

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:46:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548950.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_SRR1548950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:46:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,766,216
Mapped reads	8,341,845 / 85.42%
Unmapped reads	1,424,371 / 14.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	451,053 / 4.62%
Duplication rate	4.24%
Clipped reads	486,933 / 4.99%

2.2. ACGT Content

Number/percentage of A's	94,381,834 / 28.53%
Number/percentage of C's	70,193,344 / 21.21%
Number/percentage of T's	95,500,369 / 28.86%
Number/percentage of G's	70,795,801 / 21.4%
Number/percentage of N's	520 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.1069
Standard Deviation	1.1541

2.4. Mapping Quality

Mean Mapping Quality	44.21
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2.5. Mismatches and indels

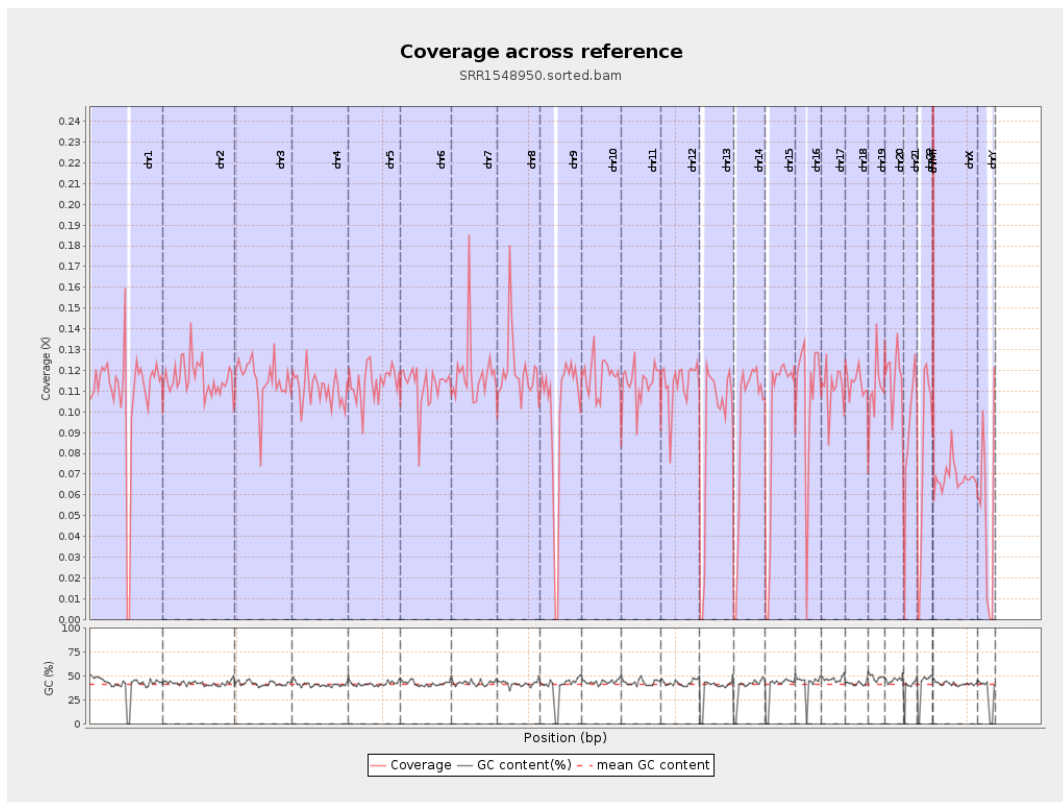
General error rate	0.22%
Mismatches	733,407
Insertions	8,933
Mapped reads with at least one insertion	0.11%
Deletions	22,990
Mapped reads with at least one deletion	0.28%
Homopolymer indels	43%

2.6. Chromosome stats

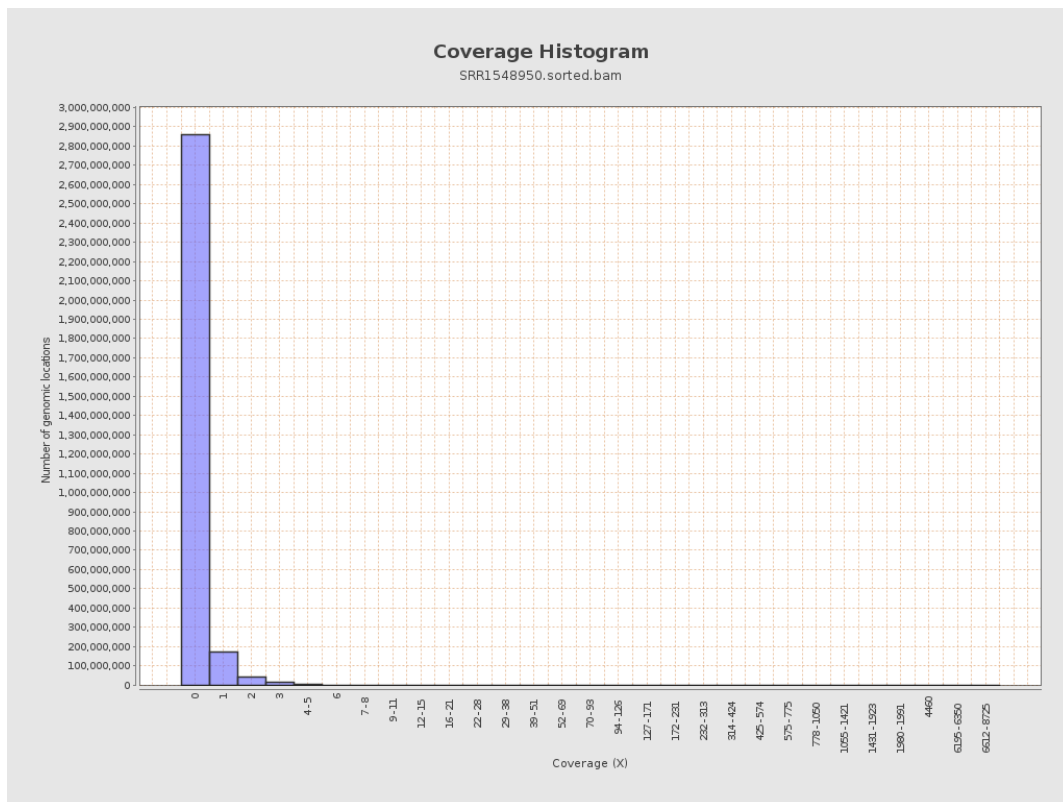
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27069799	0.1086	1.4104
chr2	243199373	28293524	0.1163	0.611
chr3	198022430	22787555	0.1151	0.4496
chr4	191154276	21298139	0.1114	0.4658
chr5	180915260	20635397	0.1141	0.4516
chr6	171115067	19308383	0.1128	0.4678
chr7	159138663	18852958	0.1185	1.1717
chr8	146364022	17529983	0.1198	4.2584

chr9	141213431	14083826	0.0997	0.5624
chr10	135534747	15843231	0.1169	0.5859
chr11	135006516	15349742	0.1137	0.6438
chr12	133851895	15305974	0.1144	0.456
chr13	115169878	10661558	0.0926	0.3979
chr14	107349540	10241254	0.0954	0.4582
chr15	102531392	9768322	0.0953	0.405
chr16	90354753	9635822	0.1066	0.4632
chr17	81195210	9089748	0.1119	0.466
chr18	78077248	8914404	0.1142	0.9909
chr19	59128983	6638599	0.1123	1.1064
chr20	63025520	7366362	0.1169	0.4663
chr21	48129895	4381927	0.091	0.4888
chr22	51304566	4076233	0.0795	0.5472
chrMT	16571	23534	1.4202	2.1675
chrX	155270560	10626031	0.0684	0.4238
chrY	59373566	3120470	0.0526	0.5875

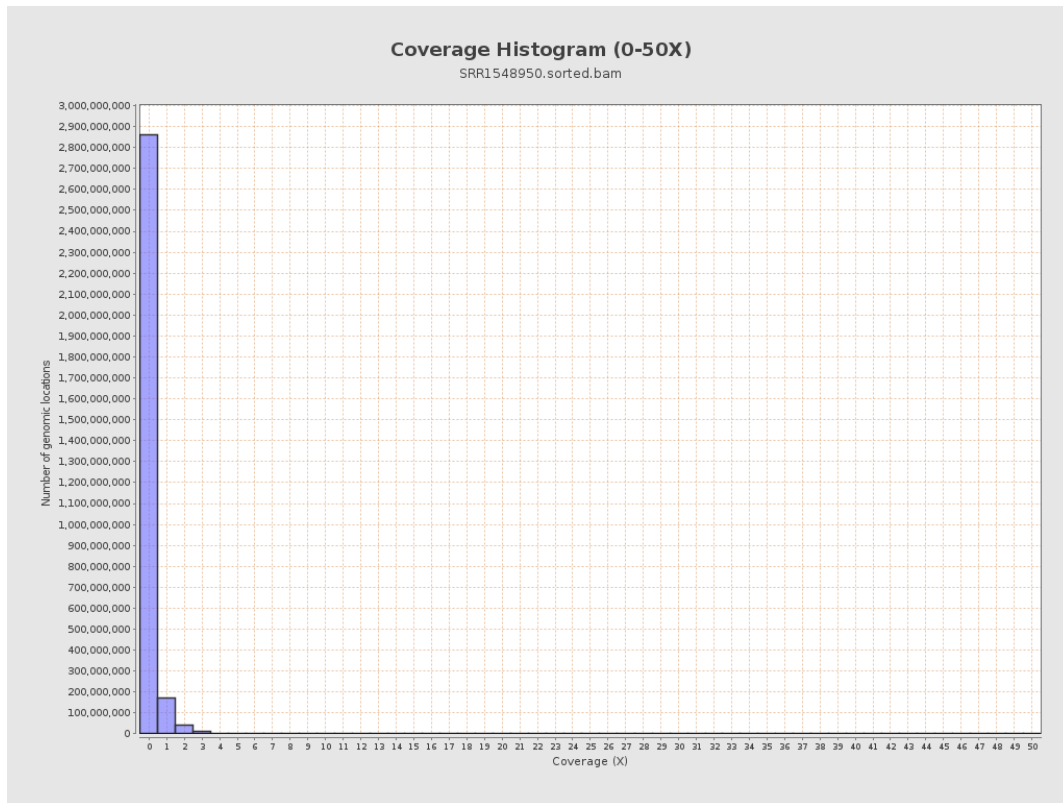
3. Results : Coverage across reference



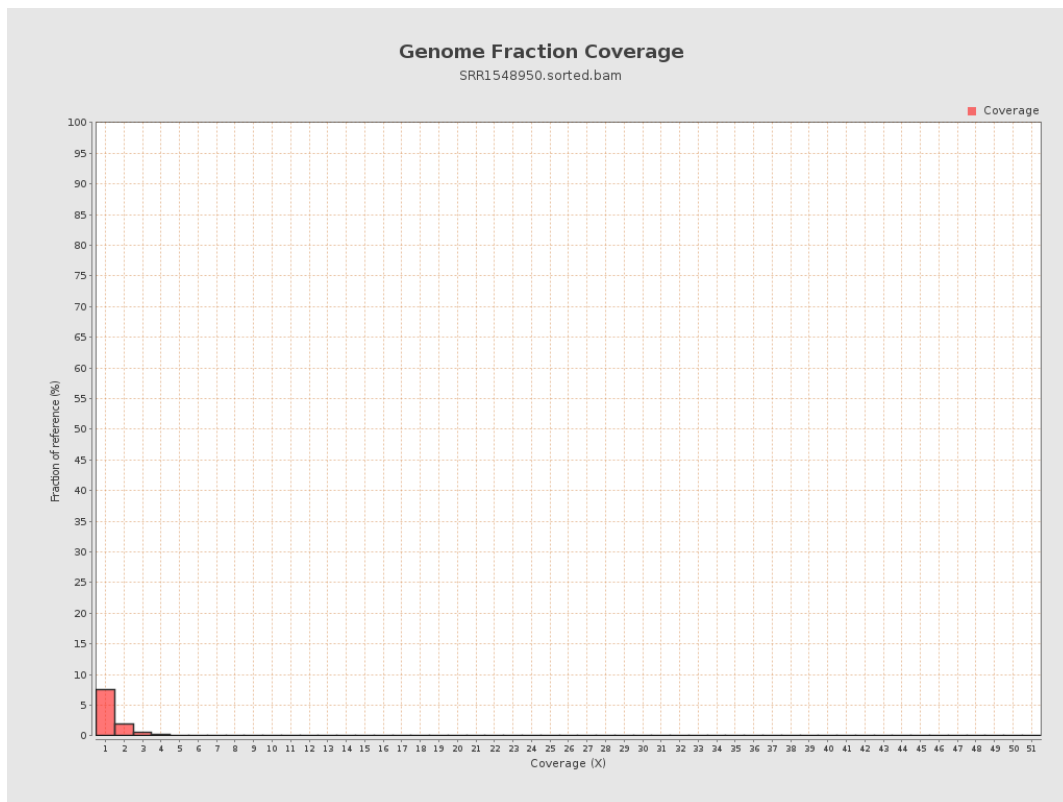
4. Results : Coverage Histogram



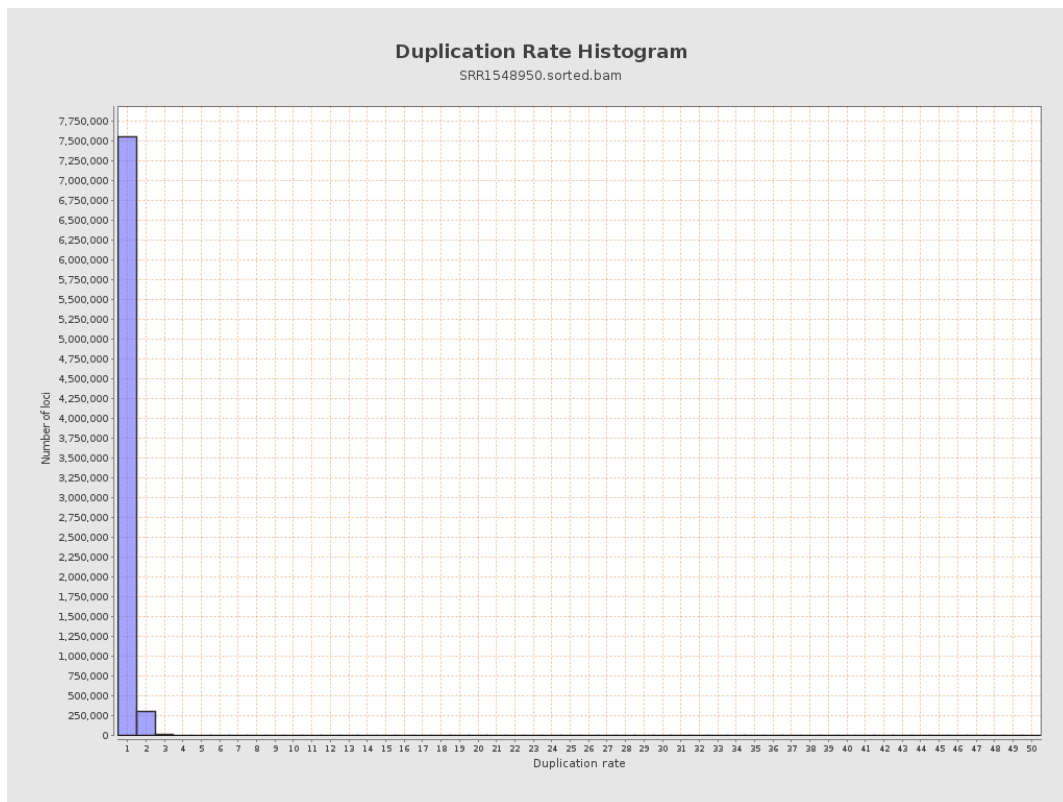
5. Results : Coverage Histogram (0-50X)



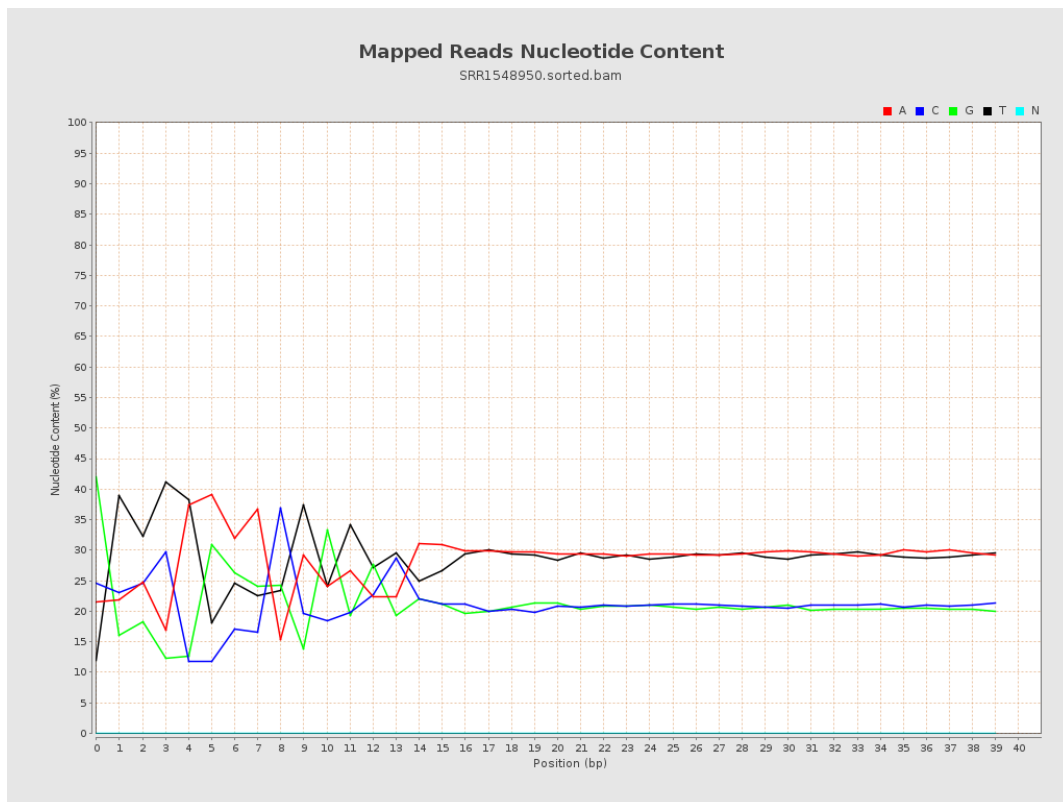
6. Results : Genome Fraction Coverage



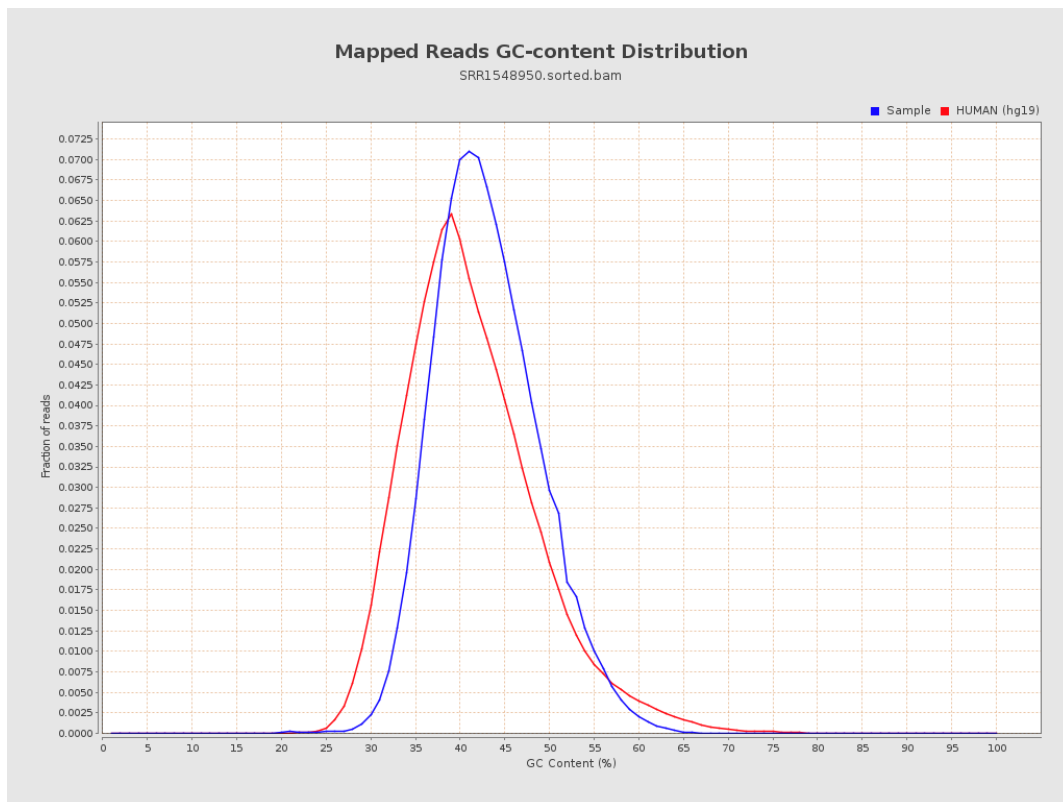
7. Results : Duplication Rate Histogram



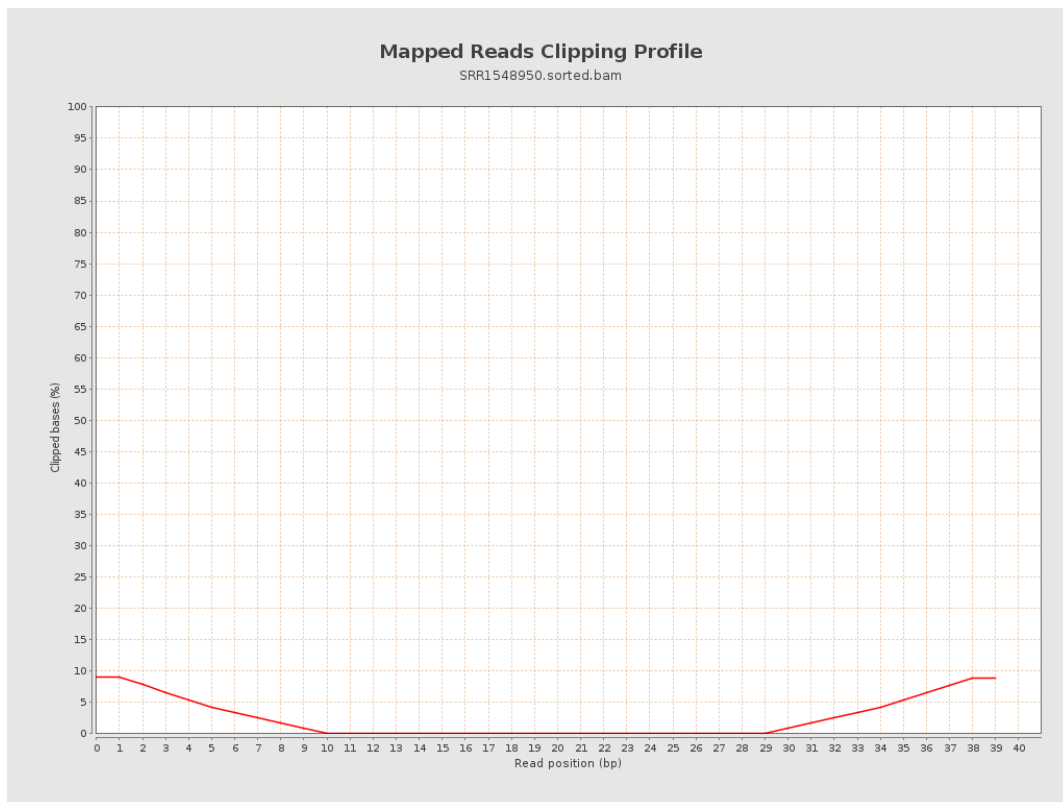
8. Results : Mapped Reads Nucleotide Content



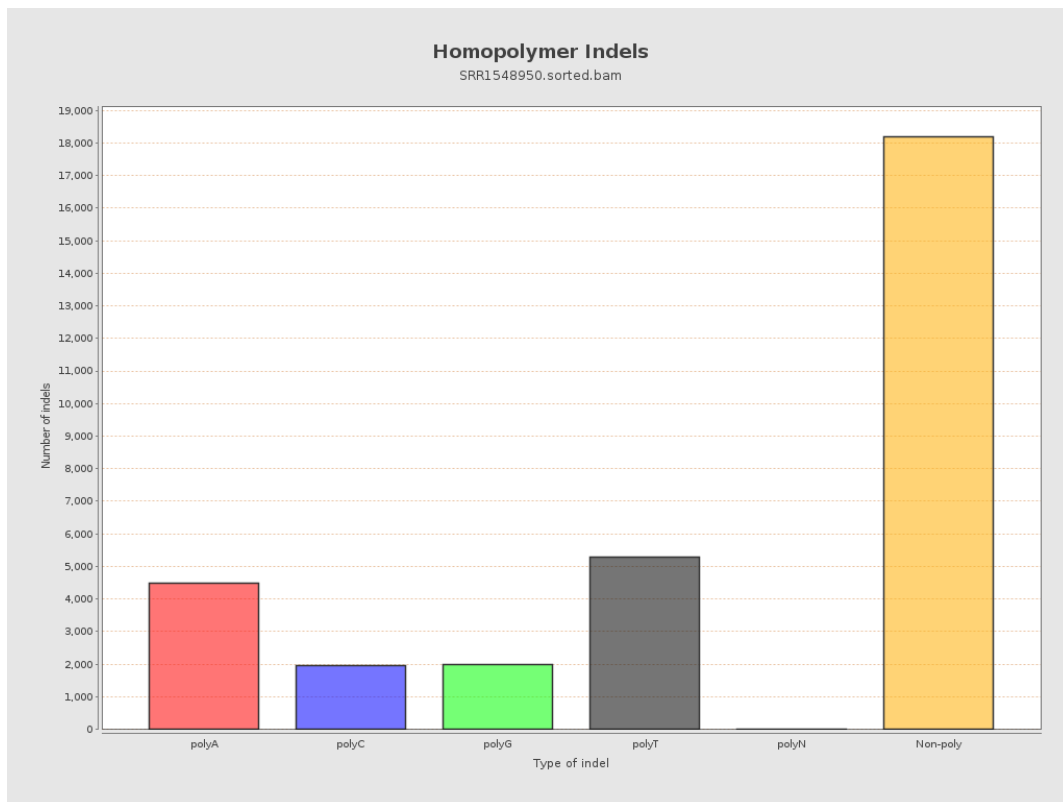
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

