

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:53:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549020.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_SRR1549020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:53:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,613,260
Mapped reads	7,452,419 / 86.52%
Unmapped reads	1,160,841 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	374,417 / 4.35%
Duplication rate	3.95%
Clipped reads	497,252 / 5.77%

2.2. ACGT Content

Number/percentage of A's	86,213,425 / 29.2%
Number/percentage of C's	61,219,053 / 20.74%
Number/percentage of T's	86,524,393 / 29.31%
Number/percentage of G's	61,272,001 / 20.75%
Number/percentage of N's	3,103 / 0%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0954
Standard Deviation	1.2774

2.4. Mapping Quality

Mean Mapping Quality	43.29
----------------------	-------

2.5. Mismatches and indels

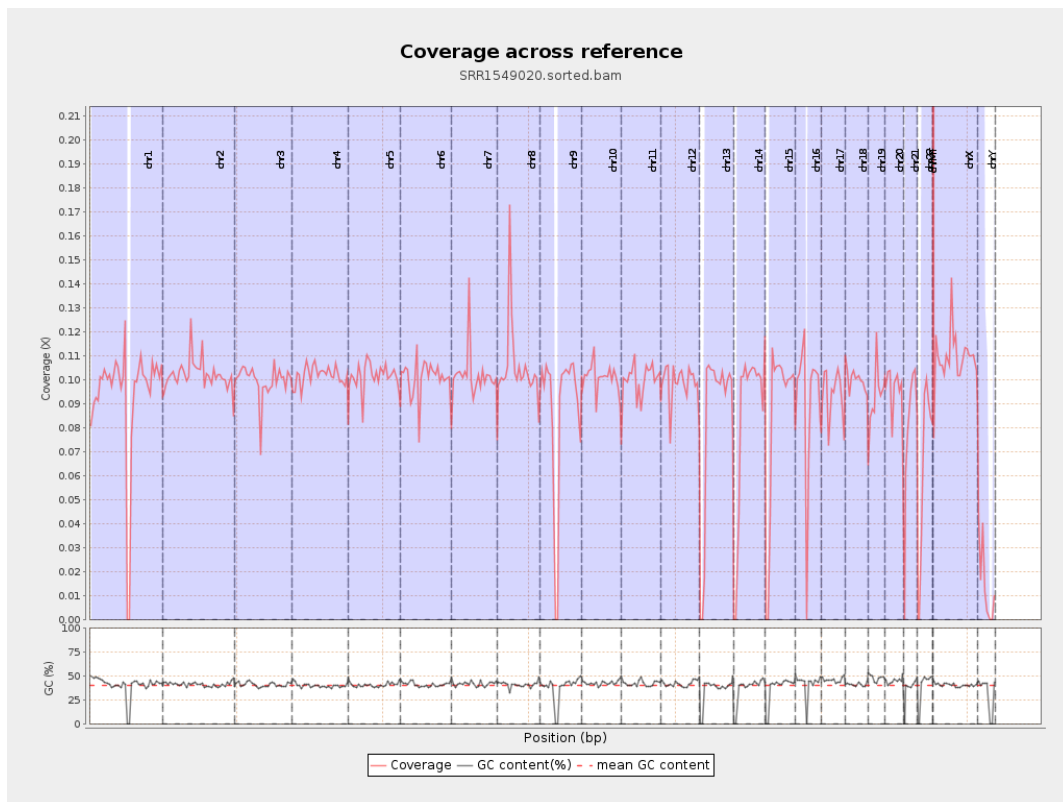
General error rate	0.26%
Mismatches	762,761
Insertions	8,731
Mapped reads with at least one insertion	0.12%
Deletions	24,336
Mapped reads with at least one deletion	0.33%
Homopolymer indels	42.45%

2.6. Chromosome stats

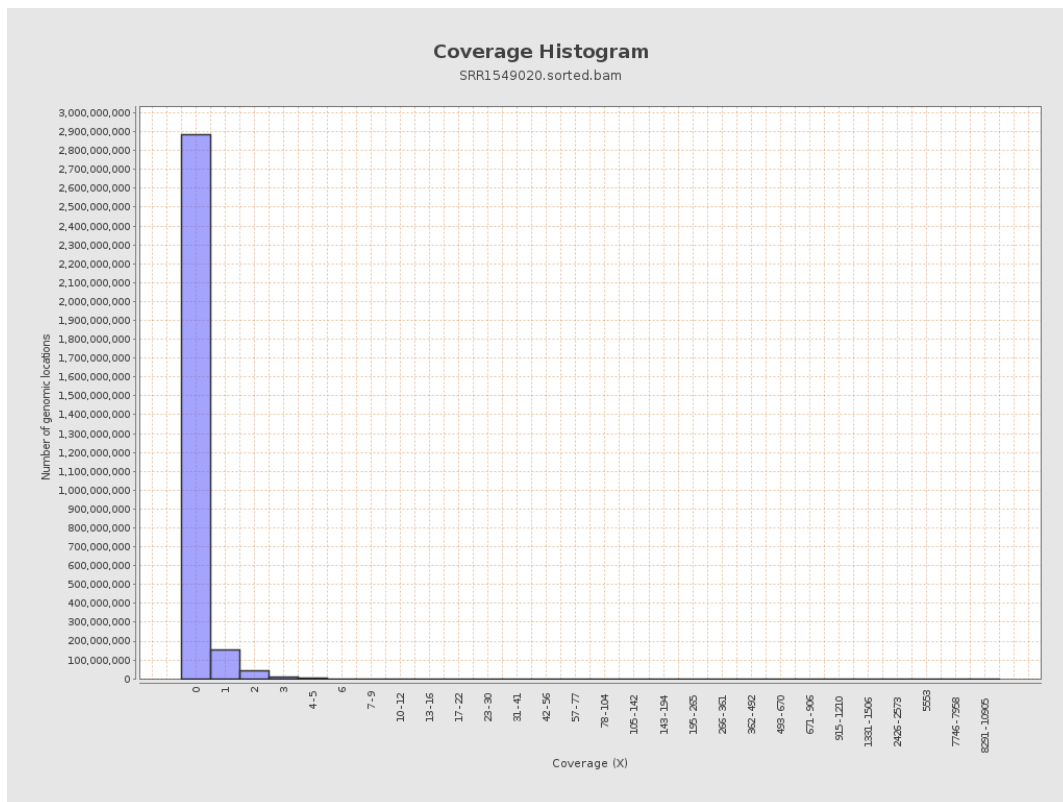
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23434247	0.094	0.9867
chr2	243199373	24885442	0.1023	0.557
chr3	198022430	19721427	0.0996	0.4223
chr4	191154276	19495000	0.102	0.4405
chr5	180915260	18322247	0.1013	0.4281
chr6	171115067	17274177	0.101	0.4577
chr7	159138663	16220555	0.1019	0.7576
chr8	146364022	15449934	0.1056	5.283

chr9	141213431	12381278	0.0877	0.5181
chr10	135534747	13678364	0.1009	0.521
chr11	135006516	13500697	0.1	0.6669
chr12	133851895	13270380	0.0991	0.4298
chr13	115169878	9707197	0.0843	0.3848
chr14	107349540	9083679	0.0846	0.4375
chr15	102531392	8634741	0.0842	0.3819
chr16	90354753	8107314	0.0897	0.4159
chr17	81195210	7687804	0.0947	0.4487
chr18	78077248	7805259	0.1	0.8707
chr19	59128983	5556473	0.094	0.8091
chr20	63025520	6029880	0.0957	0.4279
chr21	48129895	3848005	0.08	0.4098
chr22	51304566	3283999	0.064	0.3815
chrMT	16571	49225	2.9706	3.9012
chrX	155270560	16979268	0.1094	0.5226
chrY	59373566	857557	0.0144	0.2251

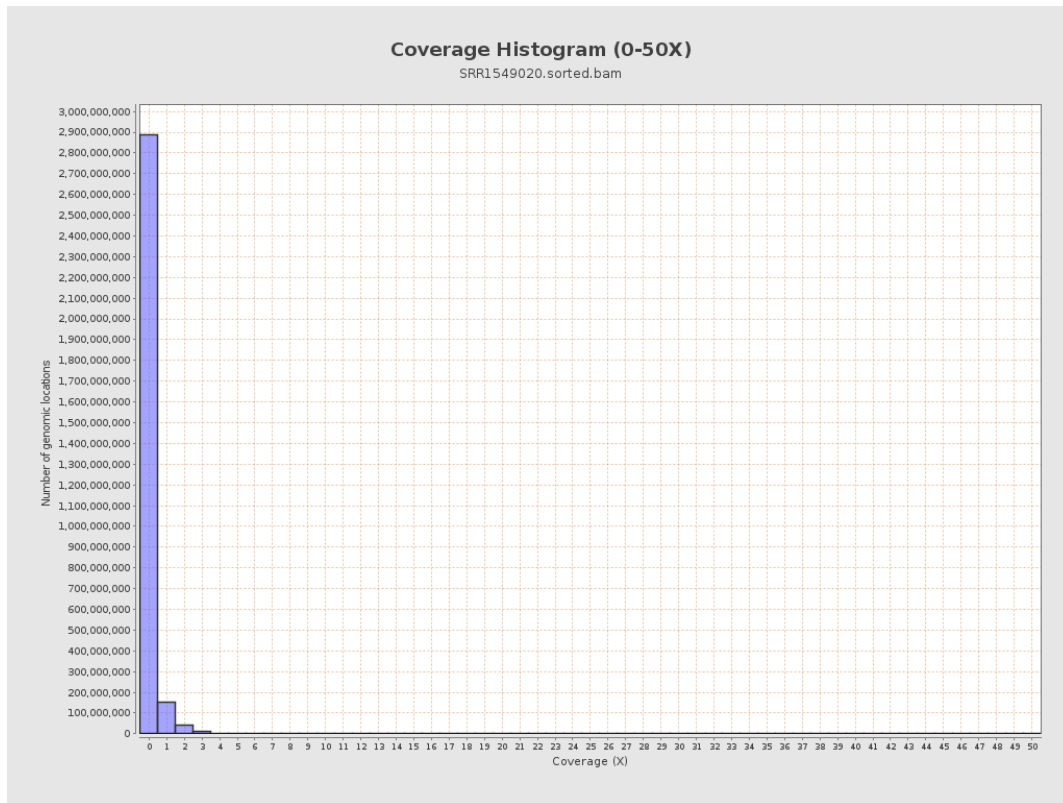
3. Results : Coverage across reference



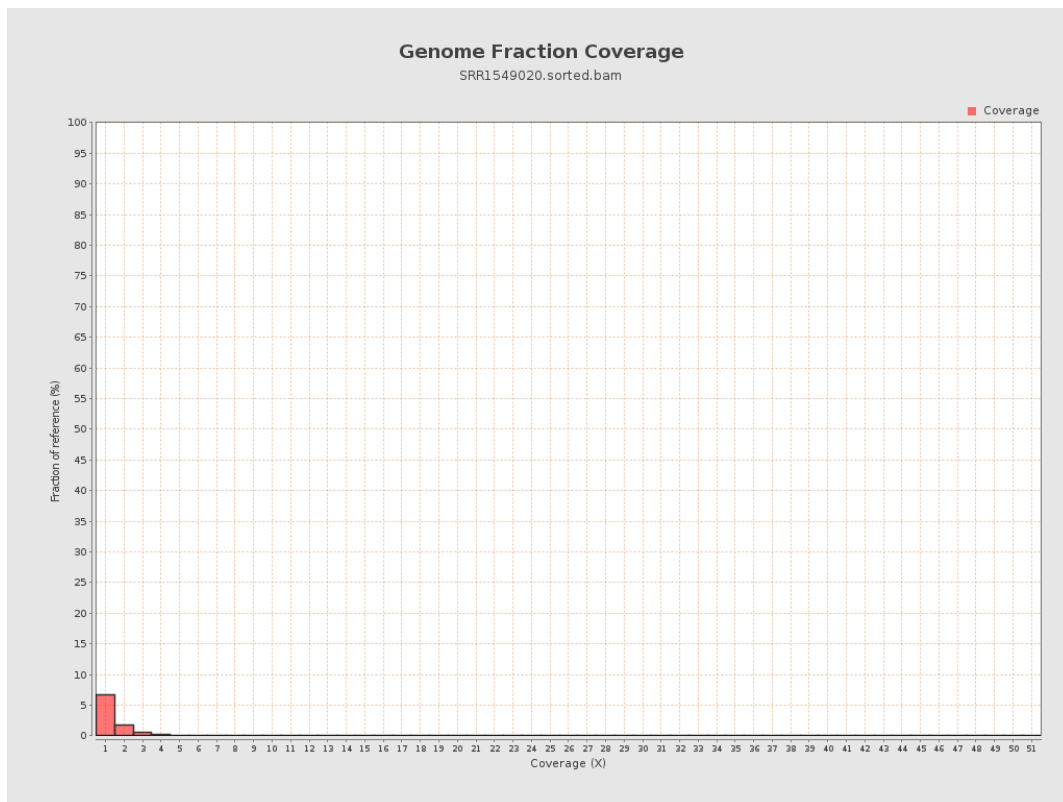
4. Results : Coverage Histogram



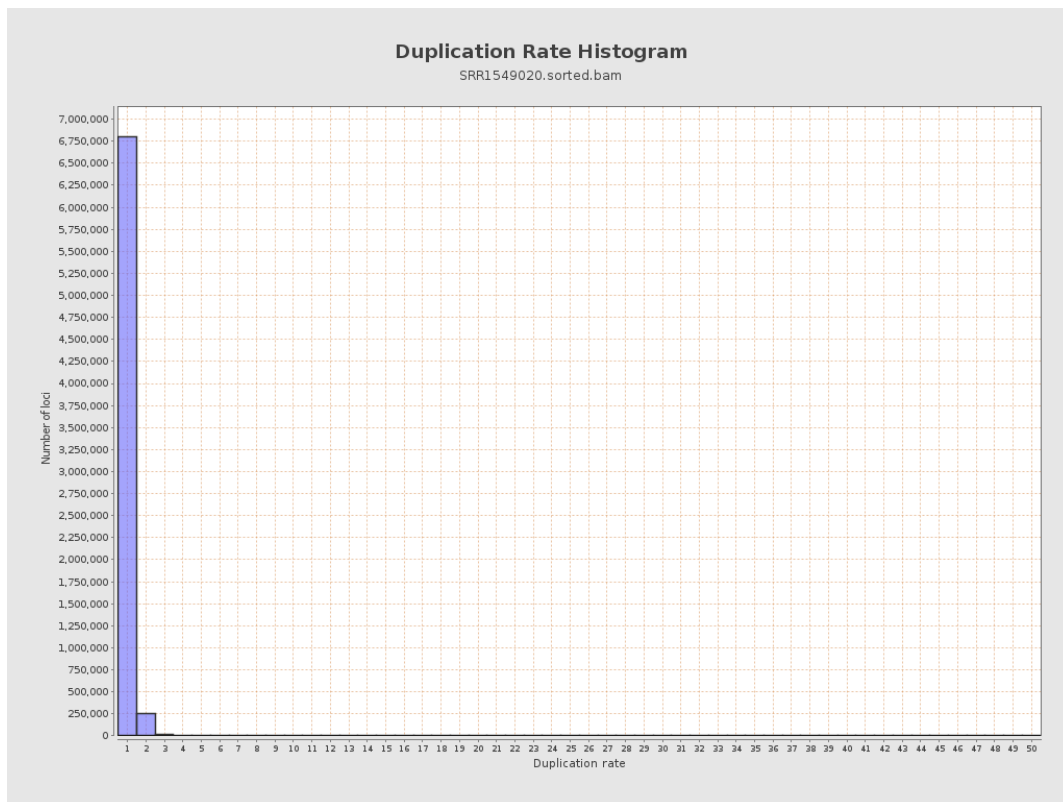
5. Results : Coverage Histogram (0-50X)



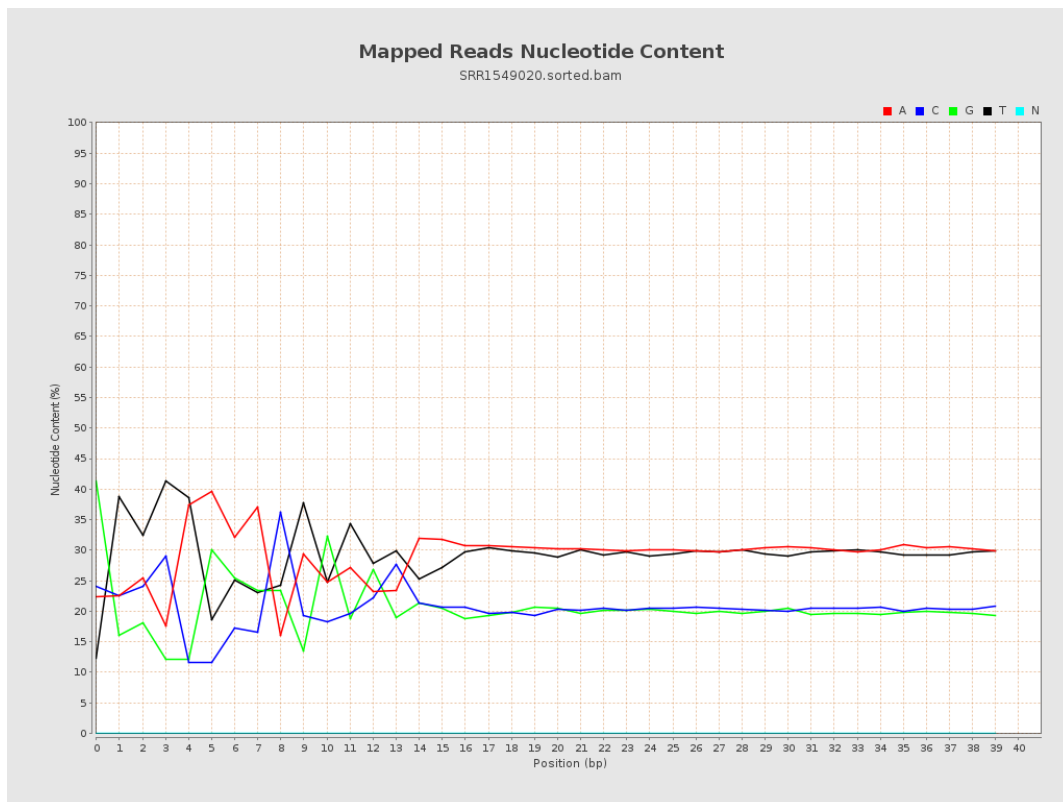
6. Results : Genome Fraction Coverage



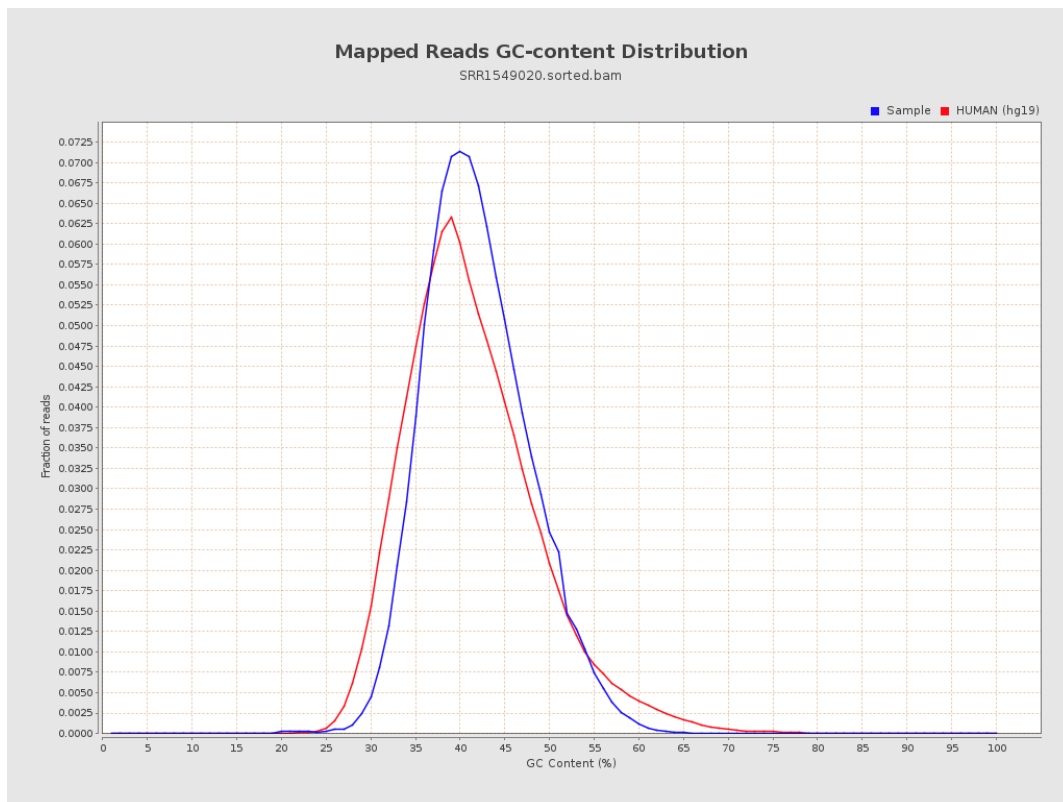
7. Results : Duplication Rate Histogram



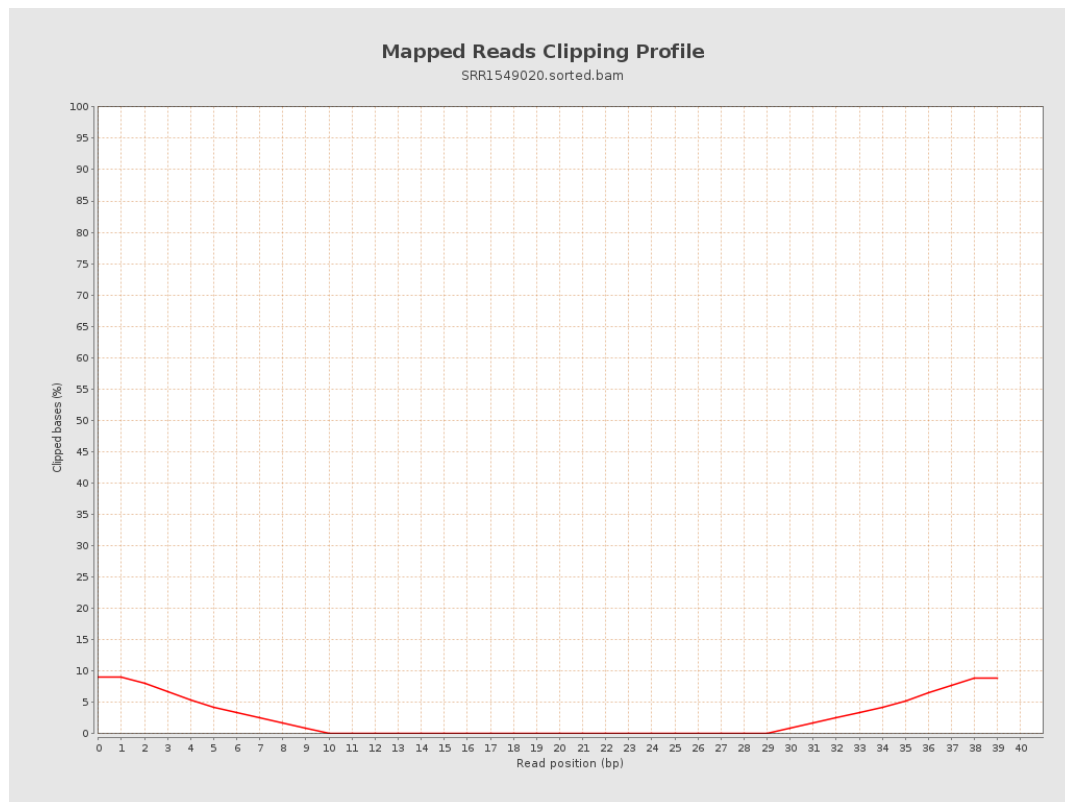
8. Results : Mapped Reads Nucleotide Content



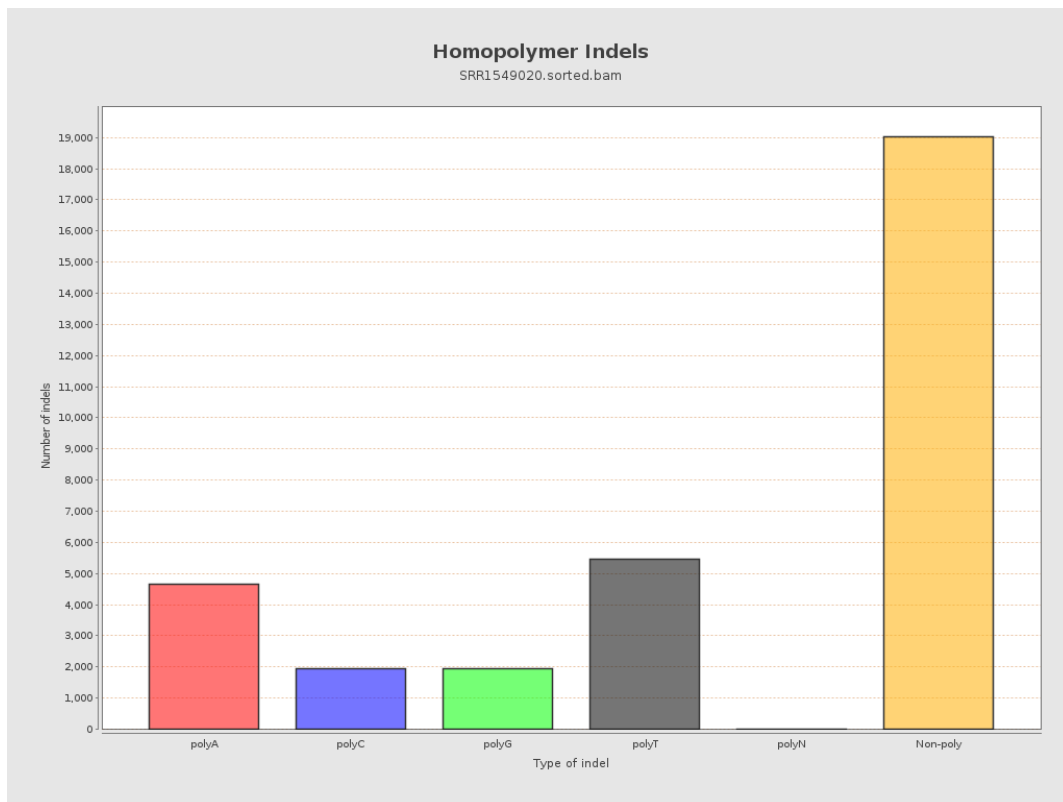
9. Results : Mapped Reads GC-content Distribution



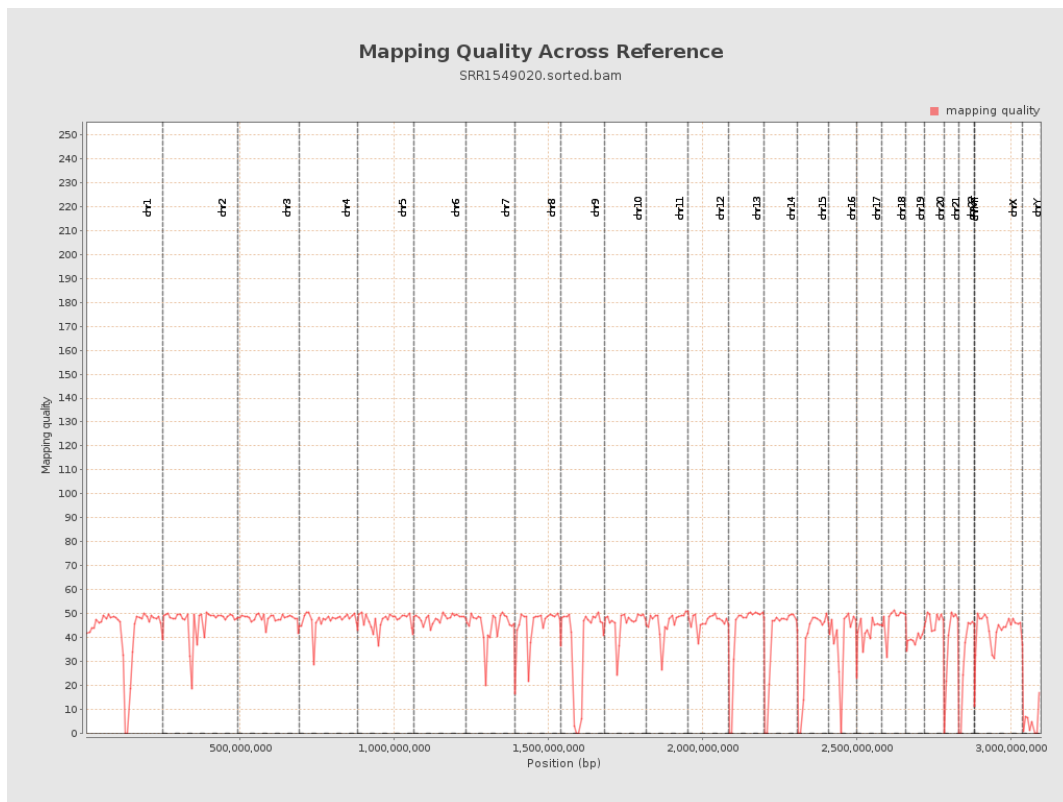
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

