

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 06:18:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618610.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_SRR618610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618610_1.fastq.gz SRR618610_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 06:18:45 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,275,028
Mapped reads	44,423,029 / 93.97%
Unmapped reads	2,851,999 / 6.03%
Mapped paired reads	44,423,029 / 93.97%
Mapped reads, first in pair	22,670,836 / 47.96%
Mapped reads, second in pair	21,752,193 / 46.01%
Mapped reads, both in pair	42,604,004 / 90.12%
Mapped reads, singletons	1,819,025 / 3.85%
Secondary alignments	0
Supplementary alignments	58,935 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	23,278,372 / 49.24%
Duplication rate	38.68%
Clipped reads	8,222,519 / 17.39%

2.2. ACGT Content

Number/percentage of A's	1,131,564,179 / 26.75%
Number/percentage of C's	973,090,950 / 23%
Number/percentage of T's	1,136,426,705 / 26.87%
Number/percentage of G's	985,585,836 / 23.3%
Number/percentage of N's	3,318,753 / 0.08%

GC Percentage	46.3%
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2.3. Coverage

Mean	1.3672
Standard Deviation	6.758

2.4. Mapping Quality

Mean Mapping Quality	53.93
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2.5. Insert size

Mean	59,625.91
Standard Deviation	2,480,000.43
P25/Median/P75	192 / 221 / 260

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	60,288,277
Insertions	748,216
Mapped reads with at least one insertion	1.66%
Deletions	1,804,305
Mapped reads with at least one deletion	3.97%
Homopolymer indels	51.43%

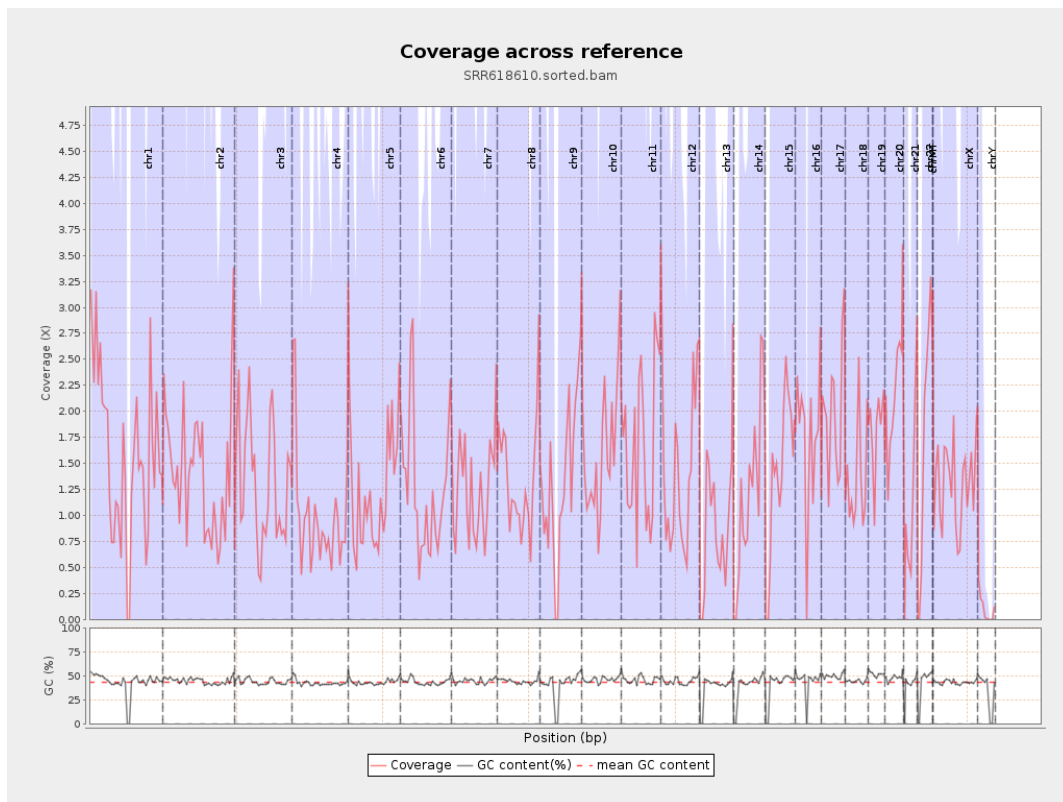
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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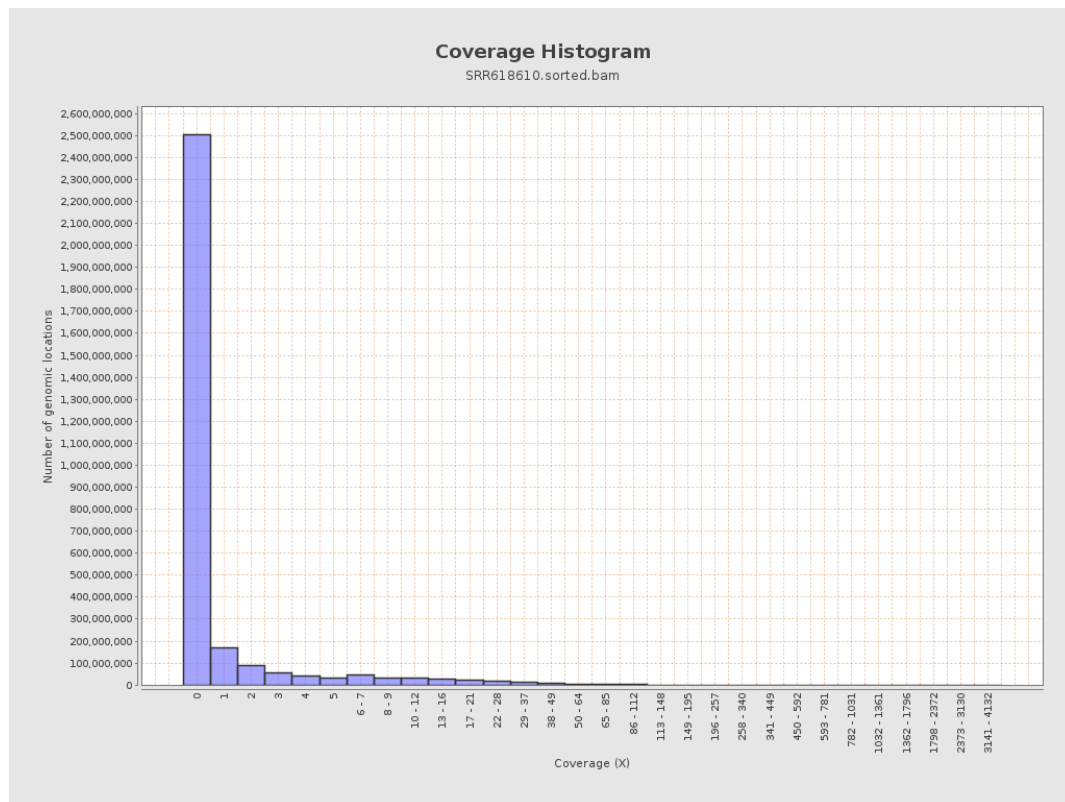
		bases	coverage	deviation
chr1	249250621	389085437	1.561	8.0317
chr2	243199373	341362852	1.4036	6.9882
chr3	198022430	257986655	1.3028	6.0104
chr4	191154276	187891859	0.9829	5.6031
chr5	180915260	227708026	1.2586	5.7952
chr6	171115067	213145861	1.2456	5.9396
chr7	159138663	200773364	1.2616	6.0393
chr8	146364022	197016221	1.3461	6.0587
chr9	141213431	186919768	1.3237	7.4208
chr10	135534747	216138395	1.5947	7.0743
chr11	135006516	227932048	1.6883	7.4444
chr12	133851895	192029606	1.4346	6.6525
chr13	115169878	100440276	0.8721	4.6289
chr14	107349540	130157362	1.2125	5.7725
chr15	102531392	143552988	1.4001	6.9691
chr16	90354753	158020736	1.7489	9.6515
chr17	81195210	159706060	1.9669	7.8109
chr18	78077248	103004693	1.3193	6.2333
chr19	59128983	106641095	1.8035	8.0886
chr20	63025520	136405076	2.1643	8.6457
chr21	48129895	55972302	1.1629	8.7118
chr22	51304566	91134705	1.7763	8.0224
chrMT	16571	52411	3.1628	13.9417
chrX	155270560	203574335	1.3111	5.8387

chrY	59373566	5875723	0.099	2.7869
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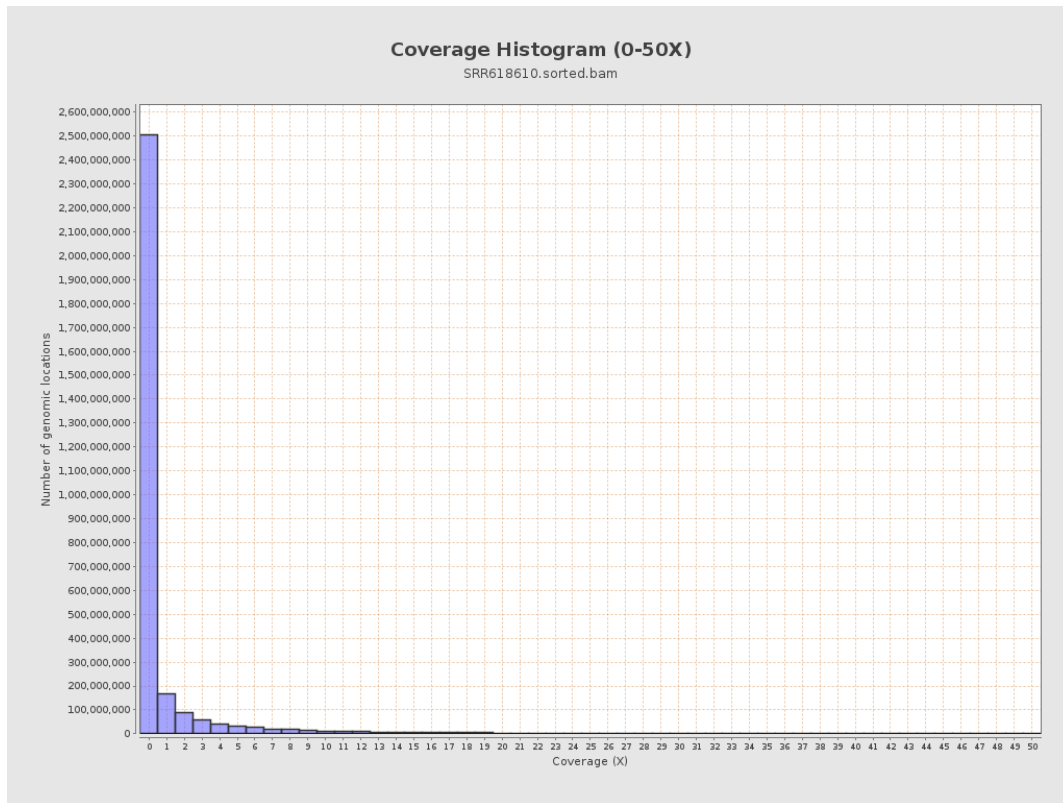
3. Results : Coverage across reference



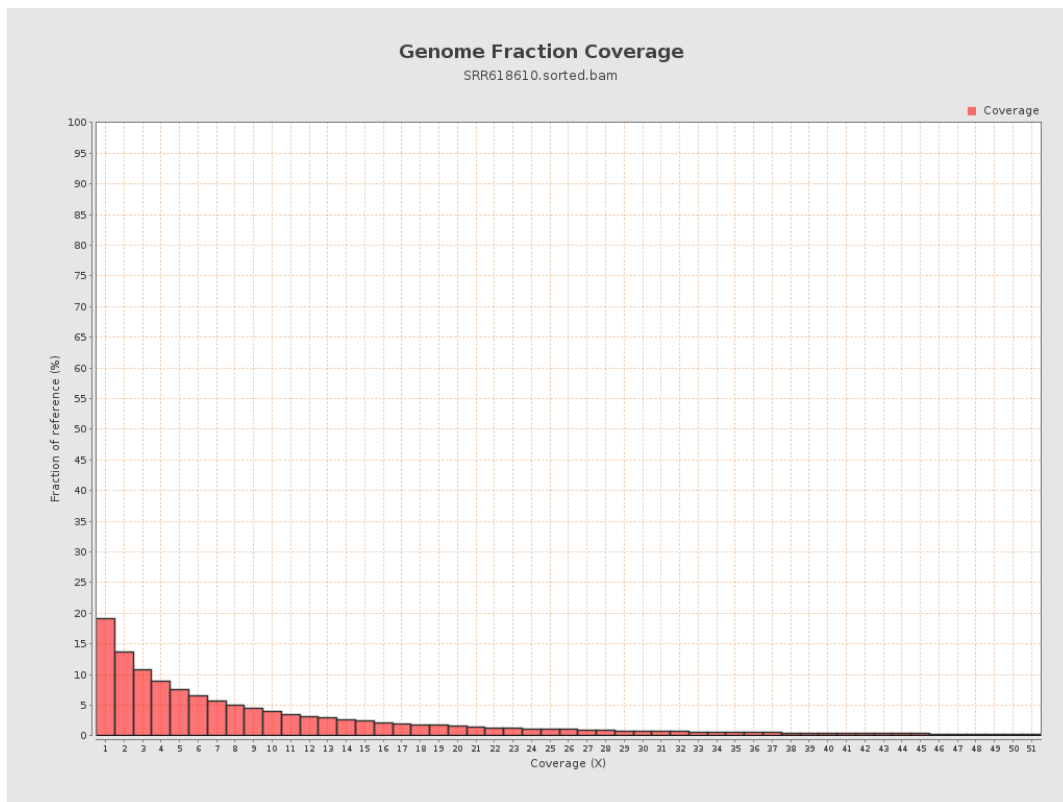
4. Results : Coverage Histogram



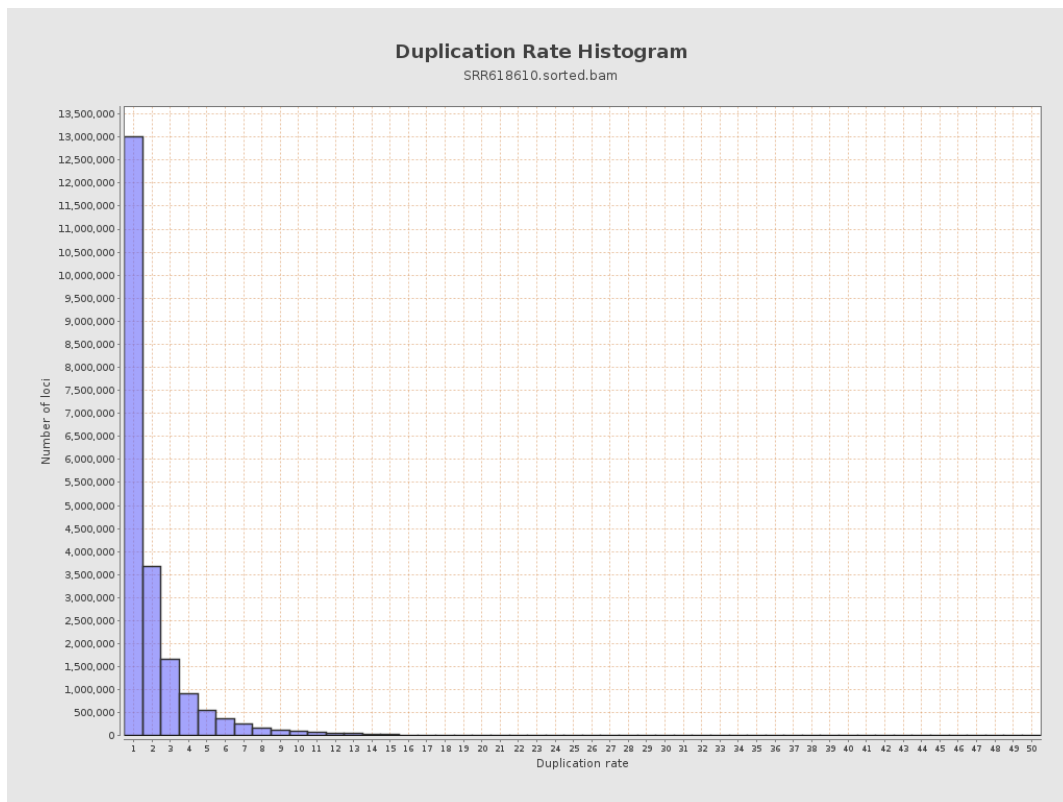
5. Results : Coverage Histogram (0-50X)



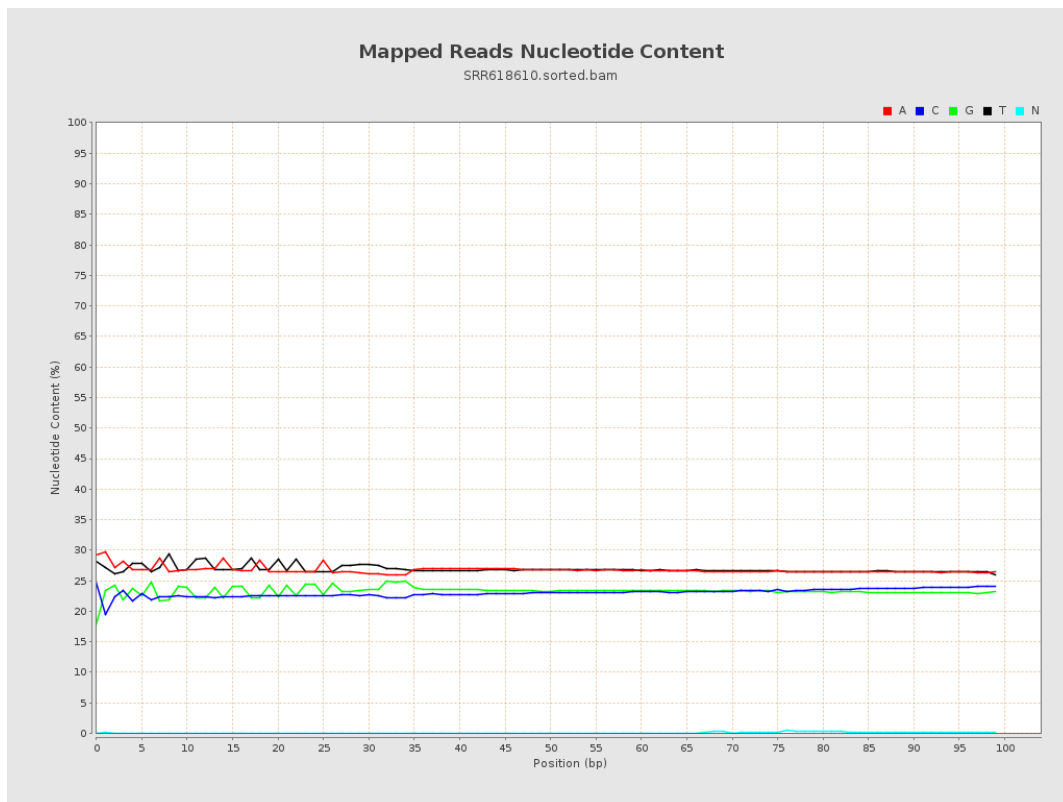
6. Results : Genome Fraction Coverage



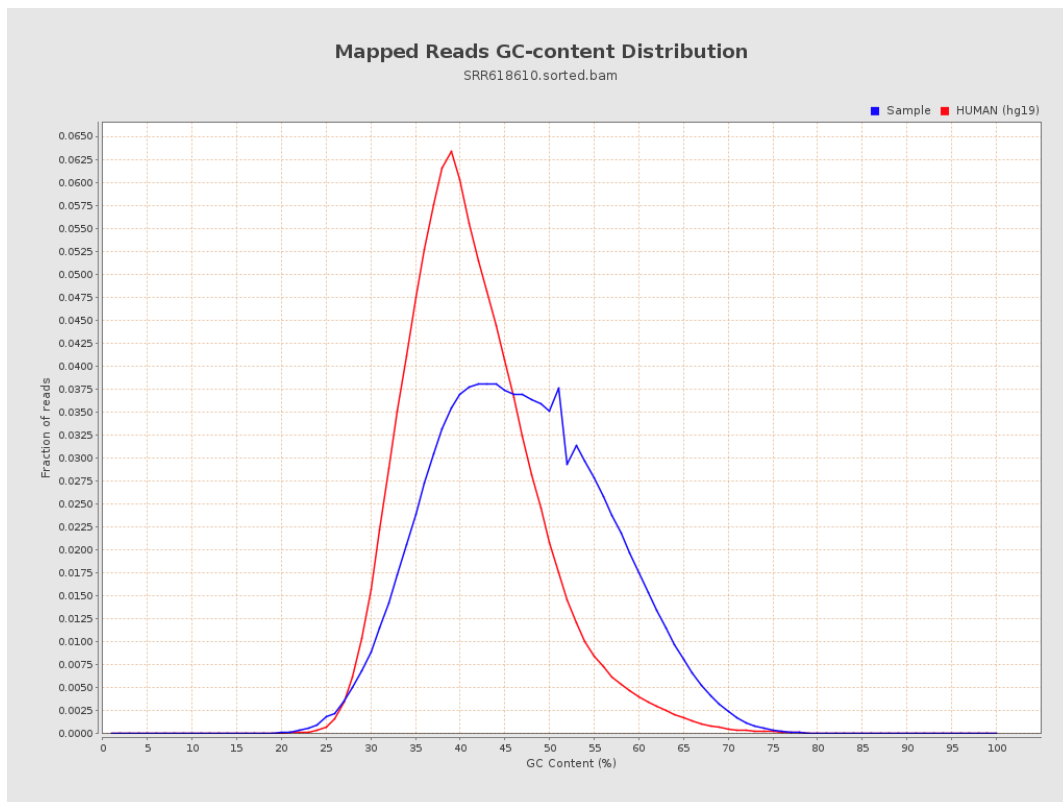
7. Results : Duplication Rate Histogram



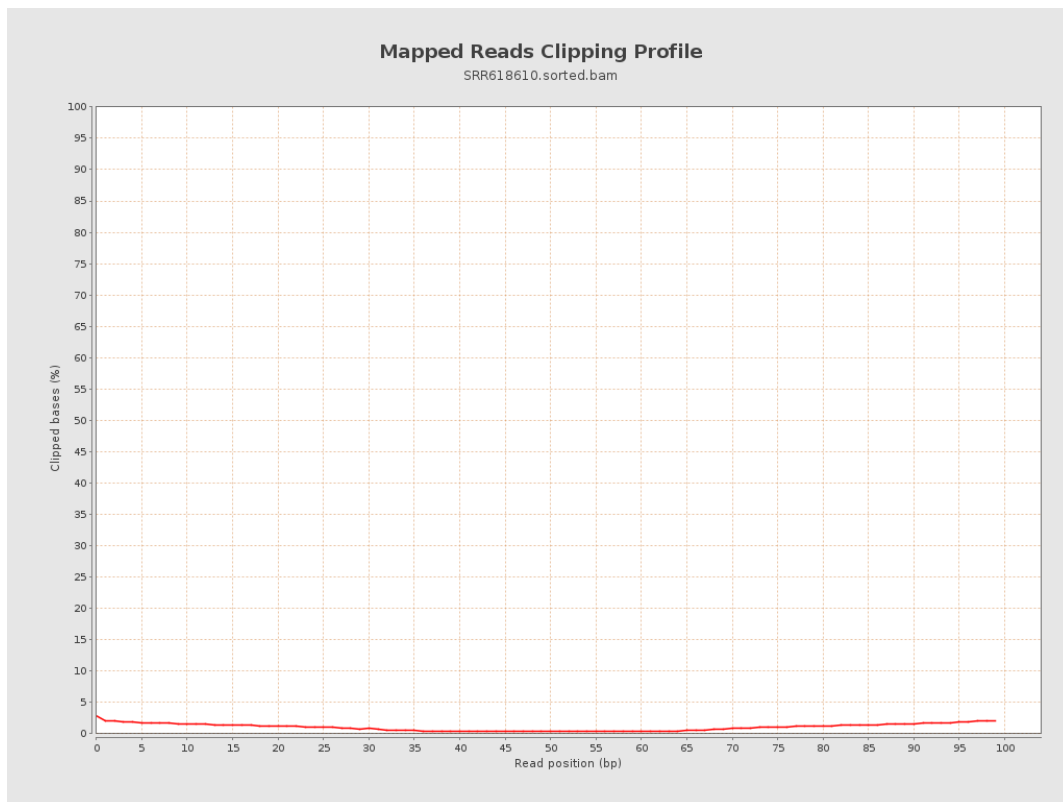
8. Results : Mapped Reads Nucleotide Content



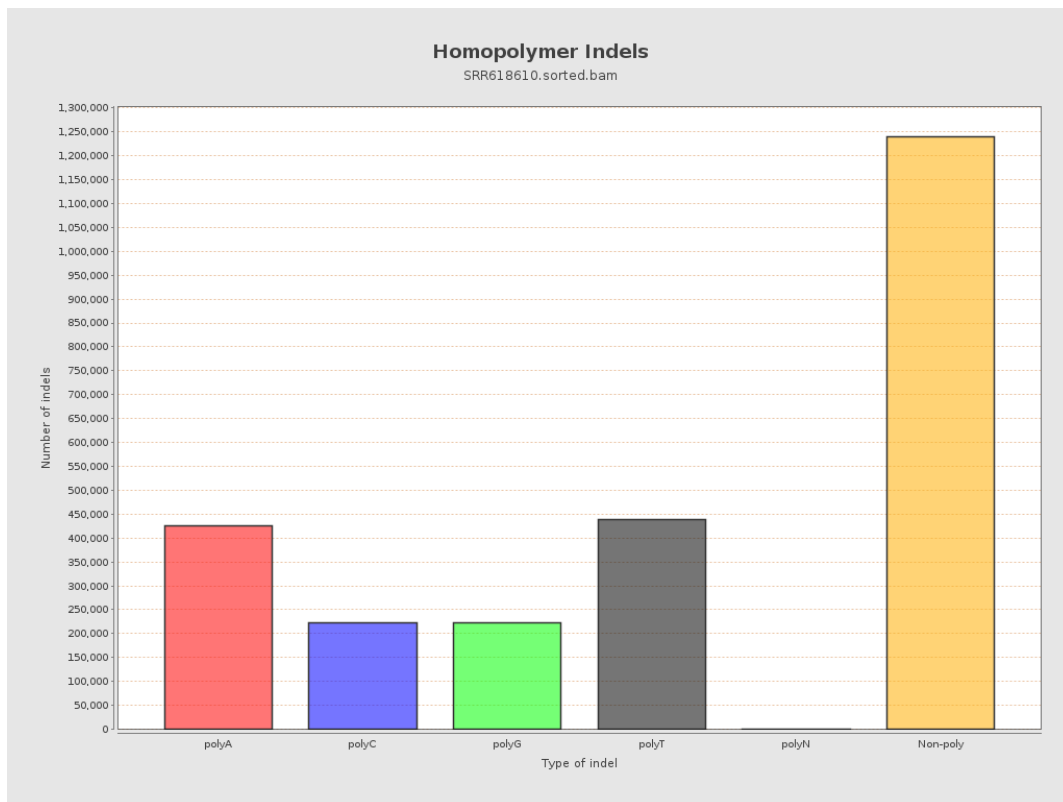
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



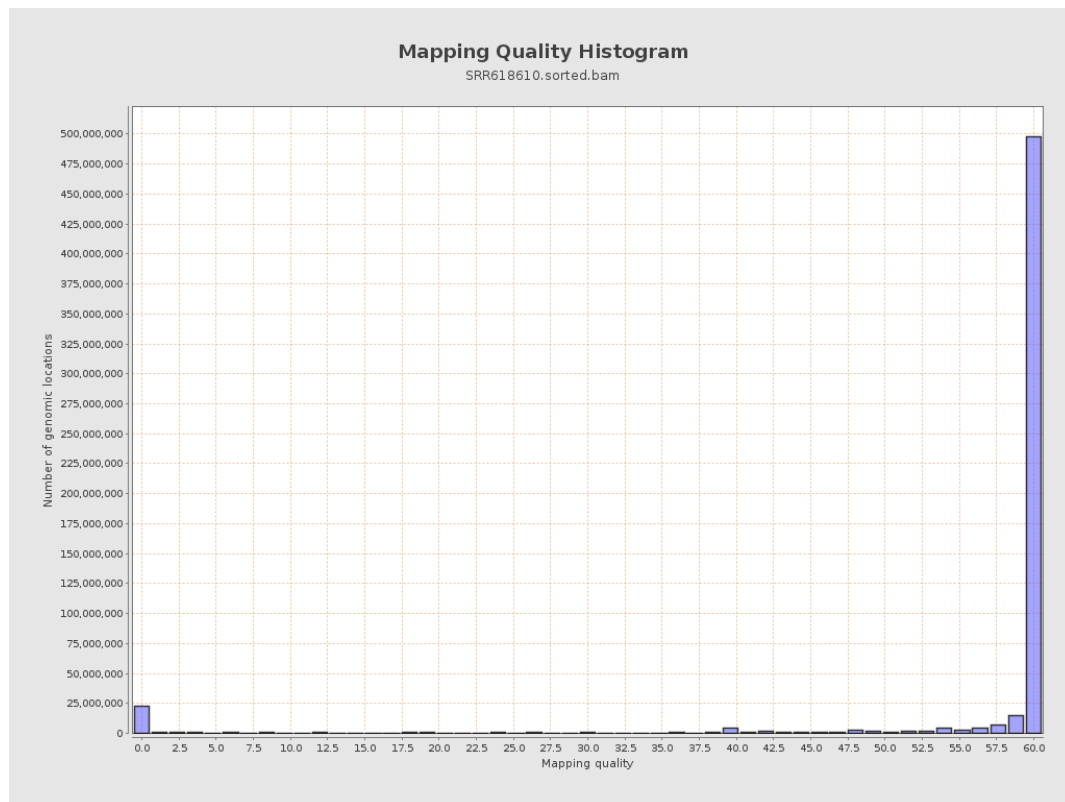
11. Results : Homopolymer Indels



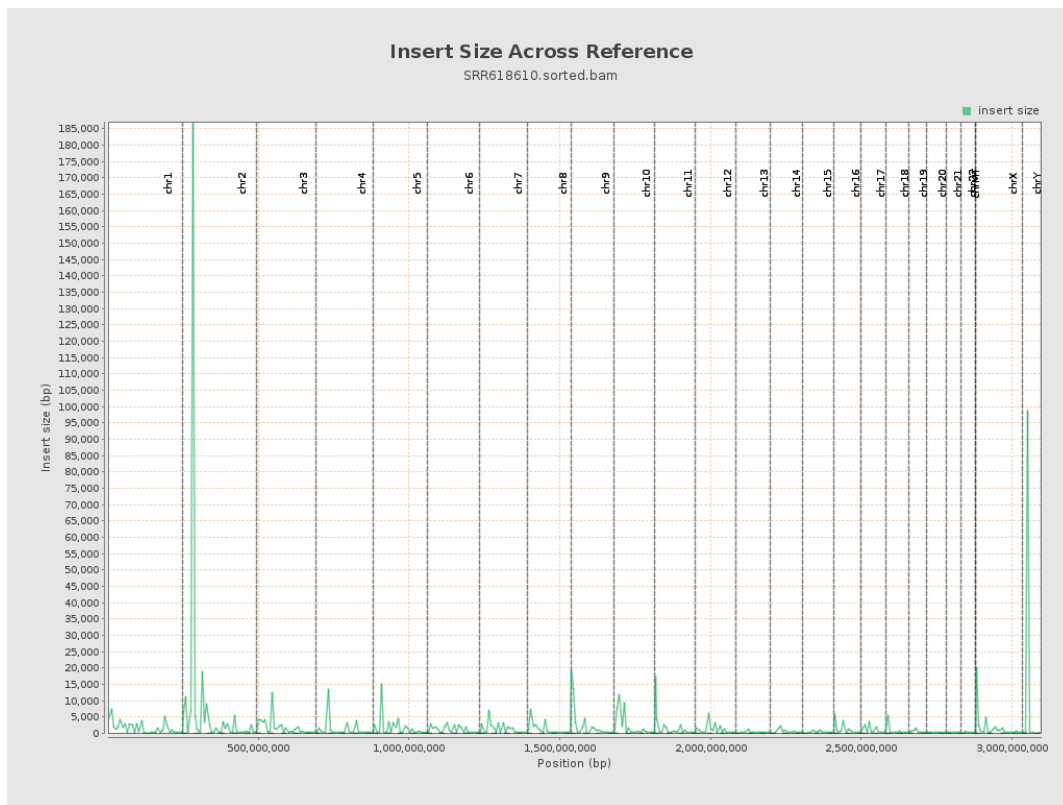
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

