Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 07:21:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617730.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_SRR8617730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617730_1.fastq.gz SRR8617730_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 07:21:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,598,236
Mapped reads	48,658,923 / 98.11%
Unmapped reads	939,313 / 1.89%
Mapped paired reads	48,658,923 / 98.11%
Mapped reads, first in pair	24,605,726 / 49.61%
Mapped reads, second in pair	24,053,197 / 48.5%
Mapped reads, both in pair	48,018,940 / 96.82%
Mapped reads, singletons	639,983 / 1.29%
Secondary alignments	0
Supplementary alignments	1,086,585 / 2.19%
Read min/max/mean length	30 / 150 / 151.06
Duplicated reads (estimated)	16,778,473 / 33.83%
Duplication rate	25.69%
Clipped reads	26,639,828 / 53.71%

2.2. ACGT Content

Number/percentage of A's	1,858,174,552 / 28.75%
Number/percentage of C's	1,233,296,894 / 19.08%
Number/percentage of T's	1,927,179,817 / 29.82%
Number/percentage of G's	1,444,165,626 / 22.34%
Number/percentage of N's	269,176 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	2.0894
Standard Deviation	20.7841

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	143,483.89
Standard Deviation	3,621,942.19
P25/Median/P75	213 / 268 / 337

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	75,280,211
Insertions	1,140,797
Mapped reads with at least one insertion	2.21%
Deletions	2,604,898
Mapped reads with at least one deletion	5.14%
Homopolymer indels	45.97%

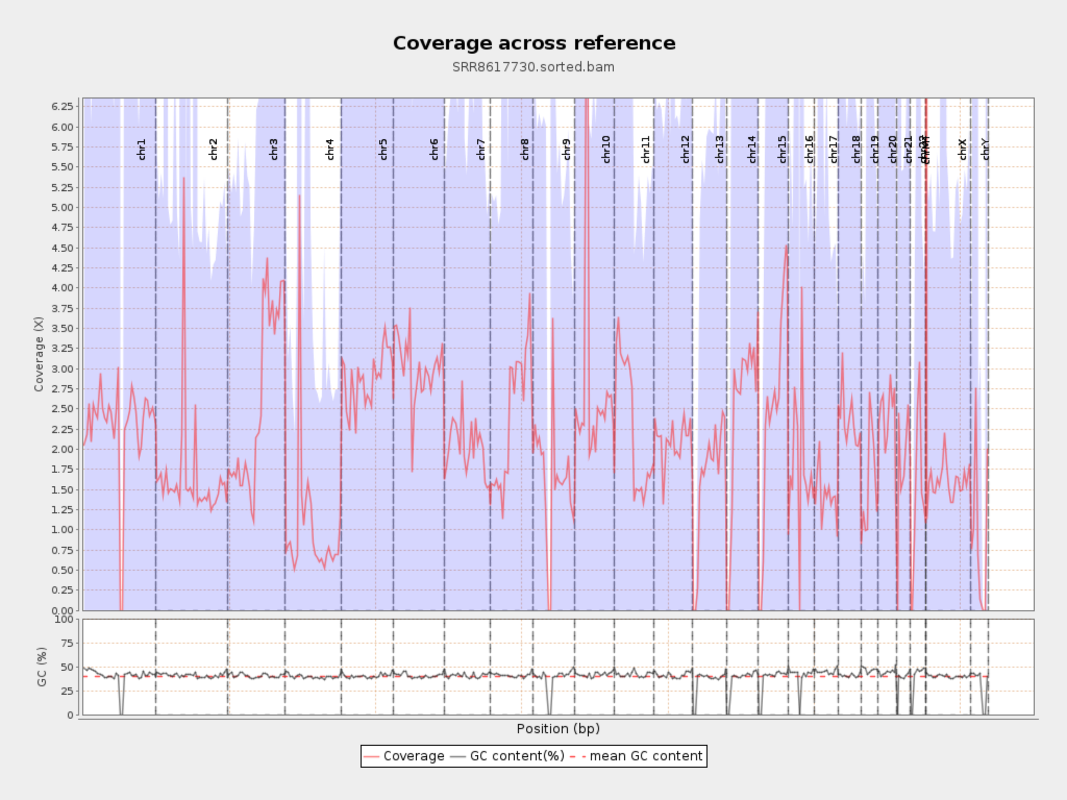
2.7. Chromosome stats

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

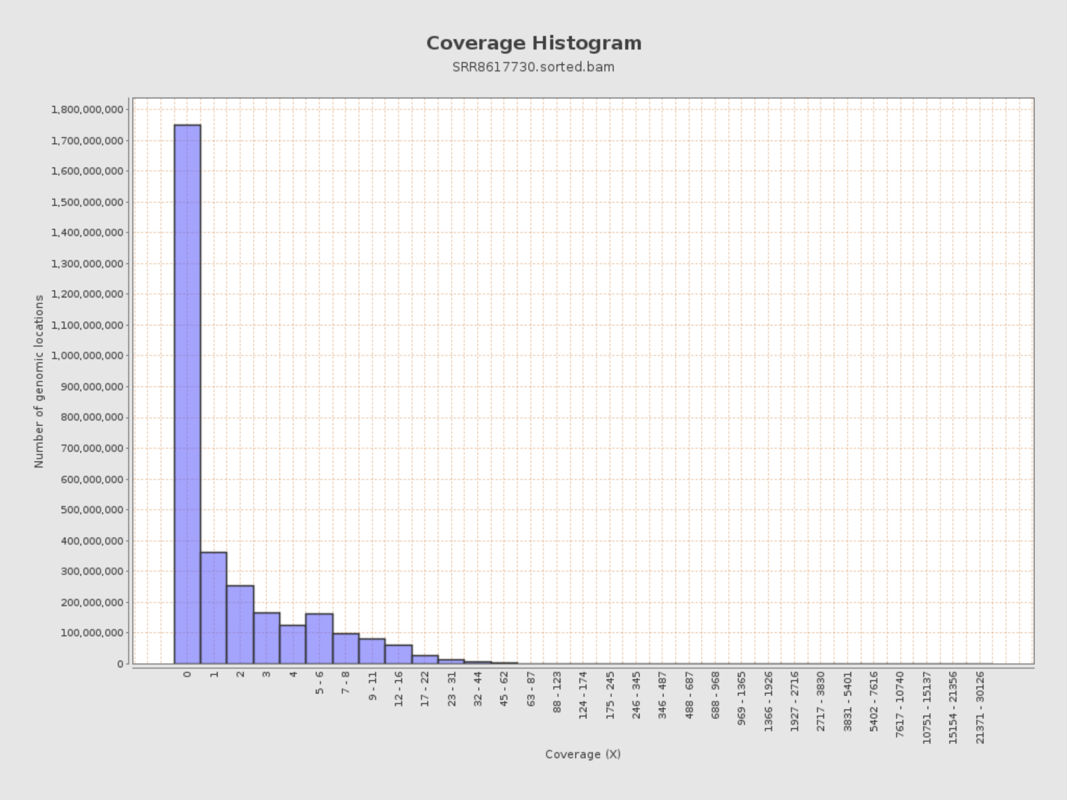
		bases	coverage	deviation
chr1	249250621	568420999	2.2805	14.7643
chr2	243199373	401939011	1.6527	24.7158
chr3	198022430	511073749	2.5809	5.0039
chr4	191154276	195194663	1.0211	23.4354
chr5	180915260	519393102	2.8709	5.1743
chr6	171115067	515621699	3.0133	11.4482
chr7	159138663	322546565	2.0268	20.6894
chr8	146364022	355169257	2.4266	6.2558
chr9	141213431	230195171	1.6301	37.5376
chr10	135534747	374229851	2.7611	59.1025
chr11	135006516	308350423	2.284	18.41
chr12	133851895	281739200	2.1049	9.0894
chr13	115169878	188823889	1.6395	3.5396
chr14	107349540	266250521	2.4802	5.0258
chr15	102531392	249575160	2.4341	5.8797
chr16	90354753	159438472	1.7646	19.598
chr17	81195210	117662623	1.4491	11.4159
chr18	78077248	184281742	2.3602	30.6242
chr19	59128983	95372798	1.613	8.3857
chr20	63025520	153684590	2.4385	7.9814
chr21	48129895	88798391	1.845	11.8413
chr22	51304566	73692097	1.4364	3.8088
chrMT	16571	2781354	167.8447	90.5655
chrX	155270560	248650707	1.6014	6.3391

chrY	59373566	55254681	0.9306	27.3548

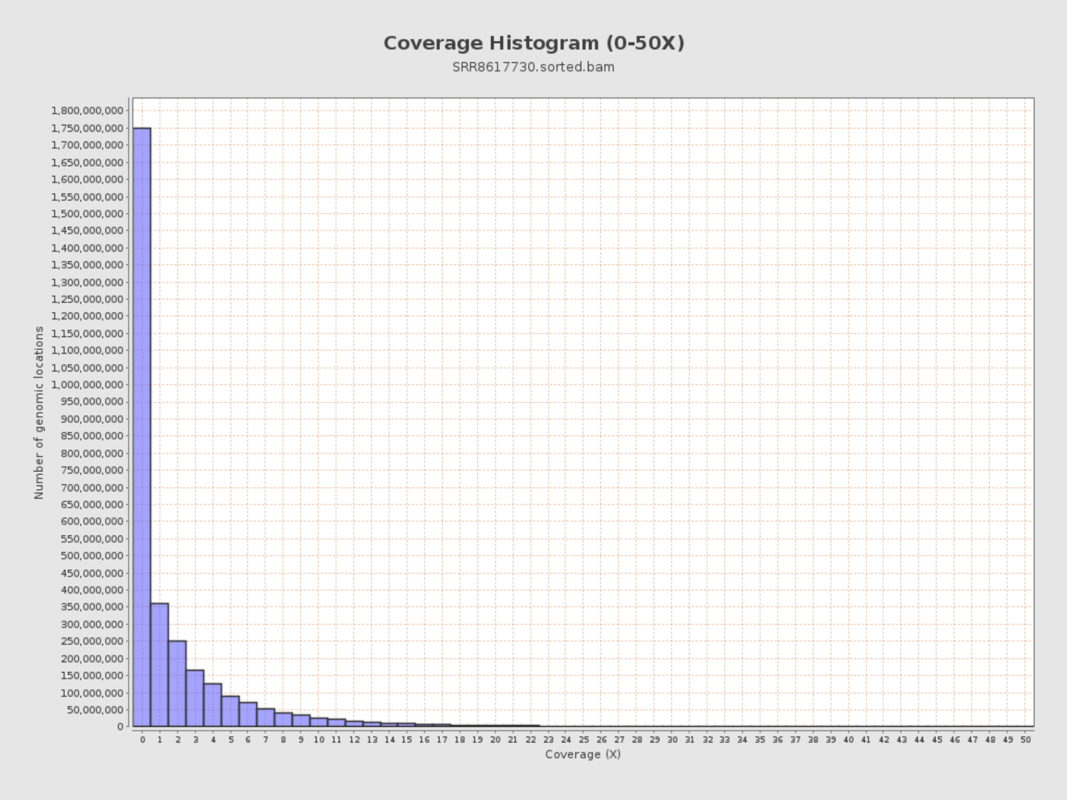
3. Results : Coverage across reference



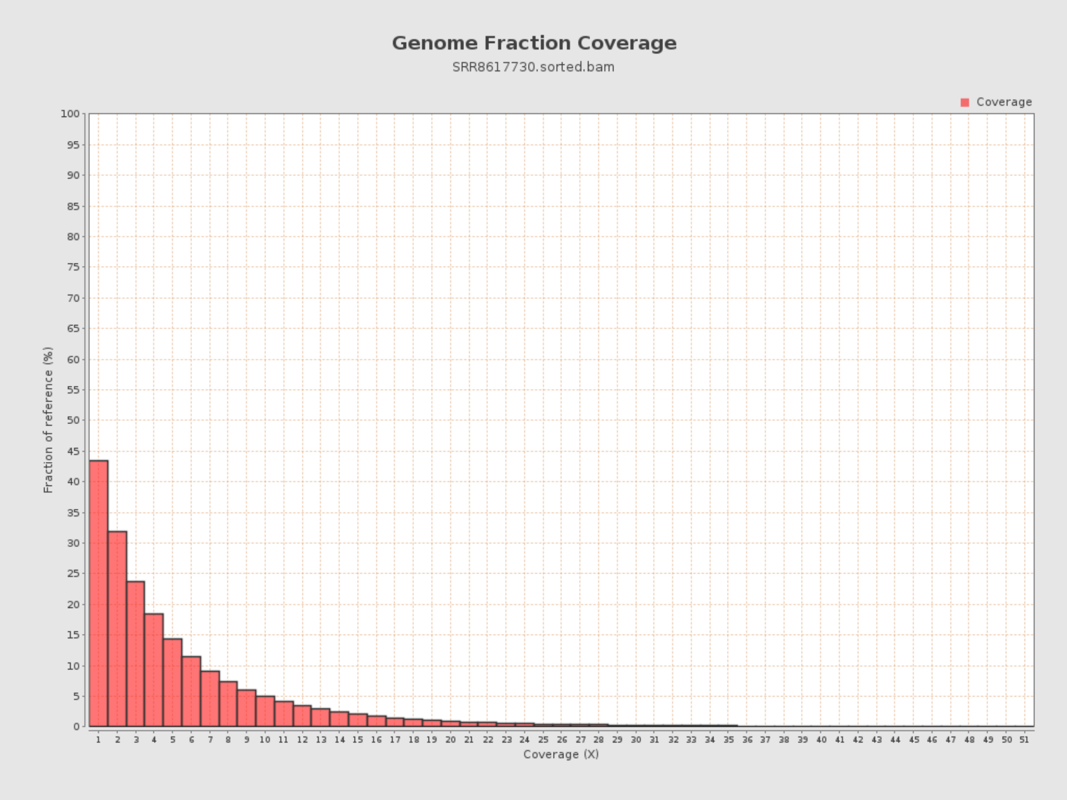
4. Results : Coverage Histogram



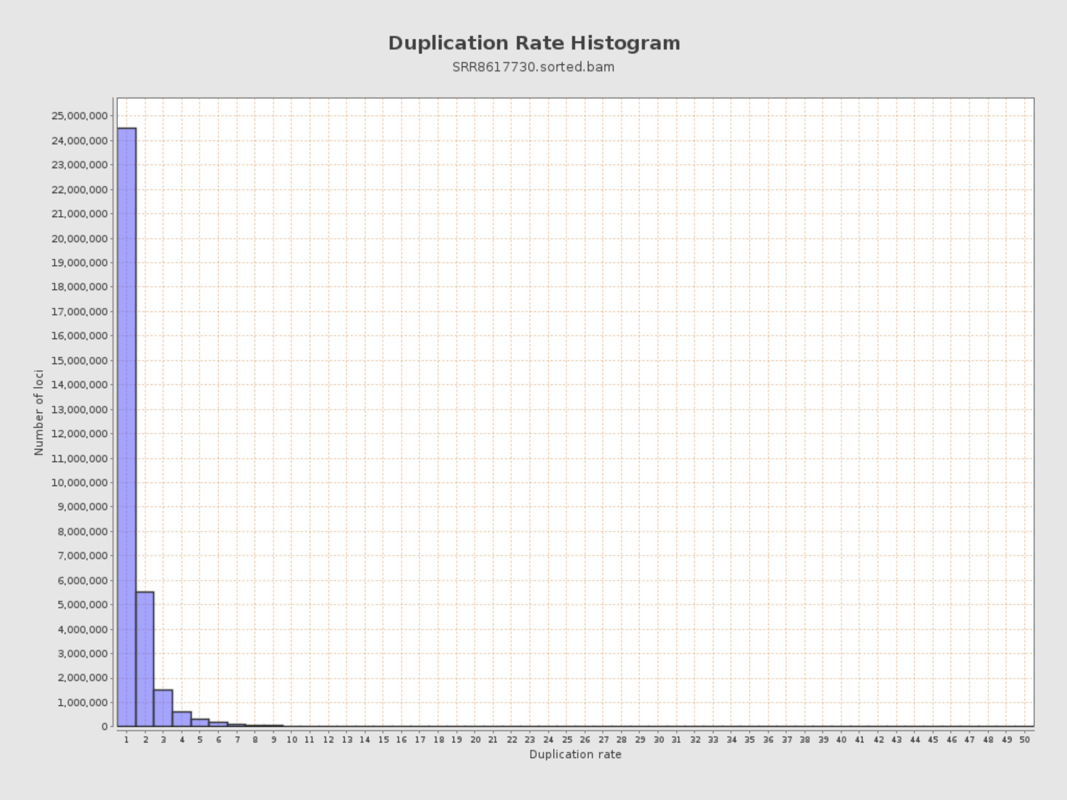
5. Results : Coverage Histogram (0-50X)



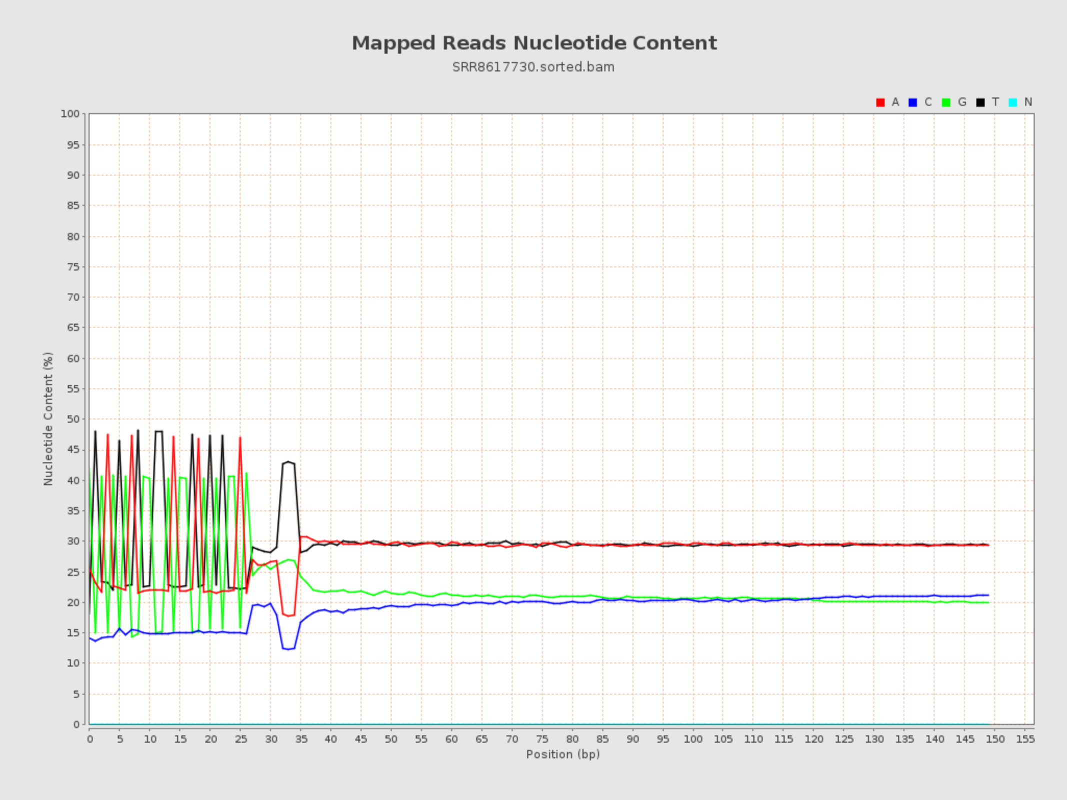
6. Results : Genome Fraction Coverage



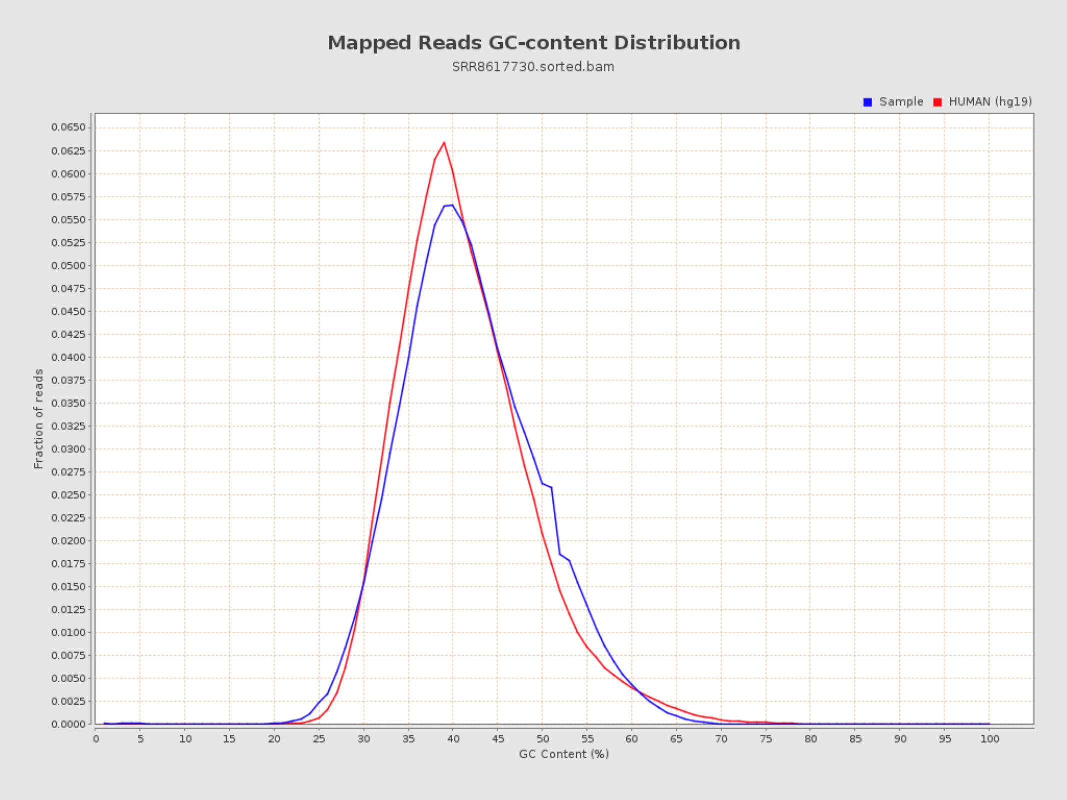
7. Results : Duplication Rate Histogram



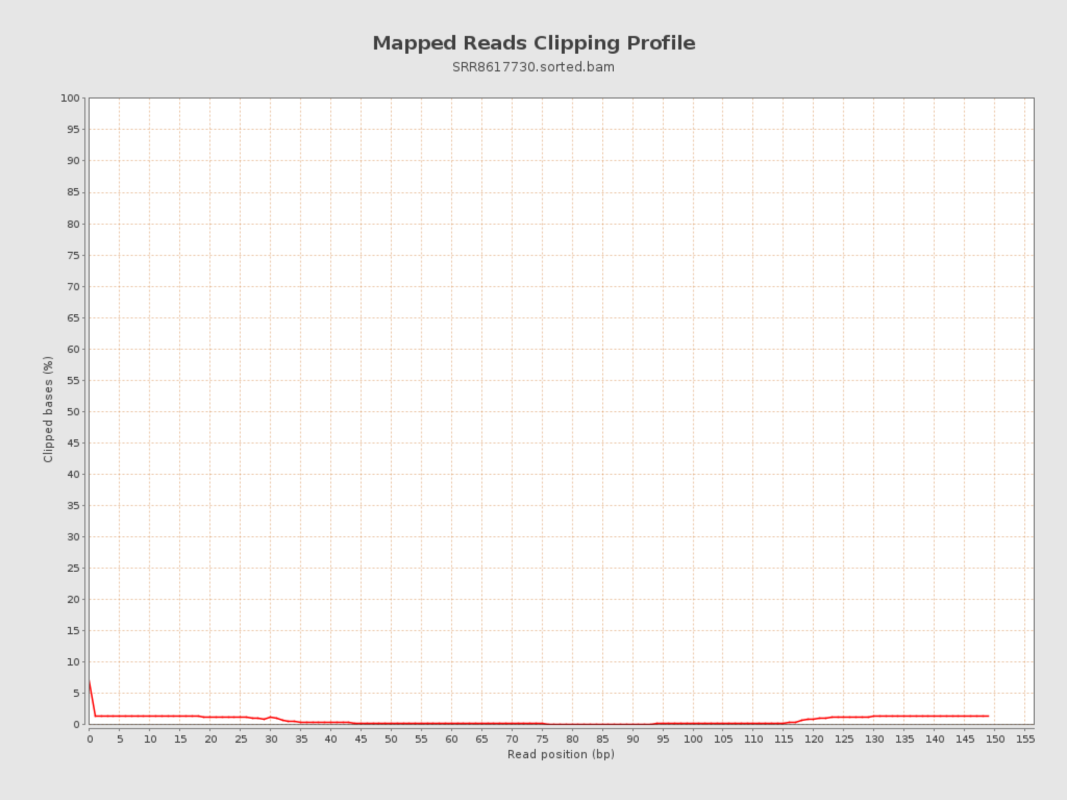
8. Results : Mapped Reads Nucleotide Content



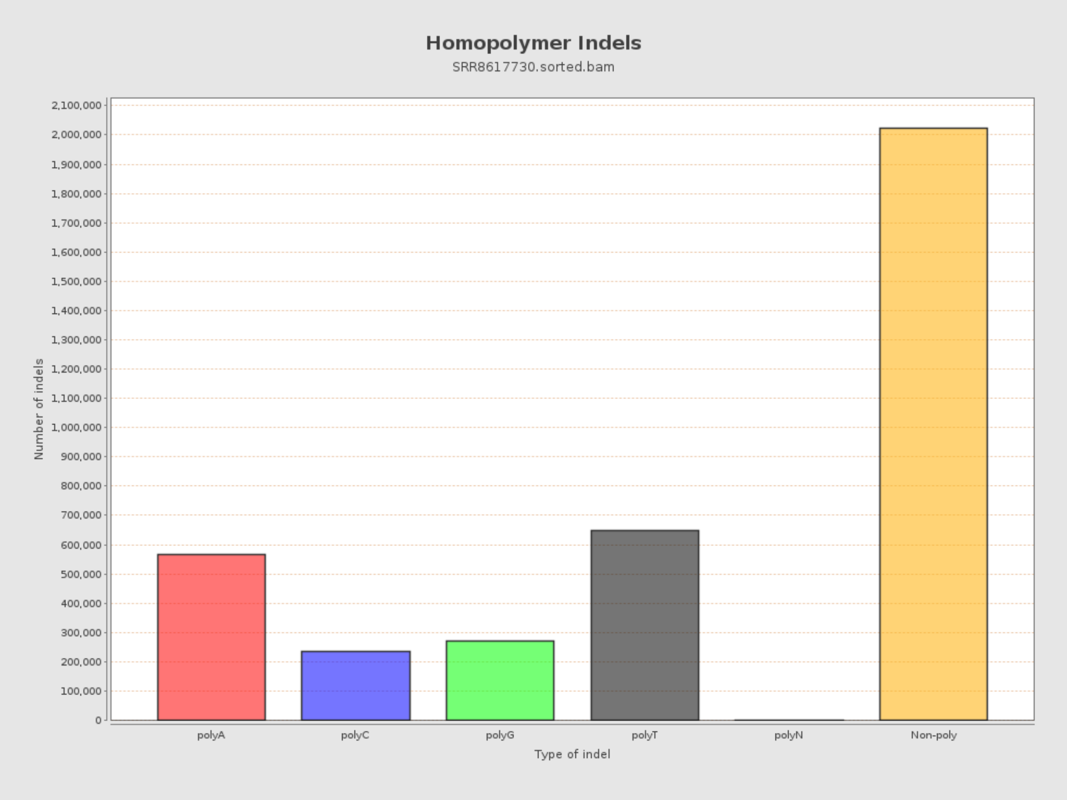
9. Results : Mapped Reads GC-content Distribution



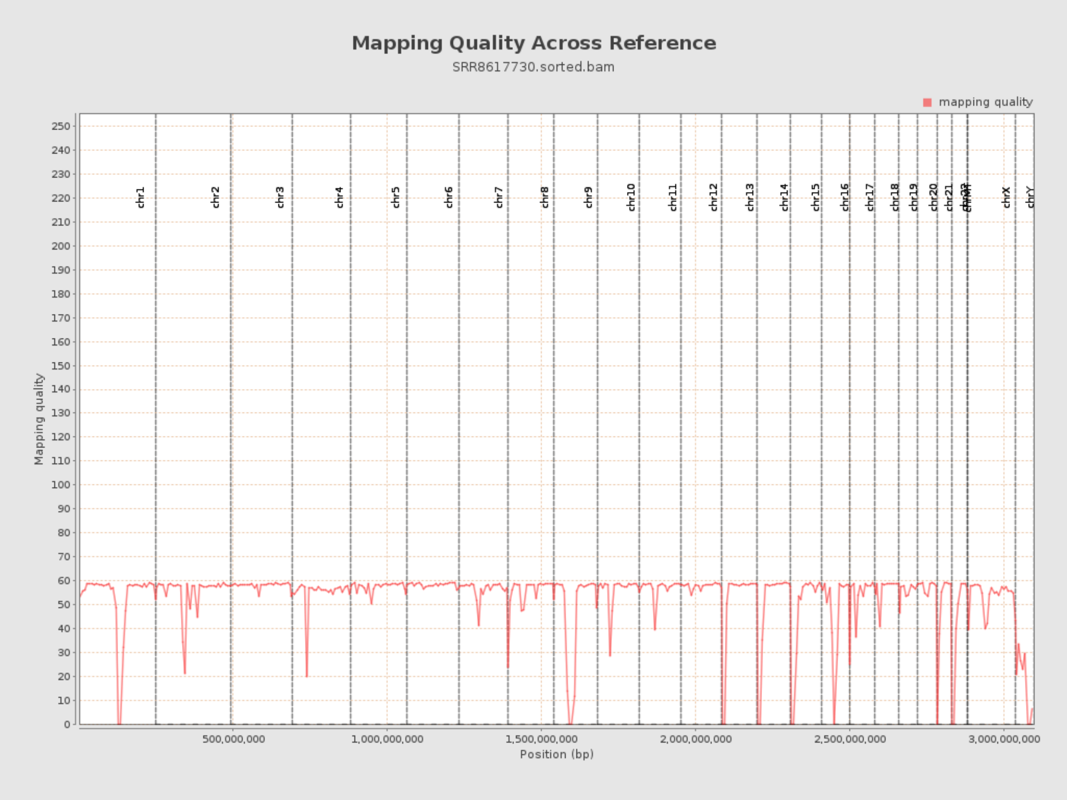
10. Results : Mapped Reads Clipping Profile



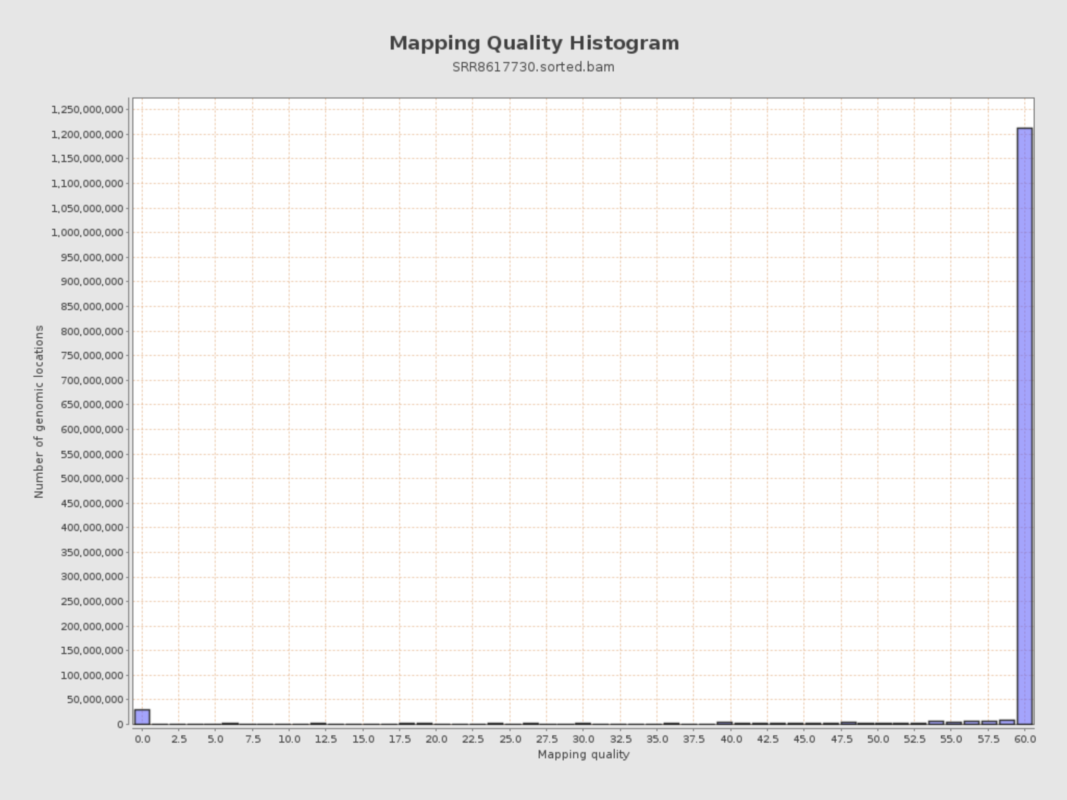
11. Results : Homopolymer Indels



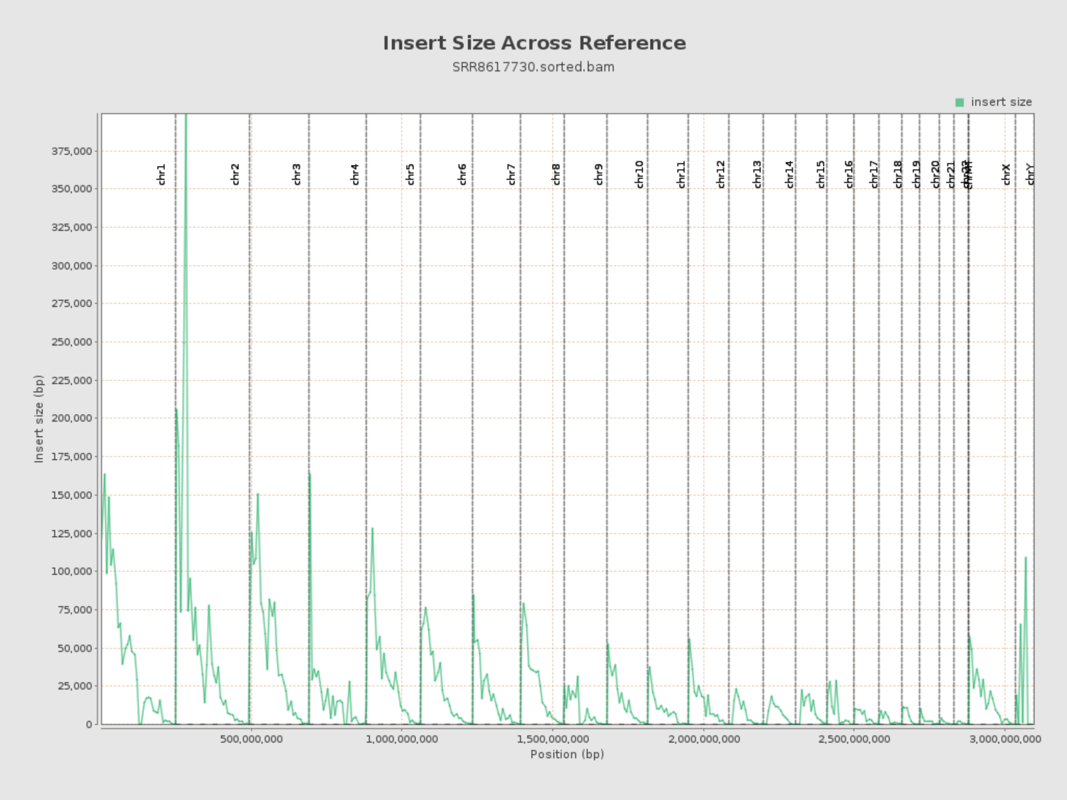
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram