Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/28 10:12:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504623.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_SRR504623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504623_1.fastq.gz SRR504623_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 28 10:12:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	567,503,902
Mapped reads	523,133,602 / 92.18%
Unmapped reads	44,370,300 / 7.82%
Mapped paired reads	523,133,602 / 92.18%
Mapped reads, first in pair	263,269,010 / 46.39%
Mapped reads, second in pair	259,864,592 / 45.79%
Mapped reads, both in pair	511,472,592 / 90.13%
Mapped reads, singletons	11,661,010 / 2.05%
Secondary alignments	0
Supplementary alignments	5,365,427 / 0.95%
Read min/max/mean length	30 / 100 / 100.38
Duplicated reads (estimated)	201,871,577 / 35.57%
Duplication rate	28.28%
Clipped reads	89,182,981 / 15.71%

2.2. ACGT Content

Number/percentage of A's	13,450,718,536 / 26.85%
Number/percentage of C's	11,542,081,110 / 23.04%
Number/percentage of T's	13,527,336,167 / 27%
Number/percentage of G's	11,563,220,475 / 23.08%
Number/percentage of N's	14,759,595 / 0.03%

GC Percentage	46.12%

2.3. Coverage

Mean	16.1972
Standard Deviation	395.6454

2.4. Mapping Quality

Mean Mapping Quality	52.21

2.5. Insert size

Mean	106,229.28
Standard Deviation	3,053,174.9
P25/Median/P75	277 / 328 / 385

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	717,207,089
Insertions	14,701,450
Mapped reads with at least one insertion	2.61%
Deletions	13,240,702
Mapped reads with at least one deletion	2.36%
Homopolymer indels	34.42%

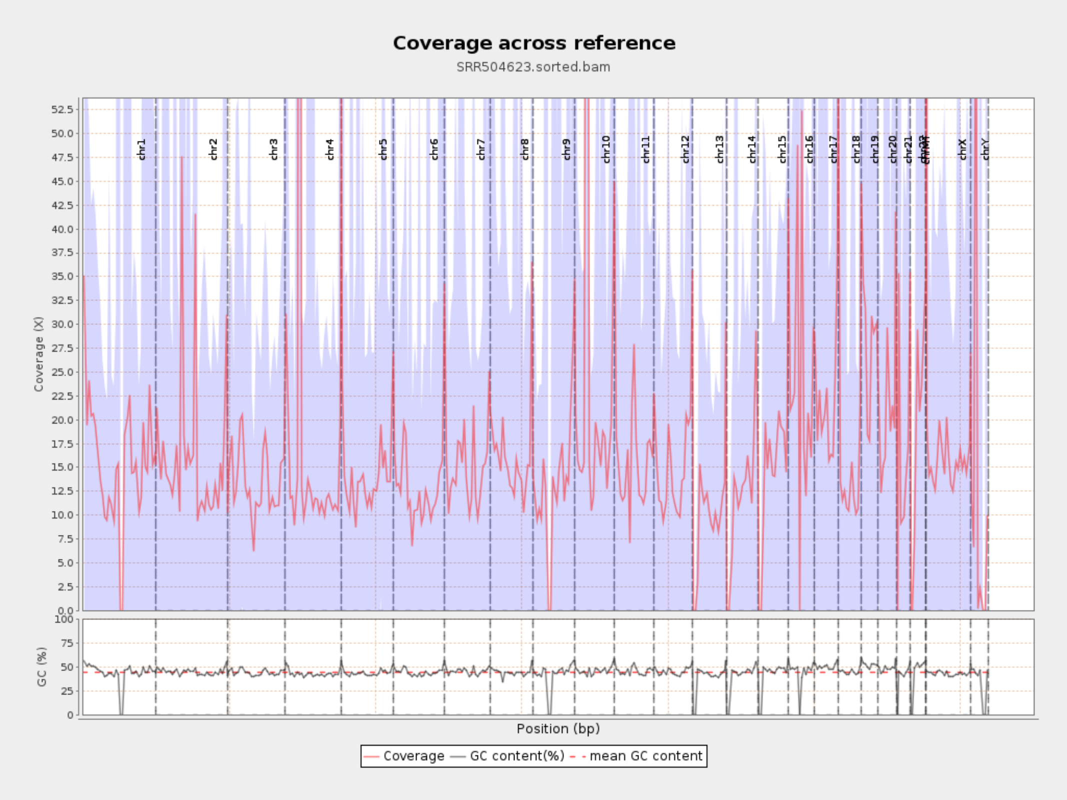
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

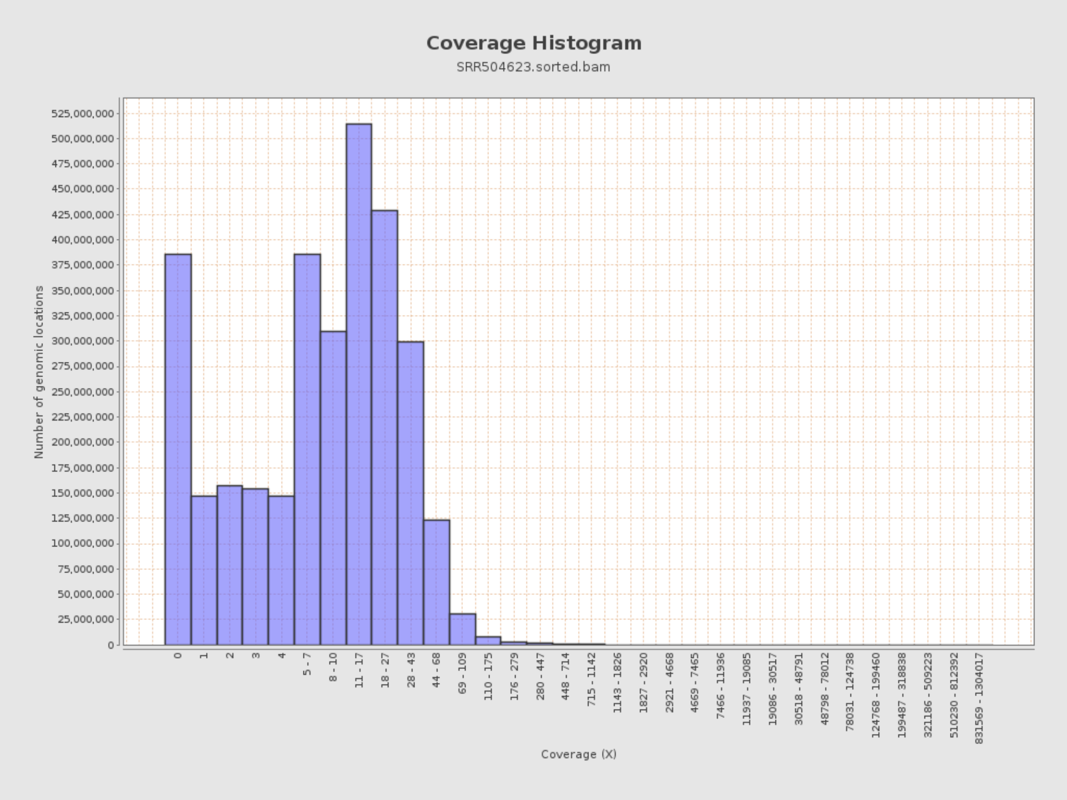
		bases	coverage	deviation
chr1	249250621	3863243104	15.4994	117.3812
chr2	243199373	3948126762	16.2341	381.3299
chr3	198022430	2679026118	13.5289	35.4605
chr4	191154276	3792864673	19.8419	1,115.9898
chr5	180915260	2607179756	14.4111	50.1792
chr6	171115067	2147962629	12.5527	49.9213
chr7	159138663	2465443943	15.4924	56.5291
chr8	146364022	2356310616	16.099	302.4415
chr9	141213431	1830970311	12.966	136.2032
chr10	135534747	3305440123	24.3881	861.0923
chr11	135006516	2150341427	15.9277	47.9825
chr12	133851895	2003195859	14.9658	28.5714
chr13	115169878	1118631853	9.7129	21.7292
chr14	107349540	1337879950	12.4628	46.2457
chr15	102531392	1459999915	14.2395	24.2449
chr16	90354753	2247082531	24.8696	302.0236
chr17	81195210	1715955784	21.1337	111.9031
chr18	78077248	1138928124	14.5872	448.7058
chr19	59128983	1669222839	28.2302	64.7861
chr20	63025520	1281241380	20.3289	272.5215
chr21	48129895	834522142	17.339	364.3659
chr22	51304566	924205647	18.0141	46.0087
chrMT	16571	18889210	1,139.8956	531.9234
chrX	155270560	2453651617	15.8024	32.6516

chrY	59373566	791342487	13.3282	937.3606

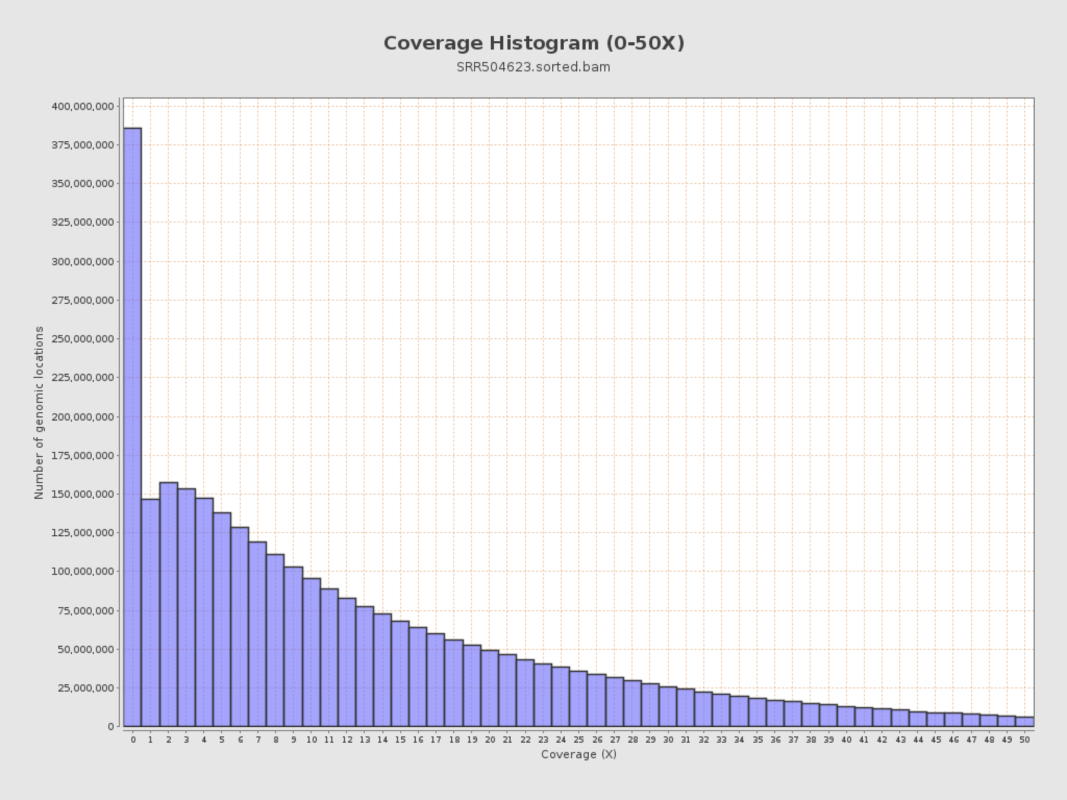
3. Results : Coverage across reference



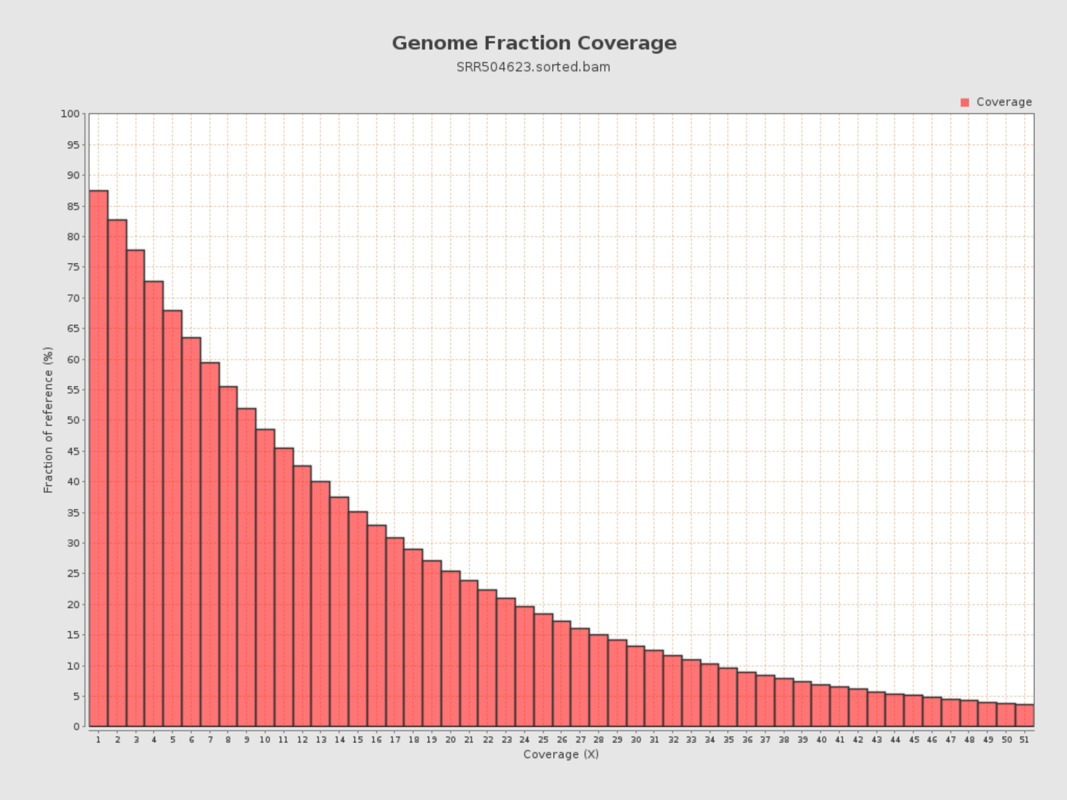
4. Results : Coverage Histogram



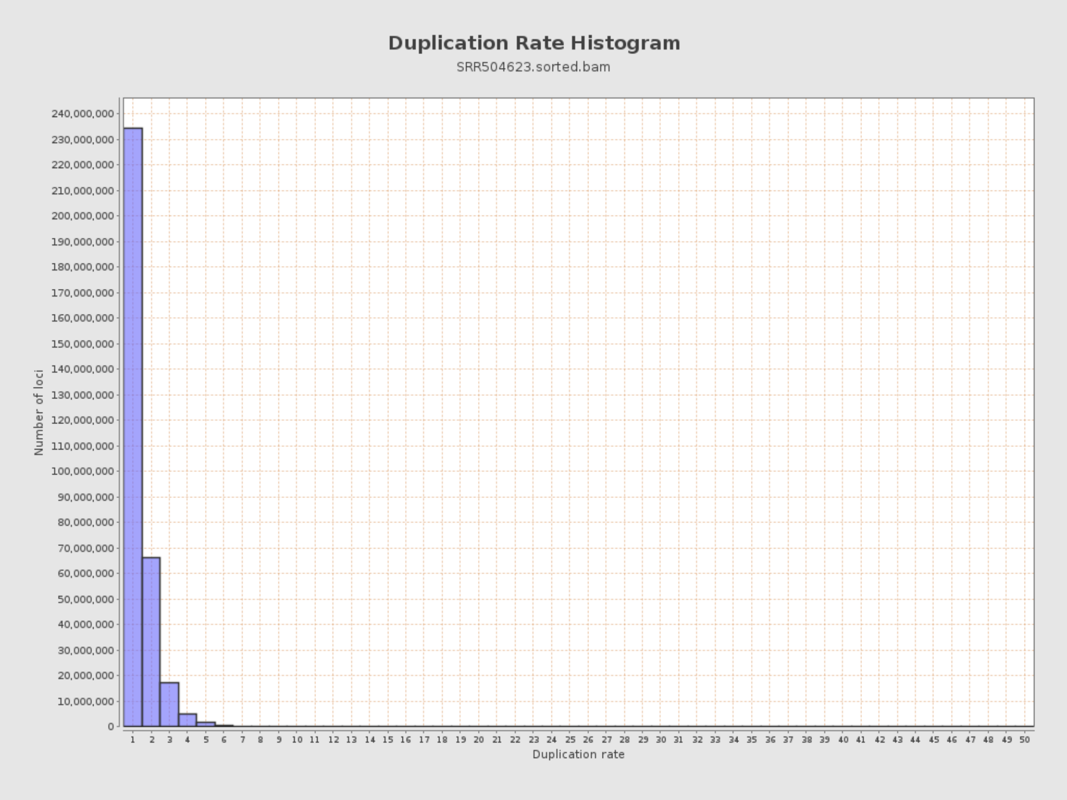
5. Results : Coverage Histogram (0-50X)



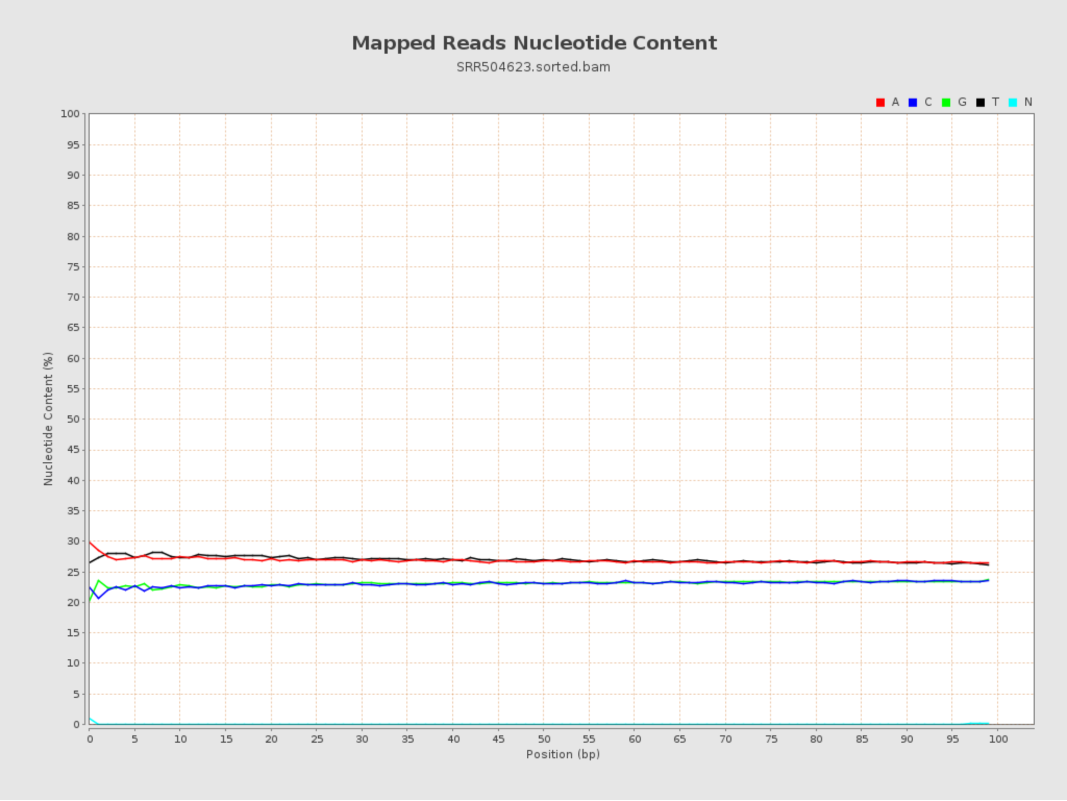
6. Results : Genome Fraction Coverage



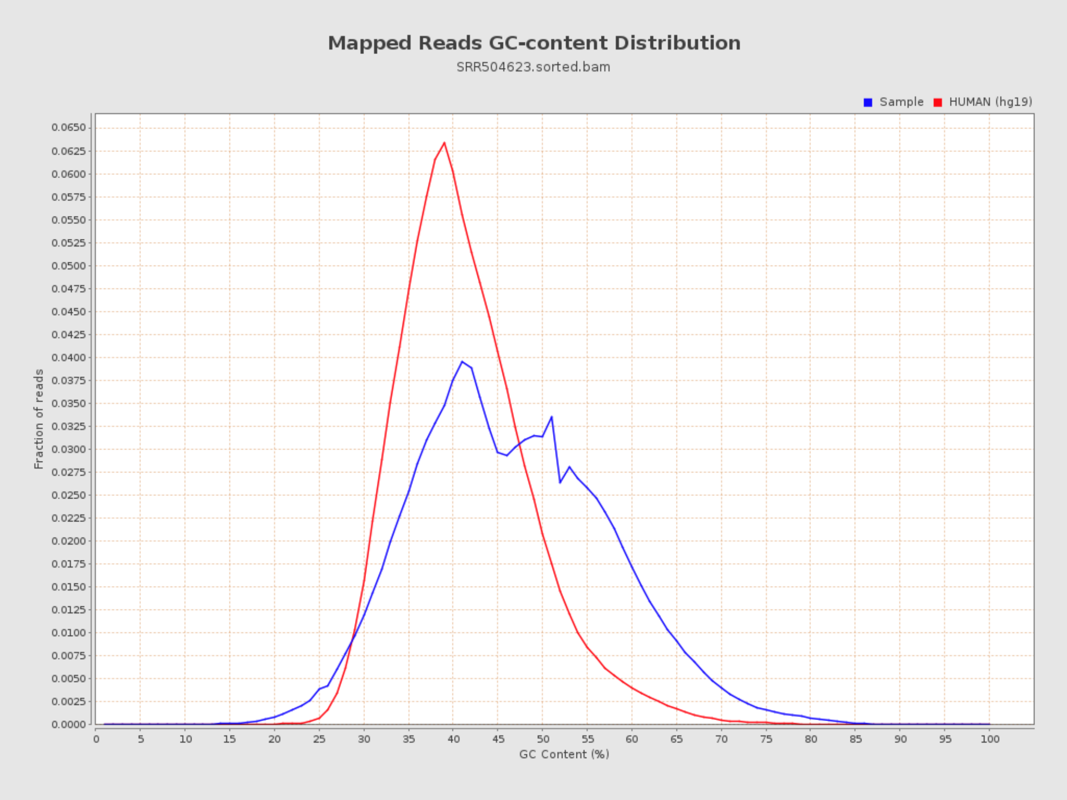
7. Results : Duplication Rate Histogram



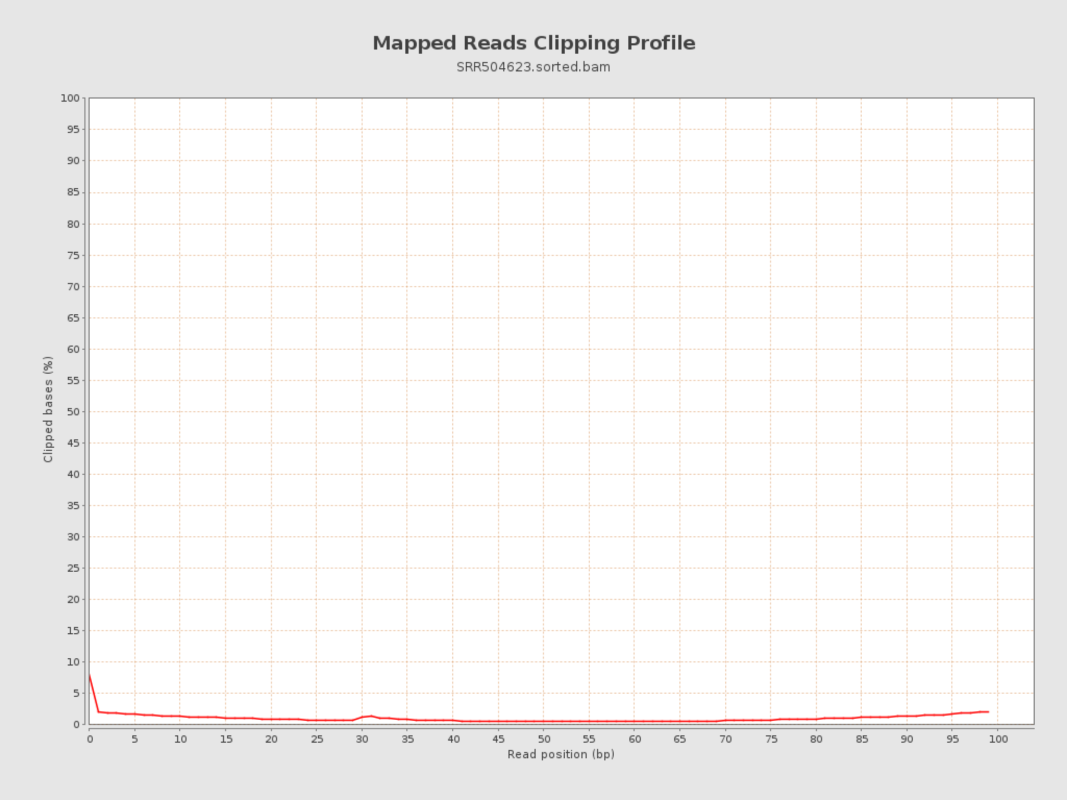
8. Results : Mapped Reads Nucleotide Content



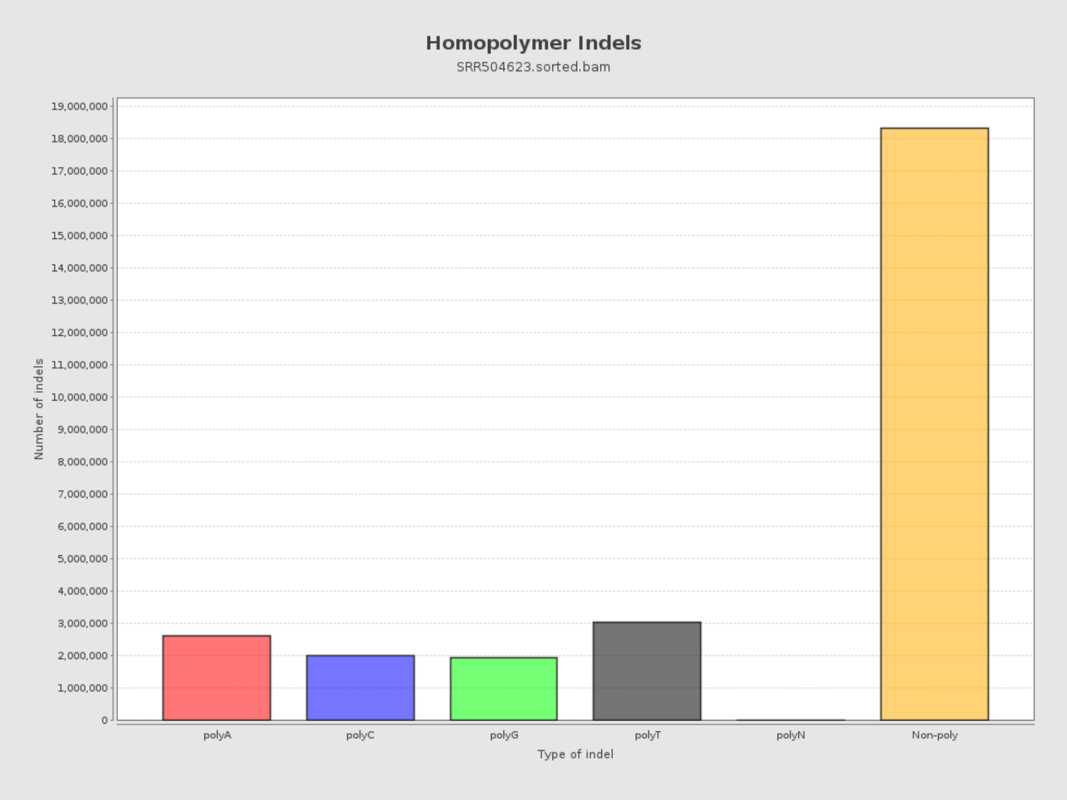
9. Results : Mapped Reads GC-content Distribution



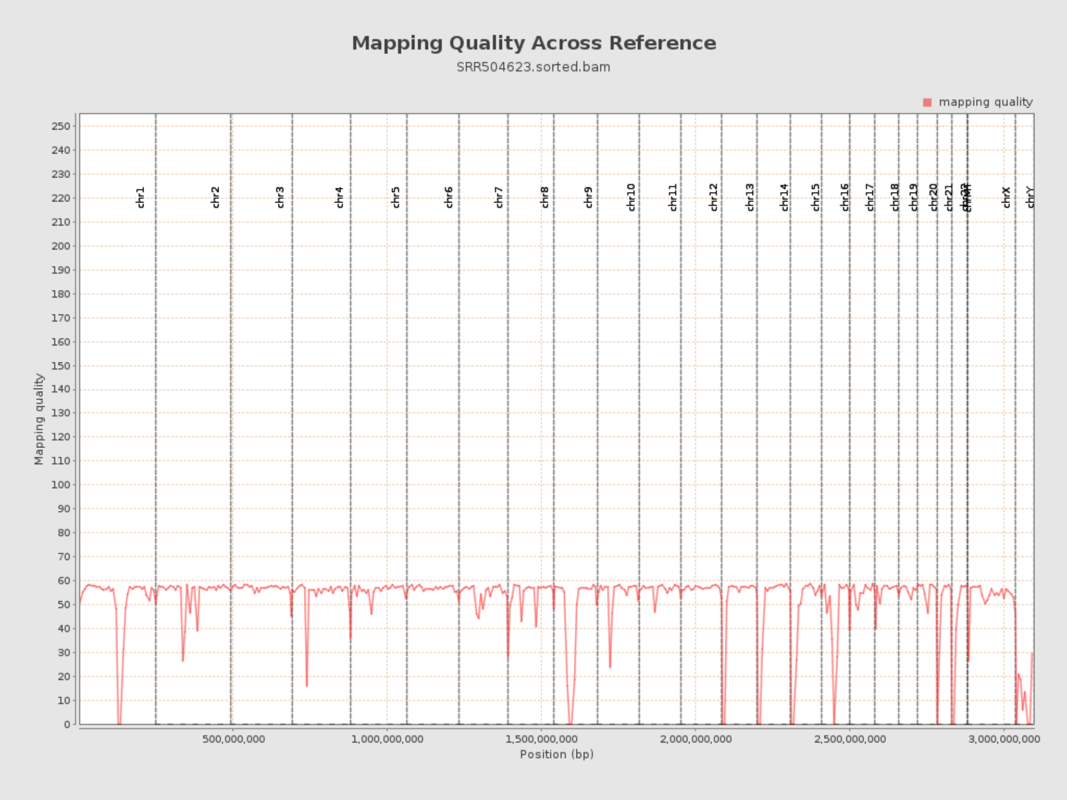
10. Results : Mapped Reads Clipping Profile



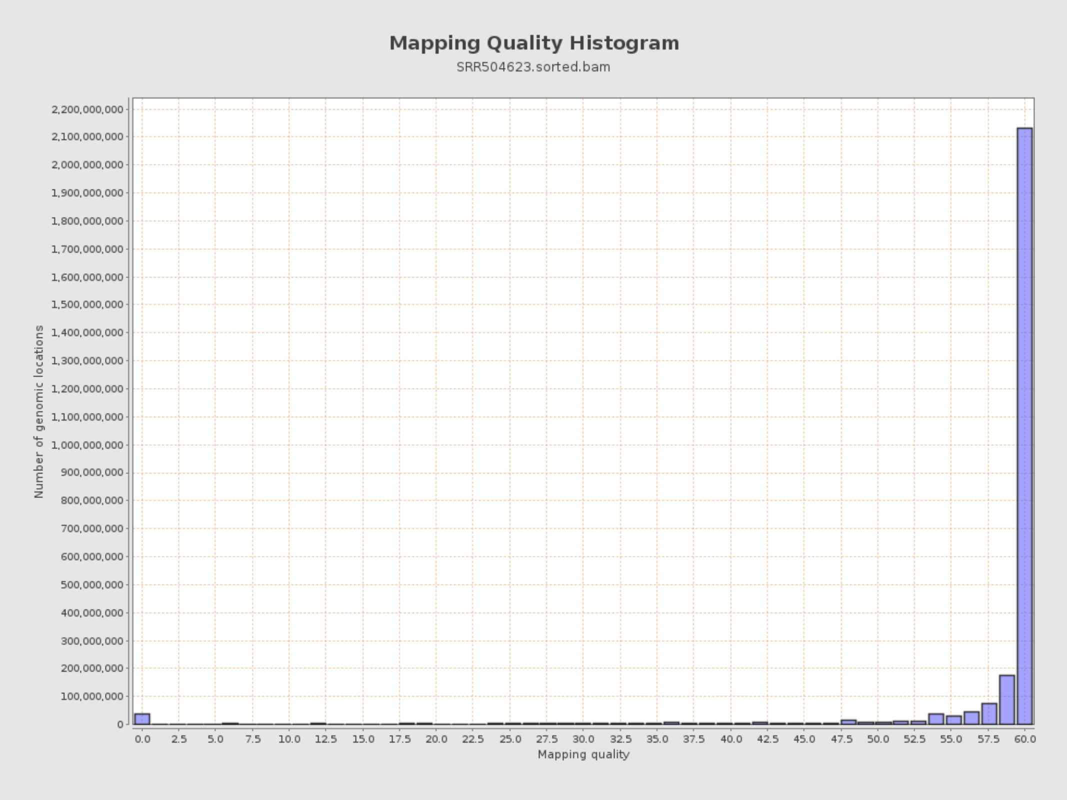
11. Results : Homopolymer Indels



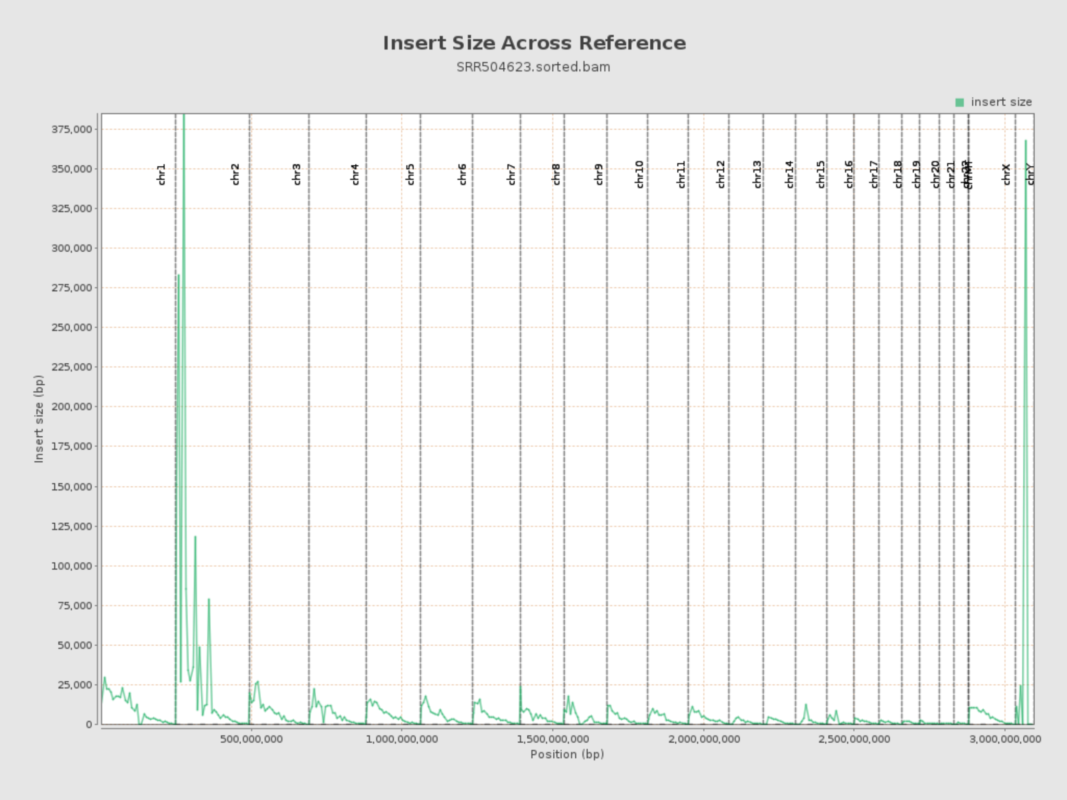
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram