Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:21:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549016.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_SRR1549016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:21:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,536,316
Mapped reads	7,437,405 / 87.13%
Unmapped reads	1,098,911 / 12.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	331,238 / 3.88%
Duplication rate	2.79%
Clipped reads	686,527 / 8.04%

2.2. ACGT Content

Number/percentage of A's	84,756,958 / 28.86%
Number/percentage of C's	61,843,485 / 21.06%
Number/percentage of T's	85,566,965 / 29.14%
Number/percentage of G's	61,480,121 / 20.94%
Number/percentage of N's	9,880 / 0%
GC Percentage	42%

2.3. Coverage

Mean	0.0949
Standard Deviation	1.192

2.4. Mapping Quality

Mean Mapping Quality	38.23

2.5. Mismatches and indels

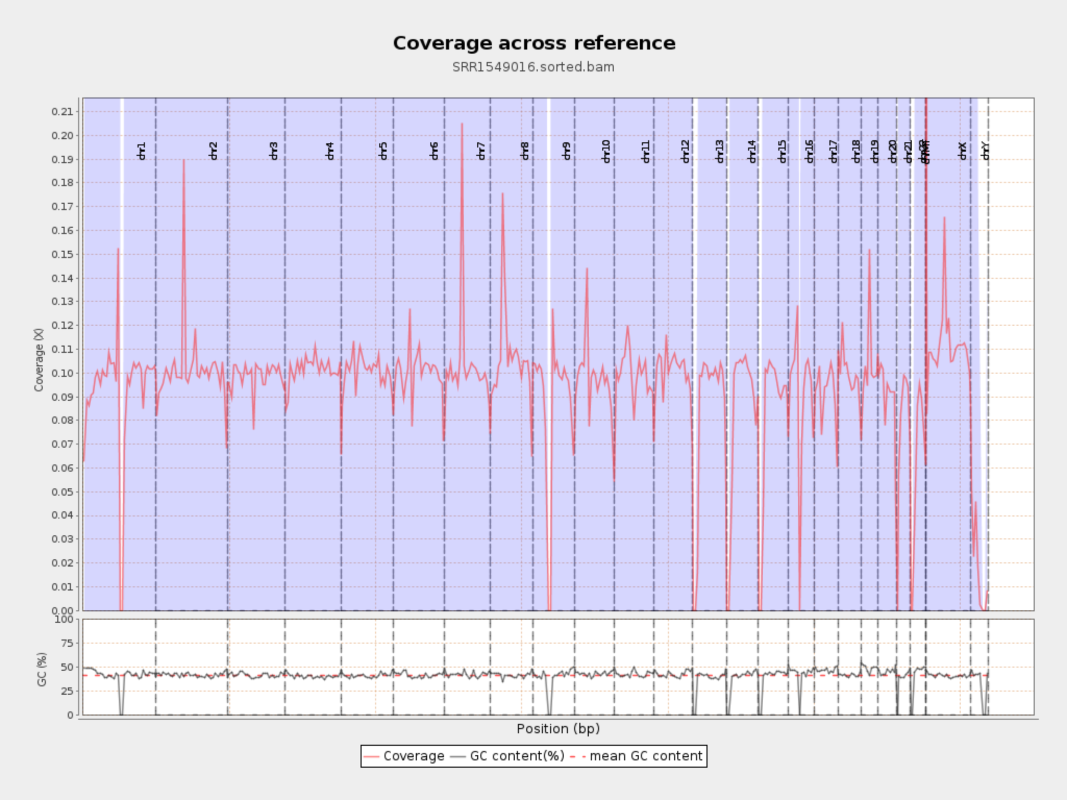
General error rate	0.31%
Mismatches	897,668
Insertions	10,695
Mapped reads with at least one insertion	0.14%
Deletions	23,608
Mapped reads with at least one deletion	0.32%
Homopolymer indels	38.88%

2.6. Chromosome stats

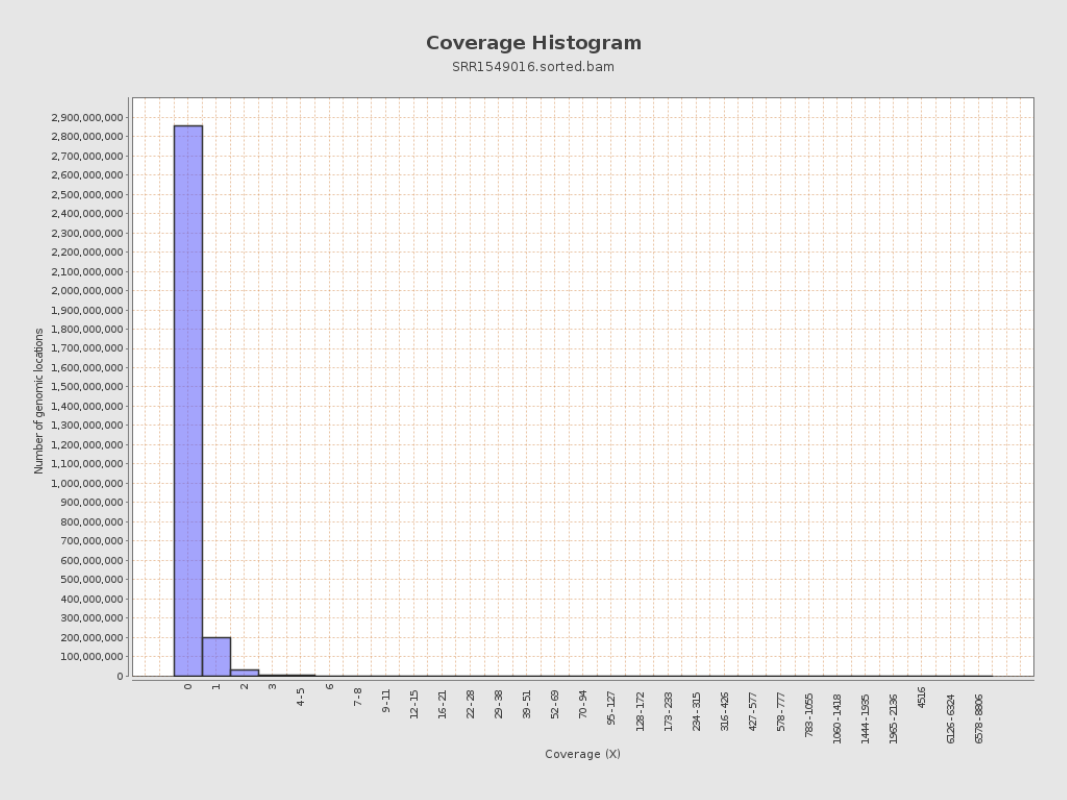
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23002726	0.0923	1.4295
chr2	243199373	24758584	0.1018	0.8028
chr3	198022430	19559471	0.0988	0.3781
chr4	191154276	19402521	0.1015	0.39
chr5	180915260	18159173	0.1004	0.4005
chr6	171115067	17258852	0.1009	0.4606
chr7	159138663	16519632	0.1038	1.1501
chr8	146364022	15602099	0.1066	4.2724

chr9	141213431	12261542	0.0868	0.7925
chr10	135534747	13289645	0.0981	0.6409
chr11	135006516	13373838	0.0991	0.7765
chr12	133851895	13538110	0.1011	0.4202
chr13	115169878	9496735	0.0825	0.33
chr14	107349540	8951985	0.0834	0.5212
chr15	102531392	8146313	0.0795	0.3322
chr16	90354753	7957910	0.0881	0.4399
chr17	81195210	7518966	0.0926	0.4181
chr18	78077248	7833149	0.1003	1.5452
chr19	59128983	6155598	0.1041	1.45
chr20	63025520	5785648	0.0918	0.3923
chr21	48129895	3679375	0.0764	0.4398
chr22	51304566	3057674	0.0596	0.3552
chrMT	16571	25721	1.5522	1.9947
chrX	155270560	17329729	0.1116	0.591
chrY	59373566	1022791	0.0172	0.2125

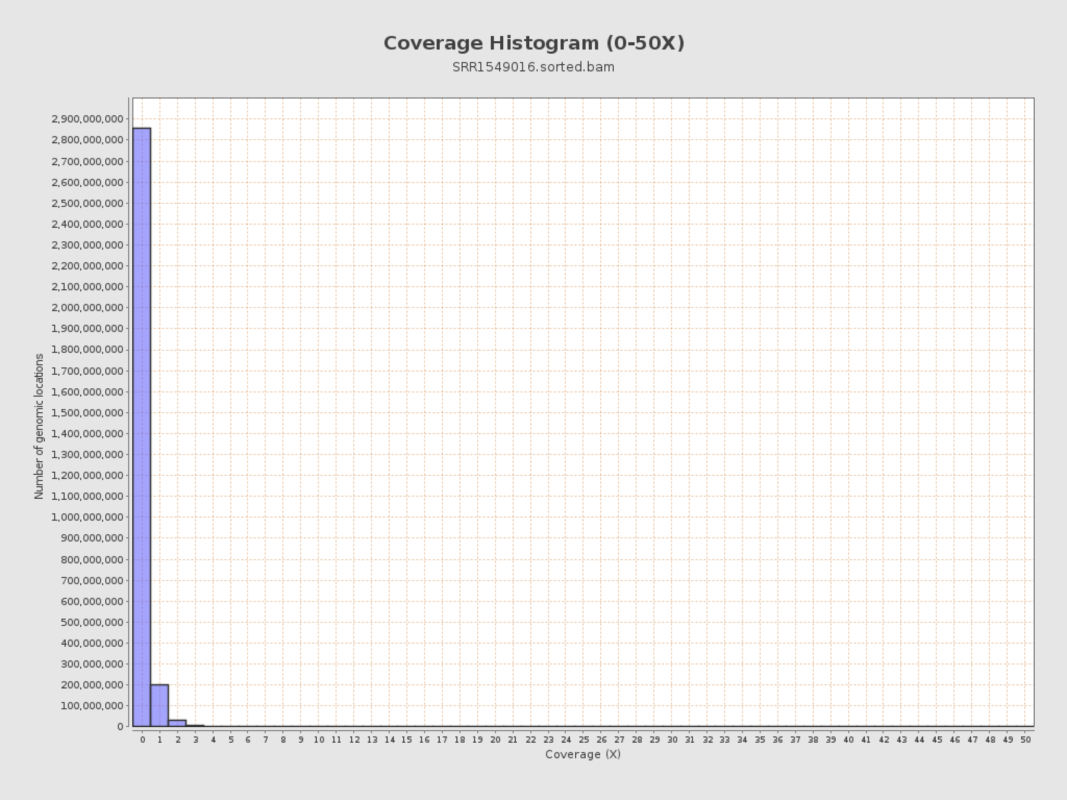
3. Results : Coverage across reference



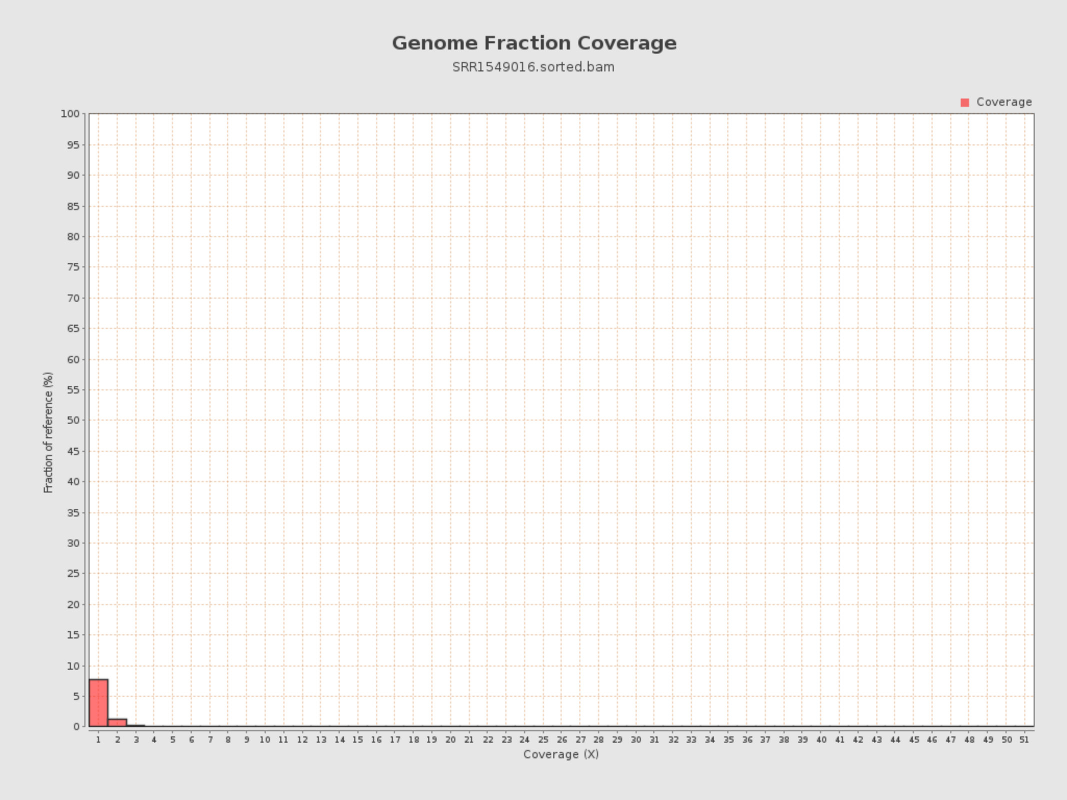
4. Results : Coverage Histogram



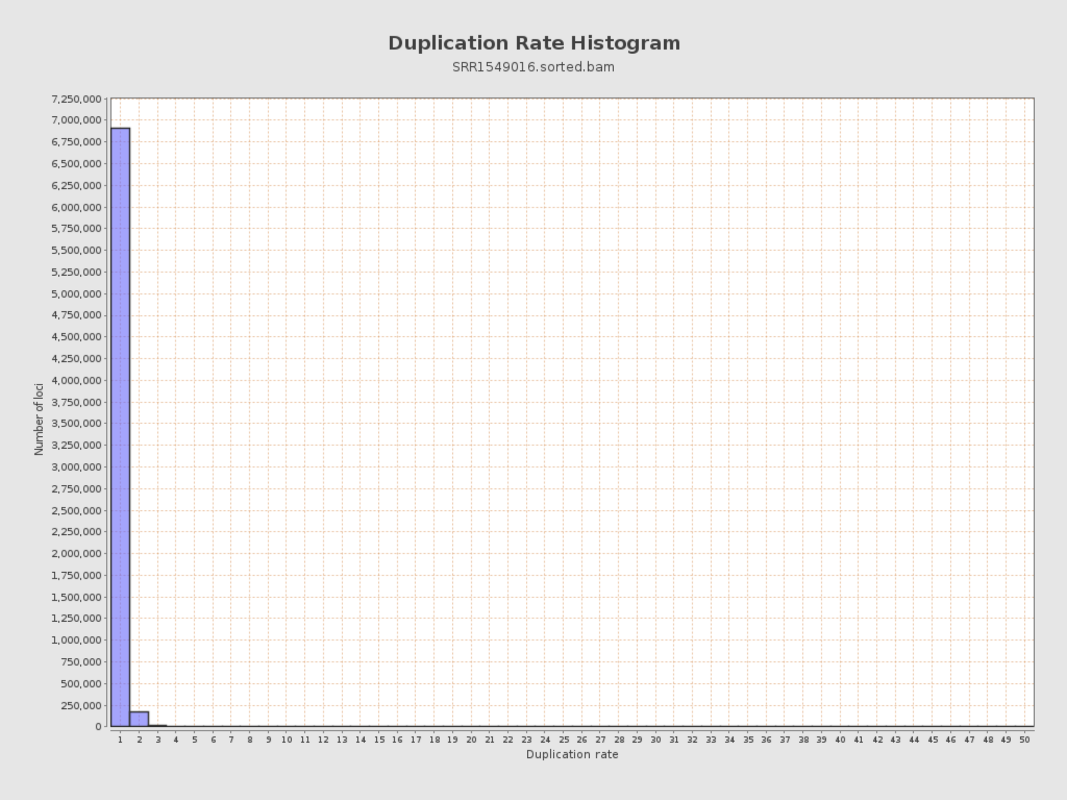
5. Results : Coverage Histogram (0-50X)



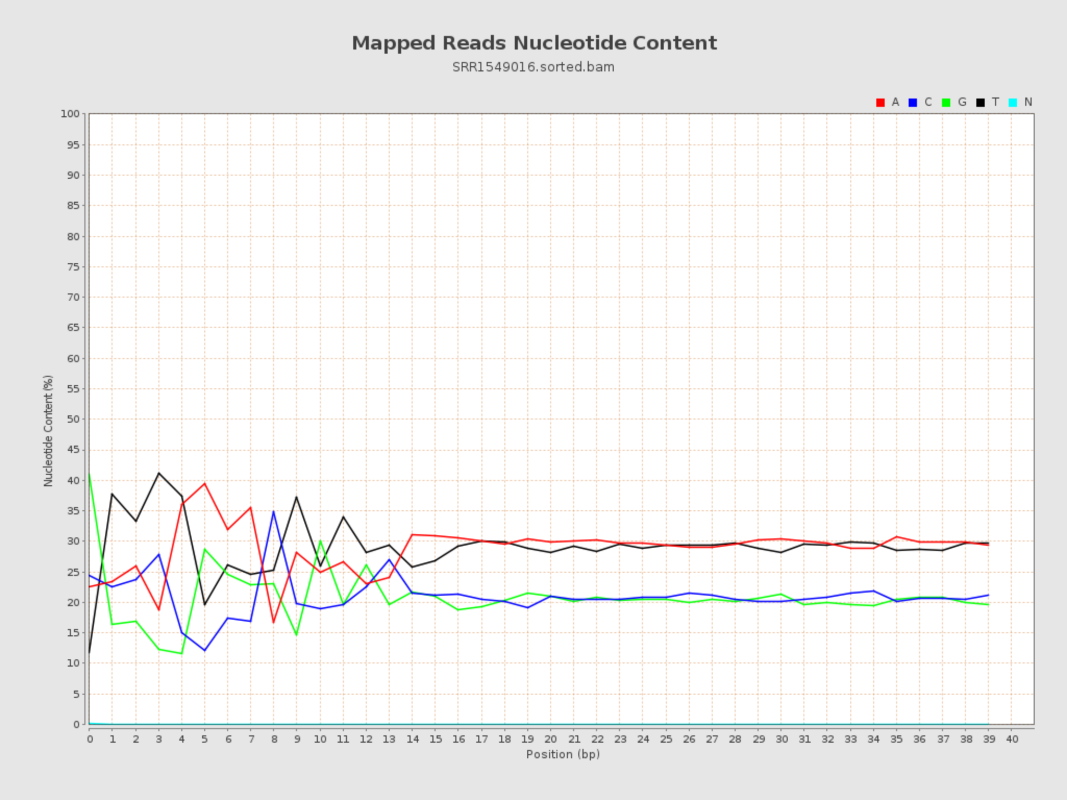
6. Results : Genome Fraction Coverage



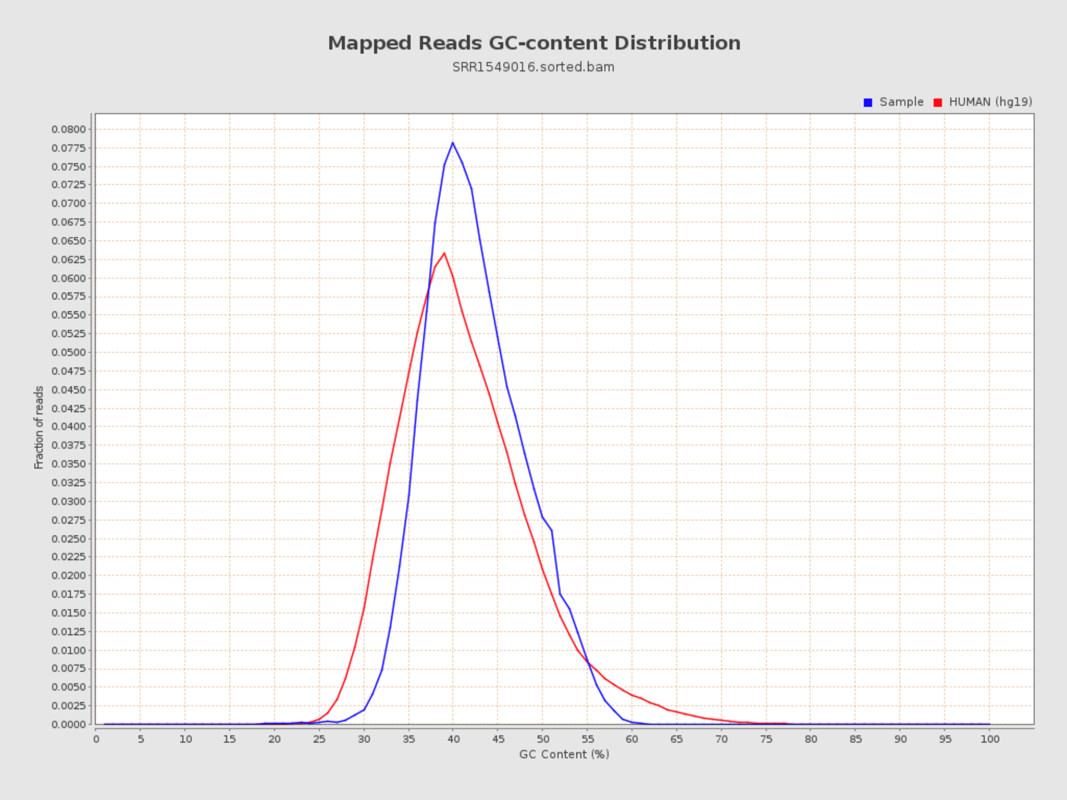
7. Results : Duplication Rate Histogram



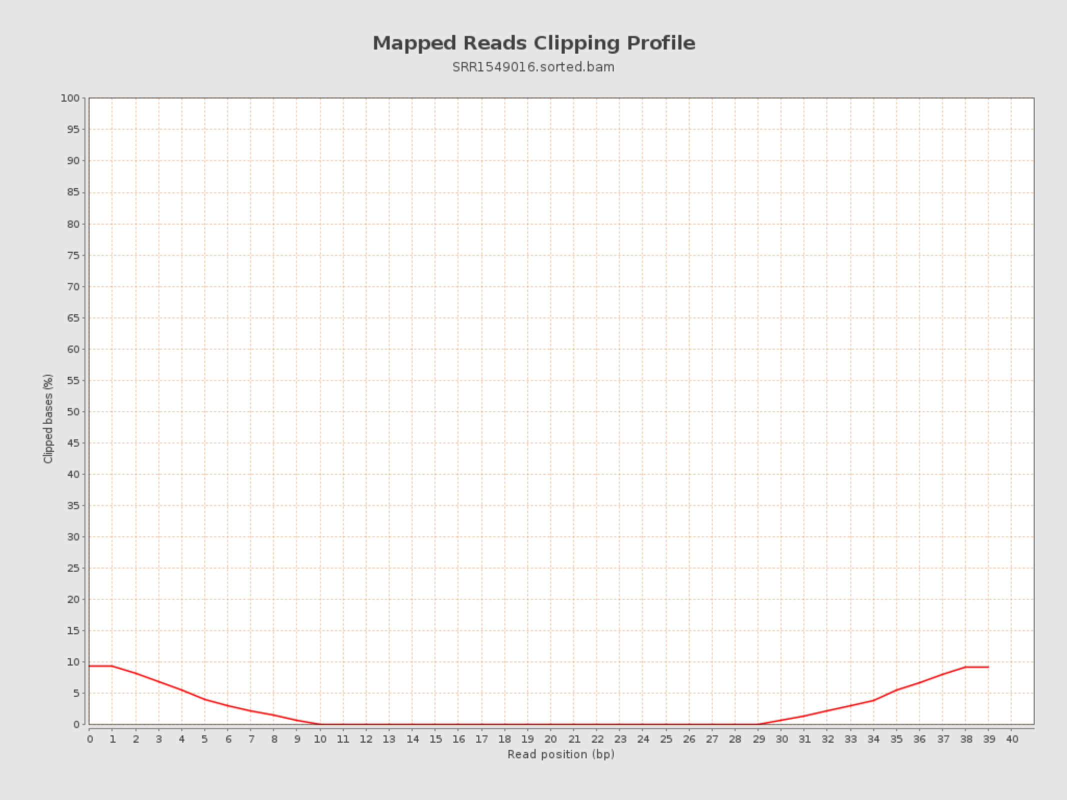
8. Results : Mapped Reads Nucleotide Content



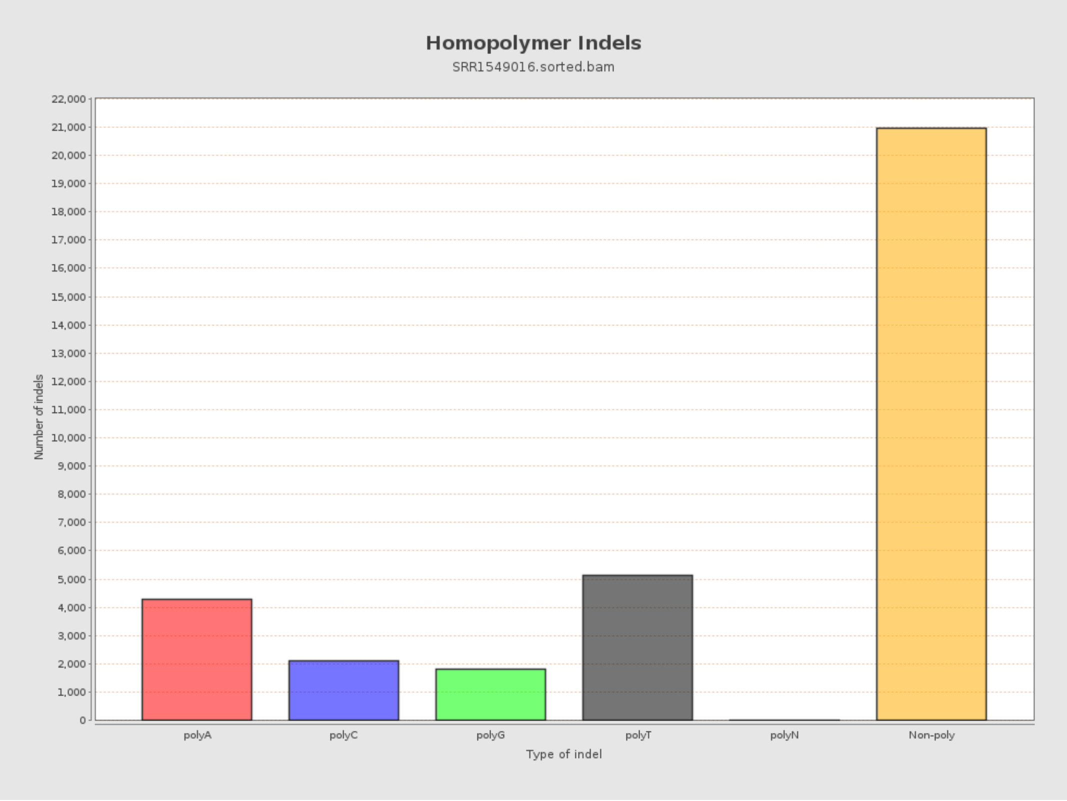
9. Results : Mapped Reads GC-content Distribution



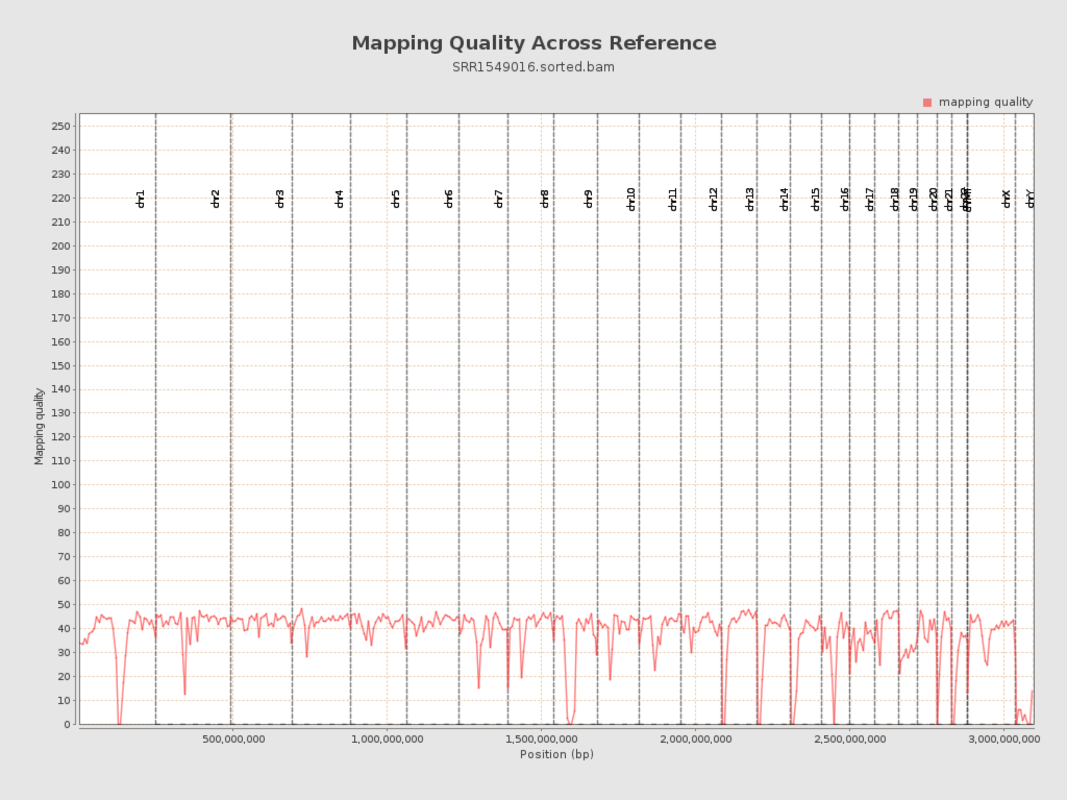
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram