

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 19:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618595.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_SRR618595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618595_1.fastq.gz SRR618595_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 19:32:04 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,607,778
Mapped reads	53,280,888 / 95.82%
Unmapped reads	2,326,890 / 4.18%
Mapped paired reads	53,280,888 / 95.82%
Mapped reads, first in pair	26,863,795 / 48.31%
Mapped reads, second in pair	26,417,093 / 47.51%
Mapped reads, both in pair	52,283,466 / 94.02%
Mapped reads, singletons	997,422 / 1.79%
Secondary alignments	0
Supplementary alignments	151,543 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	18,185,164 / 32.7%
Duplication rate	27.86%
Clipped reads	11,088,483 / 19.94%

2.2. ACGT Content

Number/percentage of A's	1,393,697,970 / 27.7%
Number/percentage of C's	1,079,530,822 / 21.45%
Number/percentage of T's	1,403,952,739 / 27.9%
Number/percentage of G's	1,154,771,137 / 22.95%
Number/percentage of N's	149,297 / 0%

GC Percentage	44.4%
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2.3. Coverage

Mean	1.6266
Standard Deviation	6.1005

2.4. Mapping Quality

Mean Mapping Quality	53.67
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2.5. Insert size

Mean	54,687.03
Standard Deviation	2,311,363.56
P25/Median/P75	178 / 206 / 243

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	61,330,009
Insertions	904,655
Mapped reads with at least one insertion	1.67%
Deletions	2,528,027
Mapped reads with at least one deletion	4.63%
Homopolymer indels	53.11%

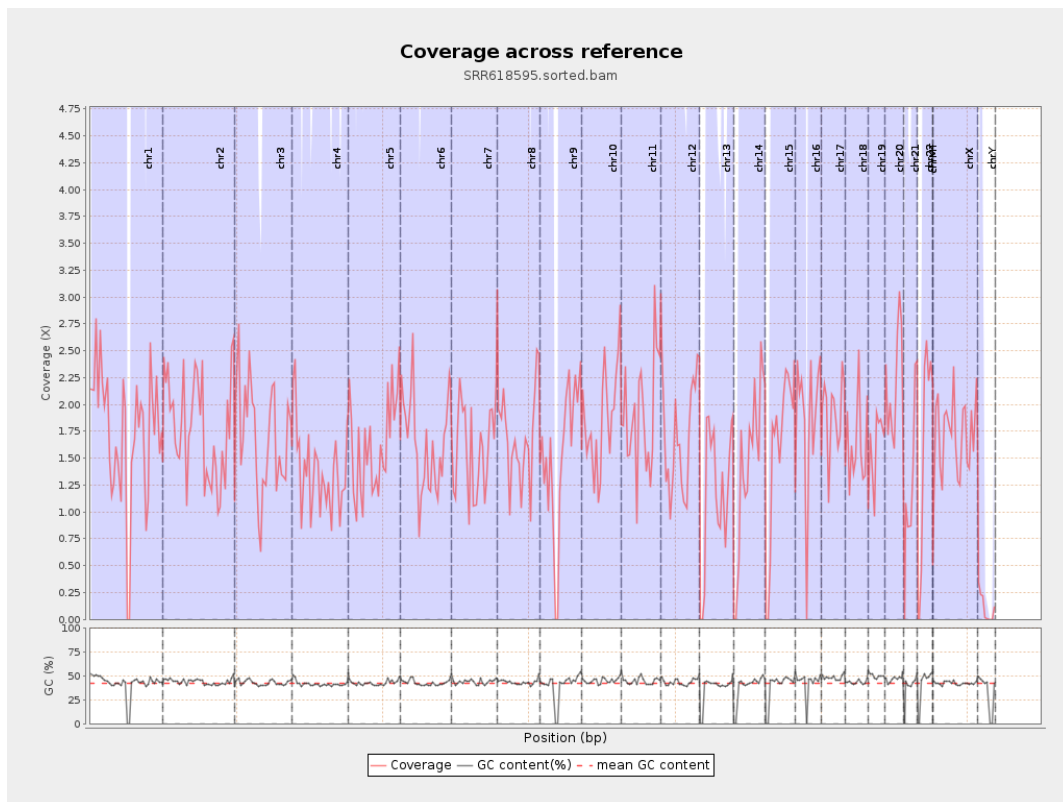
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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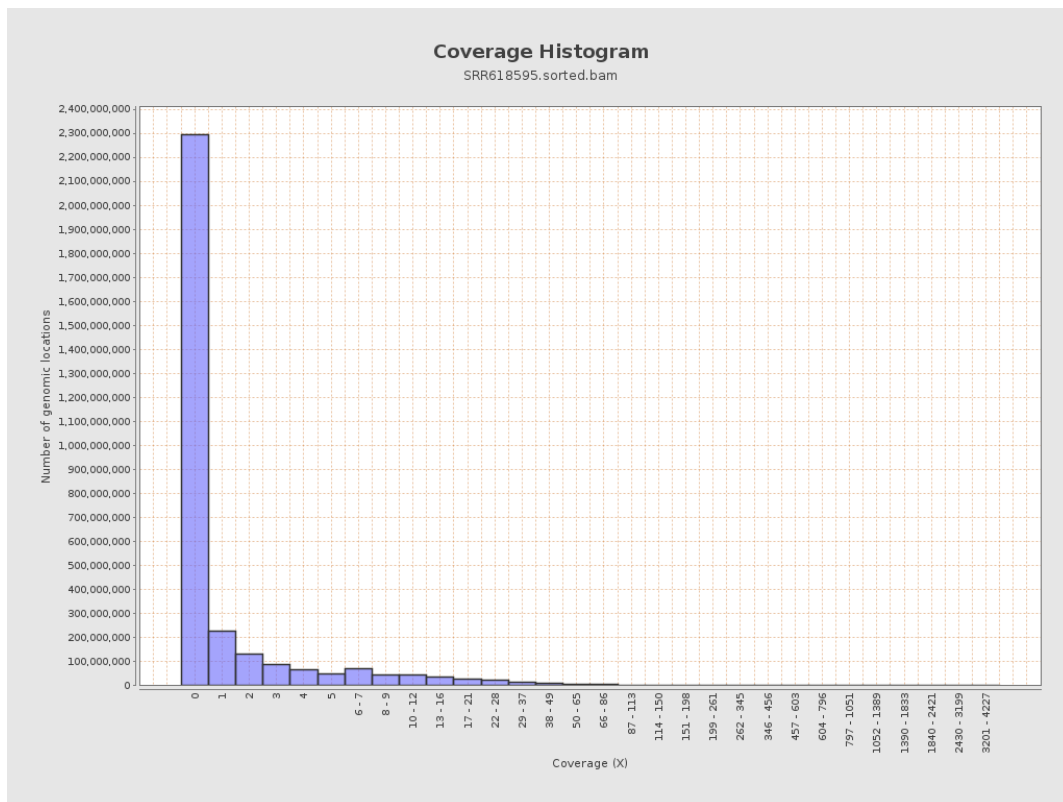
		bases	coverage	deviation
chr1	249250621	430392017	1.7267	7.1839
chr2	243199373	432734420	1.7793	6.8752
chr3	198022430	333317300	1.6832	5.392
chr4	191154276	262990661	1.3758	5.1732
chr5	180915260	292967385	1.6194	5.3524
chr6	171115067	279682257	1.6345	5.4444
chr7	159138663	252149620	1.5845	5.3305
chr8	146364022	246783548	1.6861	5.4478
chr9	141213431	215339745	1.5249	6.7026
chr10	135534747	251723869	1.8573	6.3112
chr11	135006516	256332764	1.8987	6.507
chr12	133851895	228843361	1.7097	5.6253
chr13	115169878	134029550	1.1638	4.326
chr14	107349540	154661405	1.4407	5.2047
chr15	102531392	161620728	1.5763	5.5365
chr16	90354753	167213856	1.8506	9.3229
chr17	81195210	155866239	1.9196	6.5997
chr18	78077248	125458786	1.6069	6.6239
chr19	59128983	94929600	1.6055	6.4172
chr20	63025520	140288944	2.2259	6.9649
chr21	48129895	62854616	1.3059	8.0959
chr22	51304566	82086193	1.6	6.3304
chrMT	16571	8281	0.4997	2.2297
chrX	155270560	266945408	1.7192	5.4563

chrY	59373566	6320954	0.1065	3.0909
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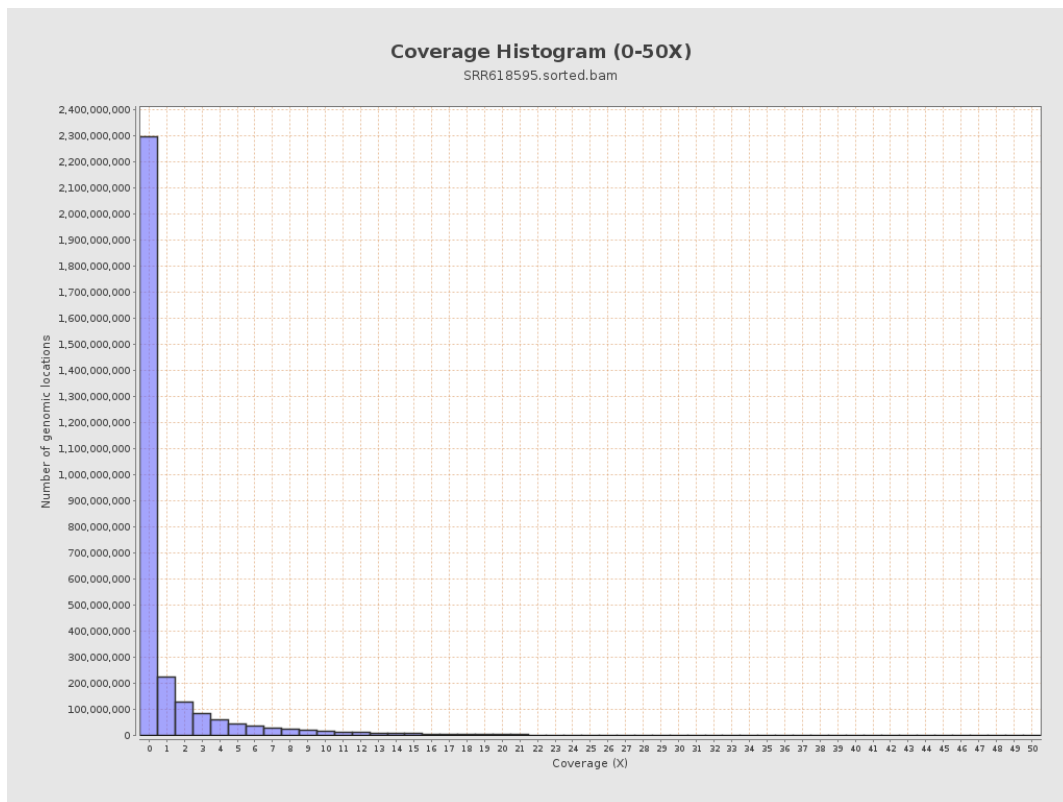
3. Results : Coverage across reference



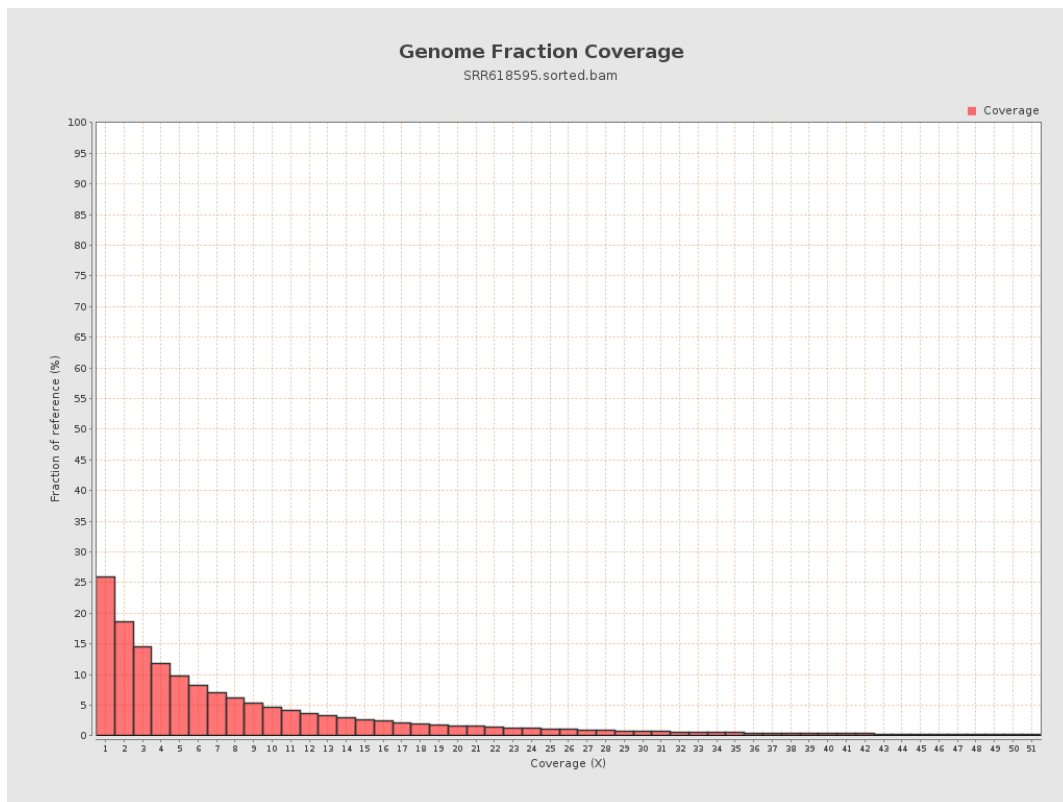
4. Results : Coverage Histogram



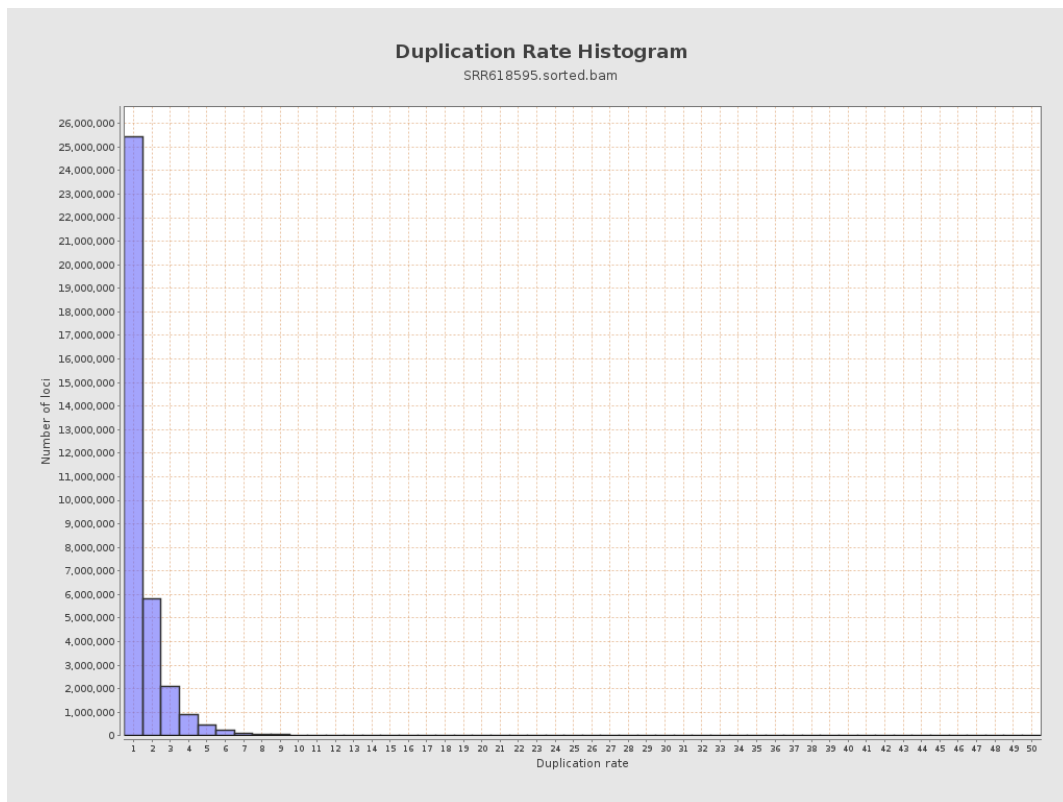
5. Results : Coverage Histogram (0-50X)



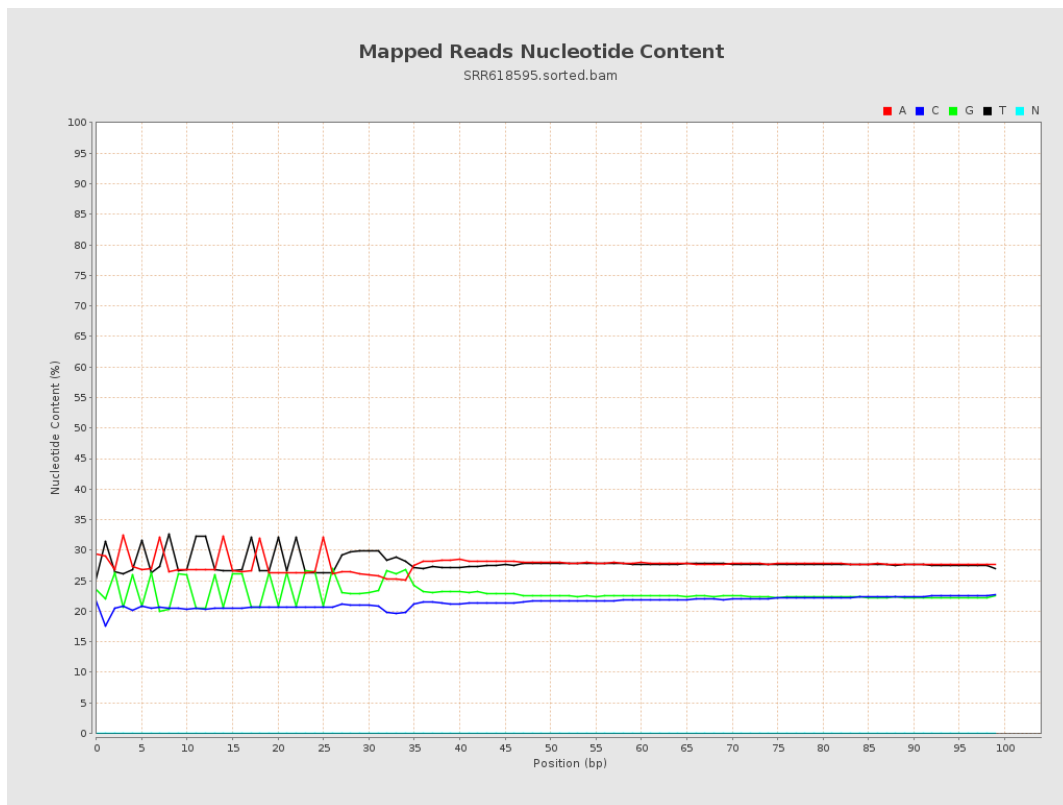
6. Results : Genome Fraction Coverage



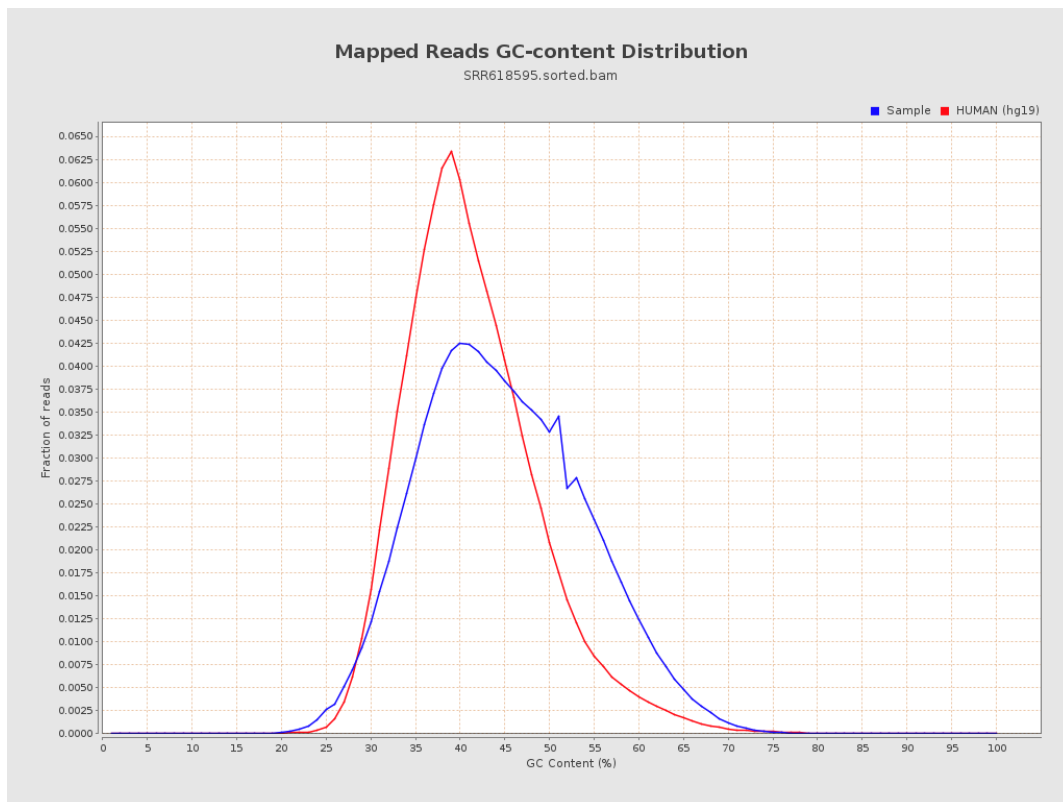
7. Results : Duplication Rate Histogram



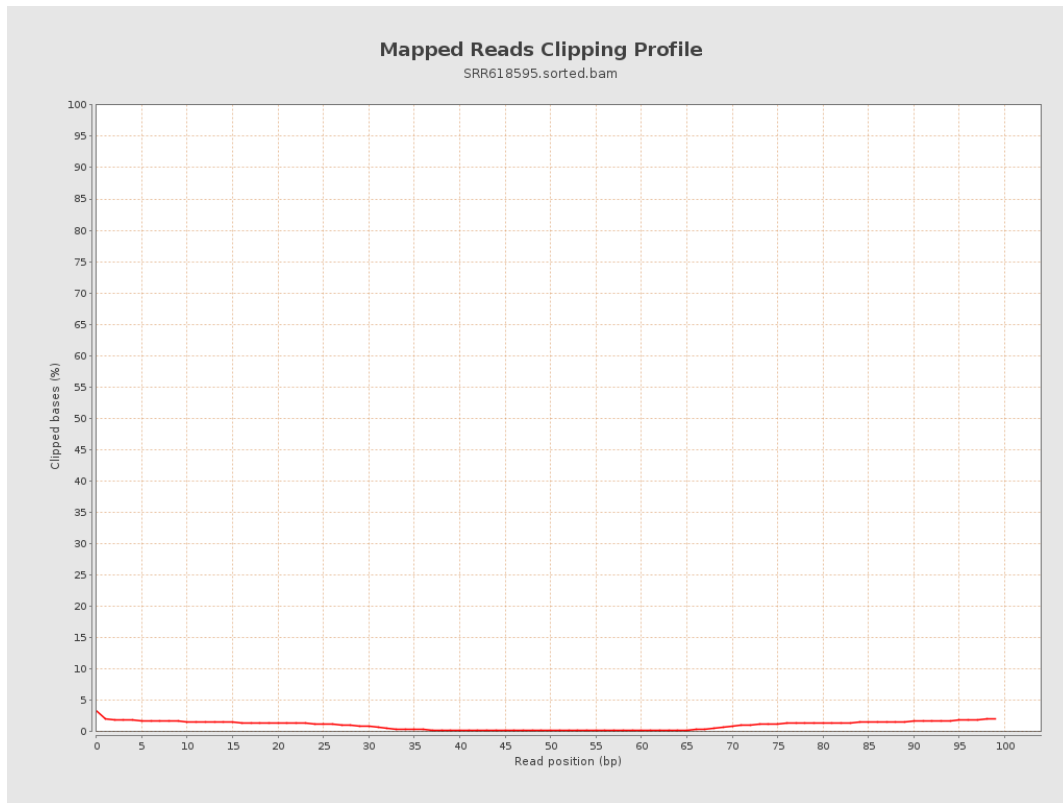
8. Results : Mapped Reads Nucleotide Content



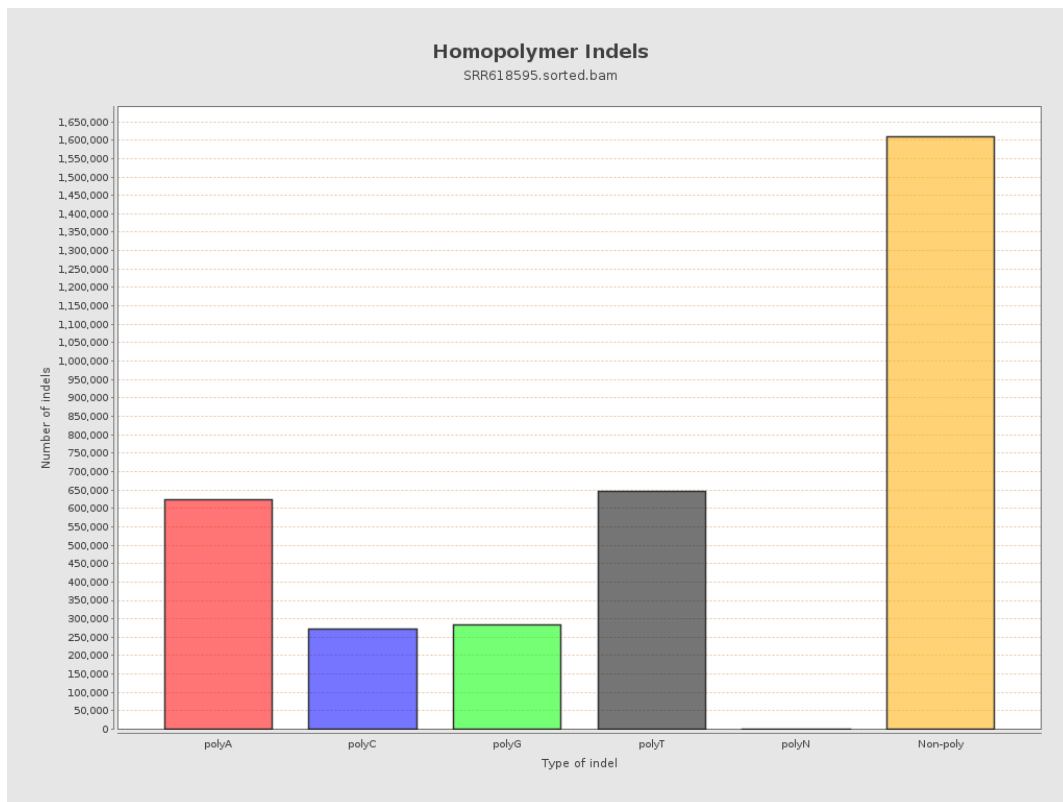
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



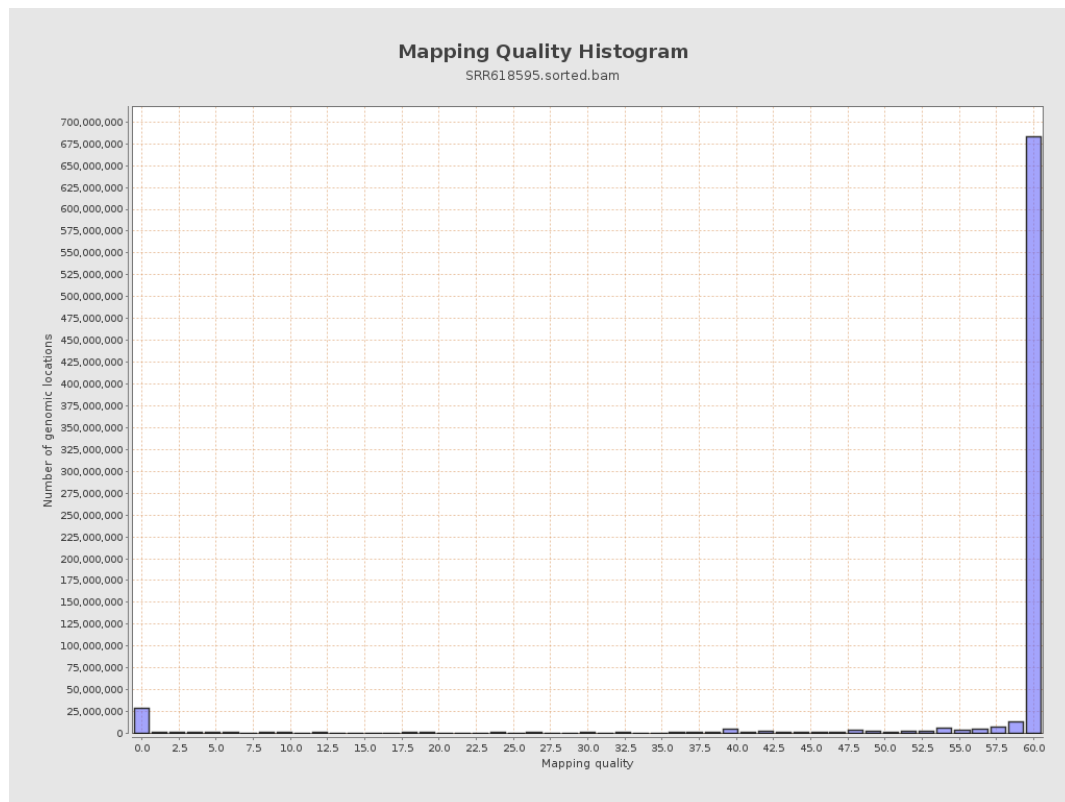
11. Results : Homopolymer Indels



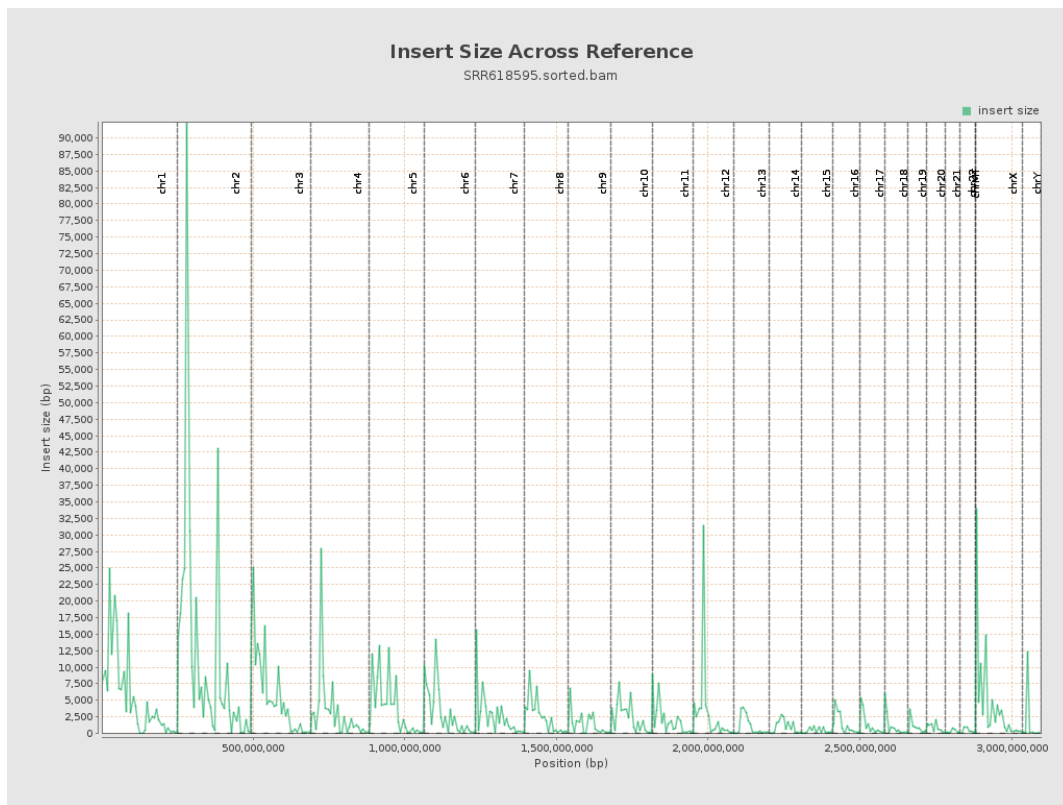
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

