

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 19:24:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630575.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_SRR630575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630575_1.fastq.gz SRR630575_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 19:24:28 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,205,002
Mapped reads	36,431,621 / 97.92%
Unmapped reads	773,381 / 2.08%
Mapped paired reads	36,431,621 / 97.92%
Mapped reads, first in pair	18,289,131 / 49.16%
Mapped reads, second in pair	18,142,490 / 48.76%
Mapped reads, both in pair	36,213,594 / 97.34%
Mapped reads, singletons	218,027 / 0.59%
Secondary alignments	0
Supplementary alignments	61,254 / 0.16%
Read min/max/mean length	30 / 101 / 101.06
Duplicated reads (estimated)	5,122,750 / 13.77%
Duplication rate	11.77%
Clipped reads	4,339,209 / 11.66%

2.2. ACGT Content

Number/percentage of A's	1,029,617,919 / 28.9%
Number/percentage of C's	727,984,945 / 20.44%
Number/percentage of T's	1,036,860,792 / 29.11%
Number/percentage of G's	767,434,204 / 21.54%
Number/percentage of N's	537,179 / 0.02%

GC Percentage	41.98%
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2.3. Coverage

Mean	1.1516
Standard Deviation	5.5811

2.4. Mapping Quality

Mean Mapping Quality	54.17
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2.5. Insert size

Mean	27,024.04
Standard Deviation	1,639,478.55
P25/Median/P75	160 / 205 / 271

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	31,504,658
Insertions	672,937
Mapped reads with at least one insertion	1.81%
Deletions	2,002,739
Mapped reads with at least one deletion	5.34%
Homopolymer indels	54.64%

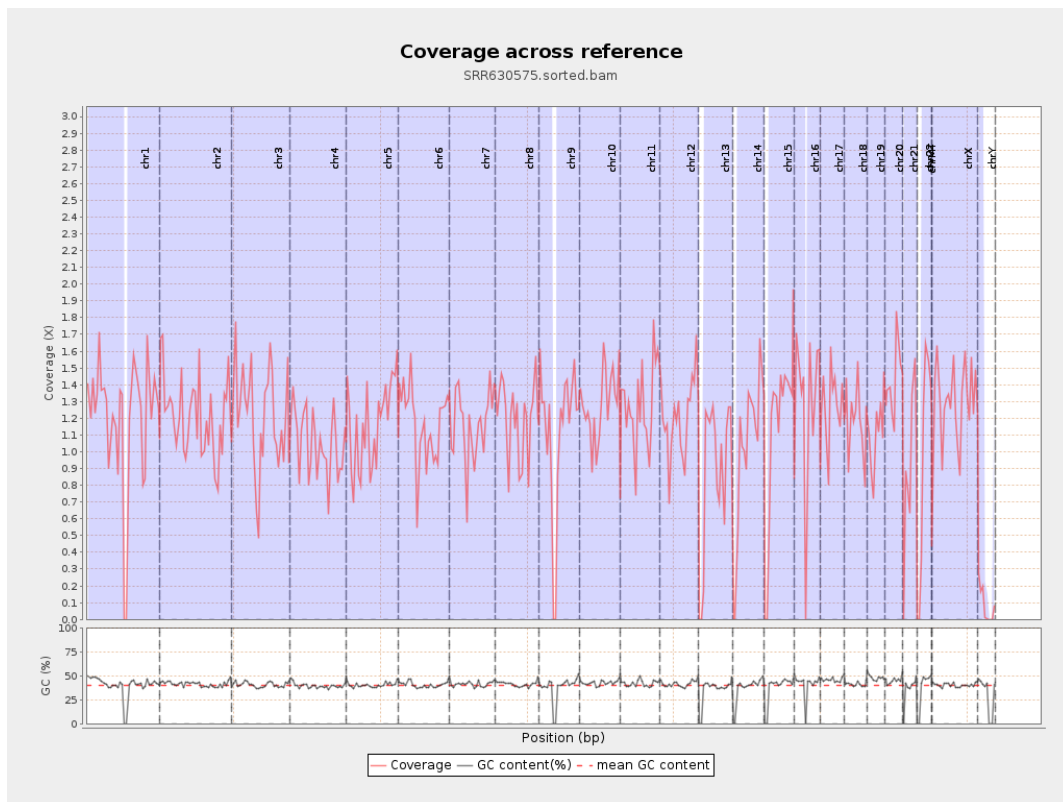
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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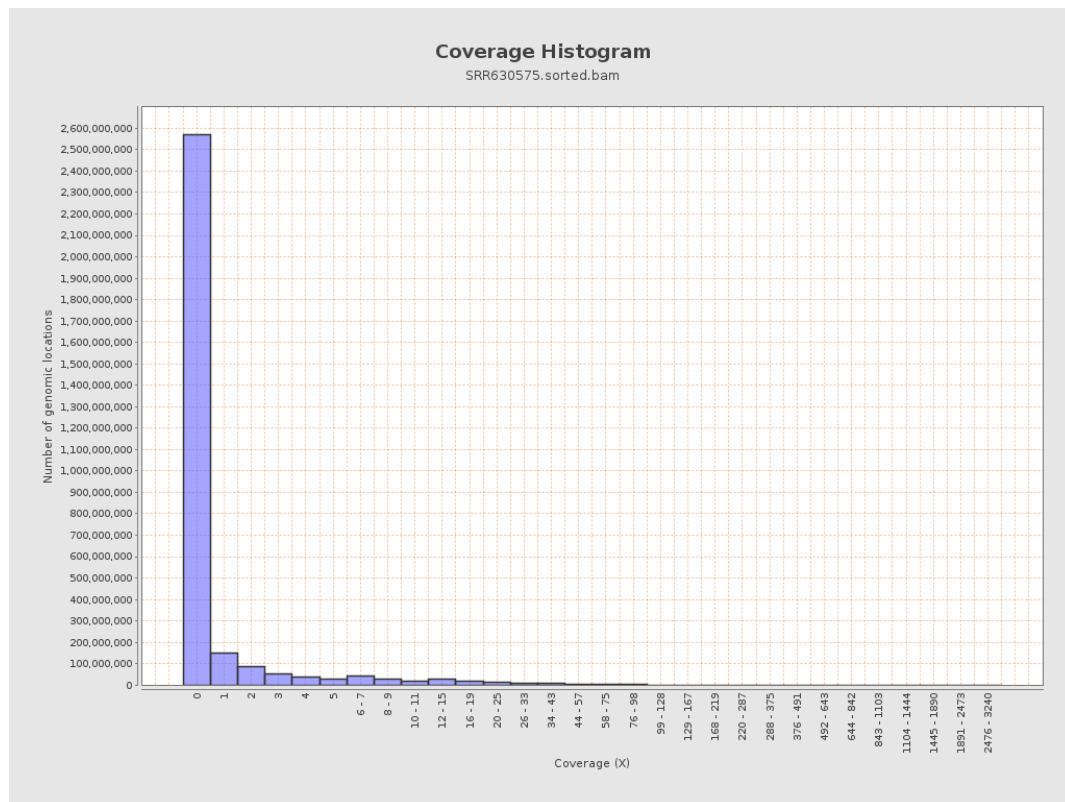
		bases	coverage	deviation
chr1	249250621	301031124	1.2077	6.2797
chr2	243199373	295154253	1.2136	6.2147
chr3	198022430	241998232	1.2221	5.283
chr4	191154276	201233952	1.0527	5.0362
chr5	180915260	210328390	1.1626	5.0529
chr6	171115067	199942668	1.1685	5.1504
chr7	159138663	184033128	1.1564	5.1909
chr8	146364022	175650397	1.2001	5.206
chr9	141213431	157469706	1.1151	6.216
chr10	135534747	173720179	1.2817	5.5412
chr11	135006516	171801867	1.2725	5.7992
chr12	133851895	161023297	1.203	5.3753
chr13	115169878	102030520	0.8859	4.3479
chr14	107349540	108759702	1.0131	4.7576
chr15	102531392	113792329	1.1098	5.0895
chr16	90354753	114639994	1.2688	7.6627
chr17	81195210	103718452	1.2774	5.8726
chr18	78077248	93155466	1.1931	5.8062
chr19	59128983	64010335	1.0826	5.8024
chr20	63025520	90359257	1.4337	6.2418
chr21	48129895	45685404	0.9492	6.6931
chr22	51304566	50607517	0.9864	5.5319
chrMT	16571	7192	0.434	2.0096
chrX	155270560	199928147	1.2876	5.5133

chrY	59373566	5056833	0.0852	2.5876
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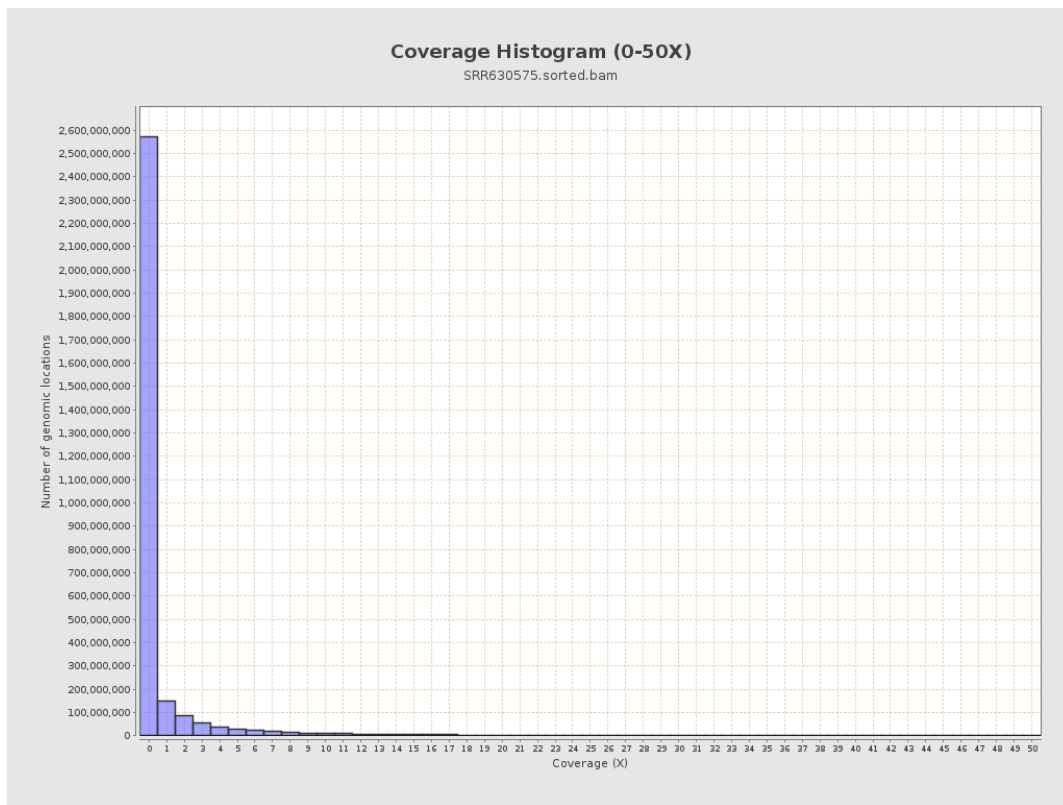
3. Results : Coverage across reference



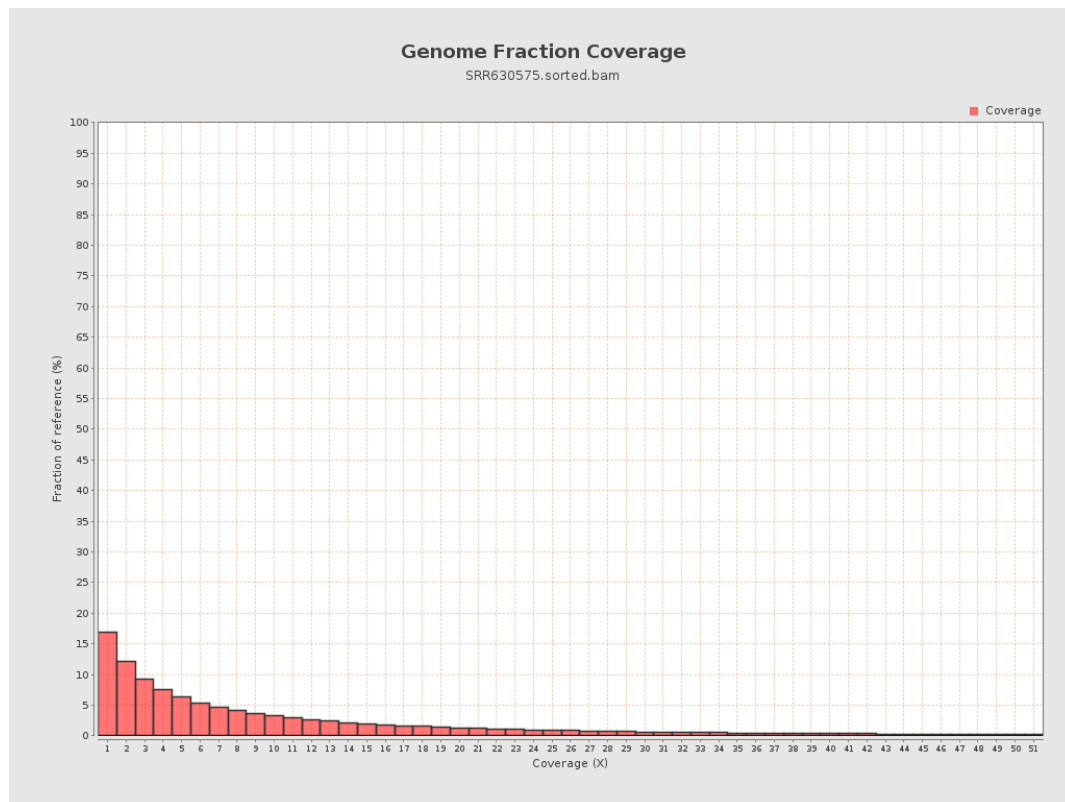
4. Results : Coverage Histogram



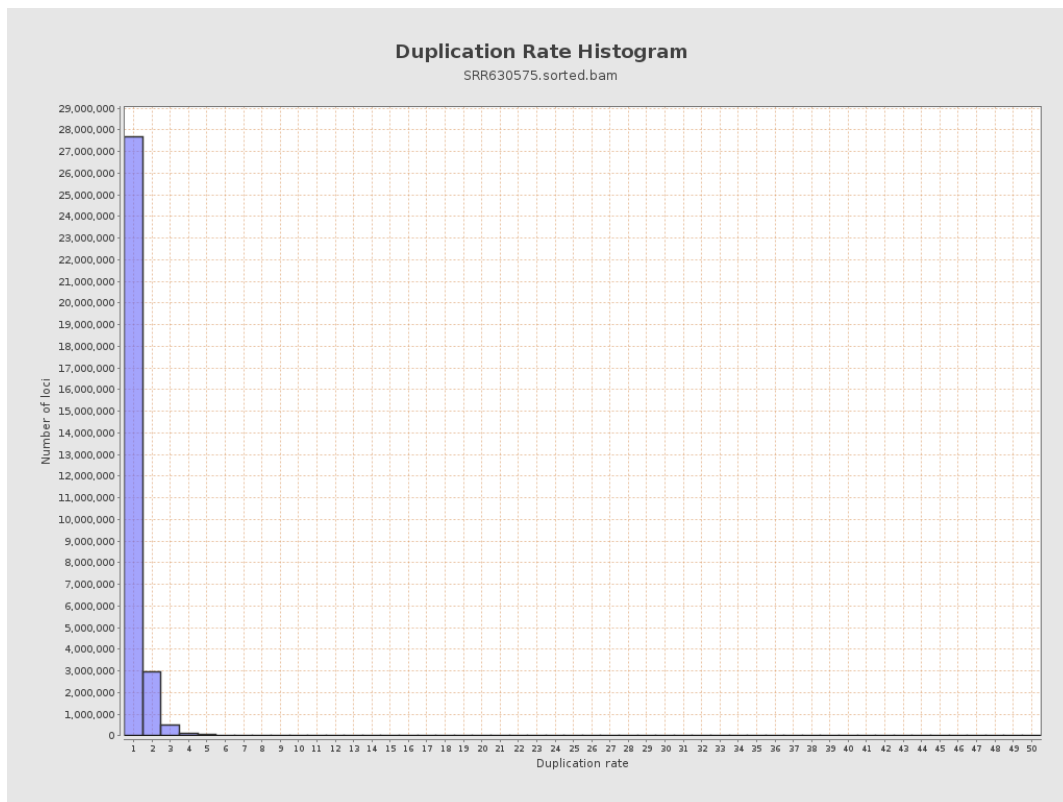
5. Results : Coverage Histogram (0-50X)



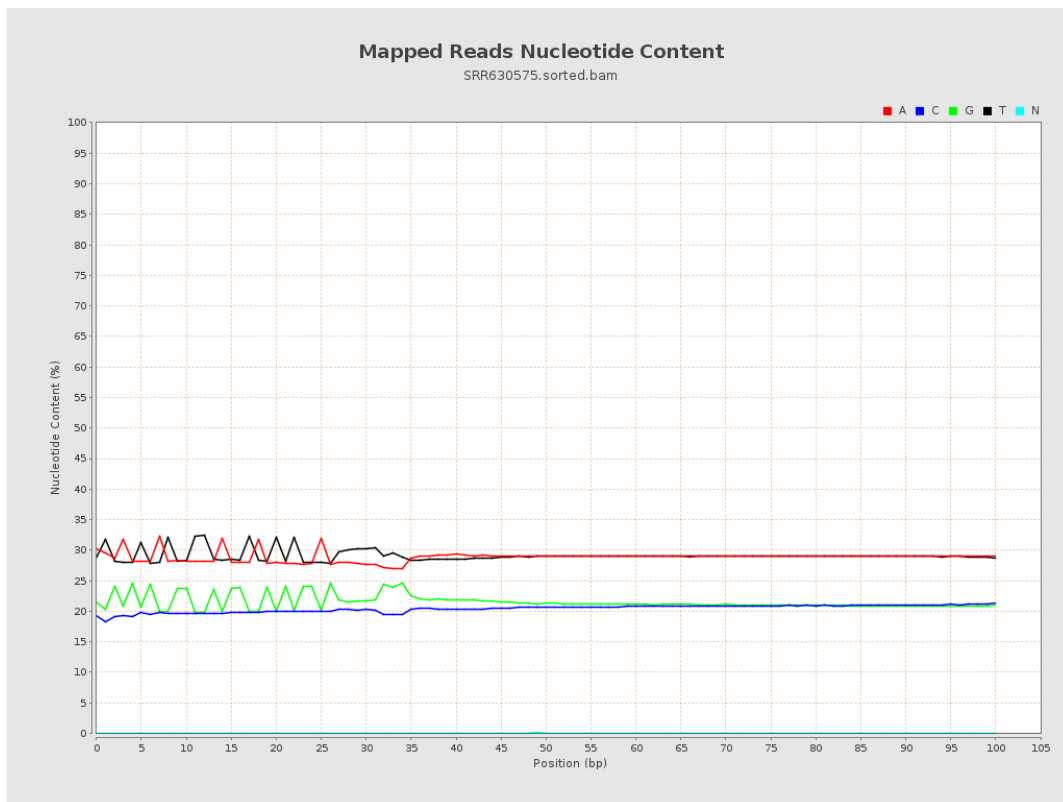
6. Results : Genome Fraction Coverage



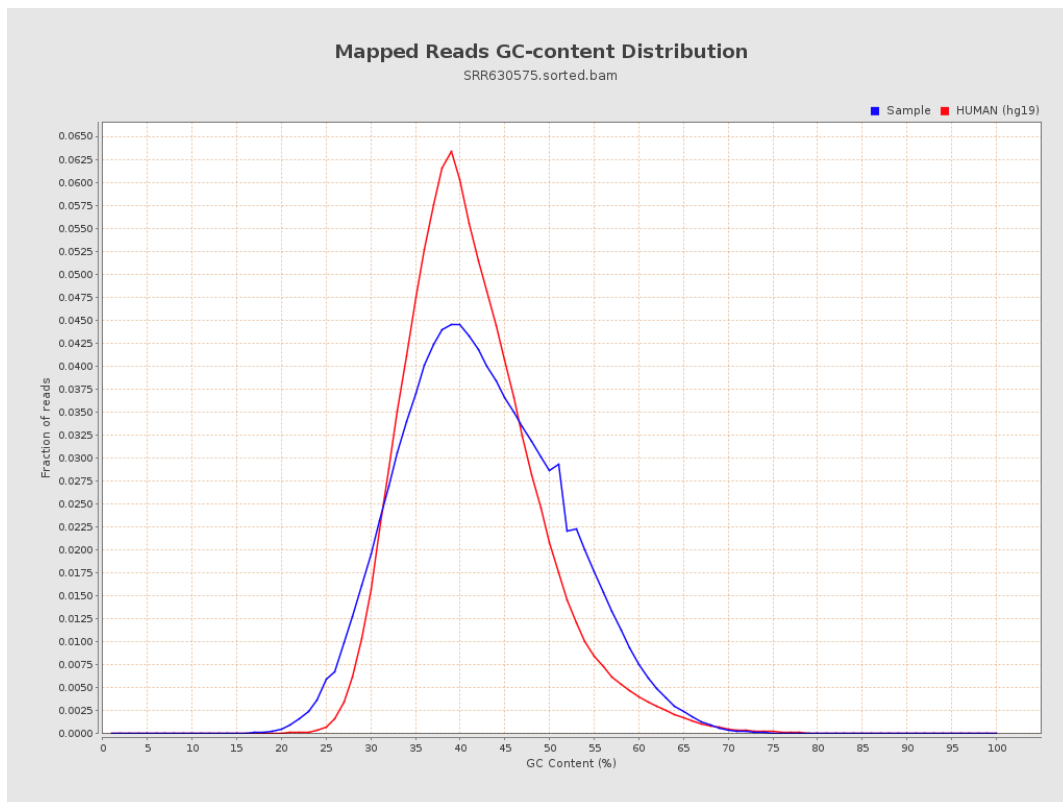
7. Results : Duplication Rate Histogram



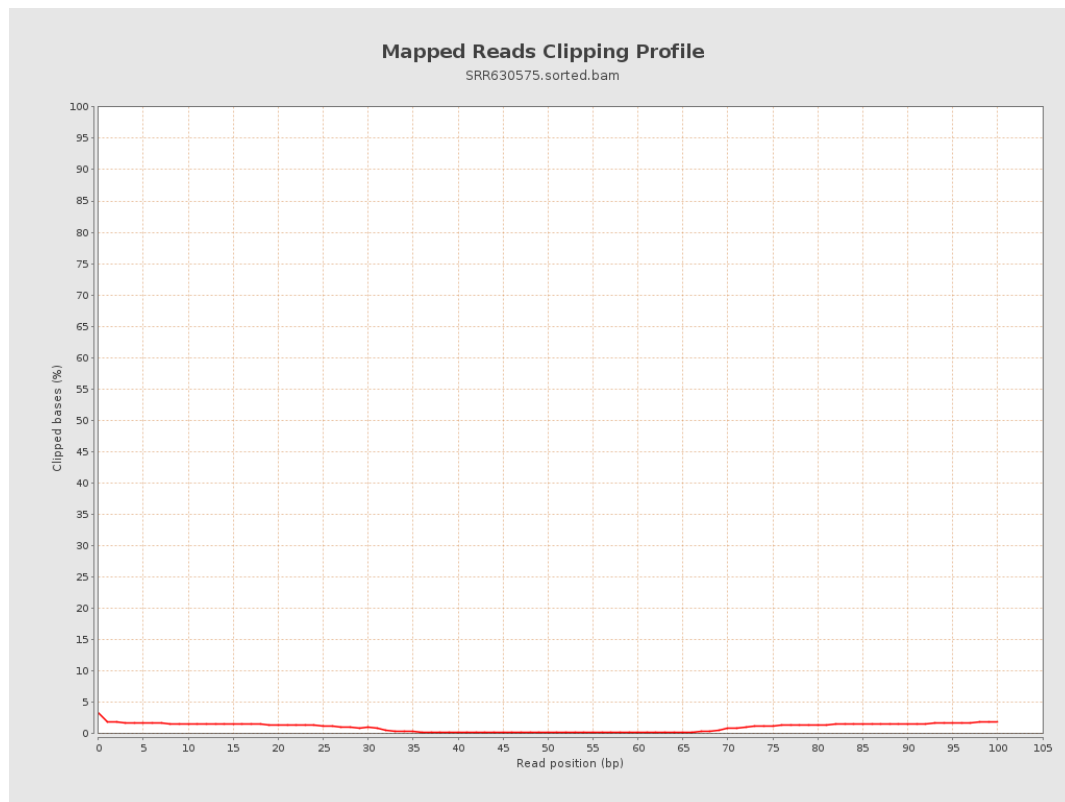
8. Results : Mapped Reads Nucleotide Content



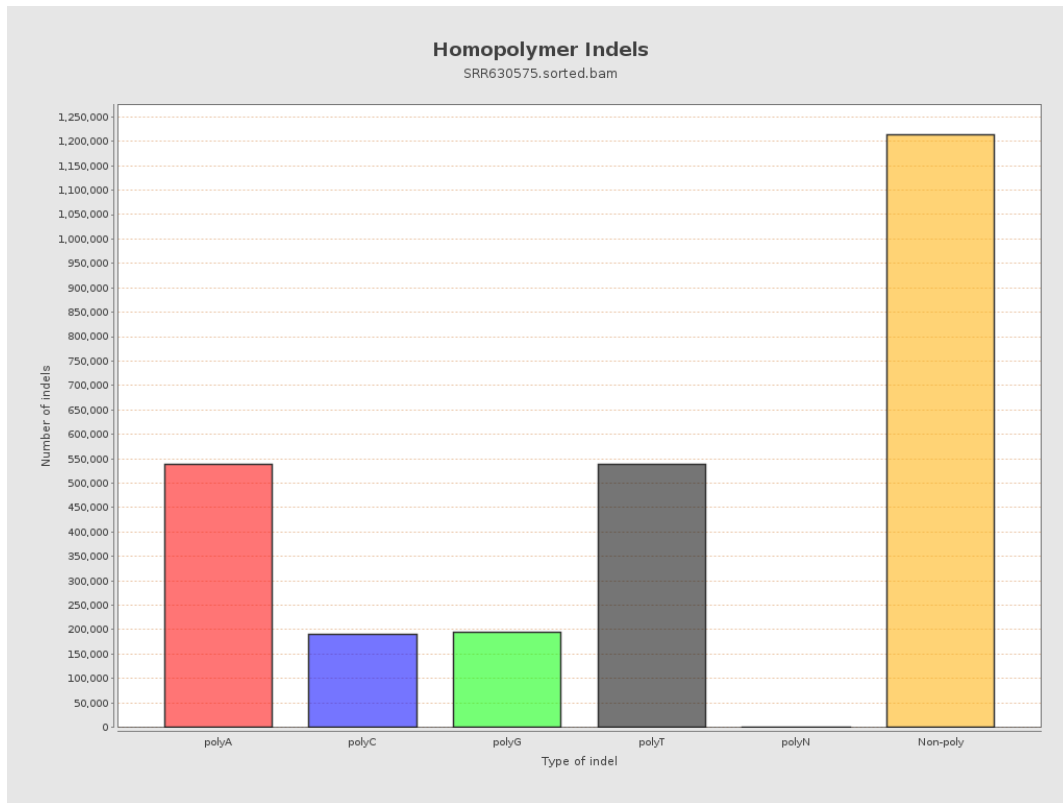
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



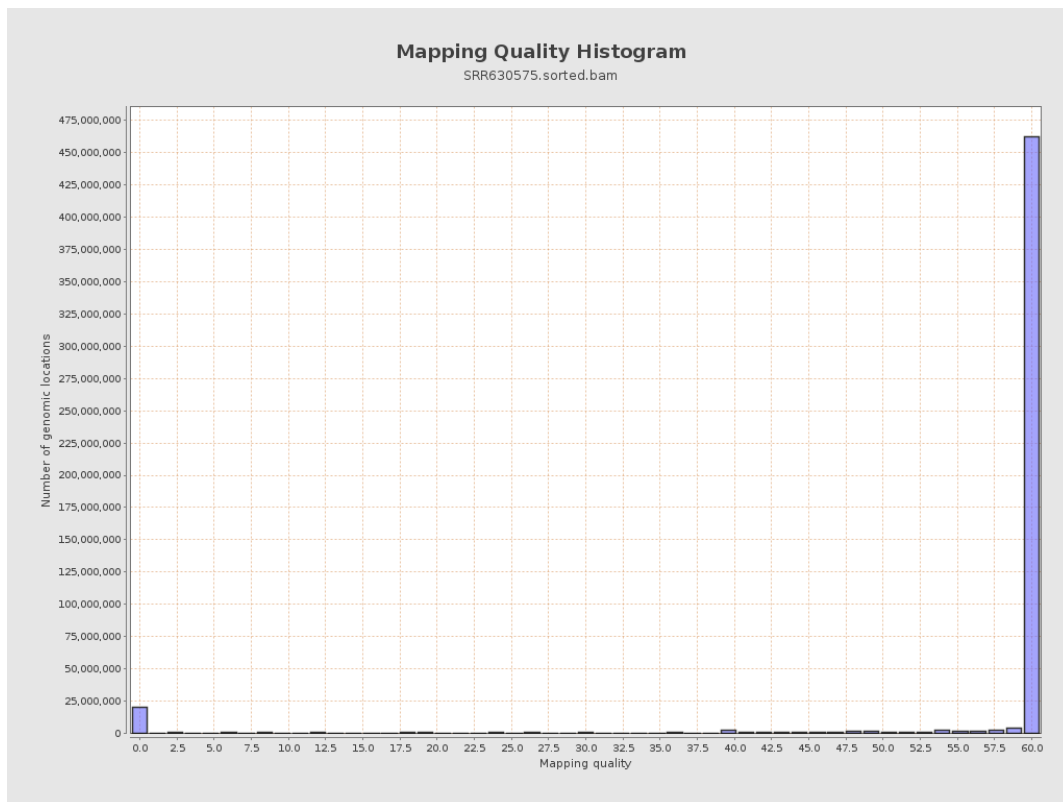
11. Results : Homopolymer Indels



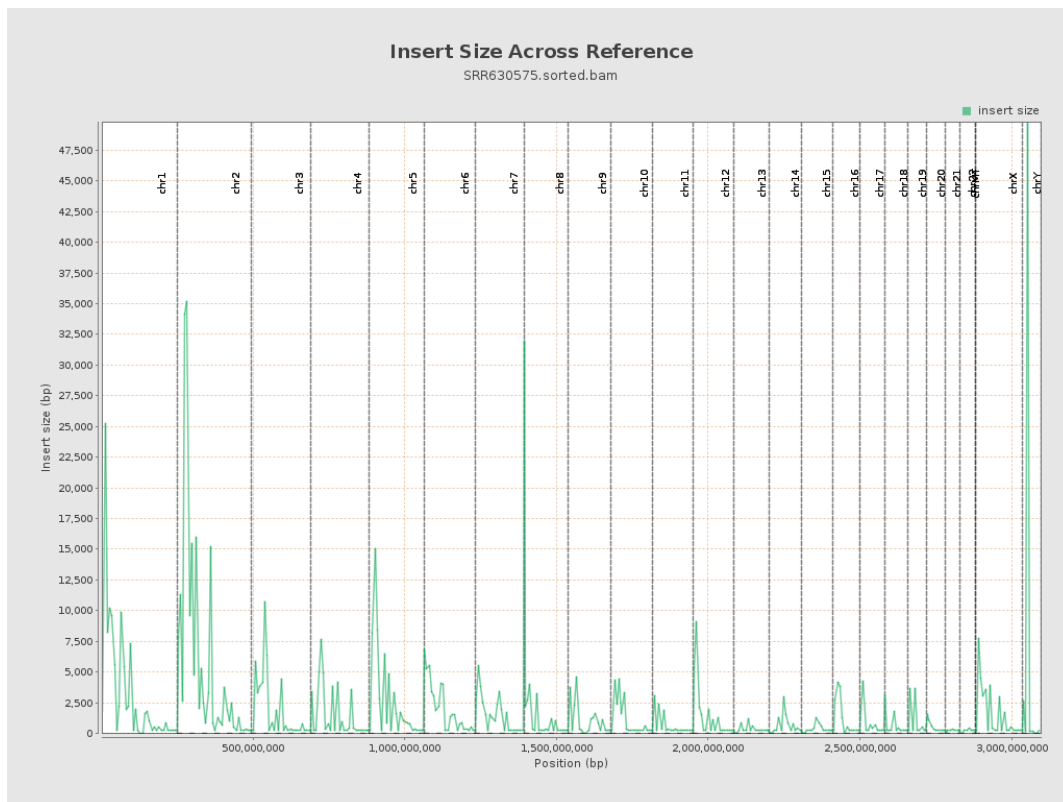
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

