Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117305.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_SRR23117305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:47:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	390,629
Mapped reads	370,298 / 94.8%
Unmapped reads	20,331 / 5.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,882 / 0.48%
Read min/max/mean length	25 / 561 / 250.02
Duplicated reads (estimated)	67,056 / 17.17%
Duplication rate	15.44%
Clipped reads	372,178 / 95.28%

2.2. ACGT Content

Number/percentage of A's	23,978,795 / 29.08%
Number/percentage of C's	17,249,006 / 20.92%
Number/percentage of T's	23,997,041 / 29.1%
Number/percentage of G's	17,228,365 / 20.89%
Number/percentage of N's	0 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.5362

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Mismatches and indels

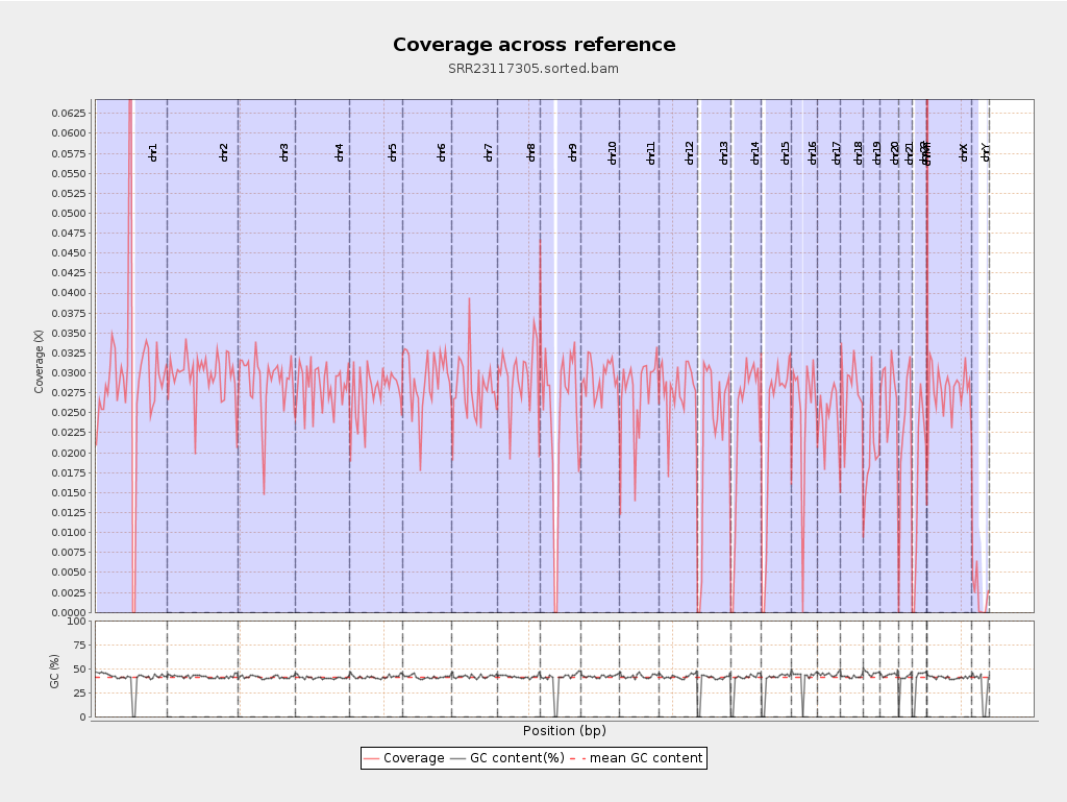
General error rate	1.47%
Mismatches	492,984
Insertions	658,398
Mapped reads with at least one insertion	67.3%
Deletions	156,060
Mapped reads with at least one deletion	28.7%
Homopolymer indels	25.99%

2.6. Chromosome stats

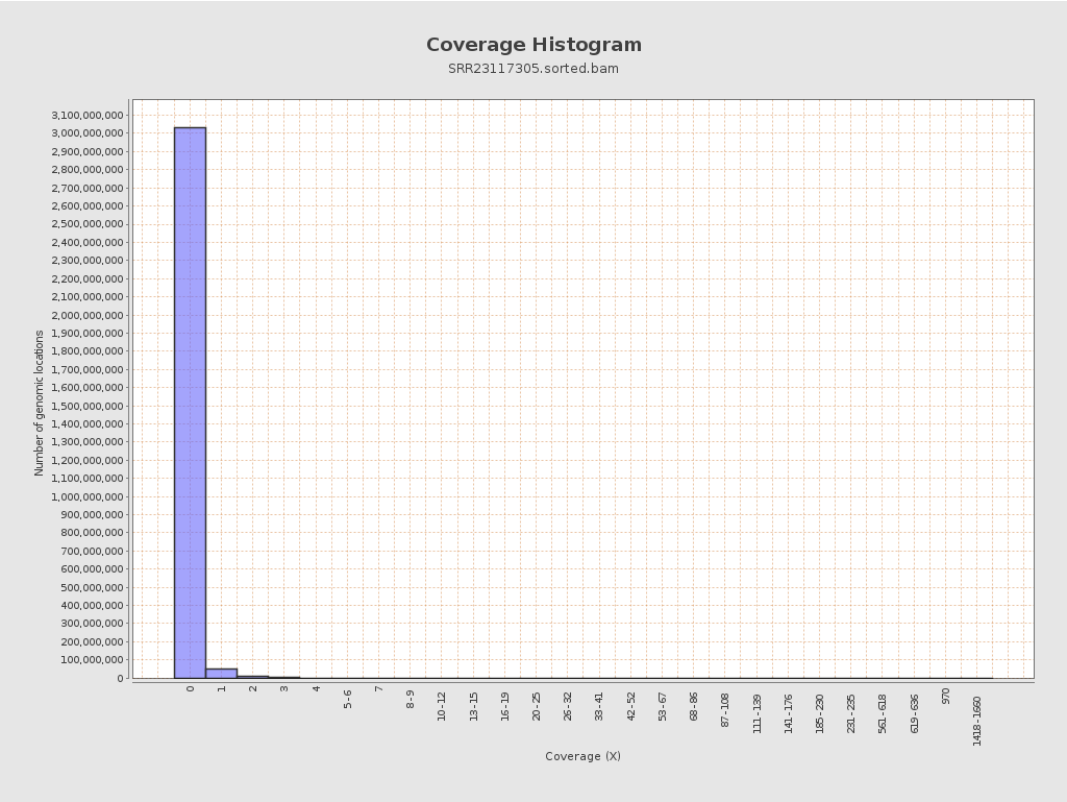
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7227090	0.029	1.6289
chr2	243199373	7245876	0.0298	0.2205
chr3	198022430	5723325	0.0289	0.2125
chr4	191154276	5416060	0.0283	0.218
chr5	180915260	5034197	0.0278	0.2077
chr6	171115067	4989610	0.0292	0.2138
chr7	159138663	4446197	0.0279	0.7855

chr8	146364022	4306689	0.0294	0.219
chr9	141213431	3513920	0.0249	0.2036
chr10	135534747	3961982	0.0292	0.2706
chr11	135006516	3737906	0.0277	0.2107
chr12	133851895	3728230	0.0279	0.2093
chr13	115169878	2611772	0.0227	0.1874
chr14	107349540	2520741	0.0235	0.1928
chr15	102531392	2395264	0.0234	0.1928
chr16	90354753	2236658	0.0248	0.231
chr17	81195210	1984156	0.0244	0.2251
chr18	78077248	2212416	0.0283	0.2475
chr19	59128983	1178715	0.0199	0.3783
chr20	63025520	1717485	0.0273	0.2205
chr21	48129895	1087831	0.0226	0.221
chr22	51304566	854205	0.0166	0.1688
chrMT	16571	68757	4.1492	10.4073
chrX	155270560	4326384	0.0279	0.2084
chrY	59373566	114097	0.0019	0.1053

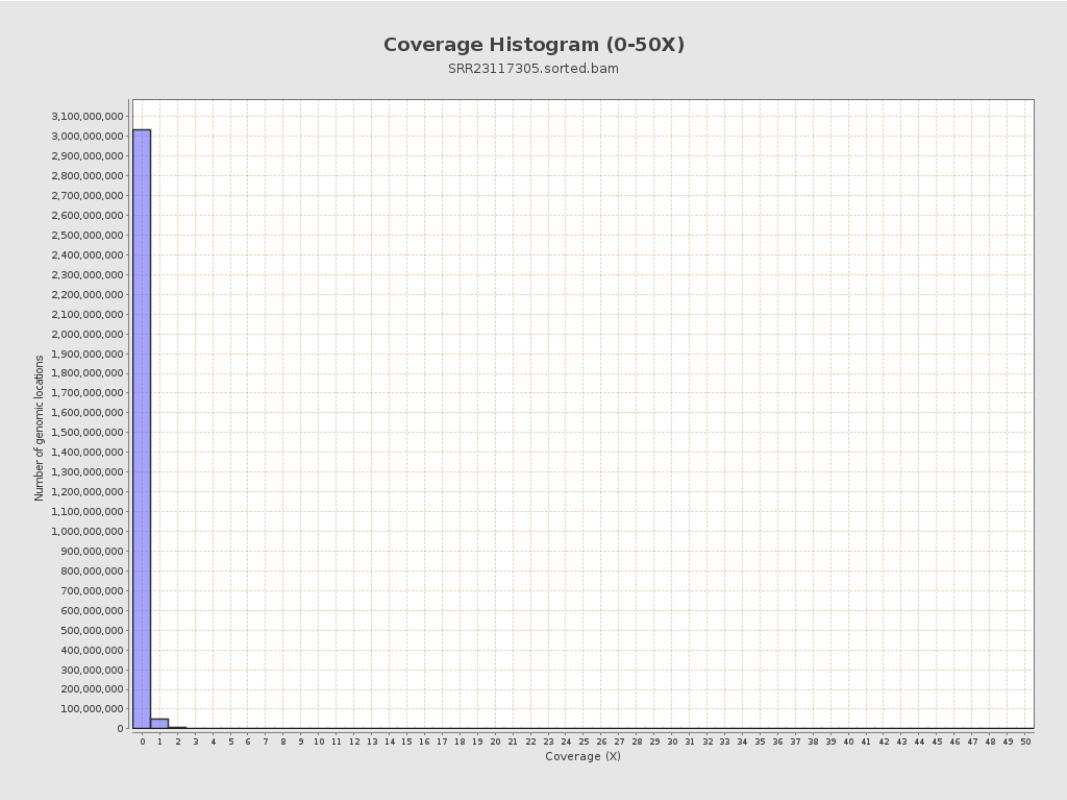
3. Results : Coverage across reference



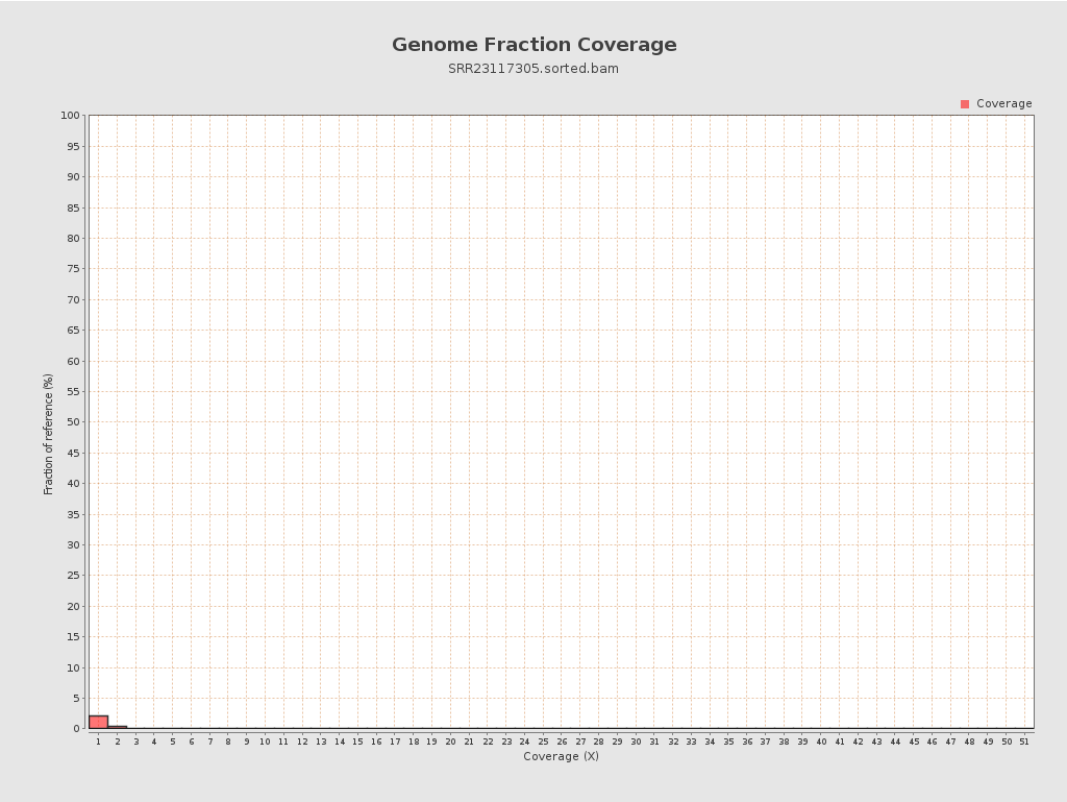
4. Results : Coverage Histogram



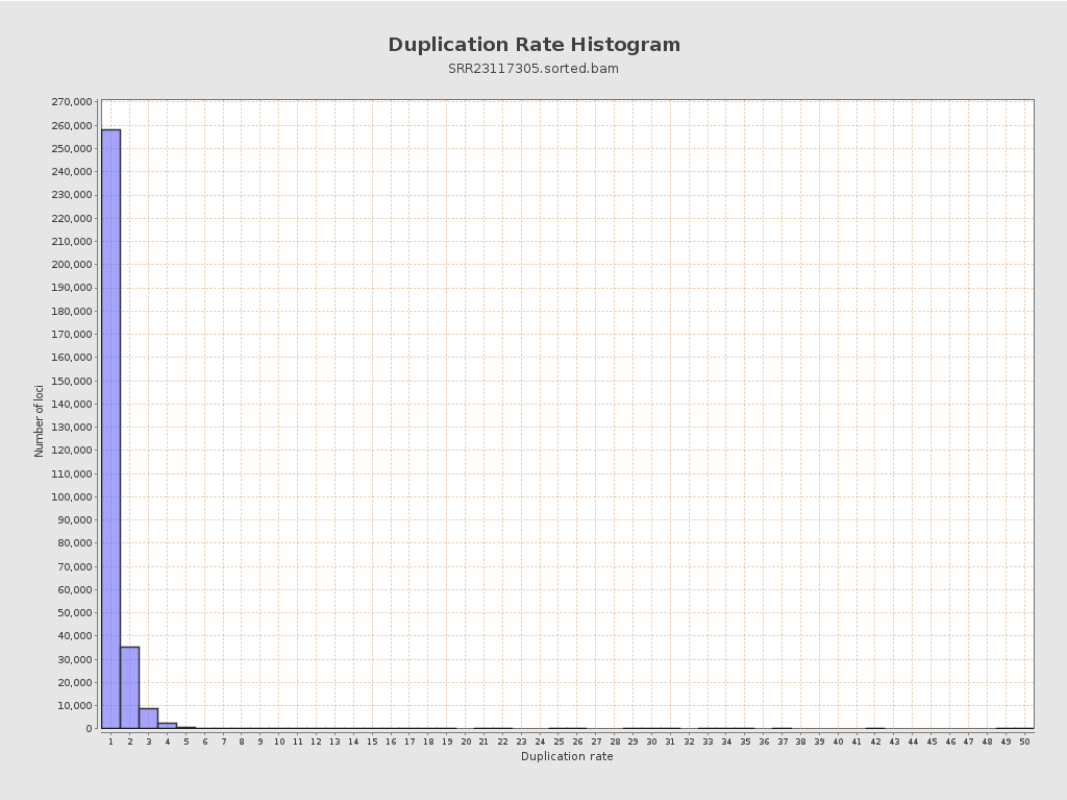
5. Results : Coverage Histogram (0-50X)



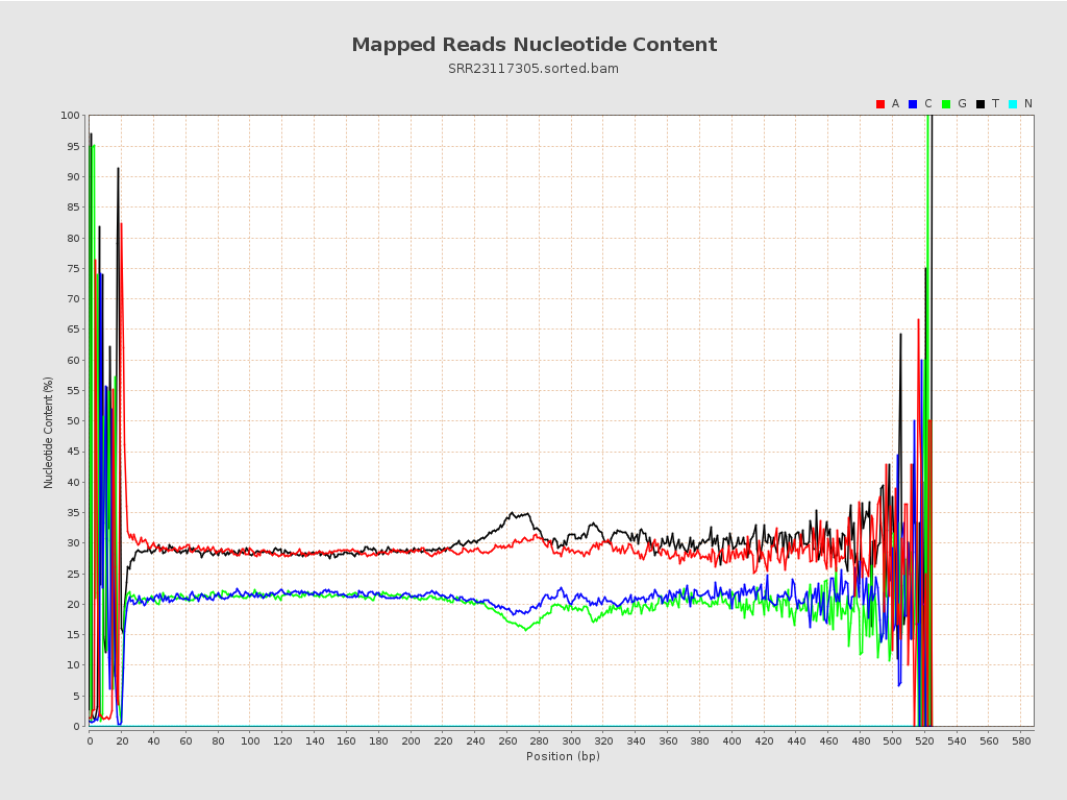
6. Results : Genome Fraction Coverage



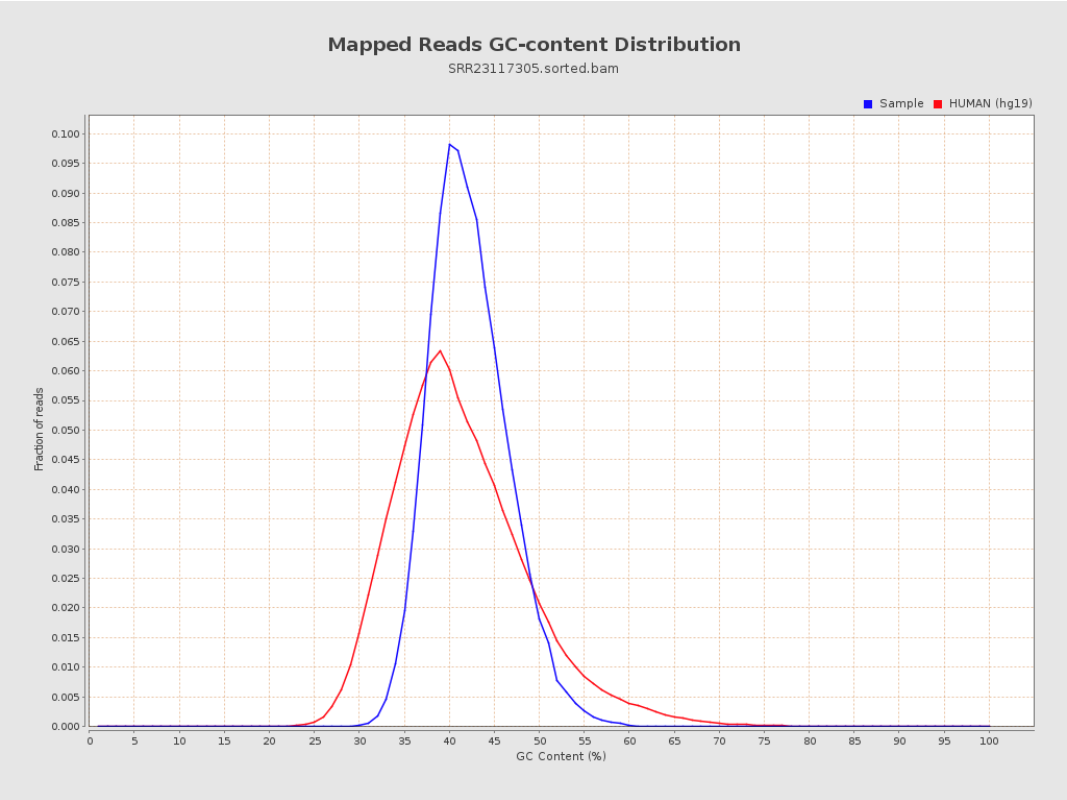
7. Results : Duplication Rate Histogram



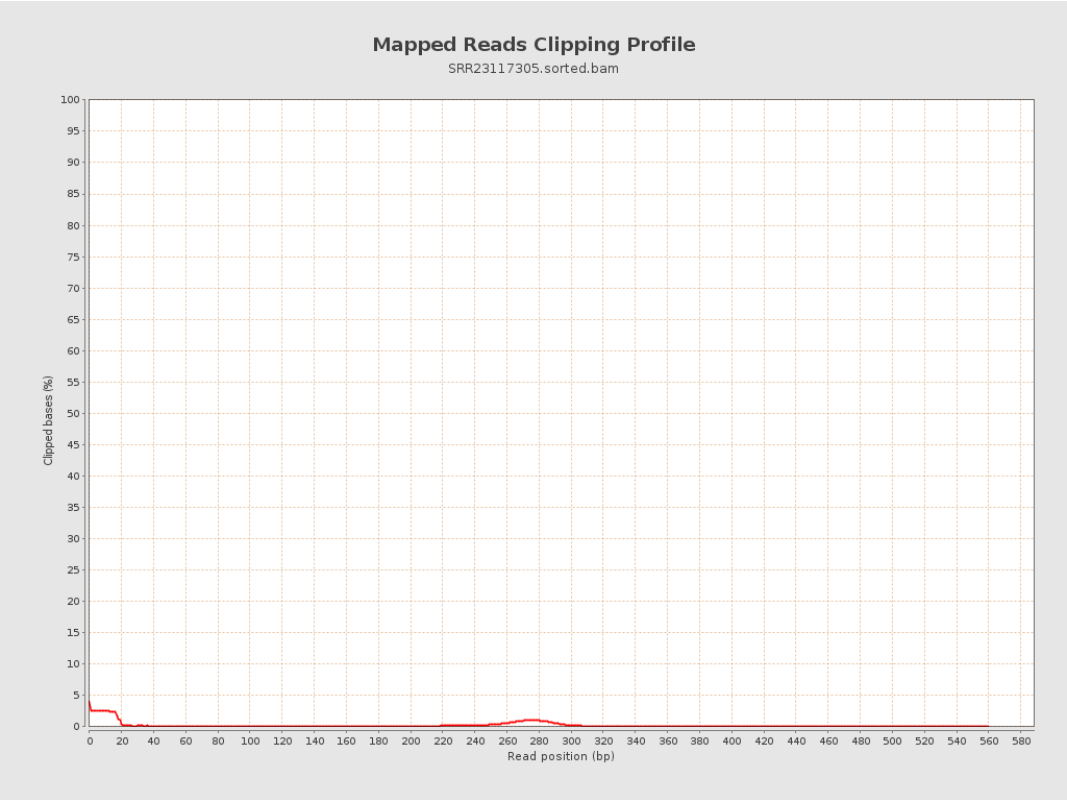
8. Results : Mapped Reads Nucleotide Content



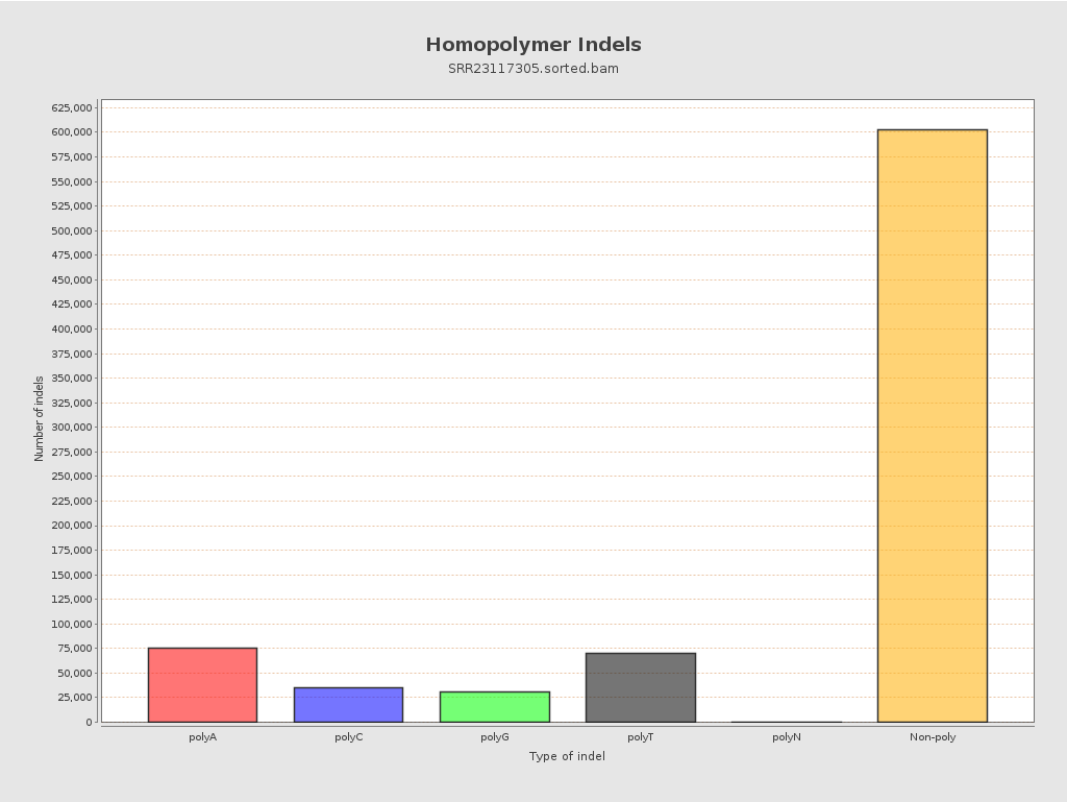
9. Results : Mapped Reads GC-content Distribution



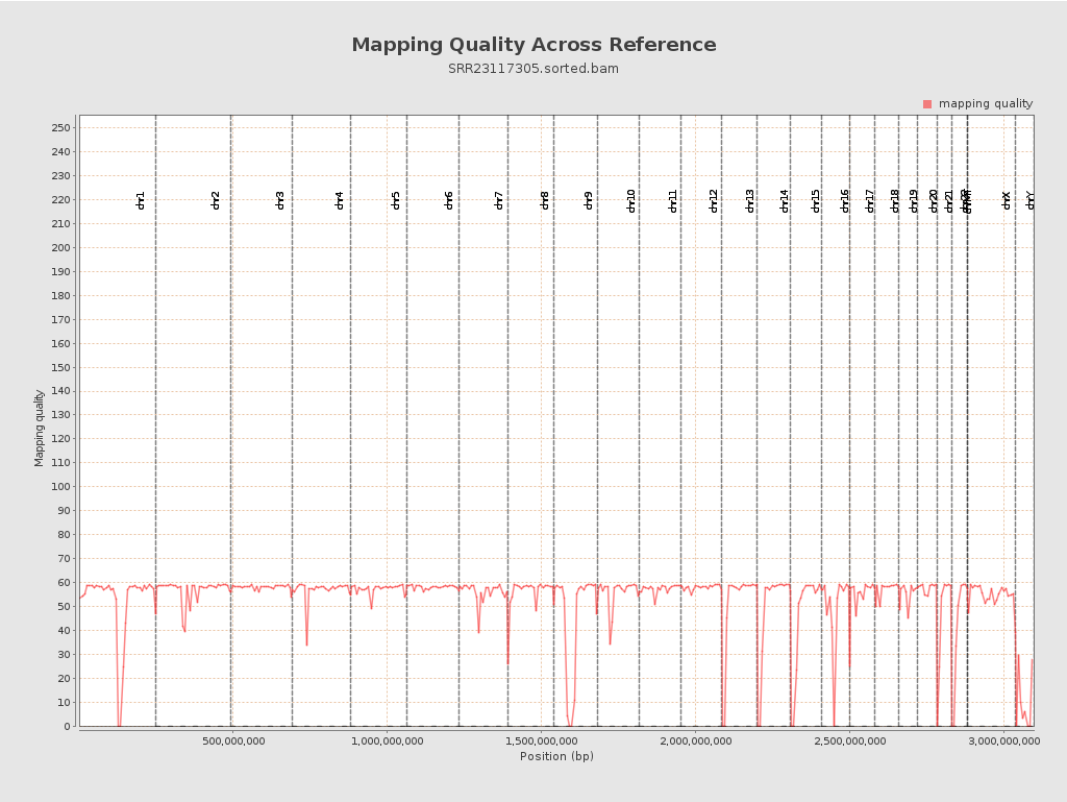
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram