

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 02:10:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618604.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_SRR618604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618604_1.fastq.gz SRR618604_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 02:10:30 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,233,946
Mapped reads	49,505,881 / 88.04%
Unmapped reads	6,728,065 / 11.96%
Mapped paired reads	49,505,881 / 88.04%
Mapped reads, first in pair	25,056,668 / 44.56%
Mapped reads, second in pair	24,449,213 / 43.48%
Mapped reads, both in pair	48,476,068 / 86.2%
Mapped reads, singletons	1,029,813 / 1.83%
Secondary alignments	0
Supplementary alignments	248,980 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	20,651,133 / 36.72%
Duplication rate	32.66%
Clipped reads	10,707,122 / 19.04%

2.2. ACGT Content

Number/percentage of A's	1,270,527,767 / 27.14%
Number/percentage of C's	1,025,865,185 / 21.92%
Number/percentage of T's	1,282,893,630 / 27.41%
Number/percentage of G's	1,101,272,332 / 23.53%
Number/percentage of N's	227,822 / 0%

GC Percentage	45.44%
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2.3. Coverage

Mean	1.5132
Standard Deviation	6.442

2.4. Mapping Quality

Mean Mapping Quality	53.44
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2.5. Insert size

Mean	89,314.55
Standard Deviation	2,963,687.21
P25/Median/P75	184 / 210 / 247

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	62,016,693
Insertions	922,398
Mapped reads with at least one insertion	1.83%
Deletions	2,784,145
Mapped reads with at least one deletion	5.46%
Homopolymer indels	52.77%

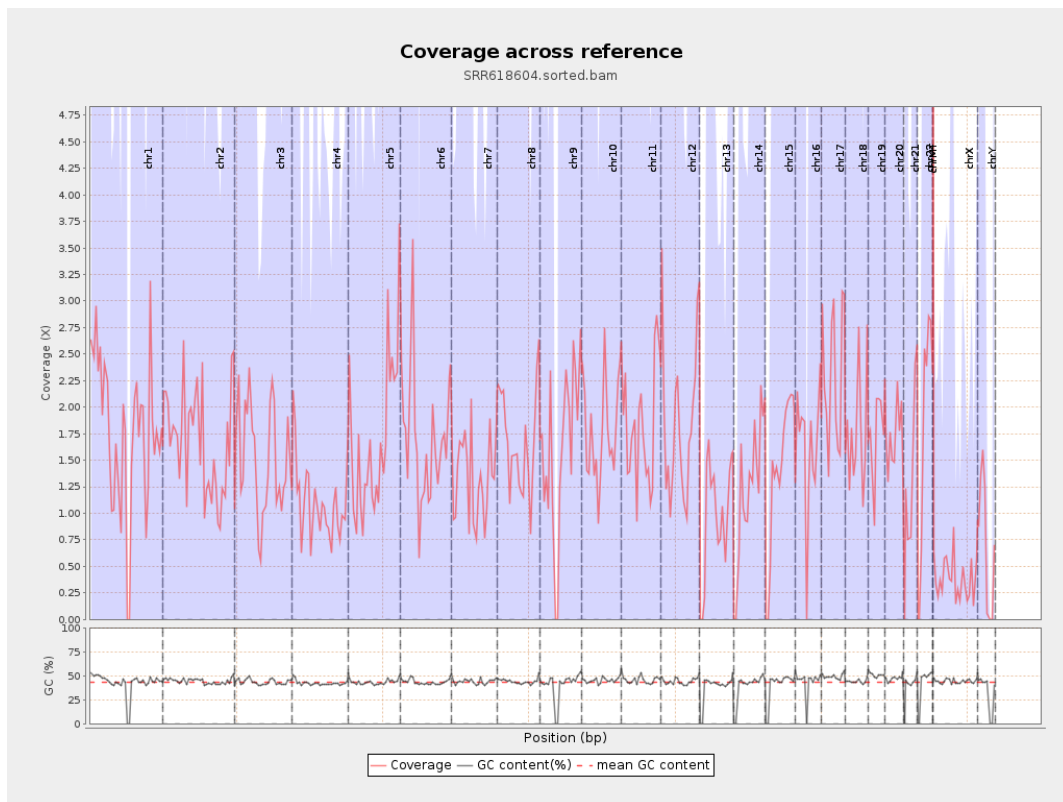
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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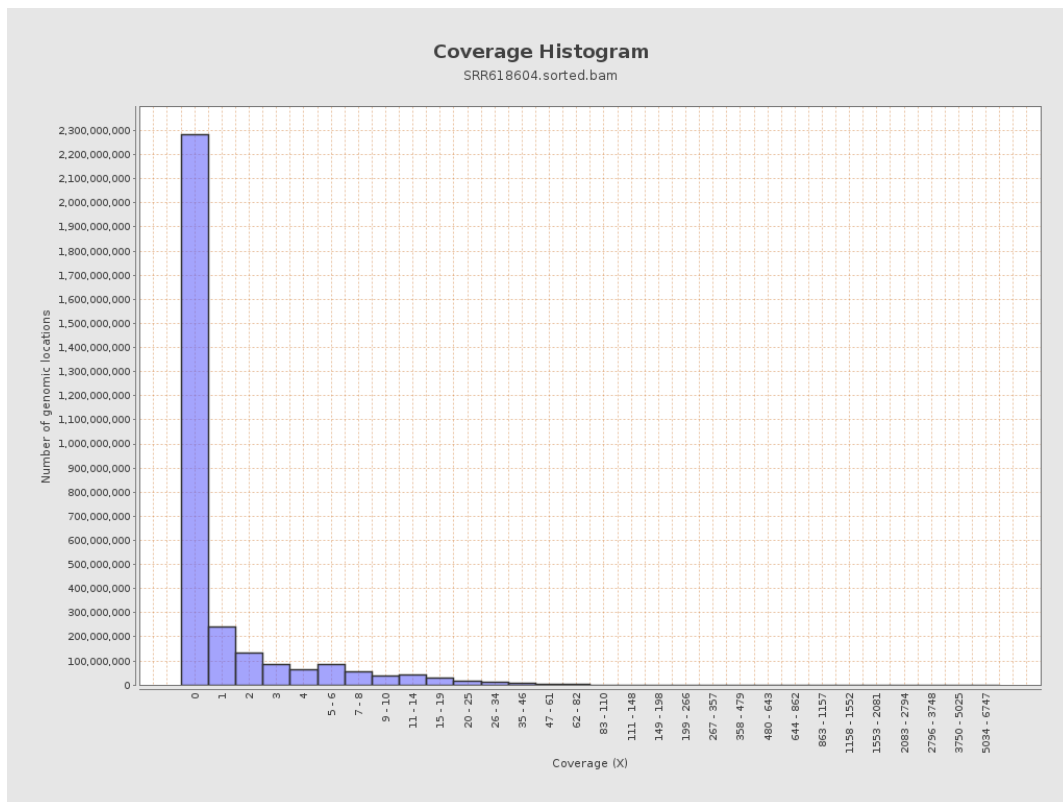
		bases	coverage	deviation
chr1	249250621	436883299	1.7528	7.6369
chr2	243199373	406689262	1.6722	7.6492
chr3	198022430	297359056	1.5016	4.8138
chr4	191154276	209179731	1.0943	4.9815
chr5	180915260	312454672	1.7271	5.6133
chr6	171115067	290002736	1.6948	7.1549
chr7	159138663	213699772	1.3429	4.5482
chr8	146364022	242763664	1.6586	5.3603
chr9	141213431	226562166	1.6044	6.9867
chr10	135534747	237115043	1.7495	6.4622
chr11	135006516	245258091	1.8166	7.2001
chr12	133851895	247151775	1.8465	6.3123
chr13	115169878	111861302	0.9713	3.6165
chr14	107349540	129719561	1.2084	4.6181
chr15	102531392	141604598	1.3811	4.8236
chr16	90354753	145520720	1.6105	12.7033
chr17	81195210	184814589	2.2762	7.5292
chr18	78077248	134385946	1.7212	7.0355
chr19	59128983	102177811	1.728	6.1432
chr20	63025520	108813096	1.7265	5.441
chr21	48129895	65252016	1.3557	9.0519
chr22	51304566	91899723	1.7913	6.7742
chrMT	16571	180523	10.8939	37.2915
chrX	155270560	60339135	0.3886	2.6485

chrY	59373566	42862498	0.7219	6.2749
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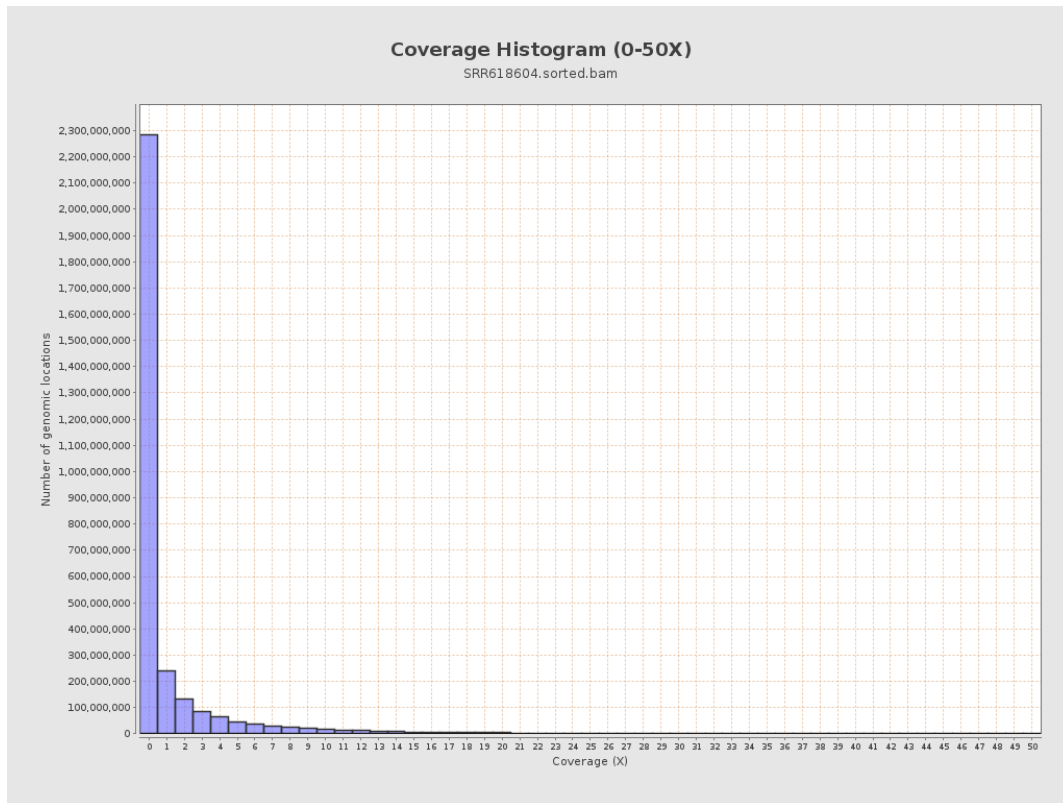
3. Results : Coverage across reference



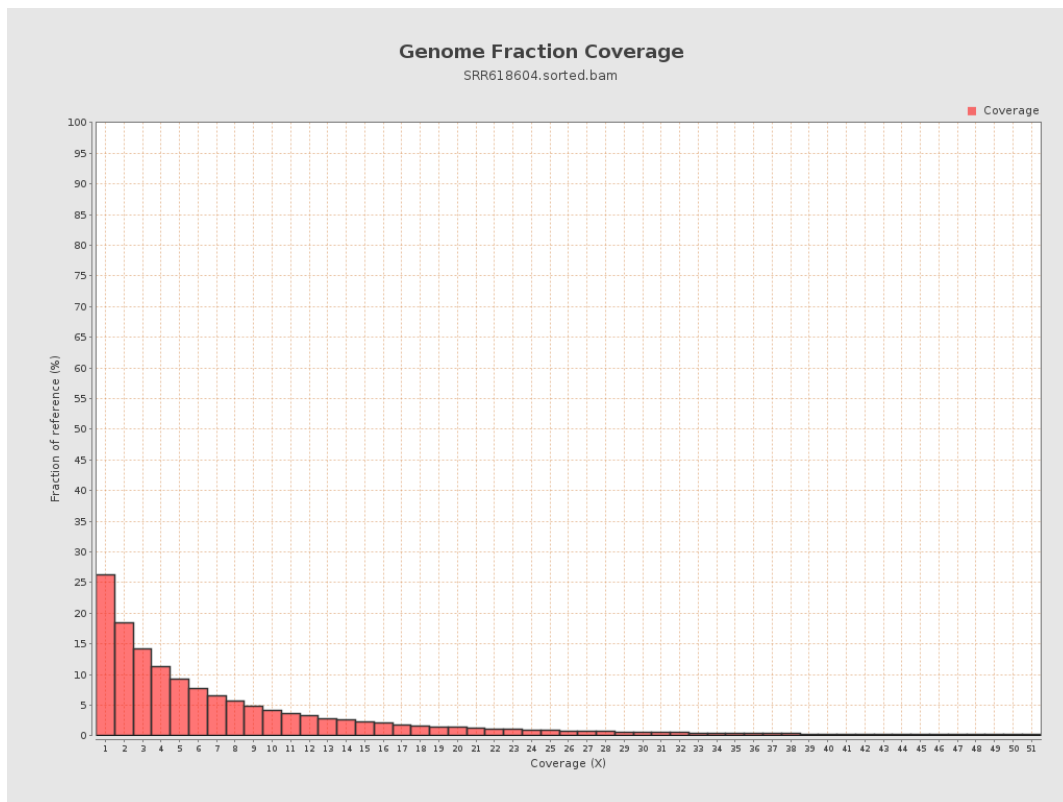
4. Results : Coverage Histogram



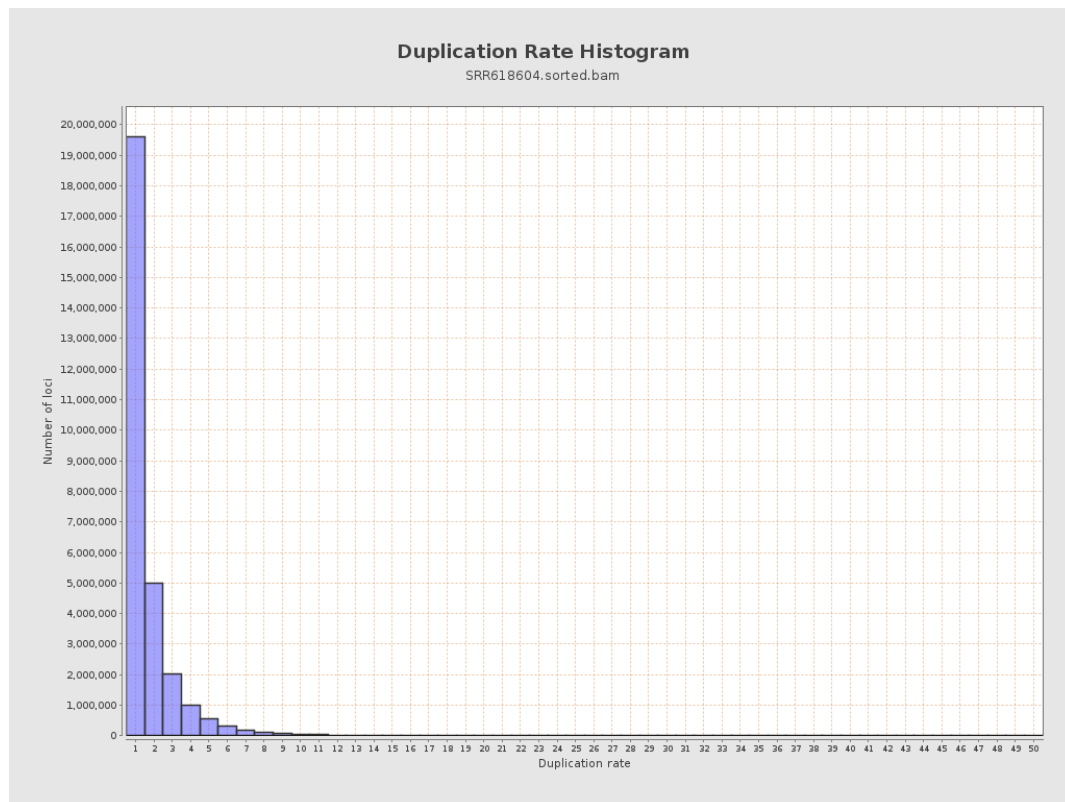
5. Results : Coverage Histogram (0-50X)



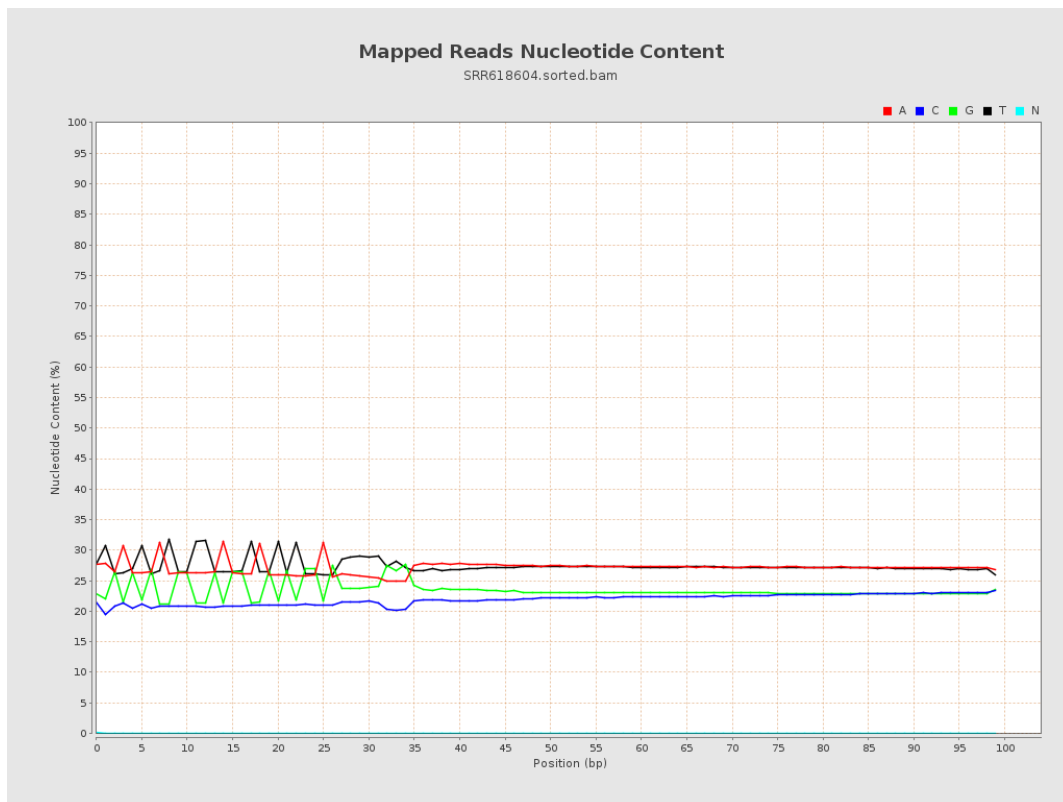
6. Results : Genome Fraction Coverage



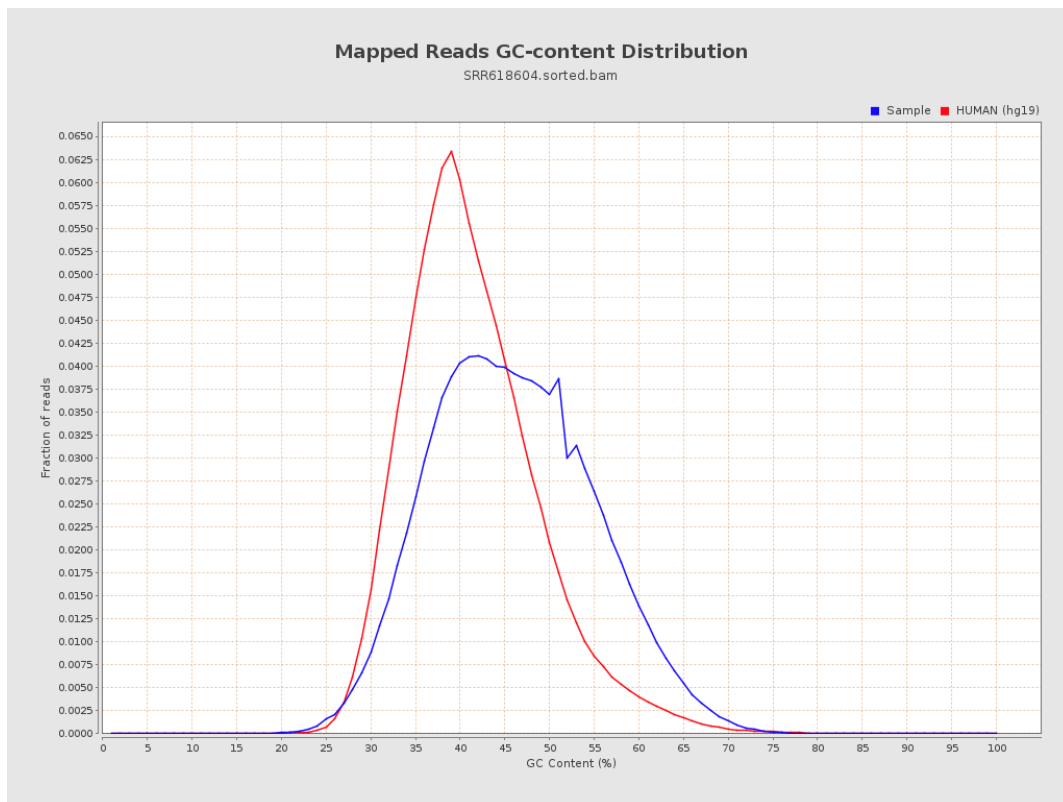
7. Results : Duplication Rate Histogram



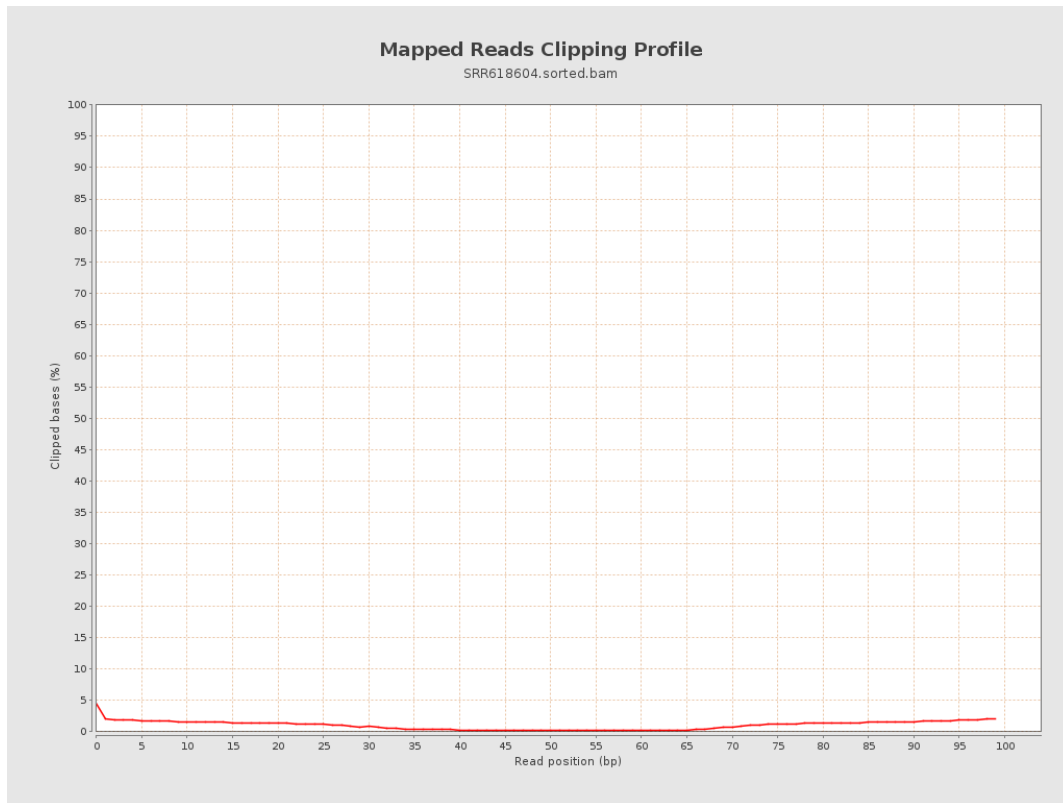
8. Results : Mapped Reads Nucleotide Content



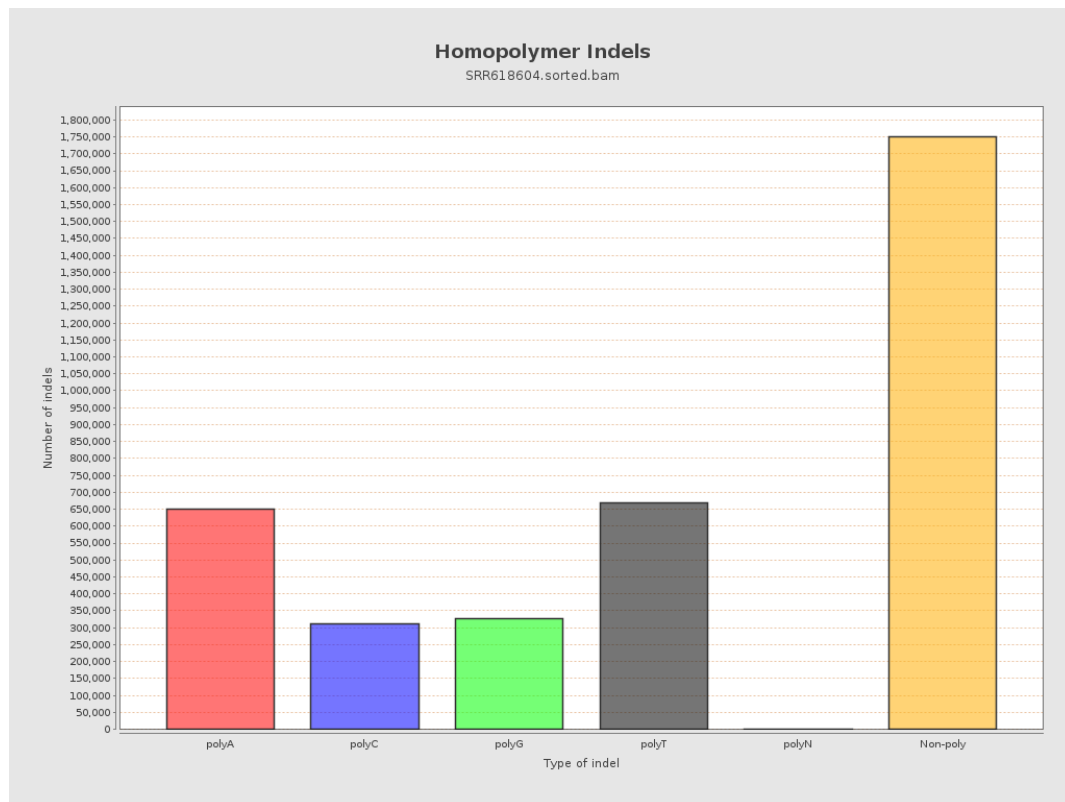
9. Results : Mapped Reads GC-content Distribution



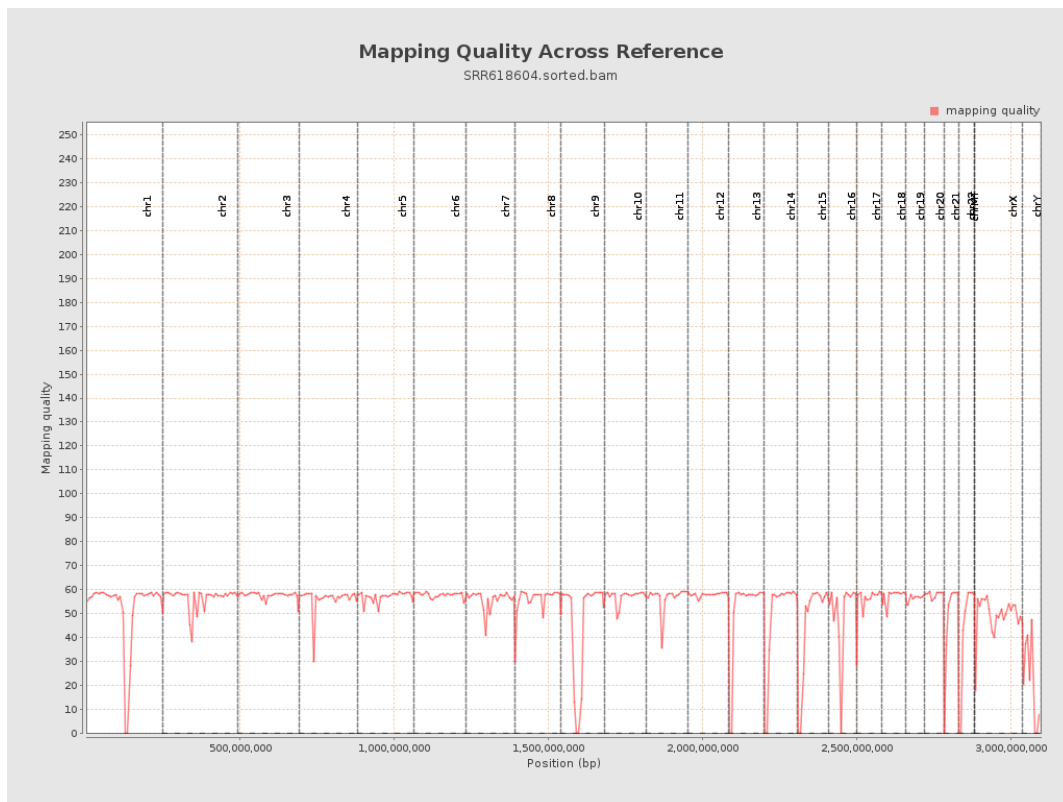
10. Results : Mapped Reads Clipping Profile



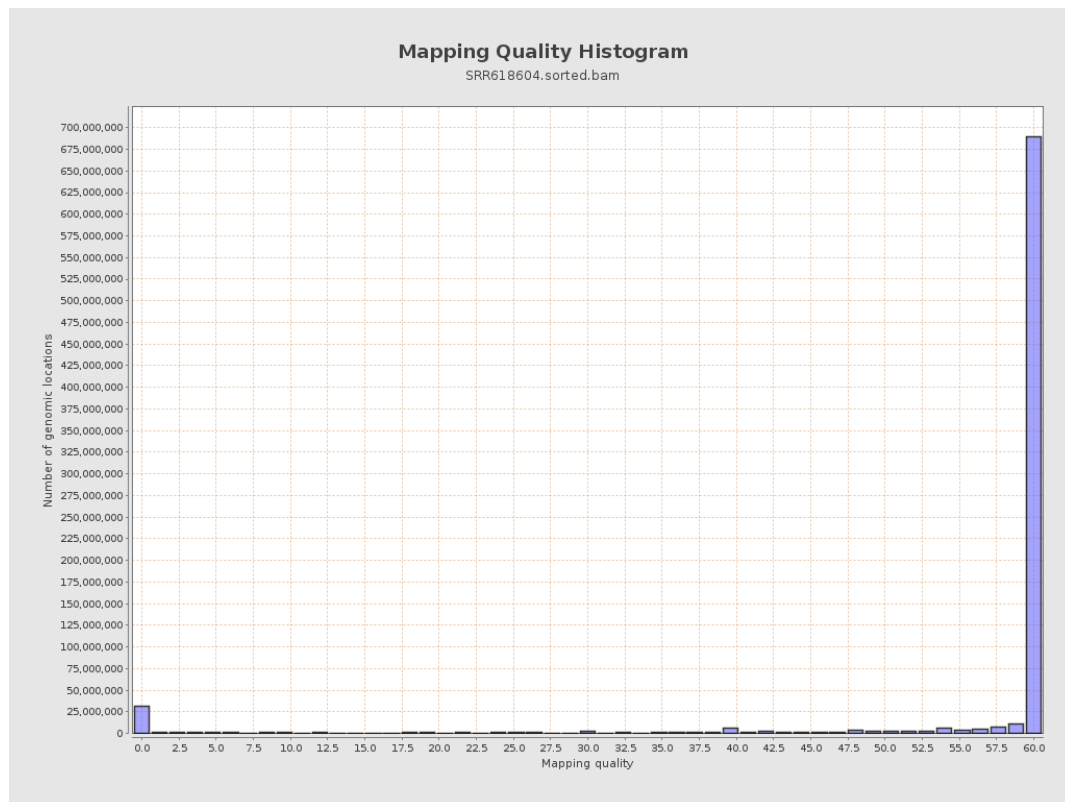
11. Results : Homopolymer Indels



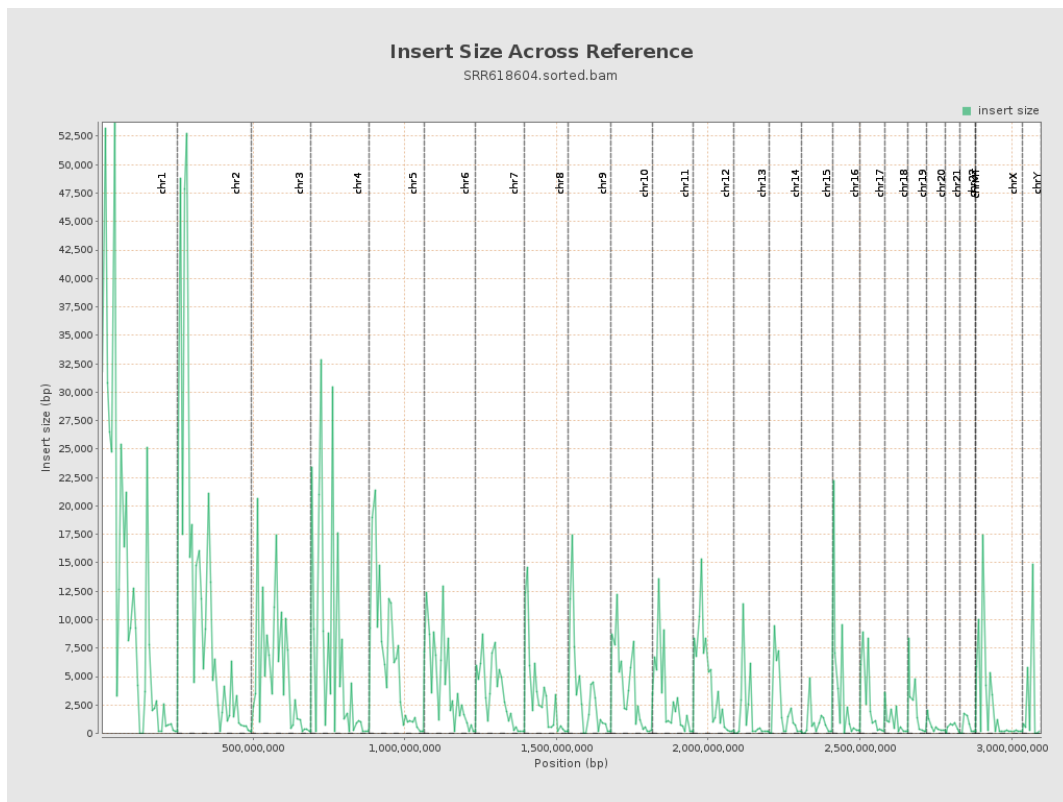
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

