Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:52:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054632.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_SRR054632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:52:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,300,816
Mapped reads	6,405,797 / 68.87%
Unmapped reads	2,895,019 / 31.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	173 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,592,130 / 17.12%
Duplication rate	17.73%
Clipped reads	669,391 / 7.2%

2.2. ACGT Content

Number/percentage of A's	92,600,446 / 30.72%
Number/percentage of C's	56,462,397 / 18.73%
Number/percentage of T's	92,444,581 / 30.67%
Number/percentage of G's	59,550,527 / 19.75%
Number/percentage of N's	394,679 / 0.13%
GC Percentage	38.48%

2.3. Coverage

Mean	0.0974

Standard Deviation	0.8203

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

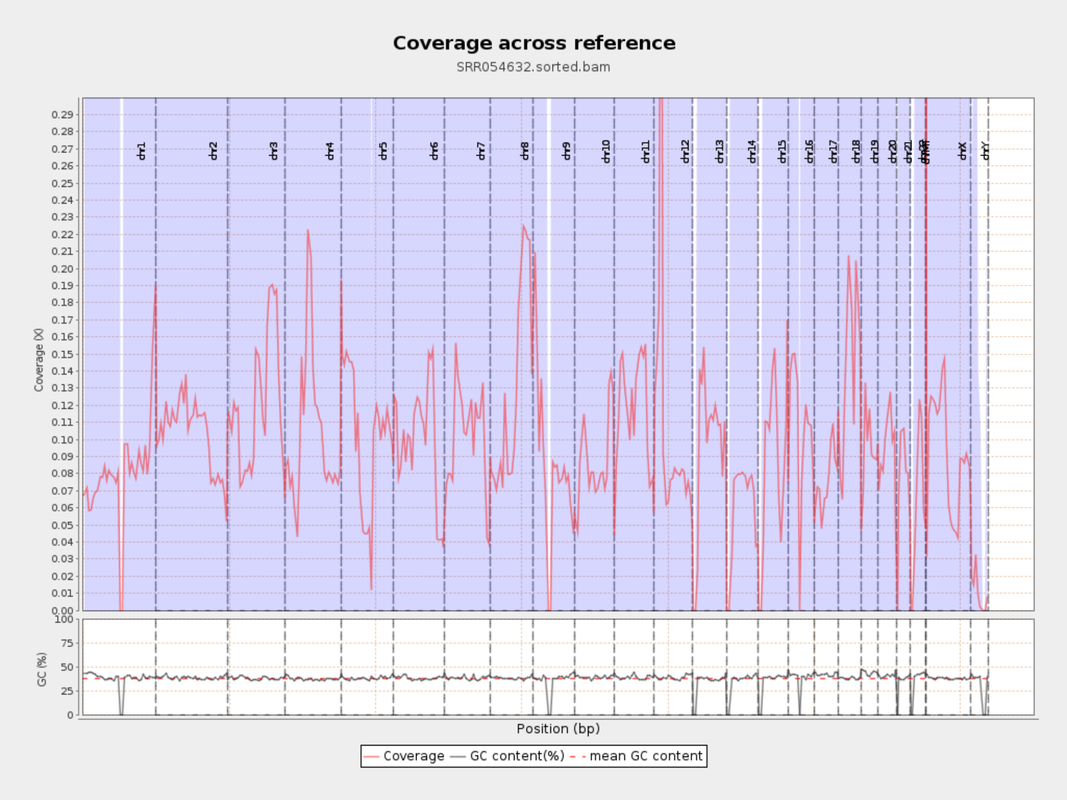
General error rate	0.83%
Mismatches	2,485,998
Insertions	14,505
Mapped reads with at least one insertion	0.23%
Deletions	43,764
Mapped reads with at least one deletion	0.68%
Homopolymer indels	47.57%

2.6. Chromosome stats

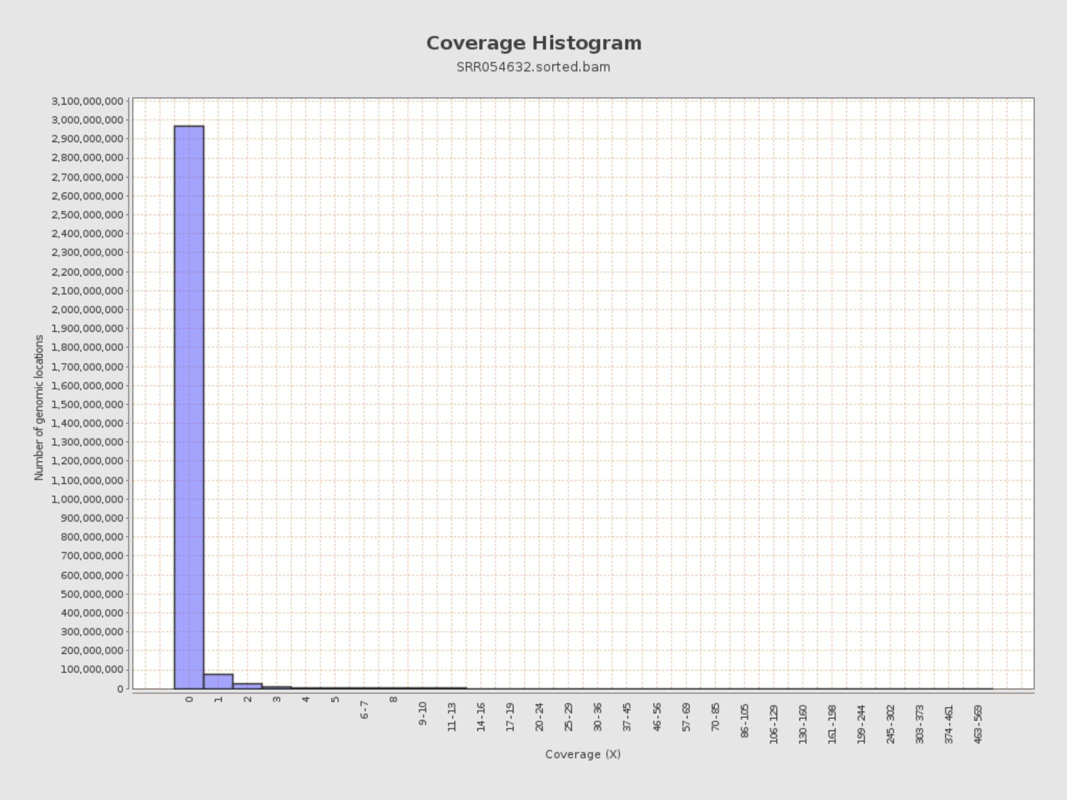
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20082226	0.0806	0.8006
chr2	243199373	25226514	0.1037	0.9194
chr3	198022430	23894588	0.1207	0.8631
chr4	191154276	19781982	0.1035	0.8421
chr5	180915260	18317302	0.1012	0.7664
chr6	171115067	17167042	0.1003	0.8305
chr7	159138663	15974004	0.1004	0.8785

chr8	146364022	18854220	0.1288	0.9502
chr9	141213431	11916308	0.0844	0.734
chr10	135534747	11788697	0.087	0.748
chr11	135006516	16048418	0.1189	0.8906
chr12	133851895	15509679	0.1159	1.0049
chr13	115169878	11126145	0.0966	0.7458
chr14	107349540	6561323	0.0611	0.6344
chr15	102531392	8775695	0.0856	0.7081
chr16	90354753	9430510	0.1044	0.8147
chr17	81195210	6221733	0.0766	0.6313
chr18	78077248	11280260	0.1445	1.0496
chr19	59128983	5673155	0.0959	0.8318
chr20	63025520	6058279	0.0961	0.7547
chr21	48129895	3667978	0.0762	0.7119
chr22	51304566	3286035	0.064	0.5805
chrMT	16571	22146	1.3364	3.5974
chrX	155270560	14222706	0.0916	0.8023
chrY	59373566	629839	0.0106	0.2559

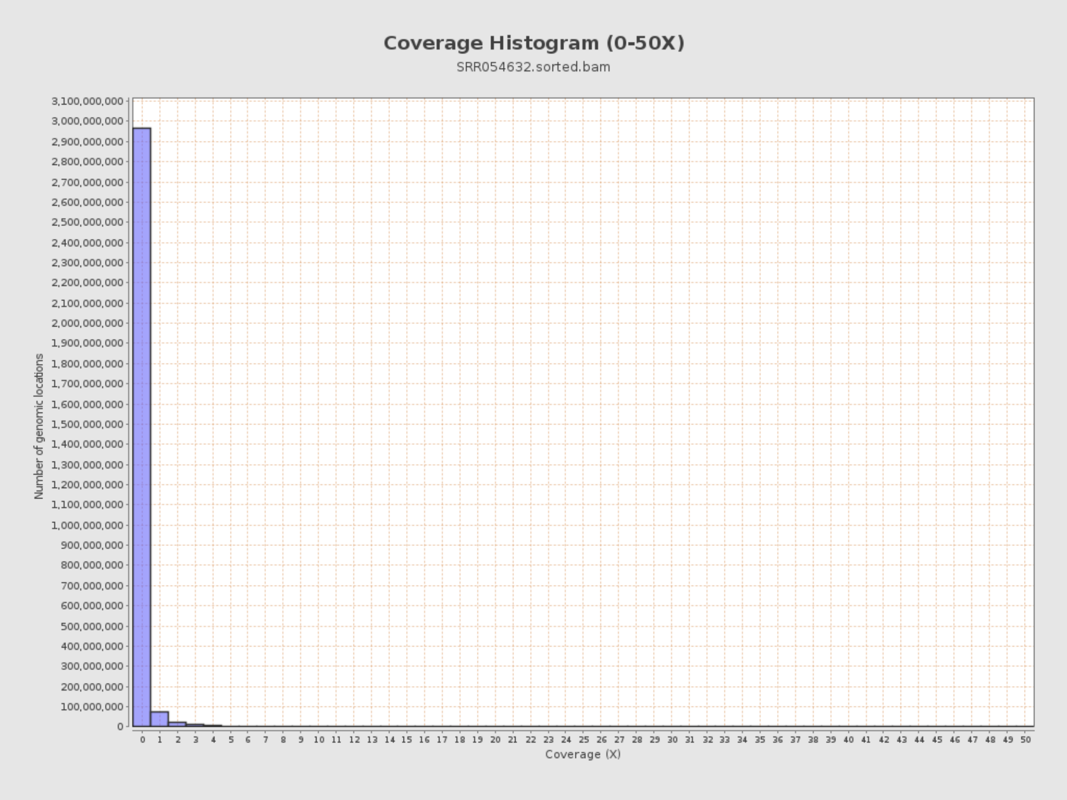
3. Results : Coverage across reference



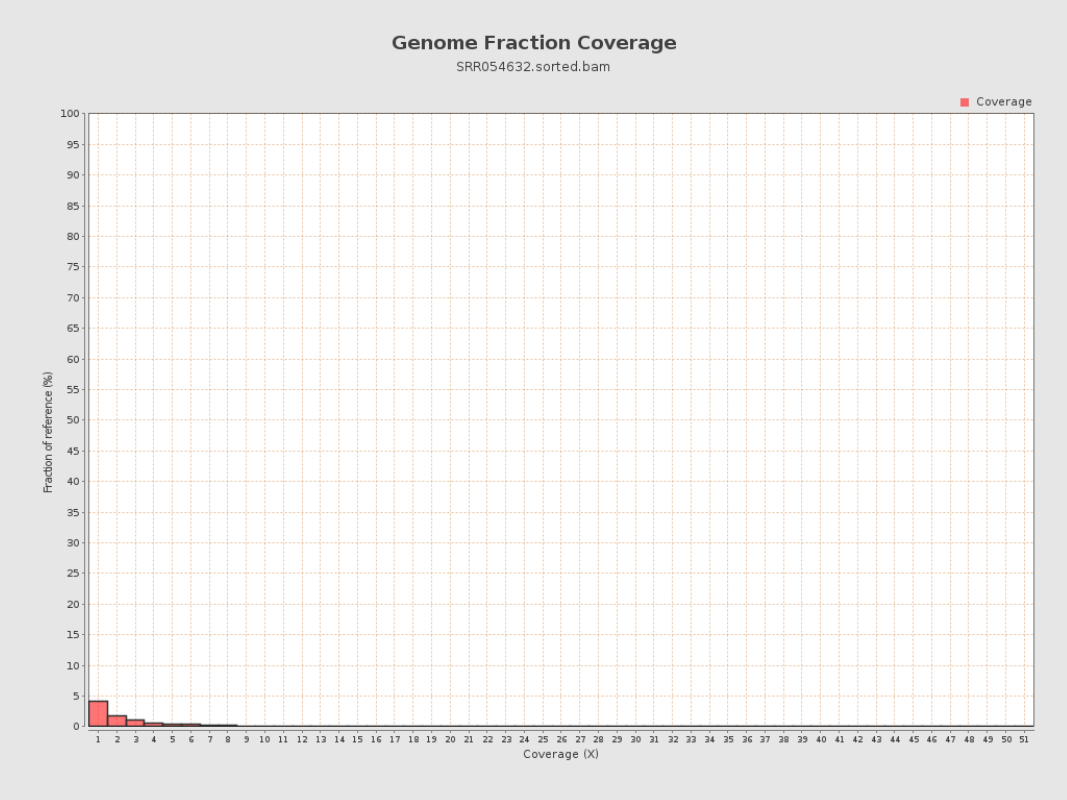
4. Results : Coverage Histogram



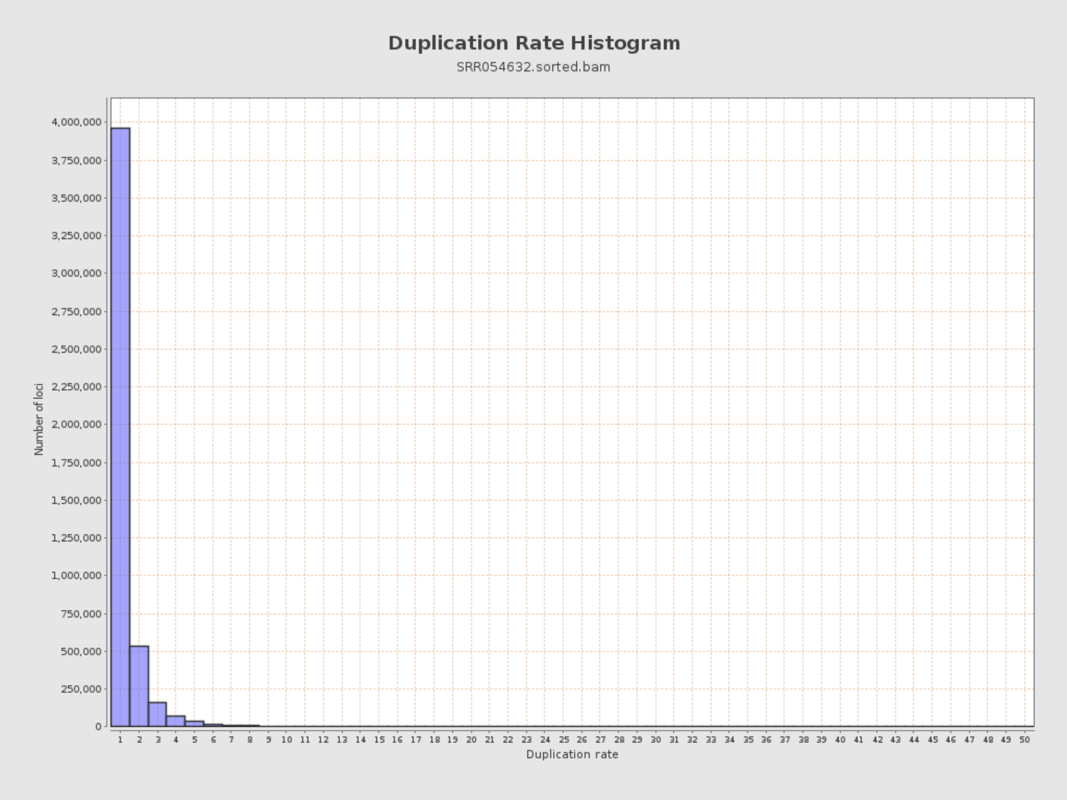
5. Results : Coverage Histogram (0-50X)



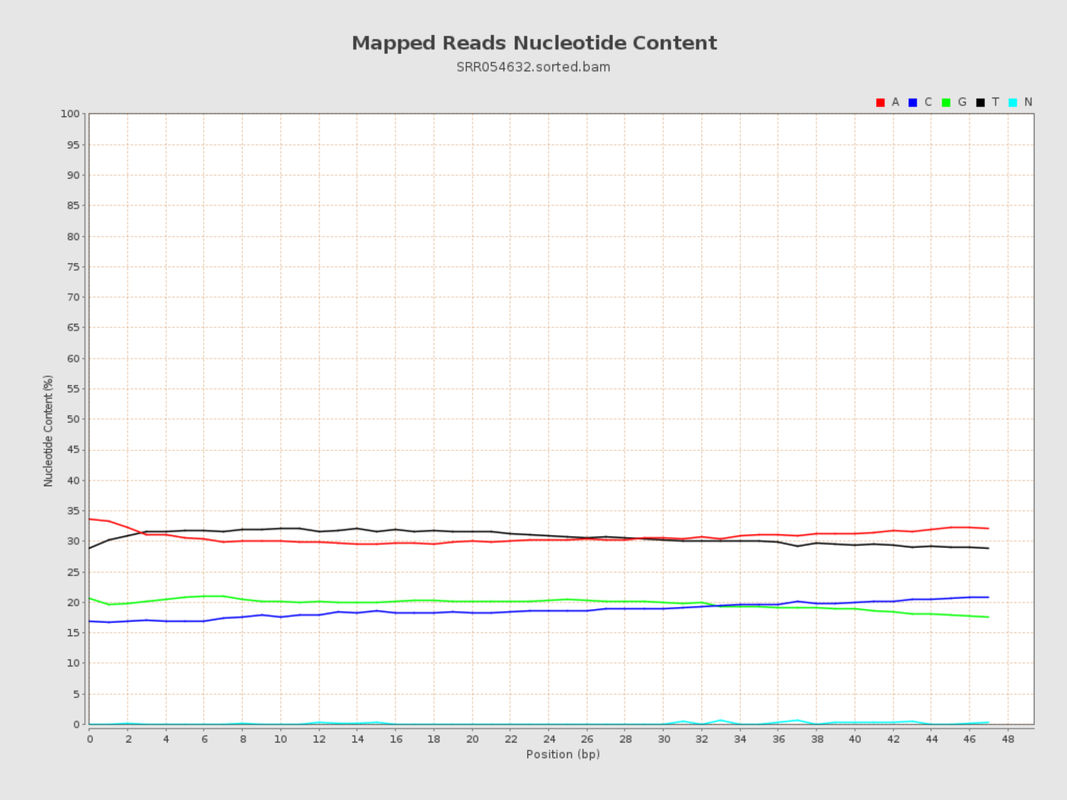
6. Results : Genome Fraction Coverage



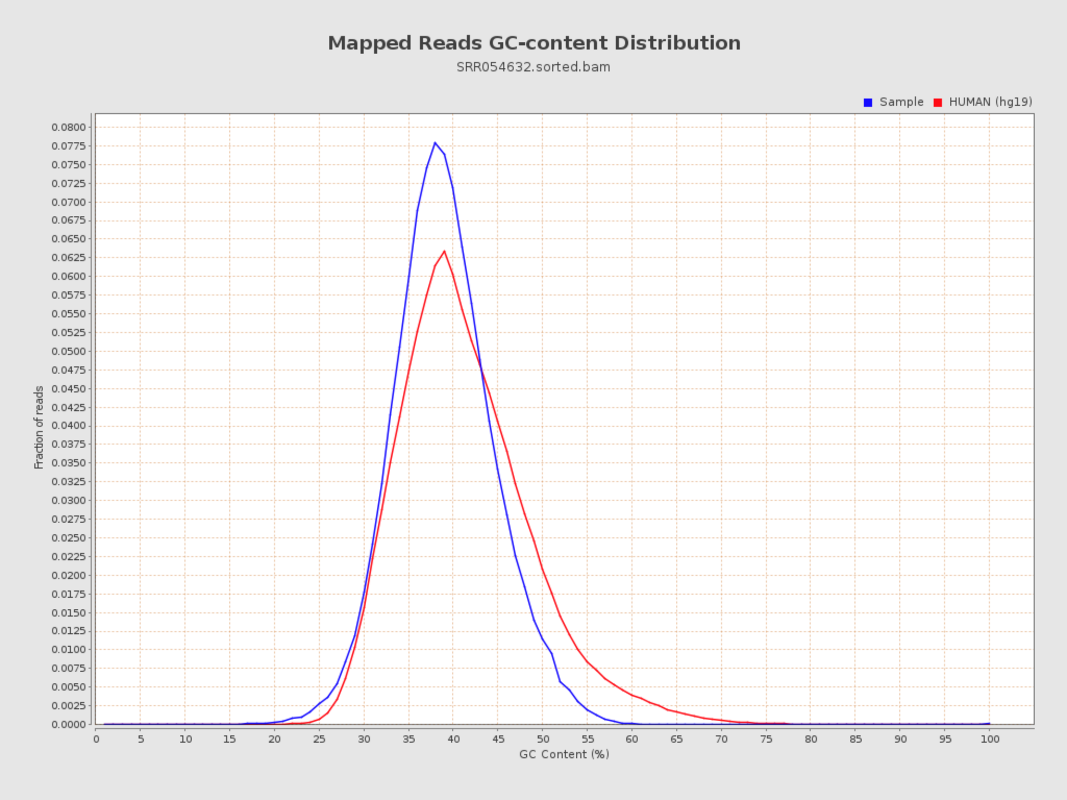
7. Results : Duplication Rate Histogram



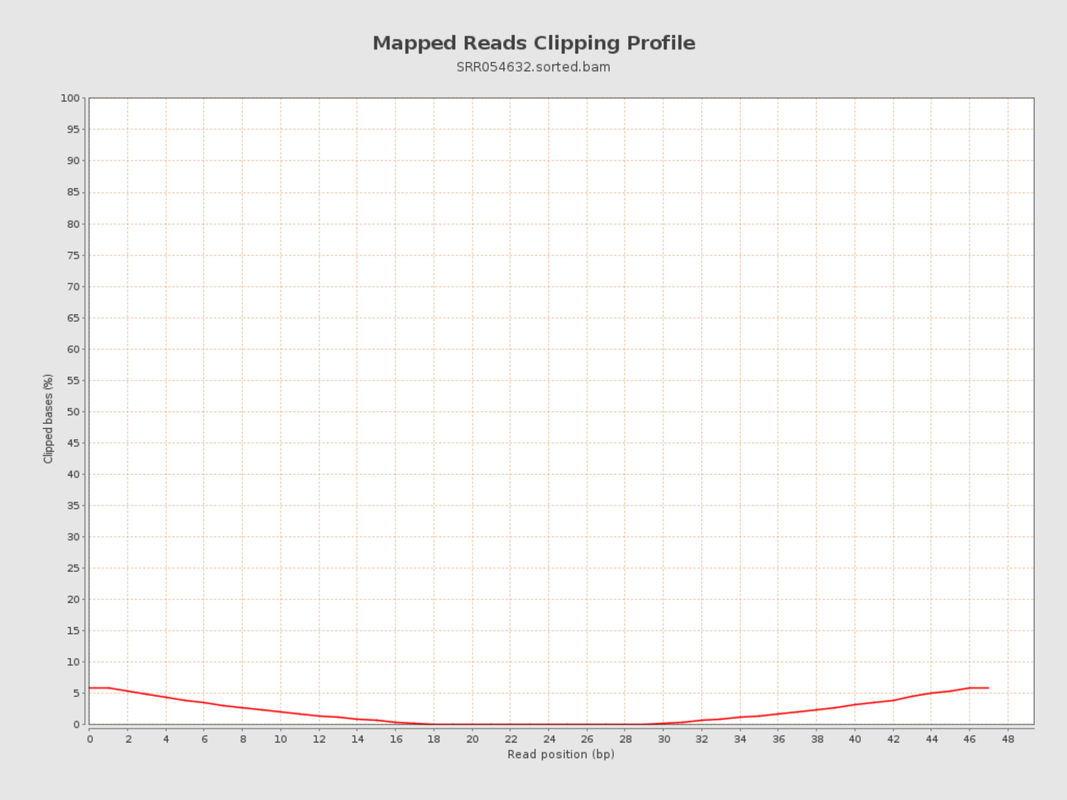
8. Results : Mapped Reads Nucleotide Content



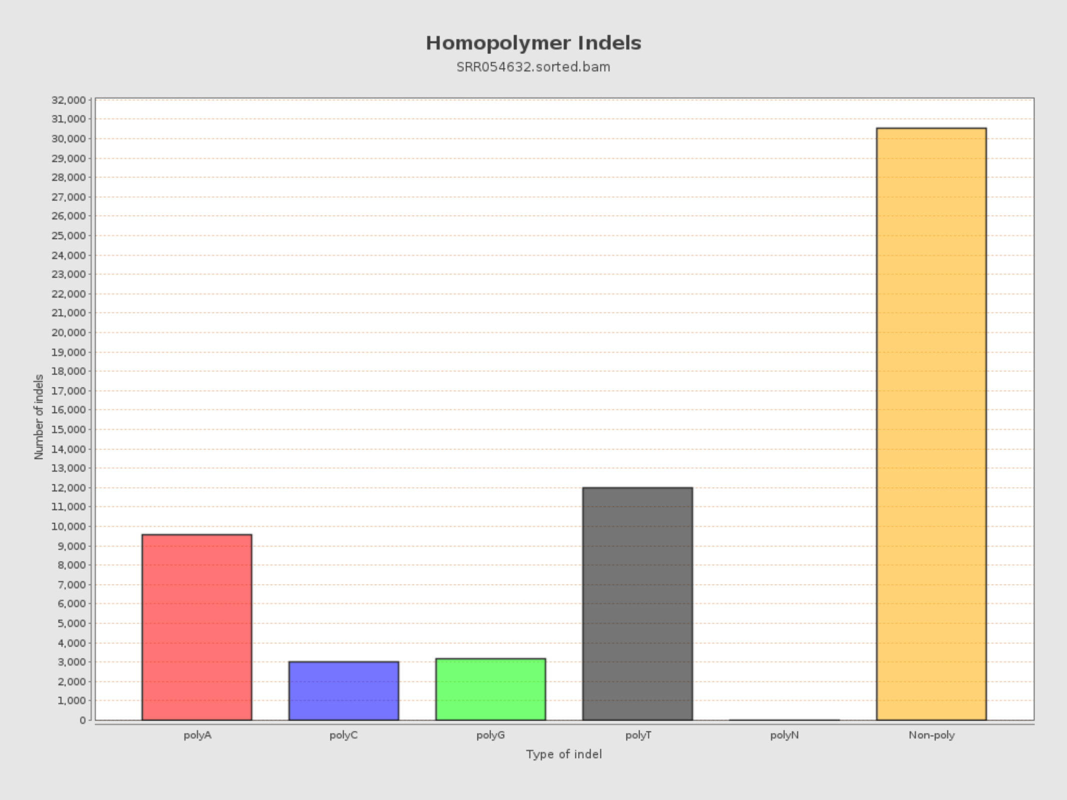
9. Results : Mapped Reads GC-content Distribution



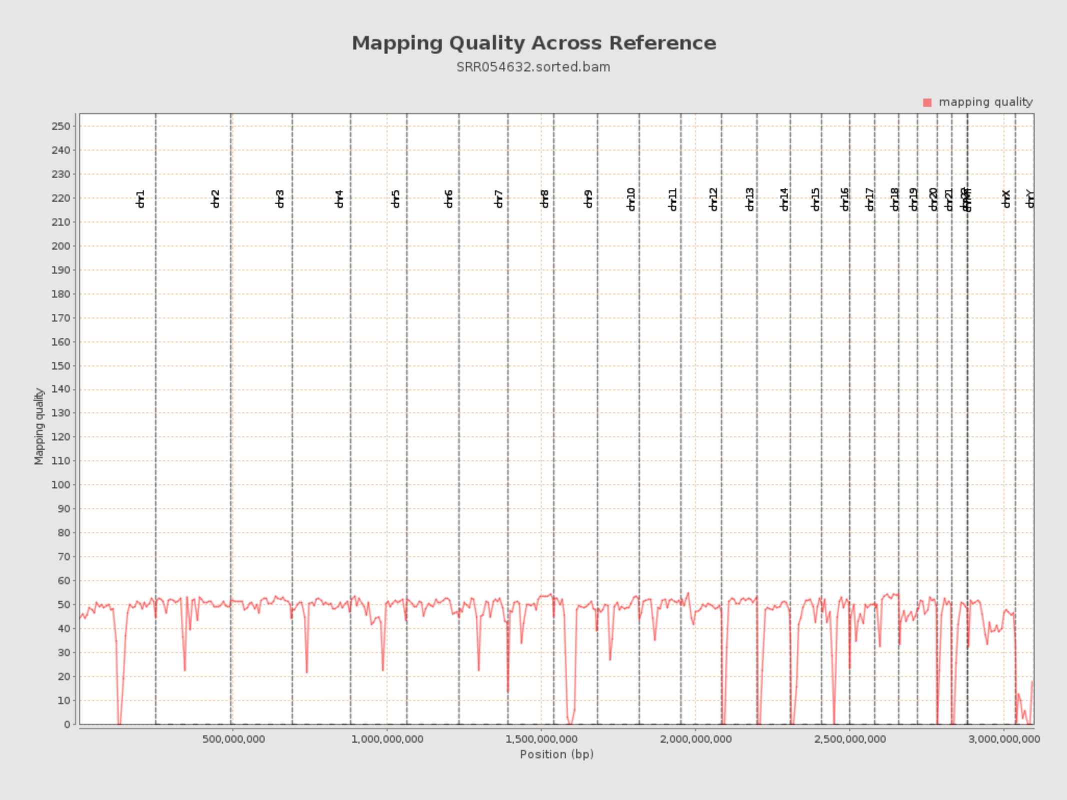
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram