Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 21:01:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536752.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_SRR536752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 21:01:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,174,906
Mapped reads	22,374,858 / 96.55%
Unmapped reads	800,048 / 3.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	551 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	190,513 / 0.82%
Duplication rate	0.84%
Clipped reads	349,673 / 1.51%

2.2. ACGT Content

Number/percentage of A's	344,239,758 / 30.85%
Number/percentage of C's	211,656,902 / 18.97%
Number/percentage of T's	343,980,386 / 30.83%
Number/percentage of G's	215,518,430 / 19.32%
Number/percentage of N's	380,408 / 0.03%
GC Percentage	38.29%

2.3. Coverage

Mean	0.3605

Standard Deviation	0.6659

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

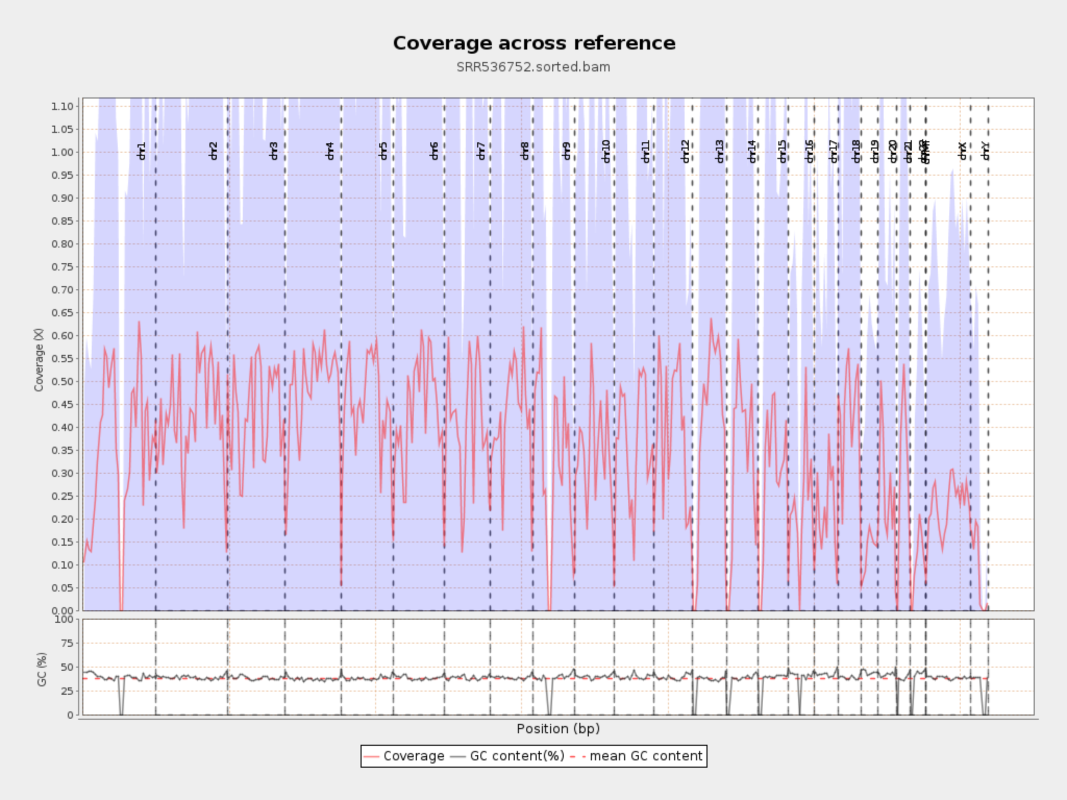
General error rate	0.34%
Mismatches	3,705,587
Insertions	58,876
Mapped reads with at least one insertion	0.26%
Deletions	56,359
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.17%

2.6. Chromosome stats

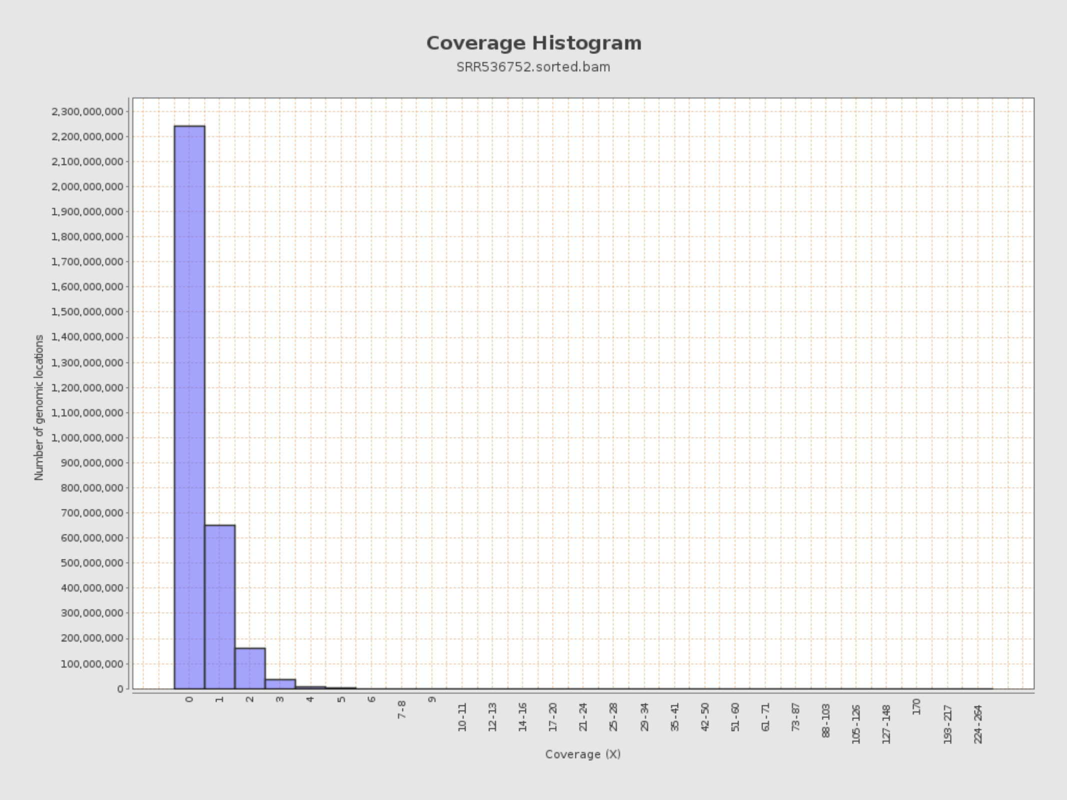
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	85566630	0.3433	0.6612
chr2	243199373	103395444	0.4251	0.7095
chr3	198022430	86378698	0.4362	0.7141
chr4	191154276	92953624	0.4863	0.7523
chr5	180915260	80149747	0.443	0.721
chr6	171115067	75851358	0.4433	0.7241
chr7	159138663	64017348	0.4023	0.6994

chr8	146364022	62397298	0.4263	0.7088
chr9	141213431	46408835	0.3286	0.6434
chr10	135534747	47612910	0.3513	0.6435
chr11	135006516	49786621	0.3688	0.6733
chr12	133851895	51552045	0.3851	0.6861
chr13	115169878	47089114	0.4089	0.7111
chr14	107349540	35629291	0.3319	0.647
chr15	102531392	29949751	0.2921	0.6095
chr16	90354753	20078042	0.2222	0.5233
chr17	81195210	17685329	0.2178	0.5222
chr18	78077248	33810957	0.433	0.7159
chr19	59128983	7775291	0.1315	0.3941
chr20	63025520	17011222	0.2699	0.5784
chr21	48129895	14288123	0.2969	0.6314
chr22	51304566	5618942	0.1095	0.366
chrMT	16571	979	0.0591	0.2554
chrX	155270560	35778938	0.2304	0.5054
chrY	59373566	5082832	0.0856	0.3274

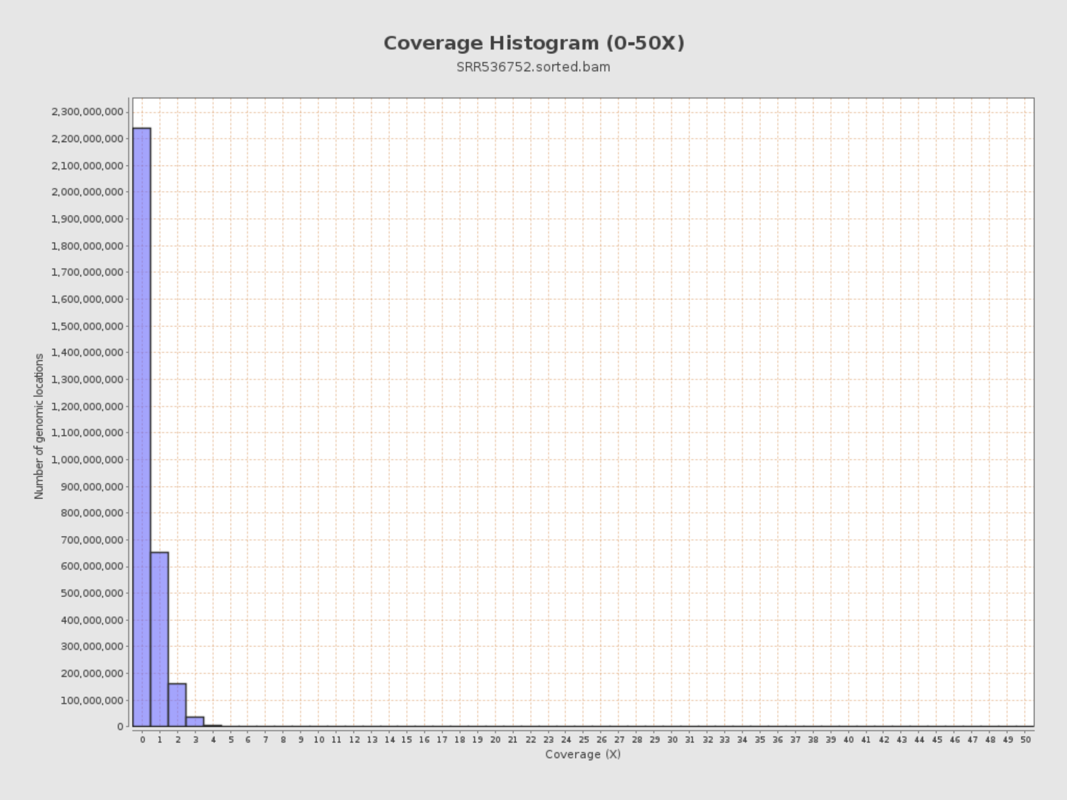
3. Results : Coverage across reference



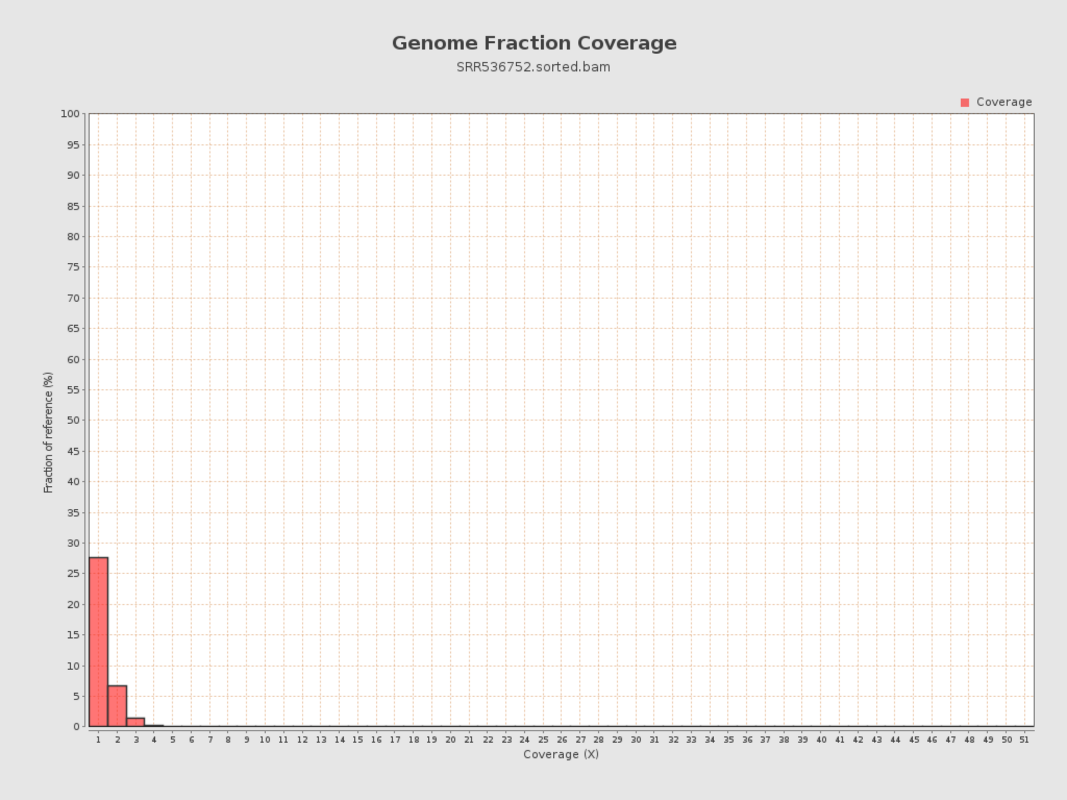
4. Results : Coverage Histogram



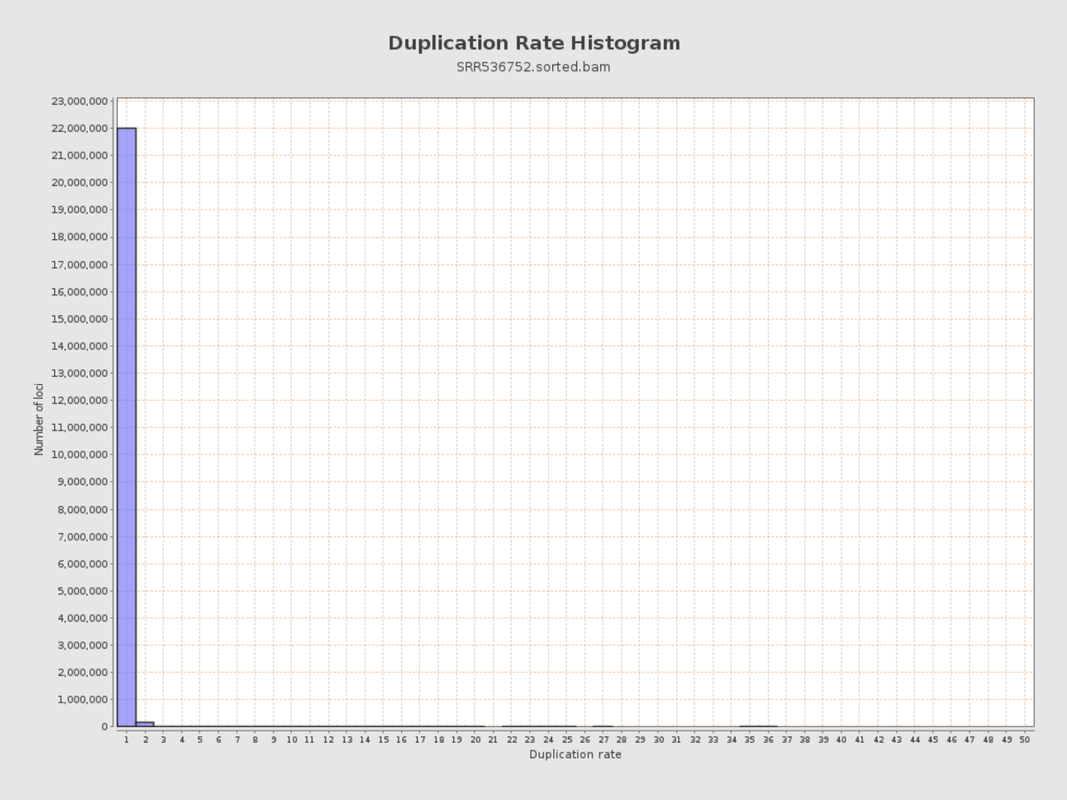
5. Results : Coverage Histogram (0-50X)



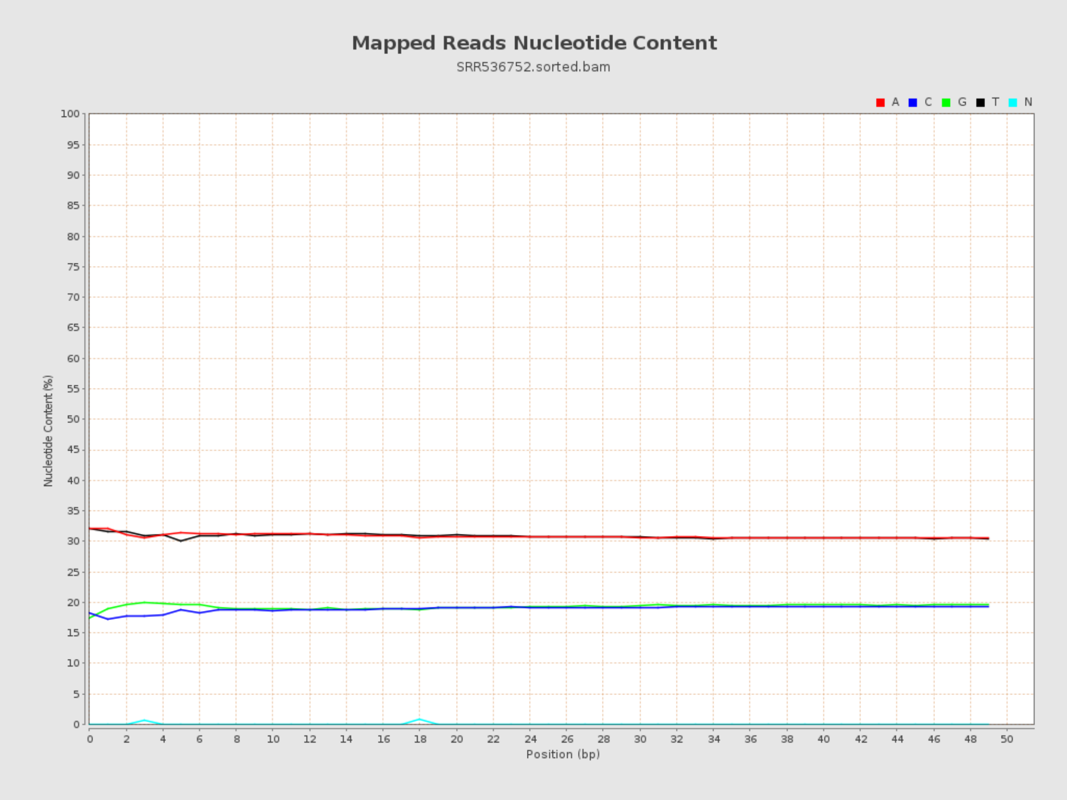
6. Results : Genome Fraction Coverage



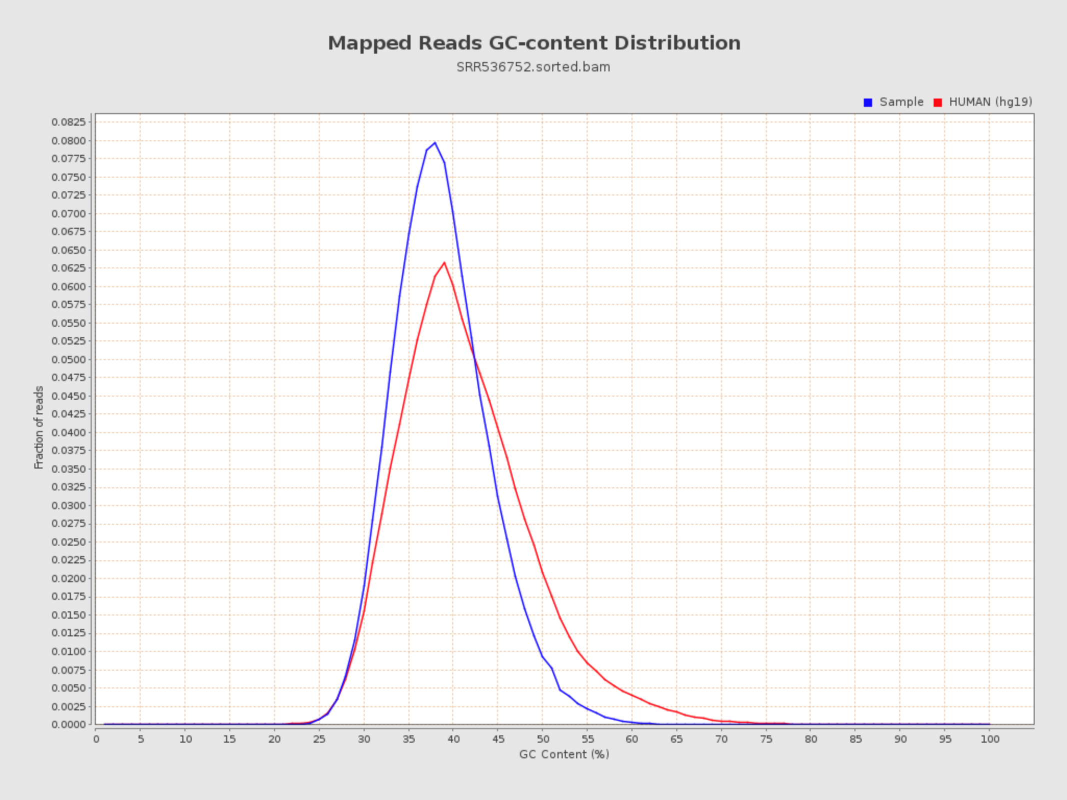
7. Results : Duplication Rate Histogram



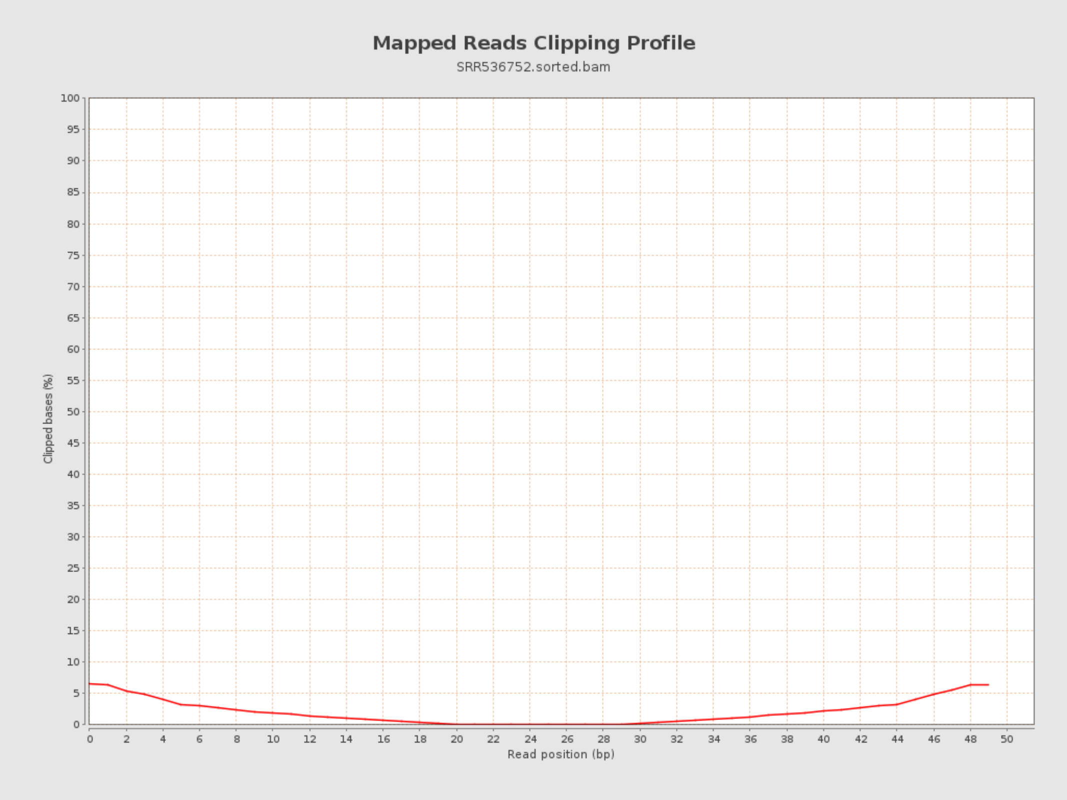
8. Results : Mapped Reads Nucleotide Content



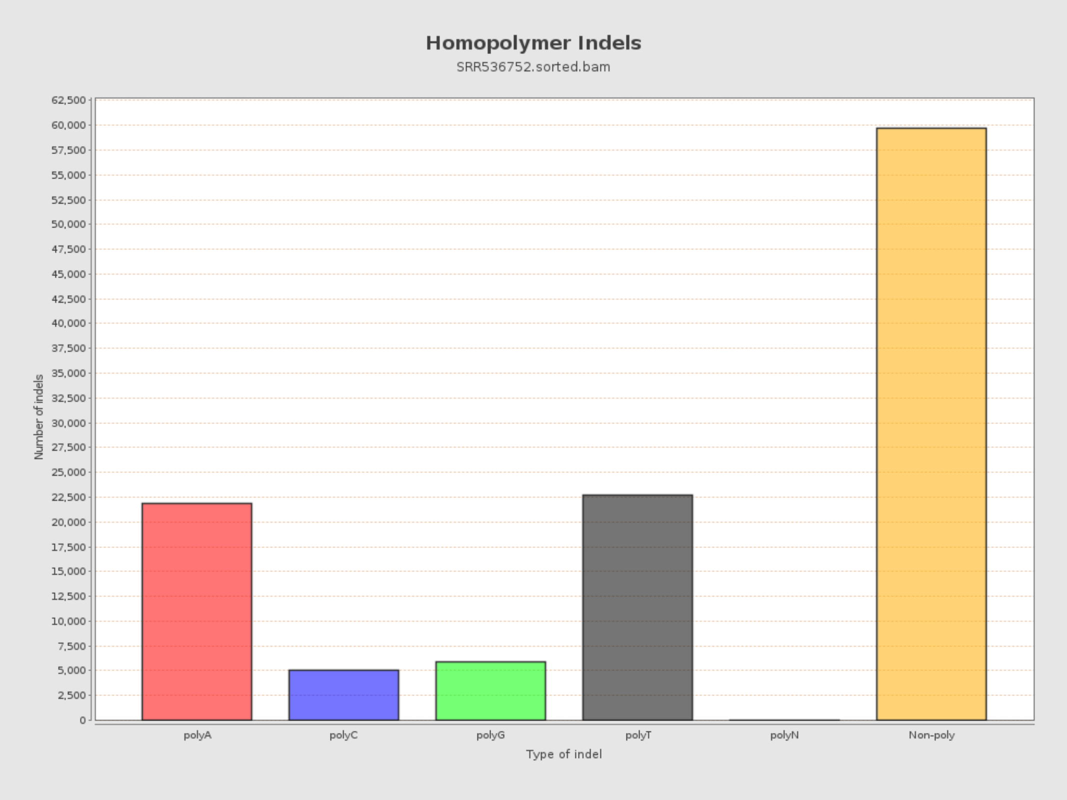
9. Results : Mapped Reads GC-content Distribution



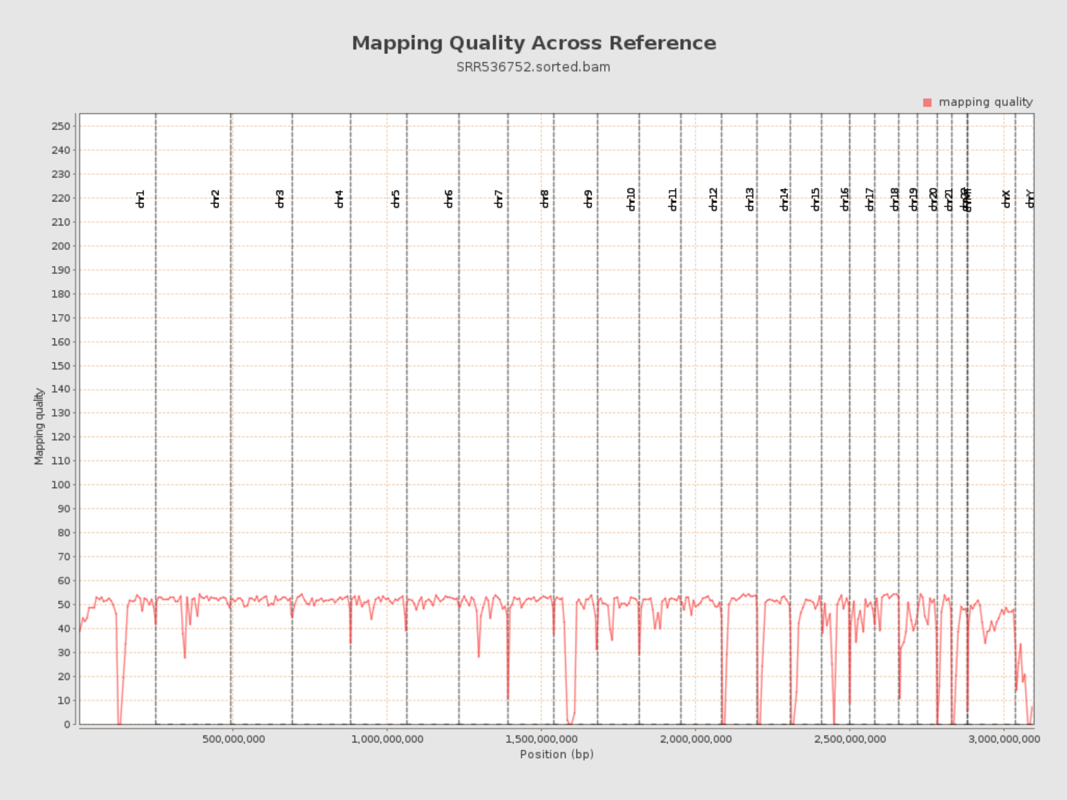
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram