Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/27 06:10:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504620.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_SRR504620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504620_1.fastq.gz SRR504620_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 27 06:10:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	551,416,168
Mapped reads	501,420,645 / 90.93%
Unmapped reads	49,995,523 / 9.07%
Mapped paired reads	501,420,645 / 90.93%
Mapped reads, first in pair	253,622,318 / 45.99%
Mapped reads, second in pair	247,798,327 / 44.94%
Mapped reads, both in pair	486,829,576 / 88.29%
Mapped reads, singletons	14,591,069 / 2.65%
Secondary alignments	0
Supplementary alignments	5,071,549 / 0.92%
Read min/max/mean length	30 / 100 / 100.37
Duplicated reads (estimated)	188,133,070 / 34.12%
Duplication rate	27.12%
Clipped reads	92,771,717 / 16.82%

2.2. ACGT Content

Number/percentage of A's	12,869,016,939 / 26.91%
Number/percentage of C's	10,969,728,458 / 22.94%
Number/percentage of T's	12,961,711,997 / 27.11%
Number/percentage of G's	10,968,020,856 / 22.94%
Number/percentage of N's	50,664,031 / 0.11%

GC Percentage	45.88%

2.3. Coverage

Mean	15.4603
Standard Deviation	364.0166

2.4. Mapping Quality

Mean Mapping Quality	52.06

2.5. Insert size

Mean	105,080.31
Standard Deviation	3,042,278.06
P25/Median/P75	276 / 327 / 384

2.6. Mismatches and indels

General error rate	1.89%
Mismatches	846,970,173
Insertions	14,064,283
Mapped reads with at least one insertion	2.6%
Deletions	12,550,138
Mapped reads with at least one deletion	2.33%
Homopolymer indels	34.09%

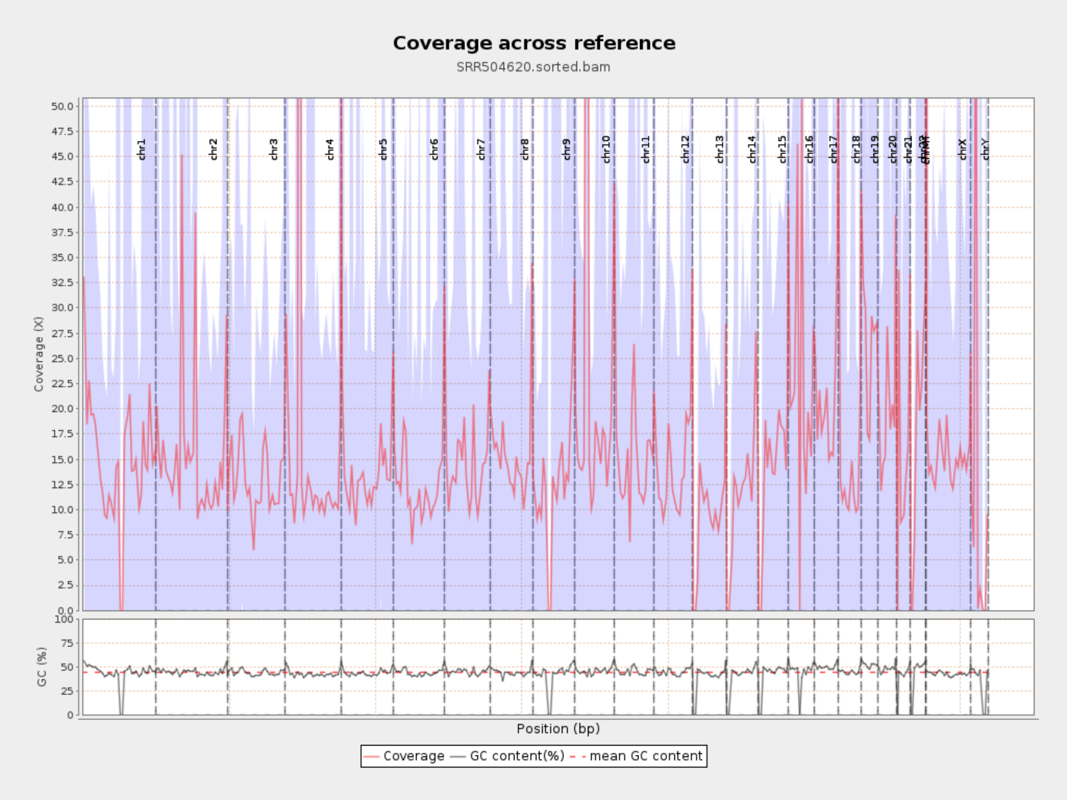
2.7. Chromosome stats

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

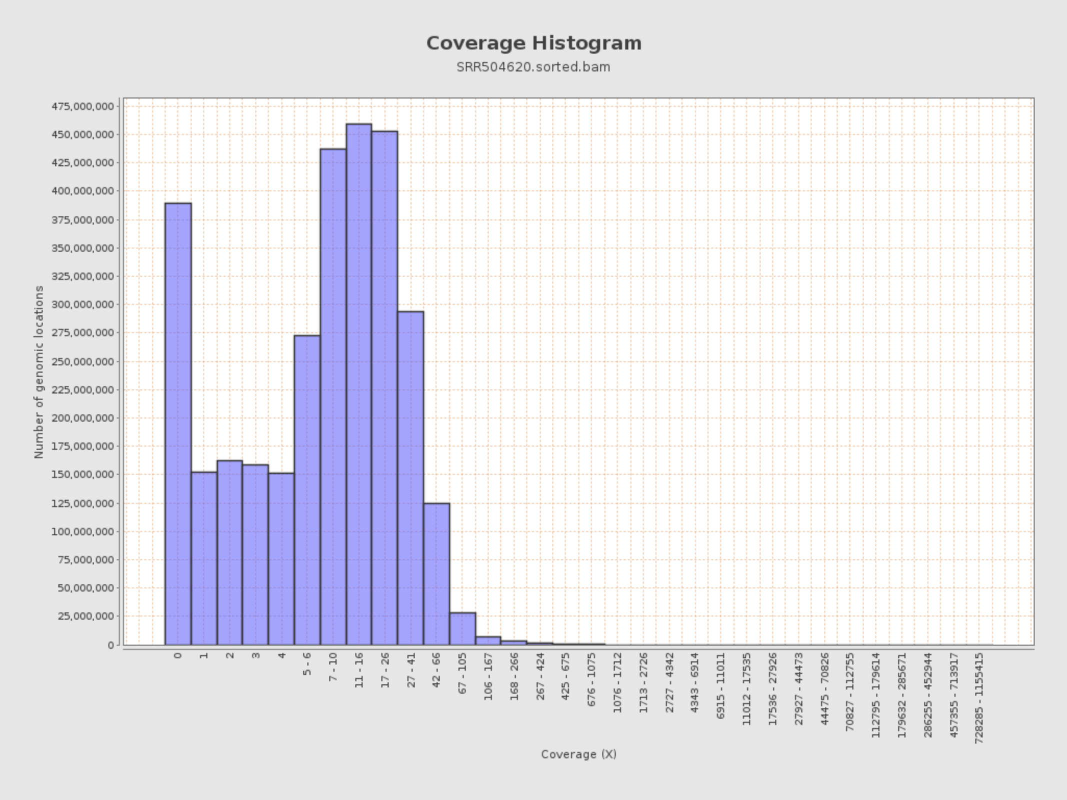
		bases	coverage	deviation
chr1	249250621	3688829426	14.7997	111.7475
chr2	243199373	3777261084	15.5315	363.8639
chr3	198022430	2567911977	12.9678	32.9595
chr4	191154276	3613246443	18.9023	1,010.8522
chr5	180915260	2498467434	13.8102	48.2928
chr6	171115067	2058609905	12.0306	46.0126
chr7	159138663	2355963038	14.8045	53.0898
chr8	146364022	2251742923	15.3845	270.9038
chr9	141213431	1745699174	12.3621	125.9601
chr10	135534747	3157030556	23.2931	810.1766
chr11	135006516	2052874435	15.2057	43.8105
chr12	133851895	1916909685	14.3211	27.4322
chr13	115169878	1072874534	9.3156	20.4803
chr14	107349540	1278090331	11.9059	44.2576
chr15	102531392	1392799818	13.5841	22.9803
chr16	90354753	2140318975	23.688	292.4089
chr17	81195210	1626074989	20.0267	104.9167
chr18	78077248	1083304560	13.8748	409.7994
chr19	59128983	1579547818	26.7136	61.2327
chr20	63025520	1218809674	19.3384	254.1755
chr21	48129895	795395731	16.526	345.6882
chr22	51304566	873896412	17.0335	44.2663
chrMT	16571	18139342	1,094.6438	503.0245
chrX	155270560	2356258088	15.1752	31.2098

chrY	59373566	740313617	12.4687	855.0746

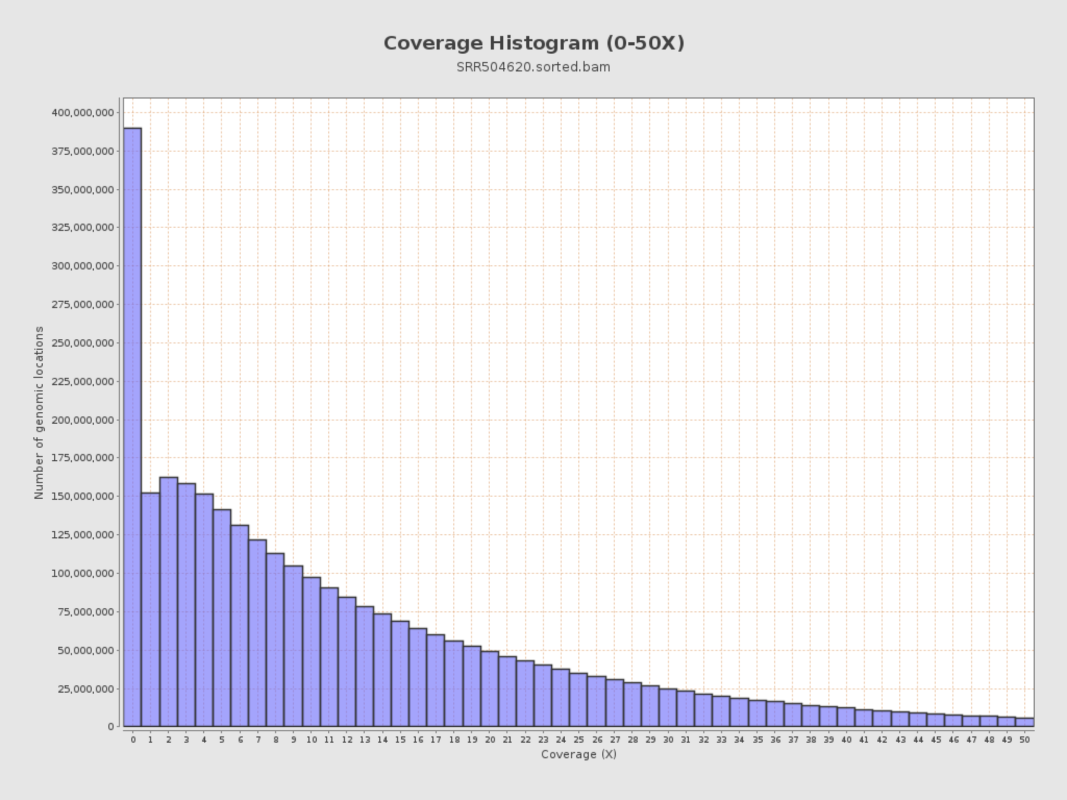
3. Results : Coverage across reference



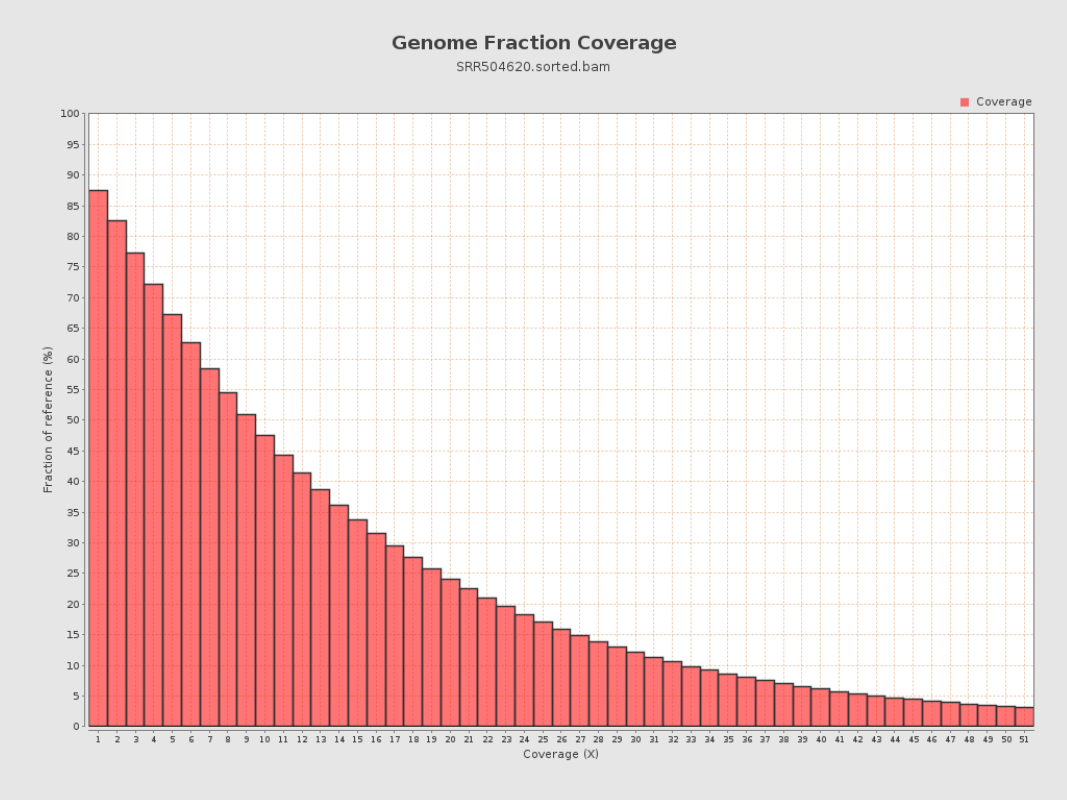
4. Results : Coverage Histogram



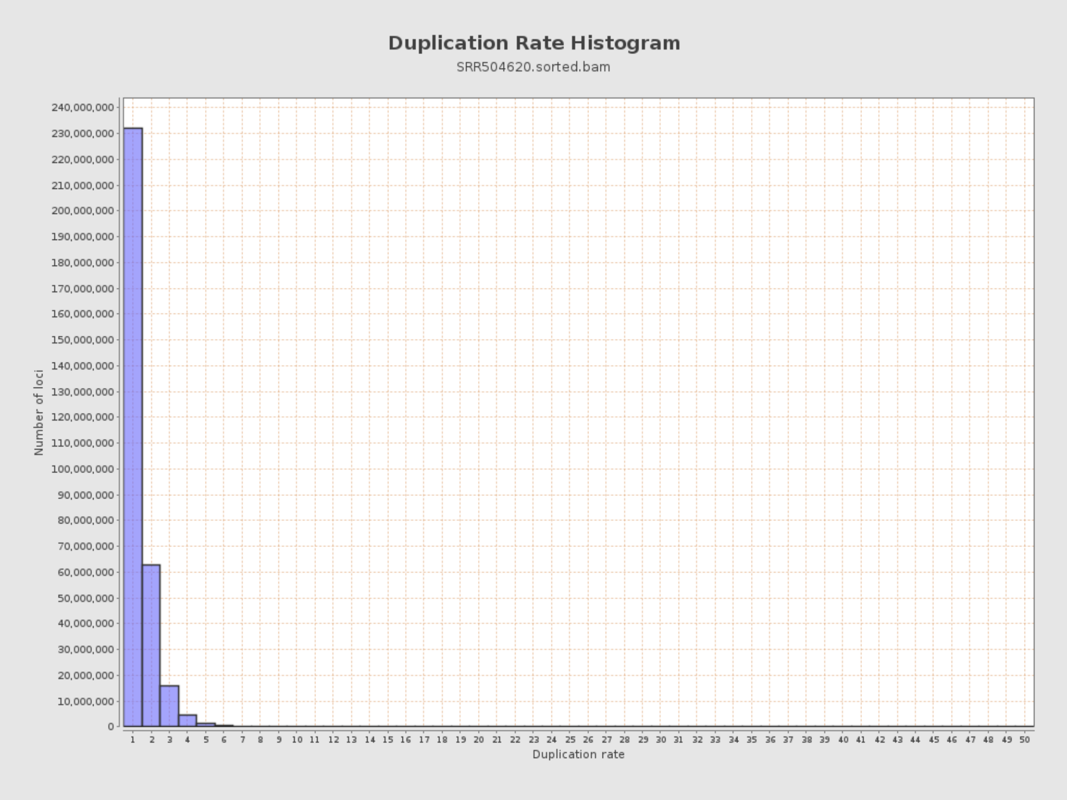
5. Results : Coverage Histogram (0-50X)



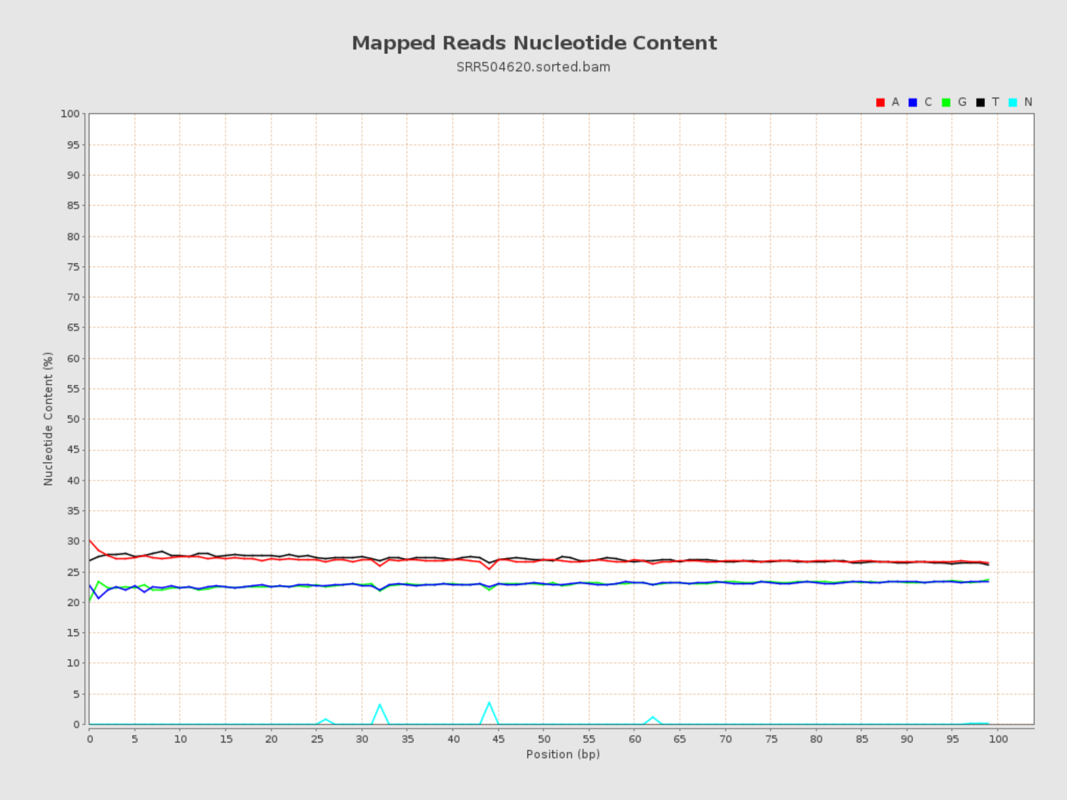
6. Results : Genome Fraction Coverage



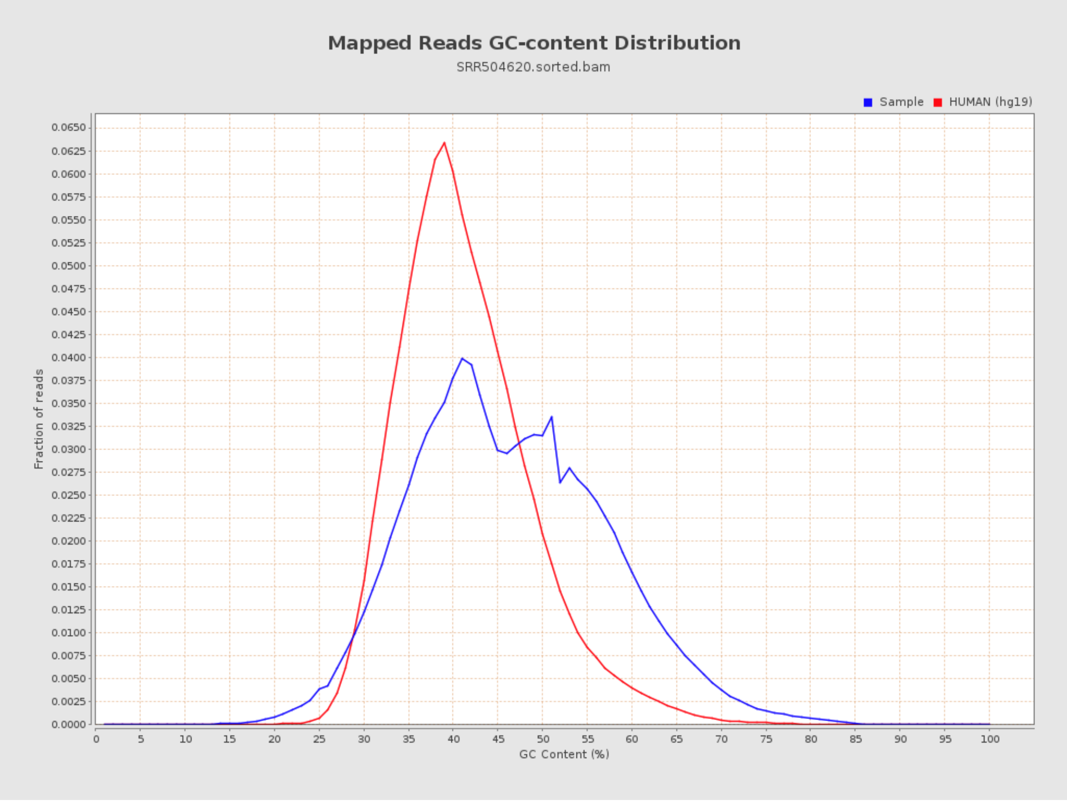
7. Results : Duplication Rate Histogram



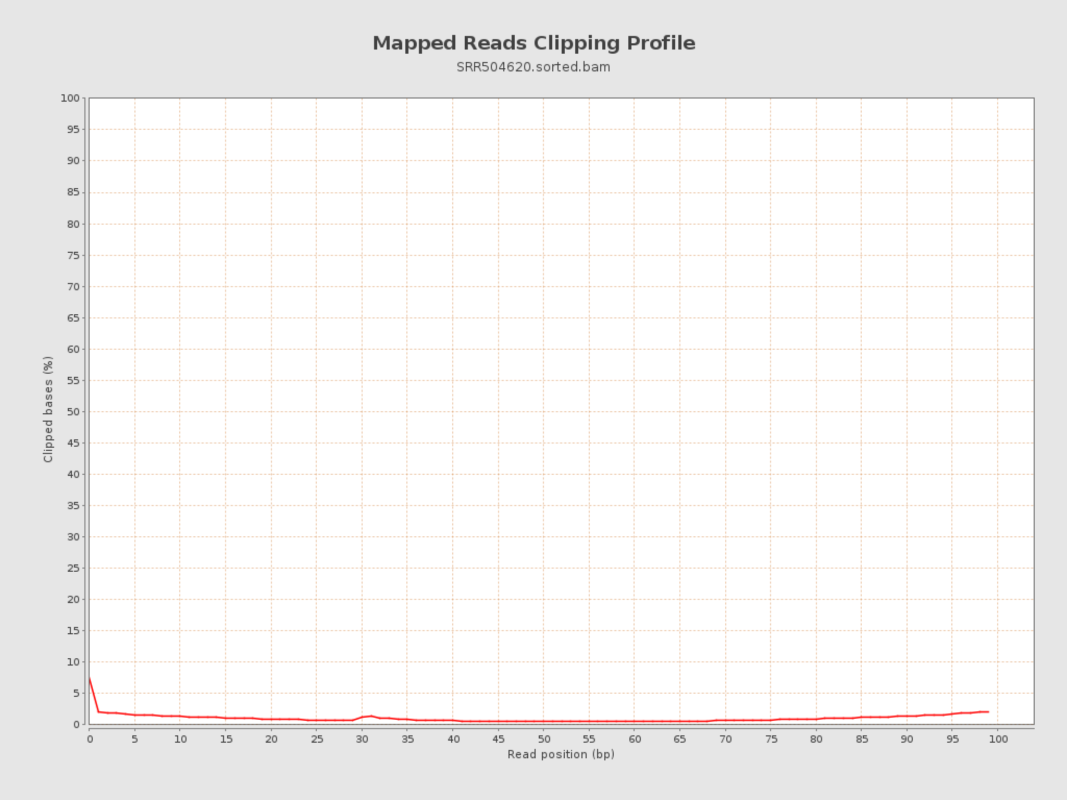
8. Results : Mapped Reads Nucleotide Content



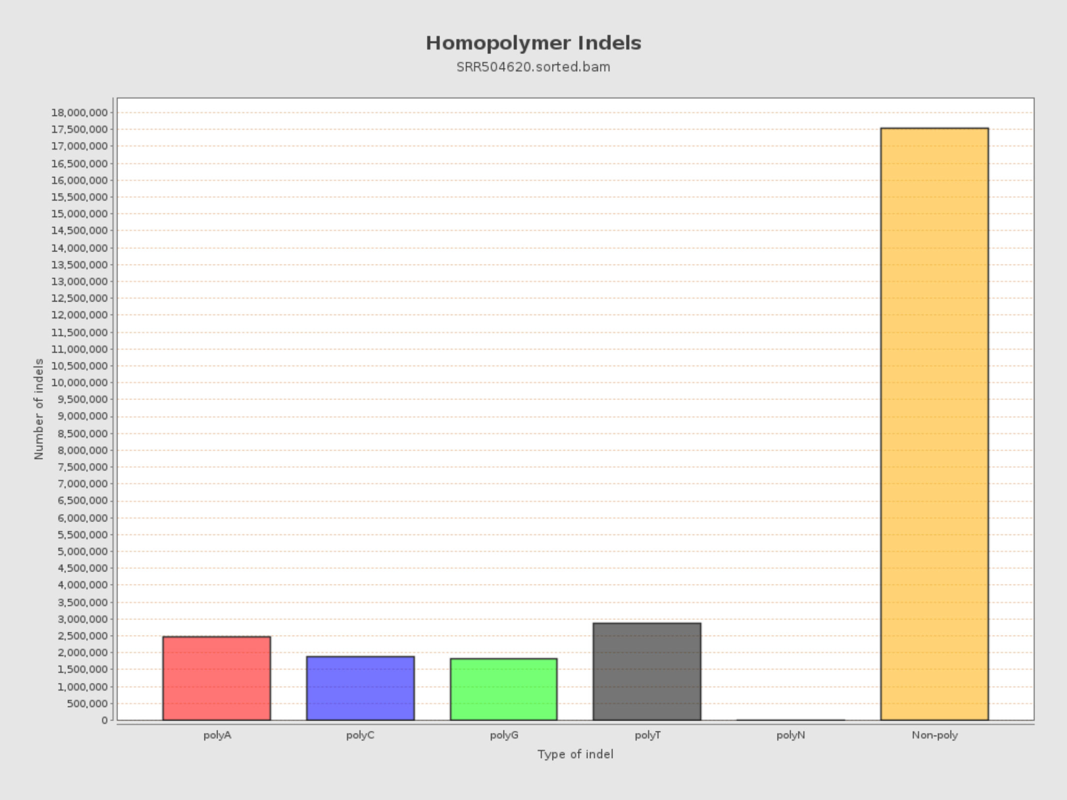
9. Results : Mapped Reads GC-content Distribution



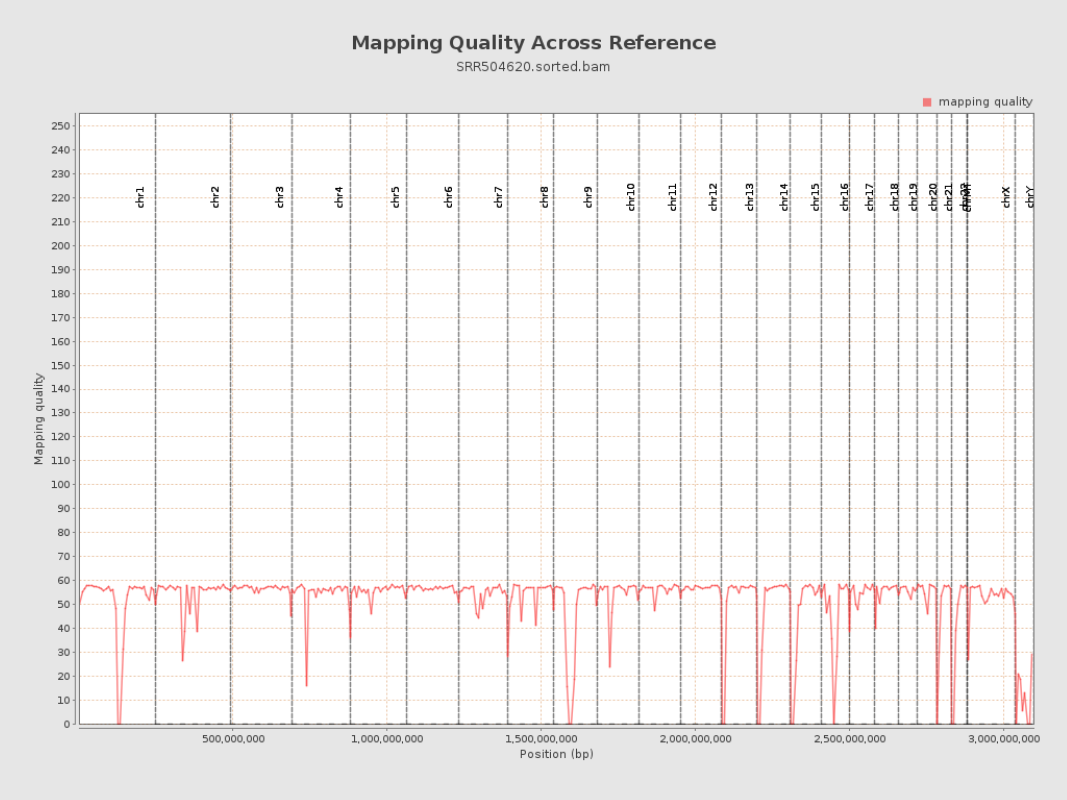
10. Results : Mapped Reads Clipping Profile



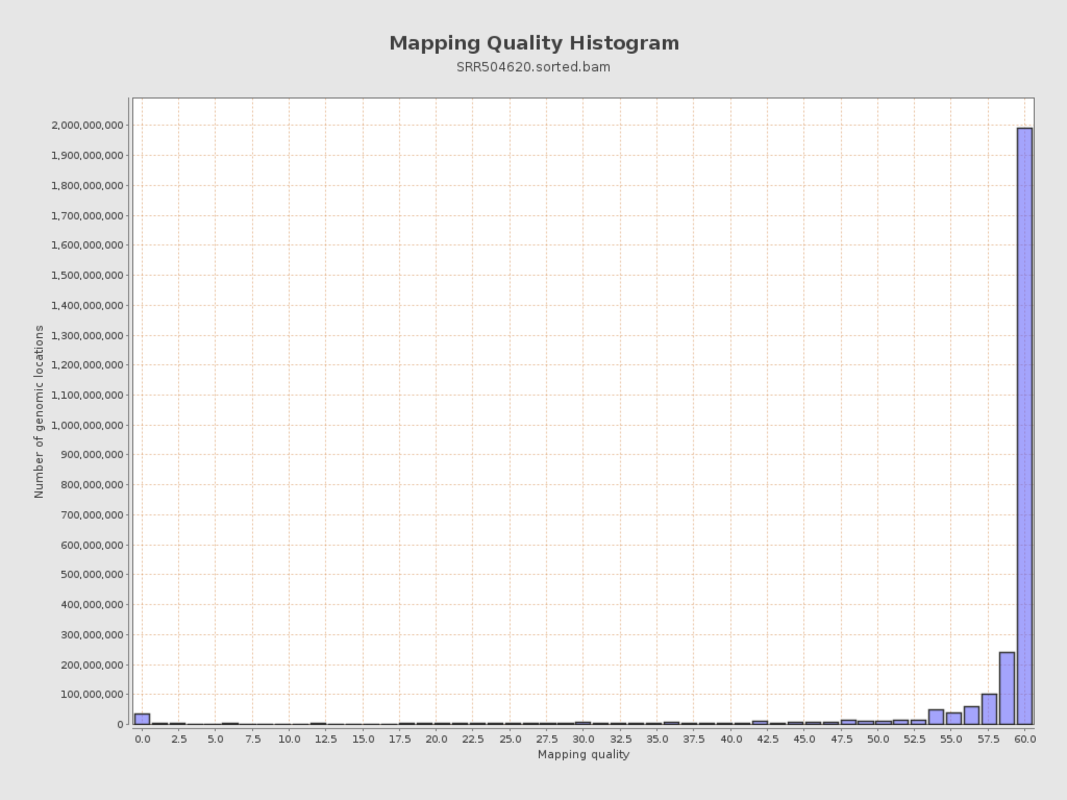
11. Results : Homopolymer Indels



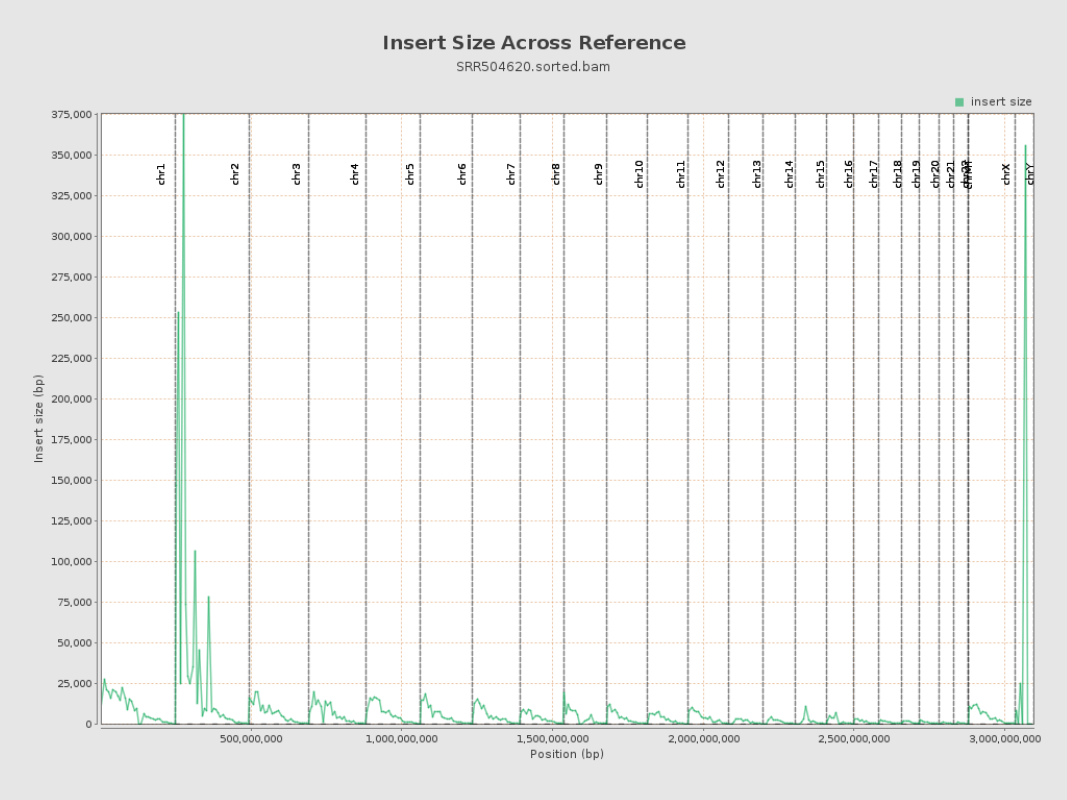
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram