Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 03:36:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504592.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_SRR504592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504592_1.fastq.gz SRR504592_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 03:36:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	362,045,086
Mapped reads	346,108,211 / 95.6%
Unmapped reads	15,936,875 / 4.4%
Mapped paired reads	346,108,211 / 95.6%
Mapped reads, first in pair	173,279,460 / 47.86%
Mapped reads, second in pair	172,828,751 / 47.74%
Mapped reads, both in pair	343,353,492 / 94.84%
Mapped reads, singletons	2,754,719 / 0.76%
Secondary alignments	0
Supplementary alignments	995,438 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	75,709,556 / 20.91%
Duplication rate	17.91%
Clipped reads	54,271,367 / 14.99%

2.2. ACGT Content

Number/percentage of A's	9,445,827,700 / 28.41%
Number/percentage of C's	7,129,467,402 / 21.45%
Number/percentage of T's	9,351,880,971 / 28.13%
Number/percentage of G's	7,307,480,760 / 21.98%
Number/percentage of N's	9,182,971 / 0.03%

GC Percentage	43.43%

2.3. Coverage

Mean	10.7422
Standard Deviation	94.5143

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	33,965.24
Standard Deviation	1,750,282.1
P25/Median/P75	133 / 189 / 246

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	191,044,541
Insertions	3,355,311
Mapped reads with at least one insertion	0.93%
Deletions	4,123,492
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.4%

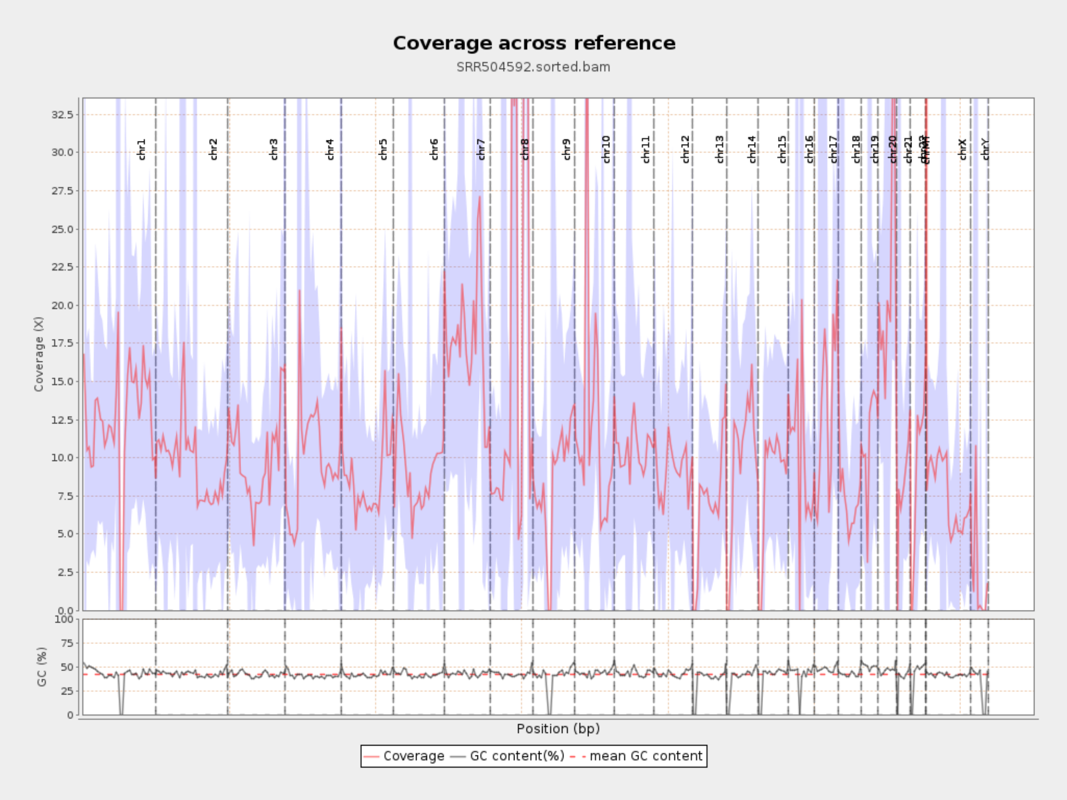
2.7. Chromosome stats

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

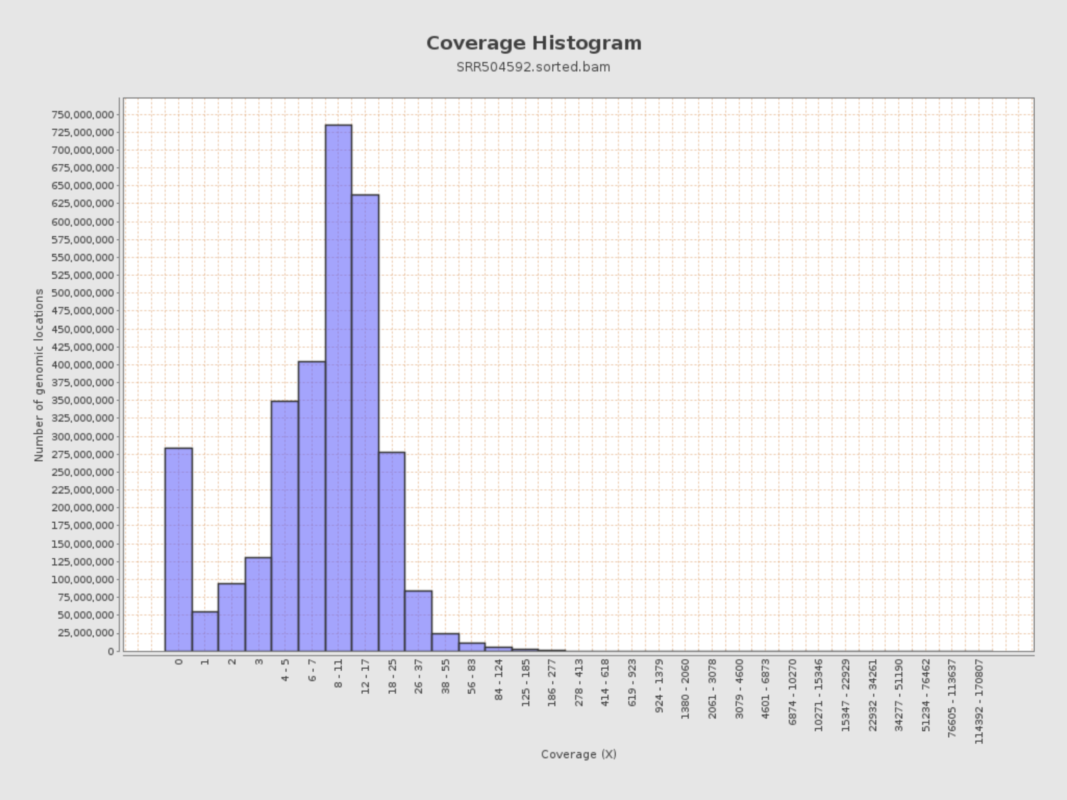
		bases	coverage	deviation
chr1	249250621	3091570943	12.4035	171.3391
chr2	243199373	2349661752	9.6615	56.9991
chr3	198022430	1966632258	9.9314	16.2485
chr4	191154276	1885613337	9.8644	113.2103
chr5	180915260	1570374551	8.6802	10.236
chr6	171115067	1558017902	9.1051	22.4515
chr7	159138663	2804925758	17.6257	135.6685
chr8	146364022	2925256669	19.9862	66.3861
chr9	141213431	1199016882	8.4908	60.2706
chr10	135534747	1619256675	11.9472	256.6989
chr11	135006516	1427703387	10.5751	38.3815
chr12	133851895	1243042224	9.2867	9.083
chr13	115169878	807192520	7.0087	6.3704
chr14	107349540	1078715208	10.0486	9.3828
chr15	102531392	869587446	8.4812	7.2072
chr16	90354753	923682038	10.2228	72.9775
chr17	81195210	1031011678	12.6979	44.5232
chr18	78077248	566939272	7.2613	93.4857
chr19	59128983	664819668	11.2435	88.8259
chr20	63025520	1397761017	22.1777	28.7387
chr21	48129895	398575670	8.2812	40.0197
chr22	51304566	448591089	8.7437	9.388
chrMT	16571	118858489	7,172.6805	1,521.5086
chrX	155270560	1180294513	7.6015	18.5533

chrY	59373566	127385876	2.1455	114.8549

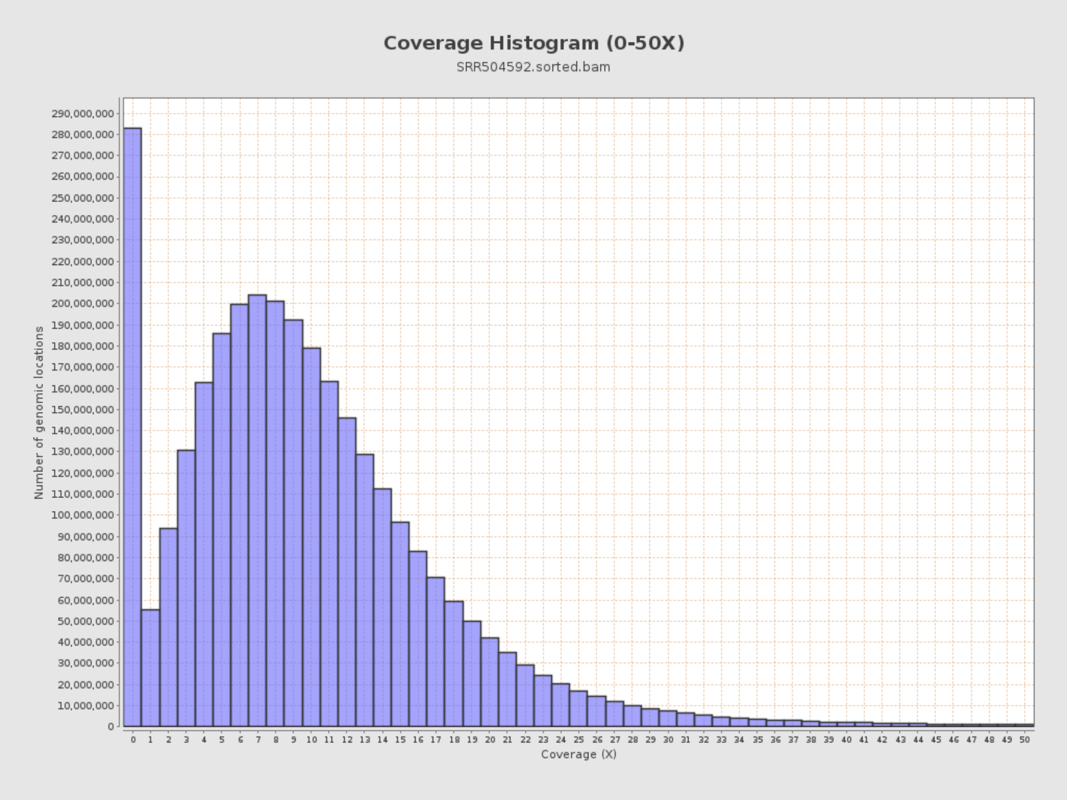
3. Results : Coverage across reference



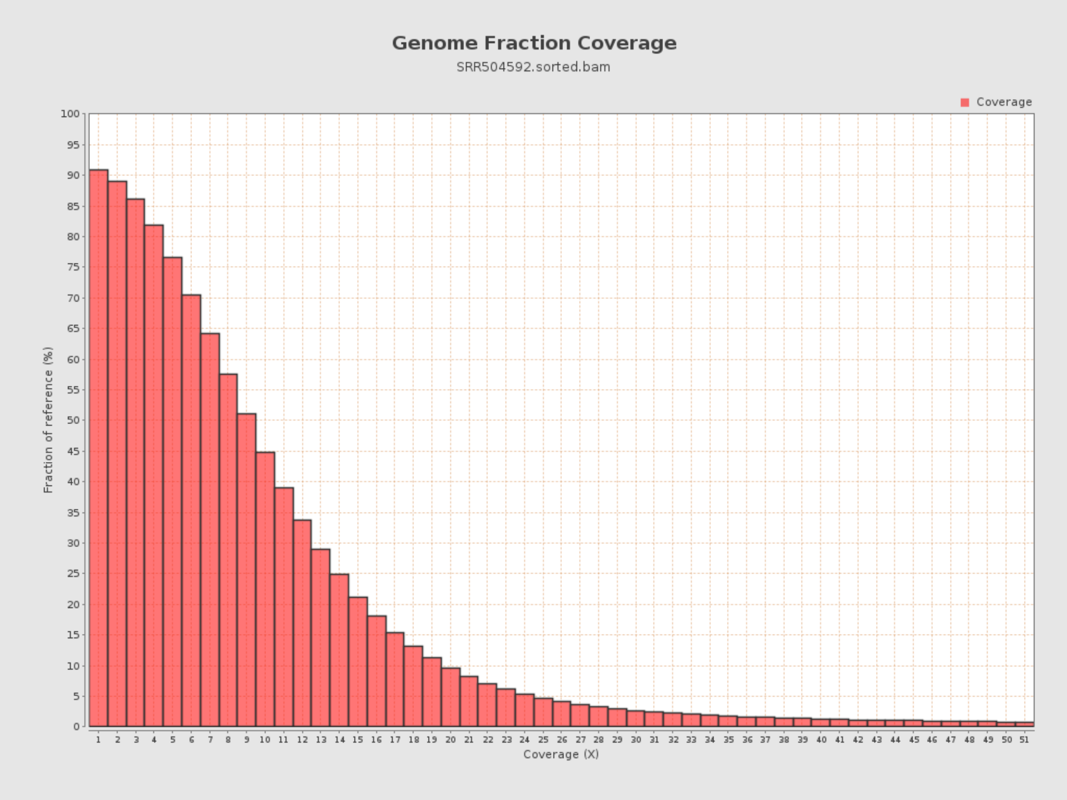
4. Results : Coverage Histogram



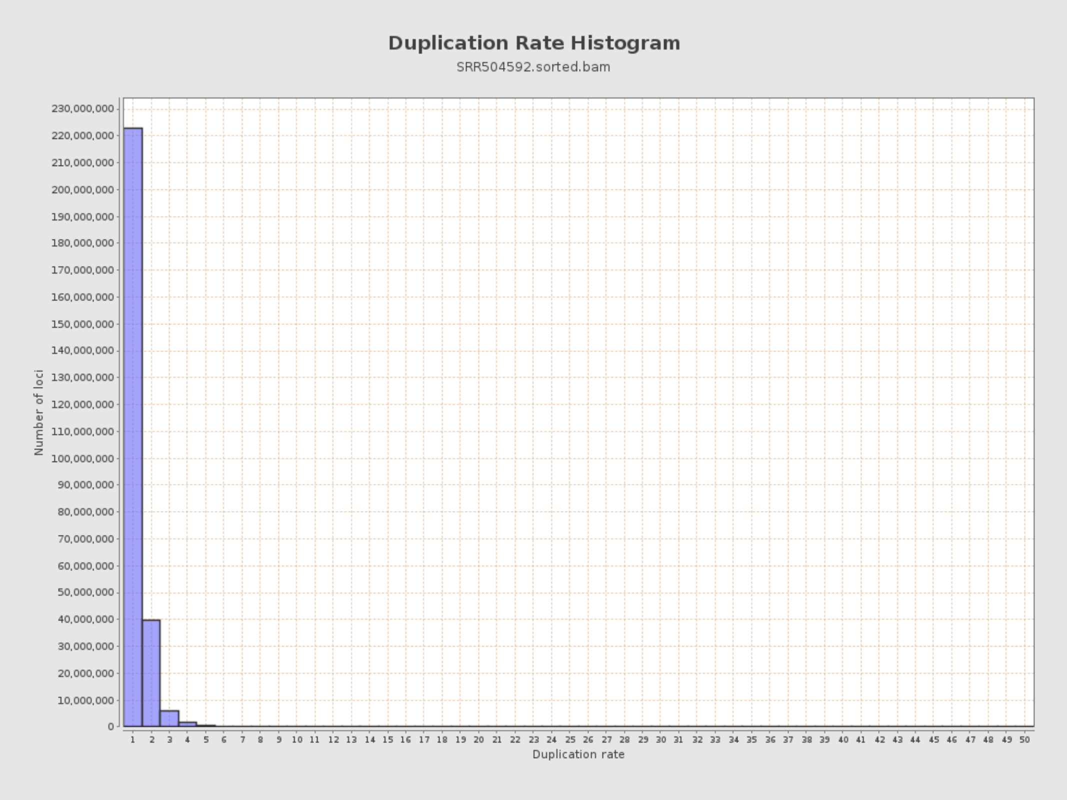
5. Results : Coverage Histogram (0-50X)



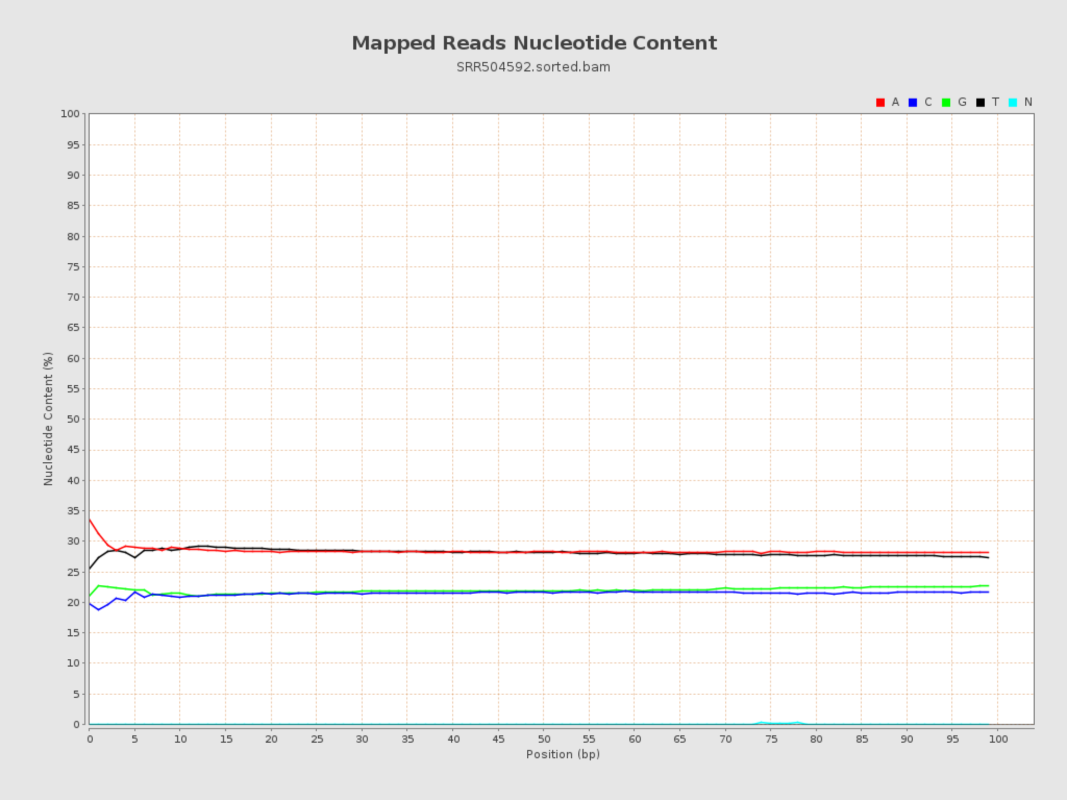
6. Results : Genome Fraction Coverage



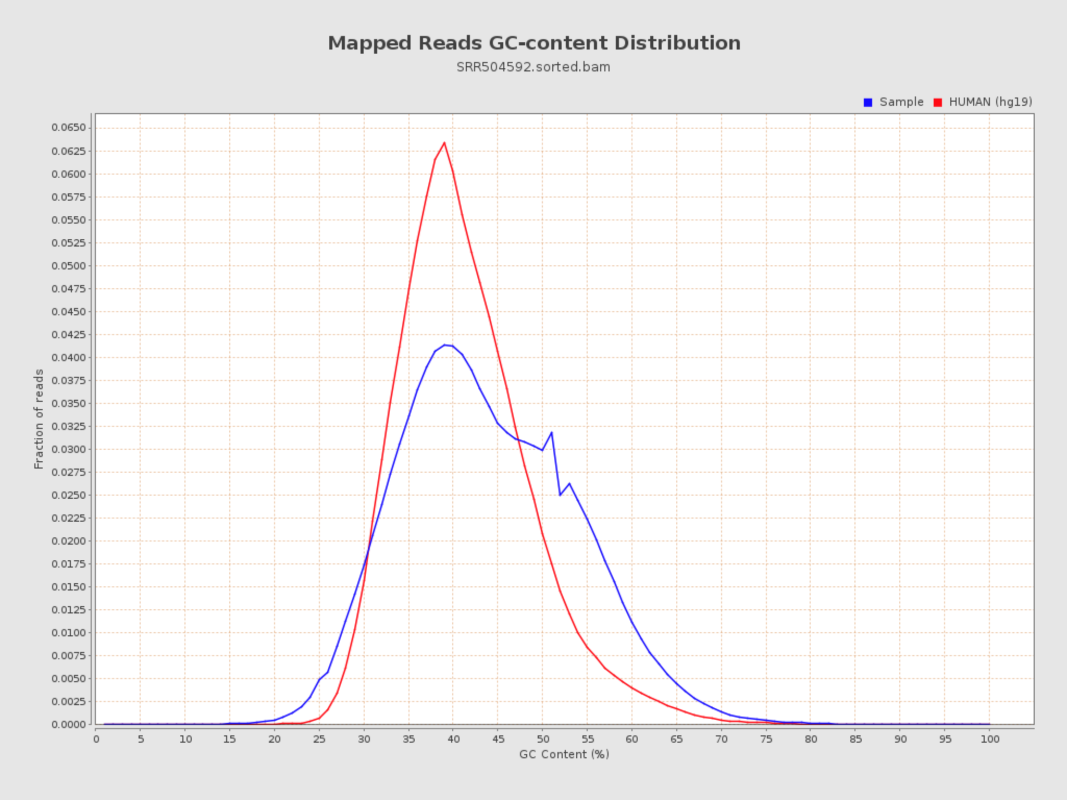
7. Results : Duplication Rate Histogram



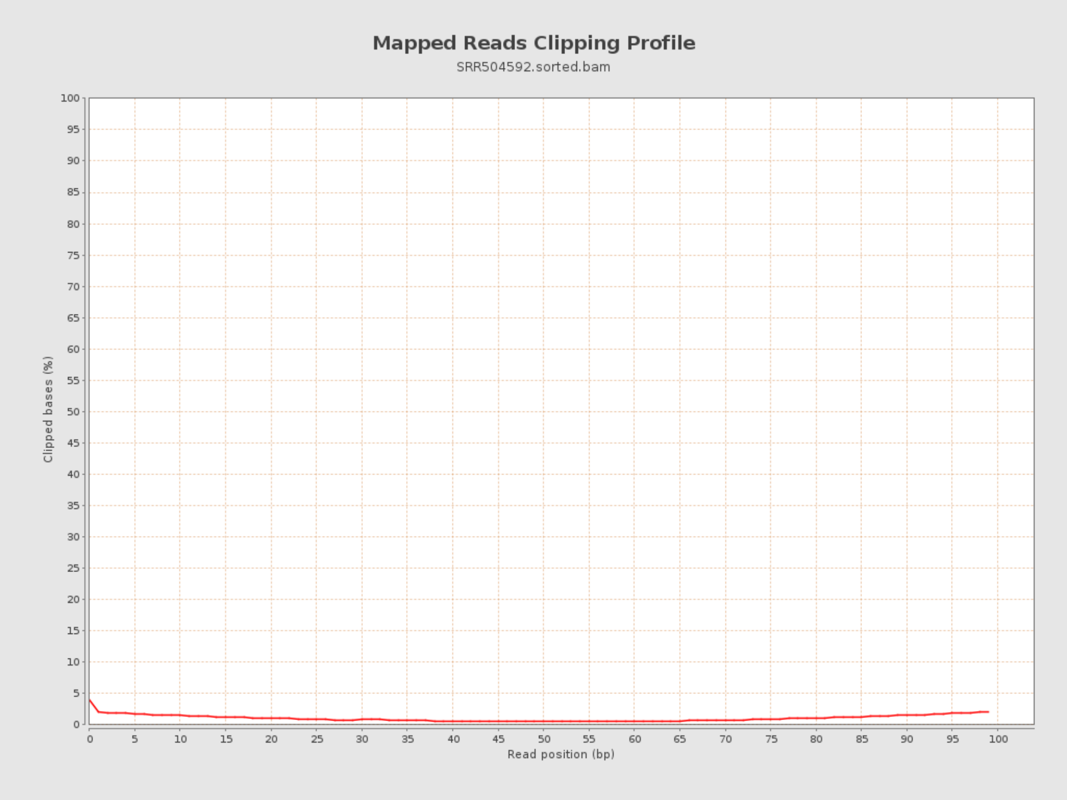
8. Results : Mapped Reads Nucleotide Content



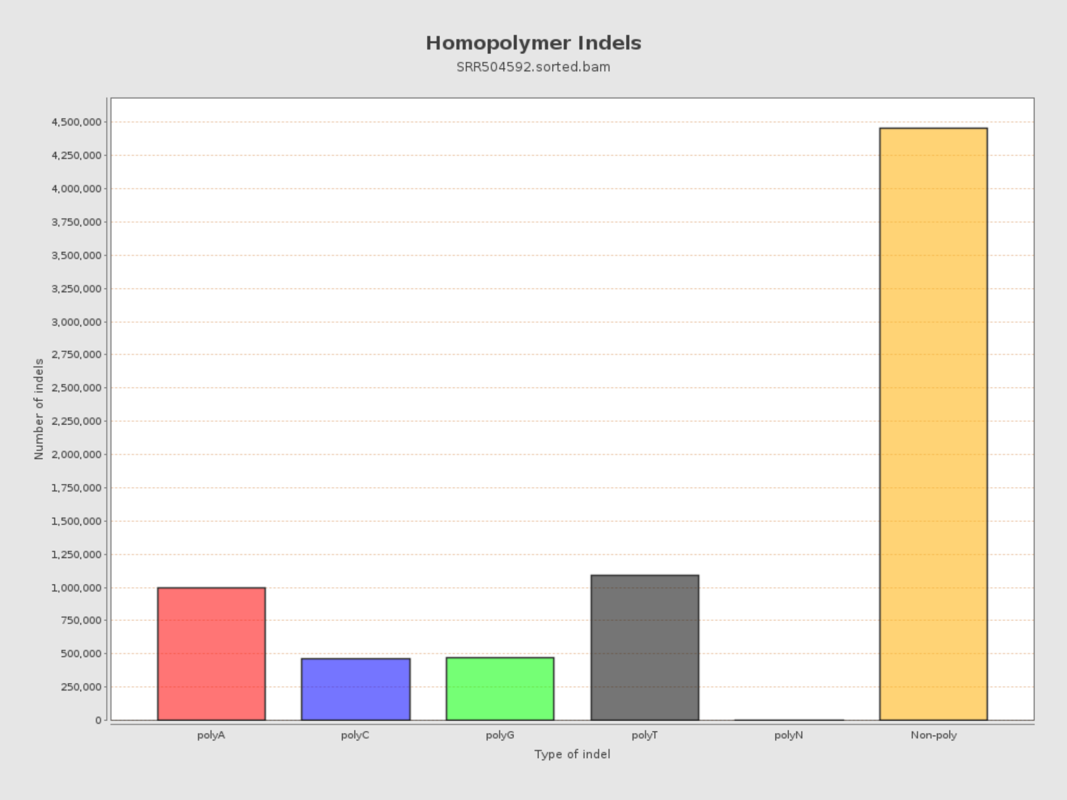
9. Results : Mapped Reads GC-content Distribution



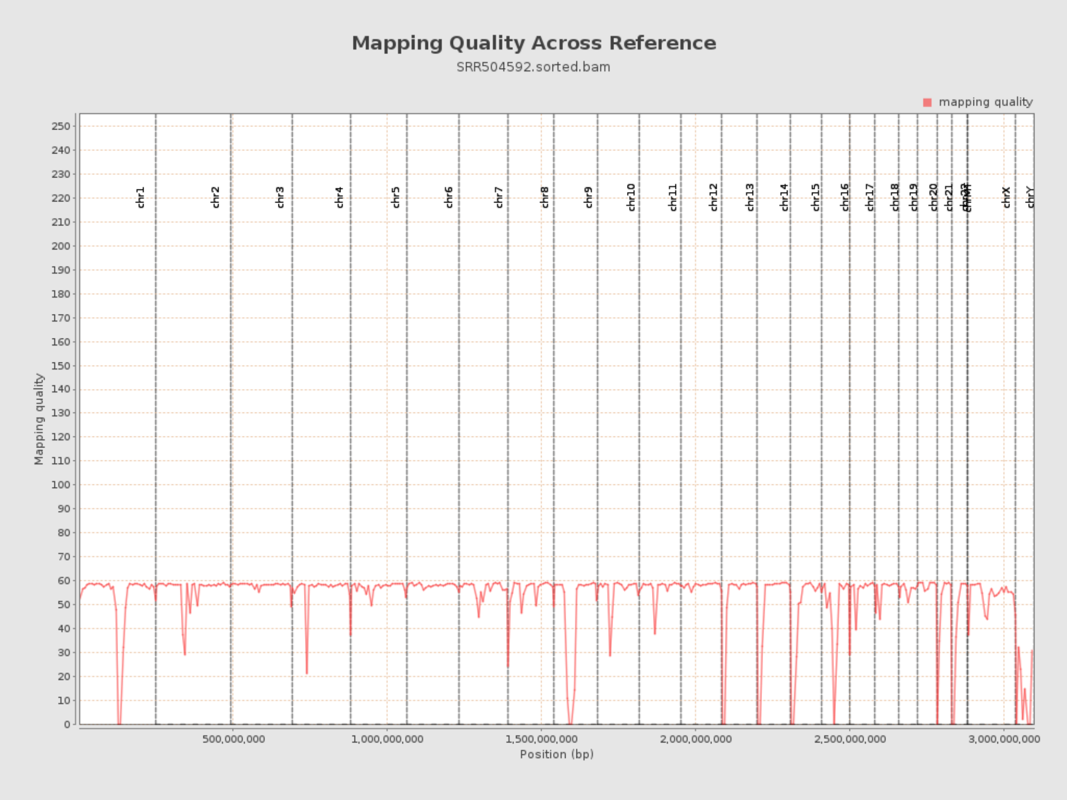
10. Results : Mapped Reads Clipping Profile



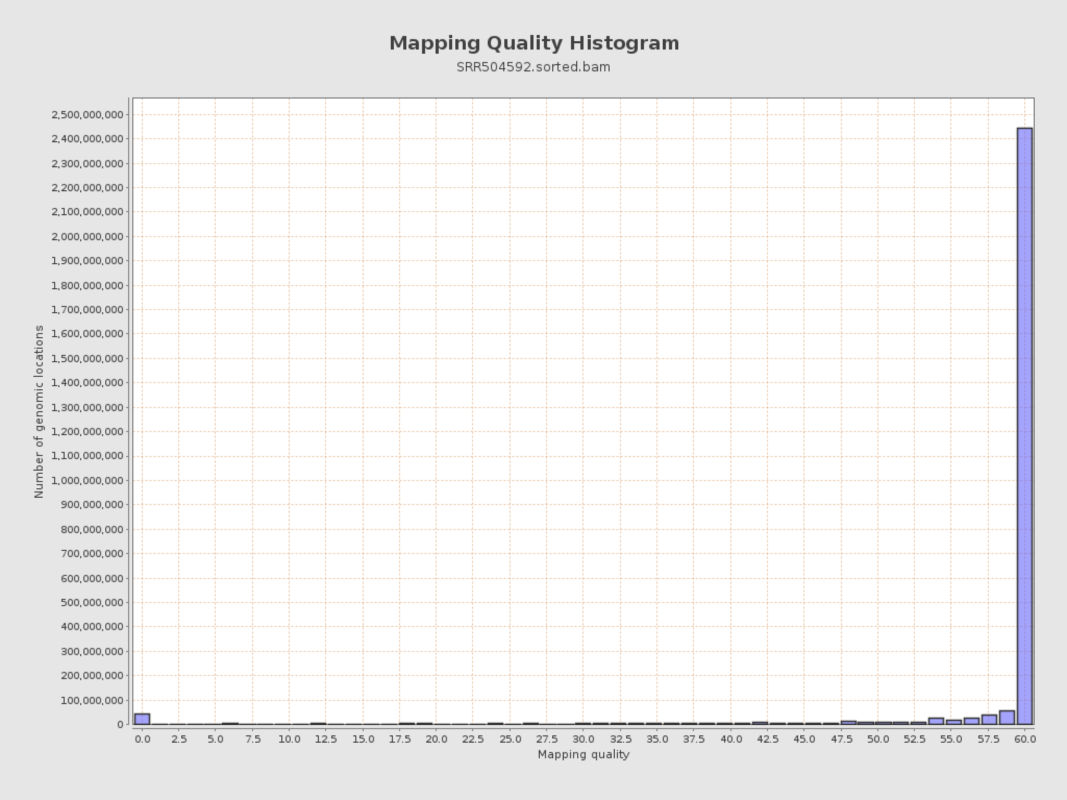
11. Results : Homopolymer Indels



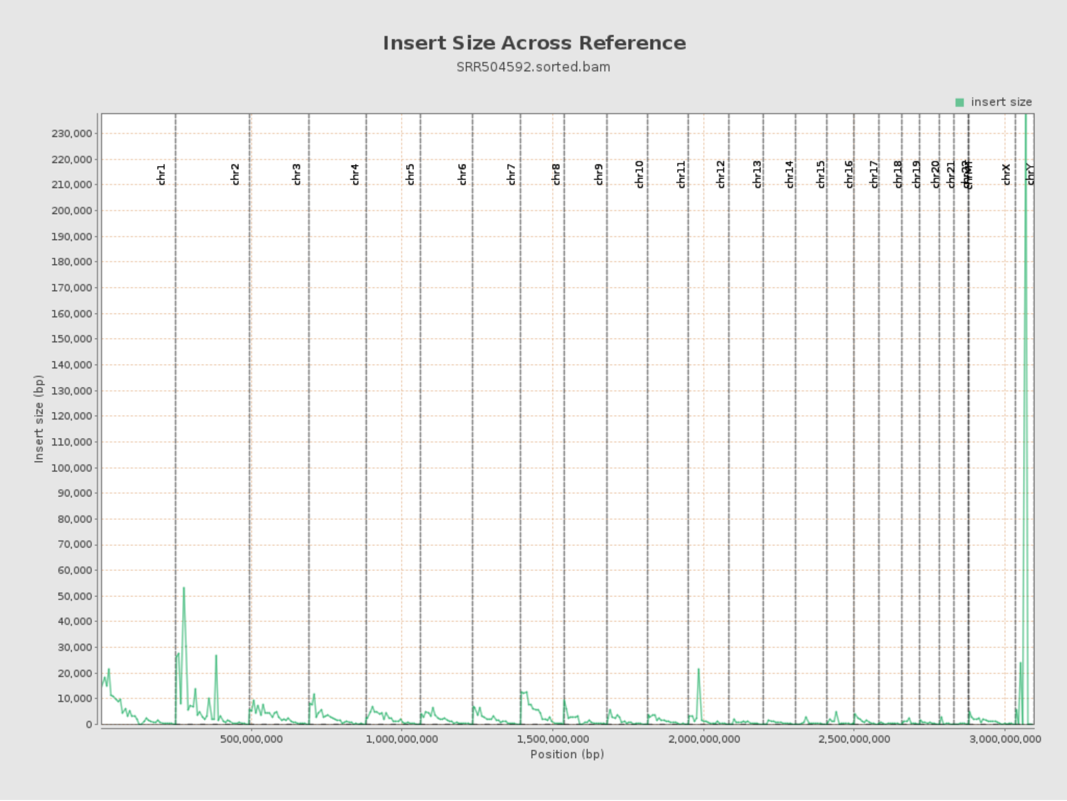
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram