Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:51:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549027.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_SRR1549027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:51:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,838,100
Mapped reads	5,148,102 / 88.18%
Unmapped reads	689,998 / 11.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	167,485 / 2.87%
Duplication rate	2.55%
Clipped reads	367,257 / 6.29%

2.2. ACGT Content

Number/percentage of A's	58,258,670 / 28.58%
Number/percentage of C's	43,232,332 / 21.21%
Number/percentage of T's	58,740,712 / 28.82%
Number/percentage of G's	43,613,822 / 21.4%
Number/percentage of N's	2,200 / 0%
GC Percentage	42.6%

2.3. Coverage

Mean	0.0659
Standard Deviation	0.5535

2.4. Mapping Quality

Mean Mapping Quality	40.85

2.5. Mismatches and indels

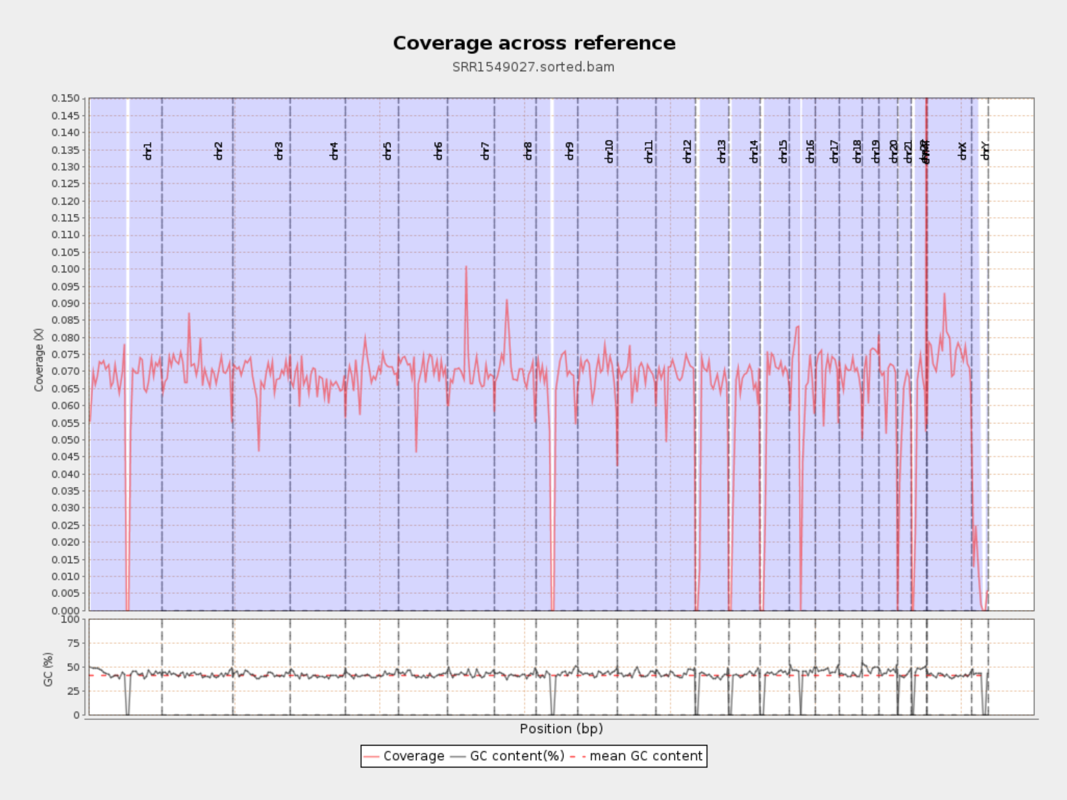
General error rate	0.28%
Mismatches	555,772
Insertions	6,319
Mapped reads with at least one insertion	0.12%
Deletions	15,810
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.95%

2.6. Chromosome stats

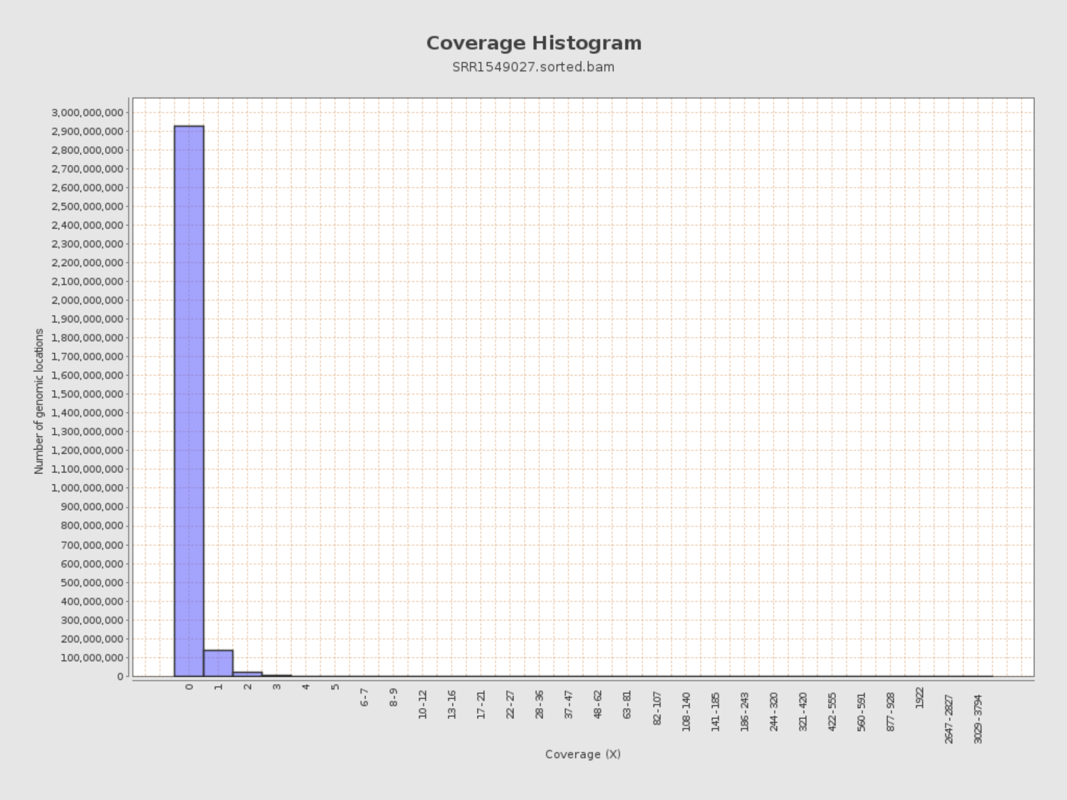
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16144388	0.0648	0.5184
chr2	243199373	17215116	0.0708	0.4039
chr3	198022430	13587891	0.0686	0.3095
chr4	191154276	12795464	0.0669	0.3106
chr5	180915260	12637483	0.0699	0.3146
chr6	171115067	12029905	0.0703	0.3318
chr7	159138663	11205633	0.0704	0.5576
chr8	146364022	10368415	0.0708	1.8601

chr9	141213431	8589561	0.0608	0.3987
chr10	135534747	9525209	0.0703	0.3498
chr11	135006516	9311260	0.069	0.4616
chr12	133851895	9262117	0.0692	0.3159
chr13	115169878	6571860	0.0571	0.2812
chr14	107349540	6052909	0.0564	0.3152
chr15	102531392	5976009	0.0583	0.2854
chr16	90354753	5689957	0.063	0.3139
chr17	81195210	5704375	0.0703	0.3328
chr18	78077248	5439469	0.0697	0.6317
chr19	59128983	4266007	0.0721	0.5172
chr20	63025520	4228575	0.0671	0.3139
chr21	48129895	2555556	0.0531	0.304
chr22	51304566	2409919	0.047	0.2847
chrMT	16571	7179	0.4332	0.7884
chrX	155270560	11692423	0.0753	0.371
chrY	59373566	601595	0.0101	0.1403

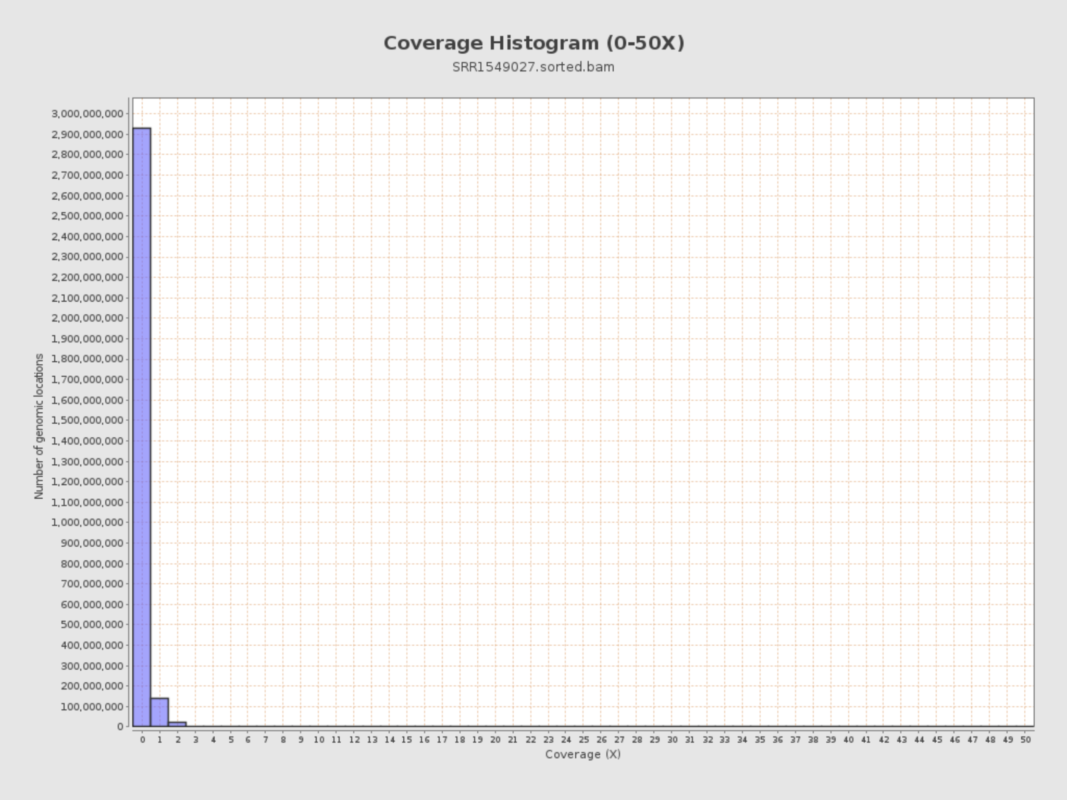
3. Results : Coverage across reference



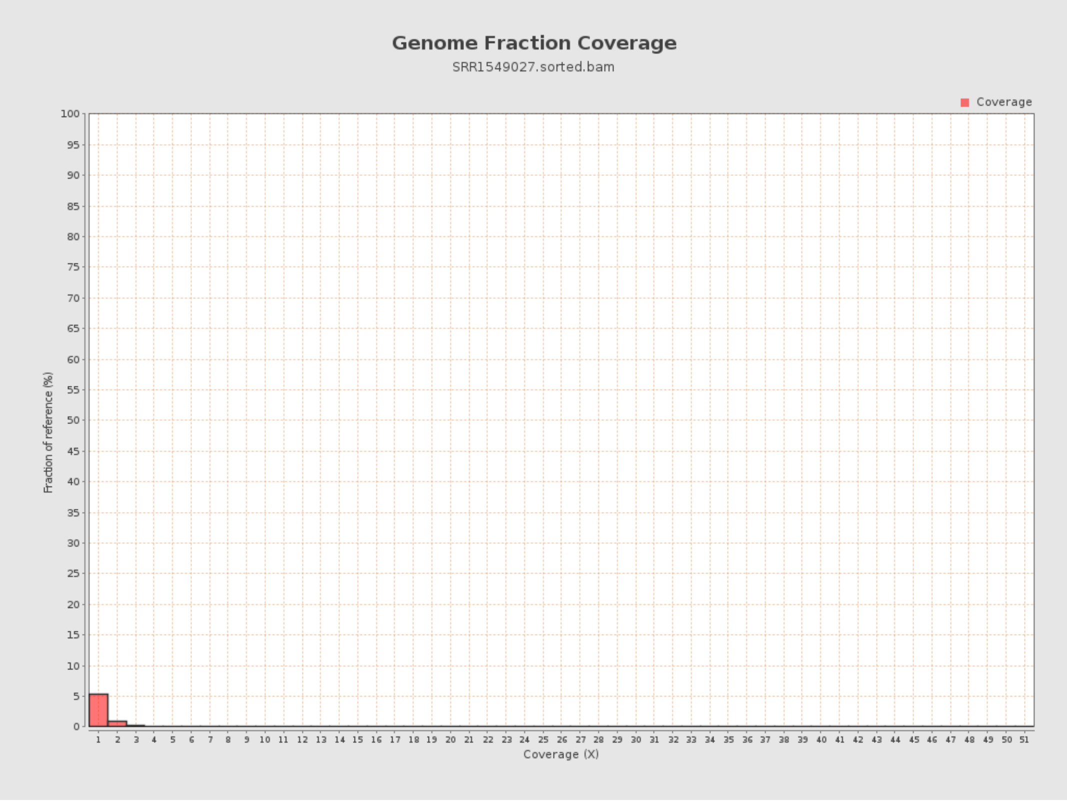
4. Results : Coverage Histogram



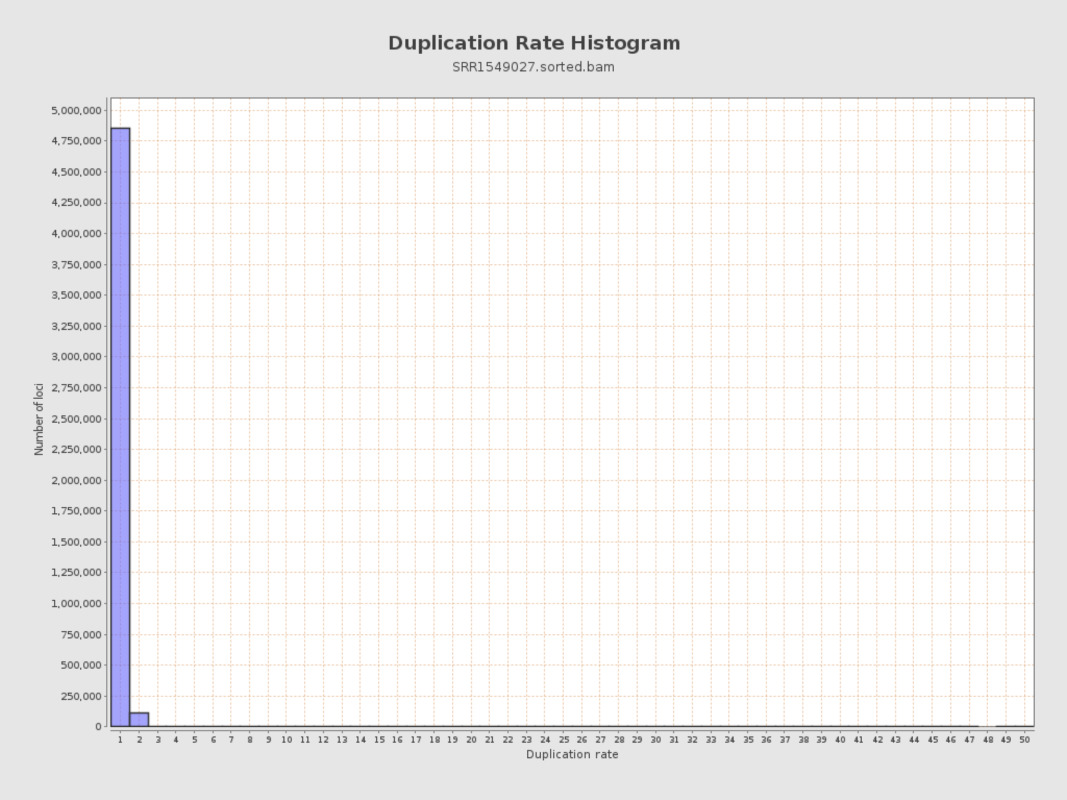
5. Results : Coverage Histogram (0-50X)



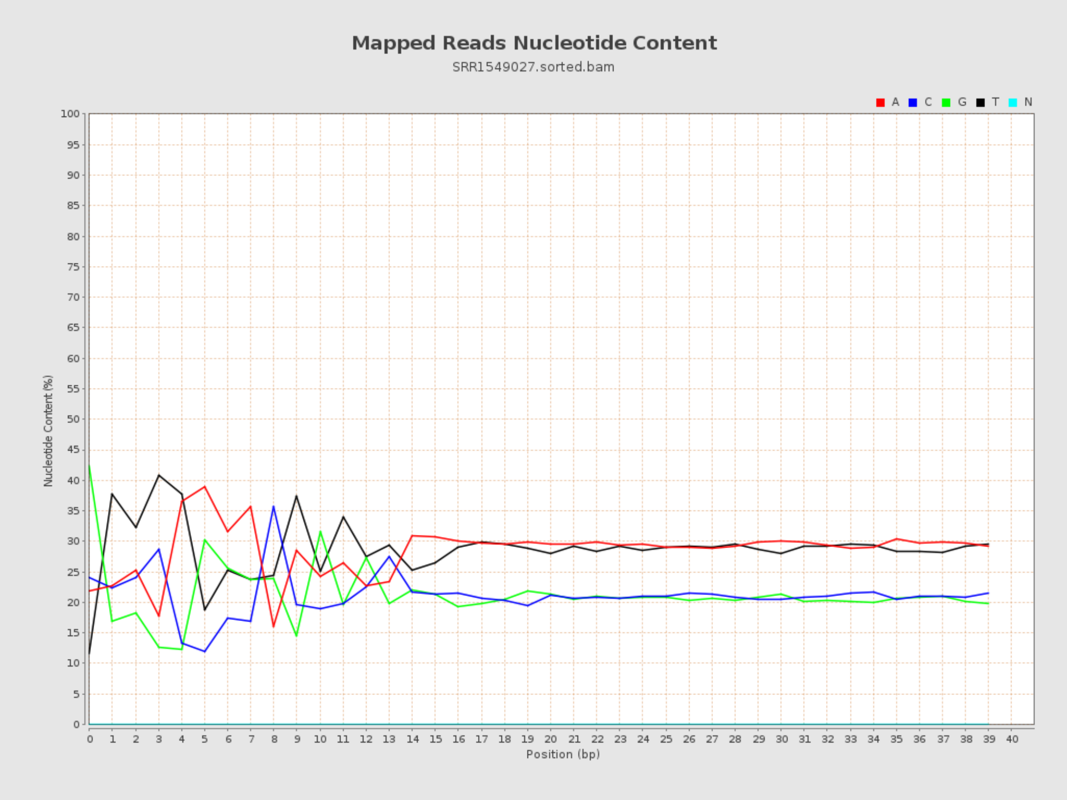
6. Results : Genome Fraction Coverage



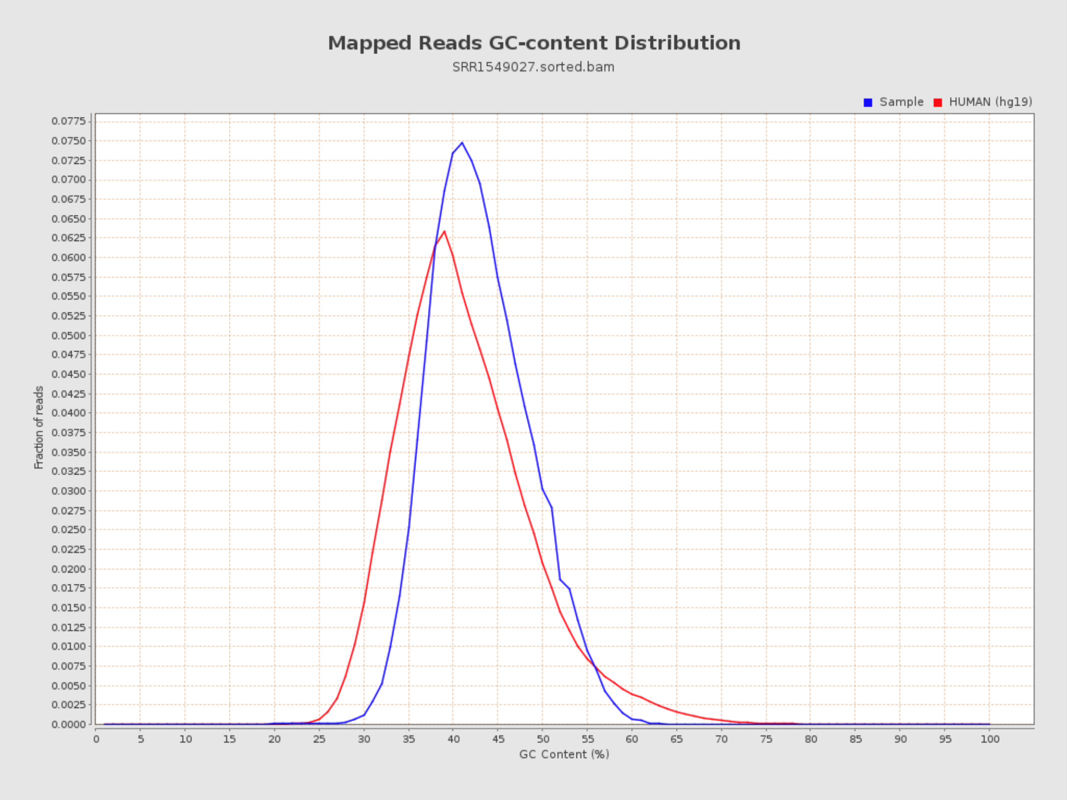
7. Results : Duplication Rate Histogram



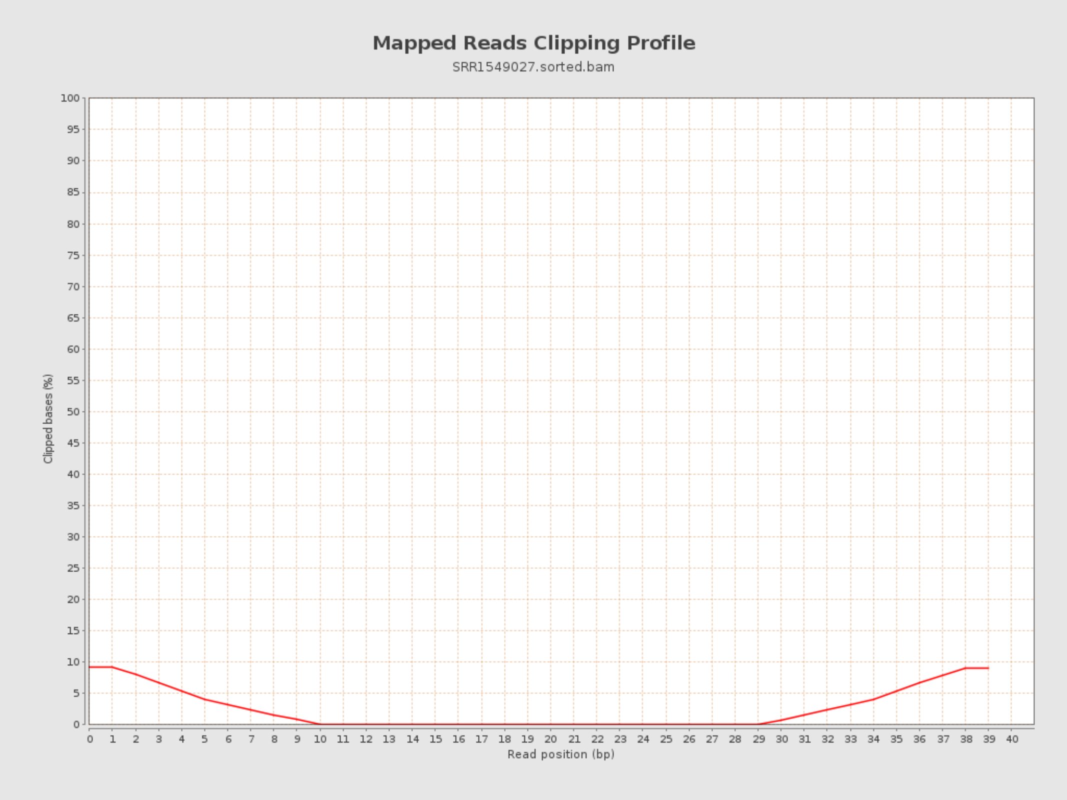
8. Results : Mapped Reads Nucleotide Content



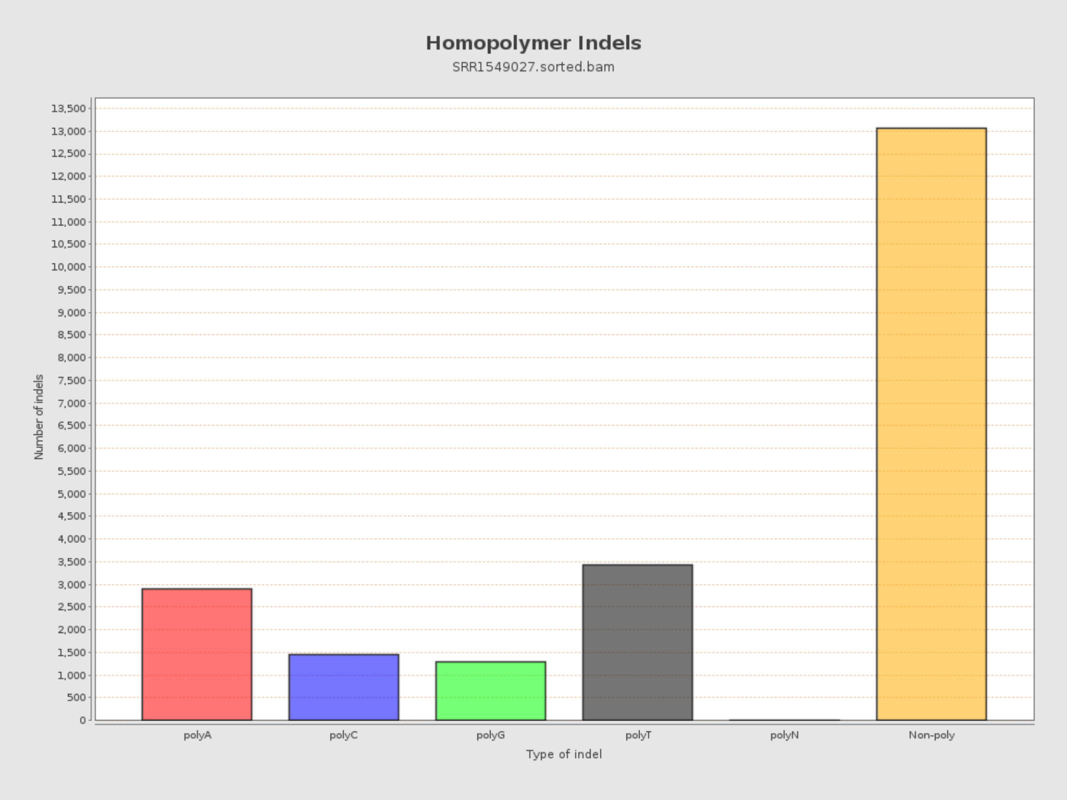
9. Results : Mapped Reads GC-content Distribution



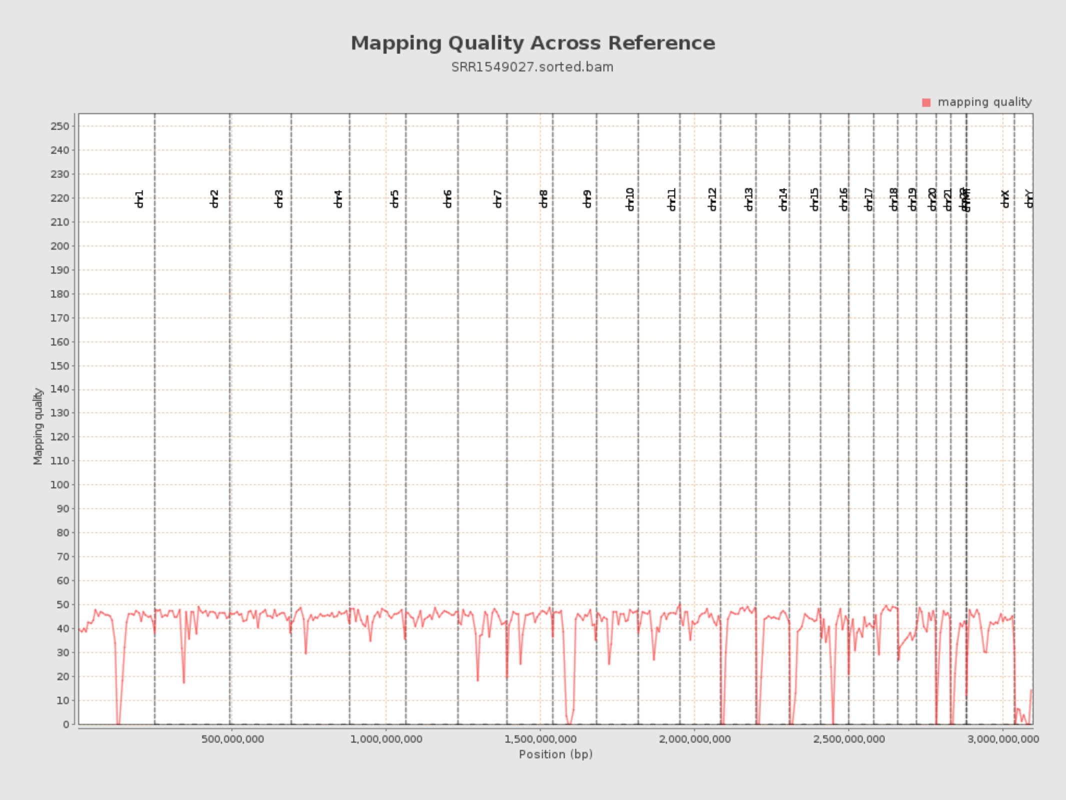
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram