

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:09:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549129.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_SRR1549129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:09:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,691,086
Mapped reads	11,994,780 / 87.61%
Unmapped reads	1,696,306 / 12.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	697,114 / 5.09%
Duplication rate	4.64%
Clipped reads	677,744 / 4.95%

2.2. ACGT Content

Number/percentage of A's	135,353,287 / 28.45%
Number/percentage of C's	101,609,918 / 21.36%
Number/percentage of T's	136,870,302 / 28.77%
Number/percentage of G's	101,812,771 / 21.4%
Number/percentage of N's	114,749 / 0.02%
GC Percentage	42.76%

2.3. Coverage

Mean	0.1537
Standard Deviation	0.8664

2.4. Mapping Quality

Mean Mapping Quality	42.86
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2.5. Mismatches and indels

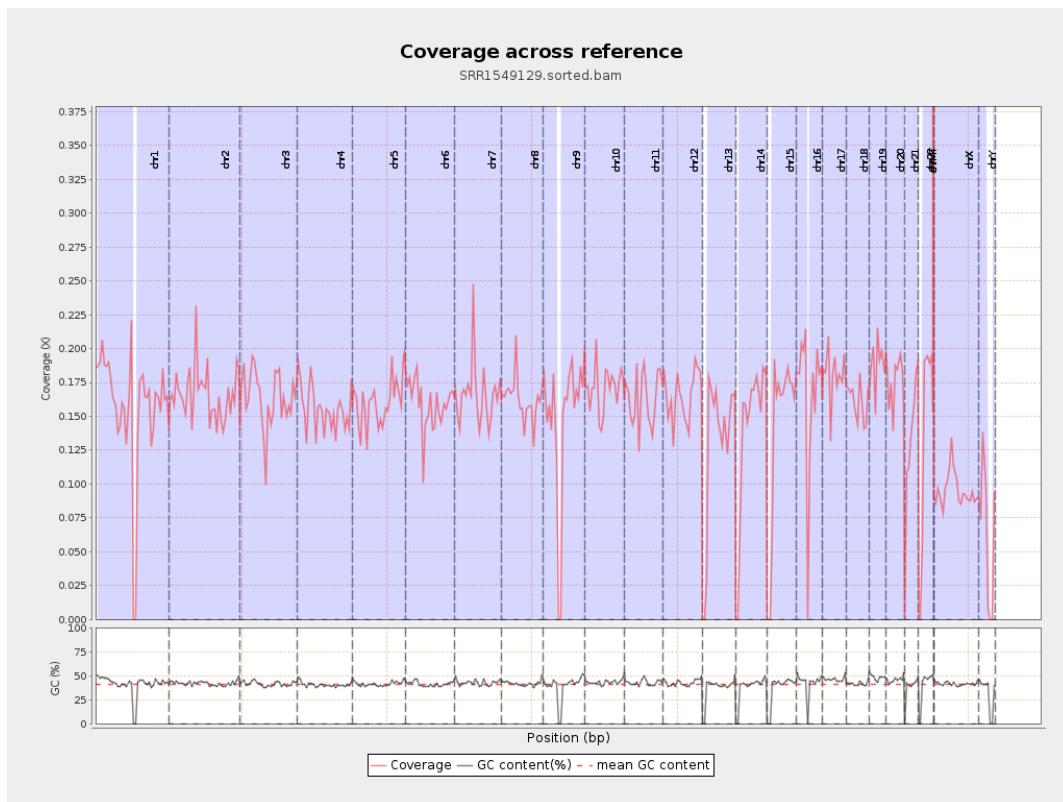
General error rate	0.34%
Mismatches	1,601,845
Insertions	12,545
Mapped reads with at least one insertion	0.1%
Deletions	36,814
Mapped reads with at least one deletion	0.31%
Homopolymer indels	45.69%

2.6. Chromosome stats

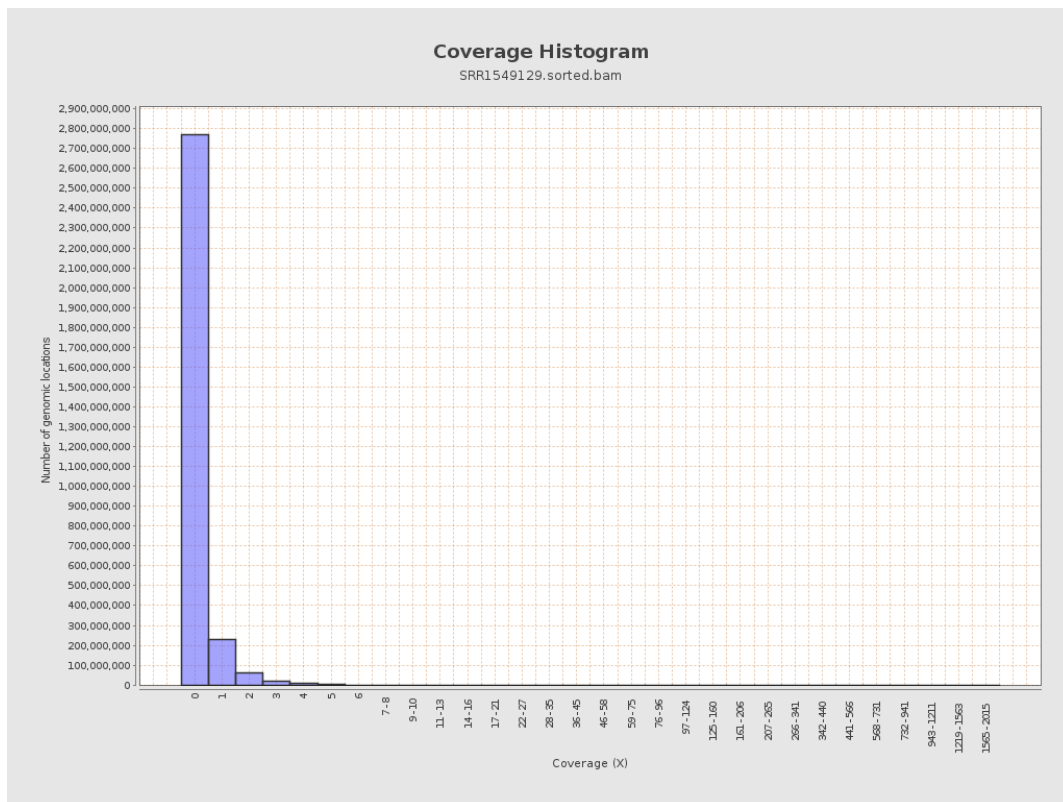
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	39066590	0.1567	1.5781
chr2	243199373	40399197	0.1661	0.8336
chr3	198022430	32321188	0.1632	0.5602
chr4	191154276	29554441	0.1546	0.58
chr5	180915260	28883638	0.1597	0.5698
chr6	171115067	27322422	0.1597	0.6218
chr7	159138663	26353976	0.1656	1.1806
chr8	146364022	23719195	0.1621	1.0247

chr9	141213431	20566914	0.1456	0.7907
chr10	135534747	23071589	0.1702	0.8177
chr11	135006516	22031901	0.1632	0.7539
chr12	133851895	22071268	0.1649	0.589
chr13	115169878	14827753	0.1287	0.4915
chr14	107349540	14828980	0.1381	0.698
chr15	102531392	14494469	0.1414	0.5104
chr16	90354753	15077676	0.1669	0.6198
chr17	81195210	14665517	0.1806	0.6471
chr18	78077248	12559312	0.1609	1.5504
chr19	59128983	11173365	0.189	1.3758
chr20	63025520	11022233	0.1749	0.6172
chr21	48129895	6334216	0.1316	0.5957
chr22	51304566	6684050	0.1303	0.5407
chrMT	16571	267320	16.1318	20.3172
chrX	155270560	14846579	0.0956	0.5395
chrY	59373566	3663376	0.0617	0.5243

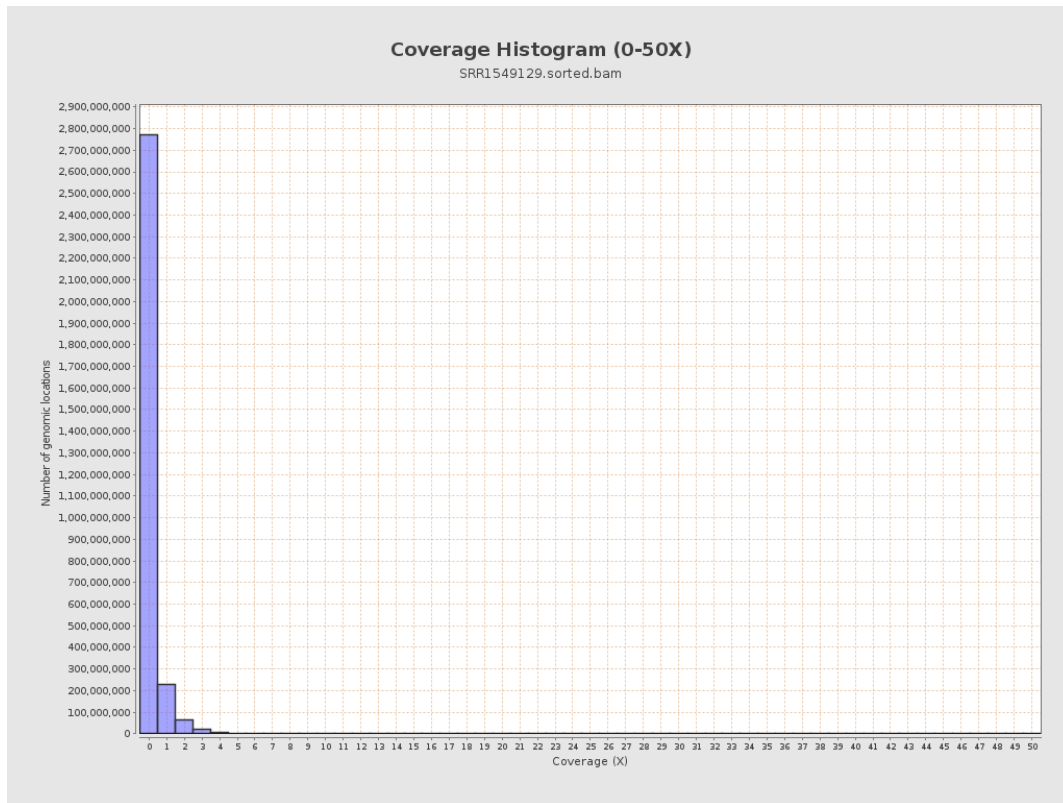
3. Results : Coverage across reference



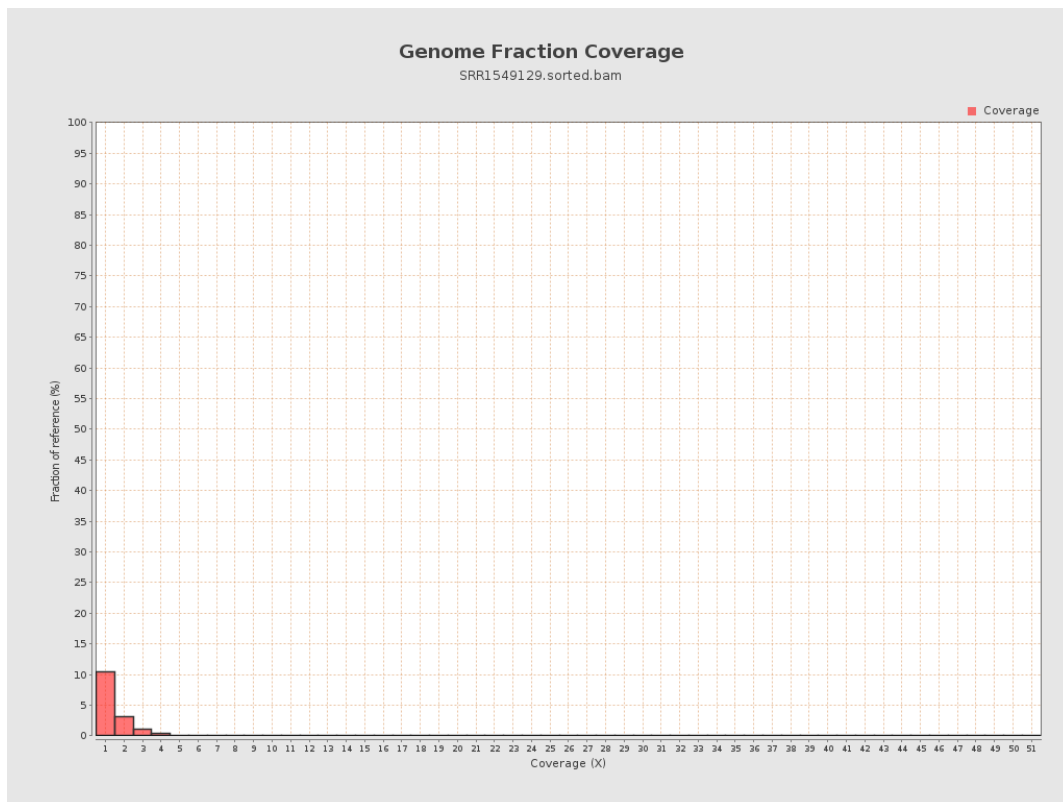
4. Results : Coverage Histogram



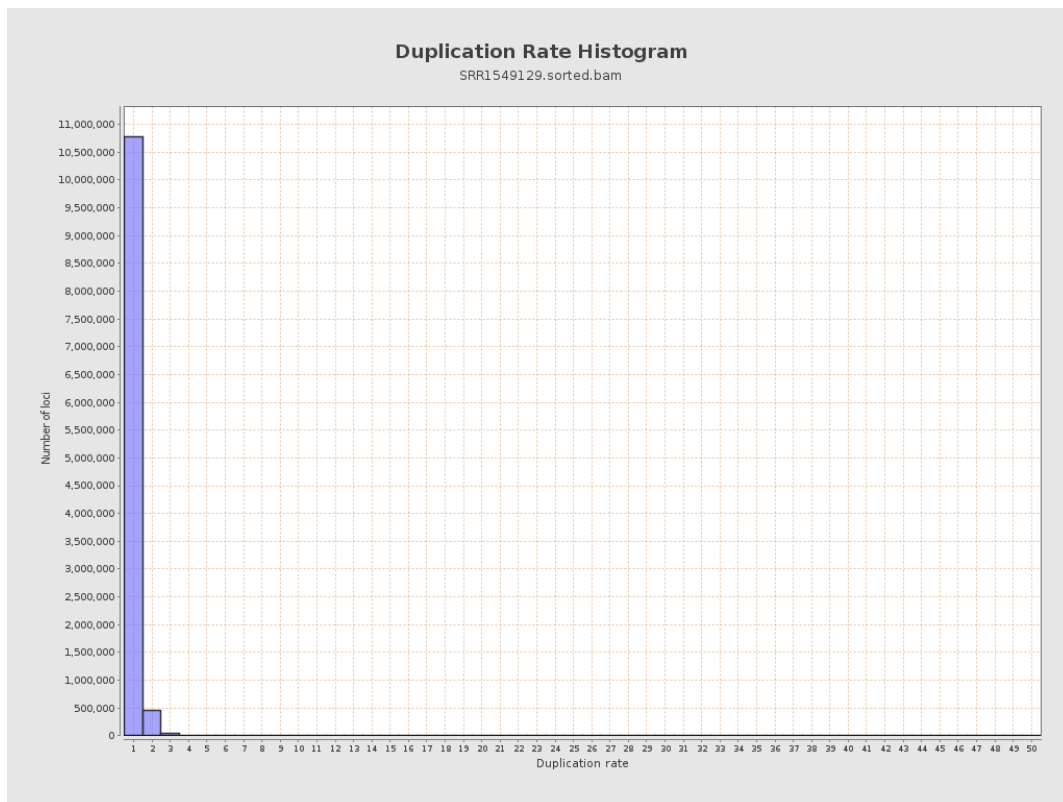
5. Results : Coverage Histogram (0-50X)



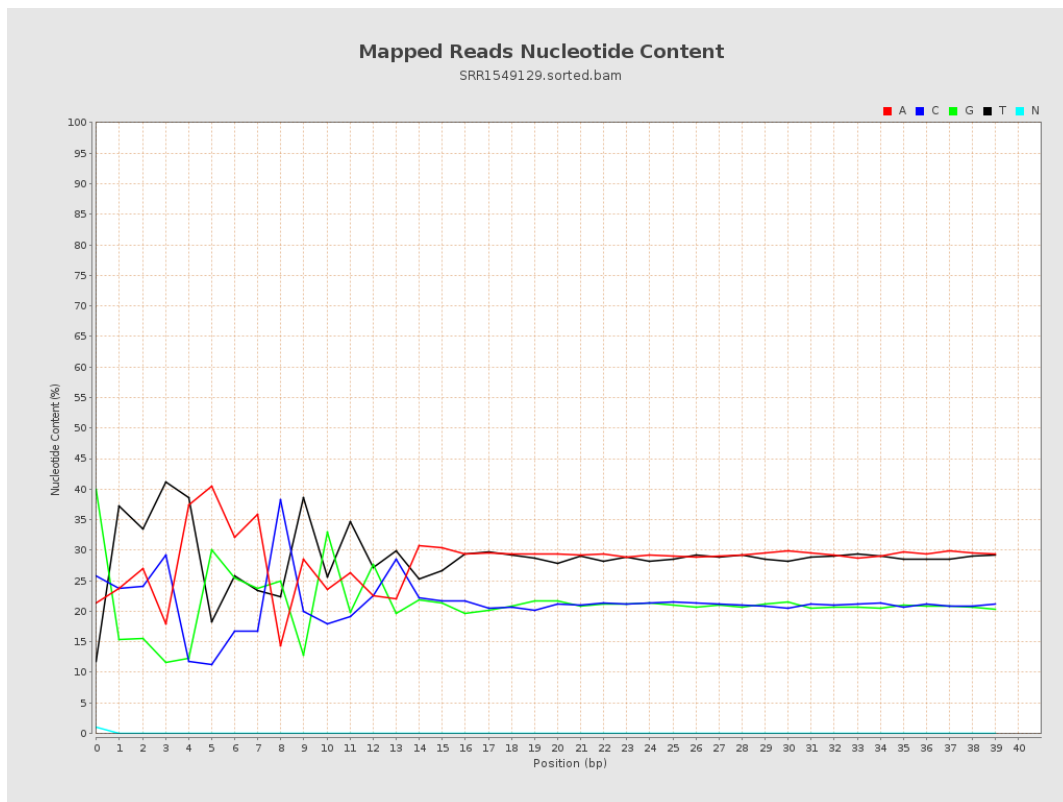
6. Results : Genome Fraction Coverage



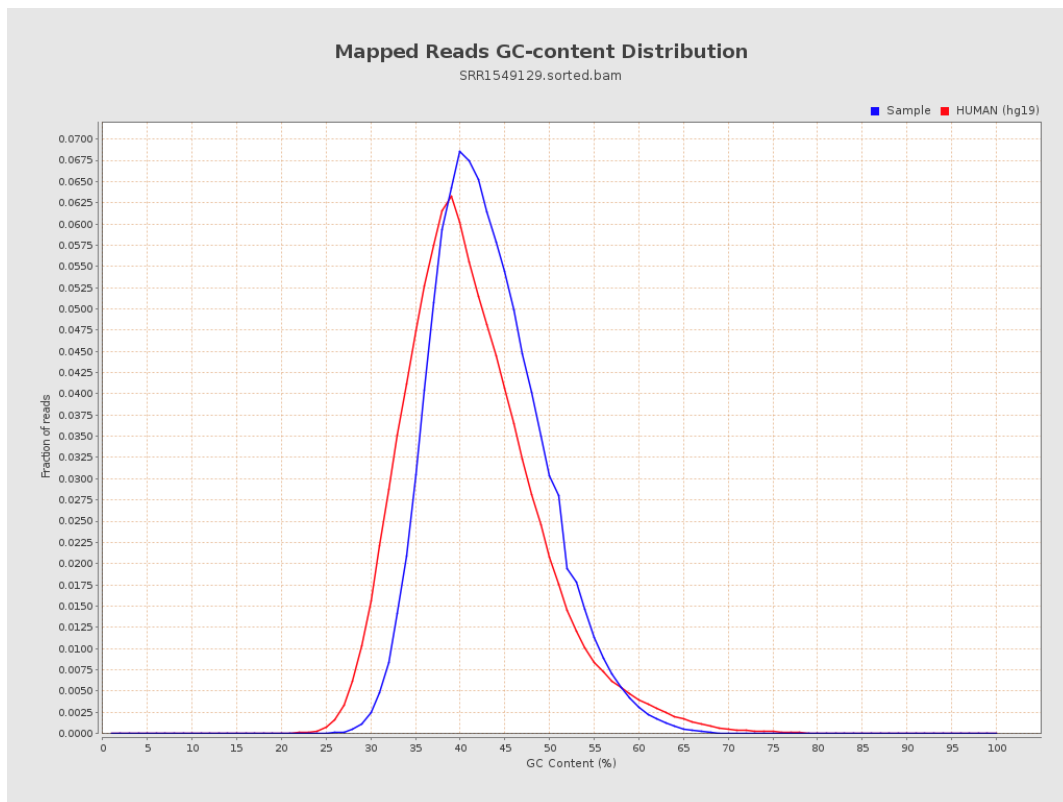
7. Results : Duplication Rate Histogram



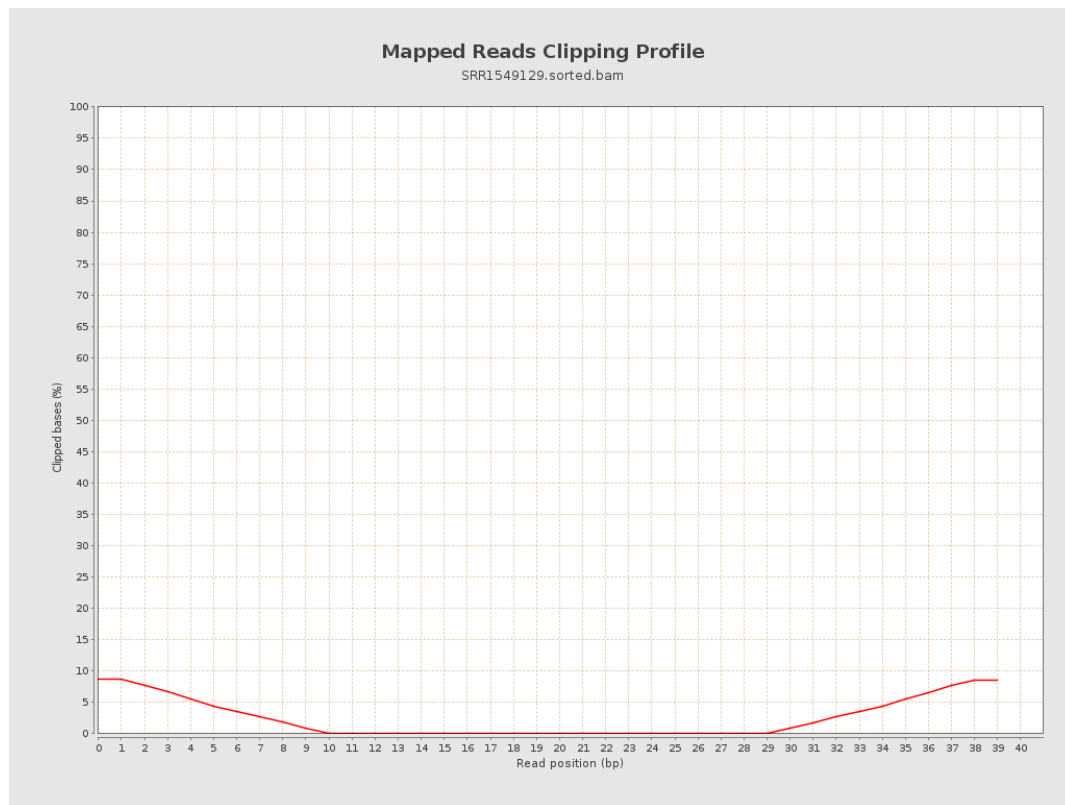
8. Results : Mapped Reads Nucleotide Content



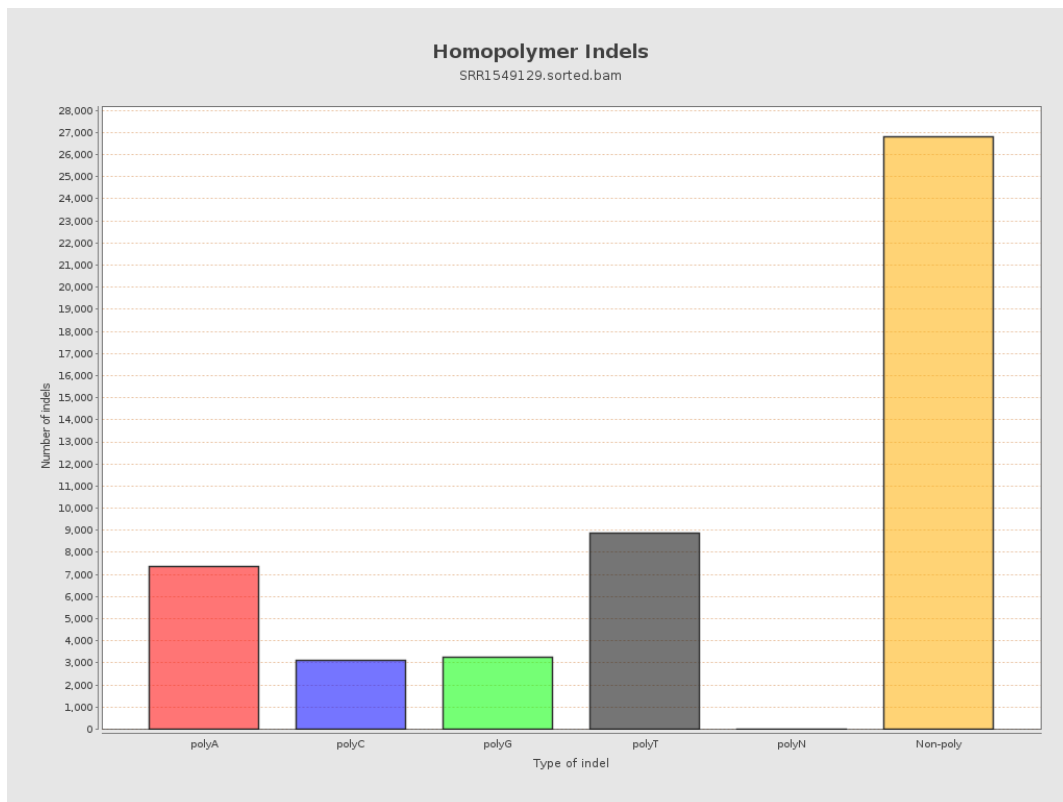
9. Results : Mapped Reads GC-content Distribution



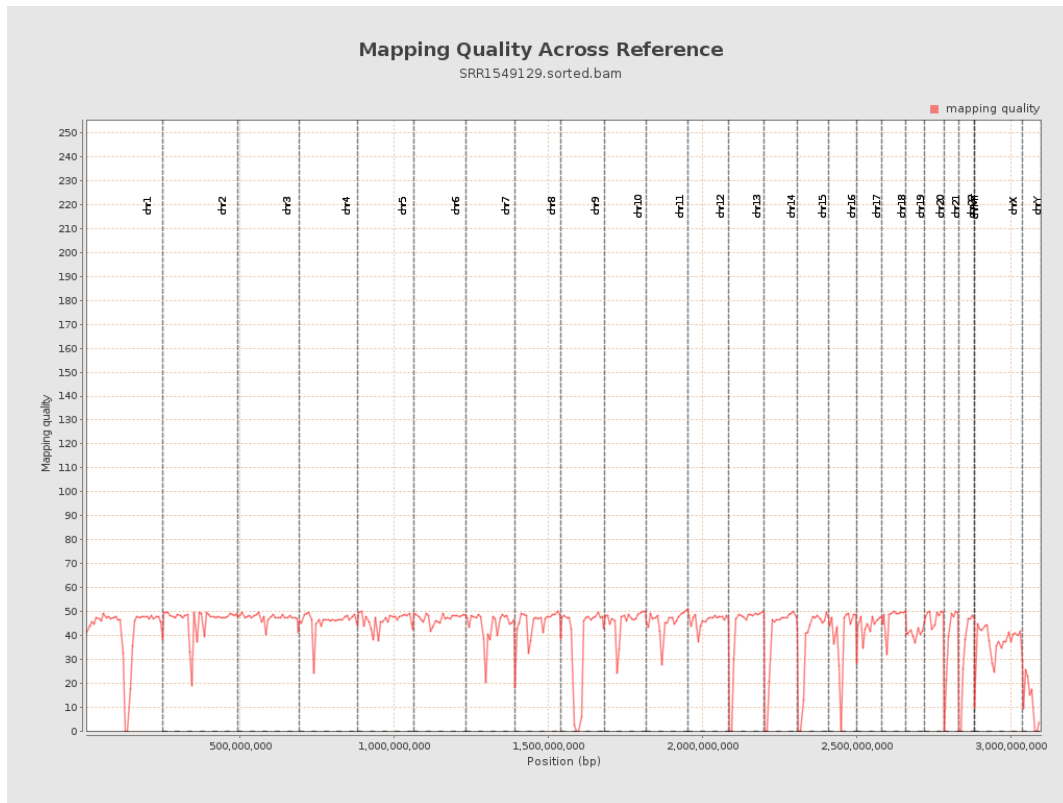
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

