Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 10:42:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617671.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_SRR617671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617671_1.fastq.gz SRR617671_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 10:42:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,386,775 / 94.96%
Unmapped reads	1,613,225 / 5.04%
Mapped paired reads	30,386,775 / 94.96%
Mapped reads, first in pair	15,385,150 / 48.08%
Mapped reads, second in pair	15,001,625 / 46.88%
Mapped reads, both in pair	29,642,822 / 92.63%
Mapped reads, singletons	743,953 / 2.32%
Secondary alignments	0
Supplementary alignments	156,106 / 0.49%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	6,986,058 / 21.83%
Duplication rate	10.73%
Clipped reads	6,324,910 / 19.77%

2.2. ACGT Content

Number/percentage of A's	869,874,906 / 29.57%
Number/percentage of C's	584,860,049 / 19.88%
Number/percentage of T's	871,965,540 / 29.64%
Number/percentage of G's	605,587,542 / 20.59%
Number/percentage of N's	9,207,815 / 0.31%

GC Percentage	40.47%

2.3. Coverage

Mean	0.9508
Standard Deviation	10.2147

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	45,451.55
Standard Deviation	2,004,715.38
P25/Median/P75	181 / 226 / 296

2.6. Mismatches and indels

General error rate	1.84%
Mismatches	53,227,782
Insertions	462,088
Mapped reads with at least one insertion	1.49%
Deletions	1,078,875
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.18%

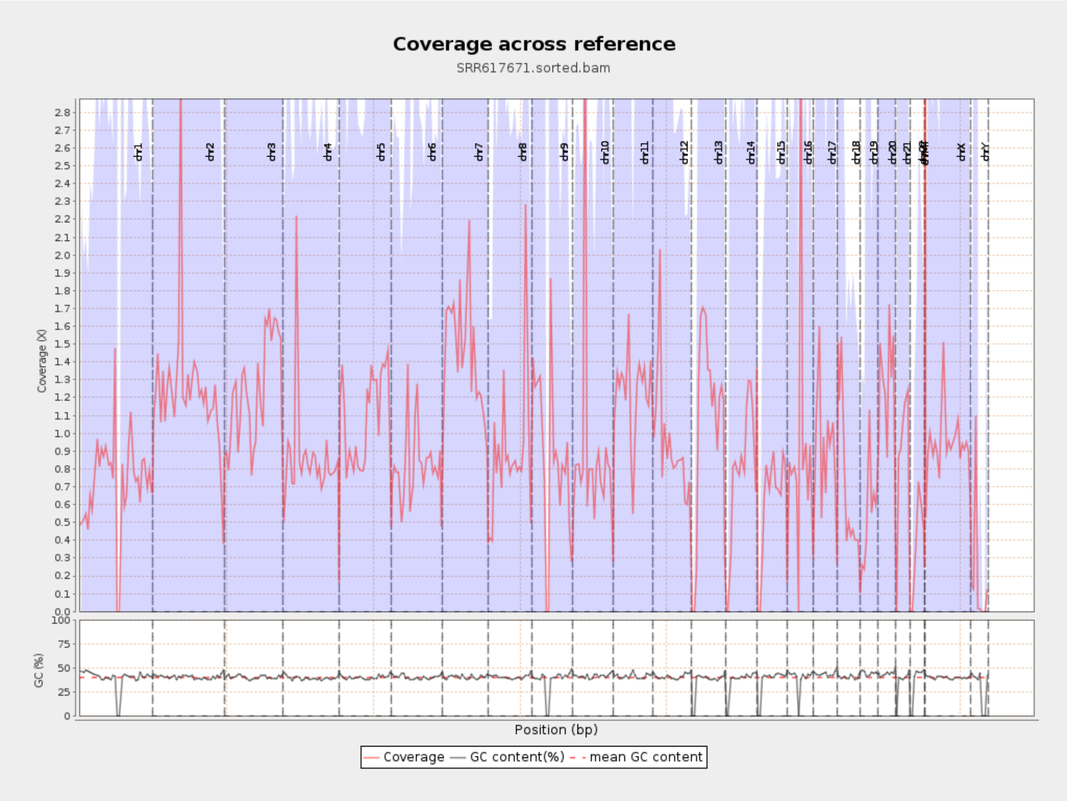
2.7. Chromosome stats

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

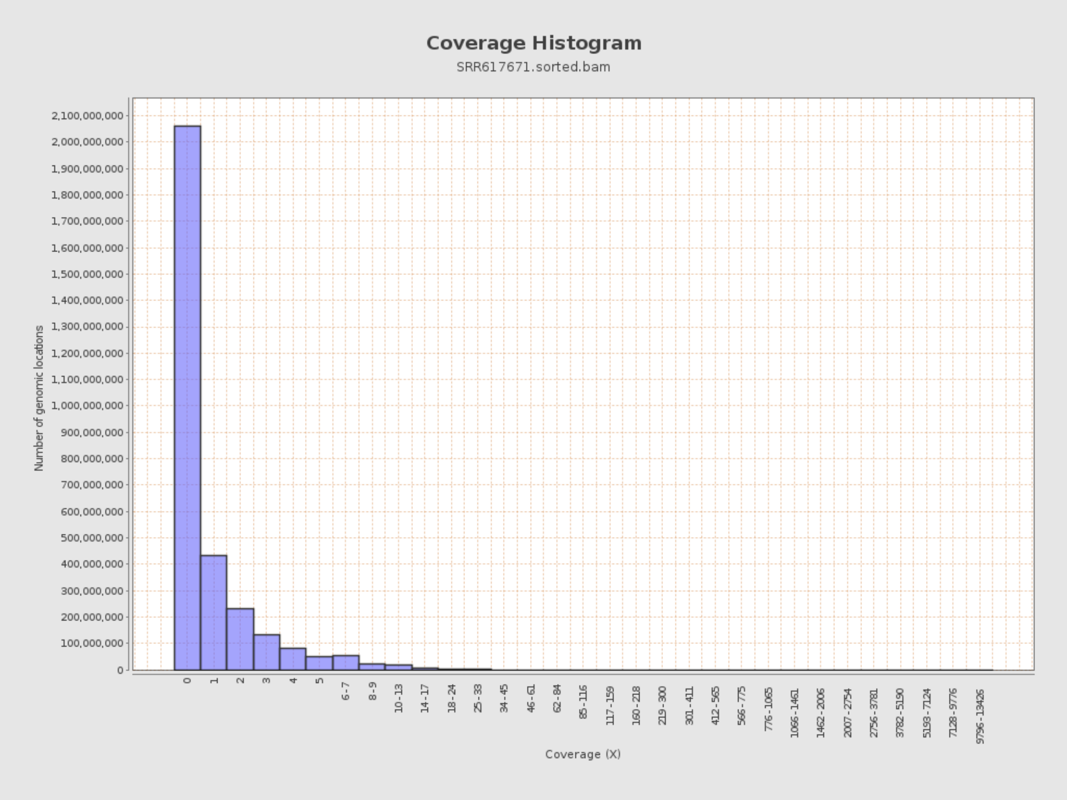
		bases	coverage	deviation
chr1	249250621	180741268	0.7251	10.0801
chr2	243199373	303563942	1.2482	11.7659
chr3	198022430	246182852	1.2432	2.494
chr4	191154276	164459785	0.8604	7.9425
chr5	180915260	194907518	1.0773	2.3437
chr6	171115067	143027822	0.8359	5.7418
chr7	159138663	230396598	1.4478	13.1672
chr8	146364022	130906395	0.8944	4.1271
chr9	141213431	120388964	0.8525	18.84
chr10	135534747	124316578	0.9172	20.7984
chr11	135006516	161661633	1.1974	11.642
chr12	133851895	125923137	0.9408	2.1895
chr13	115169878	126430628	1.0978	2.3199
chr14	107349540	84323310	0.7855	2.4942
chr15	102531392	63293874	0.6173	1.7223
chr16	90354753	81556064	0.9026	16.5109
chr17	81195210	72812627	0.8968	12.3894
chr18	78077248	54094281	0.6928	17.98
chr19	59128983	31494767	0.5326	6.0359
chr20	63025520	80116244	1.2712	3.0232
chr21	48129895	42865041	0.8906	4.2841
chr22	51304566	19119215	0.3727	1.2844
chrMT	16571	3121831	188.3912	133.2241
chrX	155270560	146133165	0.9412	4.3008

chrY	59373566	11439810	0.1927	15.7565

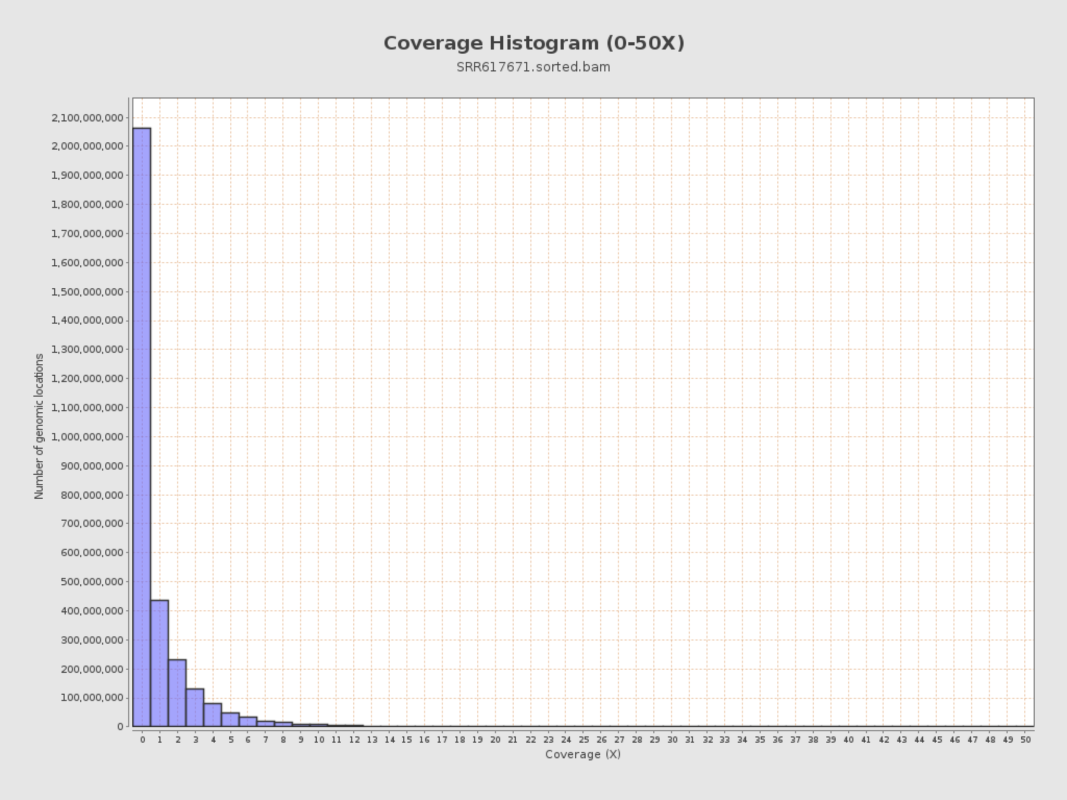
3. Results : Coverage across reference



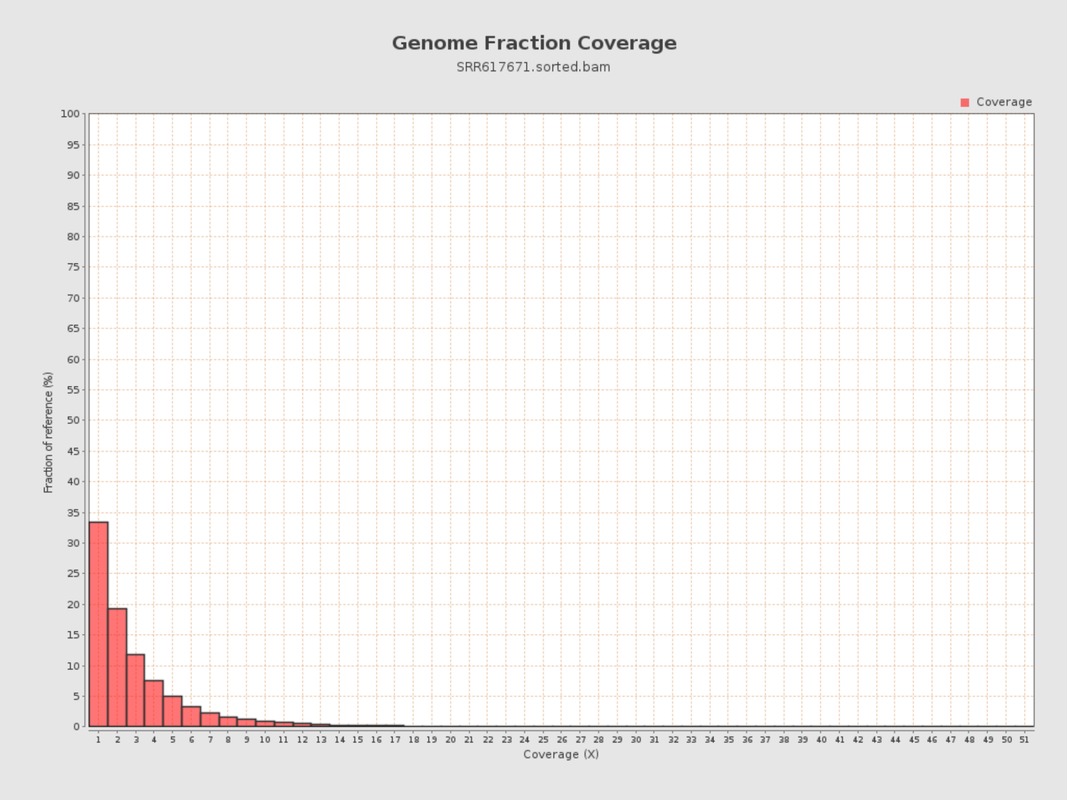
4. Results : Coverage Histogram



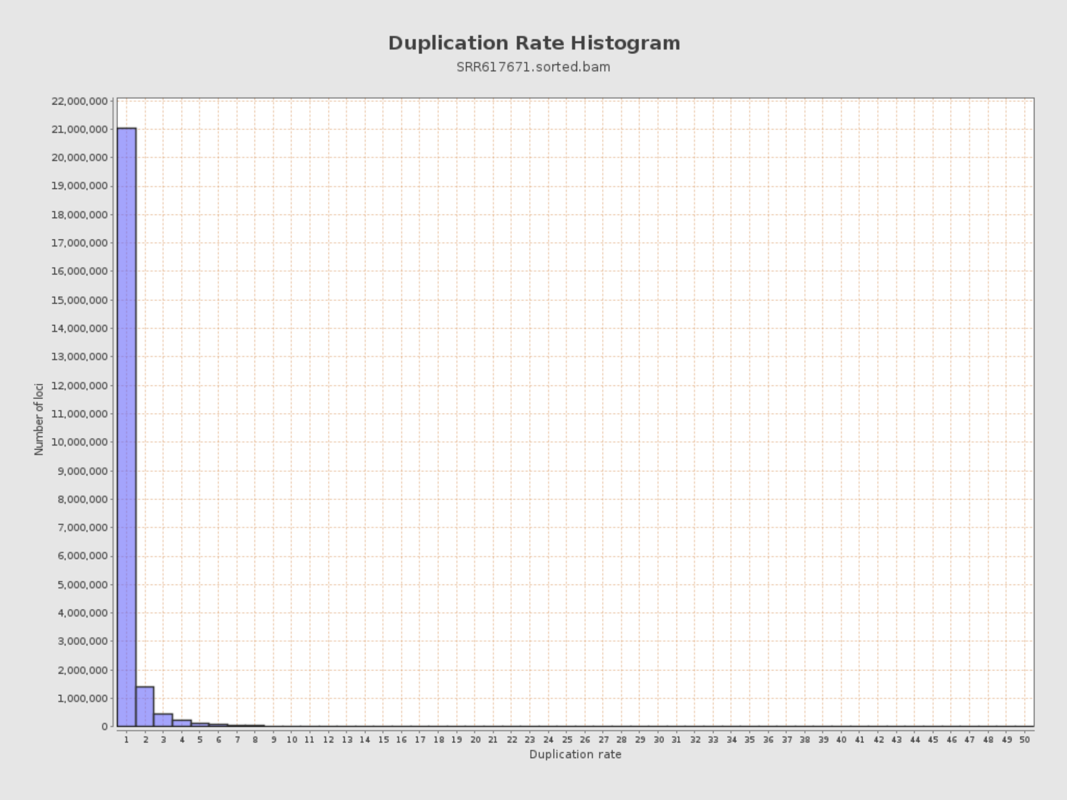
5. Results : Coverage Histogram (0-50X)



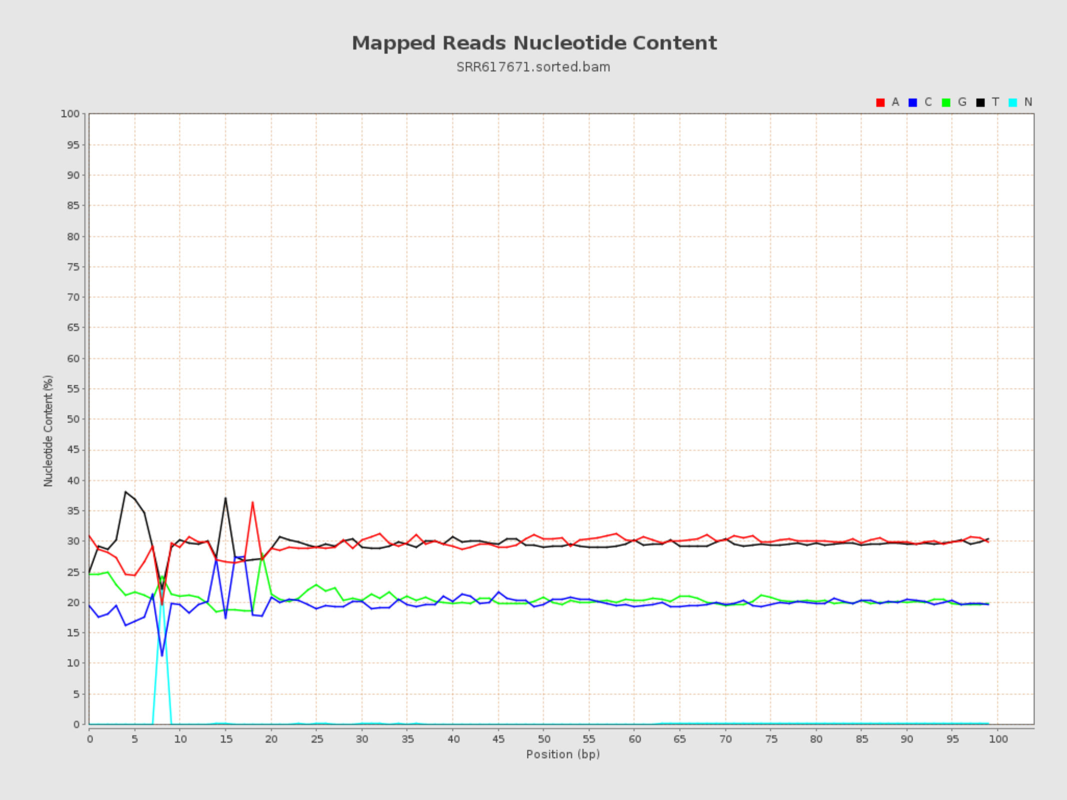
6. Results : Genome Fraction Coverage



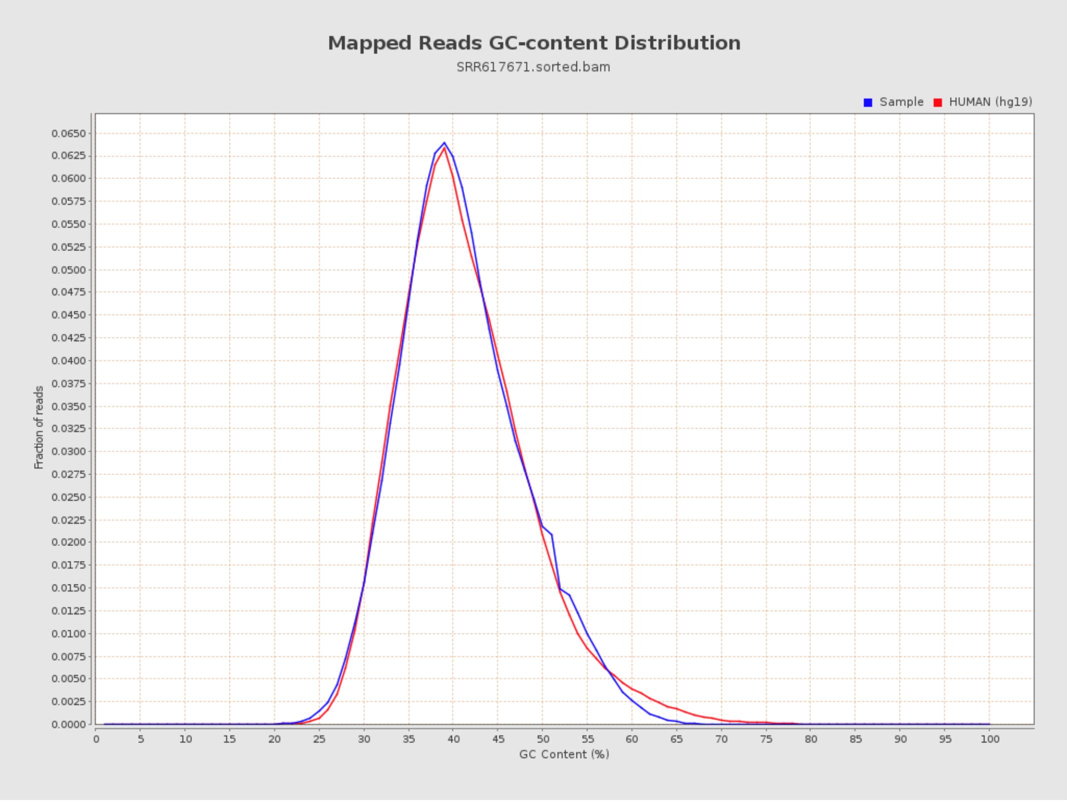
7. Results : Duplication Rate Histogram



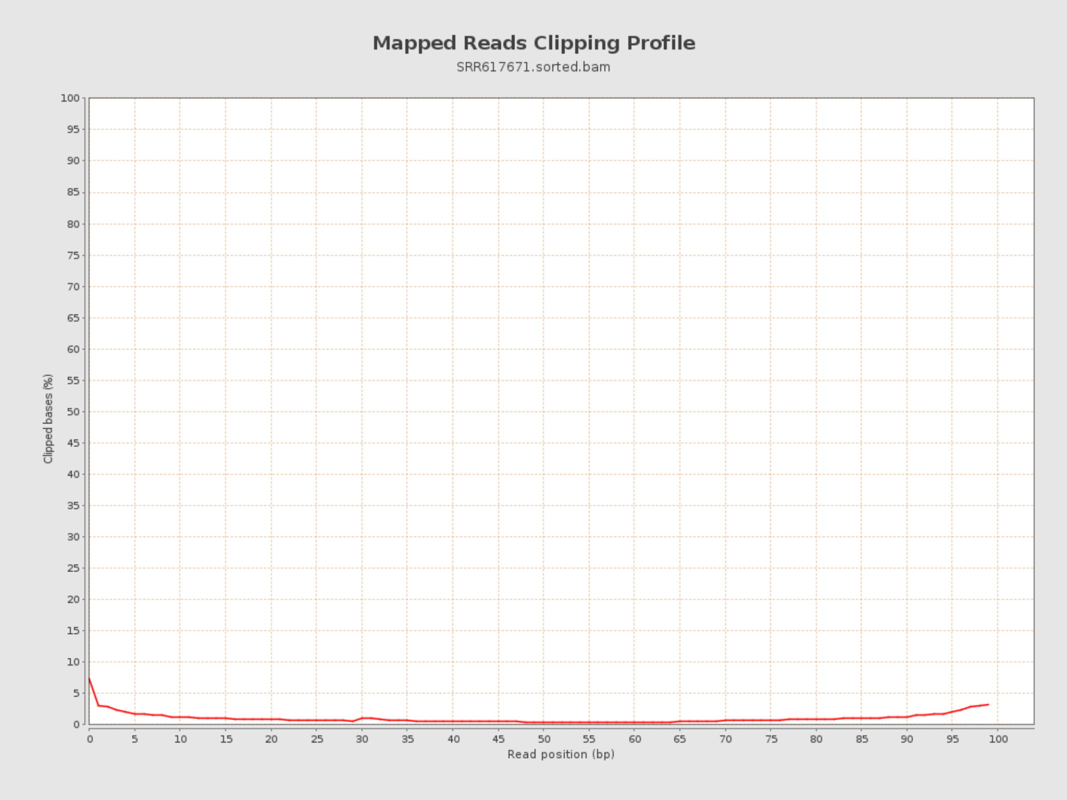
8. Results : Mapped Reads Nucleotide Content



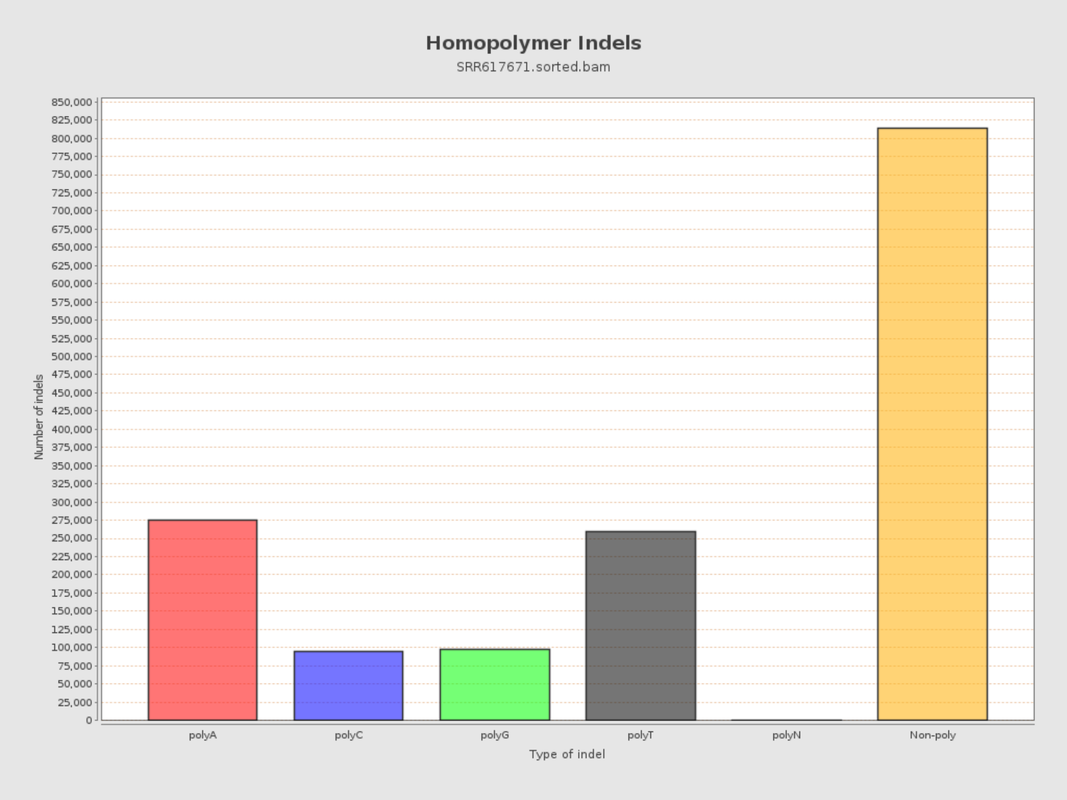
9. Results : Mapped Reads GC-content Distribution



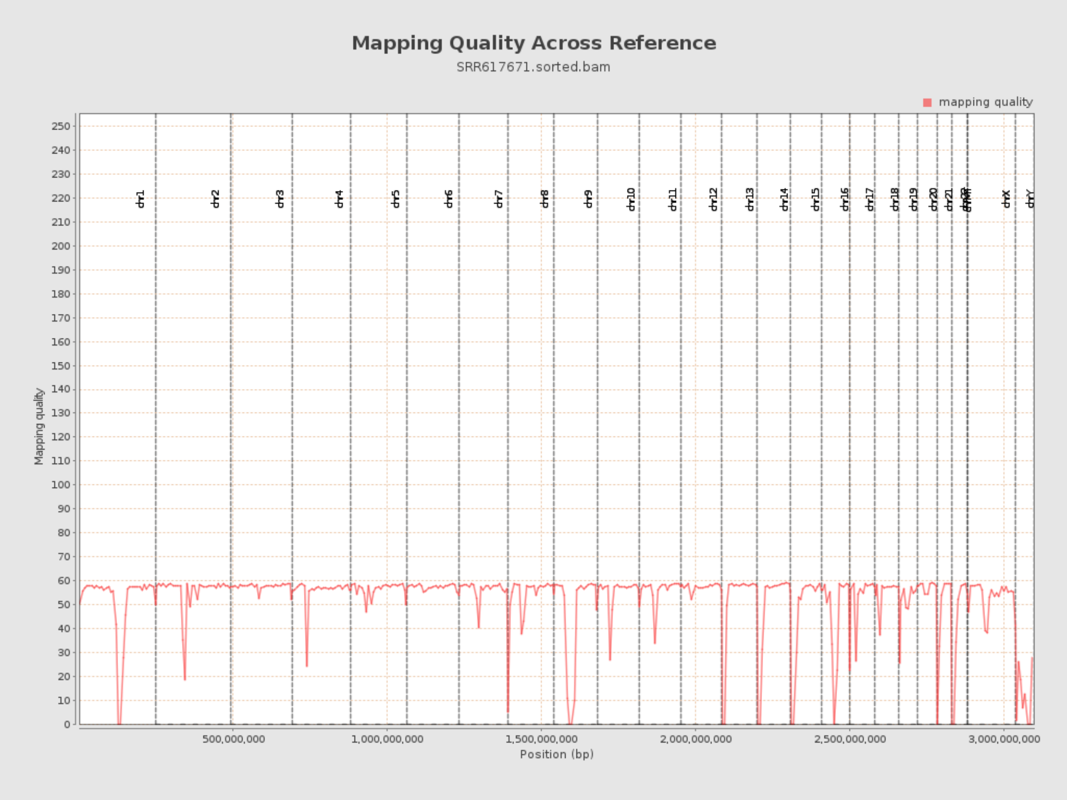
10. Results : Mapped Reads Clipping Profile



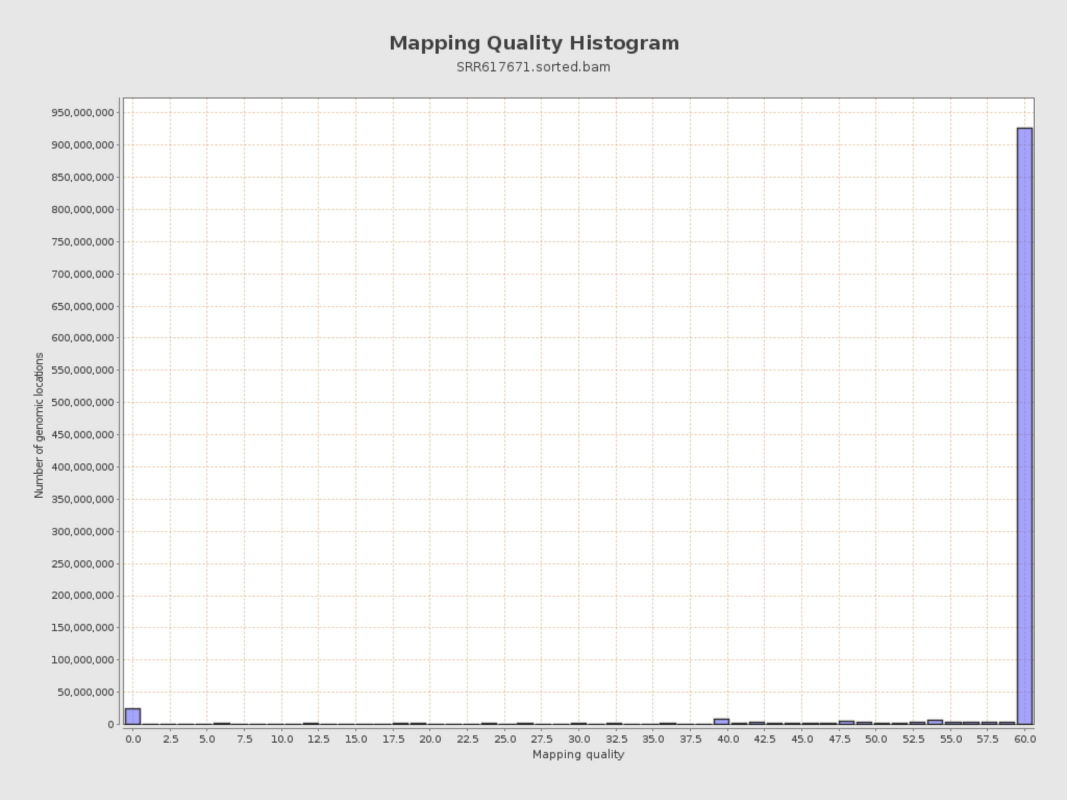
11. Results : Homopolymer Indels



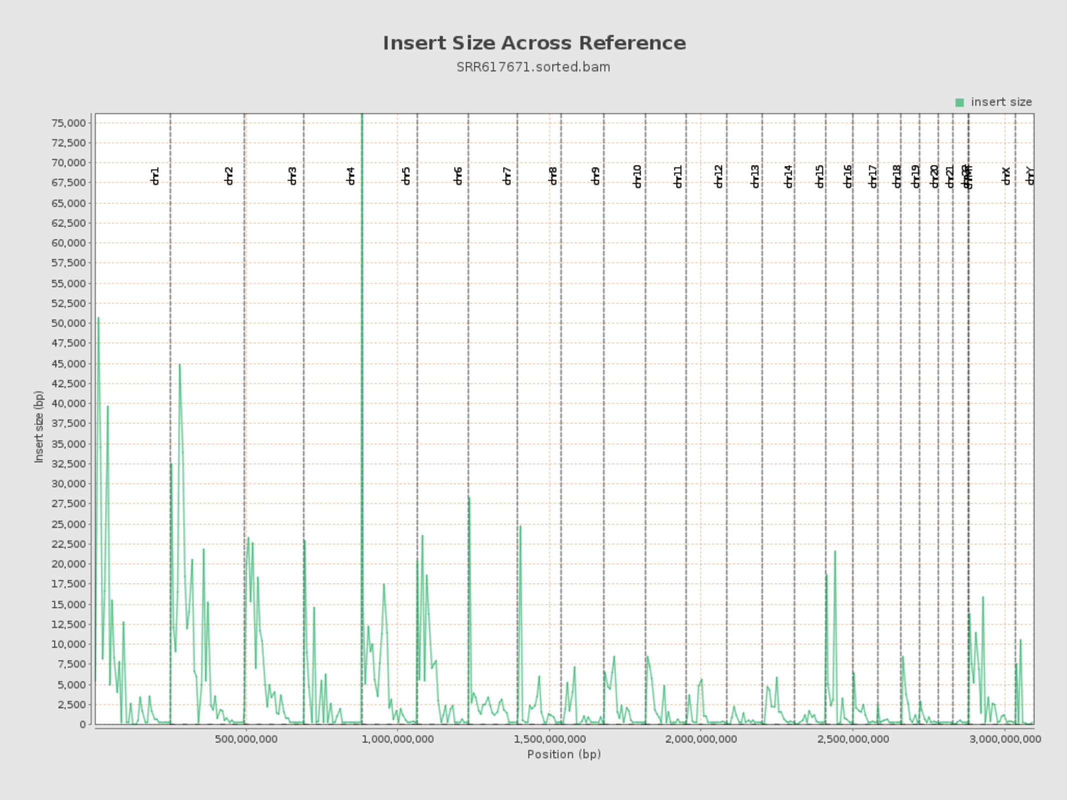
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram