

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 17:13:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618628.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_SRR618628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618628_1.fastq.gz SRR618628_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 17:13:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,266,812
Mapped reads	33,510,406 / 89.92%
Unmapped reads	3,756,406 / 10.08%
Mapped paired reads	33,510,406 / 89.92%
Mapped reads, first in pair	17,058,277 / 45.77%
Mapped reads, second in pair	16,452,129 / 44.15%
Mapped reads, both in pair	32,219,394 / 86.46%
Mapped reads, singletons	1,291,012 / 3.46%
Secondary alignments	0
Supplementary alignments	61,878 / 0.17%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	22,009,365 / 59.06%
Duplication rate	45.93%
Clipped reads	7,632,190 / 20.48%

2.2. ACGT Content

Number/percentage of A's	784,513,976 / 24.94%
Number/percentage of C's	769,593,379 / 24.46%
Number/percentage of T's	792,660,981 / 25.19%
Number/percentage of G's	796,752,040 / 25.32%
Number/percentage of N's	2,595,446 / 0.08%

GC Percentage	49.79%
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2.3. Coverage

Mean	1.0169
Standard Deviation	5.947

2.4. Mapping Quality

Mean Mapping Quality	52.89
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2.5. Insert size

Mean	63,277.78
Standard Deviation	2,583,853.33
P25/Median/P75	172 / 203 / 241

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	45,960,498
Insertions	560,514
Mapped reads with at least one insertion	1.65%
Deletions	1,398,955
Mapped reads with at least one deletion	4.08%
Homopolymer indels	51.74%

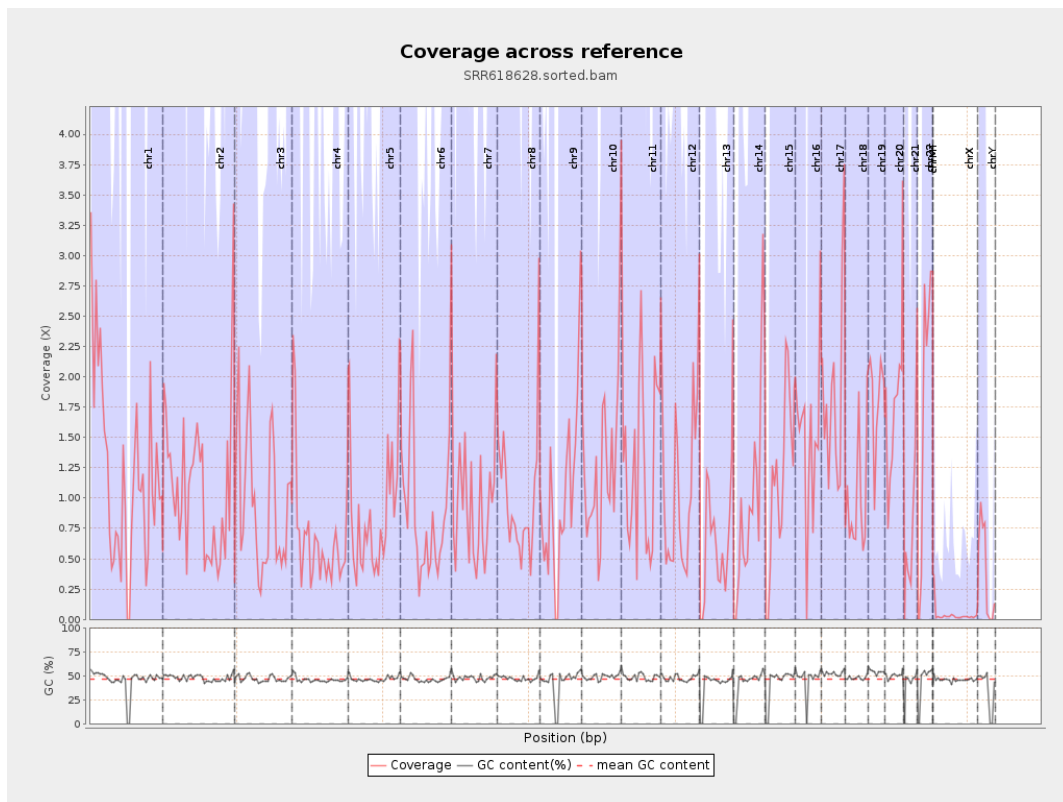
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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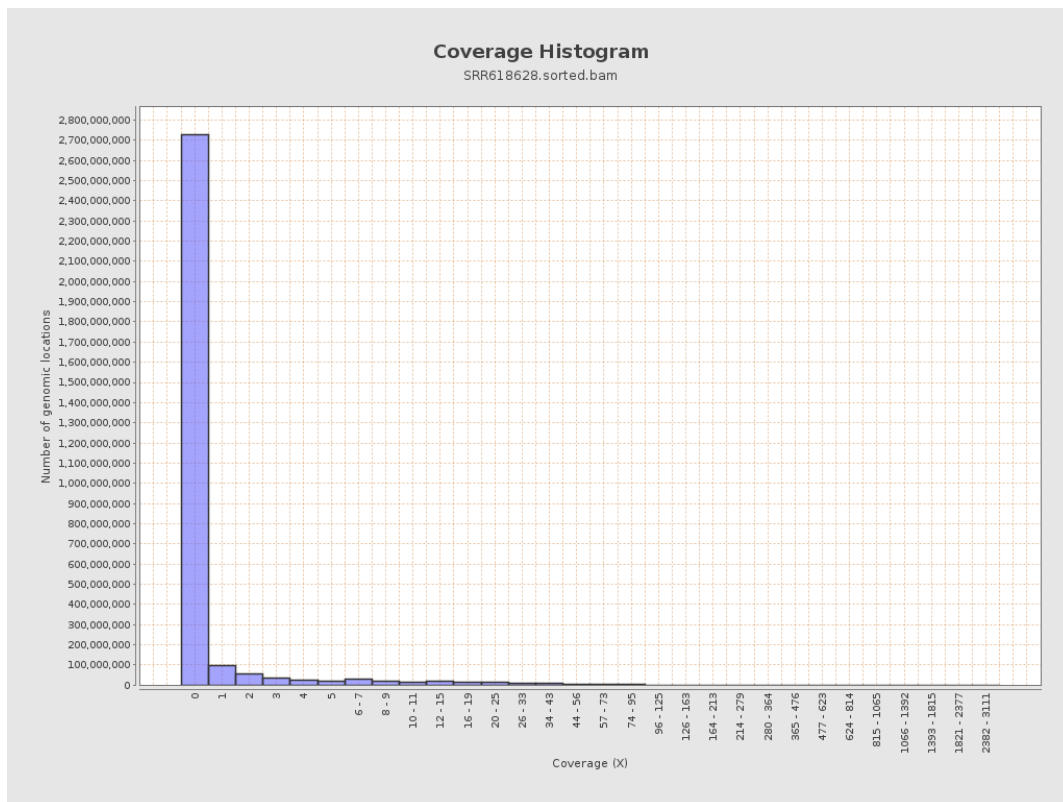
		bases	coverage	deviation
chr1	249250621	297407797	1.1932	6.8274
chr2	243199373	262548218	1.0796	6.1683
chr3	198022430	186241424	0.9405	5.3765
chr4	191154276	128113034	0.6702	4.652
chr5	180915260	160434764	0.8868	5.0487
chr6	171115067	150152438	0.8775	4.9132
chr7	159138663	158058634	0.9932	5.4806
chr8	146364022	145007228	0.9907	5.4153
chr9	141213431	143268739	1.0146	6.418
chr10	135534747	167448334	1.2355	6.2923
chr11	135006516	180027942	1.3335	7.0125
chr12	133851895	144540065	1.0799	5.8439
chr13	115169878	73087171	0.6346	3.9891
chr14	107349540	104658084	0.9749	5.8674
chr15	102531392	116038776	1.1317	6.2247
chr16	90354753	136428984	1.5099	8.1863
chr17	81195210	147397328	1.8153	8.1758
chr18	78077248	73866481	0.9461	5.2462
chr19	59128983	106231507	1.7966	8.6145
chr20	63025520	108072676	1.7147	7.7433
chr21	48129895	40113019	0.8334	6.9437
chr22	51304566	89069495	1.7361	8.3584
chrMT	16571	6221	0.3754	3.0581
chrX	155270560	5691794	0.0367	0.8479

chrY	59373566	24127096	0.4064	3.6912
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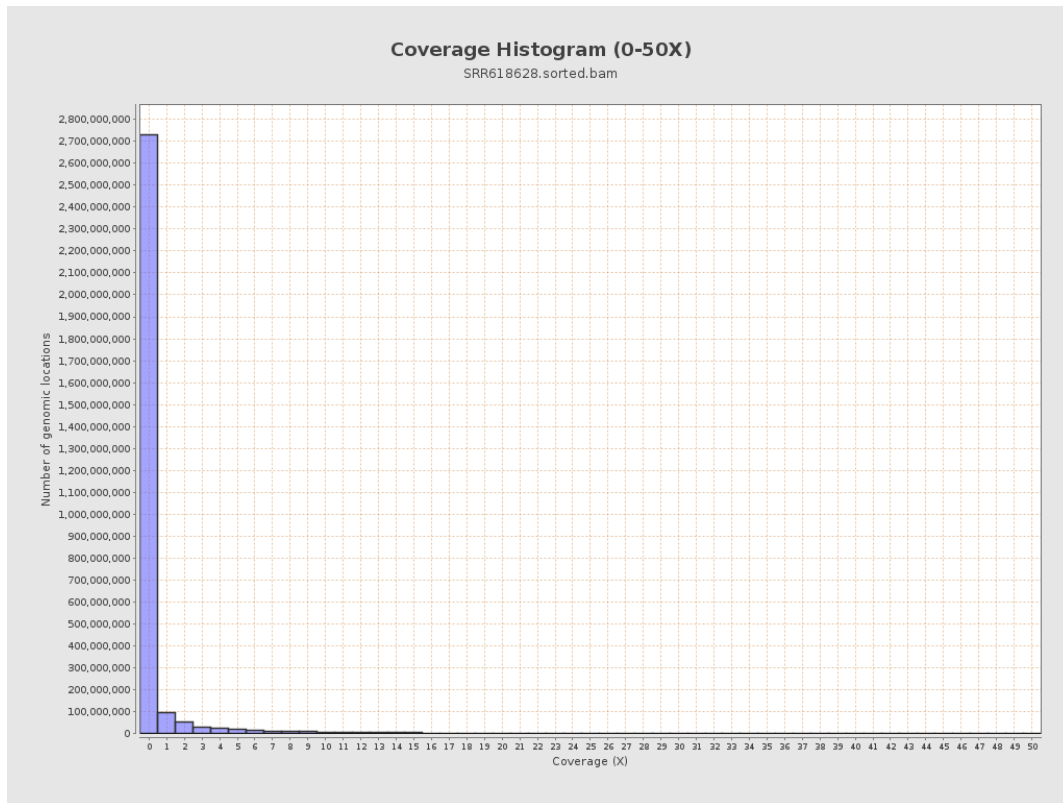
3. Results : Coverage across reference



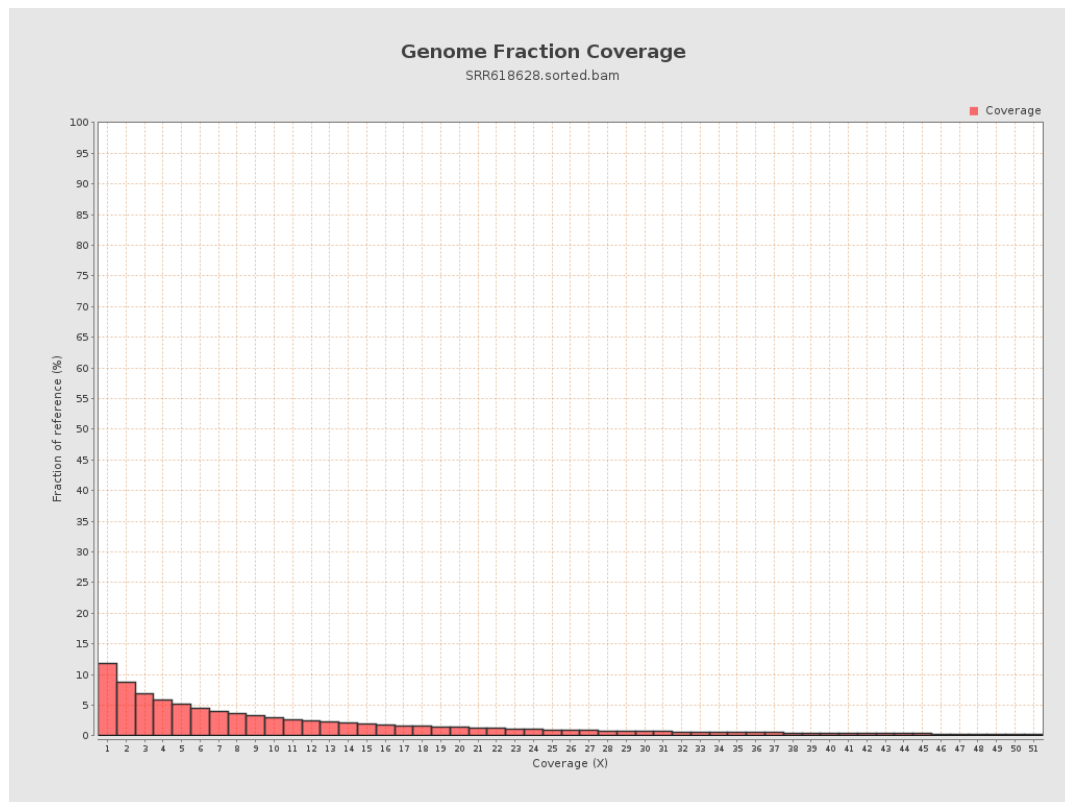
4. Results : Coverage Histogram



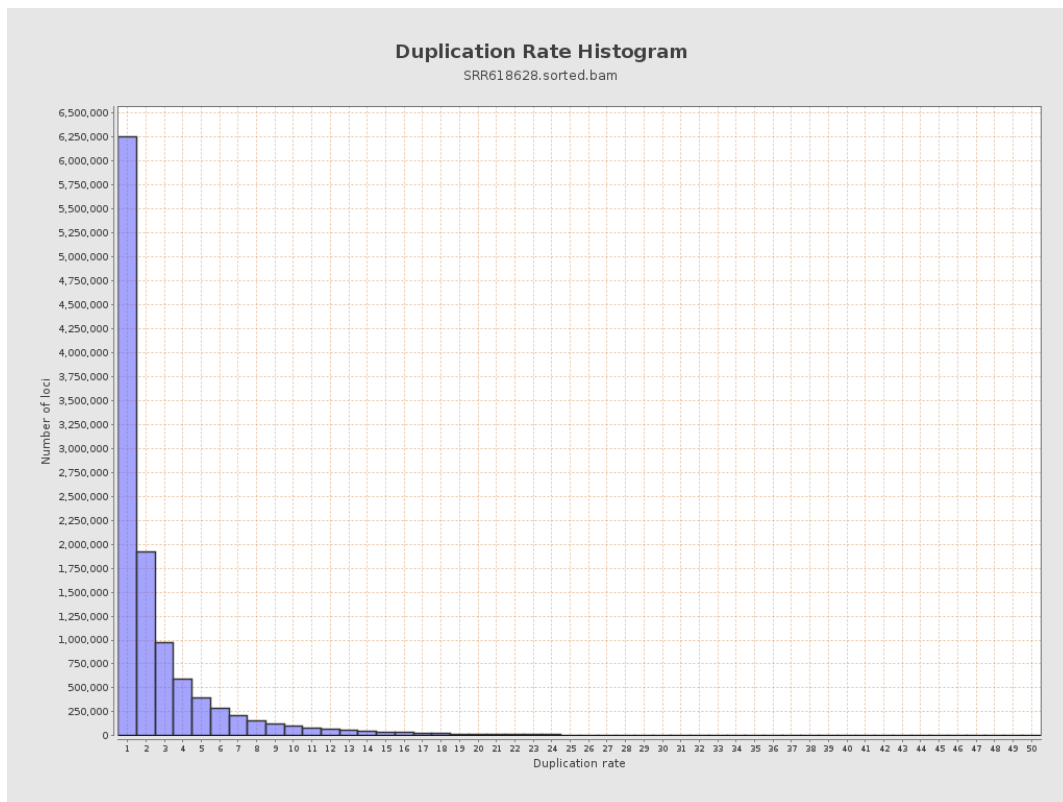
5. Results : Coverage Histogram (0-50X)



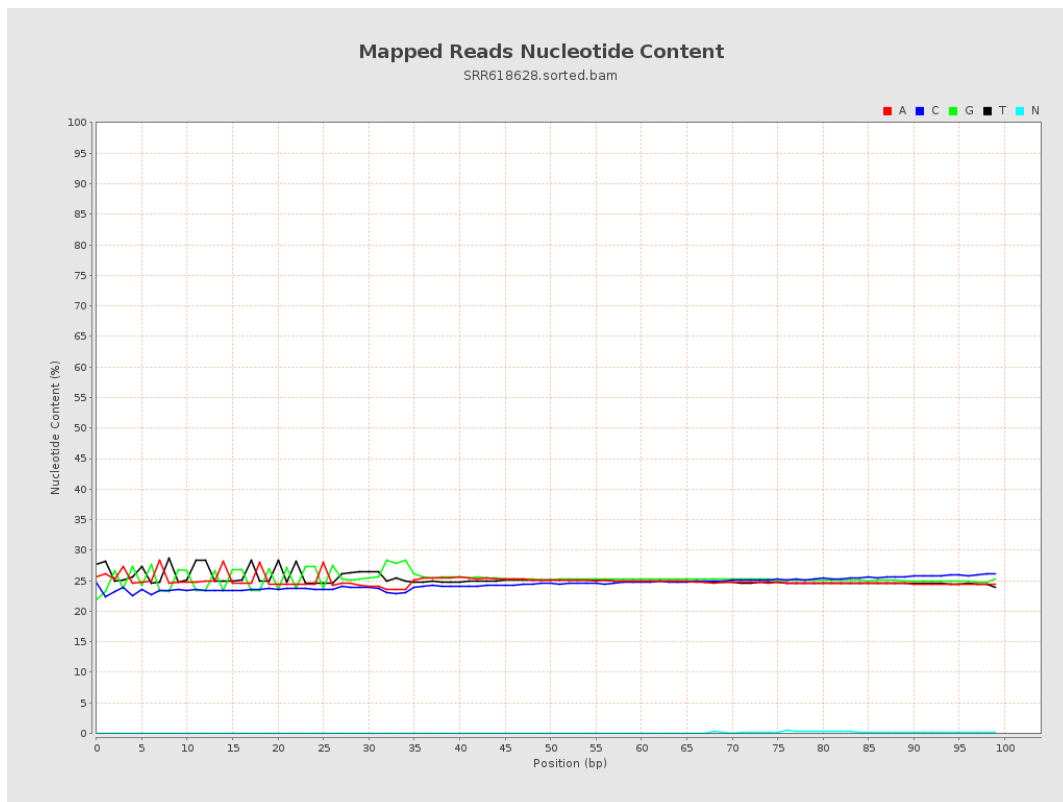
6. Results : Genome Fraction Coverage



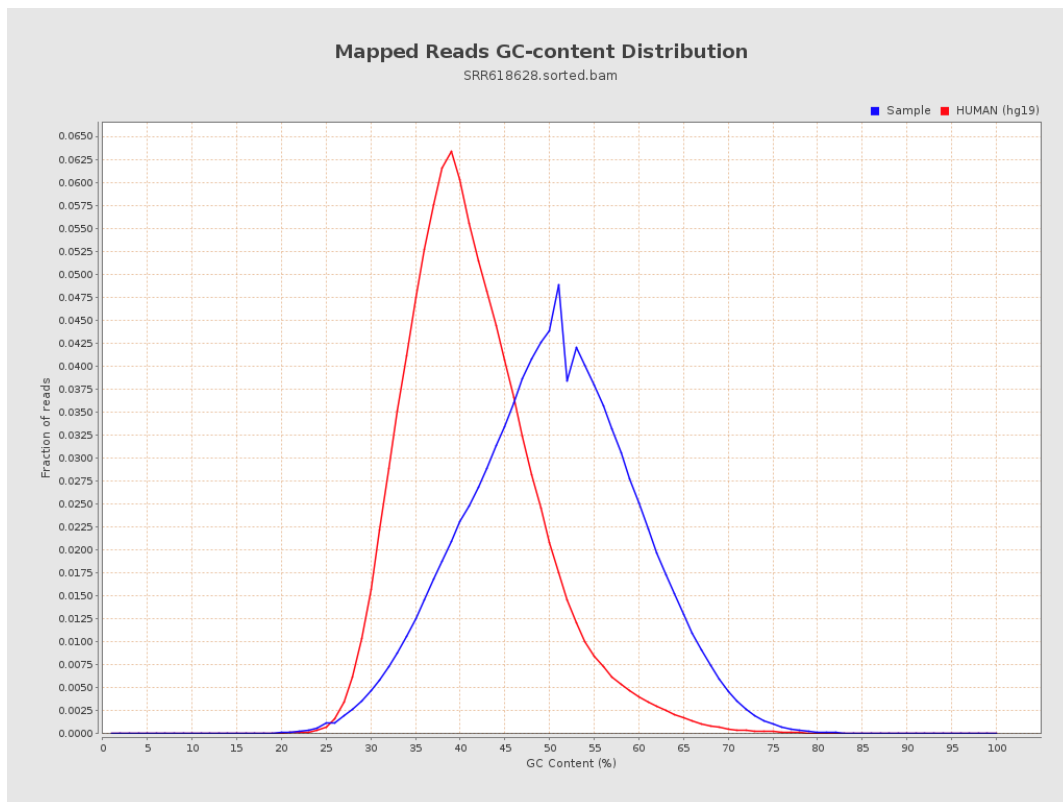
7. Results : Duplication Rate Histogram



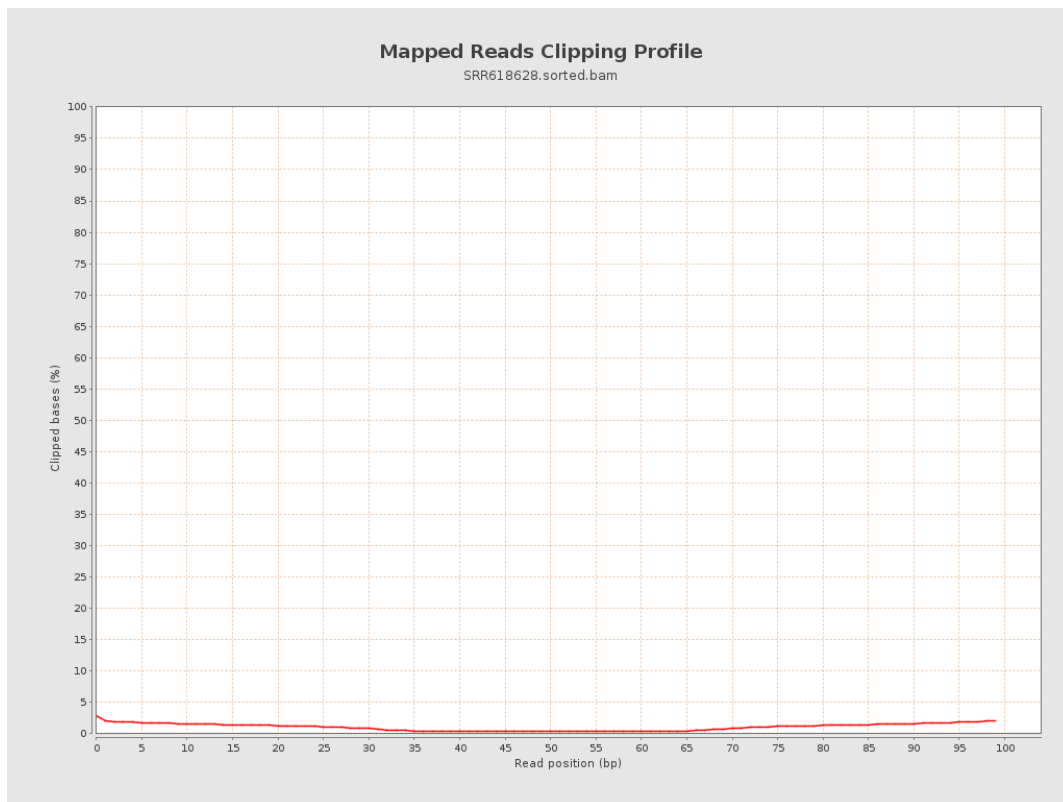
8. Results : Mapped Reads Nucleotide Content



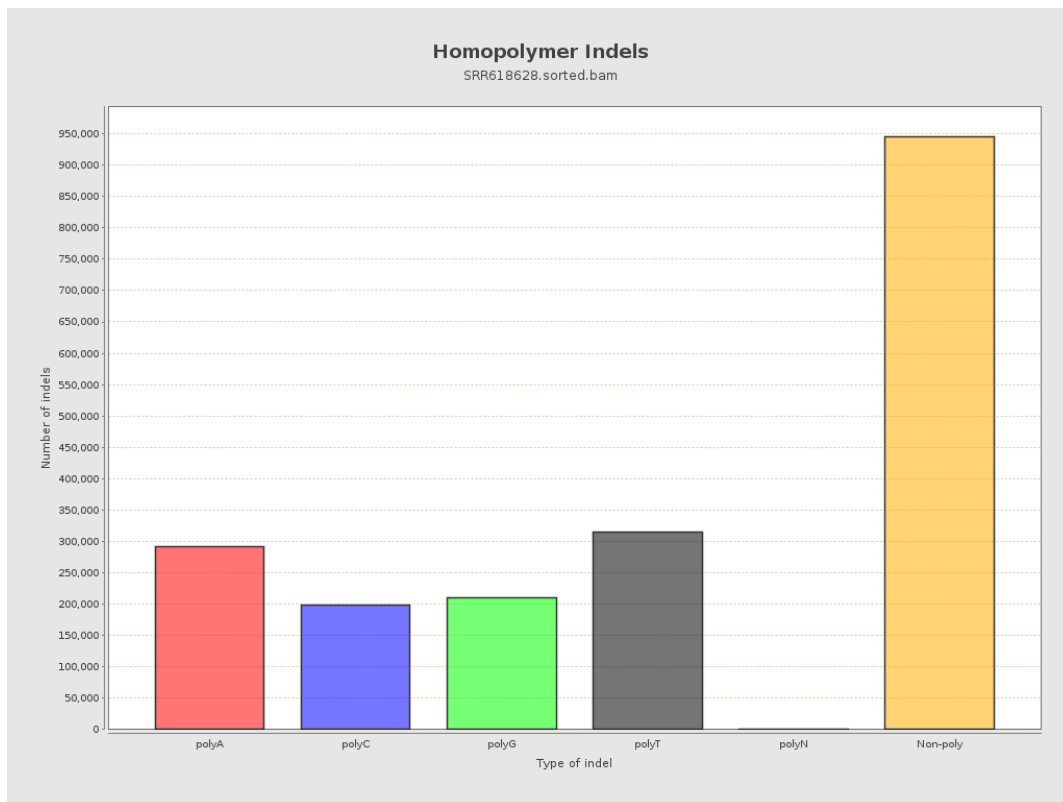
9. Results : Mapped Reads GC-content Distribution



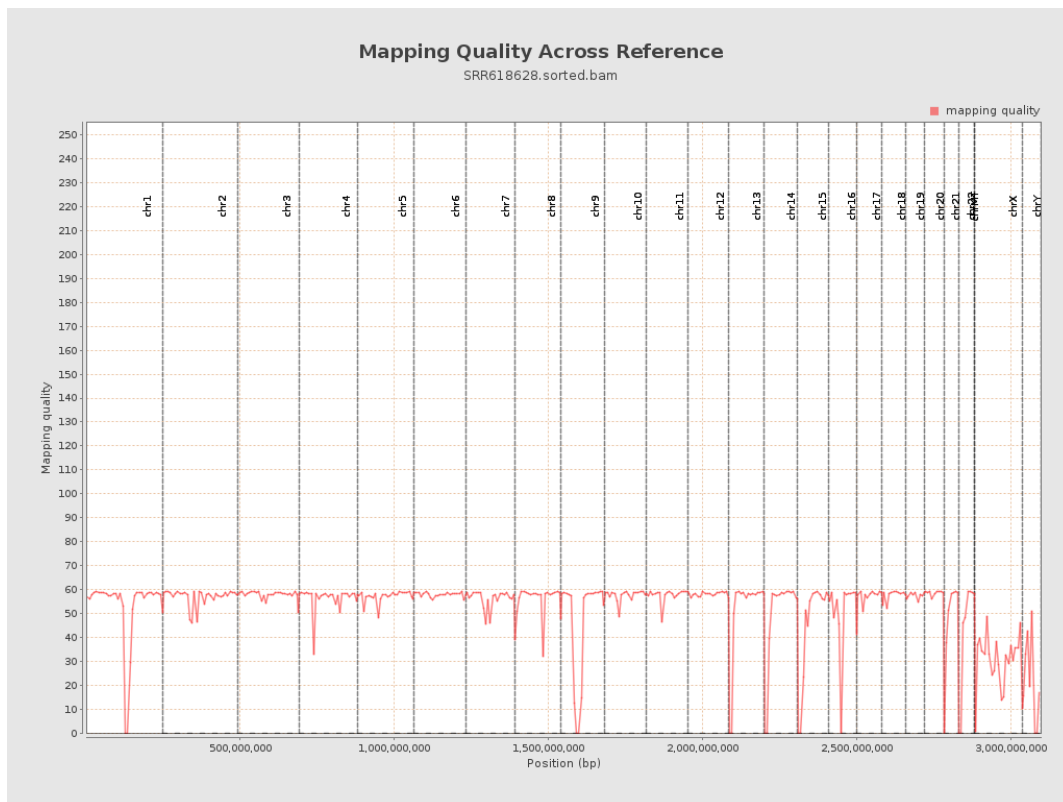
10. Results : Mapped Reads Clipping Profile



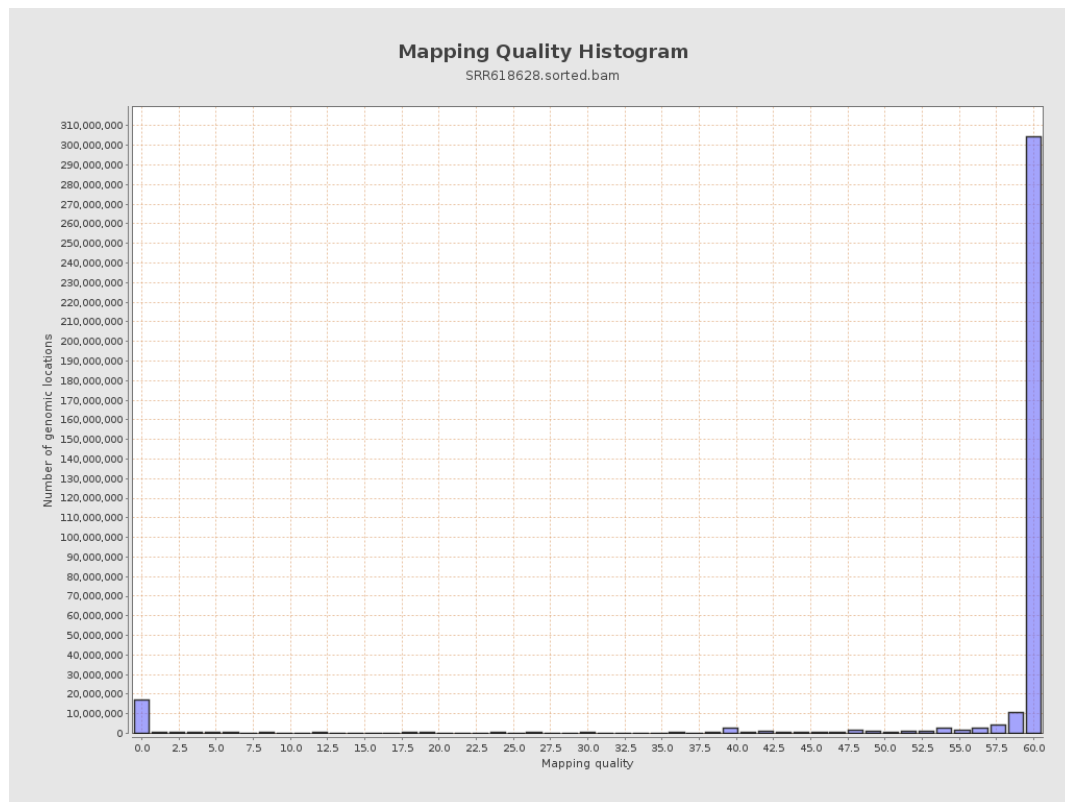
11. Results : Homopolymer Indels



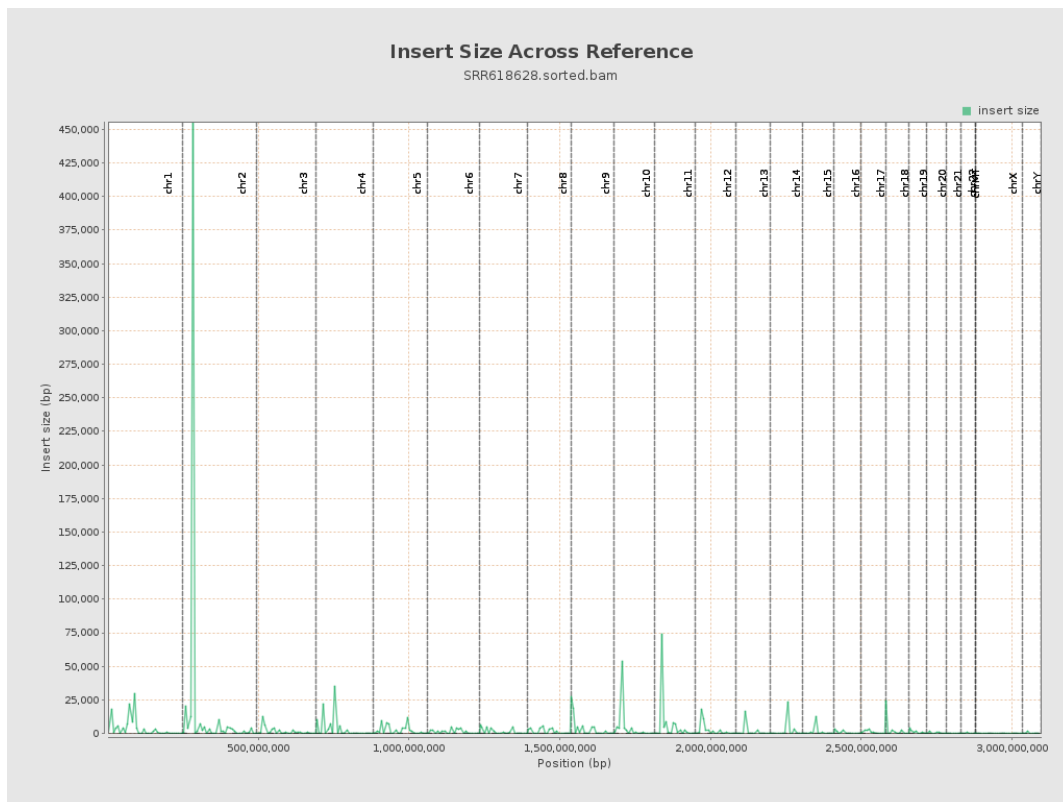
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

