Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 01:37:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264624.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_SRR1264624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264624_1.fastq.gz SRR1264624_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 01:37:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,391,545,590
Mapped reads	1,384,958,187 / 99.53%
Unmapped reads	6,587,403 / 0.47%
Mapped paired reads	1,384,958,187 / 99.53%
Mapped reads, first in pair	694,283,598 / 49.89%
Mapped reads, second in pair	690,674,589 / 49.63%
Mapped reads, both in pair	1,380,302,262 / 99.19%
Mapped reads, singletons	4,655,925 / 0.33%
Secondary alignments	0
Supplementary alignments	9,313,435 / 0.67%
Read min/max/mean length	30 / 101 / 101.28
Duplicated reads (estimated)	512,835,794 / 36.85%
Duplication rate	36.42%
Clipped reads	59,005,033 / 4.24%

2.2. ACGT Content

Number/percentage of A's	43,021,154,818 / 30.93%
Number/percentage of C's	26,440,123,874 / 19.01%
Number/percentage of T's	42,900,567,443 / 30.85%
Number/percentage of G's	26,706,739,552 / 19.2%
Number/percentage of N's	8,720,985 / 0.01%

GC Percentage	38.21%

2.3. Coverage

Mean	44.9365
Standard Deviation	47.9997

2.4. Mapping Quality

Mean Mapping Quality	54.49

2.5. Insert size

Mean	91,318.55
Standard Deviation	2,925,257.34
P25/Median/P75	288 / 315 / 348

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	509,937,520
Insertions	15,650,958
Mapped reads with at least one insertion	1.11%
Deletions	14,547,266
Mapped reads with at least one deletion	1.03%
Homopolymer indels	48.65%

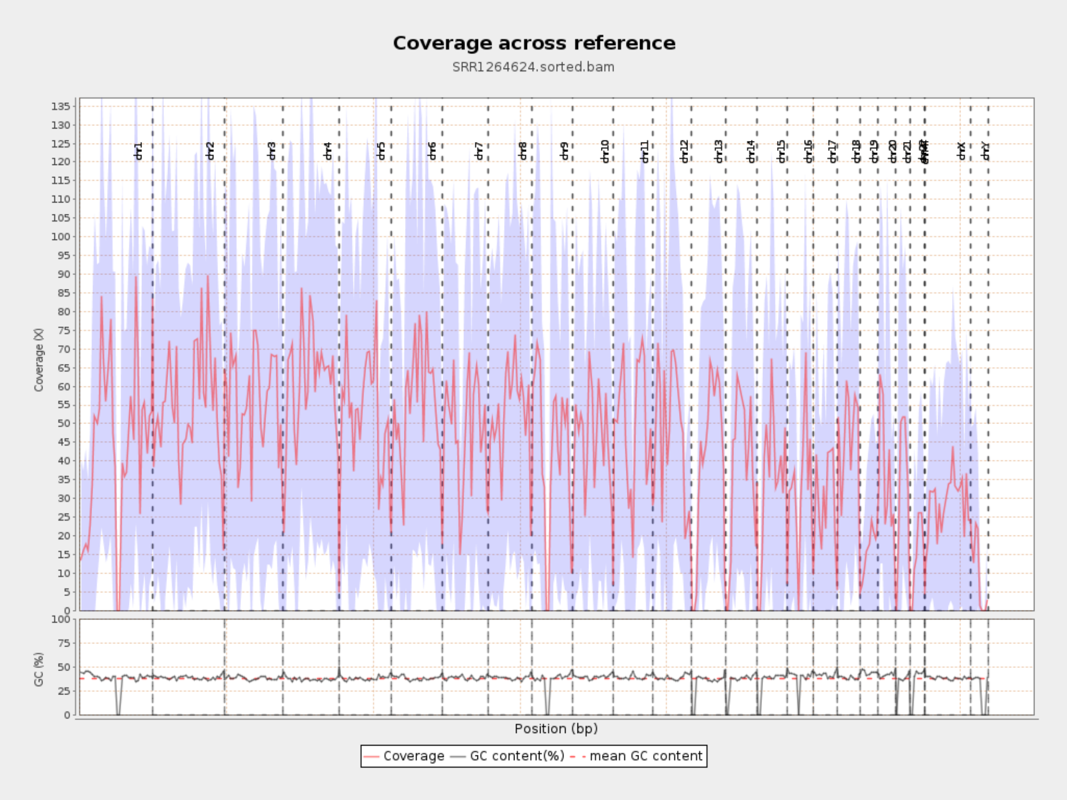
2.7. Chromosome stats

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

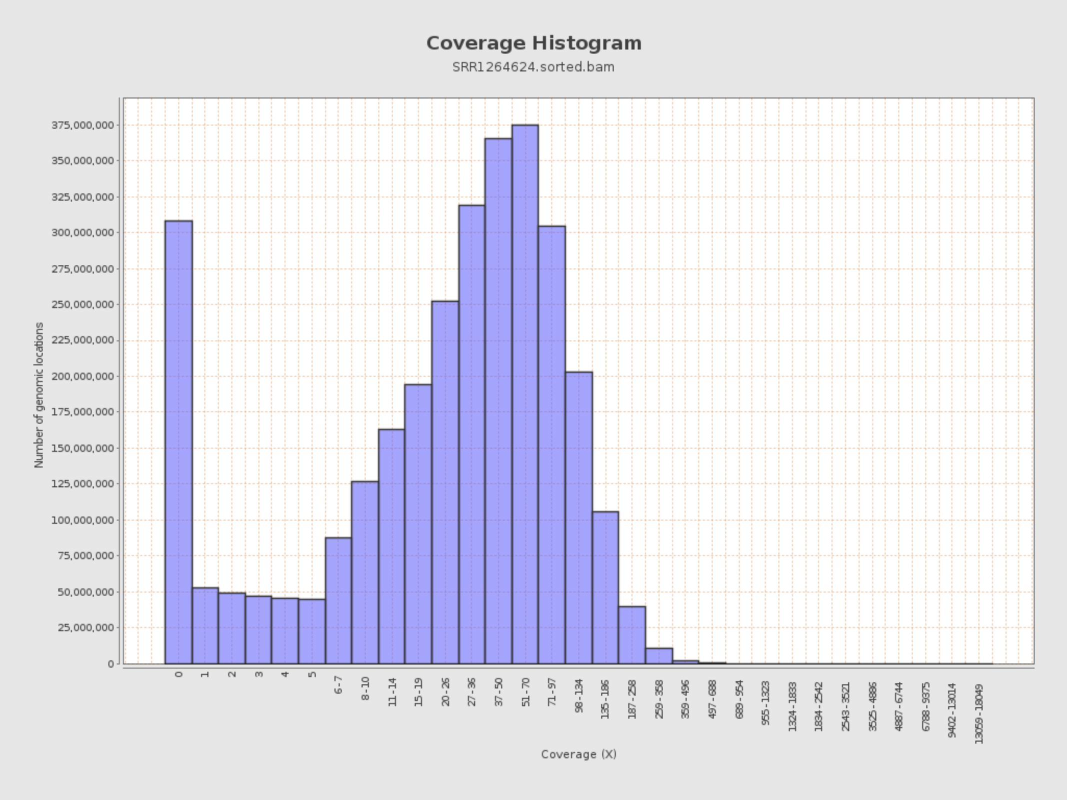
		bases	coverage	deviation
chr1	249250621	11103102855	44.5459	49.8801
chr2	243199373	13251151868	54.4868	50.7953
chr3	198022430	11140417972	56.2584	49.9304
chr4	191154276	11763517880	61.5394	51.3544
chr5	180915260	9432452997	52.1374	49.649
chr6	171115067	9583773724	56.0078	51.3786
chr7	159138663	7646290867	48.048	48.2761
chr8	146364022	7821691875	53.44	48.3601
chr9	141213431	5945373819	42.102	51.69
chr10	135534747	6299824963	46.4813	45.0162
chr11	135006516	6699712421	49.6251	49.367
chr12	133851895	6366274118	47.5621	48.2086
chr13	115169878	4800693427	41.6836	44.2648
chr14	107349540	4122323223	38.4009	44.1449
chr15	102531392	3588228189	34.9964	44.6507
chr16	90354753	2841858303	31.4522	38.3664
chr17	81195210	2348305156	28.9217	37.623
chr18	78077248	3662683242	46.911	43.1797
chr19	59128983	950402374	16.0734	23.7933
chr20	63025520	2244776074	35.6169	49.085
chr21	48129895	1663052898	34.5534	47.0428
chr22	51304566	746029081	14.5412	25.9096
chrMT	16571	70670	4.2647	8.7715
chrX	155270560	4512500029	29.0622	33.0314

chrY	59373566	575067954	9.6856	23.8857

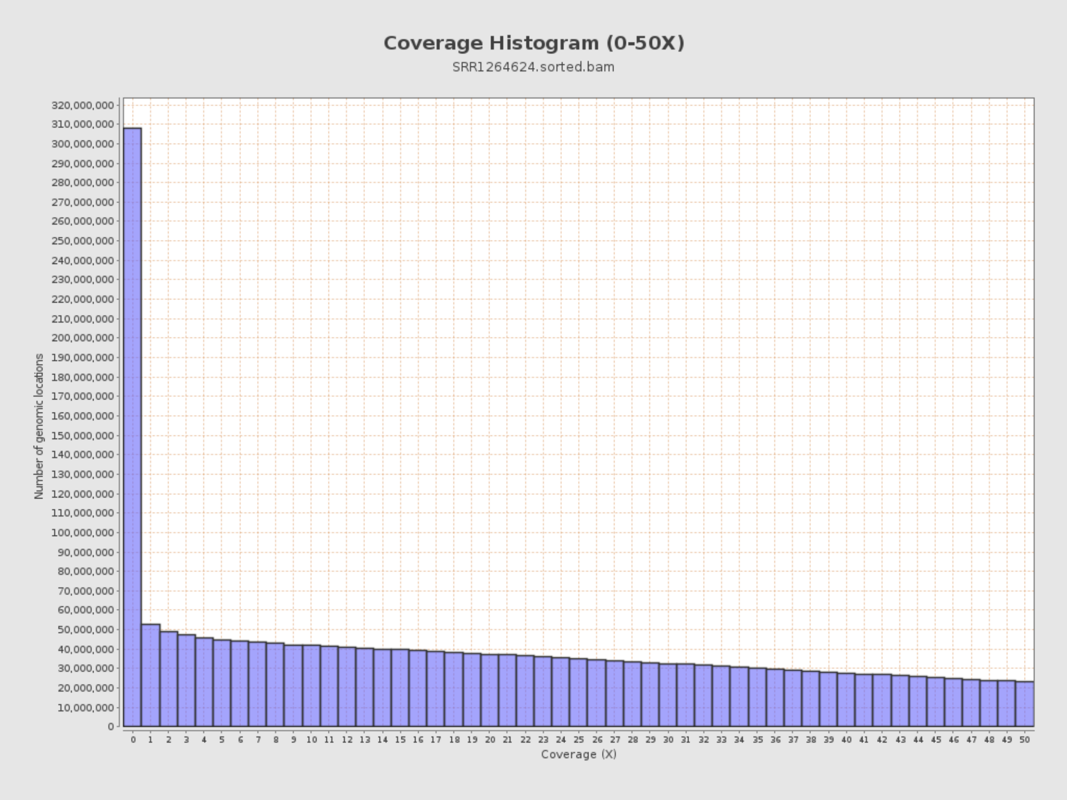
3. Results : Coverage across reference



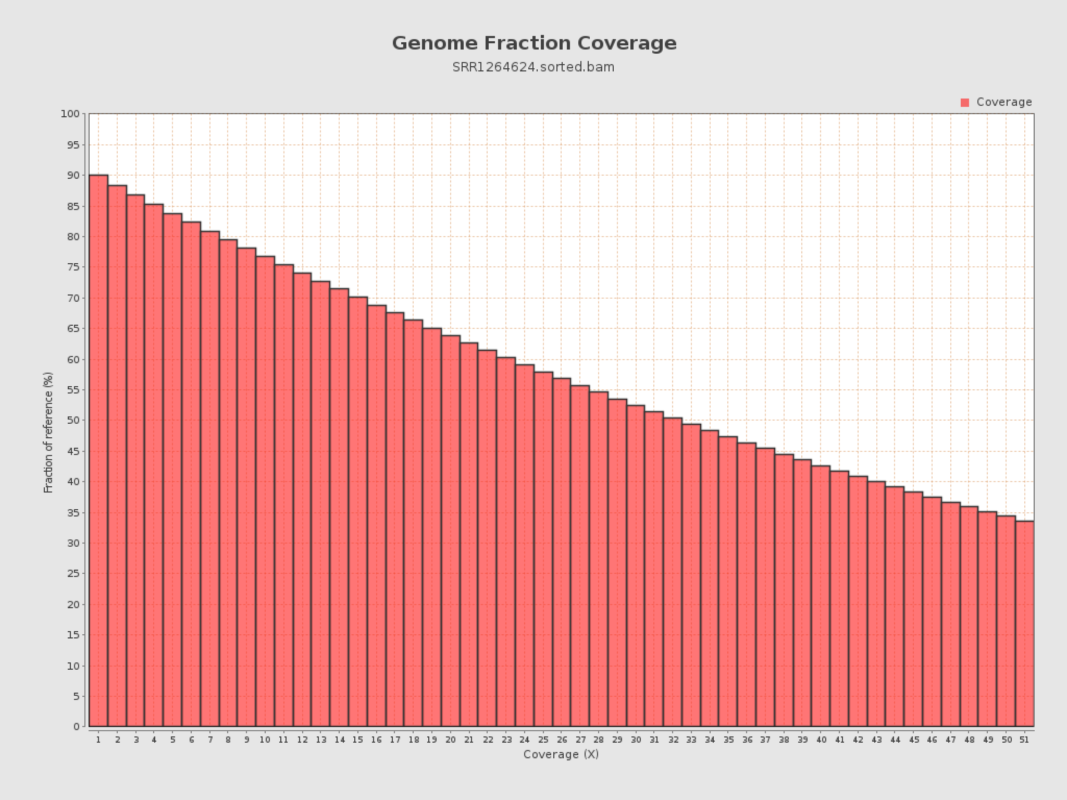
4. Results : Coverage Histogram



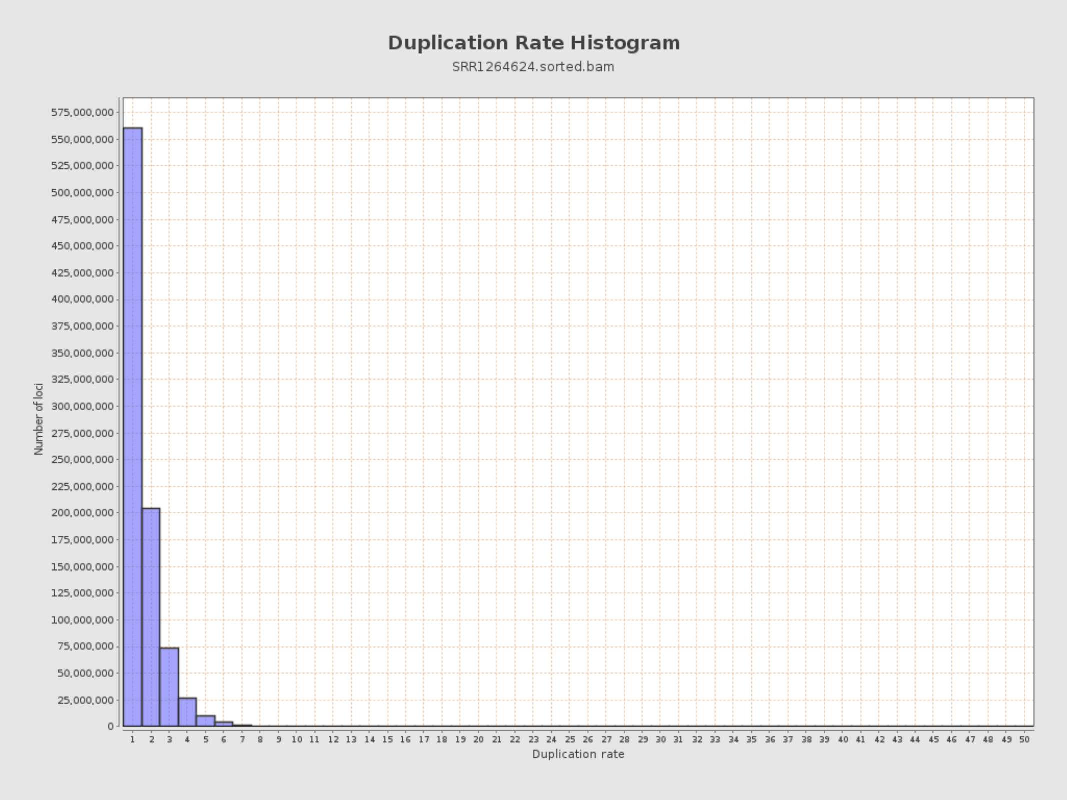
5. Results : Coverage Histogram (0-50X)



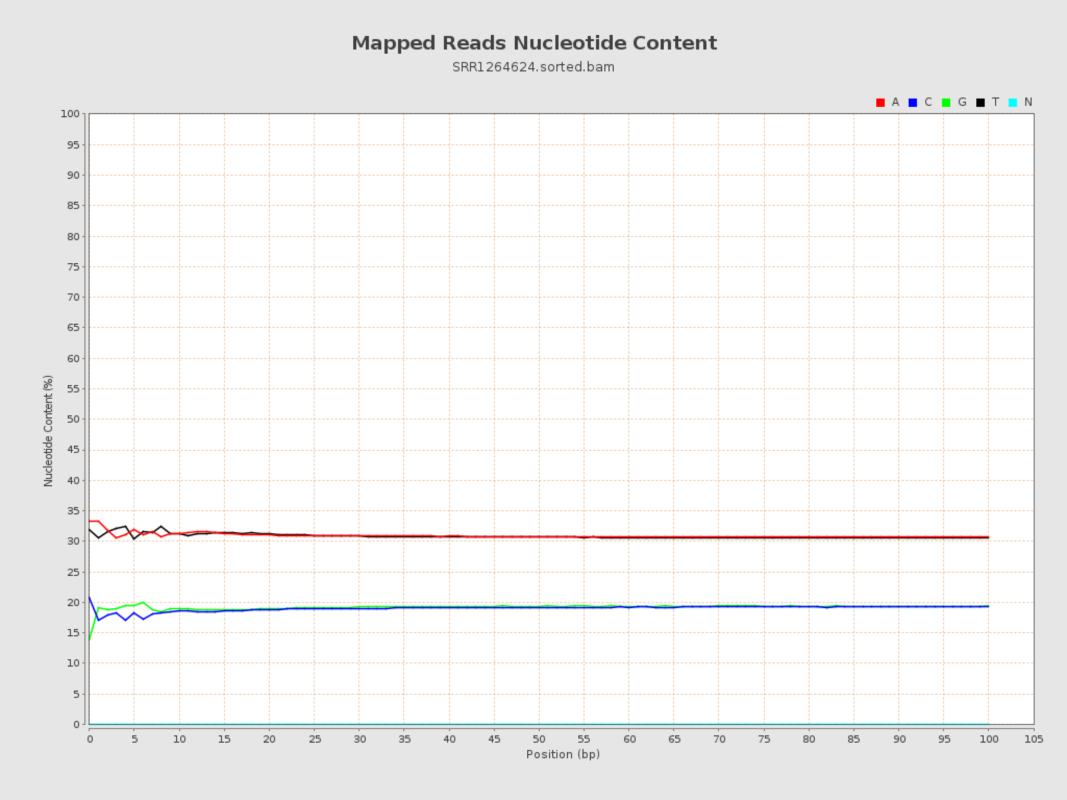
6. Results : Genome Fraction Coverage



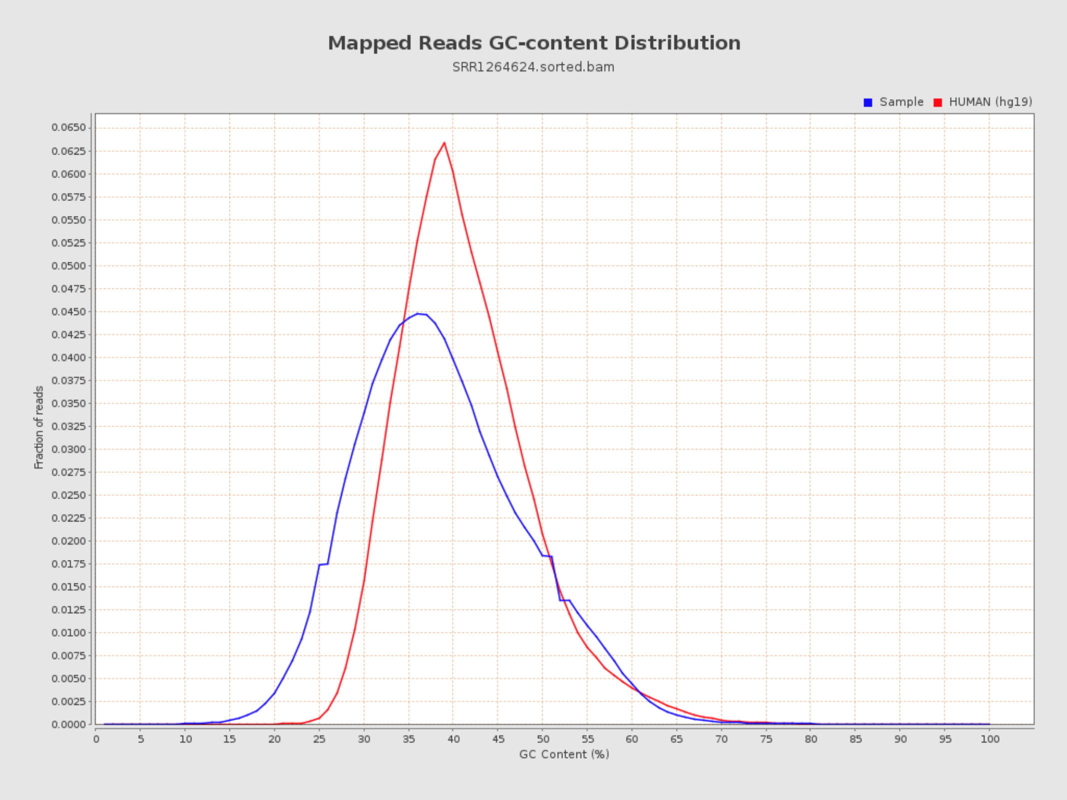
7. Results : Duplication Rate Histogram



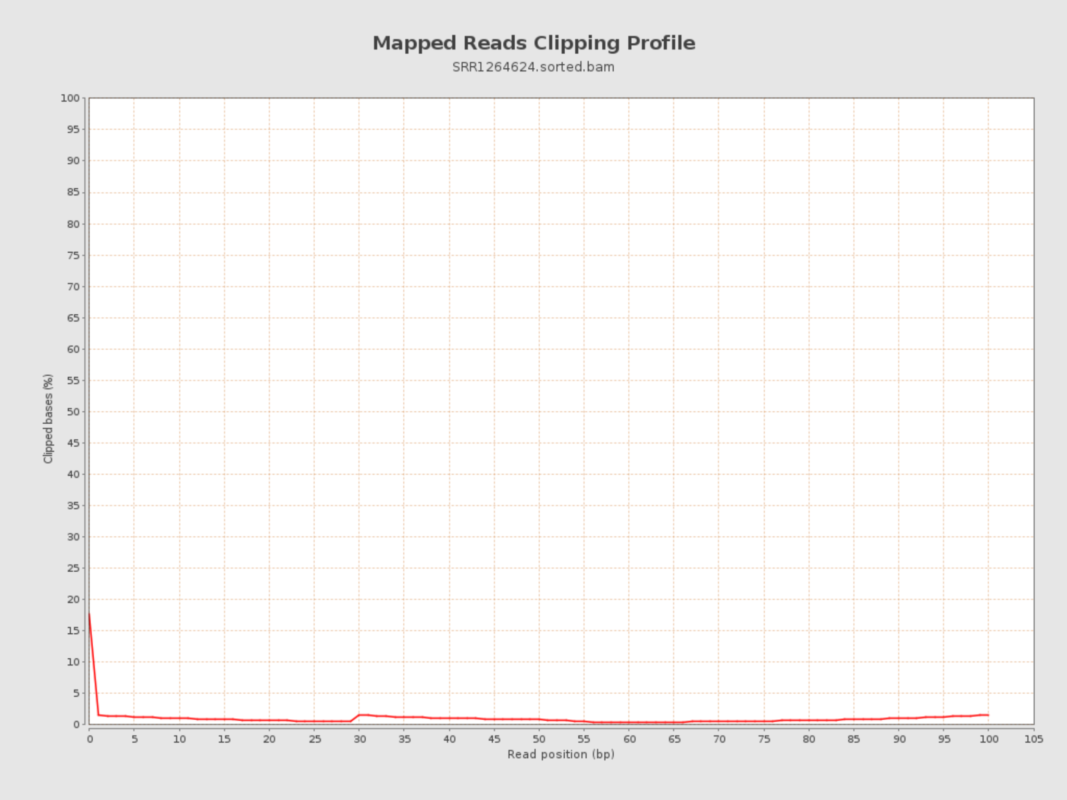
8. Results : Mapped Reads Nucleotide Content



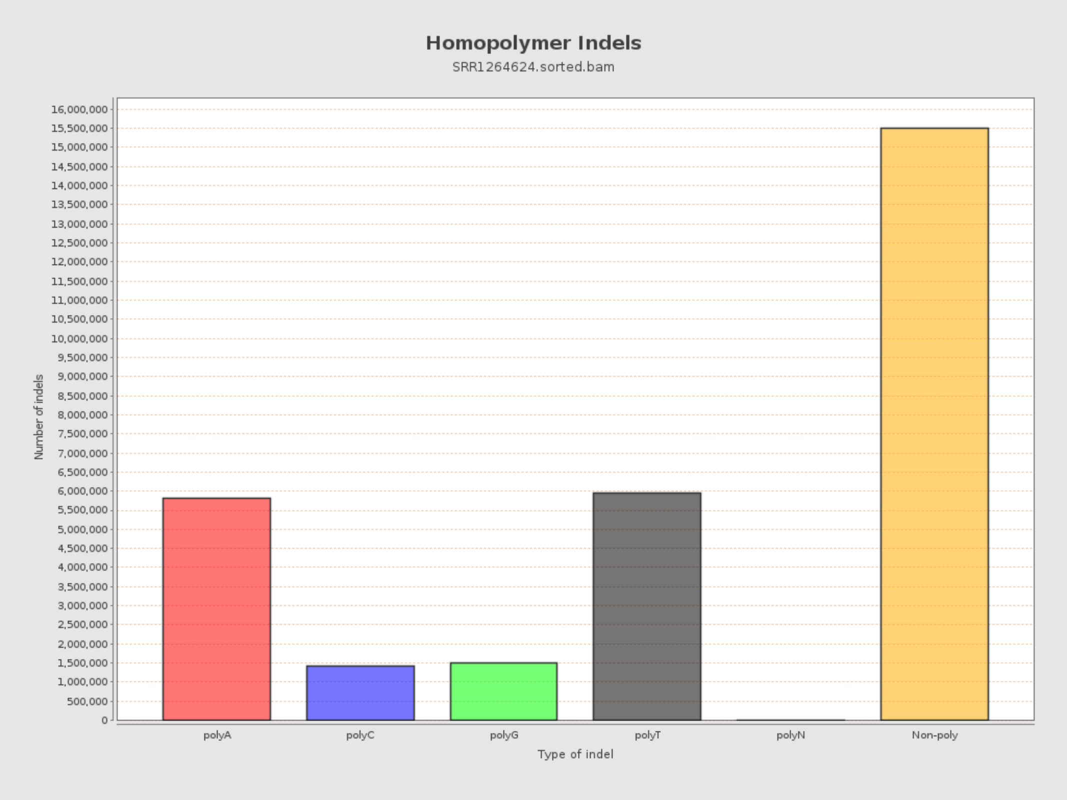
9. Results : Mapped Reads GC-content Distribution



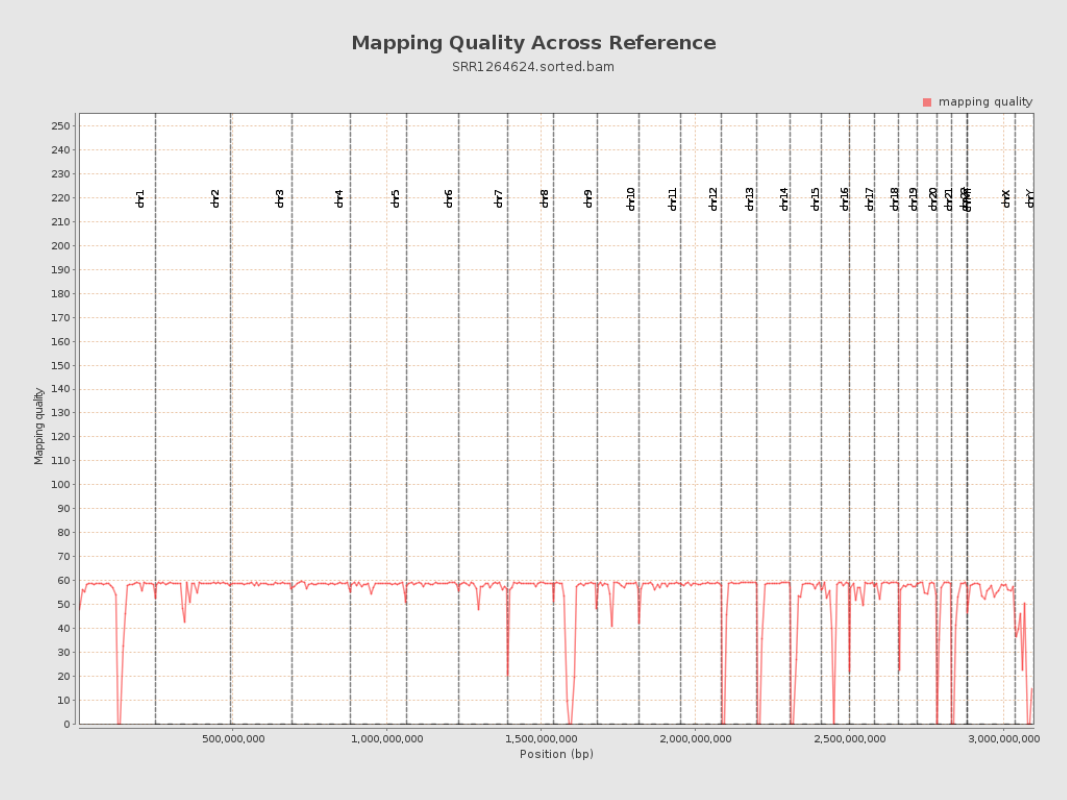
10. Results : Mapped Reads Clipping Profile



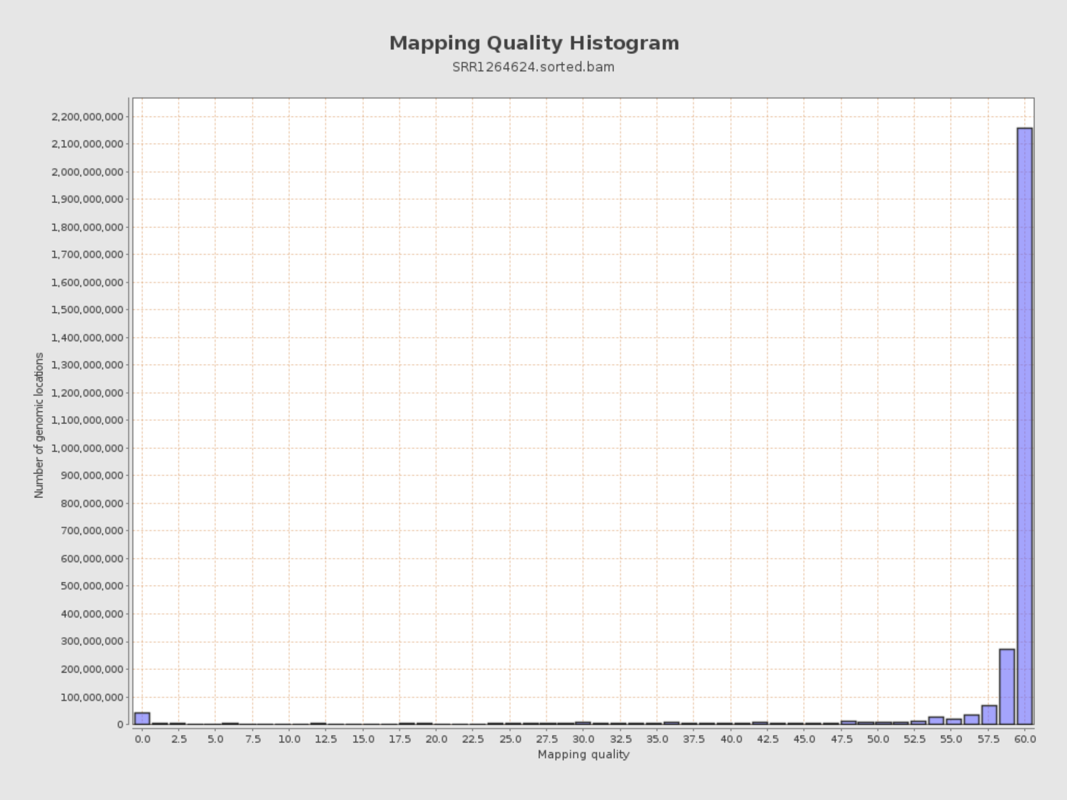
11. Results : Homopolymer Indels



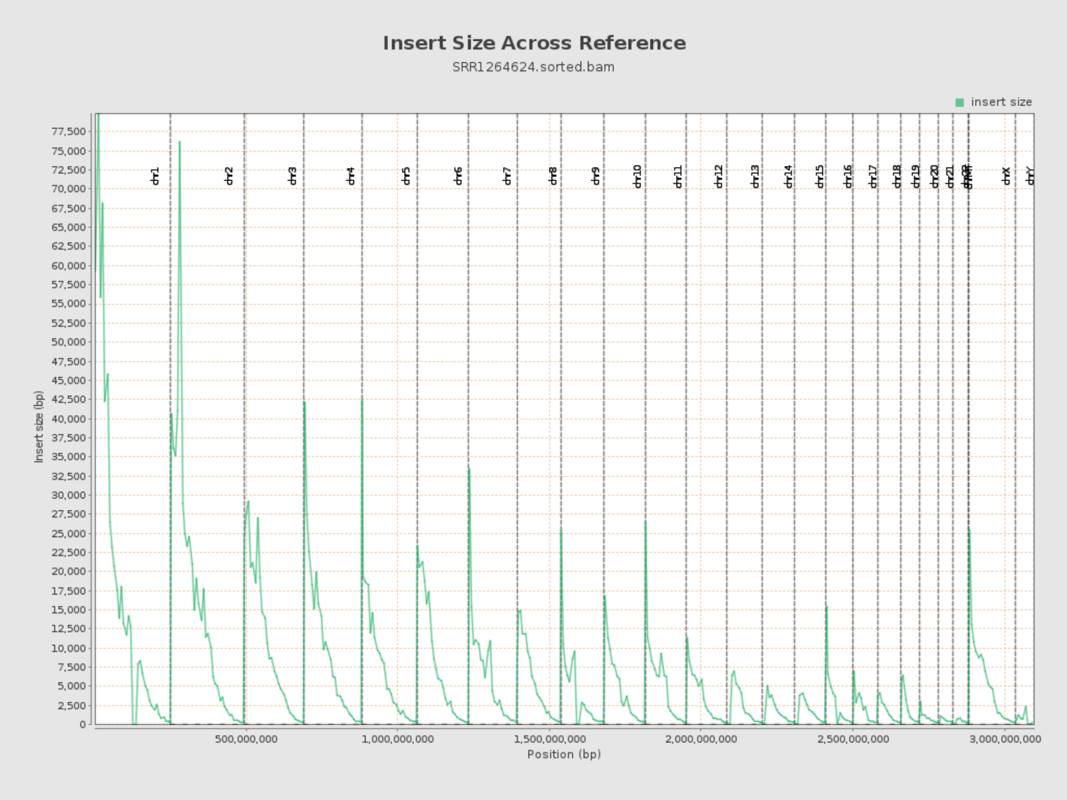
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram