

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 01:32:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618577.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_SRR618577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618577_1.fastq.gz SRR618577_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 01:32:08 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,882,138
Mapped reads	61,329,129 / 96%
Unmapped reads	2,553,009 / 4%
Mapped paired reads	61,329,129 / 96%
Mapped reads, first in pair	30,939,269 / 48.43%
Mapped reads, second in pair	30,389,860 / 47.57%
Mapped reads, both in pair	60,237,592 / 94.29%
Mapped reads, singletons	1,091,537 / 1.71%
Secondary alignments	0
Supplementary alignments	294,161 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	20,564,592 / 32.19%
Duplication rate	28.6%
Clipped reads	11,260,035 / 17.63%

2.2. ACGT Content

Number/percentage of A's	1,549,383,494 / 26.4%
Number/percentage of C's	1,347,213,812 / 22.96%
Number/percentage of T's	1,557,063,543 / 26.53%
Number/percentage of G's	1,414,375,768 / 24.1%
Number/percentage of N's	286,797 / 0%

GC Percentage	47.06%
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2.3. Coverage

Mean	1.8971
Standard Deviation	11.7985

2.4. Mapping Quality

Mean Mapping Quality	53.43
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2.5. Insert size

Mean	103,476.31
Standard Deviation	3,231,662.96
P25/Median/P75	183 / 210 / 248

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	79,156,404
Insertions	1,179,295
Mapped reads with at least one insertion	1.89%
Deletions	3,390,900
Mapped reads with at least one deletion	5.37%
Homopolymer indels	52.53%

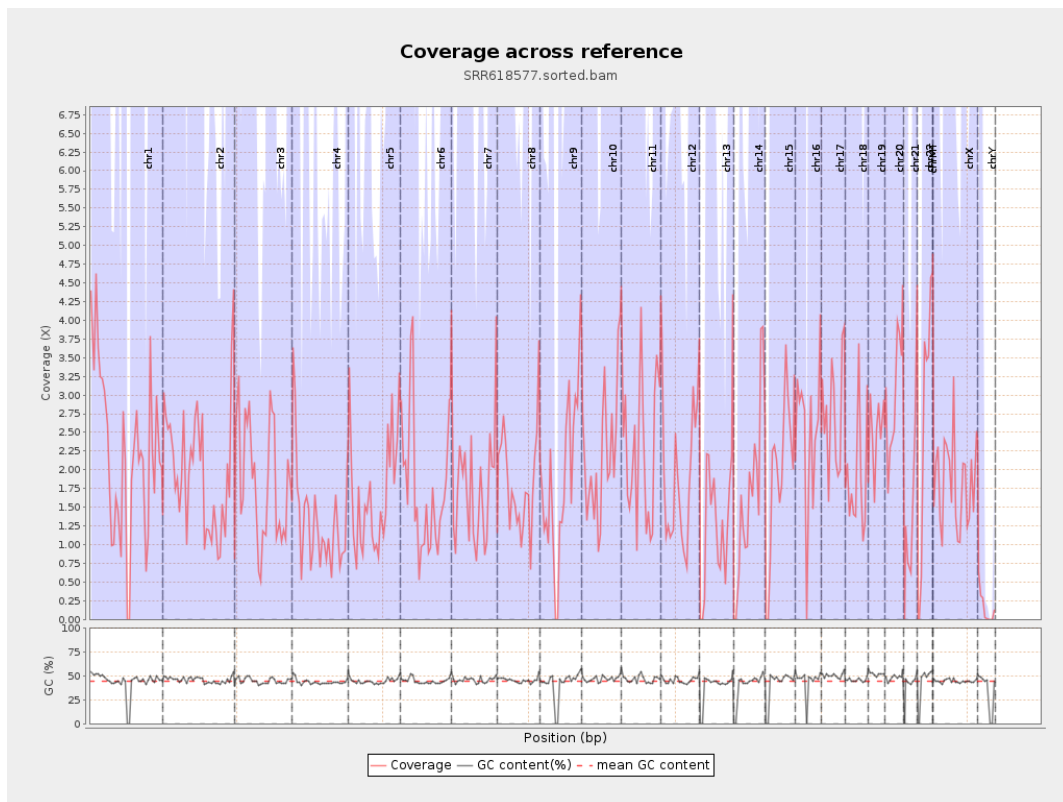
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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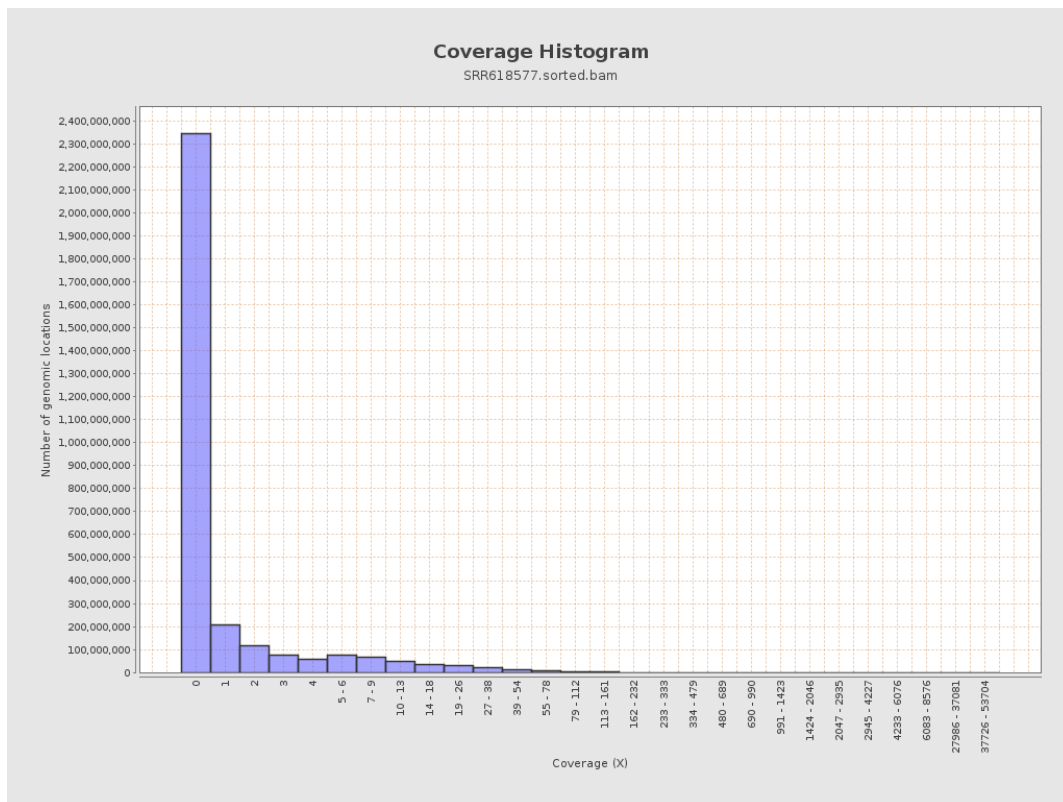
		bases	coverage	deviation
chr1	249250621	550567276	2.2089	10.5348
chr2	243199373	476988900	1.9613	10.2138
chr3	198022430	361919127	1.8277	29.8752
chr4	191154276	252041831	1.3185	7.2358
chr5	180915260	307598160	1.7002	7.2226
chr6	171115067	296976786	1.7355	7.321
chr7	159138663	287379574	1.8058	7.6917
chr8	146364022	267722061	1.8292	7.5303
chr9	141213431	262084627	1.8559	9.2693
chr10	135534747	296304817	2.1862	8.7251
chr11	135006516	308776272	2.2871	9.9748
chr12	133851895	253268013	1.8922	8.1307
chr13	115169878	147062638	1.2769	5.9949
chr14	107349540	178151145	1.6595	7.6837
chr15	102531392	200163752	1.9522	8.7038
chr16	90354753	223913653	2.4782	18.0452
chr17	81195210	220989658	2.7217	11.1863
chr18	78077248	143939910	1.8436	9.0342
chr19	59128983	148514673	2.5117	12.1368
chr20	63025520	188616563	2.9927	11.2211
chr21	48129895	75494531	1.5686	15.1301
chr22	51304566	132068080	2.5742	11.7992
chrMT	16571	81150	4.8971	16.7289
chrX	155270560	283264177	1.8243	7.2363

chrY	59373566	9062490	0.1526	6.3216
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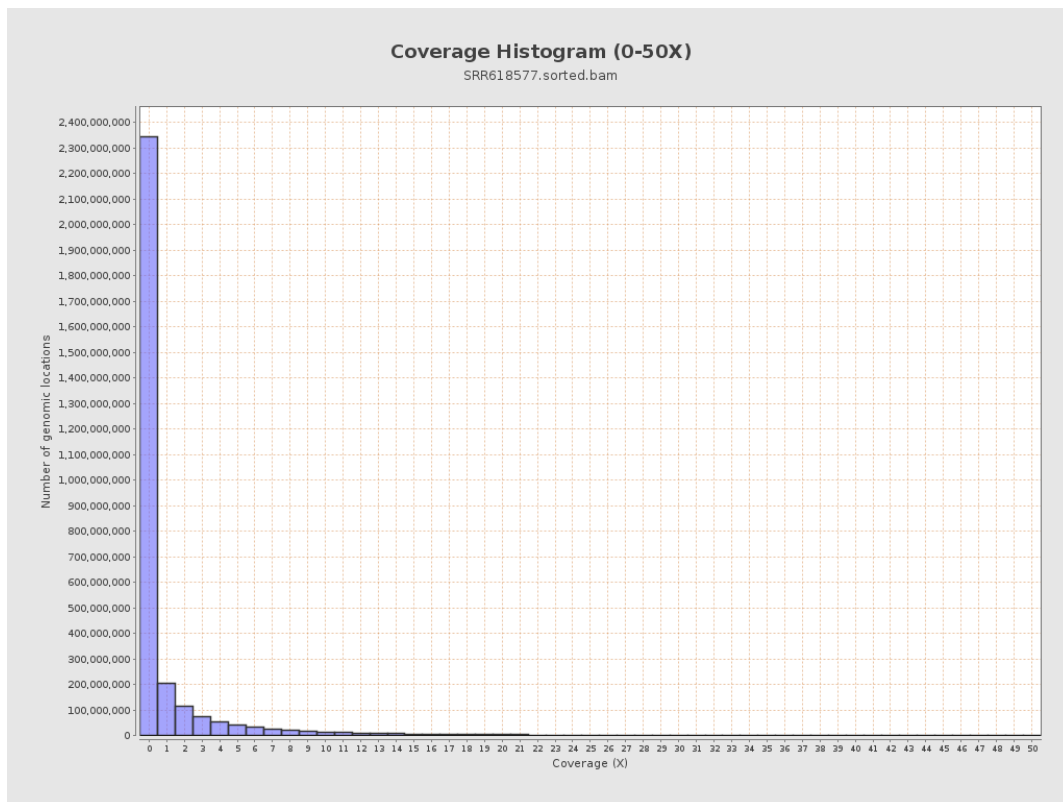
3. Results : Coverage across reference



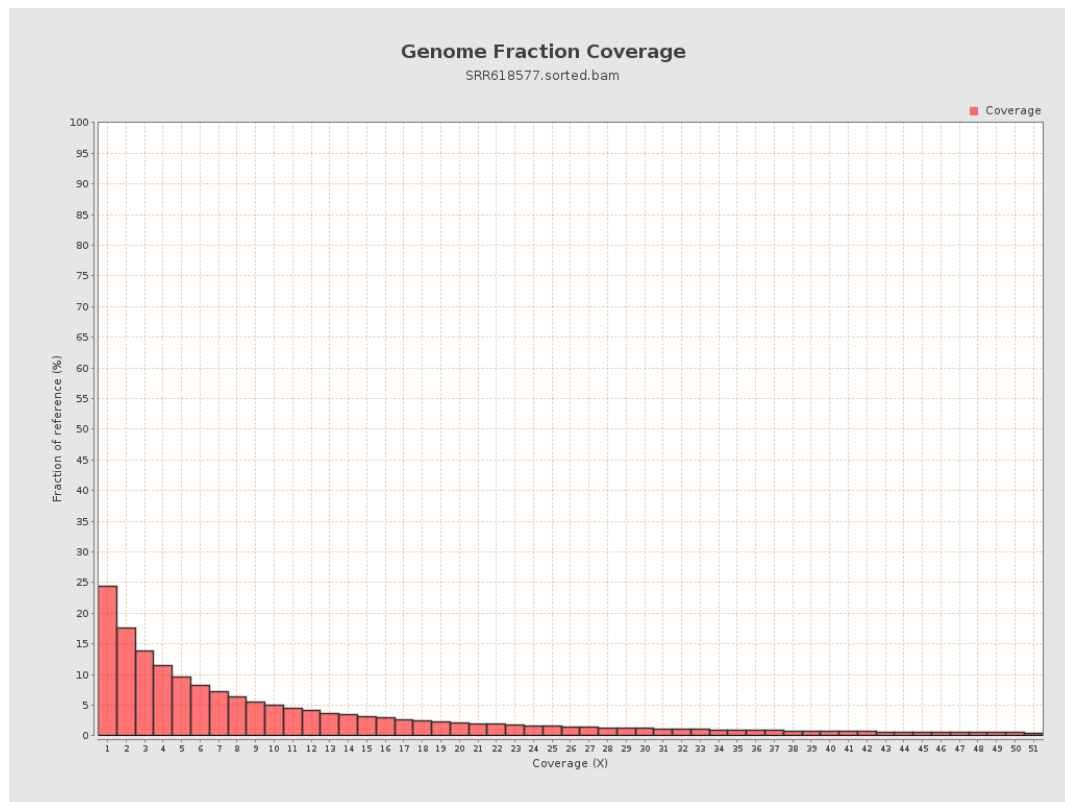
4. Results : Coverage Histogram



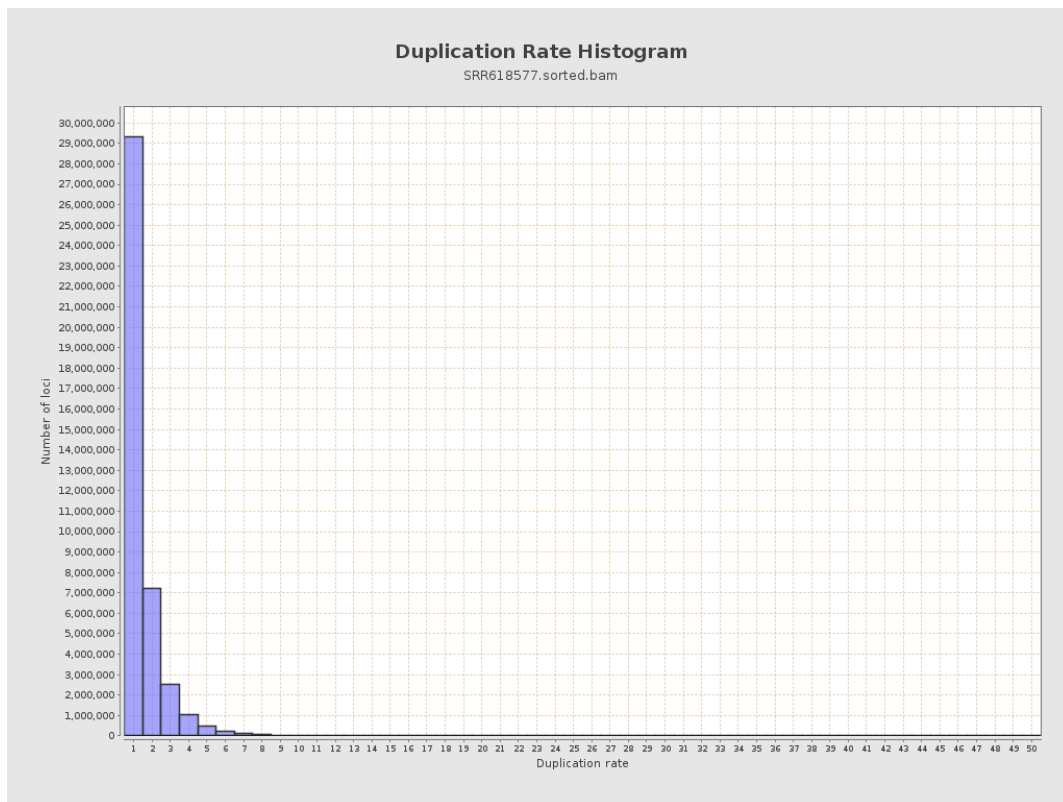
5. Results : Coverage Histogram (0-50X)



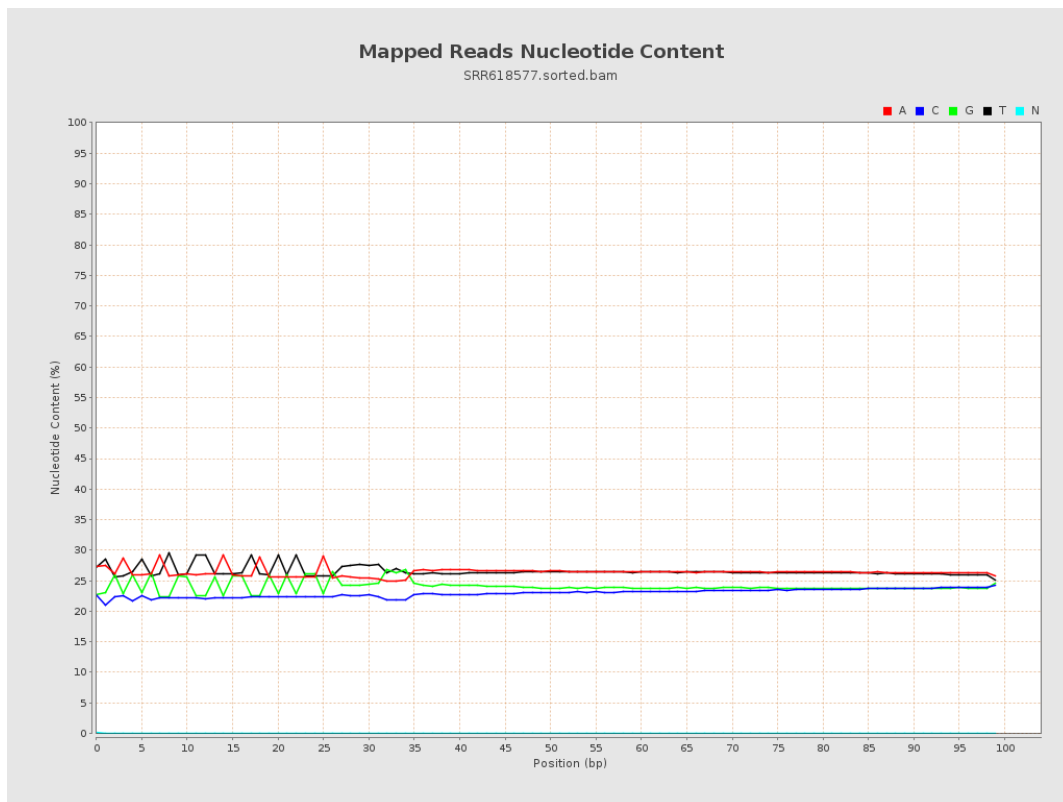
6. Results : Genome Fraction Coverage



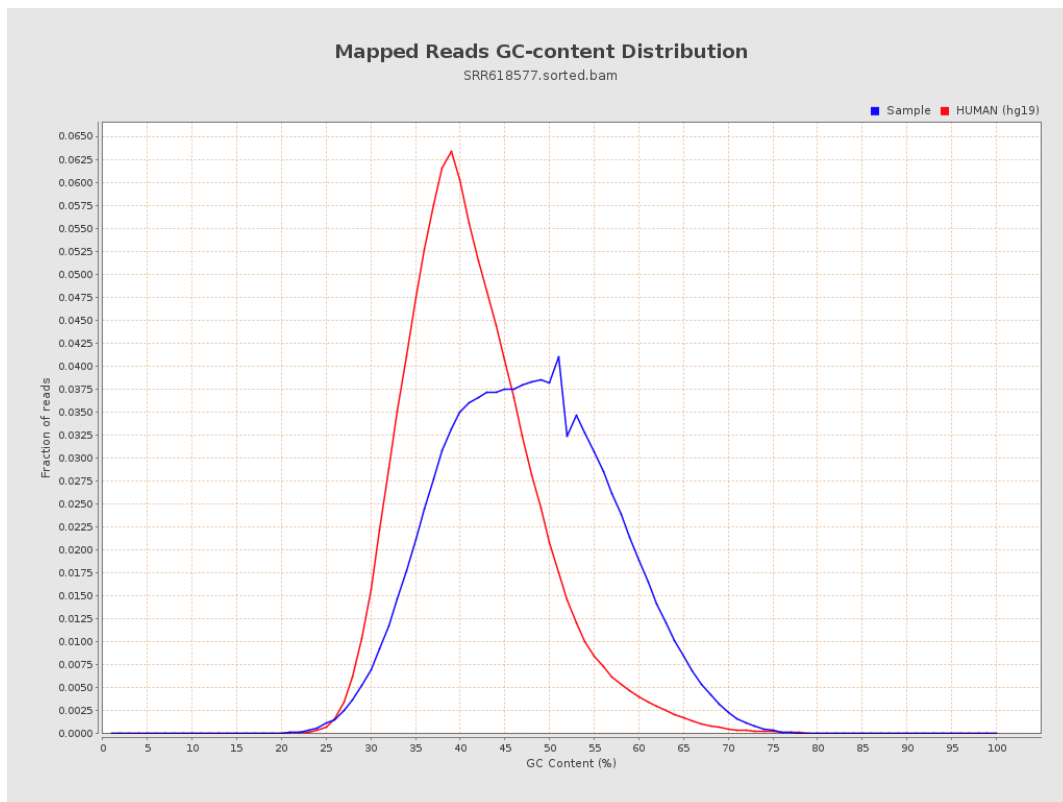
7. Results : Duplication Rate Histogram



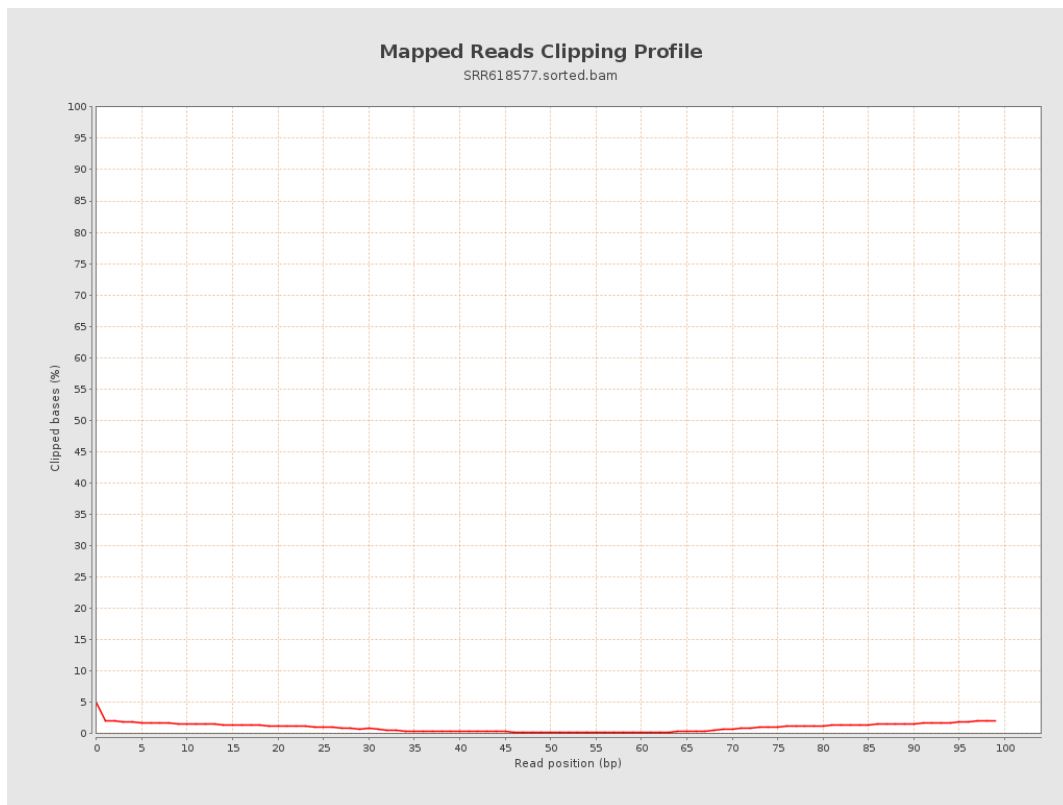
8. Results : Mapped Reads Nucleotide Content



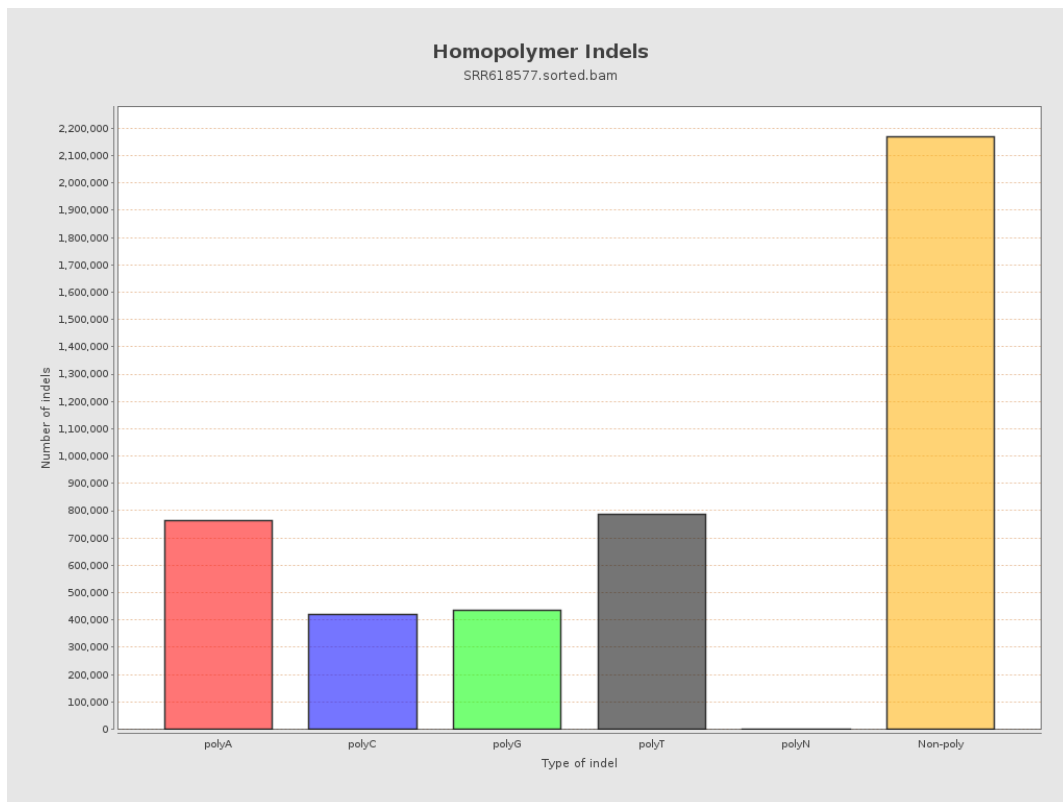
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



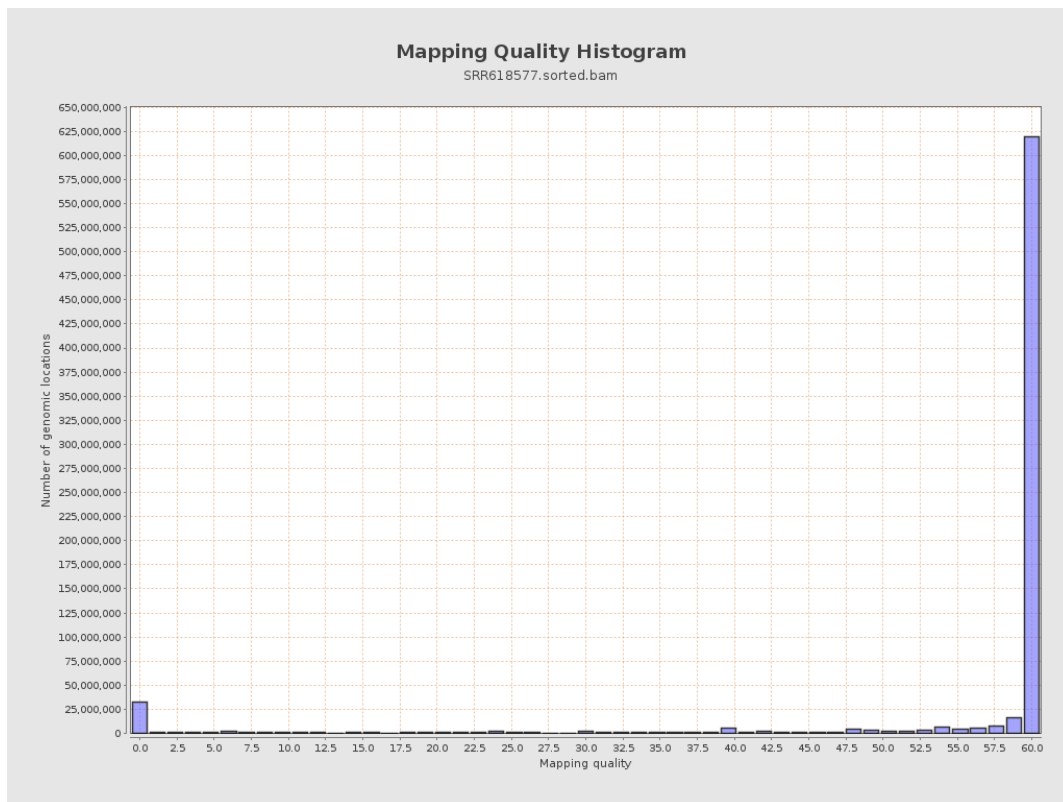
11. Results : Homopolymer Indels



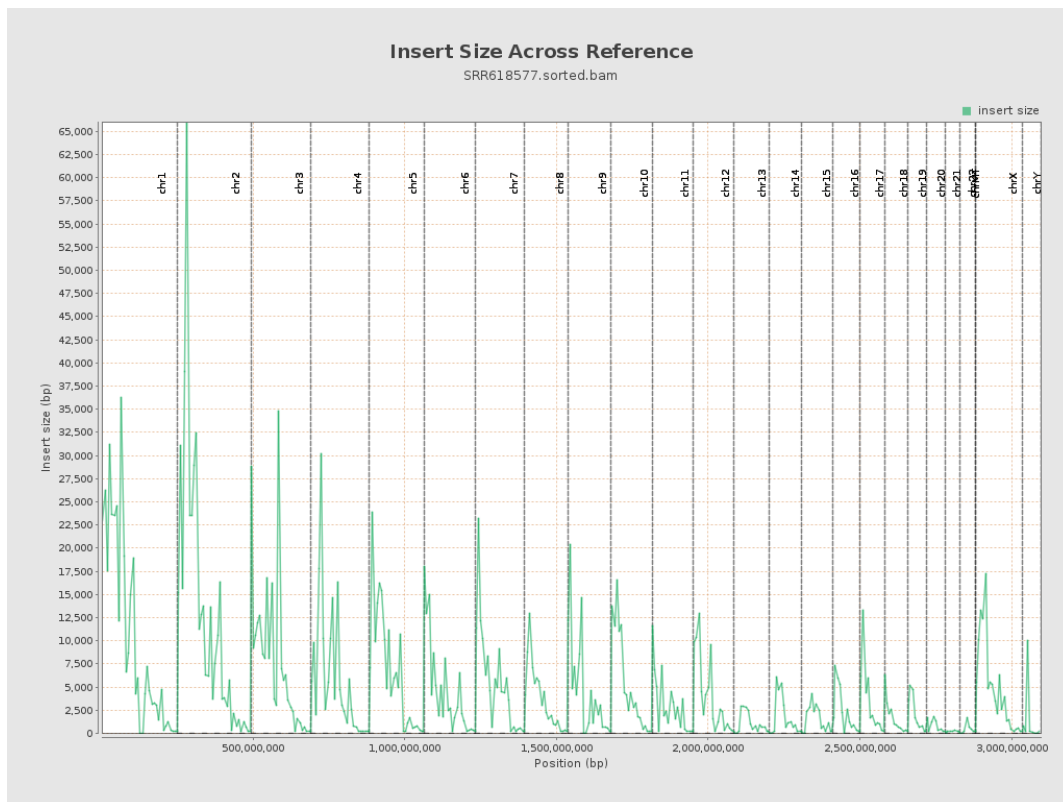
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

