

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 01:15:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472576.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_SRR3472576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472576_1.fastq.gz SRR3472576_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 01:15:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,285,174
Mapped reads	5,778,703 / 91.94%
Unmapped reads	506,471 / 8.06%
Mapped paired reads	5,778,703 / 91.94%
Mapped reads, first in pair	2,918,019 / 46.43%
Mapped reads, second in pair	2,860,684 / 45.51%
Mapped reads, both in pair	5,630,770 / 89.59%
Mapped reads, singletons	147,933 / 2.35%
Secondary alignments	0
Supplementary alignments	169,555 / 2.7%
Read min/max/mean length	30 / 100 / 101.06
Duplicated reads (estimated)	772,935 / 12.3%
Duplication rate	11.64%
Clipped reads	4,397,479 / 69.97%

2.2. ACGT Content

Number/percentage of A's	120,688,096 / 25.63%
Number/percentage of C's	94,233,265 / 20.01%
Number/percentage of T's	140,137,397 / 29.76%
Number/percentage of G's	115,482,690 / 24.53%
Number/percentage of N's	310,915 / 0.07%

GC Percentage	44.54%
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2.3. Coverage

Mean	0.1522
Standard Deviation	1.4903

2.4. Mapping Quality

Mean Mapping Quality	50.33
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2.5. Insert size

Mean	242,083.7
Standard Deviation	4,735,202.49
P25/Median/P75	93 / 132 / 184

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	5,756,245
Insertions	46,536
Mapped reads with at least one insertion	0.79%
Deletions	108,921
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.73%

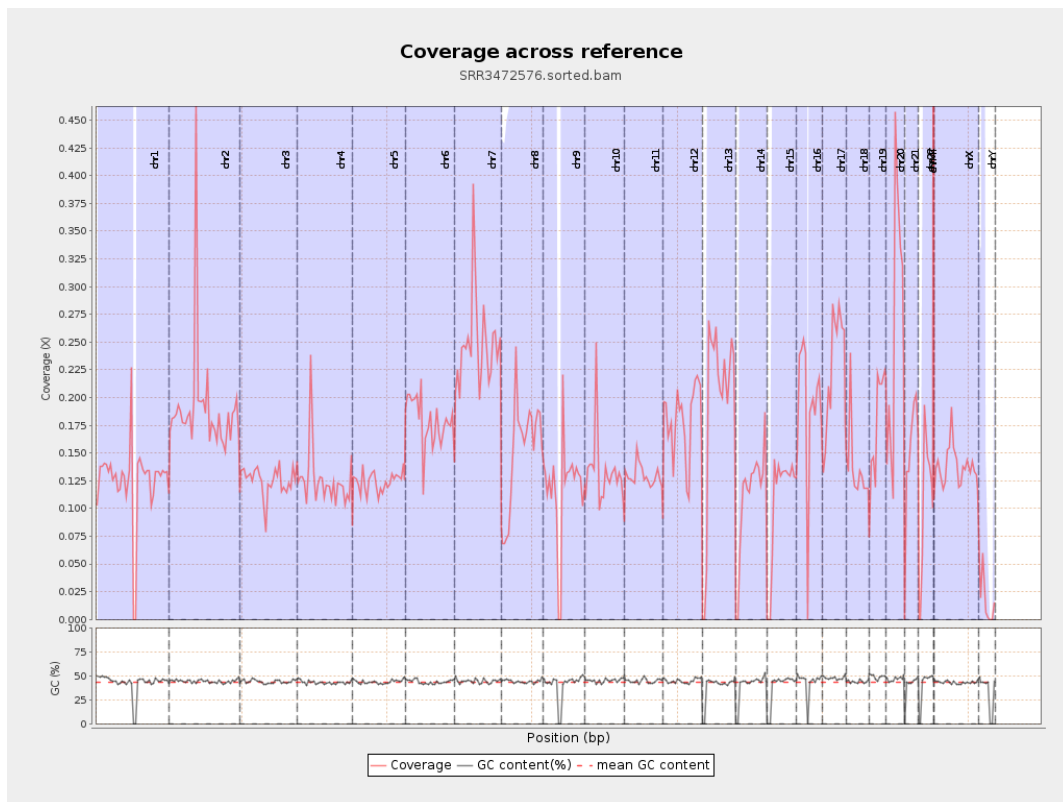
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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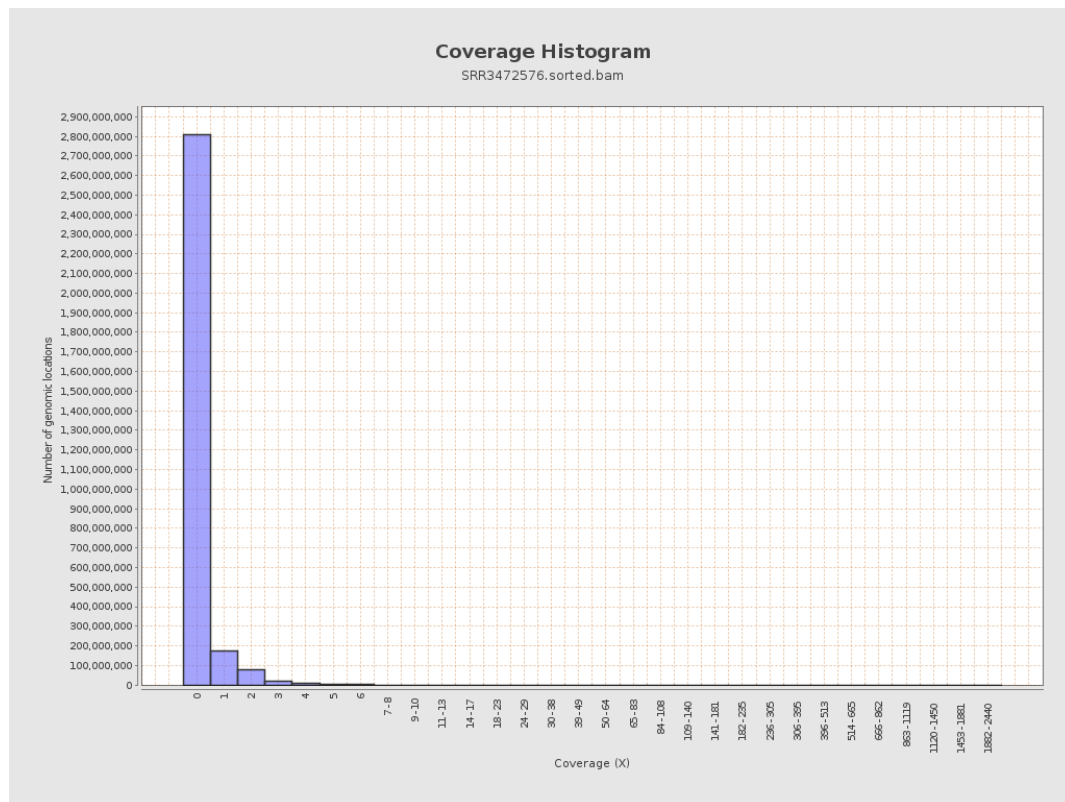
		bases	coverage	deviation
chr1	249250621	31060610	0.1246	1.8286
chr2	243199373	46309033	0.1904	2.2488
chr3	198022430	24709752	0.1248	0.4922
chr4	191154276	23857389	0.1248	0.7835
chr5	180915260	22435874	0.124	0.5265
chr6	171115067	30599156	0.1788	0.8846
chr7	159138663	39694508	0.2494	2.8413
chr8	146364022	22223213	0.1518	1.3133
chr9	141213431	16454177	0.1165	1.7102
chr10	135534747	17990095	0.1327	1.3142
chr11	135006516	17316240	0.1283	1.2414
chr12	133851895	24028531	0.1795	0.6173
chr13	115169878	22385313	0.1944	0.6479
chr14	107349540	11911976	0.111	2.6485
chr15	102531392	11122018	0.1085	0.4674
chr16	90354753	17431909	0.1929	0.8399
chr17	81195210	18531874	0.2282	1.3322
chr18	78077248	10757316	0.1378	2.9489
chr19	59128983	10561783	0.1786	1.3432
chr20	63025520	16685995	0.2647	0.9177
chr21	48129895	7232239	0.1503	0.6811
chr22	51304566	5304744	0.1034	0.4676
chrMT	16571	20384	1.2301	1.6611
chrX	155270560	21396620	0.1378	0.7472

chrY	59373566	1035469	0.0174	0.6171
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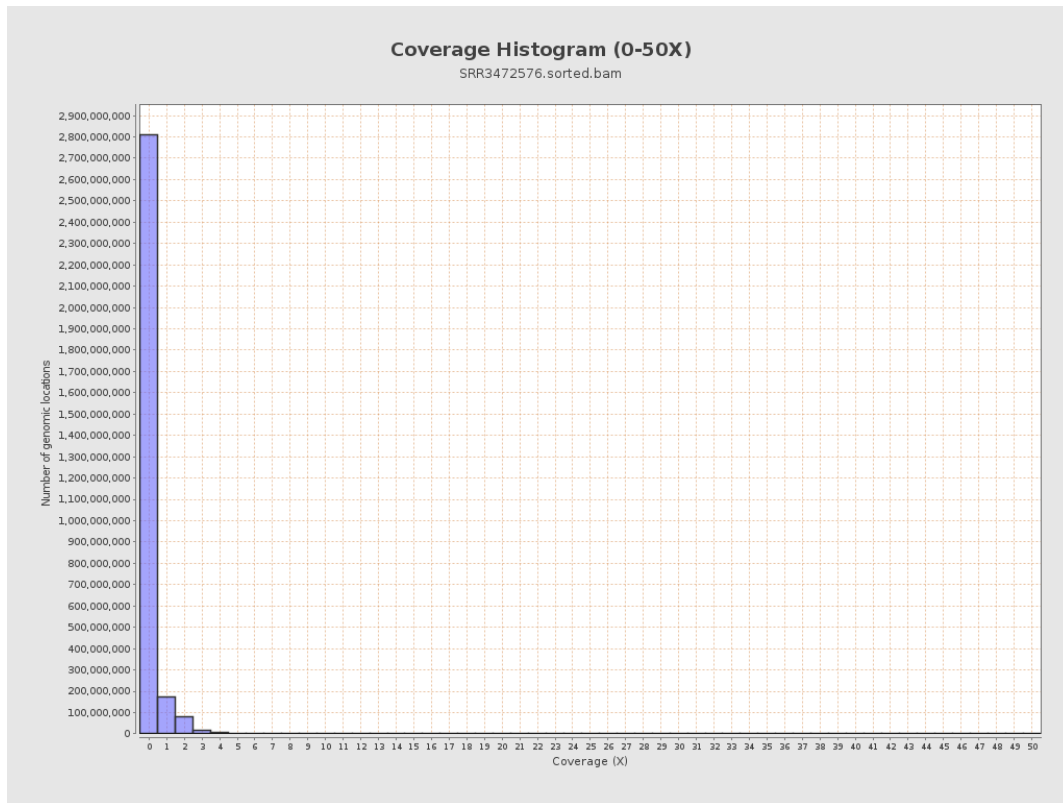
3. Results : Coverage across reference



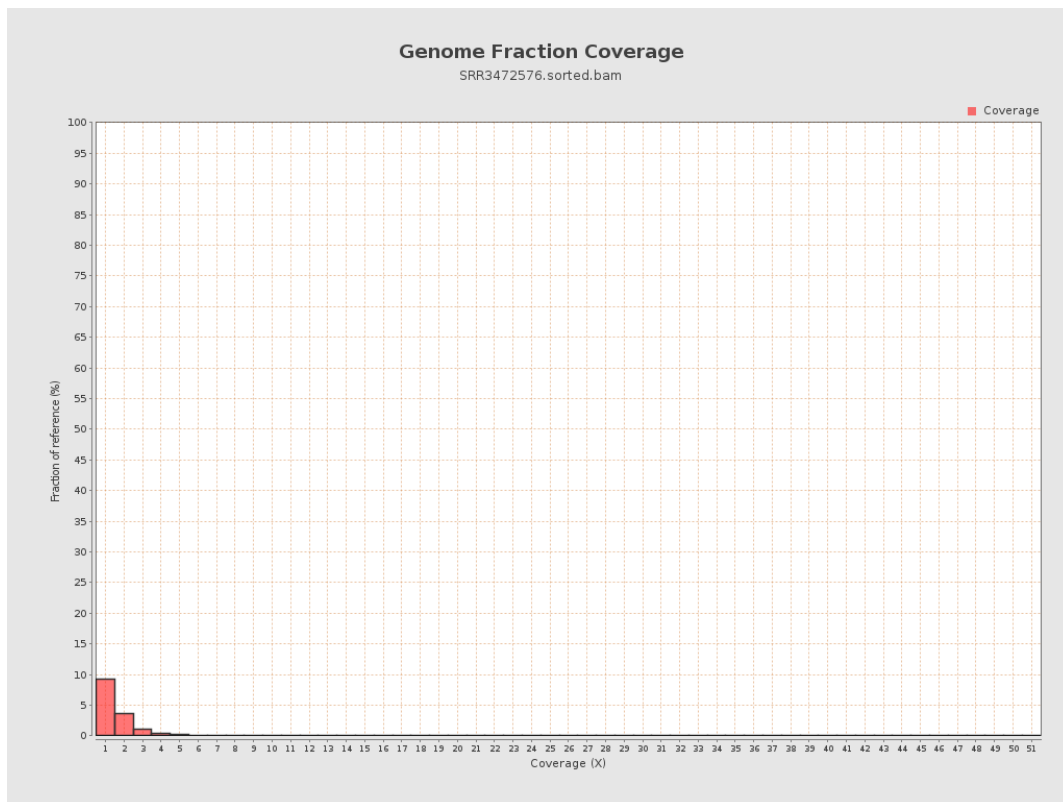
4. Results : Coverage Histogram



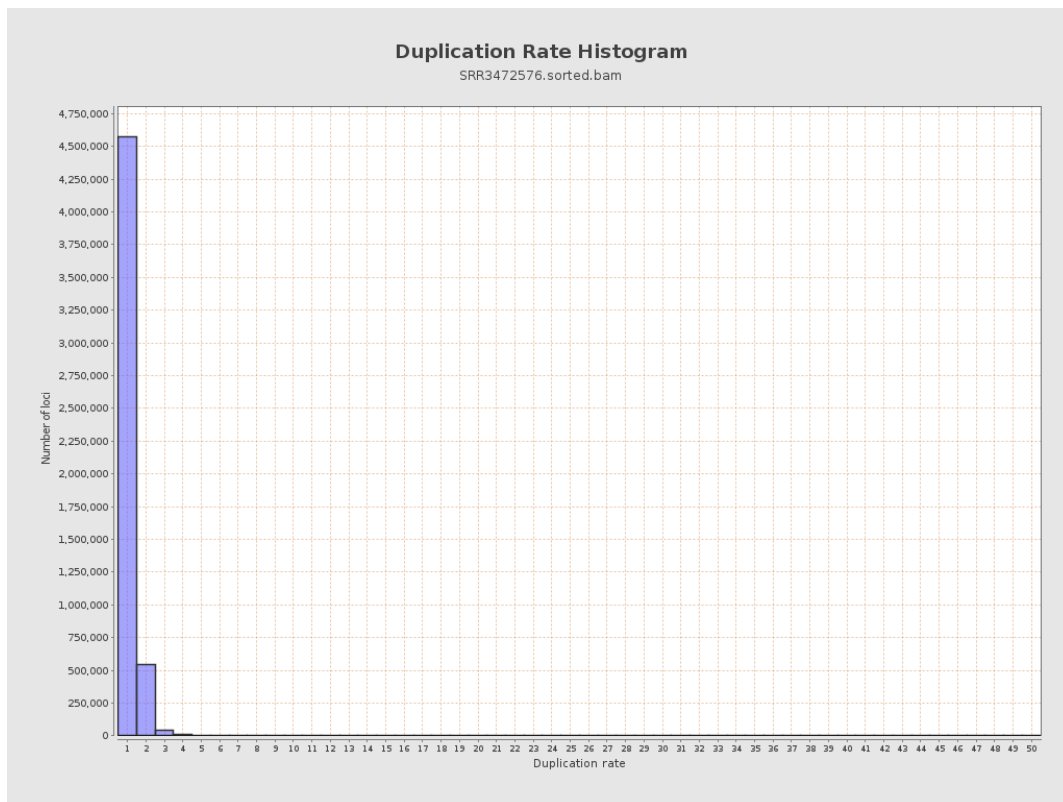
5. Results : Coverage Histogram (0-50X)



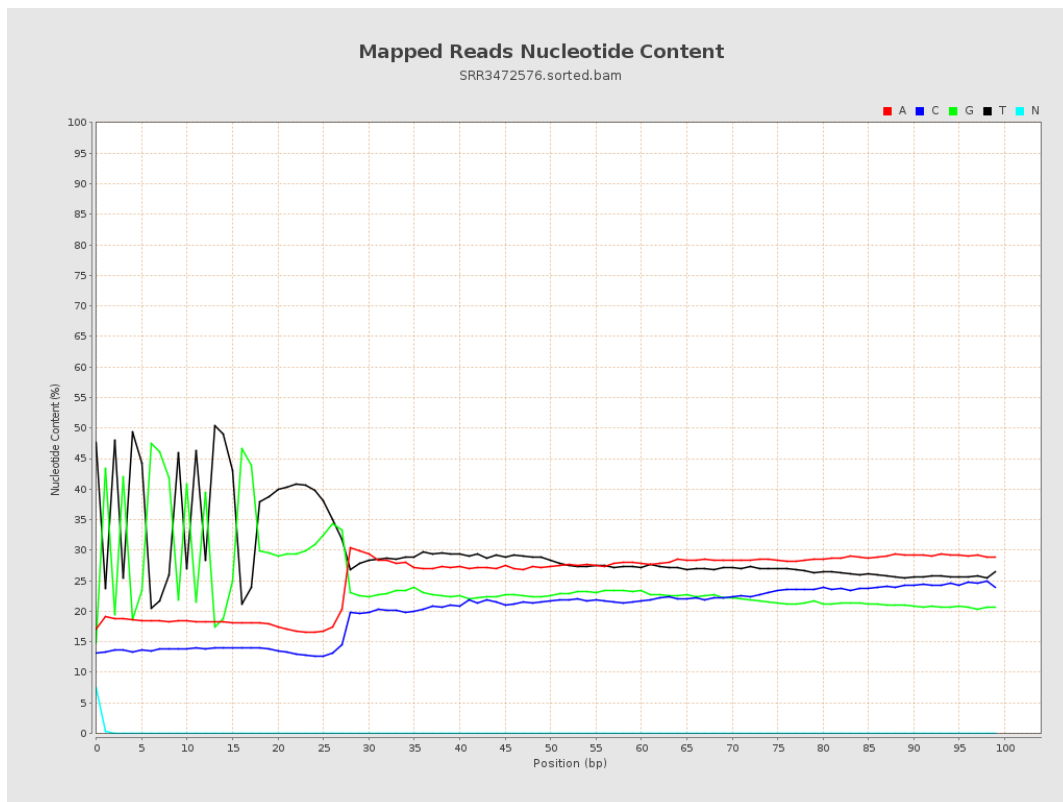
6. Results : Genome Fraction Coverage



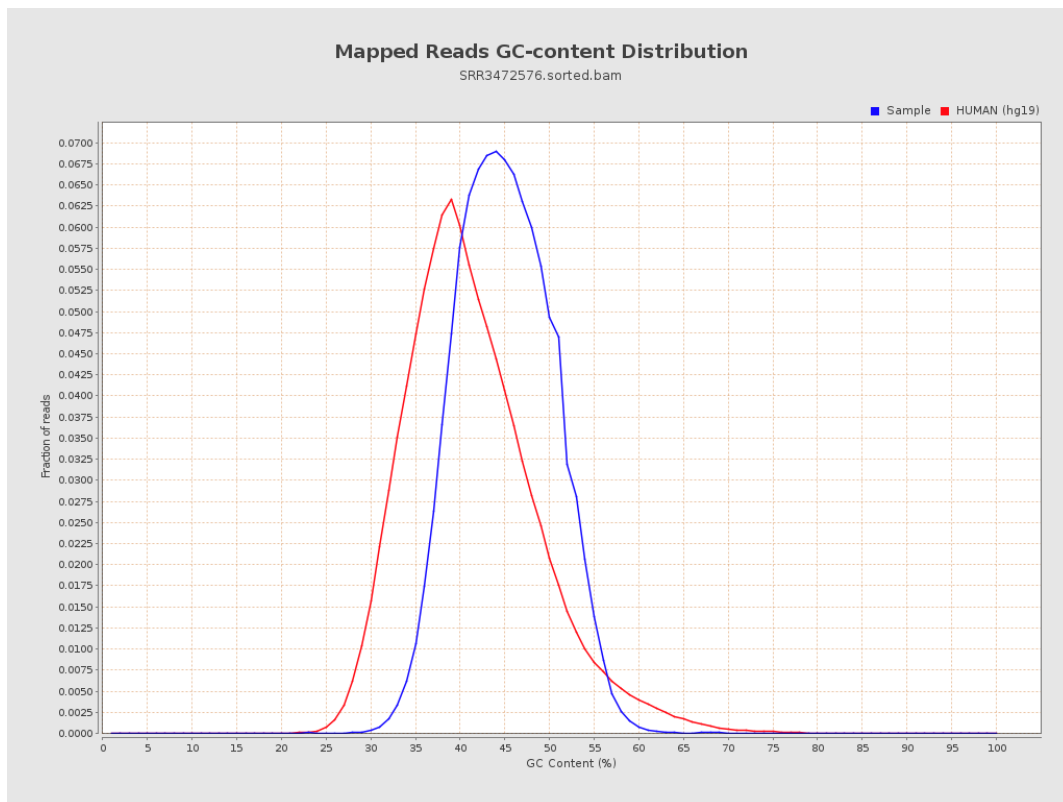
7. Results : Duplication Rate Histogram



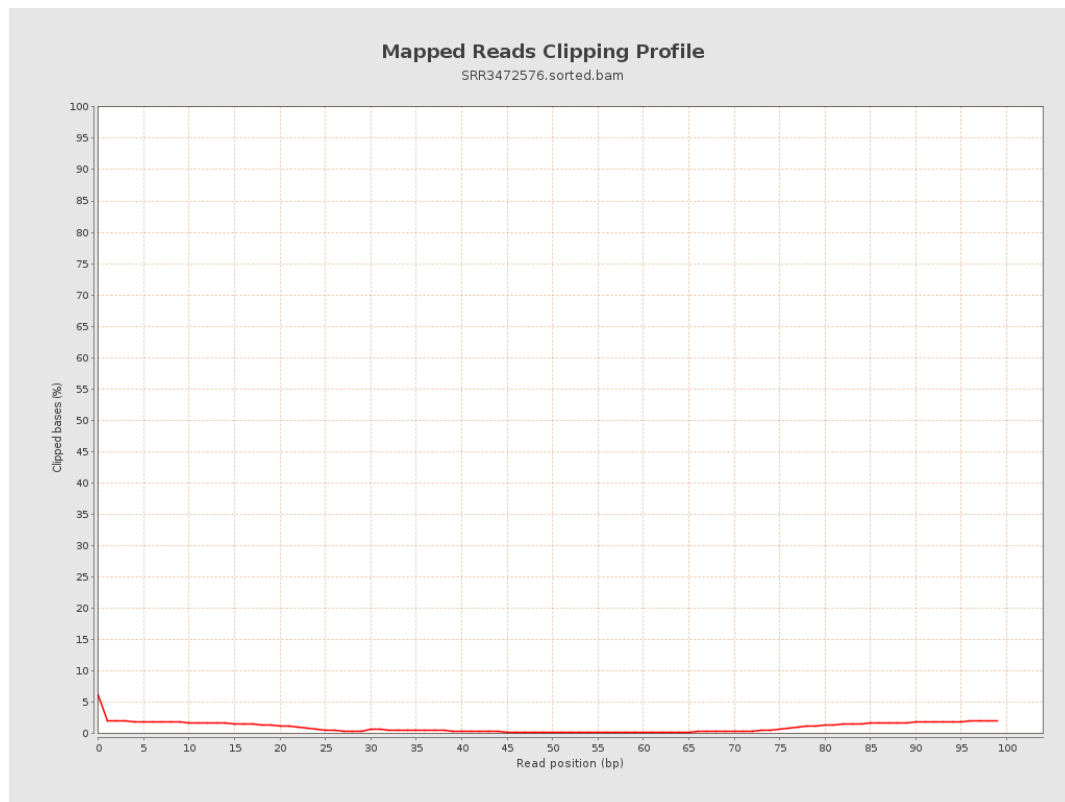
8. Results : Mapped Reads Nucleotide Content



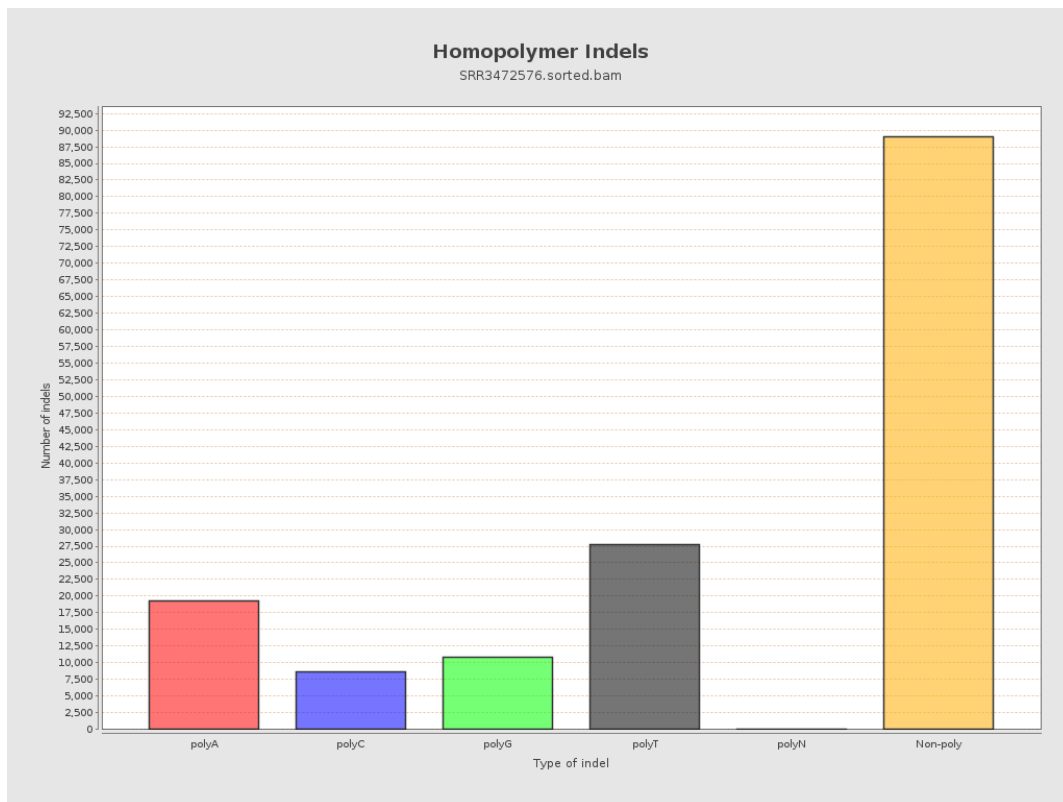
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



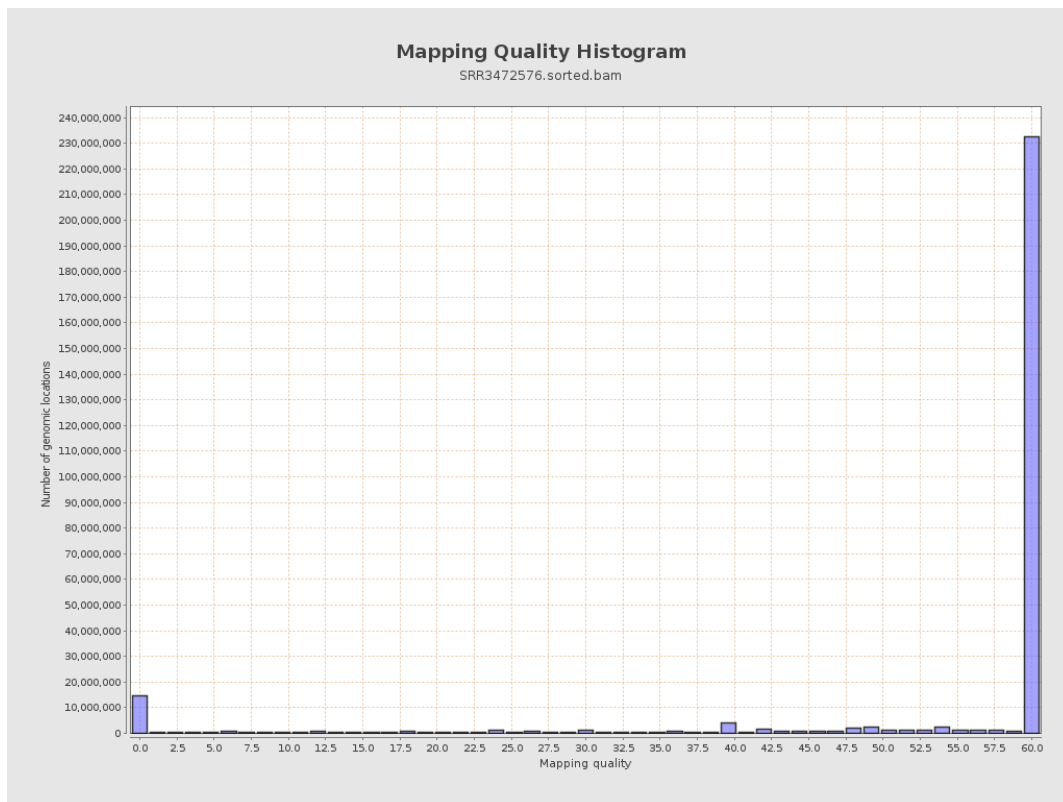
11. Results : Homopolymer Indels



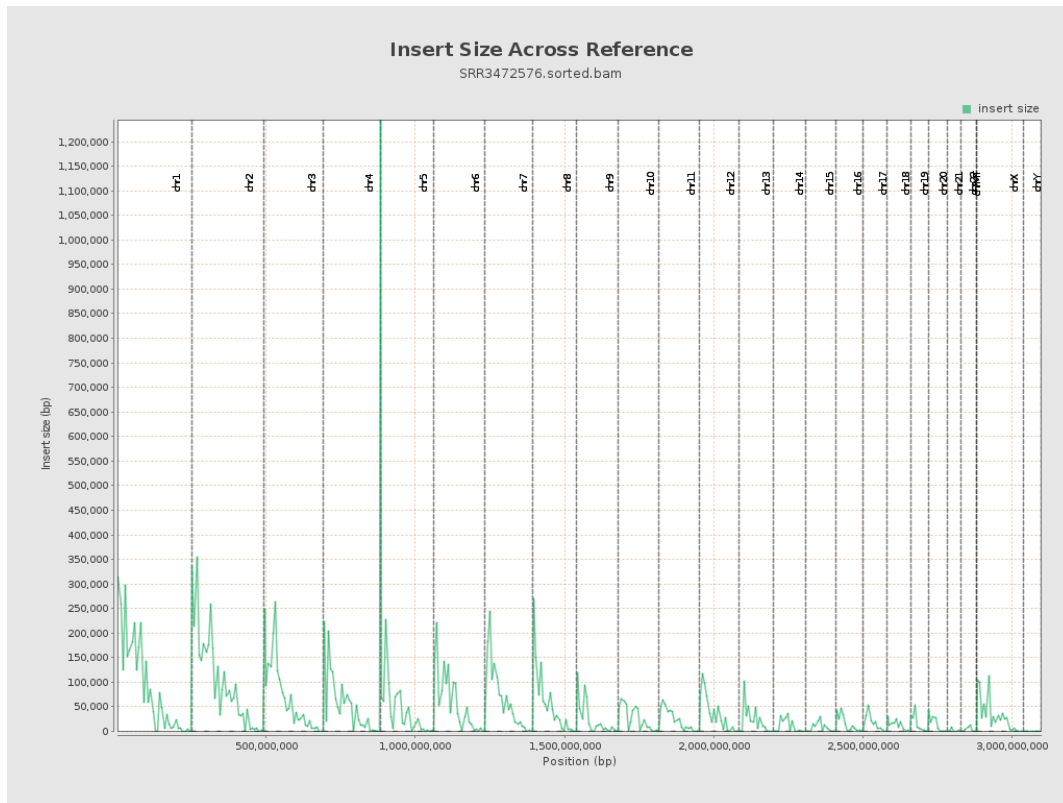
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

