Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:29:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063542.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_SRR6063542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:29:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,181,971
Mapped reads	1,834,612 / 84.08%
Unmapped reads	347,359 / 15.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,837 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	187,050 / 8.57%
Duplication rate	8.28%
Clipped reads	1,048,616 / 48.06%

2.2. ACGT Content

Number/percentage of A's	30,928,323 / 26.46%
Number/percentage of C's	20,810,137 / 17.8%
Number/percentage of T's	37,901,822 / 32.43%
Number/percentage of G's	27,246,475 / 23.31%
Number/percentage of N's	2,786 / 0%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3988

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

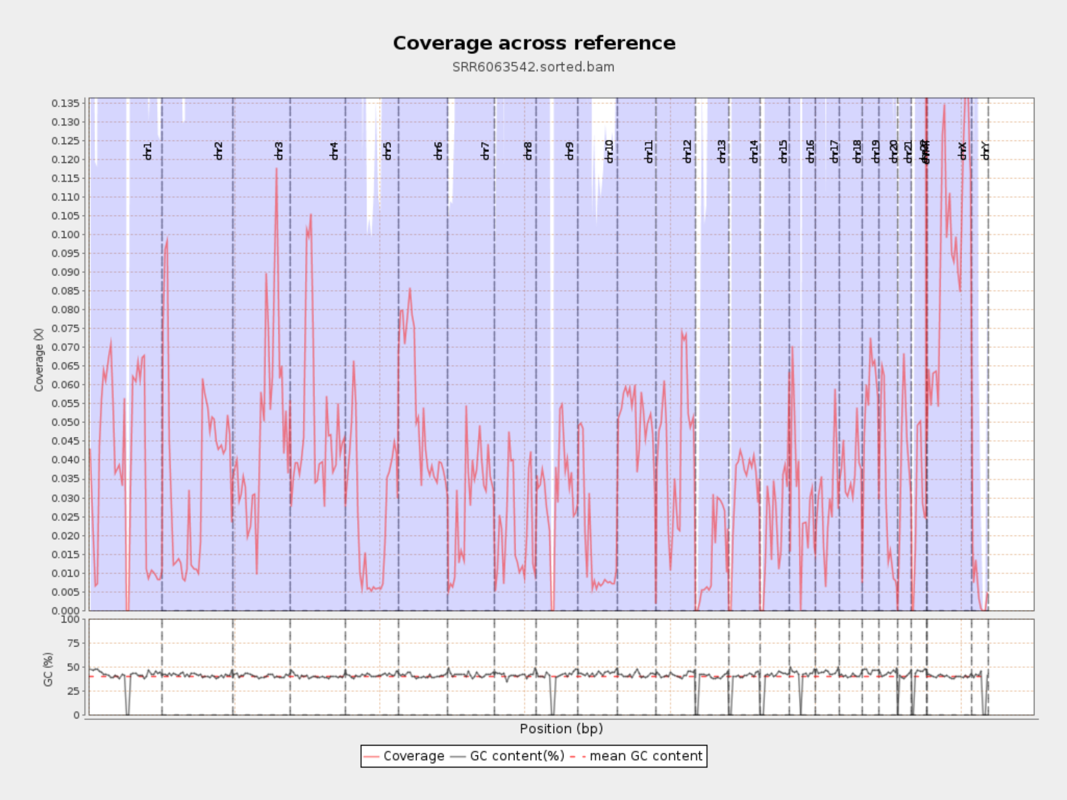
General error rate	0.86%
Mismatches	988,999
Insertions	8,517
Mapped reads with at least one insertion	0.46%
Deletions	32,221
Mapped reads with at least one deletion	1.74%
Homopolymer indels	45.83%

2.6. Chromosome stats

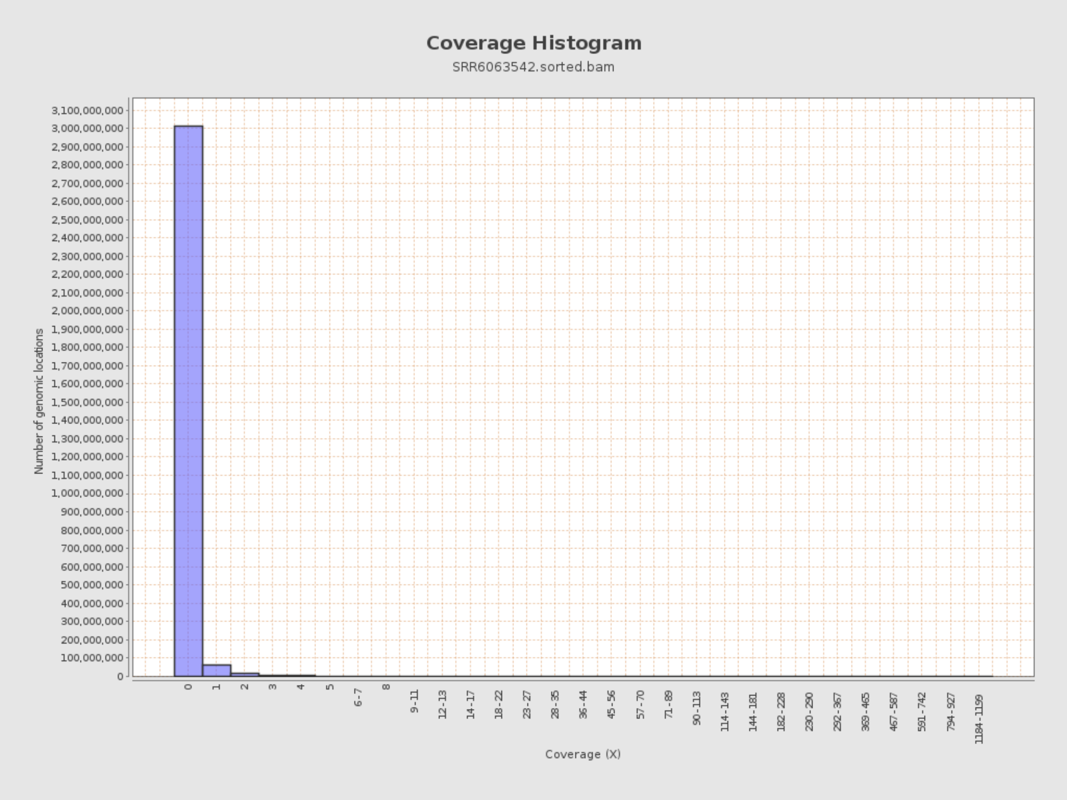
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9202596	0.0369	0.6254
chr2	243199373	8937947	0.0368	0.5623
chr3	198022430	9541967	0.0482	0.2966
chr4	191154276	9468811	0.0495	0.3088
chr5	180915260	4482284	0.0248	0.2153
chr6	171115067	9101980	0.0532	0.3707
chr7	159138663	4610799	0.029	0.4164

chr8	146364022	3130828	0.0214	0.5198
chr9	141213431	4398046	0.0311	0.3711
chr10	135534747	2220531	0.0164	0.2294
chr11	135006516	6831525	0.0506	0.4464
chr12	133851895	5874957	0.0439	0.3013
chr13	115169878	1627139	0.0141	0.1638
chr14	107349540	3444767	0.0321	0.2927
chr15	102531392	2391125	0.0233	0.2168
chr16	90354753	2709065	0.03	0.2506
chr17	81195210	2318205	0.0286	0.262
chr18	78077248	2922482	0.0374	0.5938
chr19	59128983	3351594	0.0567	0.4502
chr20	63025520	1831579	0.0291	0.2456
chr21	48129895	1853632	0.0385	0.2735
chr22	51304566	1358475	0.0265	0.2137
chrMT	16571	113080	6.824	5.6534
chrX	155270560	14897148	0.0959	0.4856
chrY	59373566	320567	0.0054	0.1342

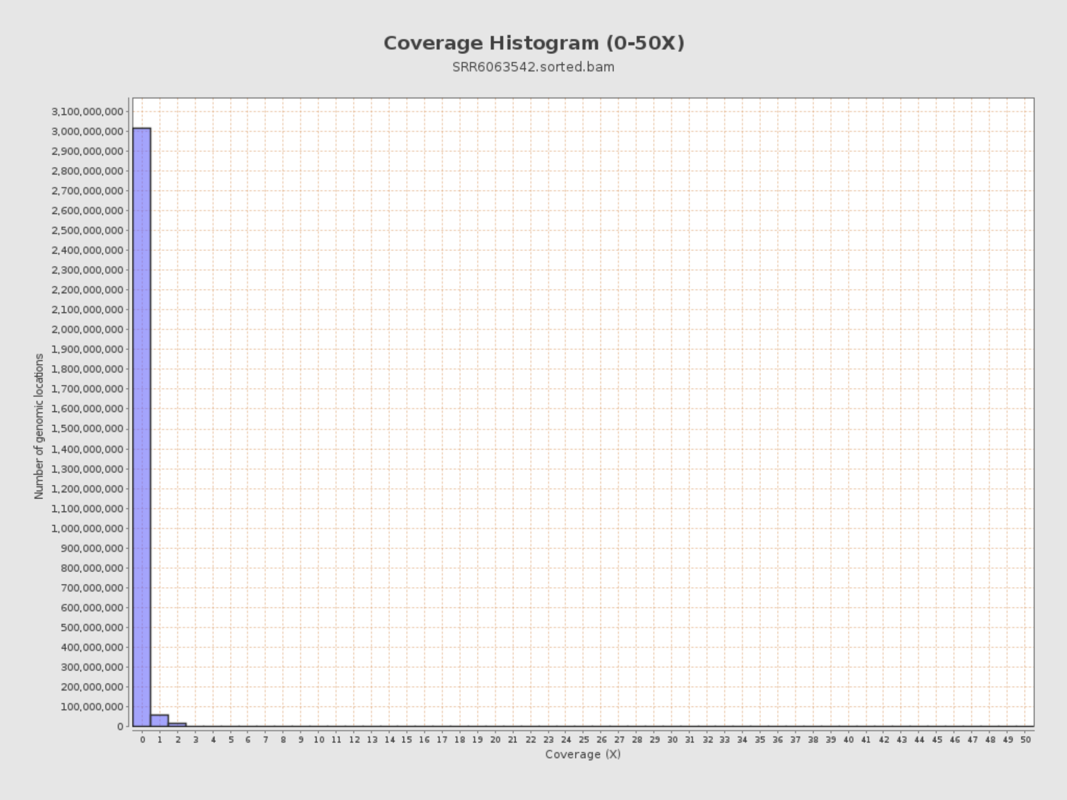
3. Results : Coverage across reference



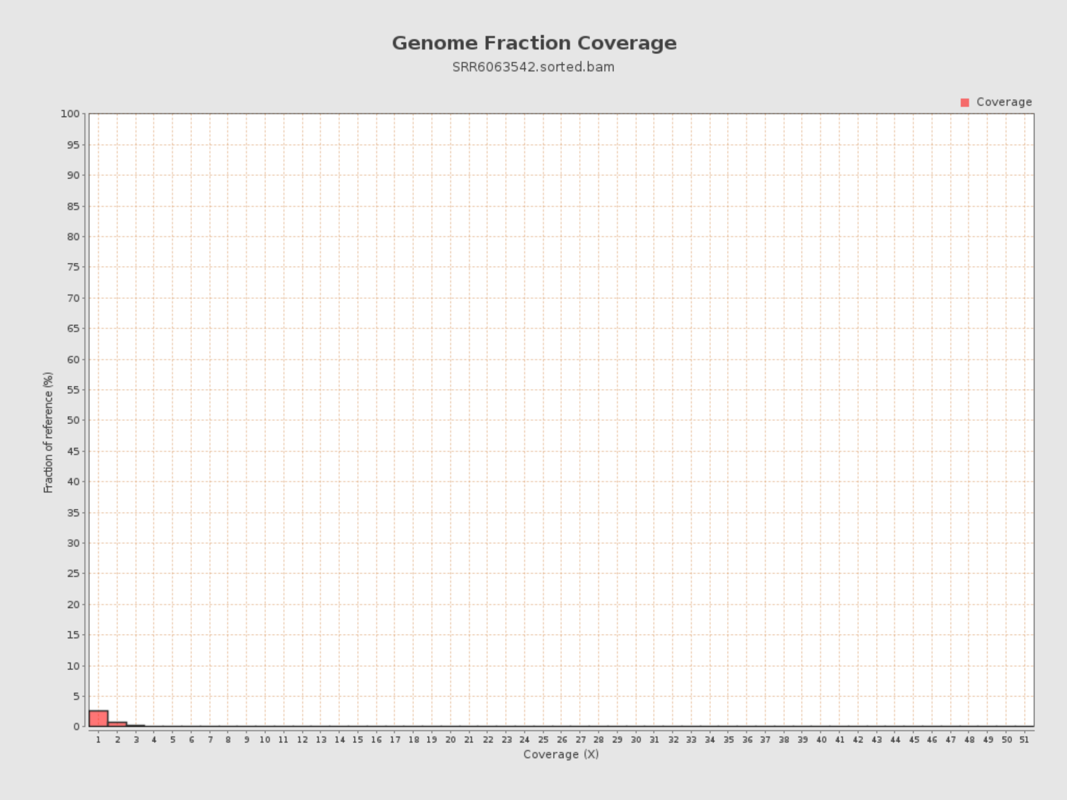
4. Results : Coverage Histogram



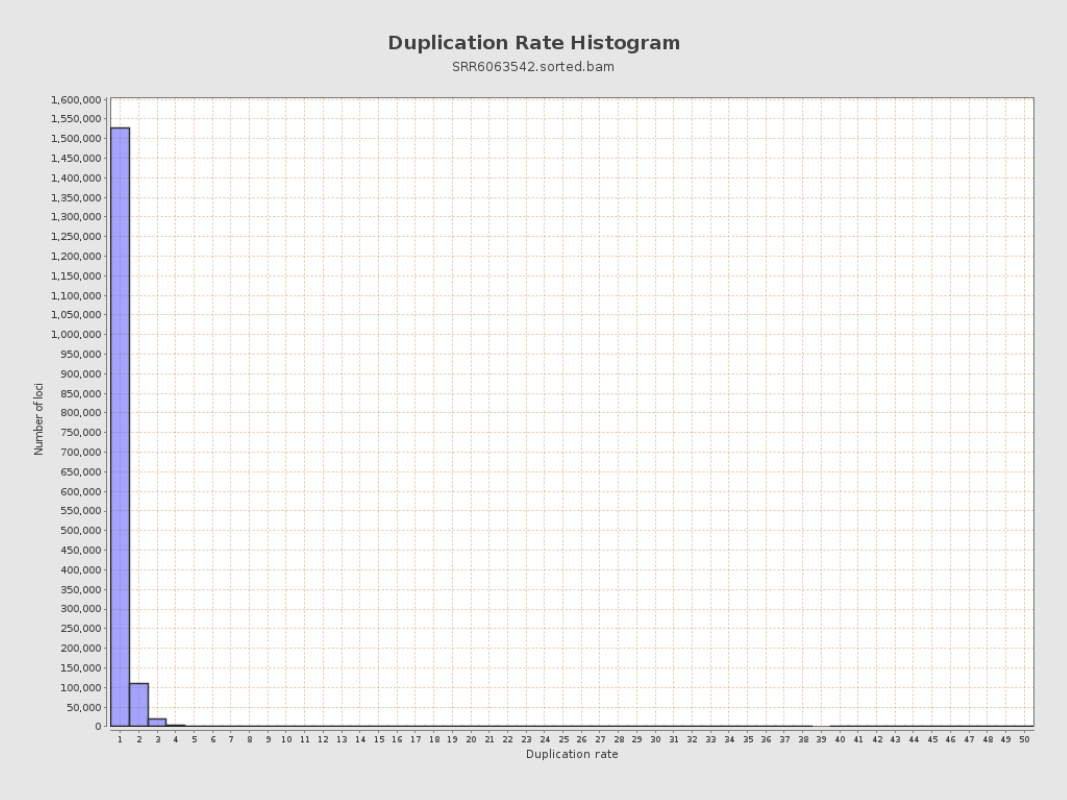
5. Results : Coverage Histogram (0-50X)



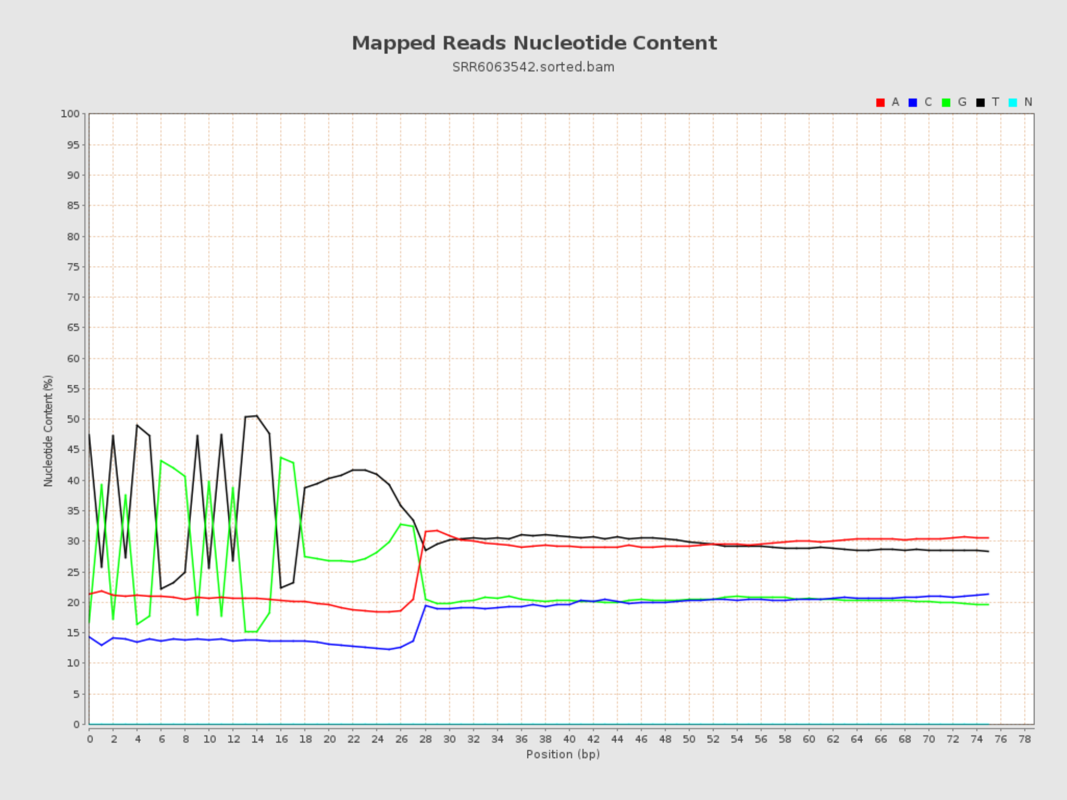
6. Results : Genome Fraction Coverage



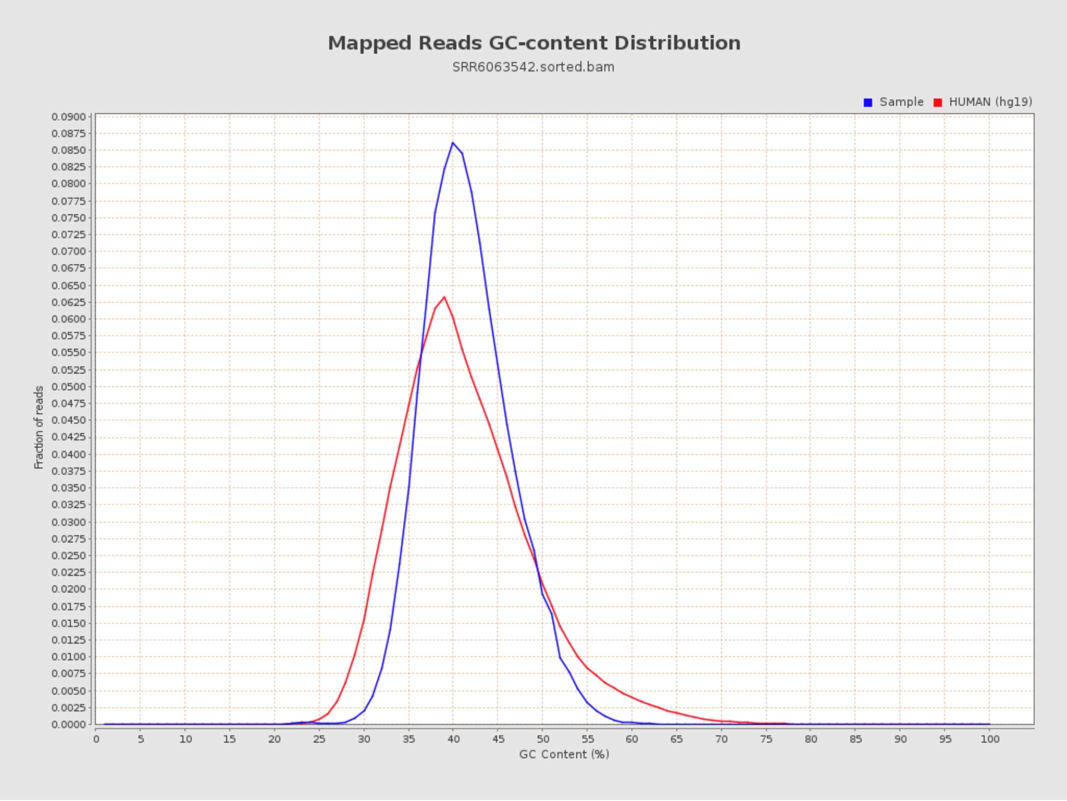
7. Results : Duplication Rate Histogram



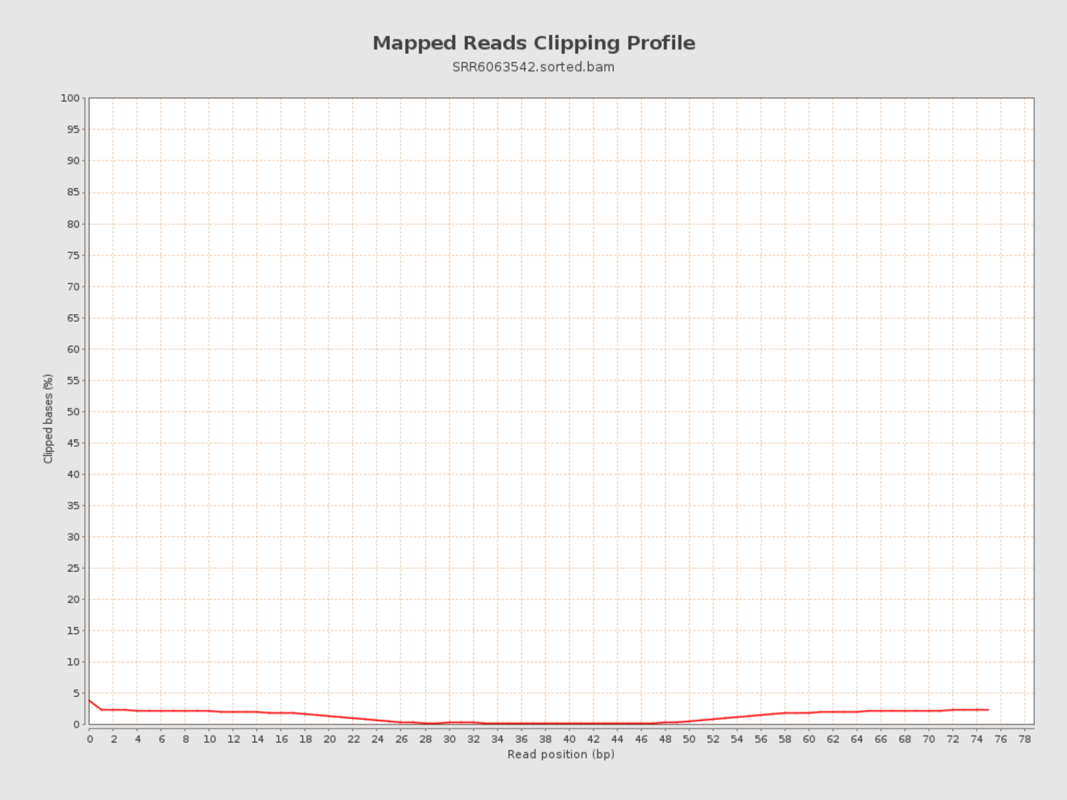
8. Results : Mapped Reads Nucleotide Content



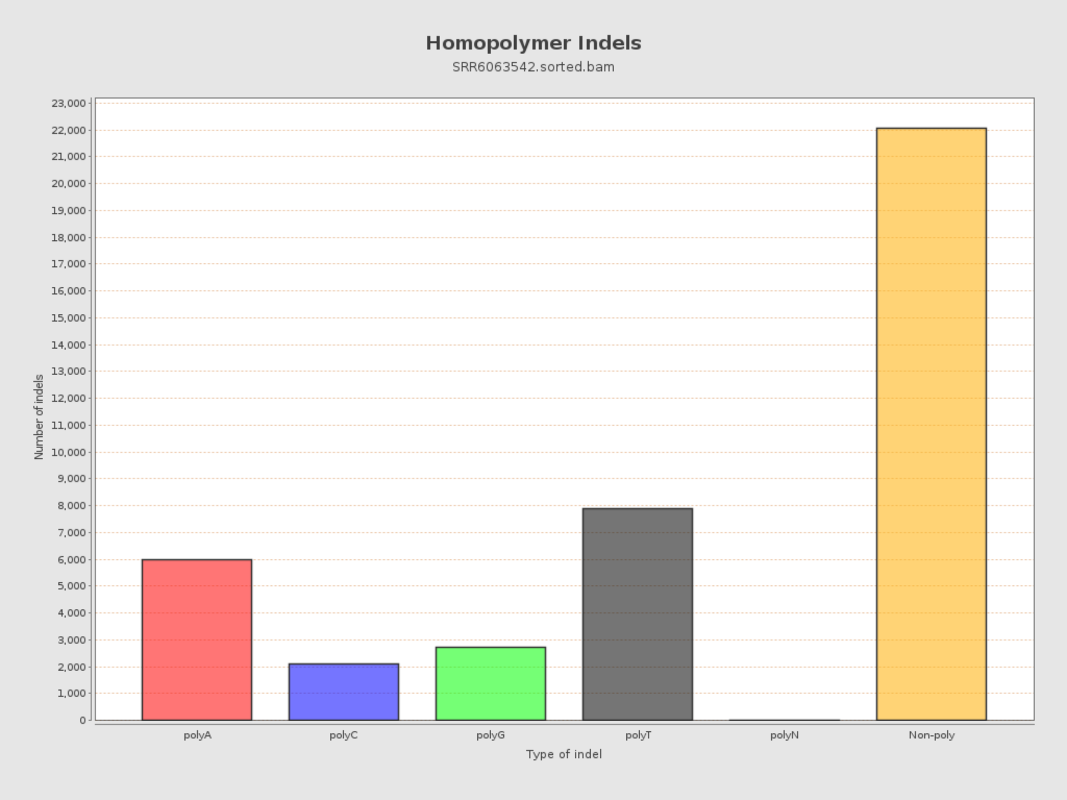
9. Results : Mapped Reads GC-content Distribution



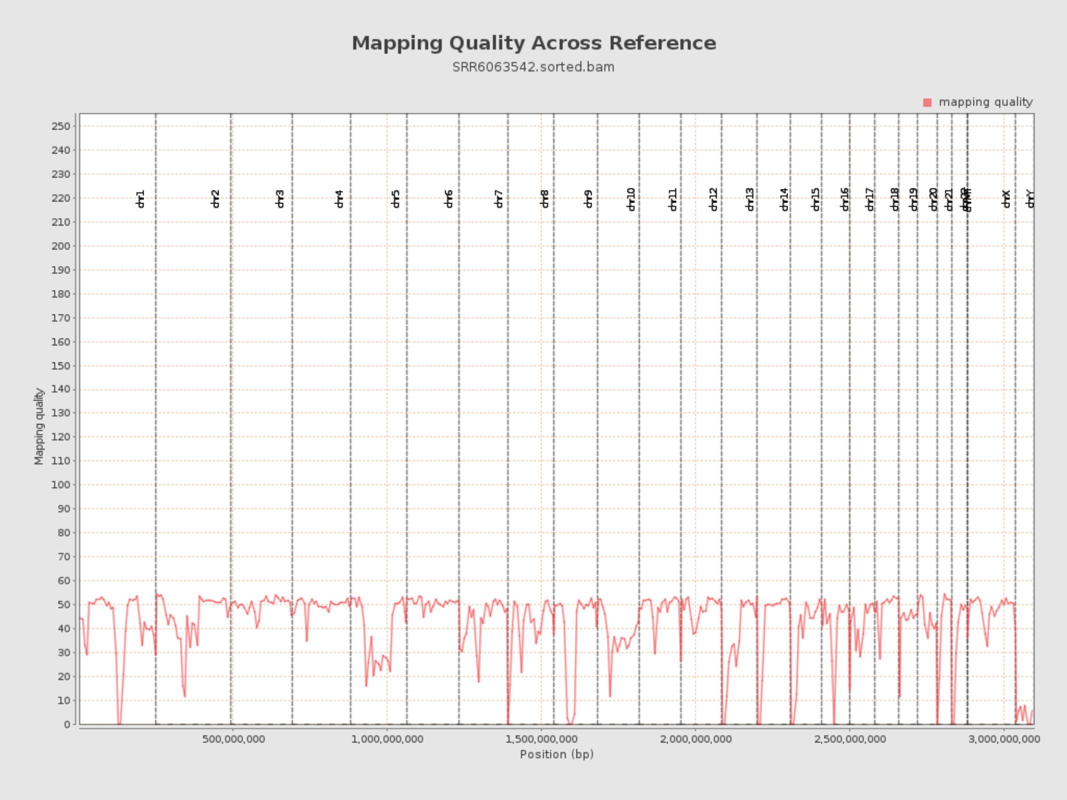
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram