Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 10:53:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438274.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_SRR8438274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438274_1.fastq.gz SRR8438274_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 10:53:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,267,395,646
Mapped reads	1,262,524,562 / 99.62%
Unmapped reads	4,871,084 / 0.38%
Mapped paired reads	1,262,524,562 / 99.62%
Mapped reads, first in pair	631,626,773 / 49.84%
Mapped reads, second in pair	630,897,789 / 49.78%
Mapped reads, both in pair	1,260,226,342 / 99.43%
Mapped reads, singletons	2,298,220 / 0.18%
Secondary alignments	0
Supplementary alignments	20,618,781 / 1.63%
Read min/max/mean length	30 / 149 / 115.21
Duplicated reads (estimated)	598,008,774 / 47.18%
Duplication rate	44.98%
Clipped reads	247,512,125 / 19.53%

2.2. ACGT Content

Number/percentage of A's	42,837,673,681 / 30.58%
Number/percentage of C's	27,398,255,971 / 19.56%
Number/percentage of T's	41,803,429,775 / 29.84%
Number/percentage of G's	28,043,157,537 / 20.02%
Number/percentage of N's	384,519 / 0%

GC Percentage	39.58%

2.3. Coverage

Mean	45.2616
Standard Deviation	597.6107

2.4. Mapping Quality

Mean Mapping Quality	53.12

2.5. Insert size

Mean	151,572.9
Standard Deviation	3,935,033.09
P25/Median/P75	77 / 125 / 202

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	448,142,150
Insertions	19,942,669
Mapped reads with at least one insertion	1.56%
Deletions	13,979,418
Mapped reads with at least one deletion	1.1%
Homopolymer indels	47.64%

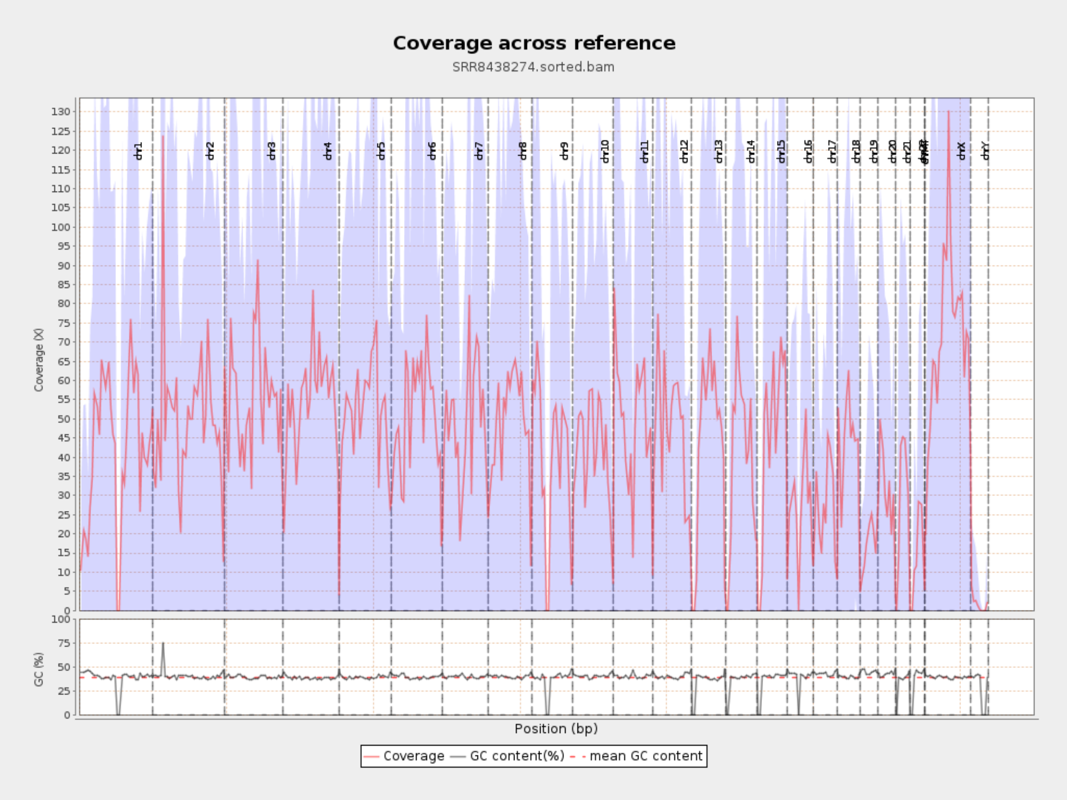
2.7. Chromosome stats

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

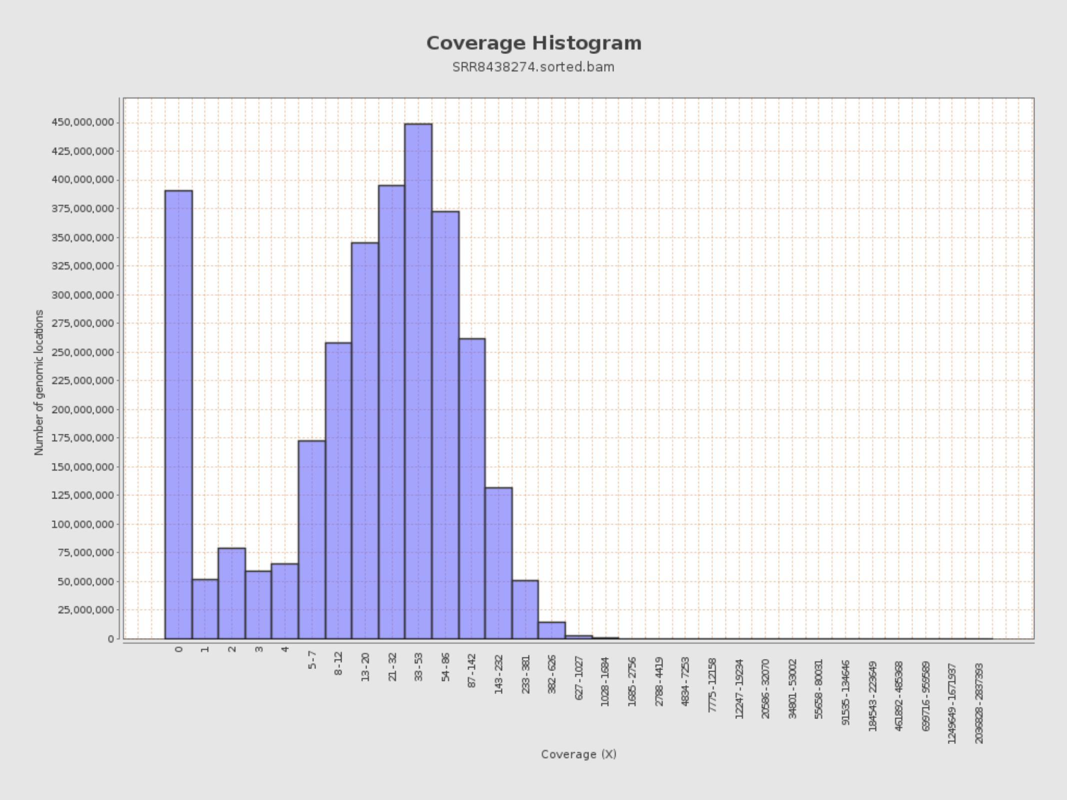
		bases	coverage	deviation
chr1	249250621	10537486520	42.2767	63.7624
chr2	243199373	12230846068	50.2914	2,120.271
chr3	198022430	10954296753	55.3185	71.2631
chr4	191154276	10529897459	55.0859	67.9485
chr5	180915260	9273247171	51.2574	64.5891
chr6	171115067	8792775015	51.3852	67.3526
chr7	159138663	7683231245	48.2801	67.3498
chr8	146364022	7289613781	49.8047	63.6083
chr9	141213431	5495516940	38.9164	59.792
chr10	135534747	5681002402	41.9155	57.4535
chr11	135006516	6692752156	49.5735	70.6807
chr12	133851895	6305179144	47.1056	64.181
chr13	115169878	5204044541	45.1858	62.6492
chr14	107349540	4320810539	40.2499	60.5753
chr15	102531392	4601070887	44.8748	70.927
chr16	90354753	2374779822	26.2828	45.4259
chr17	81195210	2182234613	26.8764	46.0827
chr18	78077248	3504265614	44.882	54.6438
chr19	59128983	991291895	16.7649	32.4244
chr20	63025520	1975857372	31.3501	49.1571
chr21	48129895	1453089273	30.191	52.8891
chr22	51304566	709135086	13.8221	34.9599
chrMT	16571	334876	20.2086	9.12
chrX	155270560	11233752468	72.3495	98.0832

chrY	59373566	99429540	1.6746	11.1945

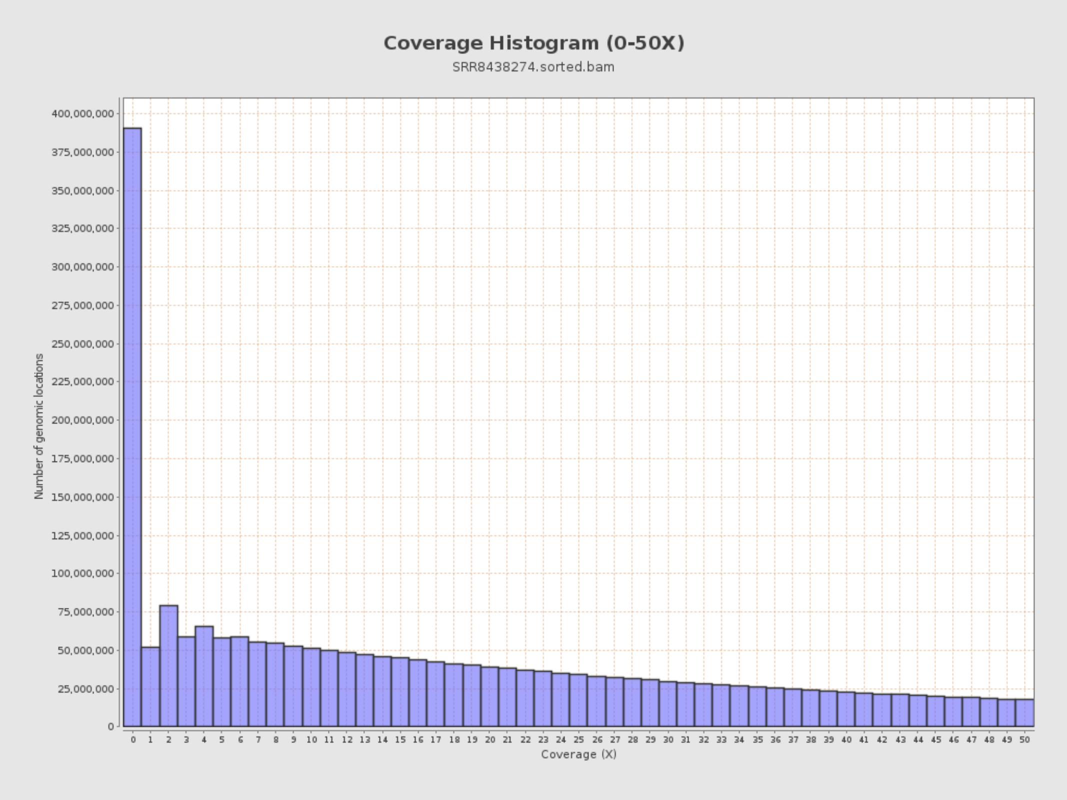
3. Results : Coverage across reference



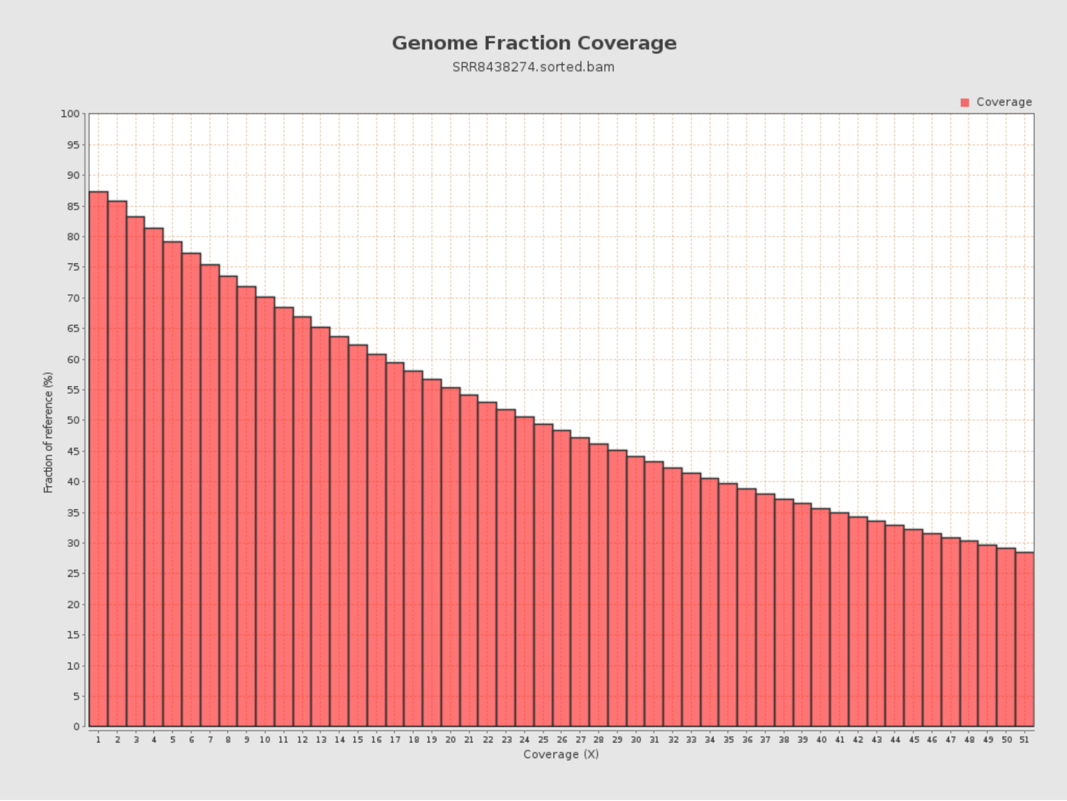
4. Results : Coverage Histogram



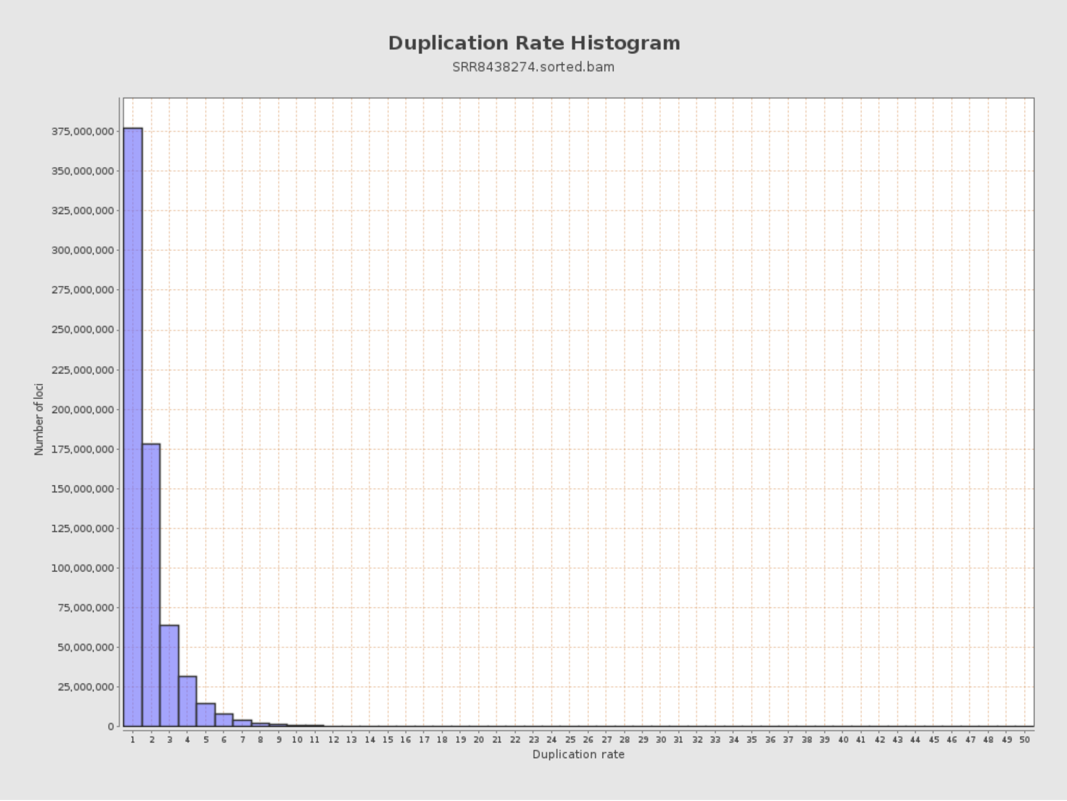
5. Results : Coverage Histogram (0-50X)



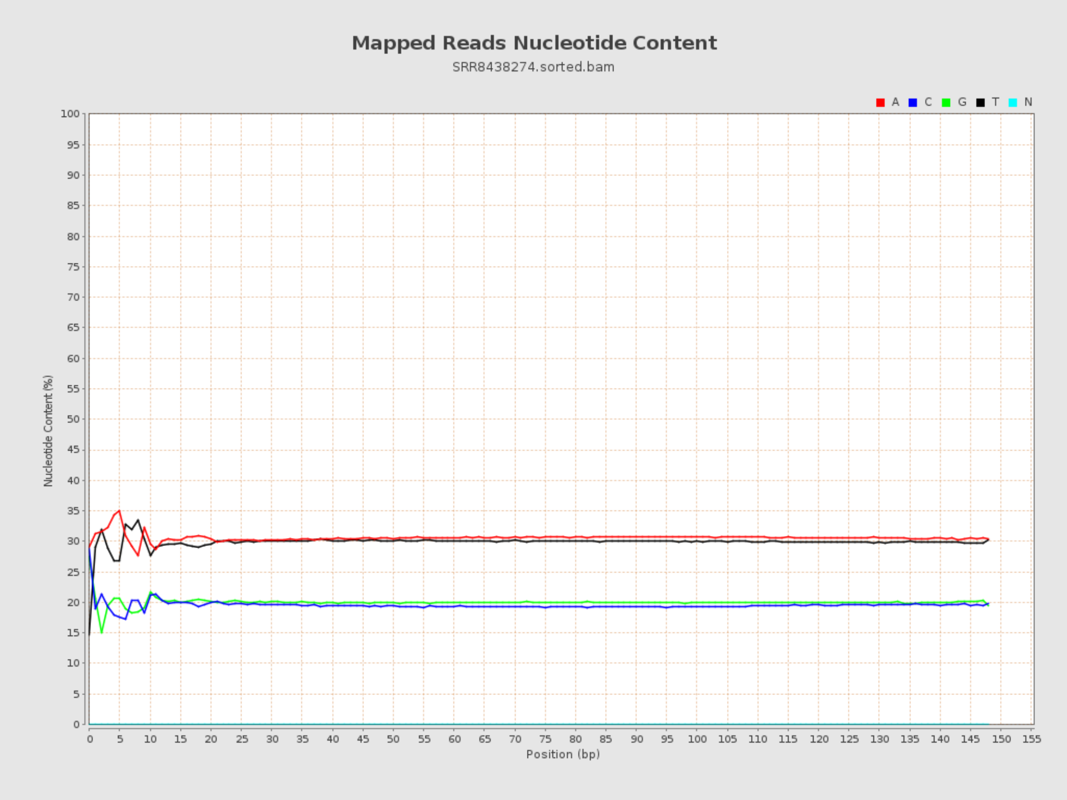
6. Results : Genome Fraction Coverage



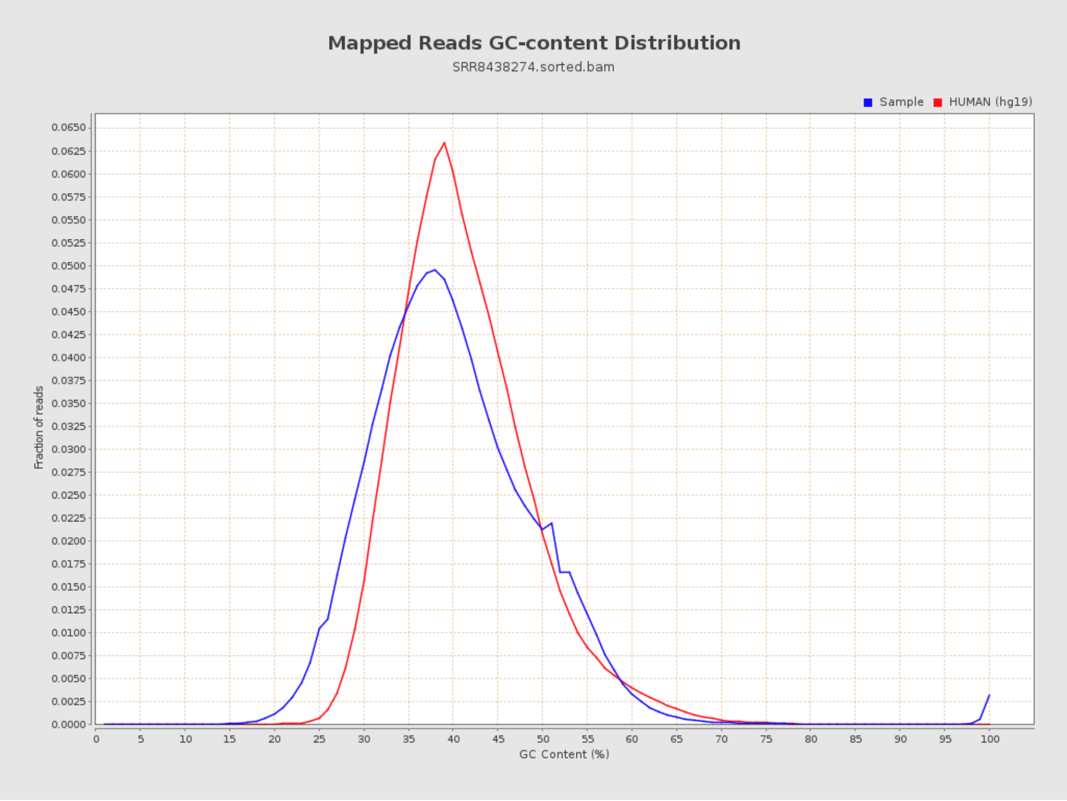
7. Results : Duplication Rate Histogram



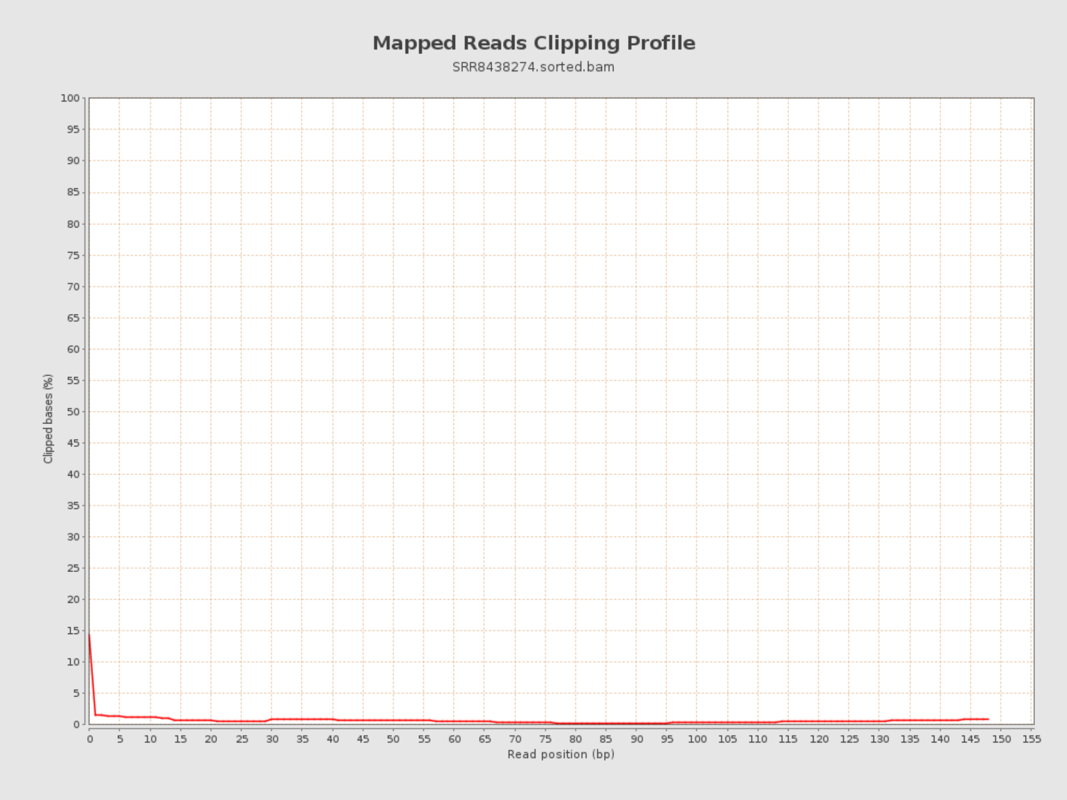
8. Results : Mapped Reads Nucleotide Content



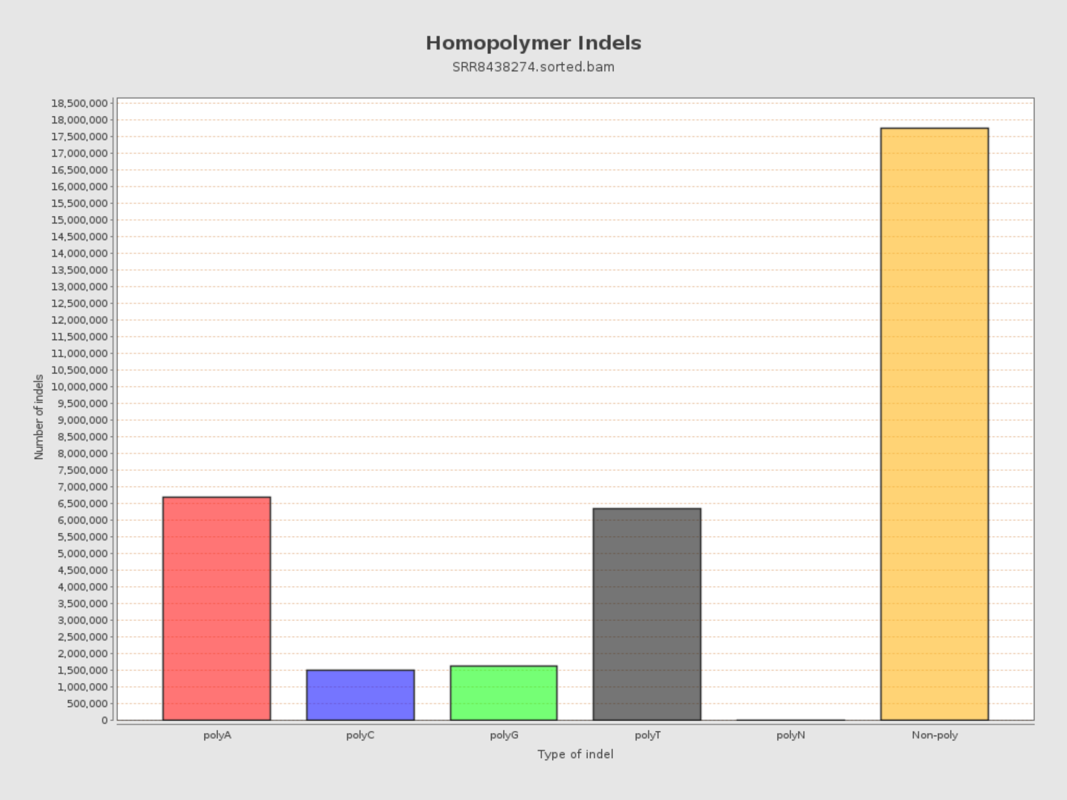
9. Results : Mapped Reads GC-content Distribution



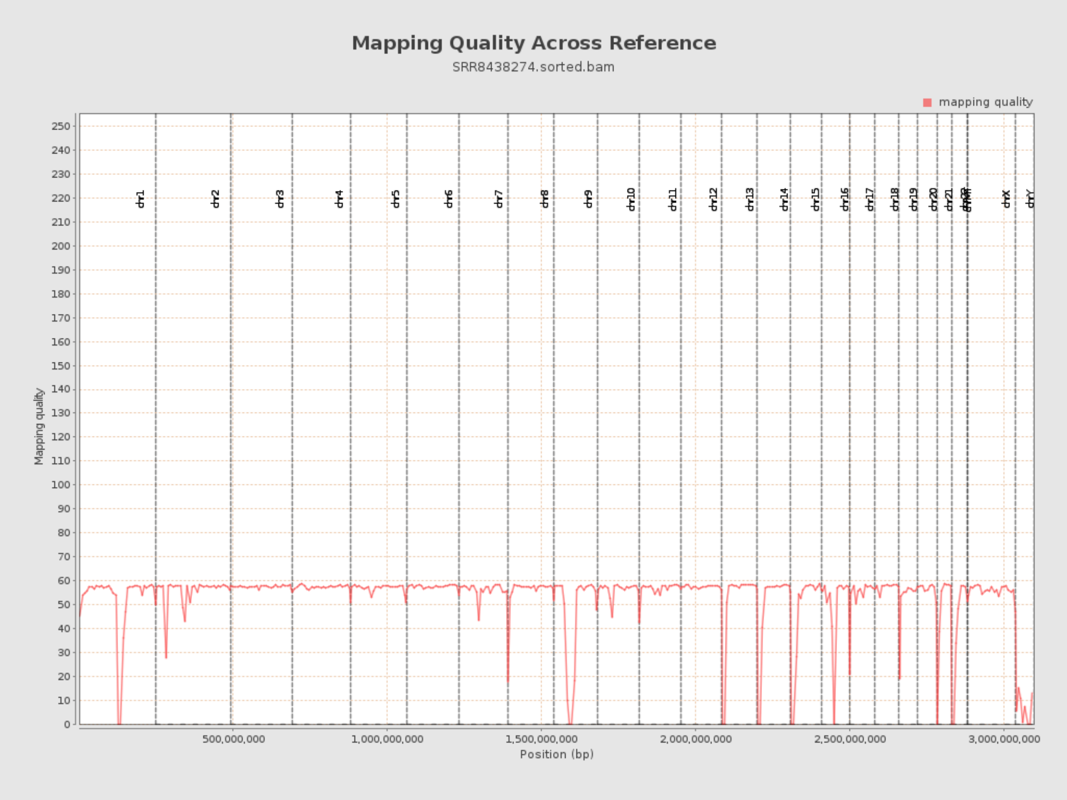
10. Results : Mapped Reads Clipping Profile



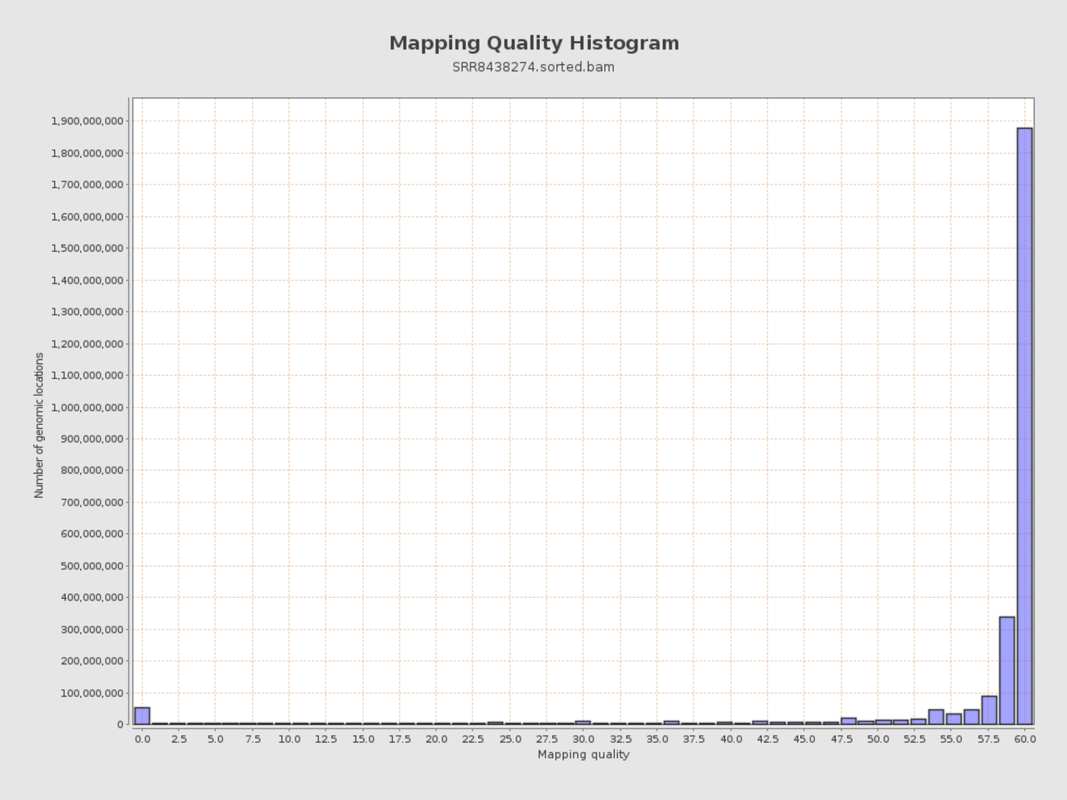
11. Results : Homopolymer Indels



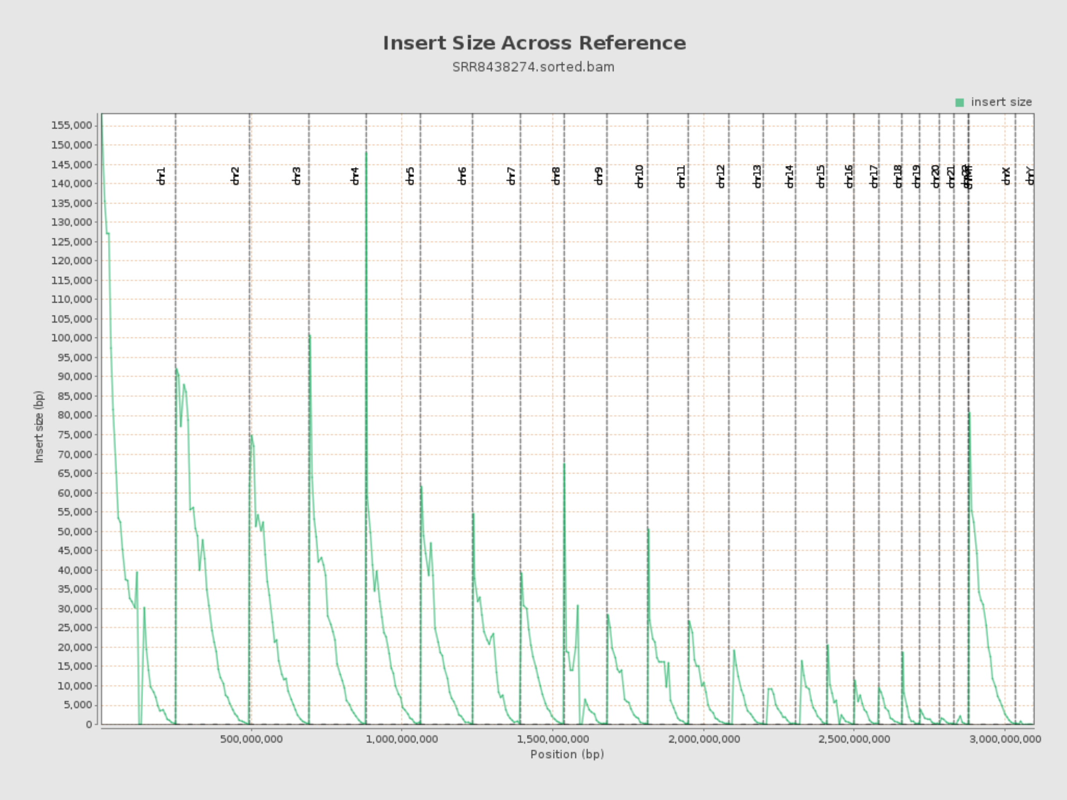
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram