Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 02:36:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038424.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_SRR5038424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038424_1.fastq.gz SRR5038424_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 02:36:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,407,816
Mapped reads	10,683,054 / 93.65%
Unmapped reads	724,762 / 6.35%
Mapped paired reads	10,683,054 / 93.65%
Mapped reads, first in pair	5,415,814 / 47.47%
Mapped reads, second in pair	5,267,240 / 46.17%
Mapped reads, both in pair	10,514,564 / 92.17%
Mapped reads, singletons	168,490 / 1.48%
Secondary alignments	0
Supplementary alignments	209,851 / 1.84%
Read min/max/mean length	30 / 150 / 150.94
Duplicated reads (estimated)	1,454,214 / 12.75%
Duplication rate	8.05%
Clipped reads	2,684,606 / 23.53%

2.2. ACGT Content

Number/percentage of A's	440,750,620 / 28.98%
Number/percentage of C's	312,787,717 / 20.57%
Number/percentage of T's	441,641,840 / 29.04%
Number/percentage of G's	325,457,700 / 21.4%
Number/percentage of N's	30,862 / 0%

GC Percentage	41.97%

2.3. Coverage

Mean	0.4916
Standard Deviation	7.2575

2.4. Mapping Quality

Mean Mapping Quality	53.77

2.5. Insert size

Mean	99,087.17
Standard Deviation	2,995,498.37
P25/Median/P75	224 / 264 / 316

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	21,682,258
Insertions	281,567
Mapped reads with at least one insertion	2.45%
Deletions	530,386
Mapped reads with at least one deletion	4.74%
Homopolymer indels	45.77%

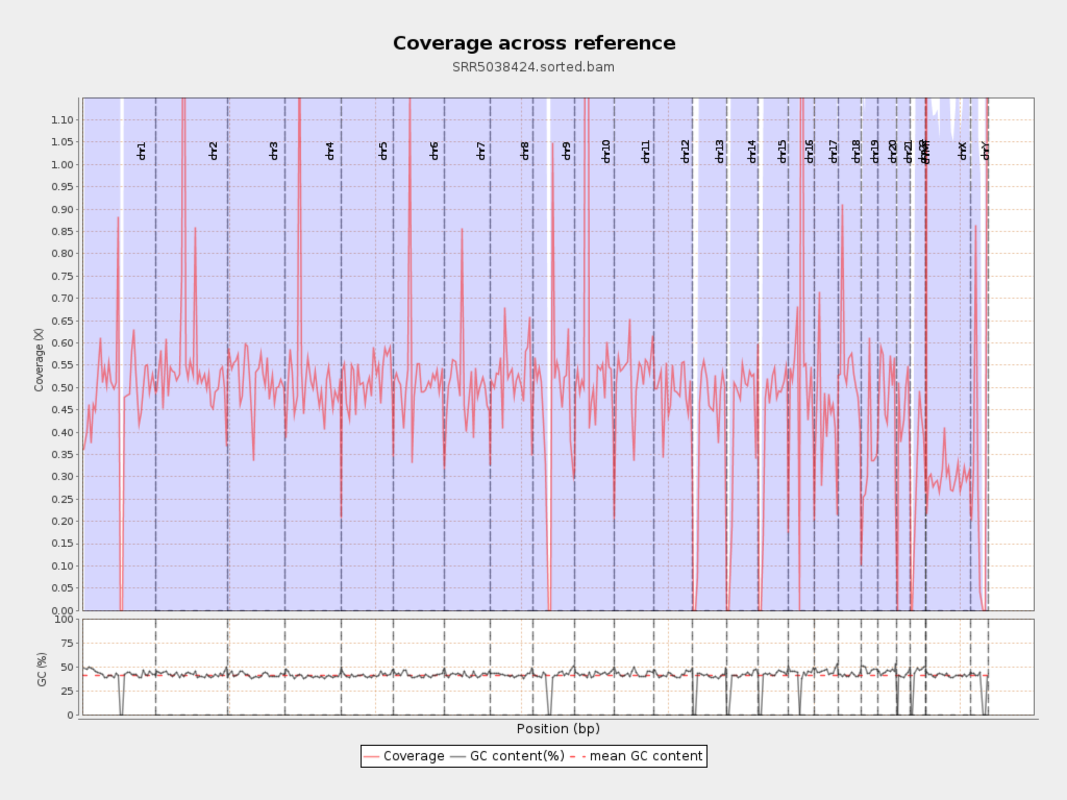
2.7. Chromosome stats

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

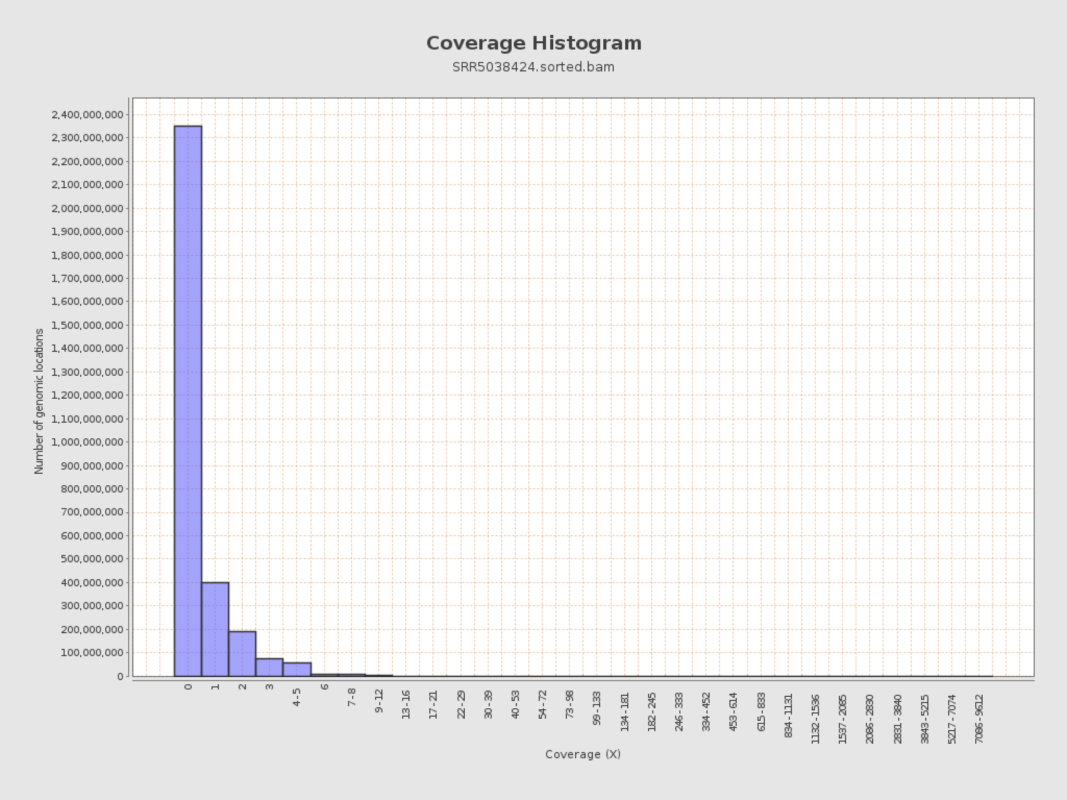
		bases	coverage	deviation
chr1	249250621	119396752	0.479	6.7593
chr2	243199373	140253476	0.5767	8.1961
chr3	198022430	102761082	0.5189	1.1982
chr4	191154276	101722787	0.5322	6.0762
chr5	180915260	93582410	0.5173	1.259
chr6	171115067	90690697	0.53	7.3542
chr7	159138663	79988812	0.5026	6.5225
chr8	146364022	77170254	0.5272	1.9423
chr9	141213431	65611952	0.4646	12.4249
chr10	135534747	87231327	0.6436	19.6736
chr11	135006516	71129434	0.5269	3.8018
chr12	133851895	65552837	0.4897	1.1433
chr13	115169878	46588536	0.4045	0.9975
chr14	107349540	44402778	0.4136	1.166
chr15	102531392	41870583	0.4084	1.0127
chr16	90354753	57601200	0.6375	13.0818
chr17	81195210	35895435	0.4421	4.6228
chr18	78077248	43561960	0.5579	10.3398
chr19	59128983	20035221	0.3388	3.5554
chr20	63025520	31788326	0.5044	2.0761
chr21	48129895	19801034	0.4114	2.9262
chr22	51304566	14637456	0.2853	1.0162
chrMT	16571	1637860	98.8389	42.3284
chrX	155270560	46151105	0.2972	1.2965

chrY	59373566	22752299	0.3832	10.7567

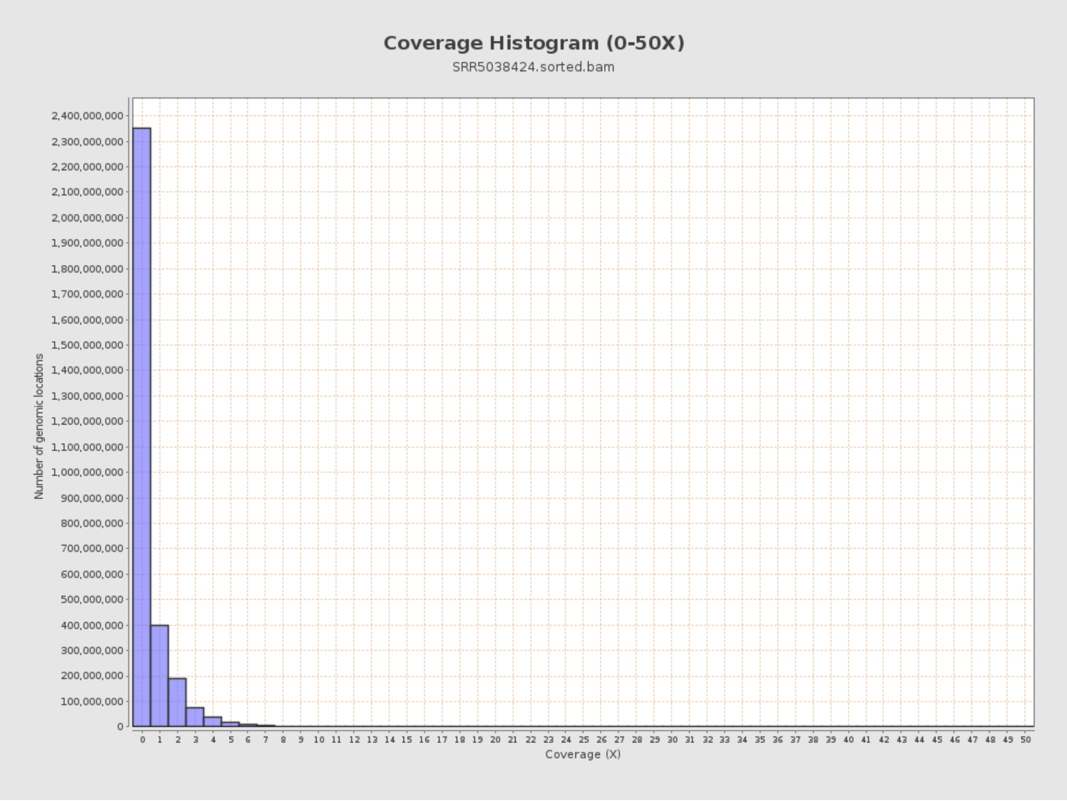
3. Results : Coverage across reference



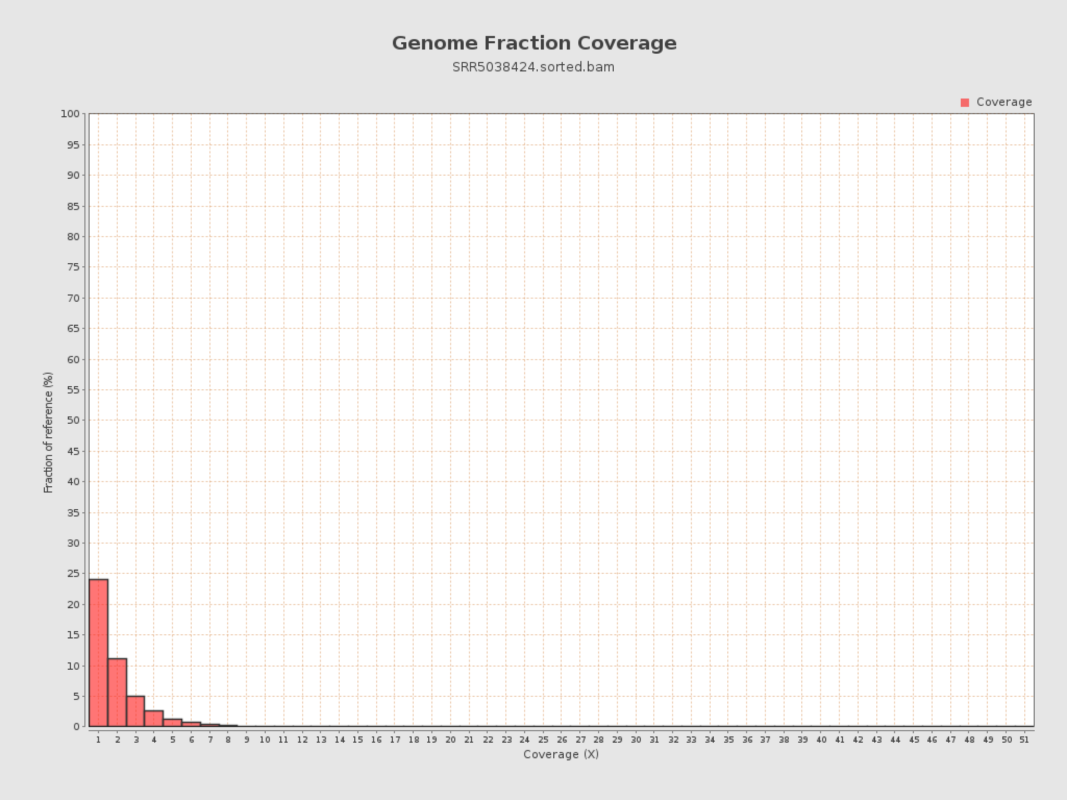
4. Results : Coverage Histogram



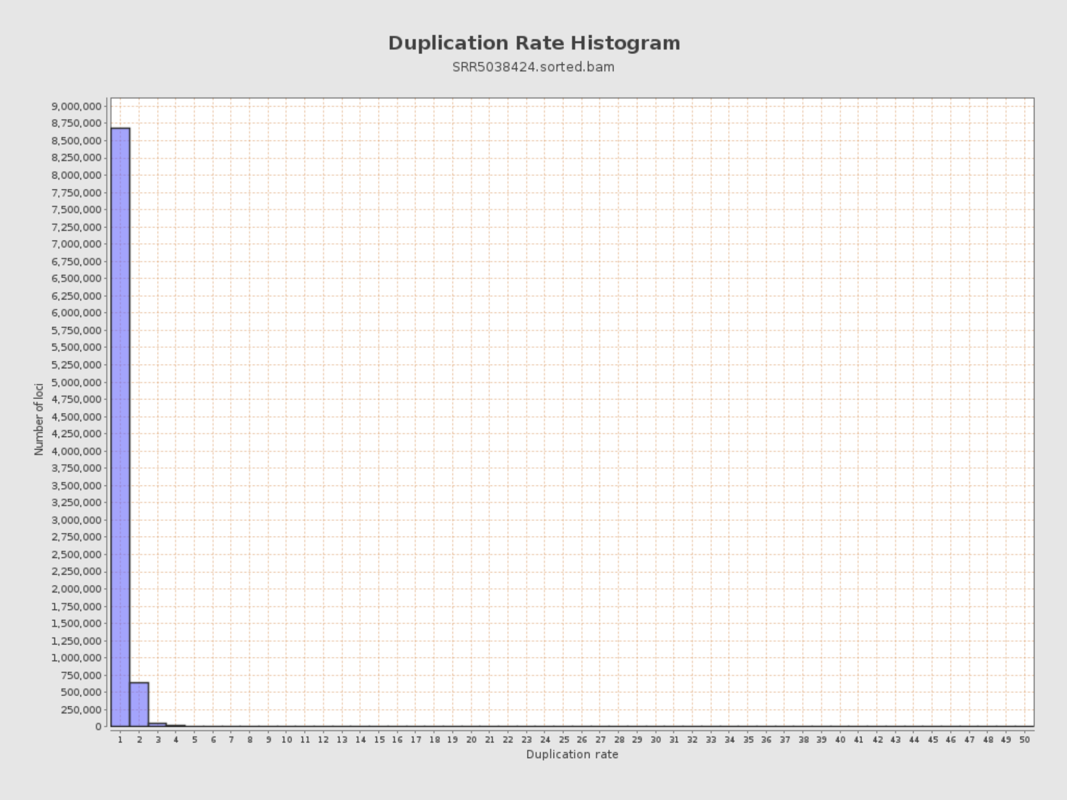
5. Results : Coverage Histogram (0-50X)



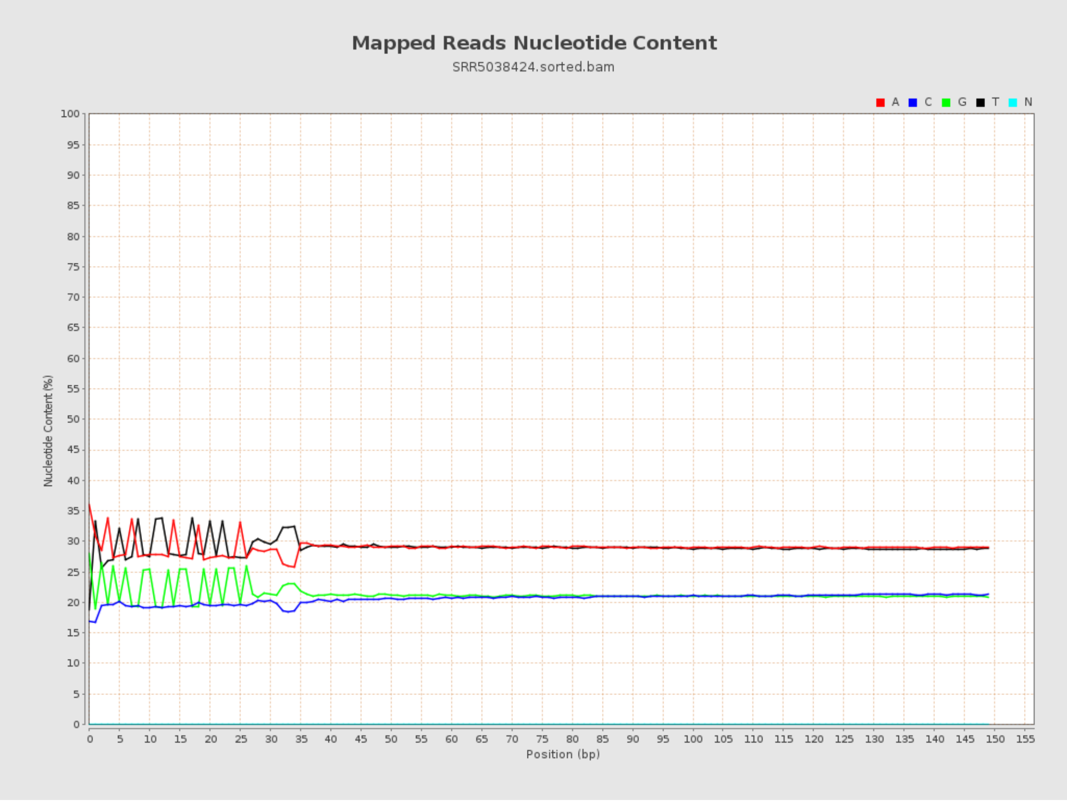
6. Results : Genome Fraction Coverage



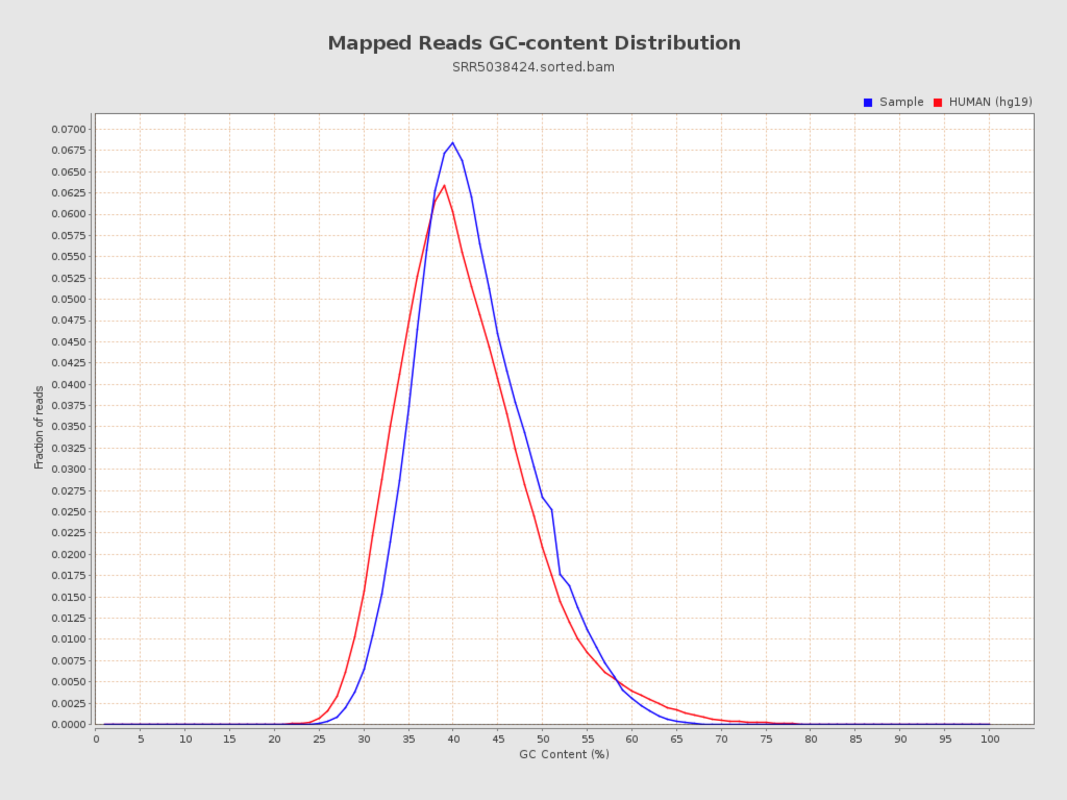
7. Results : Duplication Rate Histogram



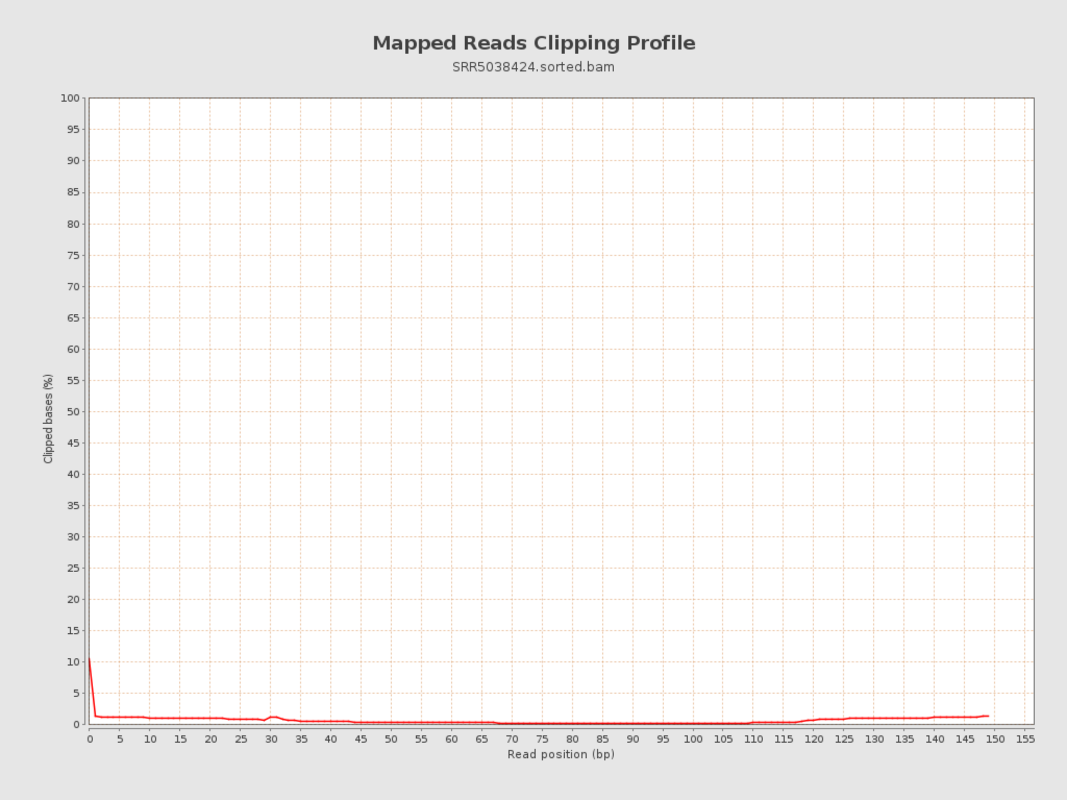
8. Results : Mapped Reads Nucleotide Content



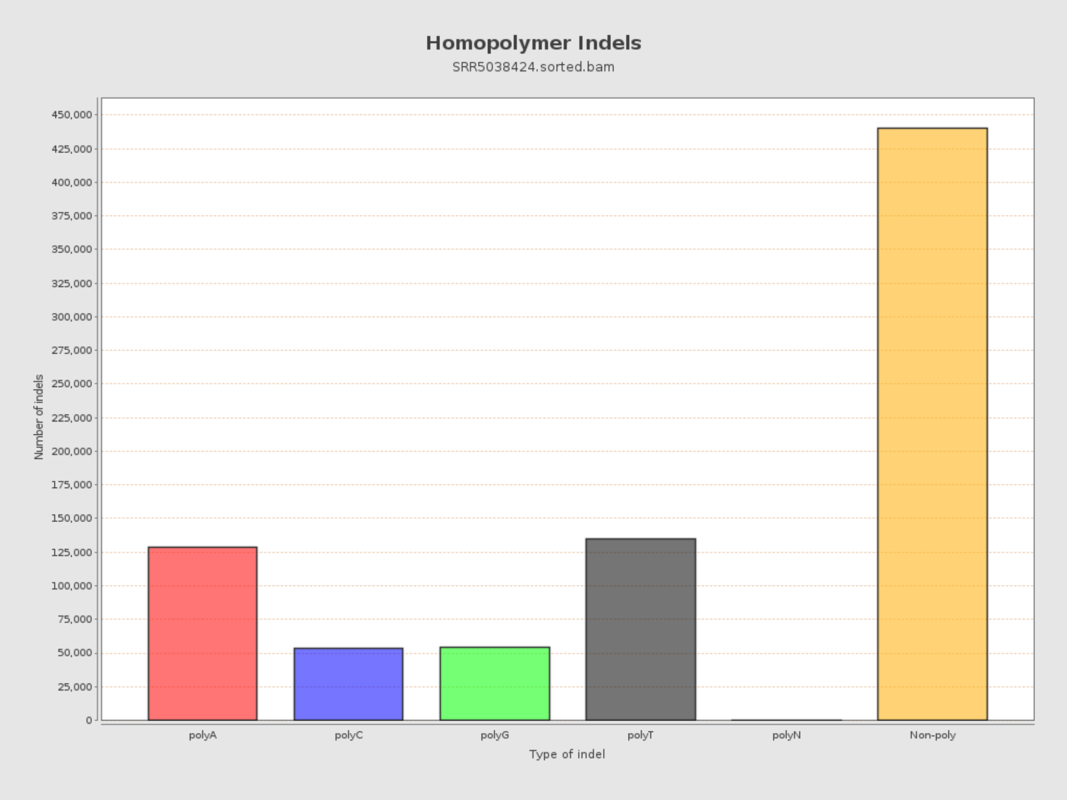
9. Results : Mapped Reads GC-content Distribution



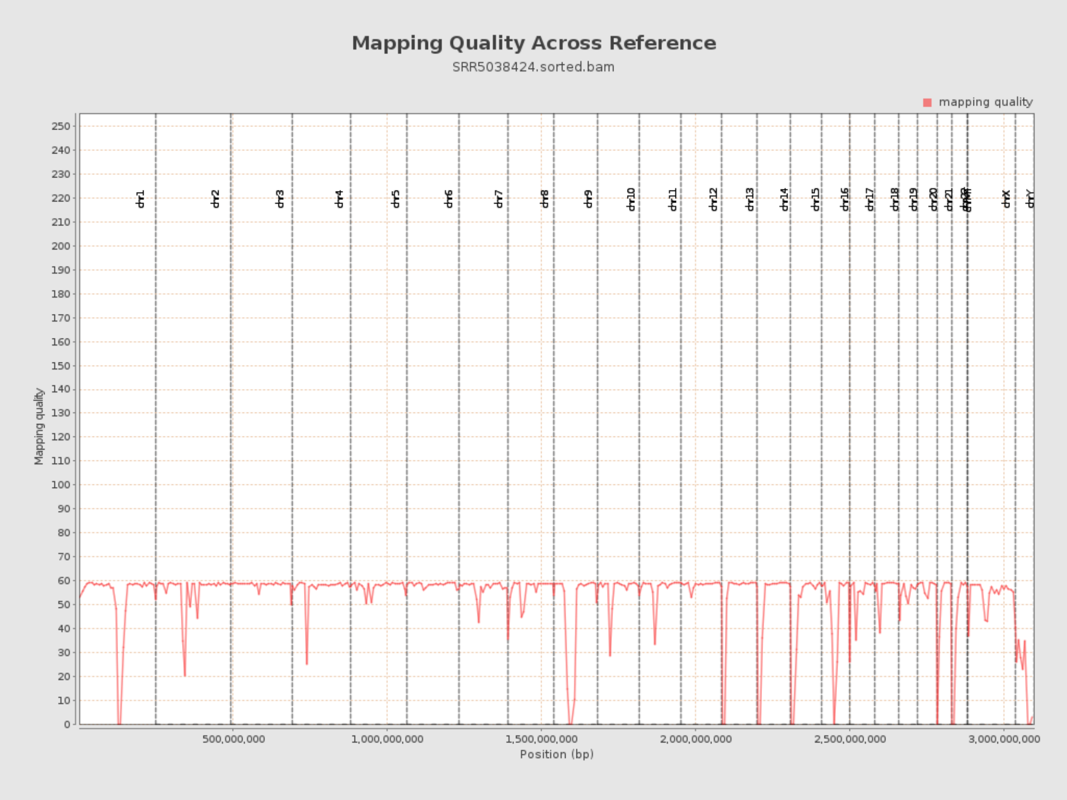
10. Results : Mapped Reads Clipping Profile



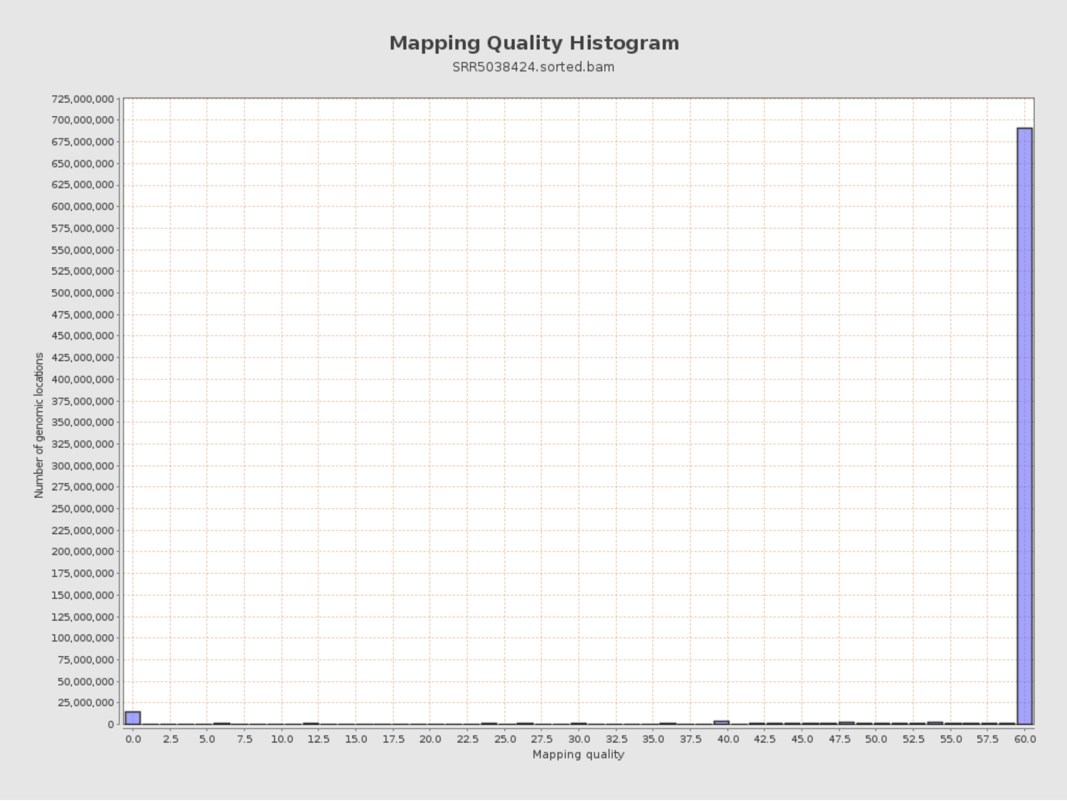
11. Results : Homopolymer Indels



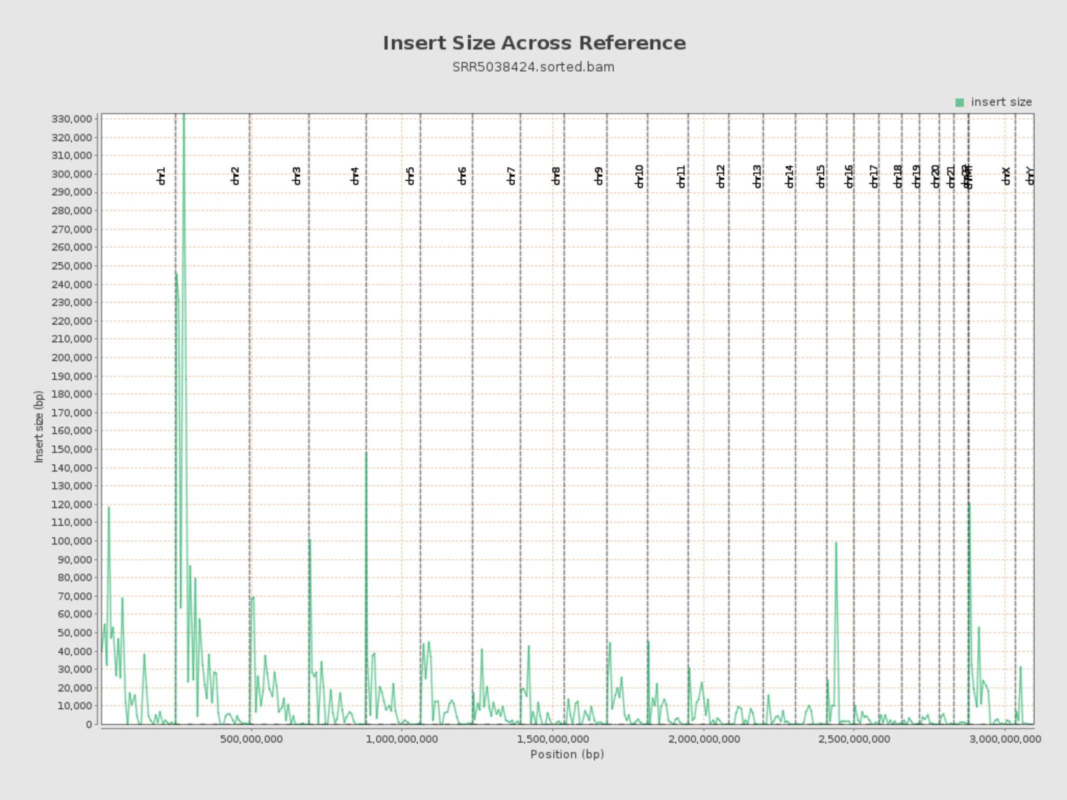
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram