Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/30 14:59:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504629.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_SRR504629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504629_1.fastq.gz SRR504629_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 30 14:59:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	570,873,916
Mapped reads	467,572,140 / 81.9%
Unmapped reads	103,301,776 / 18.1%
Mapped paired reads	467,572,140 / 81.9%
Mapped reads, first in pair	238,883,408 / 41.85%
Mapped reads, second in pair	228,688,732 / 40.06%
Mapped reads, both in pair	442,366,498 / 77.49%
Mapped reads, singletons	25,205,642 / 4.42%
Secondary alignments	0
Supplementary alignments	4,090,396 / 0.72%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	158,566,329 / 27.78%
Duplication rate	22.22%
Clipped reads	117,933,870 / 20.66%

2.2. ACGT Content

Number/percentage of A's	11,896,554,533 / 27.21%
Number/percentage of C's	9,912,479,769 / 22.67%
Number/percentage of T's	12,065,438,836 / 27.6%
Number/percentage of G's	9,782,485,515 / 22.38%
Number/percentage of N's	60,214,541 / 0.14%

GC Percentage	45.05%

2.3. Coverage

Mean	14.1334
Standard Deviation	295.4324

2.4. Mapping Quality

Mean Mapping Quality	51.27

2.5. Insert size

Mean	105,858.37
Standard Deviation	3,037,604.49
P25/Median/P75	307 / 353 / 405

2.6. Mismatches and indels

General error rate	2.75%
Mismatches	1,154,931,727
Insertions	12,024,457
Mapped reads with at least one insertion	2.4%
Deletions	11,055,191
Mapped reads with at least one deletion	2.21%
Homopolymer indels	33.11%

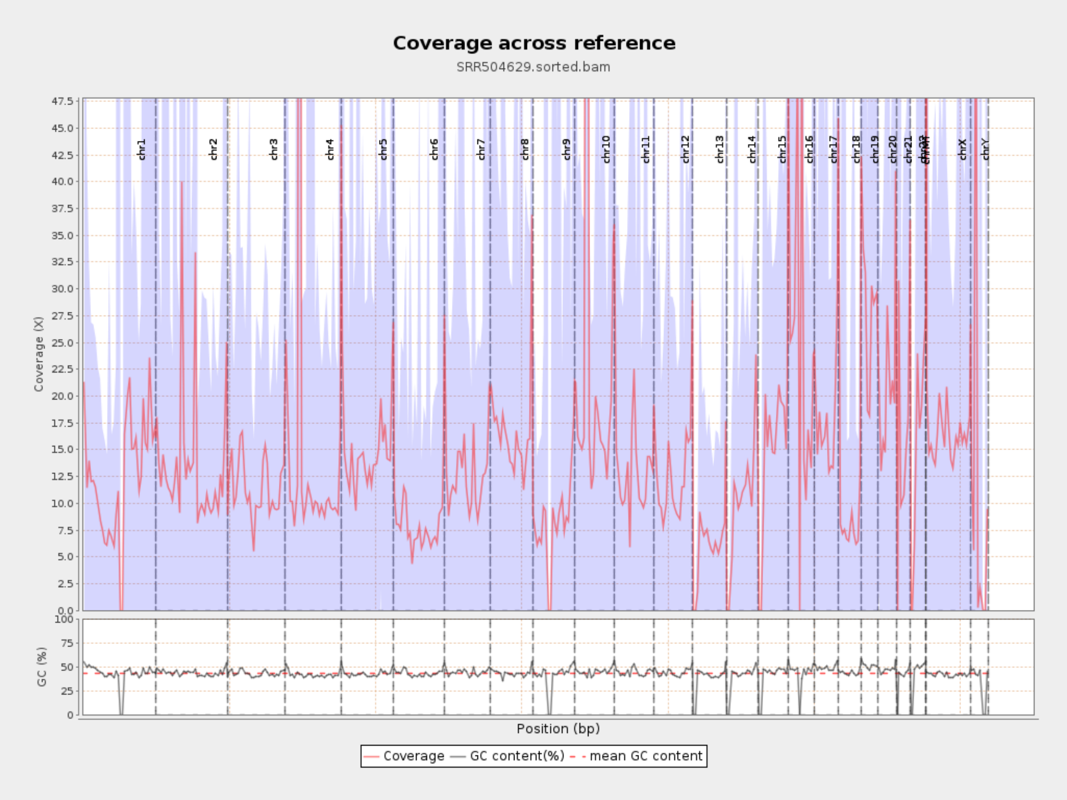
2.7. Chromosome stats

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

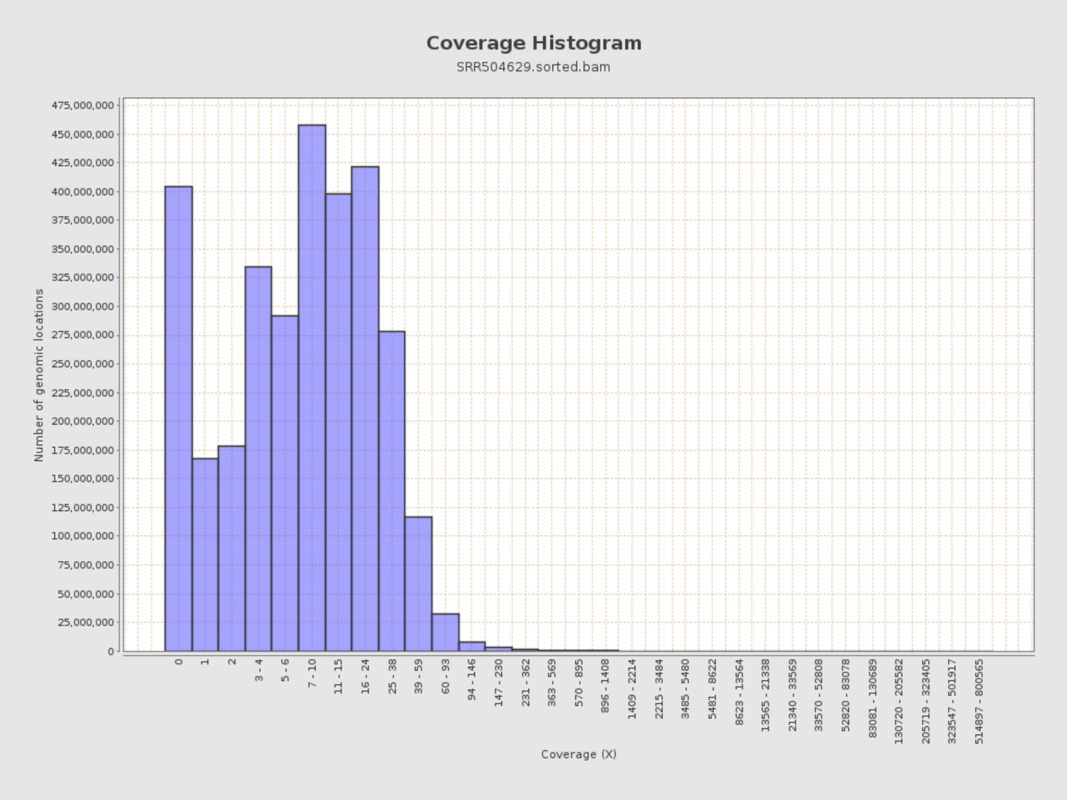
		bases	coverage	deviation
chr1	249250621	3091924158	12.4049	100.1213
chr2	243199373	3313290842	13.6238	305.4309
chr3	198022430	2269919673	11.4629	34.9482
chr4	191154276	3167217646	16.5689	746.3399
chr5	180915260	2725340462	15.0642	42.7998
chr6	171115067	1317076275	7.697	31.1091
chr7	159138663	2062596781	12.961	48.1102
chr8	146364022	2444413688	16.7009	226.6661
chr9	141213431	1149158910	8.1377	140.9755
chr10	135534747	3259026462	24.0457	726.2592
chr11	135006516	1780278371	13.1866	34.9363
chr12	133851895	1661627970	12.4139	30.9462
chr13	115169878	687668497	5.9709	14.8781
chr14	107349540	1129038475	10.5174	36.7317
chr15	102531392	1490421871	14.5362	24.2996
chr16	90354753	2300659050	25.4625	300.9959
chr17	81195210	1383535665	17.0396	95.461
chr18	78077248	728367929	9.3288	375.3387
chr19	59128983	1649440905	27.8956	60.8994
chr20	63025520	1273553510	20.2069	201.6448
chr21	48129895	828878946	17.2217	268.8932
chr22	51304566	751825477	14.6542	39.4683
chrMT	16571	14343796	865.5963	400.1245
chrX	155270560	2560325376	16.4894	33.5021

chrY	59373566	712847732	12.0061	693.5471

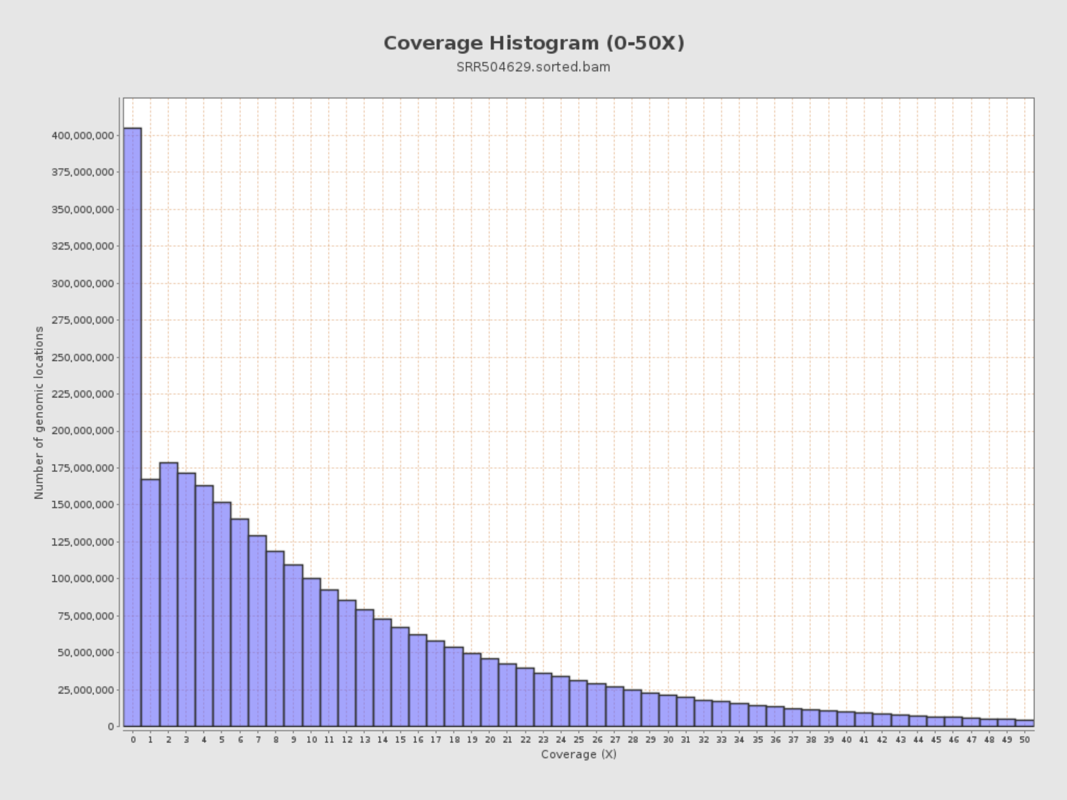
3. Results : Coverage across reference



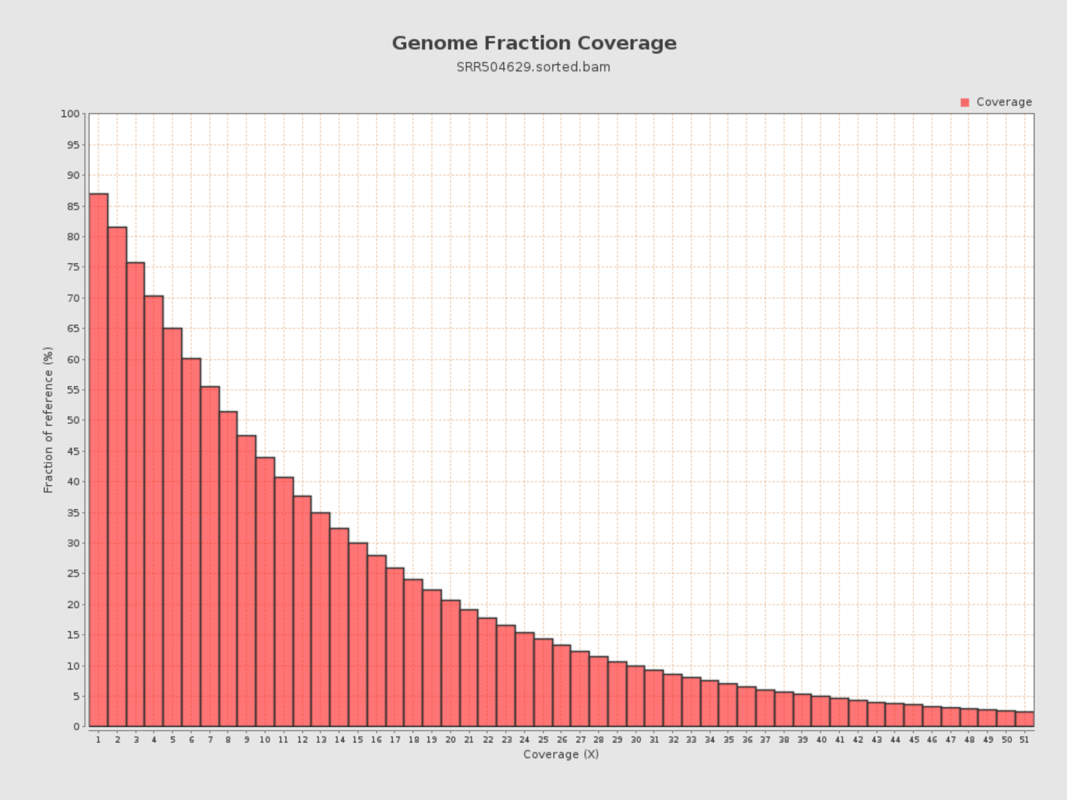
4. Results : Coverage Histogram



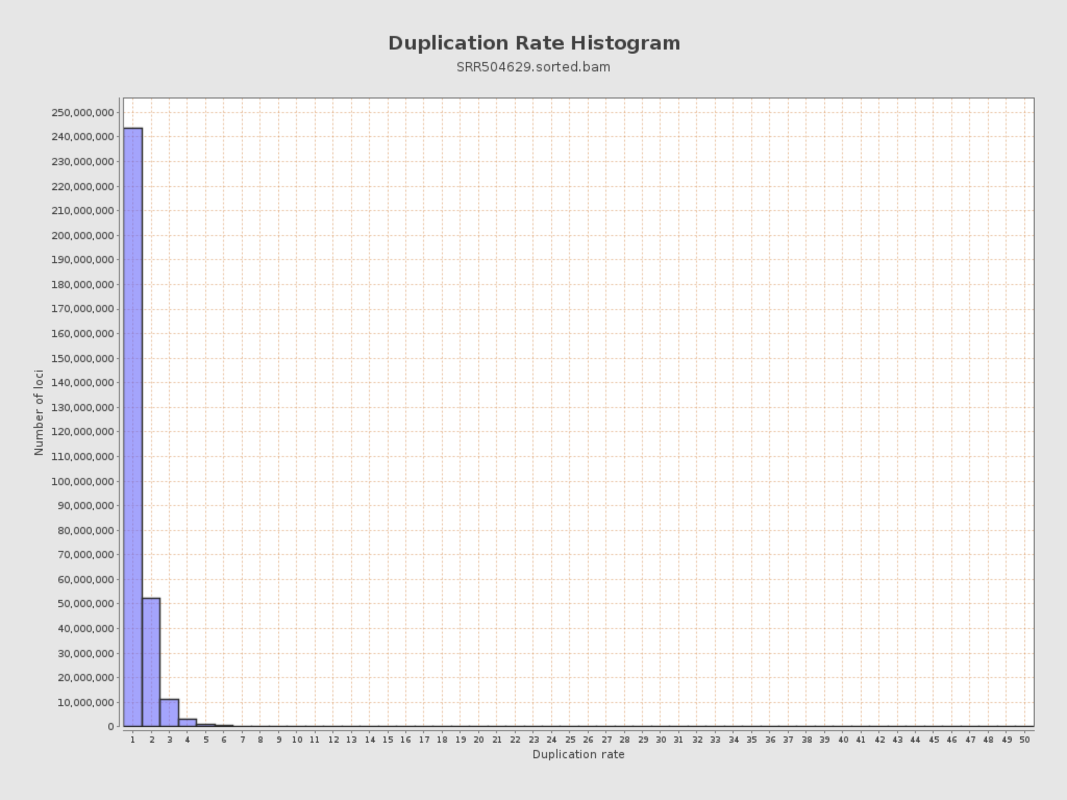
5. Results : Coverage Histogram (0-50X)



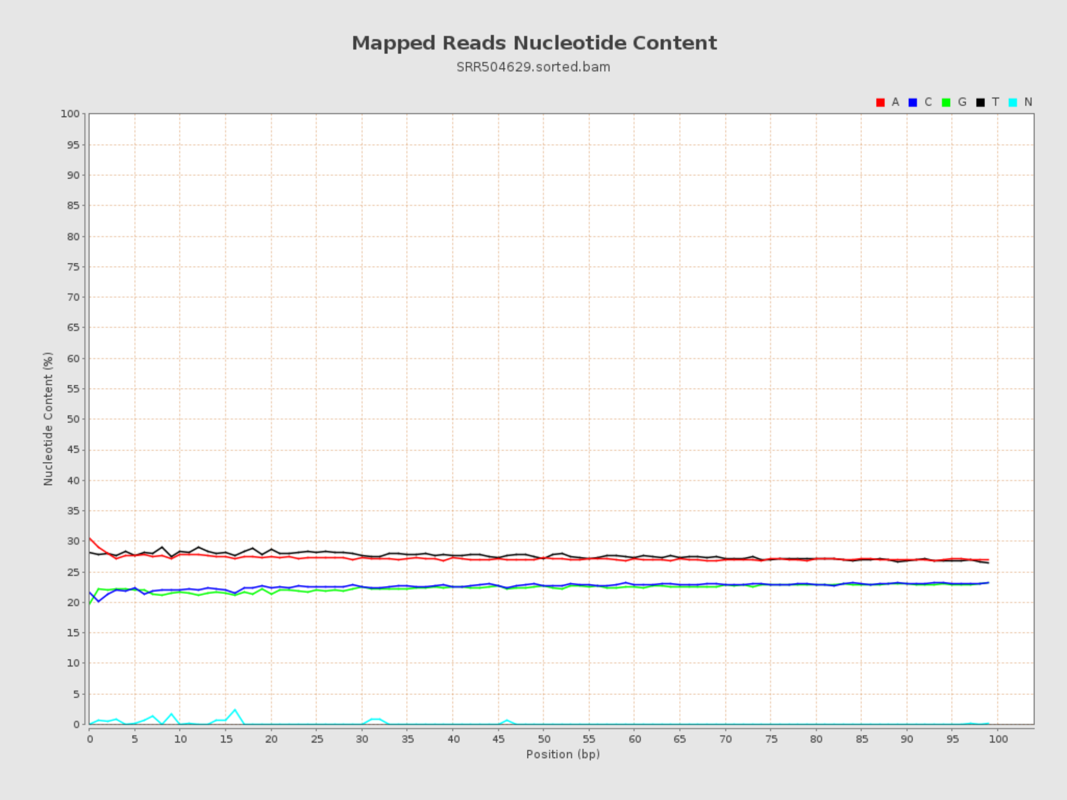
6. Results : Genome Fraction Coverage



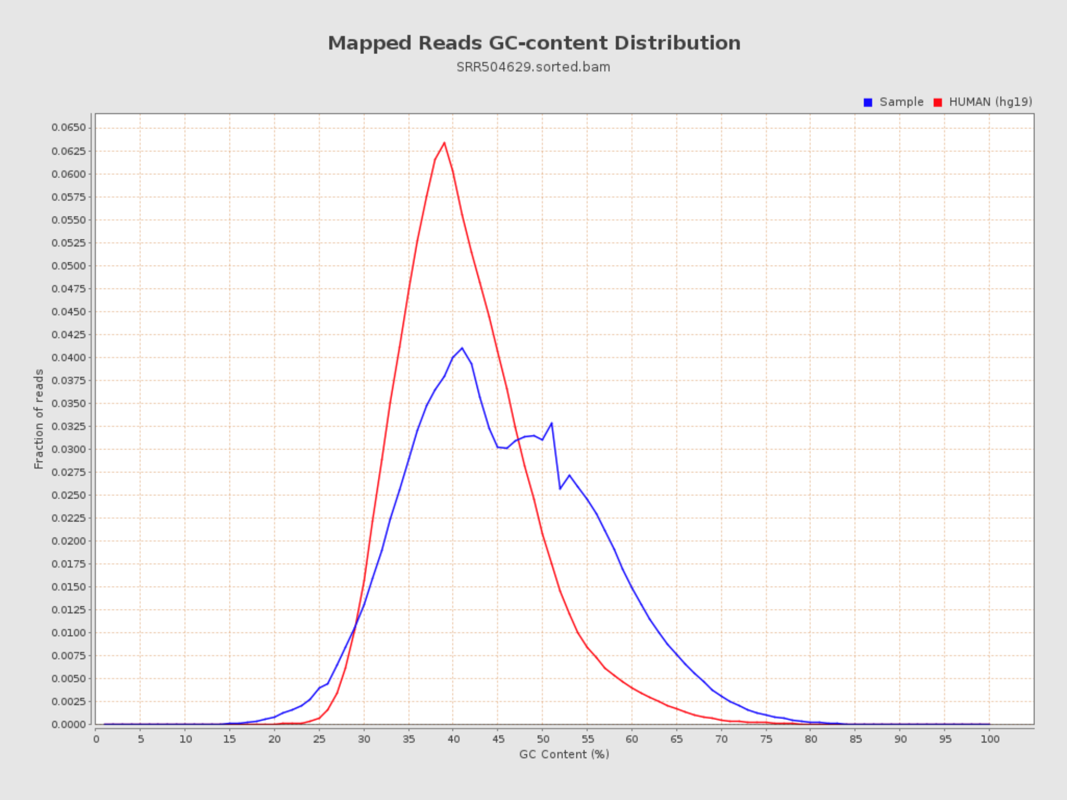
7. Results : Duplication Rate Histogram



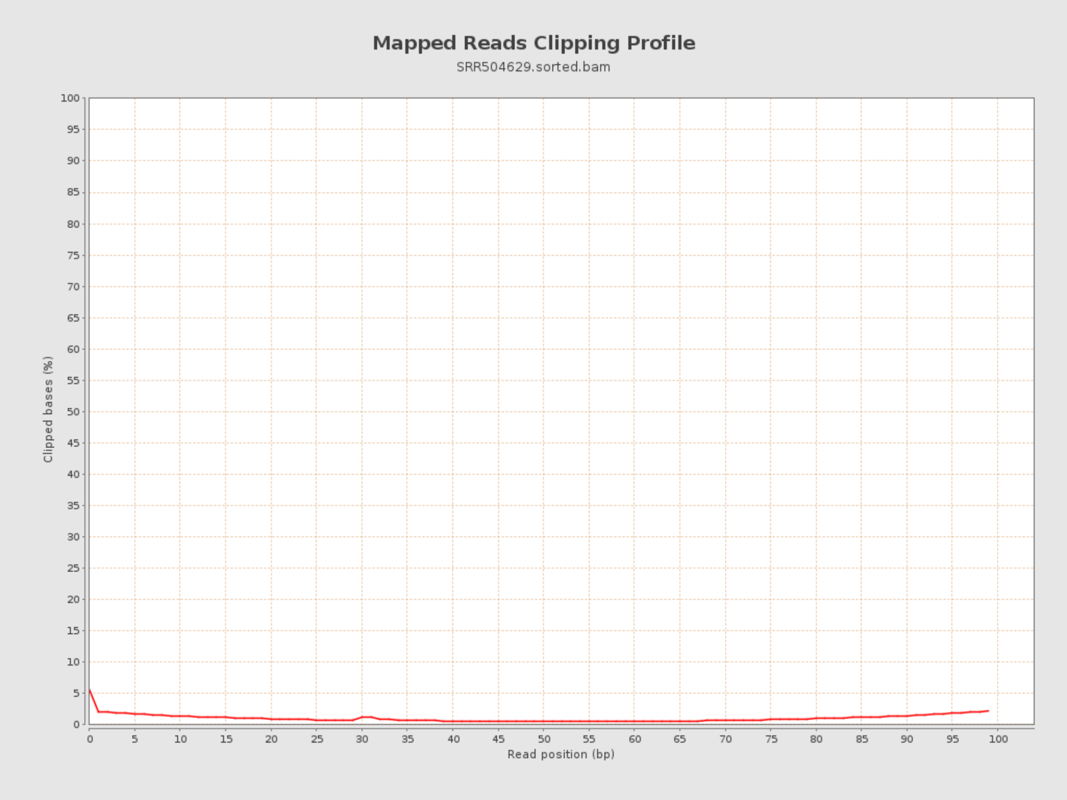
8. Results : Mapped Reads Nucleotide Content



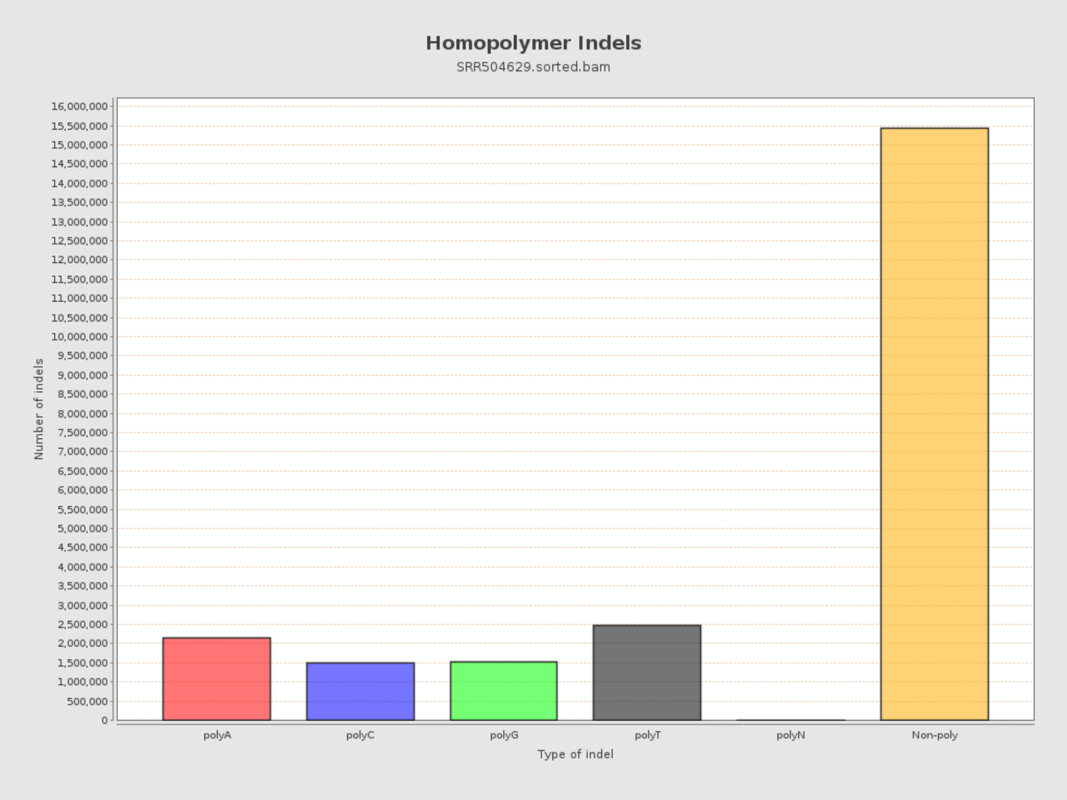
9. Results : Mapped Reads GC-content Distribution



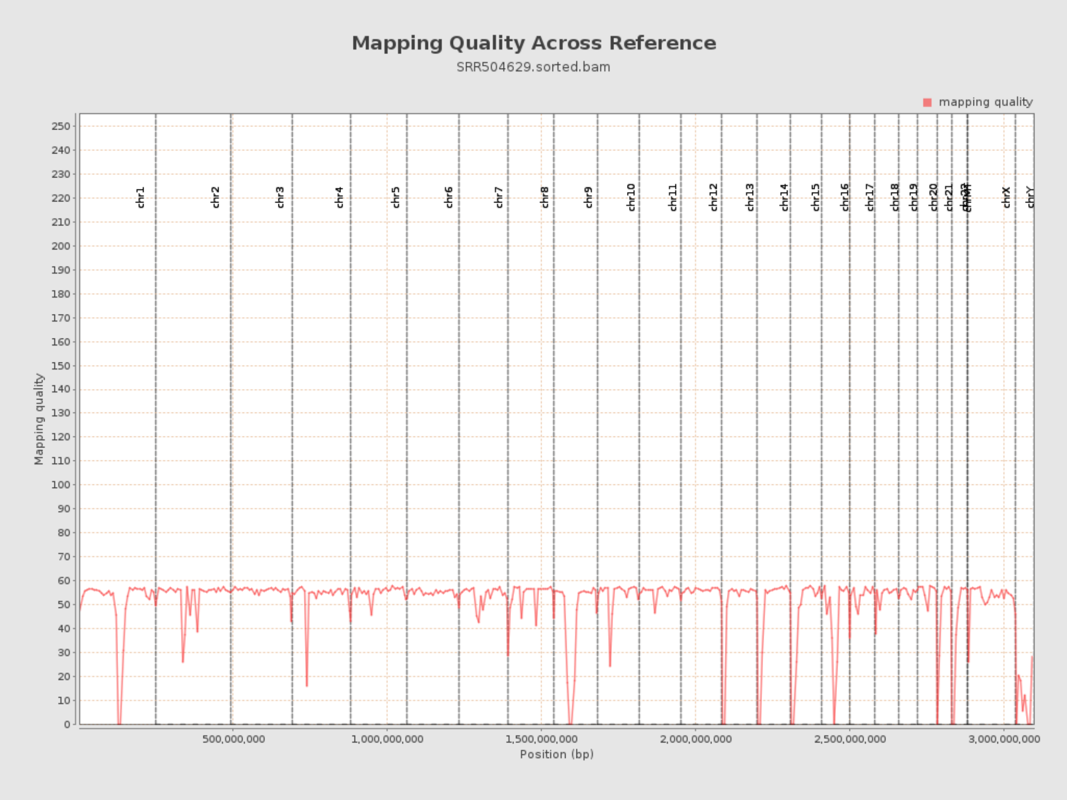
10. Results : Mapped Reads Clipping Profile



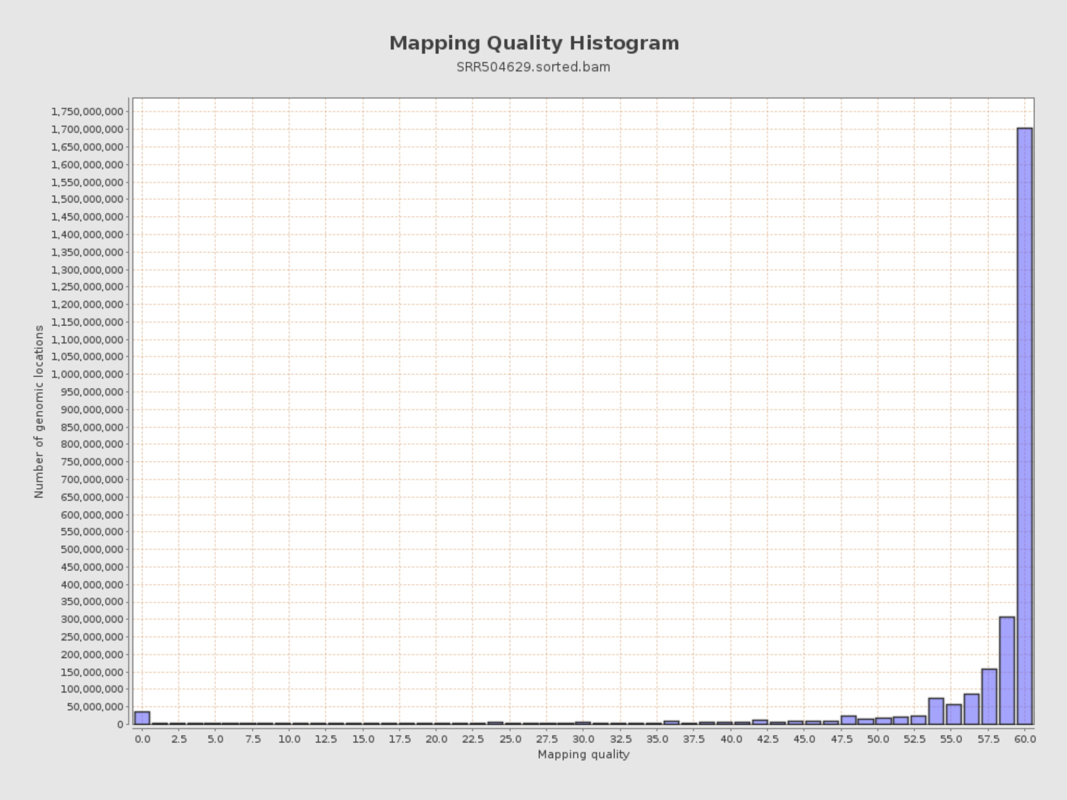
11. Results : Homopolymer Indels



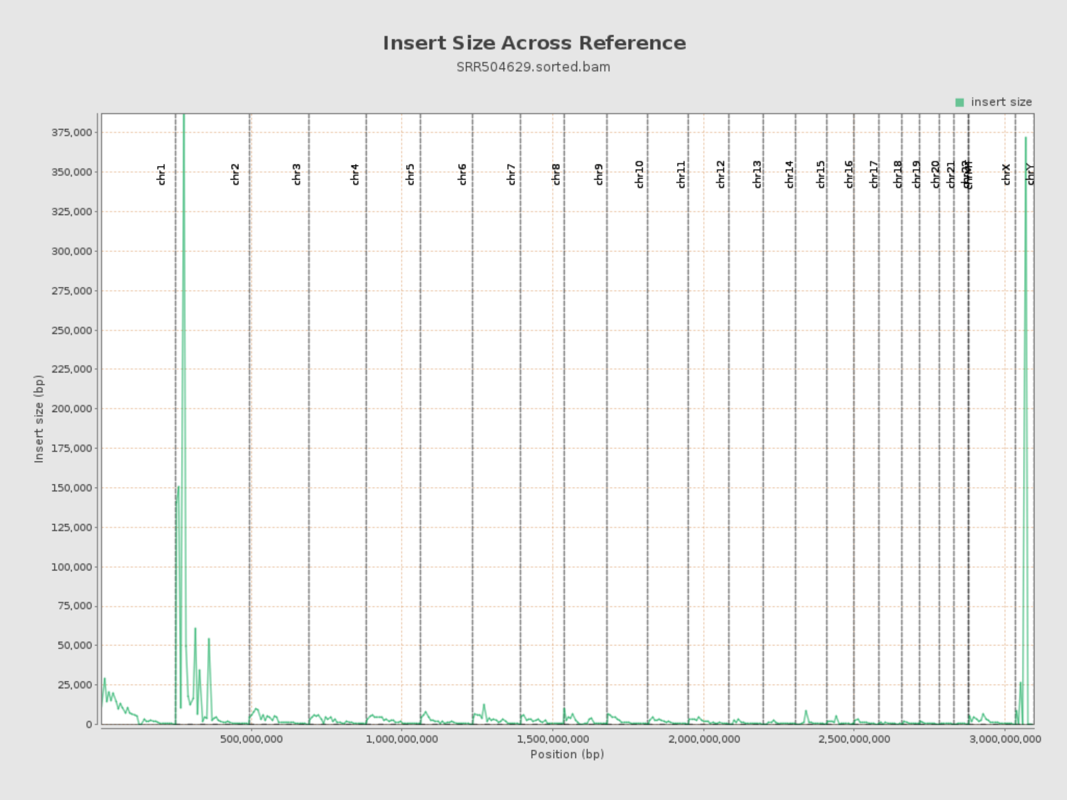
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram