Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 20:50:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504610.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_SRR504610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504610_1.fastq.gz SRR504610_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 20:50:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	442,742,124
Mapped reads	295,108,901 / 66.65%
Unmapped reads	147,633,223 / 33.35%
Mapped paired reads	295,108,901 / 66.65%
Mapped reads, first in pair	147,727,565 / 33.37%
Mapped reads, second in pair	147,381,336 / 33.29%
Mapped reads, both in pair	293,366,614 / 66.26%
Mapped reads, singletons	1,742,287 / 0.39%
Secondary alignments	0
Supplementary alignments	1,869,649 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	77,026,902 / 17.4%
Duplication rate	22.73%
Clipped reads	14,573,072 / 3.29%

2.2. ACGT Content

Number/percentage of A's	7,567,261,144 / 25.83%
Number/percentage of C's	7,018,702,208 / 23.95%
Number/percentage of T's	7,616,691,570 / 26%
Number/percentage of G's	7,092,314,858 / 24.21%
Number/percentage of N's	5,028,196 / 0.02%

GC Percentage	48.16%

2.3. Coverage

Mean	9.4672
Standard Deviation	24.3124

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	24,297.85
Standard Deviation	1,504,855.51
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	144,658,587
Insertions	2,189,914
Mapped reads with at least one insertion	0.72%
Deletions	2,883,080
Mapped reads with at least one deletion	0.95%
Homopolymer indels	39.92%

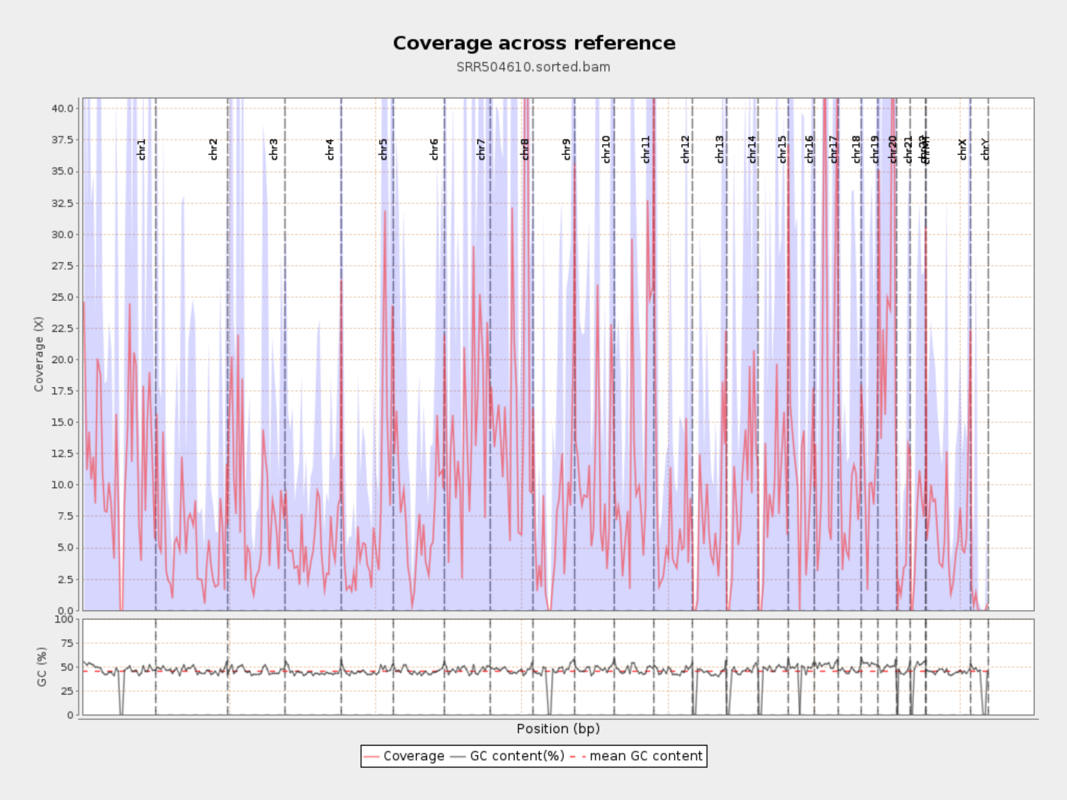
2.7. Chromosome stats

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

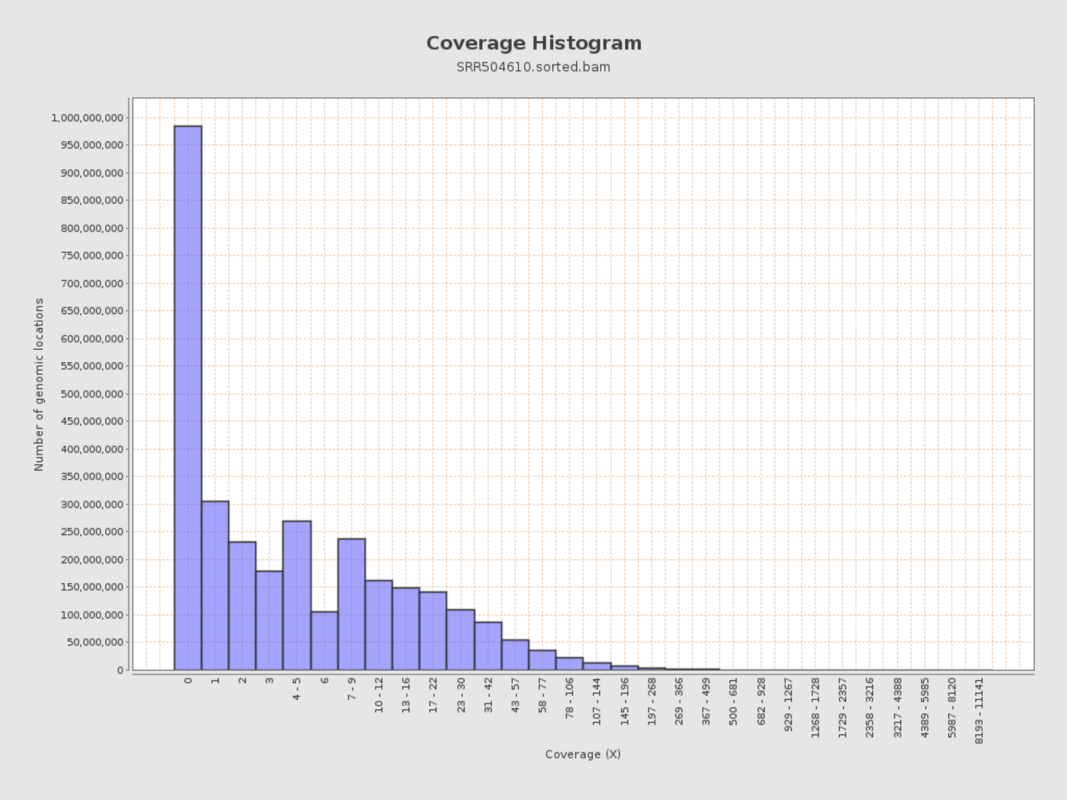
		bases	coverage	deviation
chr1	249250621	2970530031	11.9178	23.7353
chr2	243199373	1309075589	5.3827	13.4376
chr3	198022430	1655653720	8.3609	22.637
chr4	191154276	989083047	5.1743	9.8211
chr5	180915260	1429415028	7.901	22.5487
chr6	171115067	1242523603	7.2613	14.0792
chr7	159138663	2344630895	14.7333	27.195
chr8	146364022	2642930278	18.0572	43.082
chr9	141213431	894985099	6.3378	17.6839
chr10	135534747	1440980674	10.6318	21.9781
chr11	135006516	1651000676	12.229	28.0564
chr12	133851895	884095180	6.605	16.3293
chr13	115169878	801619735	6.9603	15.5135
chr14	107349540	1038234728	9.6715	19.3203
chr15	102531392	893016768	8.7097	18.1365
chr16	90354753	1092380624	12.0899	27.2848
chr17	81195210	1421647106	17.509	56.3624
chr18	78077248	669476465	8.5745	24.519
chr19	59128983	615429439	10.4083	22.2875
chr20	63025520	1663227751	26.3898	47.1125
chr21	48129895	244440594	5.0788	13.1344
chr22	51304566	322103799	6.2783	16.2133
chrMT	16571	505992	30.5348	13.4176
chrX	155270560	1062291007	6.8415	12.7865

chrY	59373566	28185856	0.4747	10.8844

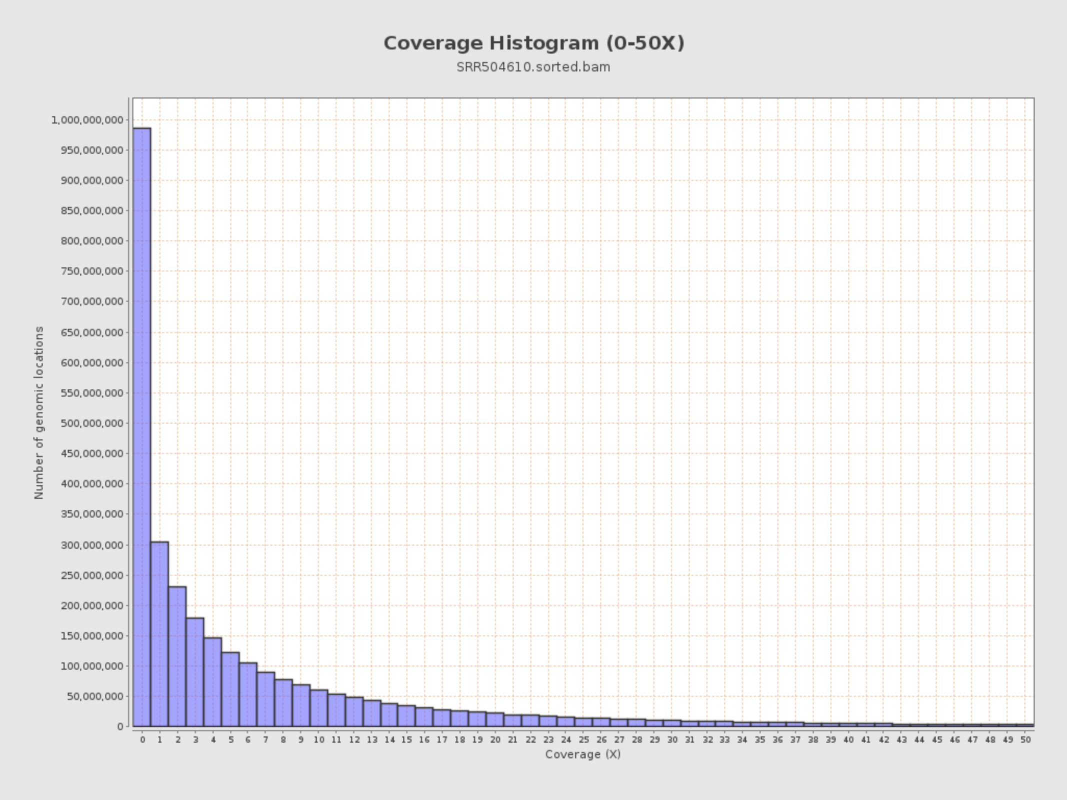
3. Results : Coverage across reference



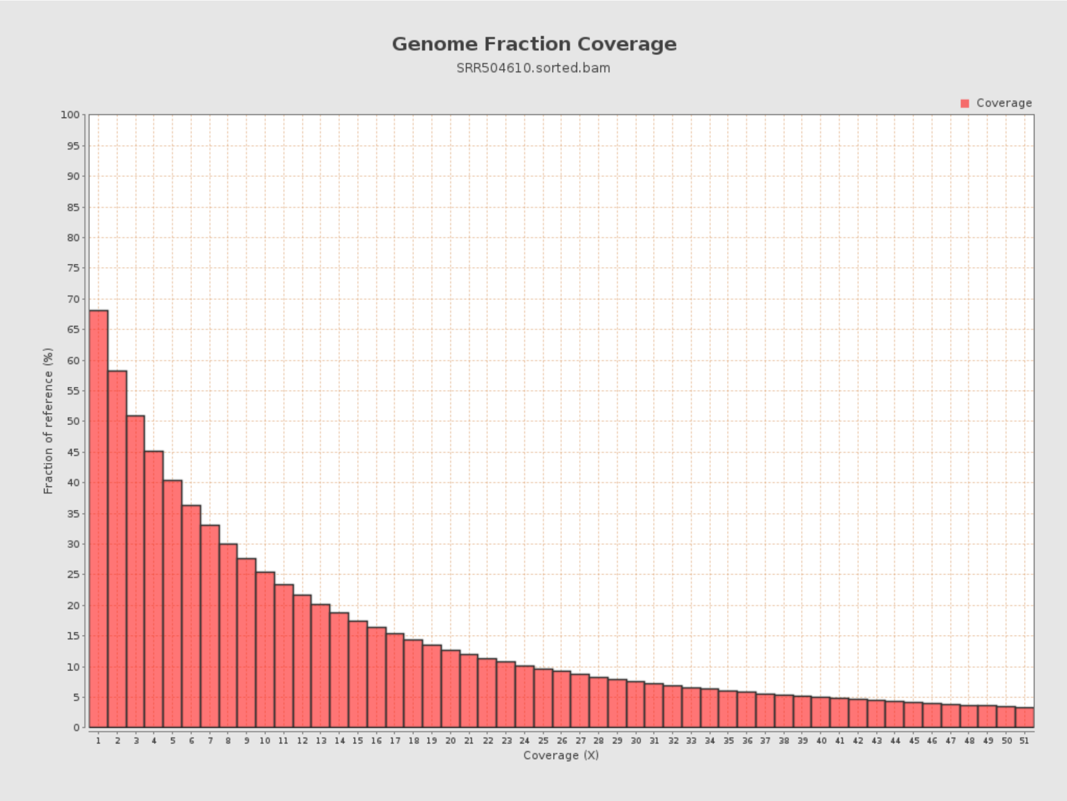
4. Results : Coverage Histogram



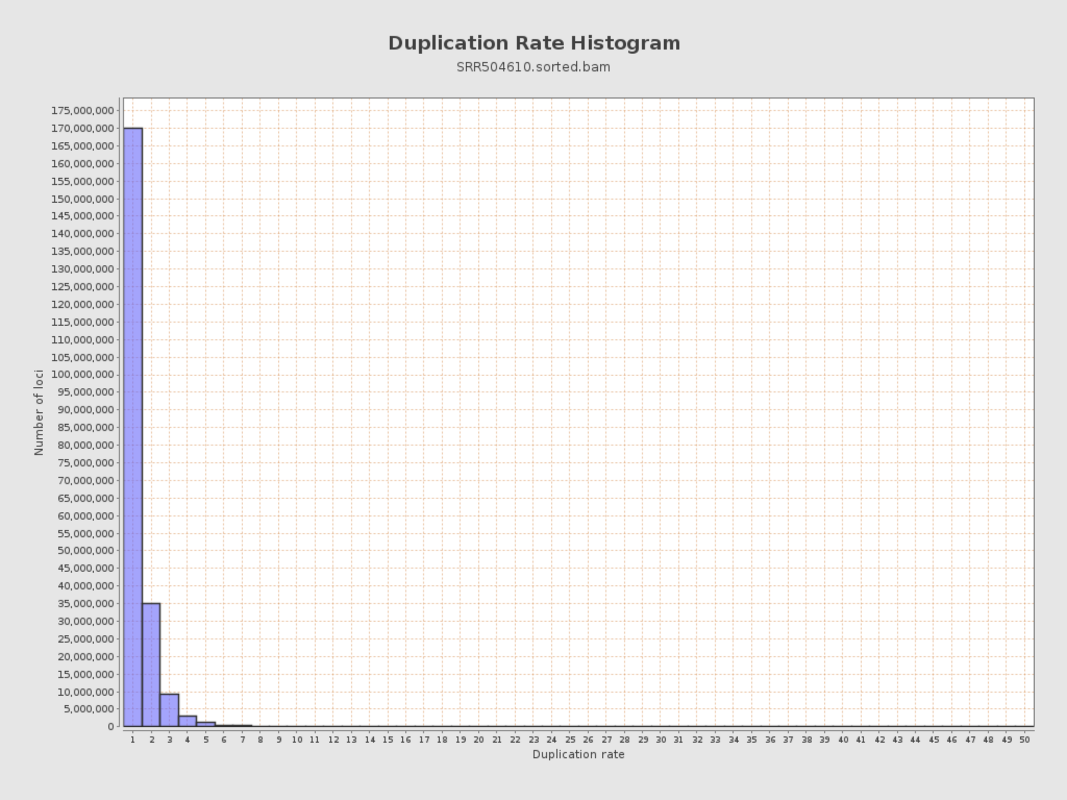
5. Results : Coverage Histogram (0-50X)



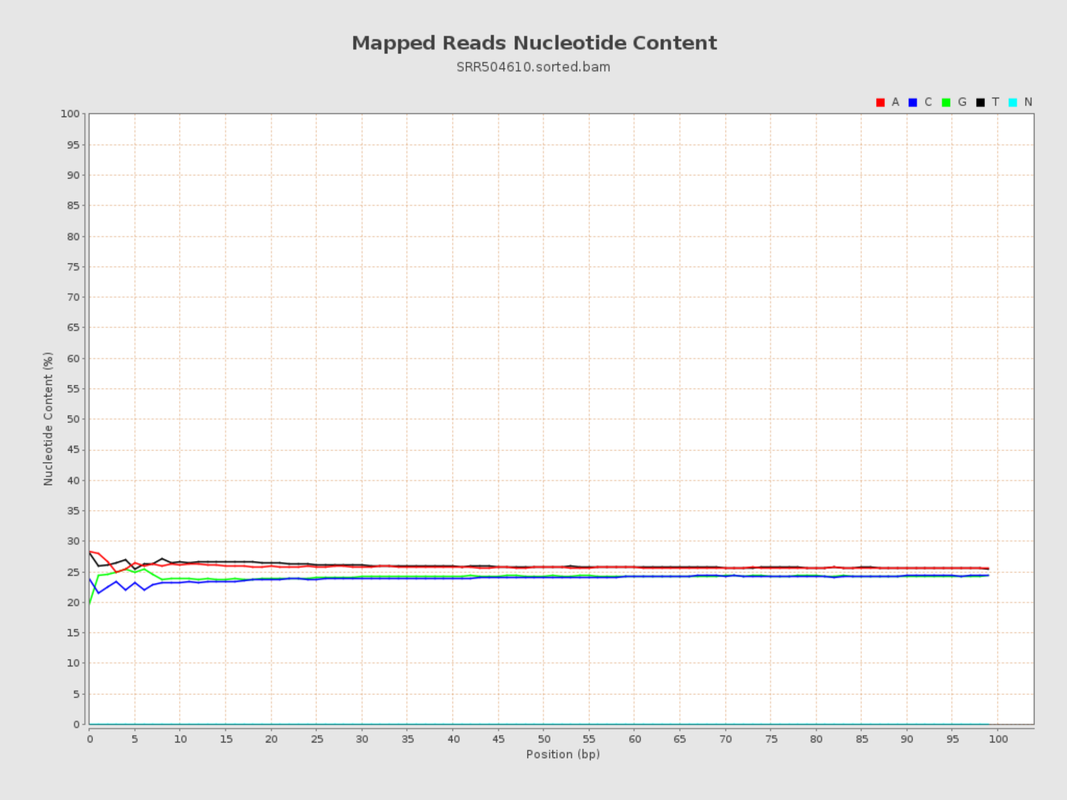
6. Results : Genome Fraction Coverage



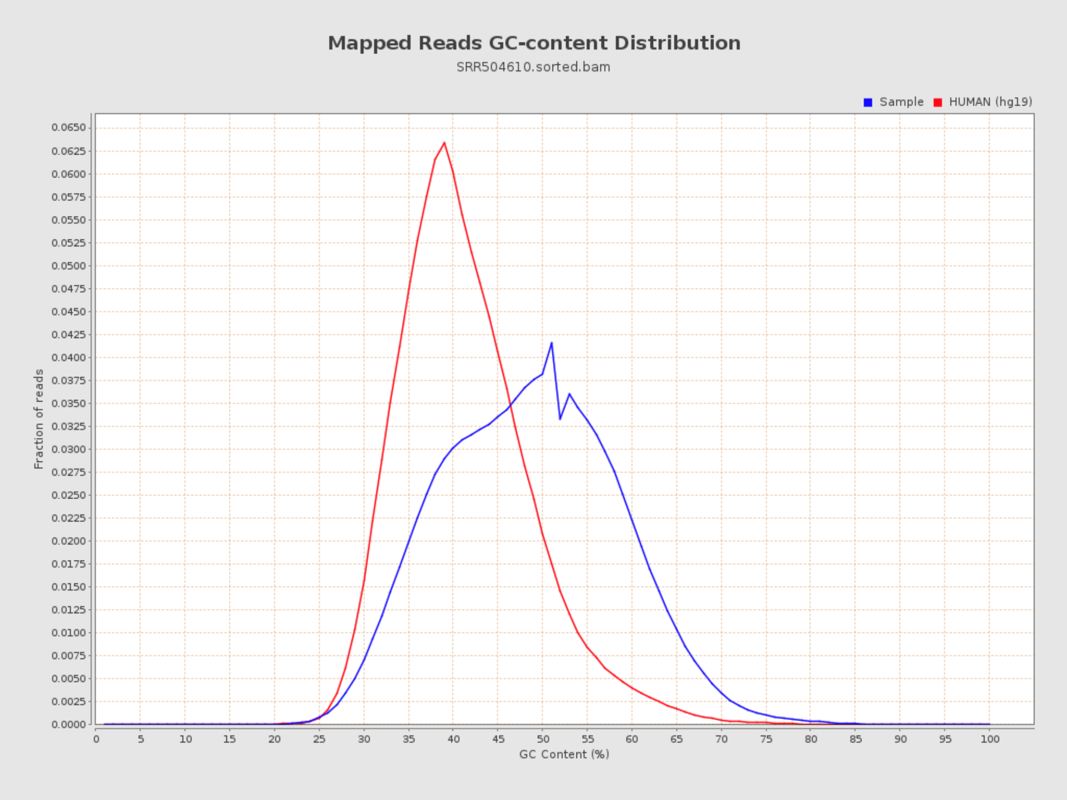
7. Results : Duplication Rate Histogram



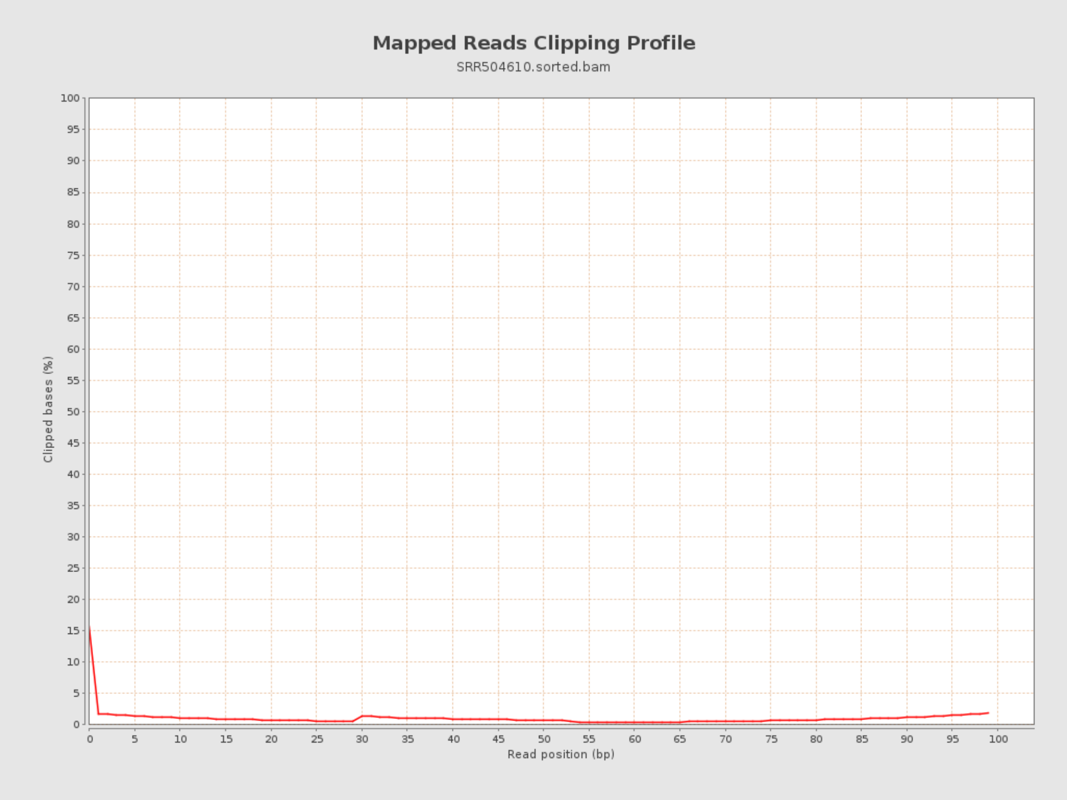
8. Results : Mapped Reads Nucleotide Content



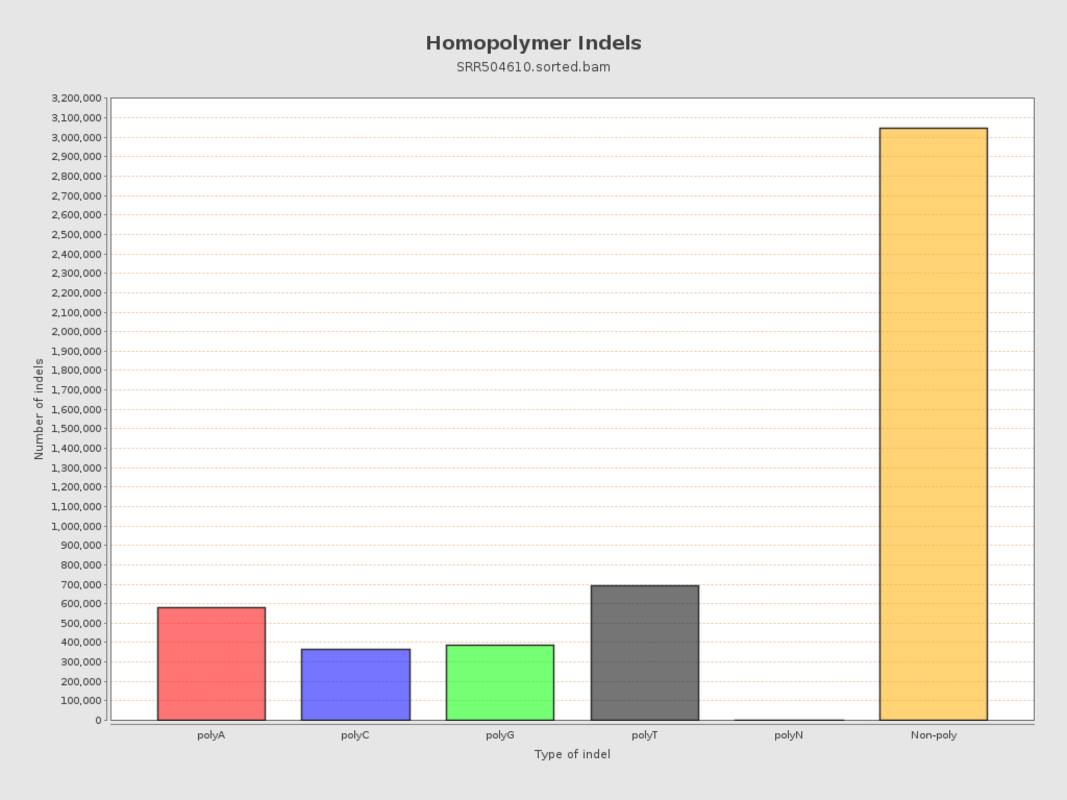
9. Results : Mapped Reads GC-content Distribution



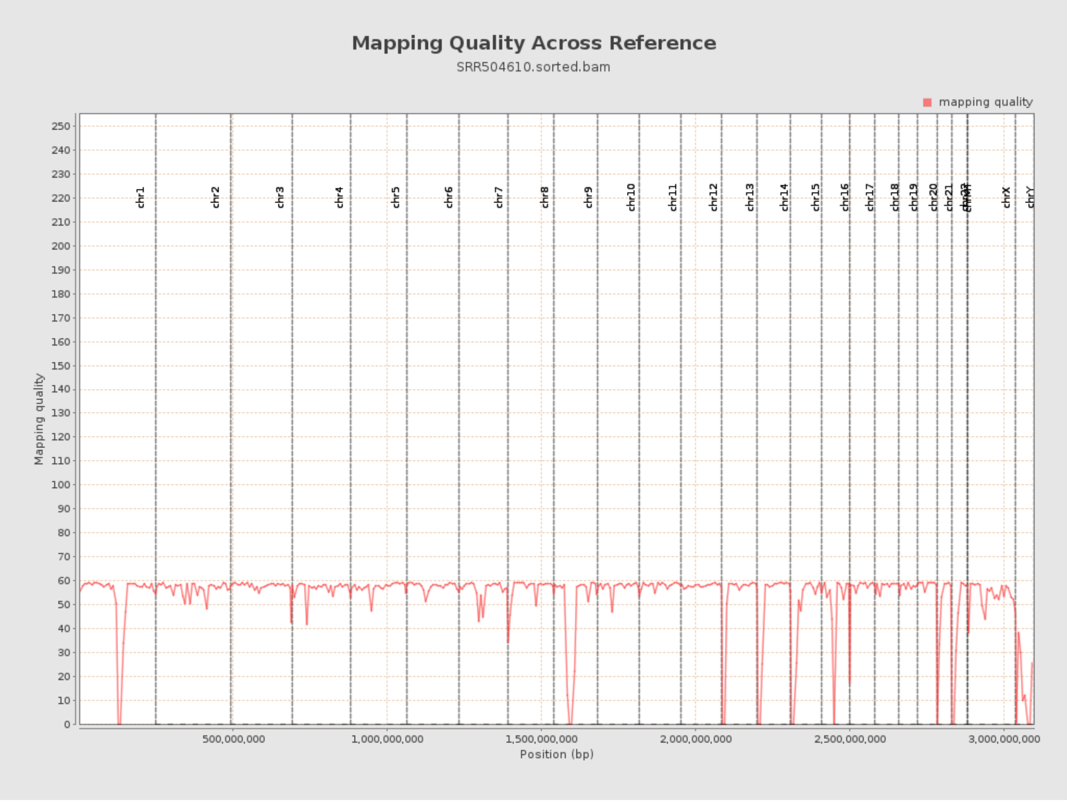
10. Results : Mapped Reads Clipping Profile



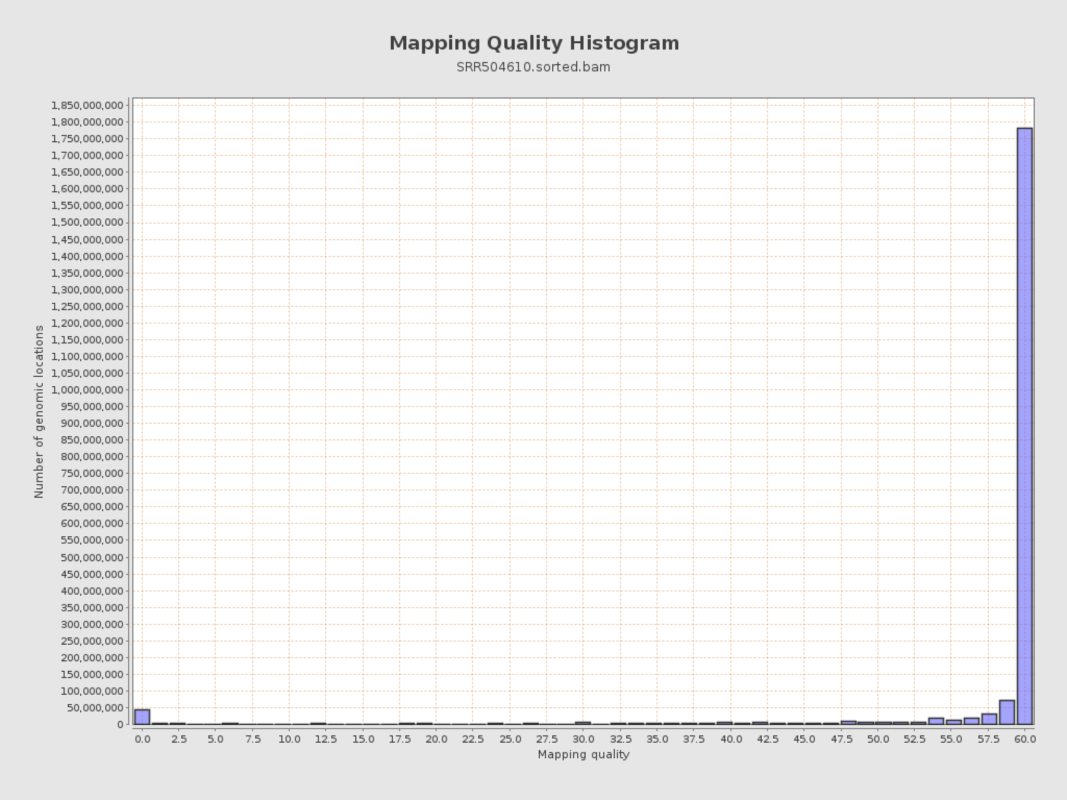
11. Results : Homopolymer Indels



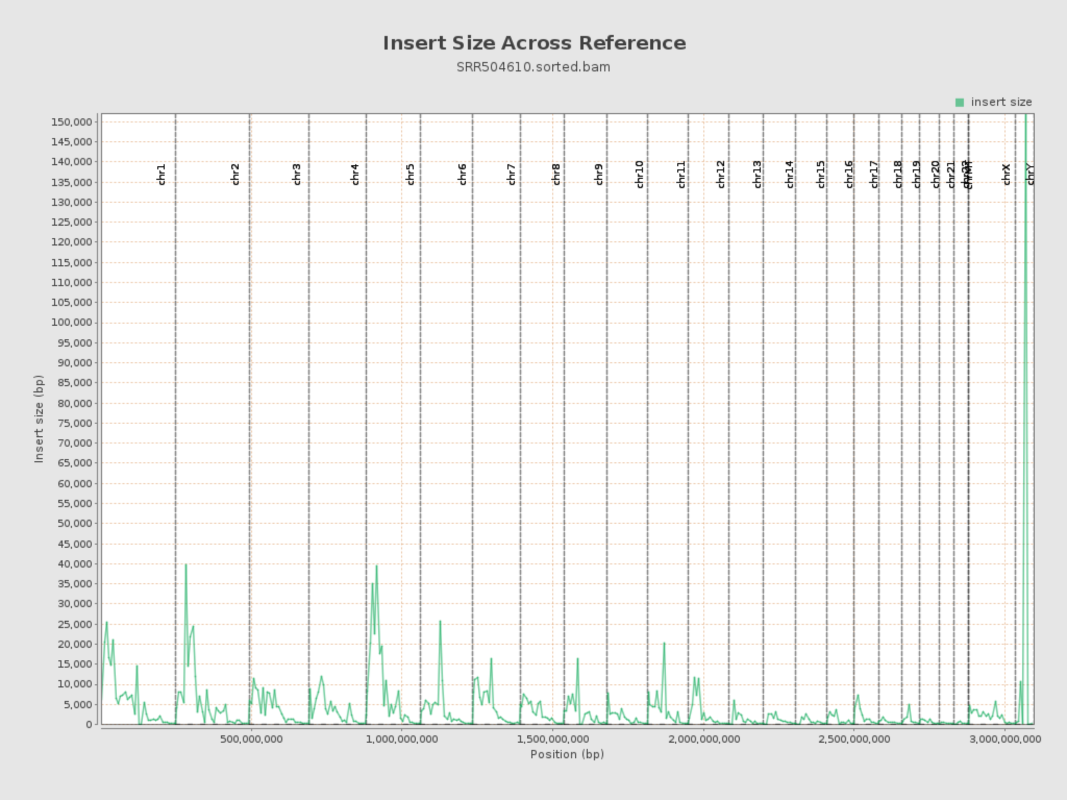
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram