

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:53:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472503.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_SRR3472503 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472503_1.fastq.gz SRR3472503_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:53:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472503.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,140,534
Mapped reads	14,941,439 / 98.69%
Unmapped reads	199,095 / 1.31%
Mapped paired reads	14,941,439 / 98.69%
Mapped reads, first in pair	7,501,819 / 49.55%
Mapped reads, second in pair	7,439,620 / 49.14%
Mapped reads, both in pair	14,832,980 / 97.97%
Mapped reads, singletons	108,459 / 0.72%
Secondary alignments	0
Supplementary alignments	61,147 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,007,826 / 59.49%
Duplication rate	44.31%
Clipped reads	1,190,570 / 7.86%

2.2. ACGT Content

Number/percentage of A's	413,233,380 / 28.09%
Number/percentage of C's	324,625,326 / 22.06%
Number/percentage of T's	411,029,625 / 27.94%
Number/percentage of G's	322,205,474 / 21.9%
Number/percentage of N's	225,664 / 0.02%

GC Percentage	43.96%
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2.3. Coverage

Mean	0.4753
Standard Deviation	16.9571

2.4. Mapping Quality

Mean Mapping Quality	55.16
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2.5. Insert size

Mean	32,943.8
Standard Deviation	1,779,536.76
P25/Median/P75	178 / 251 / 343

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	9,519,090
Insertions	85,807
Mapped reads with at least one insertion	0.57%
Deletions	80,597
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.31%

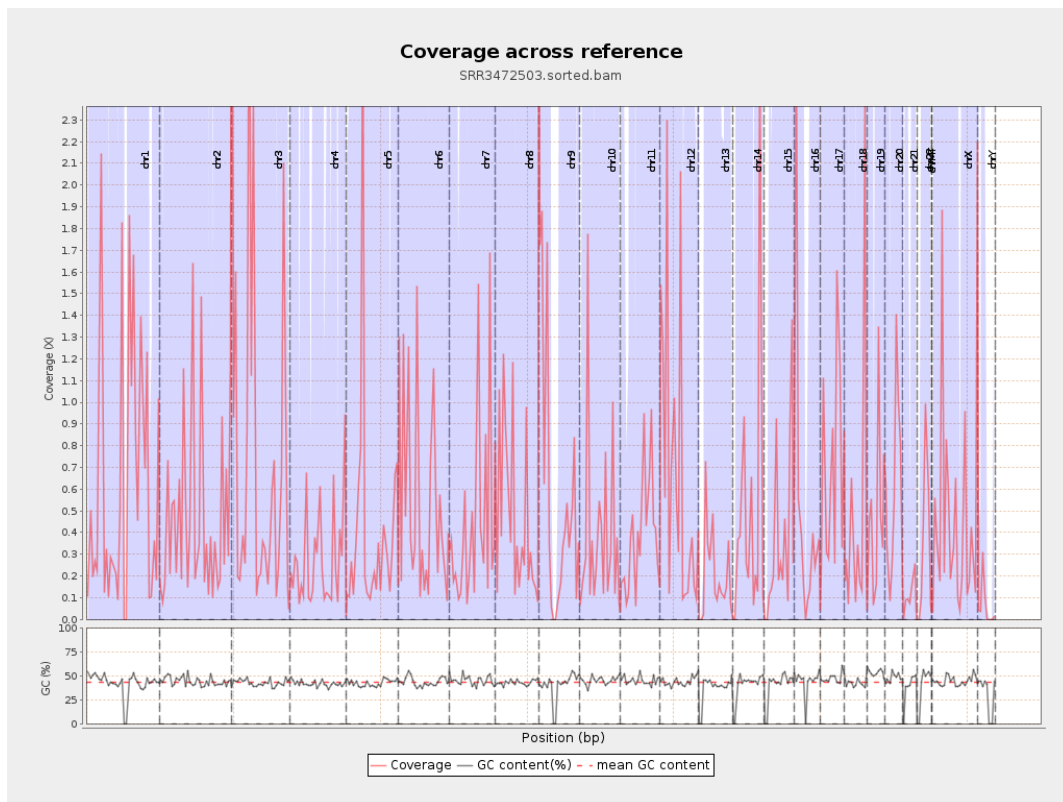
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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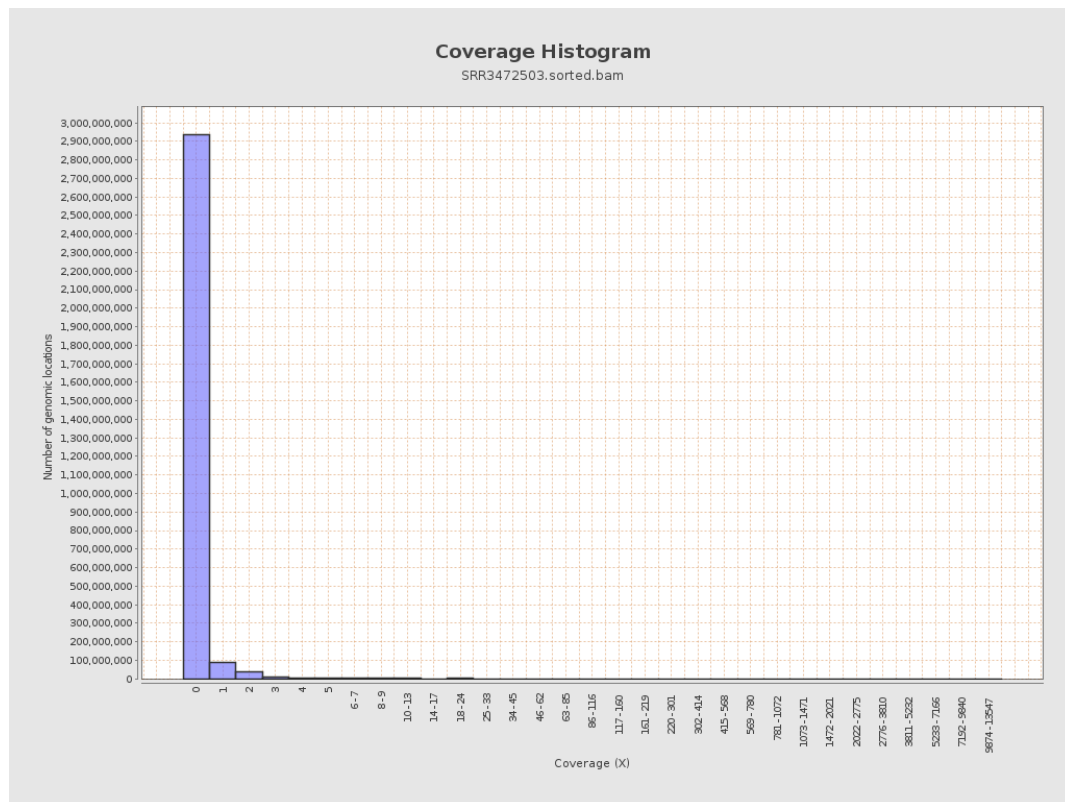
		bases	coverage	deviation
chr1	249250621	158602504	0.6363	19.8316
chr2	243199373	111223691	0.4573	14.5603
chr3	198022430	155051885	0.783	18.117
chr4	191154276	51849172	0.2712	10.8198
chr5	180915260	74868408	0.4138	11.9934
chr6	171115067	89711809	0.5243	18.6701
chr7	159138663	71368395	0.4485	13.4141
chr8	146364022	68685888	0.4693	15.3871
chr9	141213431	80544257	0.5704	15.4577
chr10	135534747	53889053	0.3976	23.0368
chr11	135006516	53295360	0.3948	13.1156
chr12	133851895	90693106	0.6776	22.5492
chr13	115169878	23606147	0.205	6.4303
chr14	107349540	50752486	0.4728	34.6344
chr15	102531392	38011333	0.3707	14.3294
chr16	90354753	44873302	0.4966	12.7336
chr17	81195210	56195968	0.6921	18.0187
chr18	78077248	36282527	0.4647	18.1541
chr19	59128983	27914864	0.4721	14.1035
chr20	63025520	38485844	0.6106	18.8649
chr21	48129895	5439734	0.113	3.3249
chr22	51304566	17089281	0.3331	13.6783
chrMT	16571	2370	0.143	0.4853
chrX	155270560	69125804	0.4452	16.2468

chrY	59373566	3952042	0.0666	3.0691
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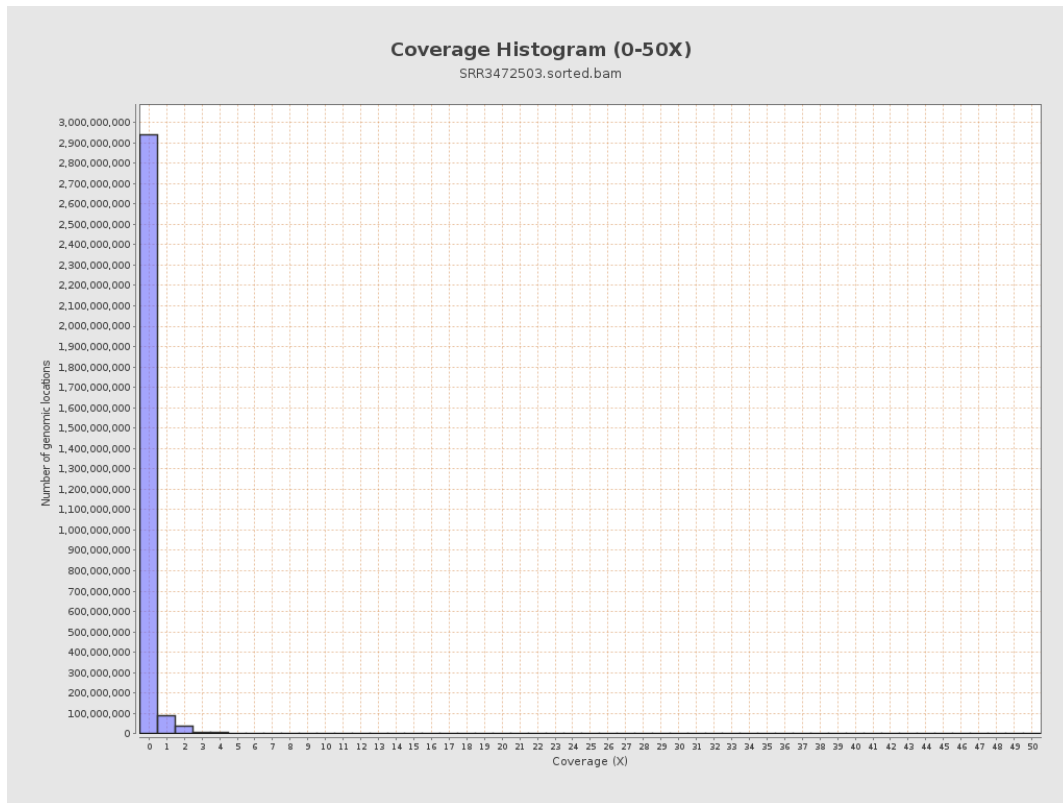
3. Results : Coverage across reference



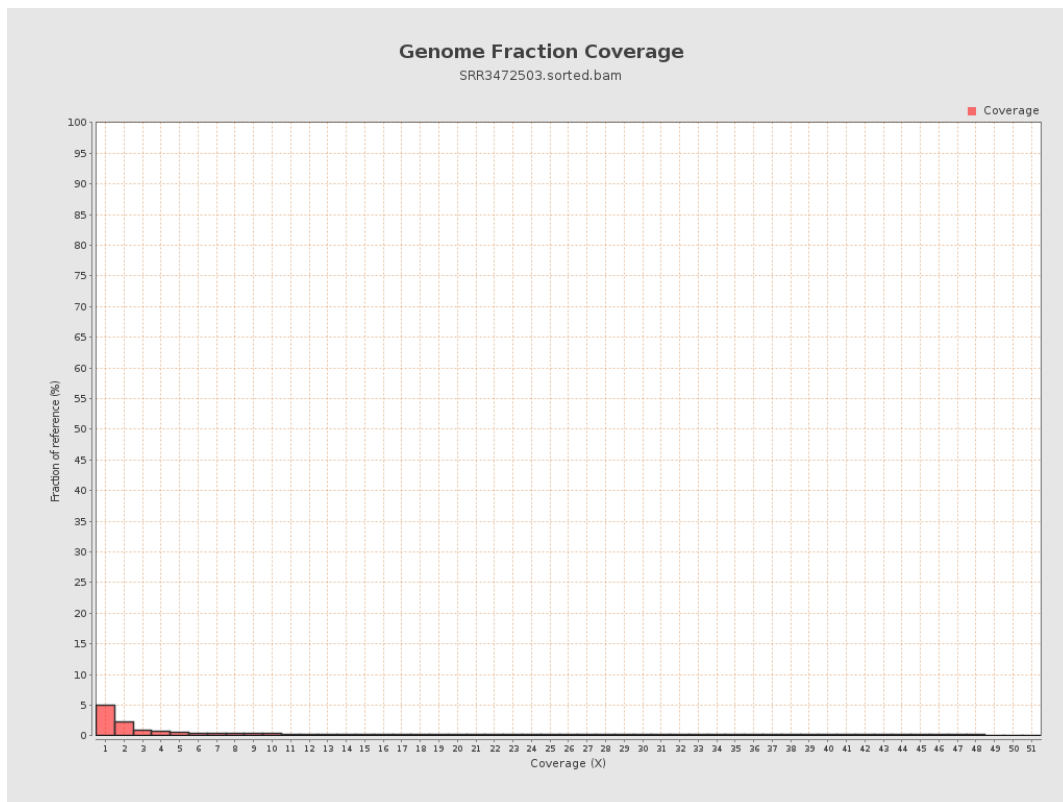
4. Results : Coverage Histogram



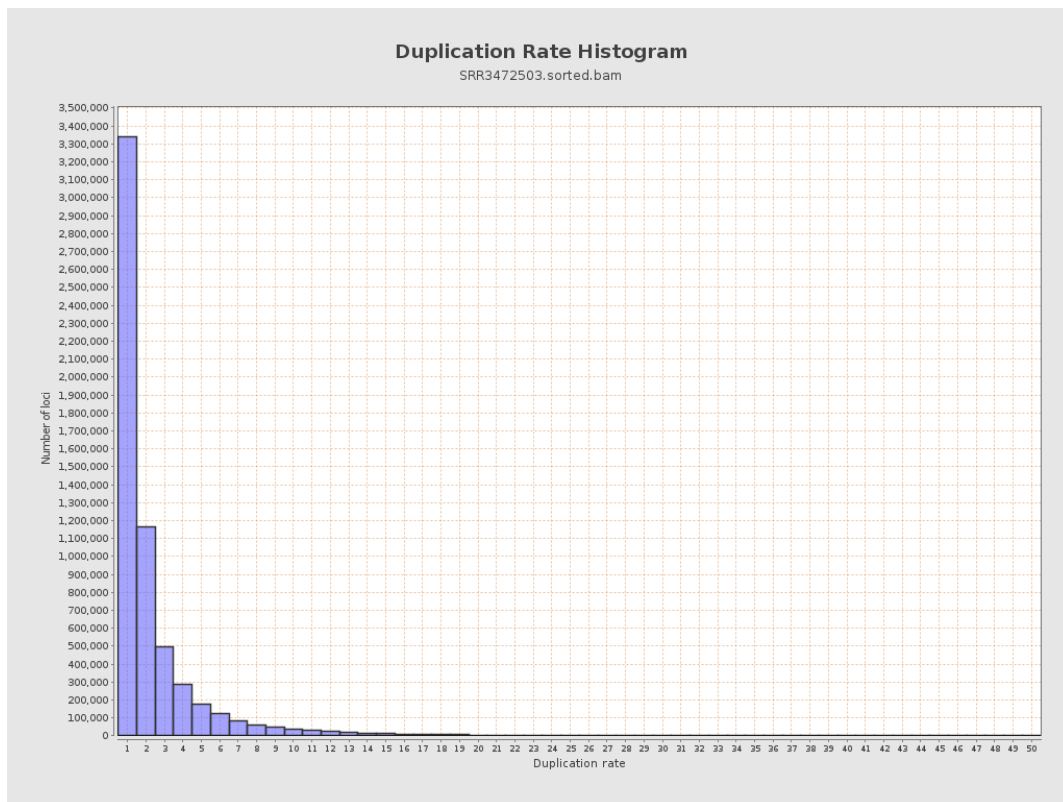
5. Results : Coverage Histogram (0-50X)



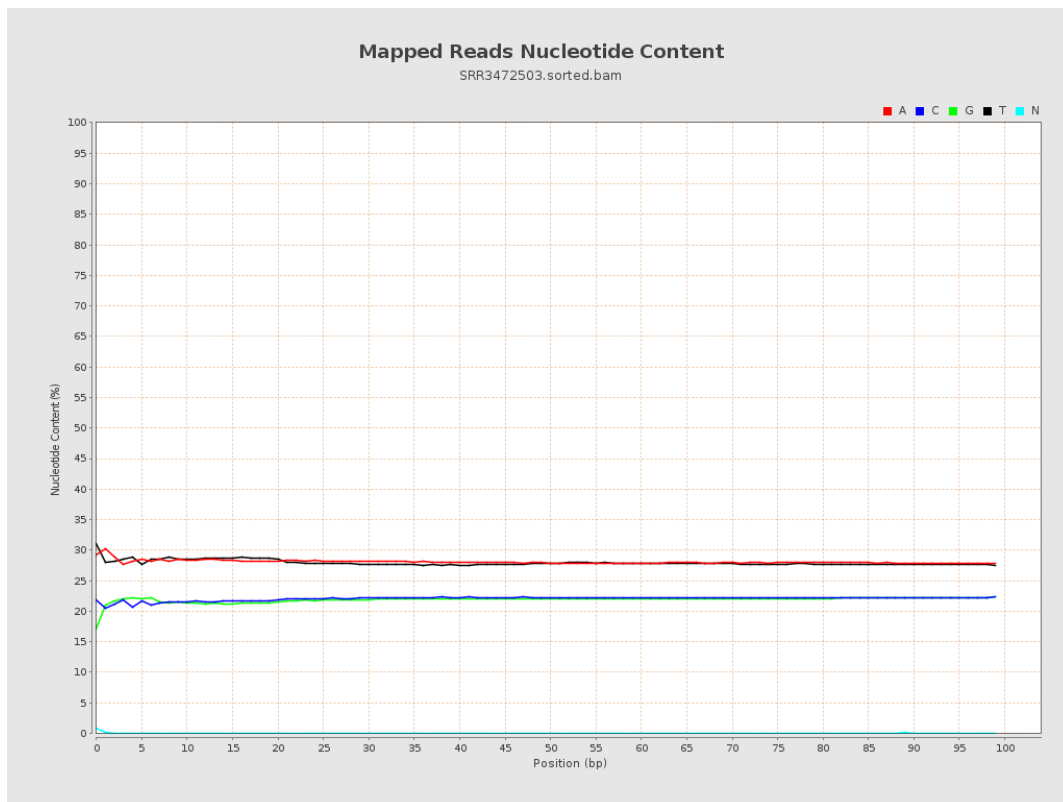
6. Results : Genome Fraction Coverage



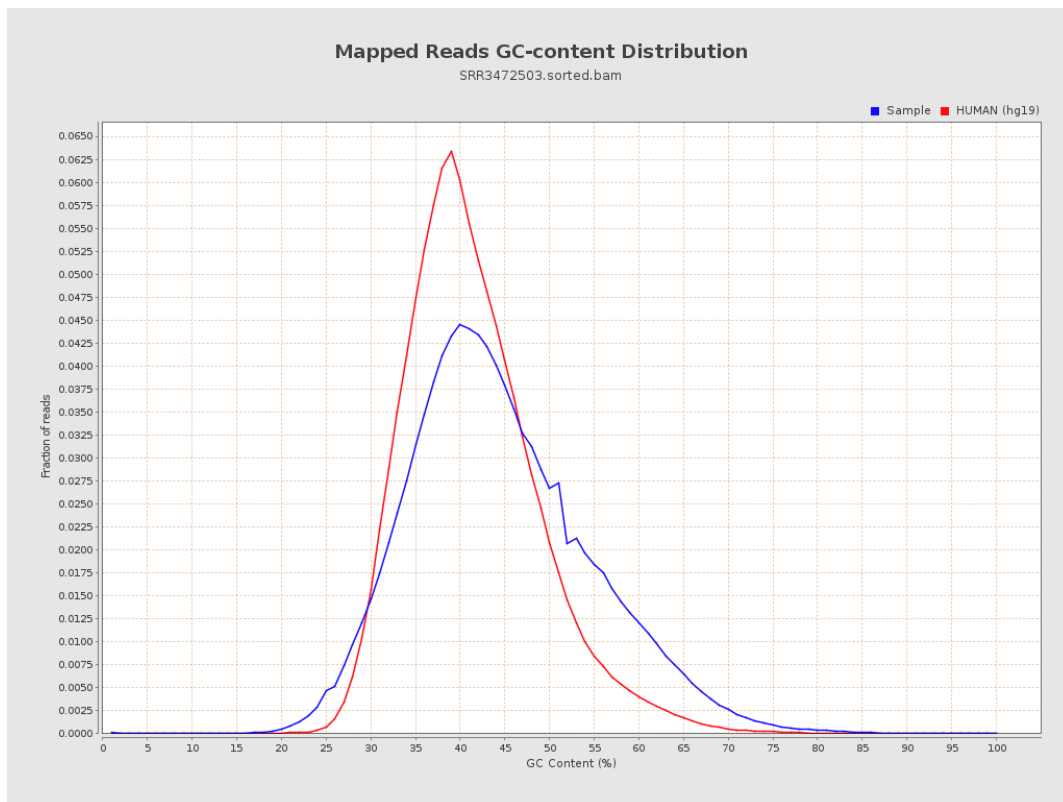
7. Results : Duplication Rate Histogram



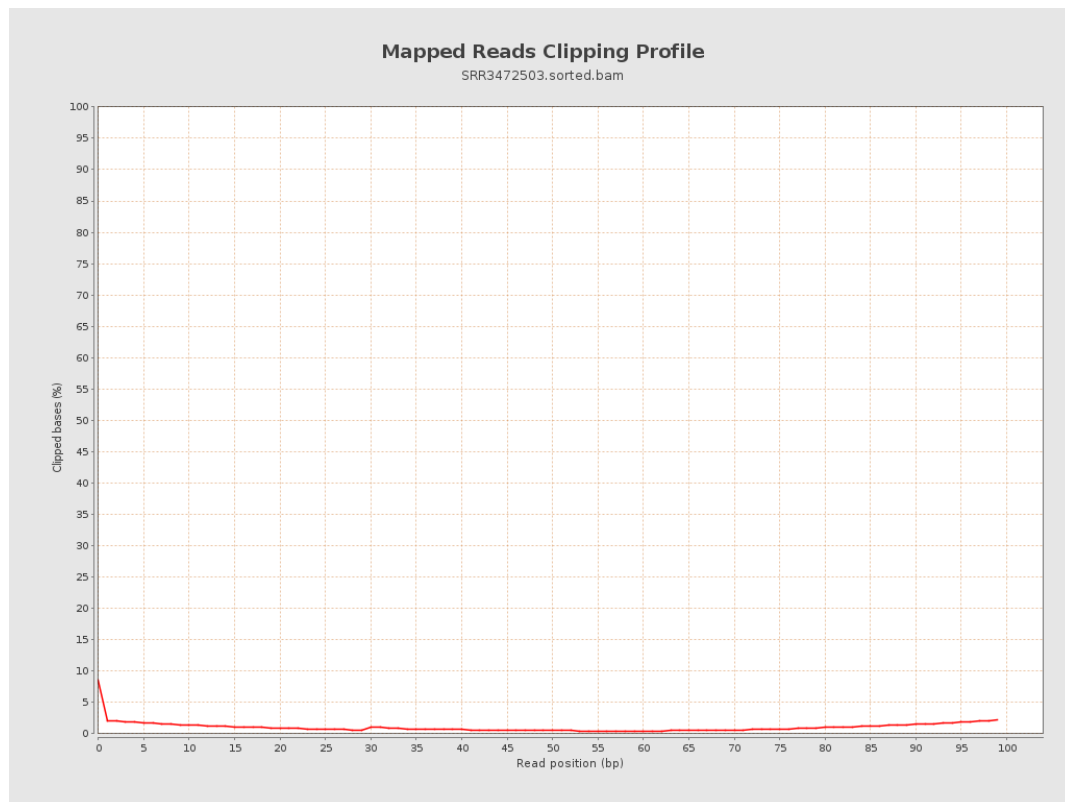
8. Results : Mapped Reads Nucleotide Content



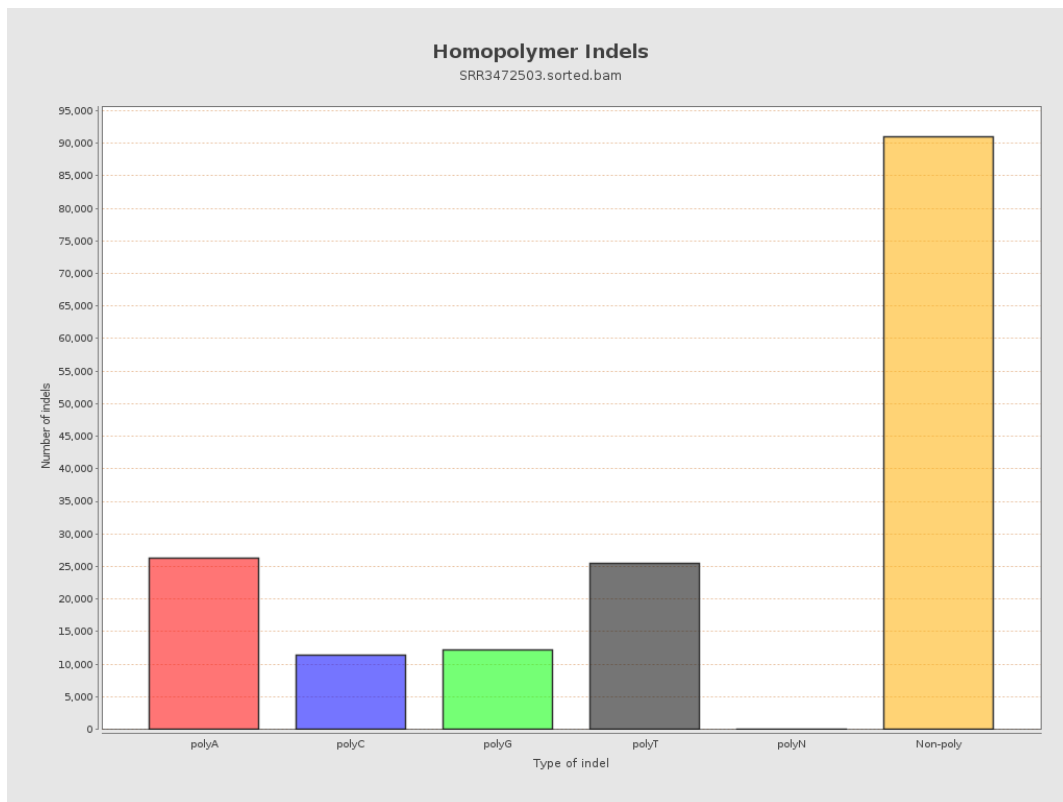
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



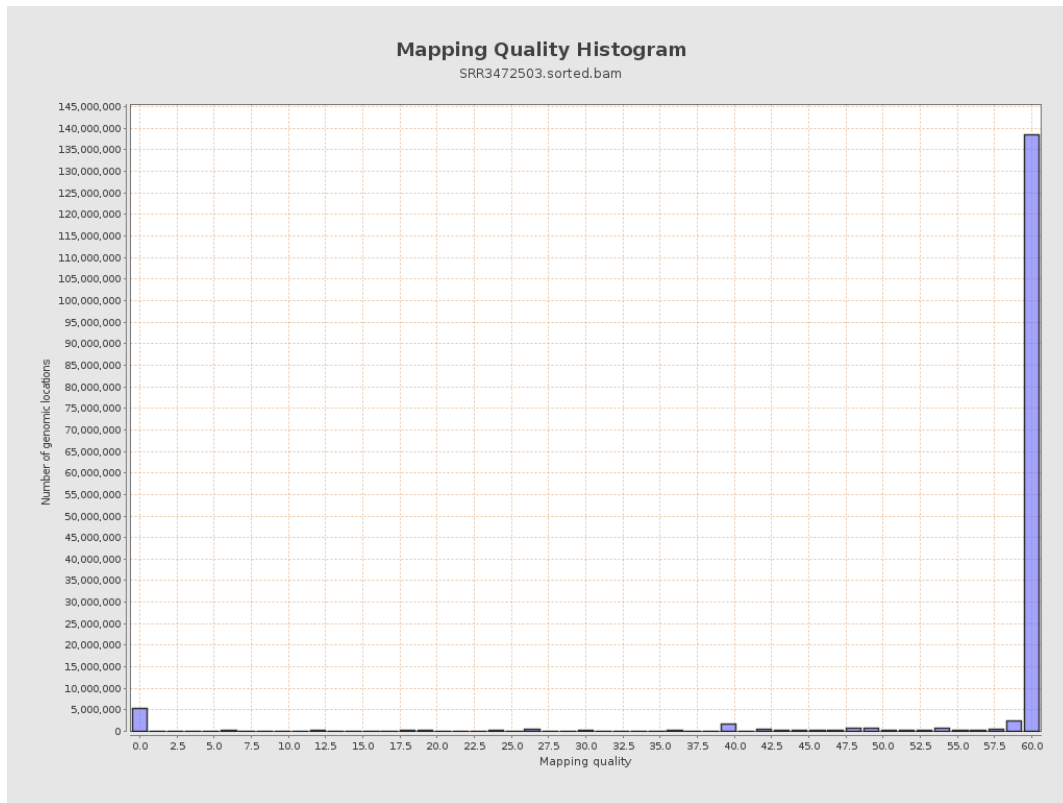
11. Results : Homopolymer Indels



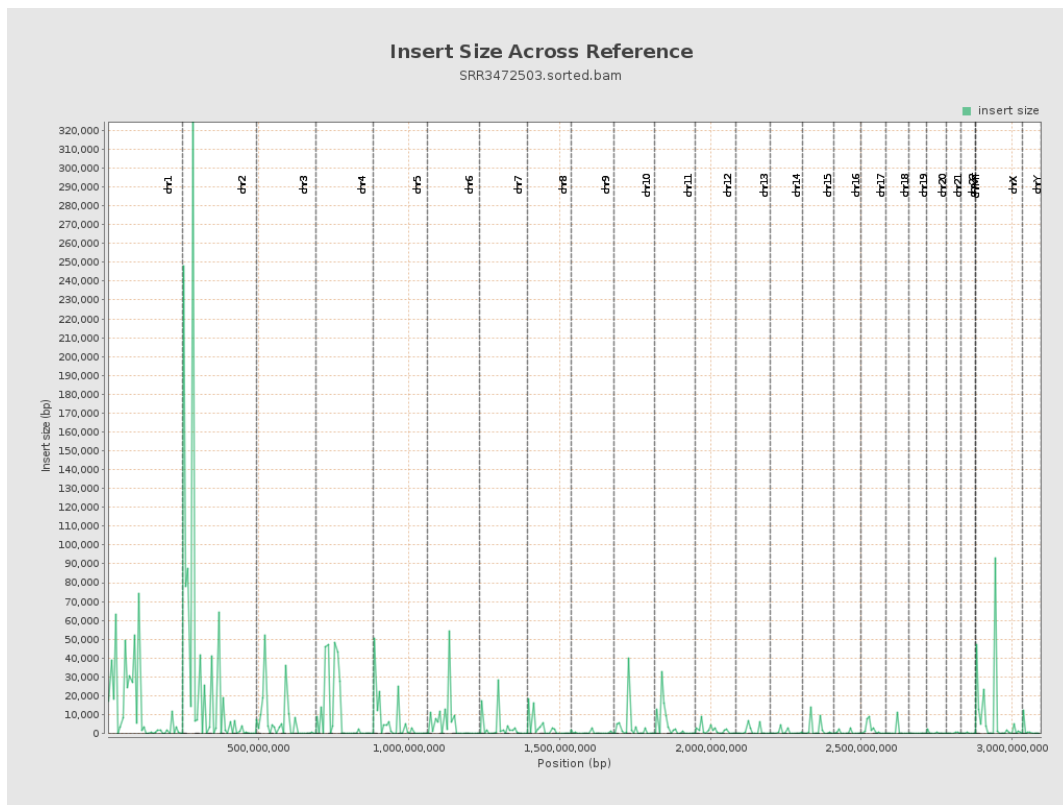
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

