Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/28 16:35:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504625.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_SRR504625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504625_1.fastq.gz SRR504625_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 28 16:35:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	302,017,412
Mapped reads	282,748,596 / 93.62%
Unmapped reads	19,268,816 / 6.38%
Mapped paired reads	282,748,596 / 93.62%
Mapped reads, first in pair	142,684,309 / 47.24%
Mapped reads, second in pair	140,064,287 / 46.38%
Mapped reads, both in pair	276,304,750 / 91.49%
Mapped reads, singletons	6,443,846 / 2.13%
Secondary alignments	0
Supplementary alignments	2,843,462 / 0.94%
Read min/max/mean length	30 / 100 / 100.38
Duplicated reads (estimated)	81,383,701 / 26.95%
Duplication rate	16.1%
Clipped reads	48,309,806 / 16%

2.2. ACGT Content

Number/percentage of A's	7,246,790,705 / 26.8%
Number/percentage of C's	6,213,311,080 / 22.98%
Number/percentage of T's	7,298,800,691 / 27%
Number/percentage of G's	6,274,170,232 / 23.21%
Number/percentage of N's	3,673,461 / 0.01%

GC Percentage	46.19%

2.3. Coverage

Mean	8.7419
Standard Deviation	205.1012

2.4. Mapping Quality

Mean Mapping Quality	52.09

2.5. Insert size

Mean	115,448.65
Standard Deviation	3,180,246.1
P25/Median/P75	320 / 367 / 424

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	325,776,922
Insertions	7,943,983
Mapped reads with at least one insertion	2.6%
Deletions	7,682,402
Mapped reads with at least one deletion	2.53%
Homopolymer indels	33.67%

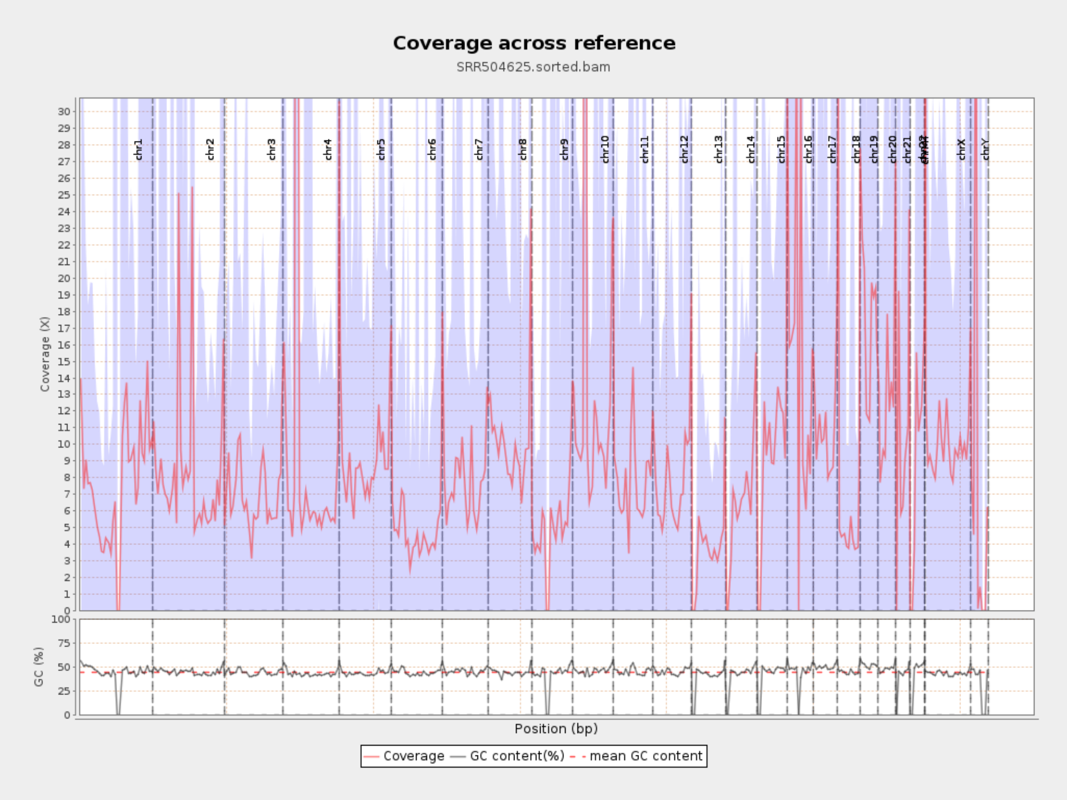
2.7. Chromosome stats

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

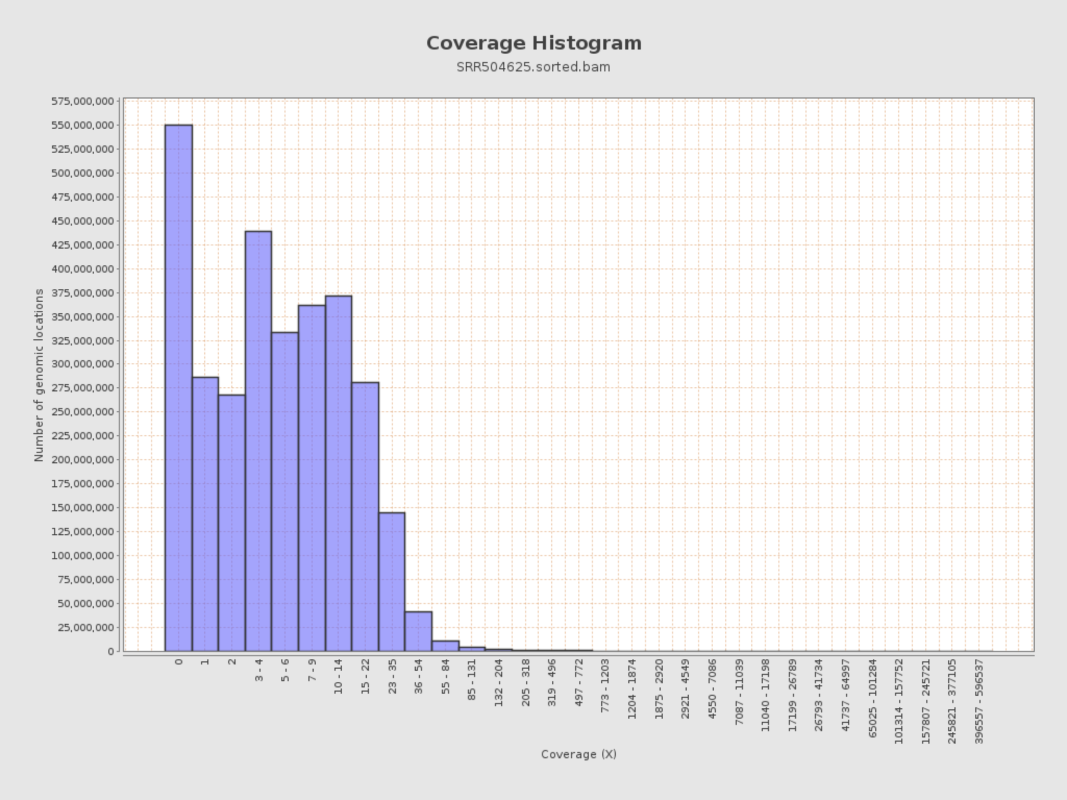
		bases	coverage	deviation
chr1	249250621	1906312754	7.6482	60.1223
chr2	243199373	2062639168	8.4813	238.0296
chr3	198022430	1367889474	6.9078	22.94
chr4	191154276	1944949726	10.1748	527.4396
chr5	180915260	1651375780	9.1279	33.793
chr6	171115067	790543465	4.62	26.1948
chr7	159138663	1267680150	7.9659	34.1304
chr8	146364022	1489205903	10.1747	138.3352
chr9	141213431	706147992	5.0006	74.878
chr10	135534747	2018361000	14.8918	470.6122
chr11	135006516	1098014396	8.133	25.2184
chr12	133851895	1018066096	7.6059	19.9828
chr13	115169878	410035276	3.5603	11.4985
chr14	107349540	693347000	6.4588	30.0201
chr15	102531392	926777763	9.039	16.8076
chr16	90354753	1453267606	16.084	201.0539
chr17	81195210	887668410	10.9325	72.2248
chr18	78077248	458217617	5.8688	278.9967
chr19	59128983	1074587233	18.1736	40.8208
chr20	63025520	801417338	12.7158	128.8552
chr21	48129895	517726309	10.7569	167.8439
chr22	51304566	486260976	9.4779	30.195
chrMT	16571	9366355	565.2257	252.0326
chrX	155270560	1538618630	9.9093	21.3395

chrY	59373566	483854093	8.1493	503.5814

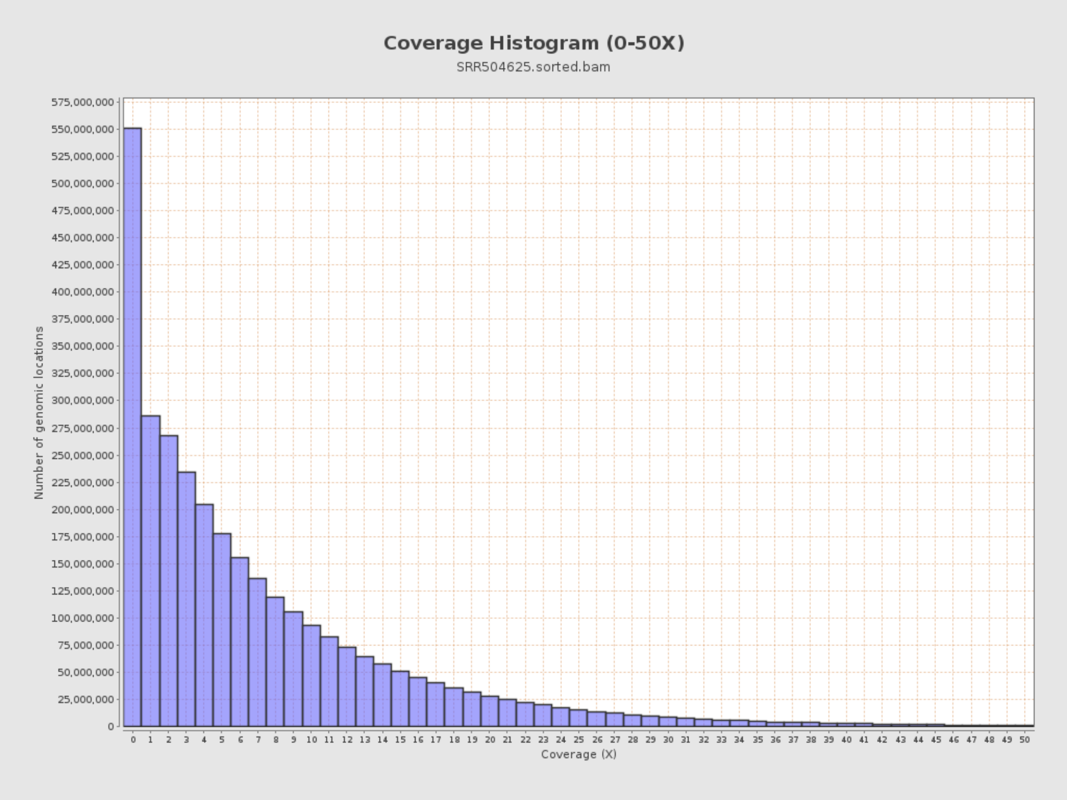
3. Results : Coverage across reference



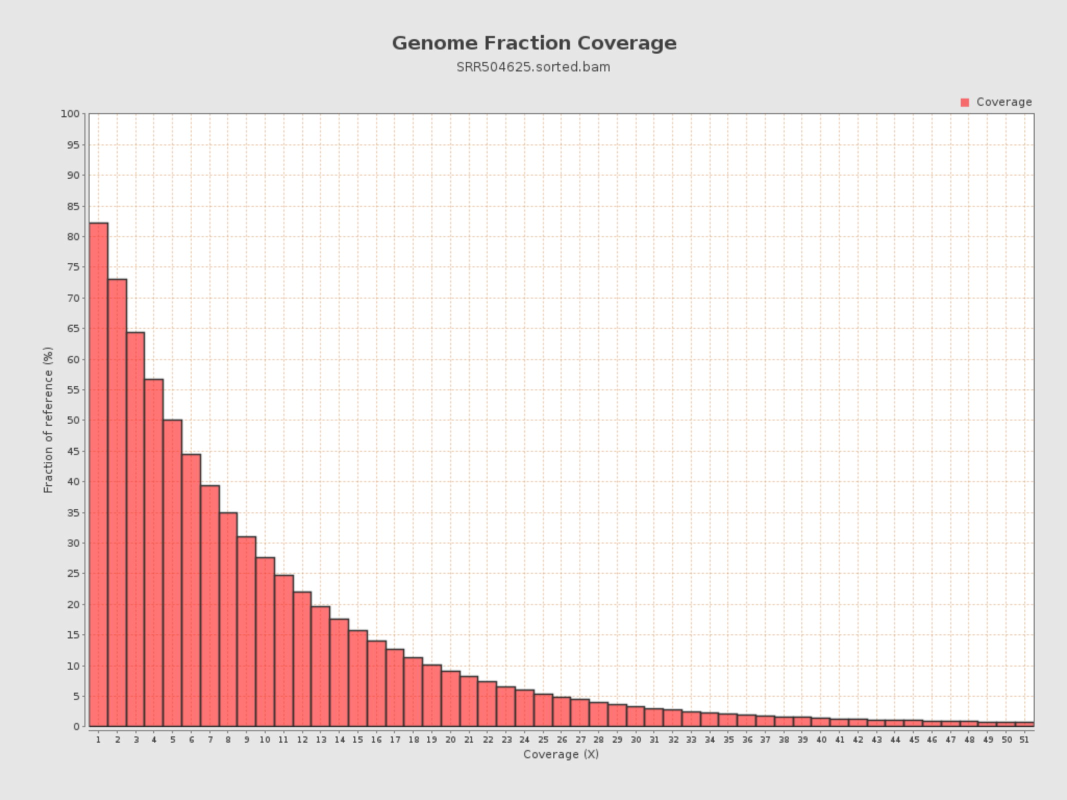
4. Results : Coverage Histogram



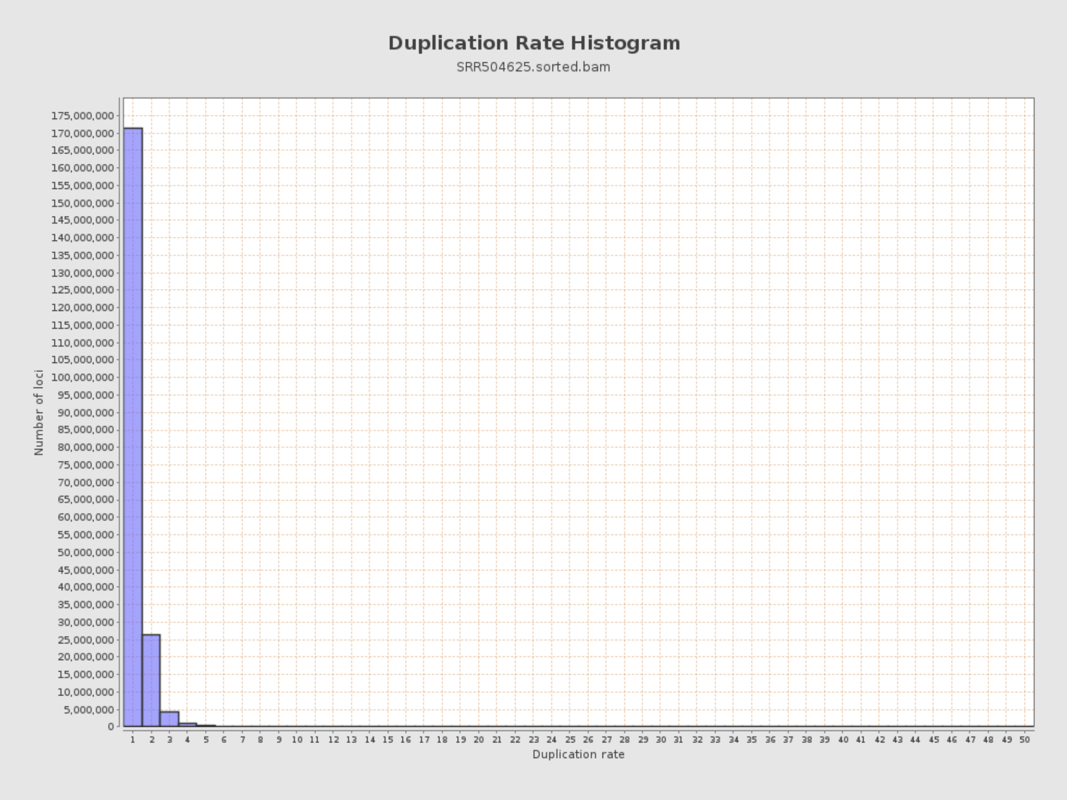
5. Results : Coverage Histogram (0-50X)



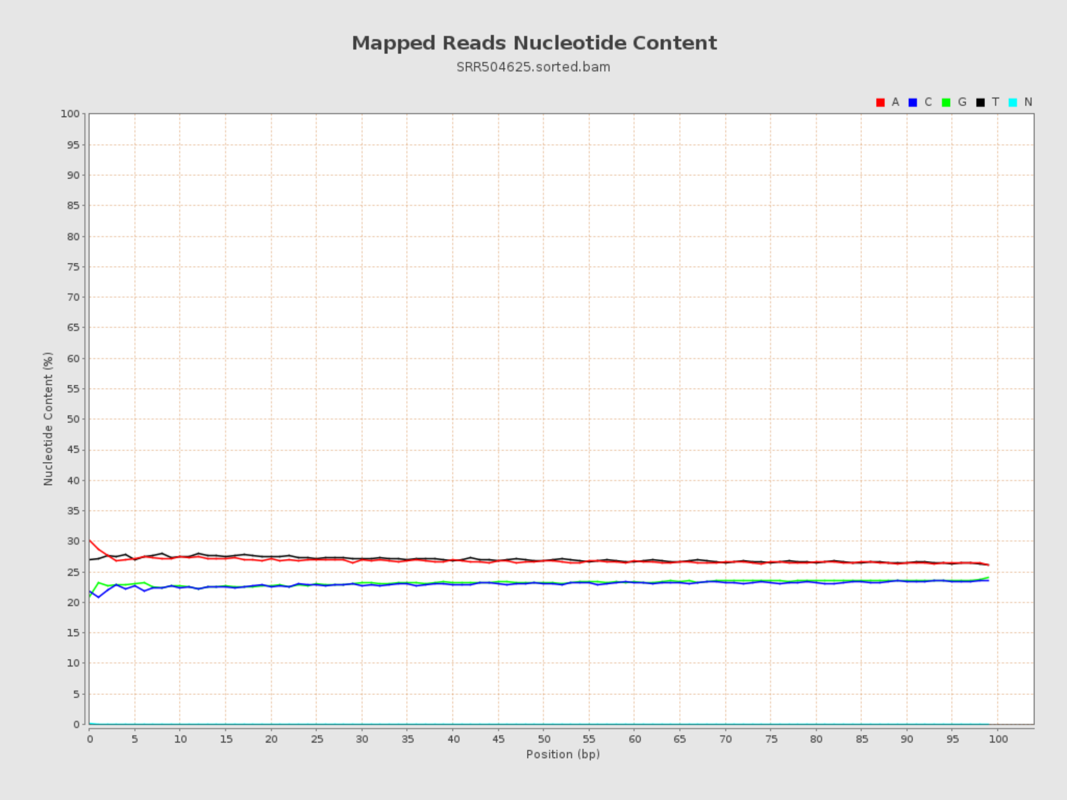
6. Results : Genome Fraction Coverage



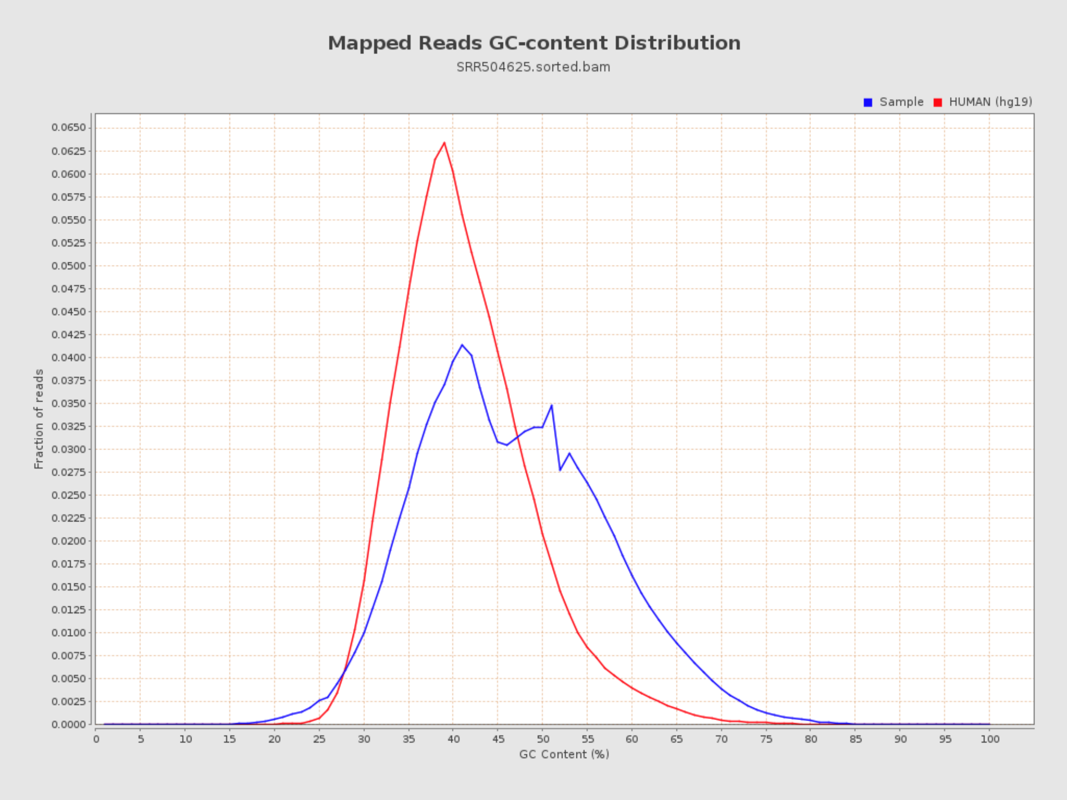
7. Results : Duplication Rate Histogram



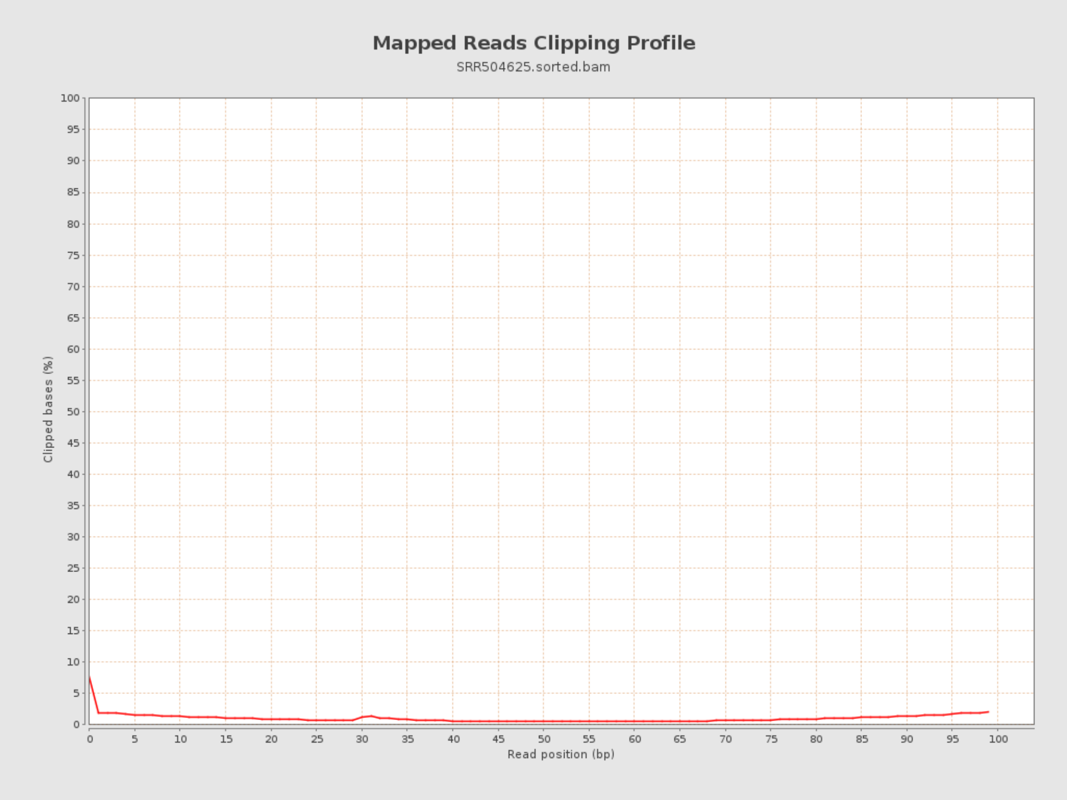
8. Results : Mapped Reads Nucleotide Content



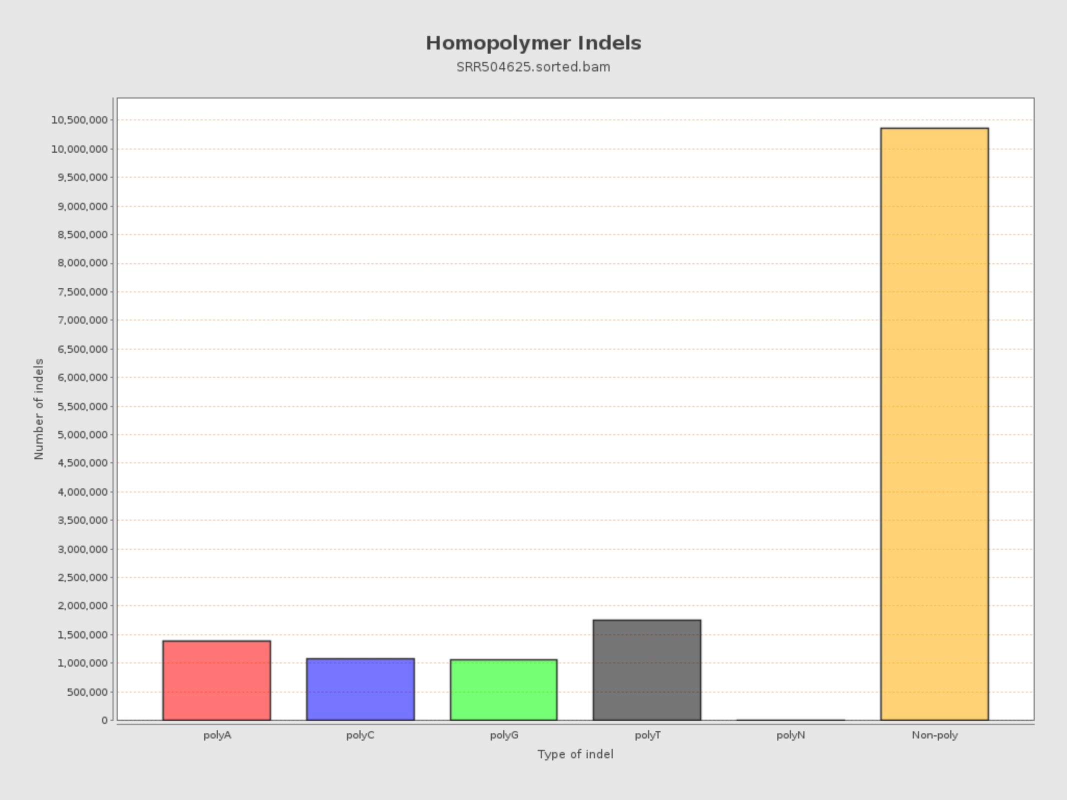
9. Results : Mapped Reads GC-content Distribution



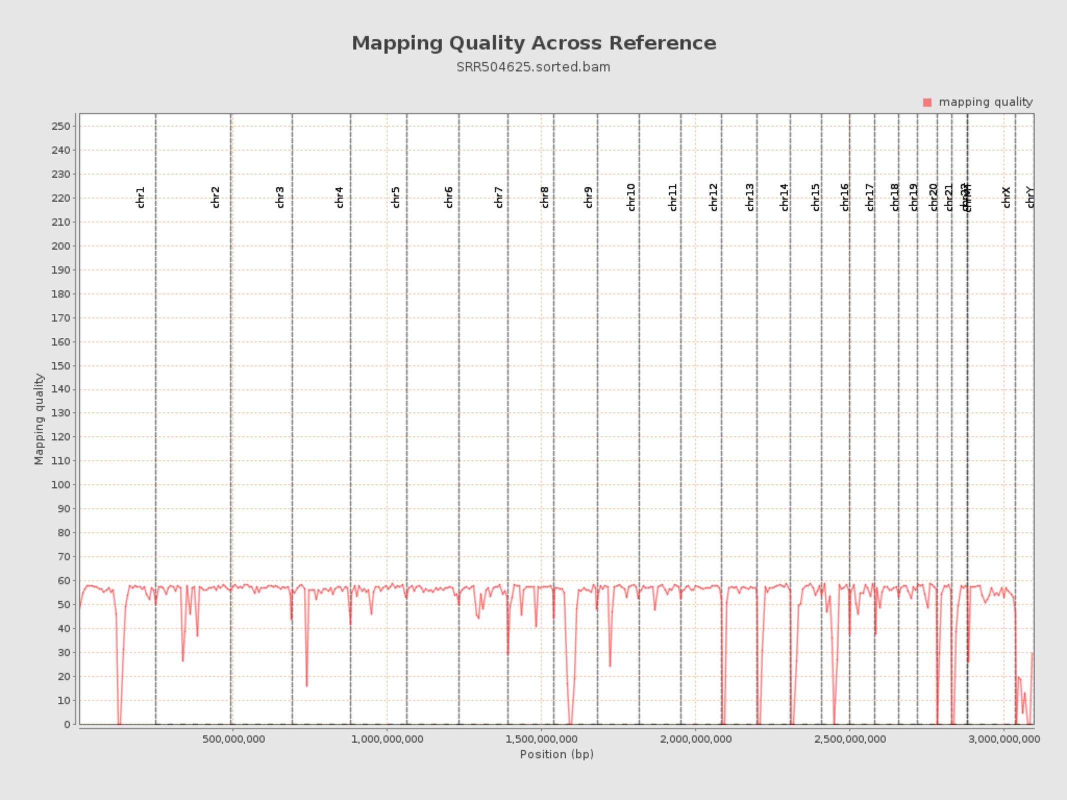
10. Results : Mapped Reads Clipping Profile



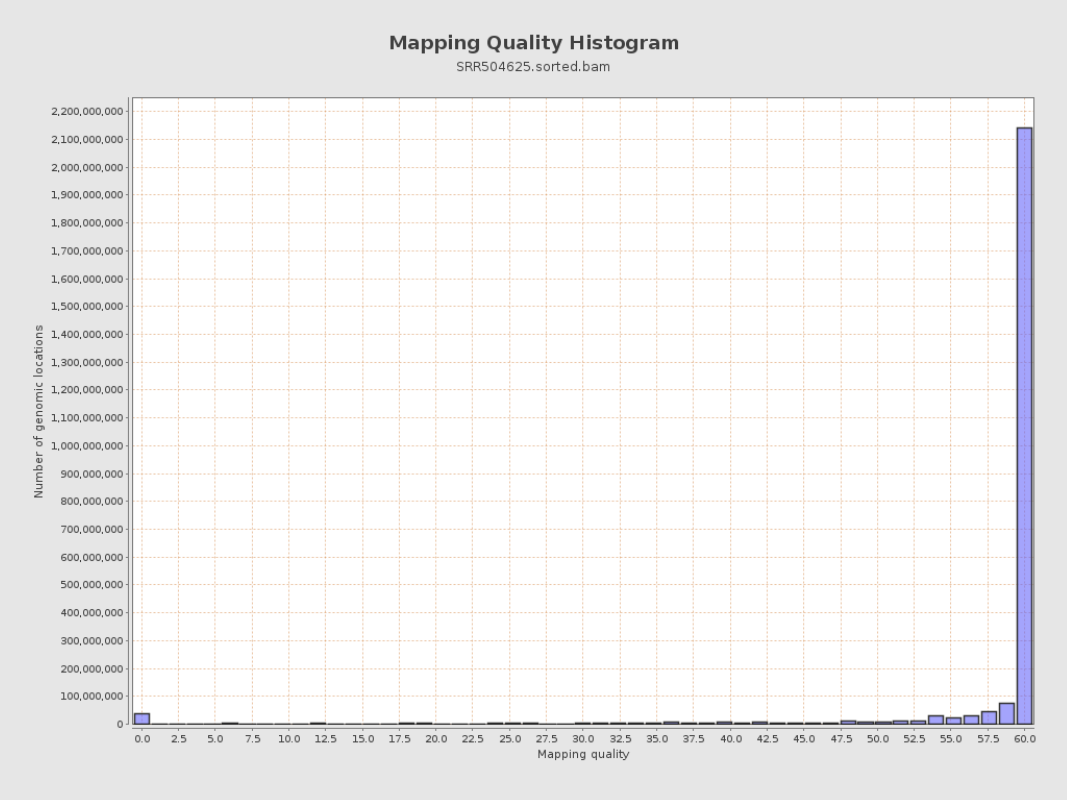
11. Results : Homopolymer Indels



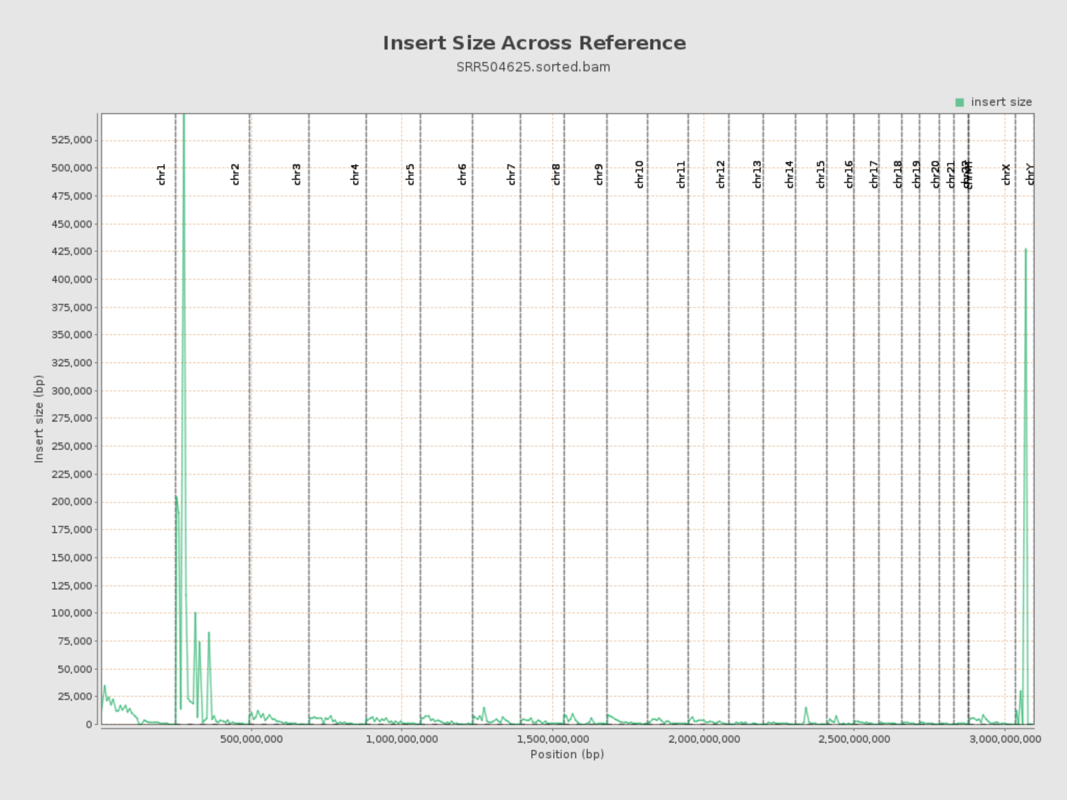
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram