Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 14:31:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617488.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_SRR617488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617488_1.fastq.gz SRR617488_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 14:31:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,438,445 / 95.12%
Unmapped reads	1,561,555 / 4.88%
Mapped paired reads	30,438,445 / 95.12%
Mapped reads, first in pair	15,357,574 / 47.99%
Mapped reads, second in pair	15,080,871 / 47.13%
Mapped reads, both in pair	29,881,072 / 93.38%
Mapped reads, singletons	557,373 / 1.74%
Secondary alignments	0
Supplementary alignments	151,318 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	6,225,214 / 19.45%
Duplication rate	9.89%
Clipped reads	6,074,776 / 18.98%

2.2. ACGT Content

Number/percentage of A's	873,315,419 / 29.48%
Number/percentage of C's	598,535,386 / 20.2%
Number/percentage of T's	873,239,640 / 29.48%
Number/percentage of G's	614,131,903 / 20.73%
Number/percentage of N's	3,409,233 / 0.12%

GC Percentage	40.93%

2.3. Coverage

Mean	0.9576
Standard Deviation	9.5896

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	34,647.71
Standard Deviation	1,734,874.55
P25/Median/P75	174 / 219 / 291

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	38,979,750
Insertions	440,911
Mapped reads with at least one insertion	1.42%
Deletions	1,030,481
Mapped reads with at least one deletion	3.32%
Homopolymer indels	47.36%

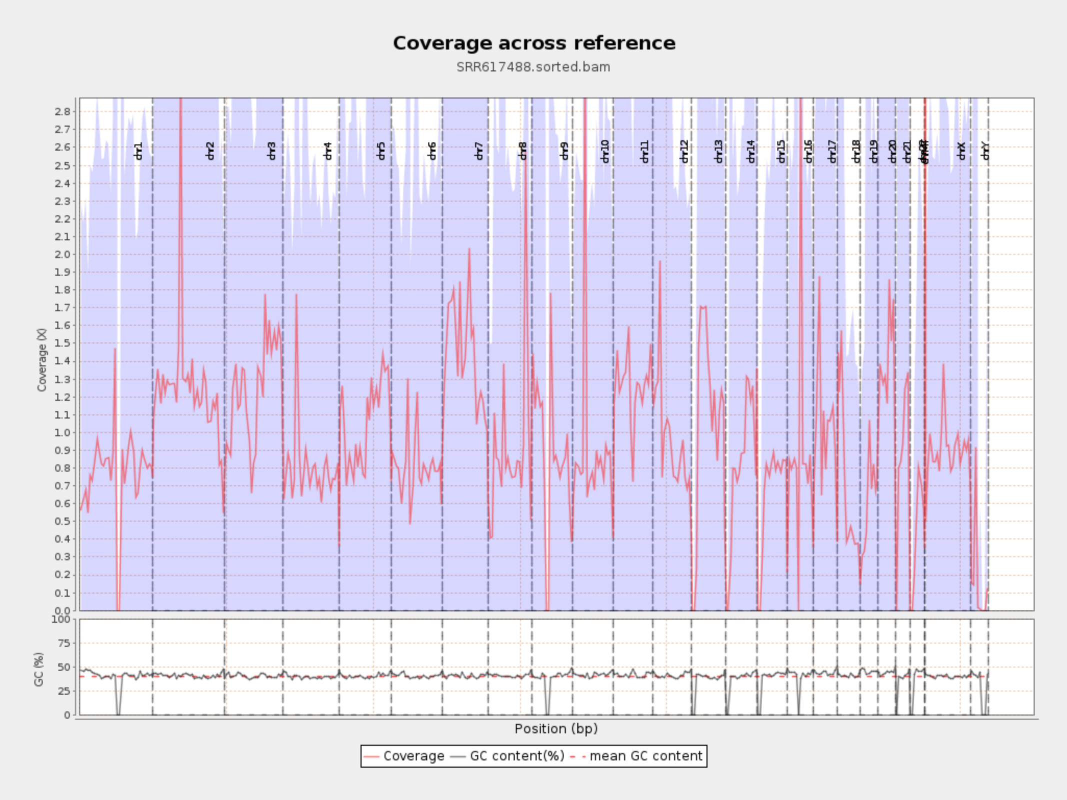
2.7. Chromosome stats

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

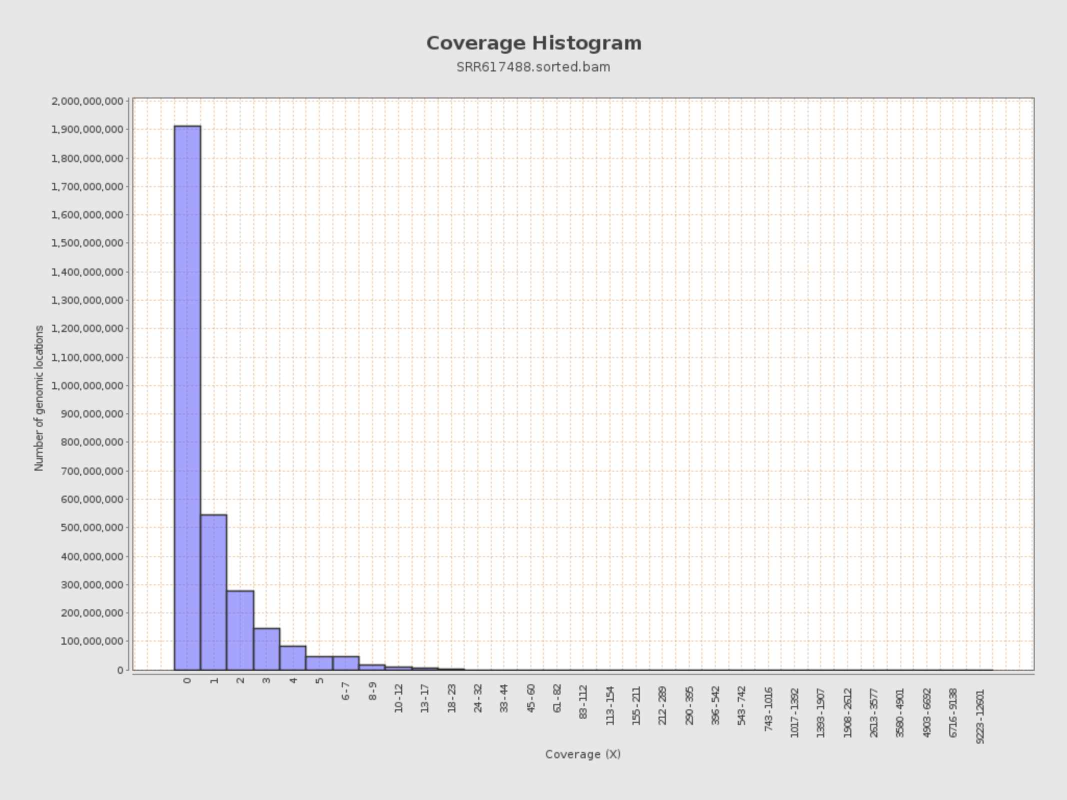
		bases	coverage	deviation
chr1	249250621	191049923	0.7665	9.4541
chr2	243199373	306212060	1.2591	11.2673
chr3	198022430	245082130	1.2376	2.2415
chr4	191154276	153136380	0.8011	5.9852
chr5	180915260	190239604	1.0515	2.0697
chr6	171115067	139873778	0.8174	5.4043
chr7	159138663	228593366	1.4364	13.1577
chr8	146364022	131832338	0.9007	3.8375
chr9	141213431	122355799	0.8665	17.8883
chr10	135534747	125347952	0.9248	18.4756
chr11	135006516	167196832	1.2384	12.5453
chr12	133851895	129384478	0.9666	1.9835
chr13	115169878	125700485	1.0914	2.1198
chr14	107349540	86159162	0.8026	2.1904
chr15	102531392	66903163	0.6525	1.4718
chr16	90354753	80098627	0.8865	14.8012
chr17	81195210	82476856	1.0158	13.2968
chr18	78077248	53200449	0.6814	16.9612
chr19	59128983	35383431	0.5984	5.7291
chr20	63025520	87711961	1.3917	2.7946
chr21	48129895	42798297	0.8892	3.7576
chr22	51304566	22242217	0.4335	1.2396
chrMT	16571	2102559	126.8818	91.6088
chrX	155270560	139135706	0.8961	4.0786

chrY	59373566	10166815	0.1712	13.4504

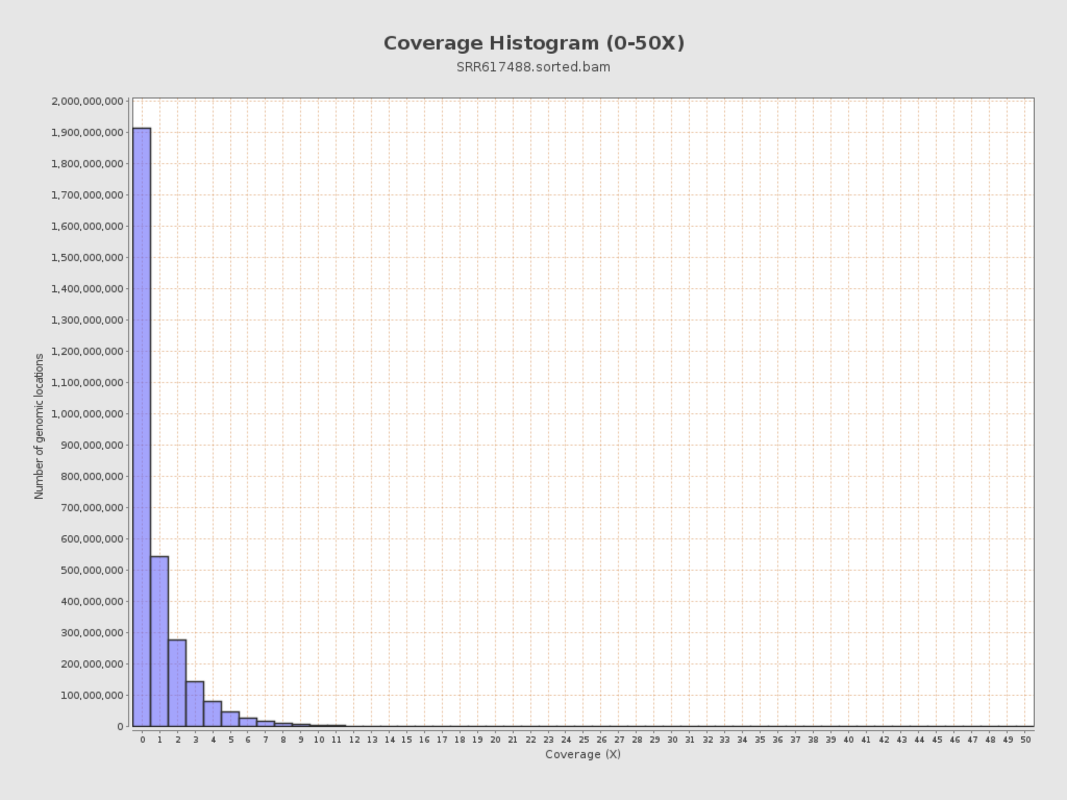
3. Results : Coverage across reference



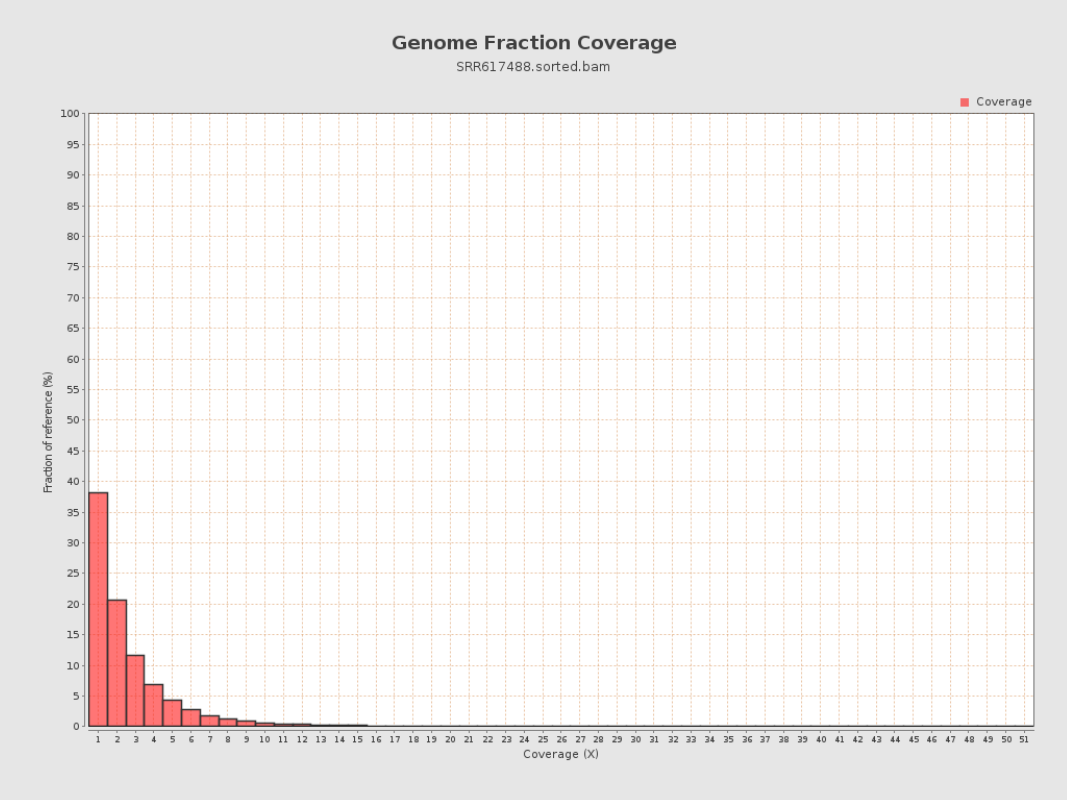
4. Results : Coverage Histogram



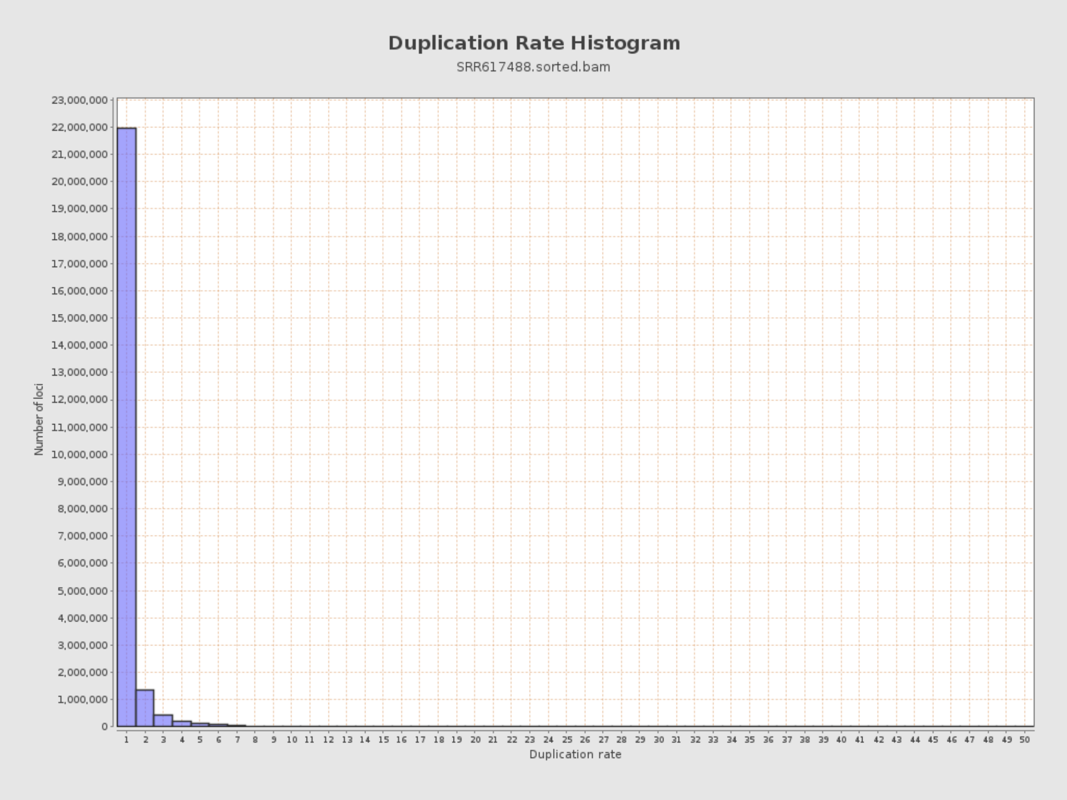
5. Results : Coverage Histogram (0-50X)



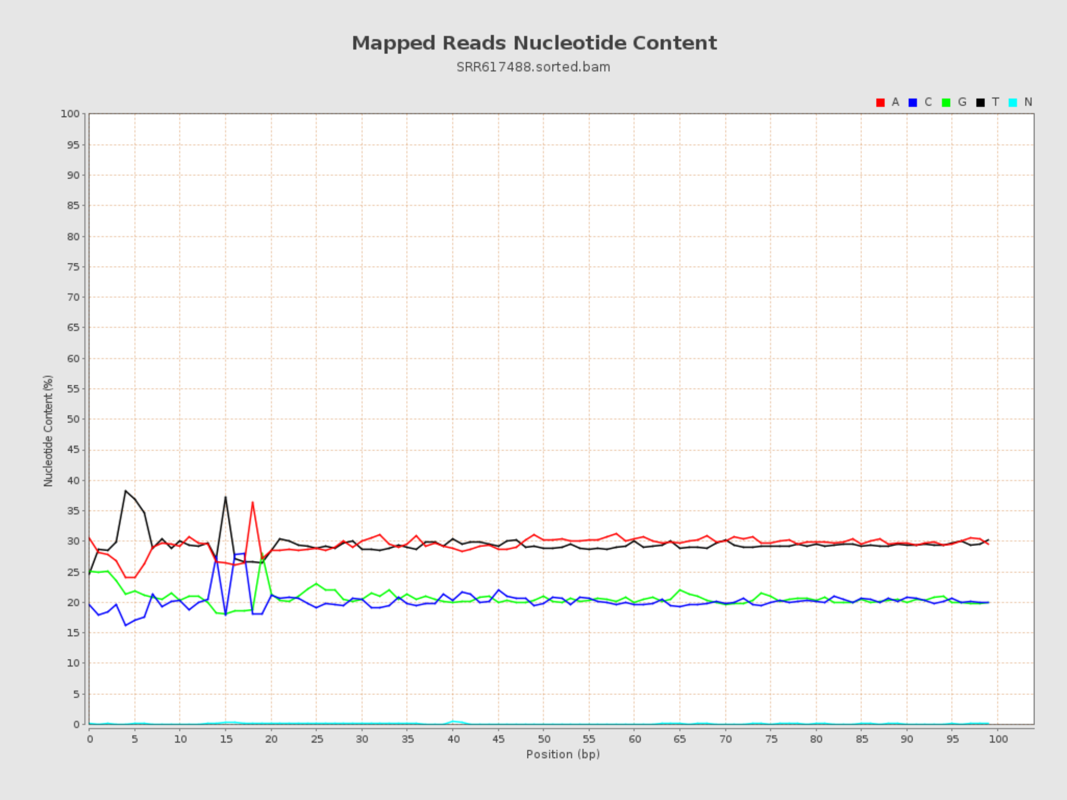
6. Results : Genome Fraction Coverage



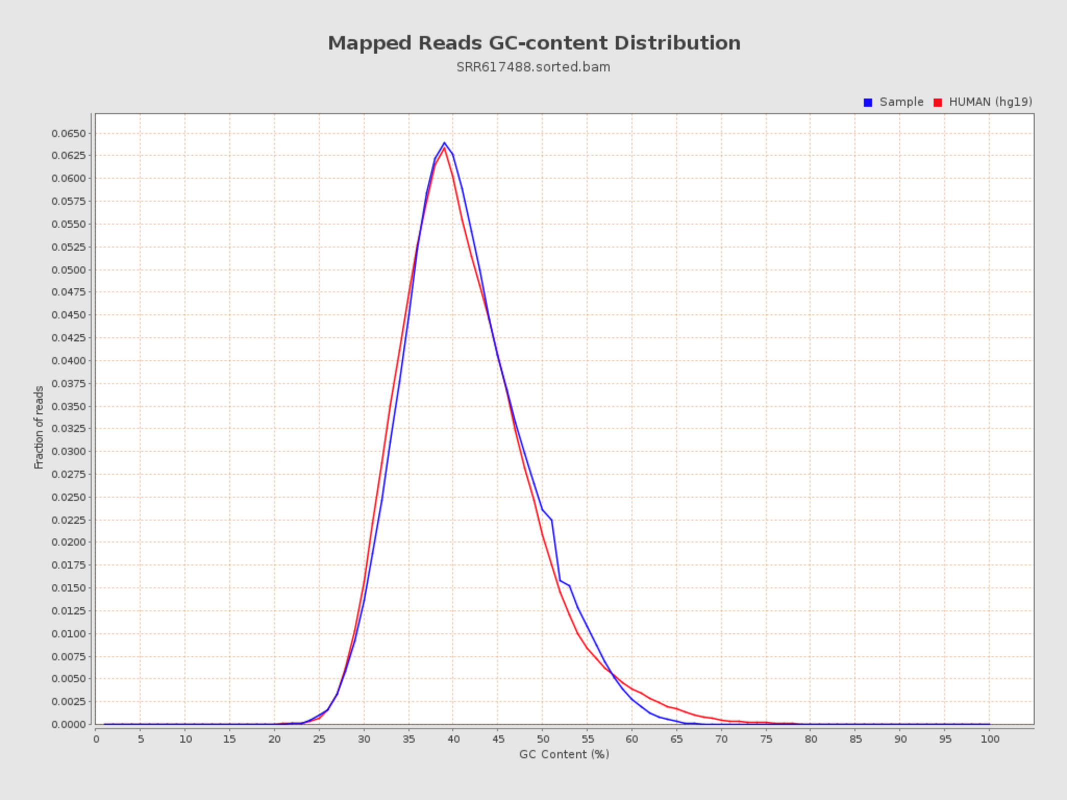
7. Results : Duplication Rate Histogram



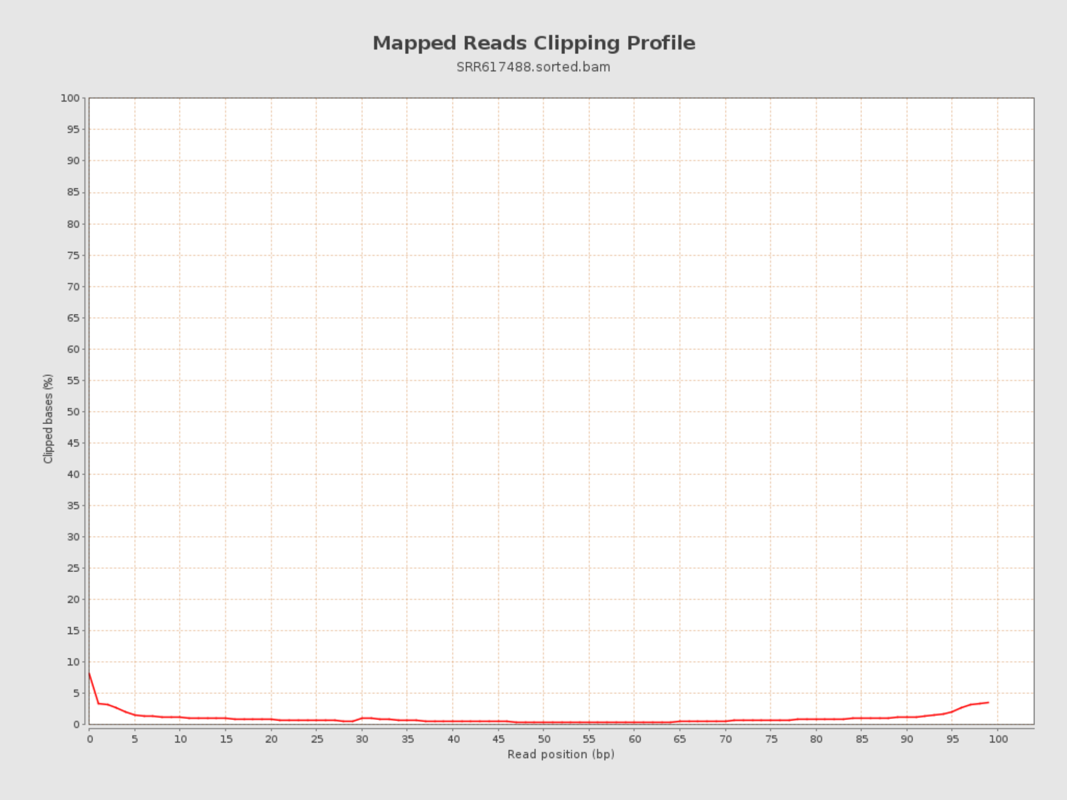
8. Results : Mapped Reads Nucleotide Content



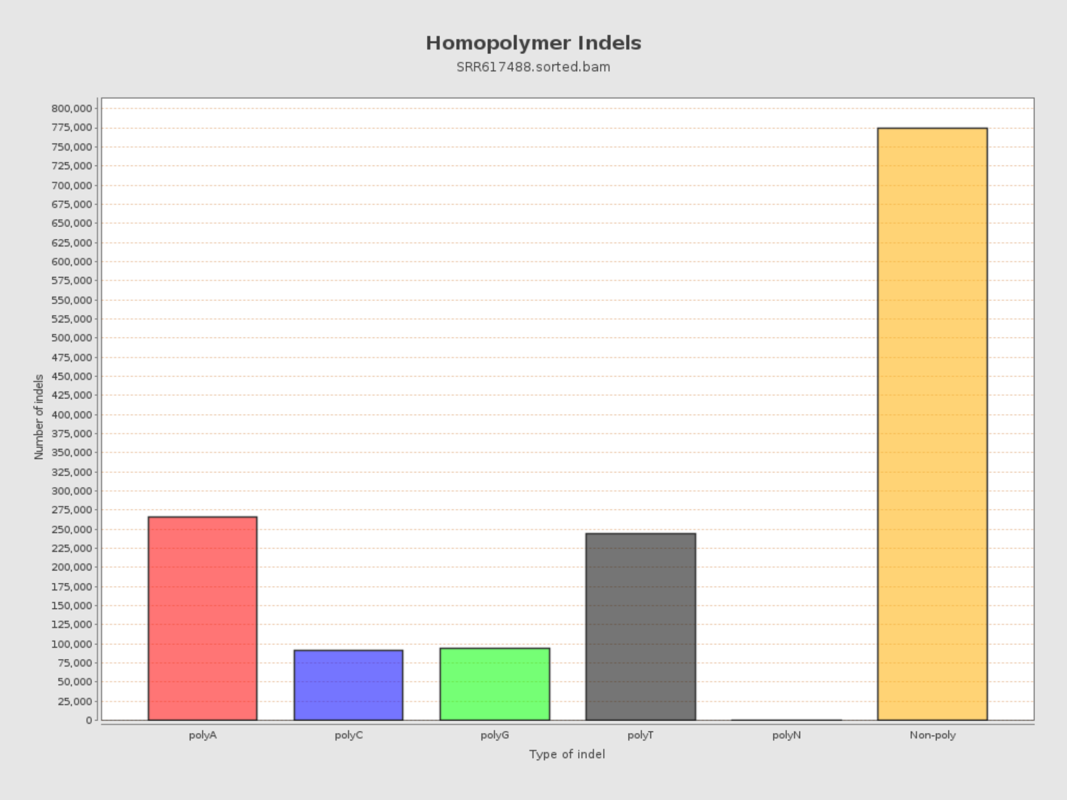
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

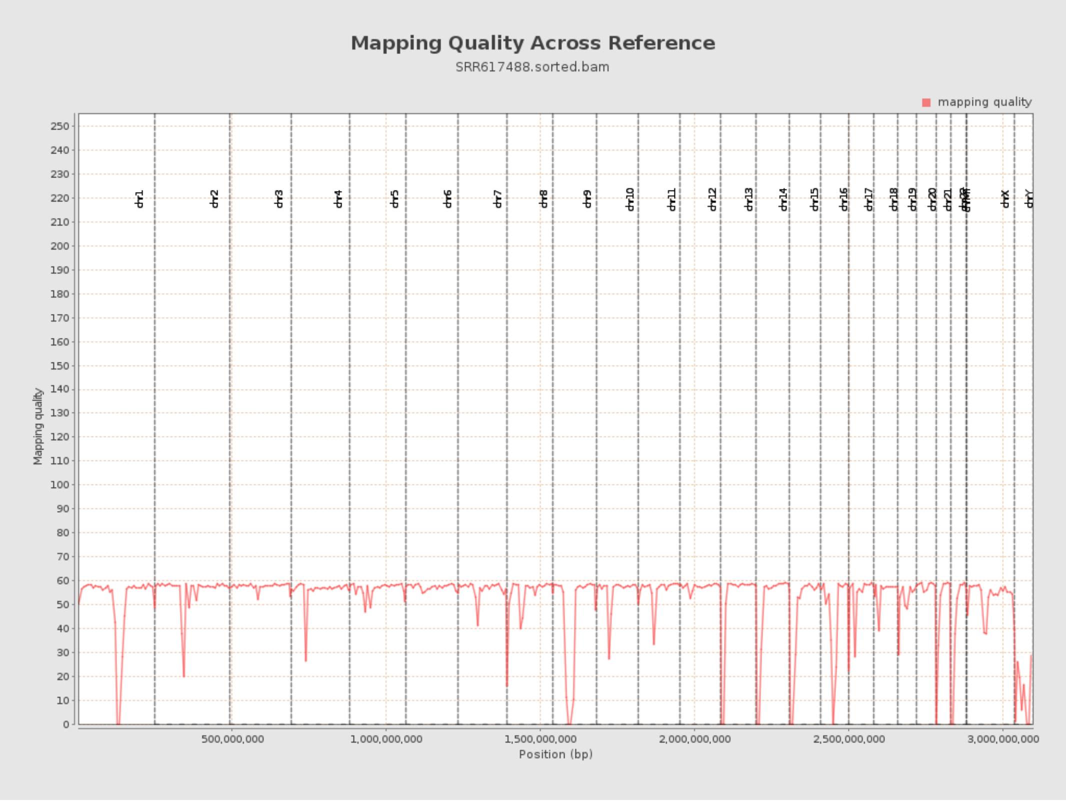


11. Results : Homopolymer Indels

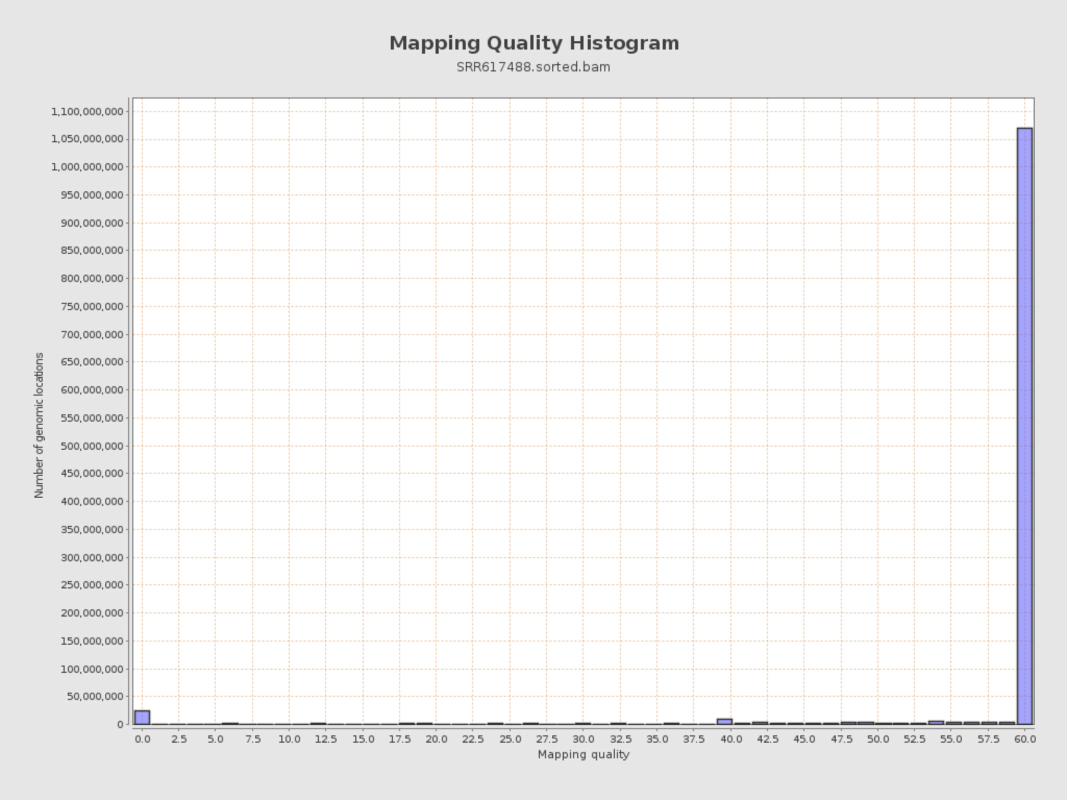


]

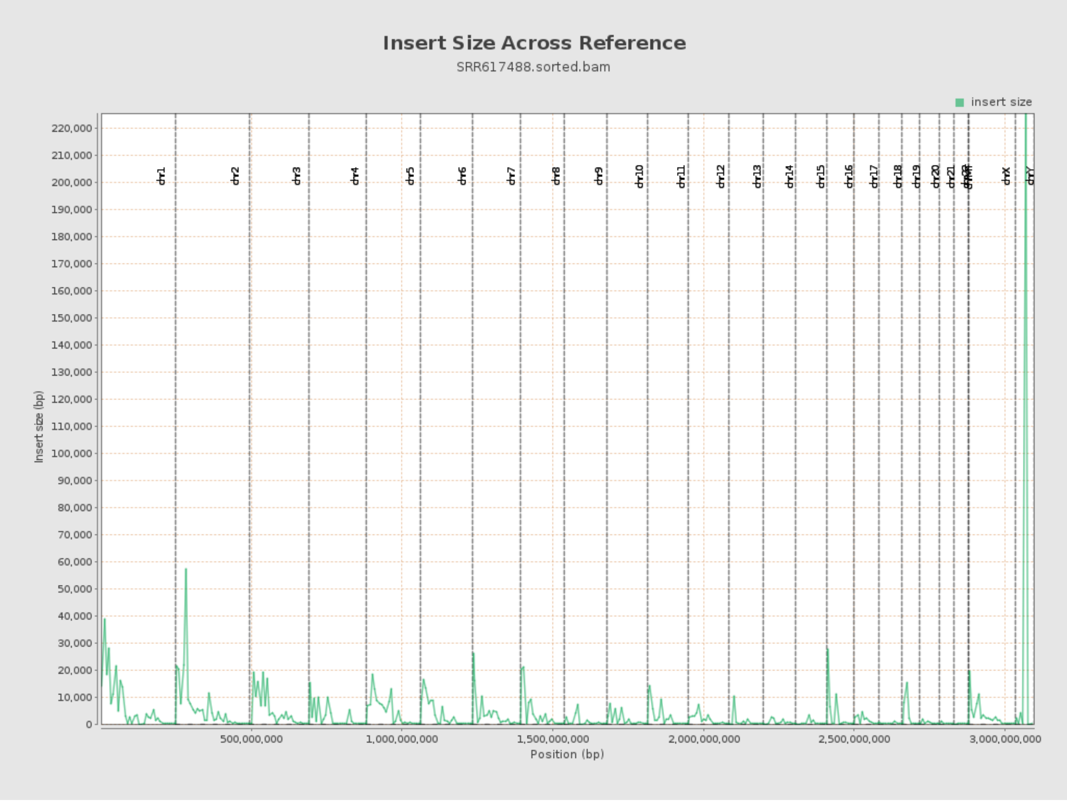
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram