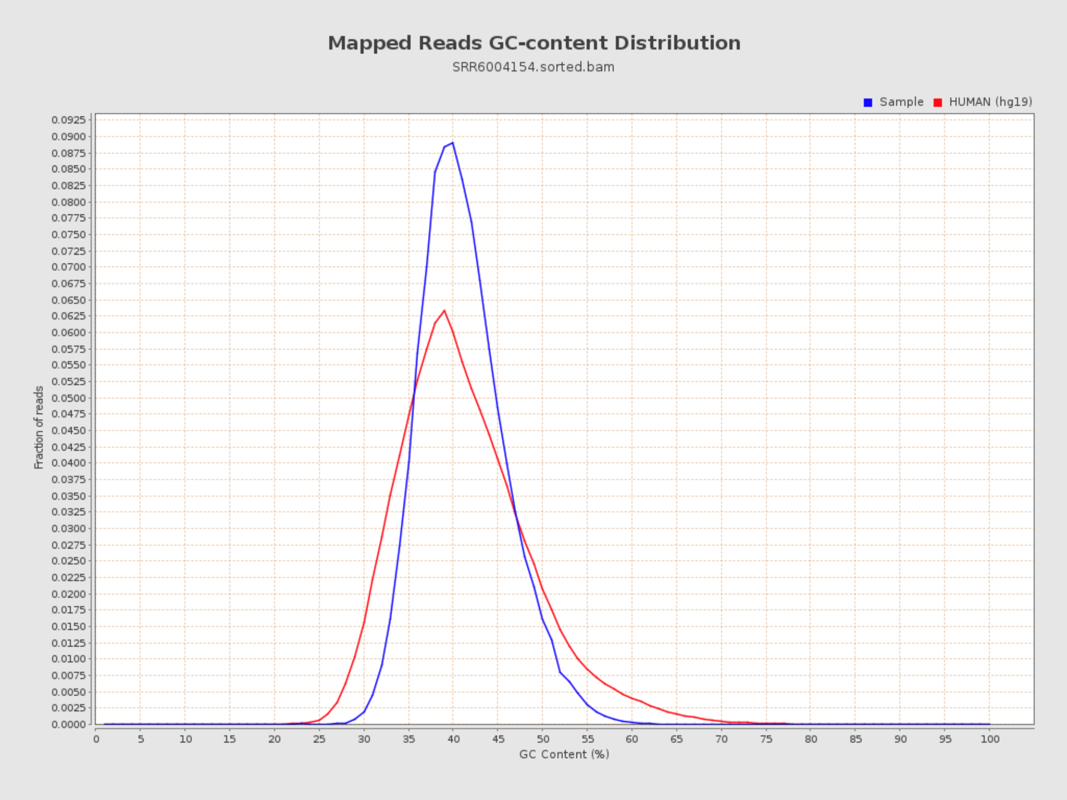
7. Results : Duplication Rate Histogram



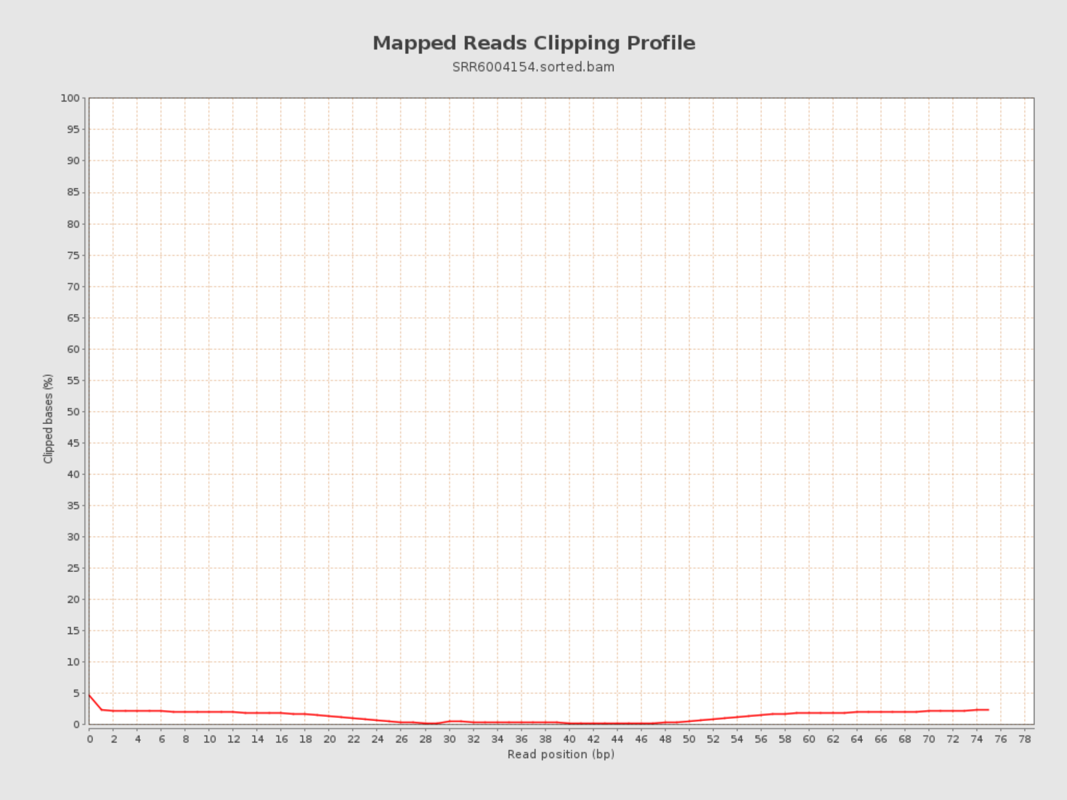
8. Results : Mapped Reads Nucleotide Content



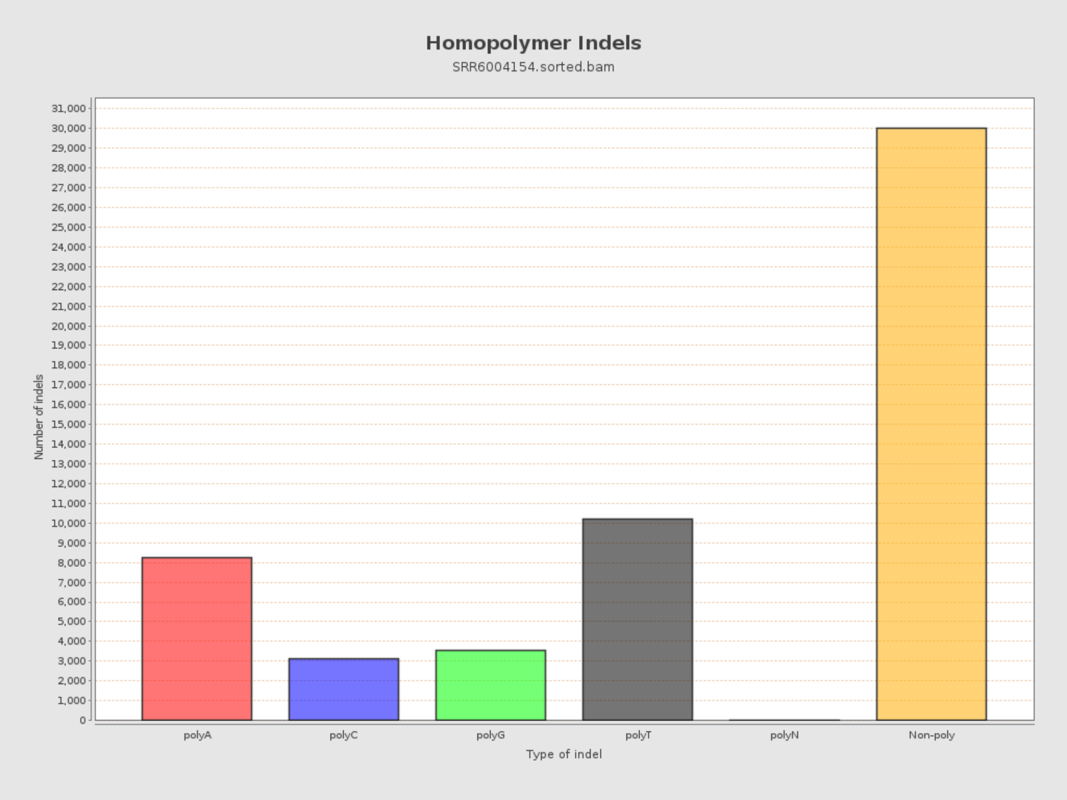
9. Results : Mapped Reads GC-content Distribution



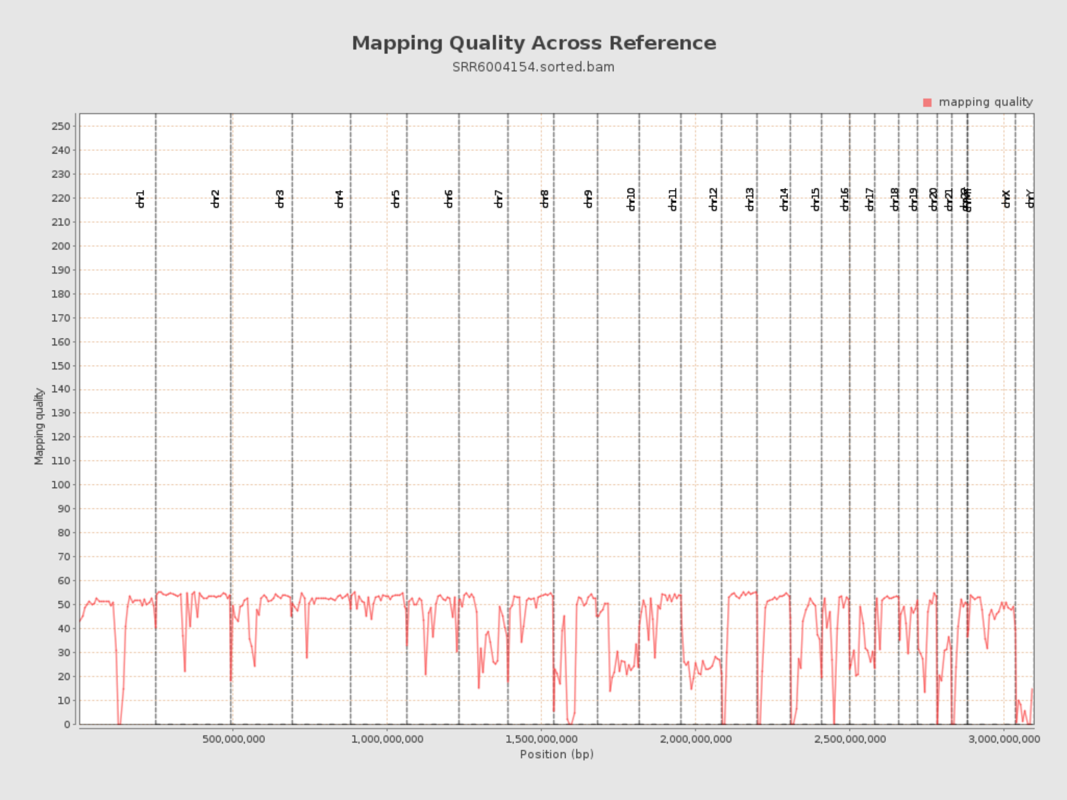
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram