Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549142.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_SRR1549142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:07:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,014,358
Mapped reads	11,417,239 / 87.73%
Unmapped reads	1,597,119 / 12.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	604,890 / 4.65%
Duplication rate	4.28%
Clipped reads	571,067 / 4.39%

2.2. ACGT Content

Number/percentage of A's	131,204,327 / 28.95%
Number/percentage of C's	94,464,648 / 20.84%
Number/percentage of T's	132,922,710 / 29.33%
Number/percentage of G's	94,567,939 / 20.86%
Number/percentage of N's	103,383 / 0.02%
GC Percentage	41.7%

2.3. Coverage

Mean	0.1464
Standard Deviation	0.8073

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

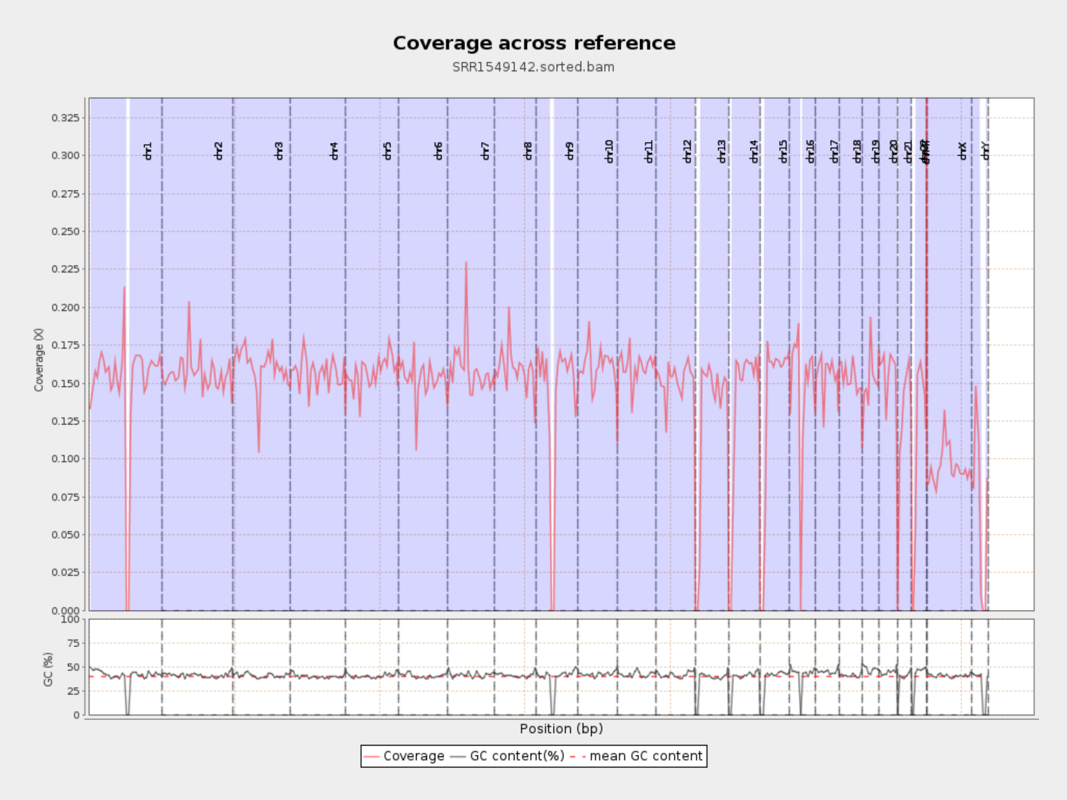
General error rate	0.32%
Mismatches	1,448,789
Insertions	11,273
Mapped reads with at least one insertion	0.1%
Deletions	34,243
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.28%

2.6. Chromosome stats

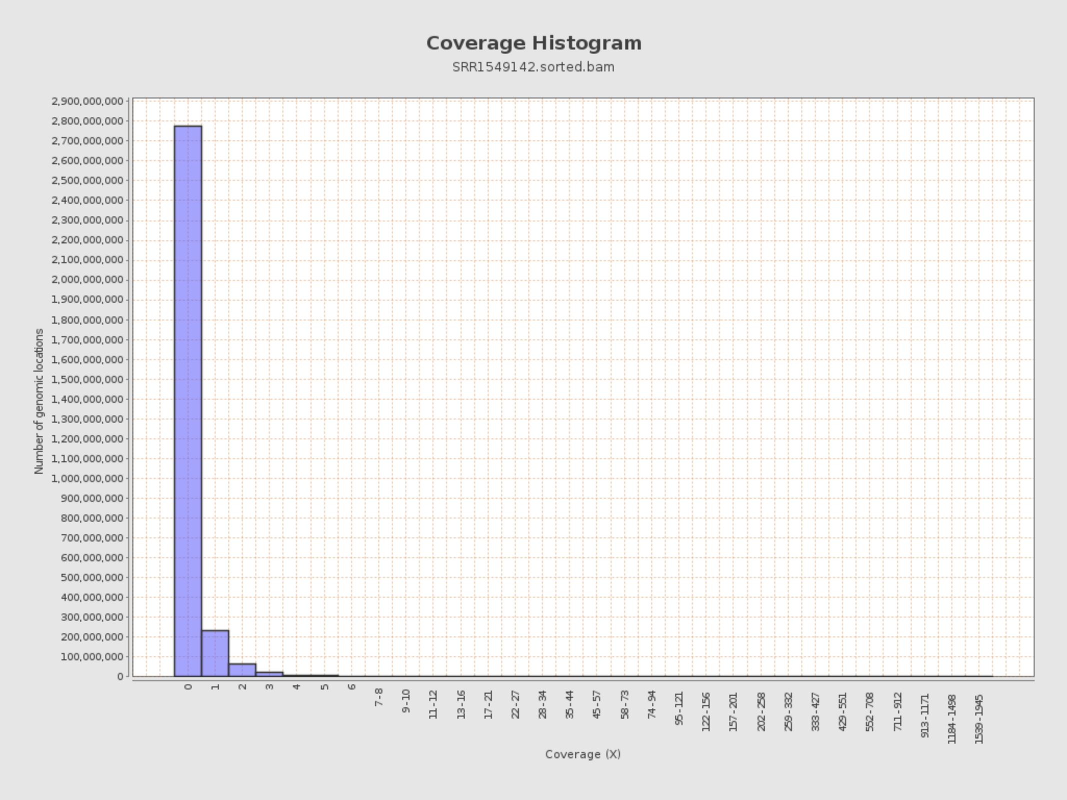
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37223498	0.1493	1.5231
chr2	243199373	38132138	0.1568	0.7626
chr3	198022430	31800445	0.1606	0.5332
chr4	191154276	29993941	0.1569	0.5638
chr5	180915260	28411687	0.157	0.537
chr6	171115067	26261878	0.1535	0.5918
chr7	159138663	25386381	0.1595	1.1686
chr8	146364022	23350245	0.1595	0.7507

chr9	141213431	19762651	0.1399	0.7289
chr10	135534747	21912935	0.1617	0.767
chr11	135006516	21611003	0.1601	0.7328
chr12	133851895	20327612	0.1519	0.5433
chr13	115169878	14478642	0.1257	0.4633
chr14	107349540	14307605	0.1333	0.6167
chr15	102531392	13779268	0.1344	0.4827
chr16	90354753	13143434	0.1455	0.5634
chr17	81195210	12569114	0.1548	0.5693
chr18	78077248	12054961	0.1544	1.4154
chr19	59128983	8994064	0.1521	1.2819
chr20	63025520	9865525	0.1565	0.5674
chr21	48129895	6003837	0.1247	0.5631
chr22	51304566	5386982	0.105	0.4593
chrMT	16571	7159	0.432	0.8748
chrX	155270560	14741818	0.0949	0.5151
chrY	59373566	3799305	0.064	0.504

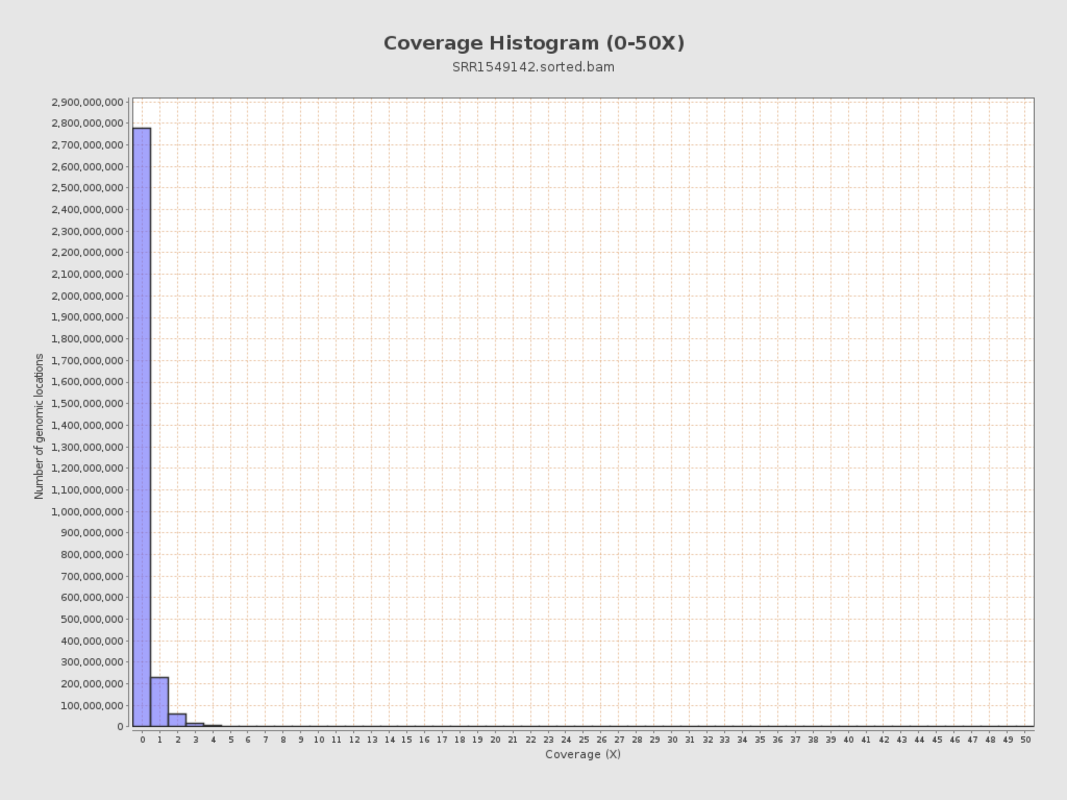
3. Results : Coverage across reference



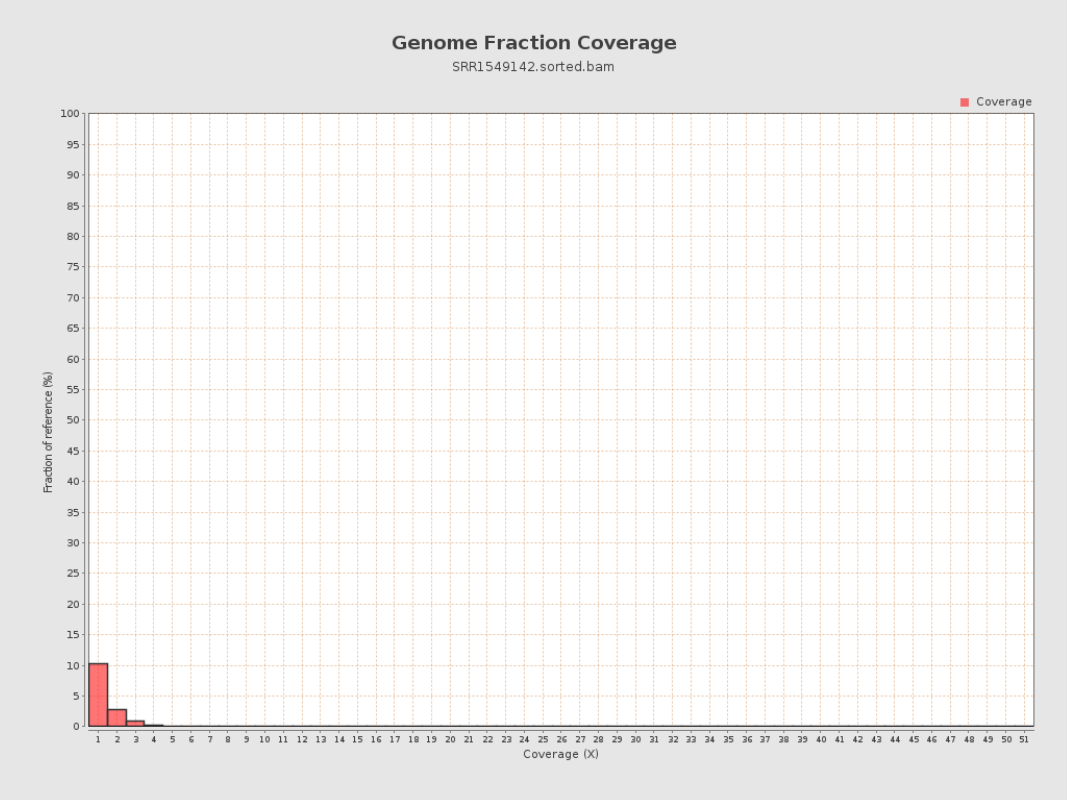
4. Results : Coverage Histogram



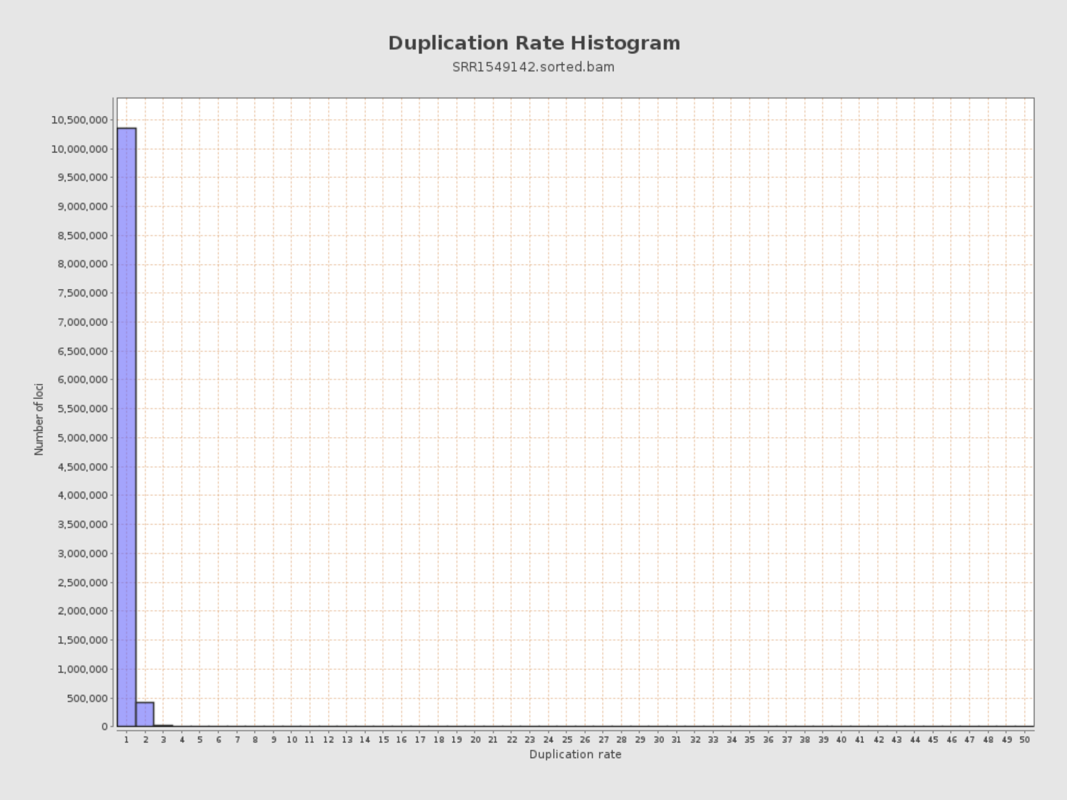
5. Results : Coverage Histogram (0-50X)



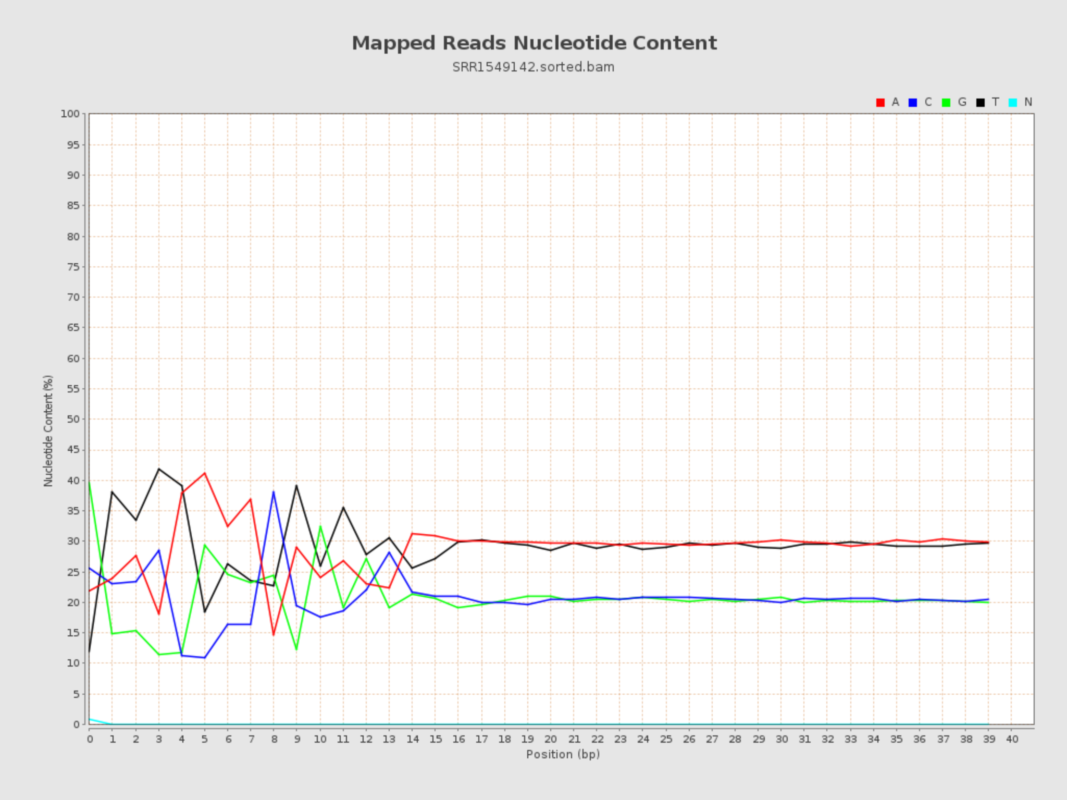
6. Results : Genome Fraction Coverage



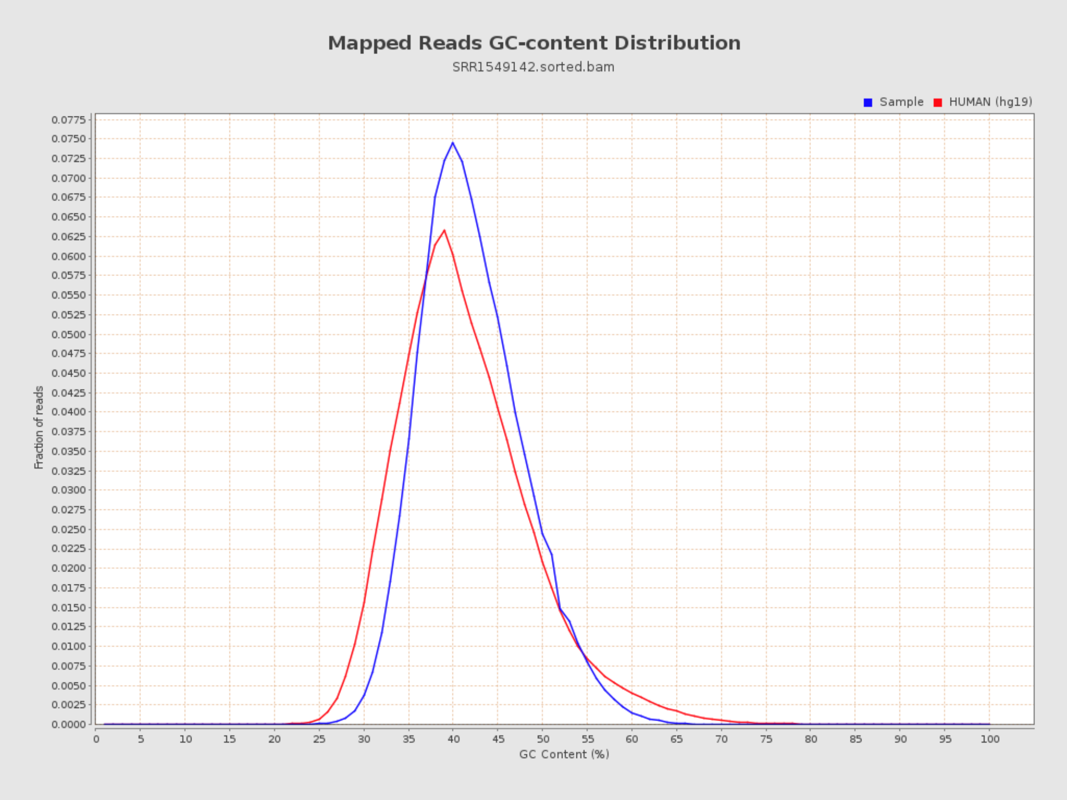
7. Results : Duplication Rate Histogram



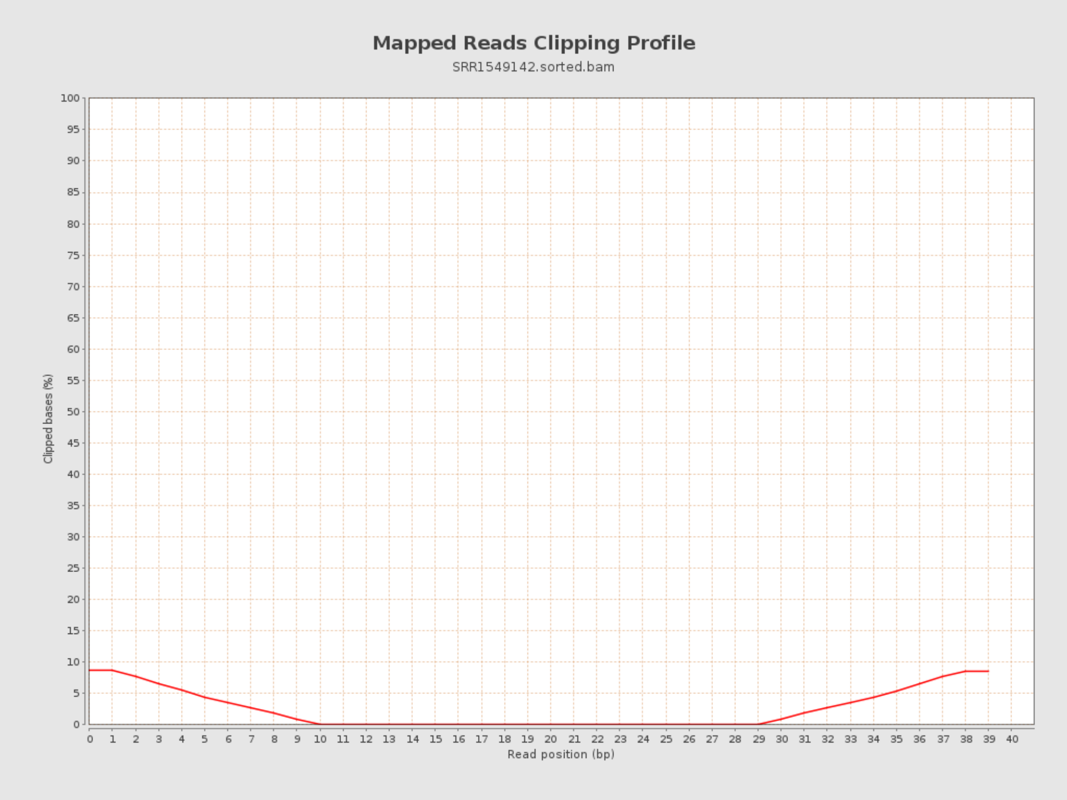
8. Results : Mapped Reads Nucleotide Content



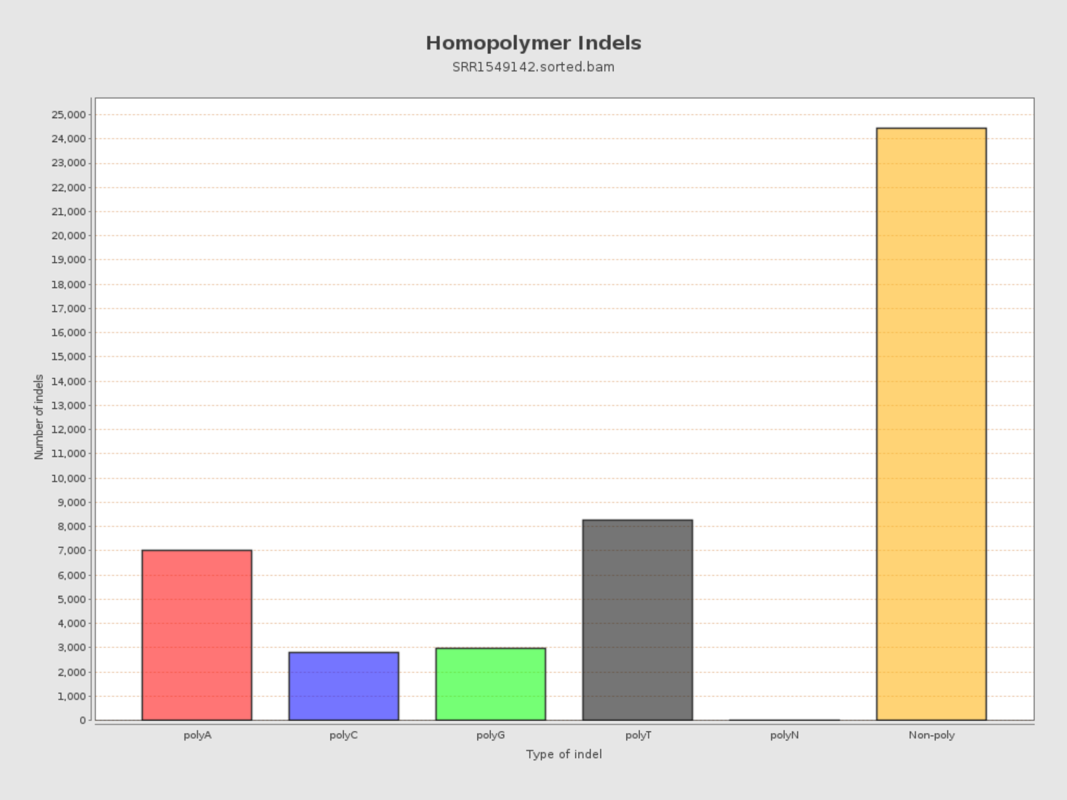
9. Results : Mapped Reads GC-content Distribution



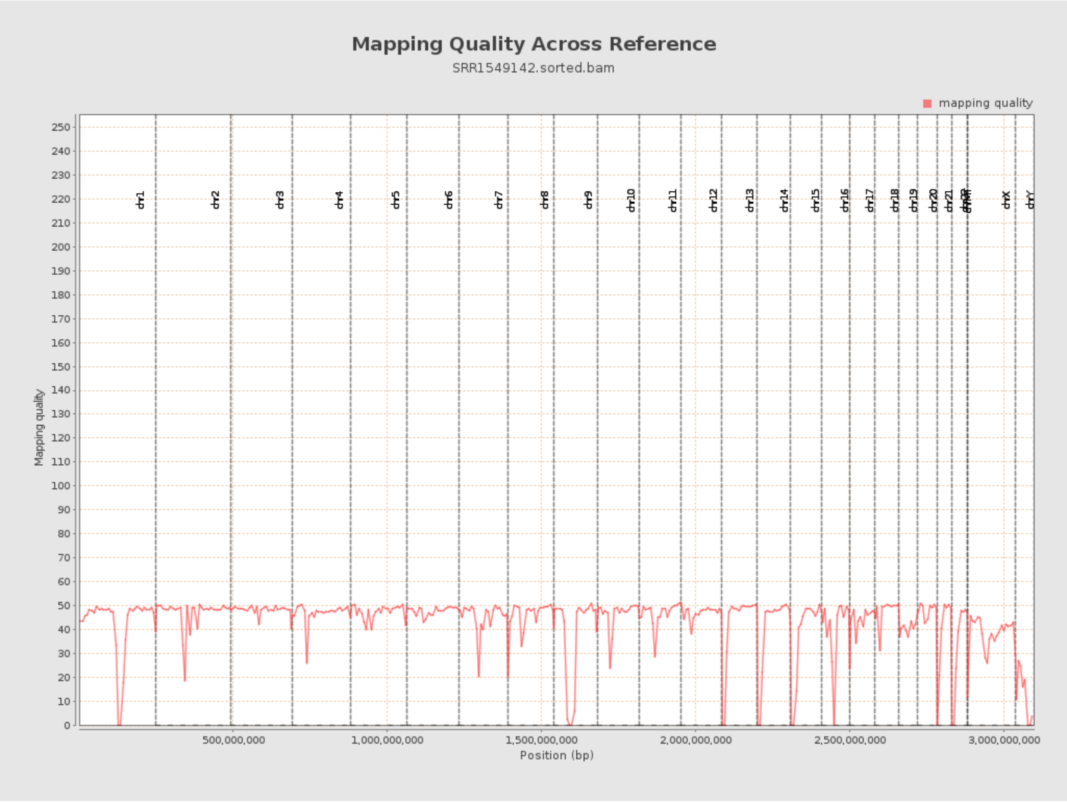
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram