Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 06:16:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124857.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_SRR3124857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124857_1.fastq.gz SRR3124857_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 06:15:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	144,422,752
Mapped reads	140,396,049 / 97.21%
Unmapped reads	4,026,703 / 2.79%
Mapped paired reads	140,396,049 / 97.21%
Mapped reads, first in pair	70,918,005 / 49.1%
Mapped reads, second in pair	69,478,044 / 48.11%
Mapped reads, both in pair	138,350,604 / 95.8%
Mapped reads, singletons	2,045,445 / 1.42%
Secondary alignments	0
Supplementary alignments	2,170,986 / 1.5%
Read min/max/mean length	30 / 150 / 150.73
Duplicated reads (estimated)	56,336,203 / 39.01%
Duplication rate	28.45%
Clipped reads	59,519,007 / 41.21%

2.2. ACGT Content

Number/percentage of A's	5,486,060,247 / 28.6%
Number/percentage of C's	3,838,074,085 / 20.01%
Number/percentage of T's	5,598,180,912 / 29.18%
Number/percentage of G's	4,260,935,630 / 22.21%
Number/percentage of N's	44,083 / 0%

GC Percentage	42.22%

2.3. Coverage

Mean	6.2018
Standard Deviation	74.4631

2.4. Mapping Quality

Mean Mapping Quality	53.77

2.5. Insert size

Mean	59,290.95
Standard Deviation	2,315,212.78
P25/Median/P75	204 / 260 / 327

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	241,298,818
Insertions	3,938,213
Mapped reads with at least one insertion	2.55%
Deletions	6,964,056
Mapped reads with at least one deletion	4.7%
Homopolymer indels	44.26%

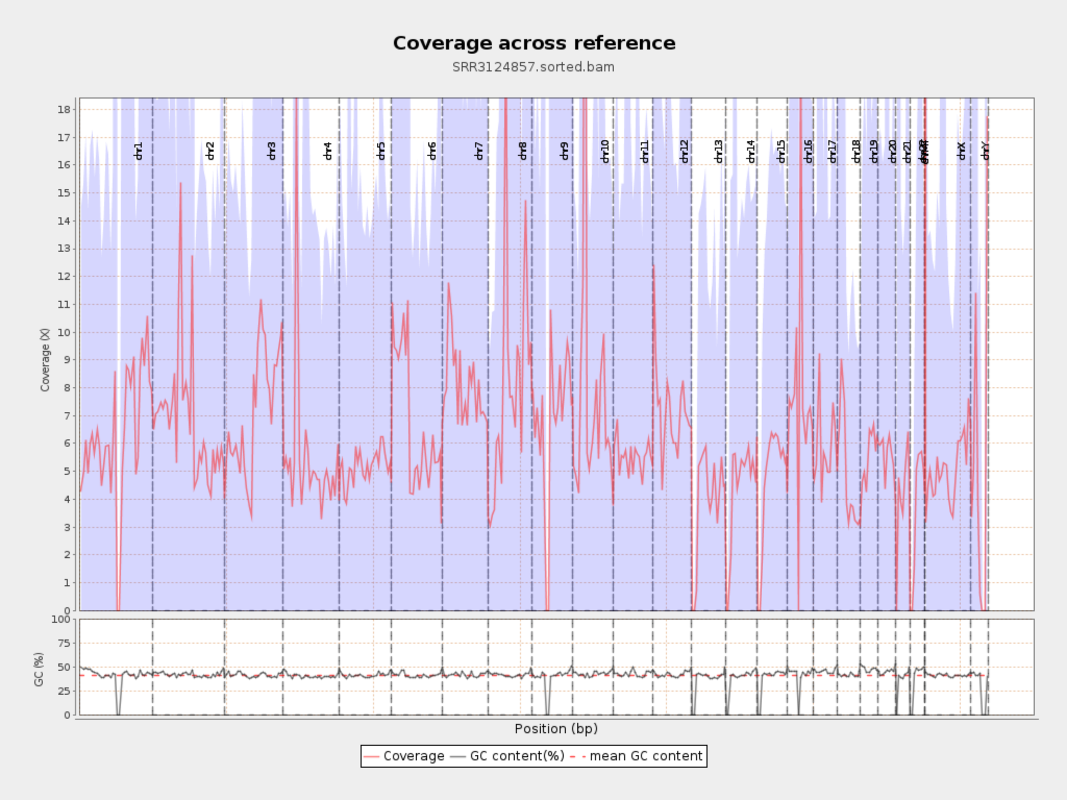
2.7. Chromosome stats

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

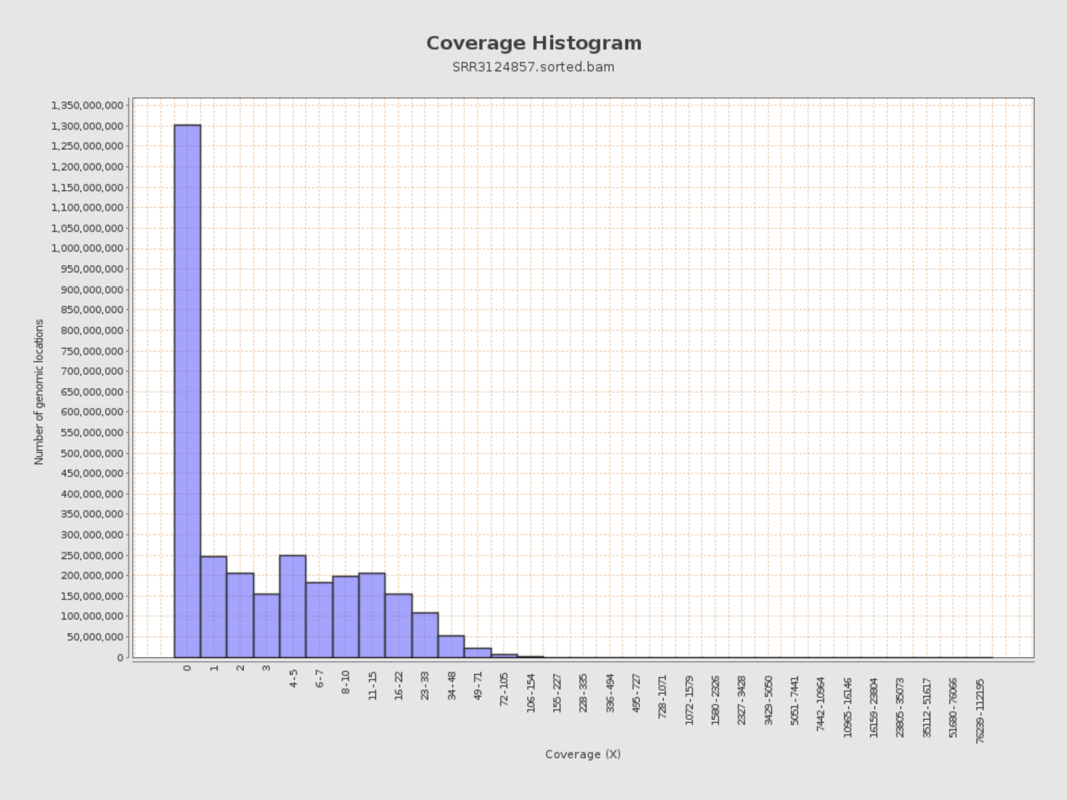
		bases	coverage	deviation
chr1	249250621	1572512095	6.309	52.2086
chr2	243199373	1681428894	6.9138	94.8168
chr3	198022430	1416047033	7.1509	12.4149
chr4	191154276	1035504269	5.4171	102.3632
chr5	180915260	937429558	5.1816	11.7992
chr6	171115067	1157888613	6.7667	31.4252
chr7	159138663	1282379128	8.0582	58.5733
chr8	146364022	1219875190	8.3345	21.3207
chr9	141213431	949477165	6.7237	112.1975
chr10	135534747	1122373403	8.2811	212.0742
chr11	135006516	745185245	5.5196	25.2677
chr12	133851895	965927062	7.2164	12.8075
chr13	115169878	452760793	3.9312	8.0924
chr14	107349540	464791484	4.3297	13.3198
chr15	102531392	474360682	4.6265	9.1378
chr16	90354753	695795189	7.7007	104.5038
chr17	81195210	469575954	5.7833	67.4038
chr18	78077248	377261247	4.8319	79.7273
chr19	59128983	324558650	5.489	28.0297
chr20	63025520	352965912	5.6004	32.3639
chr21	48129895	206545087	4.2914	47.0101
chr22	51304566	186176524	3.6288	11.4899
chrMT	16571	7256964	437.9316	196.6277
chrX	155270560	782962201	5.0426	15.4811

chrY	59373566	317905243	5.3543	149.0268

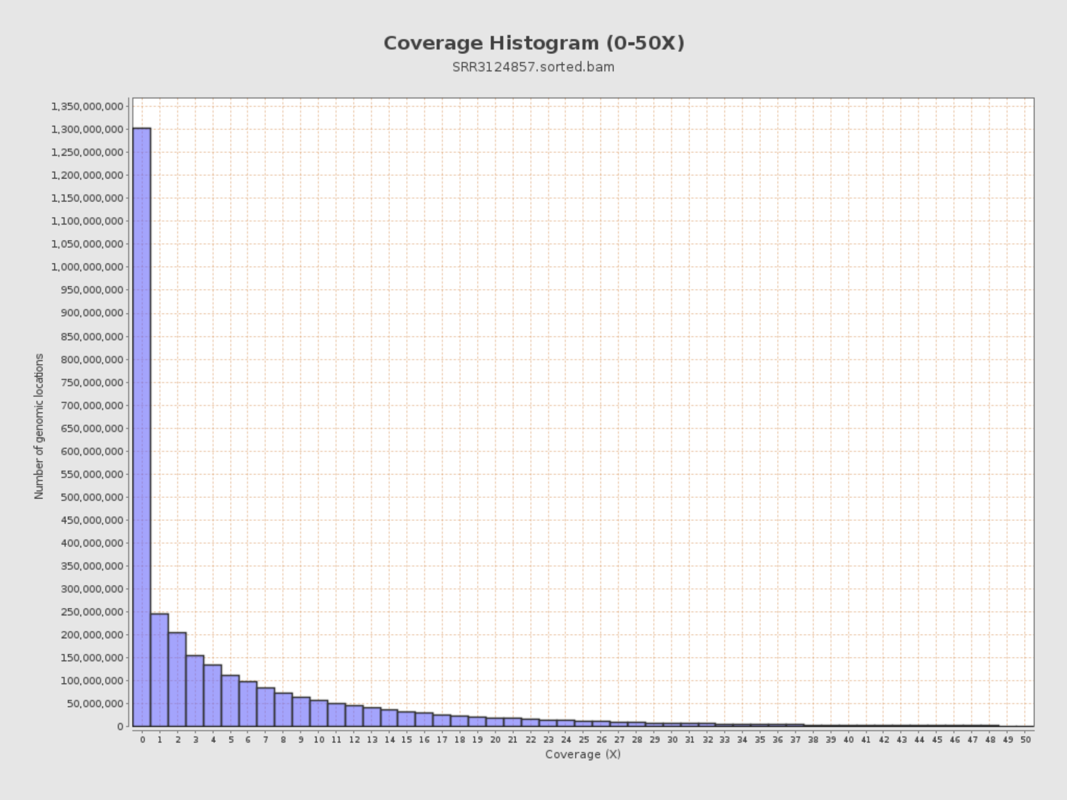
3. Results : Coverage across reference



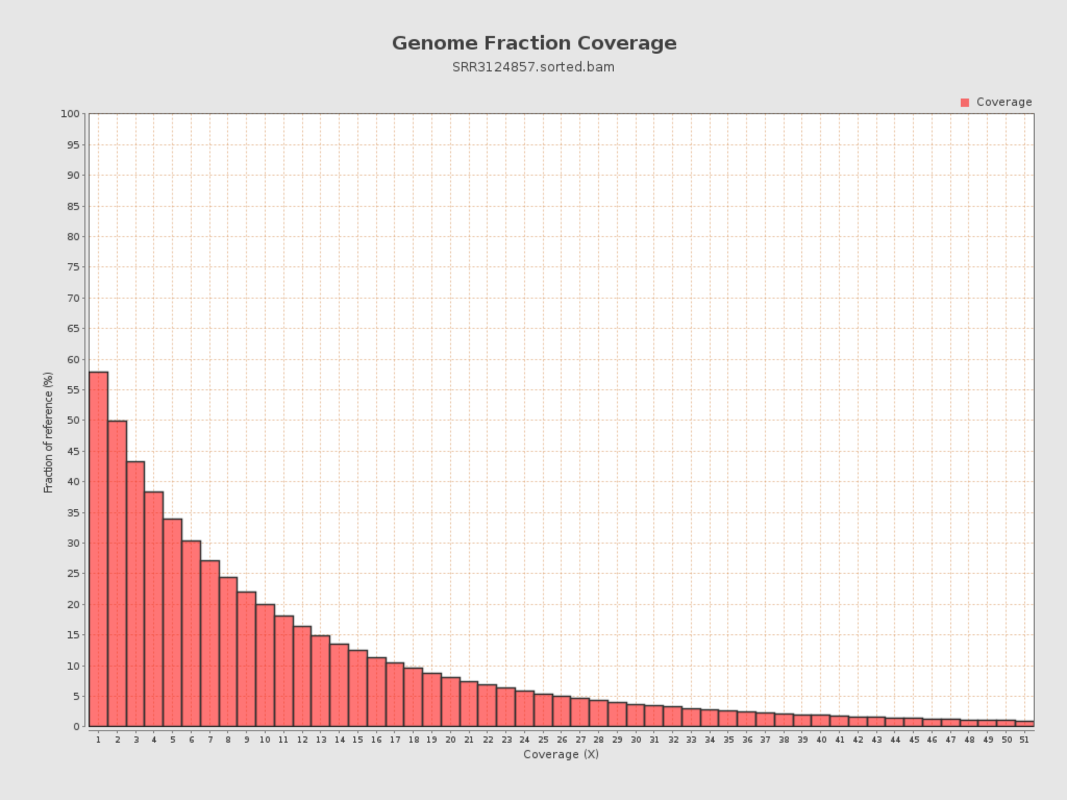
4. Results : Coverage Histogram



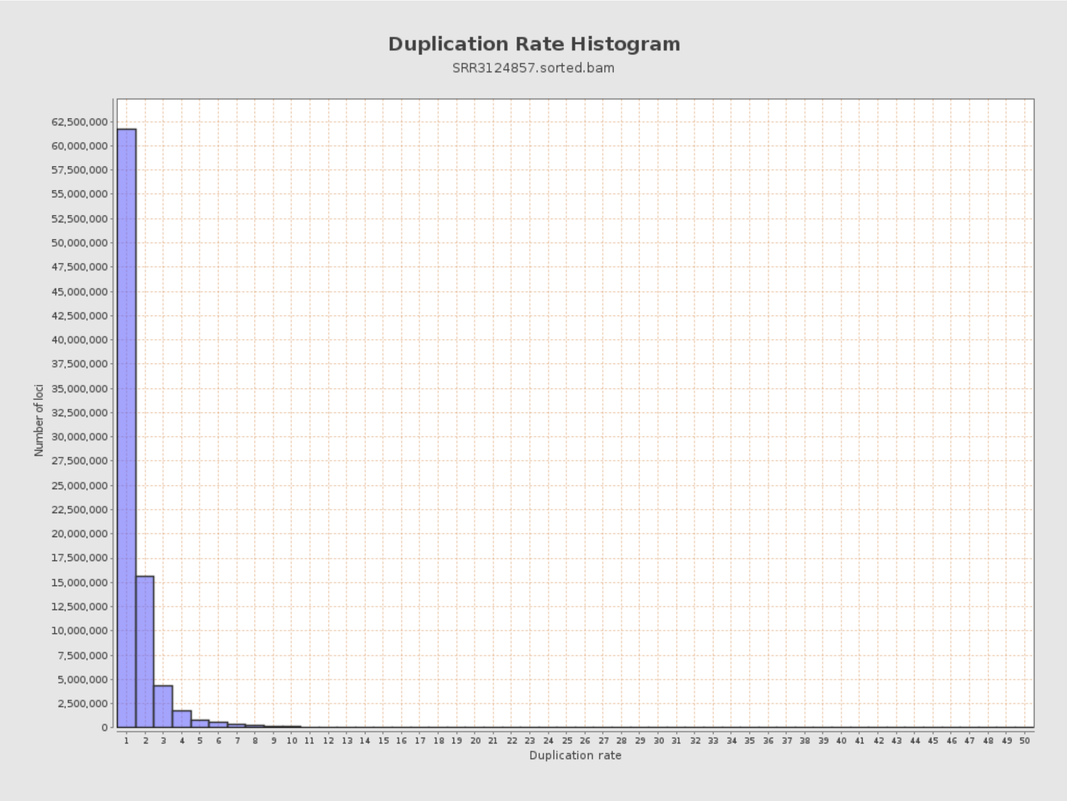
5. Results : Coverage Histogram (0-50X)



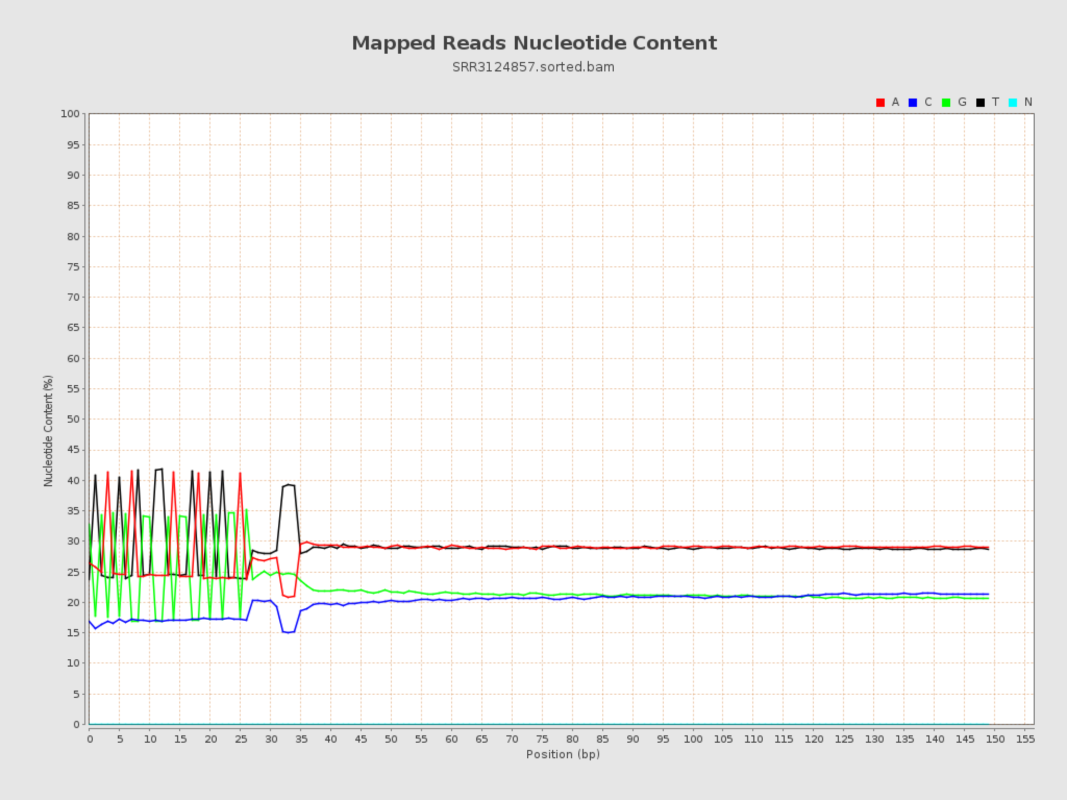
6. Results : Genome Fraction Coverage



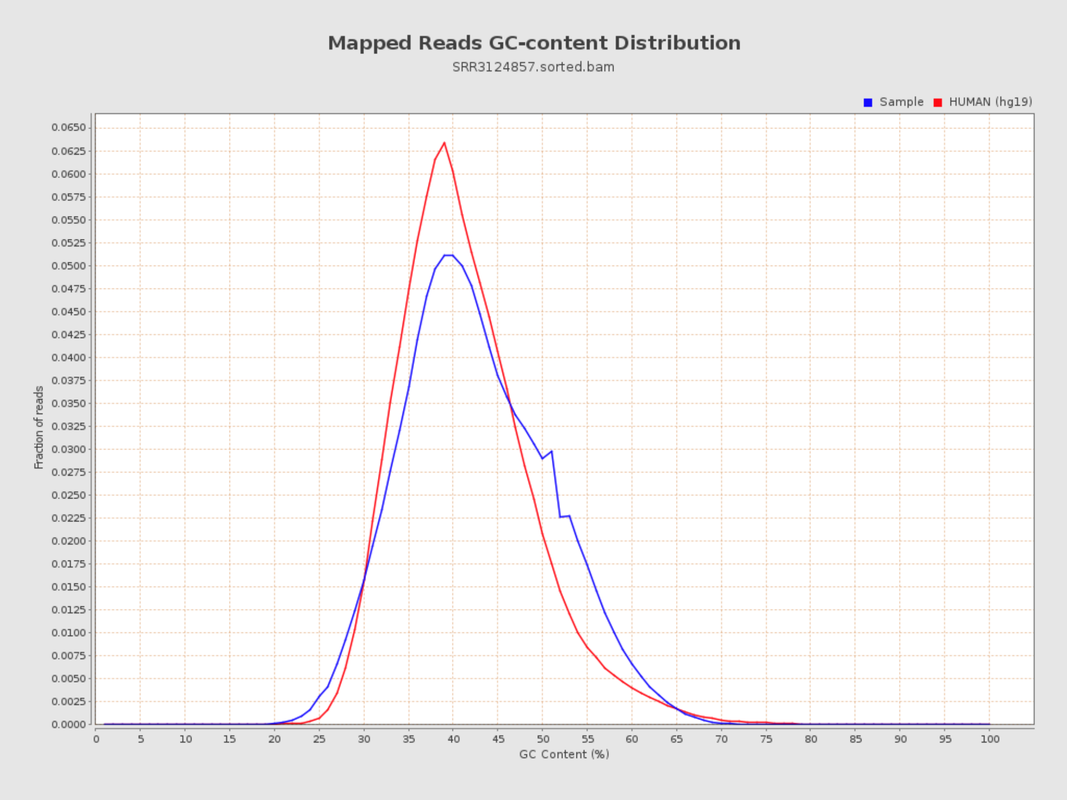
7. Results : Duplication Rate Histogram



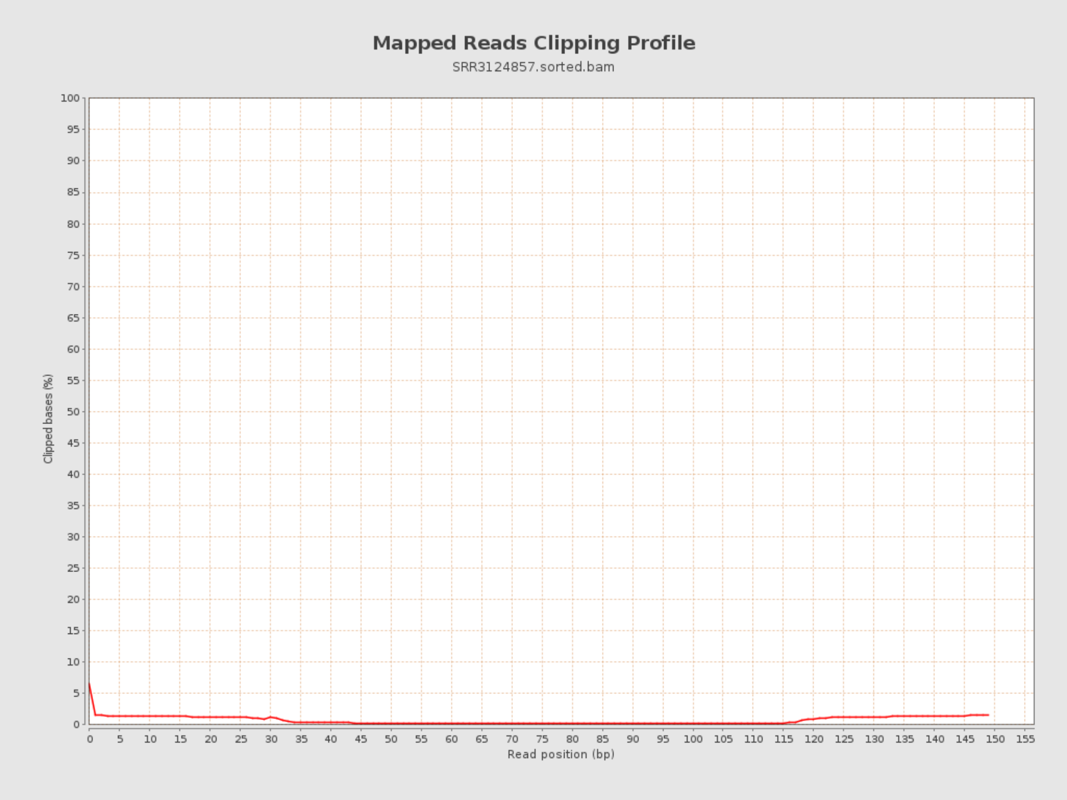
8. Results : Mapped Reads Nucleotide Content



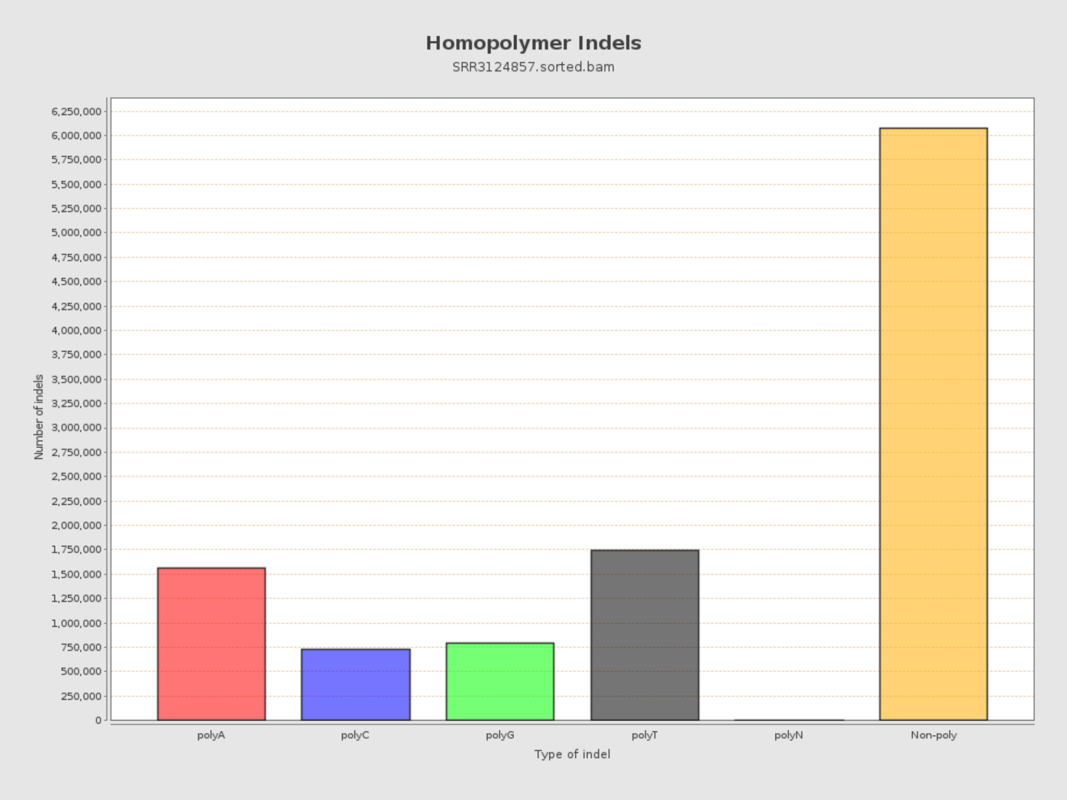
9. Results : Mapped Reads GC-content Distribution



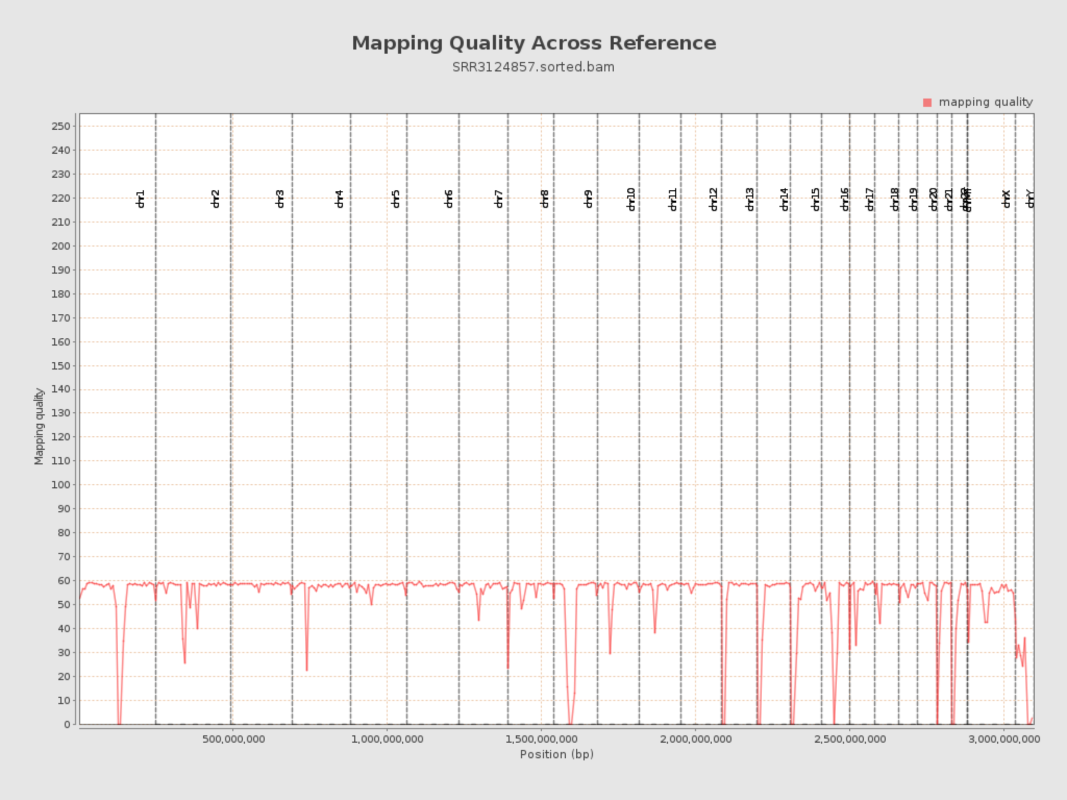
10. Results : Mapped Reads Clipping Profile



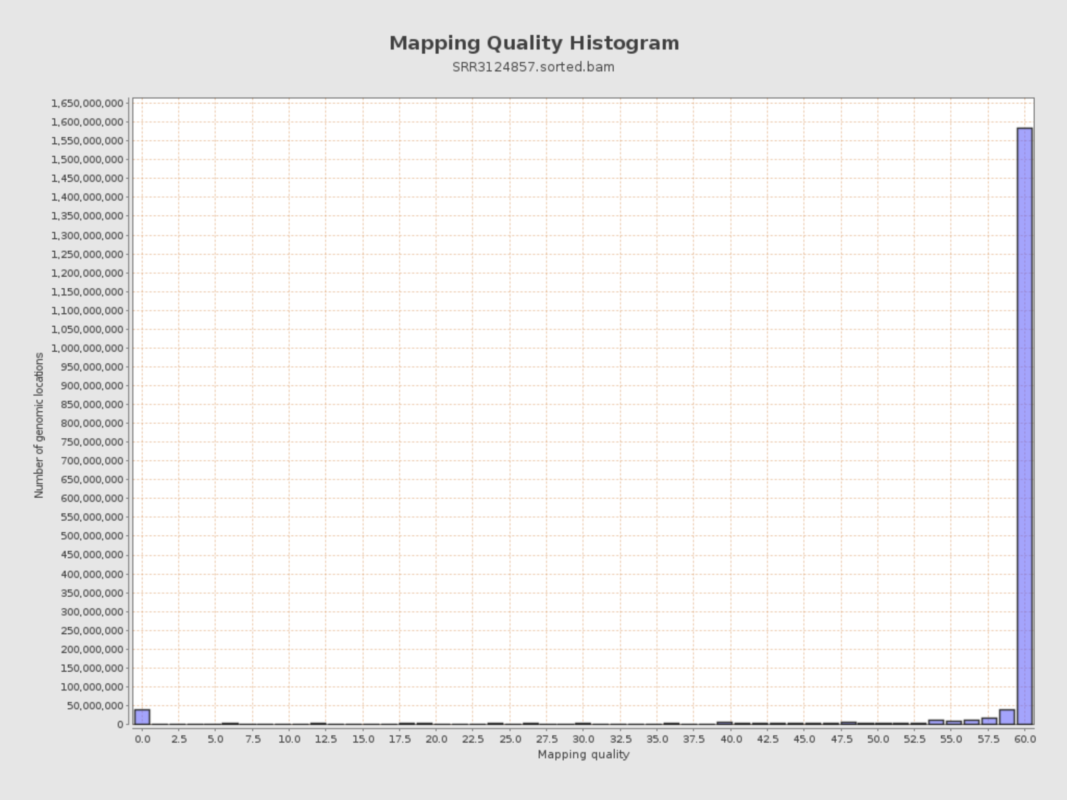
11. Results : Homopolymer Indels



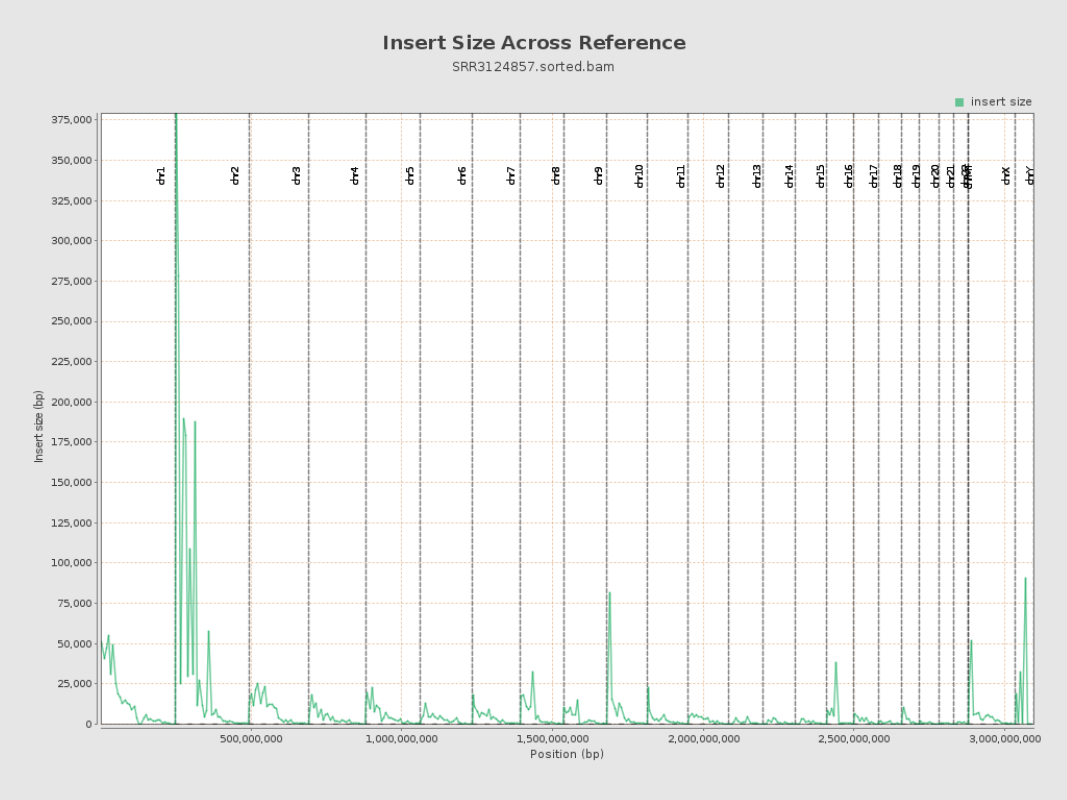
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram