

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 02:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618605.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_SRR618605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618605_1.fastq.gz SRR618605_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 02:56:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,385,178
Mapped reads	46,706,301 / 90.89%
Unmapped reads	4,678,877 / 9.11%
Mapped paired reads	46,706,301 / 90.89%
Mapped reads, first in pair	23,980,946 / 46.67%
Mapped reads, second in pair	22,725,355 / 44.23%
Mapped reads, both in pair	44,551,842 / 86.7%
Mapped reads, singletons	2,154,459 / 4.19%
Secondary alignments	0
Supplementary alignments	73,358 / 0.14%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	15,714,029 / 30.58%
Duplication rate	28.47%
Clipped reads	10,755,184 / 20.93%

2.2. ACGT Content

Number/percentage of A's	1,177,276,367 / 26.89%
Number/percentage of C's	984,537,277 / 22.48%
Number/percentage of T's	1,191,708,265 / 27.21%
Number/percentage of G's	1,022,104,626 / 23.34%
Number/percentage of N's	3,244,286 / 0.07%

GC Percentage	45.83%
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2.3. Coverage

Mean	1.4155
Standard Deviation	6.948

2.4. Mapping Quality

Mean Mapping Quality	51.95
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2.5. Insert size

Mean	62,963.79
Standard Deviation	2,603,014.5
P25/Median/P75	177 / 205 / 242

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	66,823,375
Insertions	842,944
Mapped reads with at least one insertion	1.78%
Deletions	2,233,934
Mapped reads with at least one deletion	4.66%
Homopolymer indels	51.95%

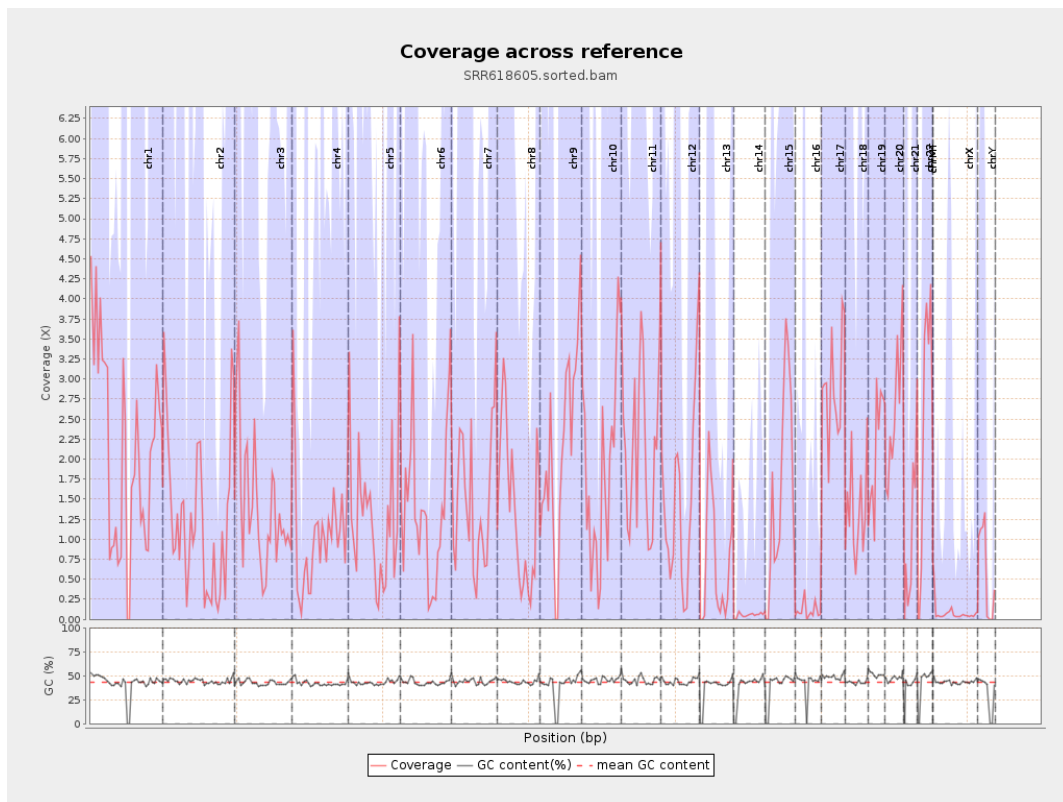
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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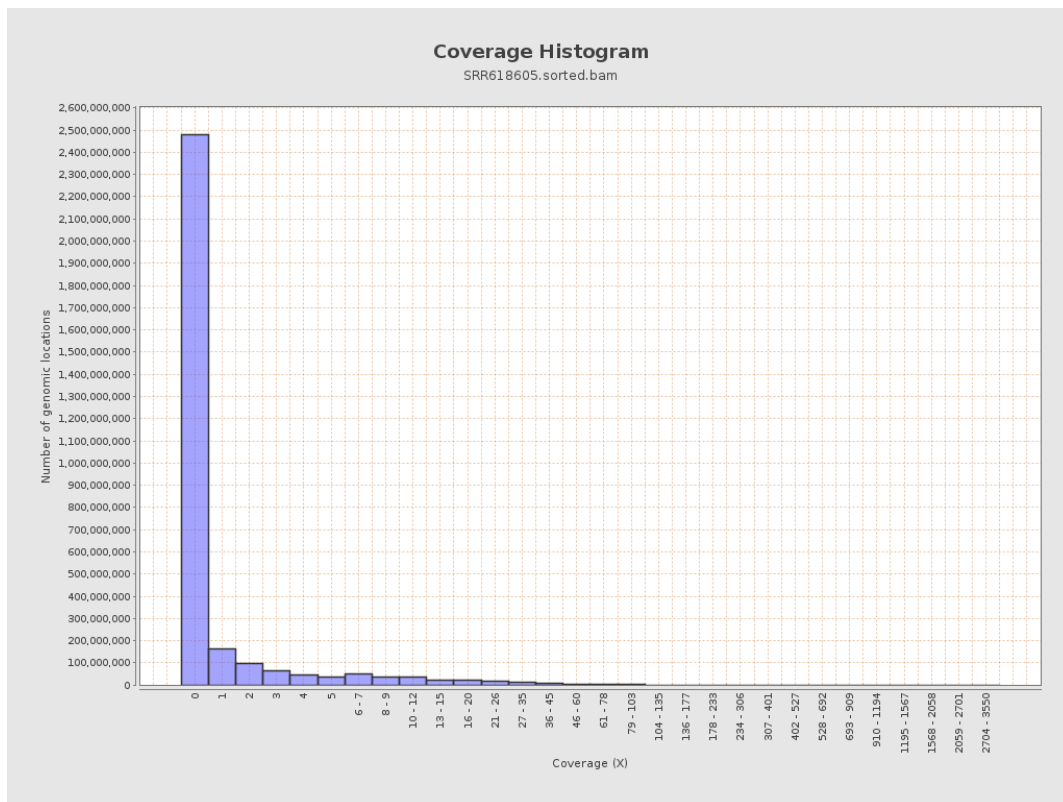
		bases	coverage	deviation
chr1	249250621	521073690	2.0906	9.4755
chr2	243199373	300773016	1.2367	6.6701
chr3	198022430	276125581	1.3944	5.8088
chr4	191154276	197952765	1.0356	6.2871
chr5	180915260	242269957	1.3391	5.898
chr6	171115067	231925430	1.3554	6.1003
chr7	159138663	245071451	1.54	6.542
chr8	146364022	200341451	1.3688	6.2118
chr9	141213431	304749024	2.1581	8.96
chr10	135534747	251063696	1.8524	7.5249
chr11	135006516	286242821	2.1202	8.704
chr12	133851895	204293547	1.5263	6.8984
chr13	115169878	81440873	0.7071	4.3072
chr14	107349540	5837020	0.0544	1.8247
chr15	102531392	167660774	1.6352	7.3977
chr16	90354753	9564200	0.1059	3.8016
chr17	81195210	233275929	2.873	9.167
chr18	78077248	106207555	1.3603	6.6941
chr19	59128983	126040905	2.1316	8.539
chr20	63025520	162996556	2.5862	9.1063
chr21	48129895	52761976	1.0962	9.1658
chr22	51304566	125991137	2.4557	9.0704
chrMT	16571	11931	0.72	3.701
chrX	155270560	11732879	0.0756	2.915

chrY	59373566	36492558	0.6146	4.1404
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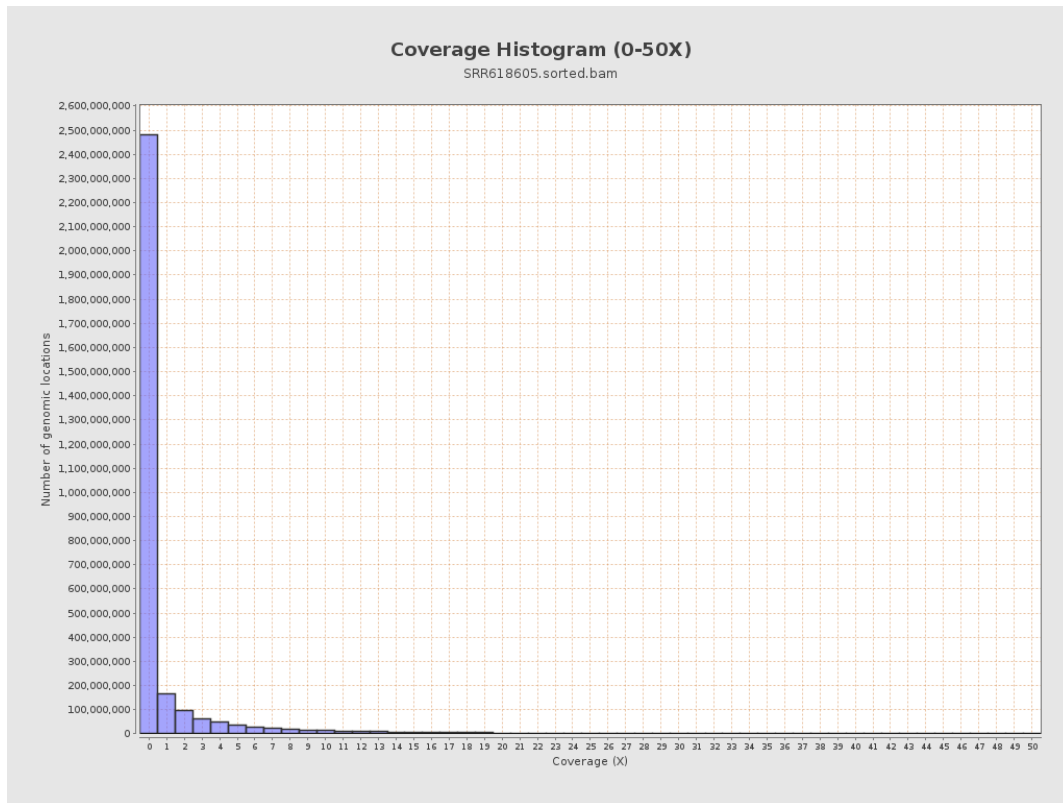
3. Results : Coverage across reference



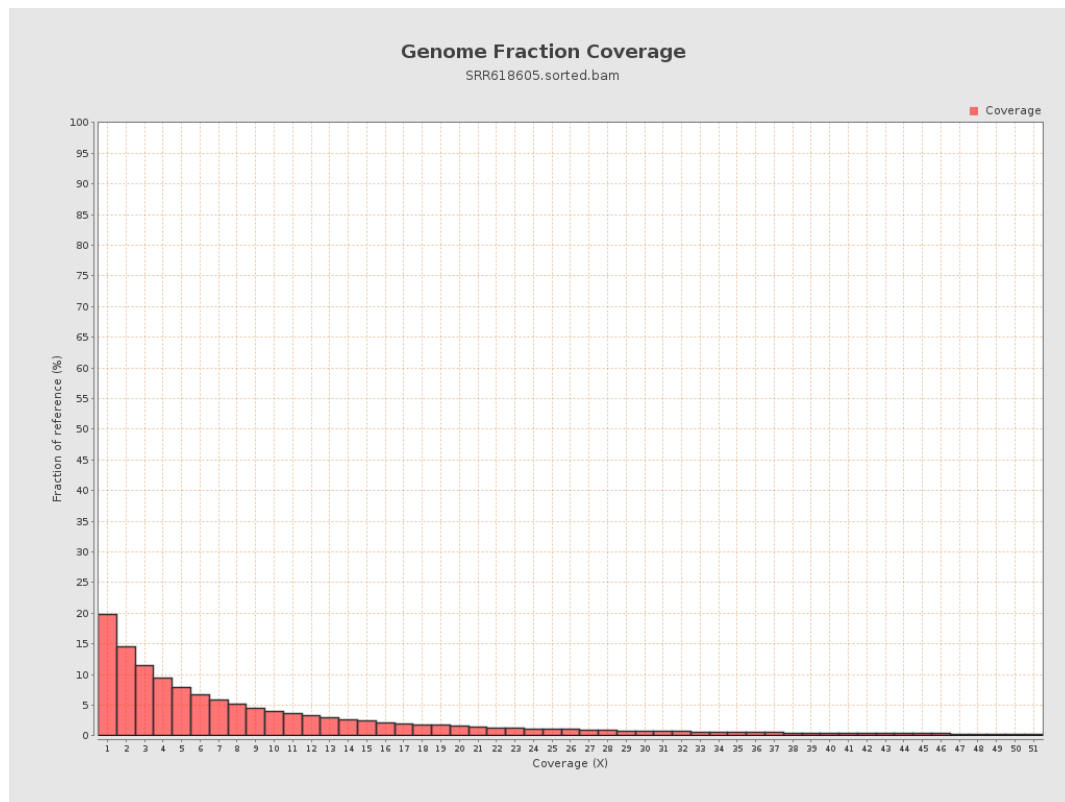
4. Results : Coverage Histogram



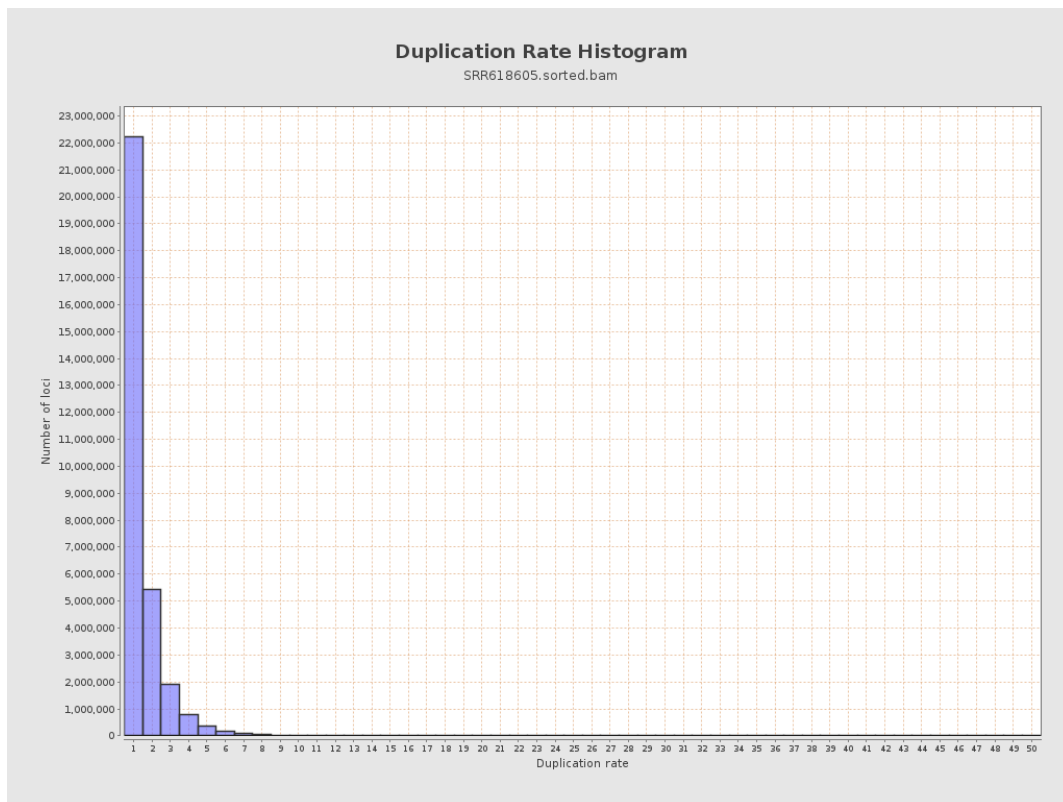
5. Results : Coverage Histogram (0-50X)



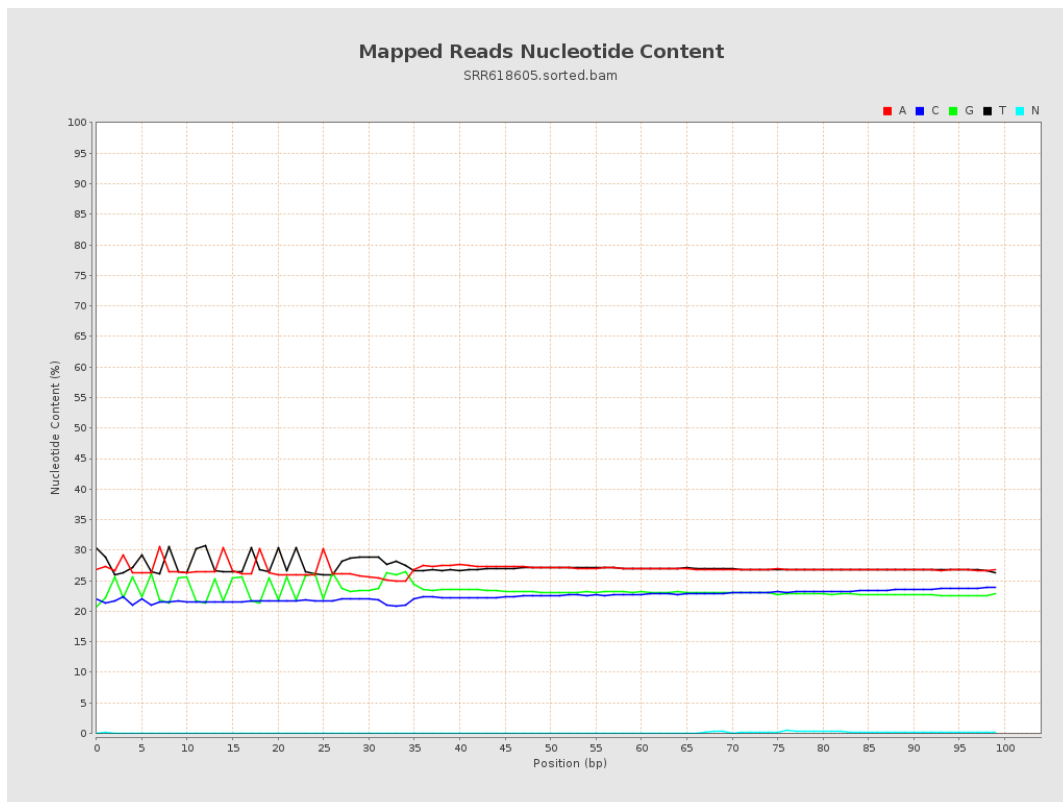
6. Results : Genome Fraction Coverage



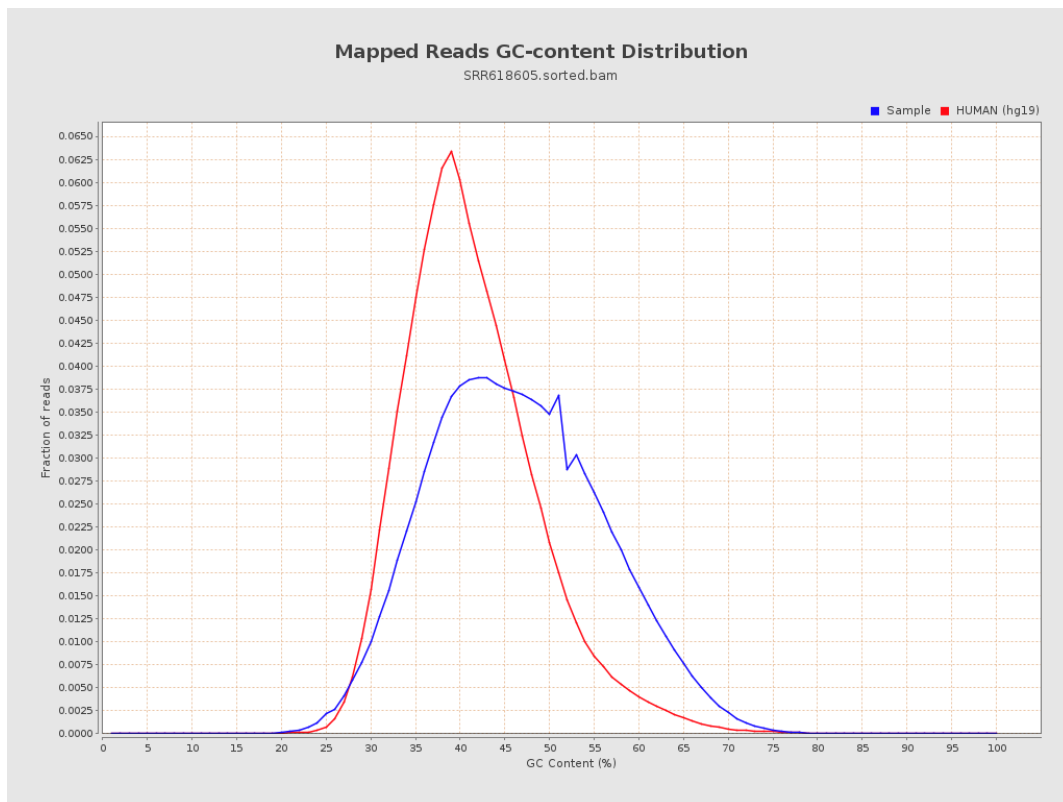
7. Results : Duplication Rate Histogram



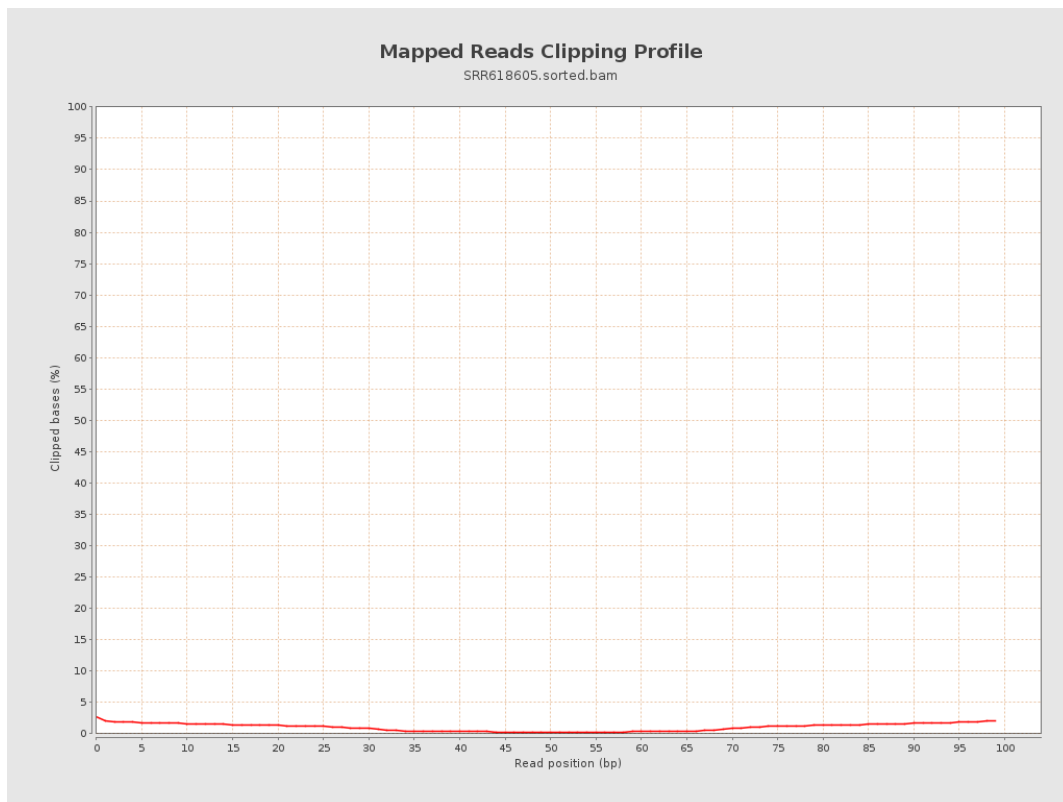
8. Results : Mapped Reads Nucleotide Content



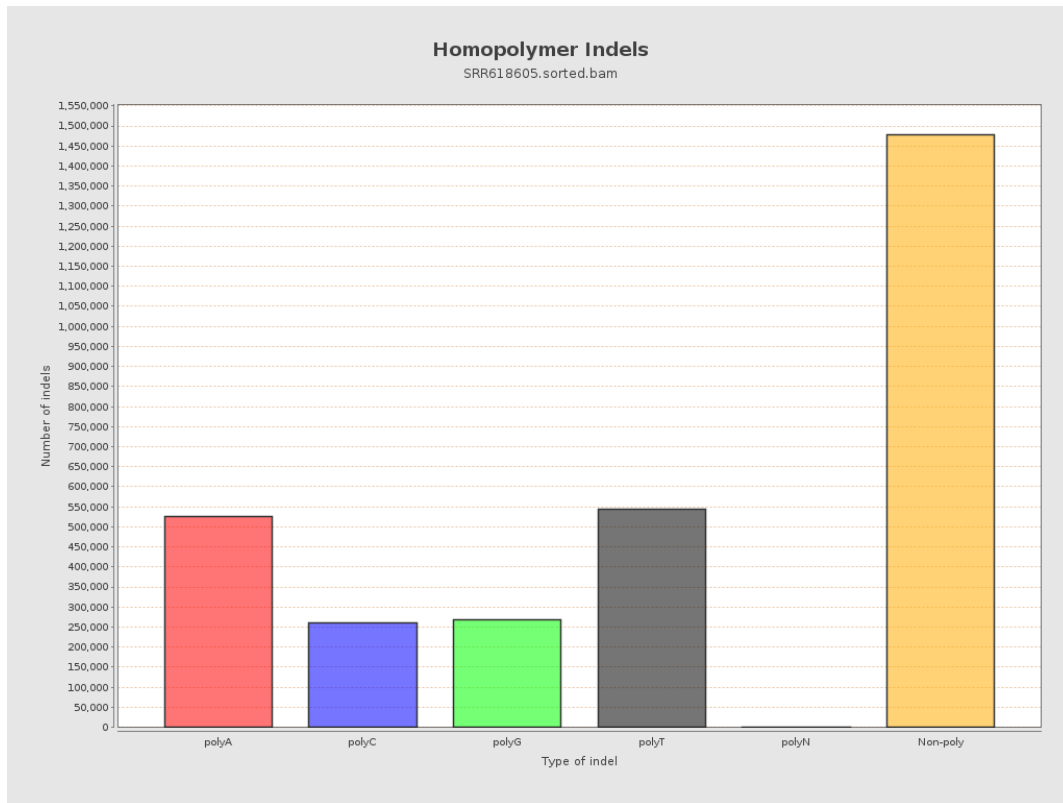
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



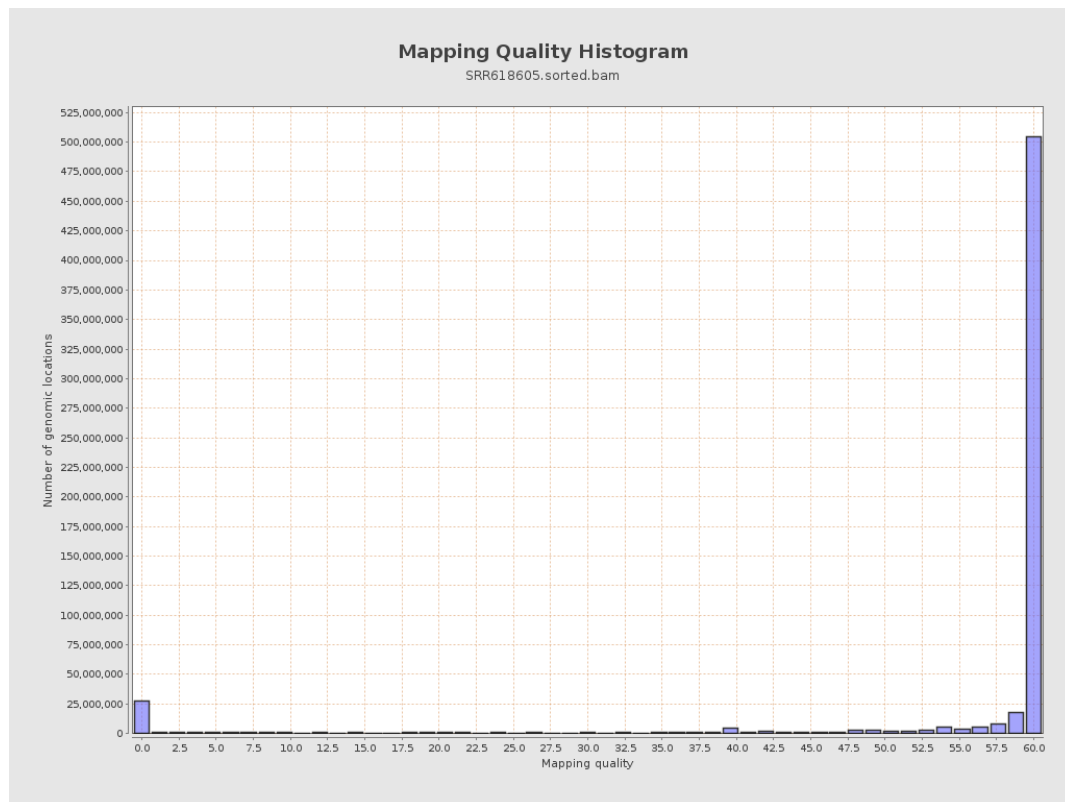
11. Results : Homopolymer Indels



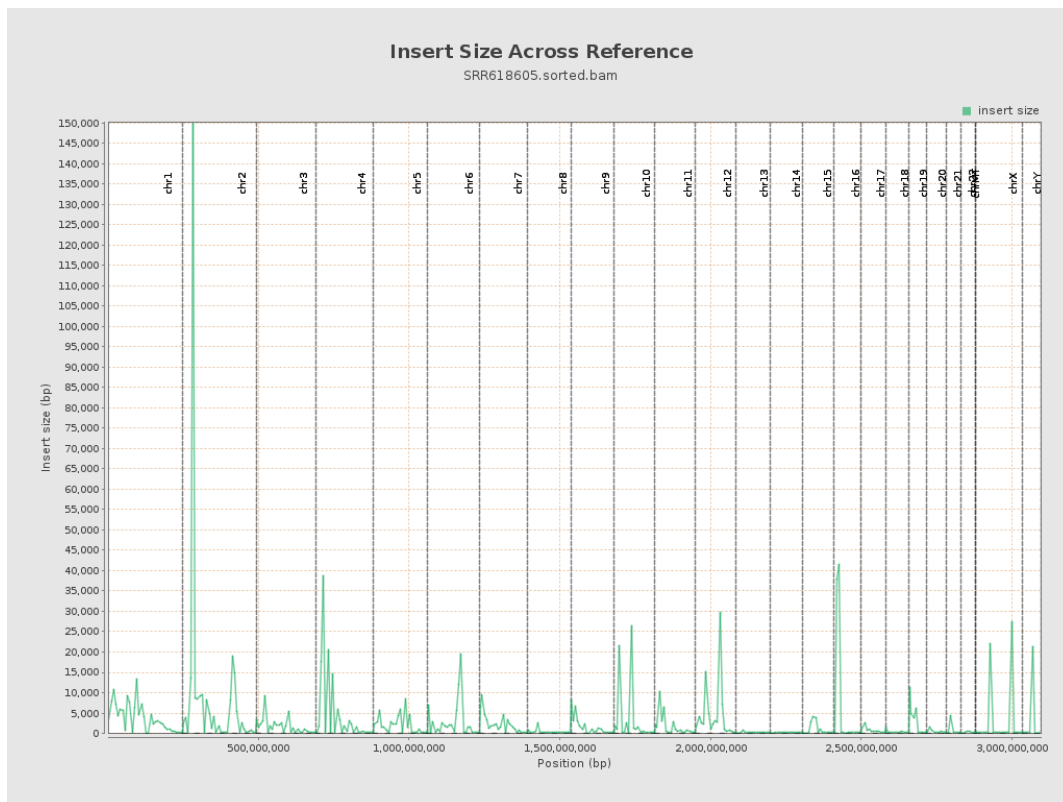
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

