Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 21:14:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504619.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_SRR504619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504619_1.fastq.gz SRR504619_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 21:14:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	299,995,974
Mapped reads	283,676,668 / 94.56%
Unmapped reads	16,319,306 / 5.44%
Mapped paired reads	283,676,668 / 94.56%
Mapped reads, first in pair	142,392,541 / 47.46%
Mapped reads, second in pair	141,284,127 / 47.1%
Mapped reads, both in pair	279,093,806 / 93.03%
Mapped reads, singletons	4,582,862 / 1.53%
Secondary alignments	0
Supplementary alignments	3,090,492 / 1.03%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	84,254,802 / 28.09%
Duplication rate	18.17%
Clipped reads	43,480,551 / 14.49%

2.2. ACGT Content

Number/percentage of A's	7,273,602,269 / 26.67%
Number/percentage of C's	6,312,022,780 / 23.15%
Number/percentage of T's	7,348,824,311 / 26.95%
Number/percentage of G's	6,332,474,387 / 23.22%
Number/percentage of N's	4,170,416 / 0.02%

GC Percentage	46.37%

2.3. Coverage

Mean	8.8176
Standard Deviation	219.2619

2.4. Mapping Quality

Mean Mapping Quality	52.31

2.5. Insert size

Mean	115,540.84
Standard Deviation	3,205,702.08
P25/Median/P75	283 / 336 / 394

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	285,842,158
Insertions	8,313,098
Mapped reads with at least one insertion	2.71%
Deletions	7,716,956
Mapped reads with at least one deletion	2.53%
Homopolymer indels	34.65%

2.7. Chromosome stats

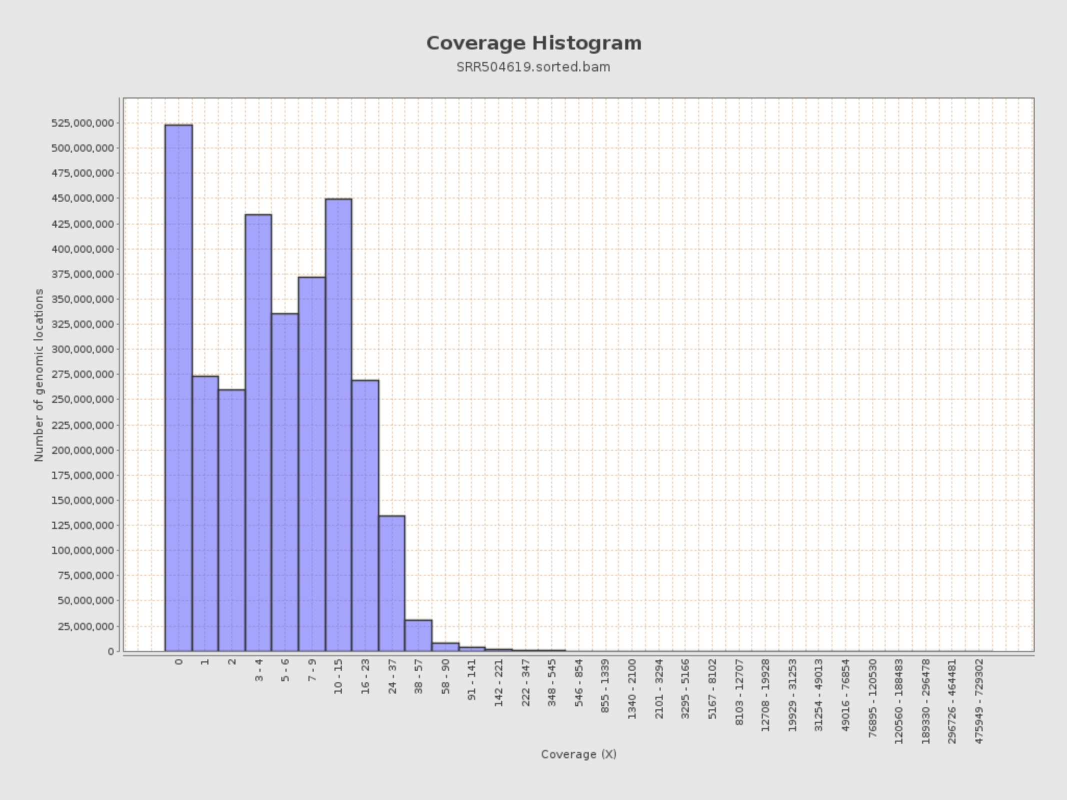
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	2103347378	8.4387	62.2466
chr2	243199373	2162895632	8.8935	229.4053
chr3	198022430	1448599307	7.3153	19.8619
chr4	191154276	2050834652	10.7287	617.9494
chr5	180915260	1413157593	7.8112	32.3466
chr6	171115067	1162463528	6.7935	30.0854
chr7	159138663	1341666441	8.4308	32.6148
chr8	146364022	1275908136	8.7174	153.8033
chr9	141213431	997055359	7.0606	65.4994
chr10	135534747	1793333212	13.2315	466.8509
chr11	135006516	1169785764	8.6647	27.1411
chr12	133851895	1090582913	8.1477	16.7553
chr13	115169878	604619129	5.2498	13.1195
chr14	107349540	727119431	6.7734	28.913
chr15	102531392	796720872	7.7705	14.2382
chr16	90354753	1231129812	13.6255	177.1228
chr17	81195210	943479057	11.6199	65.218
chr18	78077248	619530535	7.9348	251.243
chr19	59128983	922491406	15.6013	36.9119
chr20	63025520	700934741	11.1214	145.7863
chr21	48129895	455503620	9.464	196.166
chr22	51304566	509615525	9.9331	28.8001
chrMT	16571	10496502	633.426	283.1256
chrX	155270560	1326344362	8.5421	18.6382

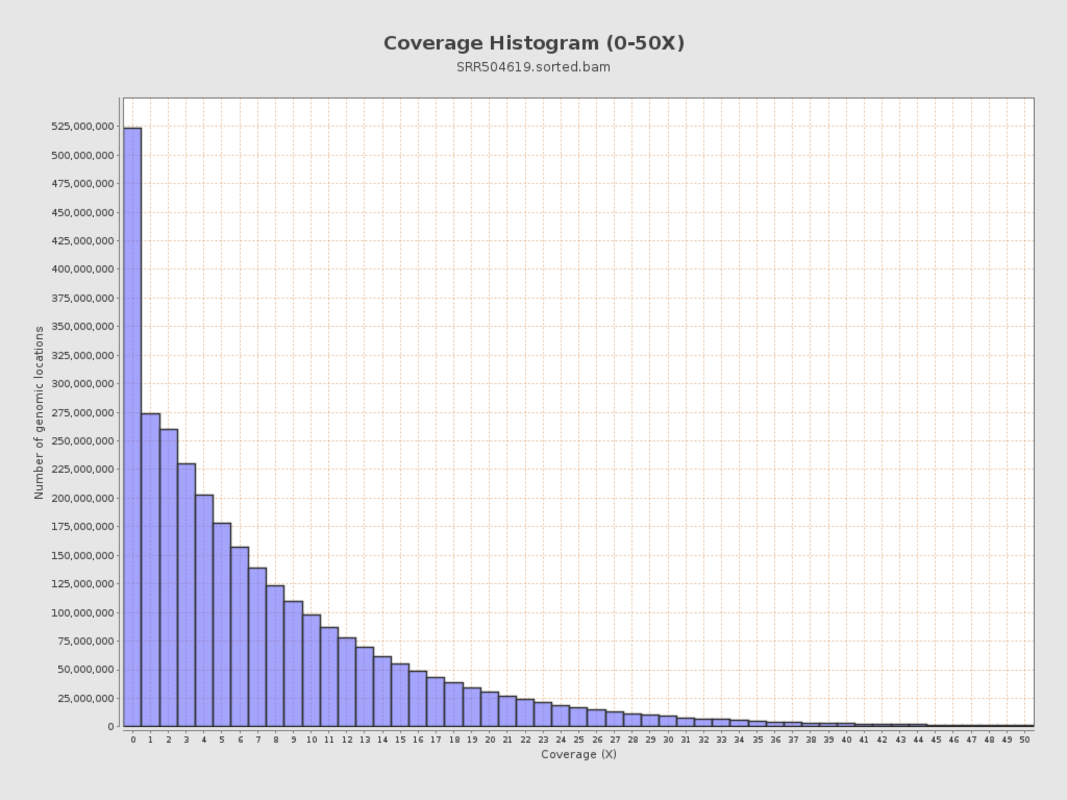
chrY	59373566	438910929	7.3924	520.7965

3. Results : Coverage across reference

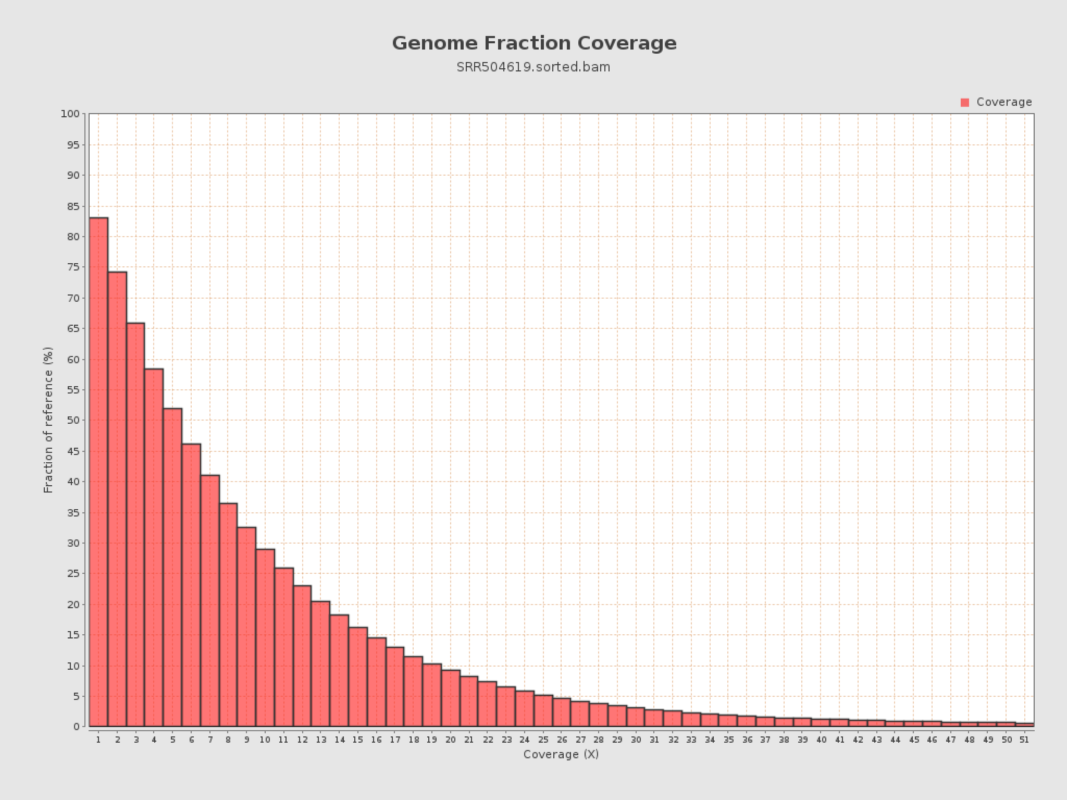
4. Results : Coverage Histogram



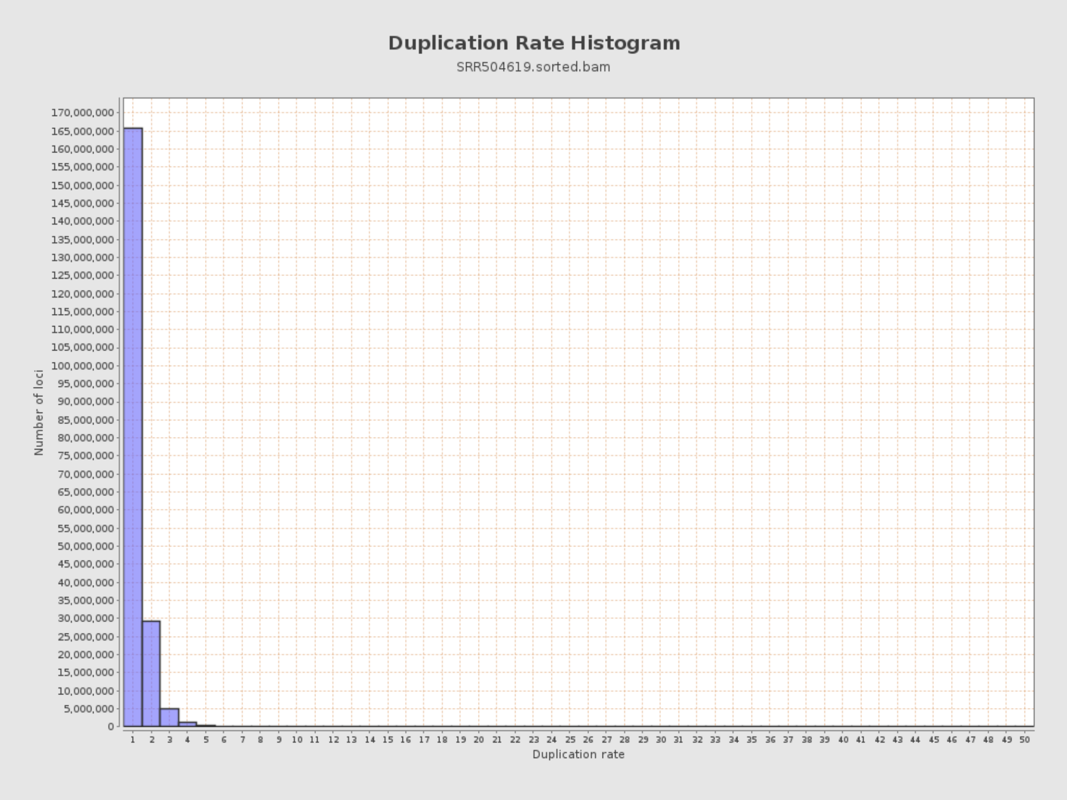
5. Results : Coverage Histogram (0-50X)



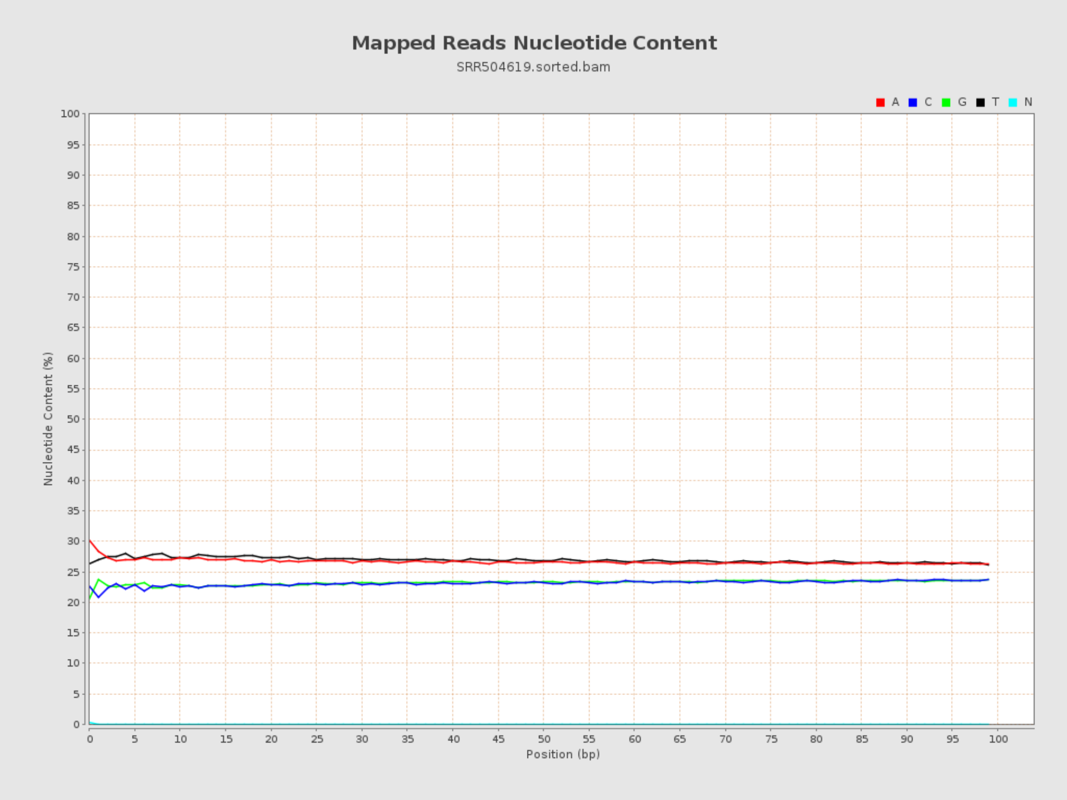
6. Results : Genome Fraction Coverage



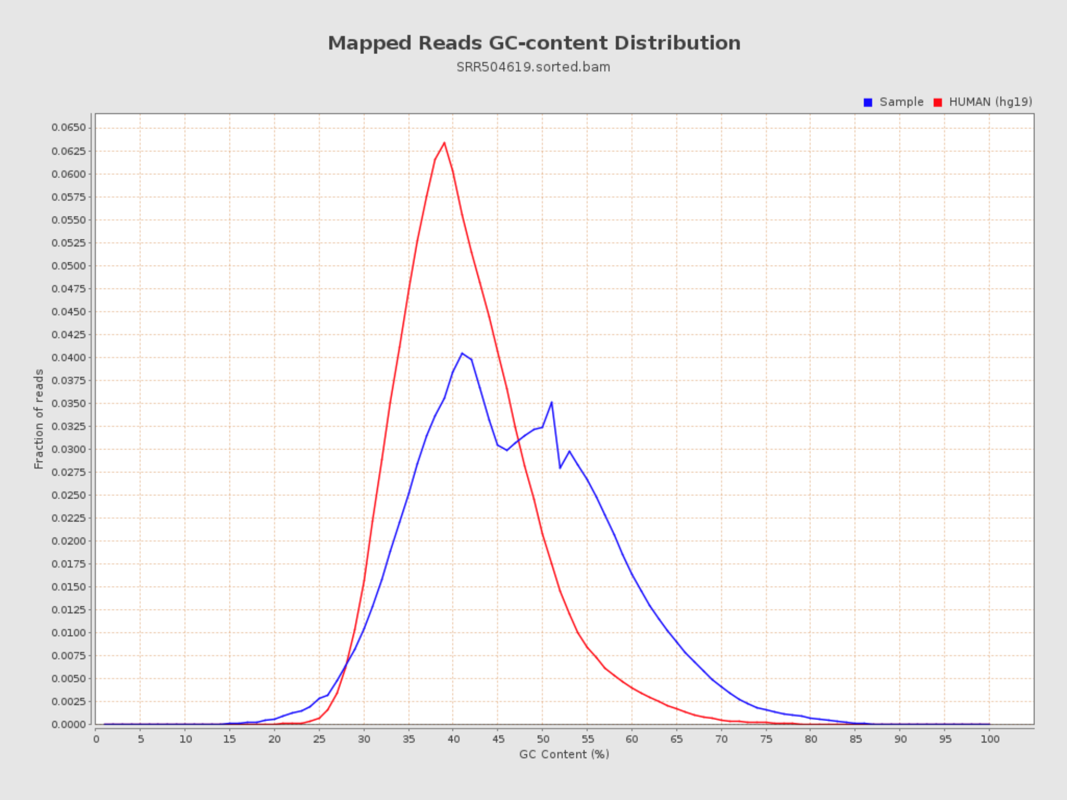
7. Results : Duplication Rate Histogram



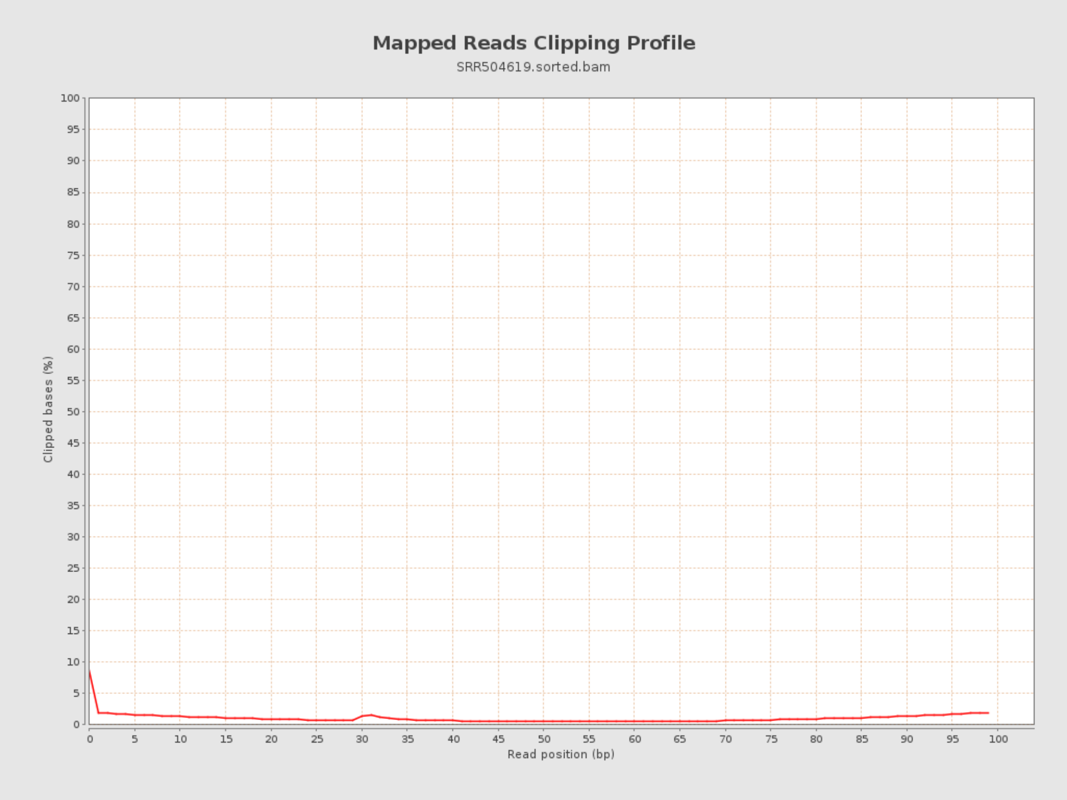
8. Results : Mapped Reads Nucleotide Content



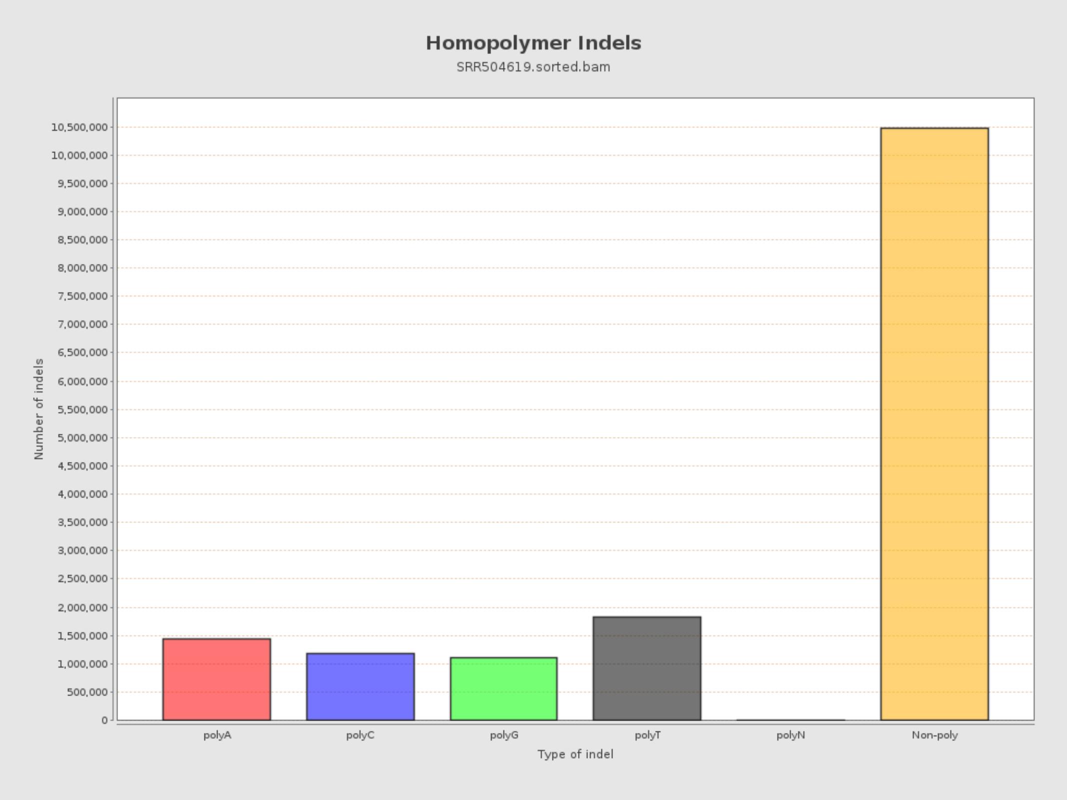
9. Results : Mapped Reads GC-content Distribution



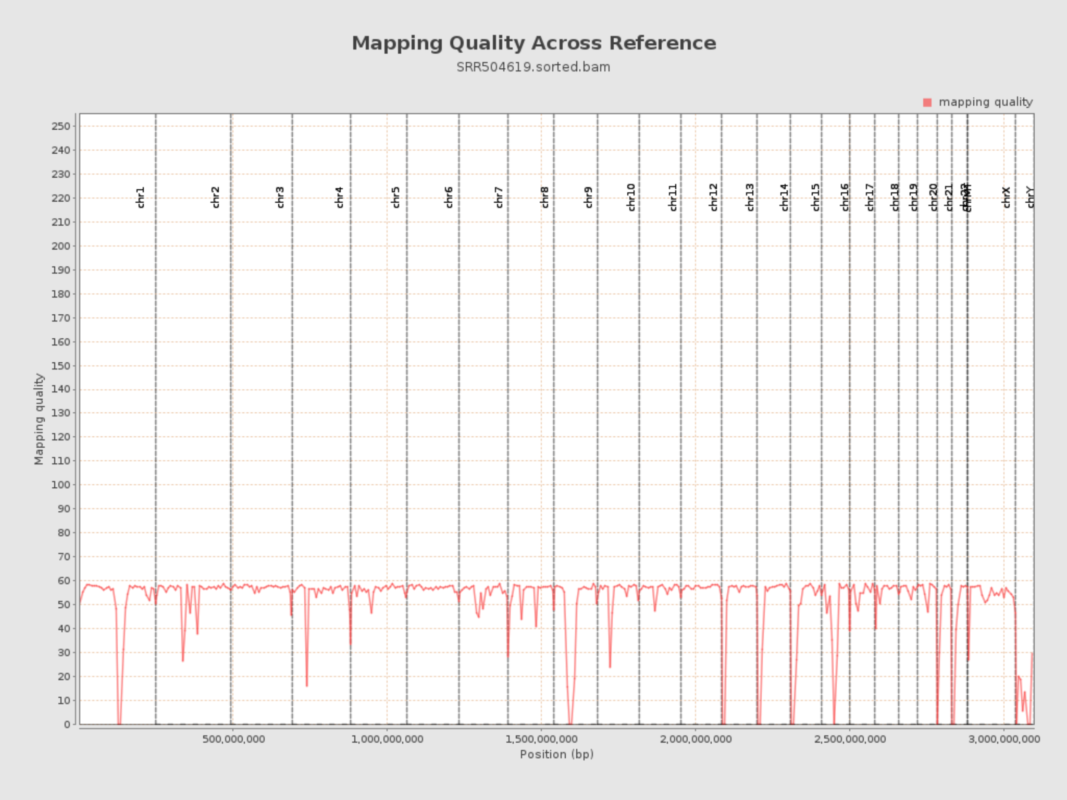
10. Results : Mapped Reads Clipping Profile



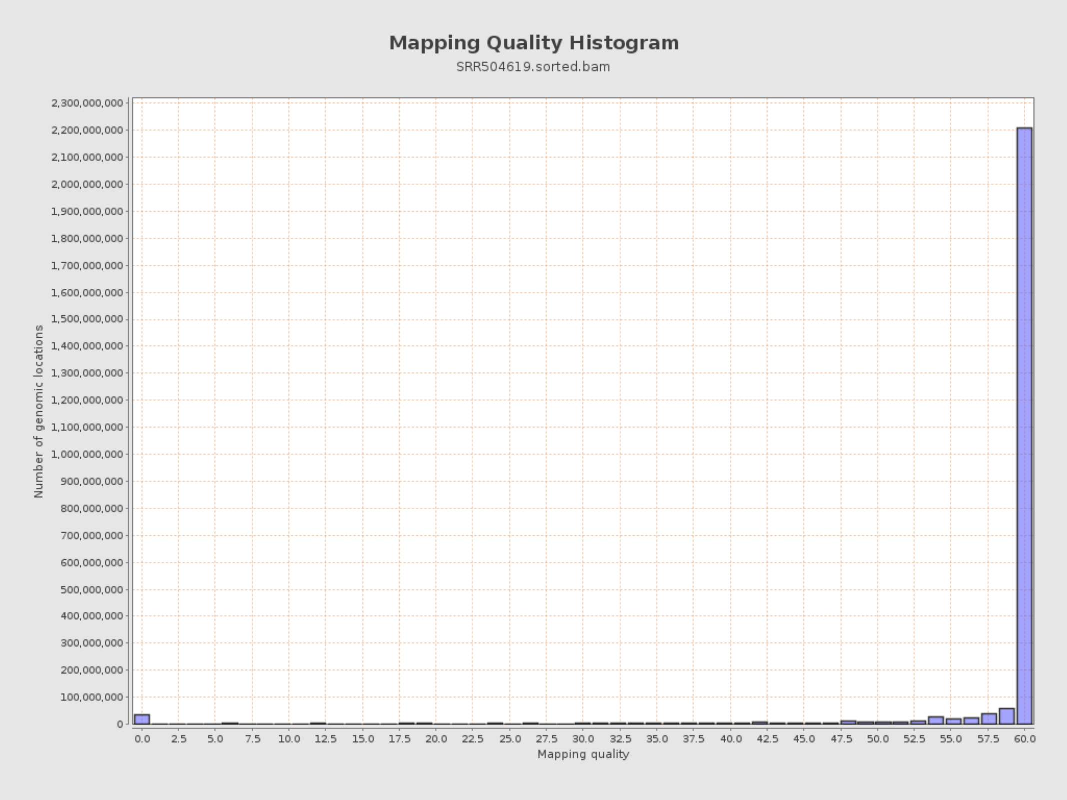
11. Results : Homopolymer Indels



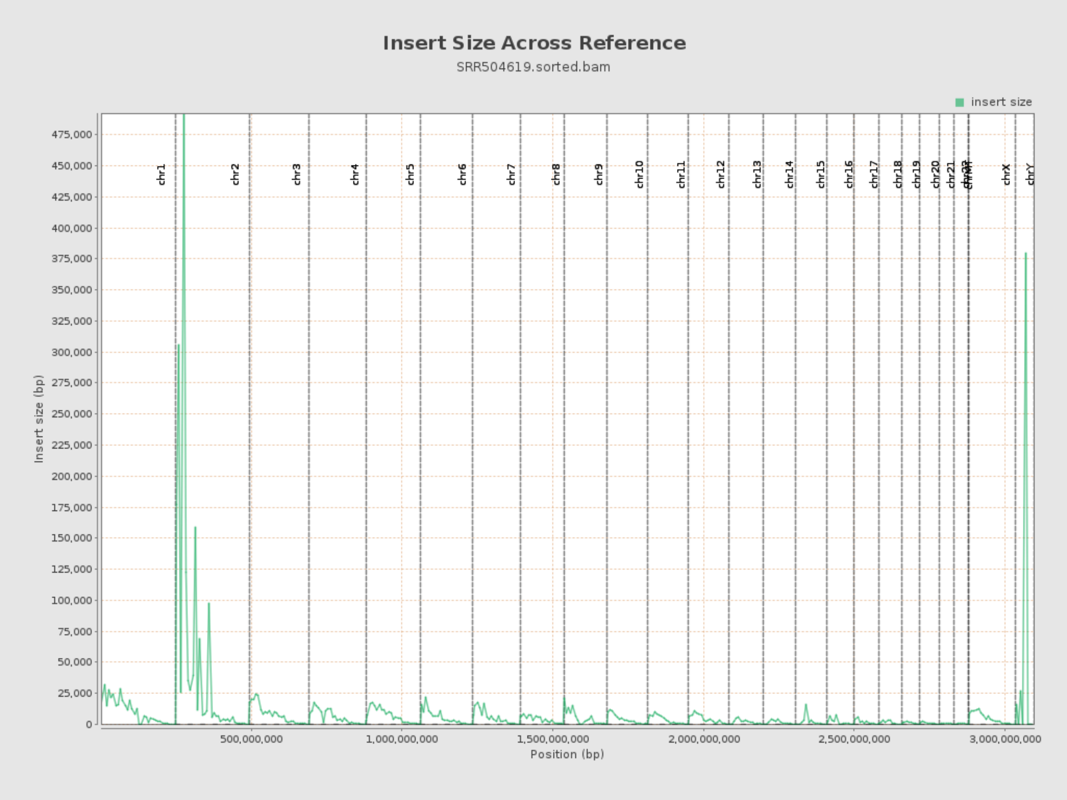
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram