Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 07:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504604.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_SRR504604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504604_1.fastq.gz SRR504604_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 07:52:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	427,936,432
Mapped reads	368,306,117 / 86.07%
Unmapped reads	59,630,315 / 13.93%
Mapped paired reads	368,306,117 / 86.07%
Mapped reads, first in pair	184,476,120 / 43.11%
Mapped reads, second in pair	183,829,997 / 42.96%
Mapped reads, both in pair	366,033,658 / 85.53%
Mapped reads, singletons	2,272,459 / 0.53%
Secondary alignments	0
Supplementary alignments	2,058,602 / 0.48%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	90,825,810 / 21.22%
Duplication rate	21.98%
Clipped reads	17,453,738 / 4.08%

2.2. ACGT Content

Number/percentage of A's	9,650,268,143 / 26.39%
Number/percentage of C's	8,556,305,784 / 23.4%
Number/percentage of T's	9,665,964,139 / 26.43%
Number/percentage of G's	8,689,859,795 / 23.76%
Number/percentage of N's	6,560,923 / 0.02%

GC Percentage	47.16%

2.3. Coverage

Mean	11.8159
Standard Deviation	24.5864

2.4. Mapping Quality

Mean Mapping Quality	53.98

2.5. Insert size

Mean	29,875.94
Standard Deviation	1,684,809.57
P25/Median/P75	180 / 213 / 267

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	172,526,973
Insertions	2,761,344
Mapped reads with at least one insertion	0.73%
Deletions	3,728,211
Mapped reads with at least one deletion	0.98%
Homopolymer indels	40.59%

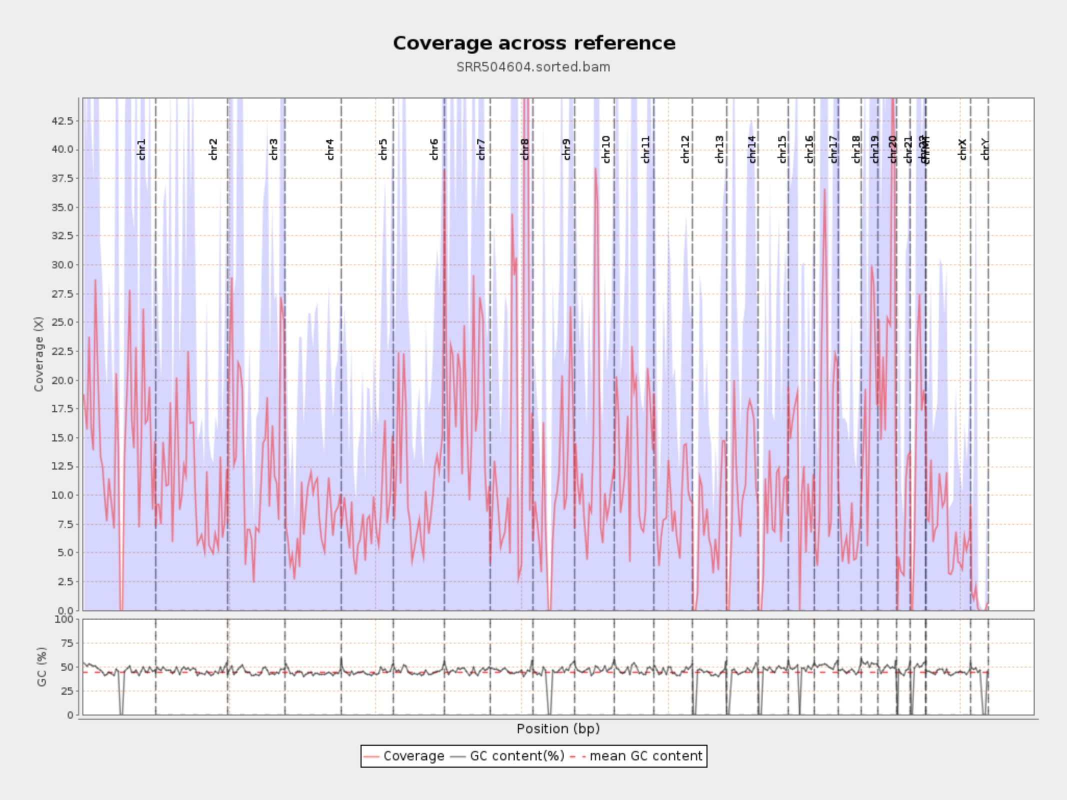
2.7. Chromosome stats

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

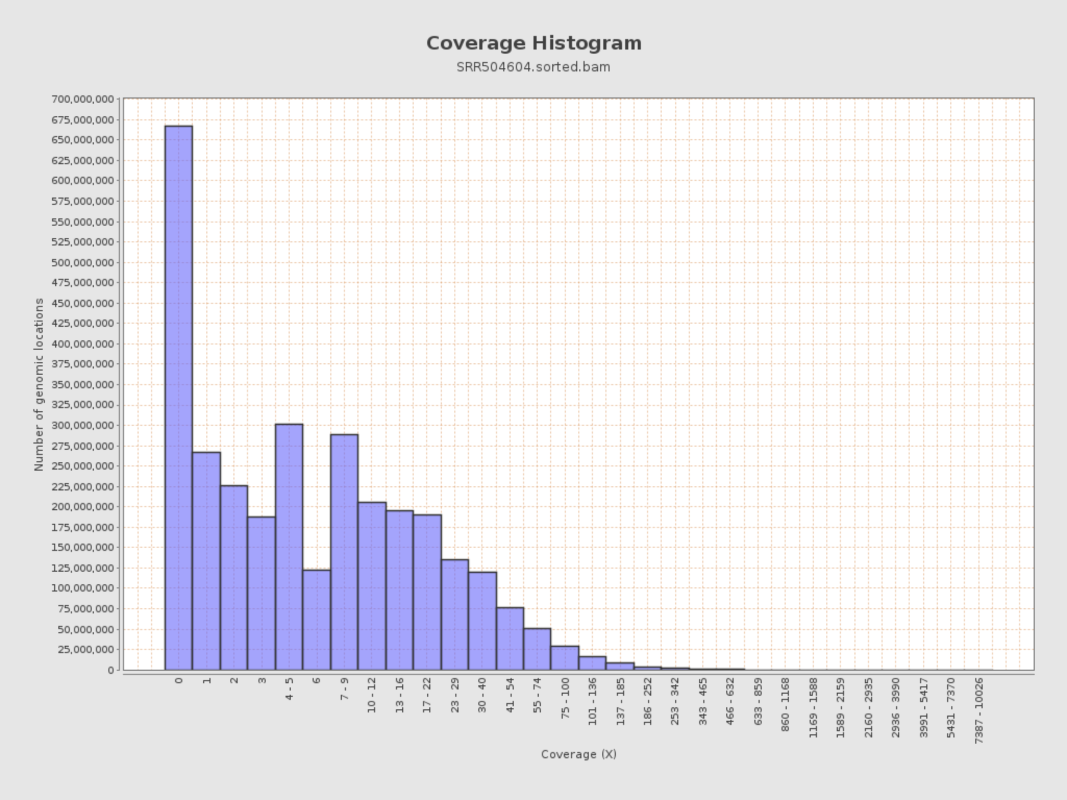
		bases	**coverage**	**deviation**
chr1	249250621	3756575245	15.0715	25.5419
chr2	243199373	2509187925	10.3174	18.8122
chr3	198022430	2705829552	13.6643	22.7438
chr4	191154276	1527198309	7.9893	12.781
chr5	180915260	1485601346	8.2116	13.9053
chr6	171115067	1868690756	10.9207	17.8961
chr7	159138663	2975900274	18.7	27.9794
chr8	146364022	2787465932	19.0447	47.0008
chr9	141213431	1438511620	10.1868	19.9651
chr10	135534747	1722316999	12.7076	24.1411
chr11	135006516	1867170594	13.8302	23.5457
chr12	133851895	1246972649	9.3161	15.8267
chr13	115169878	829798698	7.205	13.5953
chr14	107349540	1220926289	11.3734	19.8723
chr15	102531392	815231888	7.951	14.9147
chr16	90354753	1068660350	11.8274	20.4133
chr17	81195210	1330834008	16.3905	50.6667
chr18	78077248	478360779	6.1268	28.6817
chr19	59128983	1081882369	18.297	31.8974
chr20	63025520	1648393469	26.1544	39.1709
chr21	48129895	347042176	7.2105	18.4223
chr22	51304566	754154646	14.6996	27.4247
chrMT	16571	246255	14.8606	11.3553
chrX	155270560	1074710305	6.9215	12.2913

chrY	59373566	36901017	0.6215	14.8753

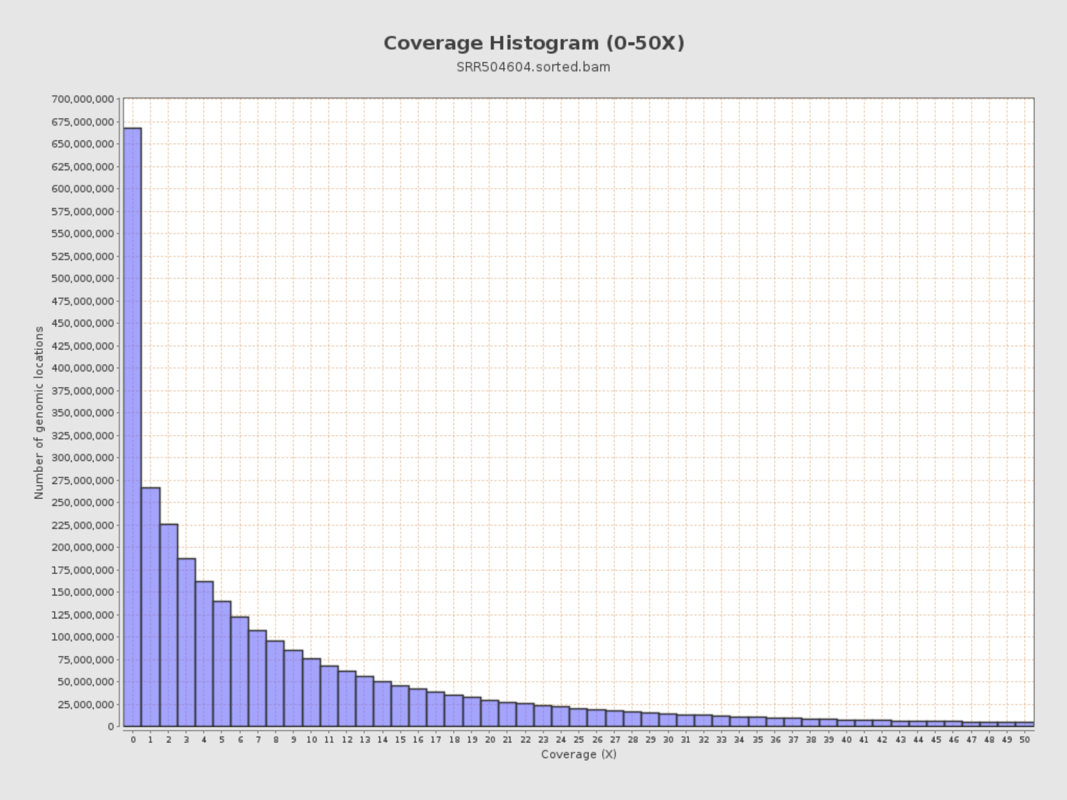
3. Results : Coverage across reference



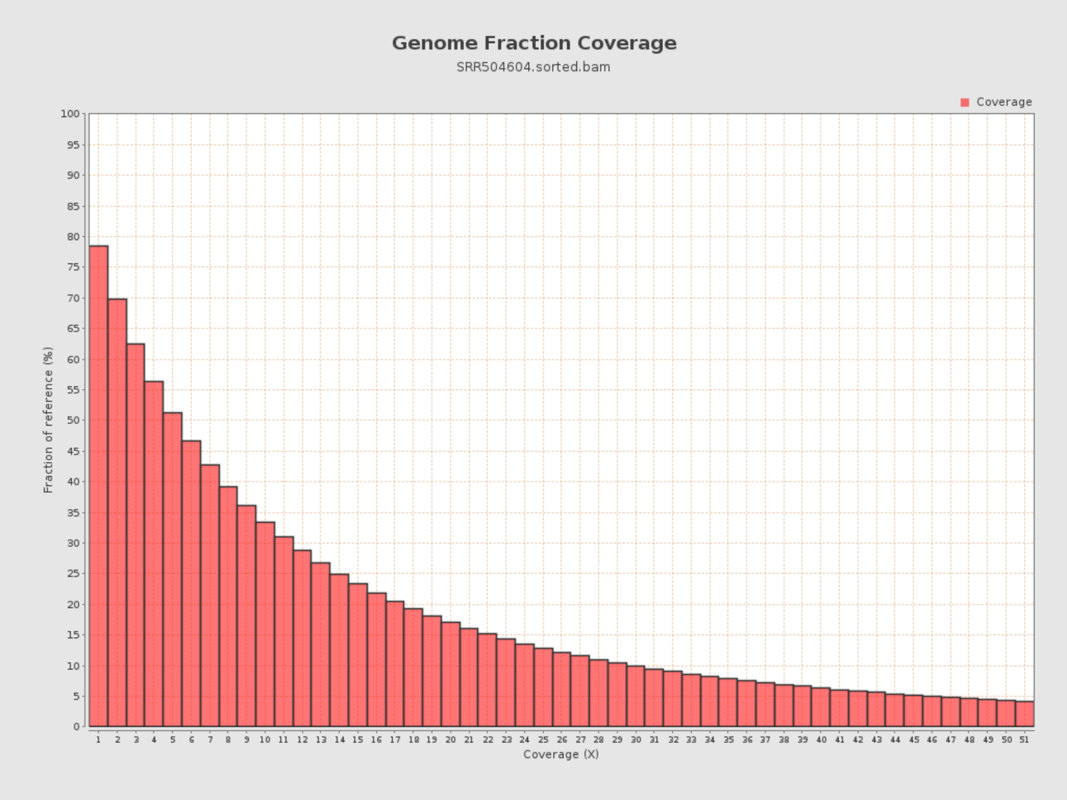
4. Results : Coverage Histogram



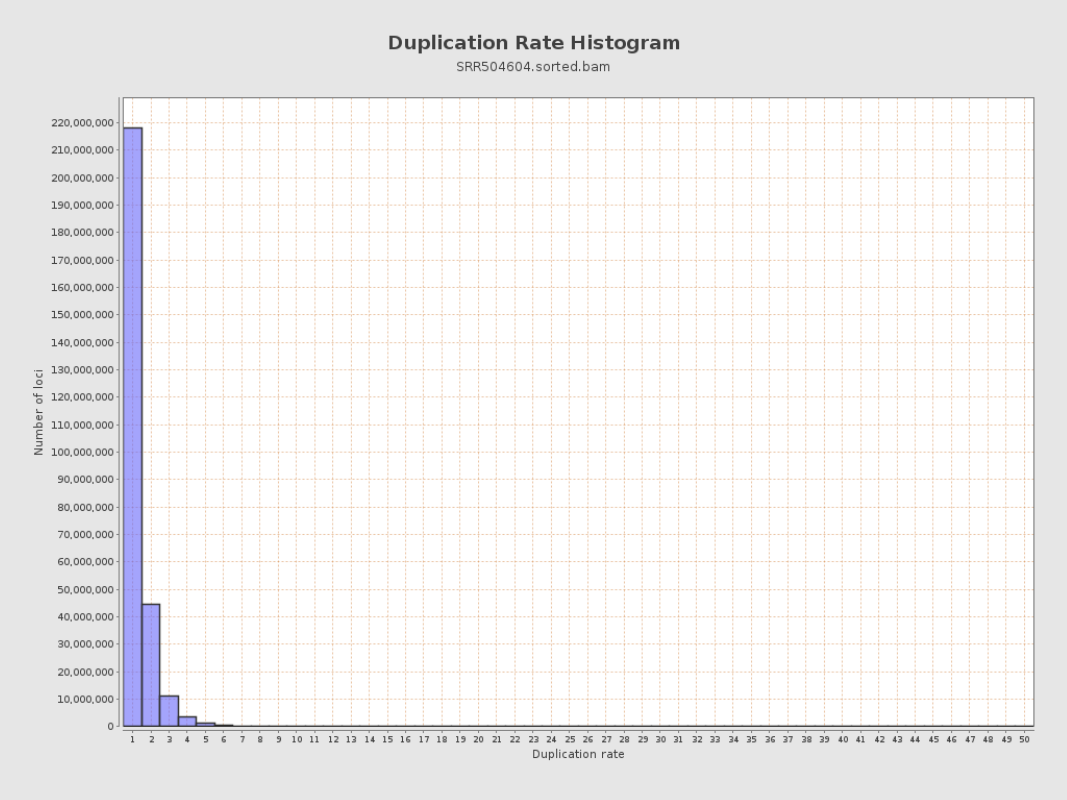
5. Results : Coverage Histogram (0-50X)



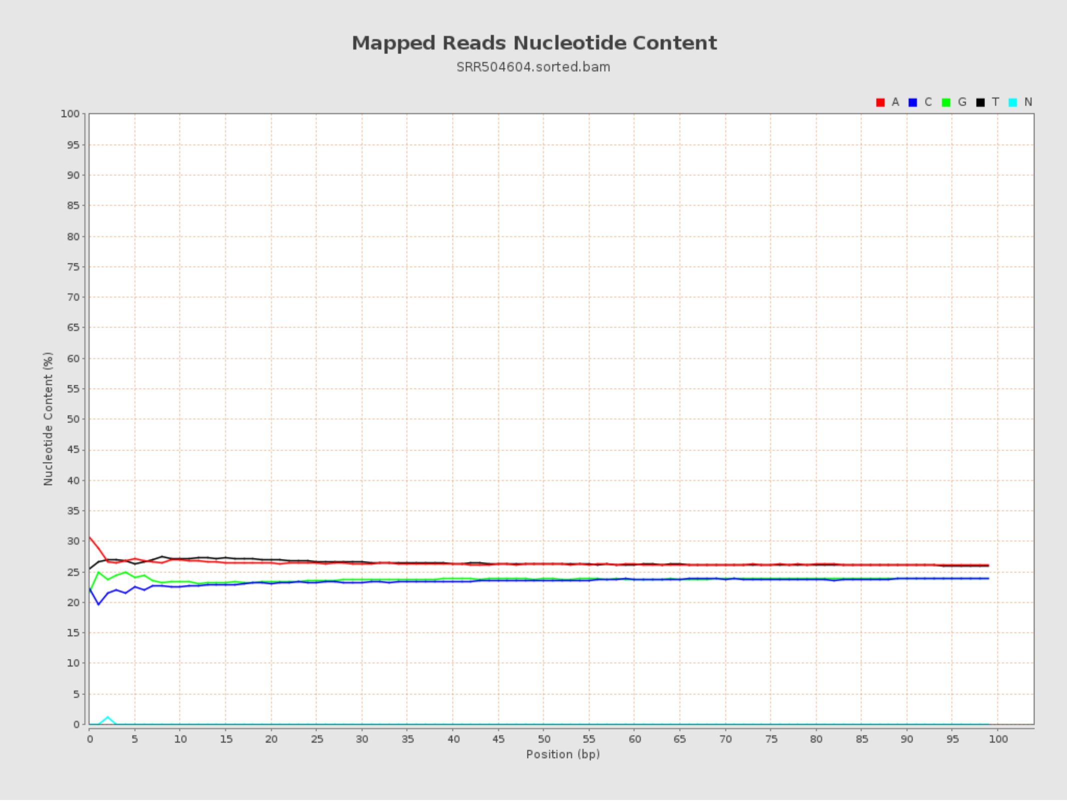
6. Results : Genome Fraction Coverage



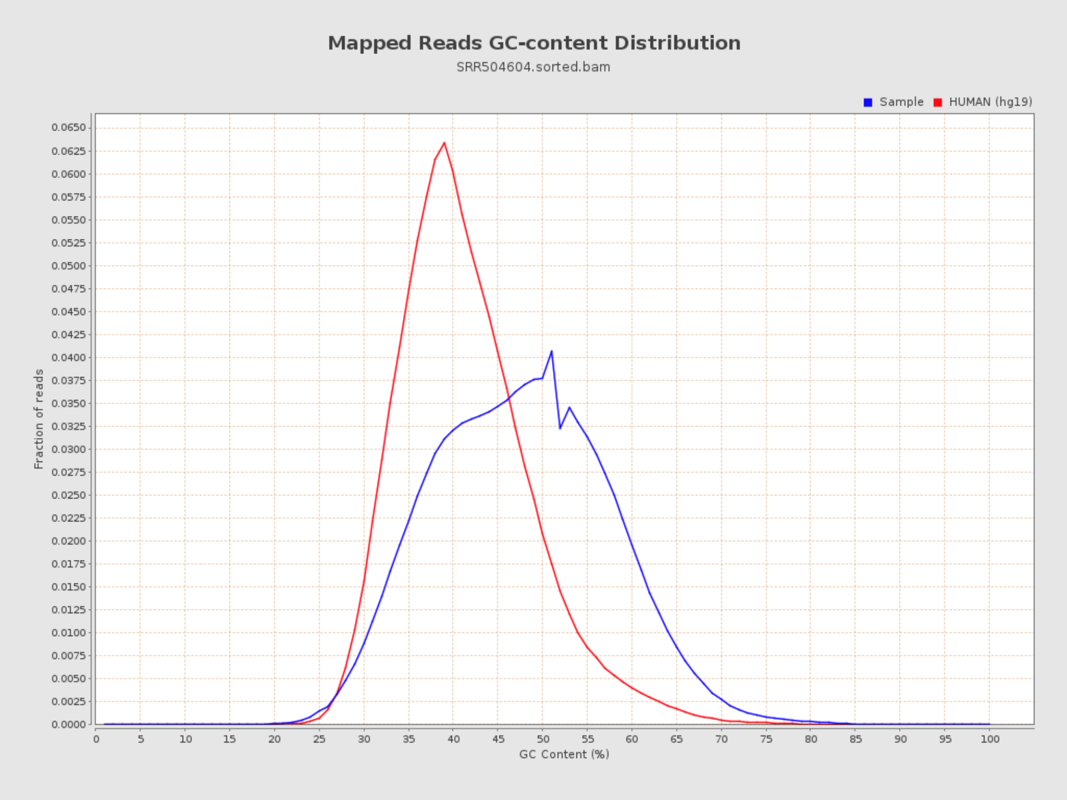
7. Results : Duplication Rate Histogram



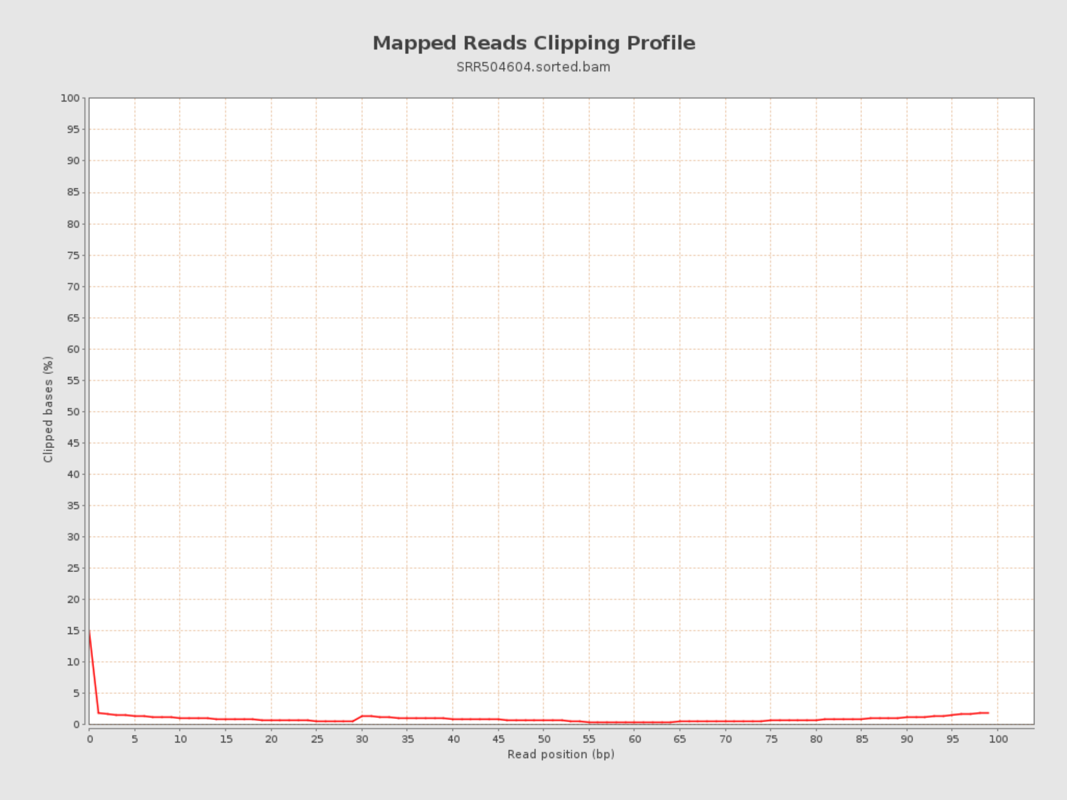
8. Results : Mapped Reads Nucleotide Content



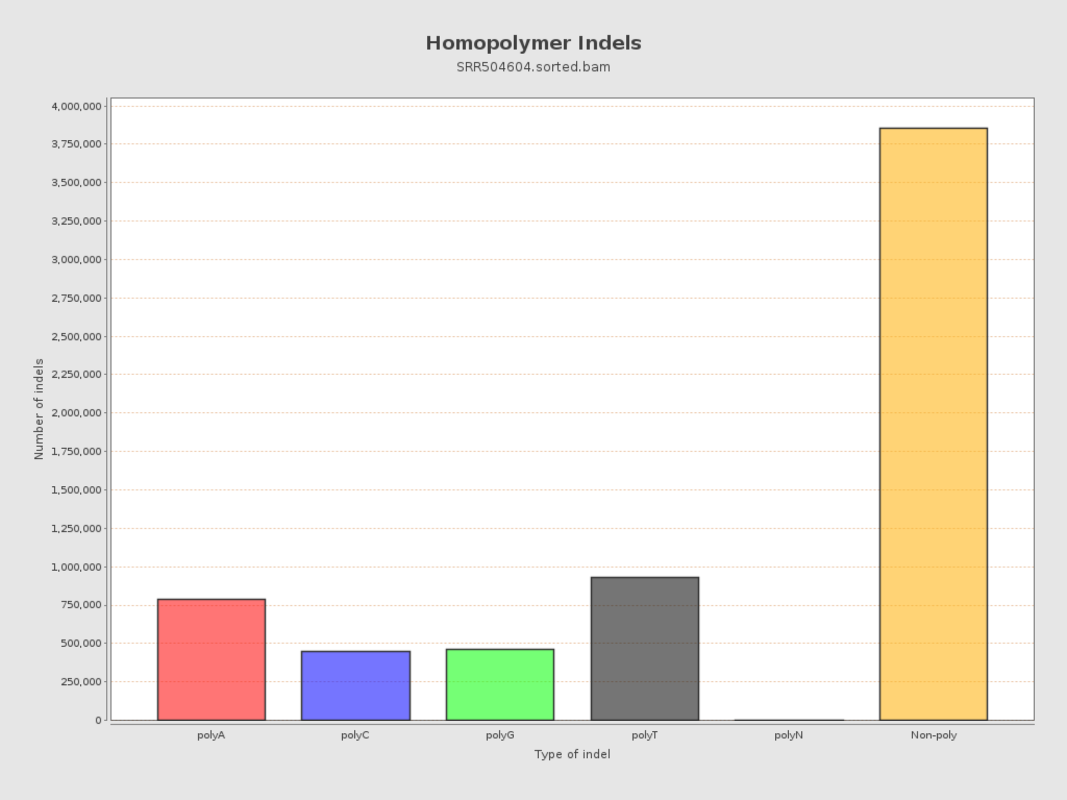
9. Results : Mapped Reads GC-content Distribution



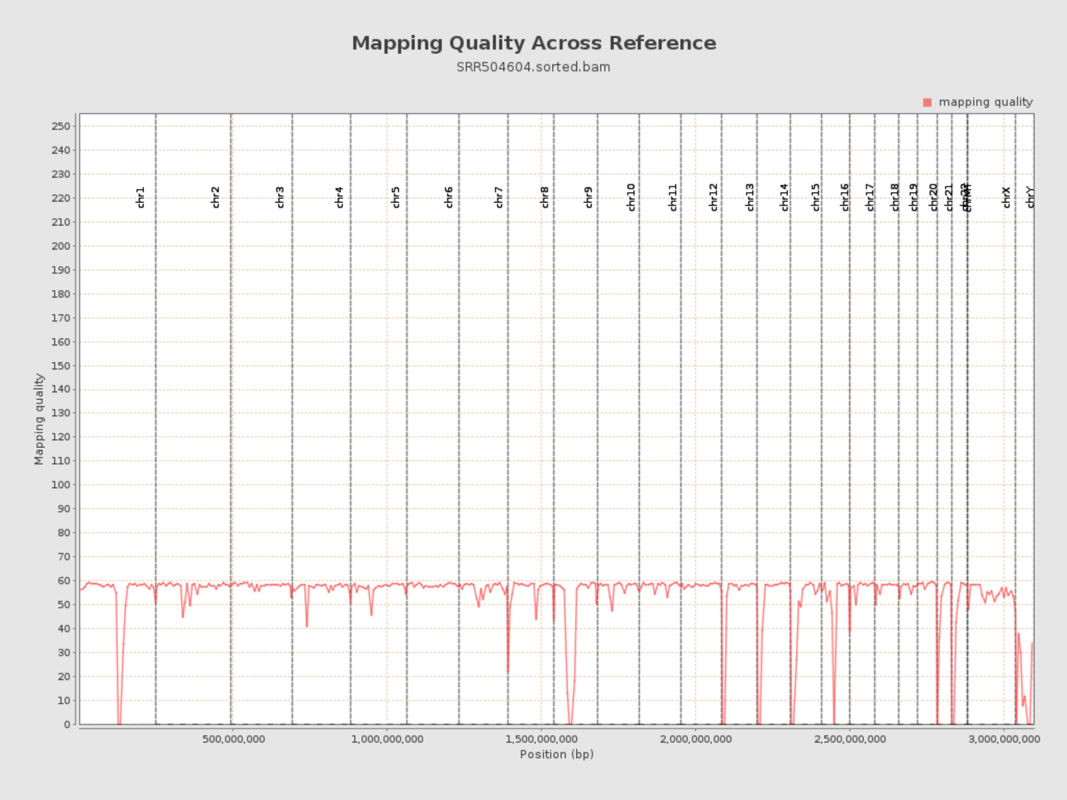
10. Results : Mapped Reads Clipping Profile



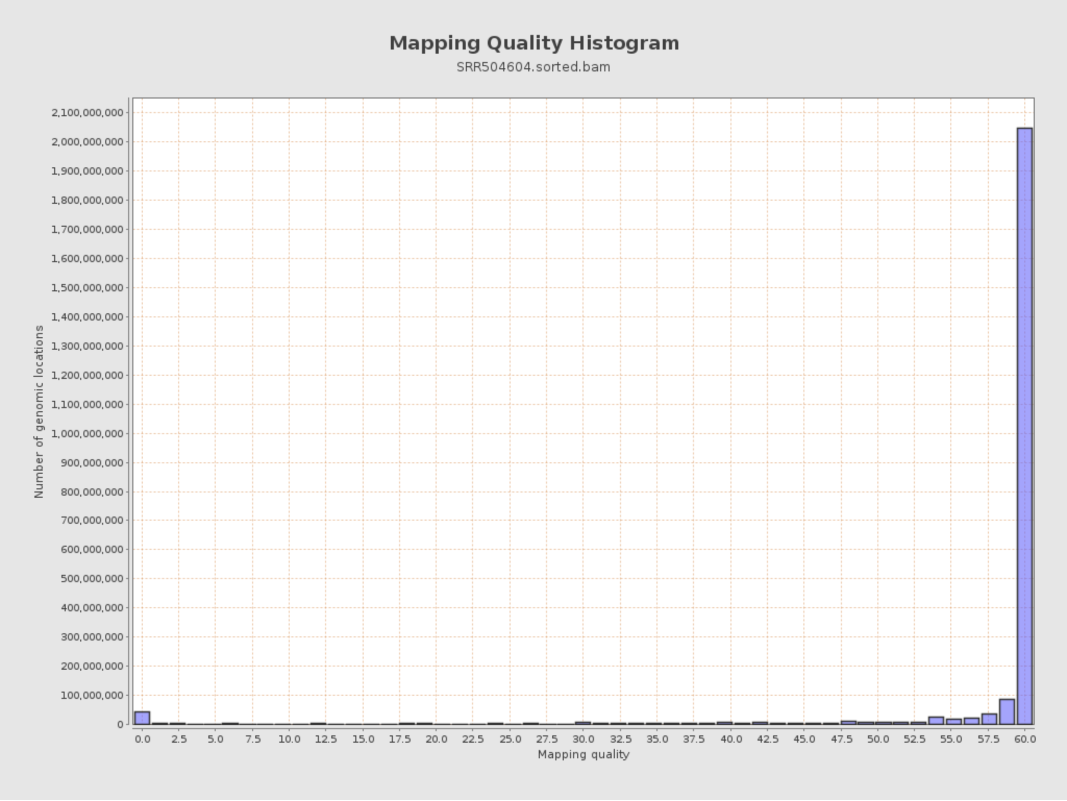
11. Results : Homopolymer Indels



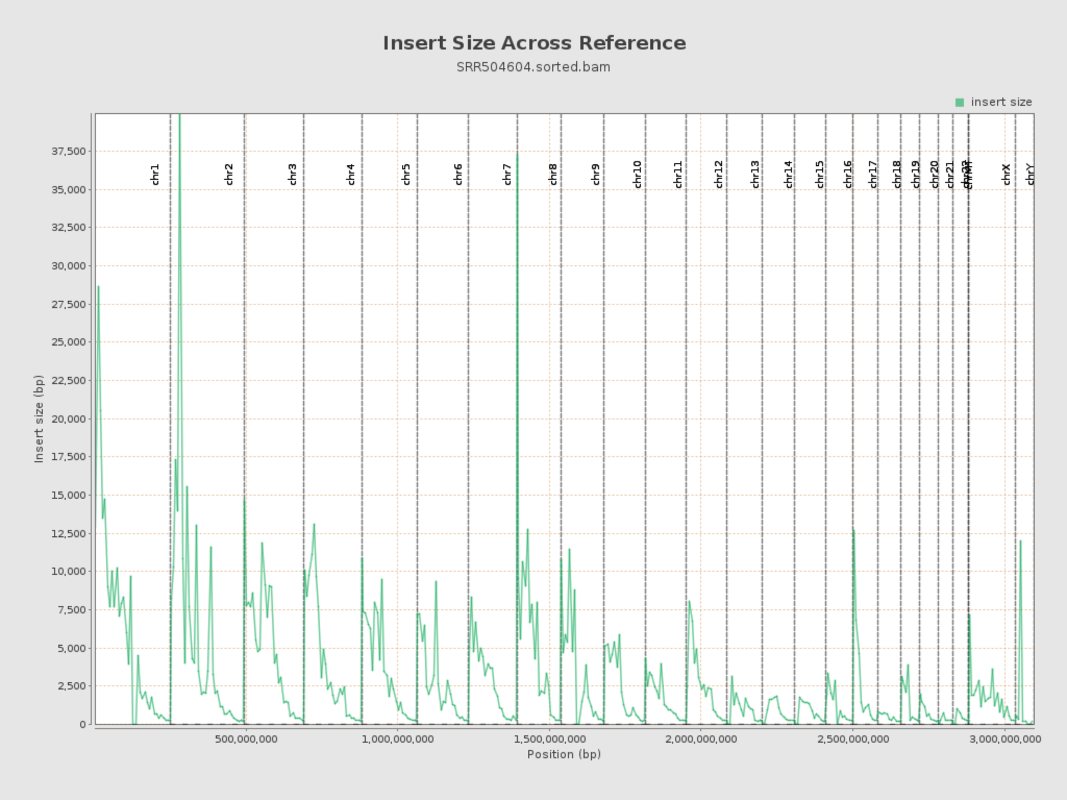
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram