

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549105.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_SRR1549105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:10:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,335,318
Mapped reads	10,646,198 / 79.83%
Unmapped reads	2,689,120 / 20.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	496,727 / 3.72%
Duplication rate	3.59%
Clipped reads	710,347 / 5.33%

2.2. ACGT Content

Number/percentage of A's	126,751,830 / 30.05%
Number/percentage of C's	83,802,472 / 19.87%
Number/percentage of T's	127,075,189 / 30.13%
Number/percentage of G's	84,159,511 / 19.95%
Number/percentage of N's	1,726 / 0%
GC Percentage	39.82%

2.3. Coverage

Mean	0.1363
Standard Deviation	1.2243

2.4. Mapping Quality

Mean Mapping Quality	42.23
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2.5. Mismatches and indels

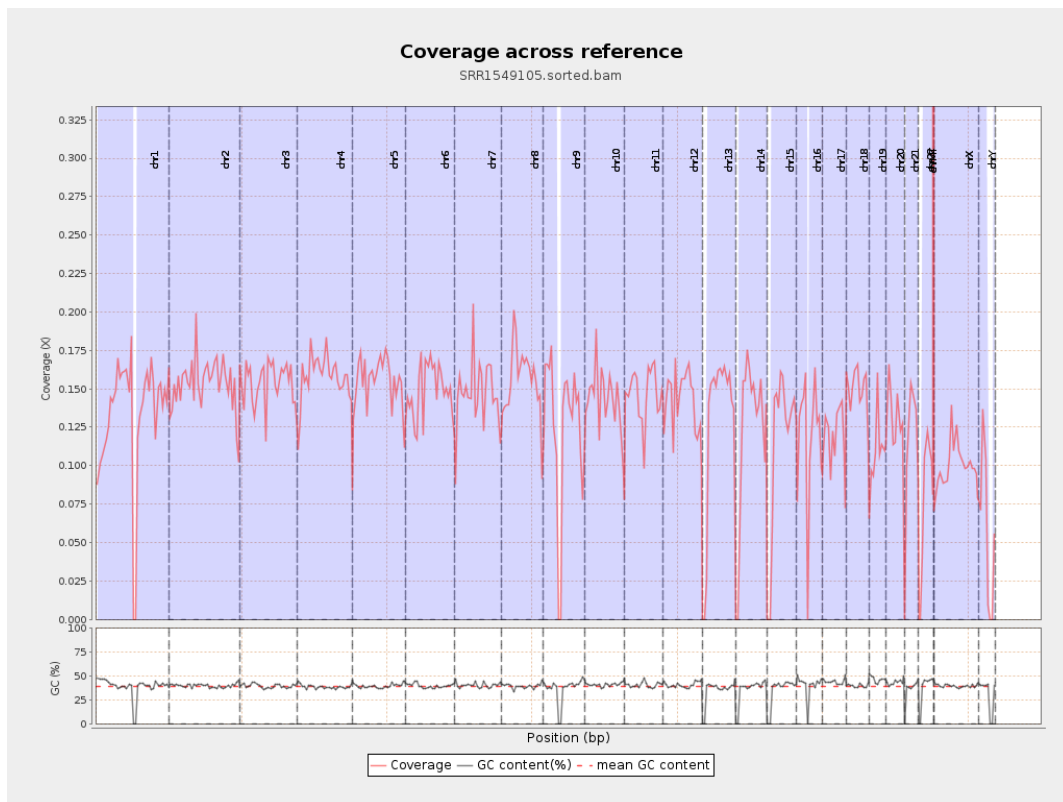
General error rate	0.34%
Mismatches	1,404,249
Insertions	13,138
Mapped reads with at least one insertion	0.12%
Deletions	34,608
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.22%

2.6. Chromosome stats

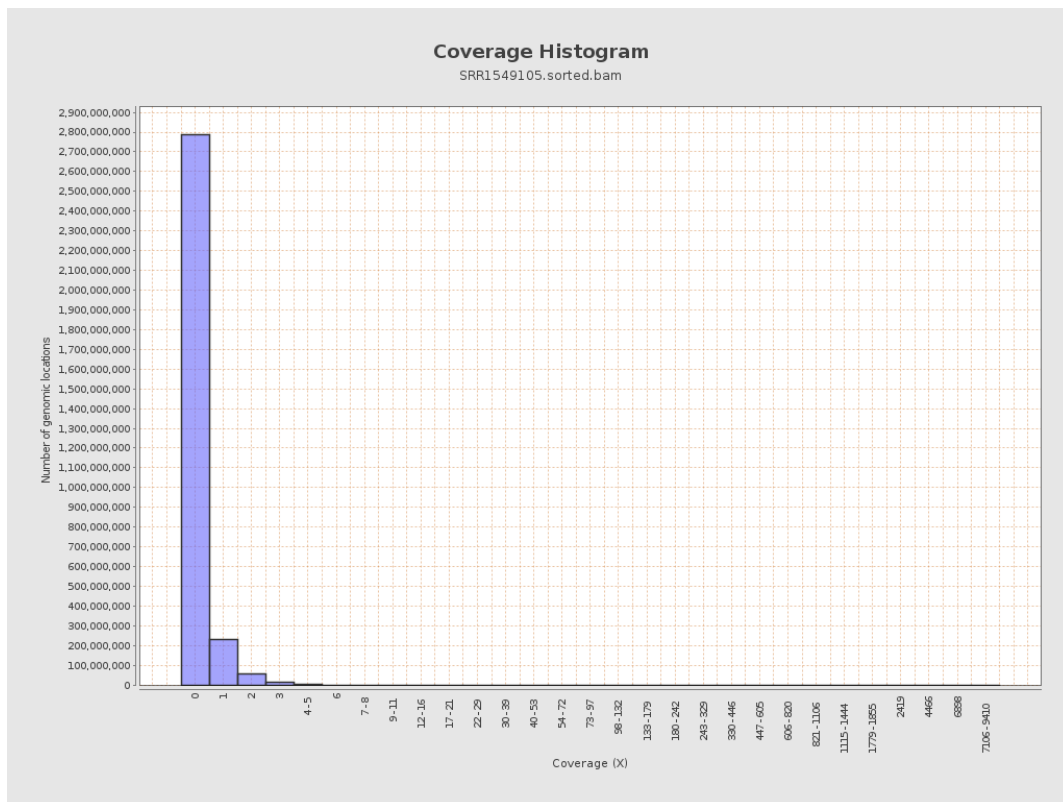
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33232220	0.1333	1.1947
chr2	243199373	37356573	0.1536	0.7762
chr3	198022430	30538536	0.1542	0.5131
chr4	191154276	30196801	0.158	0.5511
chr5	180915260	28102731	0.1553	0.5172
chr6	171115067	25450337	0.1487	0.5538
chr7	159138663	23574368	0.1481	1.0546
chr8	146364022	22718468	0.1552	4.6017

chr9	141213431	17724393	0.1255	0.734
chr10	135534747	19489368	0.1438	0.698
chr11	135006516	19687398	0.1458	0.6768
chr12	133851895	19065463	0.1424	0.5055
chr13	115169878	14625622	0.127	0.4639
chr14	107349540	13095696	0.122	0.5976
chr15	102531392	11788931	0.115	0.4402
chr16	90354753	10769220	0.1192	0.5147
chr17	81195210	9604949	0.1183	0.4661
chr18	78077248	11723719	0.1502	1.2984
chr19	59128983	6545706	0.1107	1.0705
chr20	63025520	8205306	0.1302	0.5012
chr21	48129895	5560840	0.1155	0.5425
chr22	51304566	3915605	0.0763	0.4242
chrMT	16571	47404	2.8607	3.204
chrX	155270560	15500014	0.0998	0.4908
chrY	59373566	3313880	0.0558	0.4136

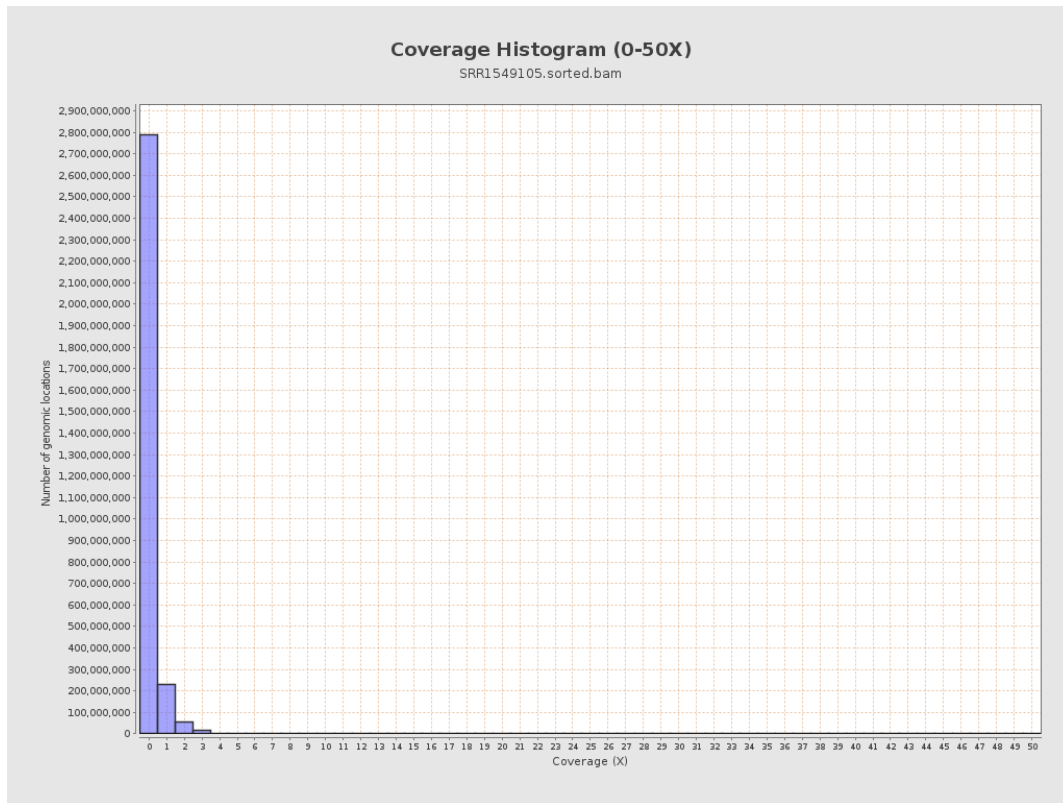
3. Results : Coverage across reference



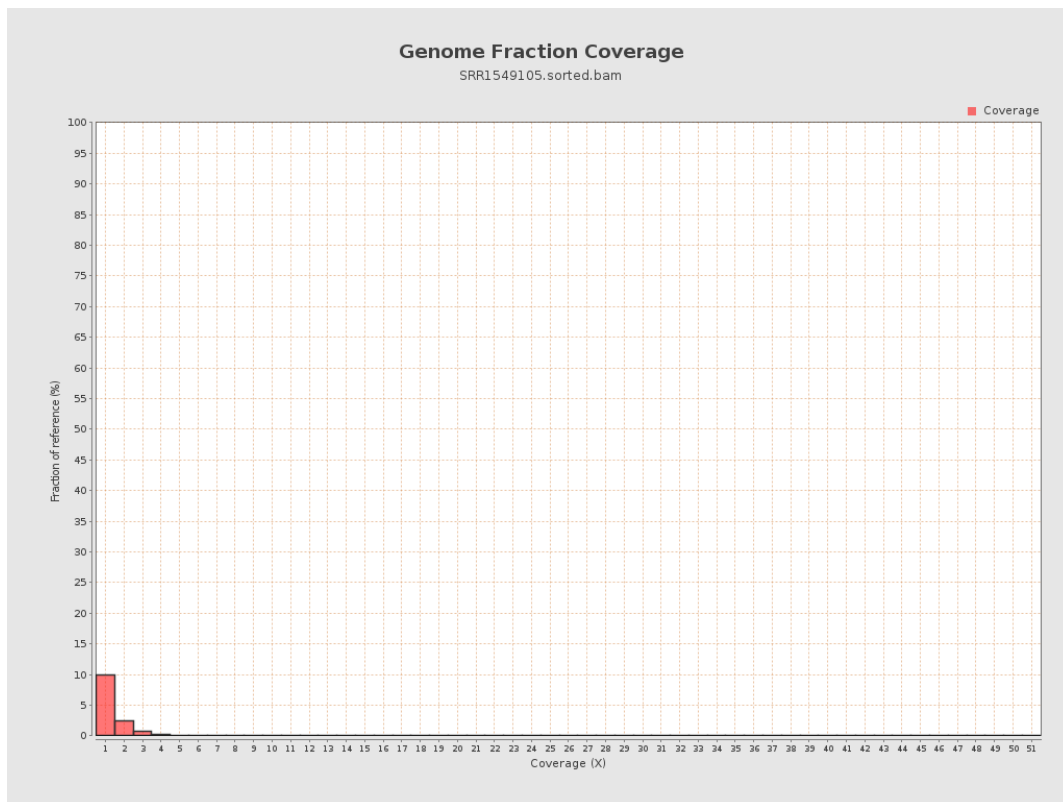
4. Results : Coverage Histogram



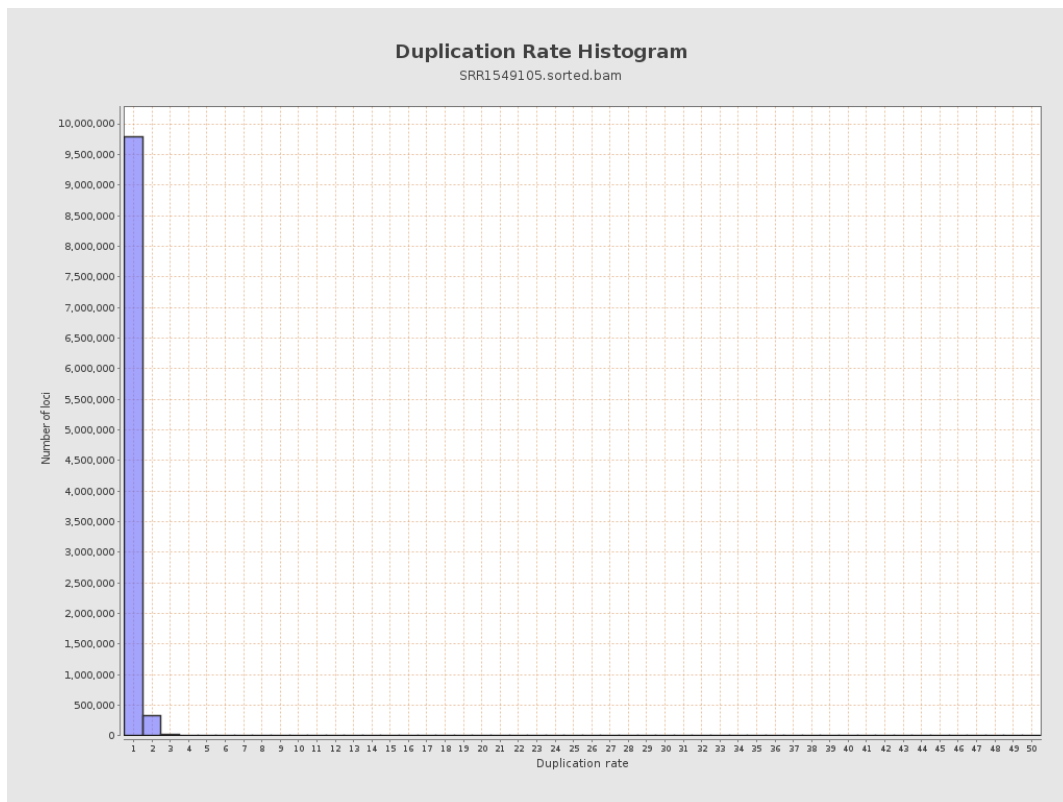
5. Results : Coverage Histogram (0-50X)



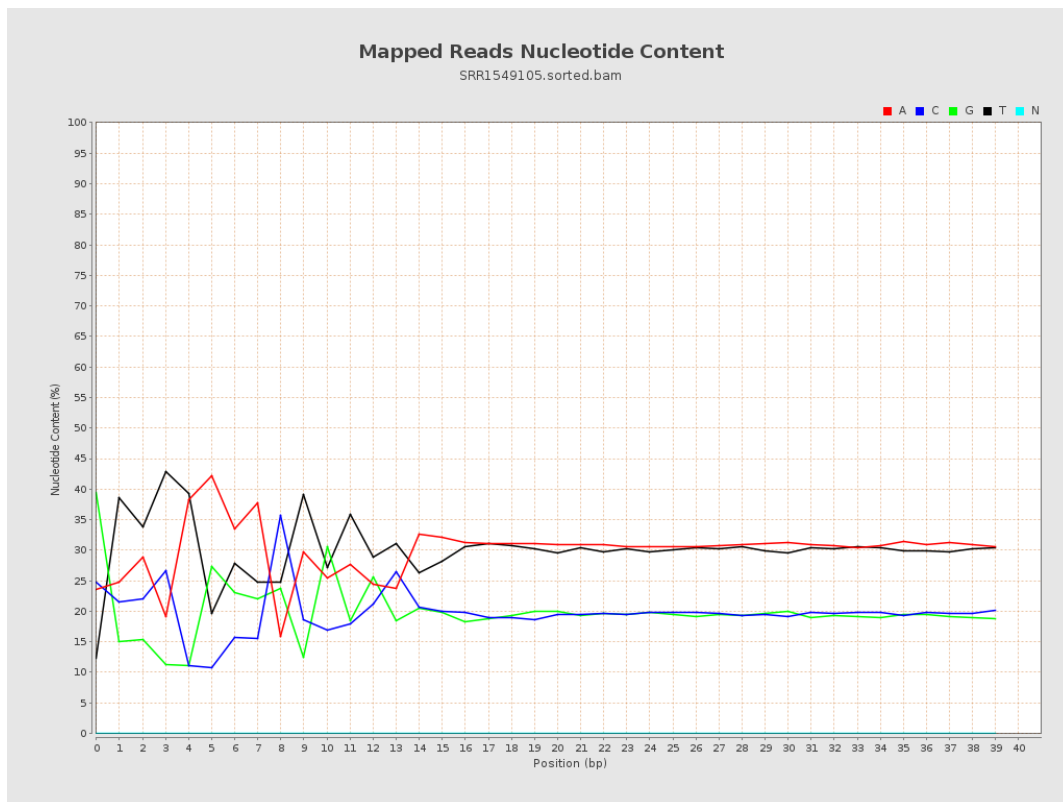
6. Results : Genome Fraction Coverage



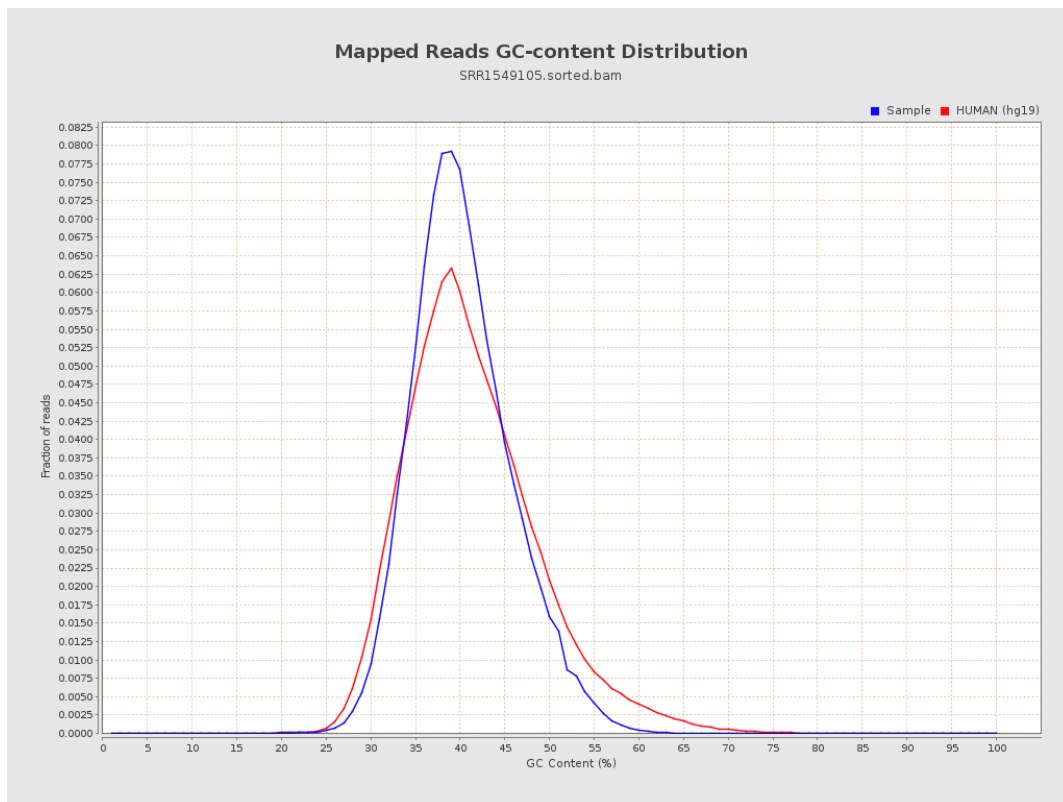
7. Results : Duplication Rate Histogram



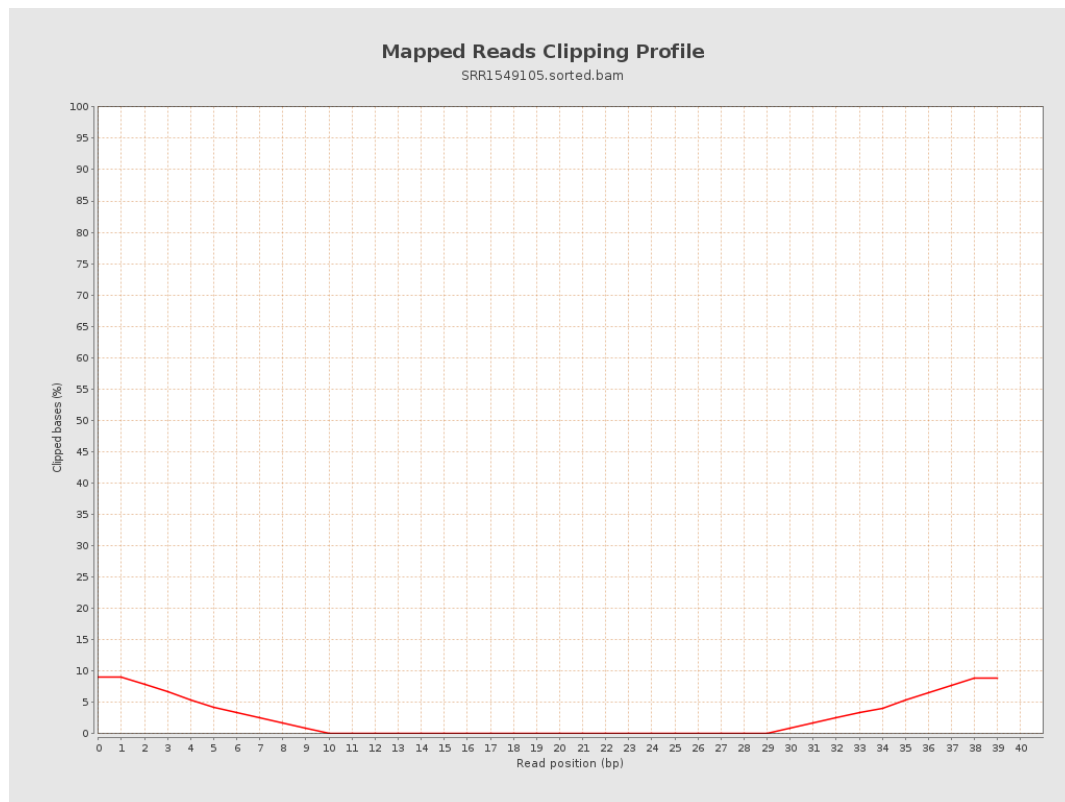
8. Results : Mapped Reads Nucleotide Content



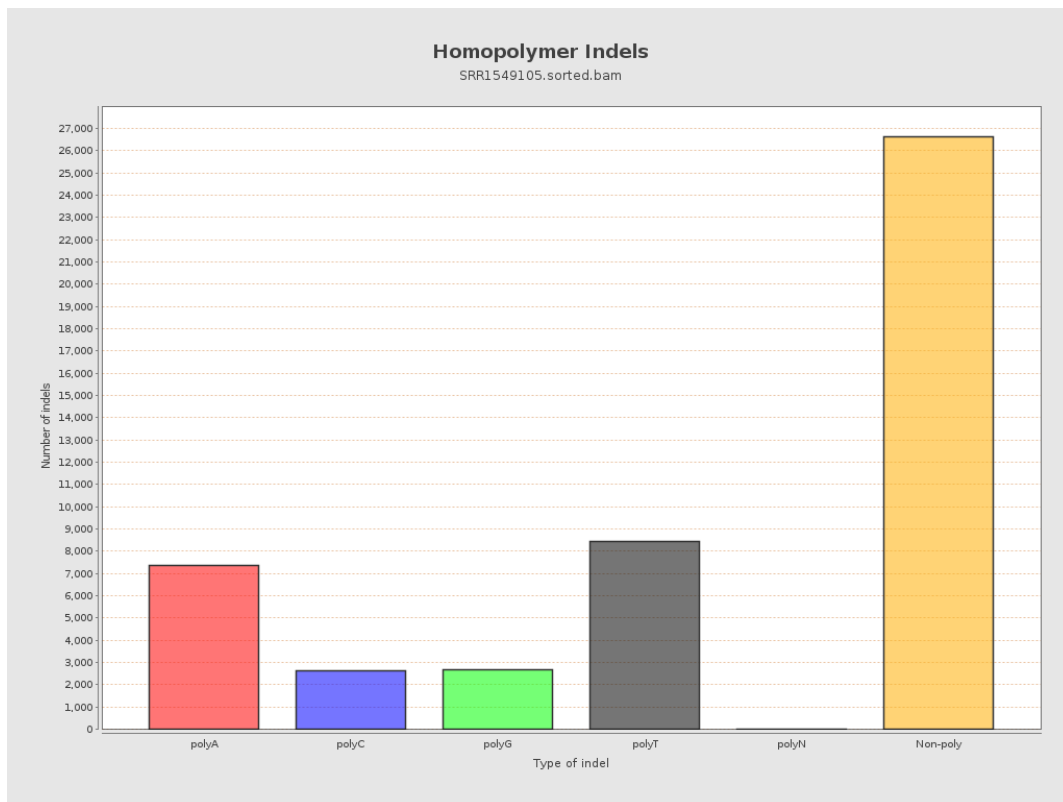
9. Results : Mapped Reads GC-content Distribution



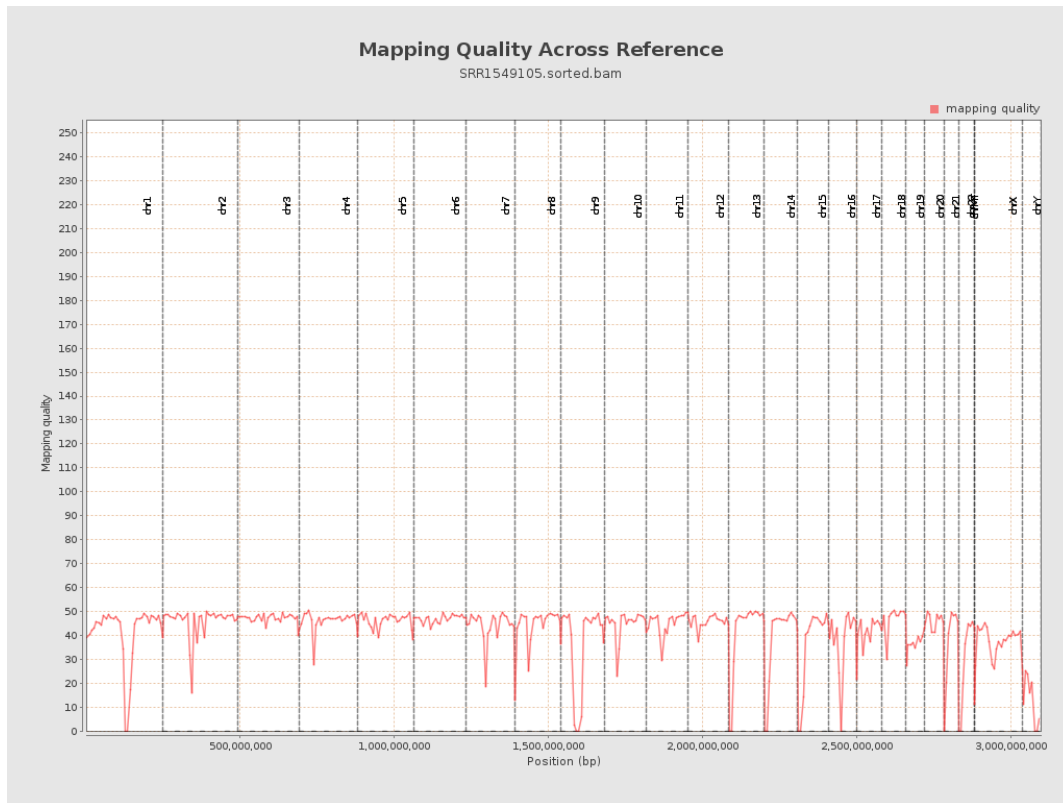
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

