

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 12:36:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617552.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_SRR8617552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617552_1.fastq.gz SRR8617552_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 12:36:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,049,146
Mapped reads	52,421,879 / 98.82%
Unmapped reads	627,267 / 1.18%
Mapped paired reads	52,421,879 / 98.82%
Mapped reads, first in pair	26,386,945 / 49.74%
Mapped reads, second in pair	26,034,934 / 49.08%
Mapped reads, both in pair	51,992,466 / 98.01%
Mapped reads, singletons	429,413 / 0.81%
Secondary alignments	0
Supplementary alignments	1,461,408 / 2.75%
Read min/max/mean length	30 / 150 / 151.34
Duplicated reads (estimated)	19,182,169 / 36.16%
Duplication rate	25.48%
Clipped reads	29,215,942 / 55.07%

2.2. ACGT Content

Number/percentage of A's	2,025,211,564 / 29.02%
Number/percentage of C's	1,313,500,922 / 18.82%
Number/percentage of T's	2,103,319,819 / 30.14%
Number/percentage of G's	1,535,419,537 / 22%
Number/percentage of N's	282,591 / 0%

GC Percentage	40.83%
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2.3. Coverage

Mean	2.2557
Standard Deviation	25.2633

2.4. Mapping Quality

Mean Mapping Quality	53.44
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2.5. Insert size

Mean	169,832.41
Standard Deviation	3,941,558.51
P25/Median/P75	213 / 272 / 343

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	77,657,788
Insertions	1,250,442
Mapped reads with at least one insertion	2.23%
Deletions	2,594,740
Mapped reads with at least one deletion	4.75%
Homopolymer indels	46.18%

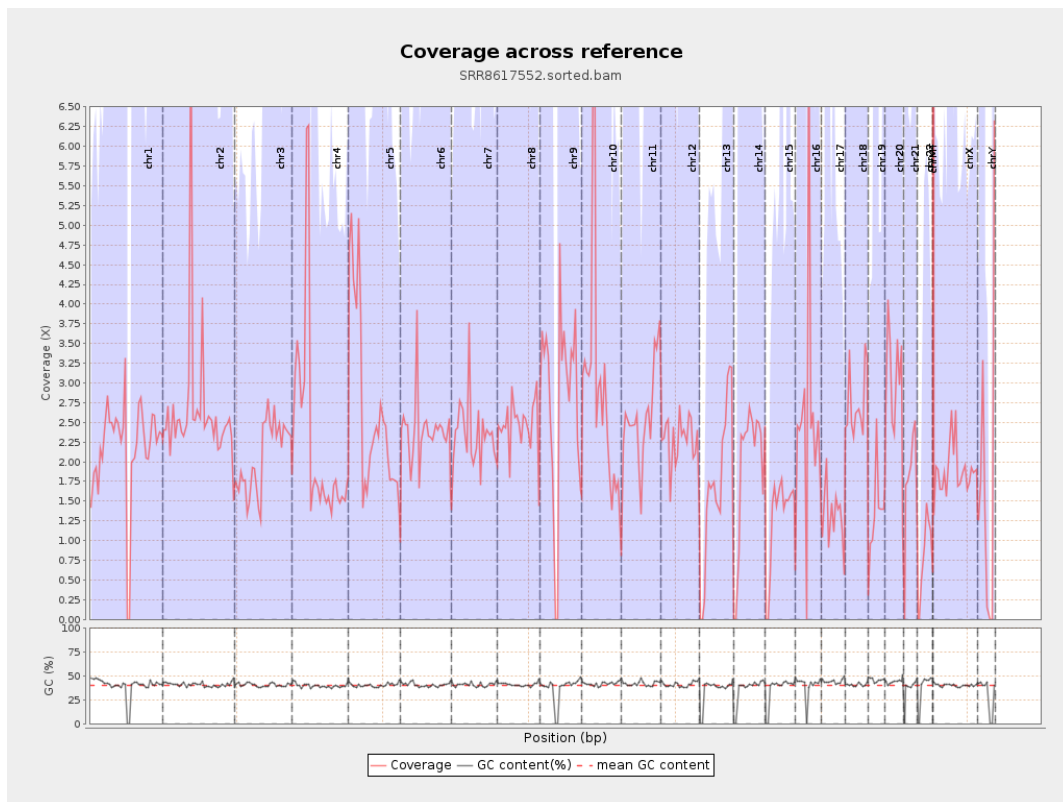
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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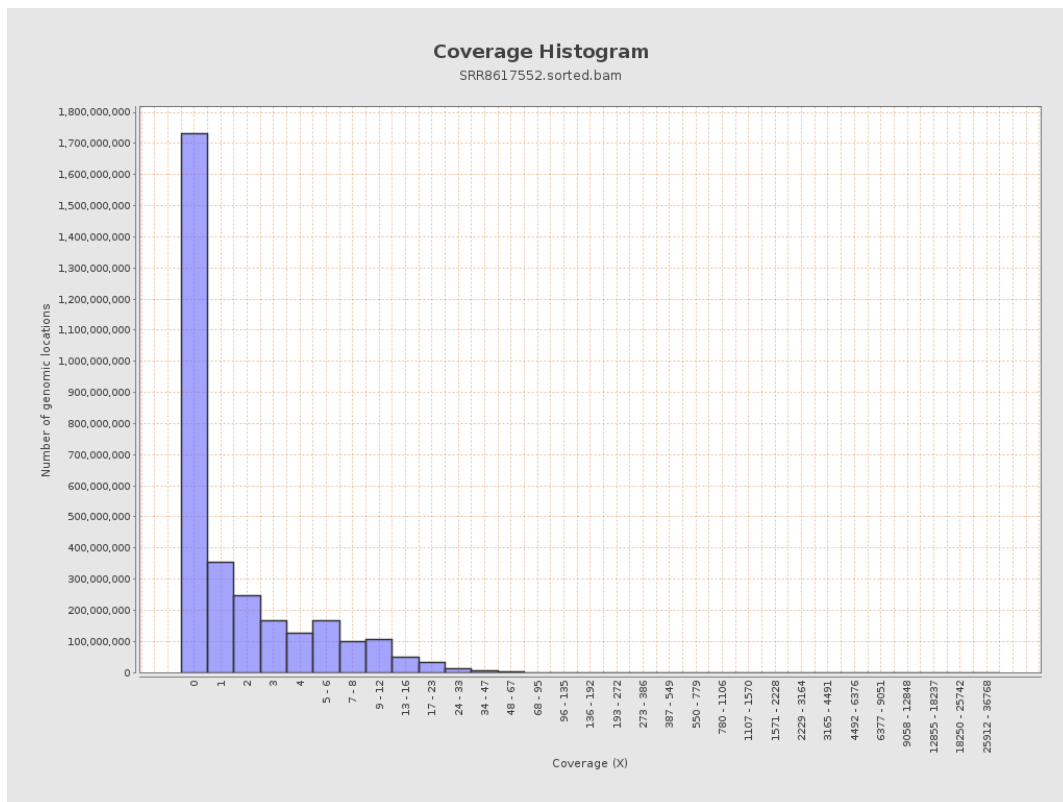
		bases	coverage	deviation
chr1	249250621	541835946	2.1739	21.3889
chr2	243199373	648598310	2.6669	35.8977
chr3	198022430	407695325	2.0588	4.212
chr4	191154276	439068854	2.2969	27.559
chr5	180915260	478605935	2.6455	5.5955
chr6	171115067	409454835	2.3929	18.028
chr7	159138663	371536593	2.3347	30.989
chr8	146364022	360356156	2.4621	7.515
chr9	141213431	396274944	2.8062	53.8368
chr10	135534747	388404683	2.8657	49.3601
chr11	135006516	345325484	2.5578	15.6814
chr12	133851895	303793170	2.2696	10.0828
chr13	115169878	198436939	1.723	3.8577
chr14	107349540	208131050	1.9388	5.0021
chr15	102531392	130350891	1.2713	5.0772
chr16	90354753	229491100	2.5399	38.7261
chr17	81195210	107983026	1.3299	14.0589
chr18	78077248	213455368	2.7339	36.0658
chr19	59128983	81760548	1.3827	13.0423
chr20	63025520	192975658	3.0619	9.9093
chr21	48129895	85533254	1.7771	11.9018
chr22	51304566	42114694	0.8209	3.3553
chrMT	16571	2359971	142.4157	71.2855
chrX	155270560	292901226	1.8864	7.9558

chrY	59373566	106463508	1.7931	40.2658
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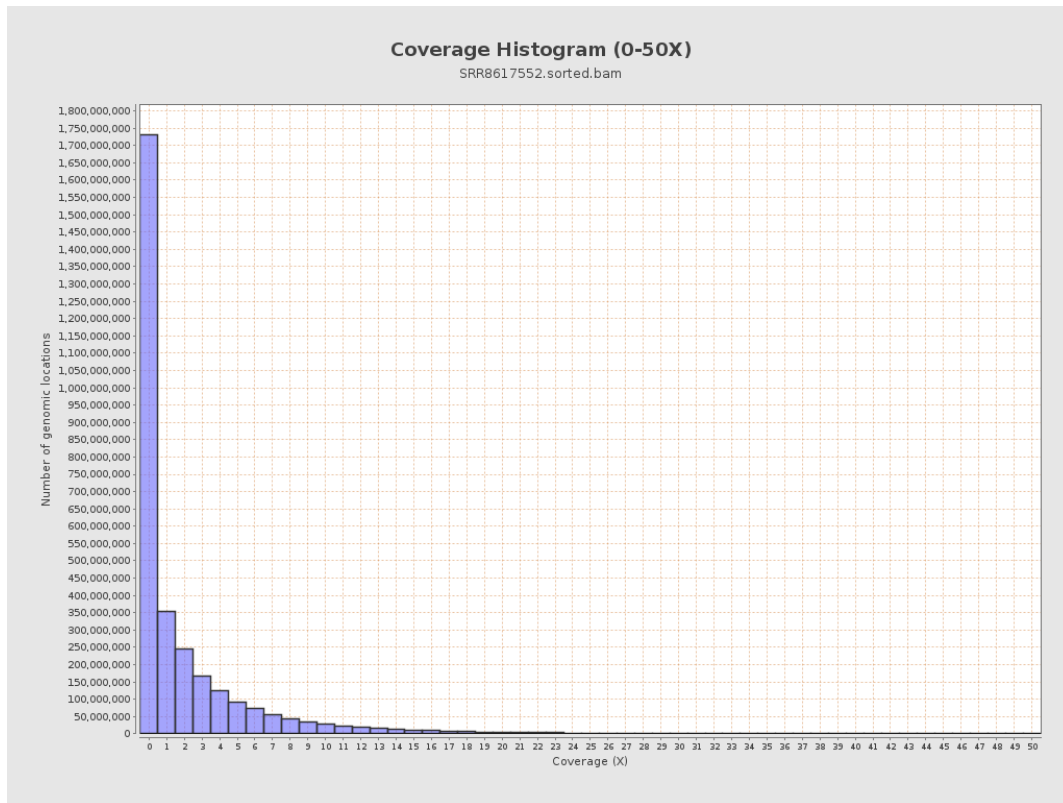
3. Results : Coverage across reference



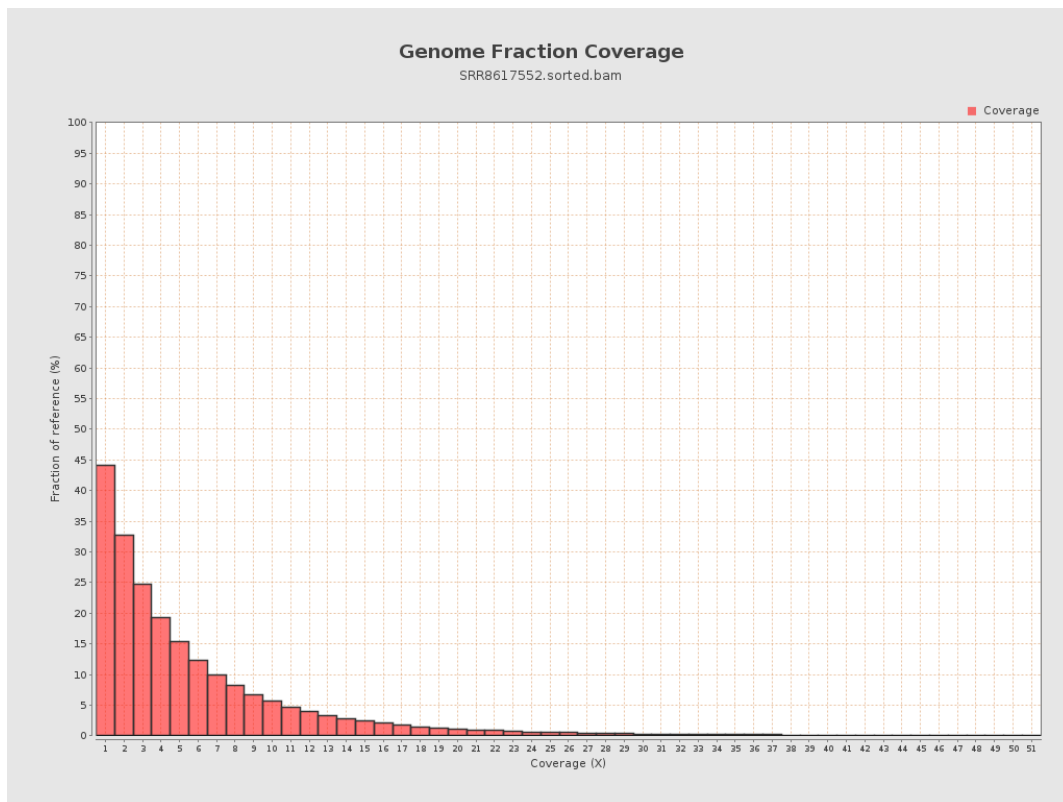
4. Results : Coverage Histogram



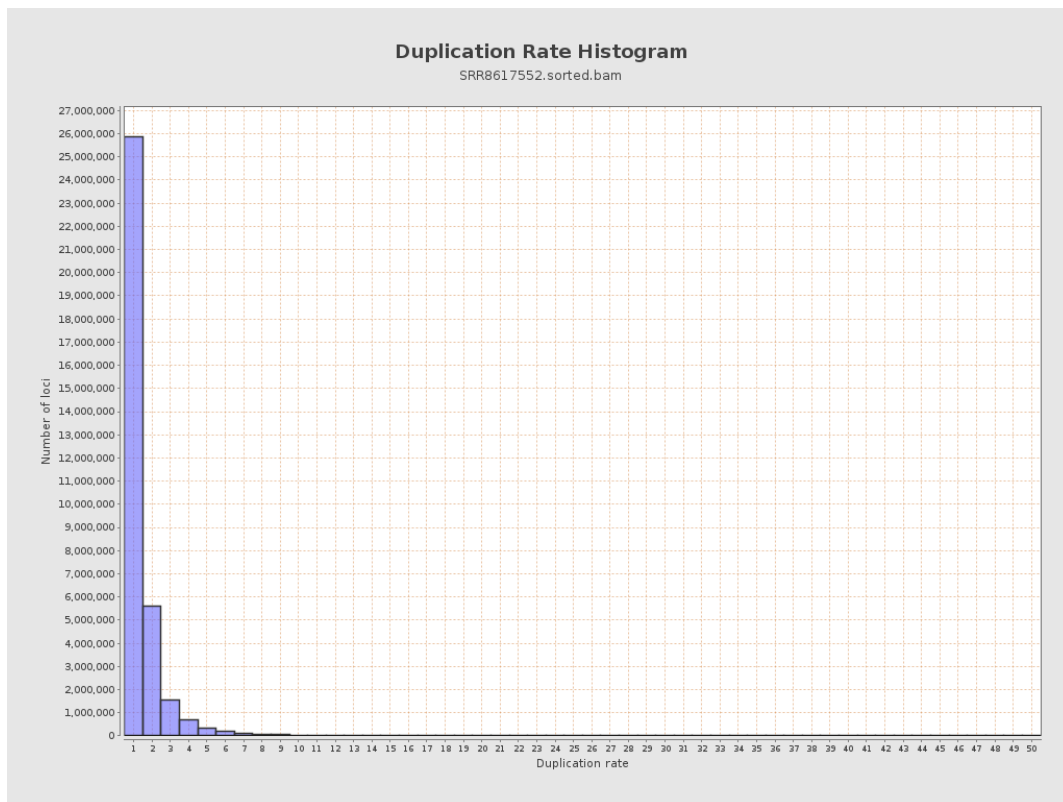
5. Results : Coverage Histogram (0-50X)



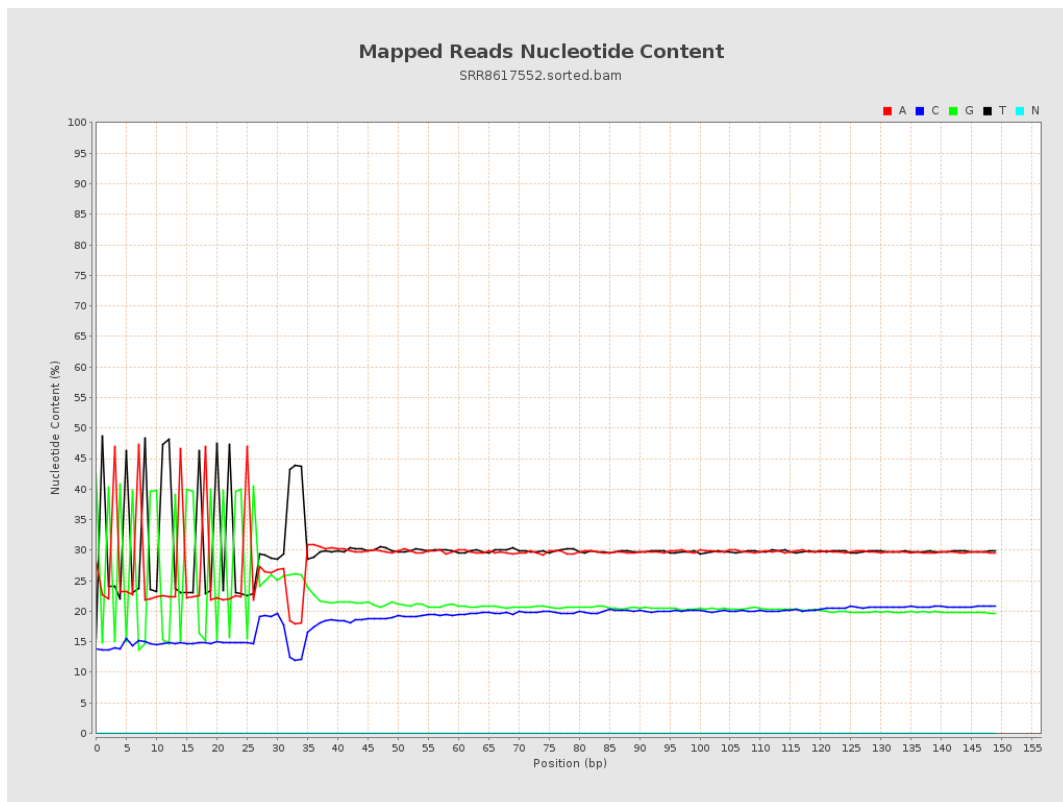
6. Results : Genome Fraction Coverage



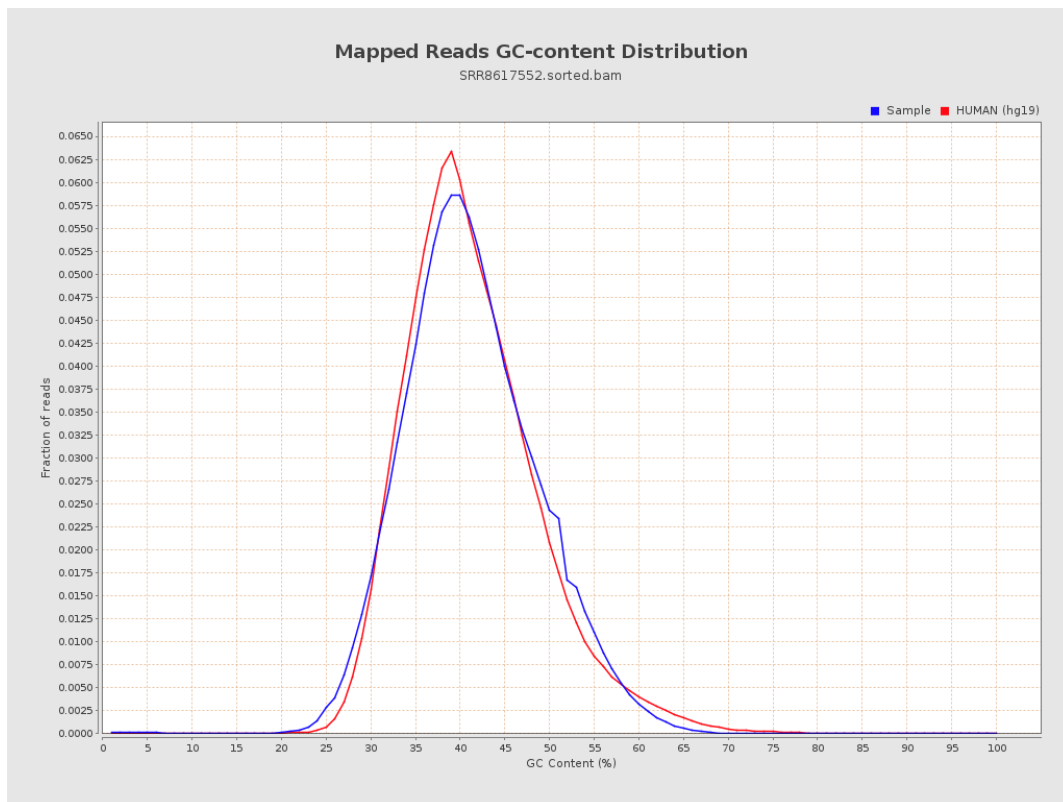
7. Results : Duplication Rate Histogram



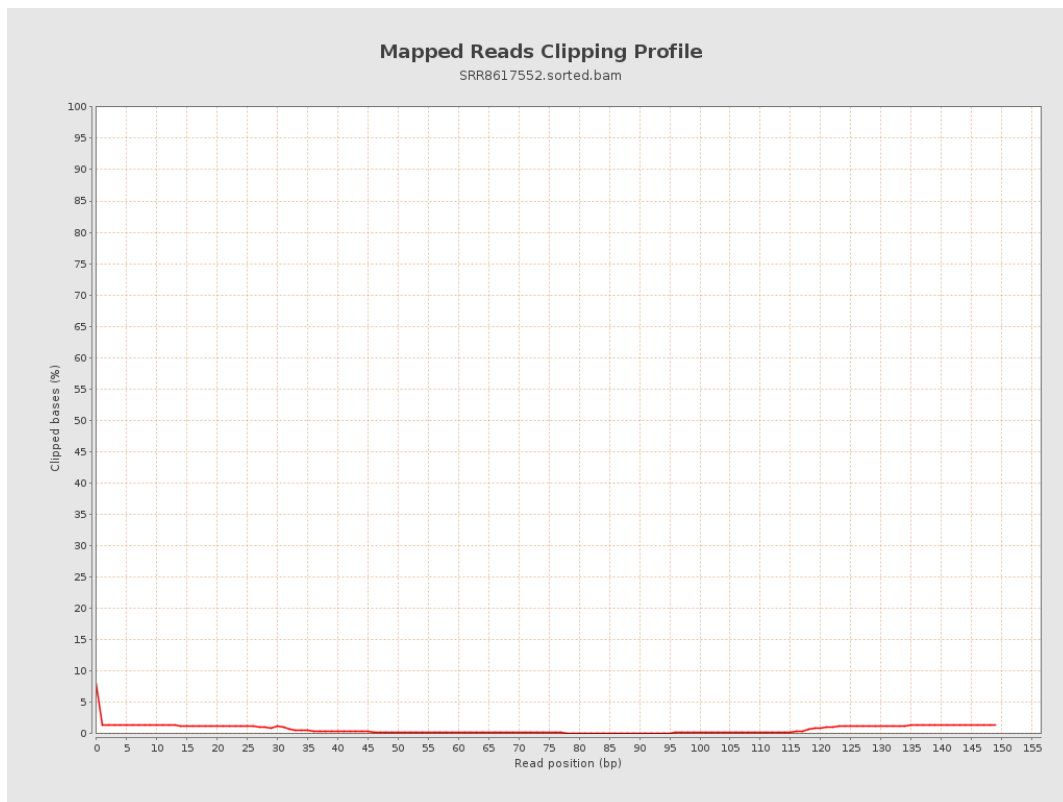
8. Results : Mapped Reads Nucleotide Content



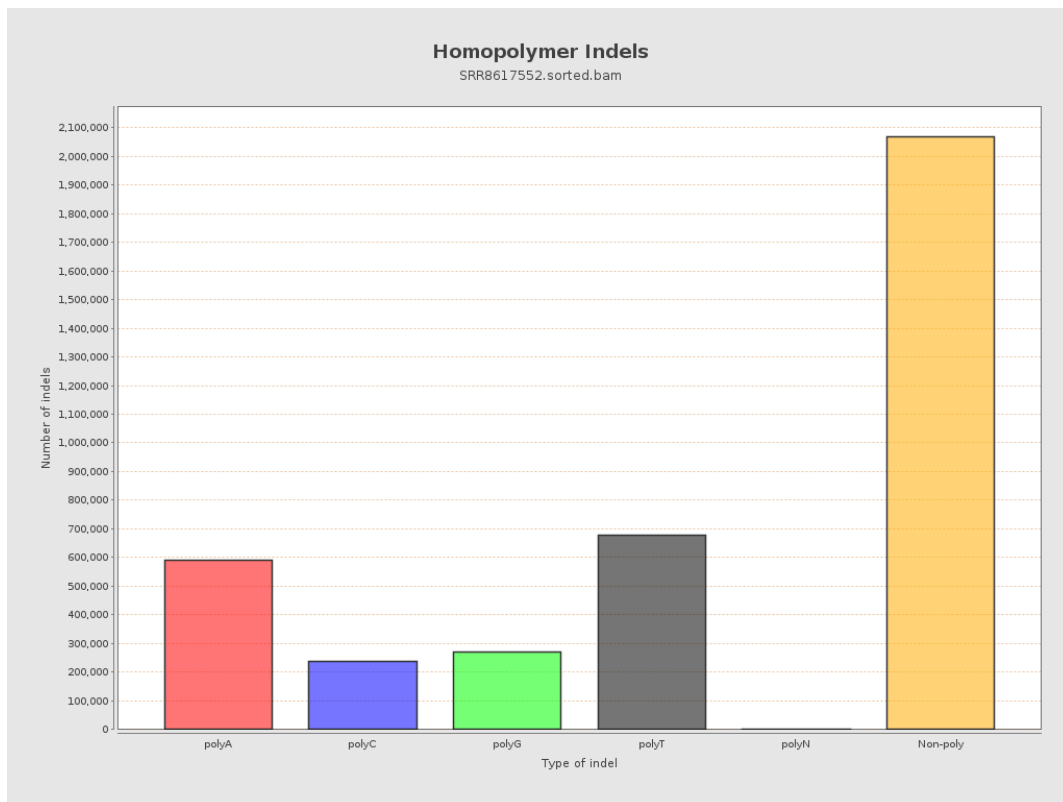
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



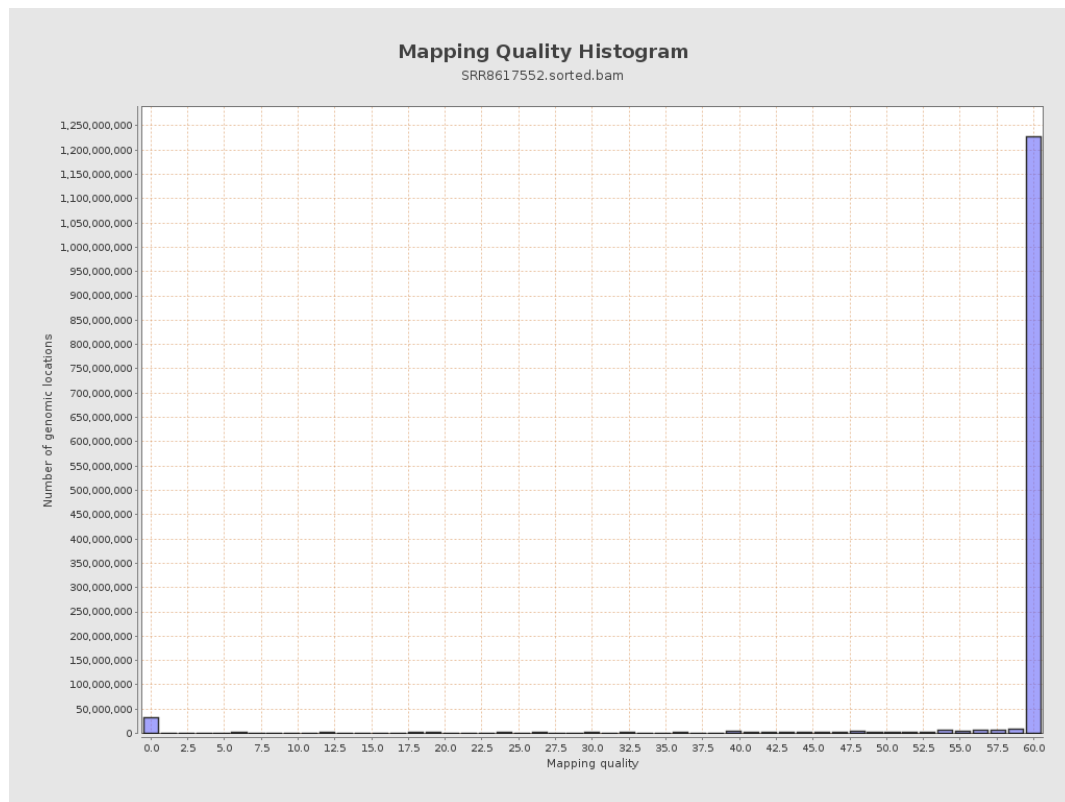
11. Results : Homopolymer Indels



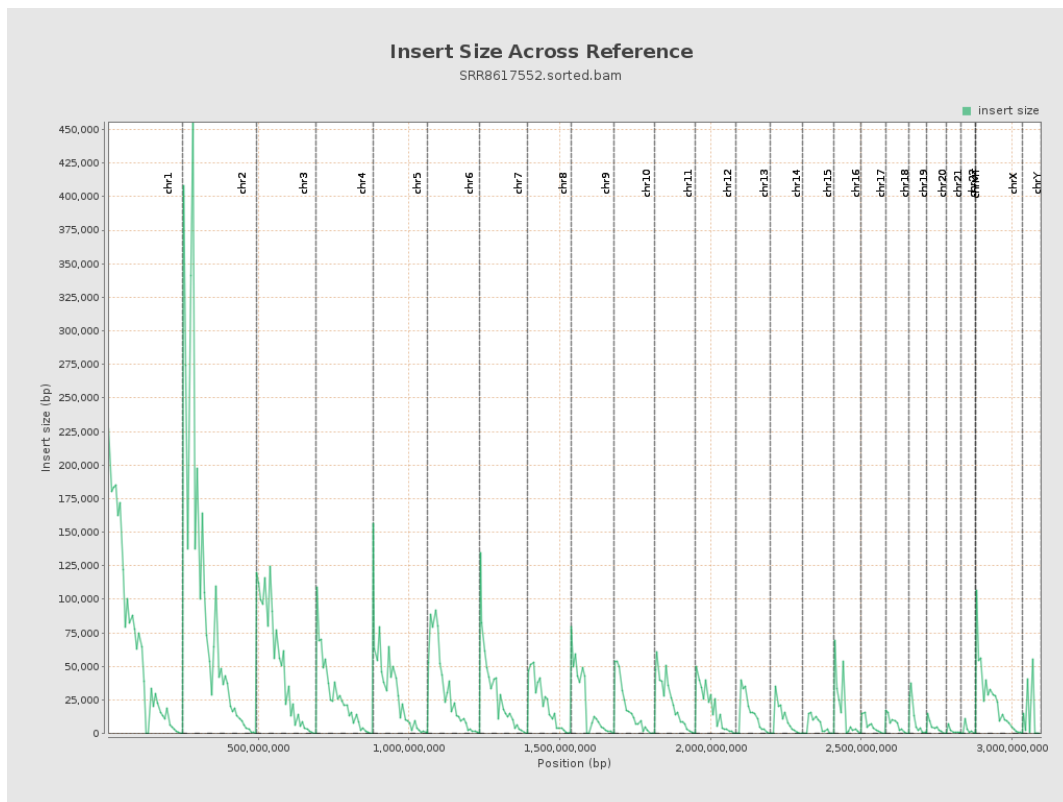
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

