Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:59:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549035.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_SRR1549035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:59:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,771,022
Mapped reads	7,525,268 / 77.02%
Unmapped reads	2,245,754 / 22.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	510,421 / 5.22%
Duplication rate	5.72%
Clipped reads	588,445 / 6.02%

2.2. ACGT Content

Number/percentage of A's	83,971,621 / 28.21%
Number/percentage of C's	63,060,505 / 21.19%
Number/percentage of T's	85,934,936 / 28.87%
Number/percentage of G's	64,646,734 / 21.72%
Number/percentage of N's	265 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0961
Standard Deviation	0.6277

2.4. Mapping Quality

Mean Mapping Quality	41.5

2.5. Mismatches and indels

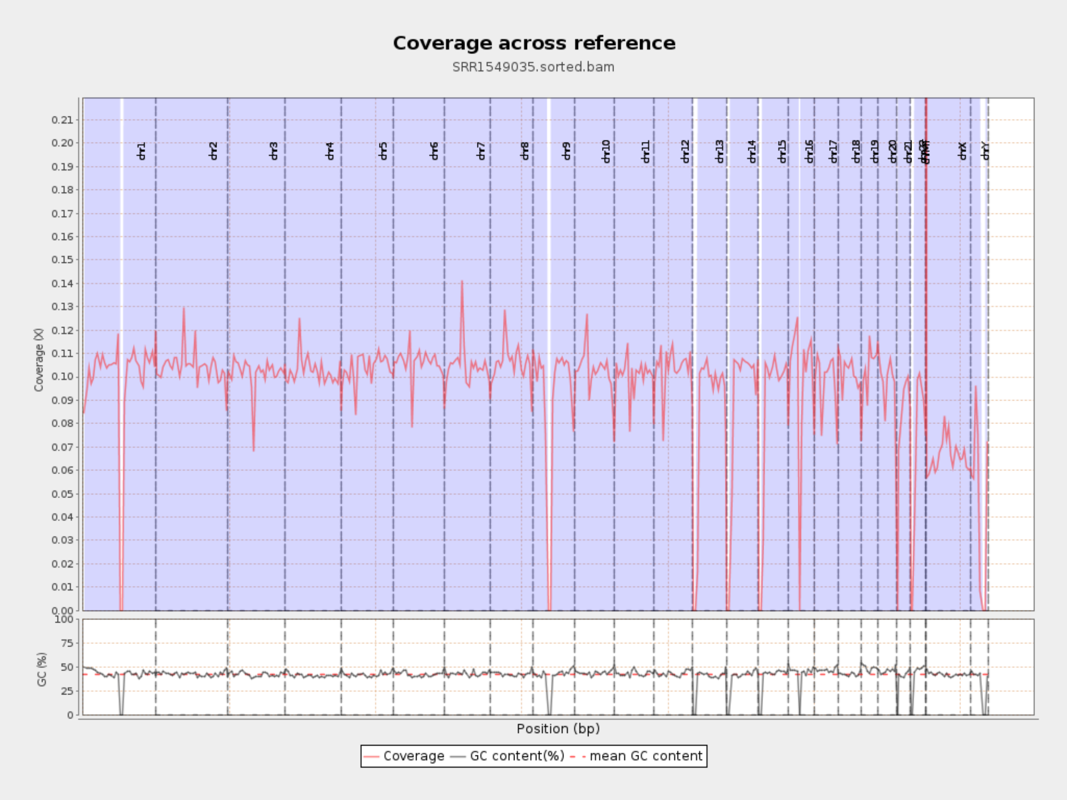
General error rate	0.26%
Mismatches	778,096
Insertions	8,454
Mapped reads with at least one insertion	0.11%
Deletions	21,167
Mapped reads with at least one deletion	0.28%
Homopolymer indels	42.12%

2.6. Chromosome stats

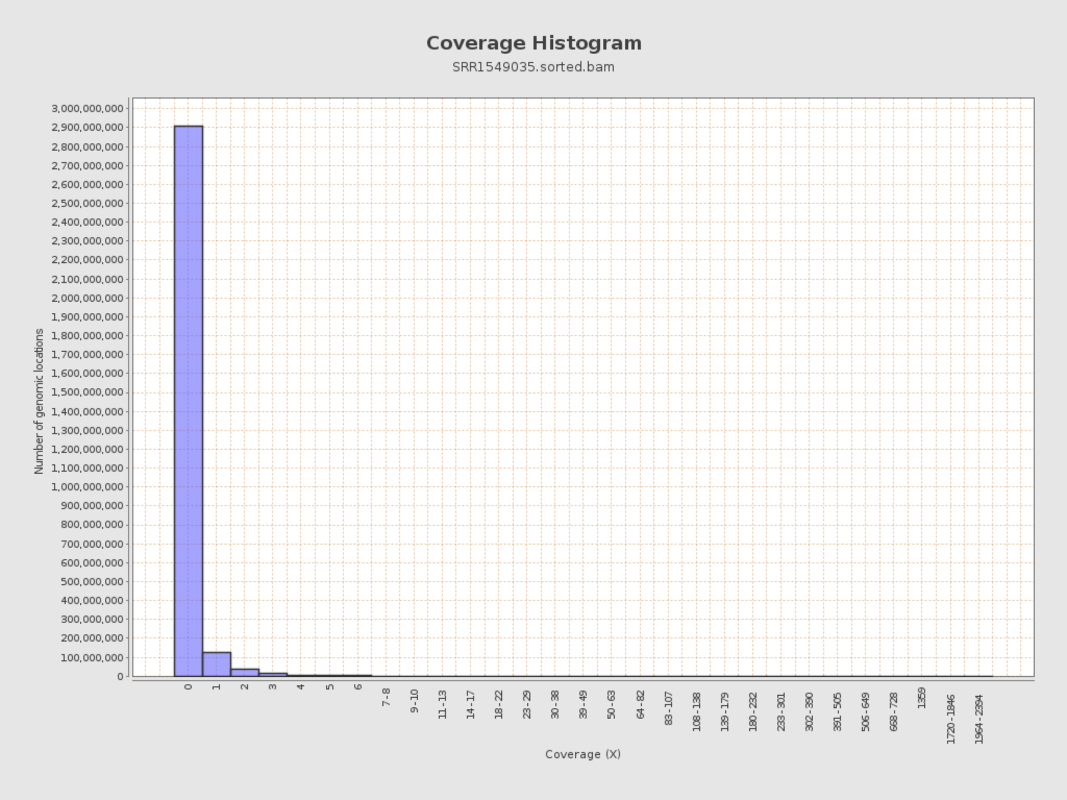
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24429283	0.098	0.7433
chr2	243199373	25416575	0.1045	0.6205
chr3	198022430	20122285	0.1016	0.4909
chr4	191154276	19643553	0.1028	0.5085
chr5	180915260	18763680	0.1037	0.4859
chr6	171115067	18160087	0.1061	0.5271
chr7	159138663	16752708	0.1053	0.8031
chr8	146364022	15511080	0.106	1.2817

chr9	141213431	12618124	0.0894	0.5683
chr10	135534747	13987229	0.1032	0.5964
chr11	135006516	13552031	0.1004	0.5474
chr12	133851895	13926369	0.104	0.4945
chr13	115169878	9600986	0.0834	0.4487
chr14	107349540	9370090	0.0873	0.4912
chr15	102531392	8519009	0.0831	0.4479
chr16	90354753	8722234	0.0965	0.5108
chr17	81195210	8052947	0.0992	0.4966
chr18	78077248	7963286	0.102	0.8376
chr19	59128983	6121676	0.1035	0.757
chr20	63025520	6162100	0.0978	0.4935
chr21	48129895	3840728	0.0798	0.515
chr22	51304566	3408104	0.0664	0.6562
chrMT	16571	37127	2.2405	2.7393
chrX	155270560	10270104	0.0661	0.4116
chrY	59373566	2690438	0.0453	0.4482

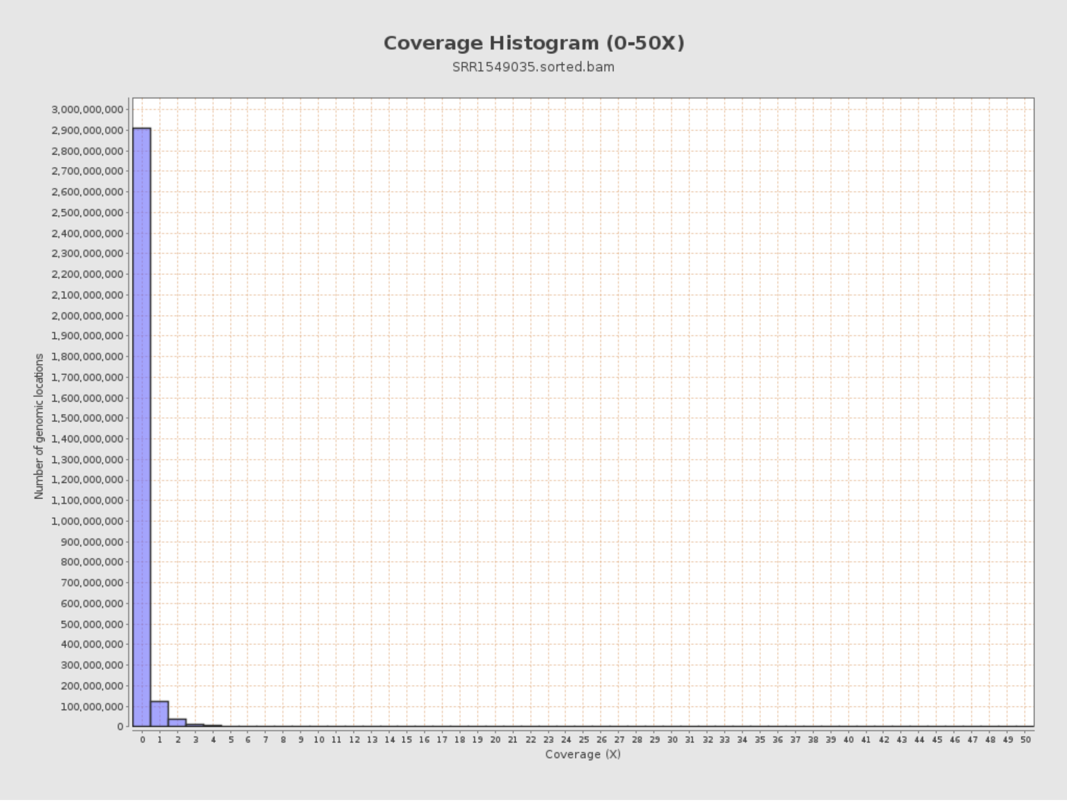
3. Results : Coverage across reference



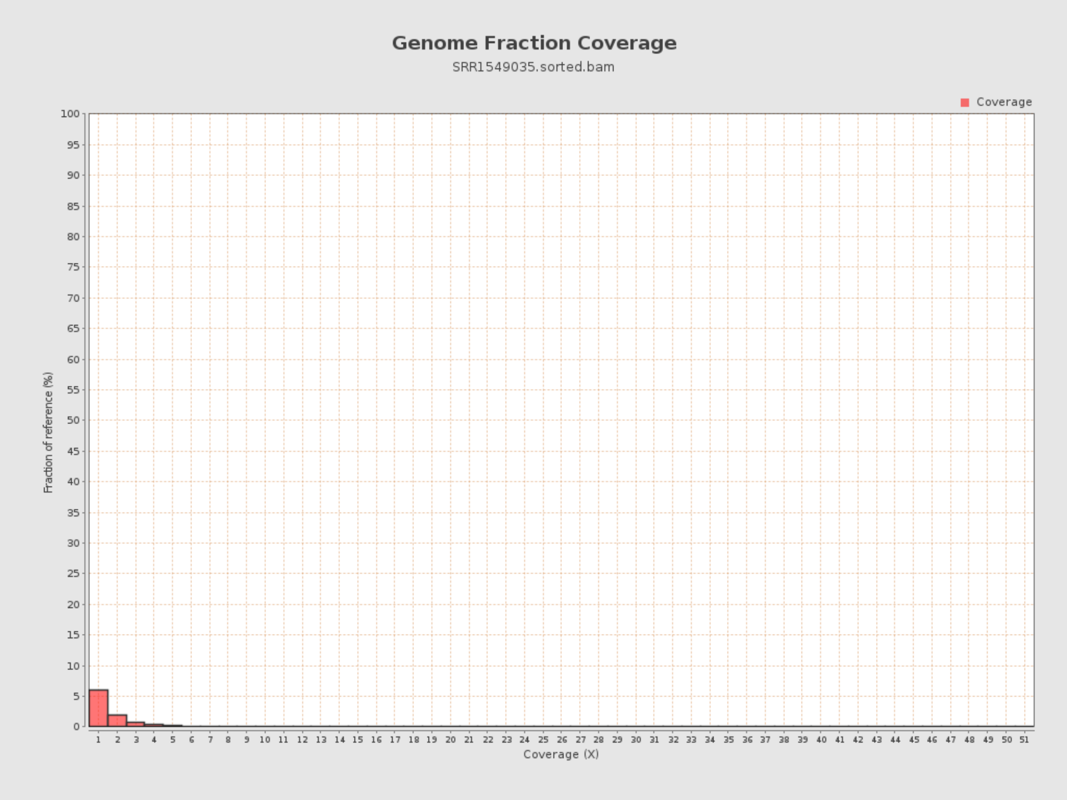
4. Results : Coverage Histogram



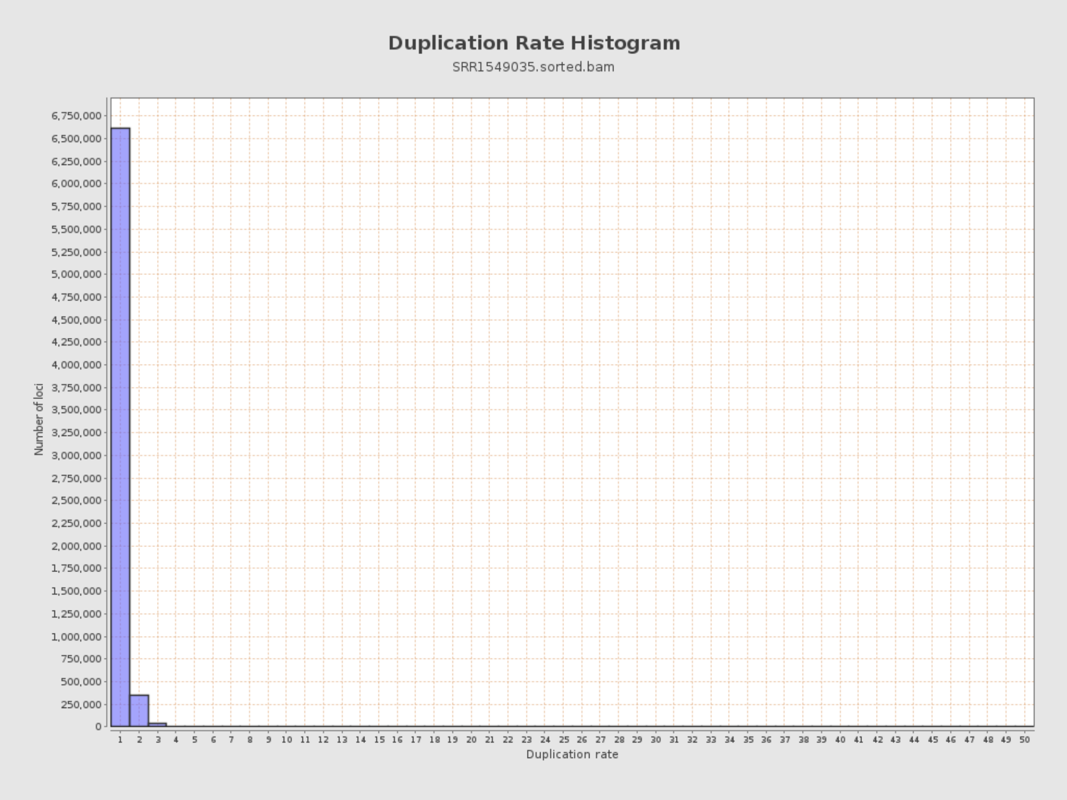
5. Results : Coverage Histogram (0-50X)



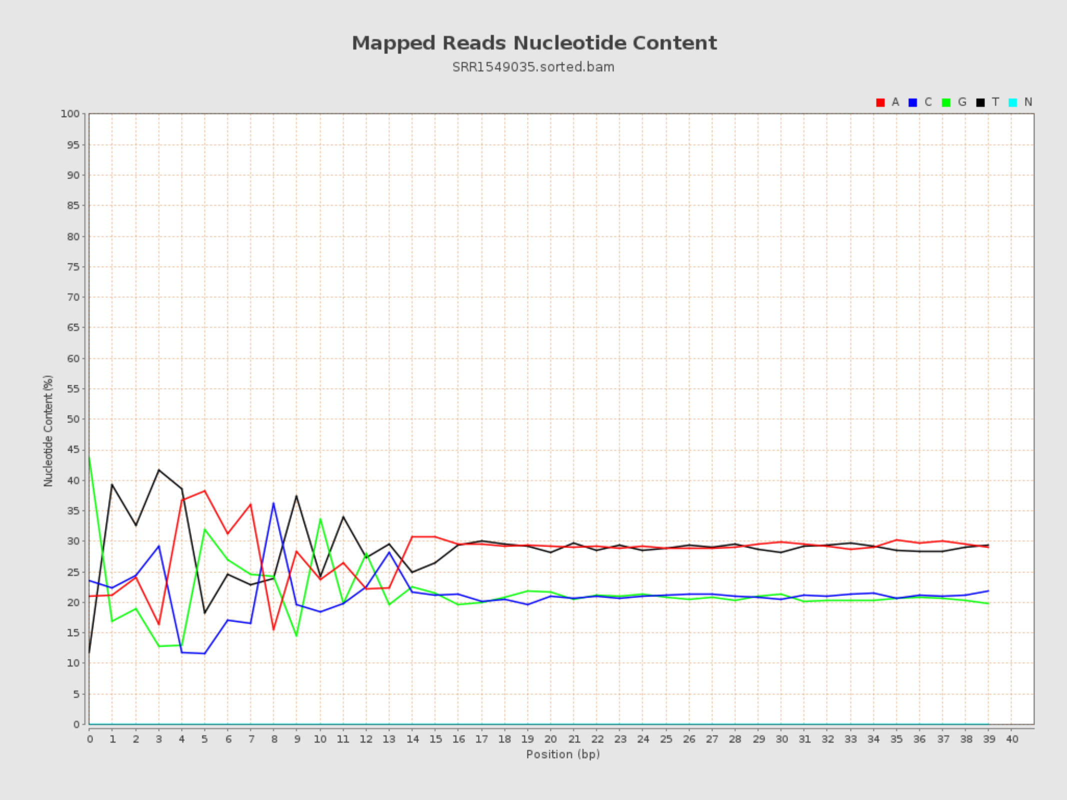
6. Results : Genome Fraction Coverage



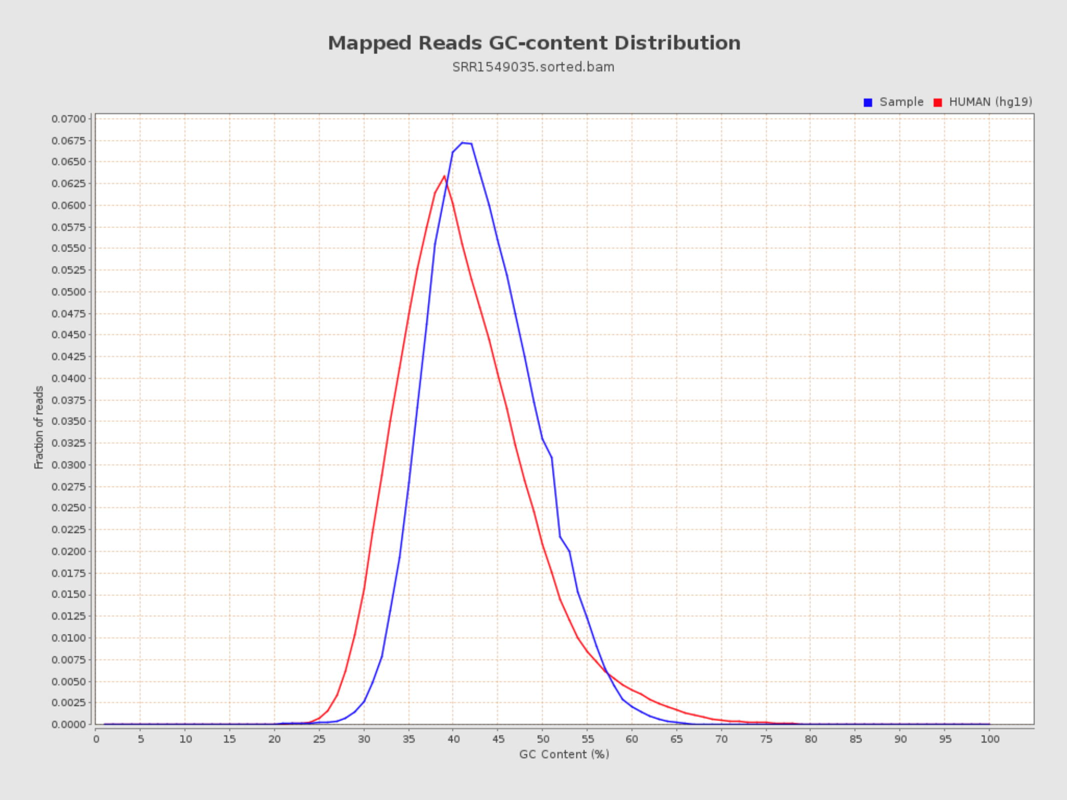
7. Results : Duplication Rate Histogram



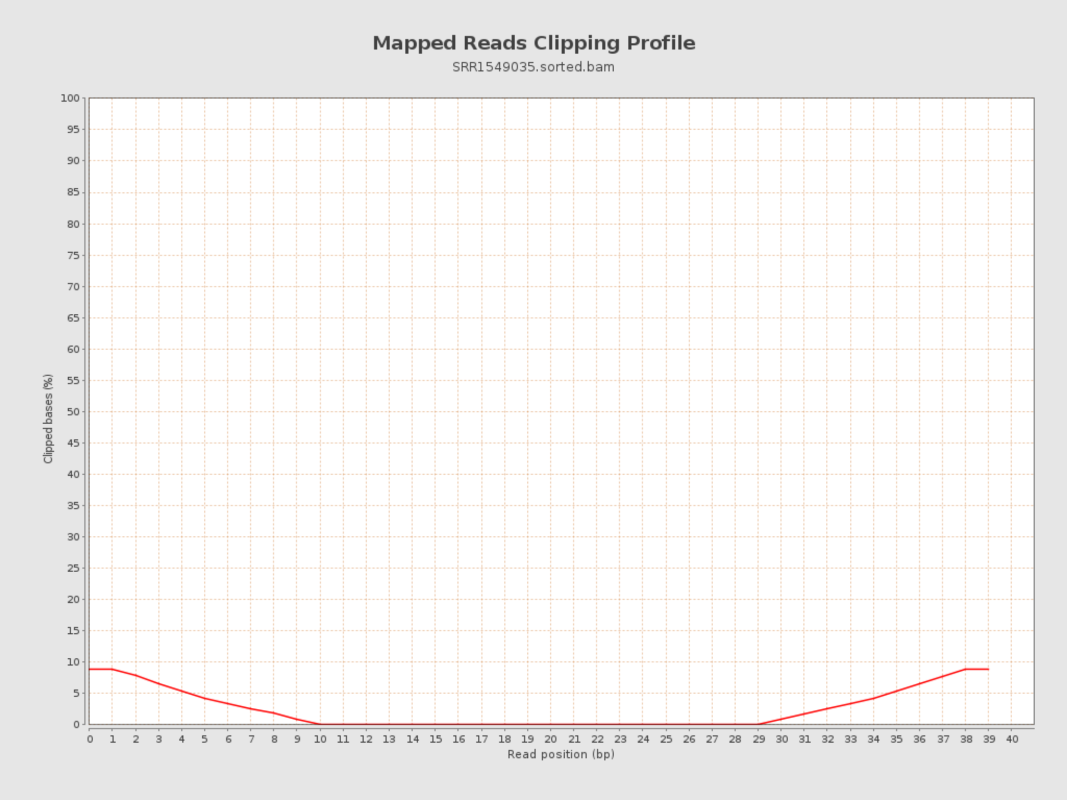
8. Results : Mapped Reads Nucleotide Content



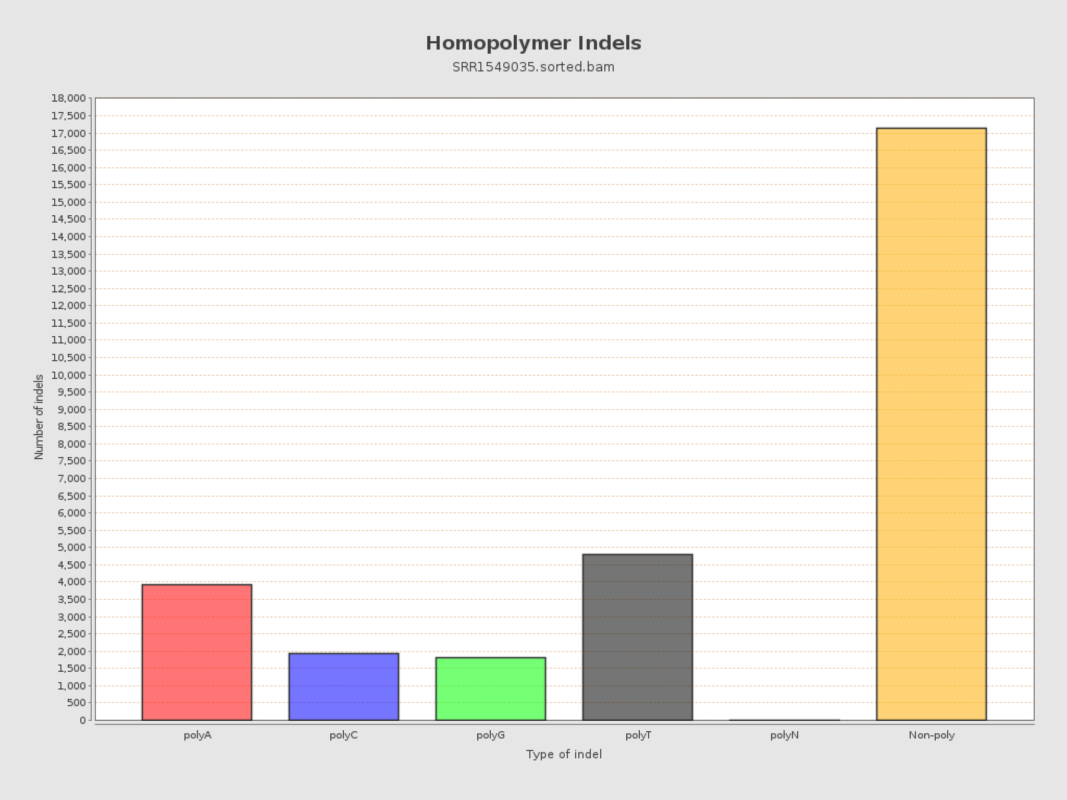
9. Results : Mapped Reads GC-content Distribution



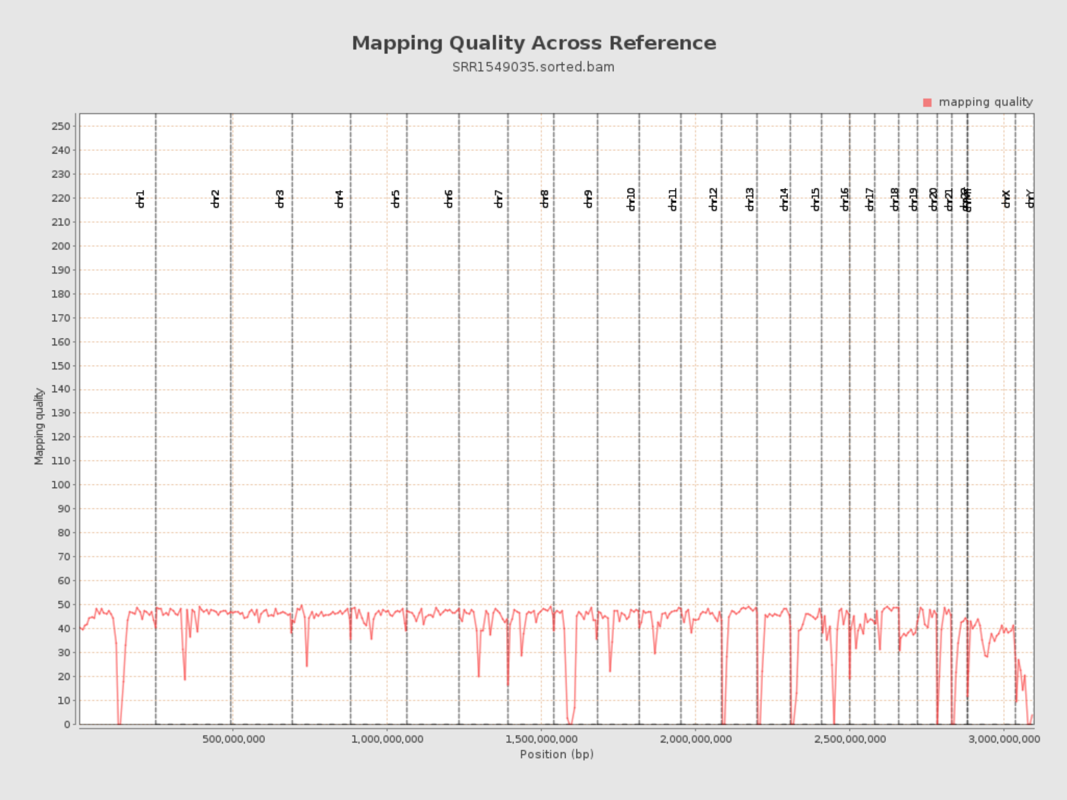
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram