

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 11:54:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618587.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_SRR618587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618587_1.fastq.gz SRR618587_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 11:54:40 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,003,888
Mapped reads	59,606,595 / 96.13%
Unmapped reads	2,397,293 / 3.87%
Mapped paired reads	59,606,595 / 96.13%
Mapped reads, first in pair	30,152,736 / 48.63%
Mapped reads, second in pair	29,453,859 / 47.5%
Mapped reads, both in pair	58,350,568 / 94.11%
Mapped reads, singletons	1,256,027 / 2.03%
Secondary alignments	0
Supplementary alignments	189,630 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	18,460,183 / 29.77%
Duplication rate	25.86%
Clipped reads	13,554,928 / 21.86%

2.2. ACGT Content

Number/percentage of A's	1,533,146,125 / 27.38%
Number/percentage of C's	1,215,316,127 / 21.7%
Number/percentage of T's	1,556,225,396 / 27.79%
Number/percentage of G's	1,295,179,594 / 23.13%
Number/percentage of N's	510,138 / 0.01%

GC Percentage	44.83%
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2.3. Coverage

Mean	1.8103
Standard Deviation	7.7978

2.4. Mapping Quality

Mean Mapping Quality	51.69
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2.5. Insert size

Mean	62,567.99
Standard Deviation	2,484,377.33
P25/Median/P75	166 / 194 / 232

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	72,697,969
Insertions	1,054,158
Mapped reads with at least one insertion	1.73%
Deletions	2,825,976
Mapped reads with at least one deletion	4.62%
Homopolymer indels	52.4%

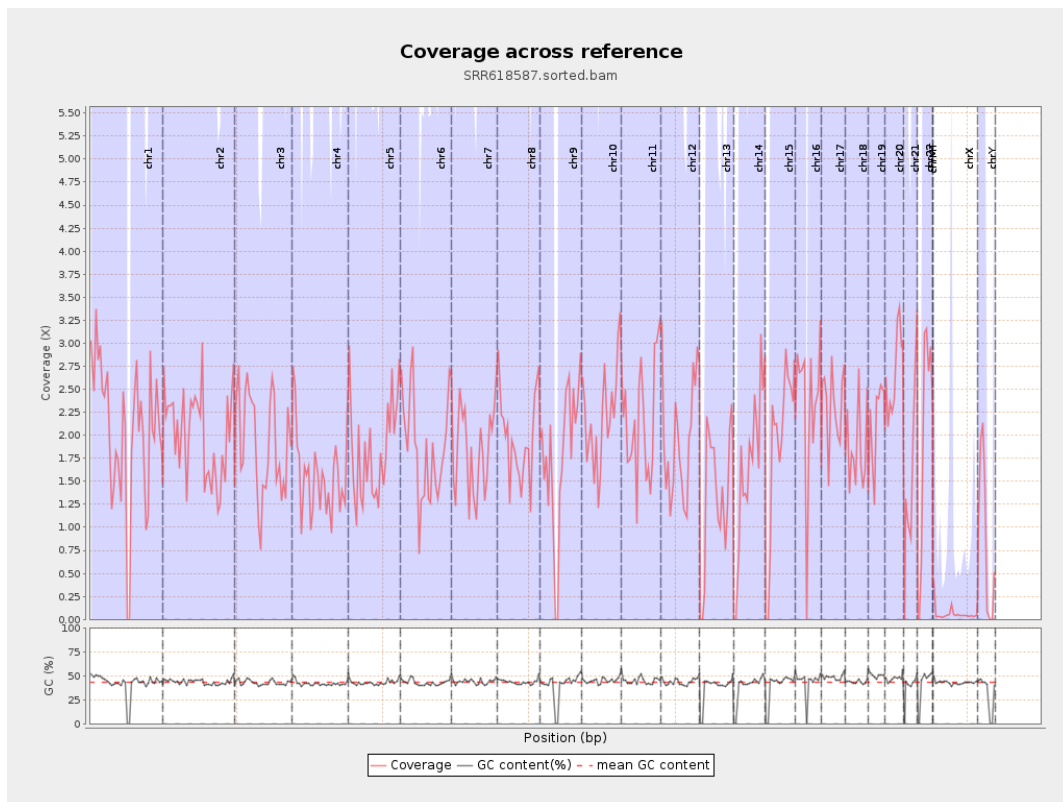
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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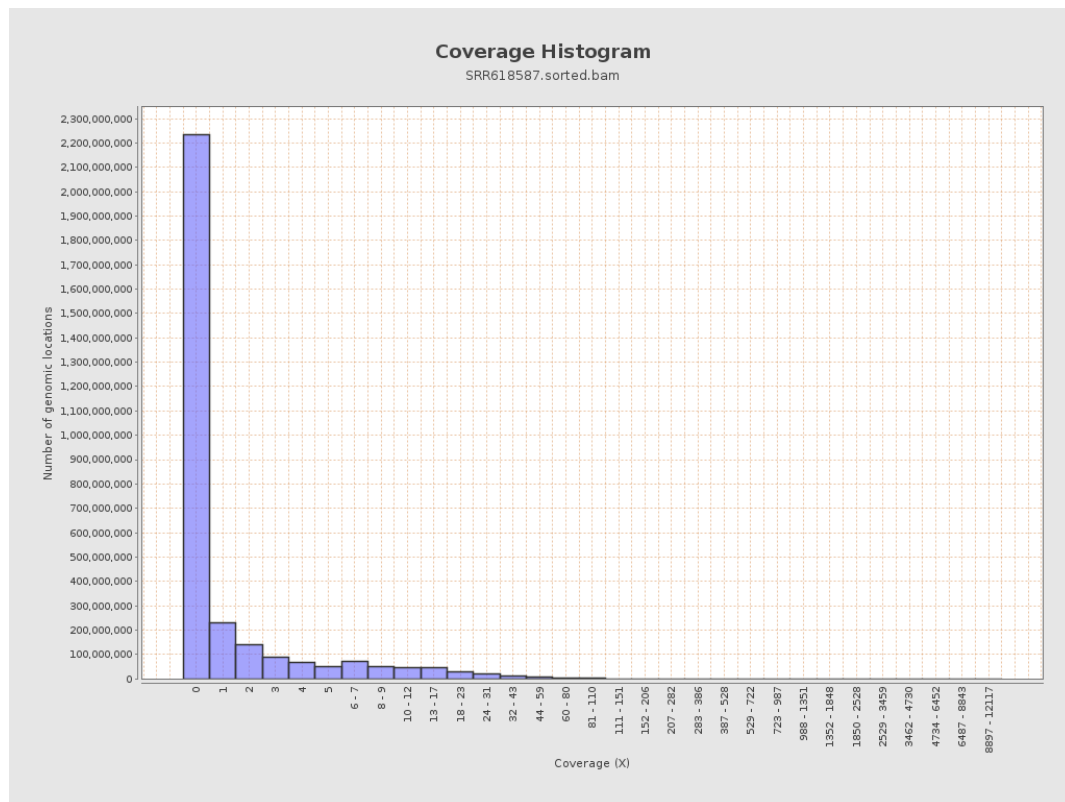
		bases	coverage	deviation
chr1	249250621	507317925	2.0354	8.9539
chr2	243199373	487708716	2.0054	10.1383
chr3	198022430	375090657	1.8942	5.7485
chr4	191154276	298954966	1.5639	5.8933
chr5	180915260	335271589	1.8532	5.8596
chr6	171115067	316435973	1.8493	6.364
chr7	159138663	294056595	1.8478	5.9503
chr8	146364022	287220997	1.9624	6.1208
chr9	141213431	250006584	1.7704	7.6373
chr10	135534747	296217947	2.1855	6.8739
chr11	135006516	291783761	2.1613	7.4387
chr12	133851895	263089472	1.9655	7.7585
chr13	115169878	155838695	1.3531	4.733
chr14	107349540	173770804	1.6187	5.5389
chr15	102531392	192478694	1.8773	6.3591
chr16	90354753	210282988	2.3273	20.5194
chr17	81195210	188428084	2.3207	7.7049
chr18	78077248	143317380	1.8356	7.3446
chr19	59128983	124906826	2.1124	7.7665
chr20	63025520	169449352	2.6886	7.7629
chr21	48129895	78052964	1.6217	8.9347
chr22	51304566	101497956	1.9783	7.1454
chrMT	16571	6243	0.3767	1.5928
chrX	155270560	9535199	0.0614	1.6614

chrY	59373566	53540029	0.9017	7.7474
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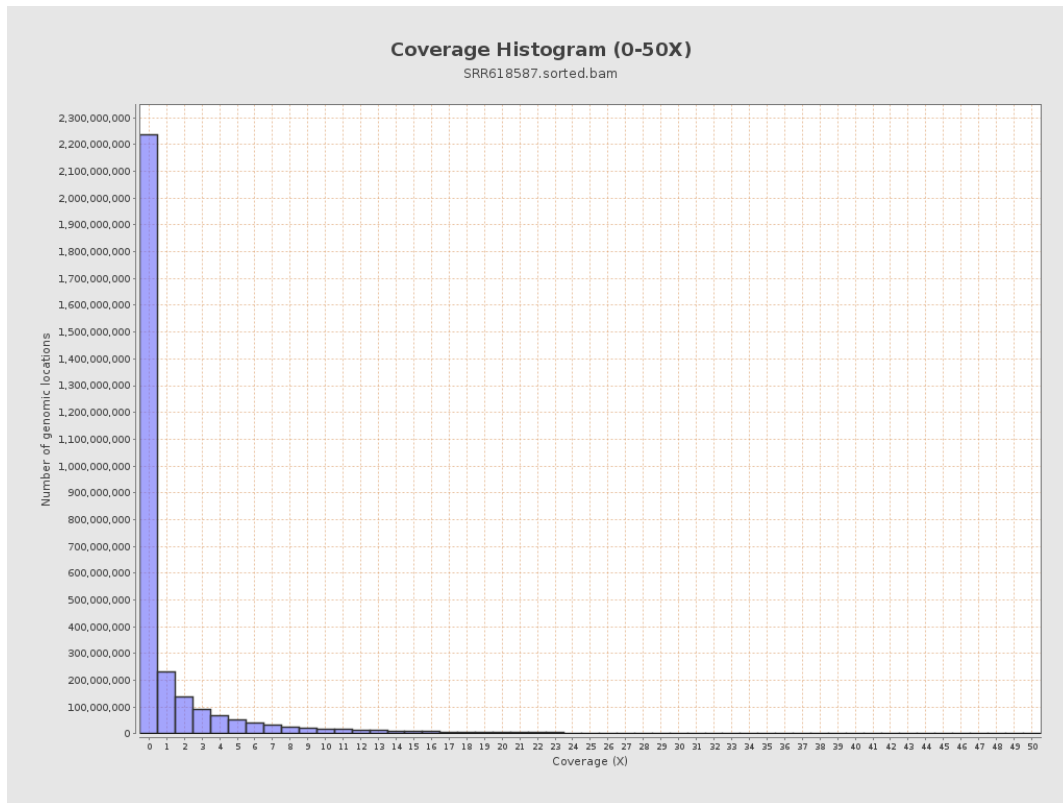
3. Results : Coverage across reference



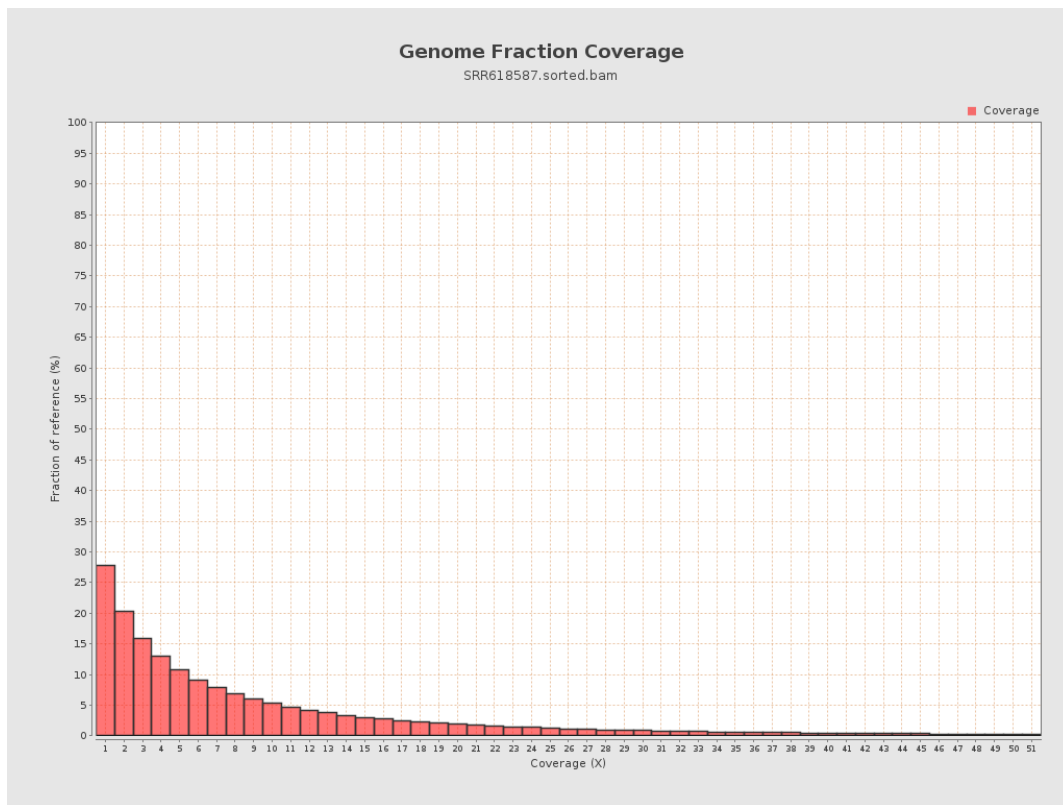
4. Results : Coverage Histogram



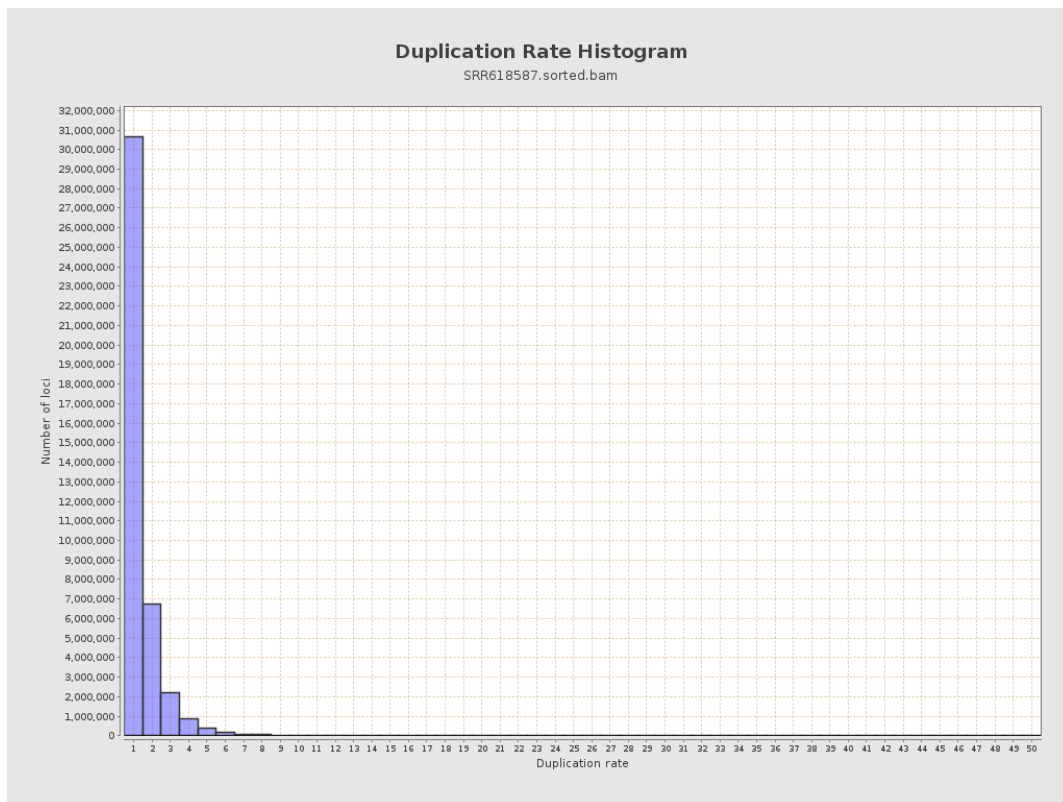
5. Results : Coverage Histogram (0-50X)



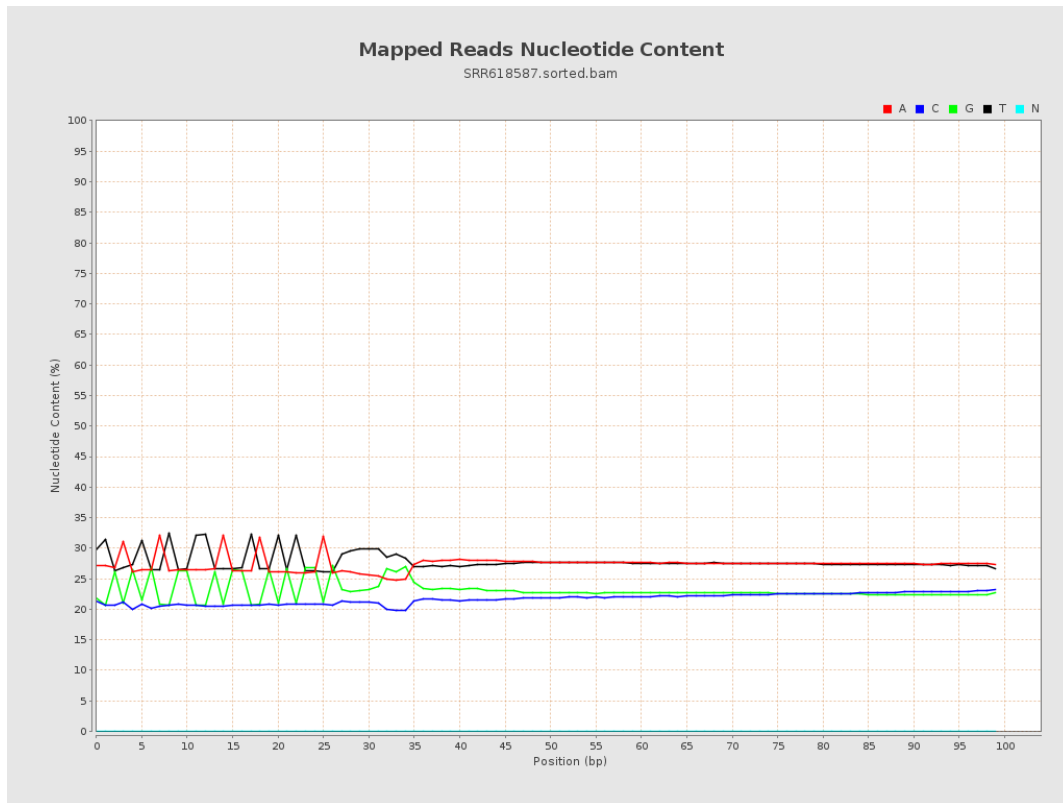
6. Results : Genome Fraction Coverage



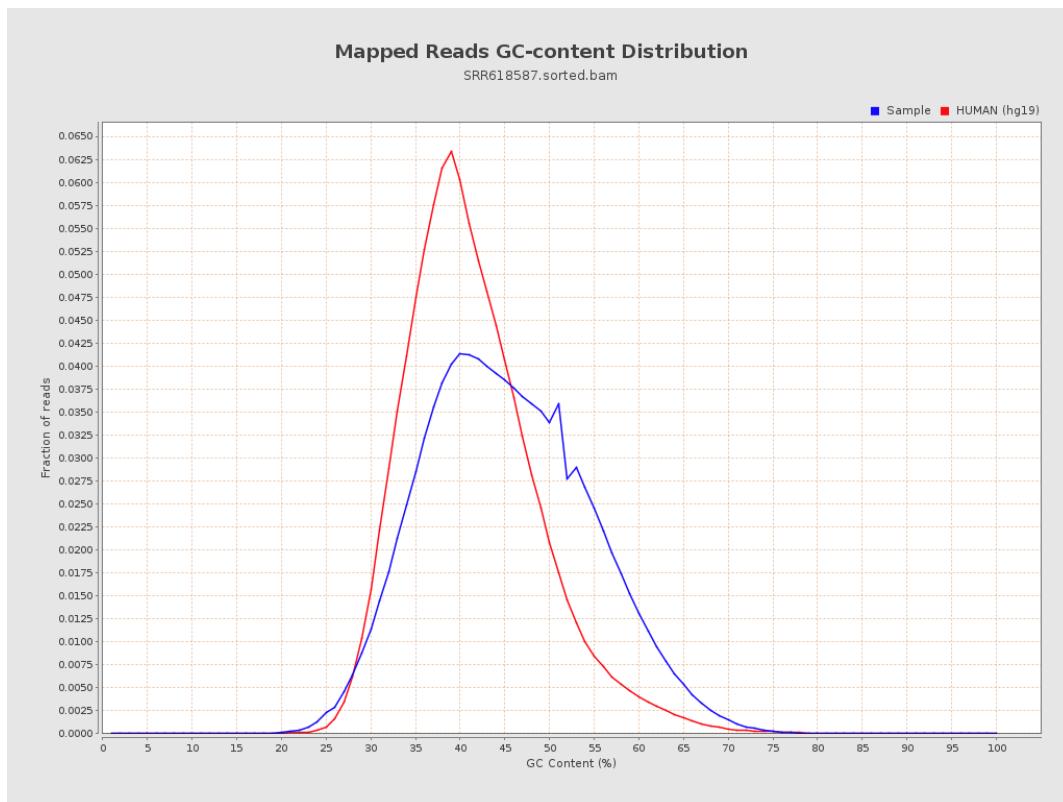
7. Results : Duplication Rate Histogram



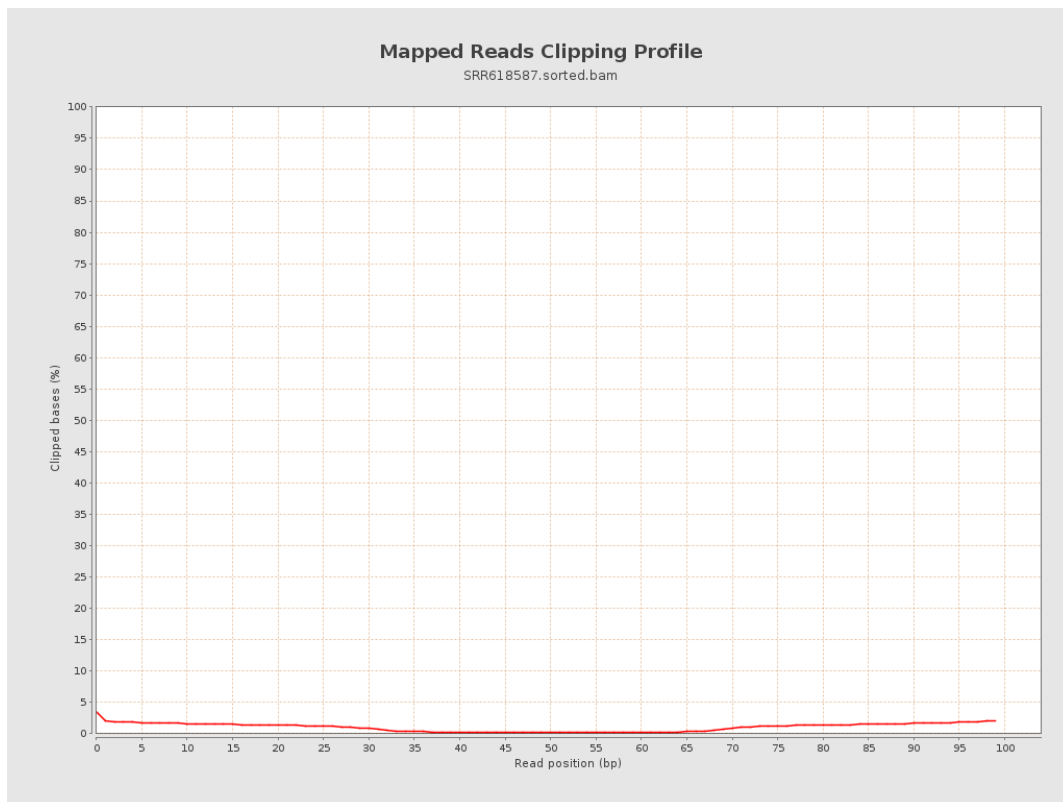
8. Results : Mapped Reads Nucleotide Content



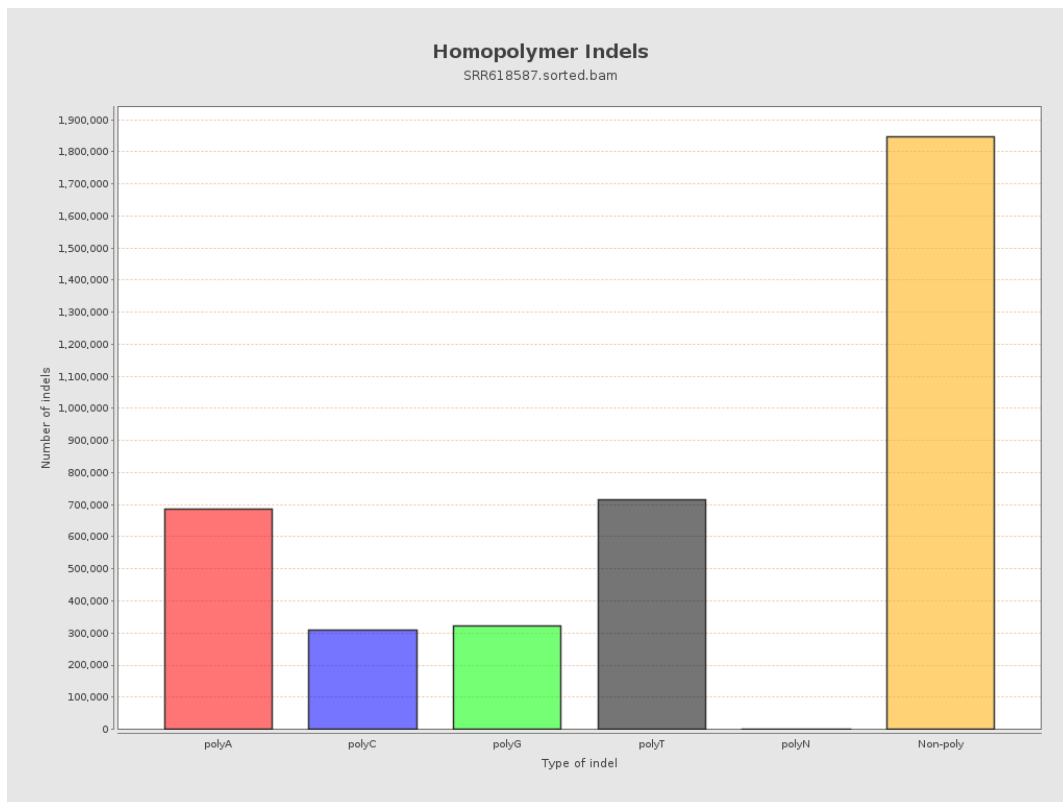
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



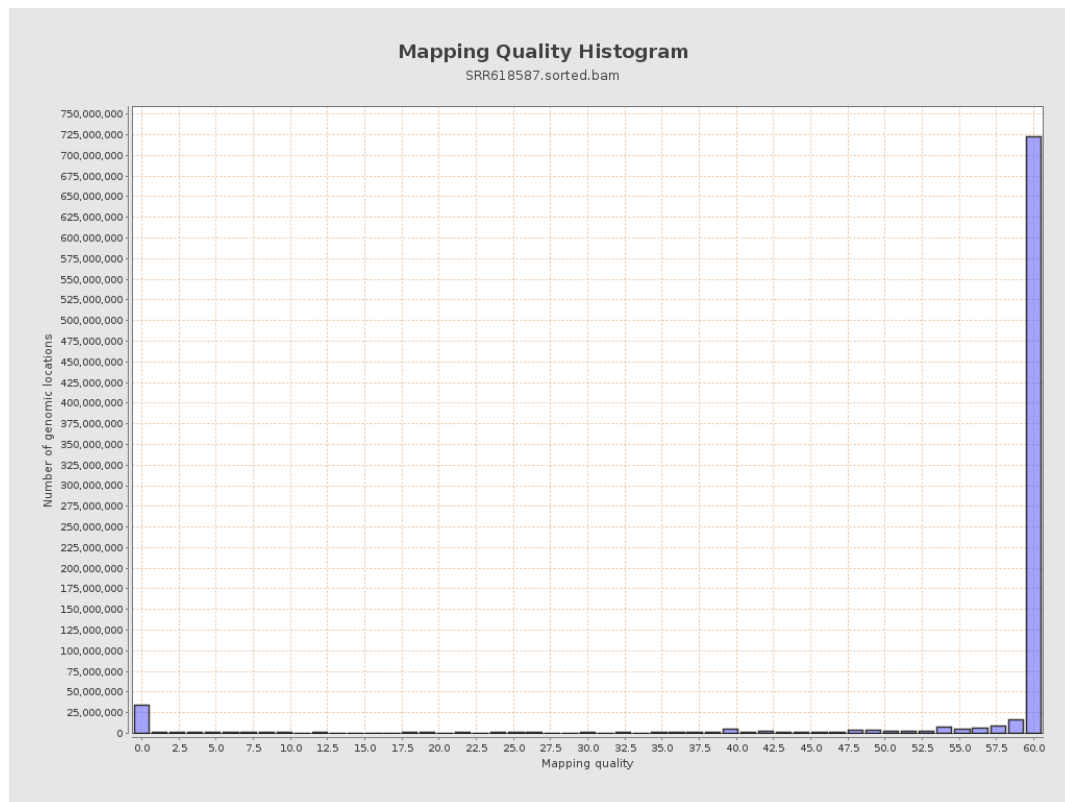
11. Results : Homopolymer Indels



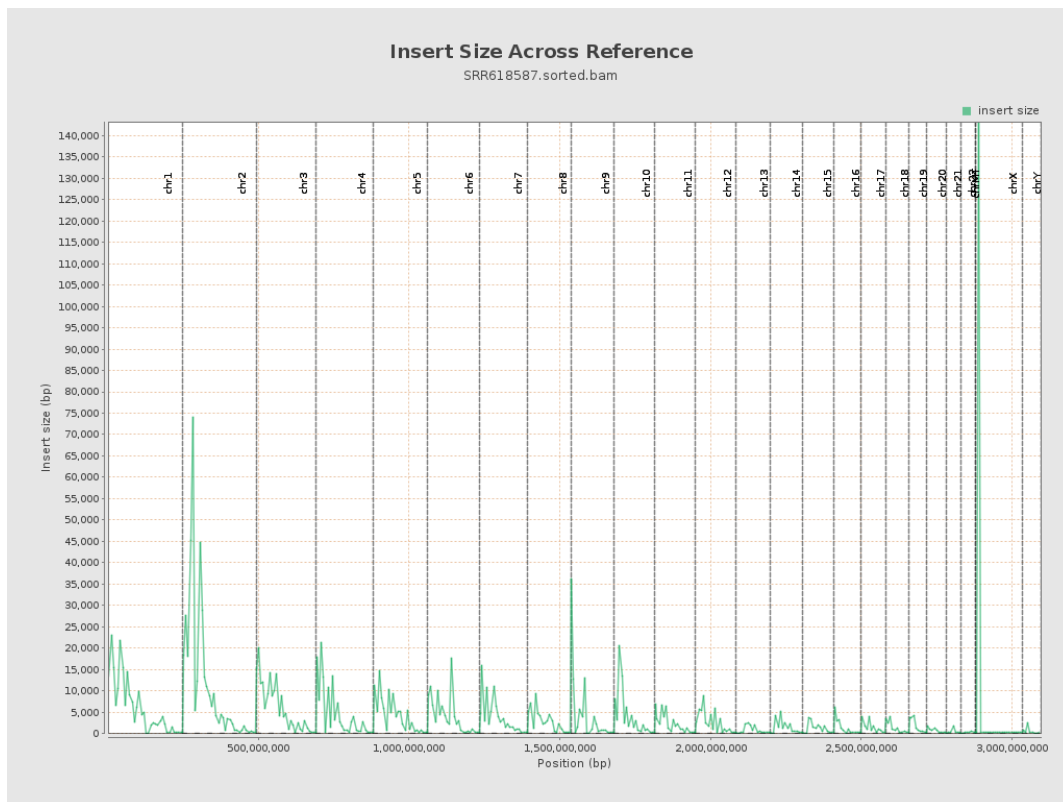
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

