Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:50:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549067.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_SRR1549067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:50:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,297,281
Mapped reads	8,885,924 / 86.29%
Unmapped reads	1,411,357 / 13.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	355,822 / 3.46%
Duplication rate	2.54%
Clipped reads	420,930 / 4.09%

2.2. ACGT Content

Number/percentage of A's	105,625,932 / 29.93%
Number/percentage of C's	70,965,040 / 20.11%
Number/percentage of T's	105,688,549 / 29.95%
Number/percentage of G's	70,621,554 / 20.01%
Number/percentage of N's	6,636 / 0%
GC Percentage	40.12%

2.3. Coverage

Mean	0.114
Standard Deviation	1.1497

2.4. Mapping Quality

Mean Mapping Quality	43.76

2.5. Mismatches and indels

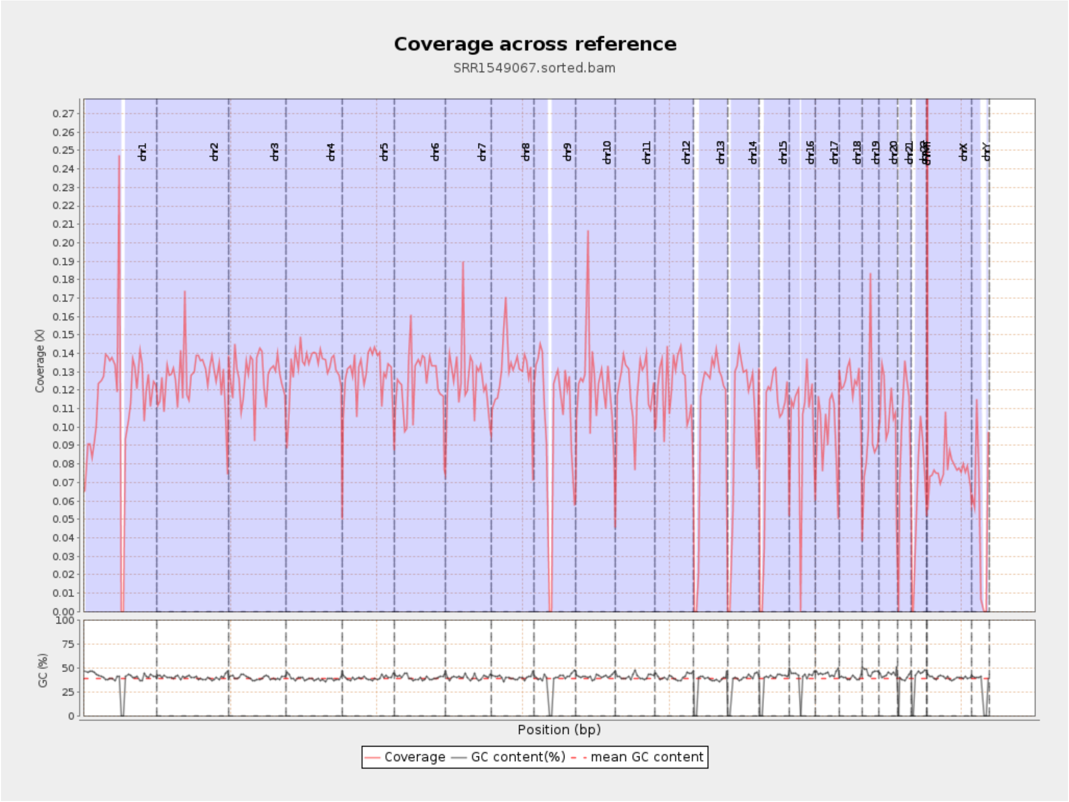
General error rate	0.31%
Mismatches	1,096,298
Insertions	8,617
Mapped reads with at least one insertion	0.1%
Deletions	26,671
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.41%

2.6. Chromosome stats

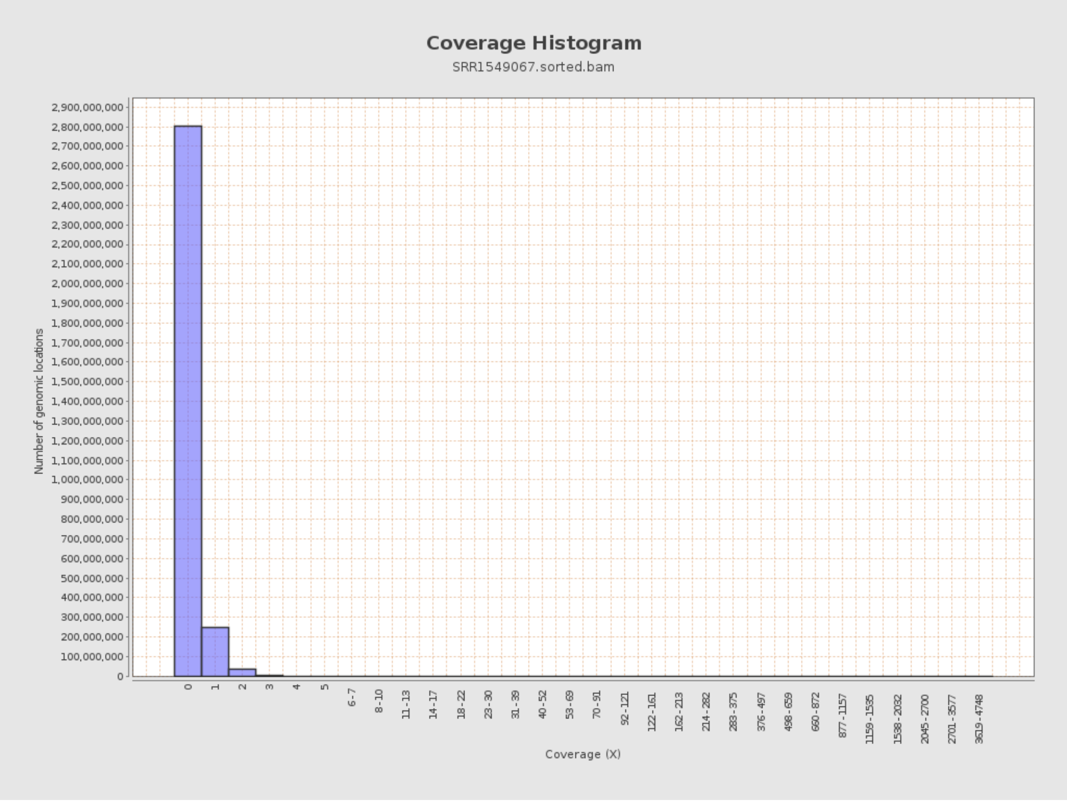
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28370740	0.1138	2.8425
chr2	243199373	30863663	0.1269	0.682
chr3	198022430	25253187	0.1275	0.4177
chr4	191154276	25434601	0.1331	0.4466
chr5	180915260	23235743	0.1284	0.4285
chr6	171115067	21477988	0.1255	0.5552
chr7	159138663	20003296	0.1257	1.0113
chr8	146364022	18948085	0.1295	2.3633

chr9	141213431	14835246	0.1051	0.6382
chr10	135534747	16795264	0.1239	0.8627
chr11	135006516	16265031	0.1205	0.6478
chr12	133851895	16274663	0.1216	0.4441
chr13	115169878	12194140	0.1059	0.3664
chr14	107349540	11091691	0.1033	0.4424
chr15	102531392	9776110	0.0953	0.3503
chr16	90354753	9049161	0.1002	0.4869
chr17	81195210	8013210	0.0987	0.424
chr18	78077248	9718772	0.1245	1.4169
chr19	59128983	5762904	0.0975	2.1297
chr20	63025520	6819632	0.1082	0.4064
chr21	48129895	4569836	0.0949	0.4388
chr22	51304566	3149865	0.0614	0.3352
chrMT	16571	39614	2.3906	2.8196
chrX	155270560	11955446	0.077	0.4634
chrY	59373566	3043507	0.0513	0.4984

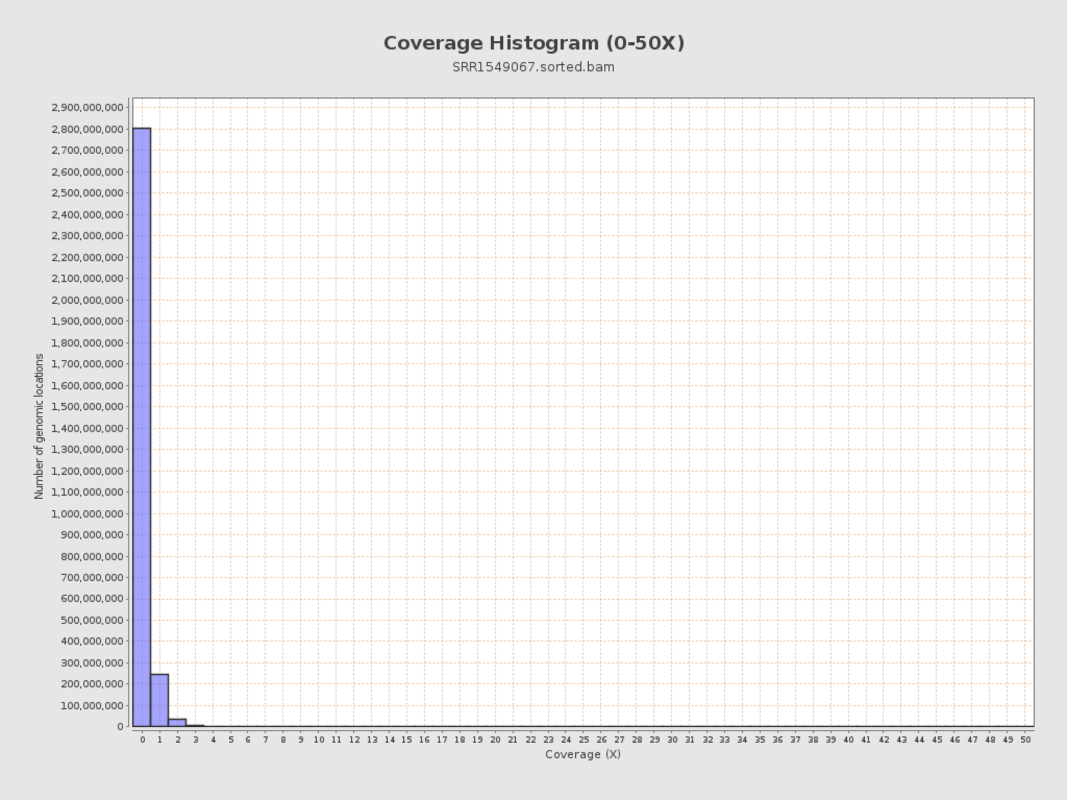
3. Results : Coverage across reference



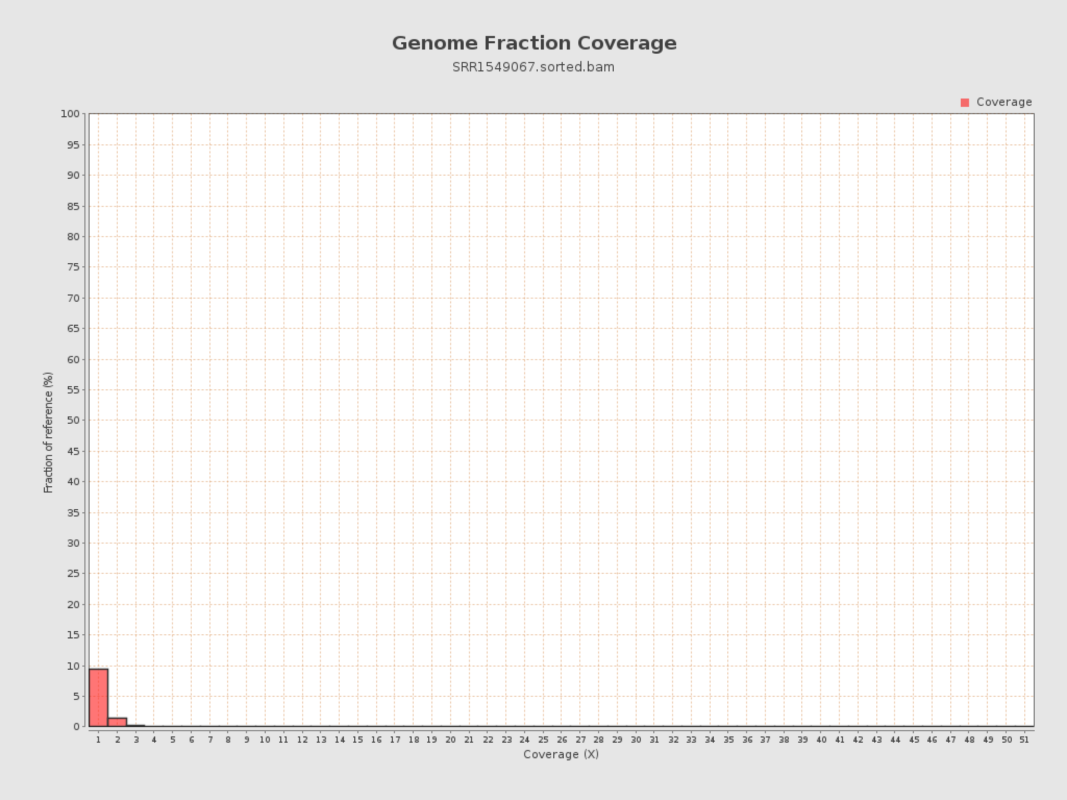
4. Results : Coverage Histogram



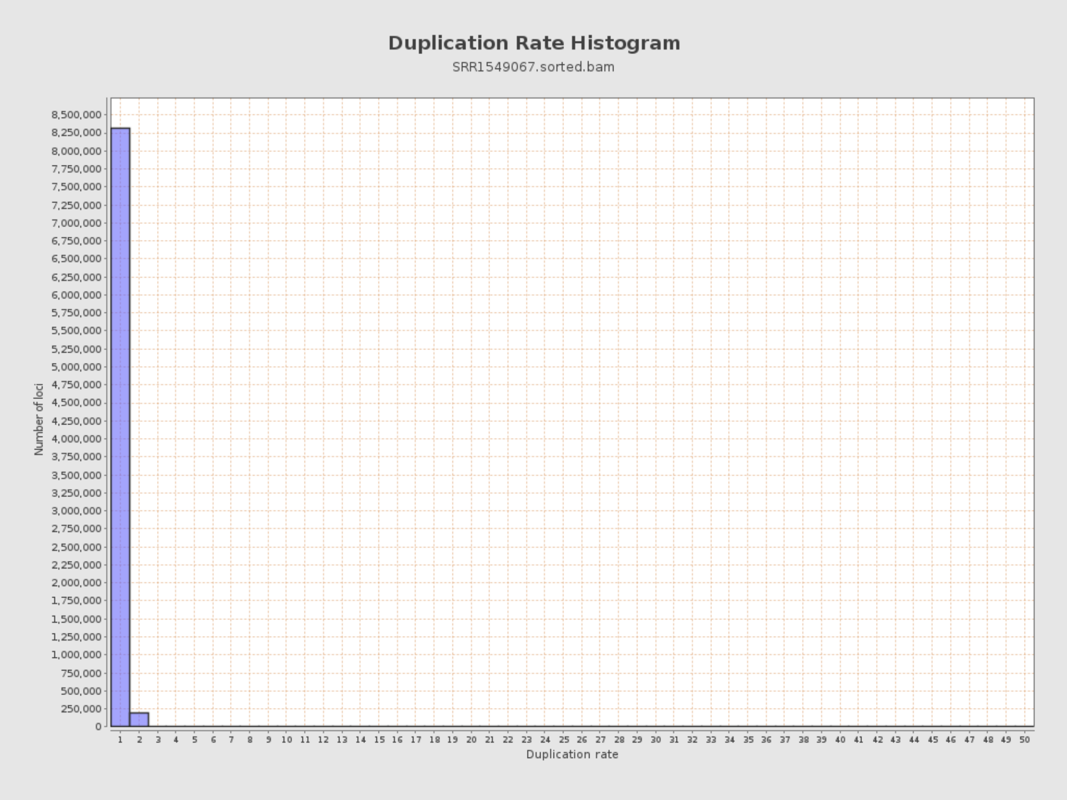
5. Results : Coverage Histogram (0-50X)



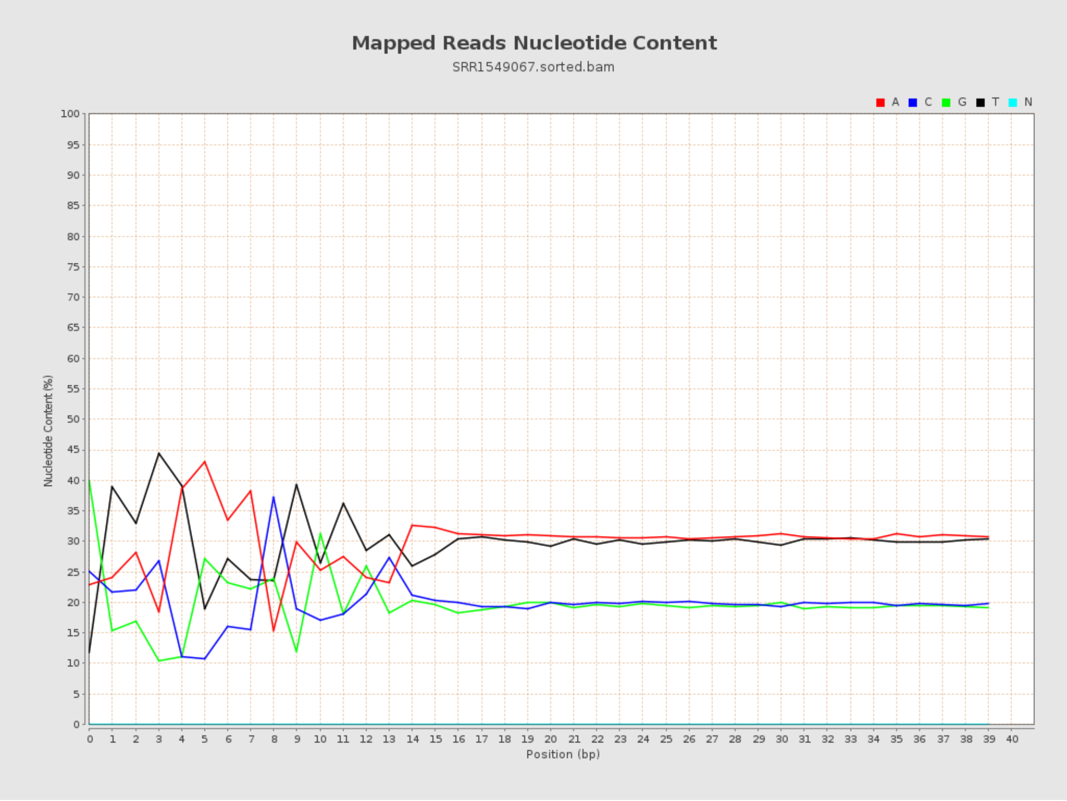
6. Results : Genome Fraction Coverage



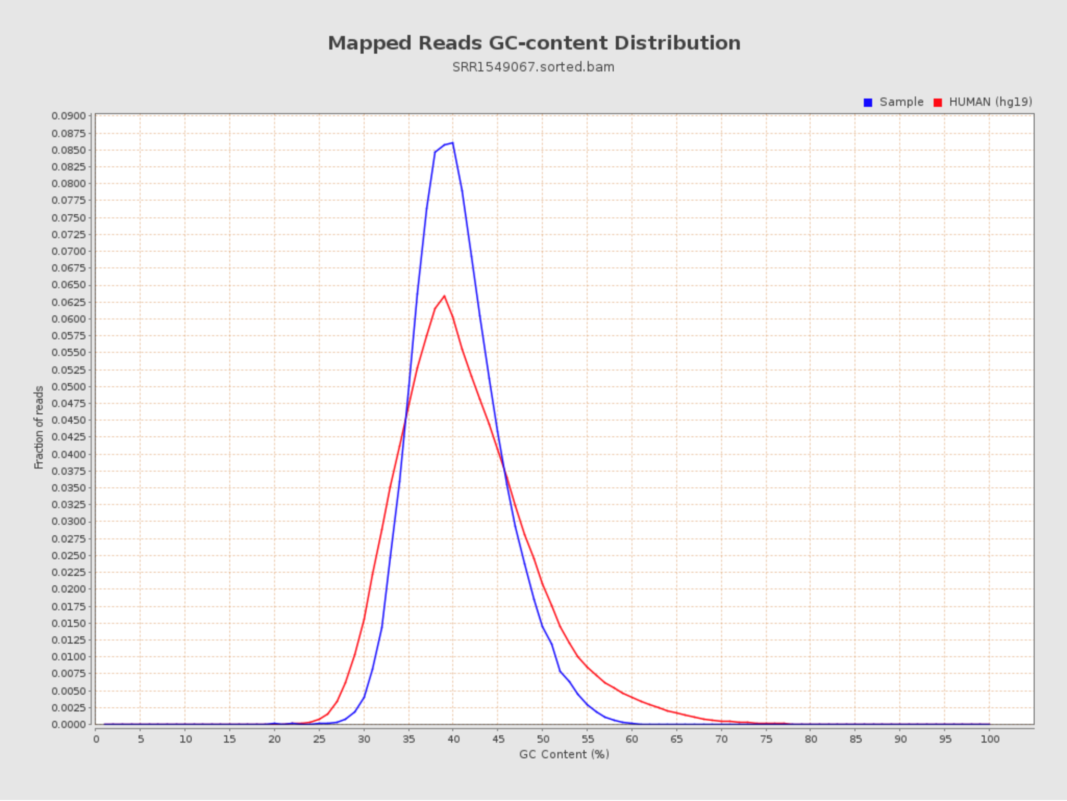
7. Results : Duplication Rate Histogram



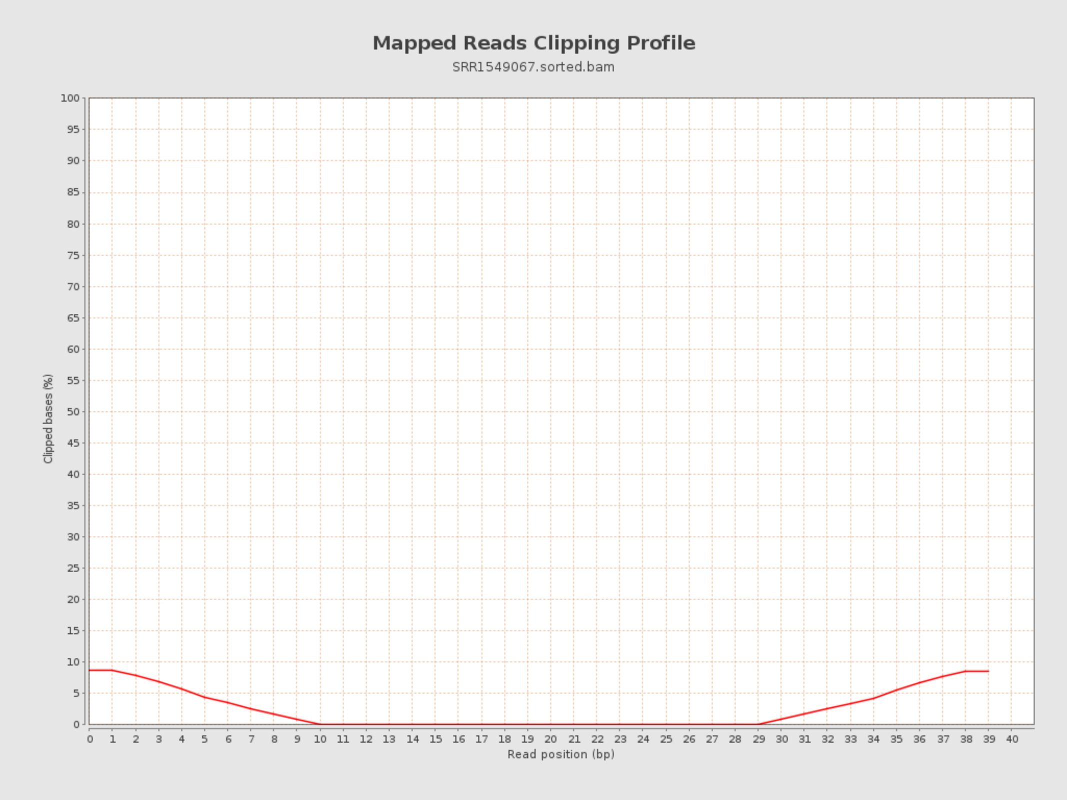
8. Results : Mapped Reads Nucleotide Content



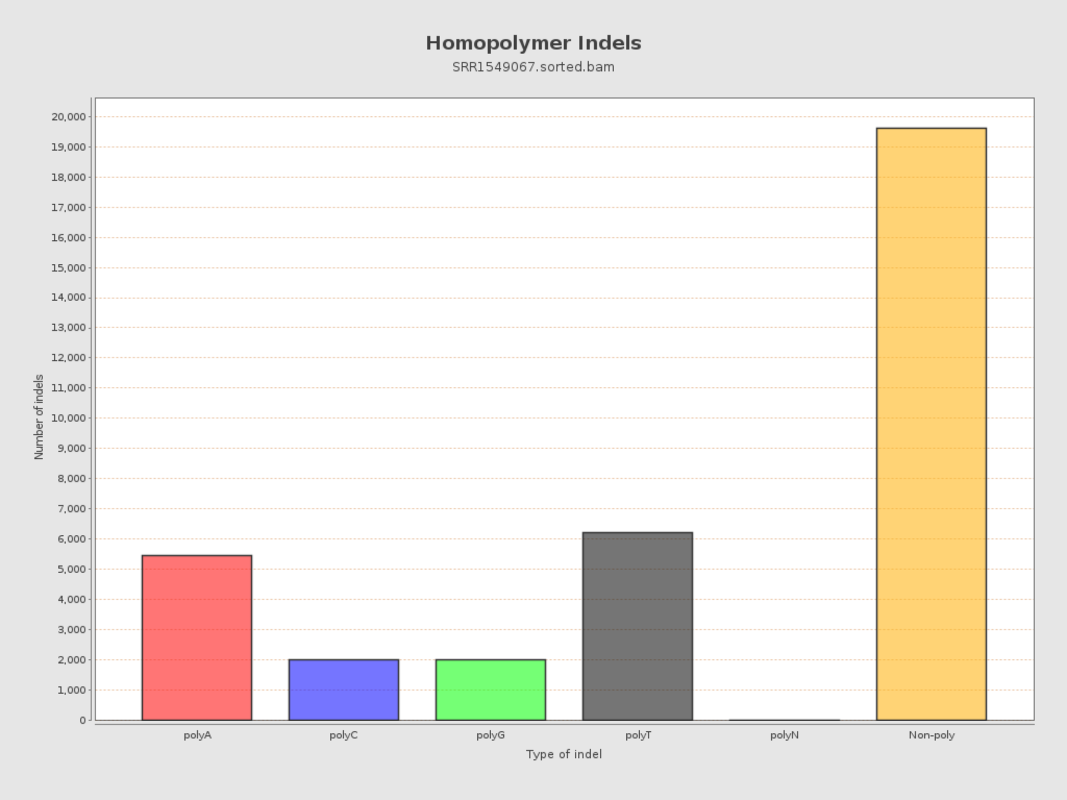
9. Results : Mapped Reads GC-content Distribution



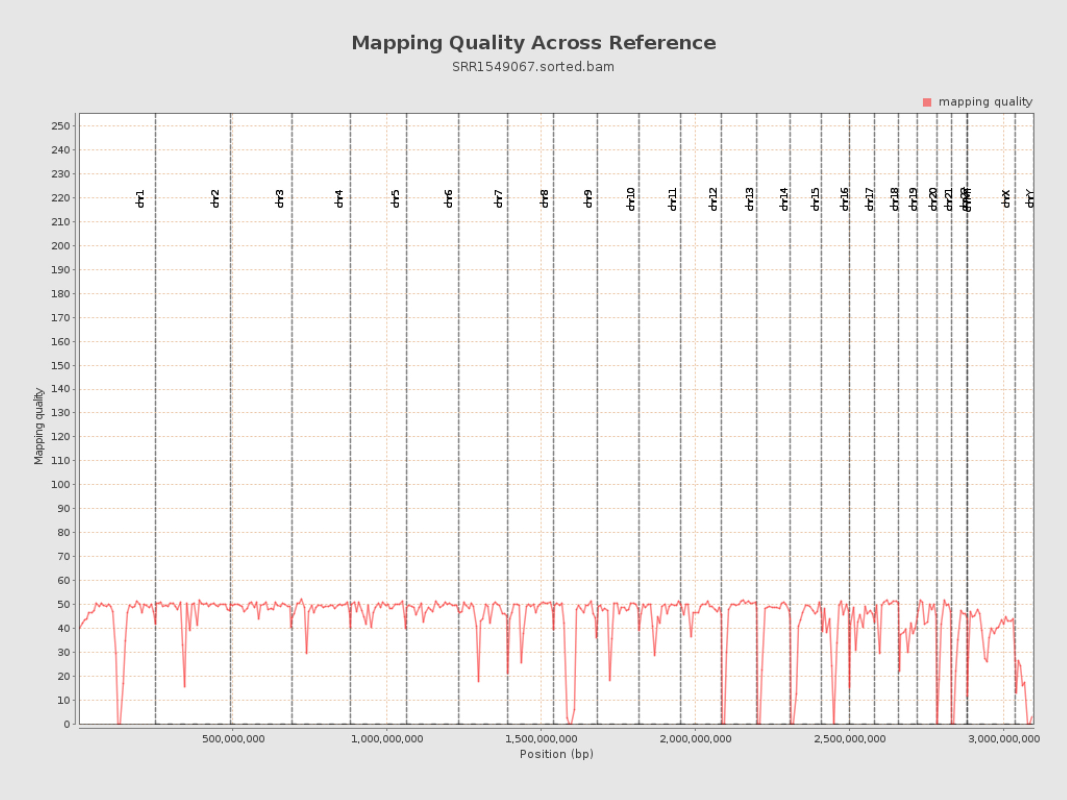
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram