

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082469.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_SRR3082469 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082469.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:20:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082469.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,005,763
Mapped reads	1,817,169 / 90.6%
Unmapped reads	188,594 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,594 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	58,502 / 2.92%
Duplication rate	2.46%
Clipped reads	711,534 / 35.47%

2.2. ACGT Content

Number/percentage of A's	36,080,437 / 29%
Number/percentage of C's	23,070,382 / 18.54%
Number/percentage of T's	38,348,245 / 30.82%
Number/percentage of G's	26,911,103 / 21.63%
Number/percentage of N's	2,600 / 0%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3486
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2.4. Mapping Quality

Mean Mapping Quality	46.76
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2.5. Mismatches and indels

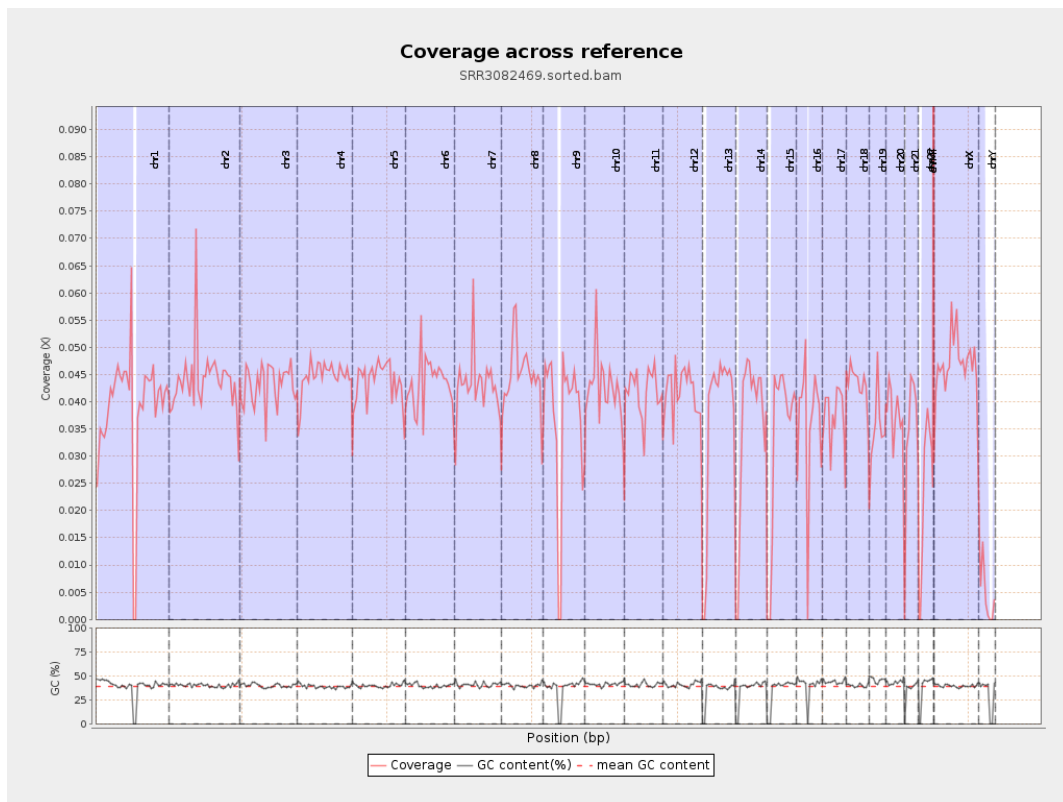
General error rate	0.85%
Mismatches	1,038,616
Insertions	10,178
Mapped reads with at least one insertion	0.56%
Deletions	27,555
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.52%

2.6. Chromosome stats

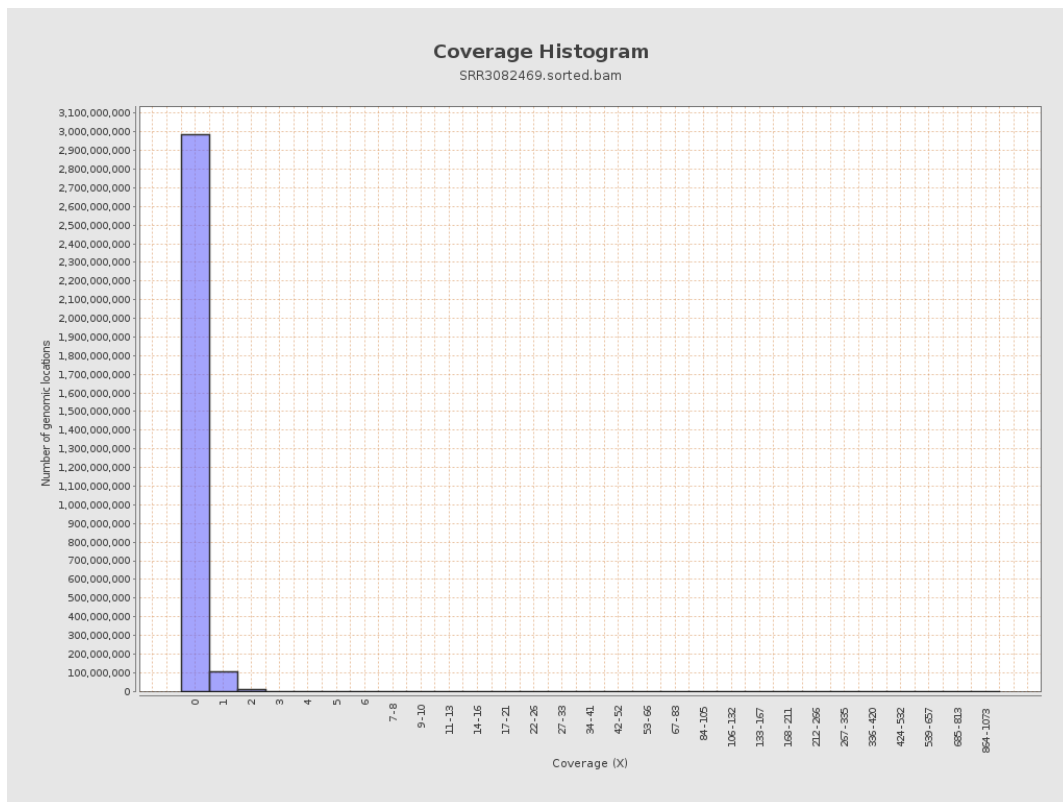
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9723334	0.039	0.5806
chr2	243199373	10695984	0.044	0.3908
chr3	198022430	8549263	0.0432	0.2255
chr4	191154276	8530703	0.0446	0.2351
chr5	180915260	7934231	0.0439	0.2273
chr6	171115067	7407968	0.0433	0.2576
chr7	159138663	6905196	0.0434	0.403

chr8	146364022	6545113	0.0447	0.6846
chr9	141213431	5234920	0.0371	0.3074
chr10	135534747	5779500	0.0426	0.3138
chr11	135006516	5618657	0.0416	0.2798
chr12	133851895	5575009	0.0417	0.2232
chr13	115169878	4194634	0.0364	0.2059
chr14	107349540	3815315	0.0355	0.2192
chr15	102531392	3453291	0.0337	0.2011
chr16	90354753	3265919	0.0361	0.229
chr17	81195210	2998150	0.0369	0.2258
chr18	78077248	3398084	0.0435	0.5345
chr19	59128983	2098765	0.0355	0.4637
chr20	63025520	2338406	0.0371	0.2131
chr21	48129895	1644176	0.0342	0.21
chr22	51304566	1209057	0.0236	0.1651
chrMT	16571	4189	0.2528	0.5537
chrX	155270560	7255630	0.0467	0.2535
chrY	59373566	282163	0.0048	0.1087

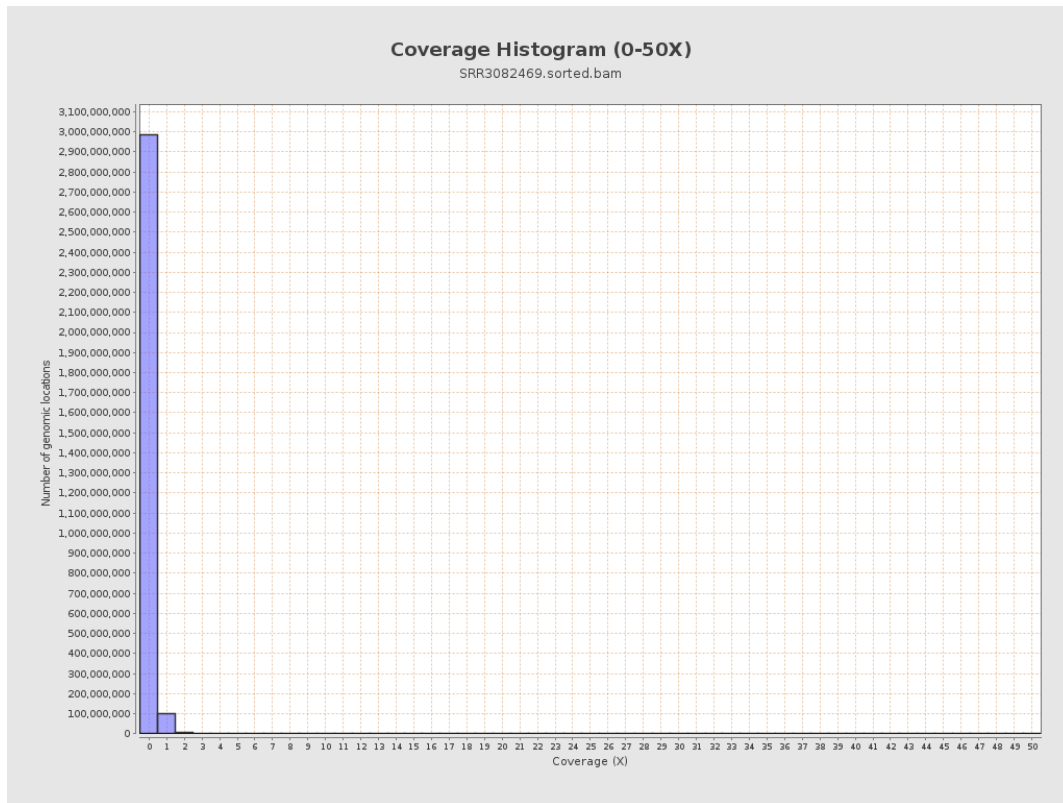
3. Results : Coverage across reference



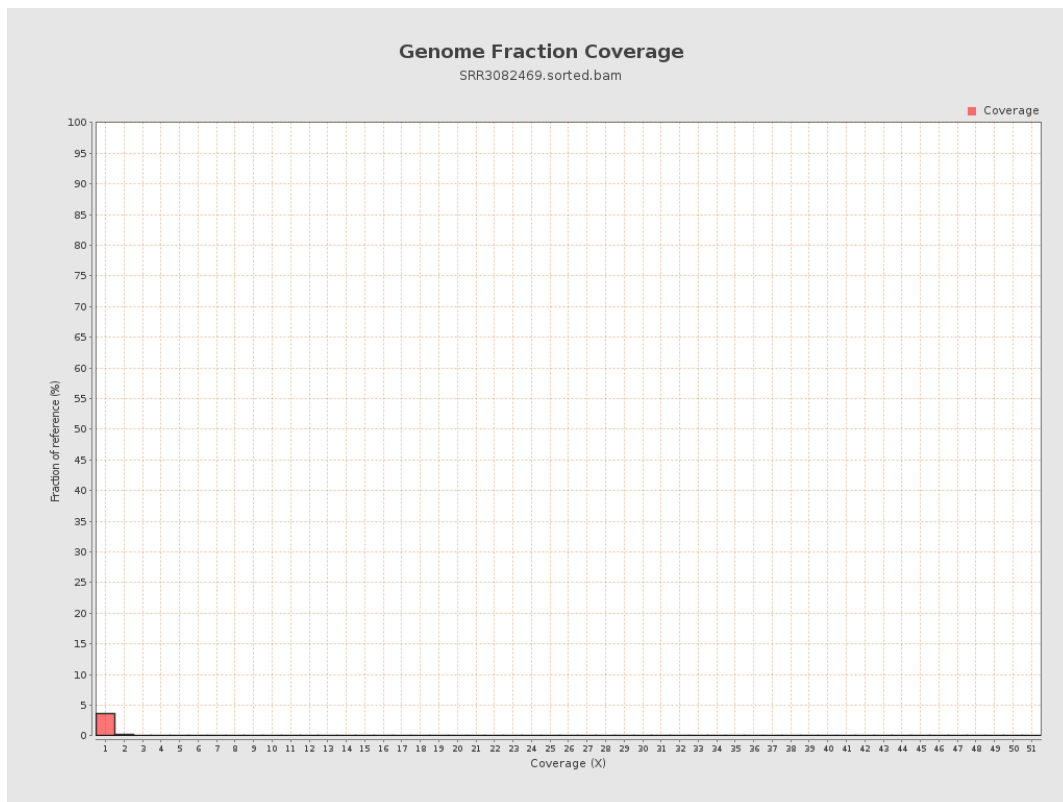
4. Results : Coverage Histogram



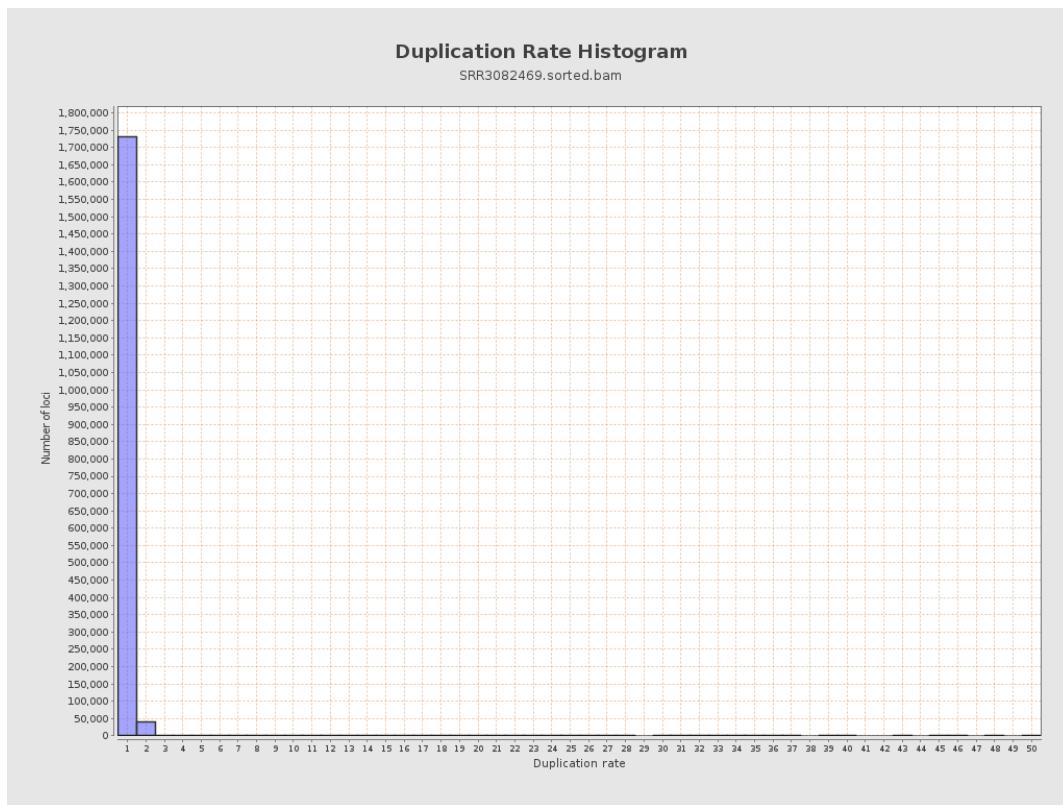
5. Results : Coverage Histogram (0-50X)



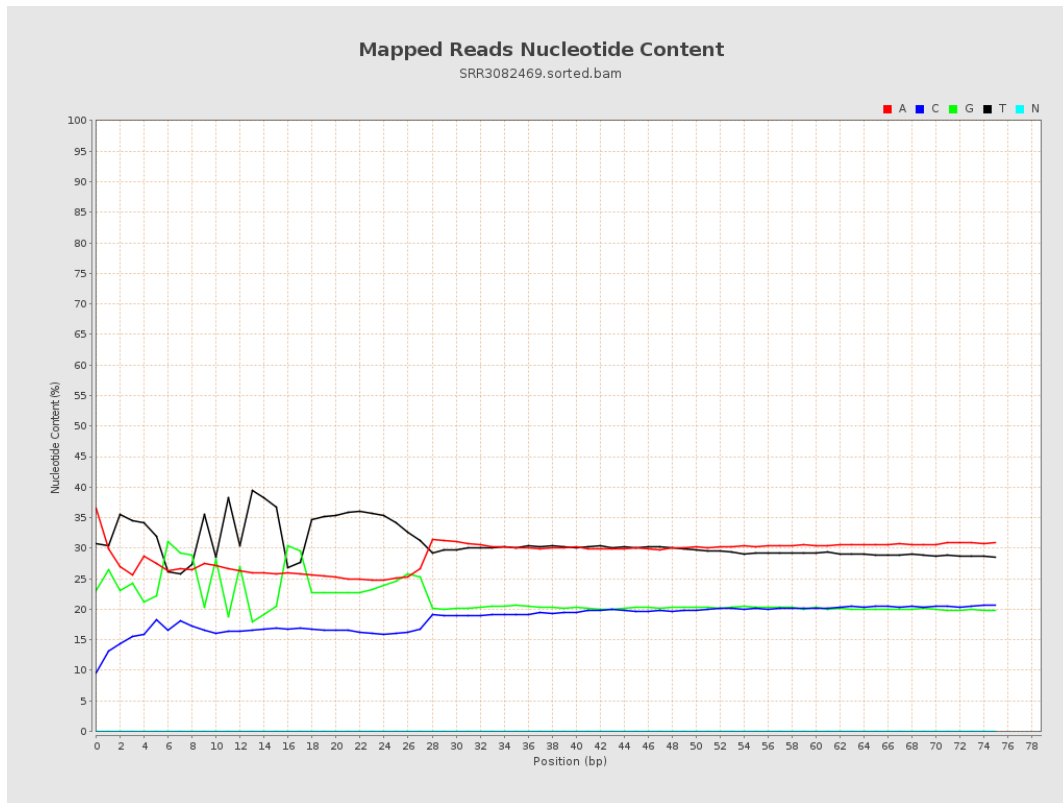
6. Results : Genome Fraction Coverage



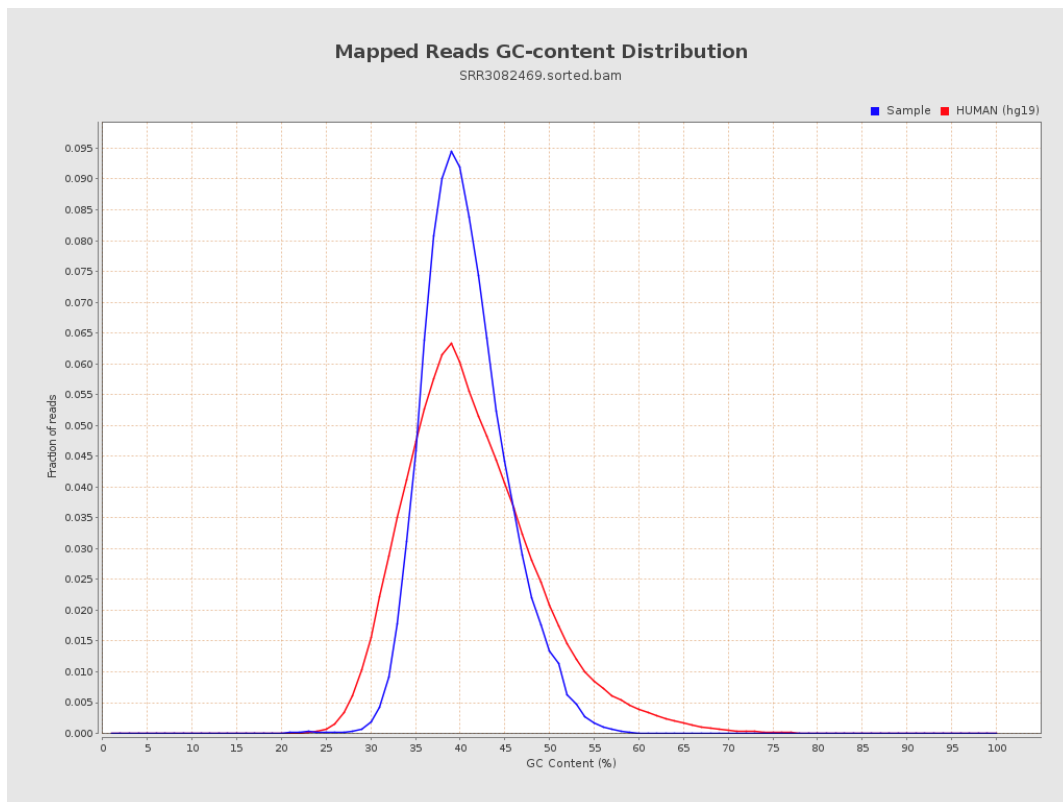
7. Results : Duplication Rate Histogram



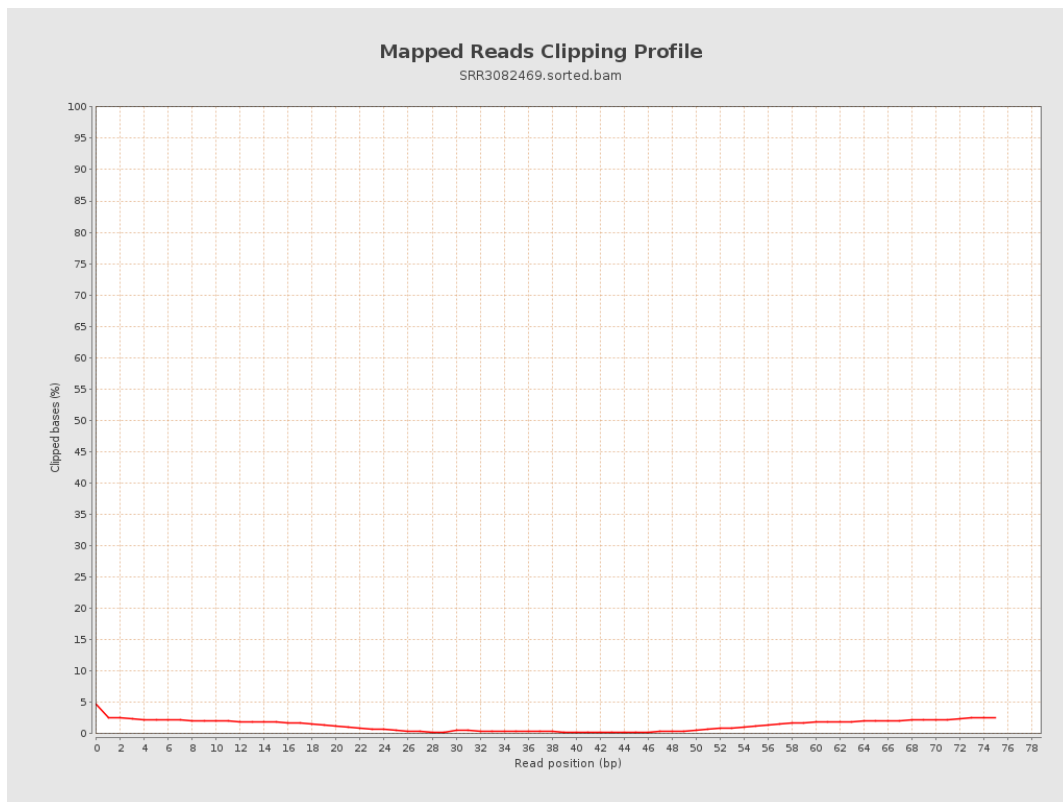
8. Results : Mapped Reads Nucleotide Content



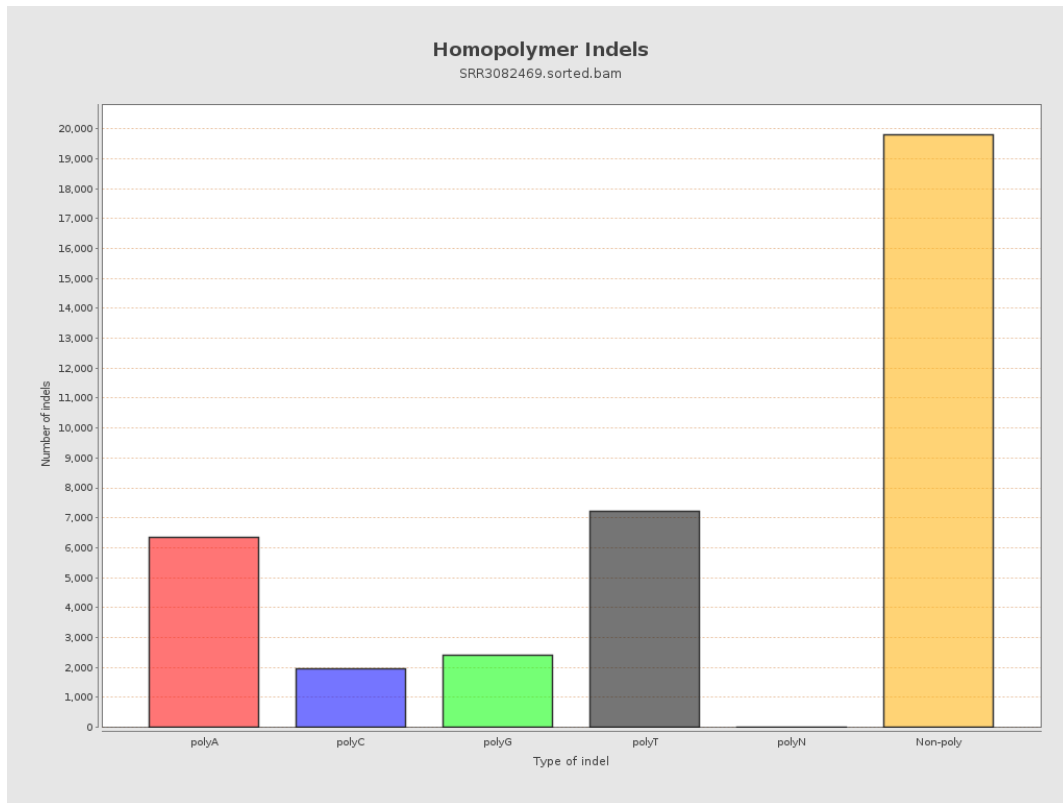
9. Results : Mapped Reads GC-content Distribution



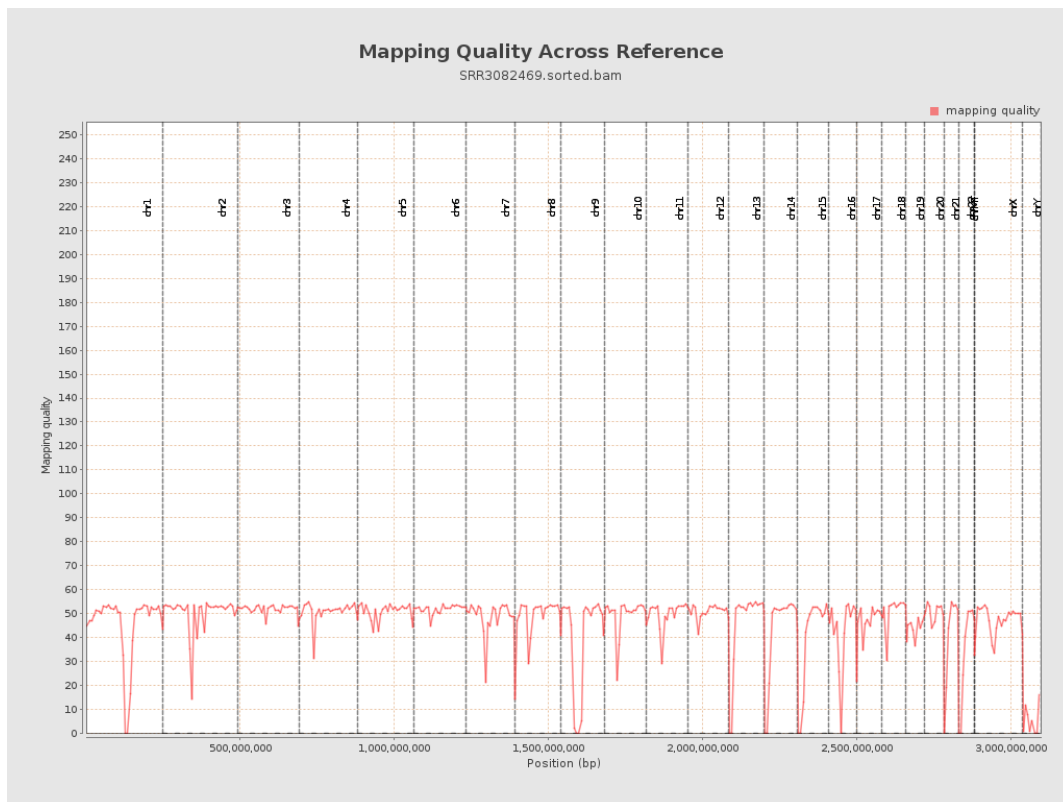
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

