

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 23:14:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630583.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_SRR630583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630583_1.fastq.gz SRR630583_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 23:14:43 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,191,046
Mapped reads	32,640,795 / 98.34%
Unmapped reads	550,251 / 1.66%
Mapped paired reads	32,640,795 / 98.34%
Mapped reads, first in pair	16,414,894 / 49.46%
Mapped reads, second in pair	16,225,901 / 48.89%
Mapped reads, both in pair	32,373,410 / 97.54%
Mapped reads, singletons	267,385 / 0.81%
Secondary alignments	0
Supplementary alignments	83,144 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	3,670,297 / 11.06%
Duplication rate	8.87%
Clipped reads	4,681,867 / 14.11%

2.2. ACGT Content

Number/percentage of A's	933,733,334 / 29.49%
Number/percentage of C's	623,282,461 / 19.68%
Number/percentage of T's	943,487,570 / 29.8%
Number/percentage of G's	665,606,449 / 21.02%
Number/percentage of N's	475,648 / 0.02%

GC Percentage	40.7%
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2.3. Coverage

Mean	1.0237
Standard Deviation	5.2288

2.4. Mapping Quality

Mean Mapping Quality	54.01
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2.5. Insert size

Mean	44,713.89
Standard Deviation	2,150,087.05
P25/Median/P75	161 / 203 / 267

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	27,857,627
Insertions	590,736
Mapped reads with at least one insertion	1.77%
Deletions	1,684,599
Mapped reads with at least one deletion	5.02%
Homopolymer indels	54%

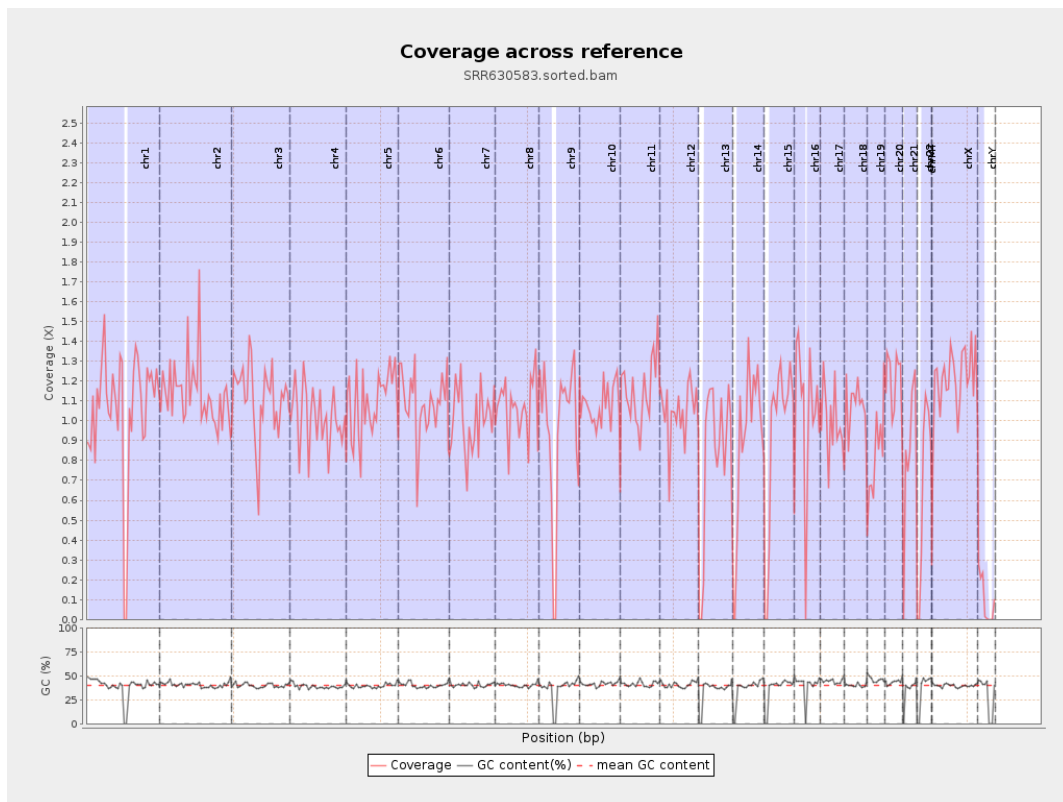
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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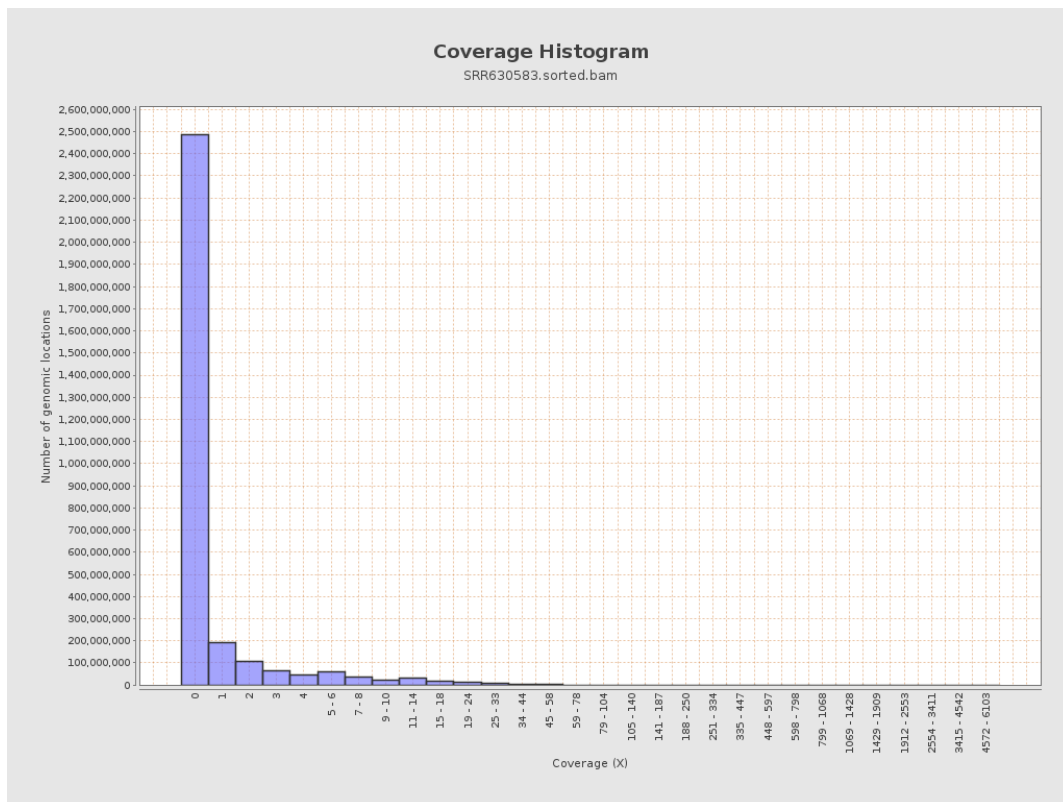
		bases	coverage	deviation
chr1	249250621	264845081	1.0626	7.3742
chr2	243199373	276903163	1.1386	7.897
chr3	198022430	220634237	1.1142	4.0139
chr4	191154276	194145758	1.0156	4.5081
chr5	180915260	197937554	1.0941	3.9178
chr6	171115067	187351215	1.0949	4.4563
chr7	159138663	159844120	1.0044	4.0486
chr8	146364022	156190587	1.0671	3.9942
chr9	141213431	133240913	0.9435	5.9895
chr10	135534747	146445877	1.0805	4.5406
chr11	135006516	154384314	1.1435	6.2037
chr12	133851895	140043203	1.0463	3.8938
chr13	115169878	94902536	0.824	3.3561
chr14	107349540	97216360	0.9056	3.7698
chr15	102531392	95429226	0.9307	3.7438
chr16	90354753	92135504	1.0197	7.7321
chr17	81195210	79766425	0.9824	4.0618
chr18	78077248	84340480	1.0802	6.5881
chr19	59128983	47726199	0.8072	4.5041
chr20	63025520	75454440	1.1972	4.4709
chr21	48129895	41467481	0.8616	4.7245
chr22	51304566	34869275	0.6797	3.4231
chrMT	16571	4491	0.271	1.0435
chrX	155270560	187871124	1.21	4.5446

chrY	59373566	5758136	0.097	3.7176
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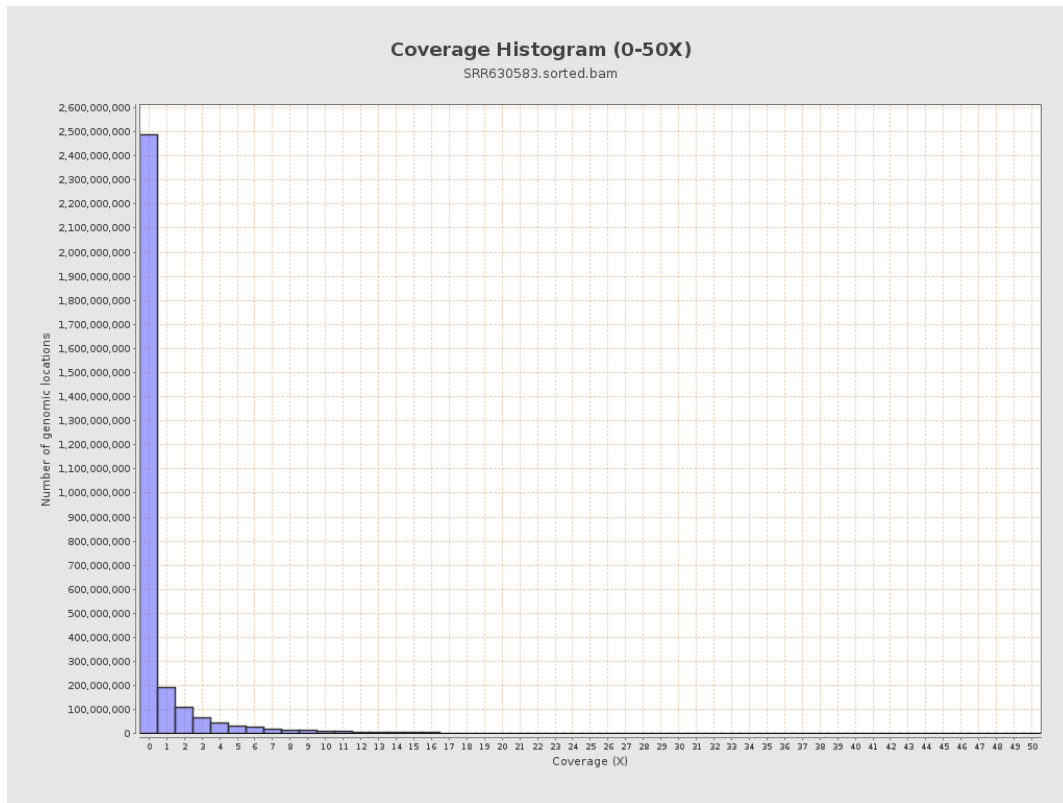
3. Results : Coverage across reference



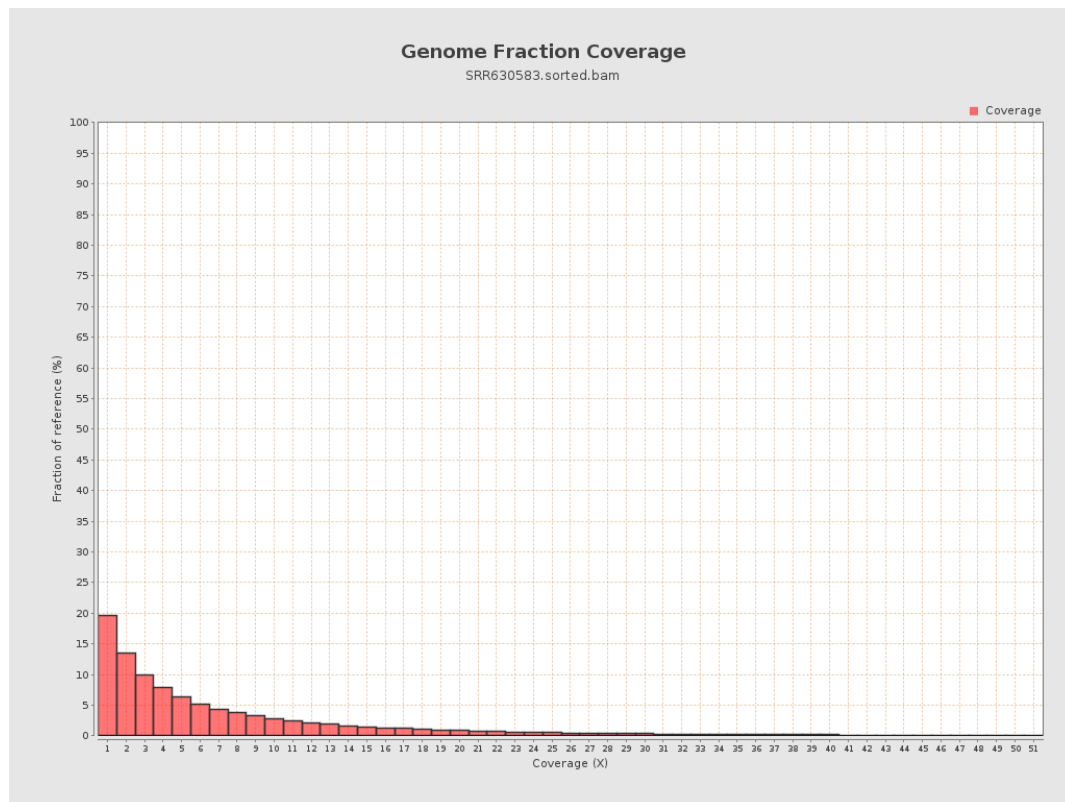
4. Results : Coverage Histogram



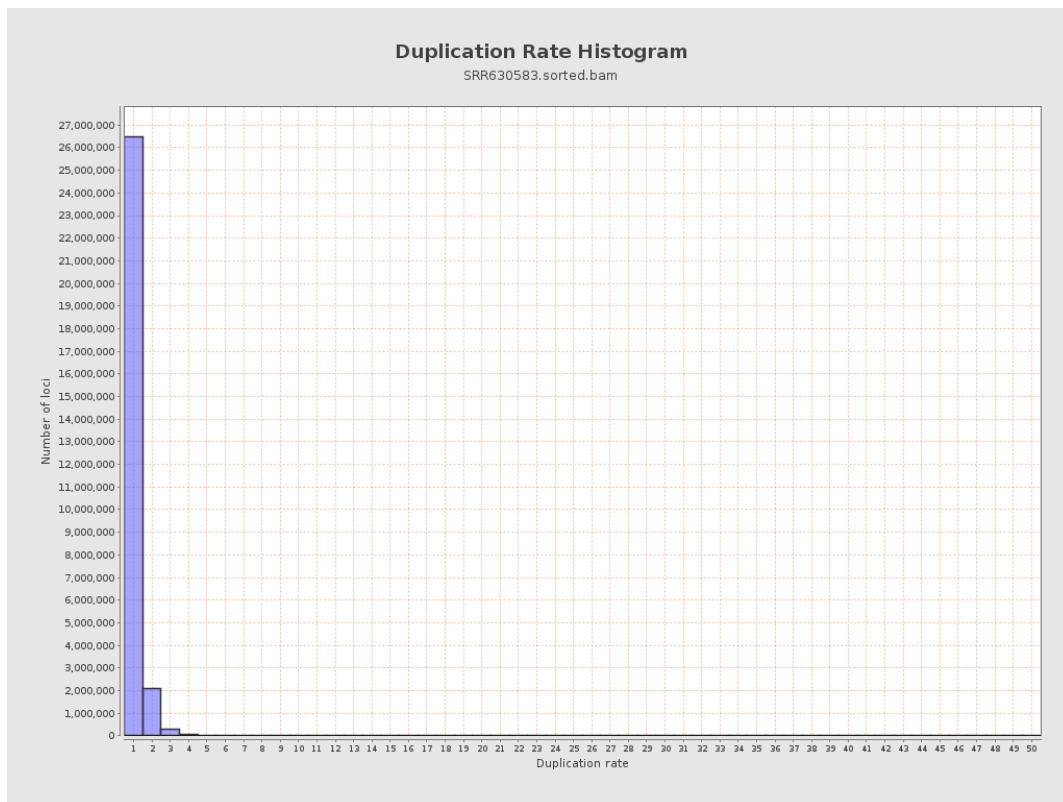
5. Results : Coverage Histogram (0-50X)



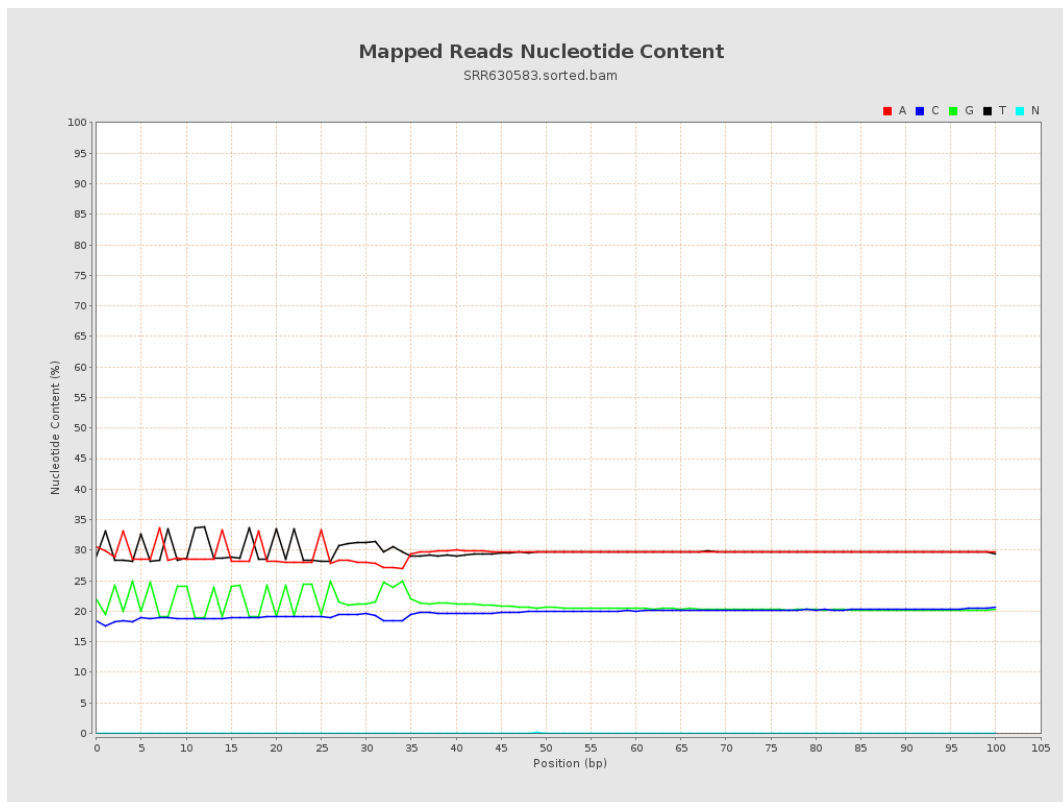
6. Results : Genome Fraction Coverage



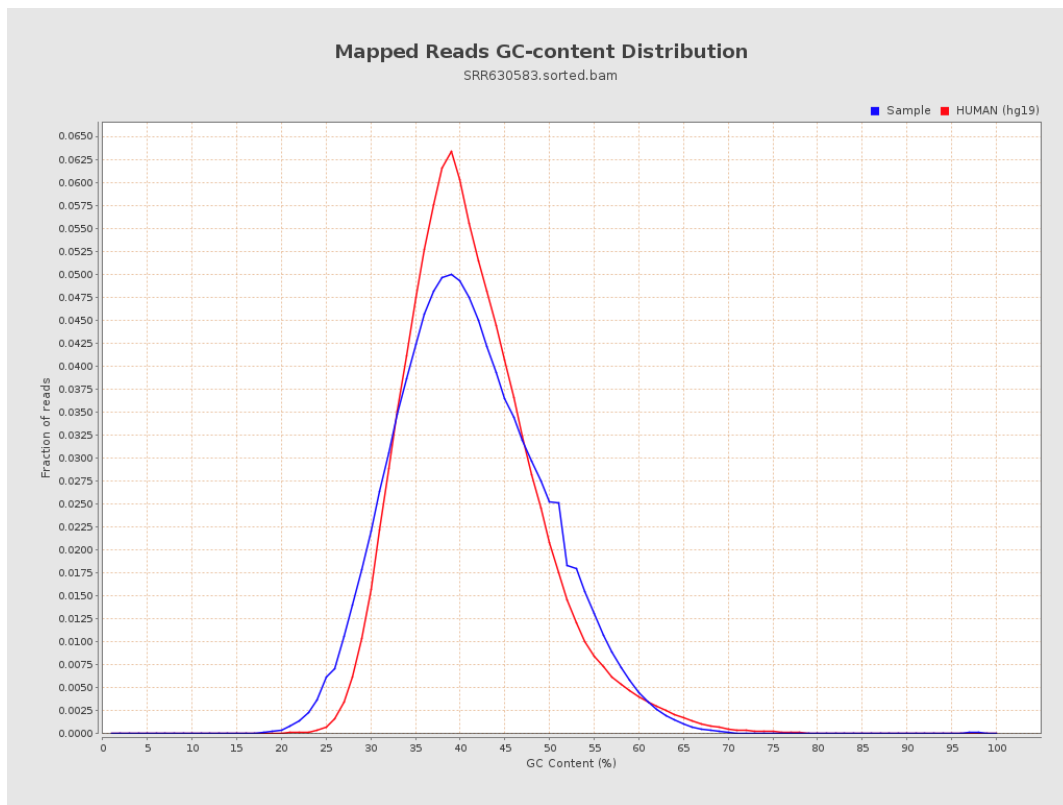
7. Results : Duplication Rate Histogram



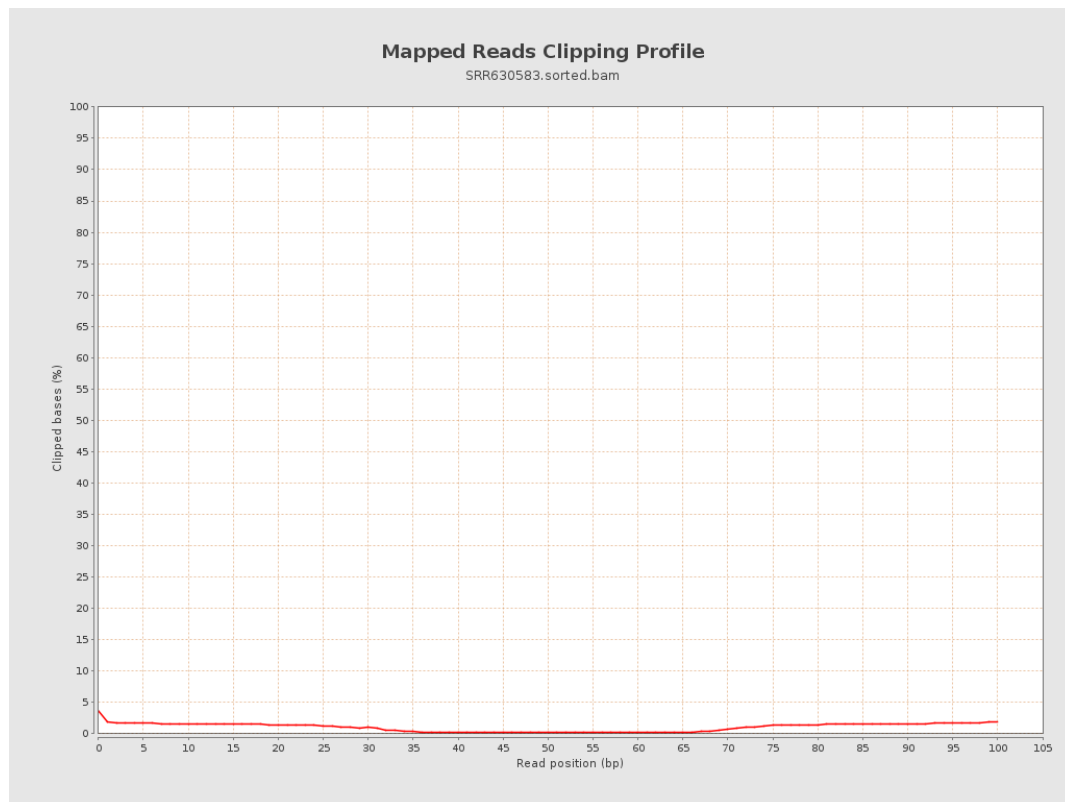
8. Results : Mapped Reads Nucleotide Content



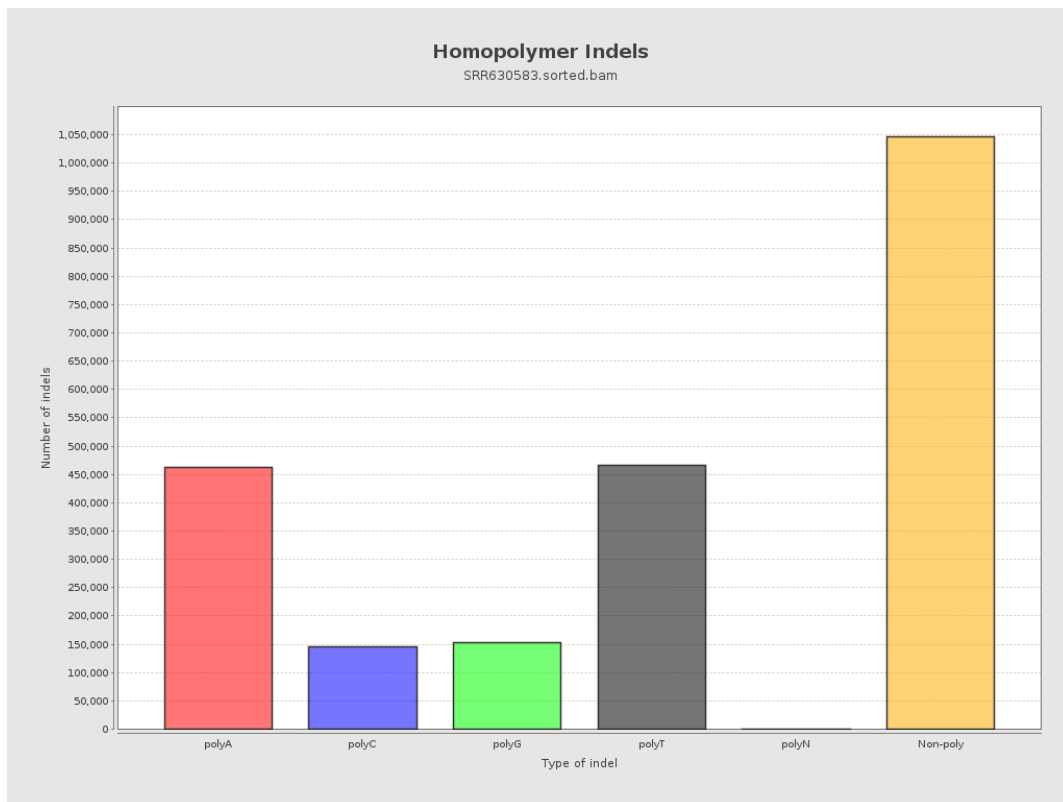
9. Results : Mapped Reads GC-content Distribution



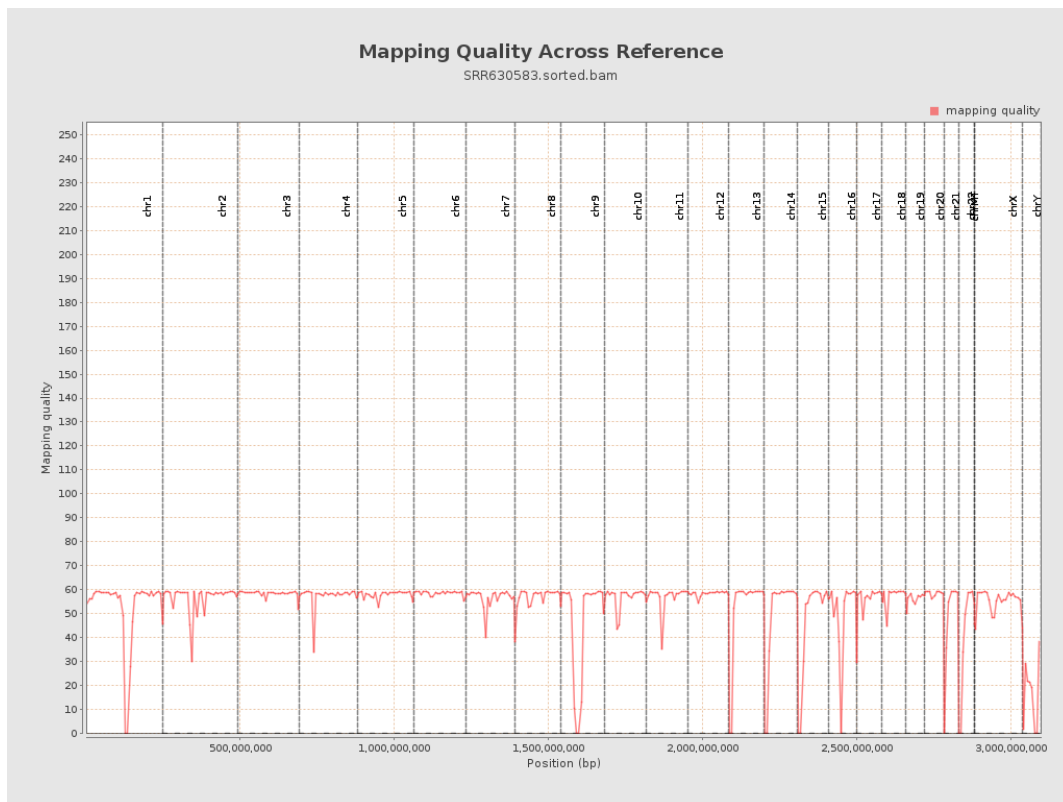
10. Results : Mapped Reads Clipping Profile



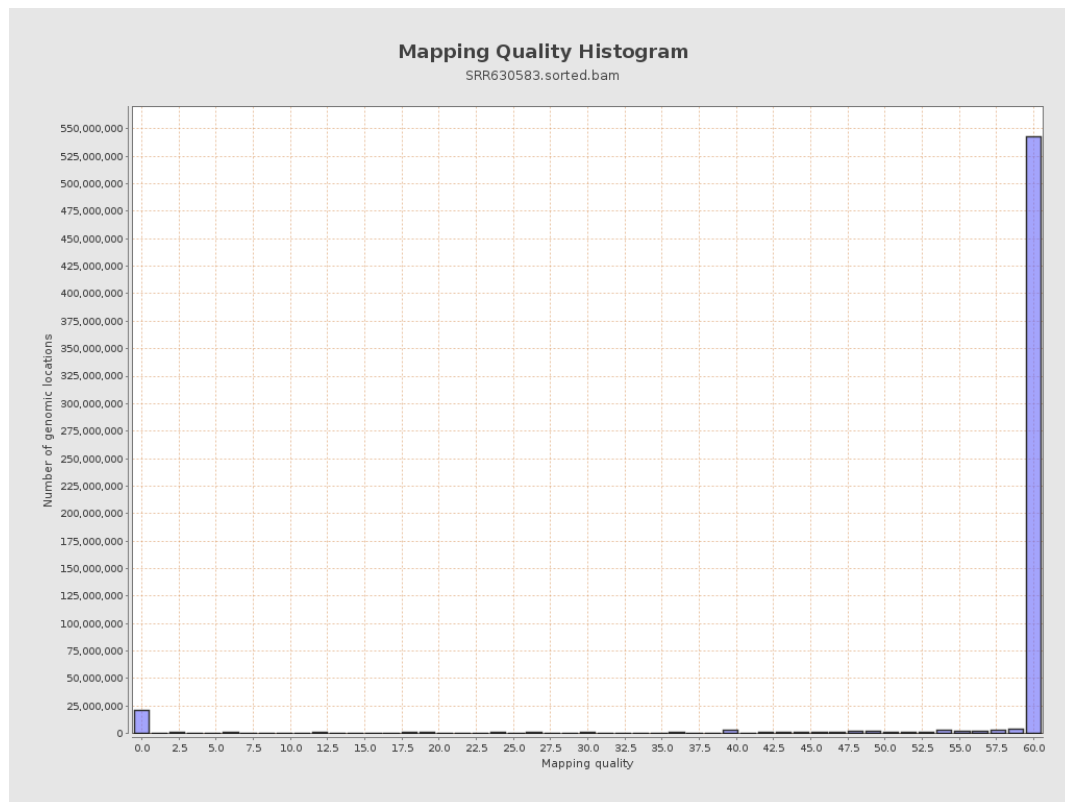
11. Results : Homopolymer Indels



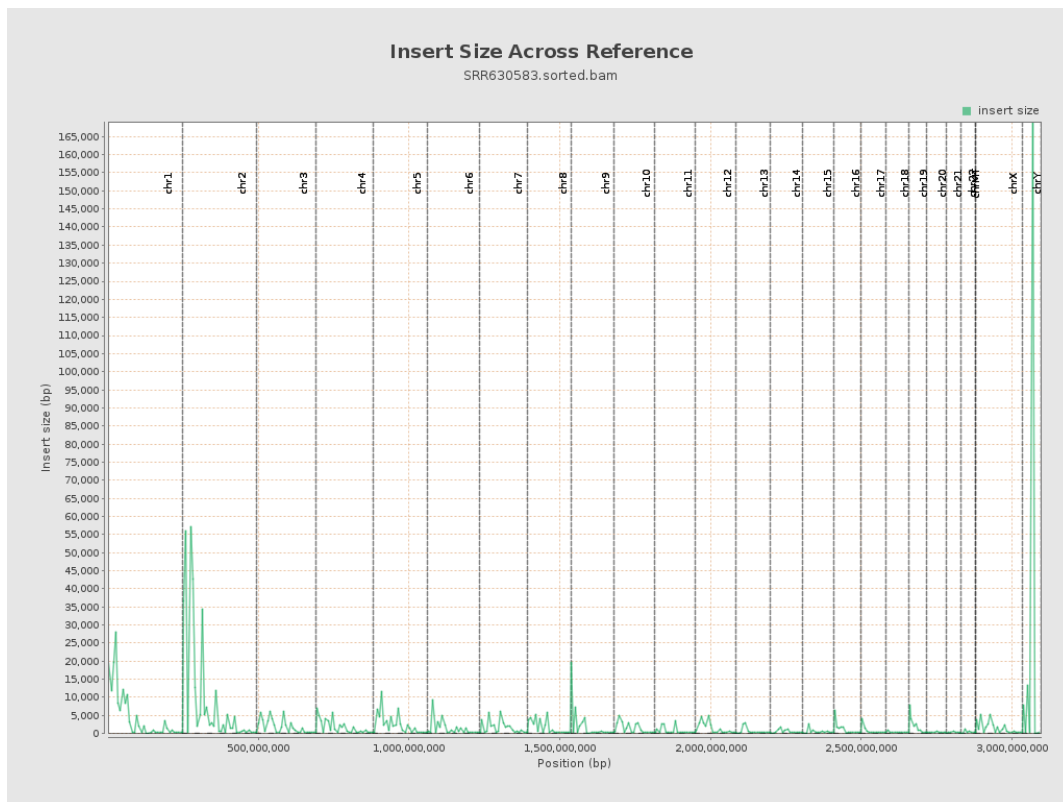
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

