Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:14:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013256.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_SRR6013256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:14:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,048,002
Mapped reads	427,276 / 20.86%
Unmapped reads	1,620,726 / 79.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,129 / 0.15%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	23,092 / 1.13%
Duplication rate	3.91%
Clipped reads	229,103 / 11.19%

2.2. ACGT Content

Number/percentage of A's	7,464,654 / 27.29%
Number/percentage of C's	4,852,828 / 17.74%
Number/percentage of T's	8,924,683 / 32.62%
Number/percentage of G's	6,113,666 / 22.35%
Number/percentage of N's	363 / 0%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1812

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

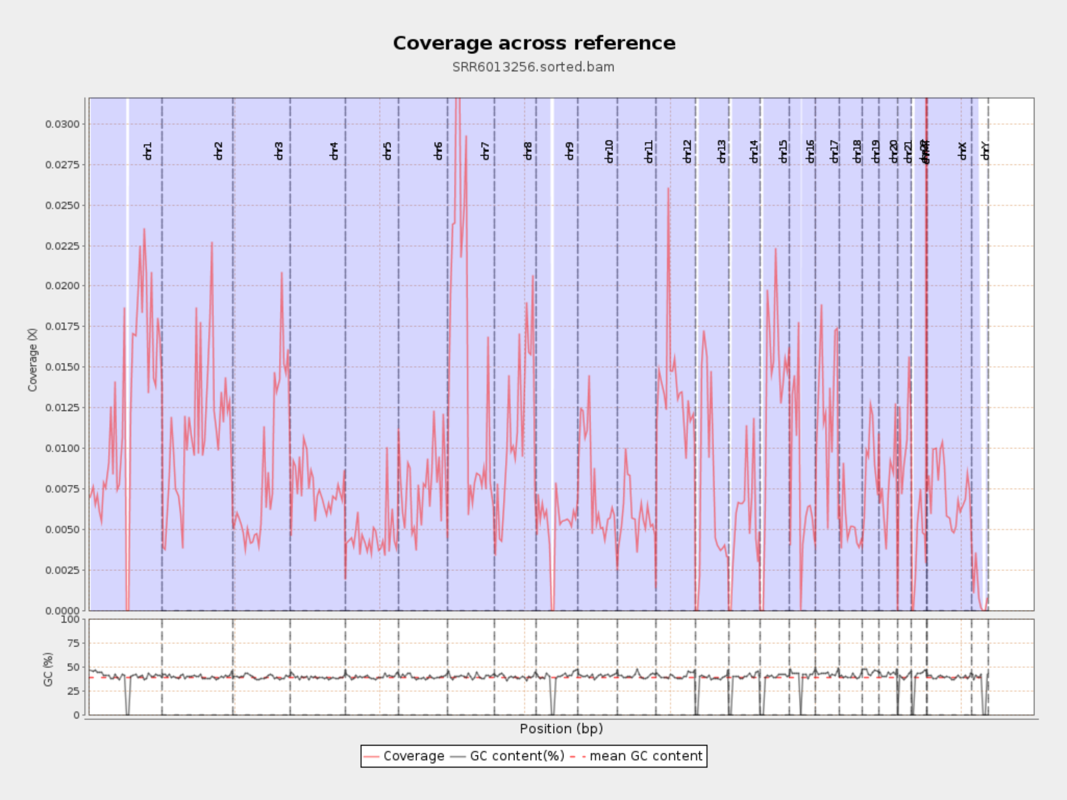
General error rate	0.87%
Mismatches	233,784
Insertions	2,085
Mapped reads with at least one insertion	0.48%
Deletions	10,368
Mapped reads with at least one deletion	2.39%
Homopolymer indels	44.37%

2.6. Chromosome stats

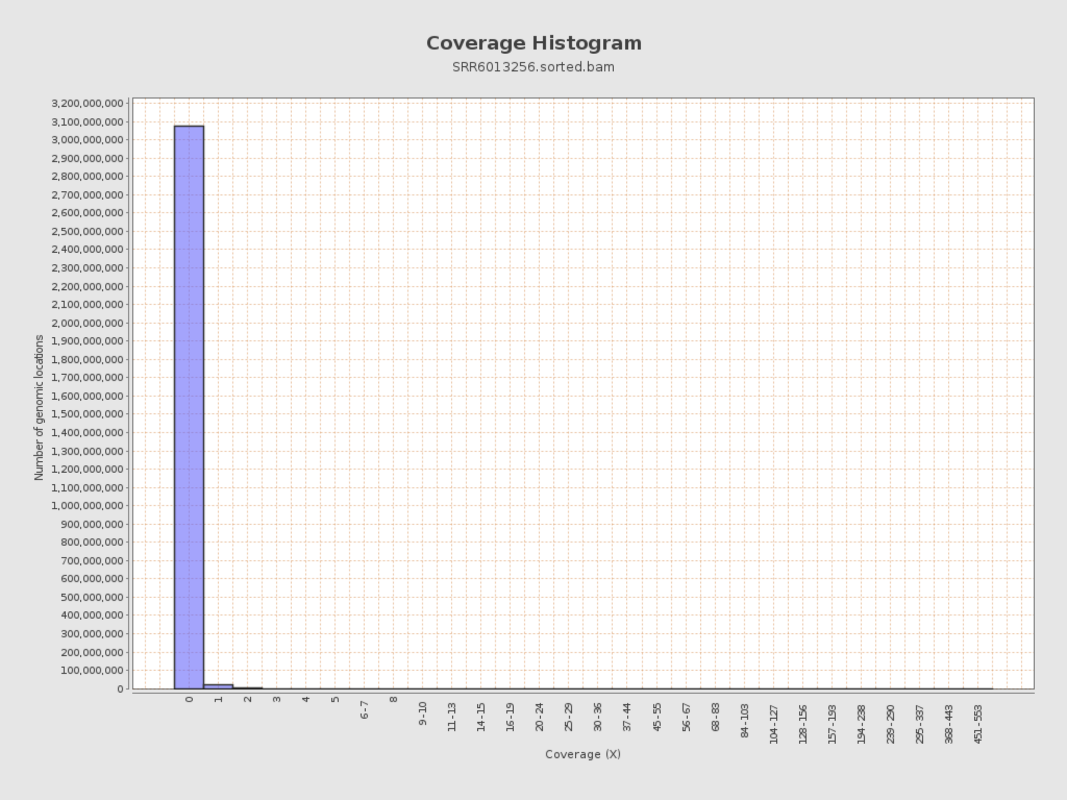
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3058255	0.0123	0.2702
chr2	243199373	2681695	0.011	0.2374
chr3	198022430	1669751	0.0084	0.1088
chr4	191154276	1438109	0.0075	0.1775
chr5	180915260	826136	0.0046	0.0857
chr6	171115067	1308328	0.0076	0.1164
chr7	159138663	2509834	0.0158	0.2775

chr8	146364022	1618292	0.0111	0.1837
chr9	141213431	740422	0.0052	0.0974
chr10	135534747	1040352	0.0077	0.1195
chr11	135006516	795954	0.0059	0.1051
chr12	133851895	1843590	0.0138	0.1618
chr13	115169878	836766	0.0073	0.1016
chr14	107349540	608336	0.0057	0.0882
chr15	102531392	1354988	0.0132	0.1348
chr16	90354753	713149	0.0079	0.3934
chr17	81195210	1017069	0.0125	0.1353
chr18	78077248	407259	0.0052	0.1429
chr19	59128983	544381	0.0092	0.2373
chr20	63025520	482915	0.0077	0.1026
chr21	48129895	479068	0.01	0.321
chr22	51304566	194305	0.0038	0.0762
chrMT	16571	2765	0.1669	0.4368
chrX	155270560	1140694	0.0073	0.1105
chrY	59373566	61557	0.001	0.04

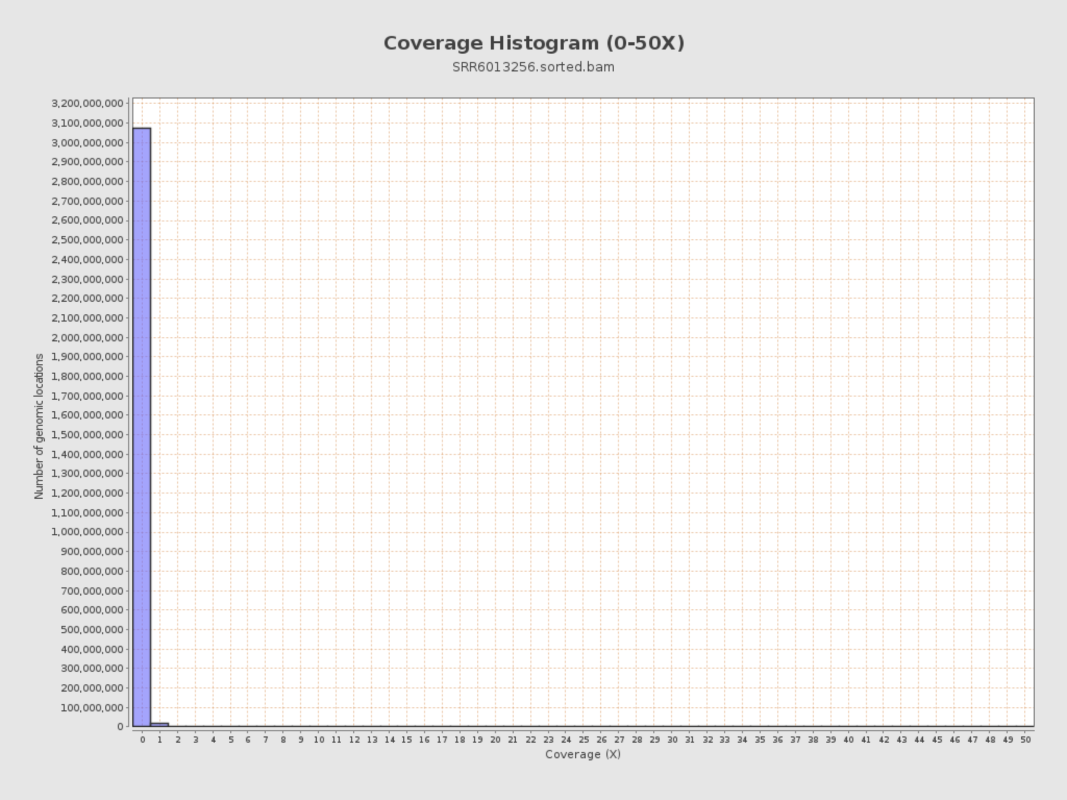
3. Results : Coverage across reference



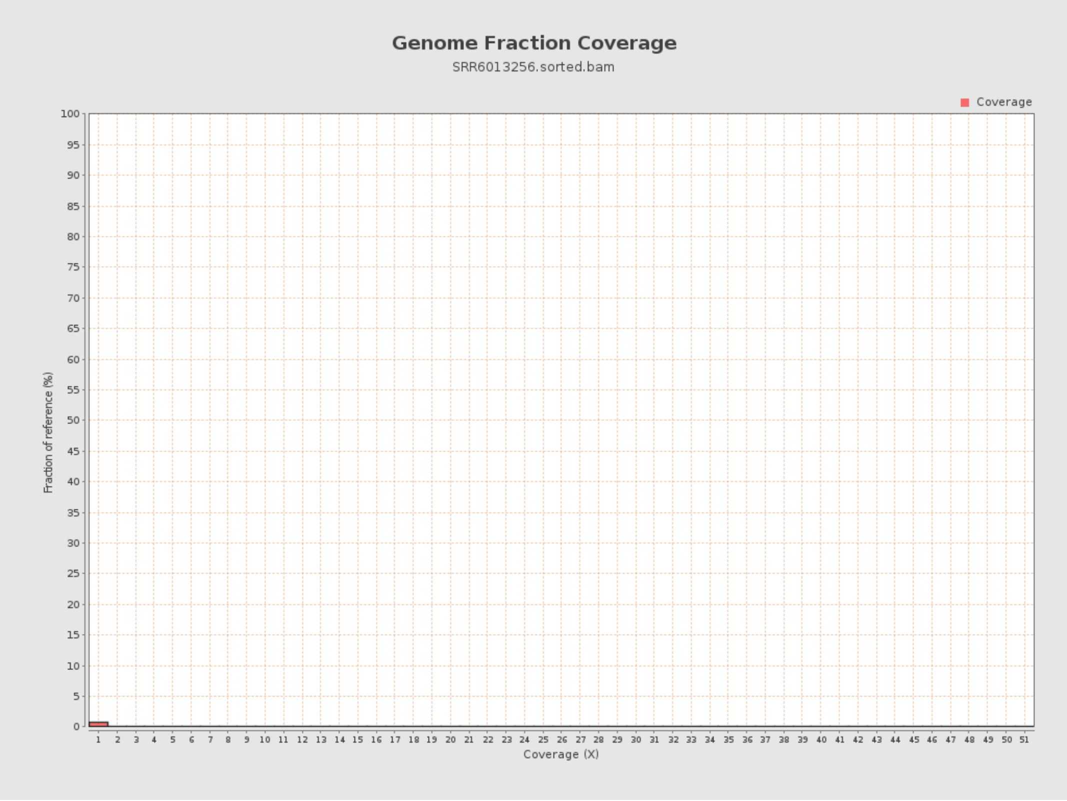
4. Results : Coverage Histogram



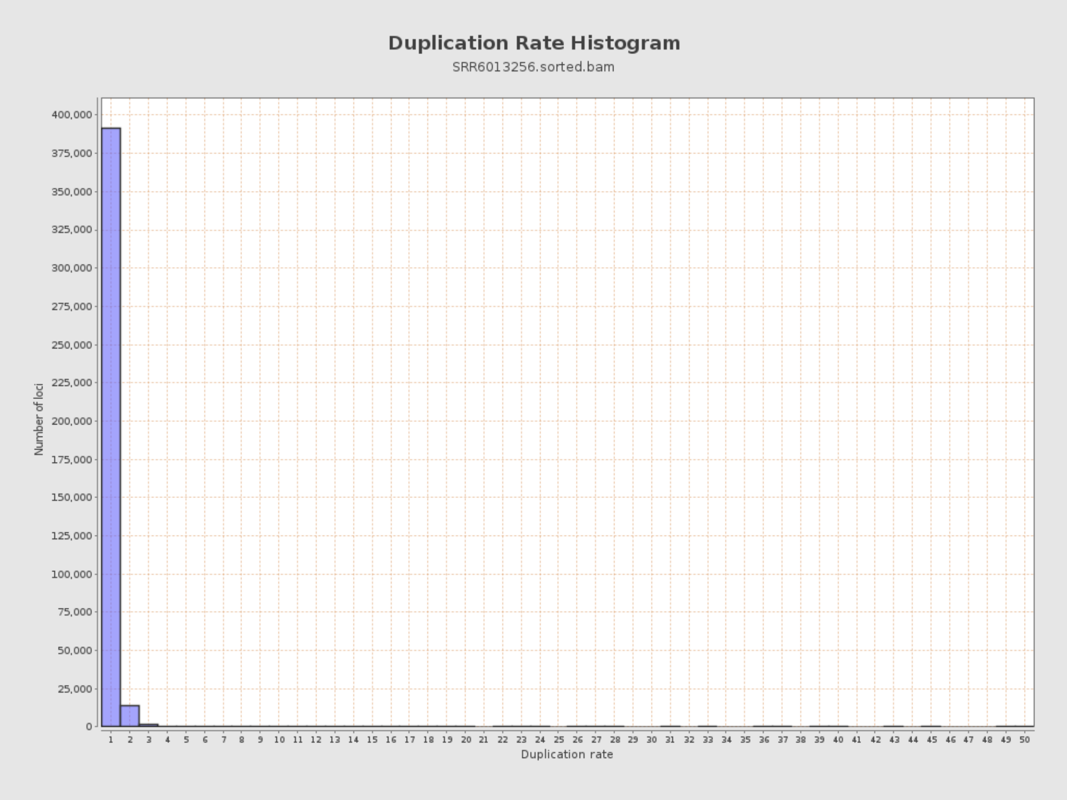
5. Results : Coverage Histogram (0-50X)



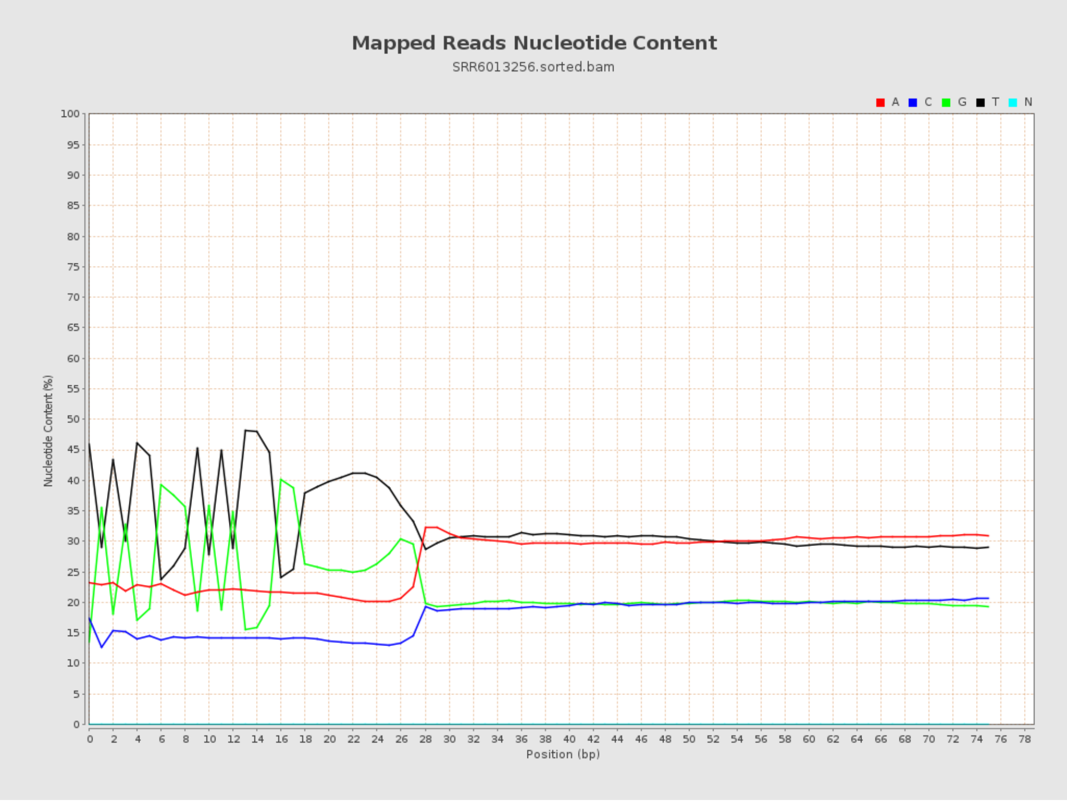
6. Results : Genome Fraction Coverage



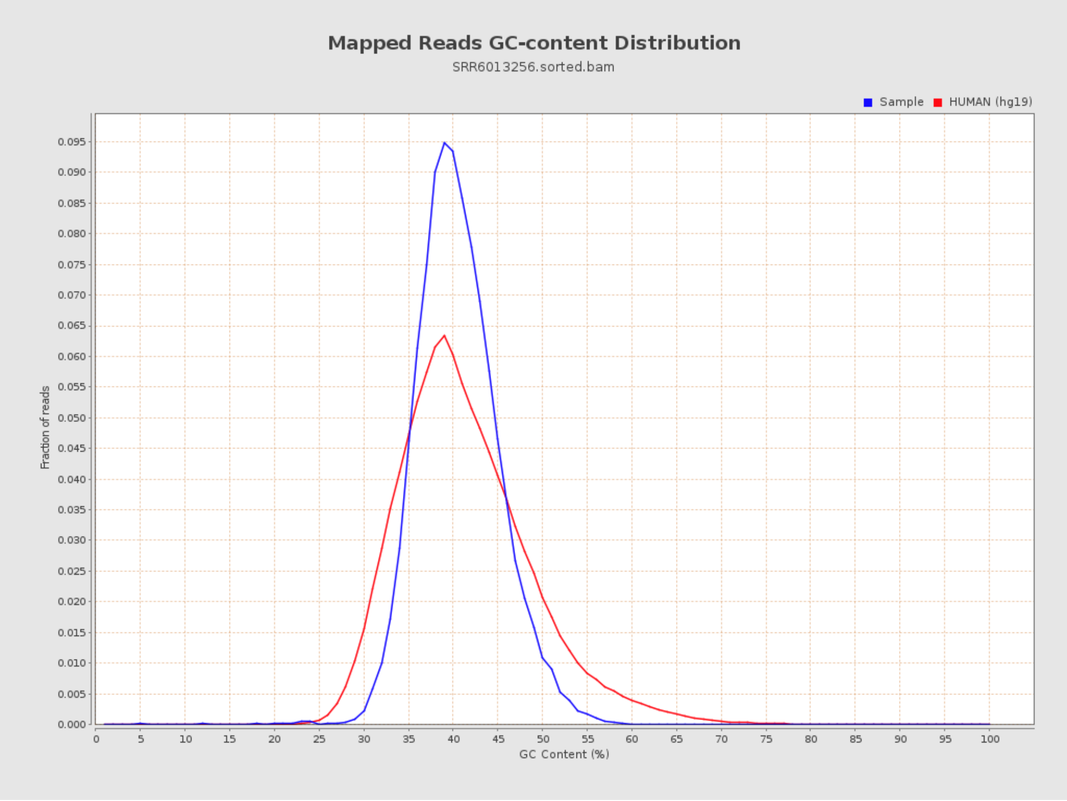
7. Results : Duplication Rate Histogram



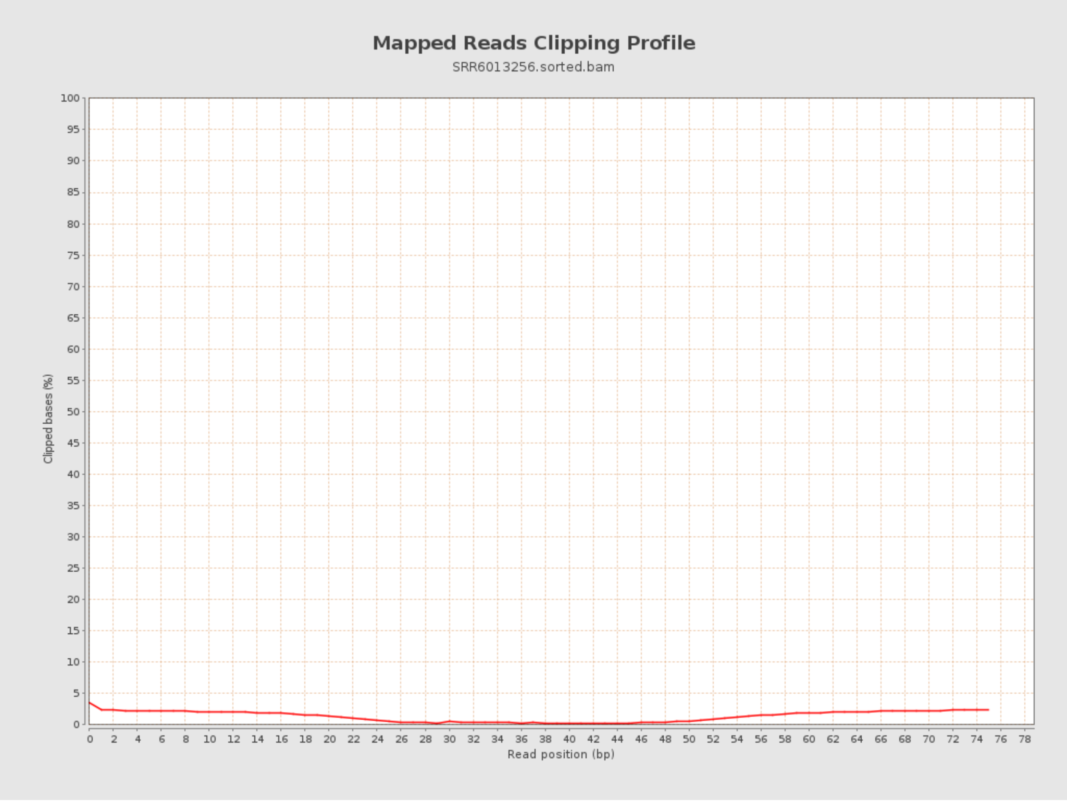
8. Results : Mapped Reads Nucleotide Content



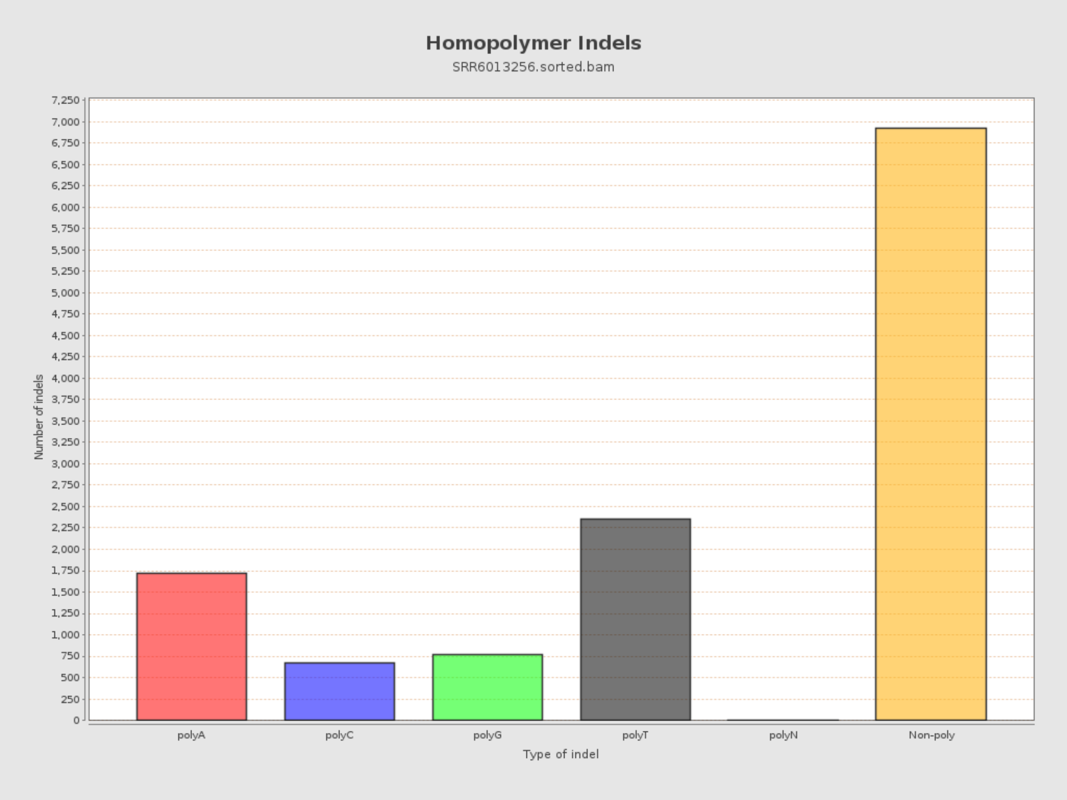
9. Results : Mapped Reads GC-content Distribution



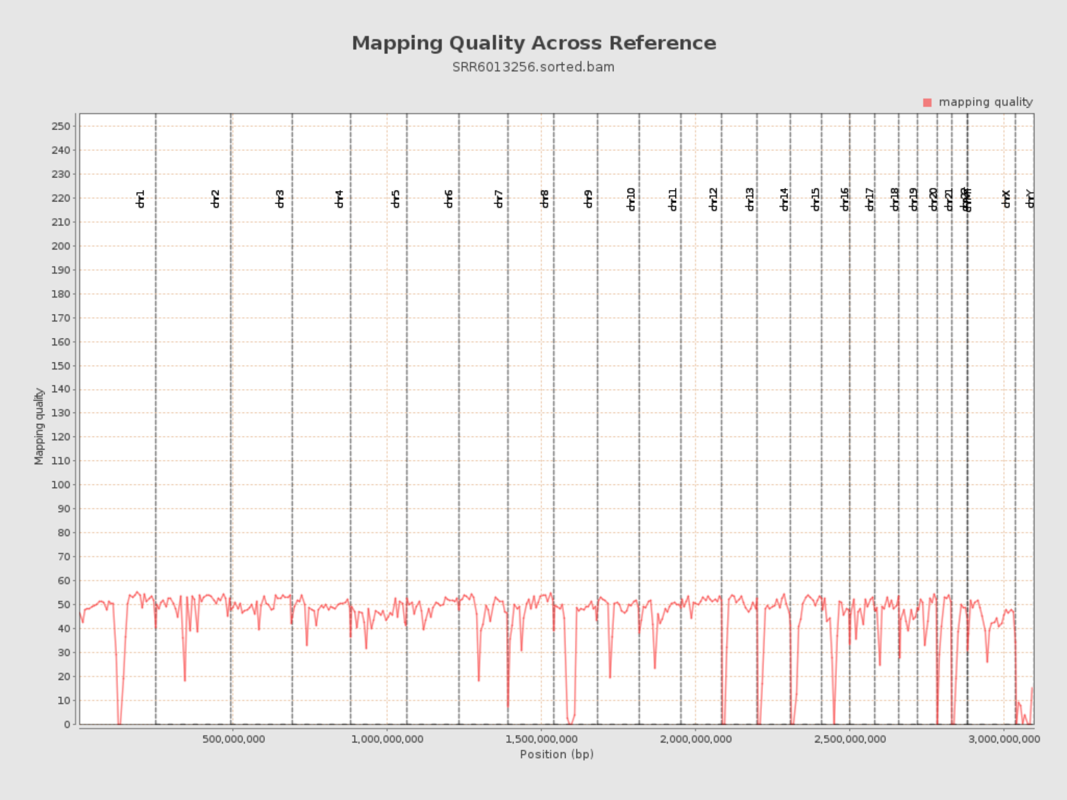
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram