Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/30 06:45:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504628.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_SRR504628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504628_1.fastq.gz SRR504628_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 30 06:45:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	291,349,294
Mapped reads	271,858,886 / 93.31%
Unmapped reads	19,490,408 / 6.69%
Mapped paired reads	271,858,886 / 93.31%
Mapped reads, first in pair	137,408,303 / 47.16%
Mapped reads, second in pair	134,450,583 / 46.15%
Mapped reads, both in pair	265,120,868 / 91%
Mapped reads, singletons	6,738,018 / 2.31%
Secondary alignments	0
Supplementary alignments	2,662,512 / 0.91%
Read min/max/mean length	30 / 100 / 100.37
Duplicated reads (estimated)	76,541,253 / 26.27%
Duplication rate	15.52%
Clipped reads	50,852,099 / 17.45%

2.2. ACGT Content

Number/percentage of A's	6,930,189,828 / 26.74%
Number/percentage of C's	5,970,667,507 / 23.04%
Number/percentage of T's	7,002,426,313 / 27.02%
Number/percentage of G's	6,004,833,629 / 23.17%
Number/percentage of N's	4,037,569 / 0.02%

GC Percentage	46.22%

2.3. Coverage

Mean	8.3782
Standard Deviation	193.2372

2.4. Mapping Quality

Mean Mapping Quality	52.04

2.5. Insert size

Mean	112,439.99
Standard Deviation	3,132,219.14
P25/Median/P75	319 / 366 / 423

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	355,044,268
Insertions	7,559,801
Mapped reads with at least one insertion	2.57%
Deletions	7,290,264
Mapped reads with at least one deletion	2.5%
Homopolymer indels	33.65%

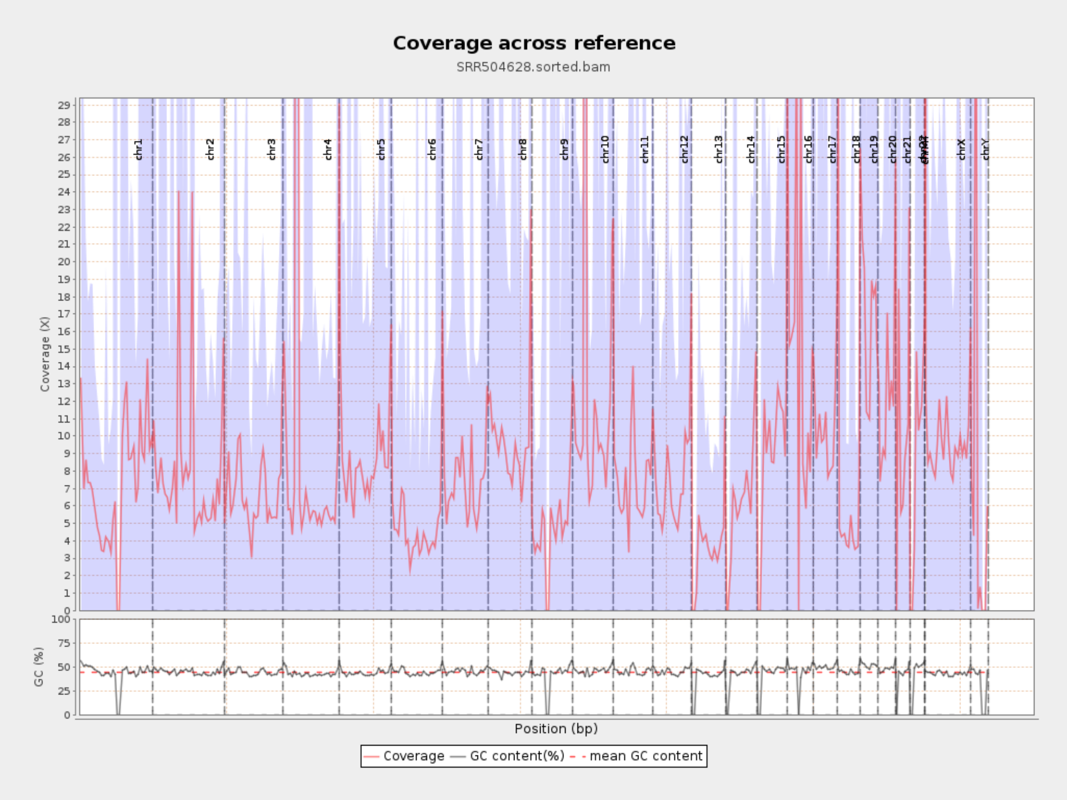
2.7. Chromosome stats

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

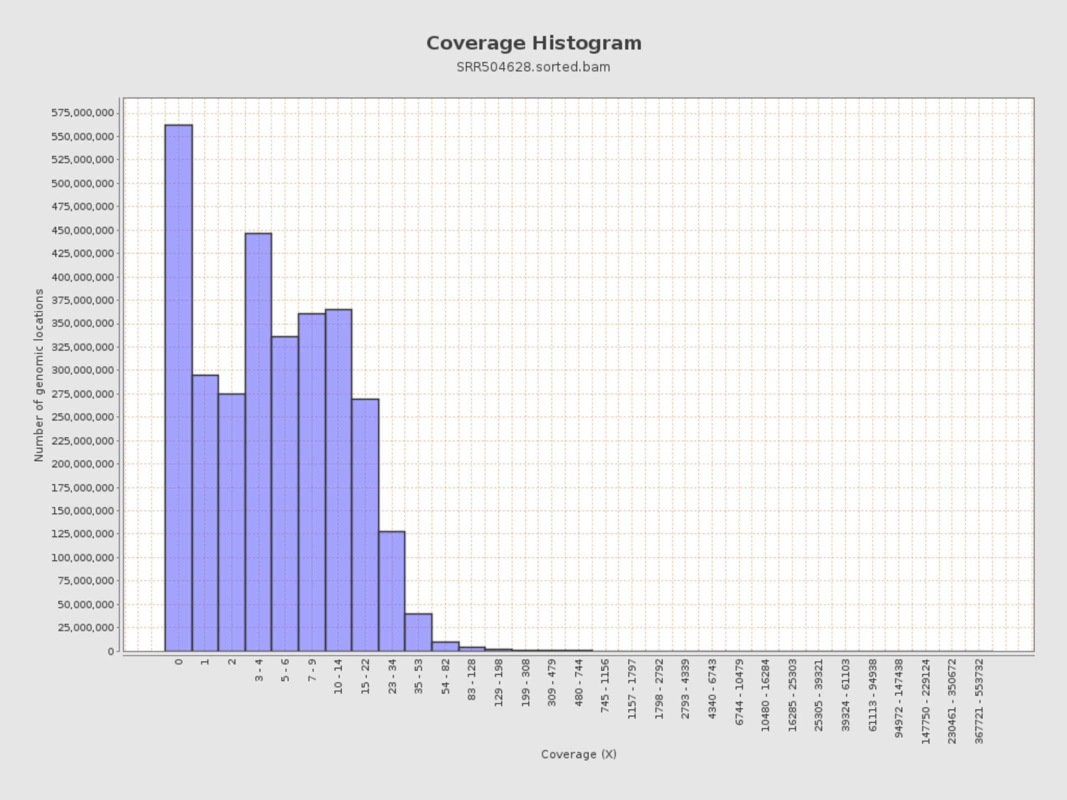
		bases	coverage	deviation
chr1	249250621	1827320305	7.3313	57.0779
chr2	243199373	1975736985	8.1239	223.9376
chr3	198022430	1313863827	6.6349	21.8409
chr4	191154276	1862429531	9.7431	494.1363
chr5	180915260	1585533887	8.764	31.8278
chr6	171115067	759693225	4.4397	24.3265
chr7	159138663	1216496135	7.6443	32.3978
chr8	146364022	1428042536	9.7568	128.485
chr9	141213431	677344913	4.7966	71.2435
chr10	135534747	1933595762	14.2664	449.1808
chr11	135006516	1051858232	7.7912	23.7831
chr12	133851895	977044530	7.2994	18.8943
chr13	115169878	393944677	3.4206	10.724
chr14	107349540	665396489	6.1984	28.2183
chr15	102531392	888910250	8.6696	16.1072
chr16	90354753	1390687939	15.3914	191.1181
chr17	81195210	849151063	10.4581	68.2931
chr18	78077248	437637867	5.6052	262.6154
chr19	59128983	1027810725	17.3825	38.7869
chr20	63025520	767494898	12.1775	121.605
chr21	48129895	496395793	10.3137	160.3003
chr22	51304566	464479498	9.0534	28.5699
chrMT	16571	8997418	542.9617	246.1407
chrX	155270560	1478499162	9.5221	20.2818

chrY	59373566	457925428	7.7126	471.1453

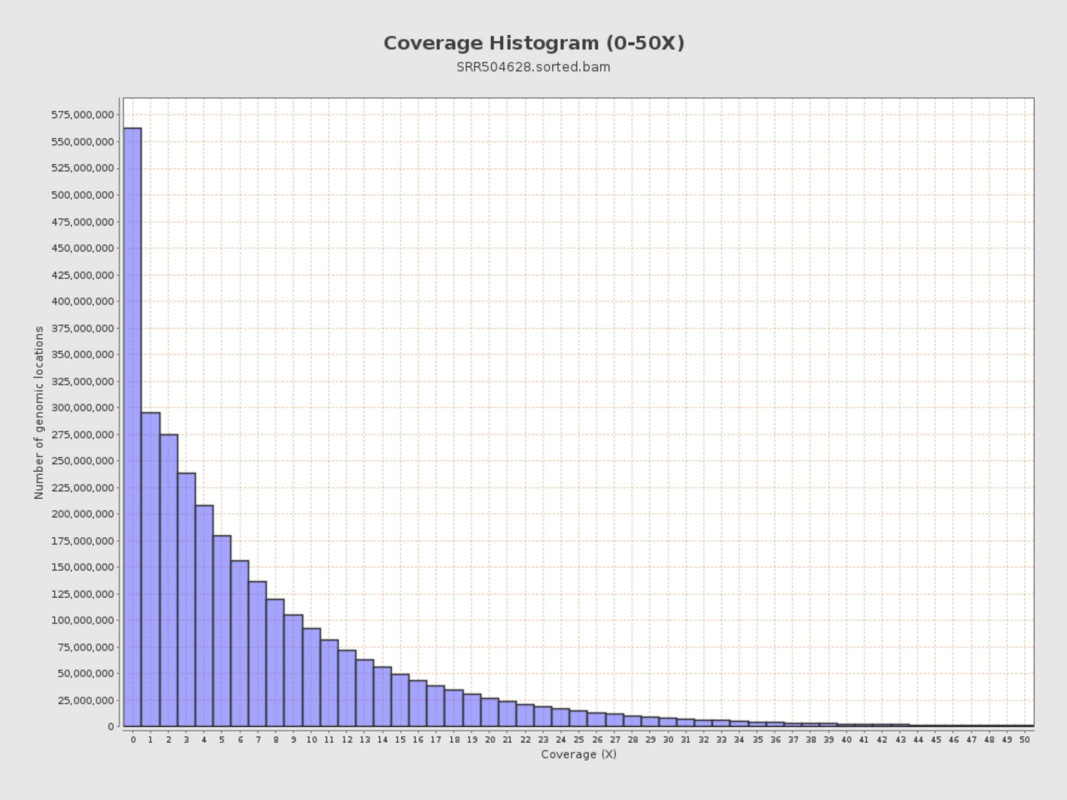
3. Results : Coverage across reference



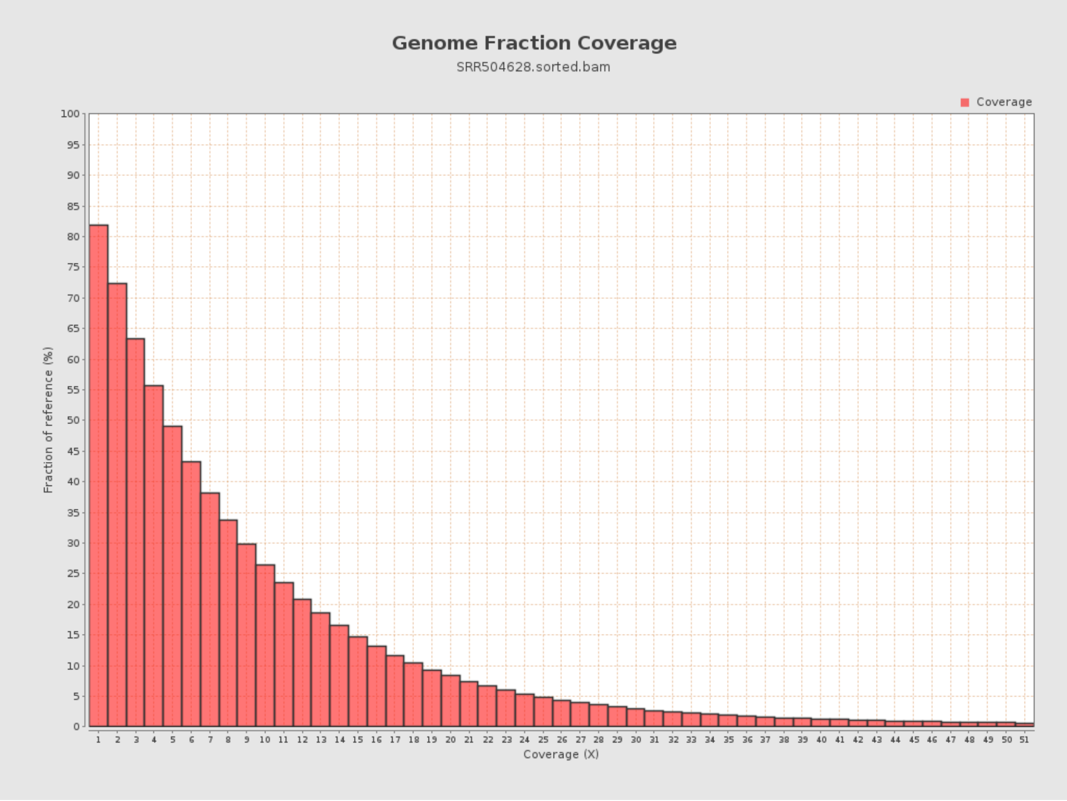
4. Results : Coverage Histogram



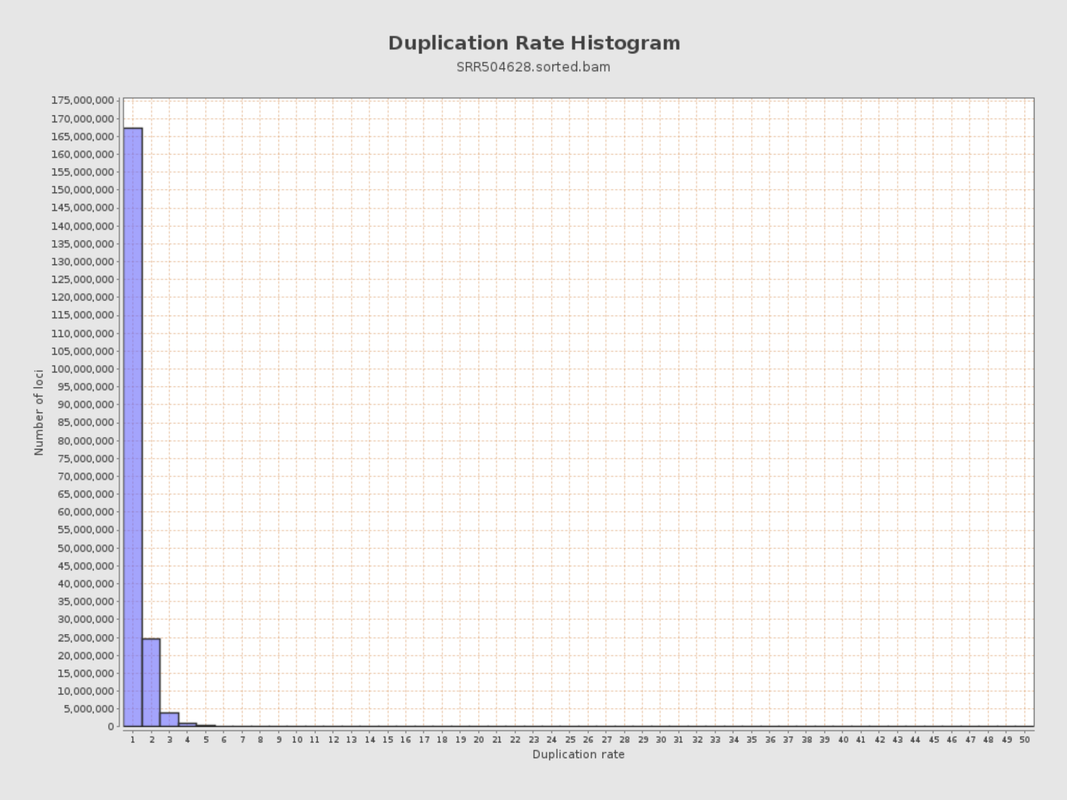
5. Results : Coverage Histogram (0-50X)



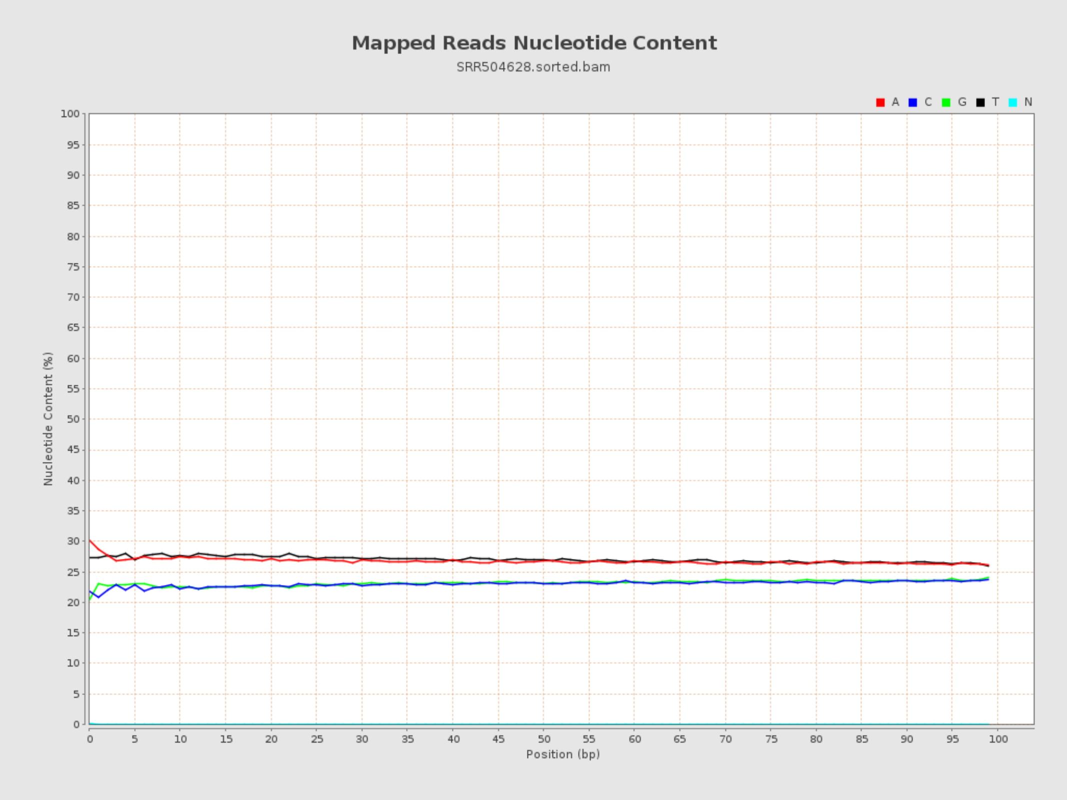
6. Results : Genome Fraction Coverage



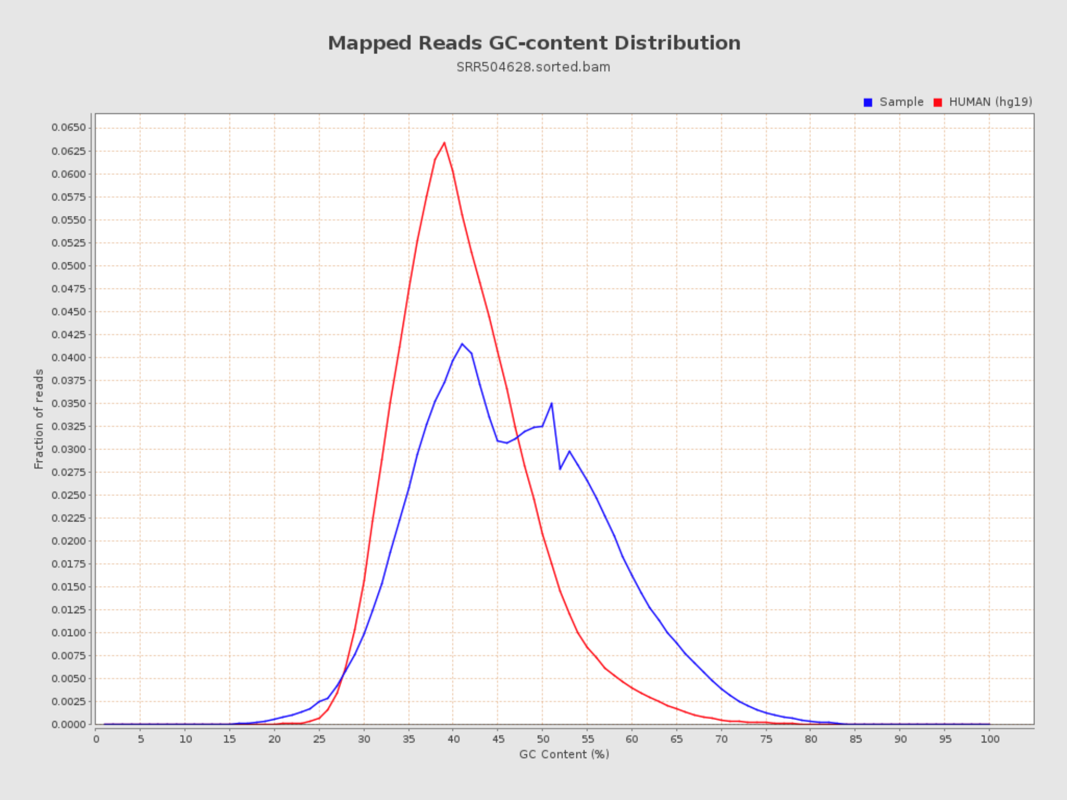
7. Results : Duplication Rate Histogram



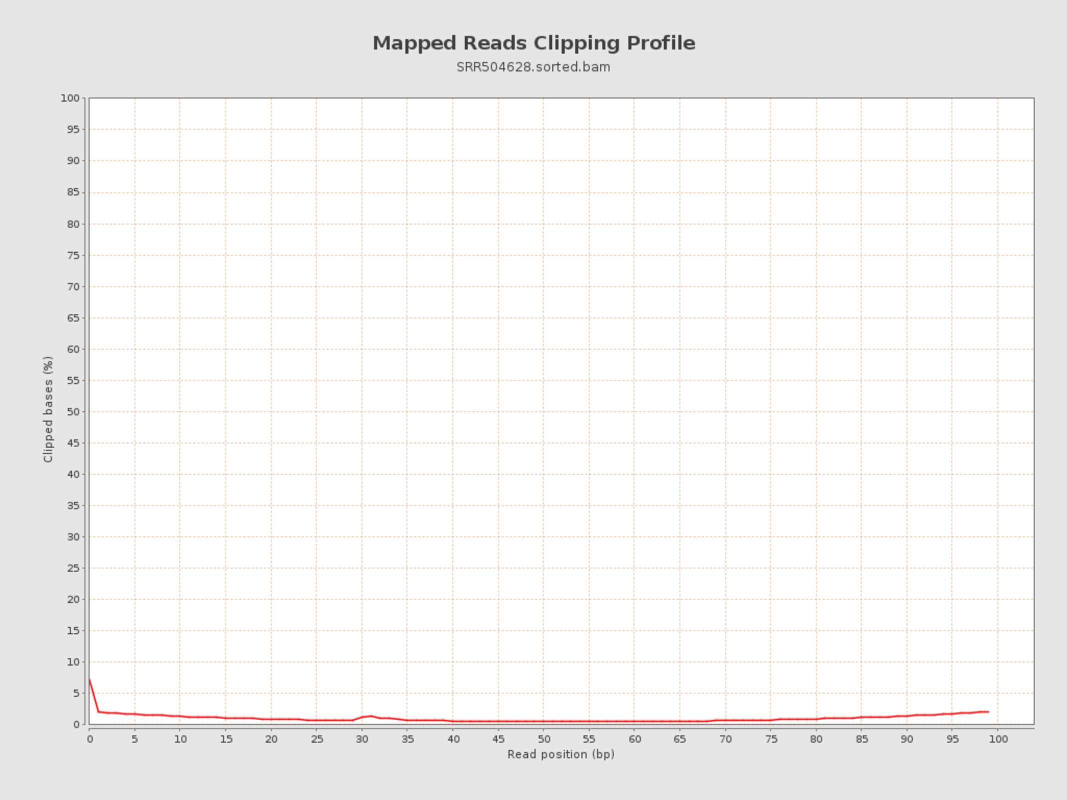
8. Results : Mapped Reads Nucleotide Content



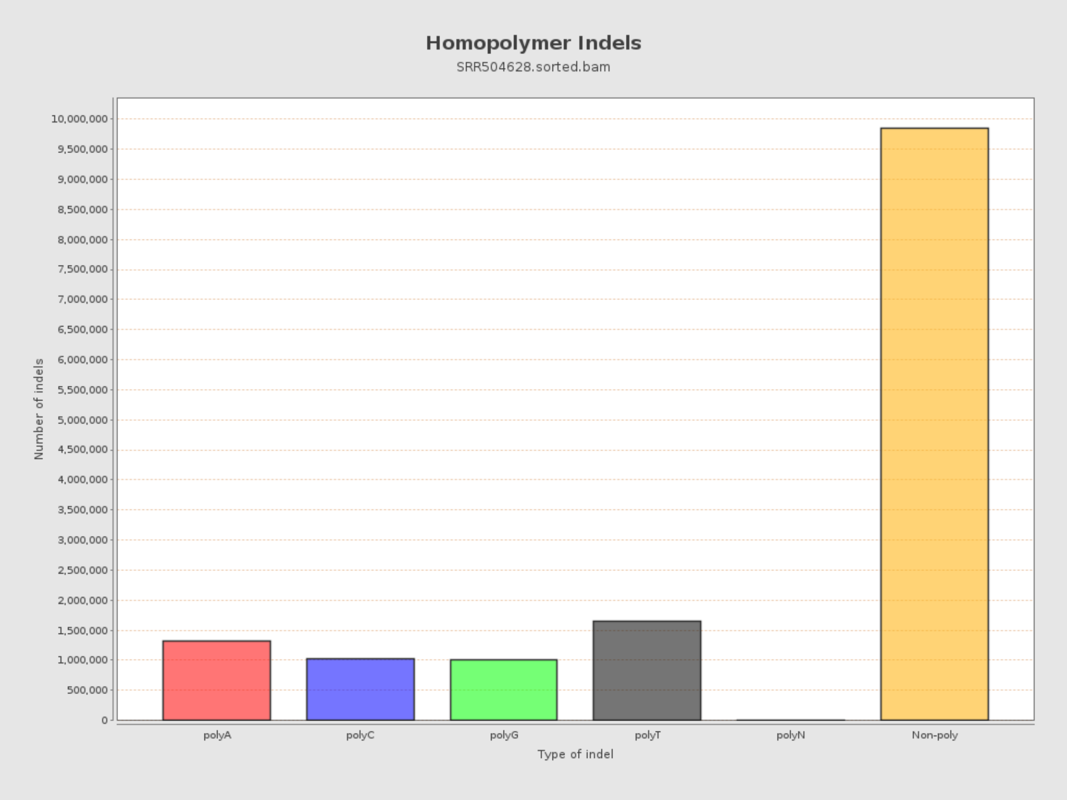
9. Results : Mapped Reads GC-content Distribution



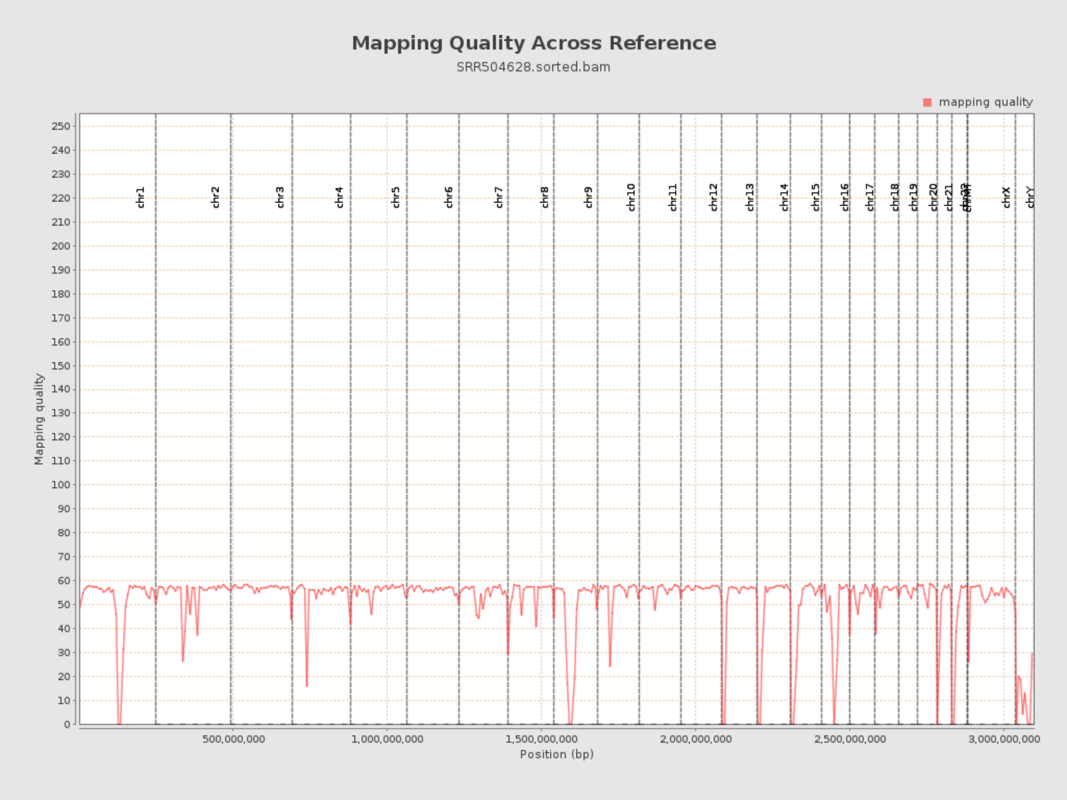
10. Results : Mapped Reads Clipping Profile



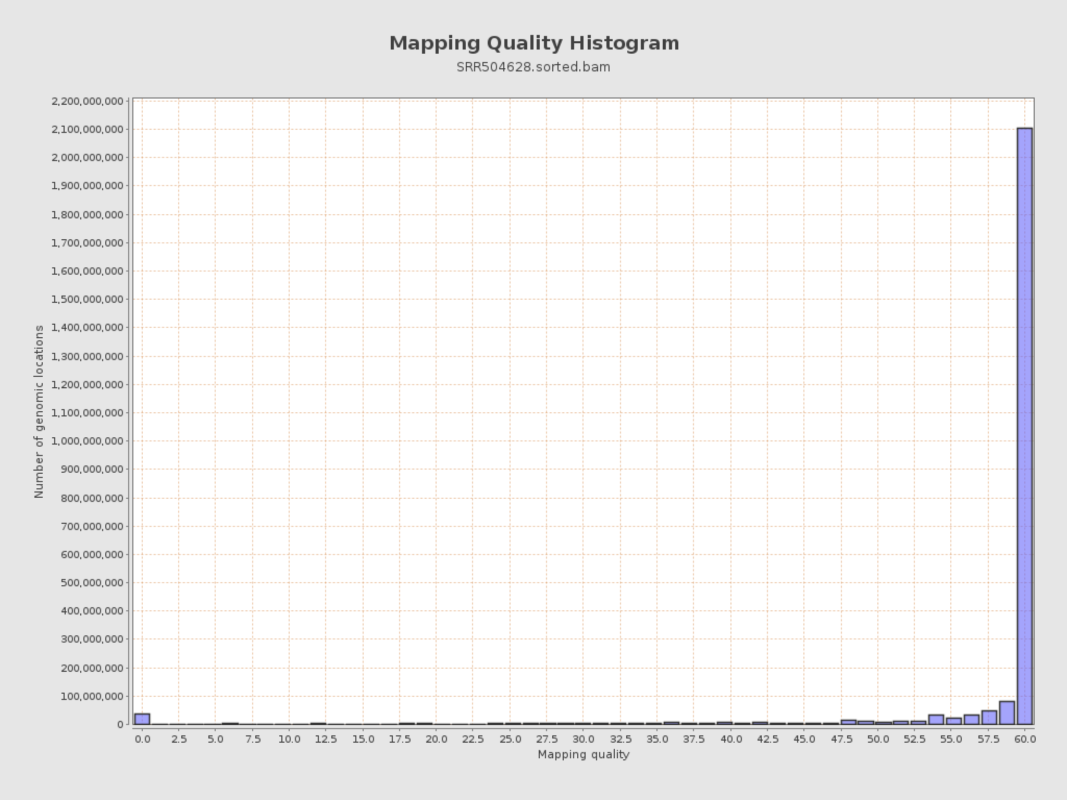
11. Results : Homopolymer Indels



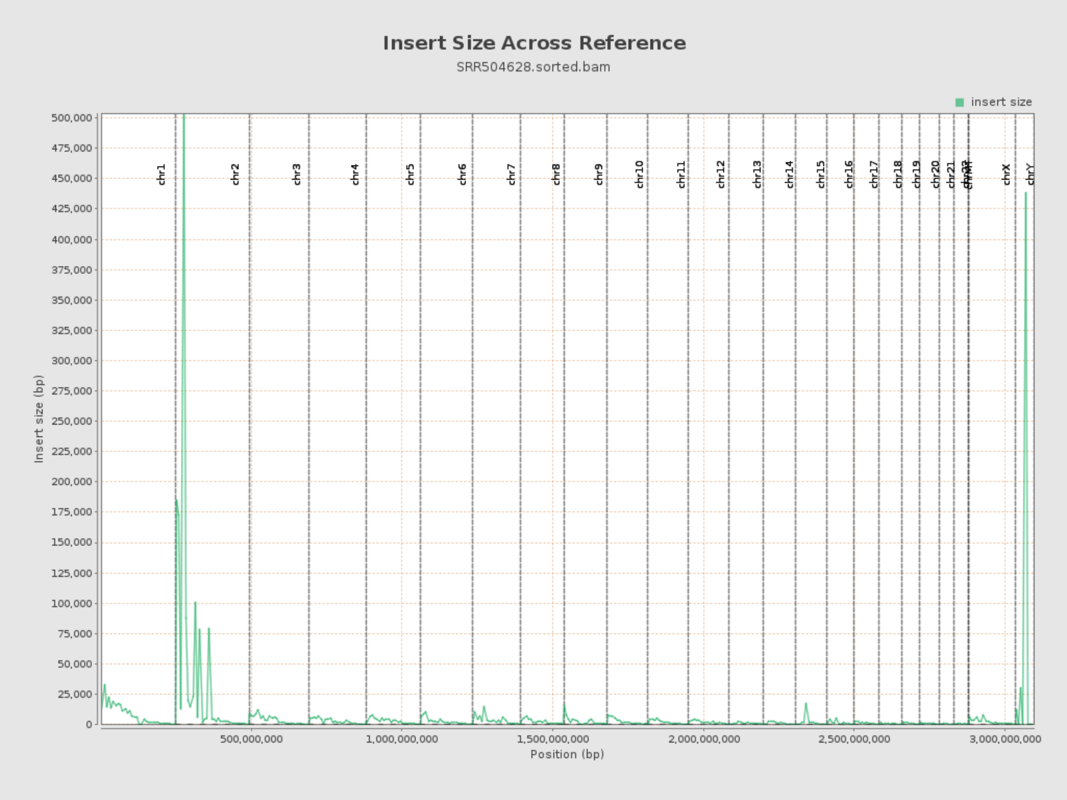
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram