

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:24:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240226.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_SRR6240226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240226.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:24:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,778,129
Mapped reads	1,506,059 / 84.7%
Unmapped reads	272,070 / 15.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,534 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	163,993 / 9.22%
Duplication rate	8.62%
Clipped reads	785,768 / 44.19%

2.2. ACGT Content

Number/percentage of A's	27,250,772 / 27.9%
Number/percentage of C's	17,650,756 / 18.07%
Number/percentage of T's	31,291,850 / 32.04%
Number/percentage of G's	21,447,153 / 21.96%
Number/percentage of N's	24,599 / 0.03%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3654
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2.4. Mapping Quality

Mean Mapping Quality	46.45
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2.5. Mismatches and indels

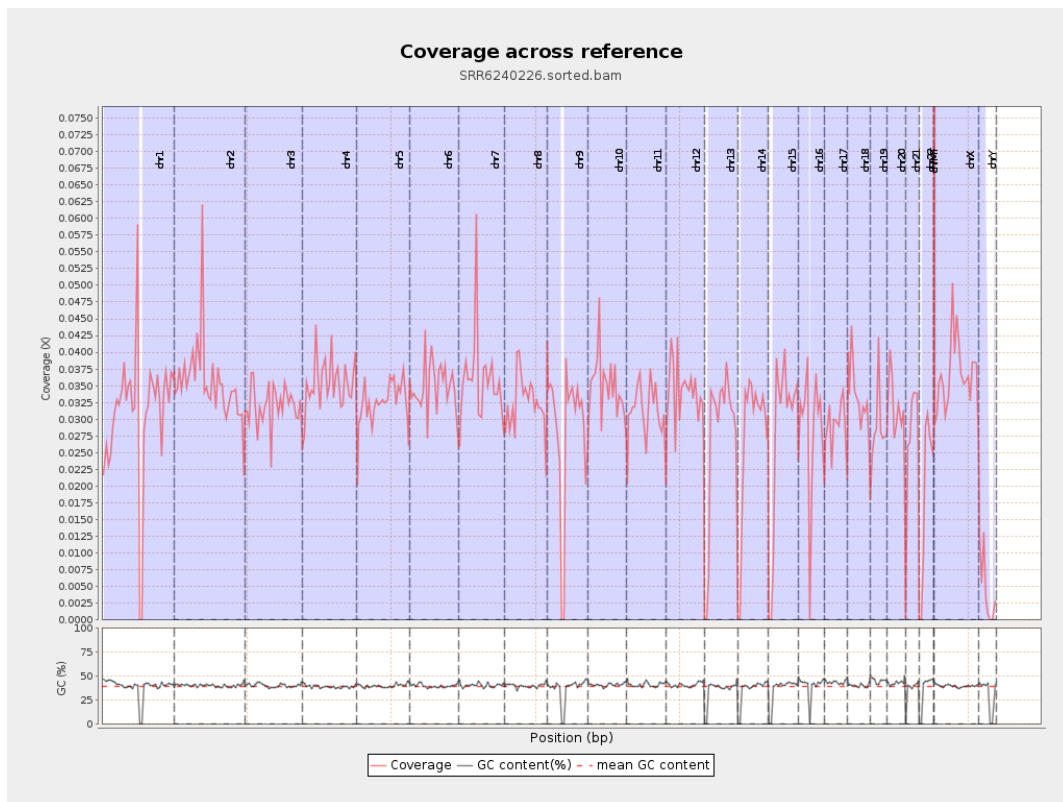
General error rate	0.79%
Mismatches	759,253
Insertions	7,236
Mapped reads with at least one insertion	0.48%
Deletions	22,273
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.4%

2.6. Chromosome stats

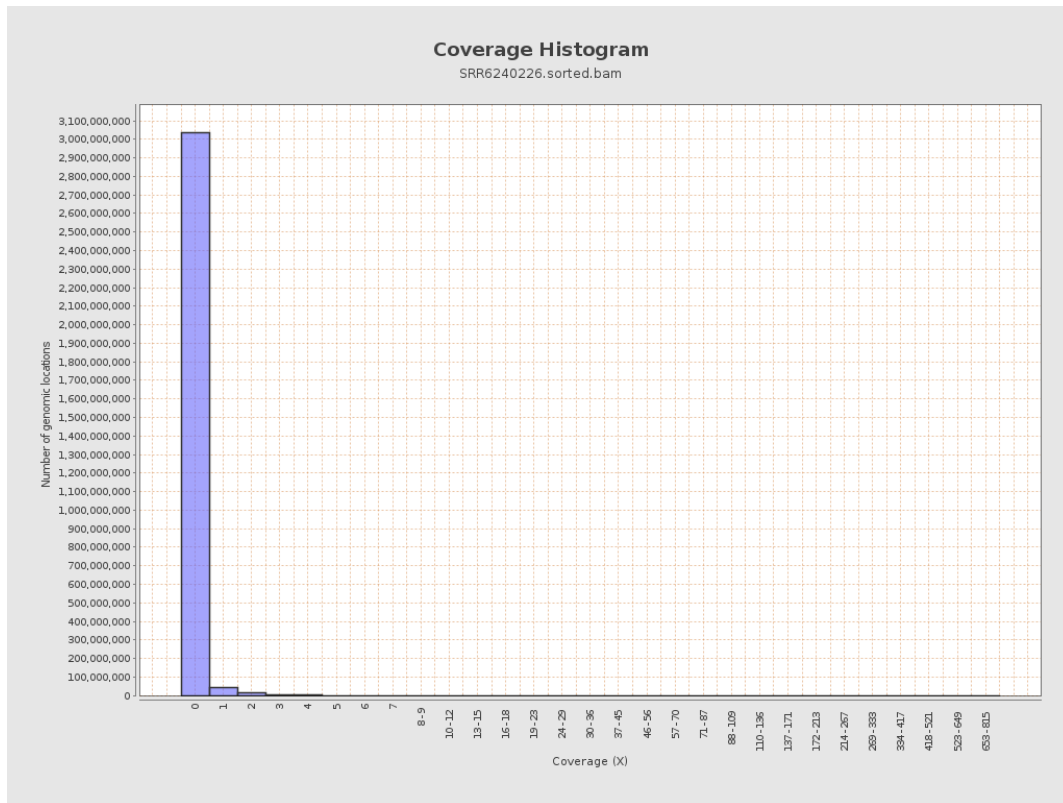
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7691351	0.0309	0.6136
chr2	243199373	8624124	0.0355	0.4007
chr3	198022430	6354437	0.0321	0.2609
chr4	191154276	6730472	0.0352	0.2831
chr5	180915260	5934477	0.0328	0.2655
chr6	171115067	5961330	0.0348	0.3005
chr7	159138663	5711488	0.0359	0.4877

chr8	146364022	4743158	0.0324	0.5523
chr9	141213431	4006061	0.0284	0.3218
chr10	135534747	4723204	0.0348	0.3224
chr11	135006516	4244947	0.0314	0.3041
chr12	133851895	4577636	0.0342	0.2741
chr13	115169878	3114782	0.027	0.2423
chr14	107349540	2925825	0.0273	0.254
chr15	102531392	2863809	0.0279	0.2466
chr16	90354753	2527538	0.028	0.2498
chr17	81195210	2356491	0.029	0.2567
chr18	78077248	2594958	0.0332	0.5629
chr19	59128983	1704087	0.0288	0.4133
chr20	63025520	1994821	0.0317	0.2661
chr21	48129895	1311634	0.0273	0.246
chr22	51304566	994402	0.0194	0.1957
chrMT	16571	22150	1.3367	1.9081
chrX	155270560	5733411	0.0369	0.2974
chrY	59373566	256871	0.0043	0.1029

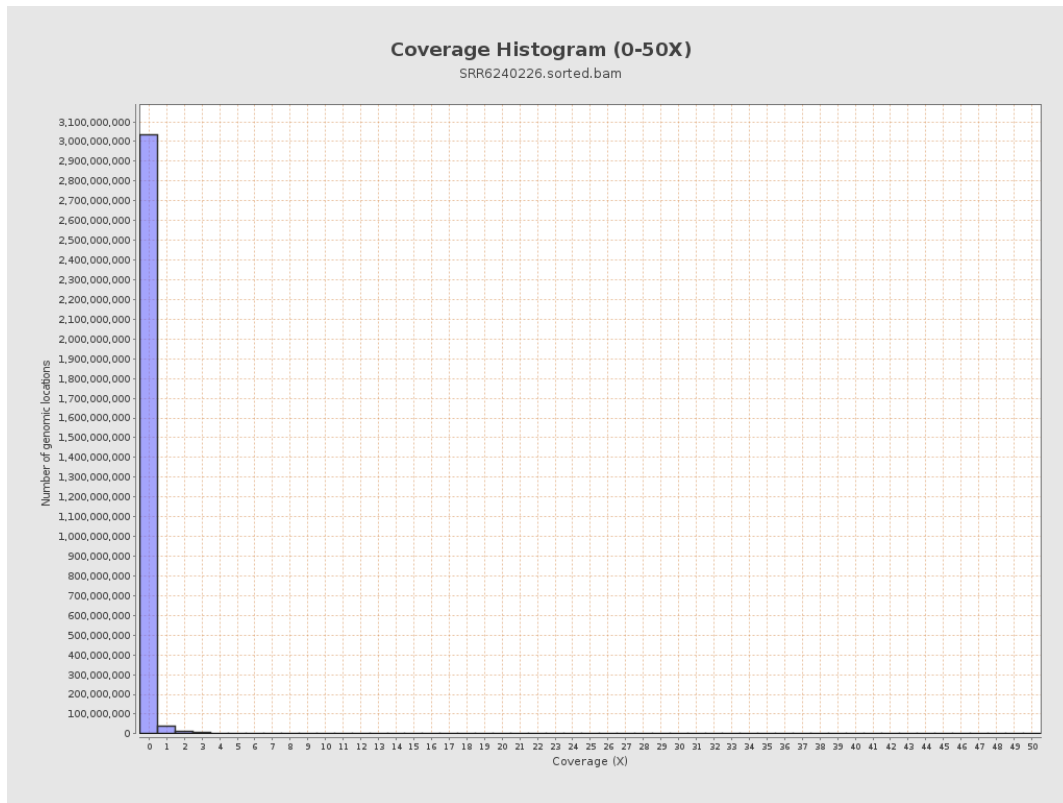
3. Results : Coverage across reference



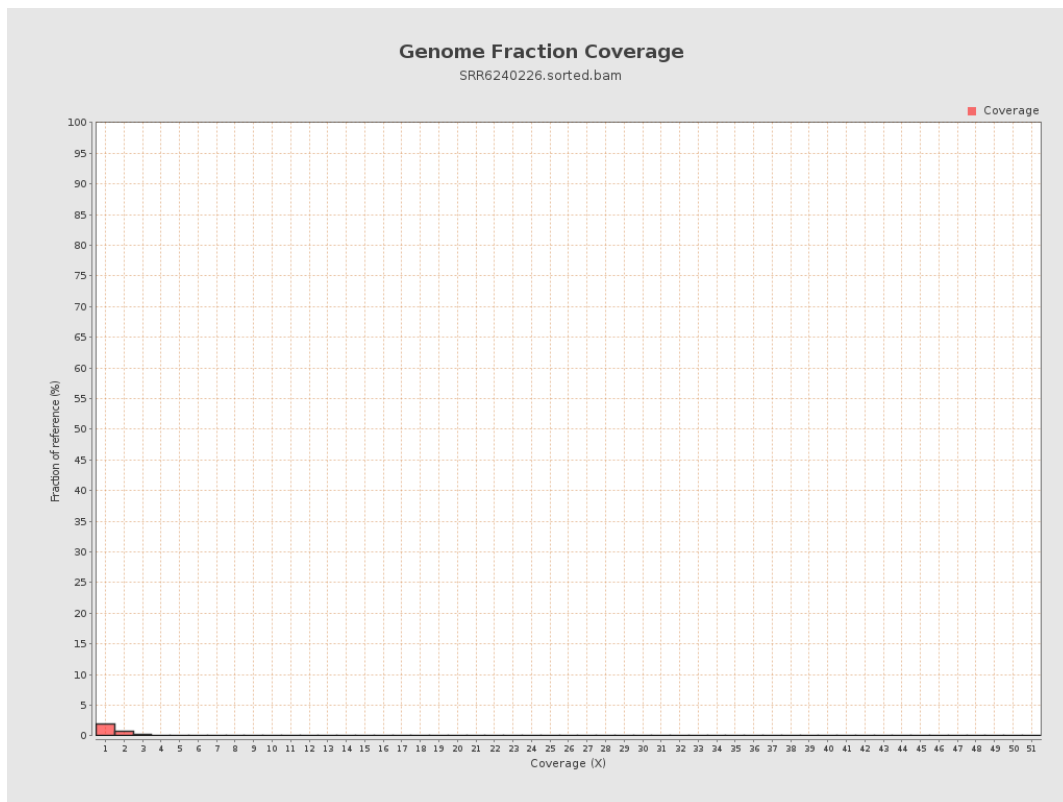
4. Results : Coverage Histogram



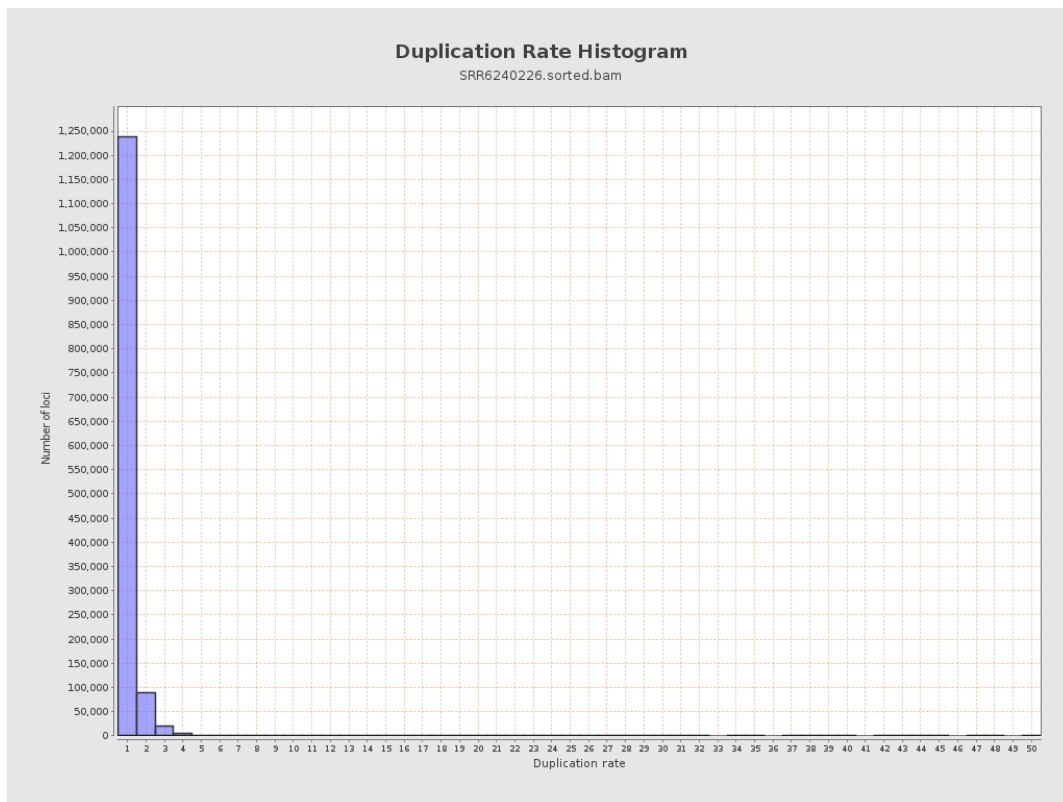
5. Results : Coverage Histogram (0-50X)



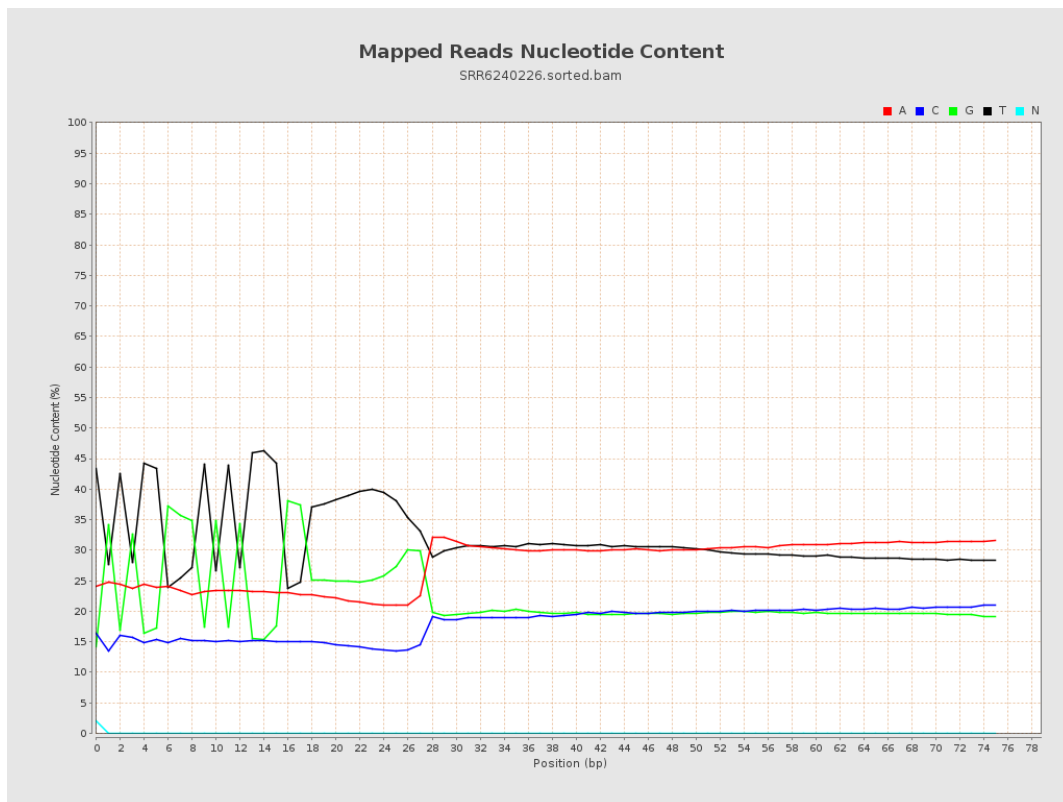
6. Results : Genome Fraction Coverage



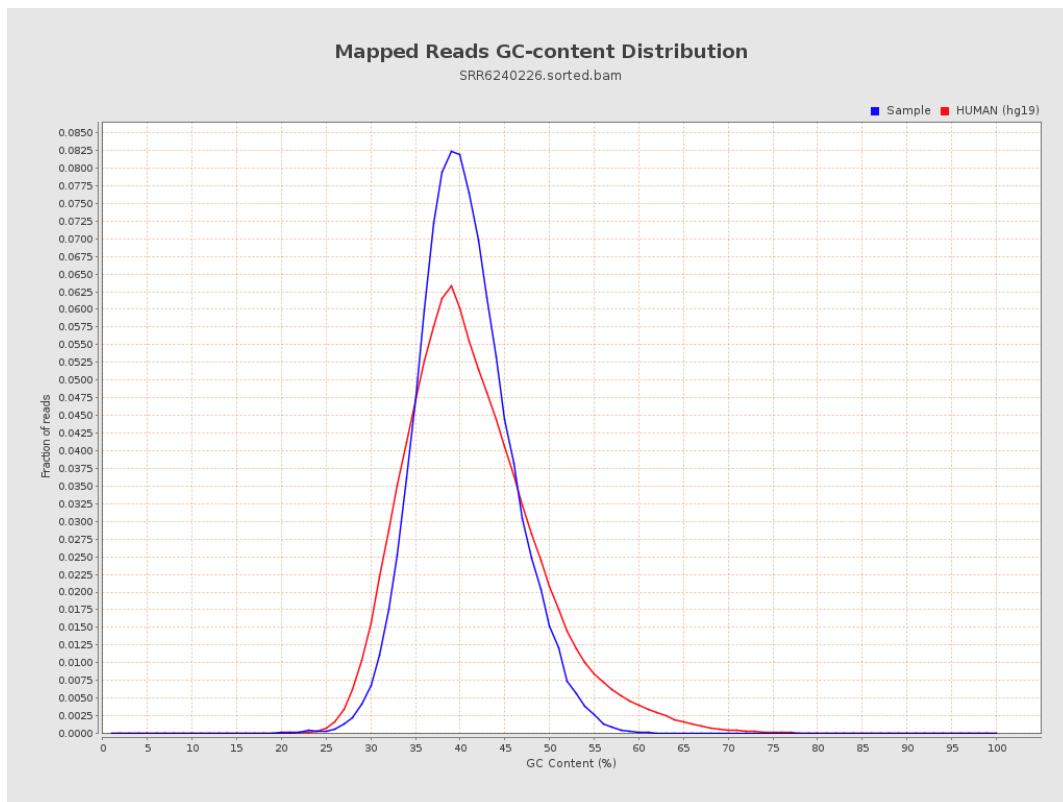
7. Results : Duplication Rate Histogram



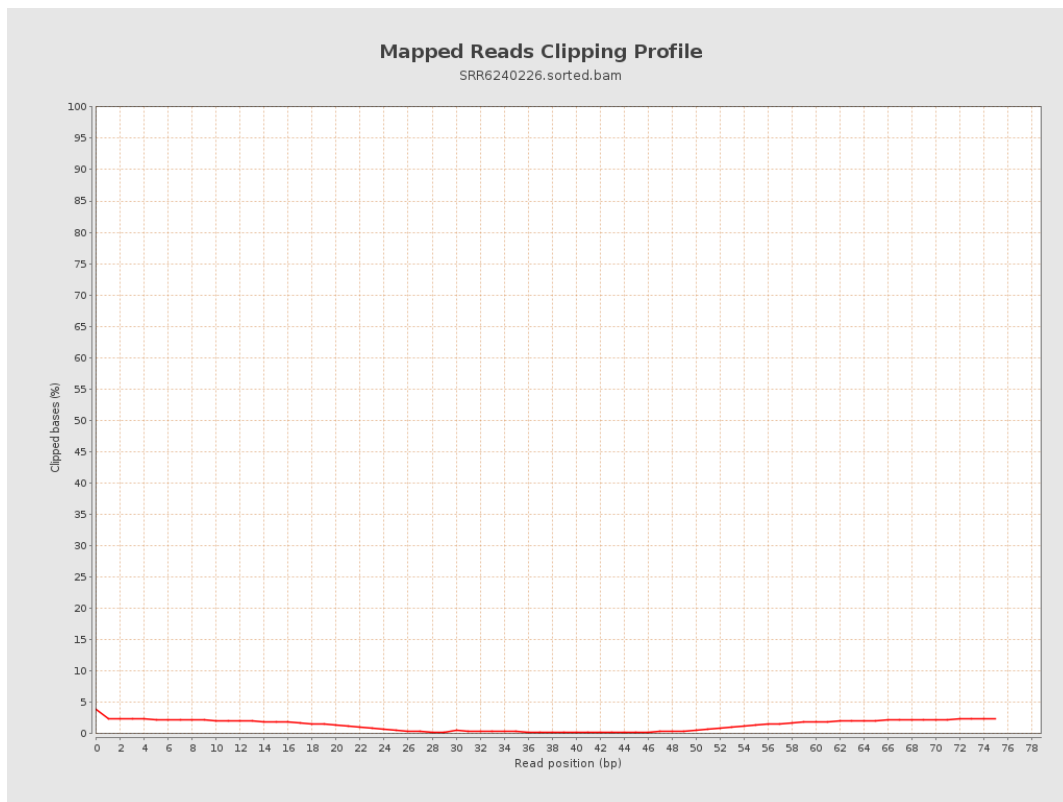
8. Results : Mapped Reads Nucleotide Content



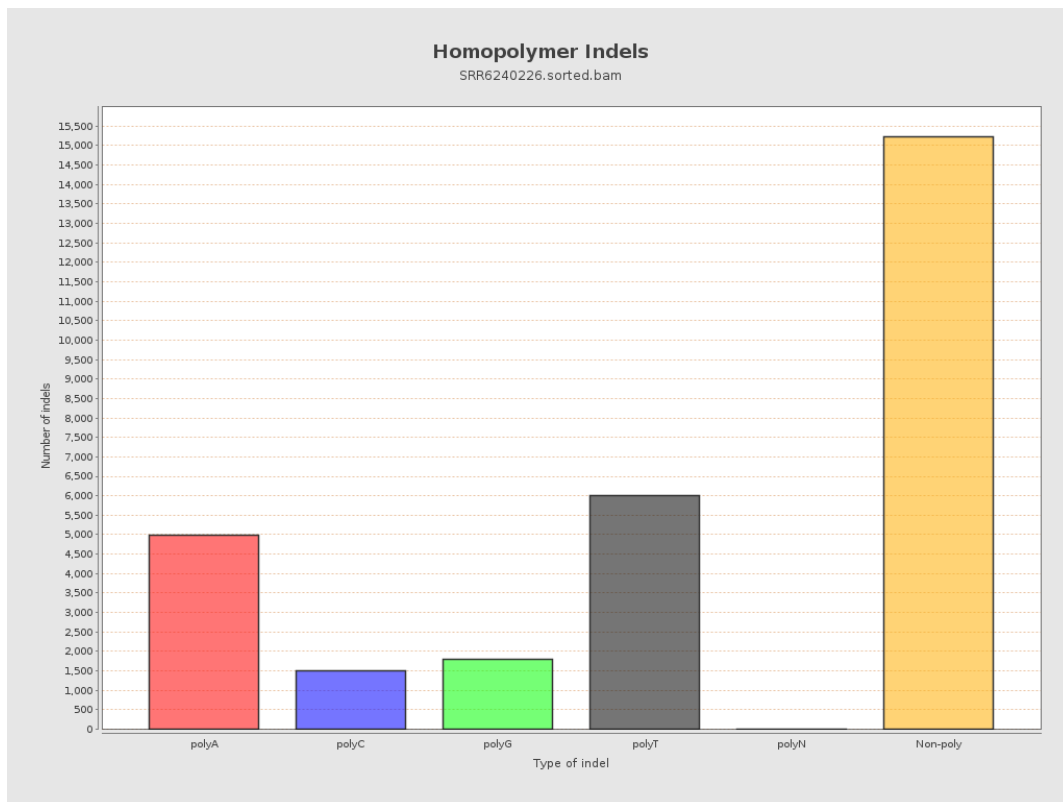
9. Results : Mapped Reads GC-content Distribution



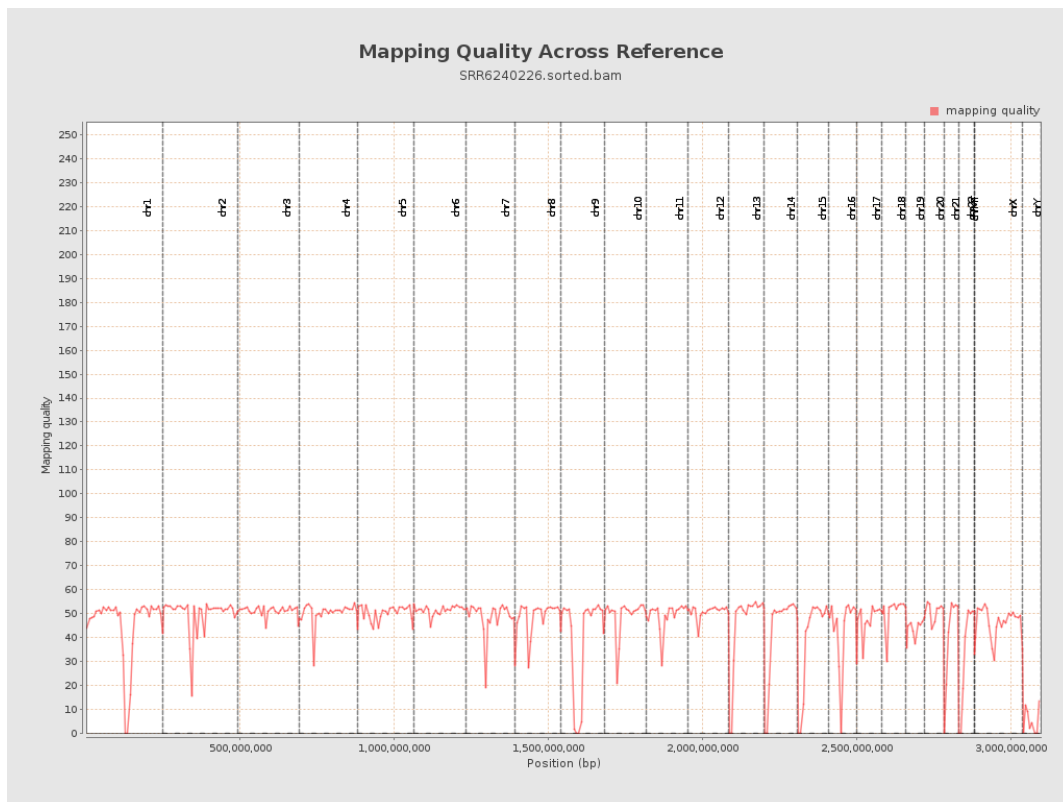
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

