

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:00:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548926.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_SRR1548926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:00:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,438,433
Mapped reads	5,605,462 / 87.06%
Unmapped reads	832,971 / 12.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	164,884 / 2.56%
Duplication rate	2.1%
Clipped reads	391,107 / 6.07%

2.2. ACGT Content

Number/percentage of A's	65,371,386 / 29.44%
Number/percentage of C's	45,557,140 / 20.52%
Number/percentage of T's	65,637,537 / 29.56%
Number/percentage of G's	45,456,118 / 20.47%
Number/percentage of N's	2,046 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0717
Standard Deviation	0.818

2.4. Mapping Quality

Mean Mapping Quality	42.7
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2.5. Mismatches and indels

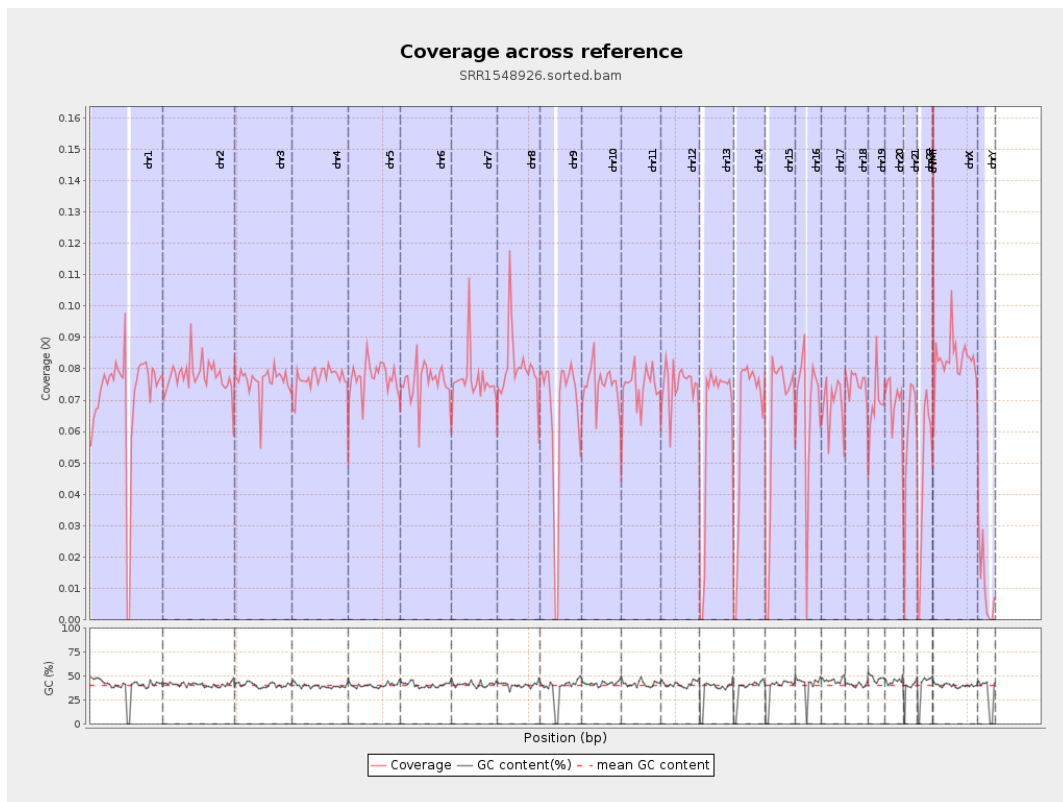
General error rate	0.27%
Mismatches	589,908
Insertions	6,854
Mapped reads with at least one insertion	0.12%
Deletions	18,477
Mapped reads with at least one deletion	0.33%
Homopolymer indels	41.59%

2.6. Chromosome stats

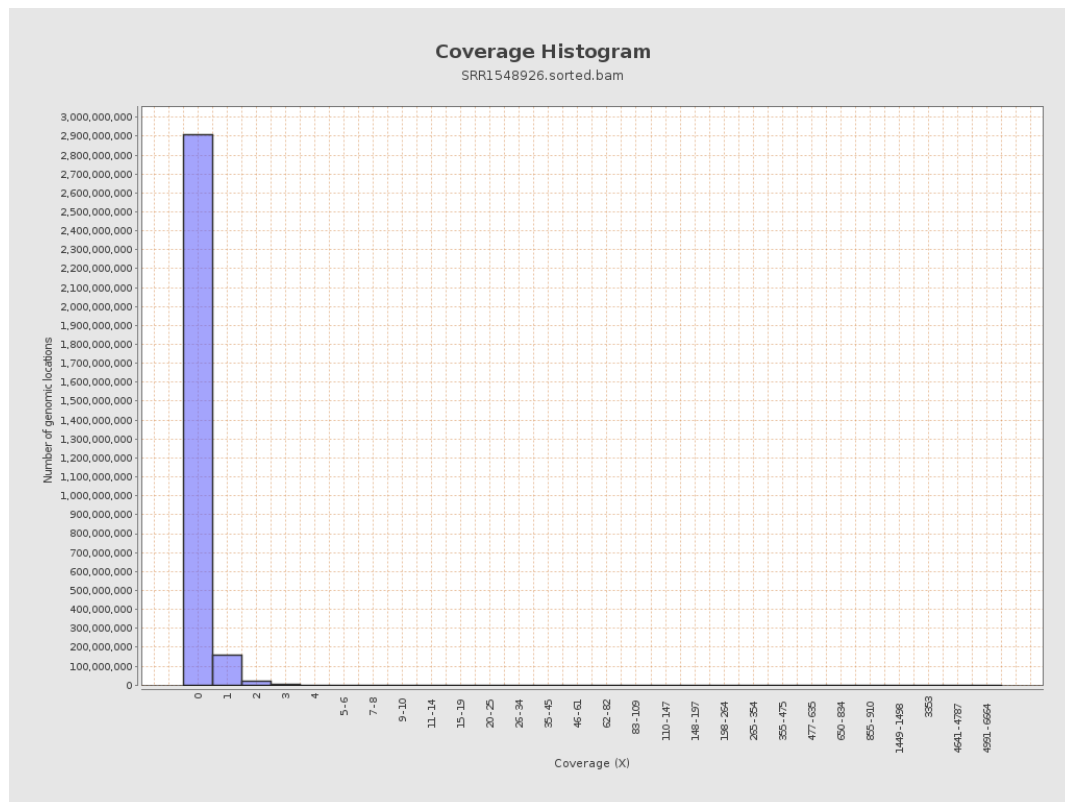
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17716645	0.0711	0.7613
chr2	243199373	18891447	0.0777	0.4125
chr3	198022430	15095582	0.0762	0.3168
chr4	191154276	14717240	0.077	0.3256
chr5	180915260	13935024	0.077	0.3221
chr6	171115067	13014003	0.0761	0.3472
chr7	159138663	12166299	0.0765	0.5742
chr8	146364022	11760667	0.0804	3.226

chr9	141213431	9275074	0.0657	0.3893
chr10	135534747	10164712	0.075	0.3893
chr11	135006516	10025216	0.0743	0.442
chr12	133851895	10041976	0.075	0.3216
chr13	115169878	7211543	0.0626	0.2835
chr14	107349540	6838340	0.0637	0.327
chr15	102531392	6466340	0.0631	0.2876
chr16	90354753	6020653	0.0666	0.3151
chr17	81195210	5611186	0.0691	0.3196
chr18	78077248	5897358	0.0755	0.6747
chr19	59128983	4105336	0.0694	0.6767
chr20	63025520	4401498	0.0698	0.311
chr21	48129895	2805223	0.0583	0.3001
chr22	51304566	2366381	0.0461	0.2825
chrMT	16571	9319	0.5624	1.0725
chrX	155270560	12878615	0.0829	0.383
chrY	59373566	633184	0.0107	0.152

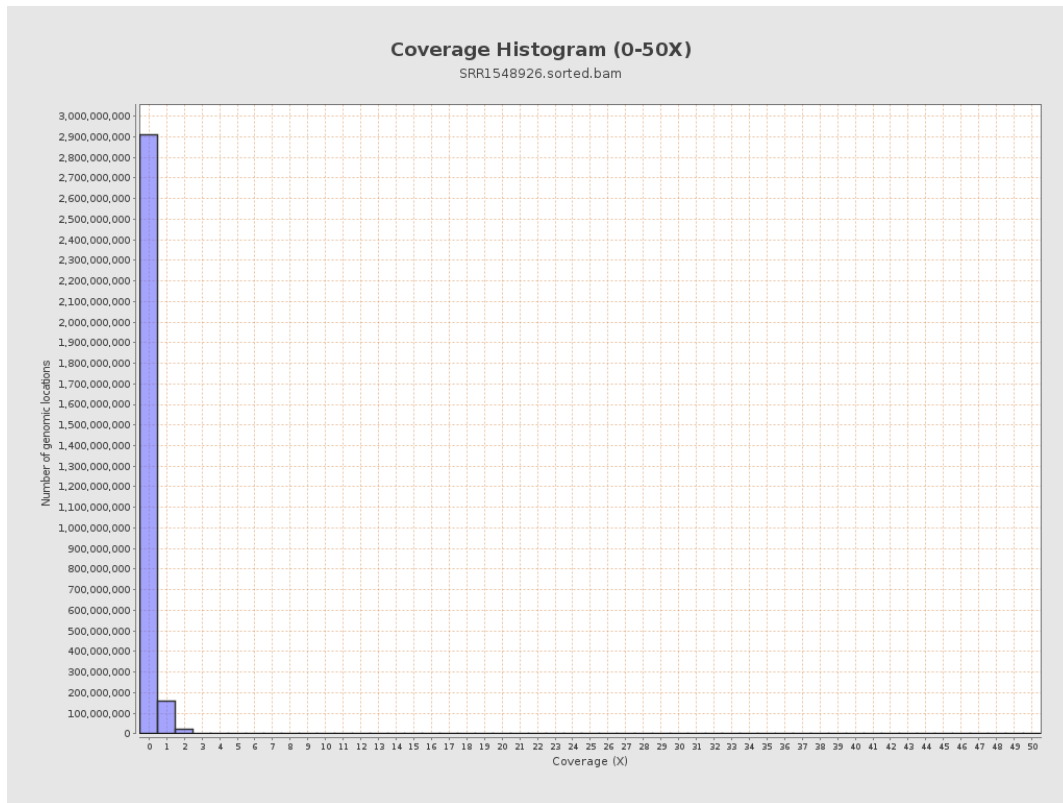
3. Results : Coverage across reference



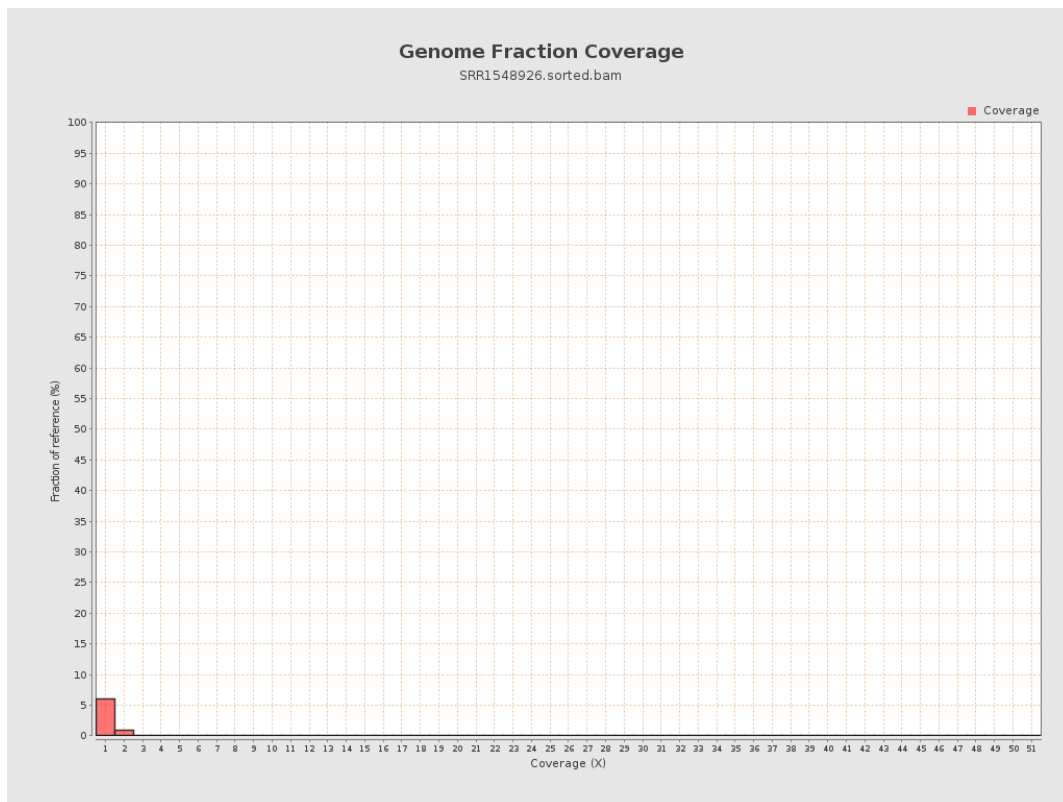
4. Results : Coverage Histogram



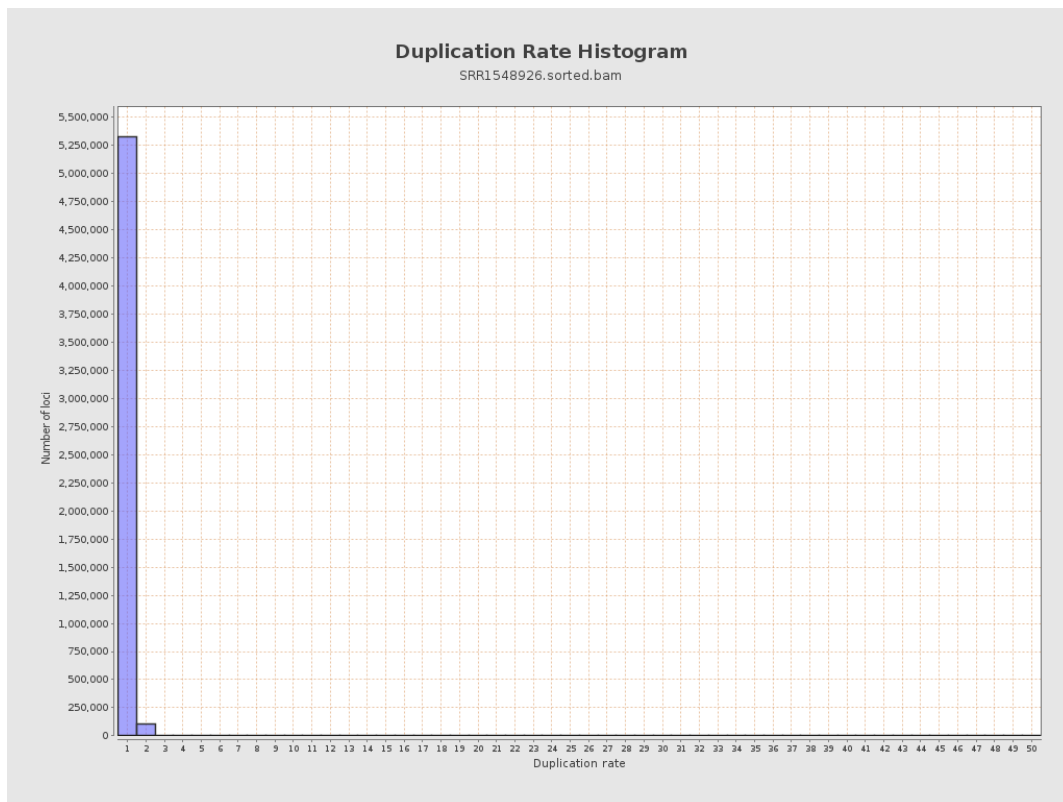
5. Results : Coverage Histogram (0-50X)



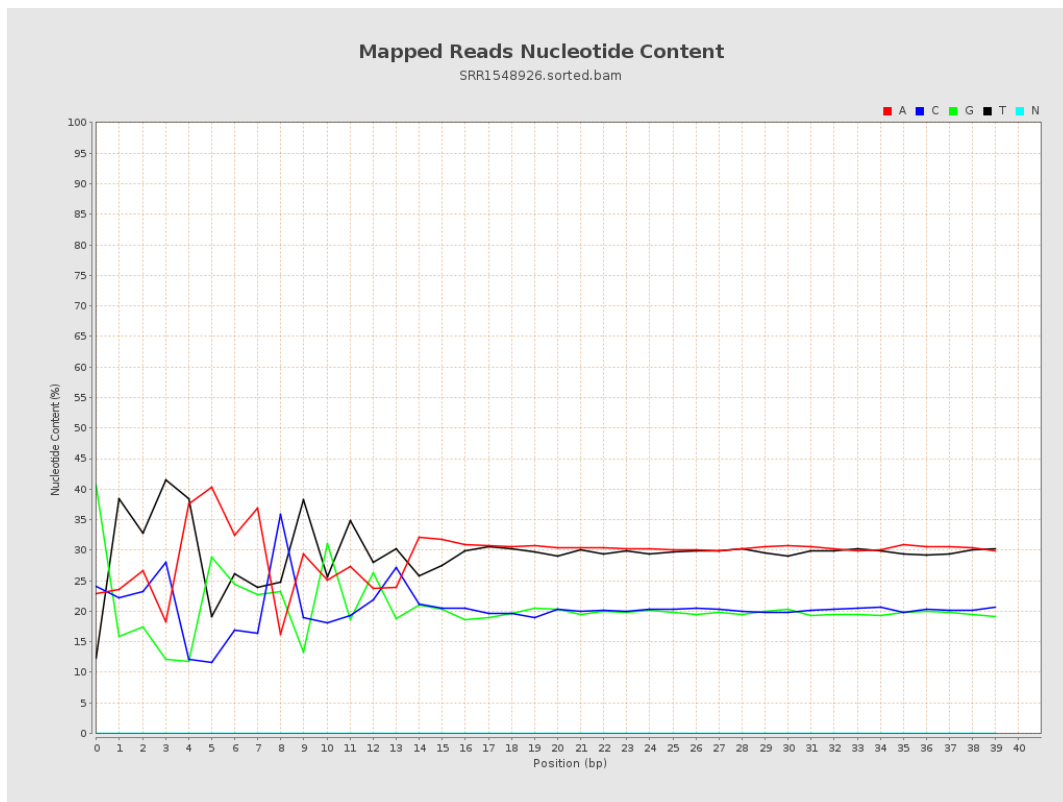
6. Results : Genome Fraction Coverage



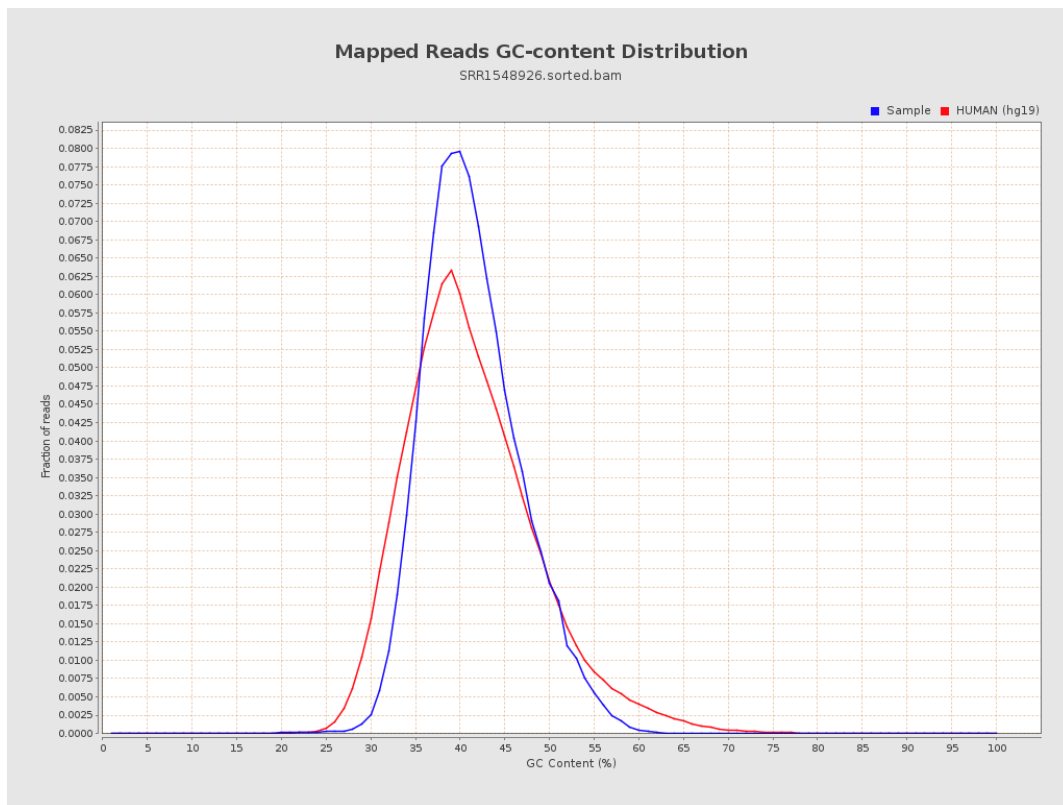
7. Results : Duplication Rate Histogram



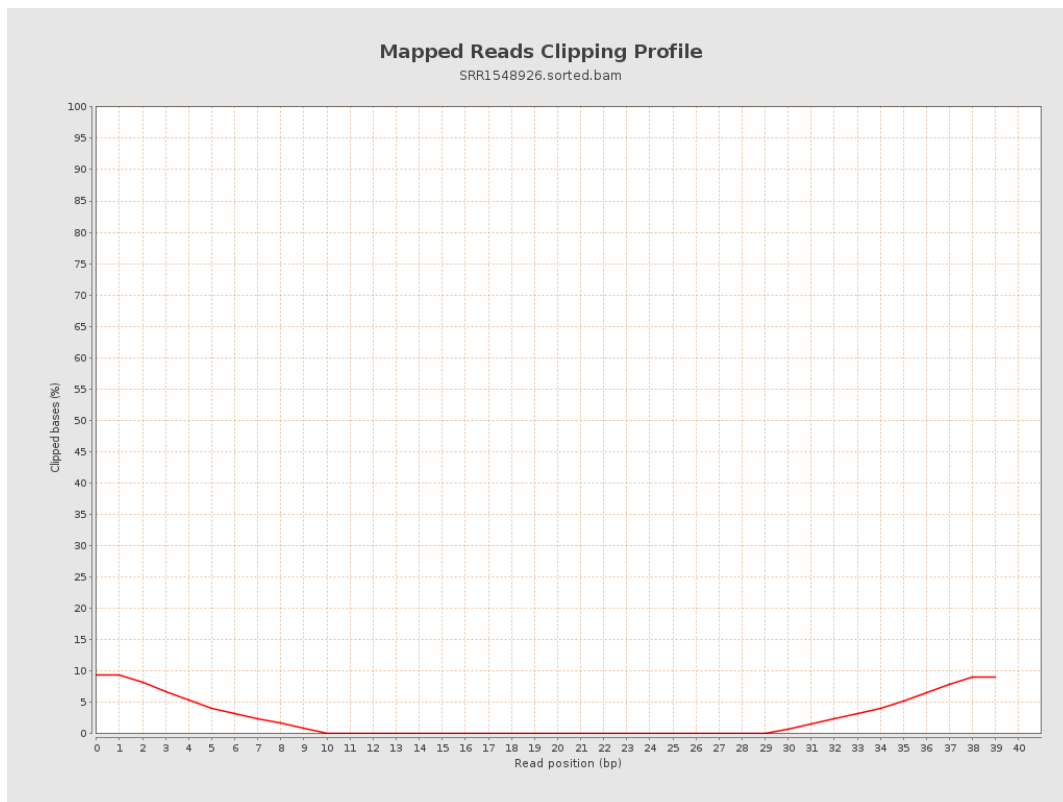
8. Results : Mapped Reads Nucleotide Content



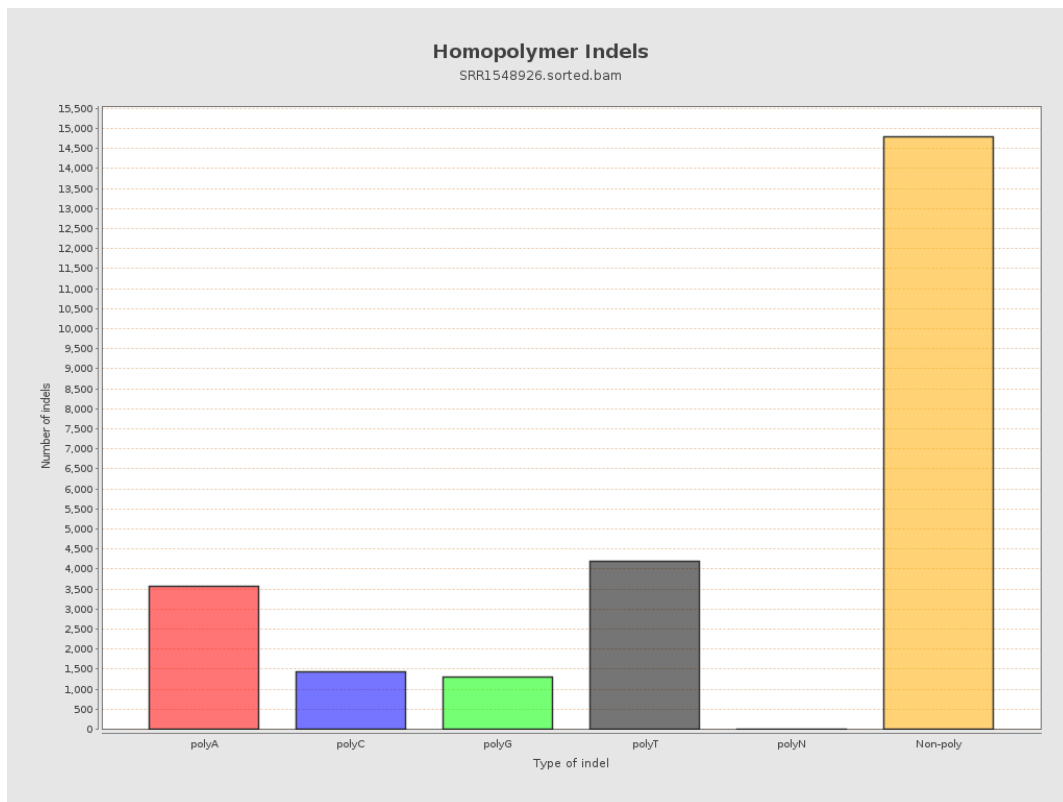
9. Results : Mapped Reads GC-content Distribution



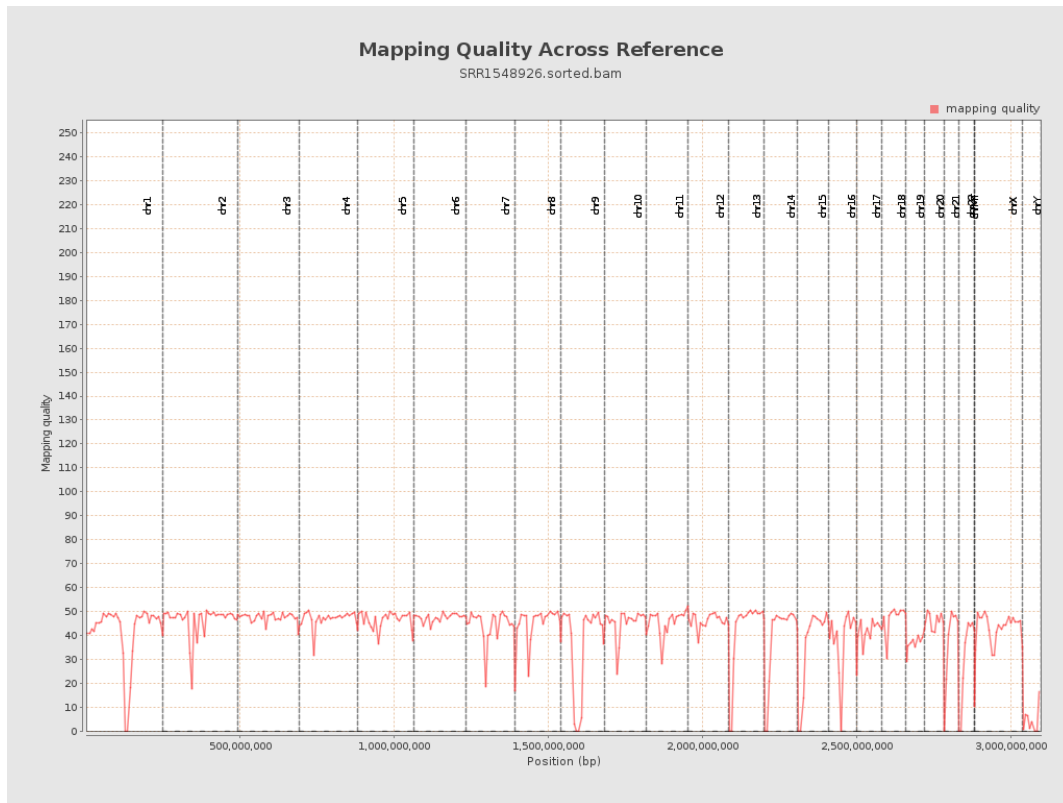
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

