Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 15:55:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504613.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_SRR504613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504613_1.fastq.gz SRR504613_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 15:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	479,878,740
Mapped reads	318,951,734 / 66.47%
Unmapped reads	160,927,006 / 33.53%
Mapped paired reads	318,951,734 / 66.47%
Mapped reads, first in pair	159,756,071 / 33.29%
Mapped reads, second in pair	159,195,663 / 33.17%
Mapped reads, both in pair	316,820,240 / 66.02%
Mapped reads, singletons	2,131,494 / 0.44%
Secondary alignments	0
Supplementary alignments	2,056,872 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	87,866,397 / 18.31%
Duplication rate	23.93%
Clipped reads	15,436,963 / 3.22%

2.2. ACGT Content

Number/percentage of A's	8,187,809,421 / 25.85%
Number/percentage of C's	7,579,442,928 / 23.93%
Number/percentage of T's	8,226,662,777 / 25.97%
Number/percentage of G's	7,676,058,059 / 24.24%
Number/percentage of N's	1,813,592 / 0.01%

GC Percentage	48.17%

2.3. Coverage

Mean	10.2335
Standard Deviation	26.4255

2.4. Mapping Quality

Mean Mapping Quality	53.76

2.5. Insert size

Mean	25,631.82
Standard Deviation	1,547,673.6
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	154,216,235
Insertions	2,354,731
Mapped reads with at least one insertion	0.72%
Deletions	3,119,200
Mapped reads with at least one deletion	0.95%
Homopolymer indels	40.14%

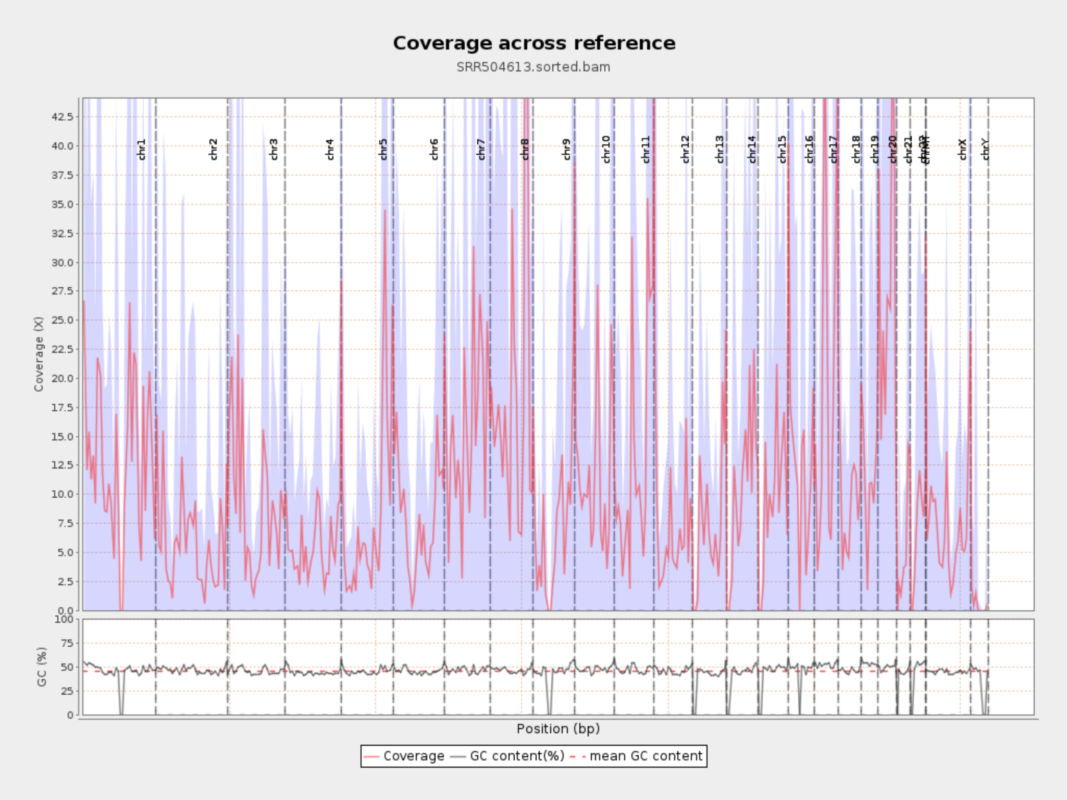
2.7. Chromosome stats

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

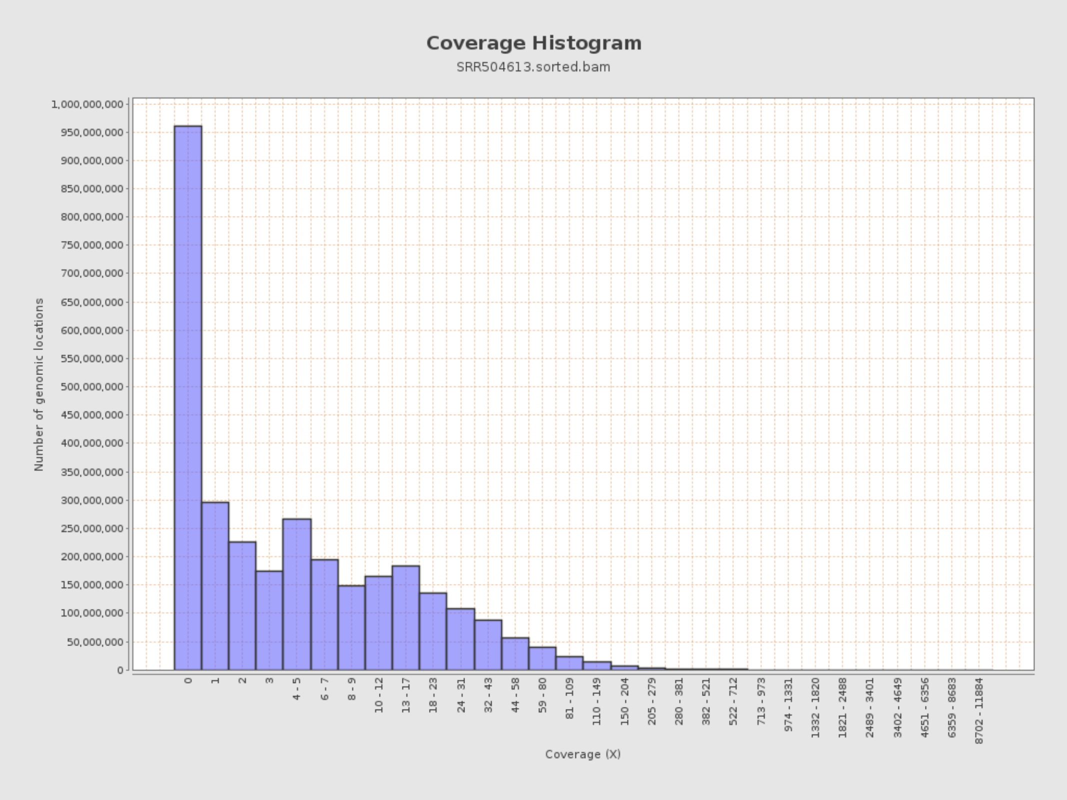
		bases	coverage	deviation
chr1	249250621	3213048875	12.8908	25.7643
chr2	243199373	1415504552	5.8203	15.6038
chr3	198022430	1788645042	9.0325	24.558
chr4	191154276	1066126069	5.5773	10.6019
chr5	180915260	1544645870	8.538	24.4782
chr6	171115067	1342114686	7.8433	15.2489
chr7	159138663	2533651741	15.921	29.4994
chr8	146364022	2852073852	19.4862	46.759
chr9	141213431	966745075	6.846	19.0821
chr10	135534747	1557321168	11.4902	23.7893
chr11	135006516	1787565673	13.2406	30.4815
chr12	133851895	955365941	7.1375	17.819
chr13	115169878	865112390	7.5116	16.7935
chr14	107349540	1122502769	10.4565	20.9554
chr15	102531392	966659714	9.4279	19.6926
chr16	90354753	1183185337	13.0949	29.6452
chr17	81195210	1539873474	18.9651	61.3639
chr18	78077248	723258655	9.2634	26.5412
chr19	59128983	666679719	11.275	24.13
chr20	63025520	1800148540	28.5622	50.9899
chr21	48129895	263913705	5.4834	14.1486
chr22	51304566	348490236	6.7926	17.5406
chrMT	16571	535020	32.2865	14.3943
chrX	155270560	1146128294	7.3815	13.8457

chrY	59373566	30582311	0.5151	11.7923

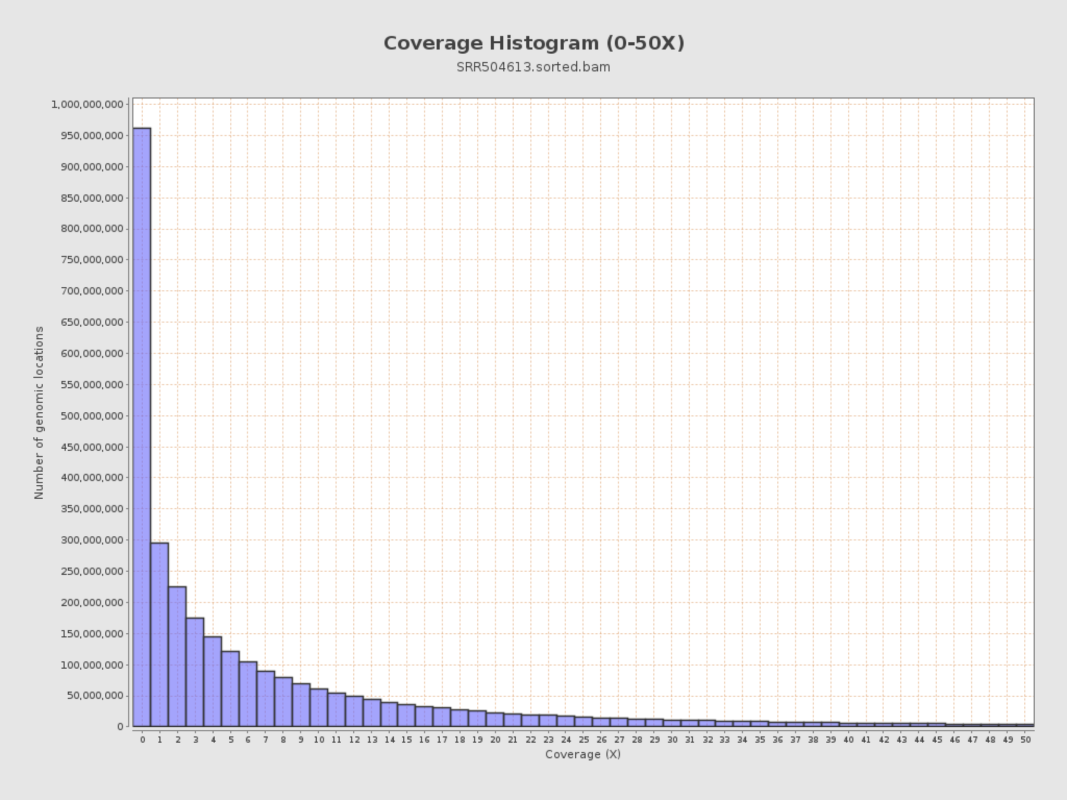
3. Results : Coverage across reference



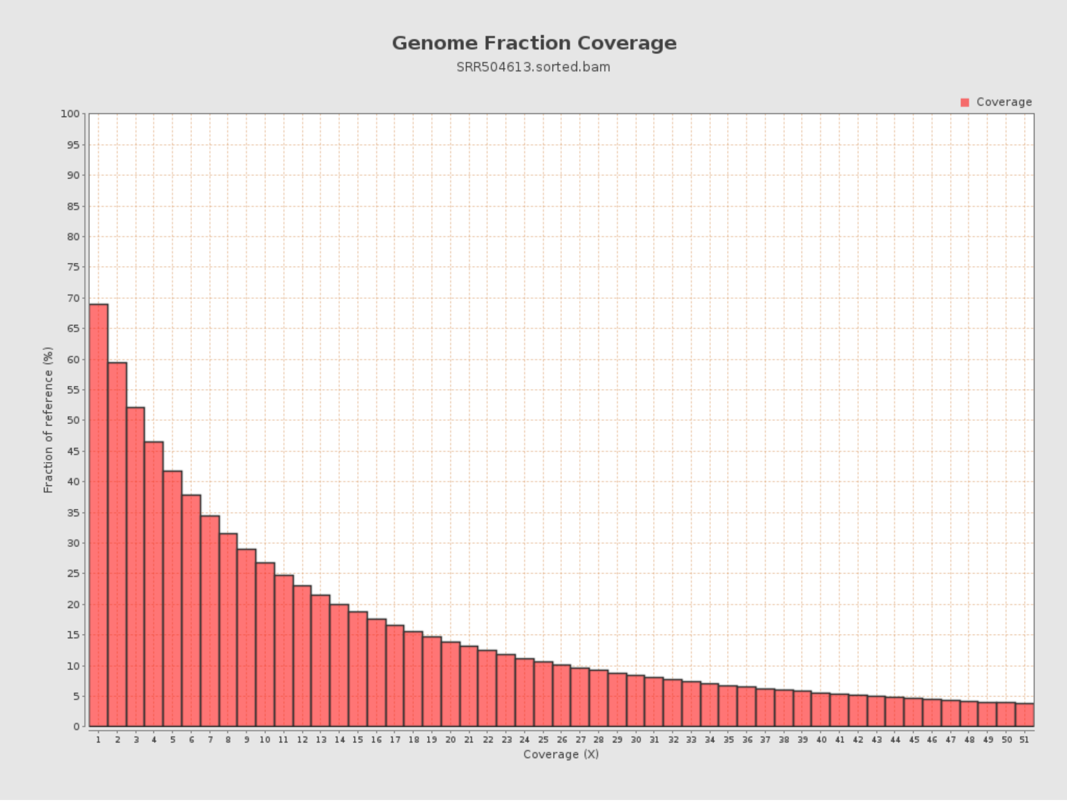
4. Results : Coverage Histogram



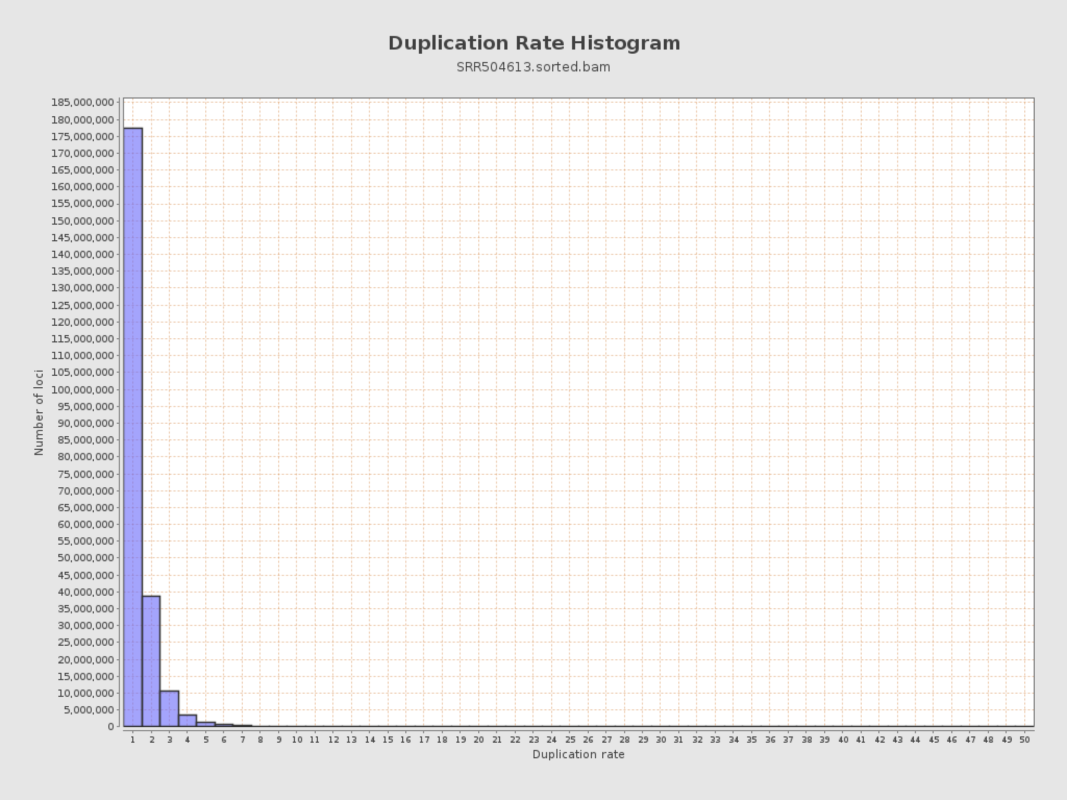
5. Results : Coverage Histogram (0-50X)



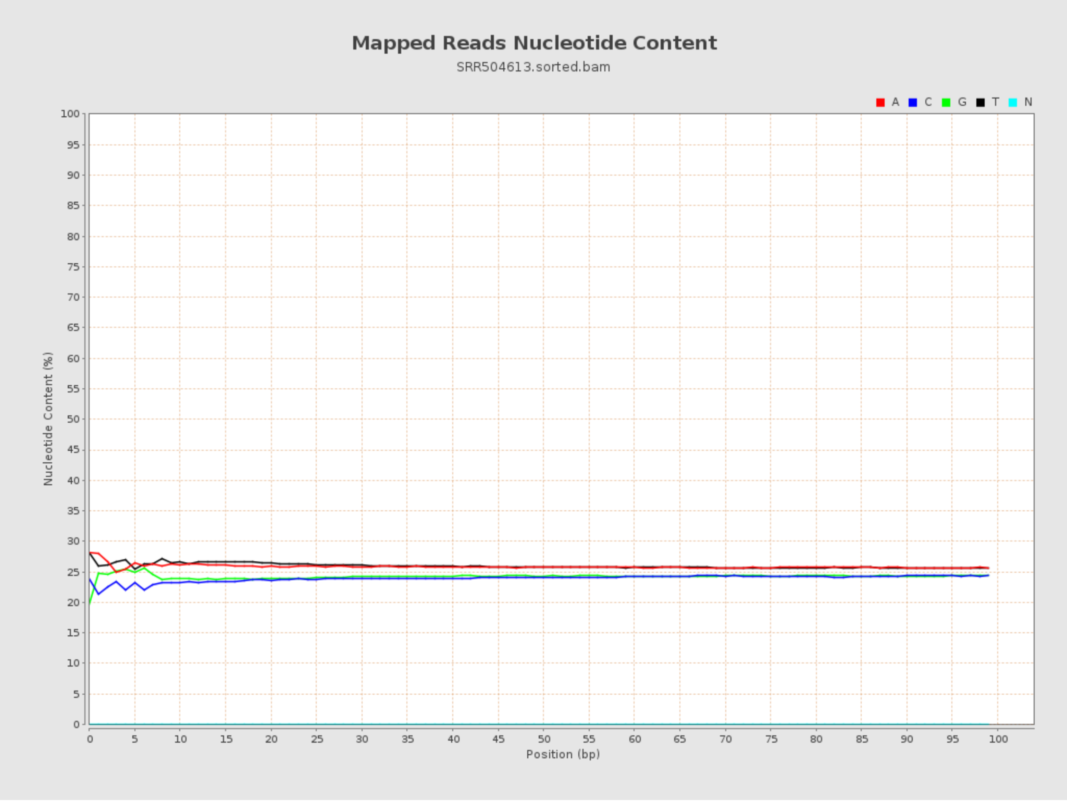
6. Results : Genome Fraction Coverage



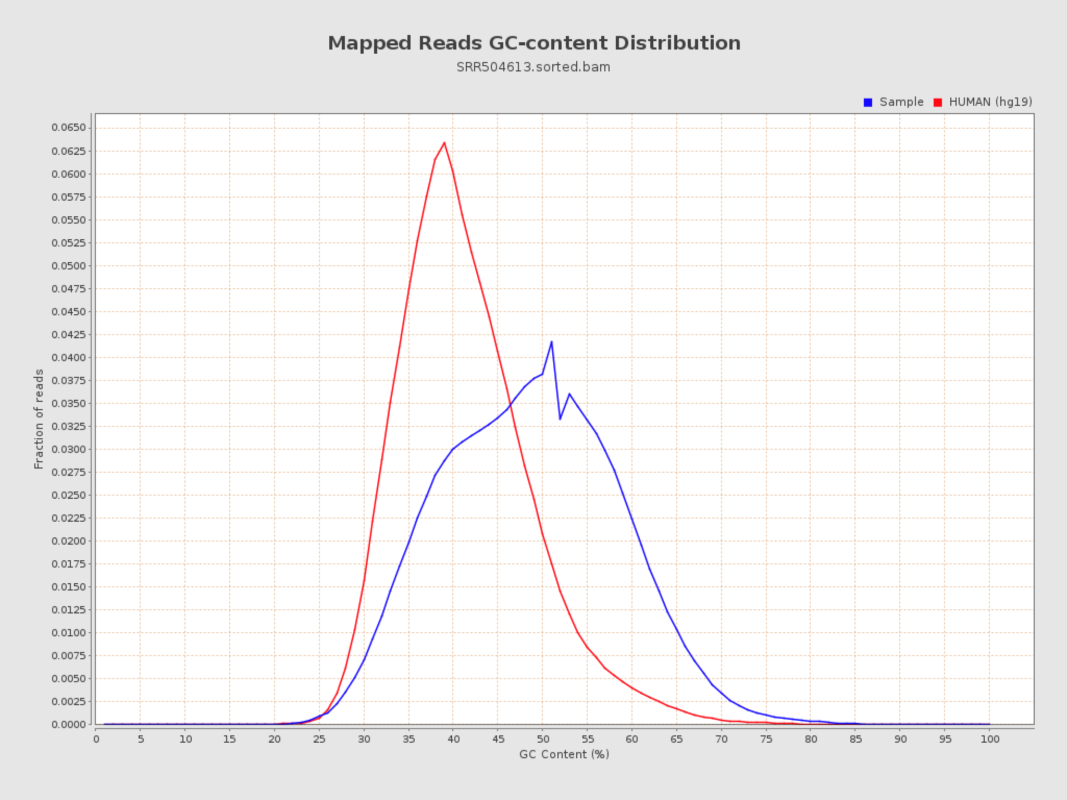
7. Results : Duplication Rate Histogram



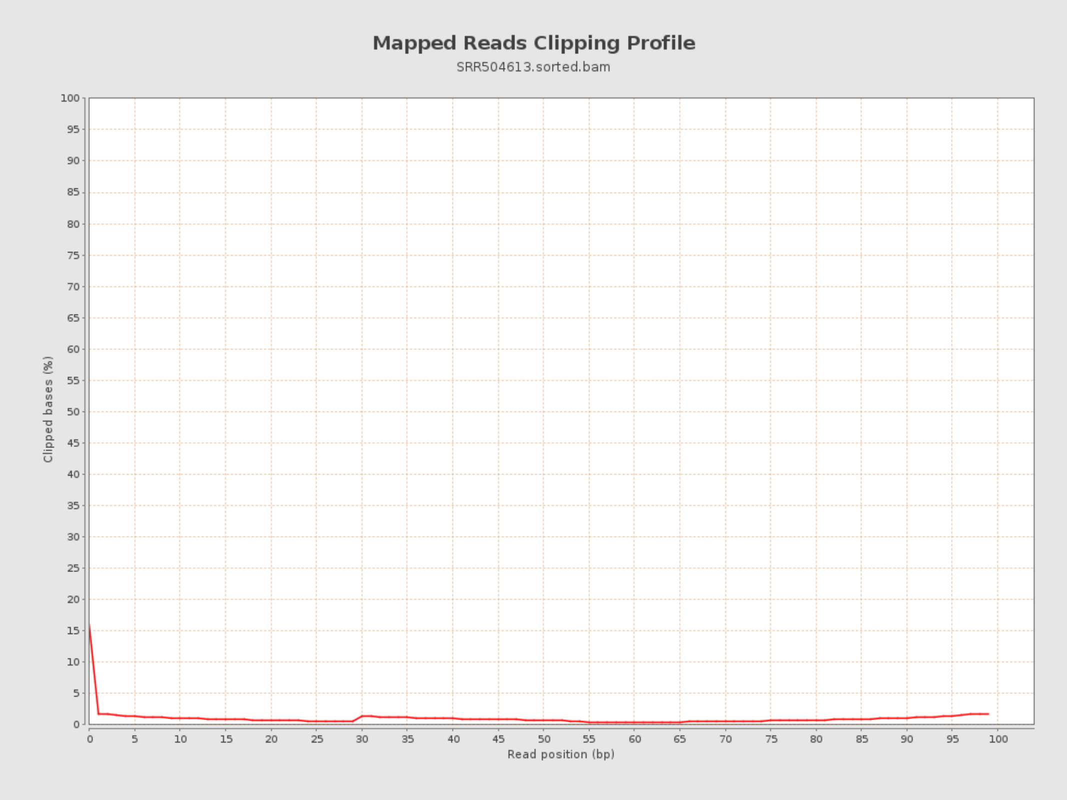
8. Results : Mapped Reads Nucleotide Content



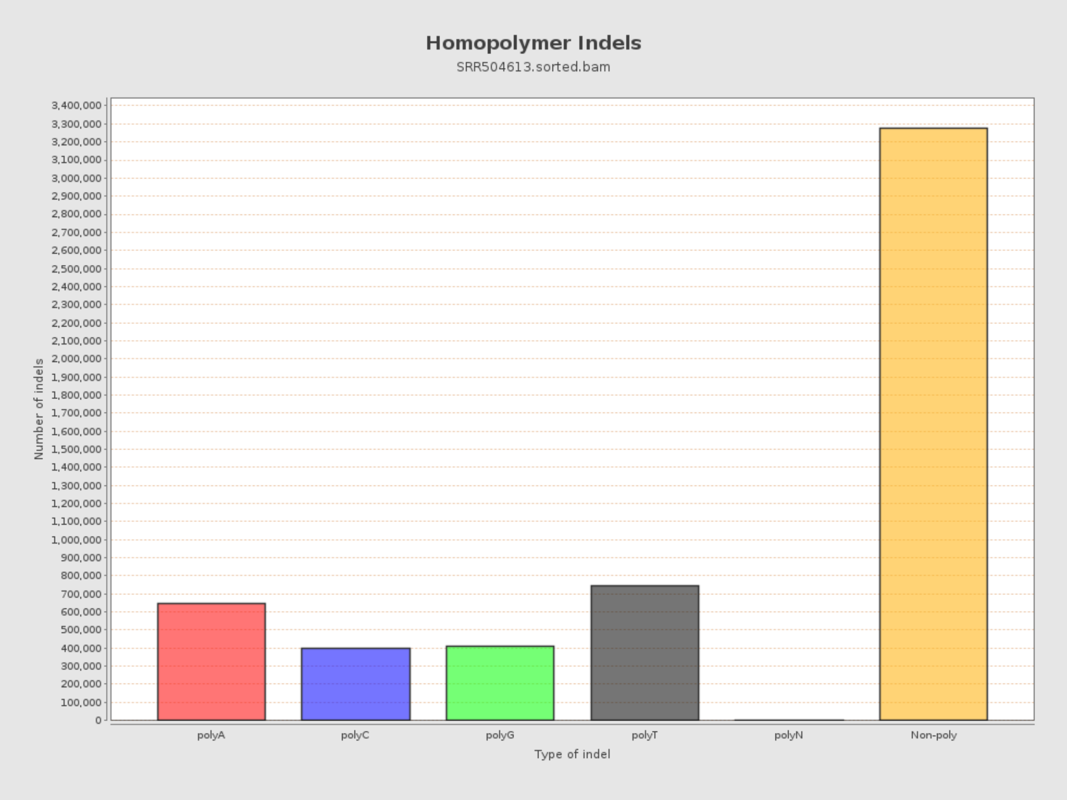
9. Results : Mapped Reads GC-content Distribution



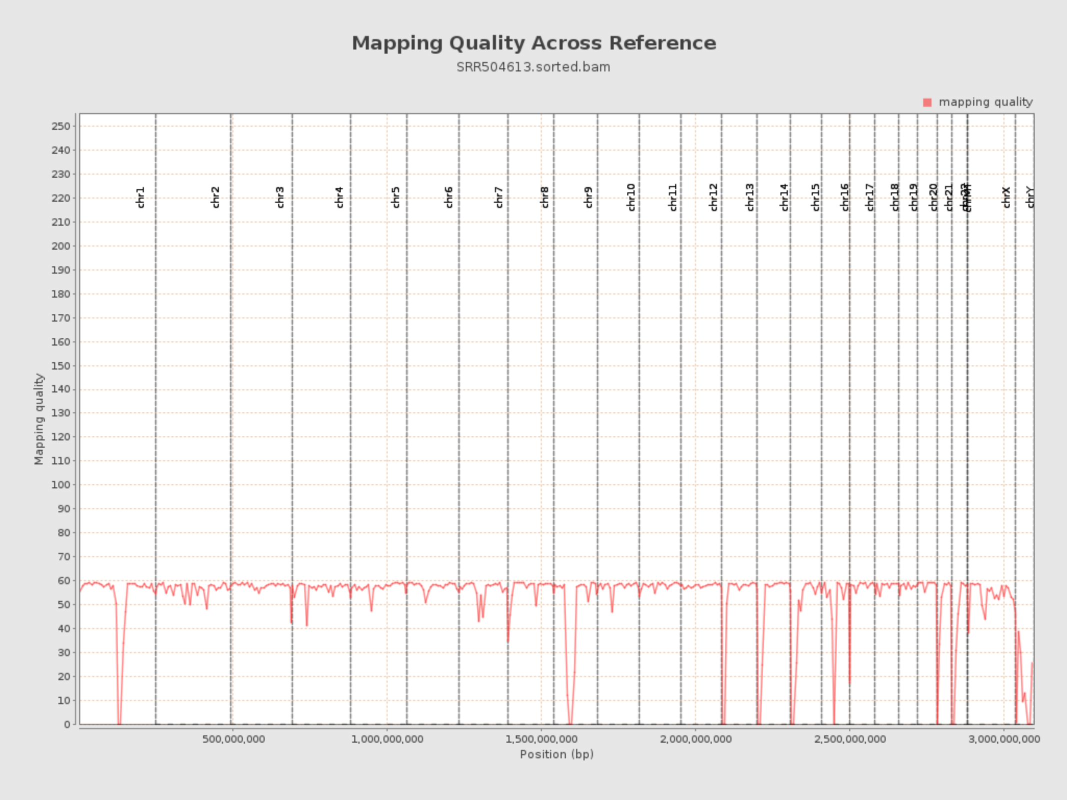
10. Results : Mapped Reads Clipping Profile



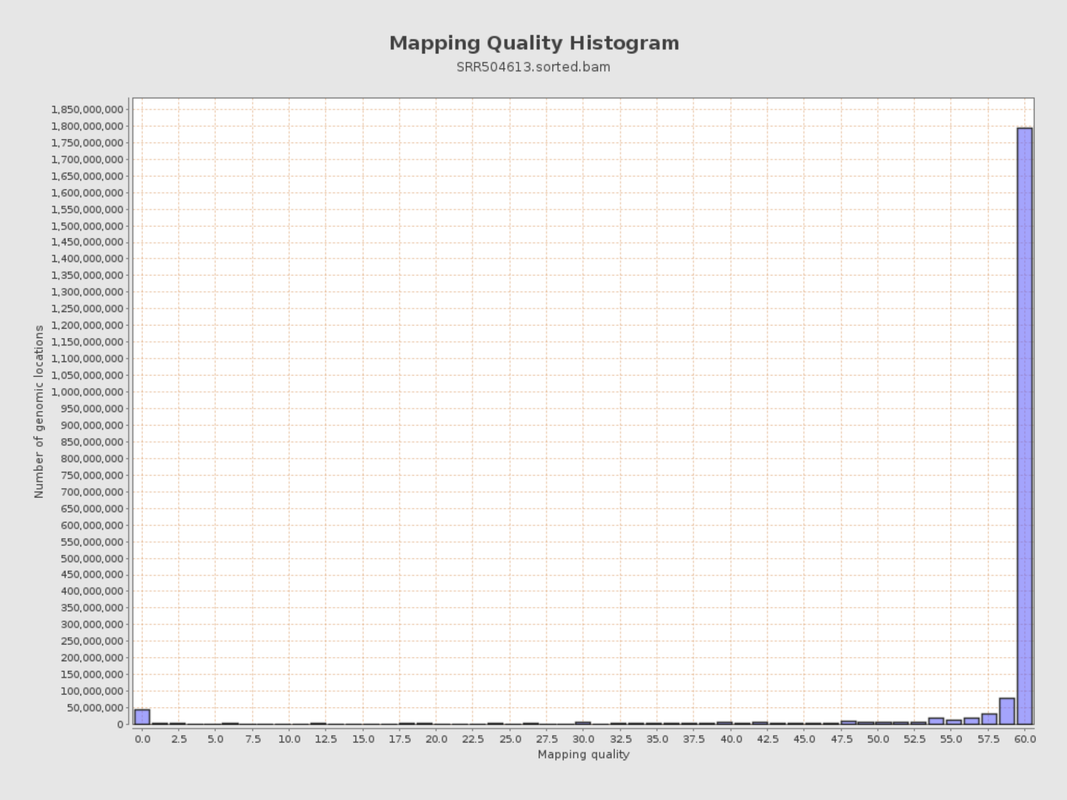
11. Results : Homopolymer Indels



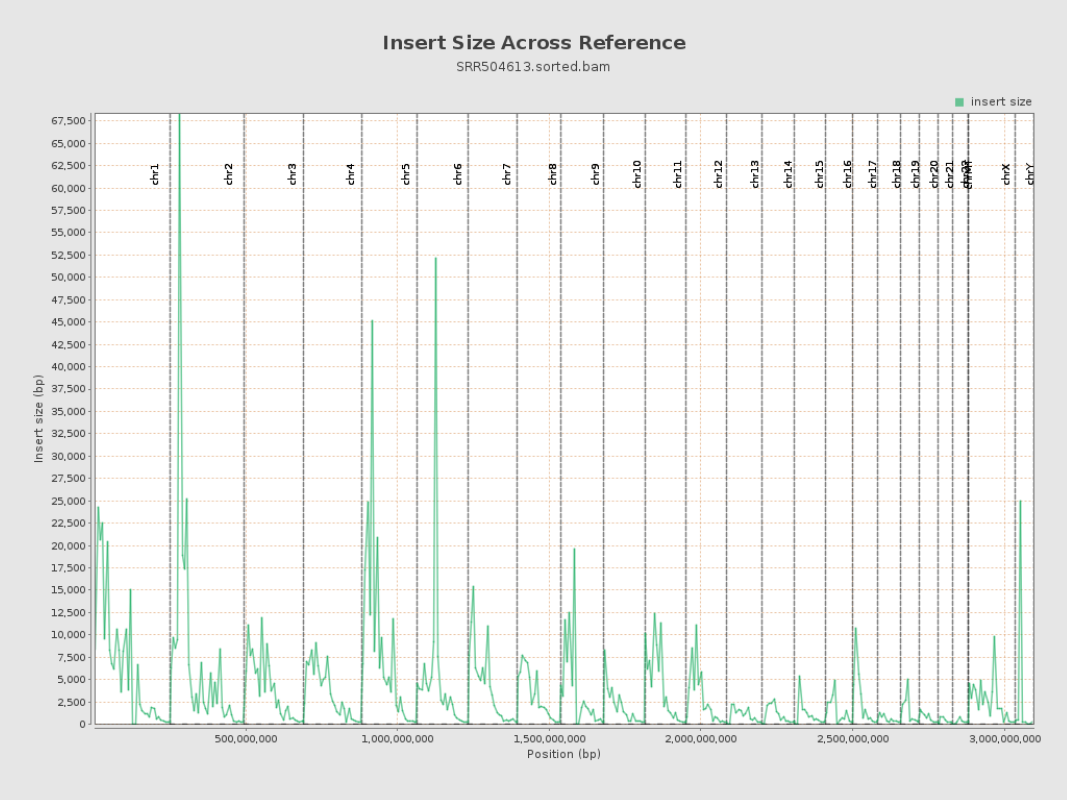
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram