Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/28 01:22:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504622.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_SRR504622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504622_1.fastq.gz SRR504622_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 28 01:21:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	529,249,188
Mapped reads	483,330,488 / 91.32%
Unmapped reads	45,918,700 / 8.68%
Mapped paired reads	483,330,488 / 91.32%
Mapped reads, first in pair	242,805,082 / 45.88%
Mapped reads, second in pair	240,525,406 / 45.45%
Mapped reads, both in pair	472,651,096 / 89.31%
Mapped reads, singletons	10,679,392 / 2.02%
Secondary alignments	0
Supplementary alignments	4,956,749 / 0.94%
Read min/max/mean length	30 / 100 / 100.38
Duplicated reads (estimated)	179,979,487 / 34.01%
Duplication rate	26.71%
Clipped reads	82,562,848 / 15.6%

2.2. ACGT Content

Number/percentage of A's	12,411,655,007 / 26.8%
Number/percentage of C's	10,669,718,573 / 23.04%
Number/percentage of T's	12,490,028,087 / 26.97%
Number/percentage of G's	10,683,888,174 / 23.07%
Number/percentage of N's	50,637,941 / 0.11%

GC Percentage	46.11%

2.3. Coverage

Mean	14.9712
Standard Deviation	367.3502

2.4. Mapping Quality

Mean Mapping Quality	52.22

2.5. Insert size

Mean	106,072.38
Standard Deviation	3,050,182.12
P25/Median/P75	277 / 328 / 385

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	664,133,264
Insertions	13,575,049
Mapped reads with at least one insertion	2.61%
Deletions	12,266,140
Mapped reads with at least one deletion	2.37%
Homopolymer indels	34.49%

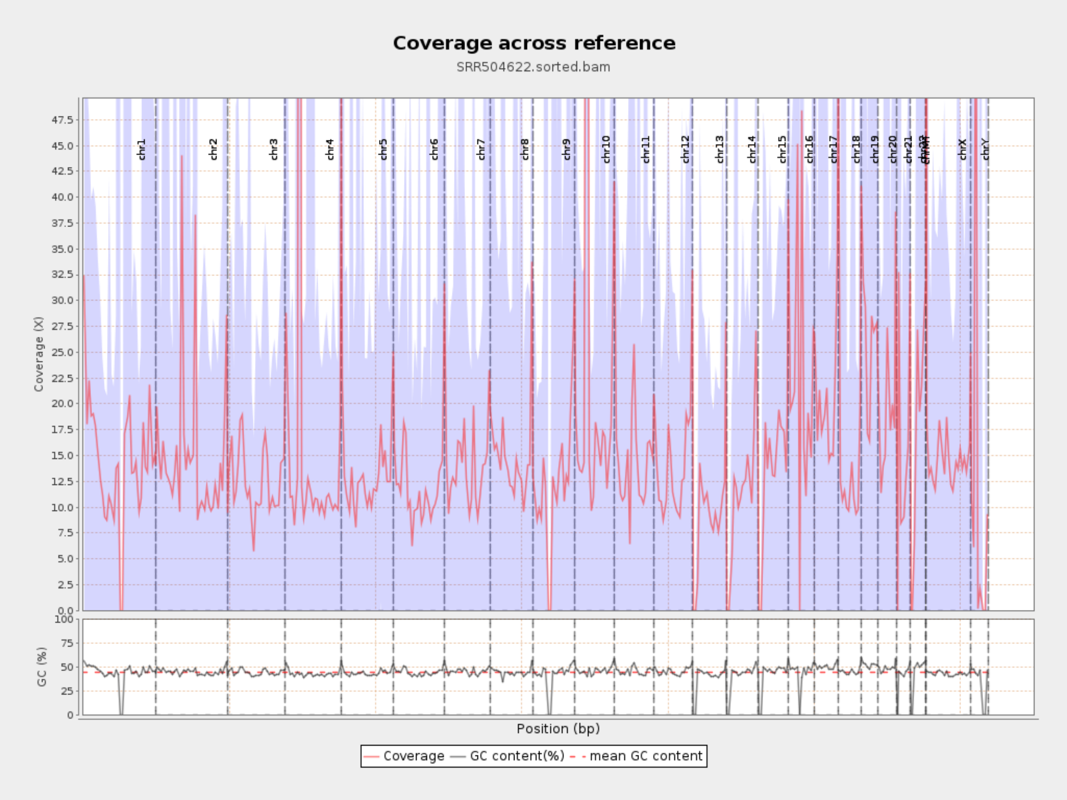
2.7. Chromosome stats

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

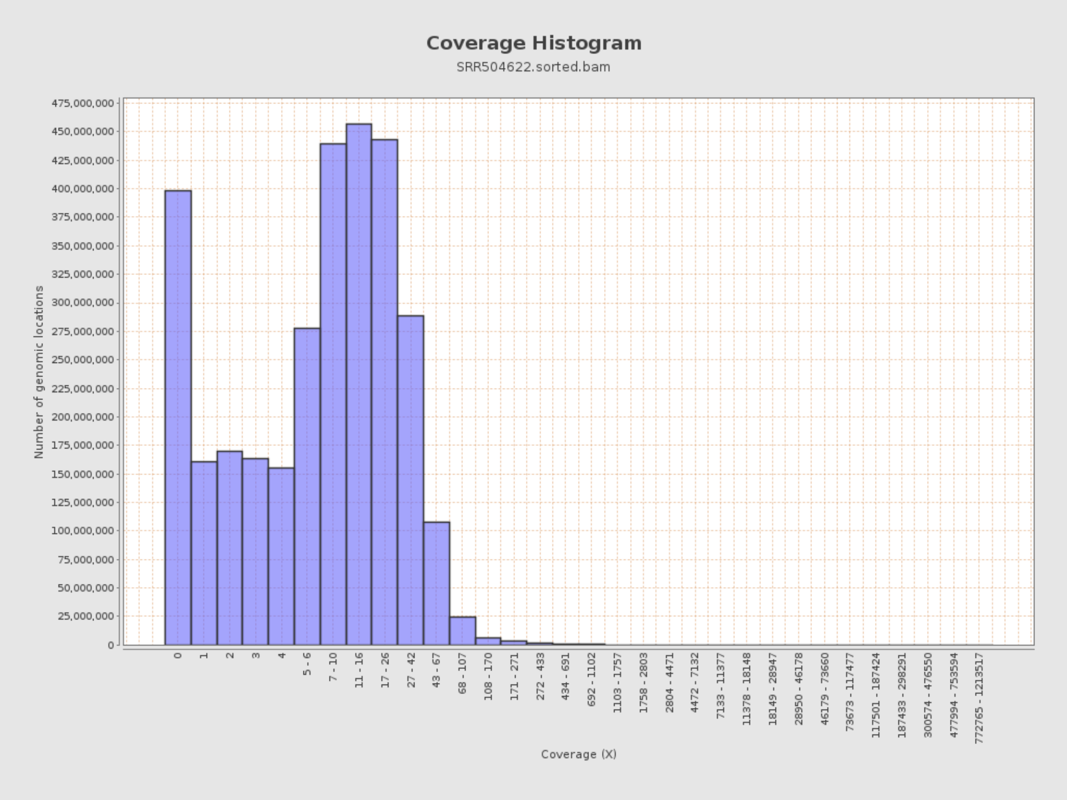
		bases	coverage	deviation
chr1	249250621	3570258235	14.324	108.9348
chr2	243199373	3648254813	15.0011	351.3521
chr3	198022430	2475195132	12.4996	33.0733
chr4	191154276	3510760911	18.3661	1,036.9889
chr5	180915260	2408682006	13.3139	46.4254
chr6	171115067	1985731047	11.6047	46.2382
chr7	159138663	2279098376	14.3215	52.4823
chr8	146364022	2177409548	14.8767	280.9655
chr9	141213431	1691470082	11.9781	126.8023
chr10	135534747	3056197917	22.5492	800.4506
chr11	135006516	1985998474	14.7104	44.8522
chr12	133851895	1851577366	13.833	26.3792
chr13	115169878	1034303671	8.9807	20.2136
chr14	107349540	1235611192	11.5102	43.1198
chr15	102531392	1349563831	13.1624	22.5298
chr16	90354753	2076818372	22.9852	278.7967
chr17	81195210	1586371952	19.5378	104.6111
chr18	78077248	1053212619	13.4894	417.7564
chr19	59128983	1543152836	26.0981	59.8915
chr20	63025520	1184114939	18.7879	249.5639
chr21	48129895	771173361	16.0228	335.7959
chr22	51304566	853603912	16.638	42.4557
chrMT	16571	17586343	1,061.2723	494.1971
chrX	155270560	2266006312	14.5939	30.2669

chrY	59373566	734107389	12.3642	871.3478

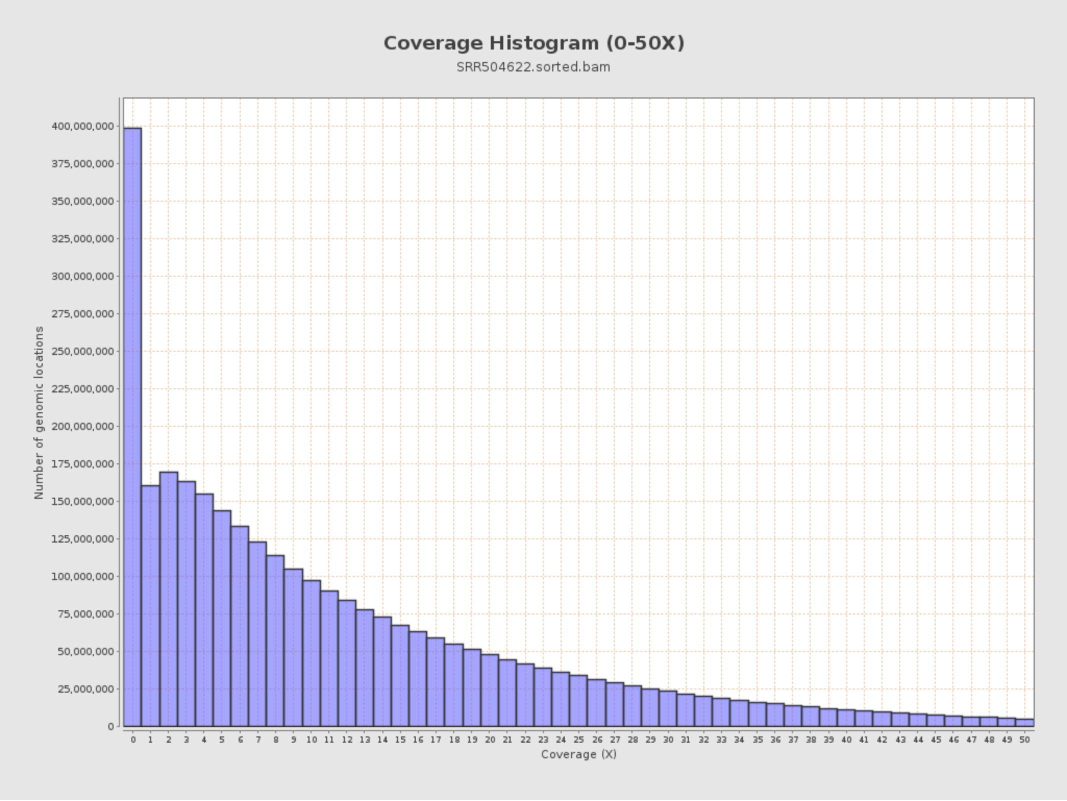
3. Results : Coverage across reference



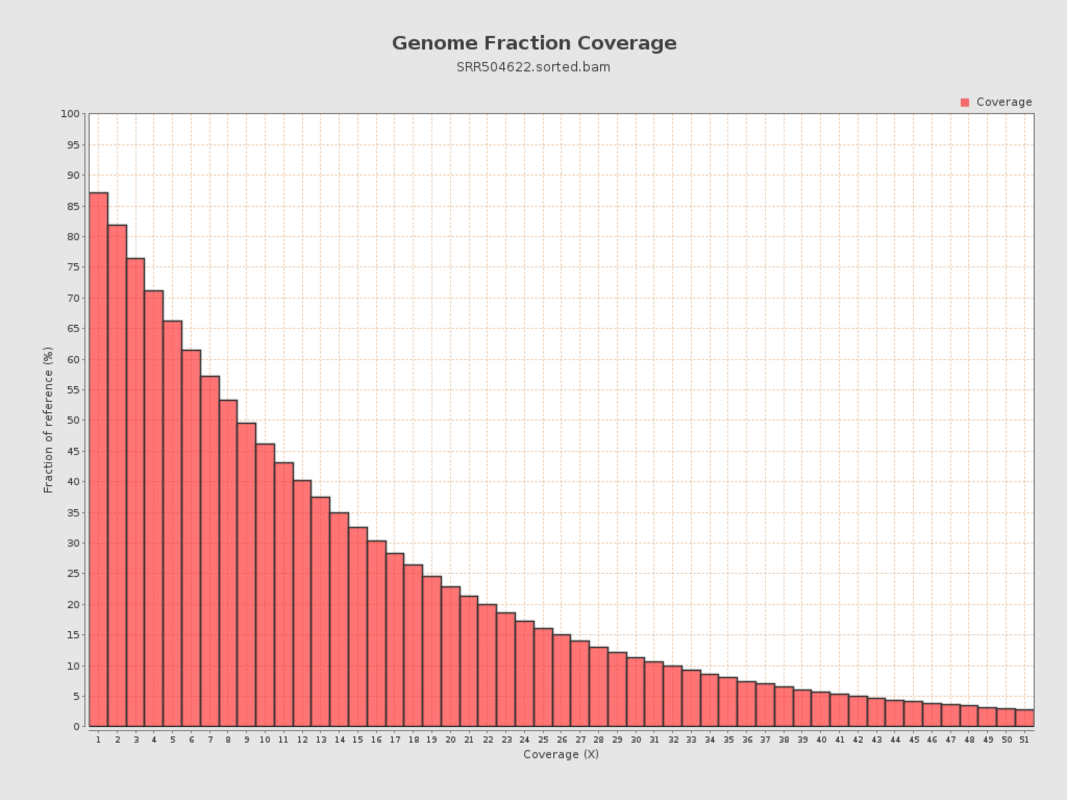
4. Results : Coverage Histogram



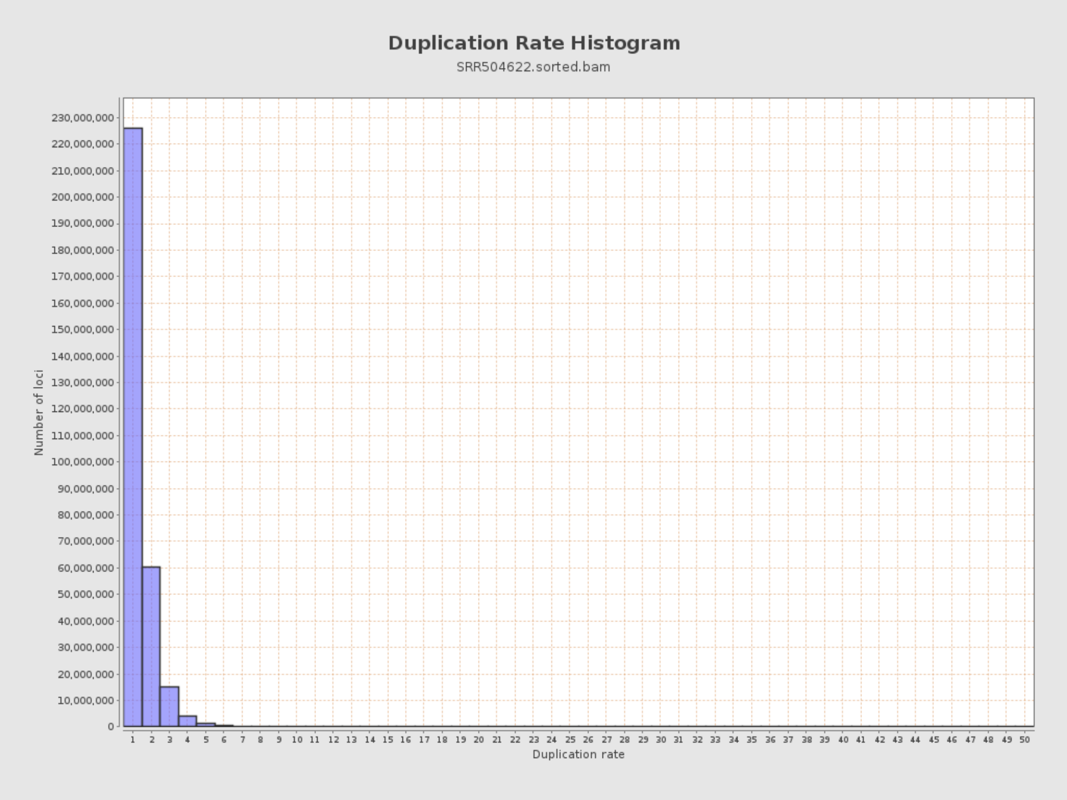
5. Results : Coverage Histogram (0-50X)



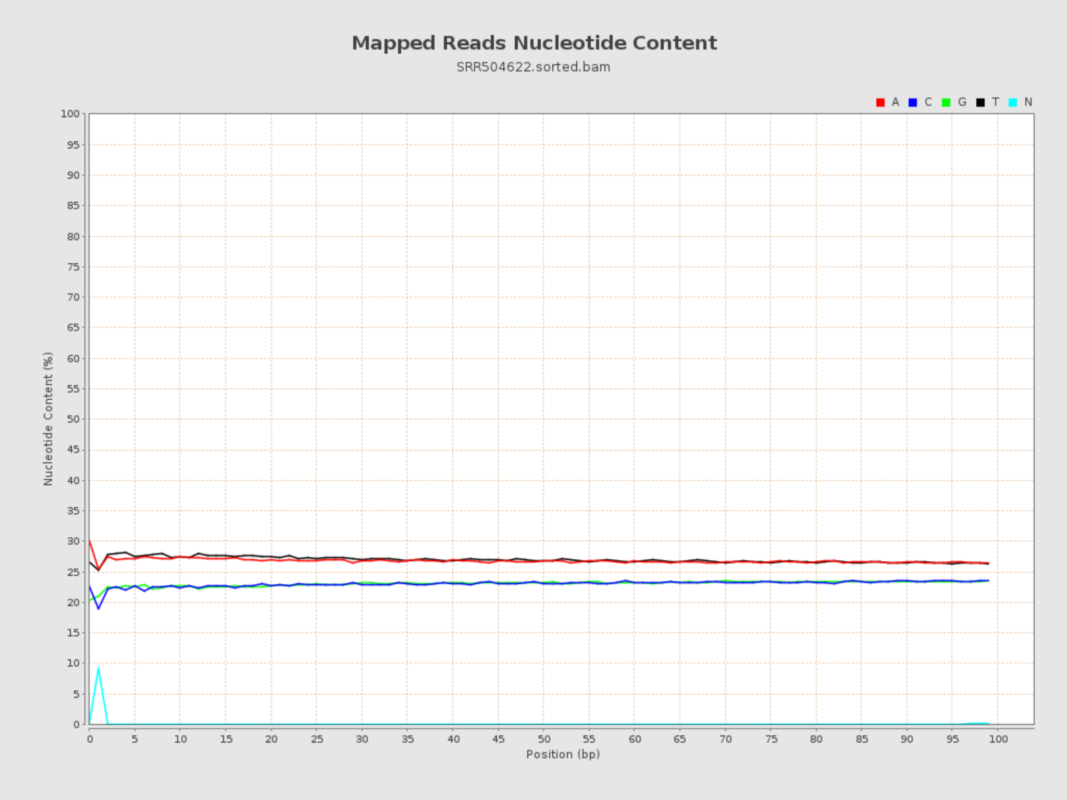
6. Results : Genome Fraction Coverage



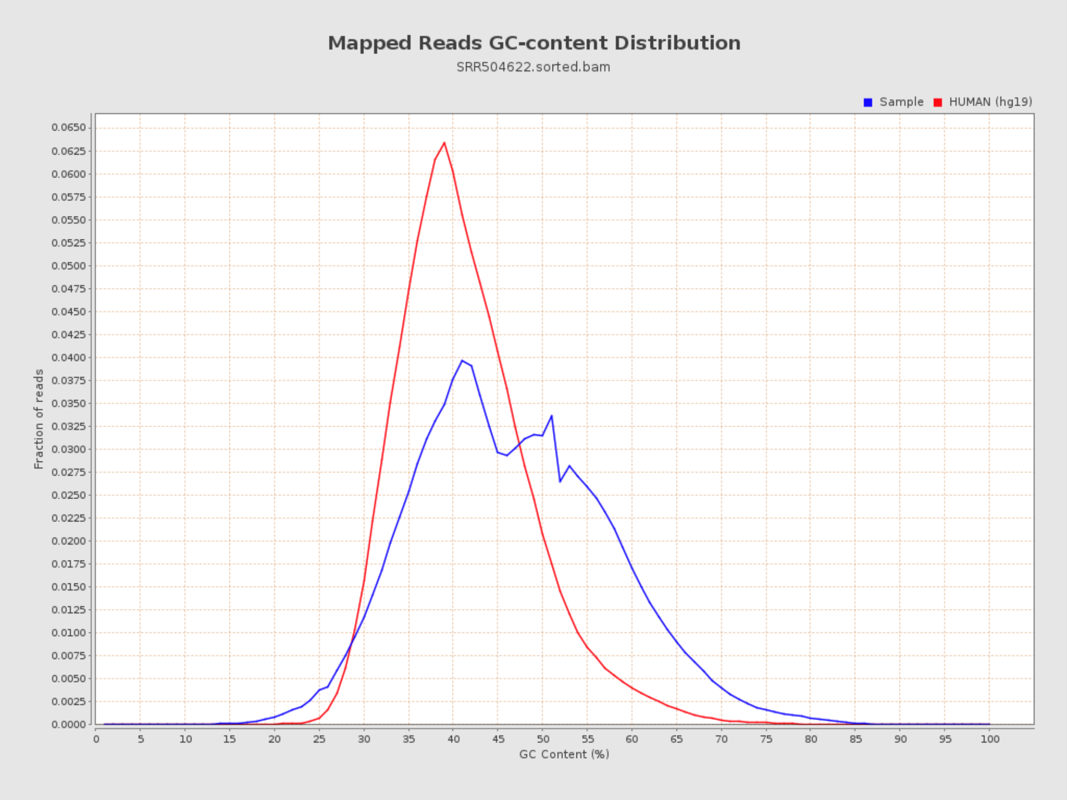
7. Results : Duplication Rate Histogram



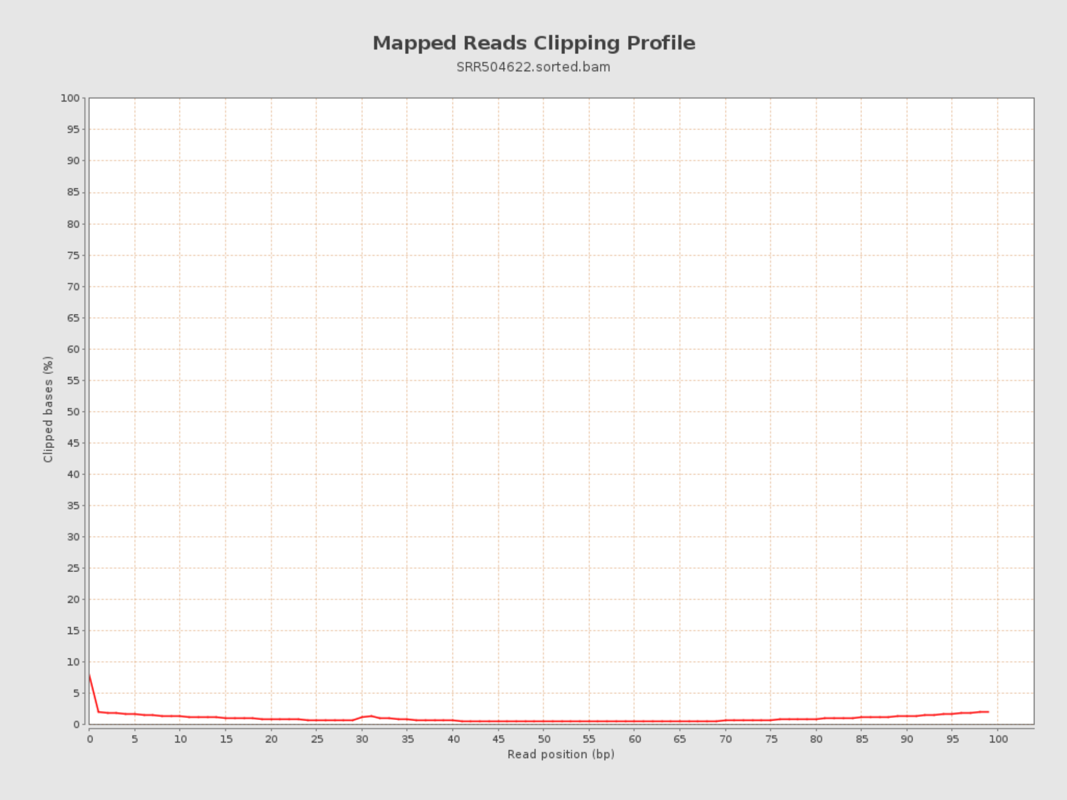
8. Results : Mapped Reads Nucleotide Content



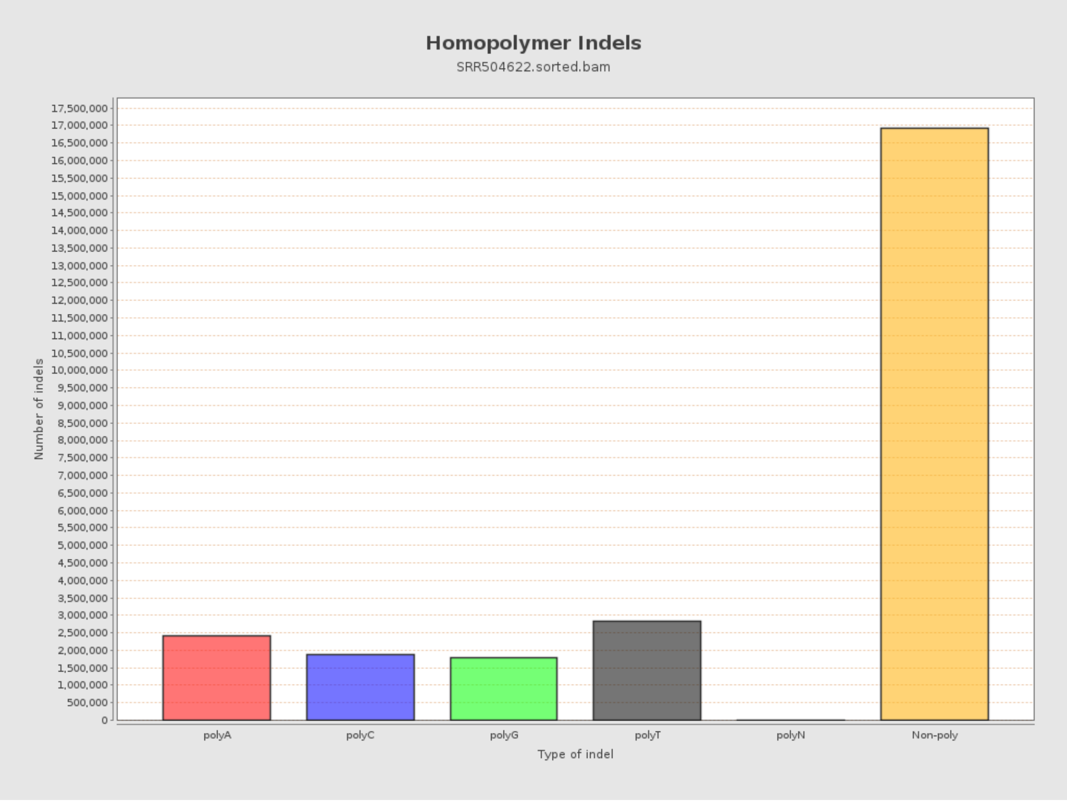
9. Results : Mapped Reads GC-content Distribution



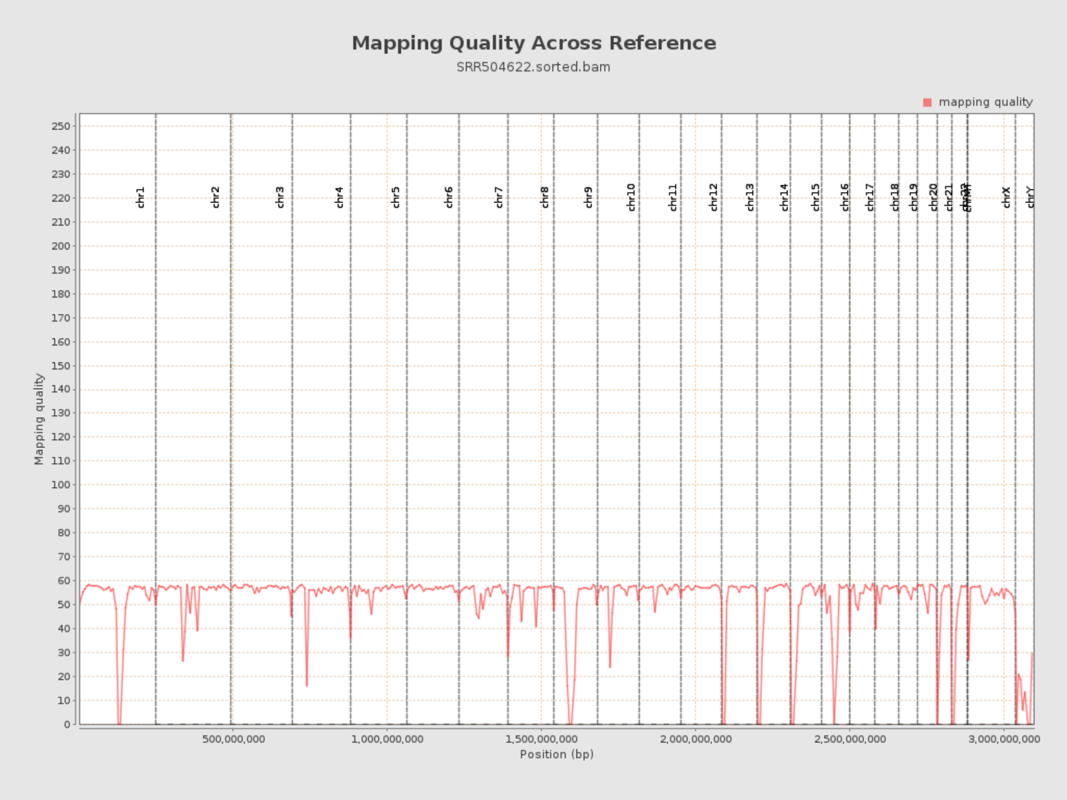
10. Results : Mapped Reads Clipping Profile



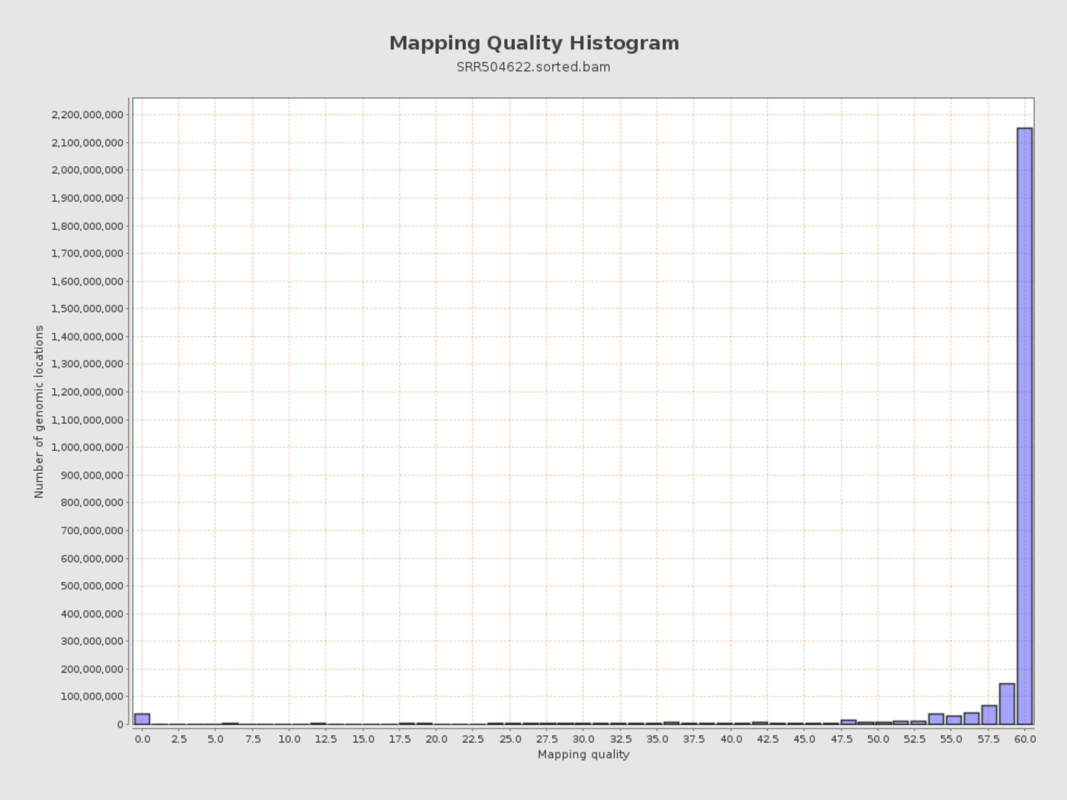
11. Results : Homopolymer Indels



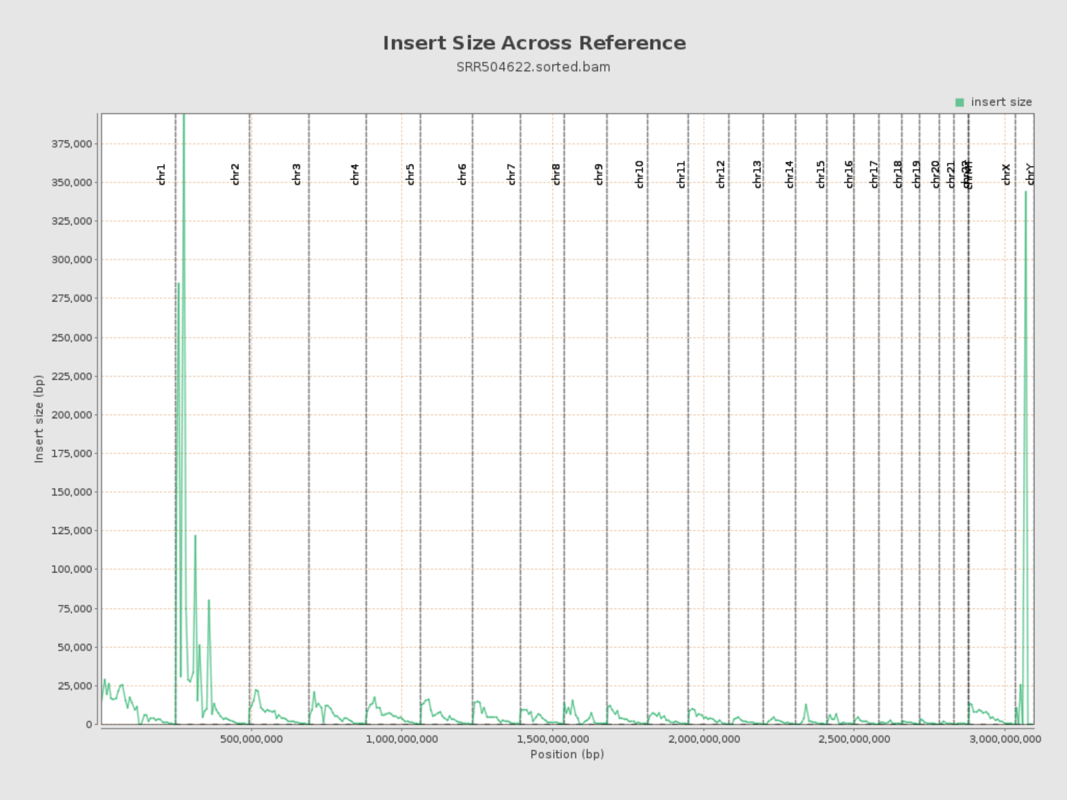
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram