Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 01:00:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264627.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_SRR1264627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264627_1.fastq.gz SRR1264627_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 01:00:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,440,914,148
Mapped reads	1,433,354,639 / 99.48%
Unmapped reads	7,559,509 / 0.52%
Mapped paired reads	1,433,354,639 / 99.48%
Mapped reads, first in pair	718,714,019 / 49.88%
Mapped reads, second in pair	714,640,620 / 49.6%
Mapped reads, both in pair	1,427,920,234 / 99.1%
Mapped reads, singletons	5,434,405 / 0.38%
Secondary alignments	0
Supplementary alignments	7,975,327 / 0.55%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	537,461,986 / 37.3%
Duplication rate	37.25%
Clipped reads	57,668,780 / 4%

2.2. ACGT Content

Number/percentage of A's	44,491,082,206 / 30.92%
Number/percentage of C's	27,408,871,596 / 19.05%
Number/percentage of T's	44,293,049,284 / 30.78%
Number/percentage of G's	27,689,656,783 / 19.24%
Number/percentage of N's	15,016,769 / 0.01%

GC Percentage	38.29%

2.3. Coverage

Mean	46.4939
Standard Deviation	46.435

2.4. Mapping Quality

Mean Mapping Quality	54.51

2.5. Insert size

Mean	64,967.5
Standard Deviation	2,449,130.86
P25/Median/P75	280 / 307 / 339

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	537,571,743
Insertions	15,888,566
Mapped reads with at least one insertion	1.09%
Deletions	14,911,058
Mapped reads with at least one deletion	1.02%
Homopolymer indels	48.58%

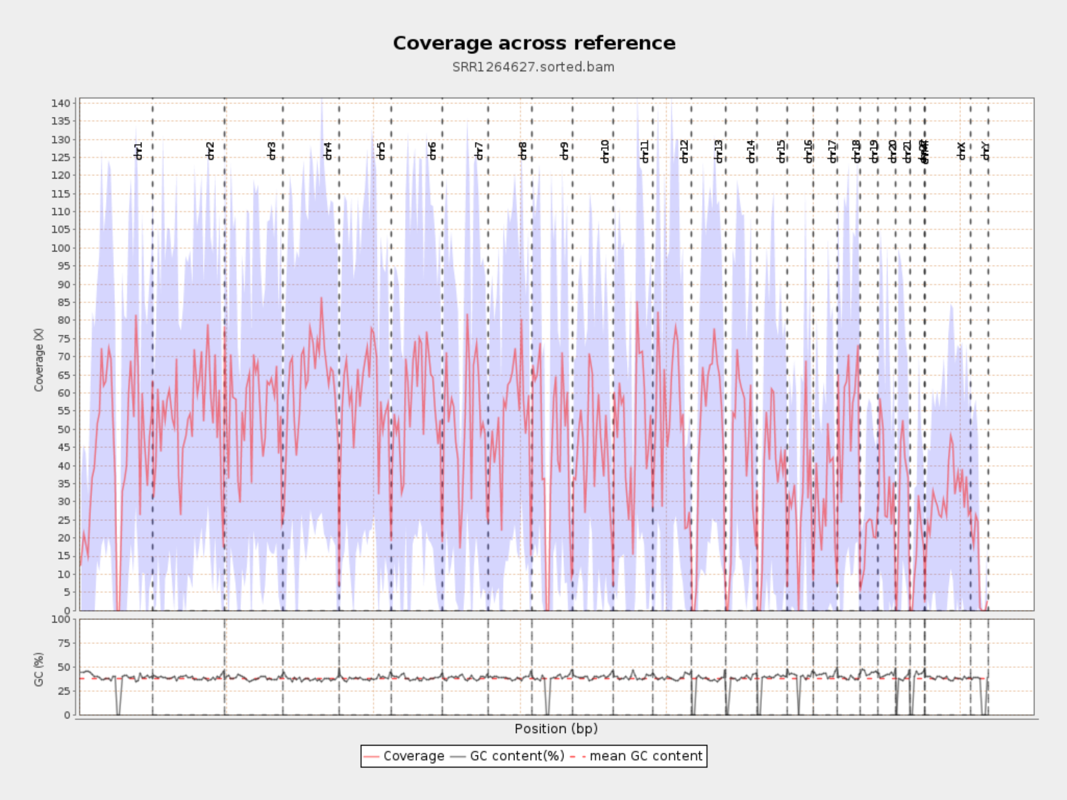
2.7. Chromosome stats

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

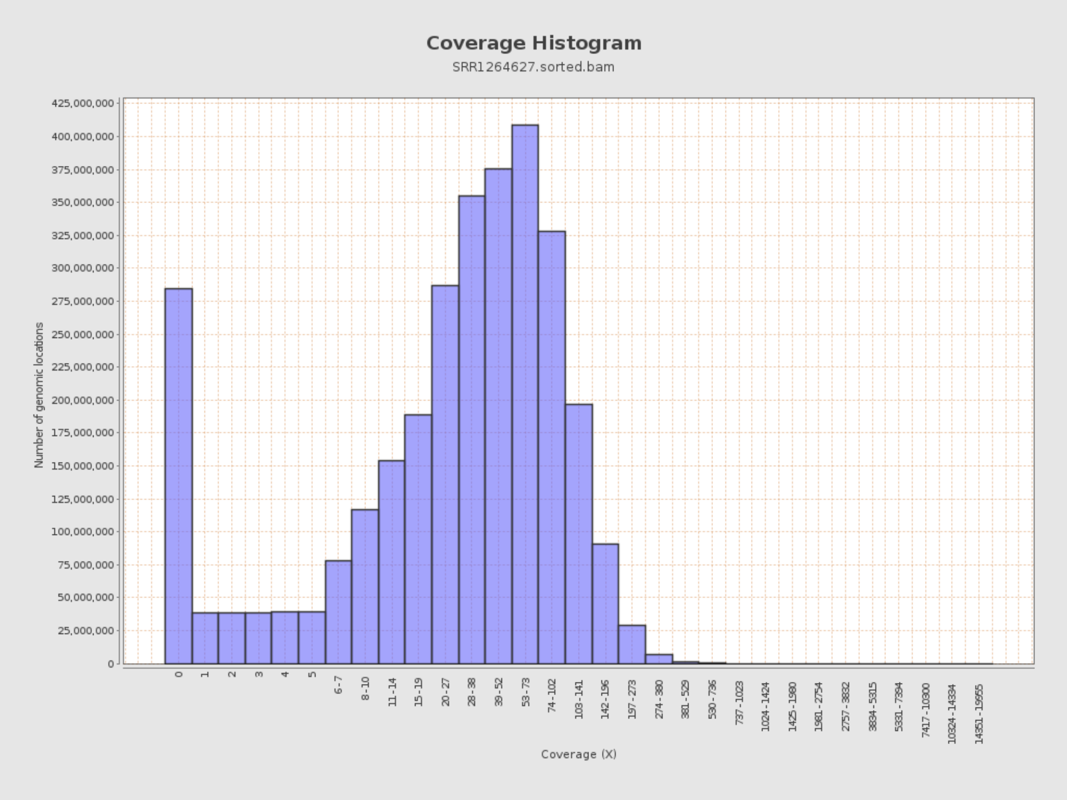
		bases	coverage	deviation
chr1	249250621	11065745851	44.3961	46.8453
chr2	243199373	13006821145	53.4821	47.1707
chr3	198022430	10822179040	54.6513	45.9488
chr4	191154276	12115124974	63.3788	48.4454
chr5	180915260	10440011985	57.7066	46.4547
chr6	171115067	9905684130	57.889	48.8434
chr7	159138663	8155734641	51.2492	47.5103
chr8	146364022	7804529678	53.3227	45.1454
chr9	141213431	6209288676	43.9709	49.0268
chr10	135534747	6098776396	44.9979	42.3846
chr11	135006516	6772243349	50.1623	47.1547
chr12	133851895	6961534955	52.0092	51.0363
chr13	115169878	5721547869	49.6792	47.4754
chr14	107349540	4439139277	41.3522	44.8417
chr15	102531392	3751942994	36.5931	43.4359
chr16	90354753	2641542192	29.2352	37.1702
chr17	81195210	2389198678	29.4254	37.2162
chr18	78077248	4357323225	55.8078	48.5808
chr19	59128983	1109173716	18.7585	26.7913
chr20	63025520	2183135224	34.6389	43.7956
chr21	48129895	1632403262	33.9166	47.1051
chr22	51304566	757810978	14.7708	25.9081
chrMT	16571	38366	2.3152	7.8005
chrX	155270560	4914442875	31.6508	32.7079

chrY	59373566	675627904	11.3793	24.5339

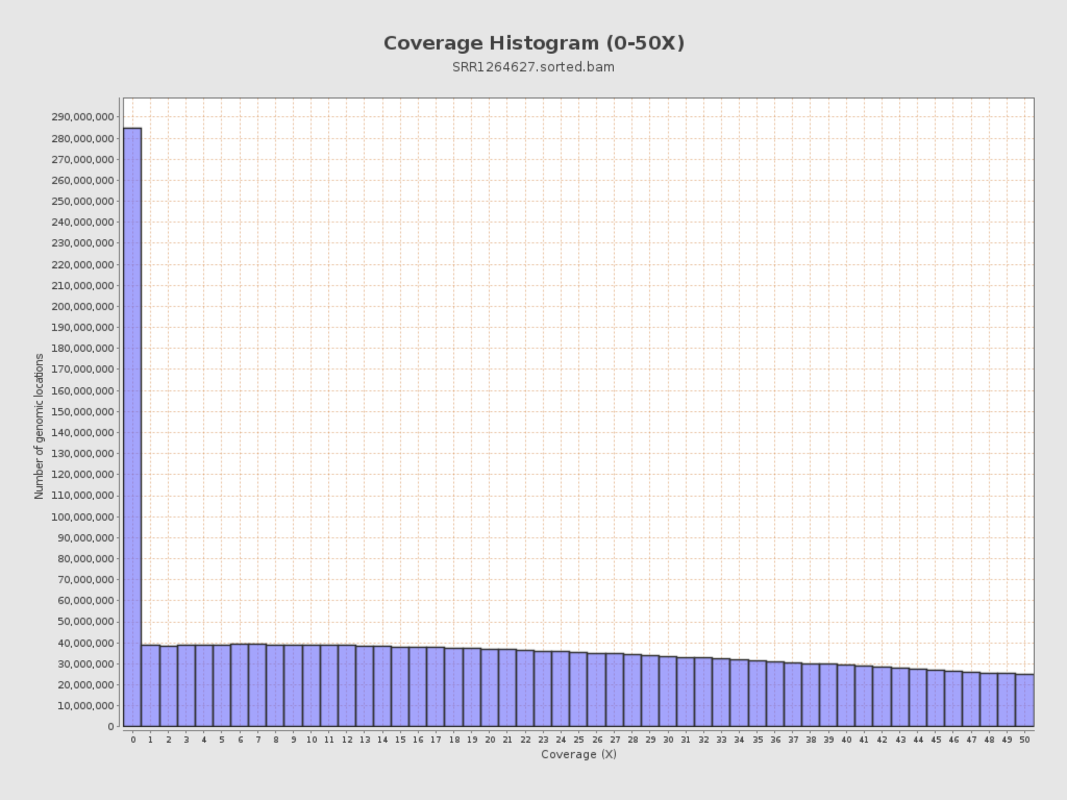
3. Results : Coverage across reference



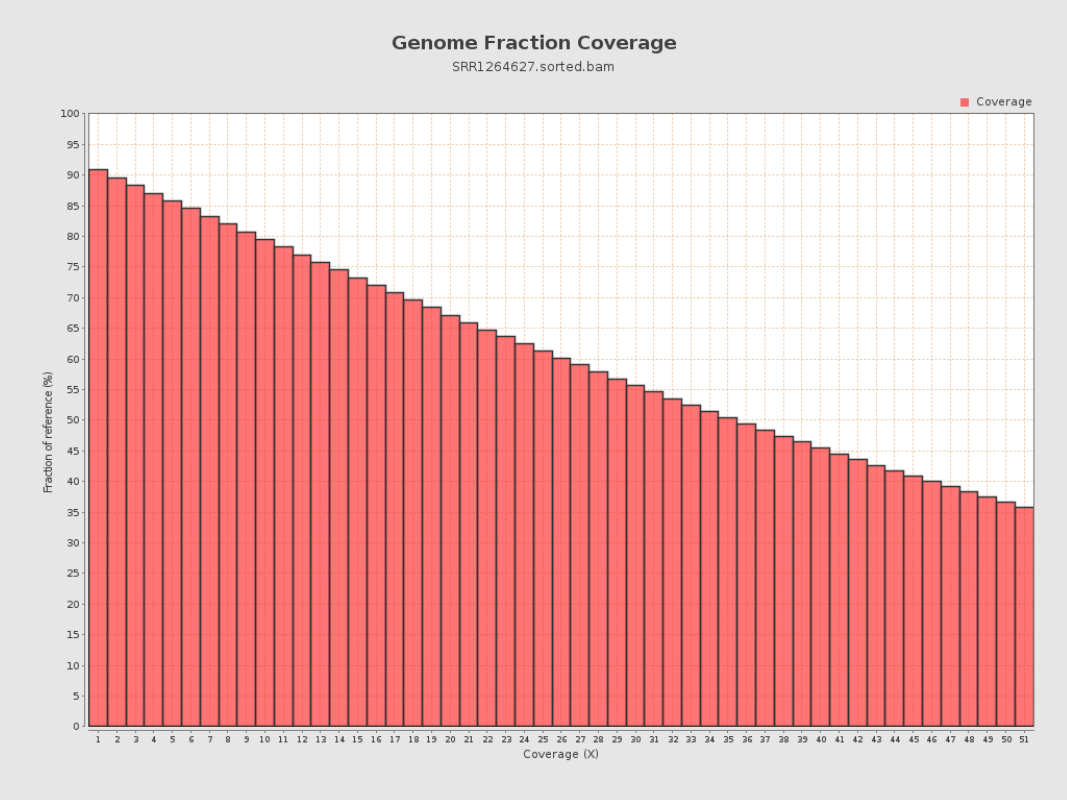
4. Results : Coverage Histogram



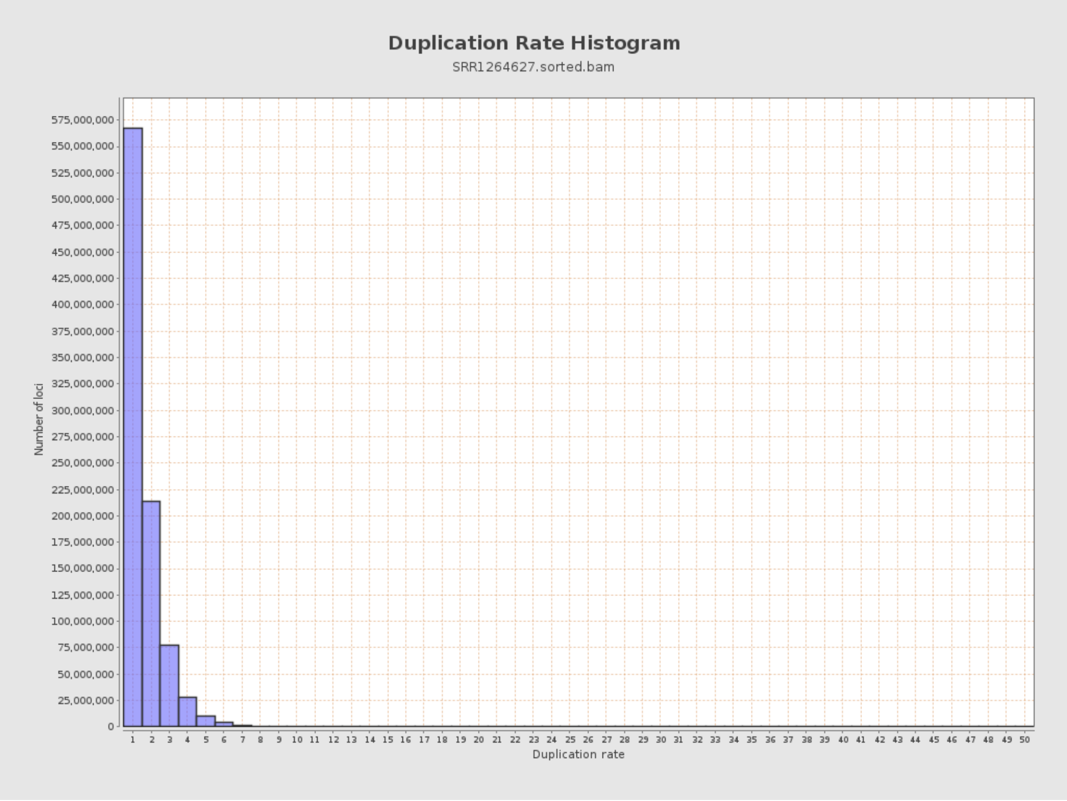
5. Results : Coverage Histogram (0-50X)



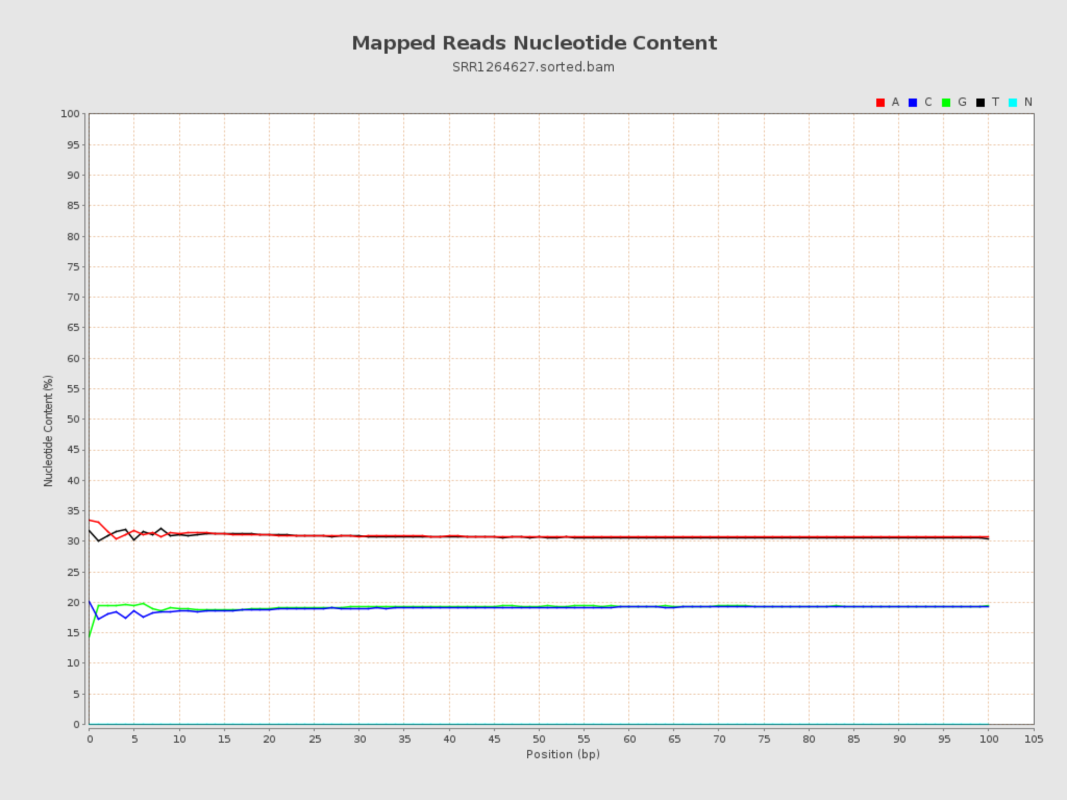
6. Results : Genome Fraction Coverage



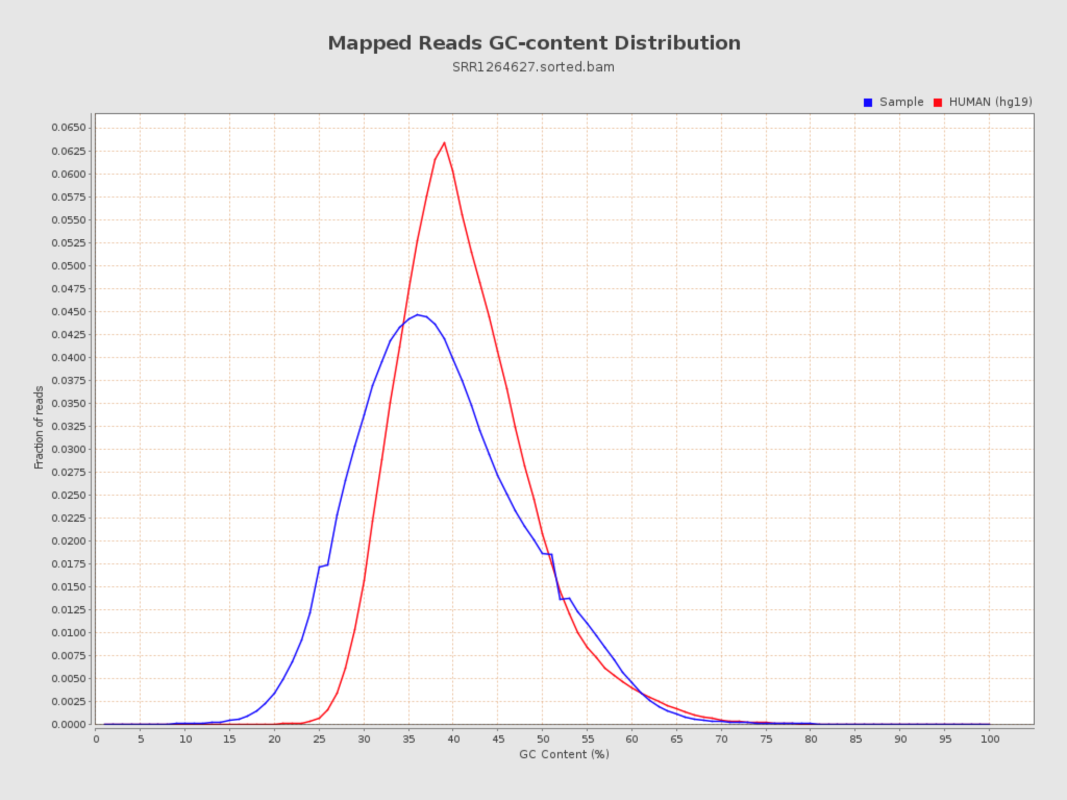
7. Results : Duplication Rate Histogram



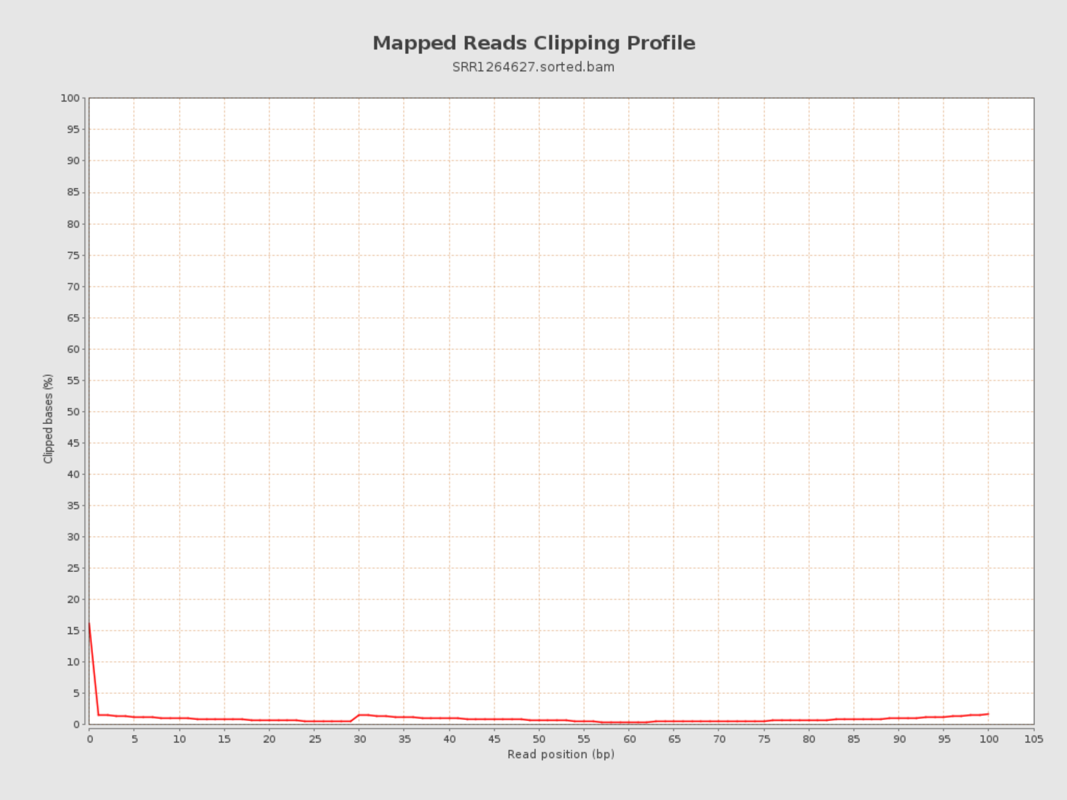
8. Results : Mapped Reads Nucleotide Content



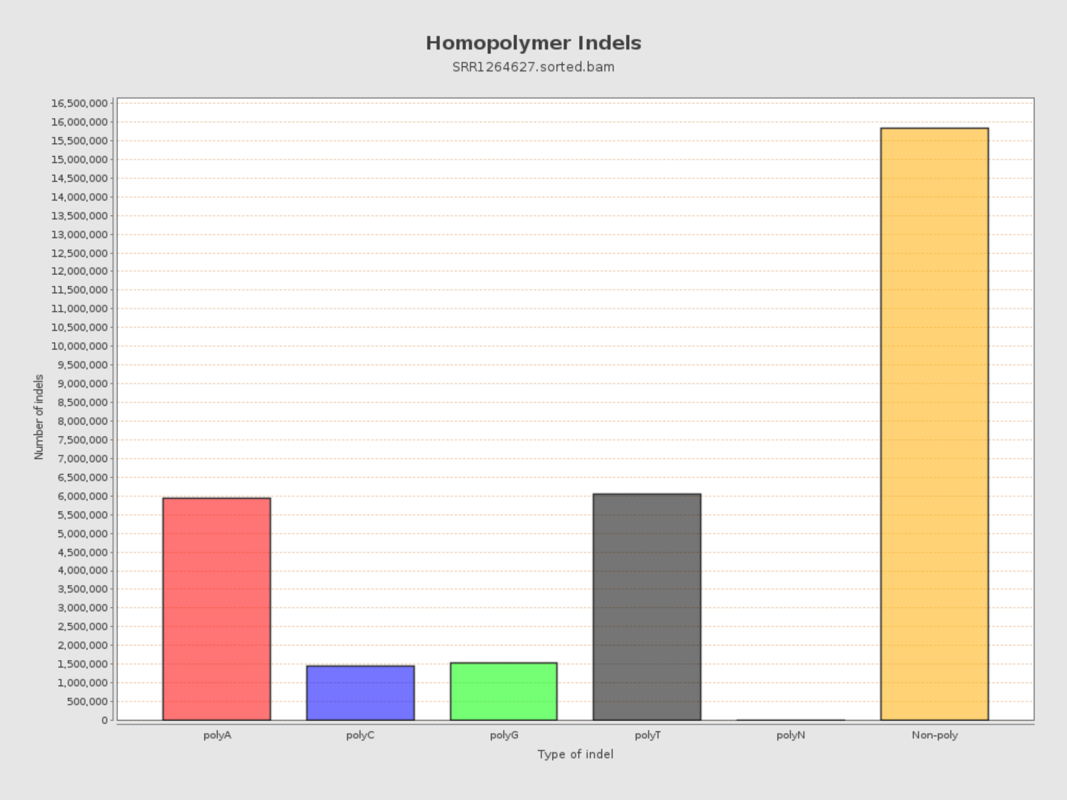
9. Results : Mapped Reads GC-content Distribution



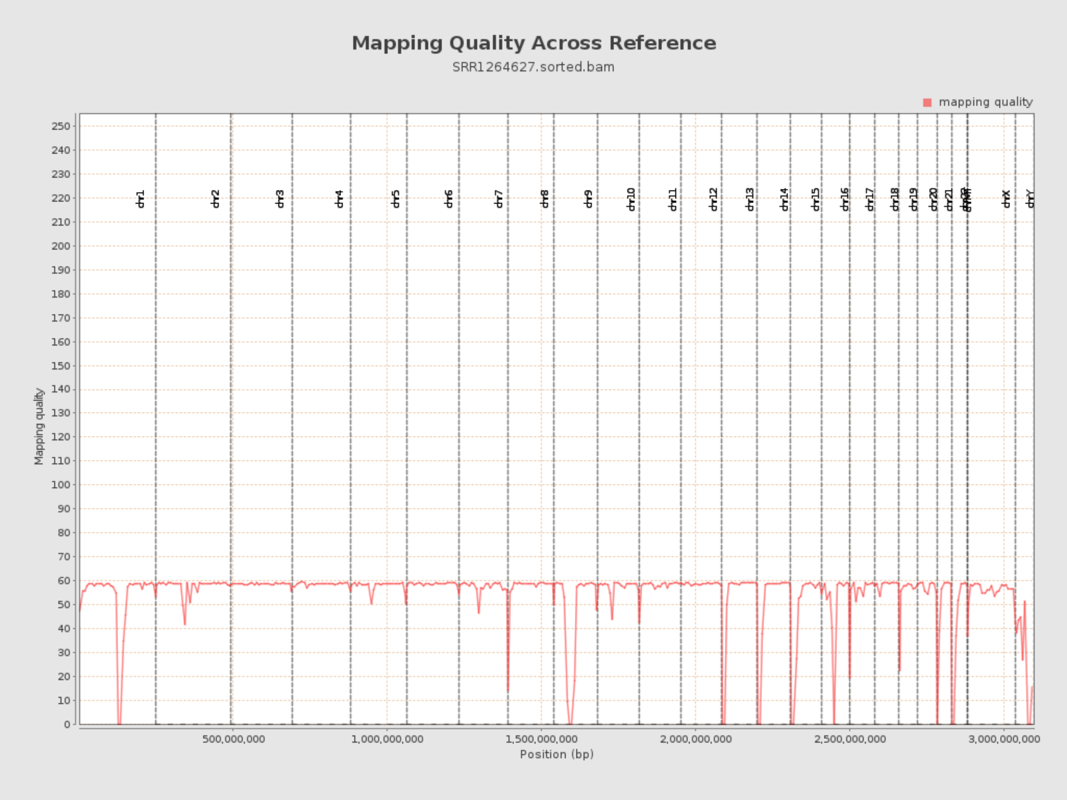
10. Results : Mapped Reads Clipping Profile



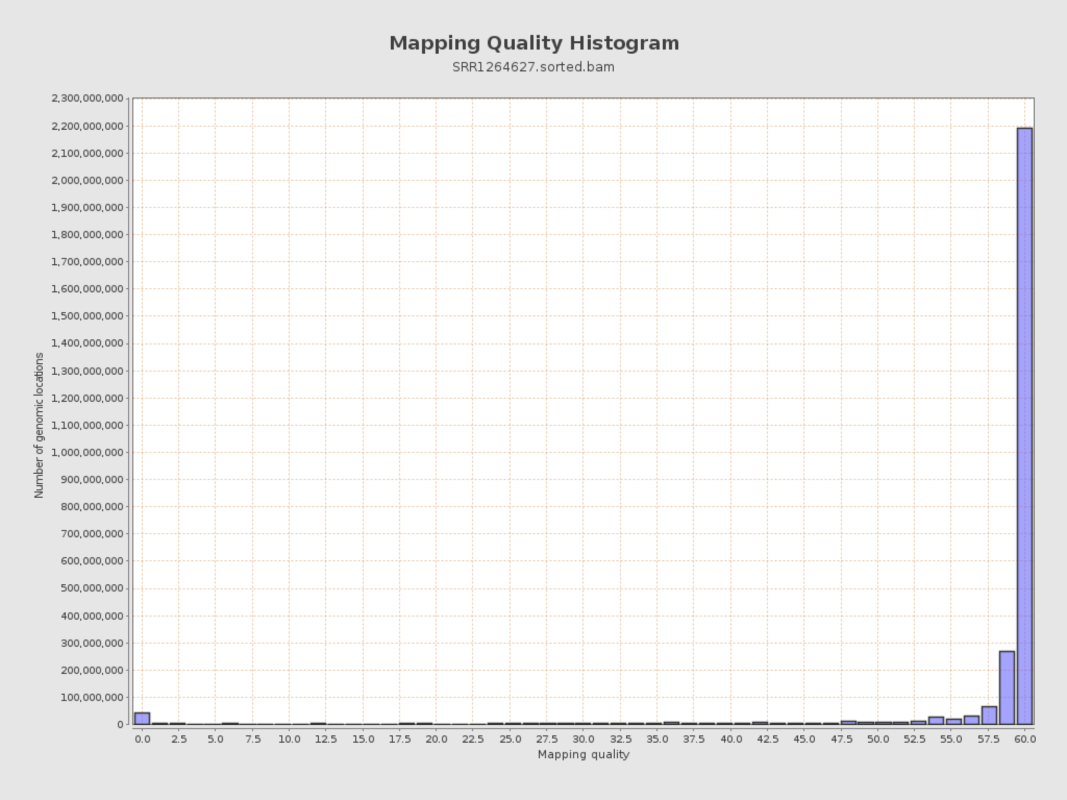
11. Results : Homopolymer Indels



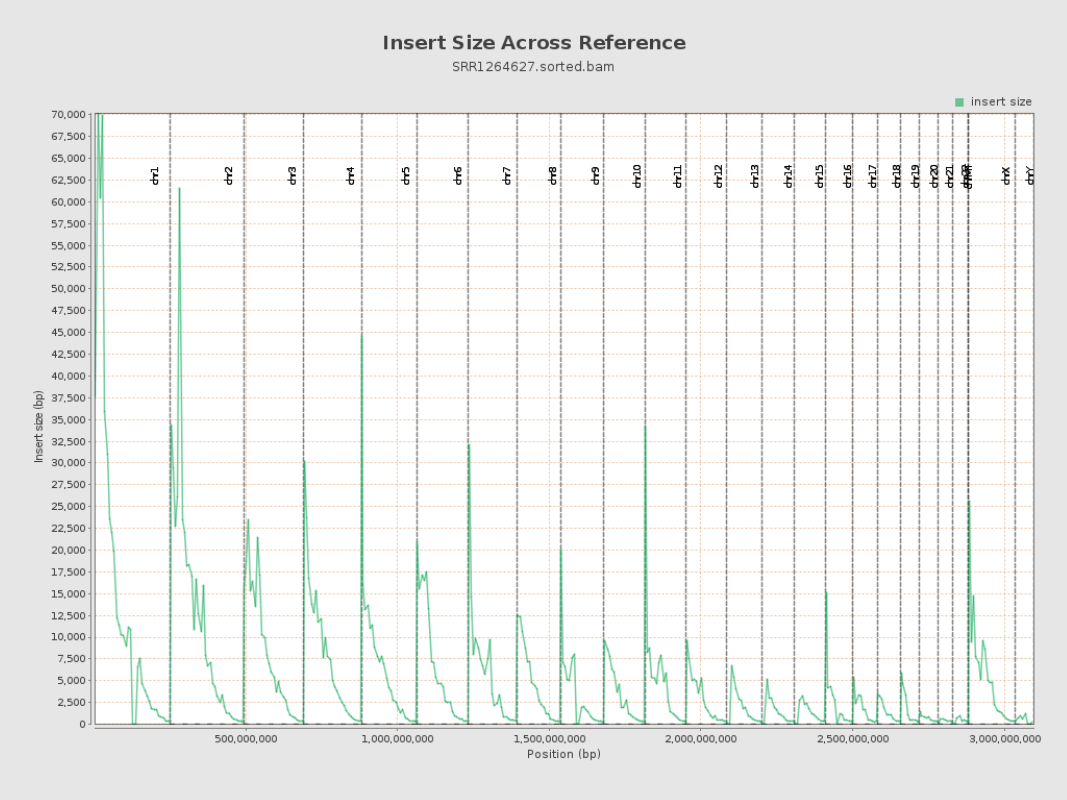
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram