Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 01:52:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617580.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_SRR8617580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617580_1.fastq.gz SRR8617580_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 01:52:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,353,382
Mapped reads	47,974,583 / 97.21%
Unmapped reads	1,378,799 / 2.79%
Mapped paired reads	47,974,583 / 97.21%
Mapped reads, first in pair	24,252,873 / 49.14%
Mapped reads, second in pair	23,721,710 / 48.07%
Mapped reads, both in pair	47,114,368 / 95.46%
Mapped reads, singletons	860,215 / 1.74%
Secondary alignments	0
Supplementary alignments	3,675,650 / 7.45%
Read min/max/mean length	30 / 150 / 153.83
Duplicated reads (estimated)	13,451,316 / 27.26%
Duplication rate	17.26%
Clipped reads	30,245,876 / 61.28%

2.2. ACGT Content

Number/percentage of A's	1,837,590,243 / 28.72%
Number/percentage of C's	1,252,888,600 / 19.58%
Number/percentage of T's	1,870,954,513 / 29.24%
Number/percentage of G's	1,436,635,186 / 22.45%
Number/percentage of N's	101,698 / 0%

GC Percentage	42.04%

2.3. Coverage

Mean	2.0684
Standard Deviation	26.9717

2.4. Mapping Quality

Mean Mapping Quality	52.15

2.5. Insert size

Mean	690,208.61
Standard Deviation	8,056,426.51
P25/Median/P75	204 / 272 / 354

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	84,413,835
Insertions	1,126,098
Mapped reads with at least one insertion	2.23%
Deletions	2,417,555
Mapped reads with at least one deletion	4.84%
Homopolymer indels	44.89%

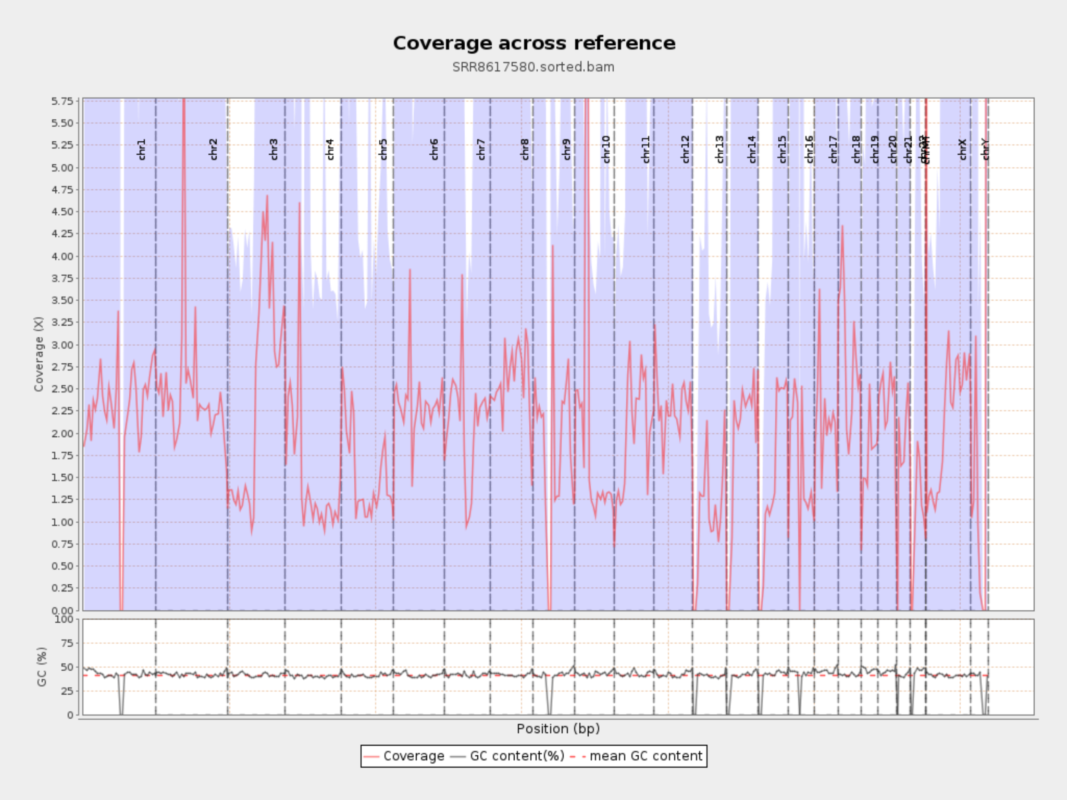
2.7. Chromosome stats

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

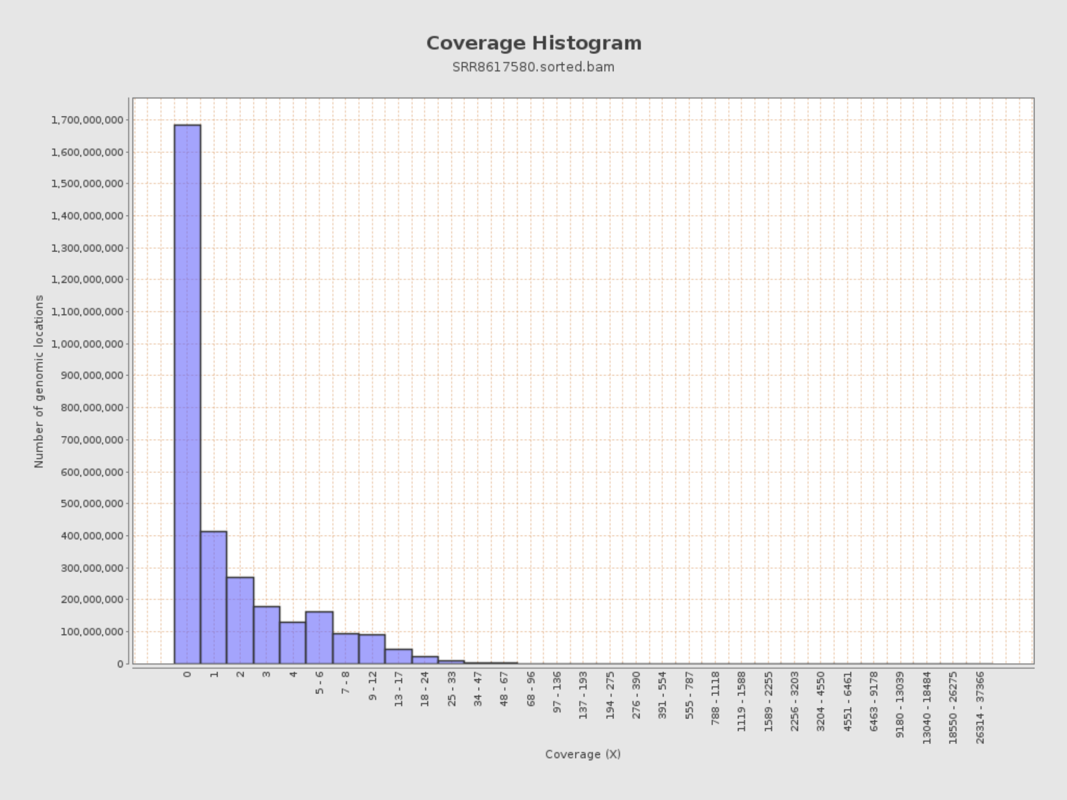
		bases	**coverage**	**deviation**
chr1	249250621	560597038	2.2491	16.8025
chr2	243199373	607175309	2.4966	26.6564
chr3	198022430	477708603	2.4124	5.4832
chr4	191154276	290714991	1.5208	15.8195
chr5	180915260	281045192	1.5535	3.7051
chr6	171115067	400477146	2.3404	18.325
chr7	159138663	339821948	2.1354	29.7174
chr8	146364022	379735389	2.5945	8.4202
chr9	141213431	264229410	1.8711	46.4049
chr10	135534747	282320528	2.083	78.6122
chr11	135006516	272625424	2.0194	20.2283
chr12	133851895	310579389	2.3203	9.8981
chr13	115169878	126383996	1.0974	2.6252
chr14	107349540	204676034	1.9066	4.3713
chr15	102531392	153425972	1.4964	5.9863
chr16	90354753	142689983	1.5792	12.0375
chr17	81195210	177603299	2.1874	22.7239
chr18	78077248	228171064	2.9224	37.9052
chr19	59128983	102865300	1.7397	10.1124
chr20	63025520	152499328	2.4196	6.5146
chr21	48129895	87908926	1.8265	8.7858
chr22	51304566	52974752	1.0326	3.3347
chrMT	16571	562568	33.9489	16.8454
chrX	155270560	332358020	2.1405	7.4897

chrY	59373566	173989158	2.9304	75.4641

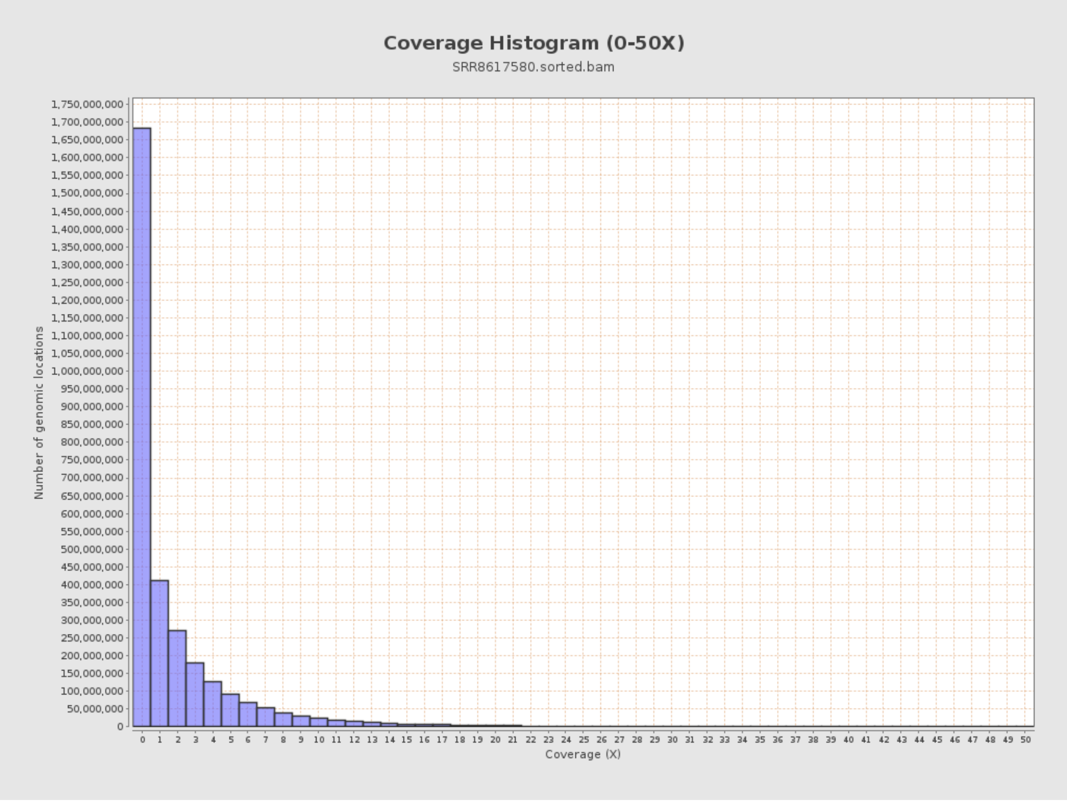
3. Results : Coverage across reference



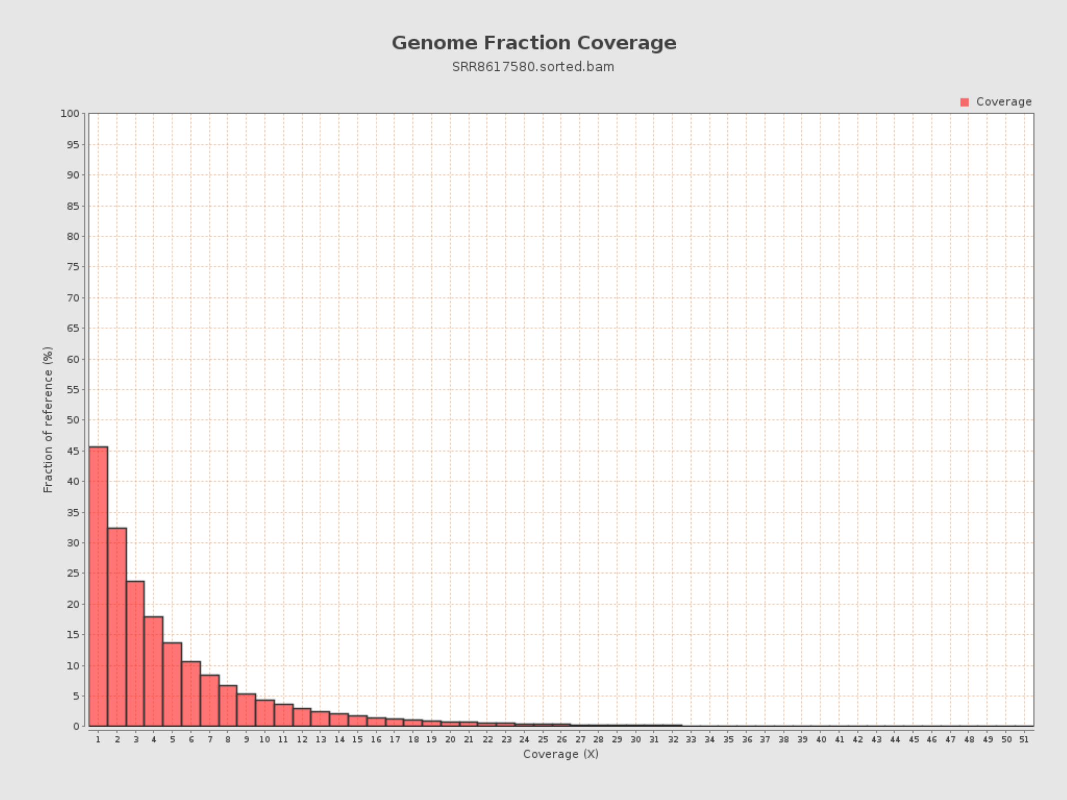
4. Results : Coverage Histogram



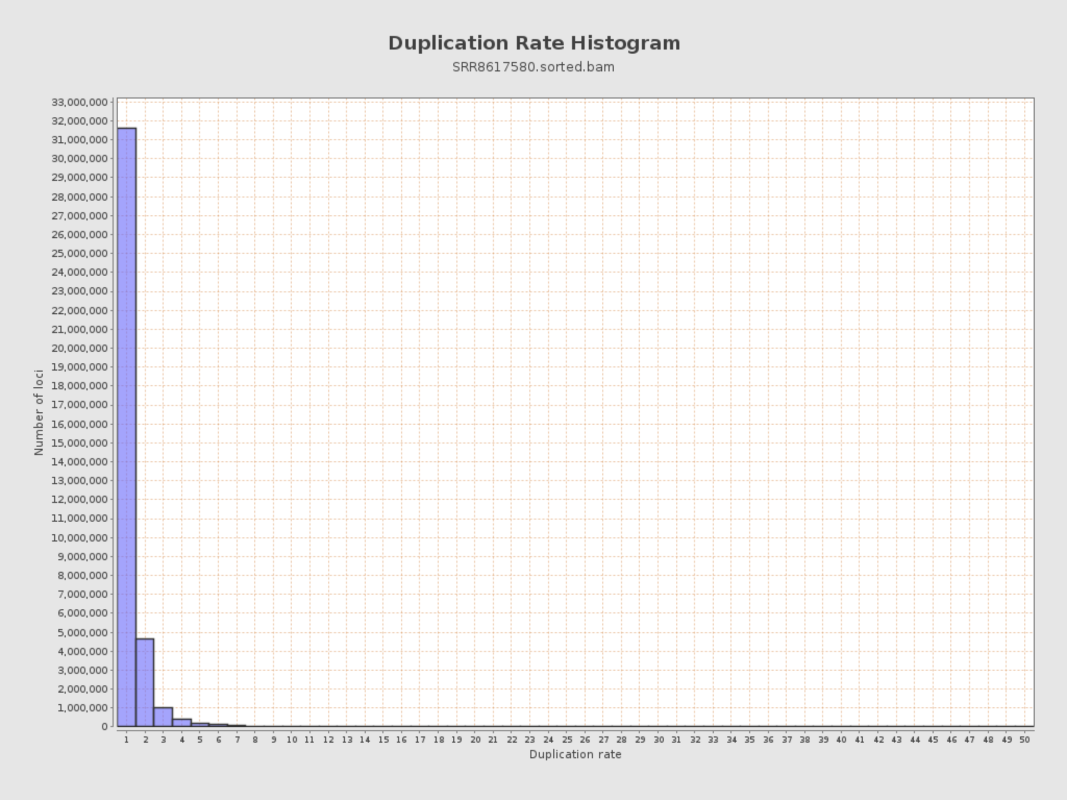
5. Results : Coverage Histogram (0-50X)



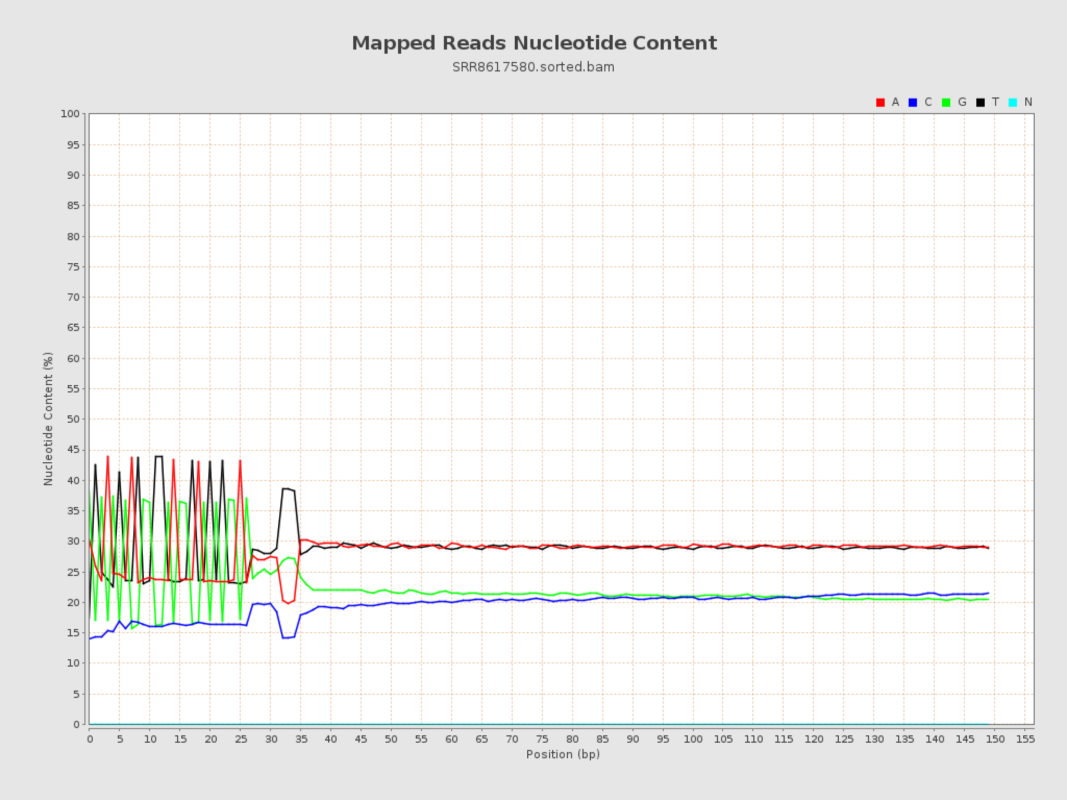
6. Results : Genome Fraction Coverage



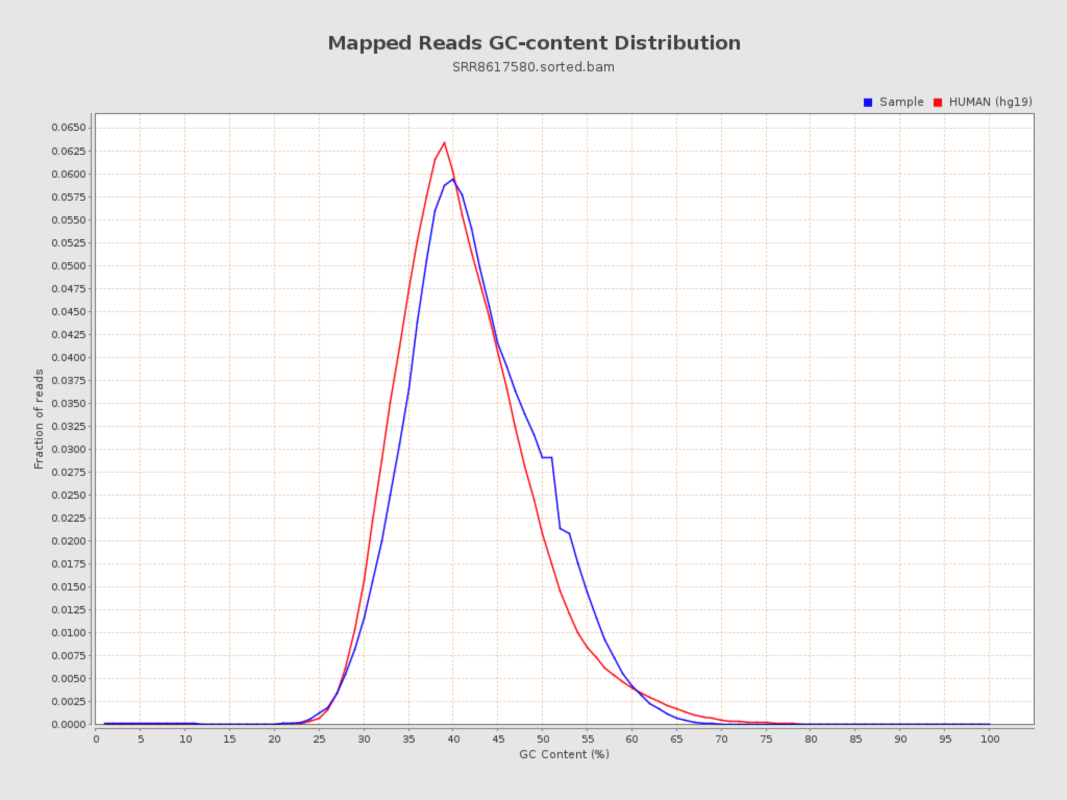
7. Results : Duplication Rate Histogram



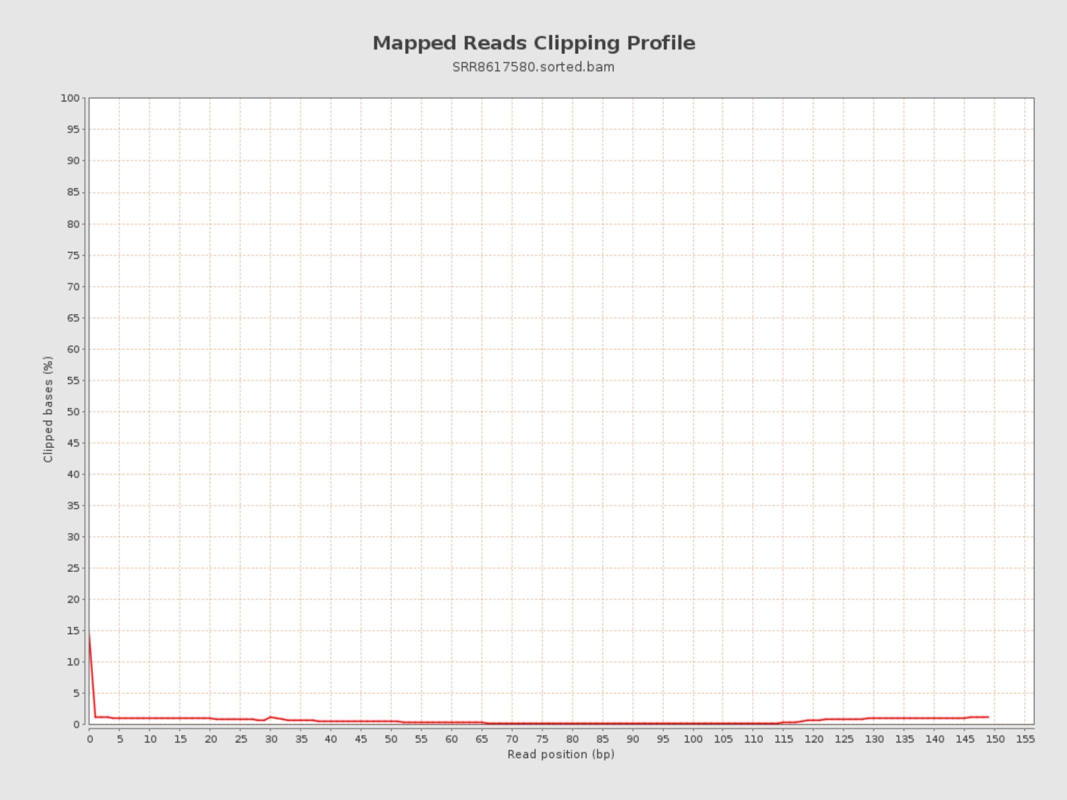
8. Results : Mapped Reads Nucleotide Content



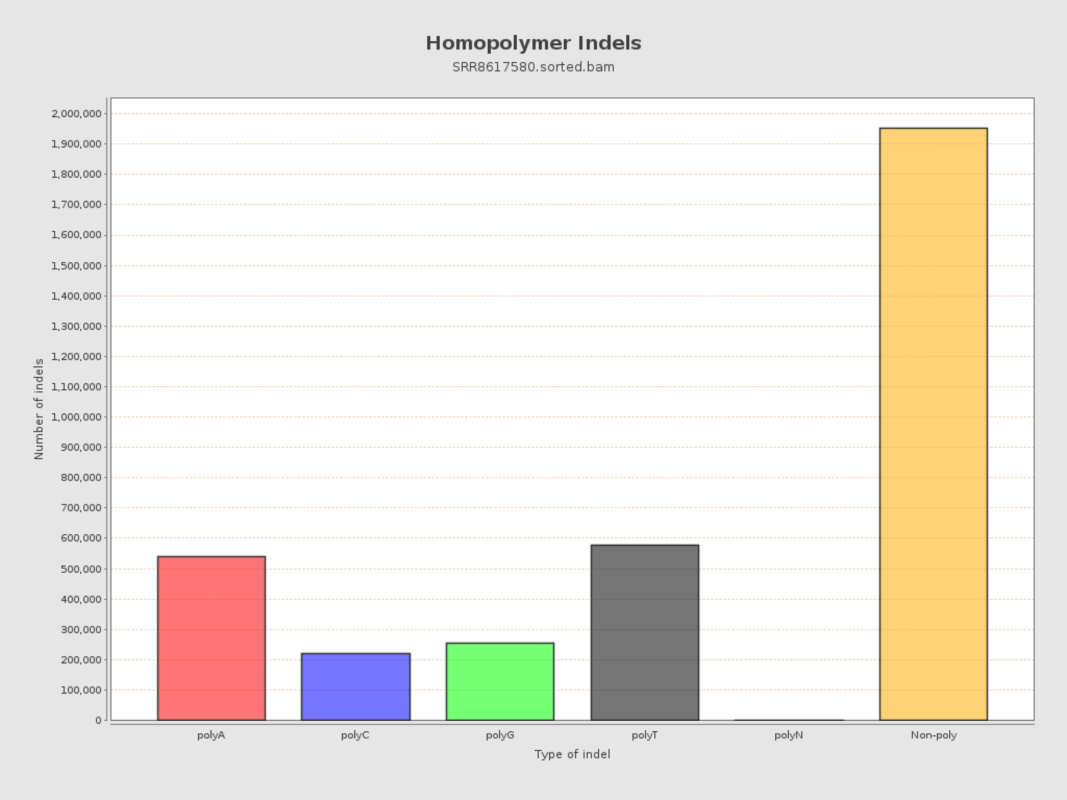
9. Results : Mapped Reads GC-content Distribution



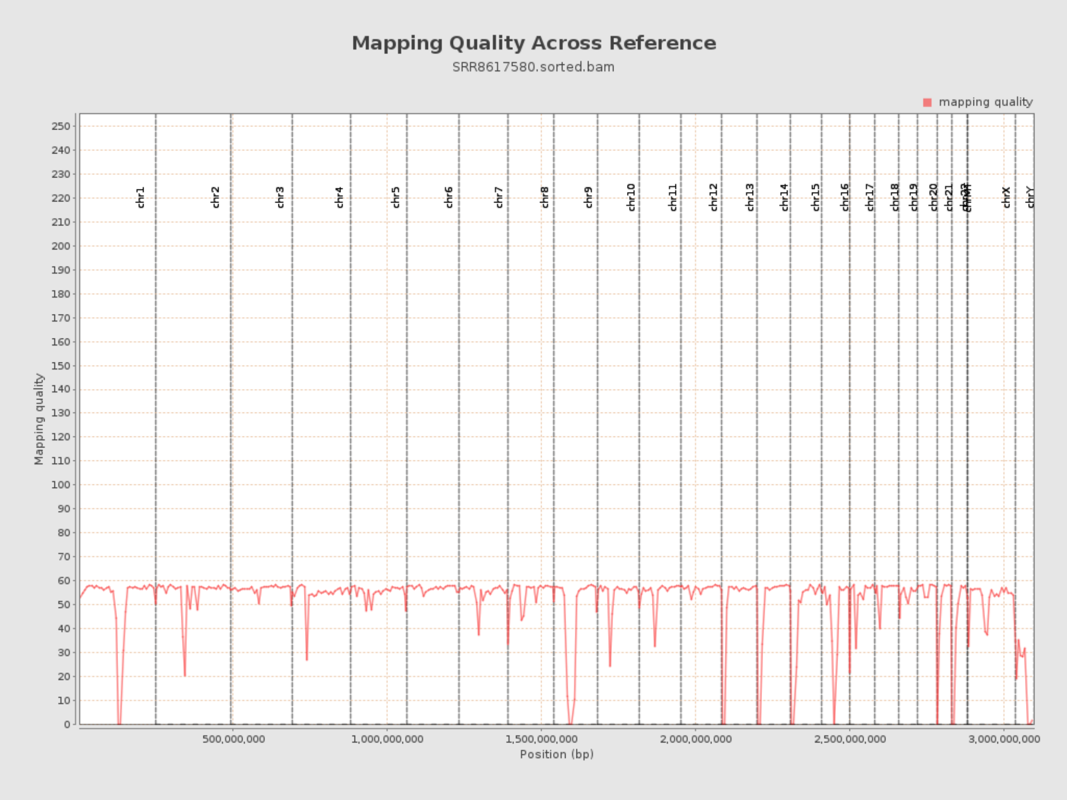
10. Results : Mapped Reads Clipping Profile



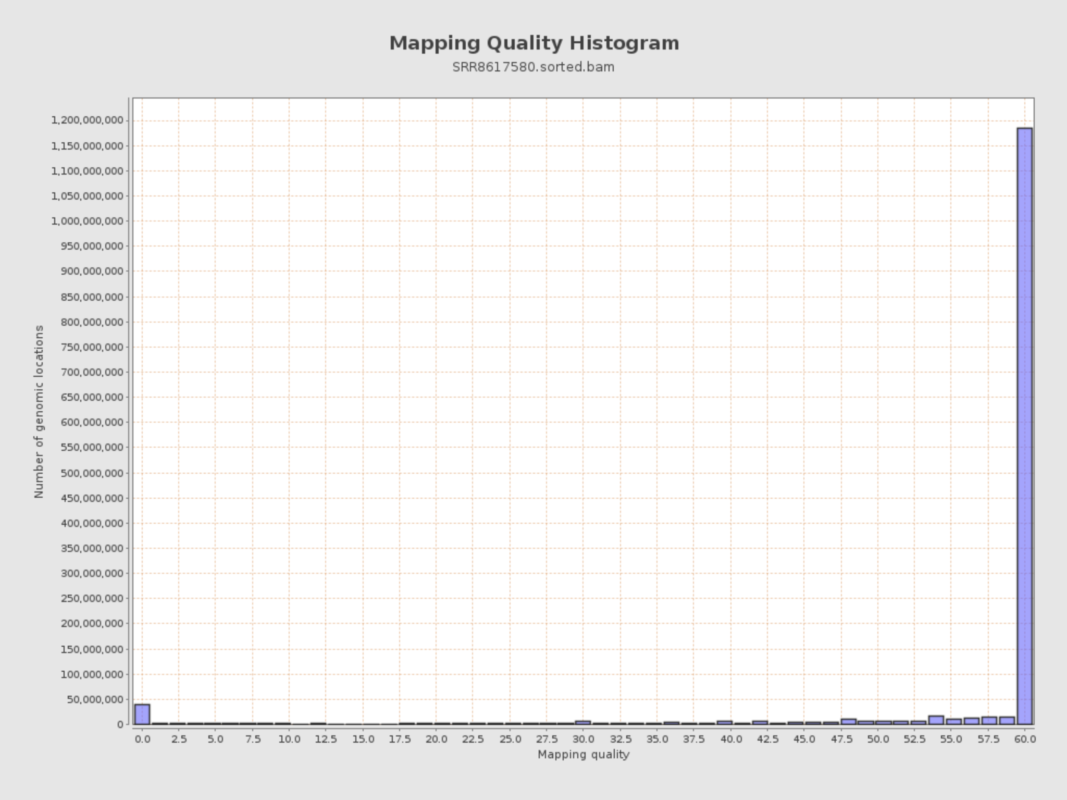
11. Results : Homopolymer Indels



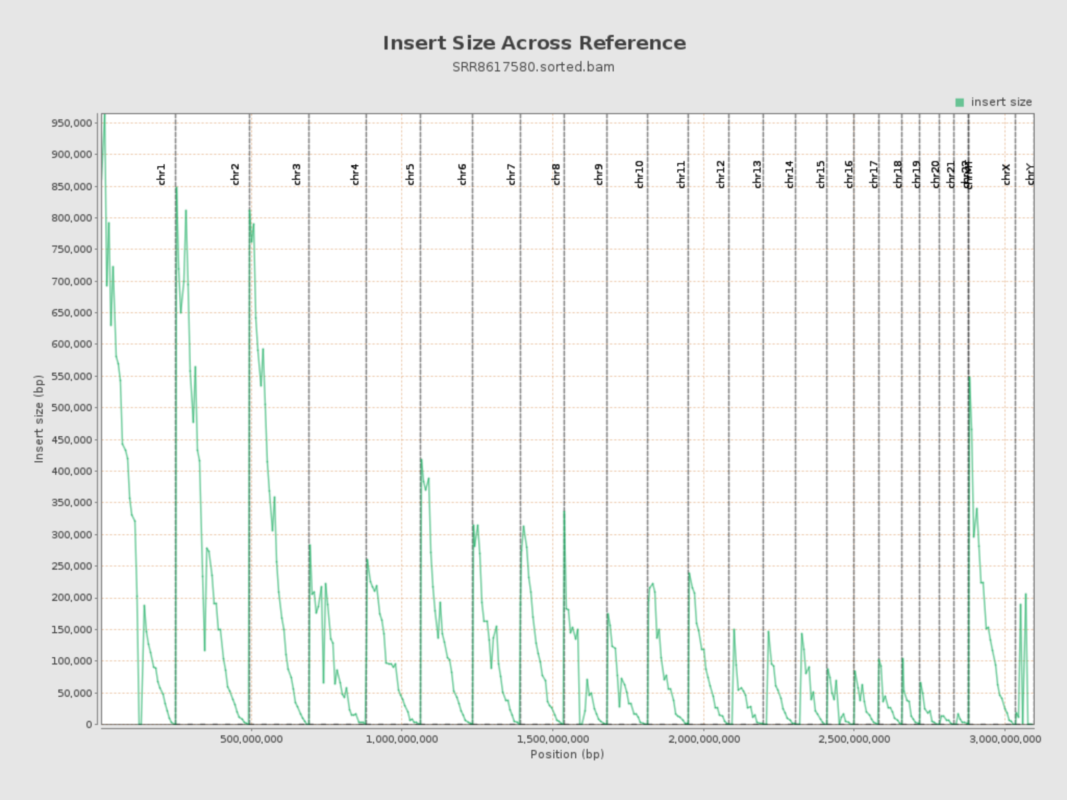
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram