Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:43:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549155.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_SRR1549155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:43:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,265,329
Mapped reads	11,631,909 / 87.69%
Unmapped reads	1,633,420 / 12.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	694,854 / 5.24%
Duplication rate	4.89%
Clipped reads	609,862 / 4.6%

2.2. ACGT Content

Number/percentage of A's	130,855,102 / 28.34%
Number/percentage of C's	98,447,420 / 21.32%
Number/percentage of T's	133,127,869 / 28.84%
Number/percentage of G's	99,139,189 / 21.47%
Number/percentage of N's	90,545 / 0.02%
GC Percentage	42.8%

2.3. Coverage

Mean	0.1491
Standard Deviation	0.8132

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

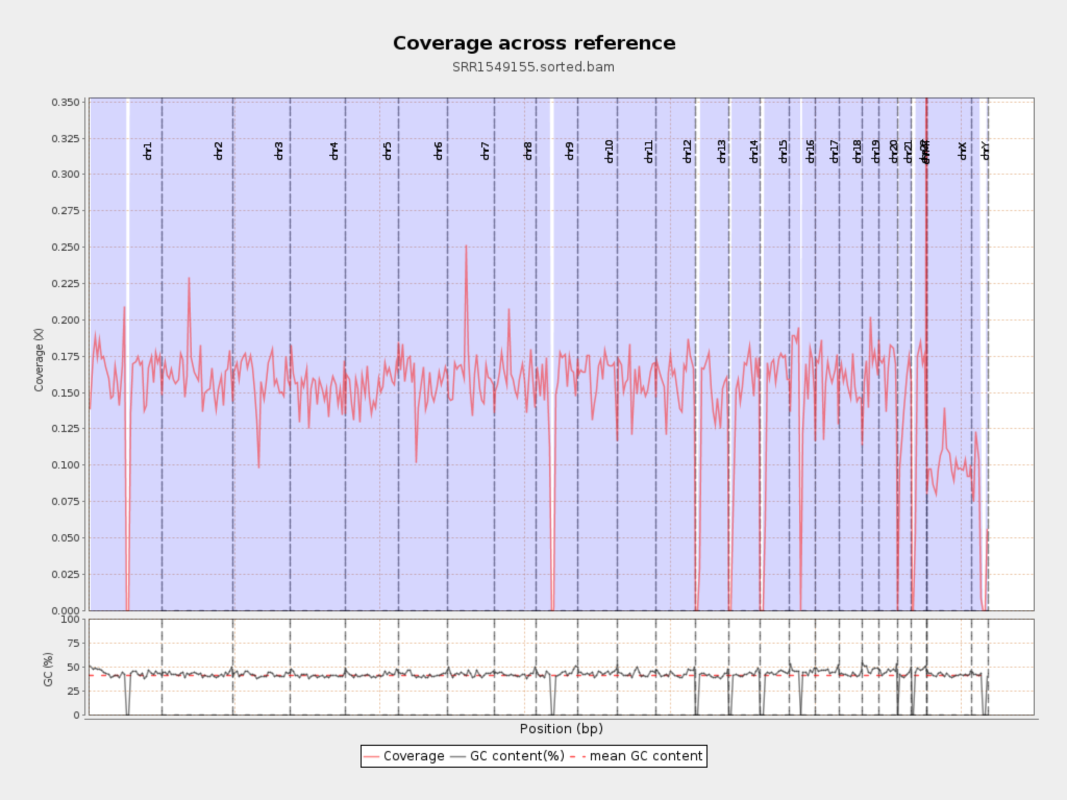
General error rate	0.31%
Mismatches	1,422,492
Insertions	11,573
Mapped reads with at least one insertion	0.1%
Deletions	34,676
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.23%

2.6. Chromosome stats

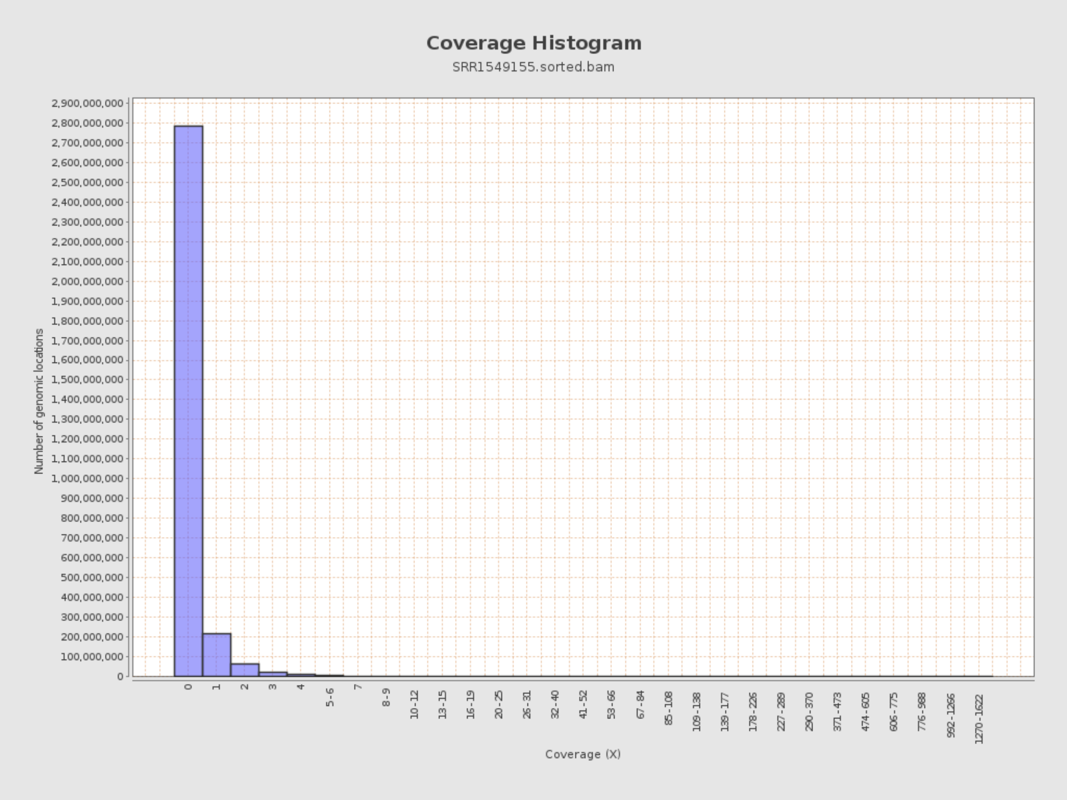
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38722694	0.1554	1.3538
chr2	243199373	39457796	0.1622	0.8537
chr3	198022430	31530679	0.1592	0.5562
chr4	191154276	29142593	0.1525	0.5567
chr5	180915260	27778497	0.1535	0.5577
chr6	171115067	26955062	0.1575	0.6327
chr7	159138663	25873109	0.1626	1.2496
chr8	146364022	23563914	0.161	0.7627

chr9	141213431	20066822	0.1421	0.8244
chr10	135534747	22092861	0.163	0.7401
chr11	135006516	21360591	0.1582	0.7298
chr12	133851895	21410767	0.16	0.5819
chr13	115169878	14742936	0.128	0.4922
chr14	107349540	14426441	0.1344	0.6615
chr15	102531392	14018082	0.1367	0.5159
chr16	90354753	13861936	0.1534	0.6053
chr17	81195210	13133130	0.1617	0.6155
chr18	78077248	12227356	0.1566	1.5443
chr19	59128983	9856510	0.1667	1.2086
chr20	63025520	10535521	0.1672	0.6078
chr21	48129895	6114236	0.127	0.5831
chr22	51304566	6110841	0.1191	0.5154
chrMT	16571	16280	0.9824	1.6594
chrX	155270560	15456717	0.0995	0.5391
chrY	59373566	3247941	0.0547	0.3809

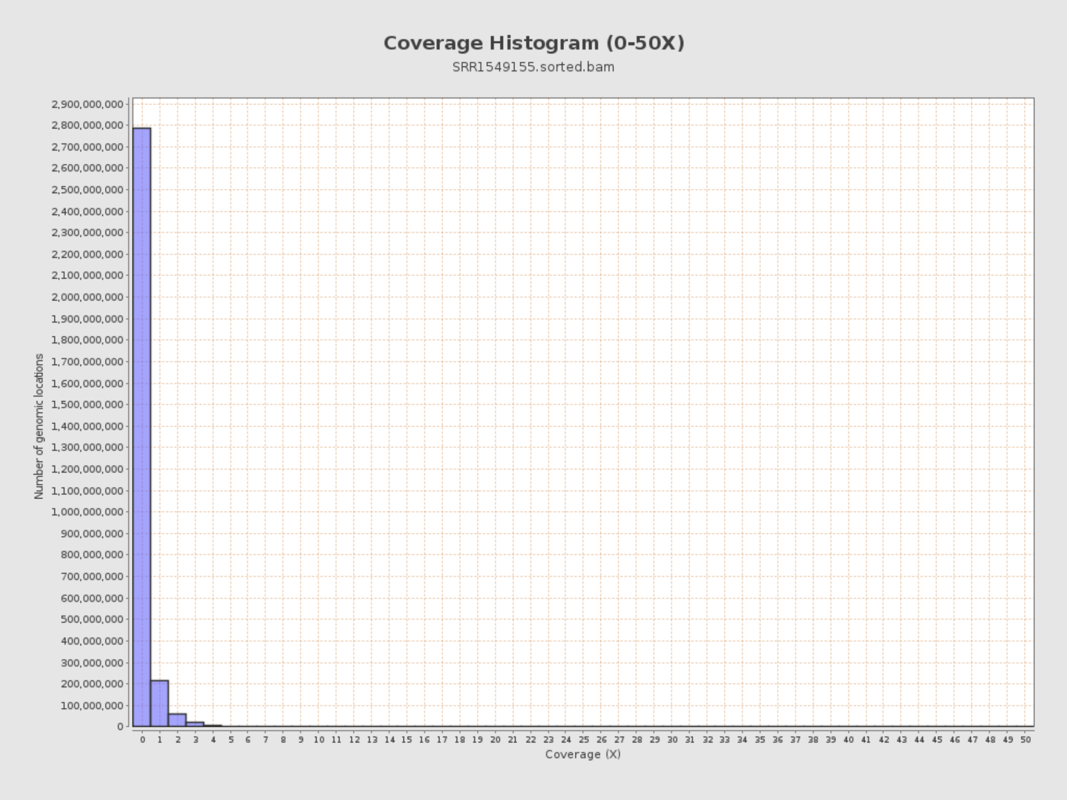
3. Results : Coverage across reference



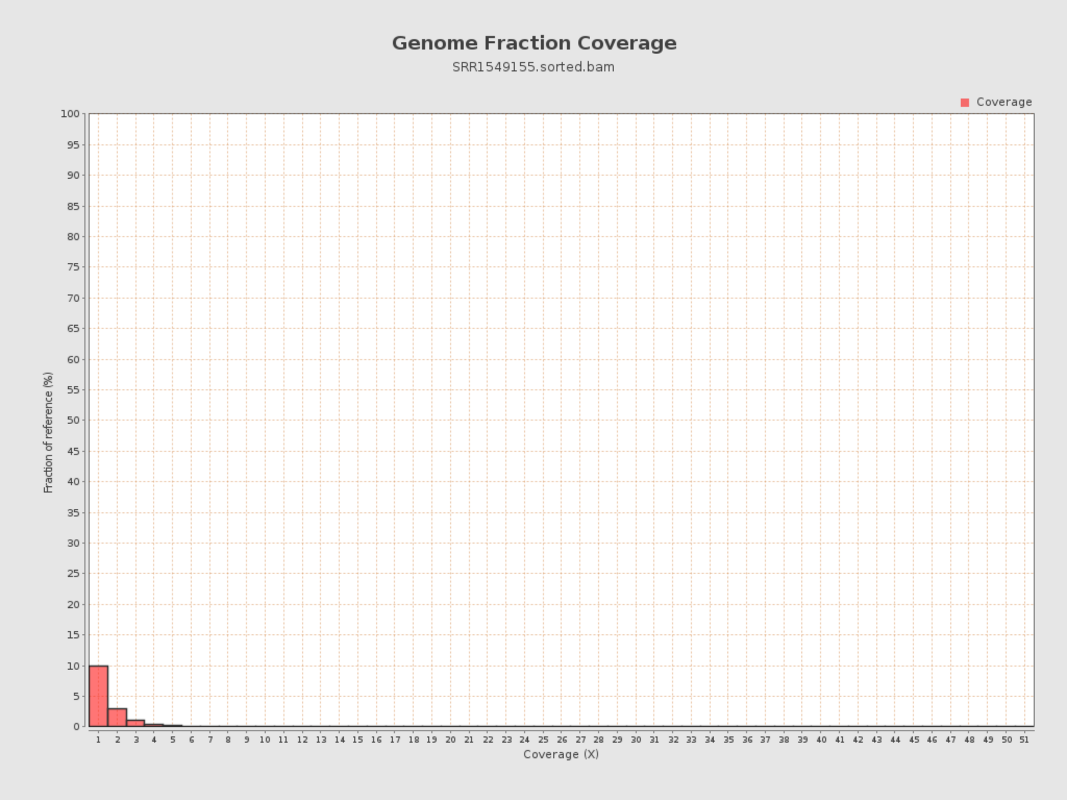
4. Results : Coverage Histogram



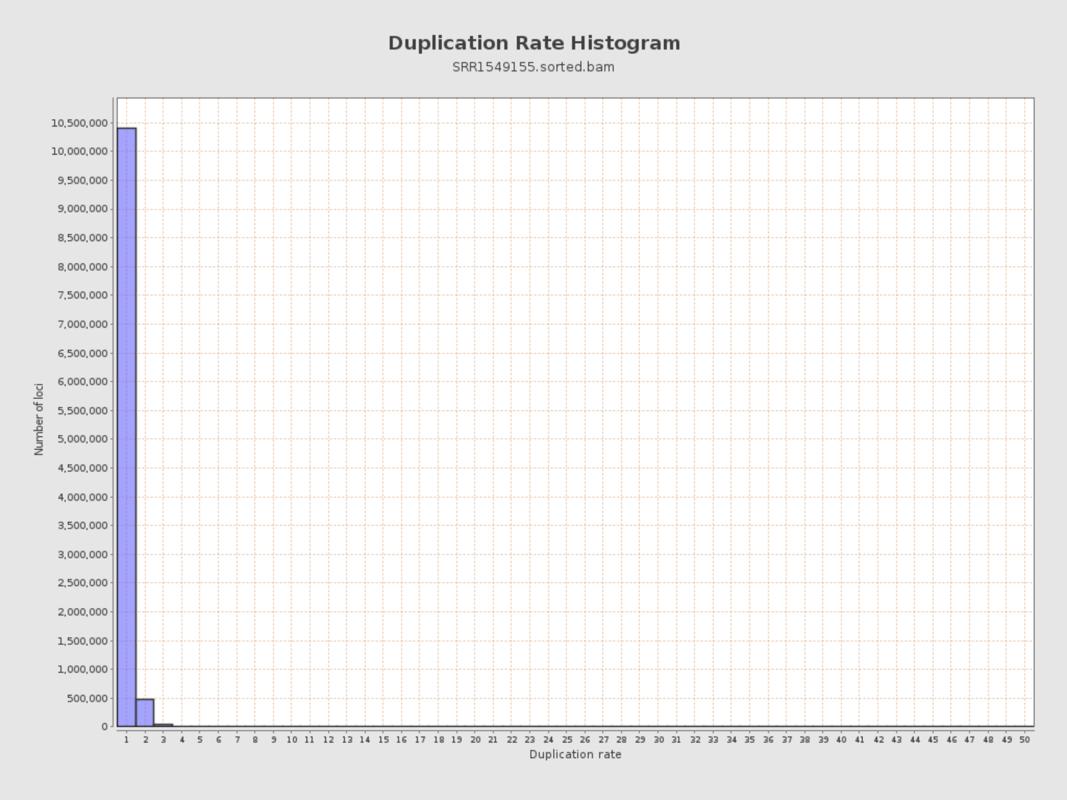
5. Results : Coverage Histogram (0-50X)



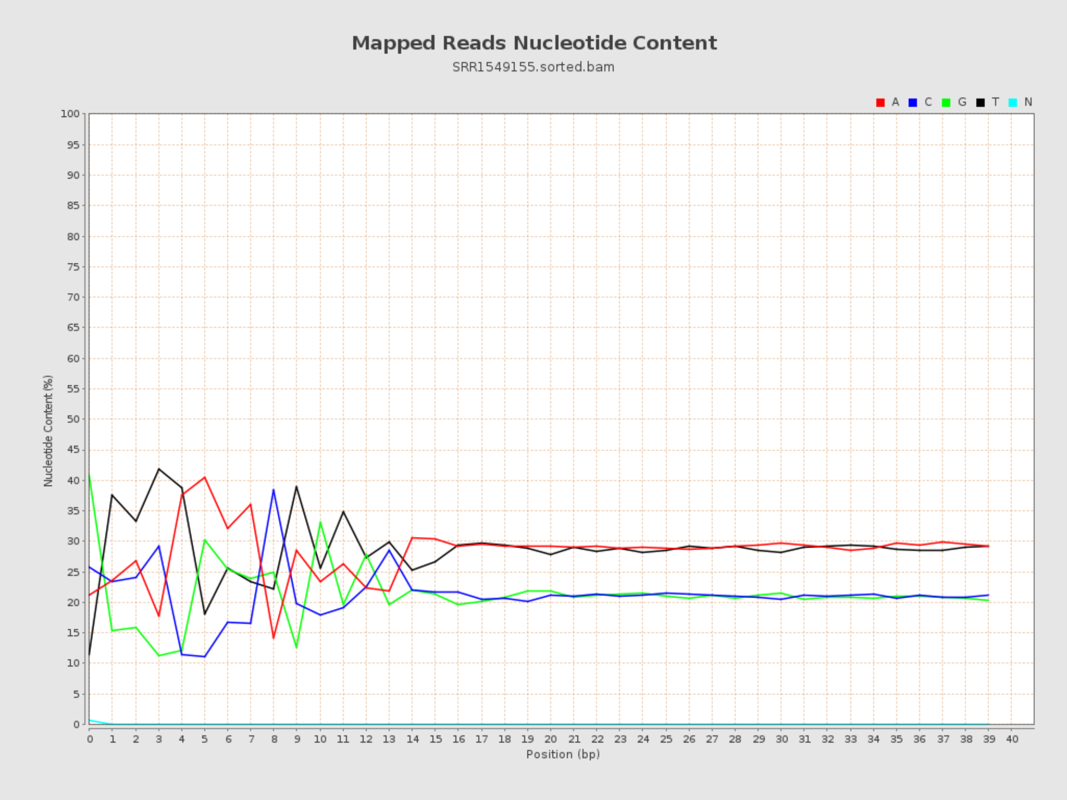
6. Results : Genome Fraction Coverage



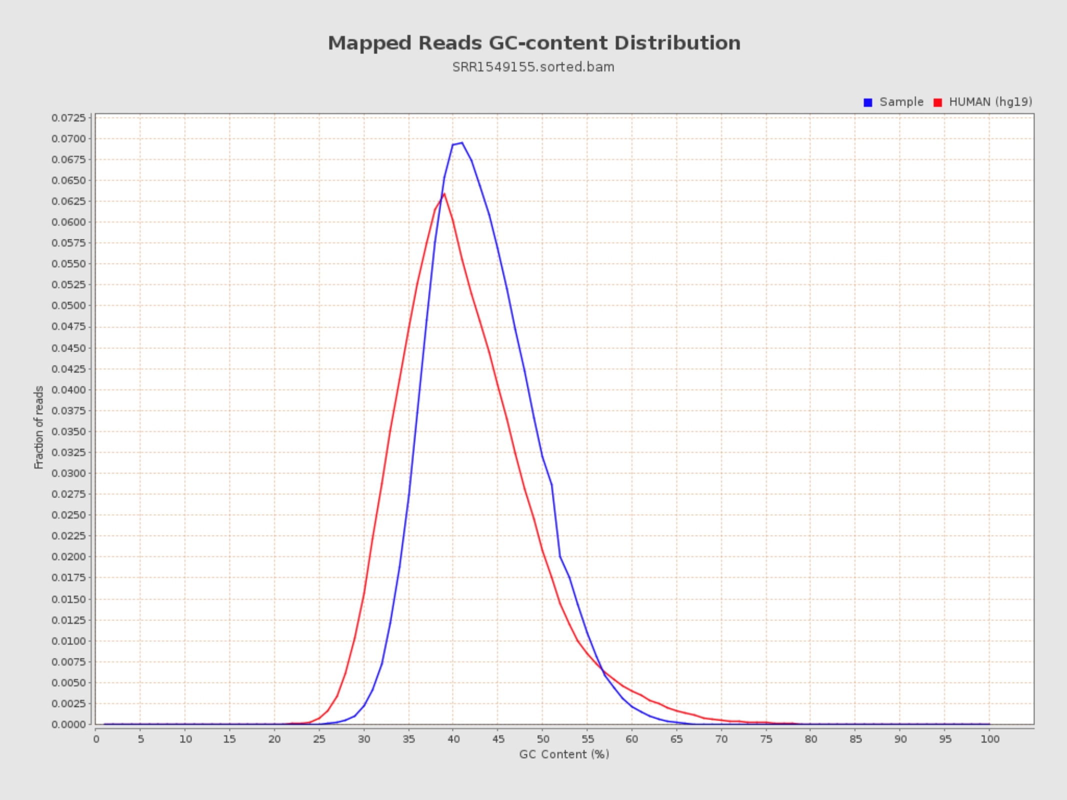
7. Results : Duplication Rate Histogram



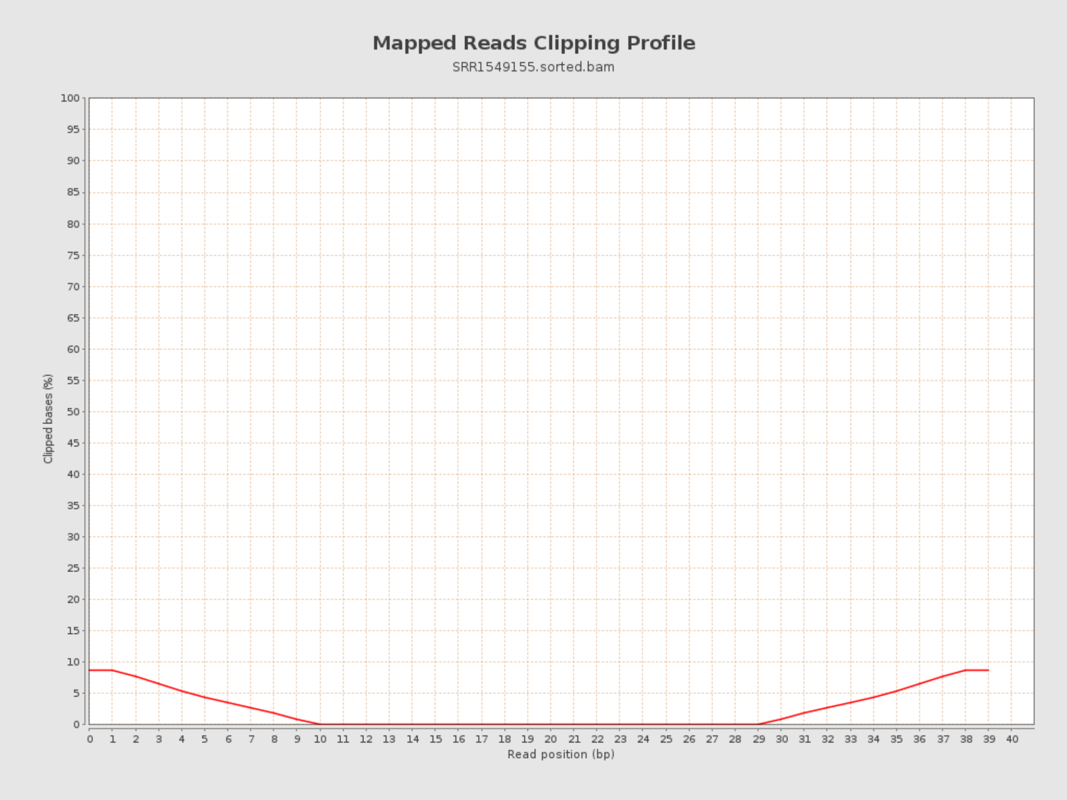
8. Results : Mapped Reads Nucleotide Content



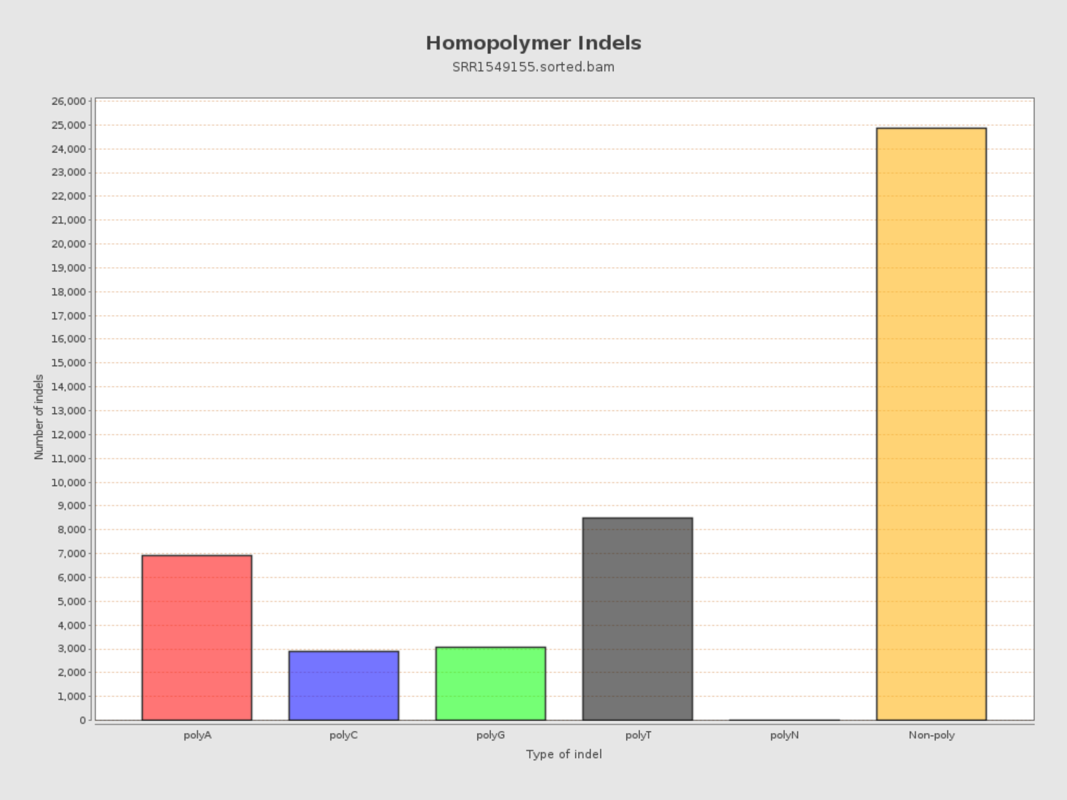
9. Results : Mapped Reads GC-content Distribution



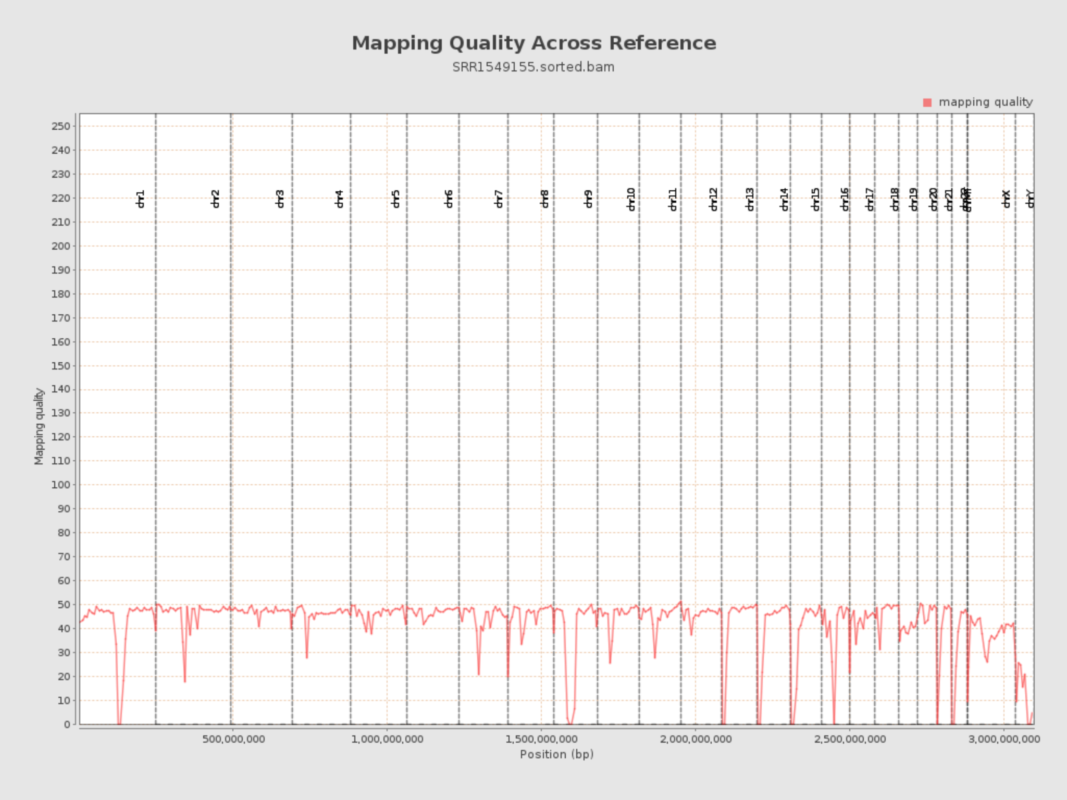
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram