Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 00:09:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617723.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_SRR8617723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617723_1.fastq.gz SRR8617723_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 00:09:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,586,162
Mapped reads	41,723,338 / 97.97%
Unmapped reads	862,824 / 2.03%
Mapped paired reads	41,723,338 / 97.97%
Mapped reads, first in pair	21,082,071 / 49.5%
Mapped reads, second in pair	20,641,267 / 48.47%
Mapped reads, both in pair	41,207,092 / 96.76%
Mapped reads, singletons	516,246 / 1.21%
Secondary alignments	0
Supplementary alignments	997,218 / 2.34%
Read min/max/mean length	30 / 150 / 151.13
Duplicated reads (estimated)	15,247,308 / 35.8%
Duplication rate	25.6%
Clipped reads	22,842,419 / 53.64%

2.2. ACGT Content

Number/percentage of A's	1,604,100,845 / 28.91%
Number/percentage of C's	1,054,652,441 / 19%
Number/percentage of T's	1,657,727,074 / 29.87%
Number/percentage of G's	1,232,739,731 / 22.21%
Number/percentage of N's	230,990 / 0%

GC Percentage	41.22%

2.3. Coverage

Mean	1.7941
Standard Deviation	20.3181

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	148,446.03
Standard Deviation	3,686,015.74
P25/Median/P75	206 / 261 / 331

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	66,192,027
Insertions	1,019,682
Mapped reads with at least one insertion	2.29%
Deletions	2,229,935
Mapped reads with at least one deletion	5.12%
Homopolymer indels	45.7%

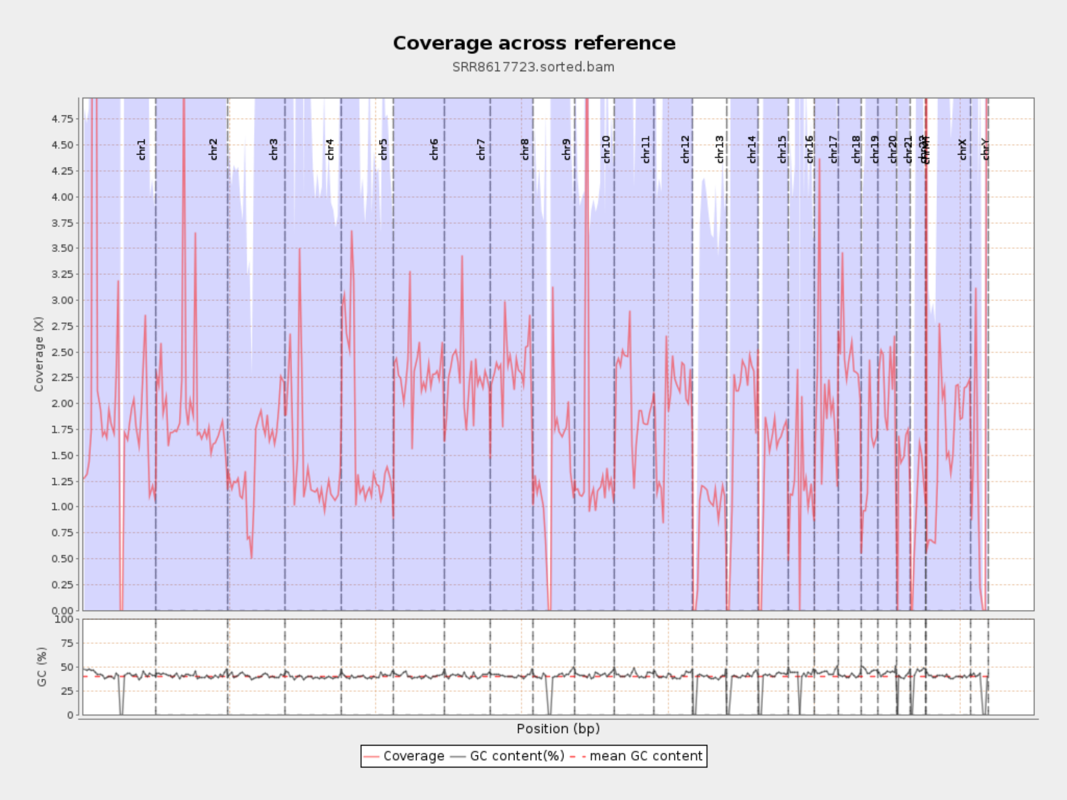
2.7. Chromosome stats

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

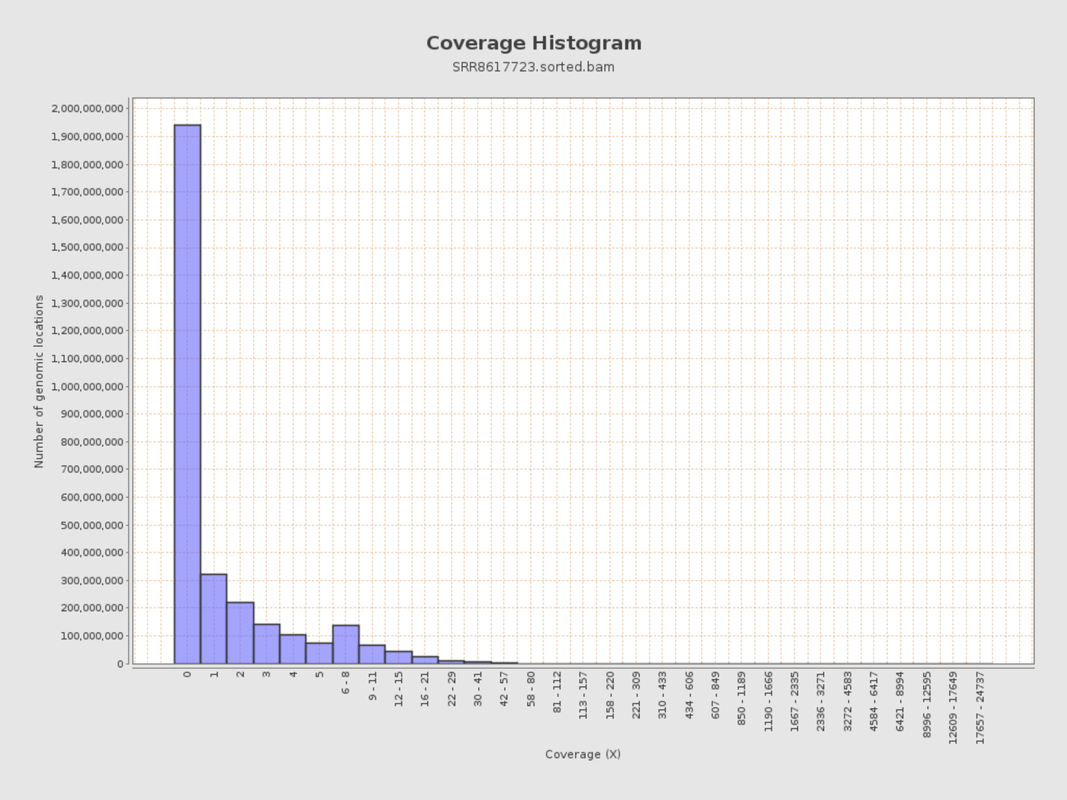
		bases	coverage	deviation
chr1	249250621	543196615	2.1793	20.111
chr2	243199373	484733146	1.9932	27.2896
chr3	198022430	291029401	1.4697	3.4576
chr4	191154276	280122027	1.4654	13.3042
chr5	180915260	299562744	1.6558	4.2565
chr6	171115067	394839704	2.3075	12.5007
chr7	159138663	357621933	2.2472	26.2569
chr8	146364022	343890108	2.3496	7.7168
chr9	141213431	192443903	1.3628	36.3897
chr10	135534747	194680028	1.4364	36.6397
chr11	135006516	276646052	2.0491	22.3777
chr12	133851895	260620525	1.9471	8.2636
chr13	115169878	104833141	0.9102	2.558
chr14	107349540	199904614	1.8622	4.8958
chr15	102531392	145660928	1.4206	4.4809
chr16	90354753	106966857	1.1839	14.9322
chr17	81195210	170623923	2.1014	36.5292
chr18	78077248	193605935	2.4797	33.8091
chr19	59128983	86467666	1.4624	9.5937
chr20	63025520	140659027	2.2318	5.6796
chr21	48129895	67784812	1.4084	6.8554
chr22	51304566	49583538	0.9665	3.6236
chrMT	16571	1313885	79.2882	41.4803
chrX	155270560	250390176	1.6126	7.683

chrY	59373566	116705245	1.9656	45.3967

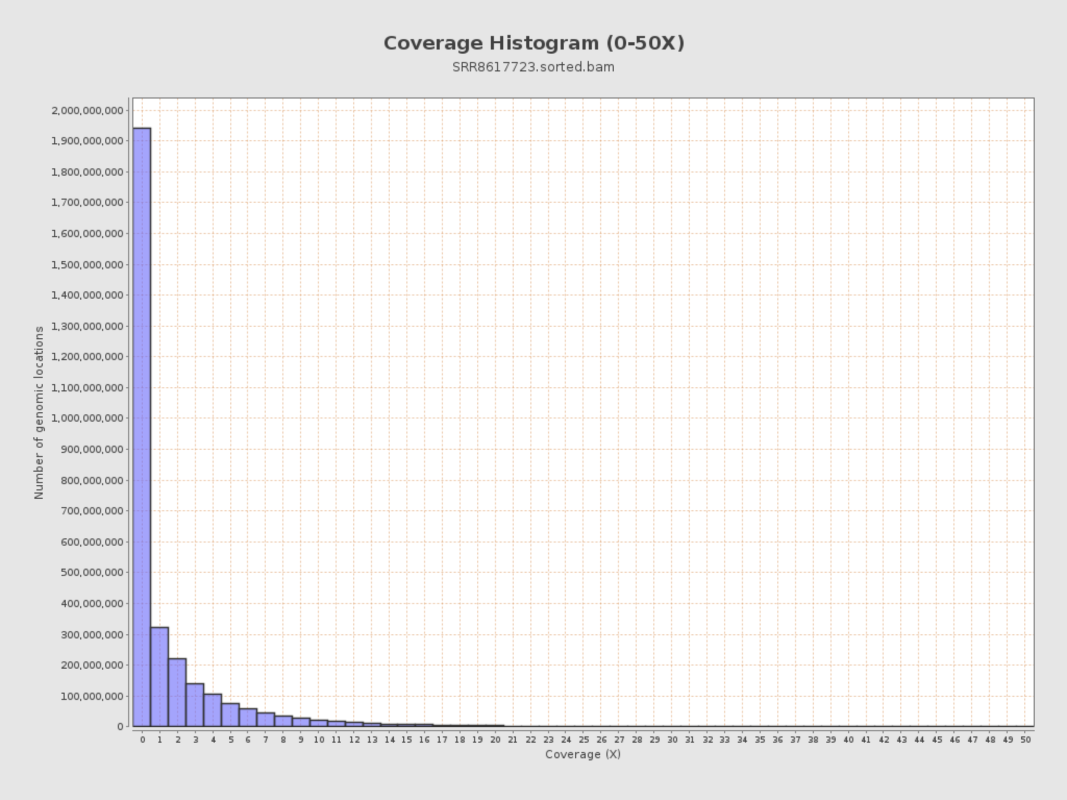
3. Results : Coverage across reference



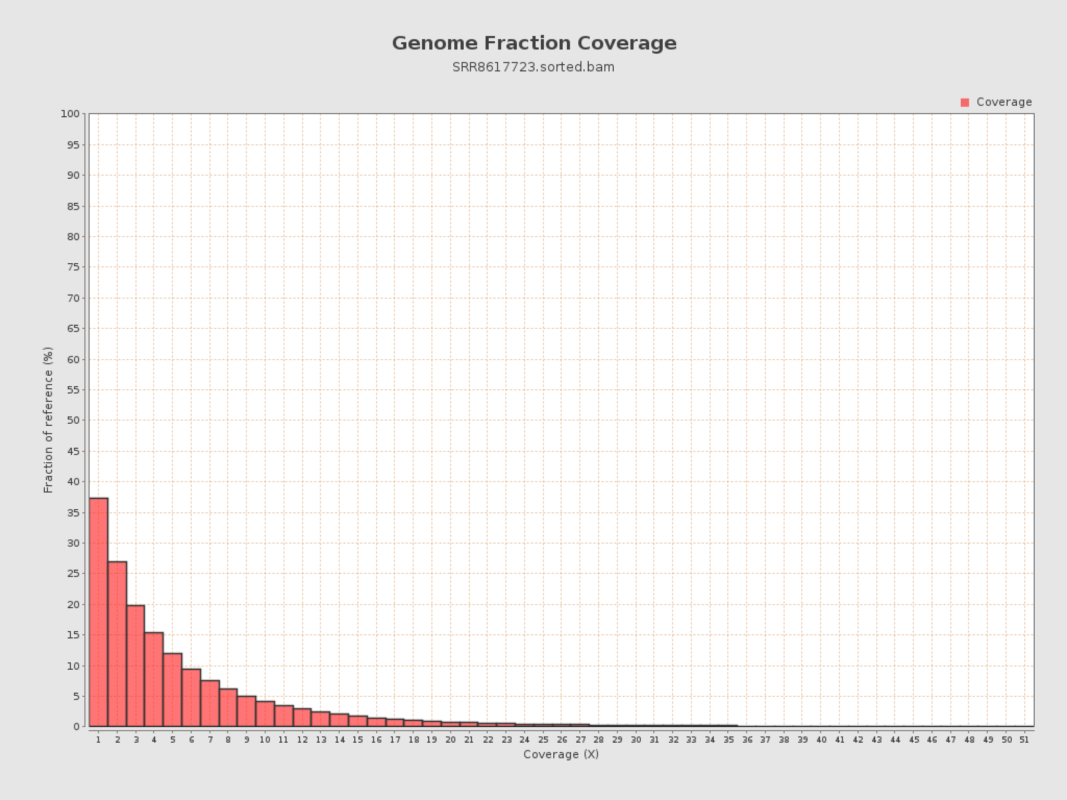
4. Results : Coverage Histogram



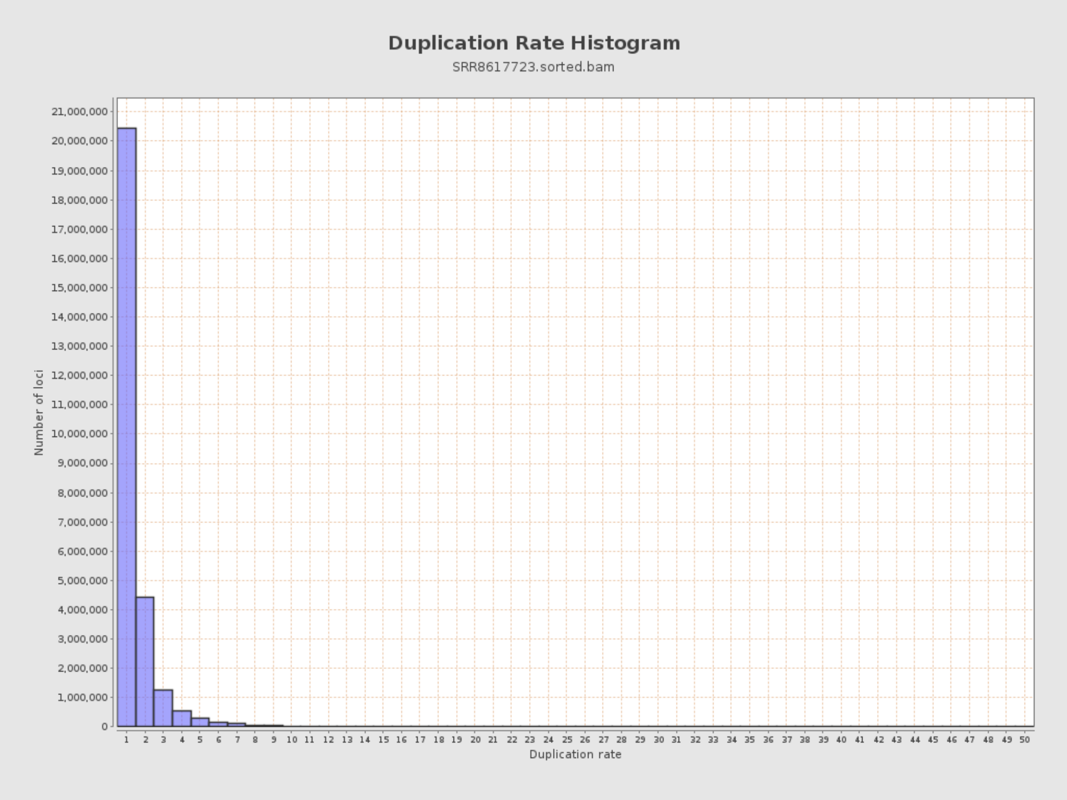
5. Results : Coverage Histogram (0-50X)



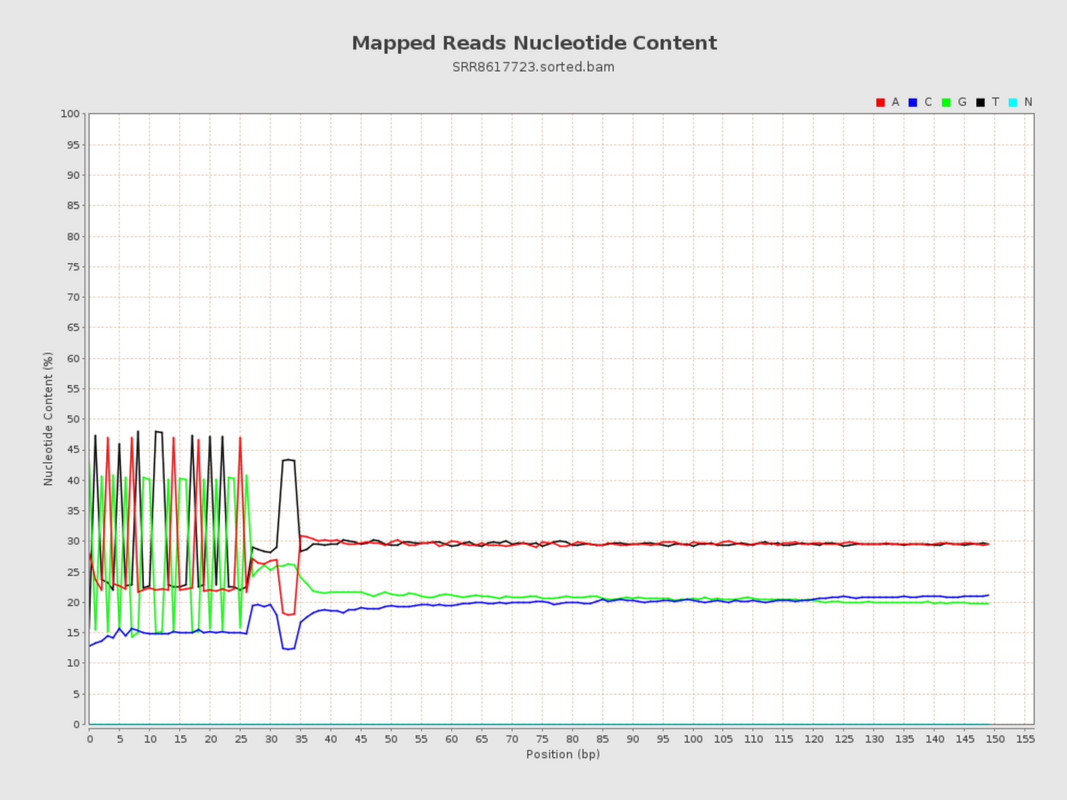
6. Results : Genome Fraction Coverage



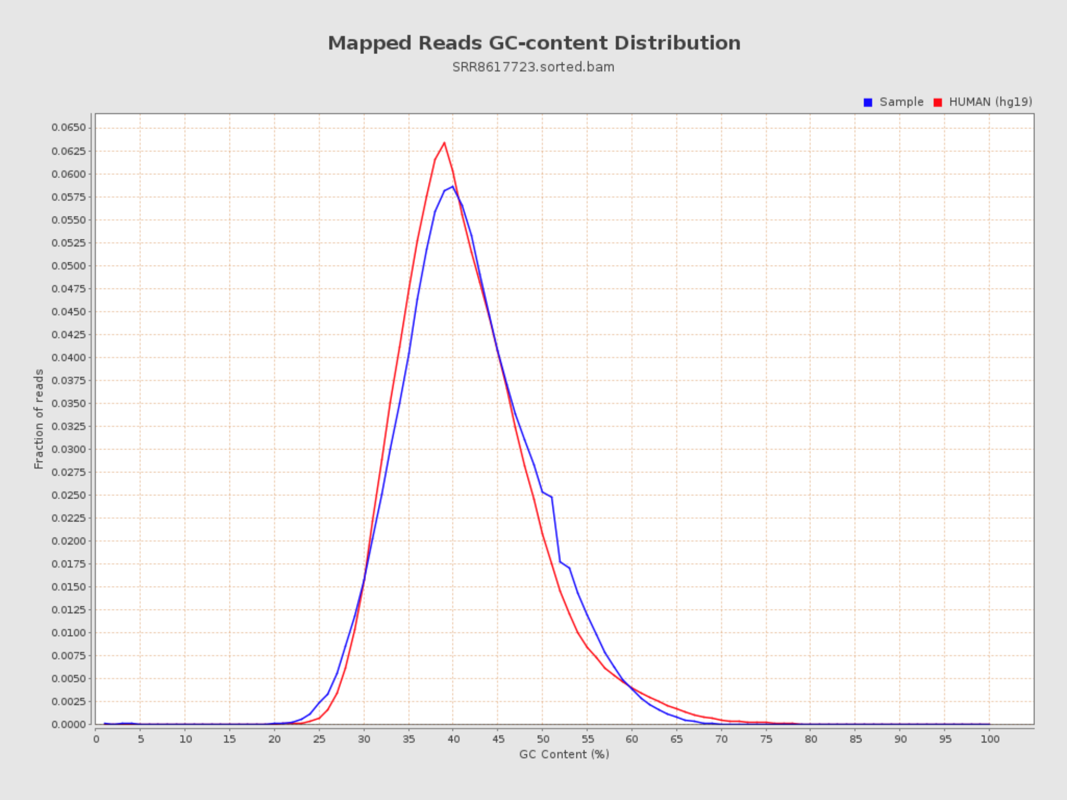
7. Results : Duplication Rate Histogram



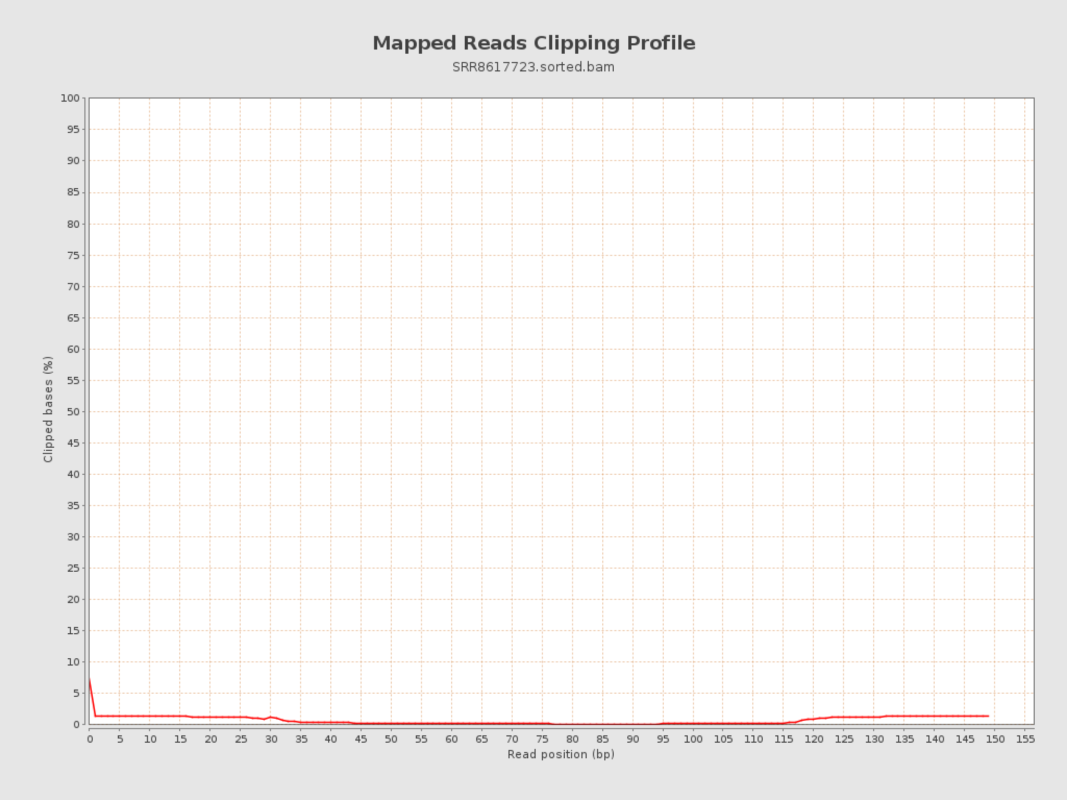
8. Results : Mapped Reads Nucleotide Content



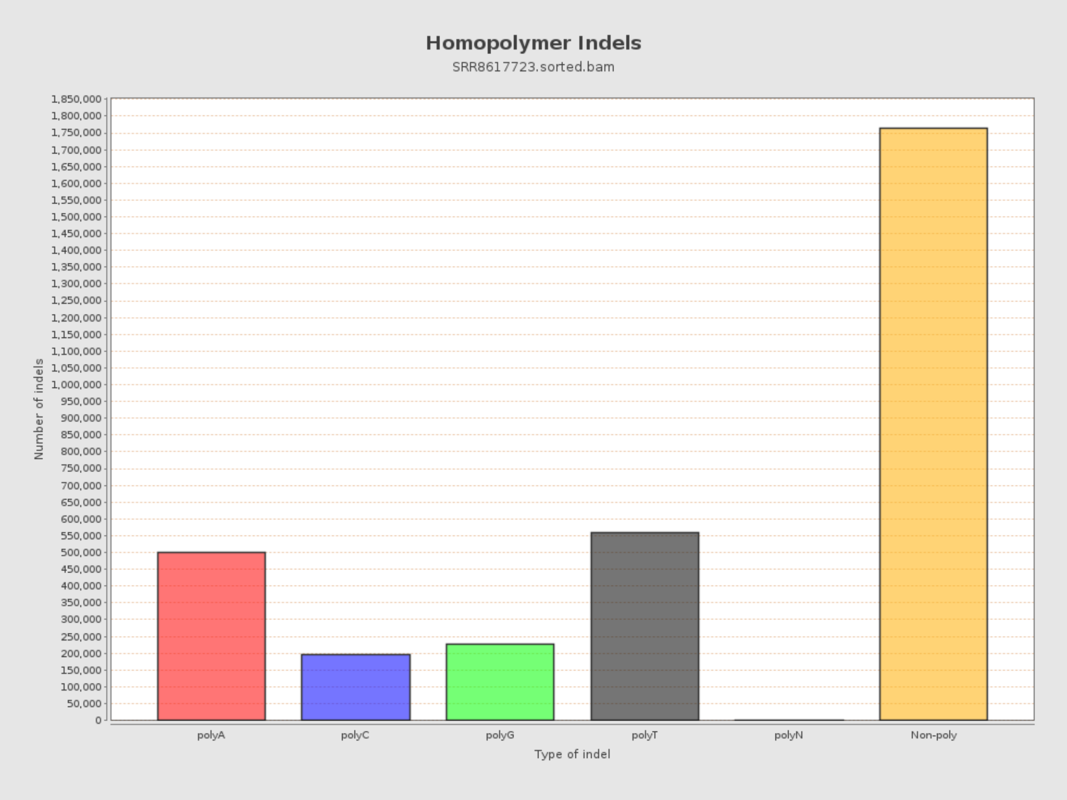
9. Results : Mapped Reads GC-content Distribution



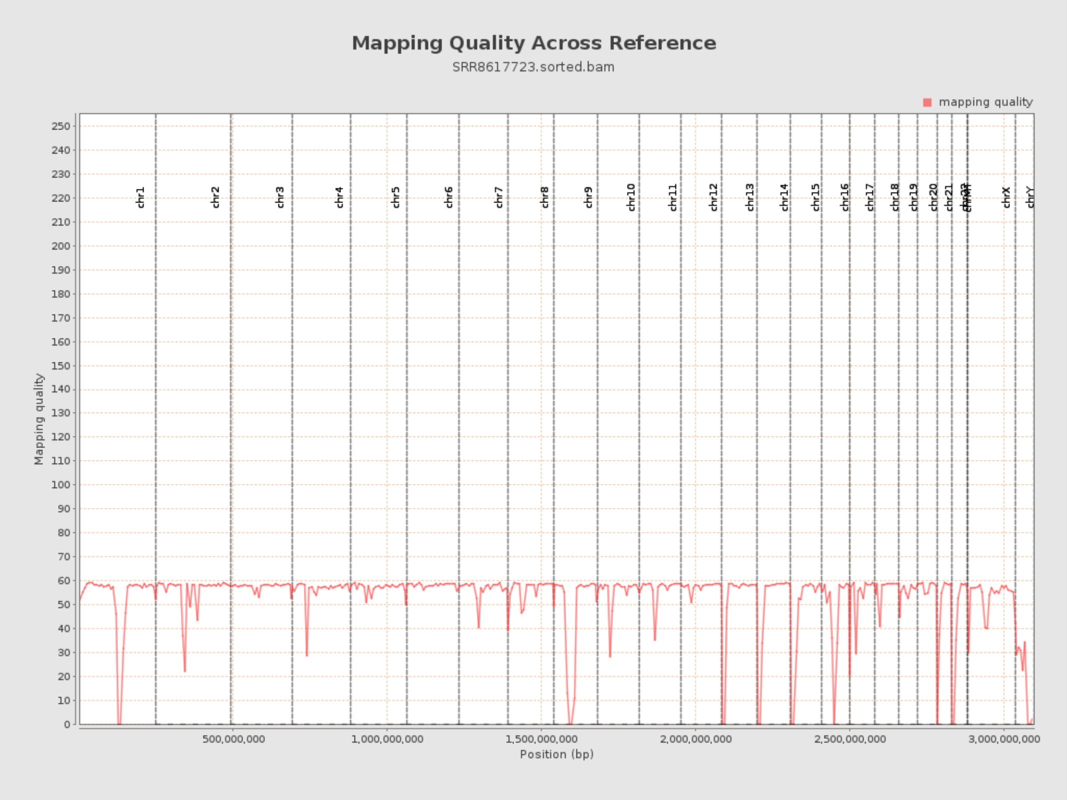
10. Results : Mapped Reads Clipping Profile



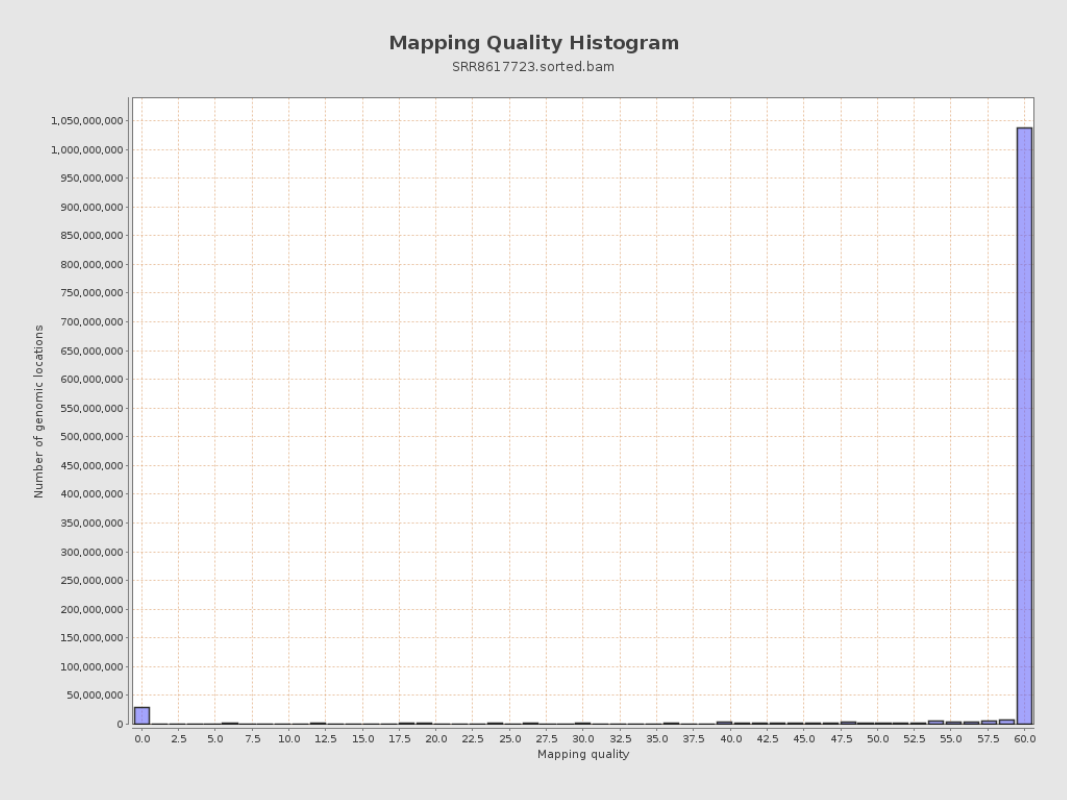
11. Results : Homopolymer Indels



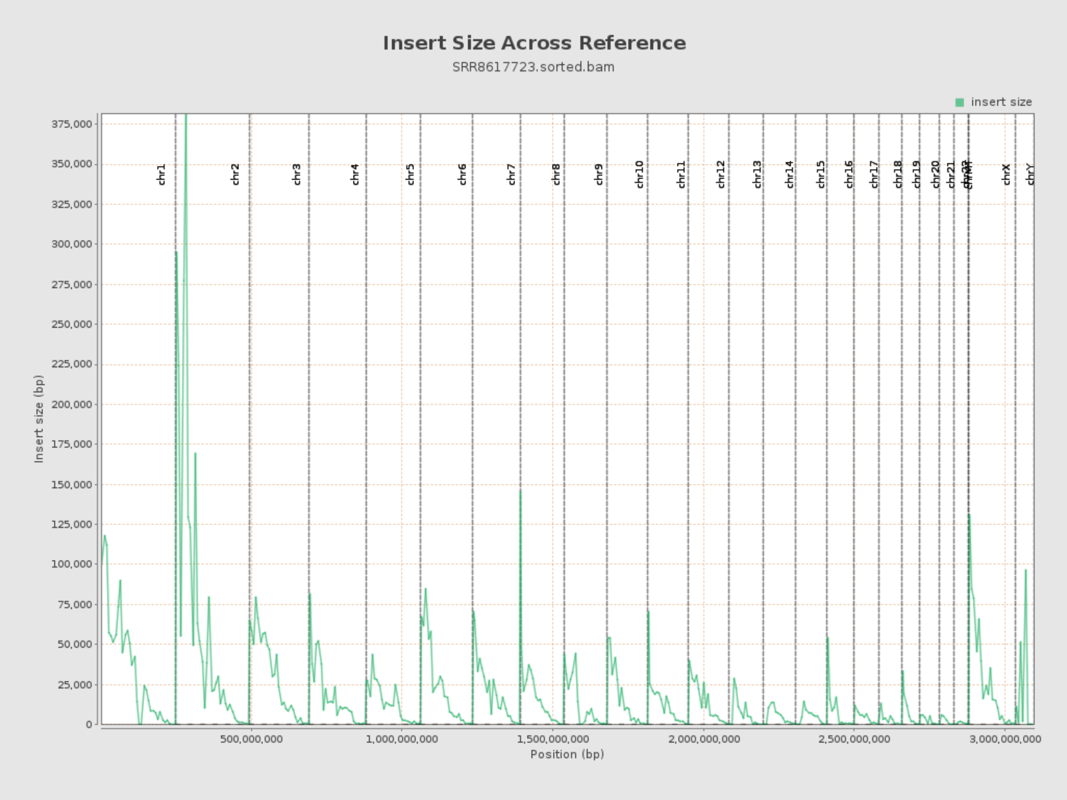
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram