

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 18:41:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618594.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_SRR618594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618594_1.fastq.gz SRR618594_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 18:41:18 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,908,148
Mapped reads	49,232,334 / 96.71%
Unmapped reads	1,675,814 / 3.29%
Mapped paired reads	49,232,334 / 96.71%
Mapped reads, first in pair	24,838,215 / 48.79%
Mapped reads, second in pair	24,394,119 / 47.92%
Mapped reads, both in pair	48,344,634 / 94.96%
Mapped reads, singletons	887,700 / 1.74%
Secondary alignments	0
Supplementary alignments	179,310 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,668,942 / 22.92%
Duplication rate	20.48%
Clipped reads	10,992,919 / 21.59%

2.2. ACGT Content

Number/percentage of A's	1,267,528,056 / 27.34%
Number/percentage of C's	1,010,200,387 / 21.79%
Number/percentage of T's	1,282,011,860 / 27.65%
Number/percentage of G's	1,075,940,522 / 23.21%
Number/percentage of N's	223,156 / 0%

GC Percentage	45%
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2.3. Coverage

Mean	1.4986
Standard Deviation	5.8493

2.4. Mapping Quality

Mean Mapping Quality	53.32
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2.5. Insert size

Mean	65,152.97
Standard Deviation	2,529,470
P25/Median/P75	159 / 188 / 227

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	59,078,052
Insertions	828,299
Mapped reads with at least one insertion	1.66%
Deletions	2,310,675
Mapped reads with at least one deletion	4.58%
Homopolymer indels	52.64%

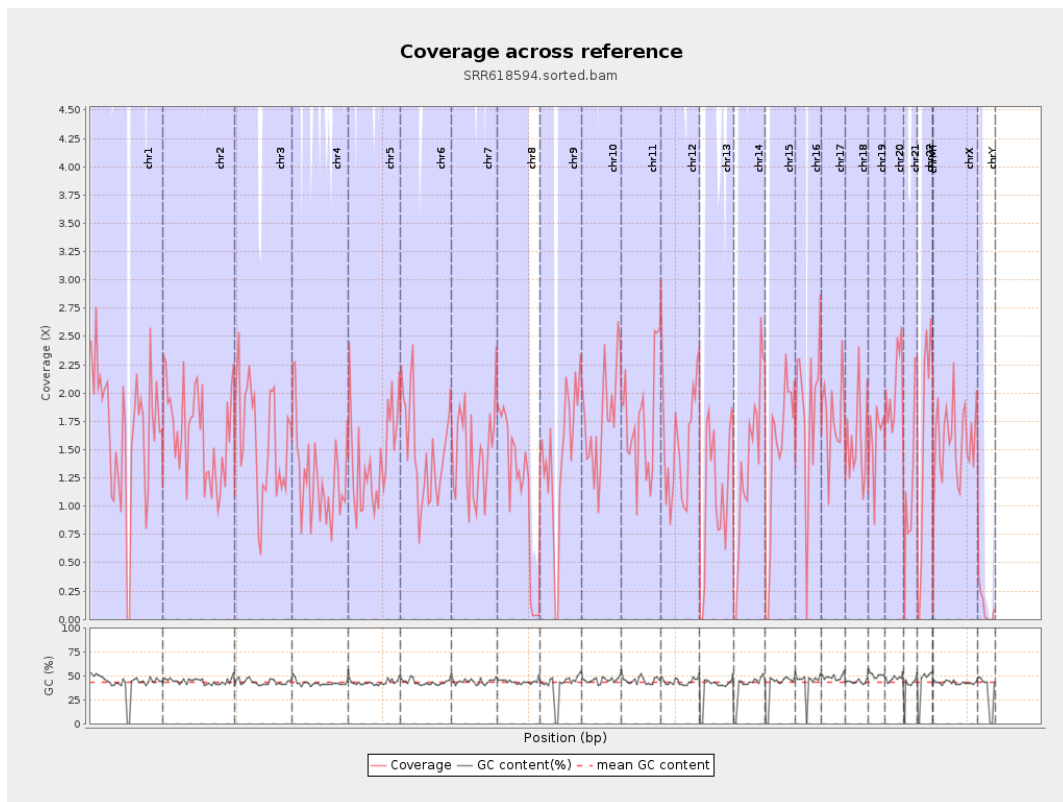
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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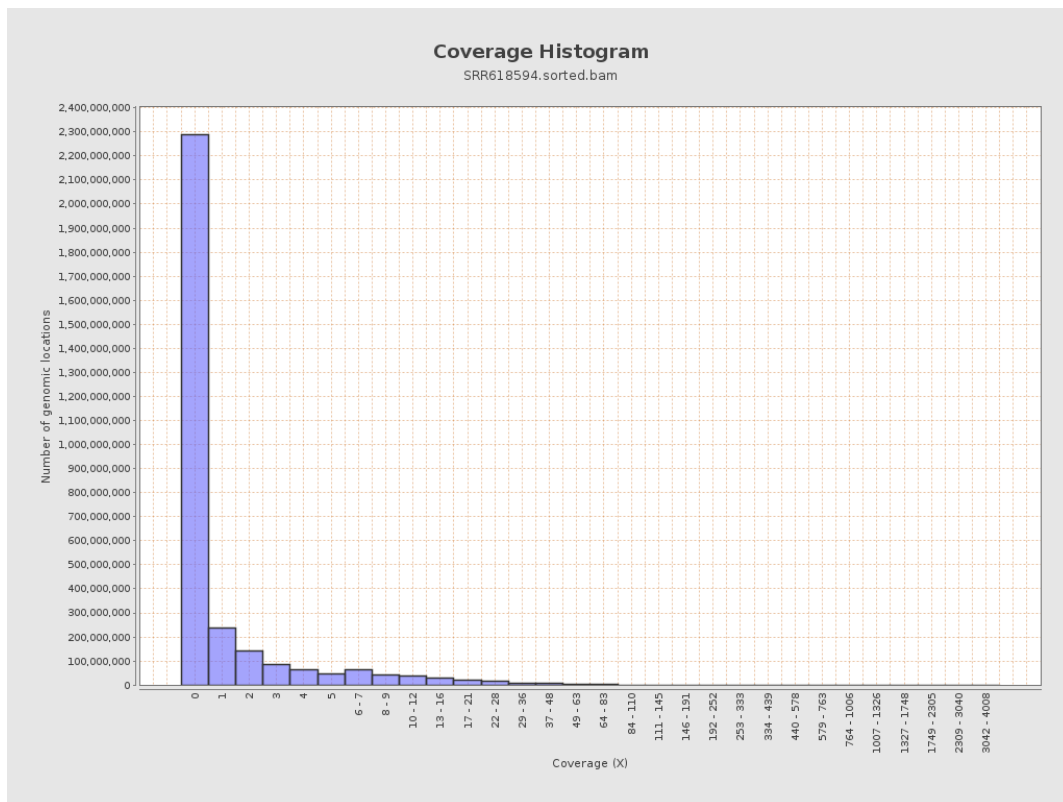
		bases	coverage	deviation
chr1	249250621	413424162	1.6587	7.3378
chr2	243199373	398685485	1.6393	6.502
chr3	198022430	311265914	1.5719	5.0269
chr4	191154276	239128904	1.251	4.9743
chr5	180915260	260706082	1.441	4.7977
chr6	171115067	252030146	1.4729	4.8924
chr7	159138663	235262735	1.4784	4.9737
chr8	146364022	163861564	1.1195	4.2671
chr9	141213431	204294074	1.4467	6.6085
chr10	135534747	239199267	1.7649	5.7222
chr11	135006516	236183284	1.7494	6.5241
chr12	133851895	208347979	1.5566	5.2046
chr13	115169878	127570823	1.1077	4.0386
chr14	107349540	146934804	1.3688	4.9971
chr15	102531392	150073874	1.4637	5.2391
chr16	90354753	166094777	1.8383	9.2874
chr17	81195210	145134308	1.7875	6.1307
chr18	78077248	120744035	1.5465	6.8029
chr19	59128983	93687081	1.5845	6.5087
chr20	63025520	130009333	2.0628	6.4128
chr21	48129895	60417391	1.2553	8.8853
chr22	51304566	82811238	1.6141	6.4925
chrMT	16571	528	0.0319	0.2221
chrX	155270560	247117126	1.5915	5.0615

chrY	59373566	6068283	0.1022	2.99
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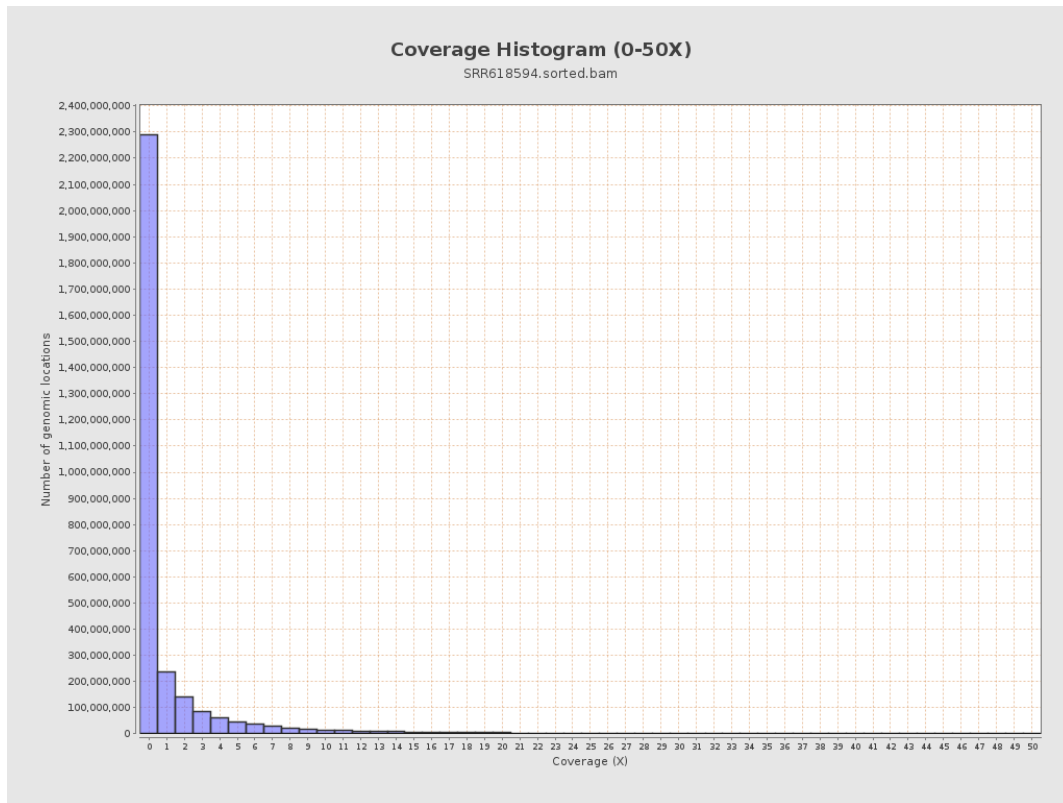
3. Results : Coverage across reference



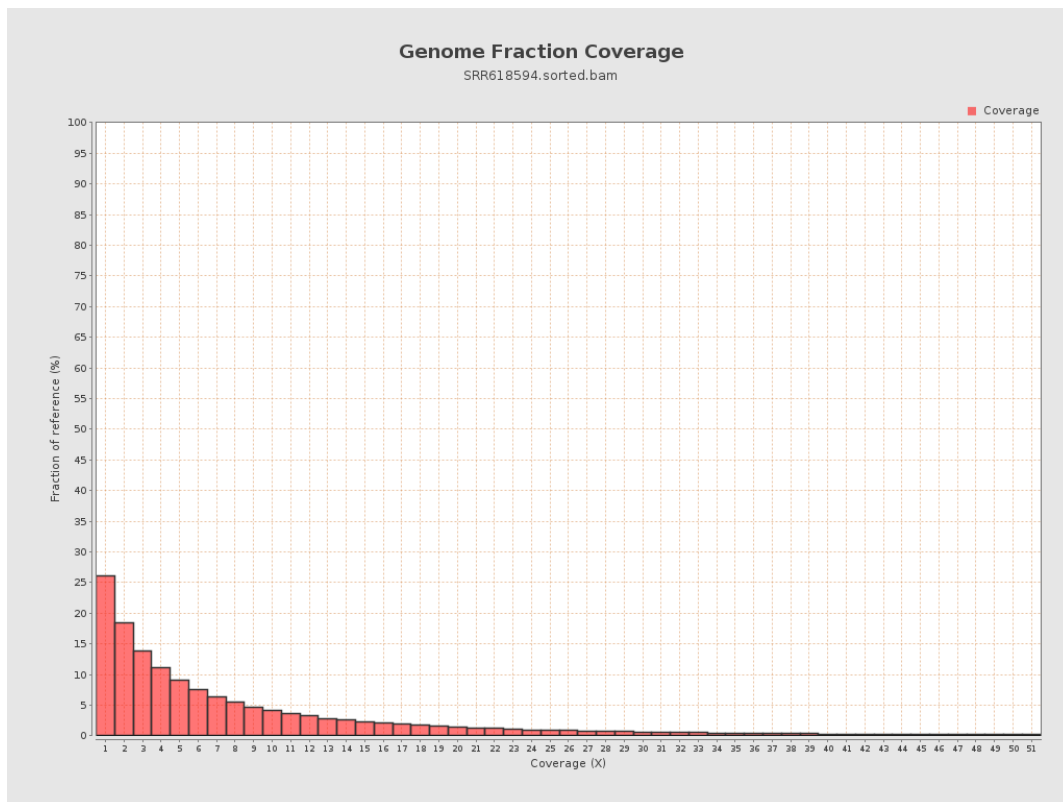
4. Results : Coverage Histogram



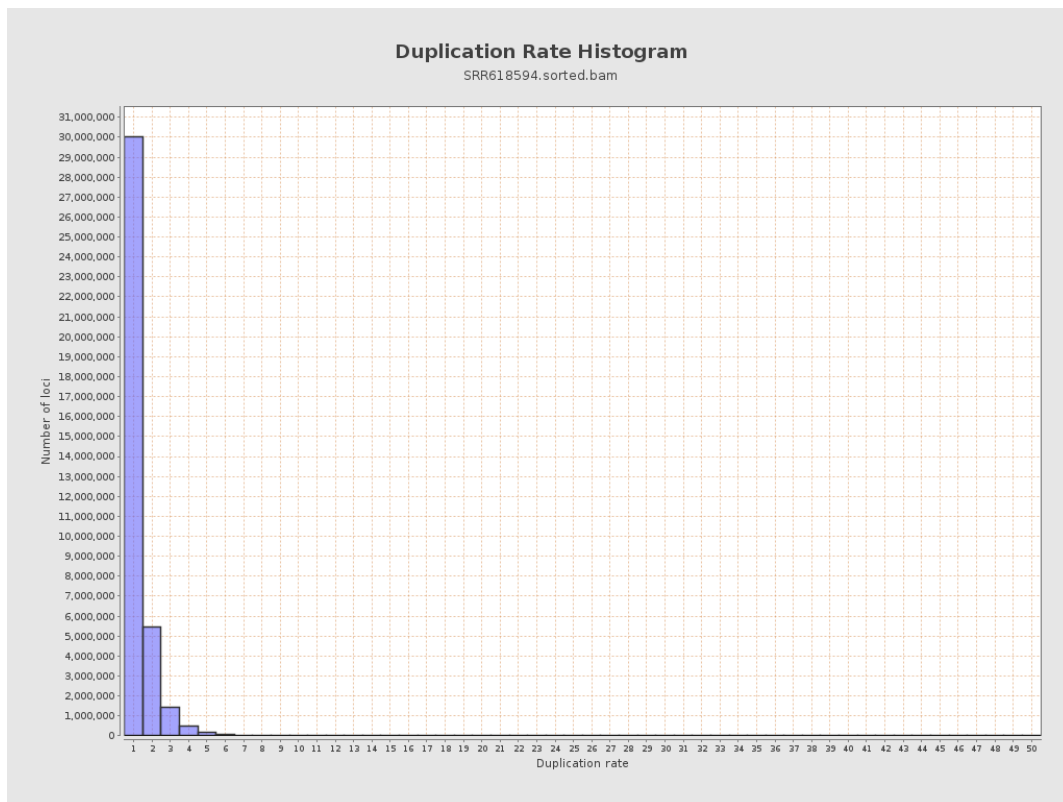
5. Results : Coverage Histogram (0-50X)



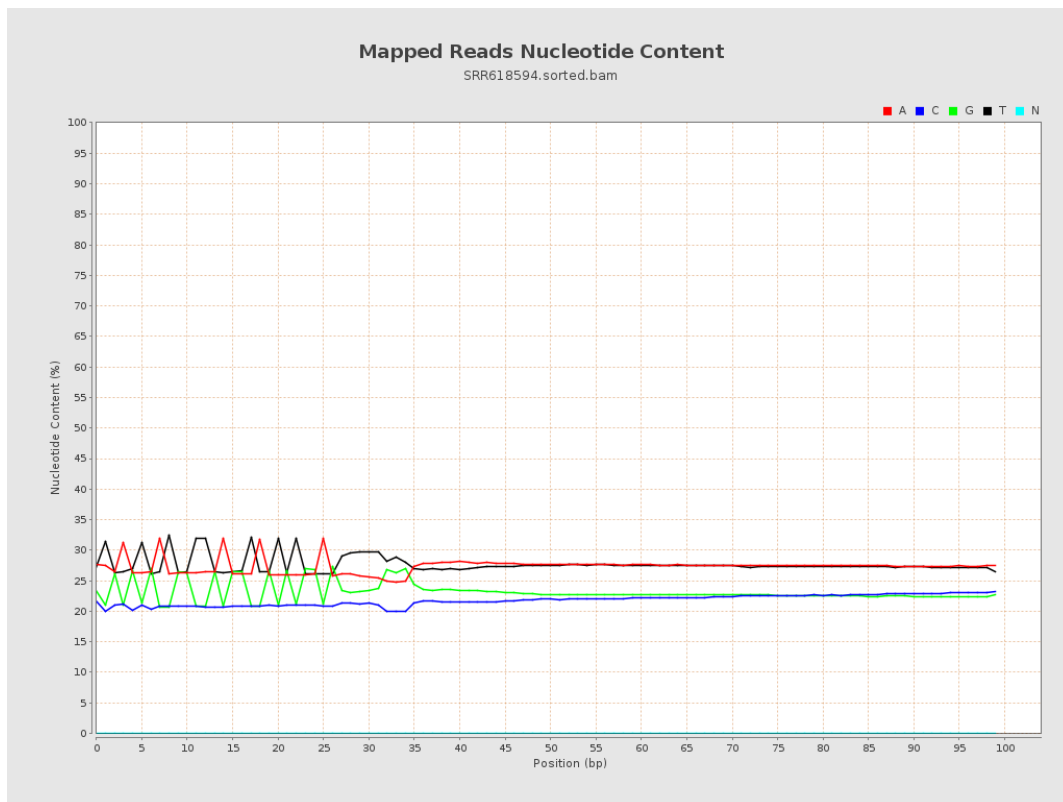
6. Results : Genome Fraction Coverage



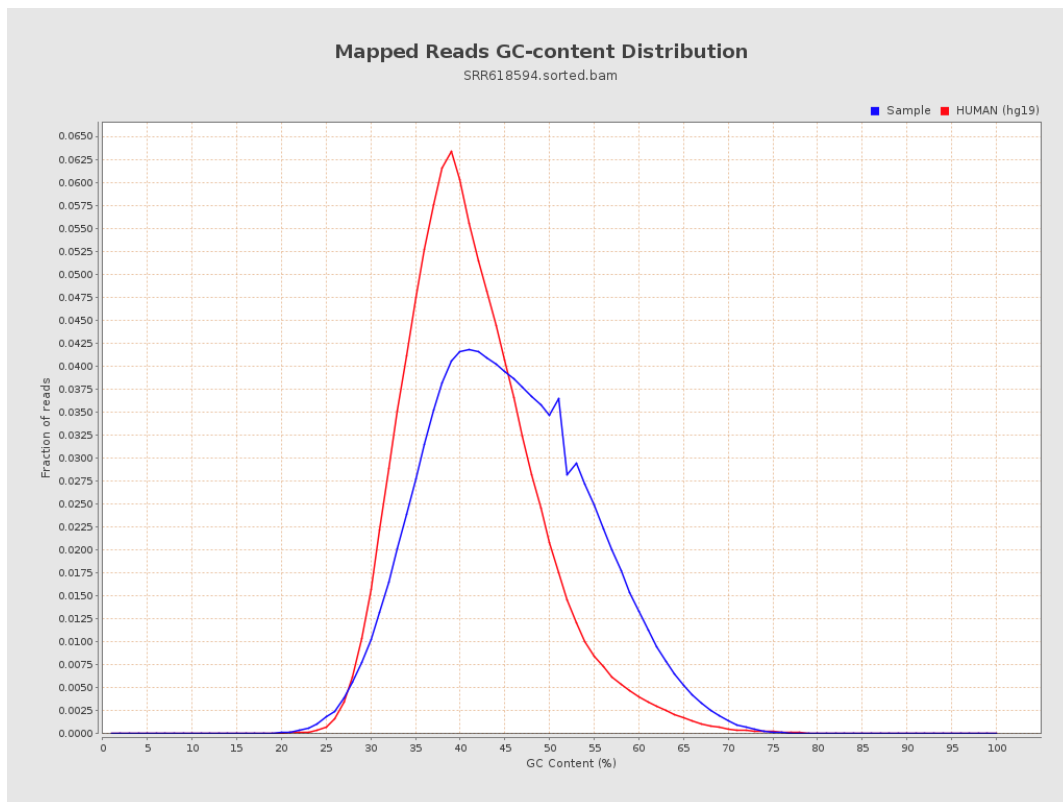
7. Results : Duplication Rate Histogram



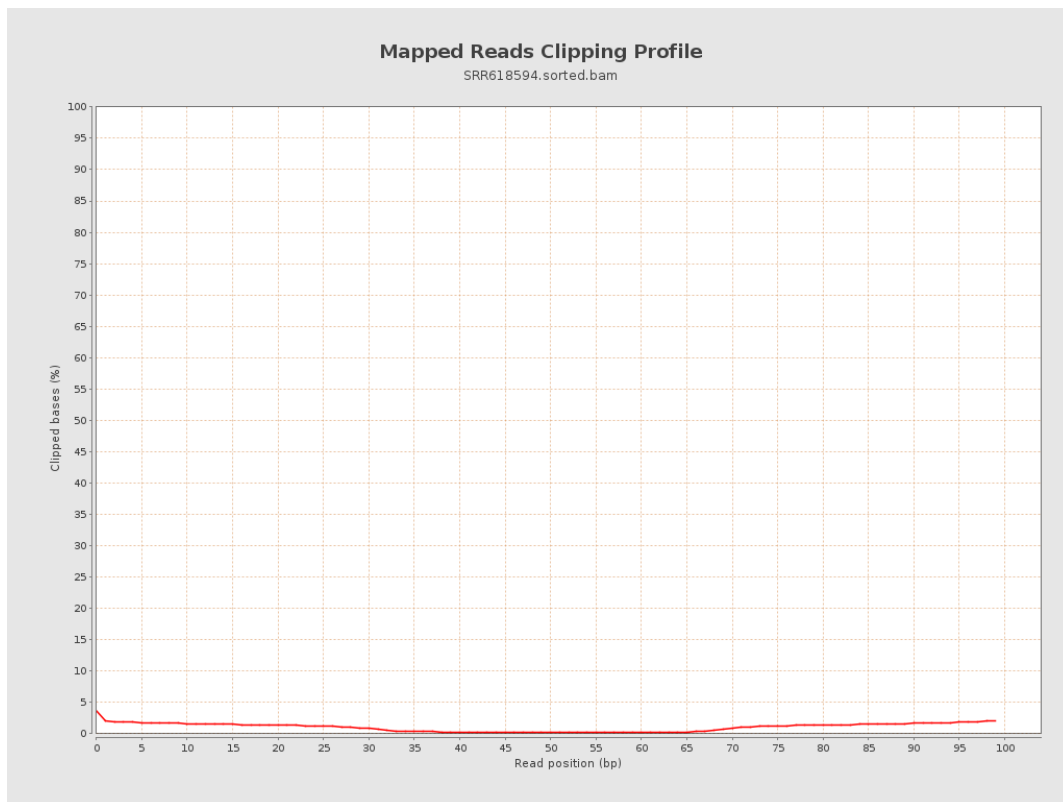
8. Results : Mapped Reads Nucleotide Content



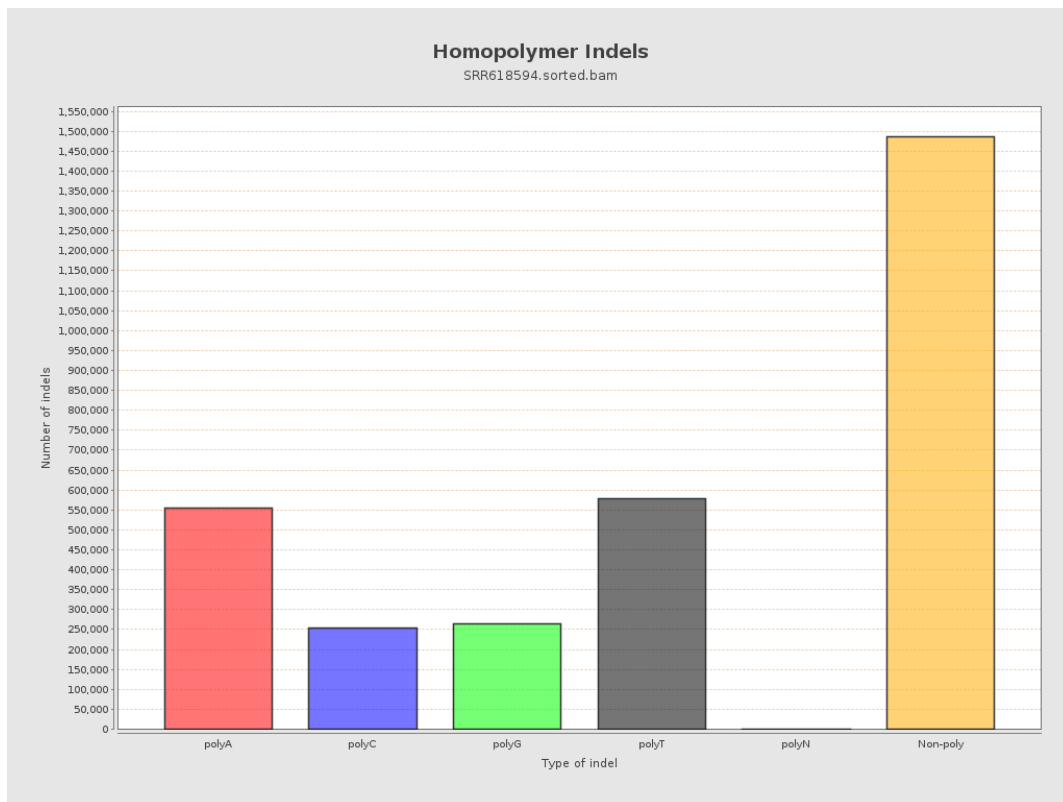
9. Results : Mapped Reads GC-content Distribution



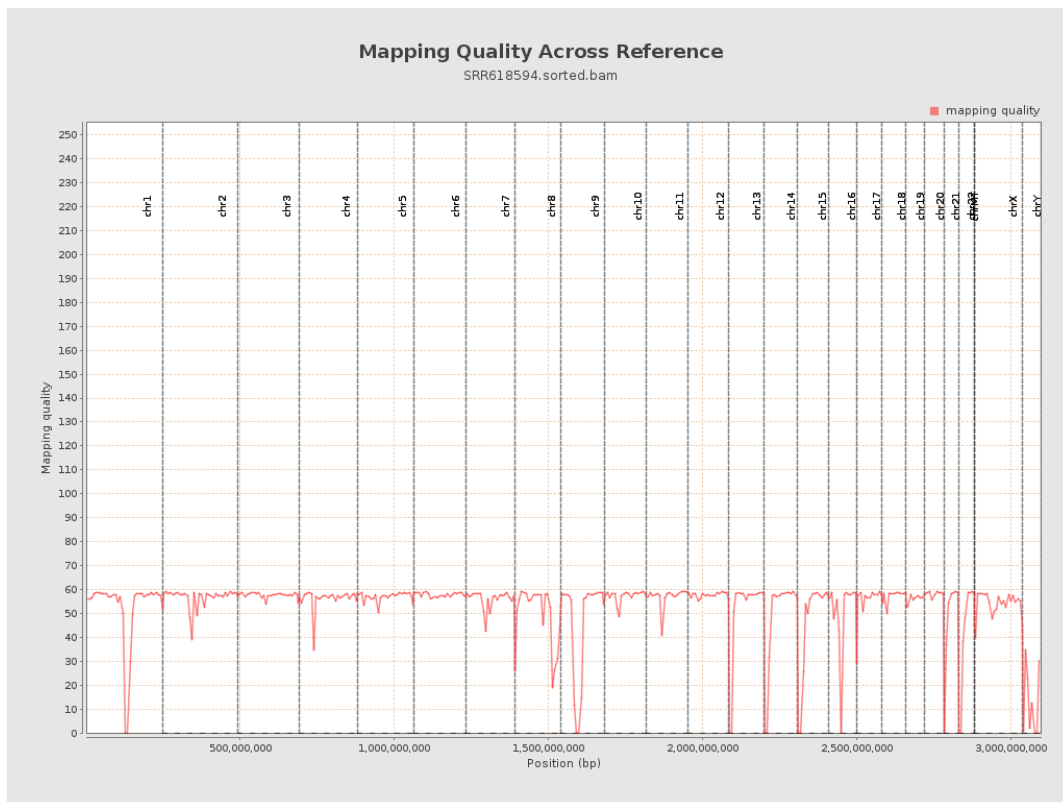
10. Results : Mapped Reads Clipping Profile



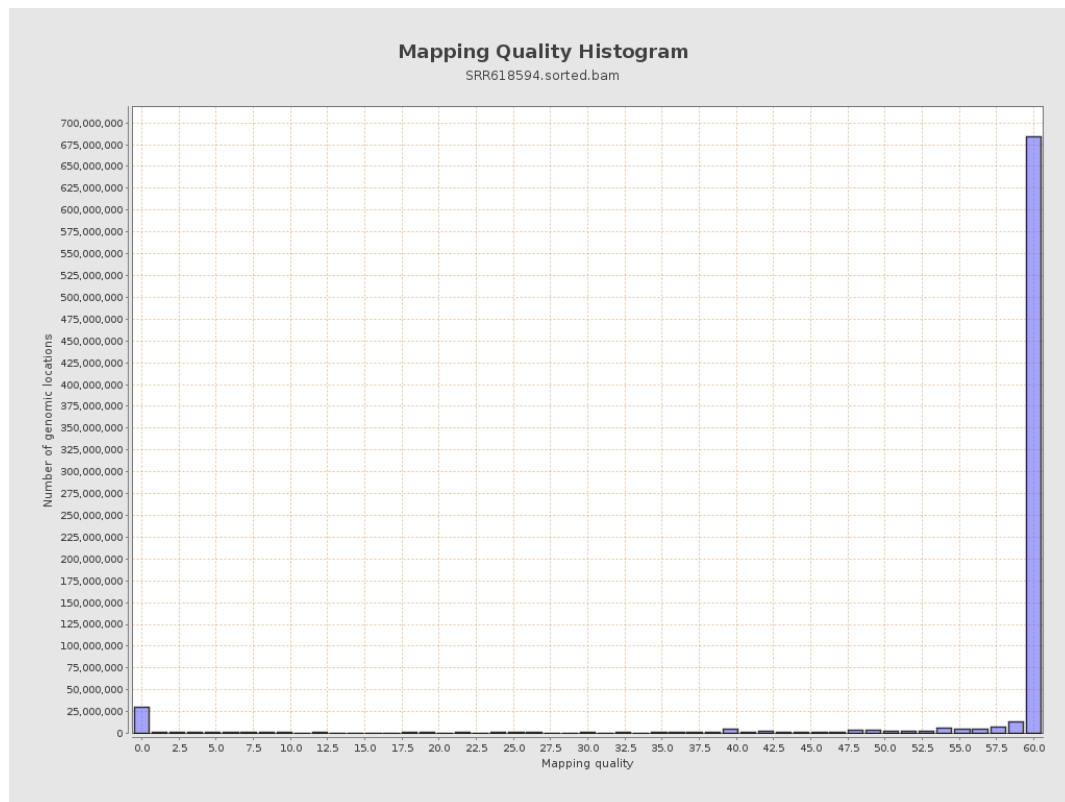
11. Results : Homopolymer Indels



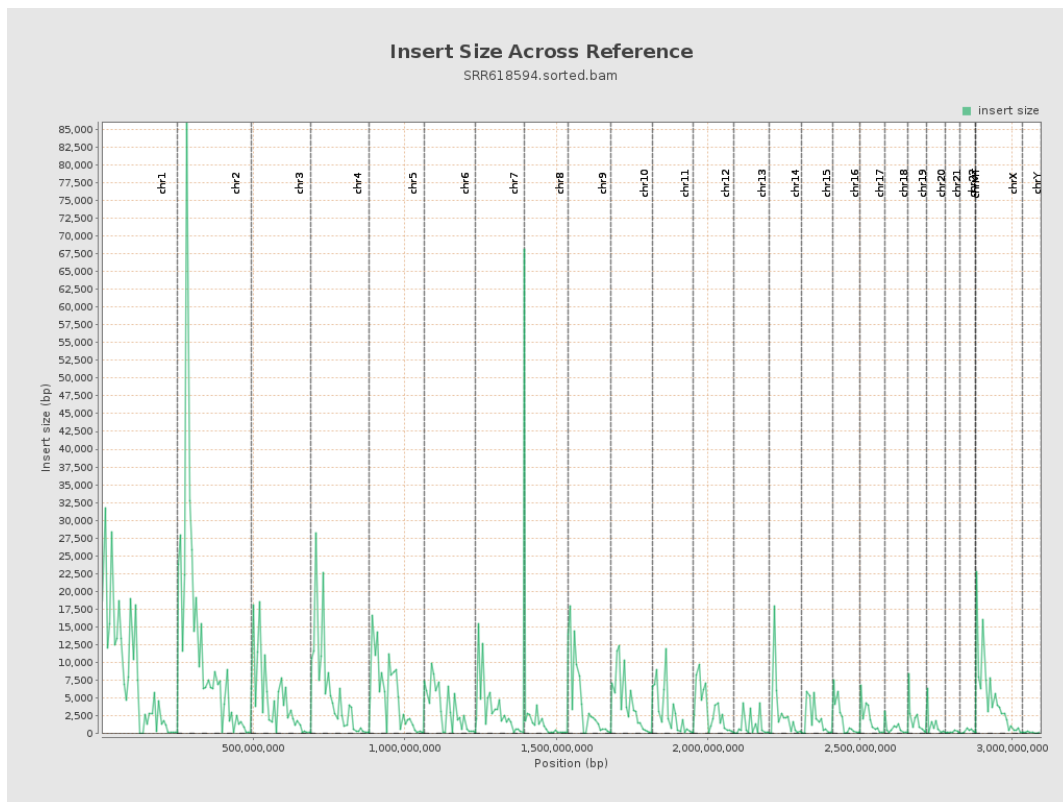
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

