

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:38:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549127.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_SRR1549127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:38:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,981,640
Mapped reads	9,387,658 / 85.49%
Unmapped reads	1,593,982 / 14.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	577,721 / 5.26%
Duplication rate	4.74%
Clipped reads	512,914 / 4.67%

2.2. ACGT Content

Number/percentage of A's	109,113,497 / 29.29%
Number/percentage of C's	76,961,885 / 20.66%
Number/percentage of T's	109,785,387 / 29.47%
Number/percentage of G's	76,550,728 / 20.55%
Number/percentage of N's	81,285 / 0.02%
GC Percentage	41.21%

2.3. Coverage

Mean	0.1203
Standard Deviation	1.5522

2.4. Mapping Quality

Mean Mapping Quality	44.28
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2.5. Mismatches and indels

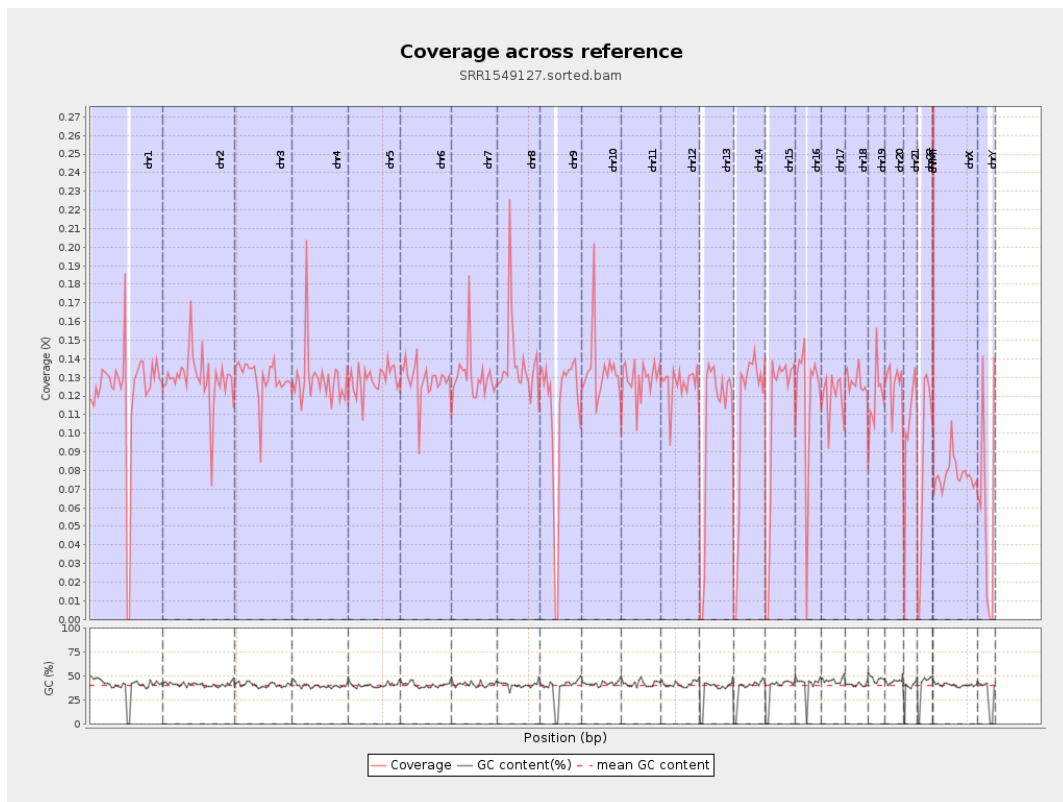
General error rate	0.34%
Mismatches	1,248,785
Insertions	9,966
Mapped reads with at least one insertion	0.11%
Deletions	31,402
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.52%

2.6. Chromosome stats

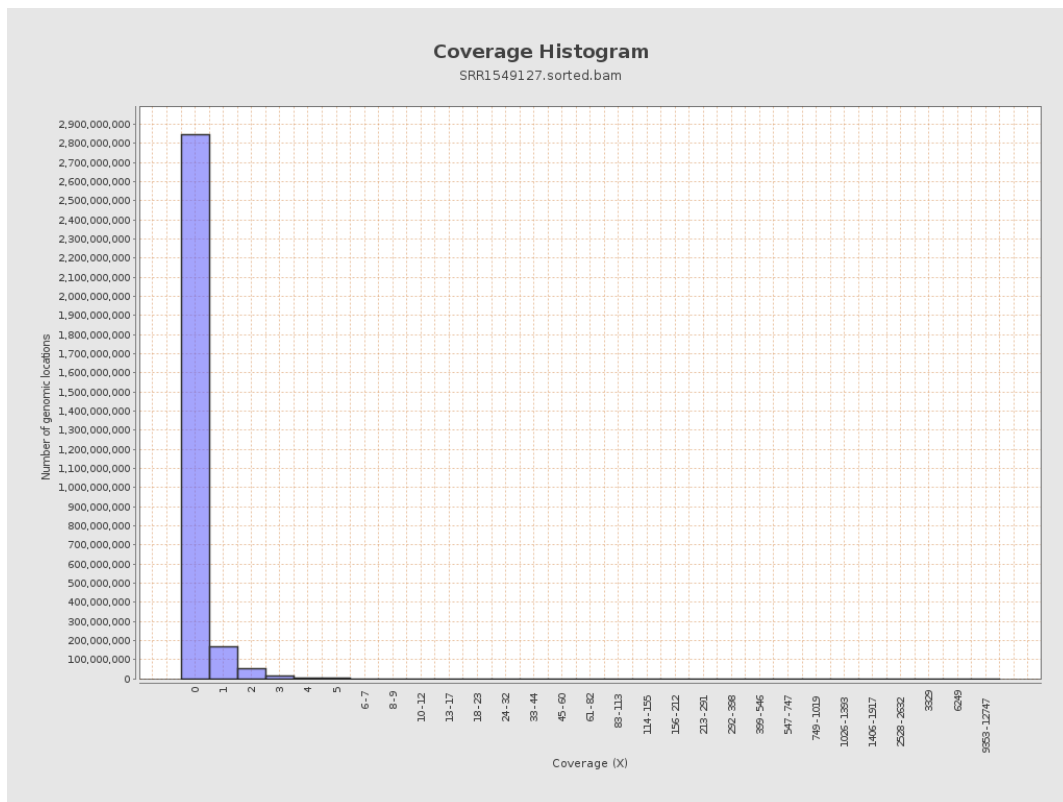
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30367040	0.1218	1.5061
chr2	243199373	31591530	0.1299	0.7525
chr3	198022430	25618456	0.1294	0.497
chr4	191154276	24787356	0.1297	0.6363
chr5	180915260	23296161	0.1288	0.5097
chr6	171115067	22020340	0.1287	0.5285
chr7	159138663	20737031	0.1303	0.9938
chr8	146364022	20122650	0.1375	6.2303

chr9	141213431	15874763	0.1124	0.6418
chr10	135534747	18055531	0.1332	0.8766
chr11	135006516	17388306	0.1288	0.6607
chr12	133851895	16952999	0.1267	0.5116
chr13	115169878	12131790	0.1053	0.4485
chr14	107349540	11779244	0.1097	0.5441
chr15	102531392	11122676	0.1085	0.4505
chr16	90354753	10590573	0.1172	0.5337
chr17	81195210	9756720	0.1202	0.5158
chr18	78077248	9958678	0.1275	1.2091
chr19	59128983	7085439	0.1198	1.17
chr20	63025520	7968346	0.1264	0.5443
chr21	48129895	4980020	0.1035	0.6037
chr22	51304566	4416150	0.0861	0.4306
chrMT	16571	169905	10.2532	12.5135
chrX	155270560	12104732	0.078	0.468
chrY	59373566	3656346	0.0616	0.7835

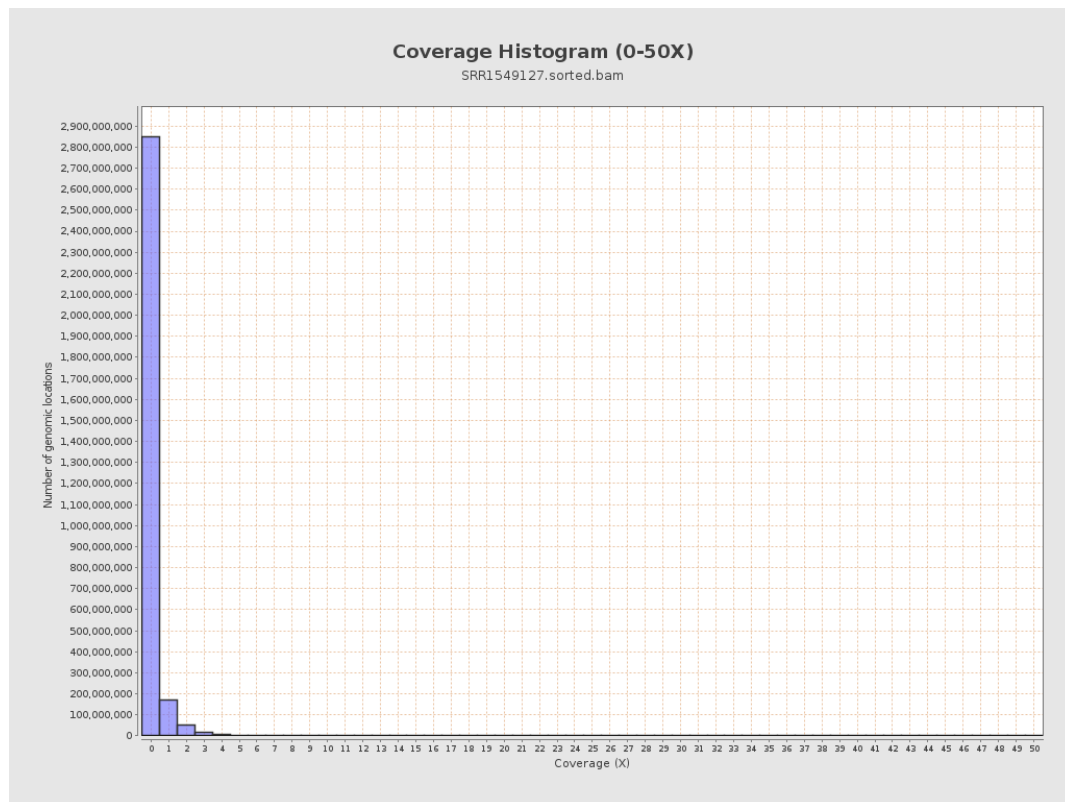
3. Results : Coverage across reference



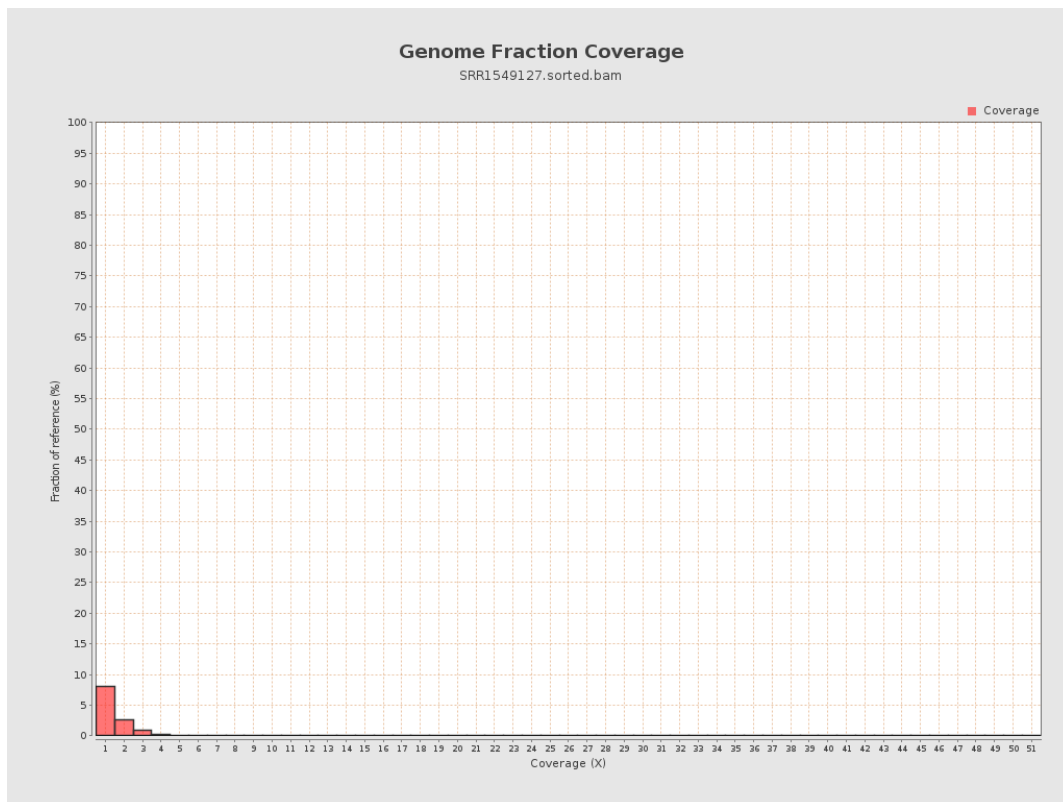
4. Results : Coverage Histogram



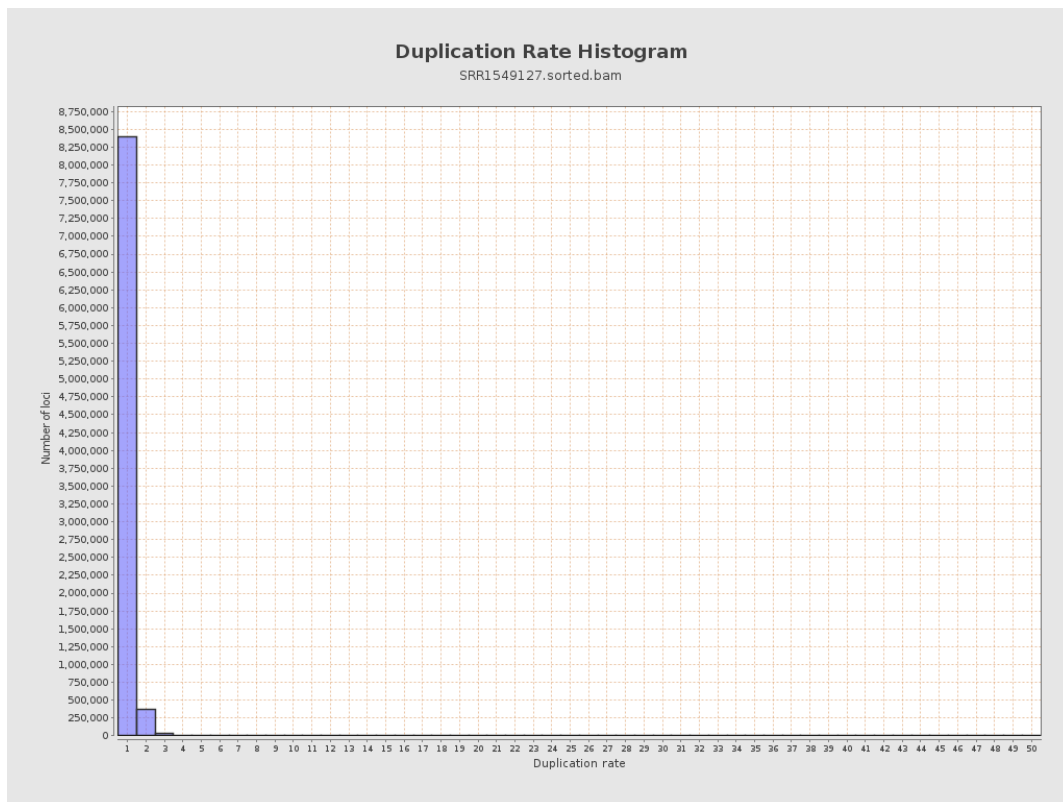
5. Results : Coverage Histogram (0-50X)



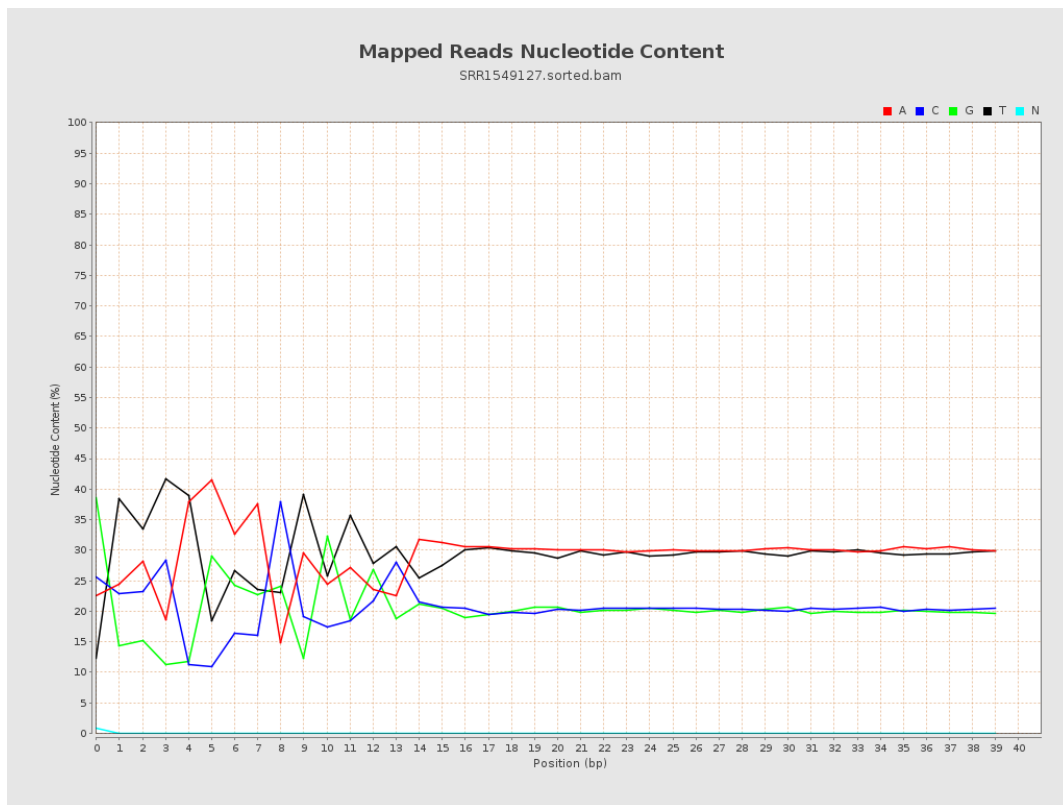
6. Results : Genome Fraction Coverage



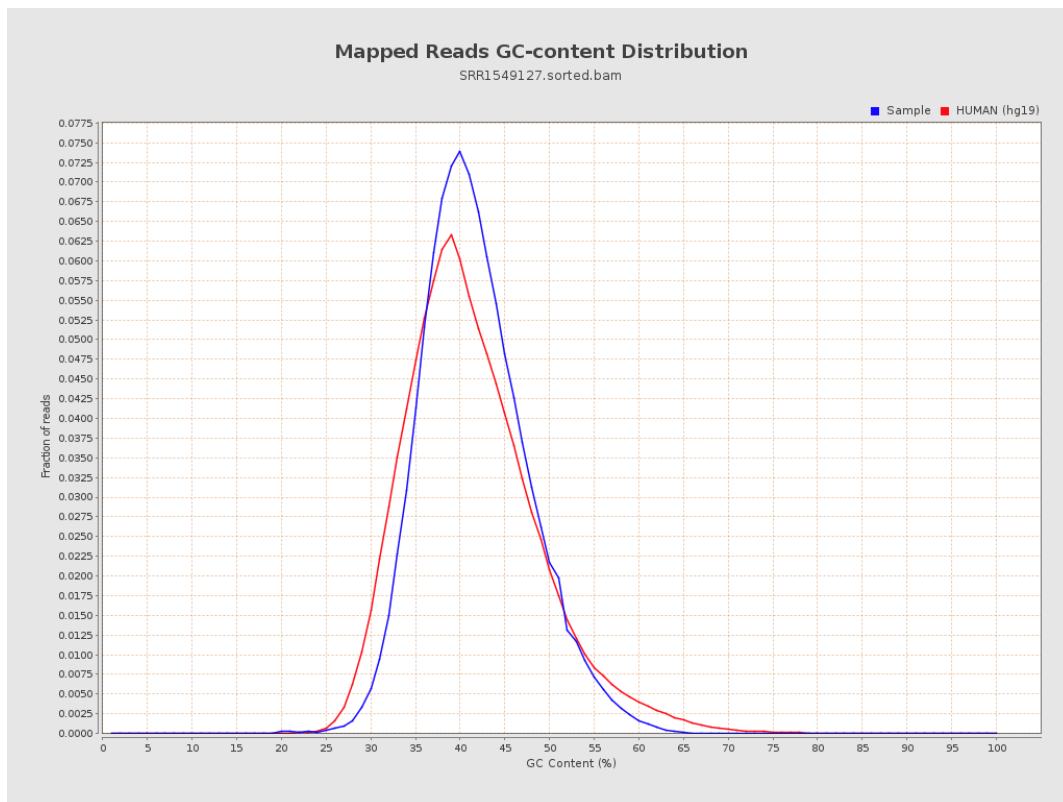
7. Results : Duplication Rate Histogram



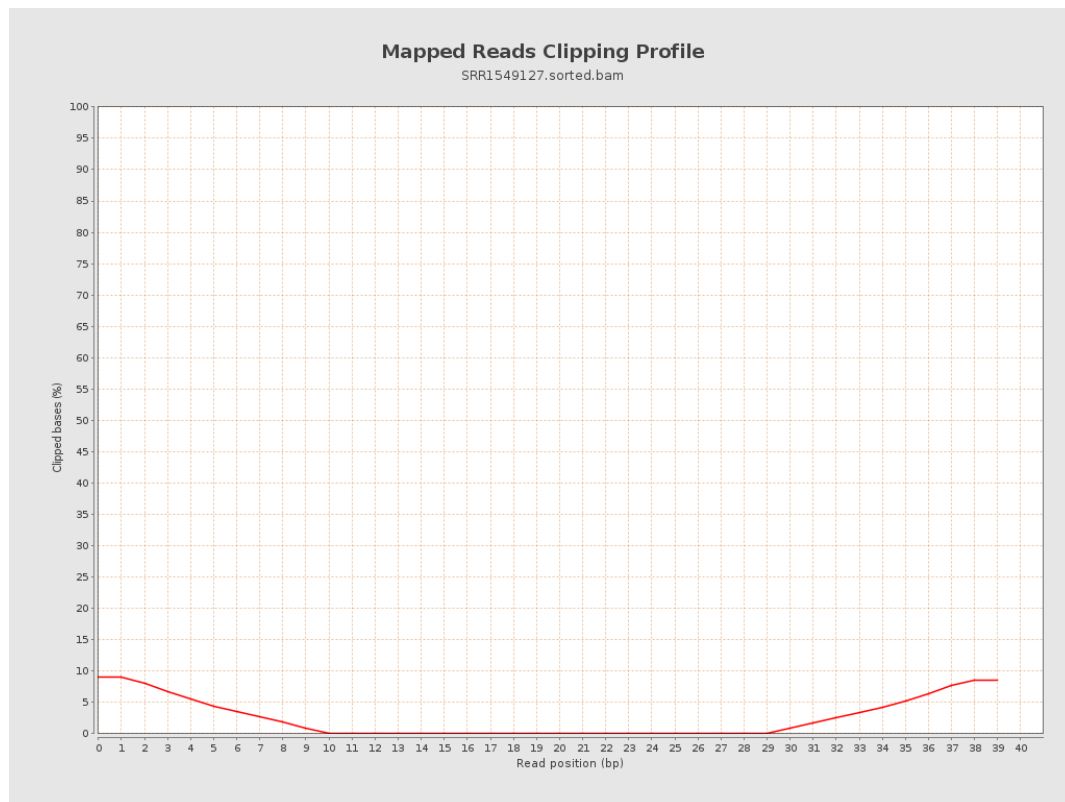
8. Results : Mapped Reads Nucleotide Content



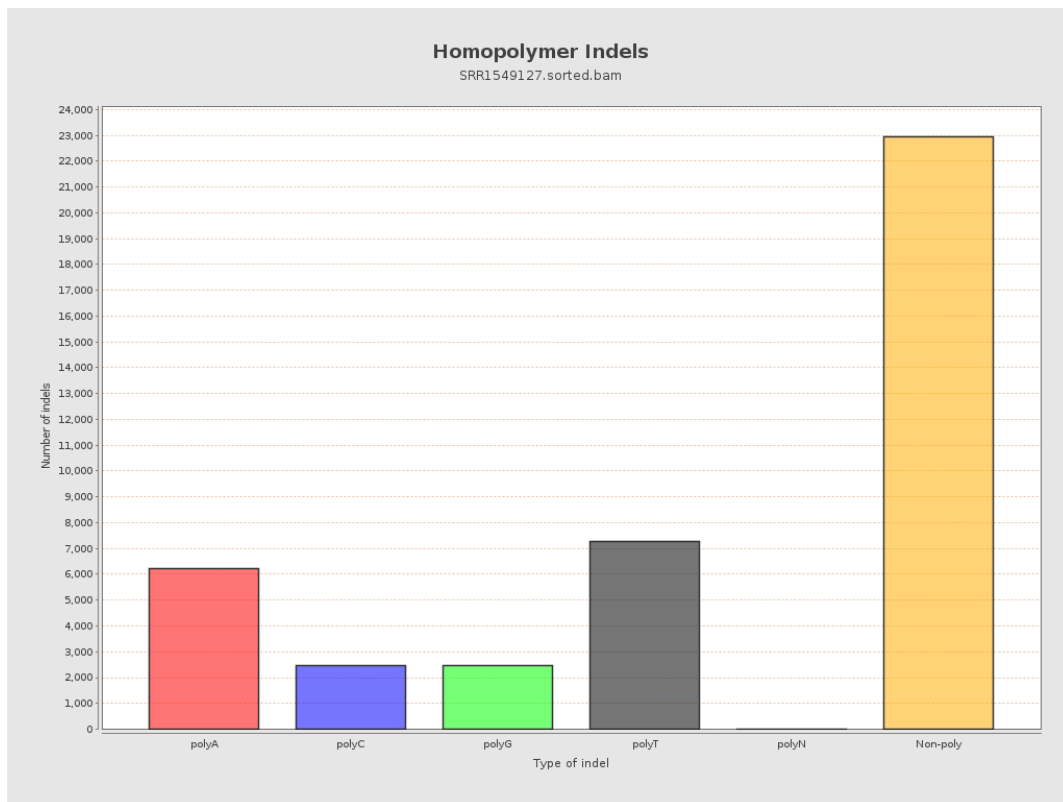
9. Results : Mapped Reads GC-content Distribution



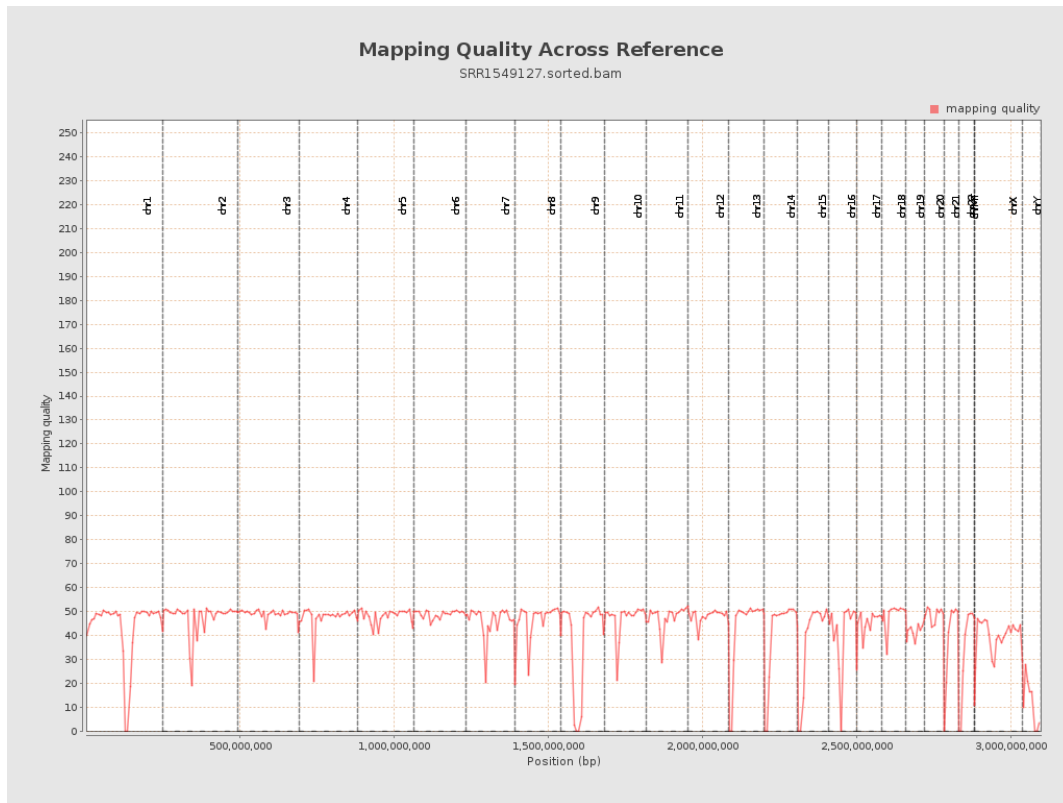
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

