Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 03:33:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264623.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_SRR1264623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264623_1.fastq.gz SRR1264623_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 03:33:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,531,466,718
Mapped reads	1,521,652,562 / 99.36%
Unmapped reads	9,814,156 / 0.64%
Mapped paired reads	1,521,652,562 / 99.36%
Mapped reads, first in pair	763,358,148 / 49.84%
Mapped reads, second in pair	758,294,414 / 49.51%
Mapped reads, both in pair	1,515,288,608 / 98.94%
Mapped reads, singletons	6,363,954 / 0.42%
Secondary alignments	0
Supplementary alignments	8,841,737 / 0.58%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	637,351,613 / 41.62%
Duplication rate	41.75%
Clipped reads	63,632,495 / 4.16%

2.2. ACGT Content

Number/percentage of A's	47,389,401,853 / 31.03%
Number/percentage of C's	28,959,583,566 / 18.96%
Number/percentage of T's	47,075,817,635 / 30.83%
Number/percentage of G's	29,261,230,478 / 19.16%
Number/percentage of N's	26,411,751 / 0.02%

GC Percentage	38.12%

2.3. Coverage

Mean	49.3419
Standard Deviation	50.153

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	68,703.18
Standard Deviation	2,516,978.88
P25/Median/P75	276 / 303 / 335

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	562,699,824
Insertions	16,822,045
Mapped reads with at least one insertion	1.09%
Deletions	15,617,909
Mapped reads with at least one deletion	1.01%
Homopolymer indels	48.66%

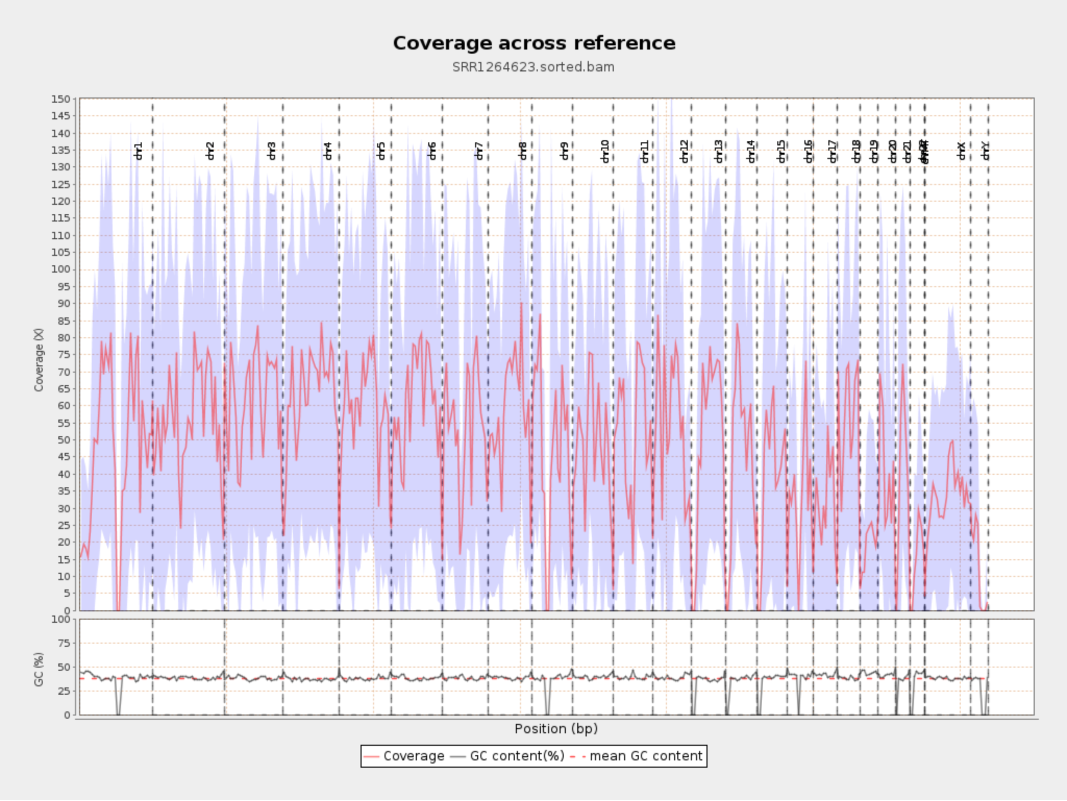
2.7. Chromosome stats

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

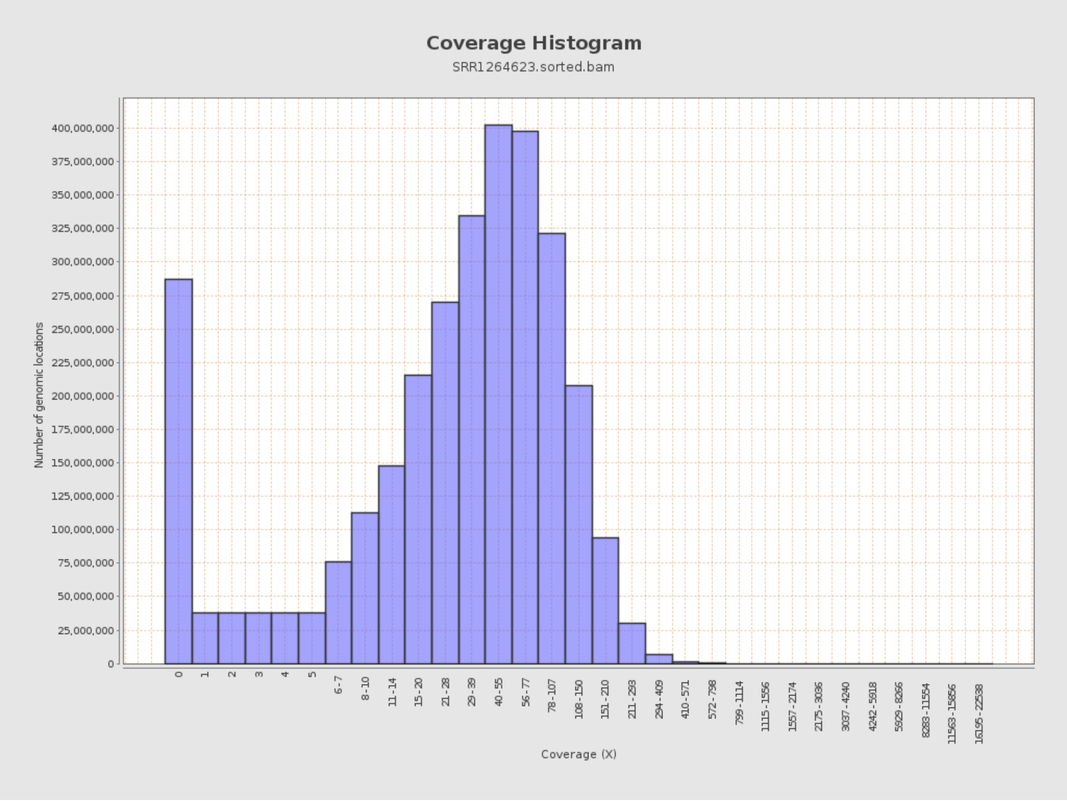
		bases	coverage	deviation
chr1	249250621	11839251300	47.4994	51.2701
chr2	243199373	13545189472	55.6958	50.3103
chr3	198022430	12216338584	61.6917	50.9726
chr4	191154276	12267642027	64.1767	50.7924
chr5	180915260	10663070404	58.9396	50.3341
chr6	171115067	10567808466	61.7585	53.163
chr7	159138663	8509816727	53.4742	51.6986
chr8	146364022	8669667233	59.2336	49.7264
chr9	141213431	6426243707	45.5073	52.3964
chr10	135534747	6643892422	49.0198	46.2161
chr11	135006516	7078253056	52.429	50.7124
chr12	133851895	7267896939	54.2981	53.6581
chr13	115169878	5944017030	51.6109	52.2004
chr14	107349540	4896109206	45.609	50.0069
chr15	102531392	4083489671	39.8267	49.1969
chr16	90354753	2853885860	31.5853	38.7786
chr17	81195210	2517898595	31.0104	40.7188
chr18	78077248	4417682955	56.5809	49.2581
chr19	59128983	1119816109	18.9385	27.407
chr20	63025520	2443821445	38.7751	50.4529
chr21	48129895	2005131025	41.6608	54.287
chr22	51304566	778675496	15.1775	26.1188
chrMT	16571	69615	4.201	7.5893
chrX	155270560	5272222506	33.9551	34.9122

chrY	59373566	719413382	12.1167	27.1426

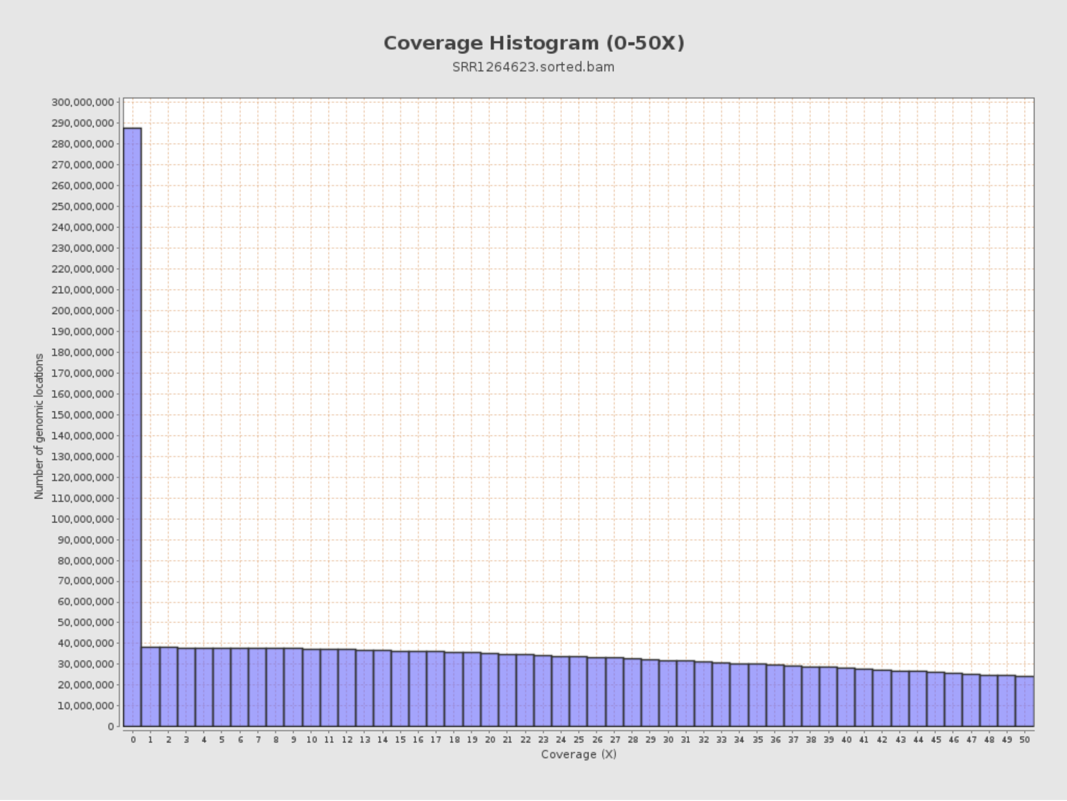
3. Results : Coverage across reference



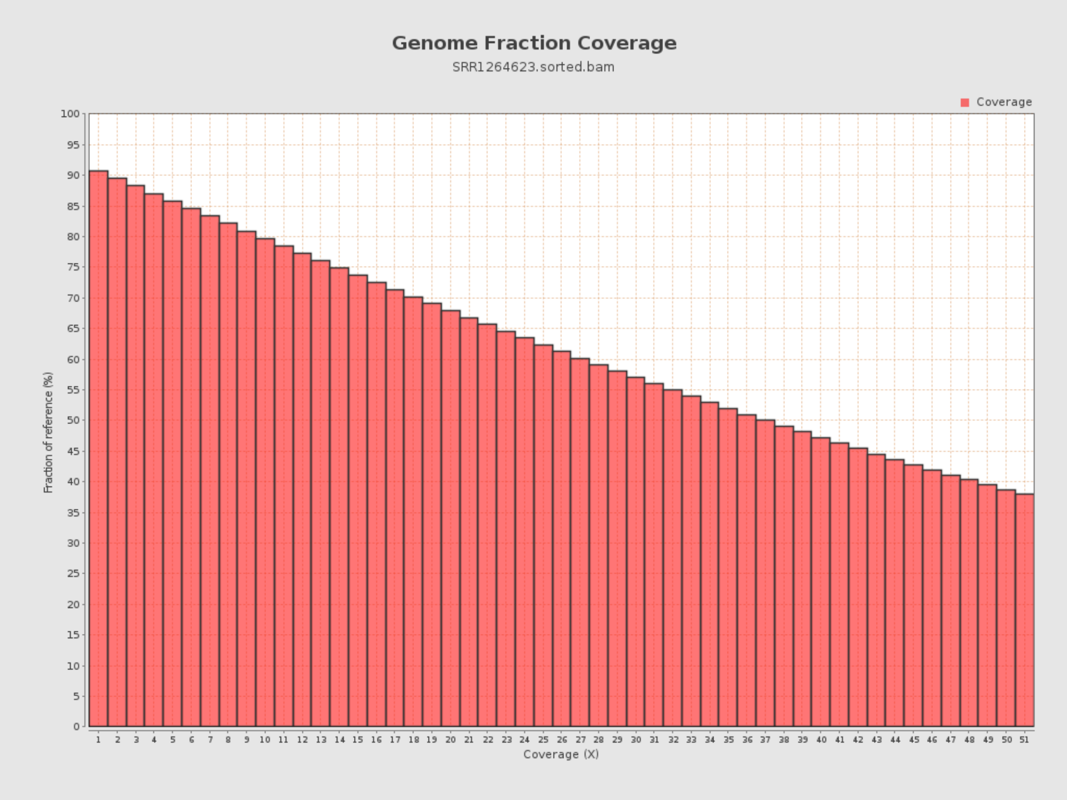
4. Results : Coverage Histogram



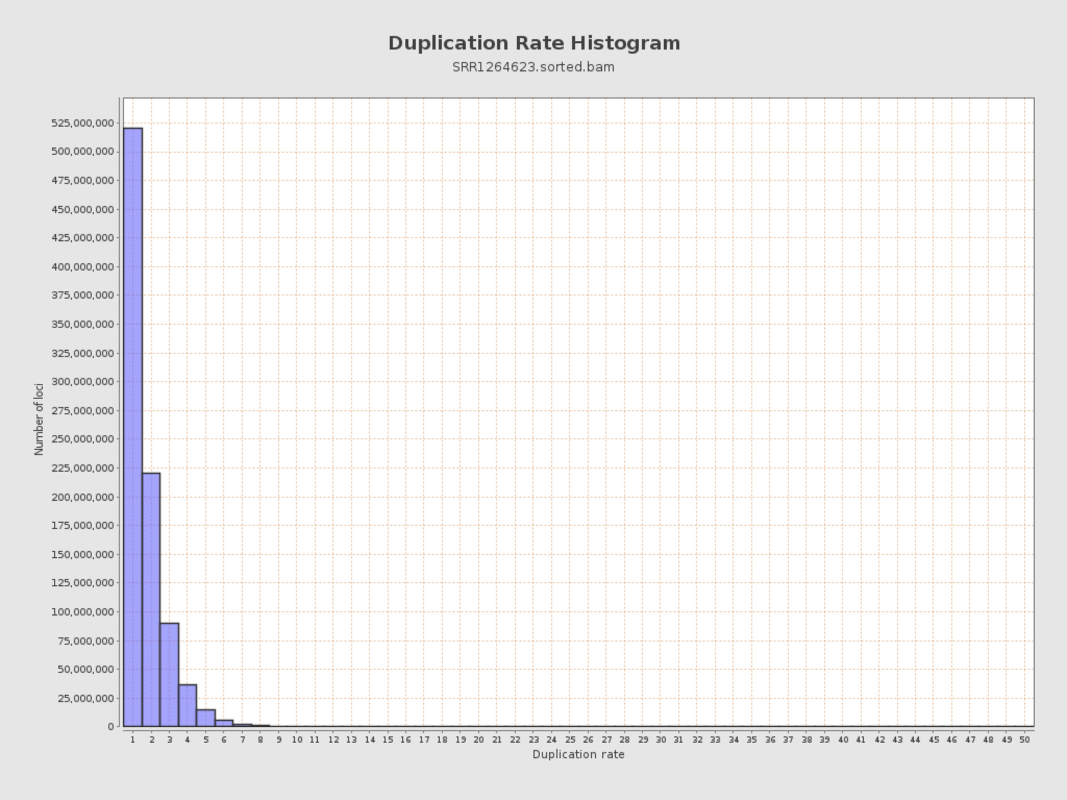
5. Results : Coverage Histogram (0-50X)



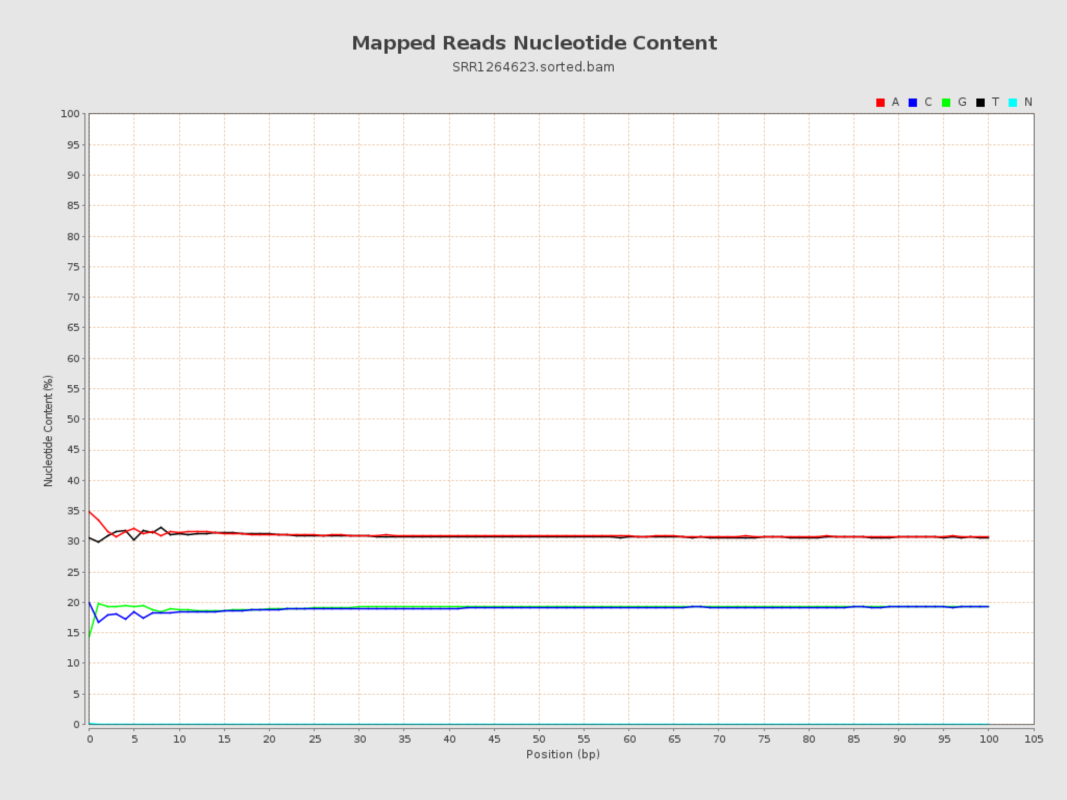
6. Results : Genome Fraction Coverage



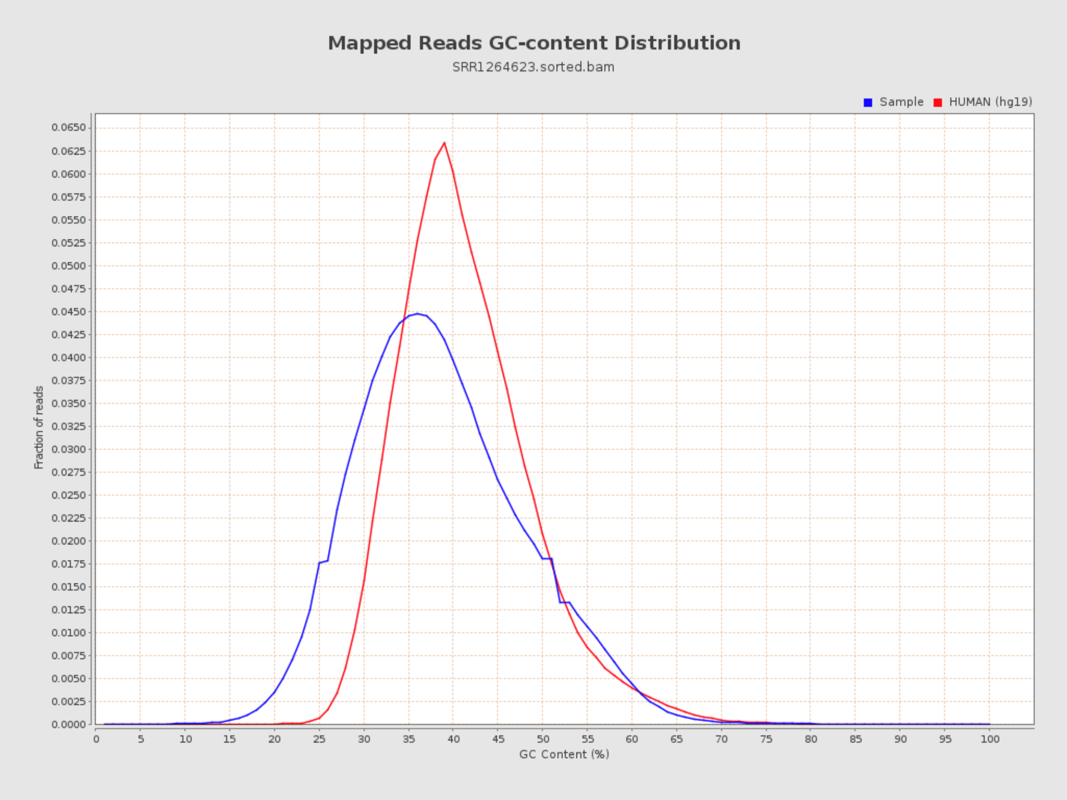
7. Results : Duplication Rate Histogram



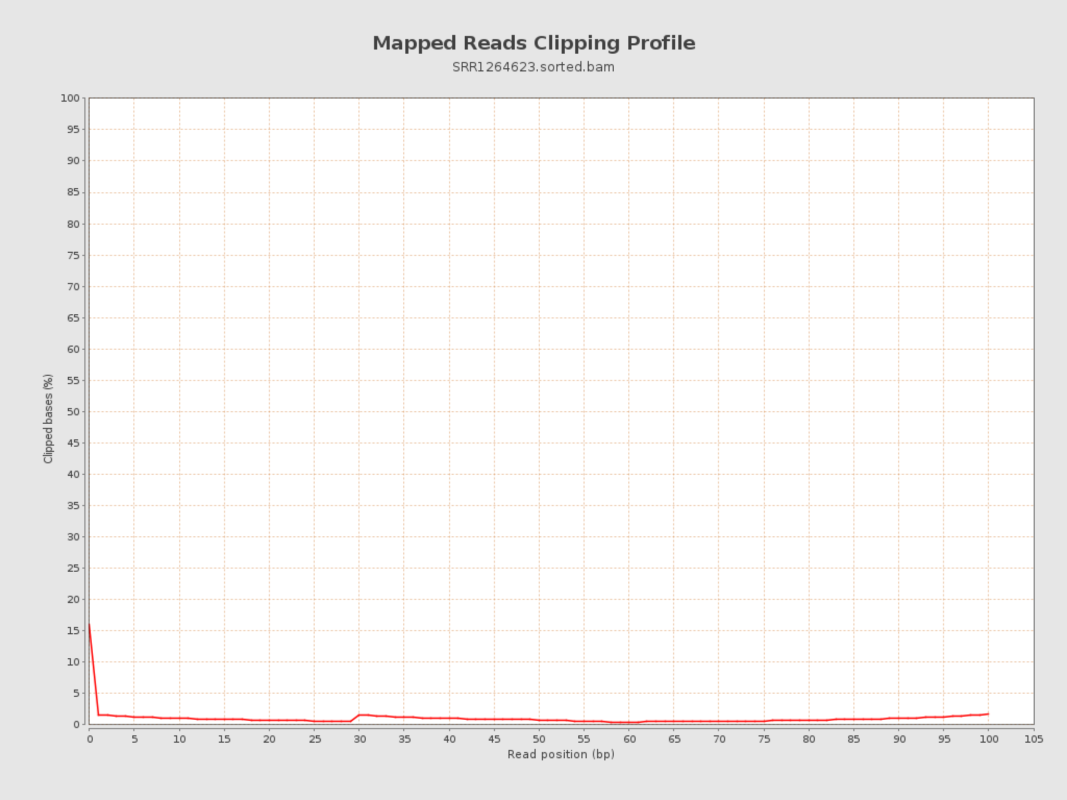
8. Results : Mapped Reads Nucleotide Content



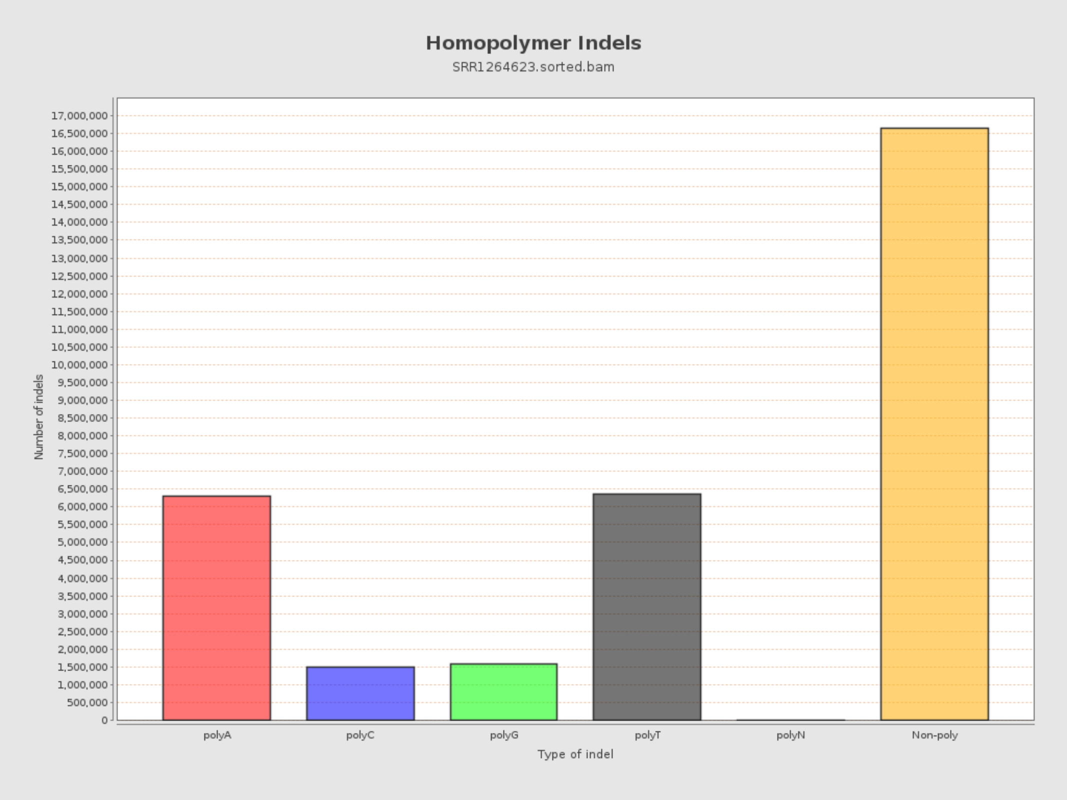
9. Results : Mapped Reads GC-content Distribution



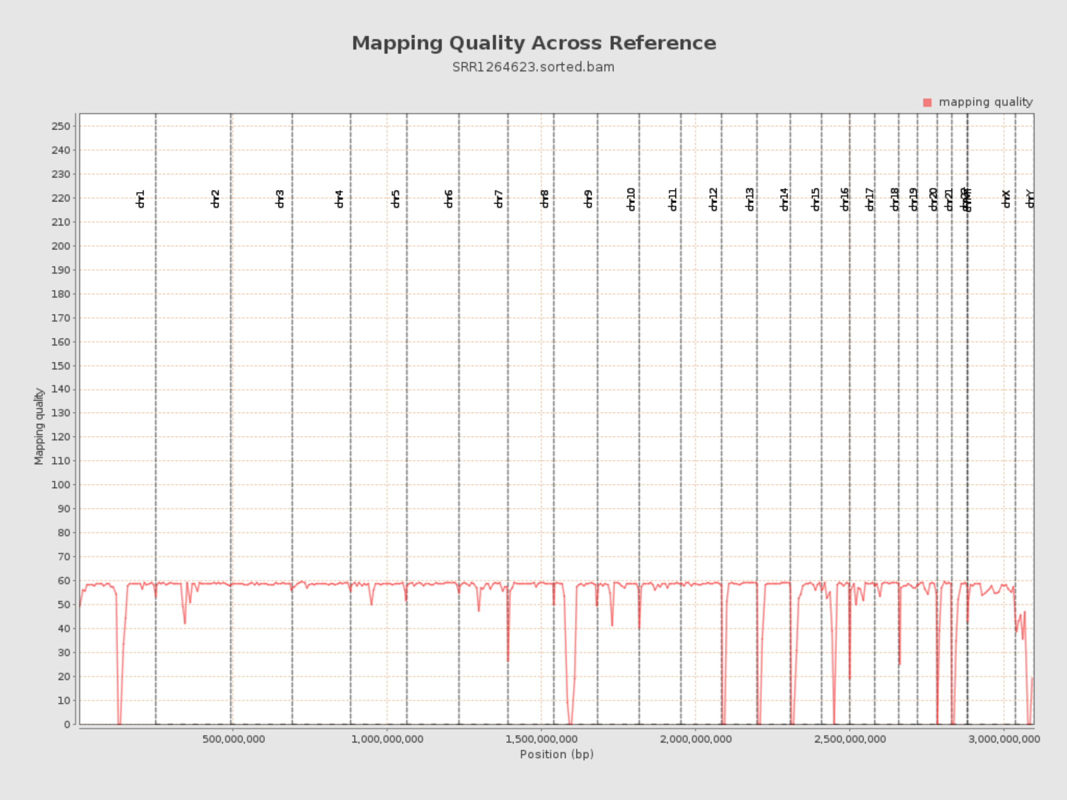
10. Results : Mapped Reads Clipping Profile



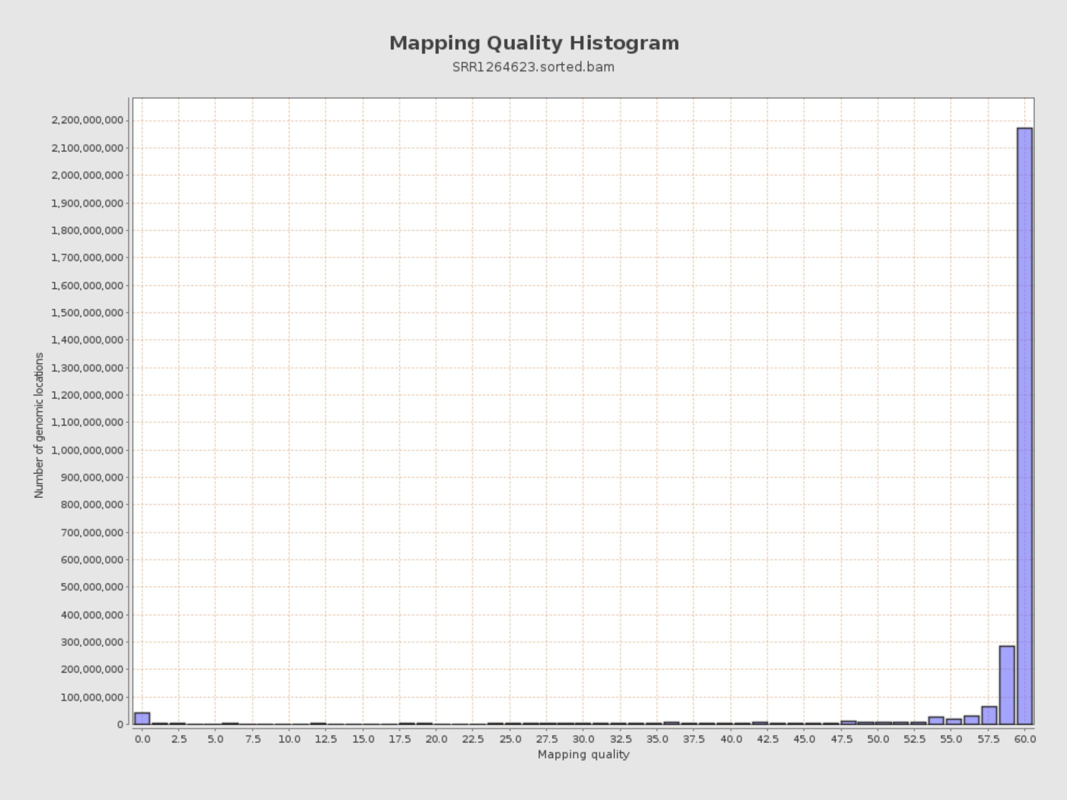
11. Results : Homopolymer Indels



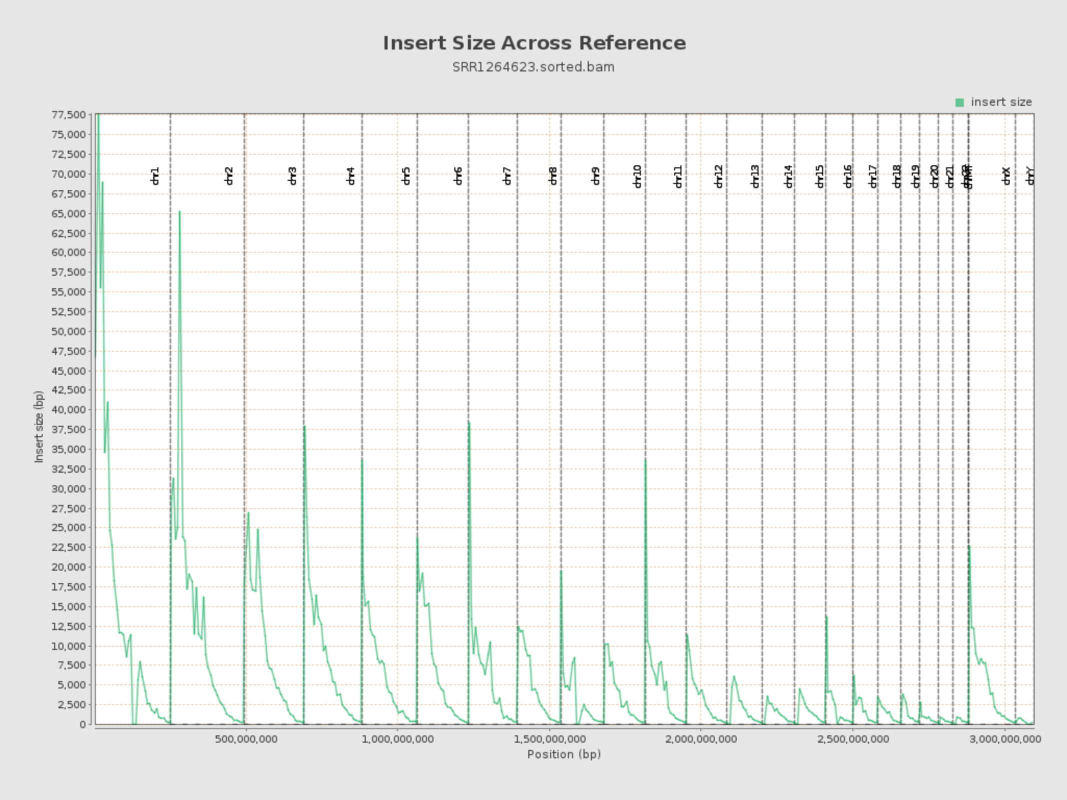
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram