Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:31:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549149.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_SRR1549149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:30:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,789,852
Mapped reads	18,334,195 / 88.19%
Unmapped reads	2,455,657 / 11.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,386,547 / 6.67%
Duplication rate	6.22%
Clipped reads	902,974 / 4.34%

2.2. ACGT Content

Number/percentage of A's	207,549,360 / 28.51%
Number/percentage of C's	155,280,731 / 21.33%
Number/percentage of T's	210,026,320 / 28.85%
Number/percentage of G's	154,911,206 / 21.28%
Number/percentage of N's	143,495 / 0.02%
GC Percentage	42.61%

2.3. Coverage

Mean	0.2352
Standard Deviation	1.2462

2.4. Mapping Quality

Mean Mapping Quality	43.13

2.5. Mismatches and indels

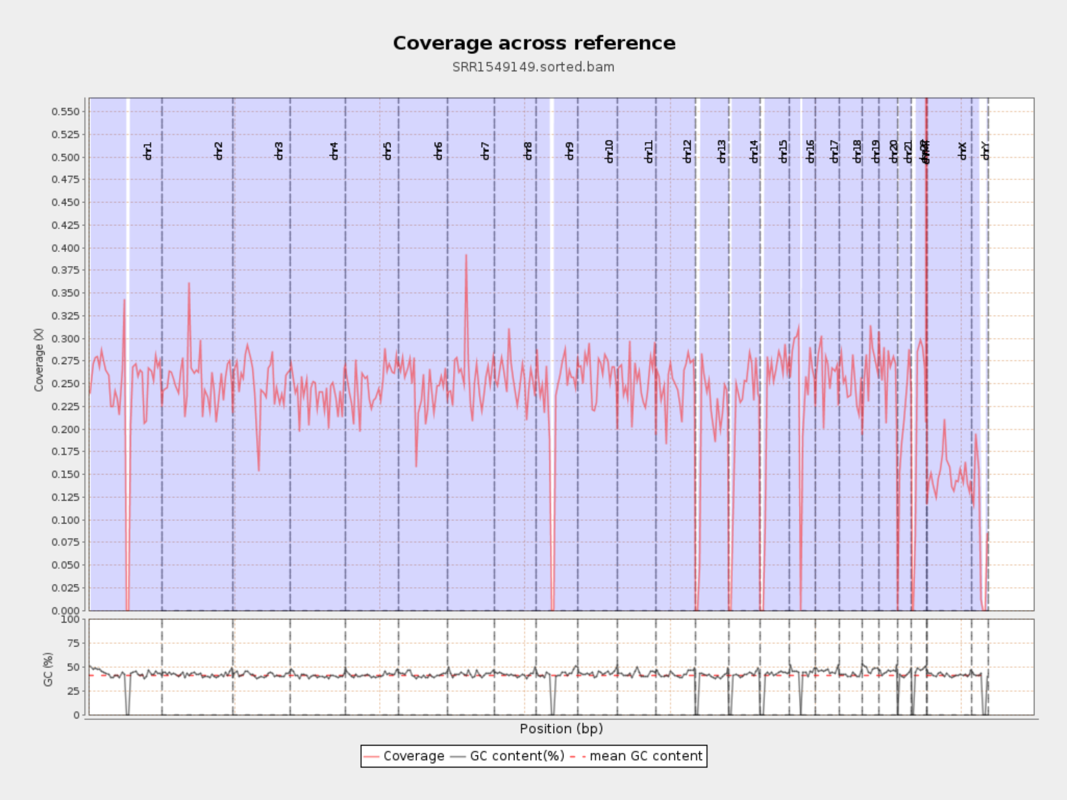
General error rate	0.31%
Mismatches	2,205,048
Insertions	18,436
Mapped reads with at least one insertion	0.1%
Deletions	55,977
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.53%

2.6. Chromosome stats

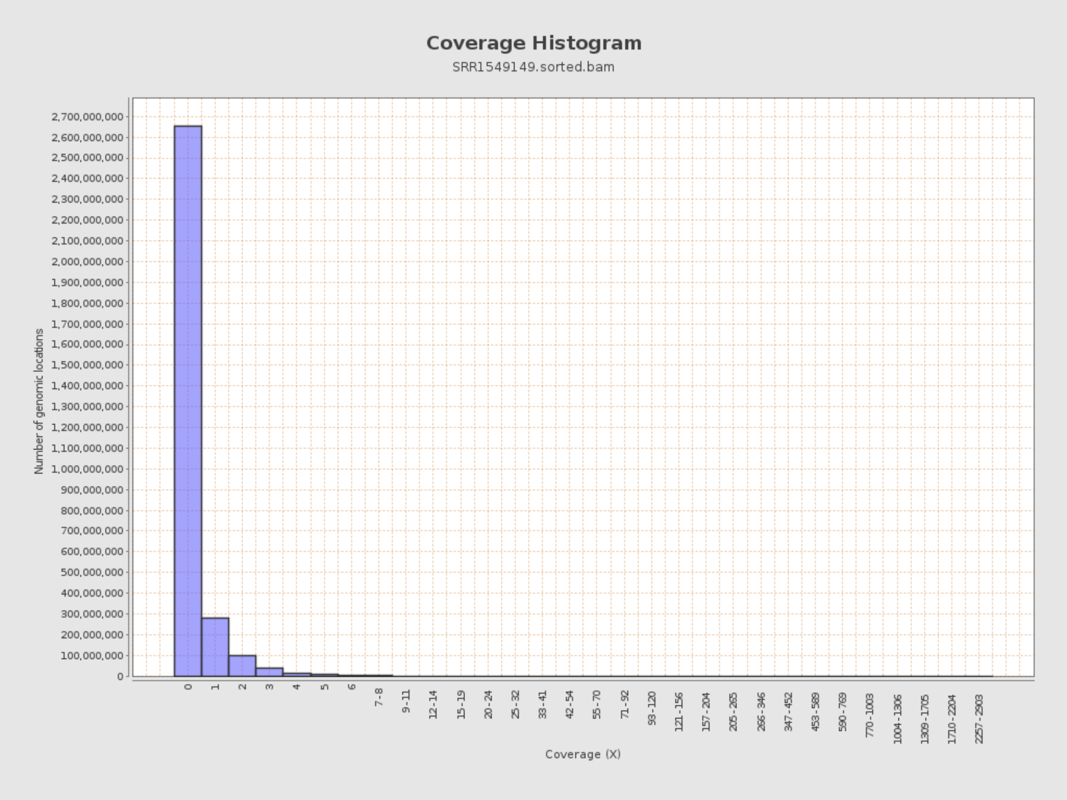
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60247950	0.2417	2.3866
chr2	243199373	61688853	0.2537	1.2263
chr3	198022430	49362439	0.2493	0.7501
chr4	191154276	45469302	0.2379	0.7447
chr5	180915260	44925069	0.2483	0.7686
chr6	171115067	42182765	0.2465	0.9153
chr7	159138663	41143175	0.2585	1.8708
chr8	146364022	37288802	0.2548	1.0347

chr9	141213431	31536404	0.2233	1.1536
chr10	135534747	35544255	0.2623	1.1405
chr11	135006516	34137287	0.2529	1.097
chr12	133851895	33656384	0.2514	0.8079
chr13	115169878	22406205	0.1945	0.6467
chr14	107349540	22423585	0.2089	0.8889
chr15	102531392	22522496	0.2197	0.6945
chr16	90354753	22253342	0.2463	0.8524
chr17	81195210	21327559	0.2627	0.8914
chr18	78077248	19556702	0.2505	2.3871
chr19	59128983	16010991	0.2708	2.0459
chr20	63025520	16631763	0.2639	0.8352
chr21	48129895	9586365	0.1992	0.7966
chr22	51304566	9882152	0.1926	0.7234
chrMT	16571	123674	7.4633	10.7152
chrX	155270560	23086514	0.1487	0.792
chrY	59373566	4987673	0.084	0.5333

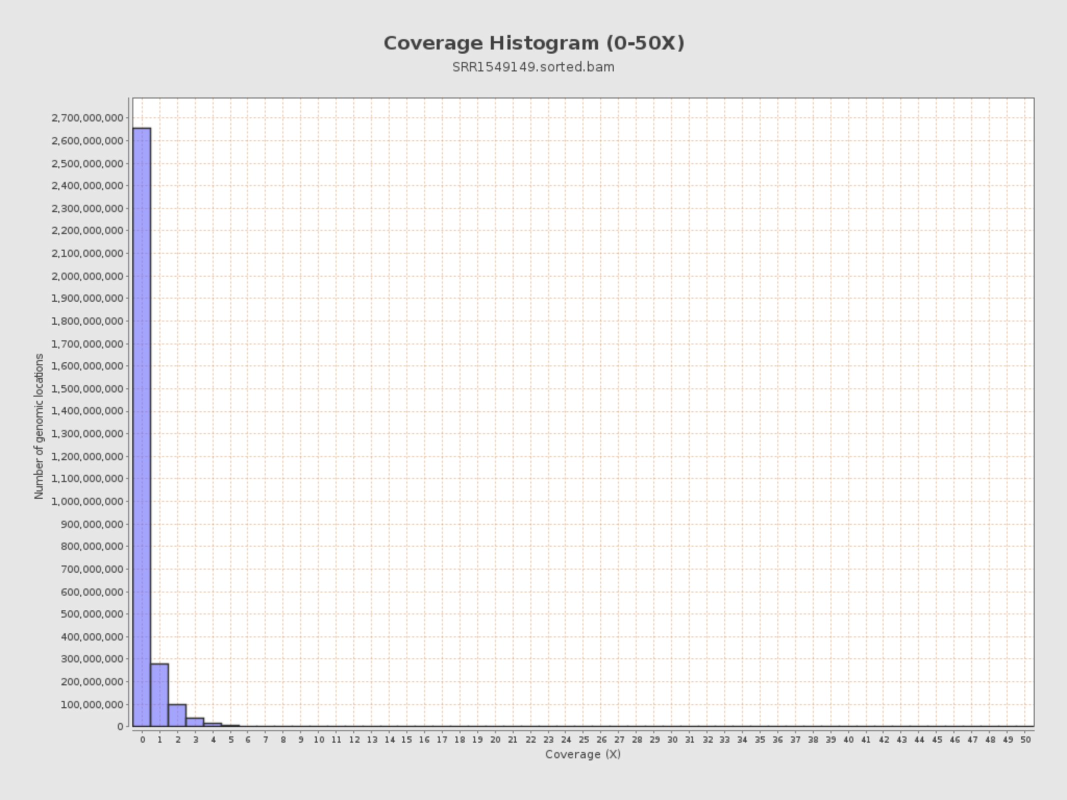
3. Results : Coverage across reference



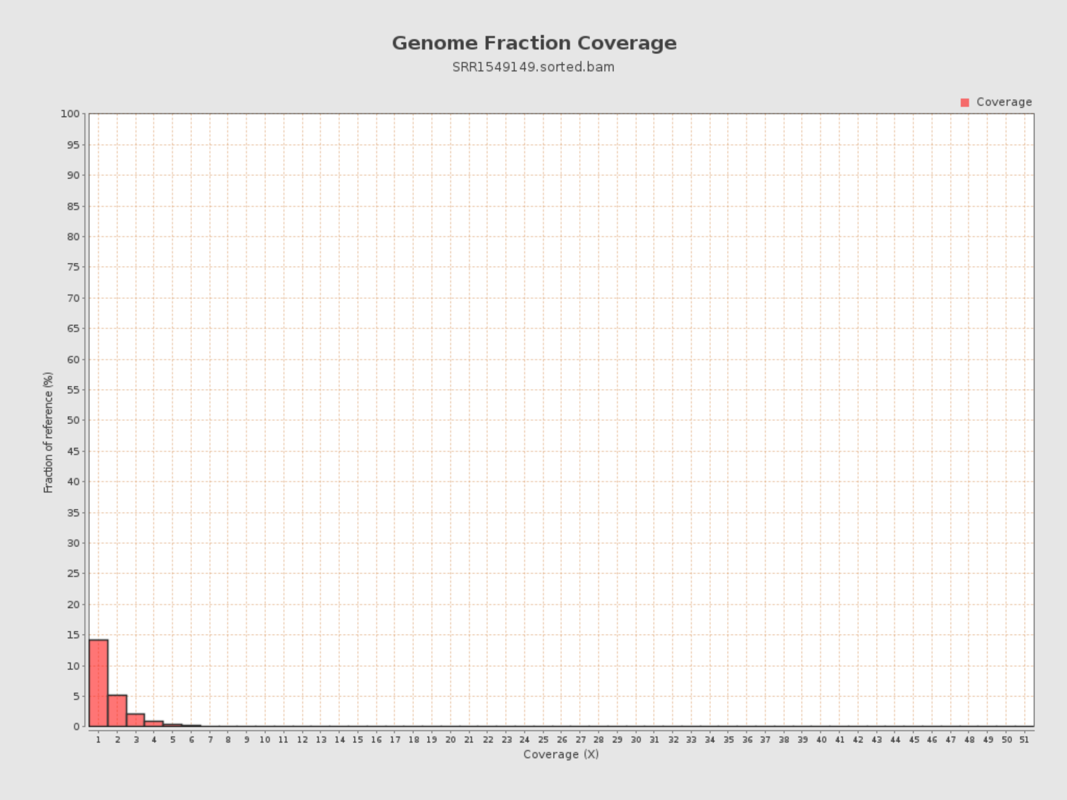
4. Results : Coverage Histogram



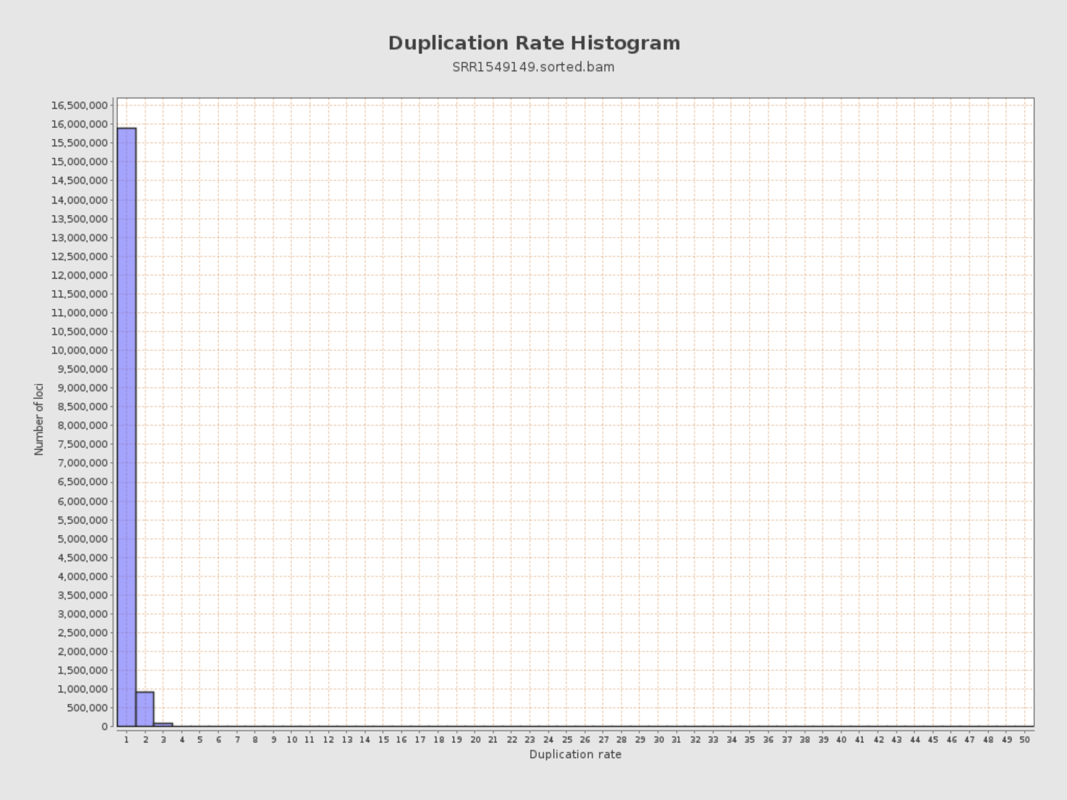
5. Results : Coverage Histogram (0-50X)



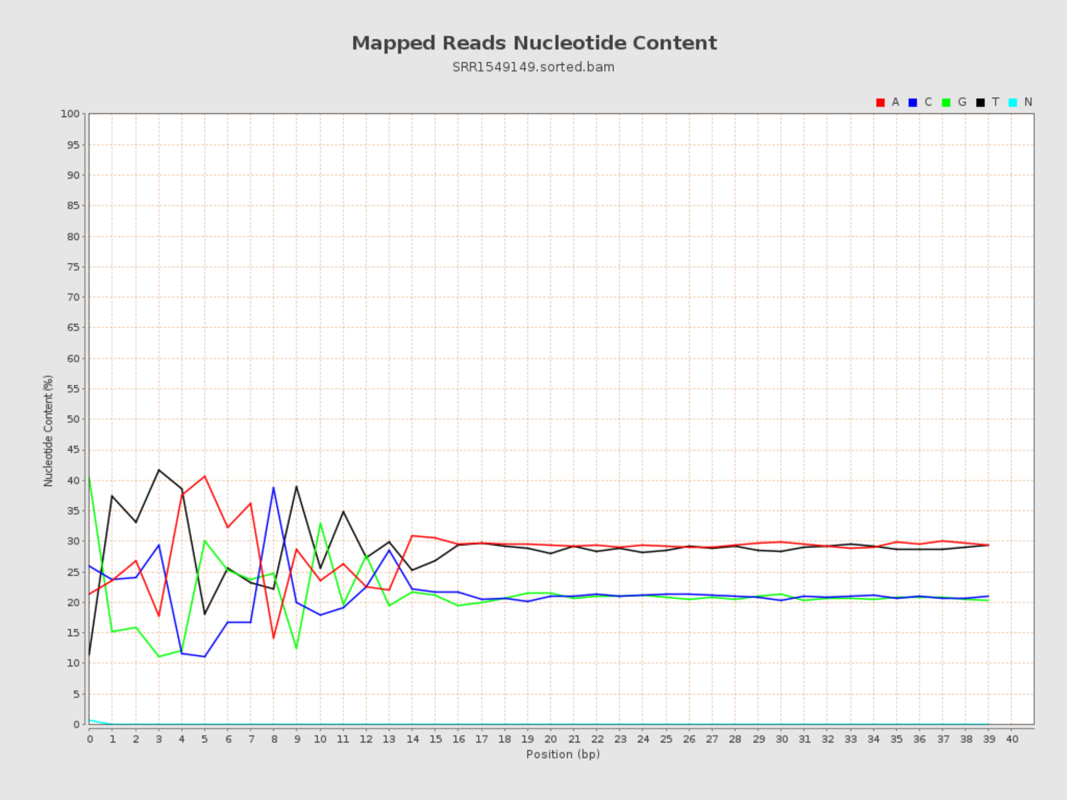
6. Results : Genome Fraction Coverage



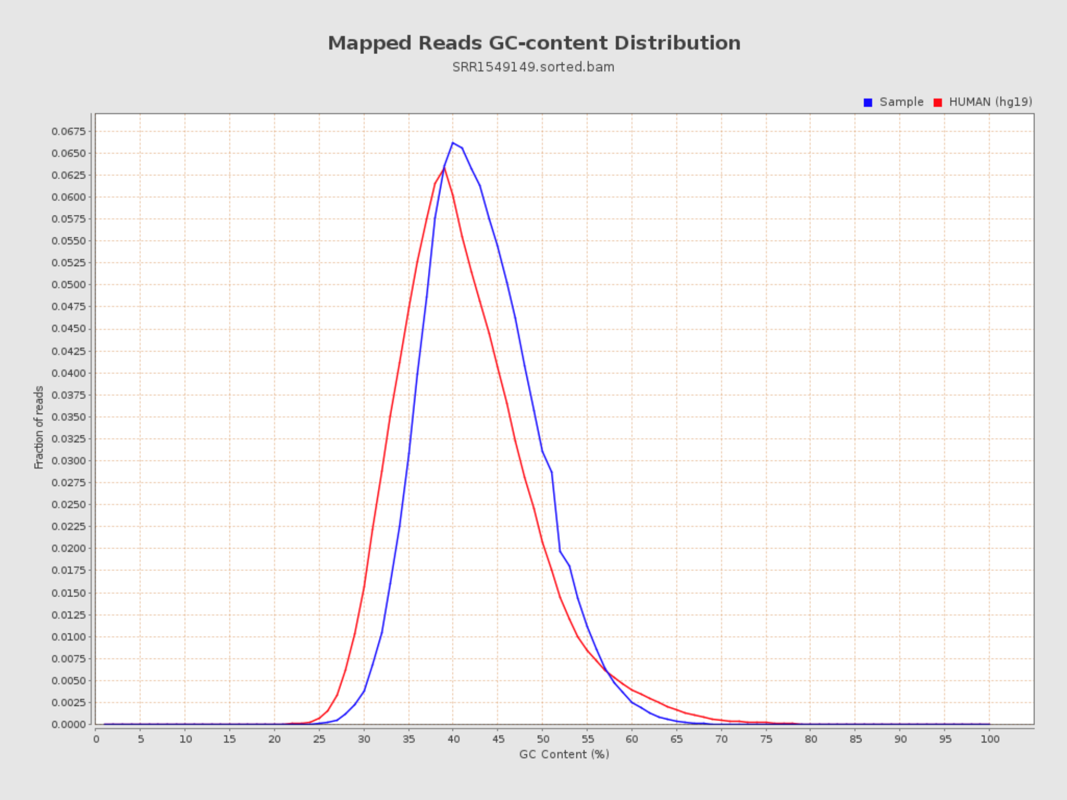
7. Results : Duplication Rate Histogram



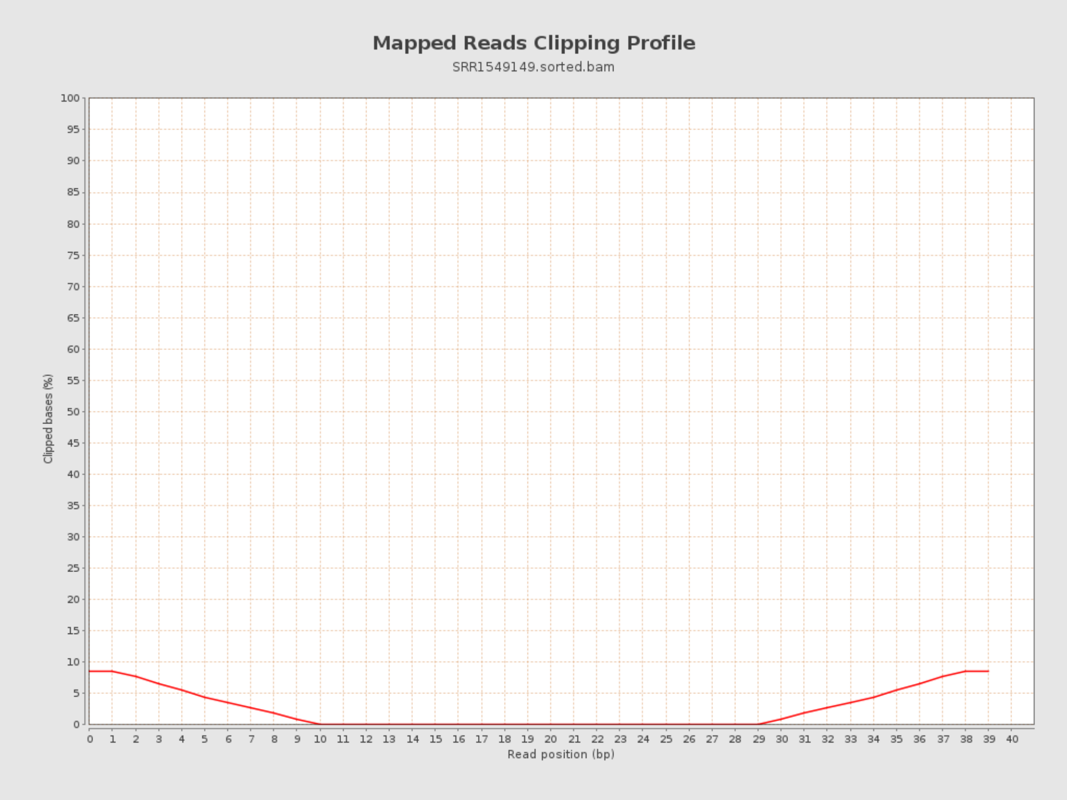
8. Results : Mapped Reads Nucleotide Content



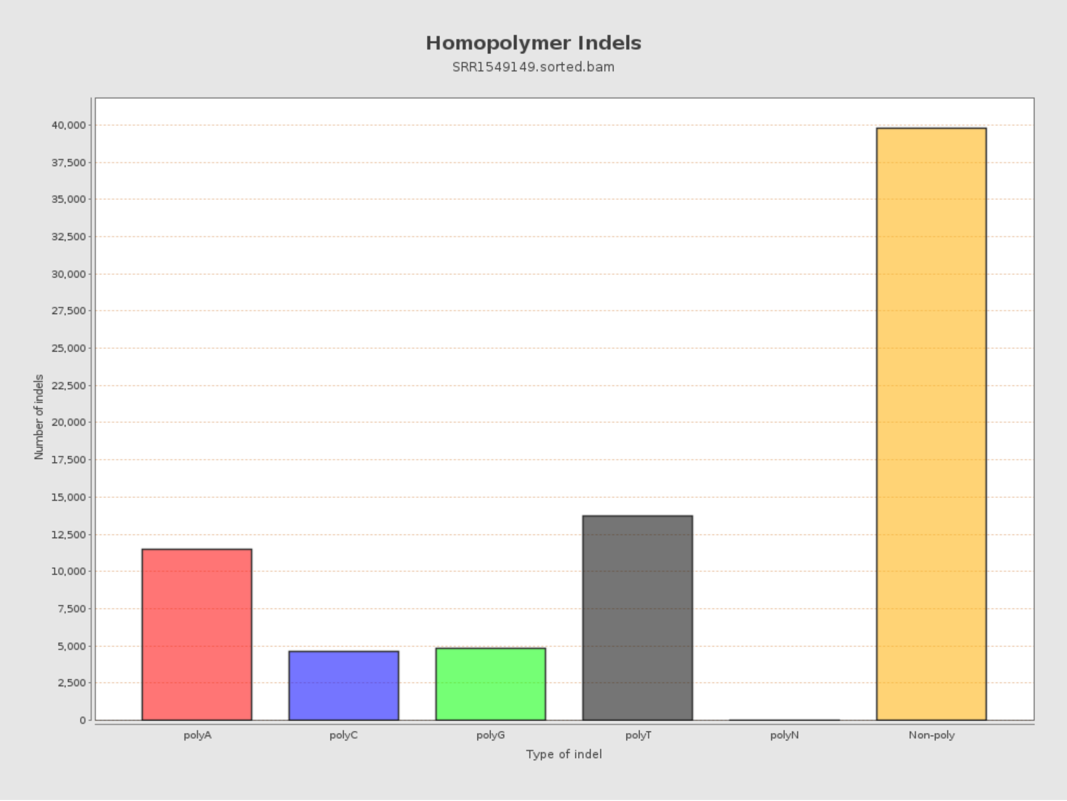
9. Results : Mapped Reads GC-content Distribution



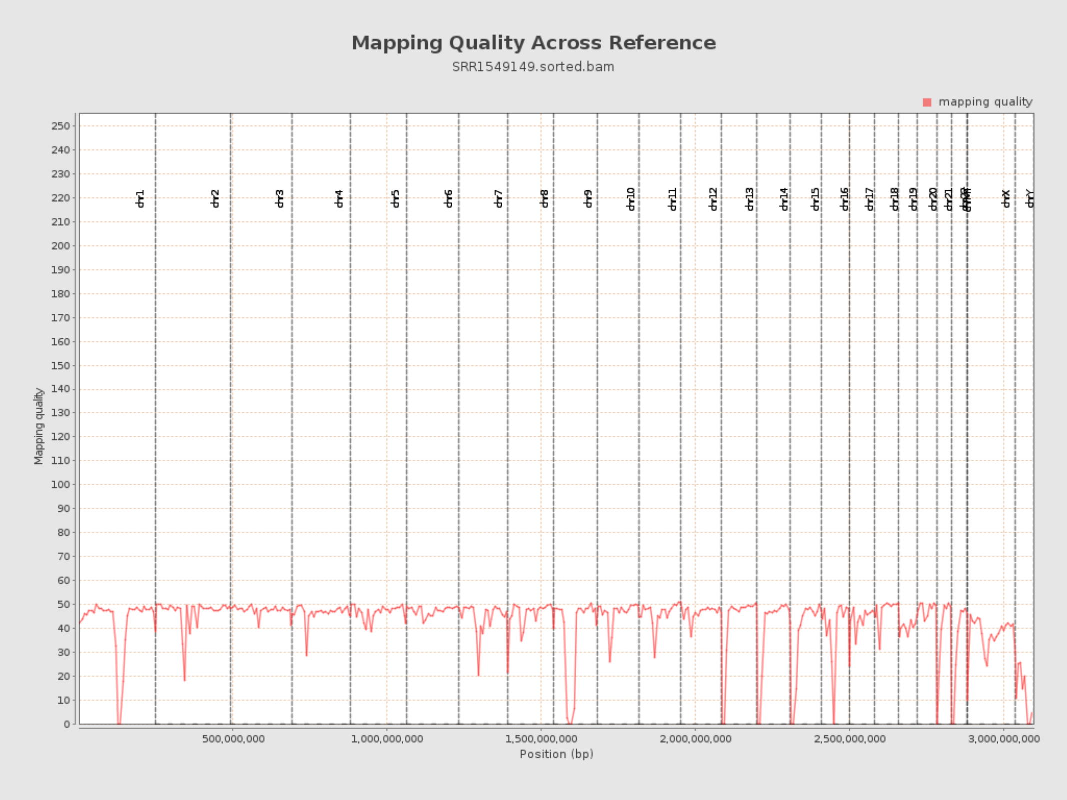
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram