Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:46:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549132.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_SRR1549132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:46:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,159,759
Mapped reads	12,303,453 / 86.89%
Unmapped reads	1,856,306 / 13.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	779,103 / 5.5%
Duplication rate	5%
Clipped reads	605,771 / 4.28%

2.2. ACGT Content

Number/percentage of A's	141,815,621 / 29.03%
Number/percentage of C's	101,856,913 / 20.85%
Number/percentage of T's	143,224,608 / 29.32%
Number/percentage of G's	101,528,079 / 20.78%
Number/percentage of N's	107,199 / 0.02%
GC Percentage	41.63%

2.3. Coverage

Mean	0.1578
Standard Deviation	1.2411

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

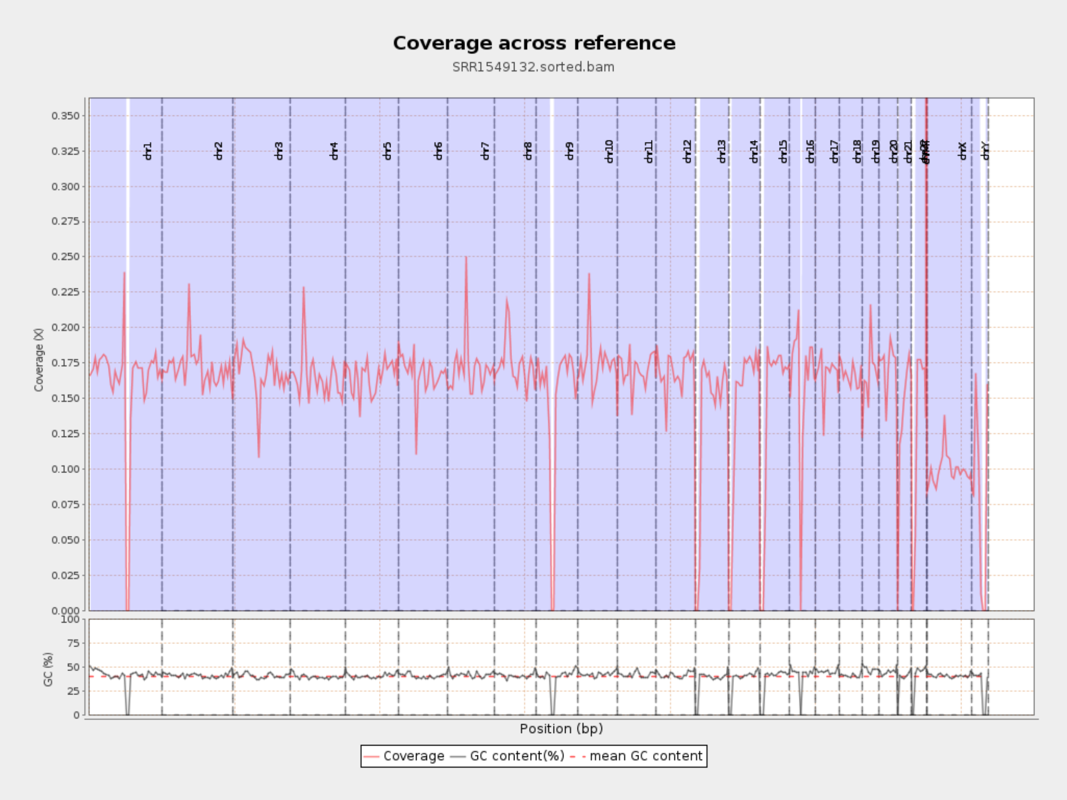
General error rate	0.33%
Mismatches	1,607,276
Insertions	12,146
Mapped reads with at least one insertion	0.1%
Deletions	41,080
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45%

2.6. Chromosome stats

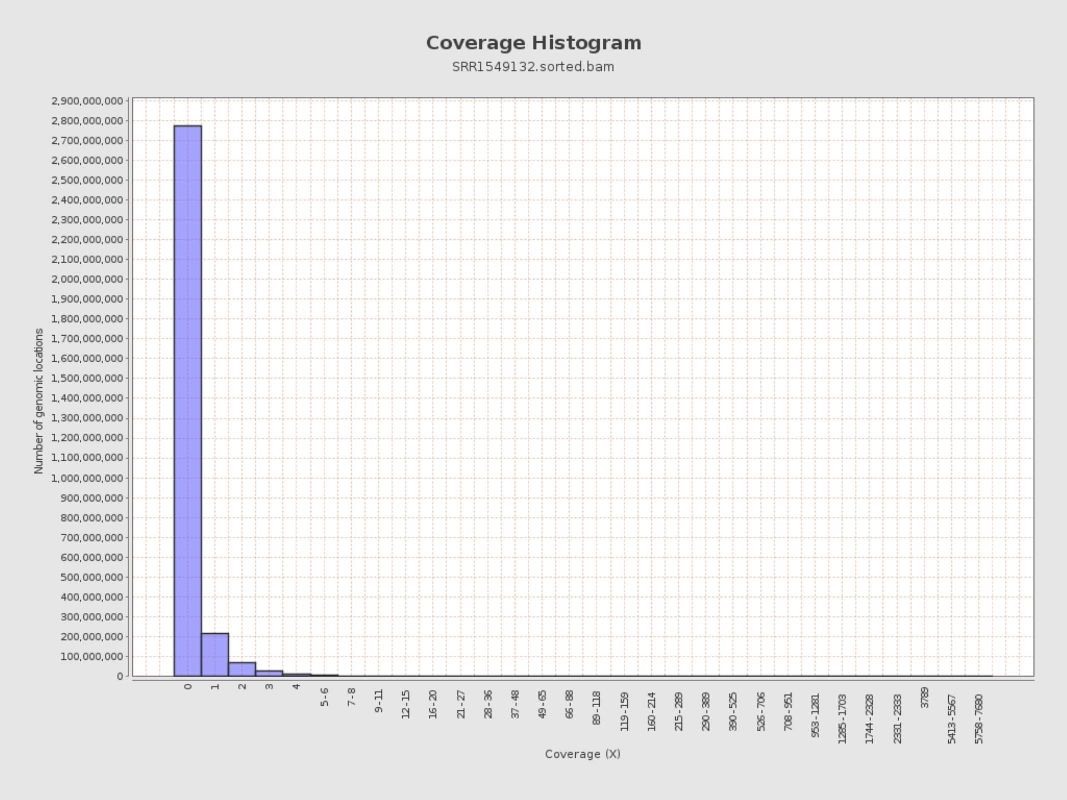
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40007867	0.1605	1.8618
chr2	243199373	41914064	0.1723	0.9057
chr3	198022430	33408565	0.1687	0.5781
chr4	191154276	31505774	0.1648	0.6843
chr5	180915260	29939496	0.1655	0.5872
chr6	171115067	28692597	0.1677	0.6318
chr7	159138663	27338079	0.1718	1.3233
chr8	146364022	25439462	0.1738	3.7974

chr9	141213431	20867212	0.1478	0.7942
chr10	135534747	23698931	0.1749	0.9681
chr11	135006516	22961937	0.1701	0.824
chr12	133851895	22652524	0.1692	0.6036
chr13	115169878	15591527	0.1354	0.5109
chr14	107349540	15200352	0.1416	0.672
chr15	102531392	14653848	0.1429	0.5216
chr16	90354753	14569666	0.1612	0.6419
chr17	81195210	13547672	0.1669	0.6254
chr18	78077248	13022396	0.1668	1.6117
chr19	59128983	9965883	0.1685	1.4964
chr20	63025520	10852214	0.1722	0.6455
chr21	48129895	6580673	0.1367	0.6721
chr22	51304566	6071993	0.1184	0.5131
chrMT	16571	177026	10.6829	13.7121
chrX	155270560	15468866	0.0996	0.5789
chrY	59373566	4456208	0.0751	0.8431

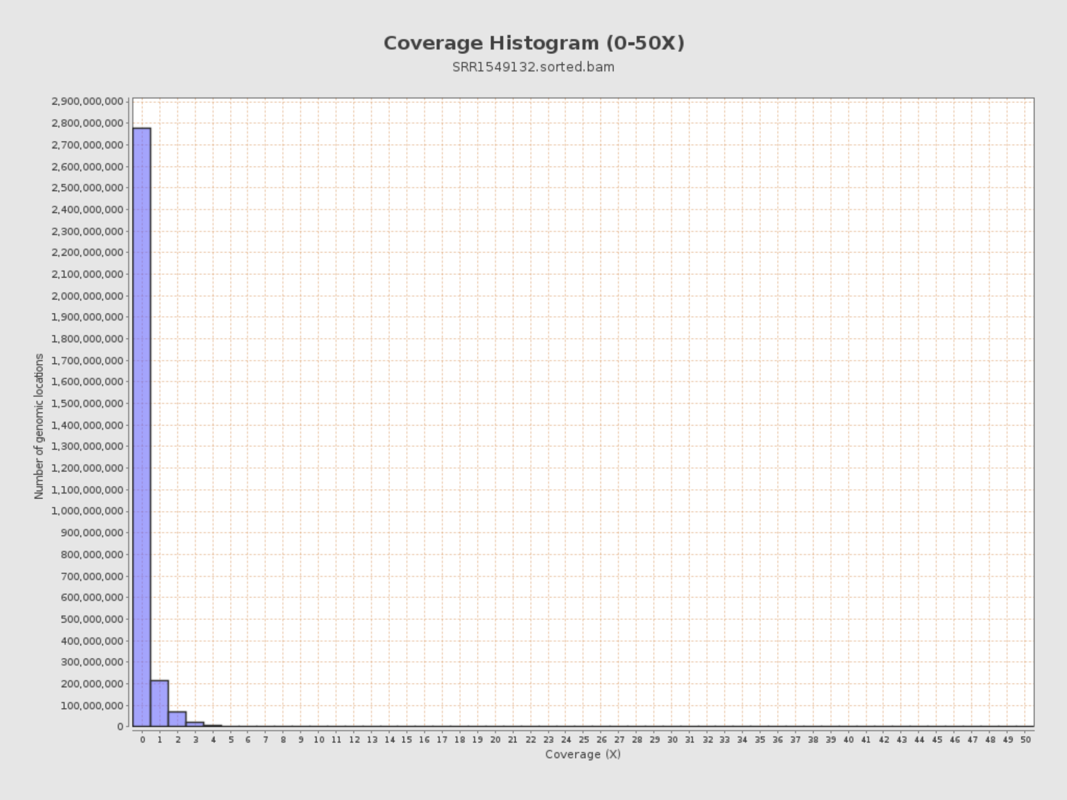
3. Results : Coverage across reference



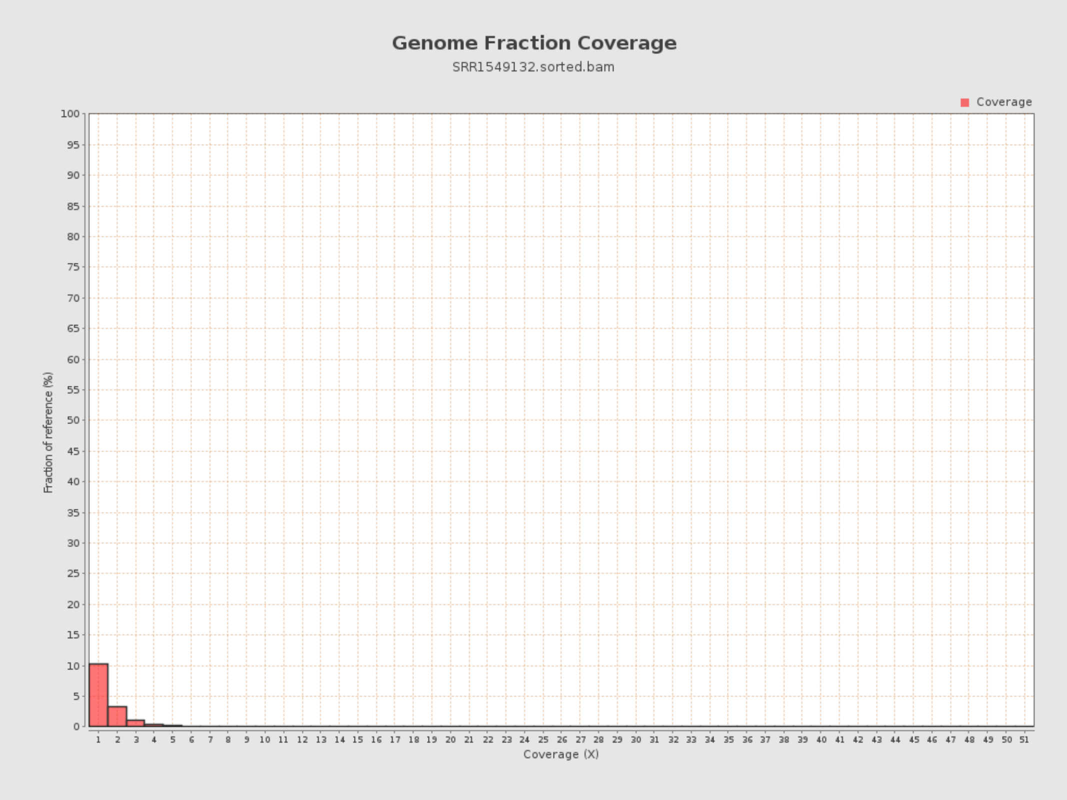
4. Results : Coverage Histogram



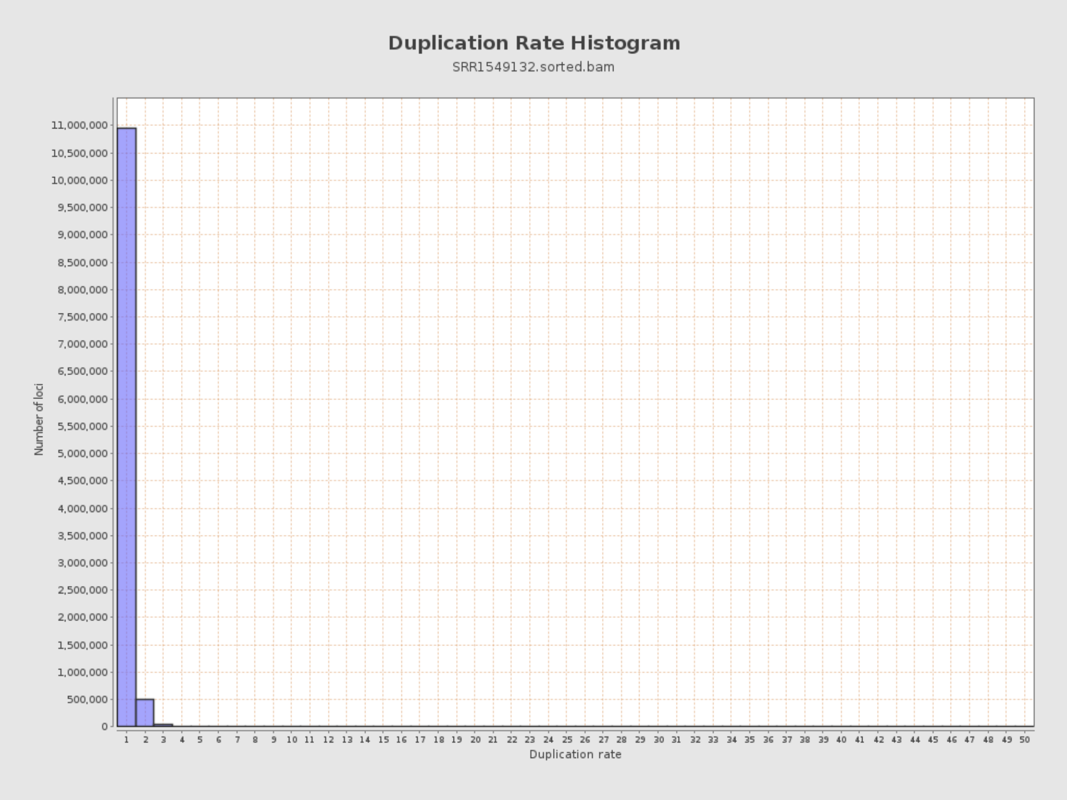
5. Results : Coverage Histogram (0-50X)



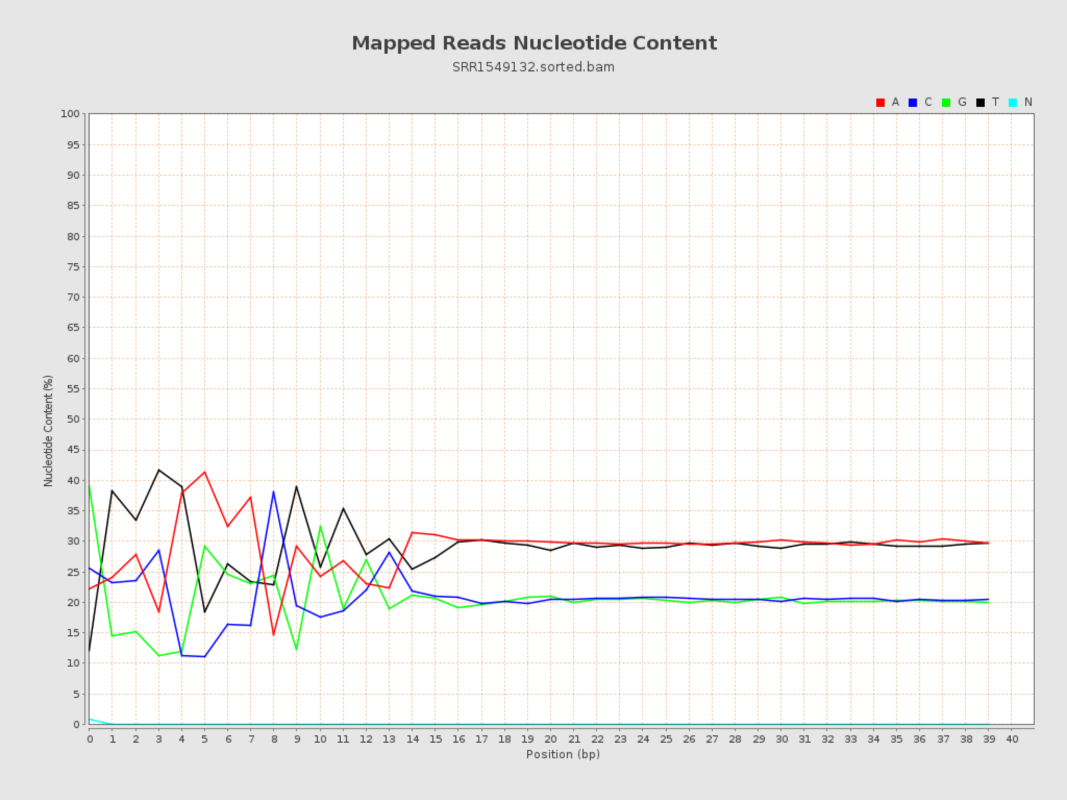
6. Results : Genome Fraction Coverage



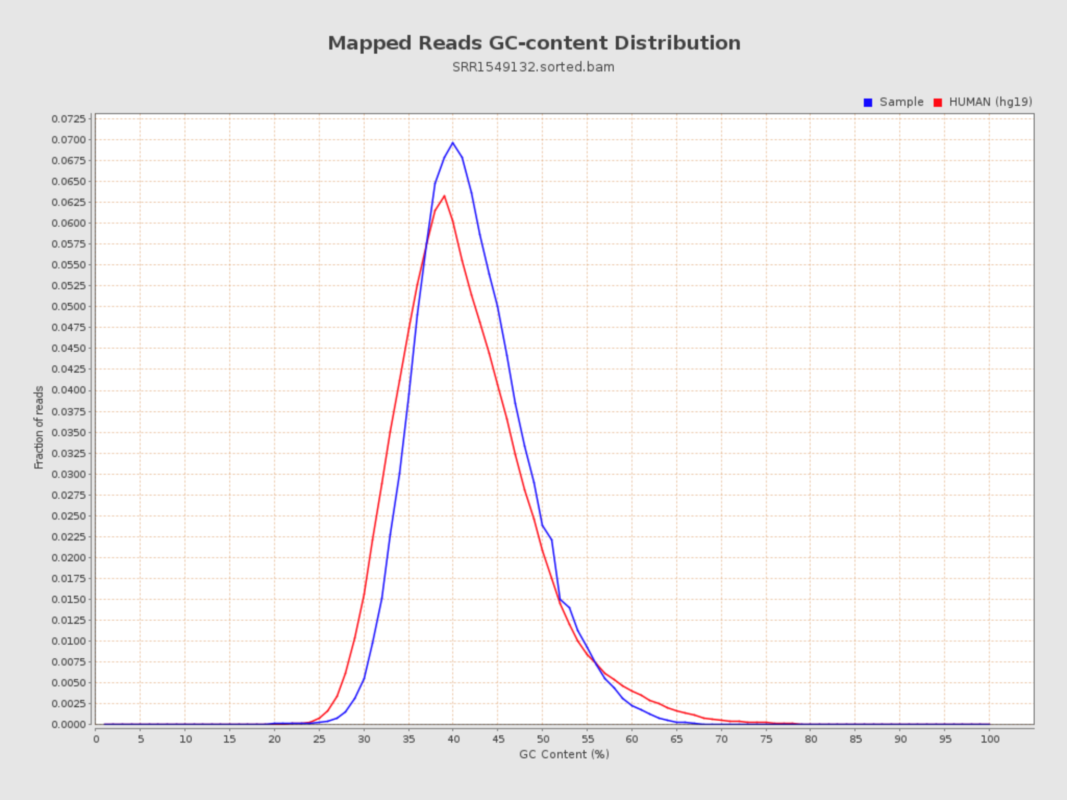
7. Results : Duplication Rate Histogram



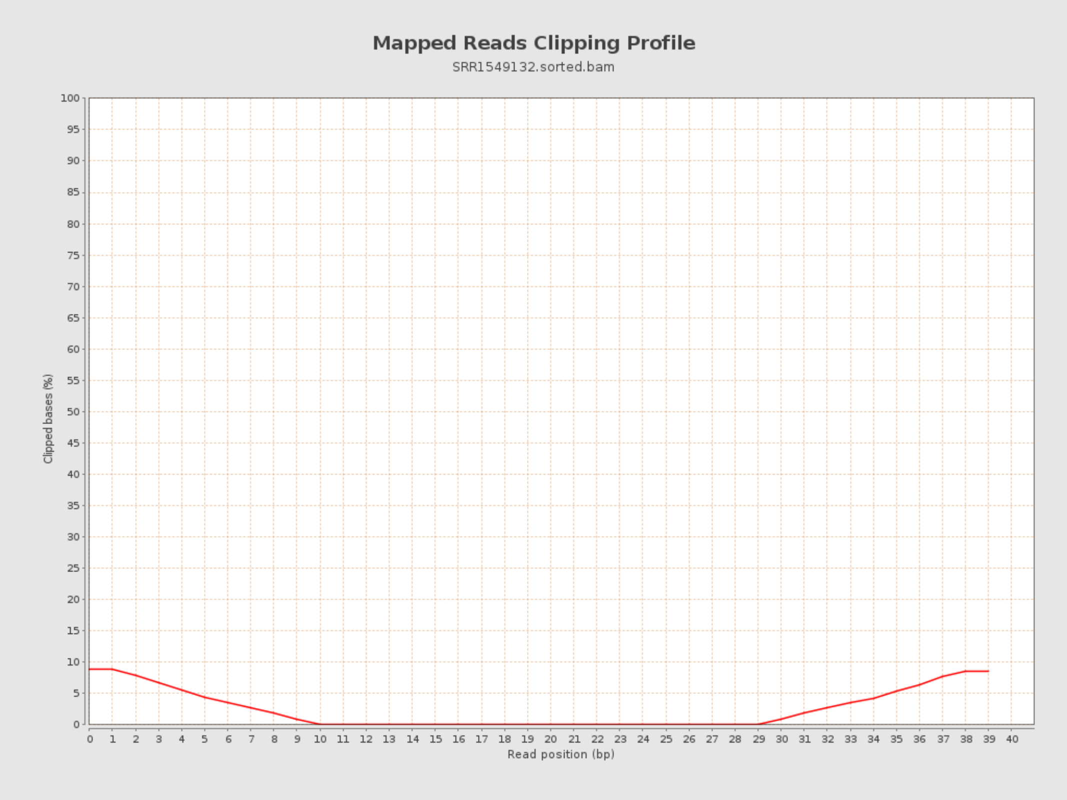
8. Results : Mapped Reads Nucleotide Content



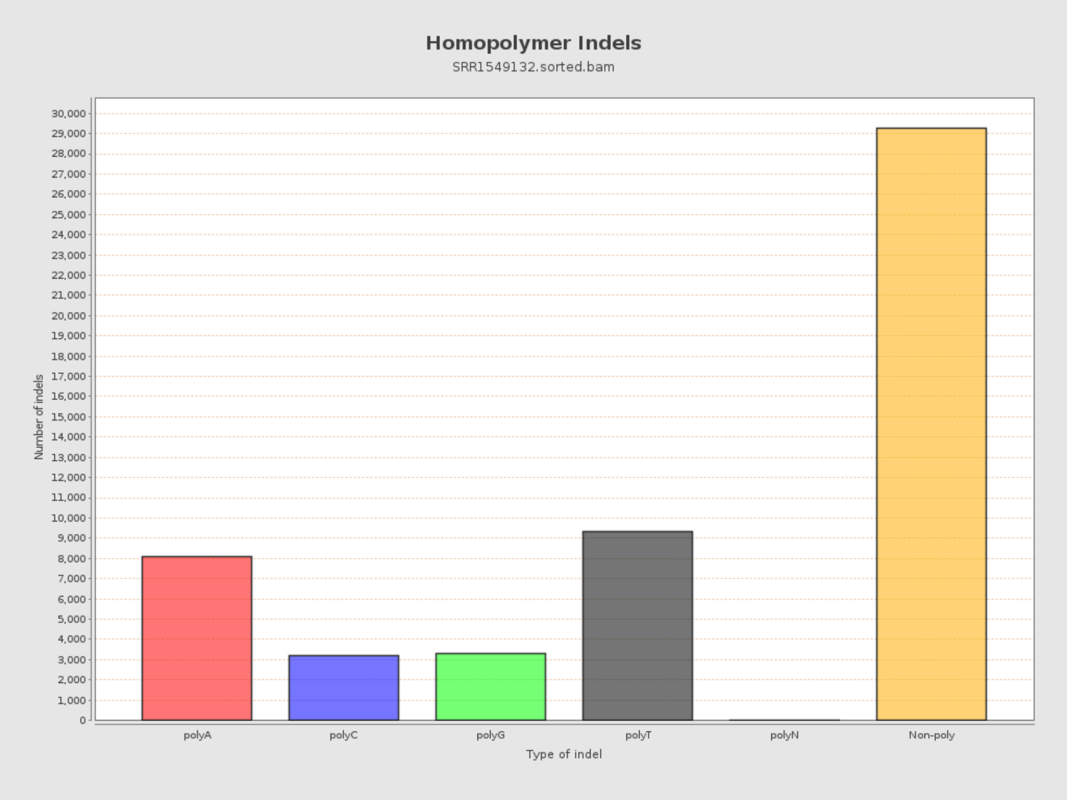
9. Results : Mapped Reads GC-content Distribution



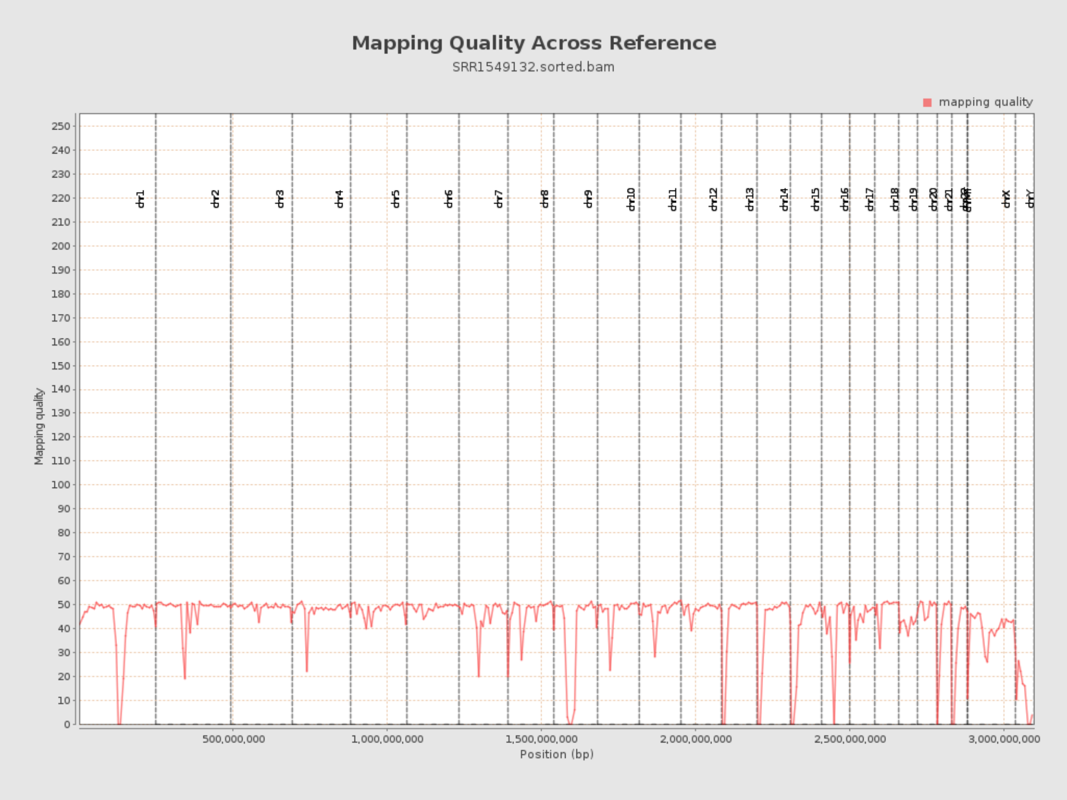
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram