Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:56:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013353.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_SRR6013353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:56:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,444,475
Mapped reads	3,102,506 / 90.07%
Unmapped reads	341,969 / 9.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,061 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	115,534 / 3.35%
Duplication rate	2.62%
Clipped reads	1,607,118 / 46.66%

2.2. ACGT Content

Number/percentage of A's	55,211,355 / 27.39%
Number/percentage of C's	38,973,280 / 19.33%
Number/percentage of T's	61,029,511 / 30.27%
Number/percentage of G's	46,338,043 / 22.99%
Number/percentage of N's	44,483 / 0.02%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0652

Standard Deviation	0.546

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Mismatches and indels

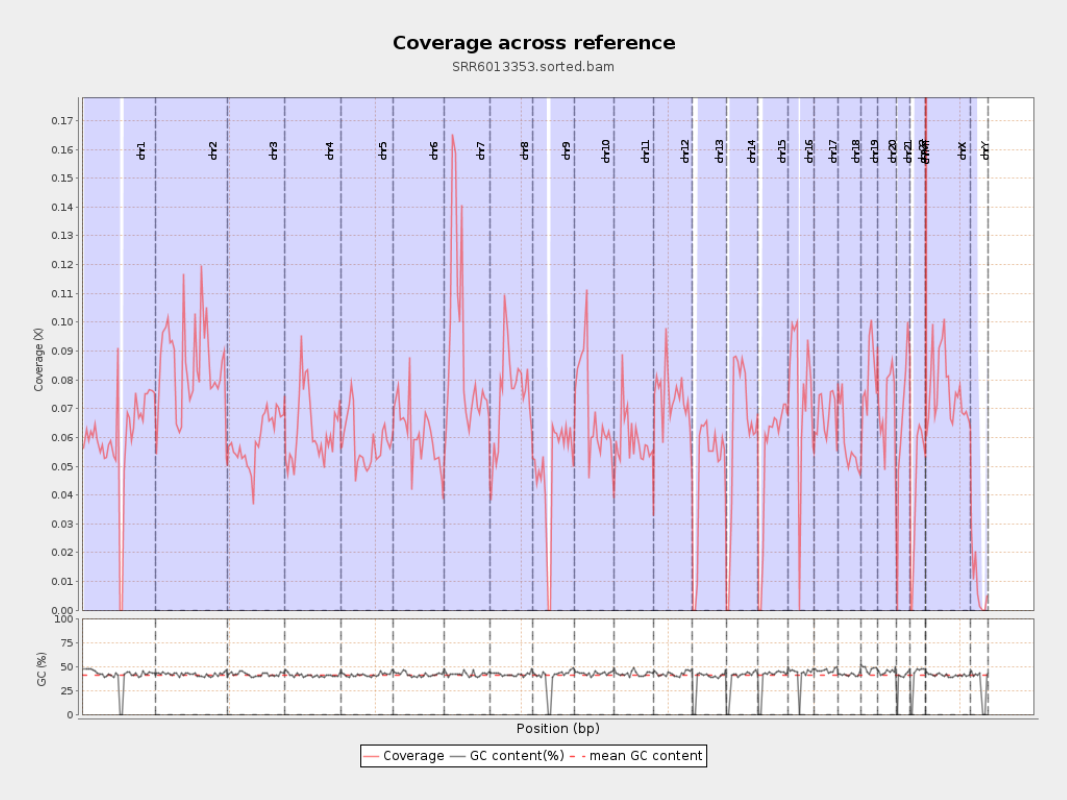
General error rate	0.83%
Mismatches	1,650,381
Insertions	14,340
Mapped reads with at least one insertion	0.46%
Deletions	51,639
Mapped reads with at least one deletion	1.65%
Homopolymer indels	44.23%

2.6. Chromosome stats

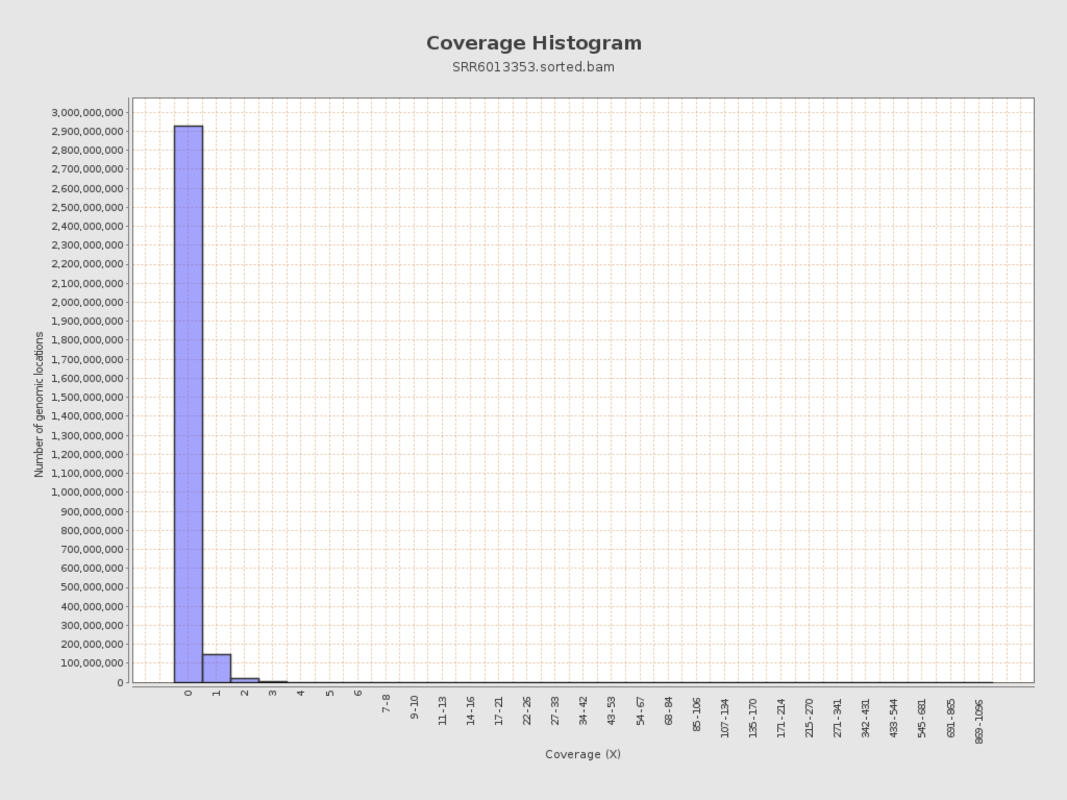
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14942733	0.06	0.9211
chr2	243199373	20700176	0.0851	0.6765
chr3	198022430	11723952	0.0592	0.2782
chr4	191154276	12043847	0.063	0.3043
chr5	180915260	10496338	0.058	0.2786
chr6	171115067	10499137	0.0614	0.3981
chr7	159138663	13939012	0.0876	1.1241

chr8	146364022	10928858	0.0747	0.4646
chr9	141213431	6958358	0.0493	0.4088
chr10	135534747	9383314	0.0692	0.5397
chr11	135006516	7968216	0.059	0.3772
chr12	133851895	9911988	0.0741	0.3187
chr13	115169878	5584002	0.0485	0.2582
chr14	107349540	6767640	0.063	0.3271
chr15	102531392	5380243	0.0525	0.2637
chr16	90354753	6707042	0.0742	0.3622
chr17	81195210	5518921	0.068	0.3415
chr18	78077248	4549616	0.0583	0.7739
chr19	59128983	4813934	0.0814	0.7187
chr20	63025520	4466385	0.0709	0.3113
chr21	48129895	3246821	0.0675	0.3215
chr22	51304566	2177088	0.0424	0.234
chrMT	16571	661794	39.9369	24.7596
chrX	155270560	11831019	0.0762	0.3602
chrY	59373566	485131	0.0082	0.1562

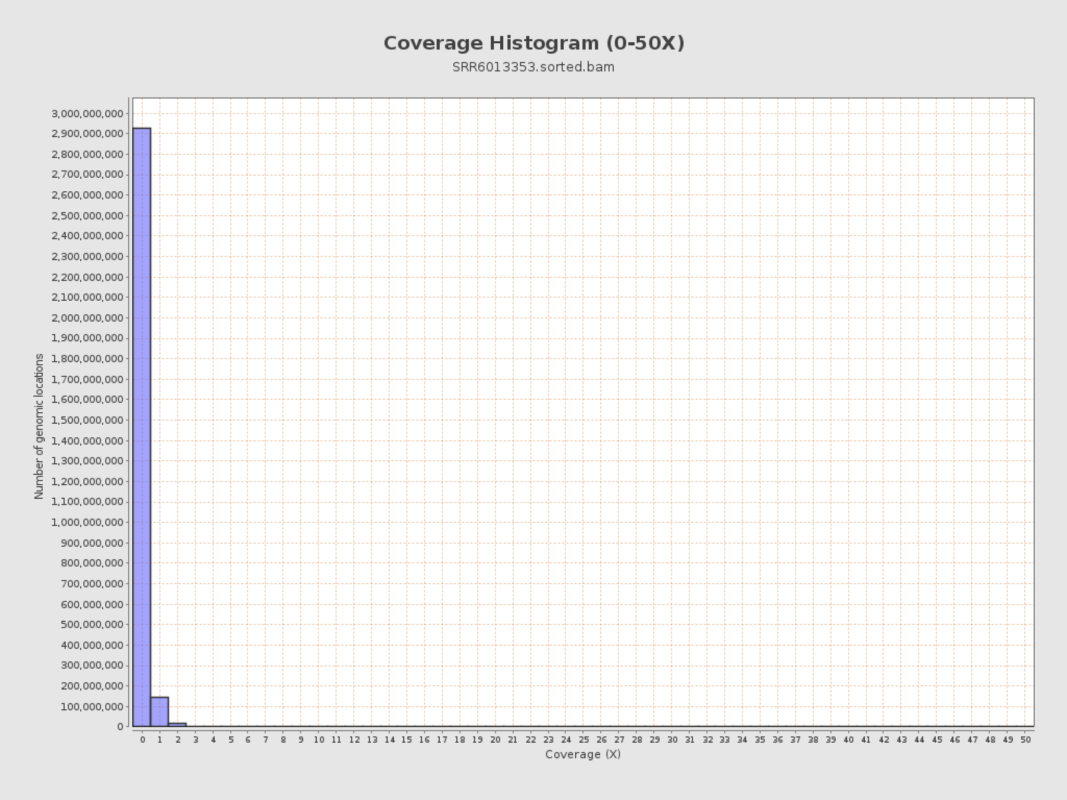
3. Results : Coverage across reference



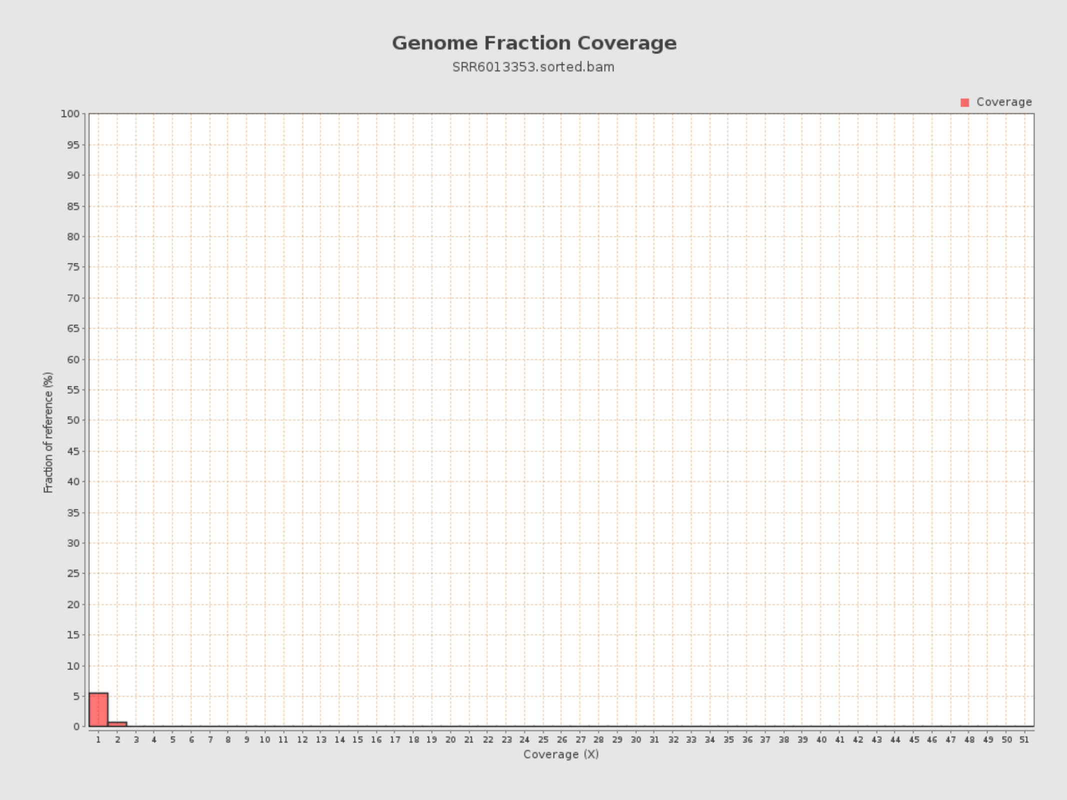
4. Results : Coverage Histogram



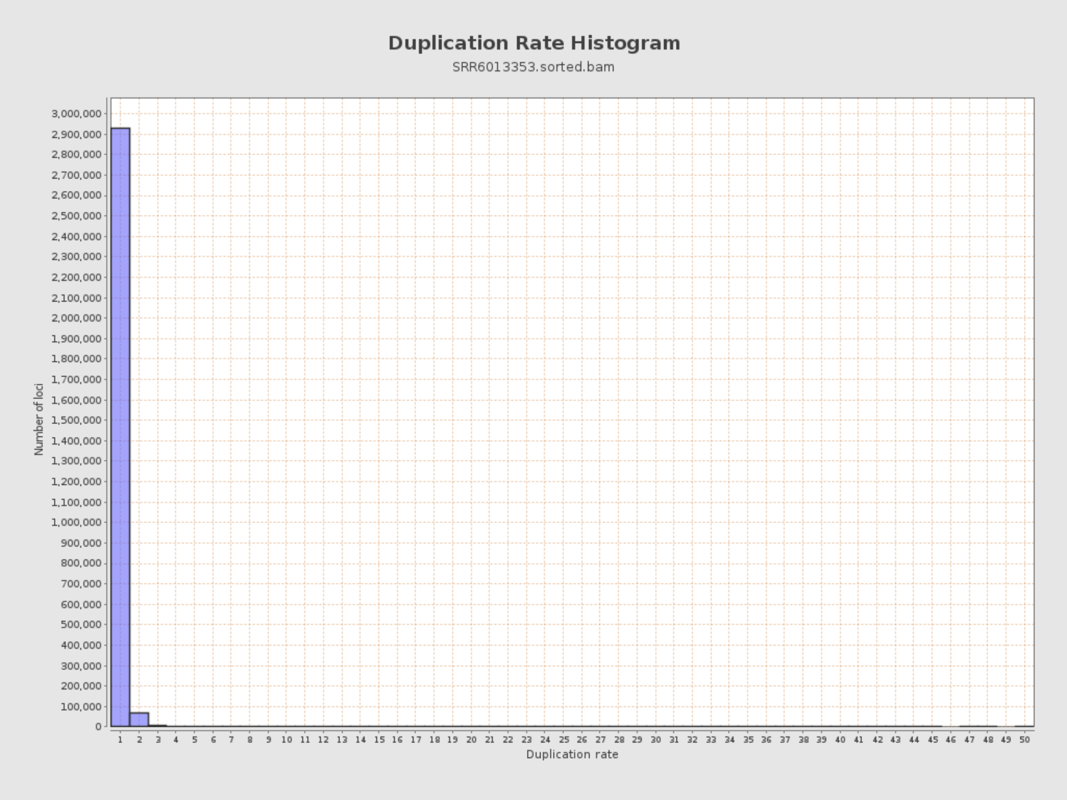
5. Results : Coverage Histogram (0-50X)



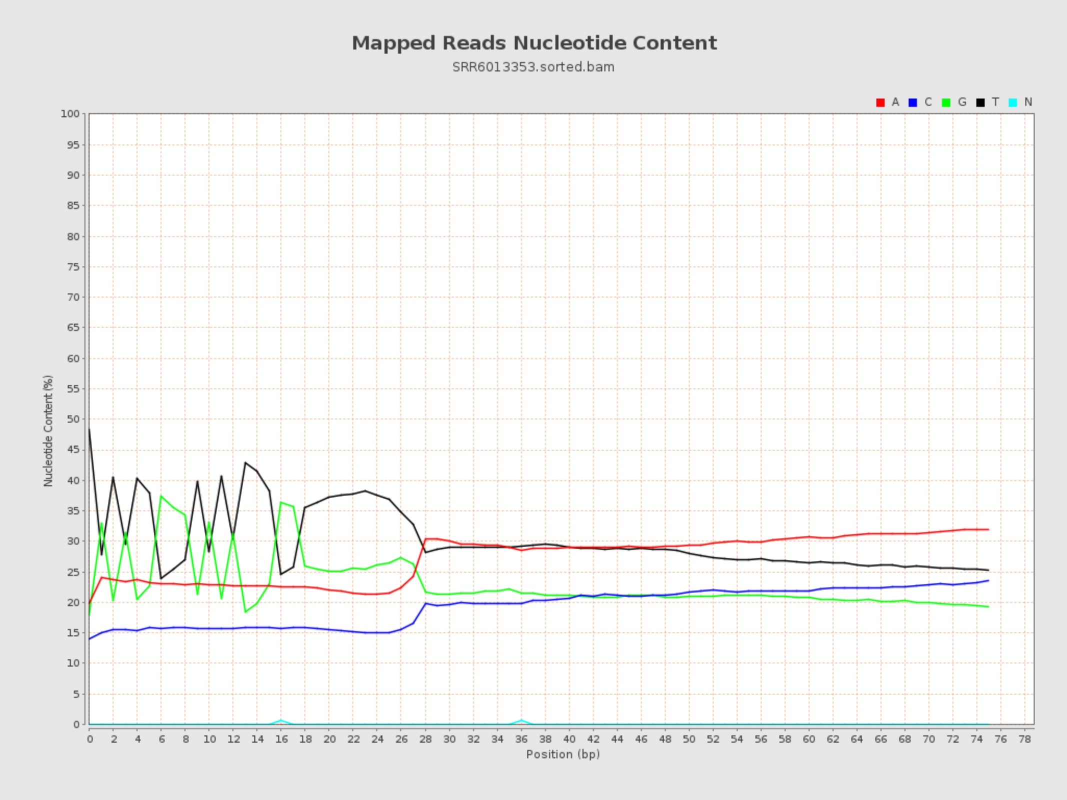
6. Results : Genome Fraction Coverage



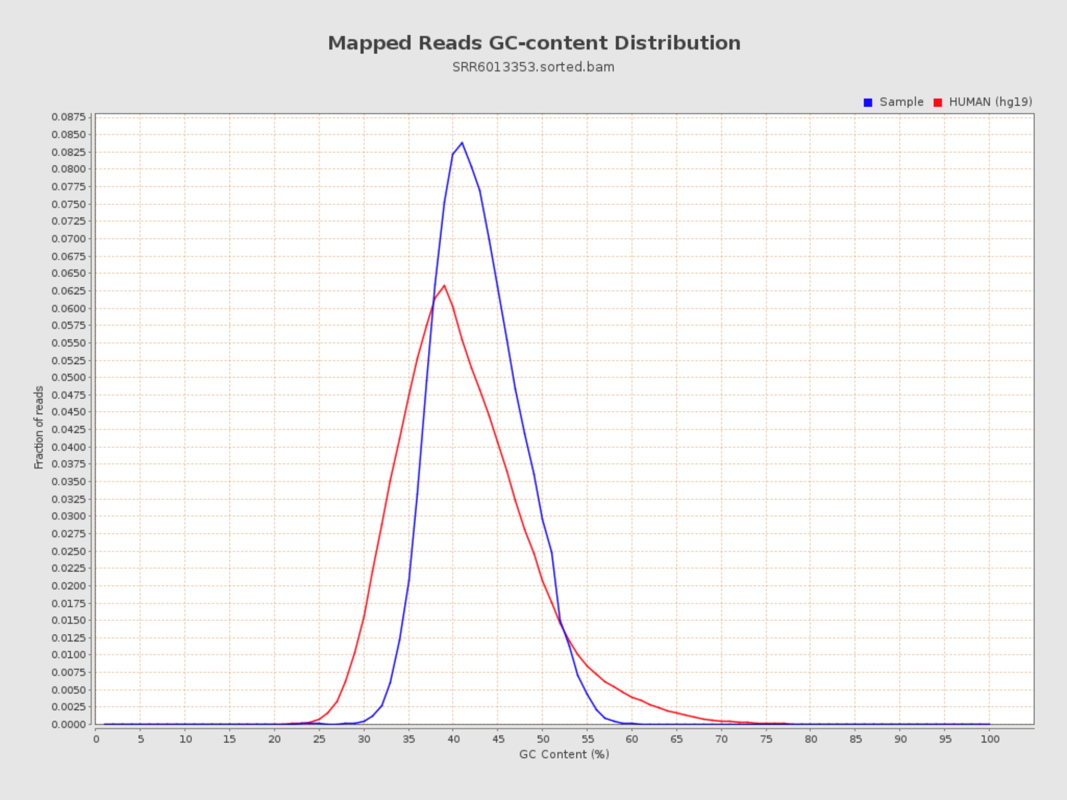
7. Results : Duplication Rate Histogram



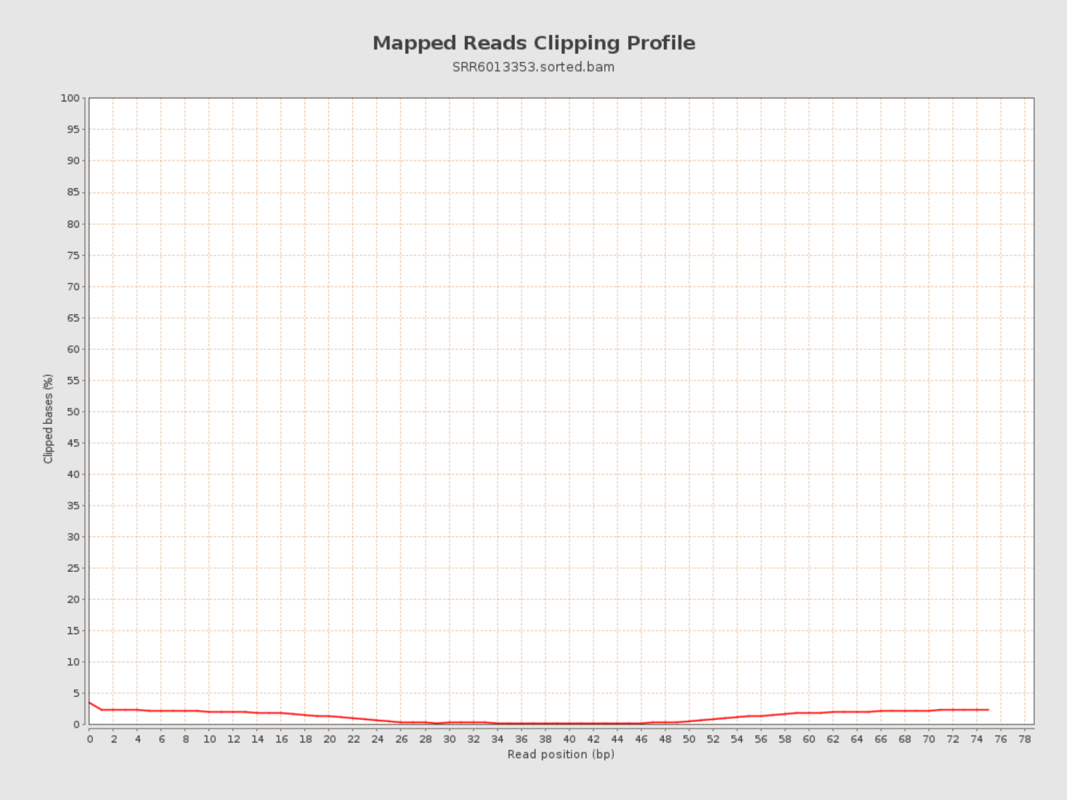
8. Results : Mapped Reads Nucleotide Content



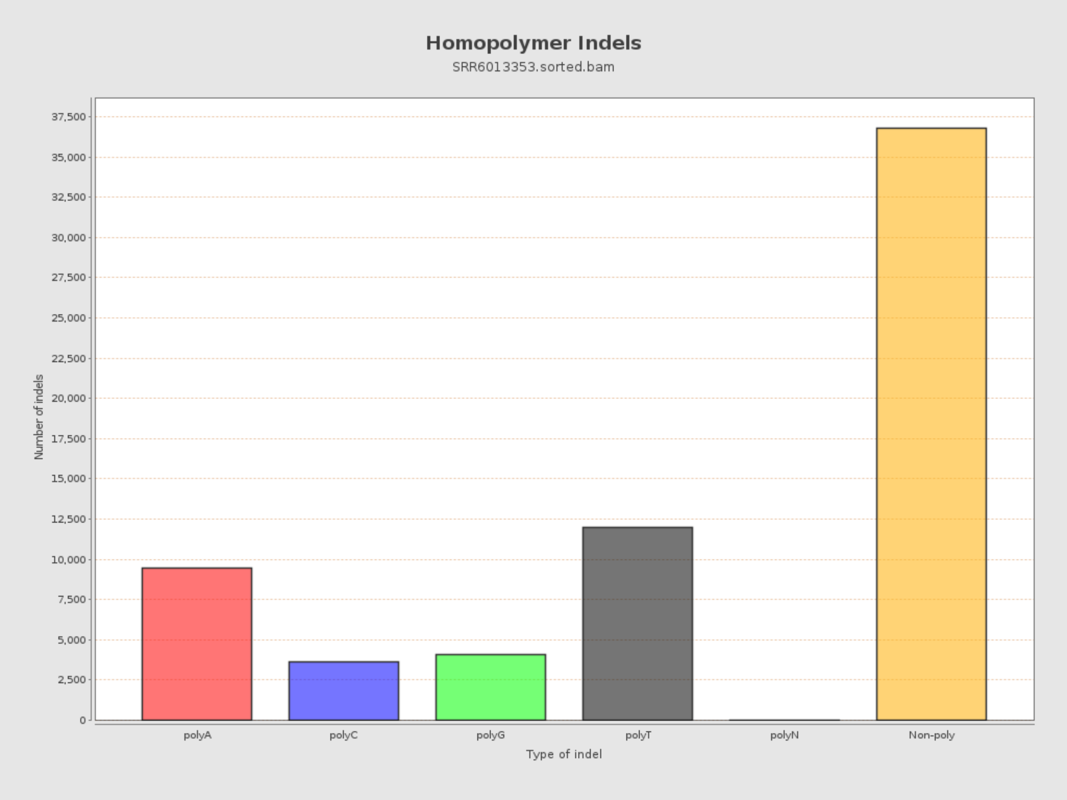
9. Results : Mapped Reads GC-content Distribution



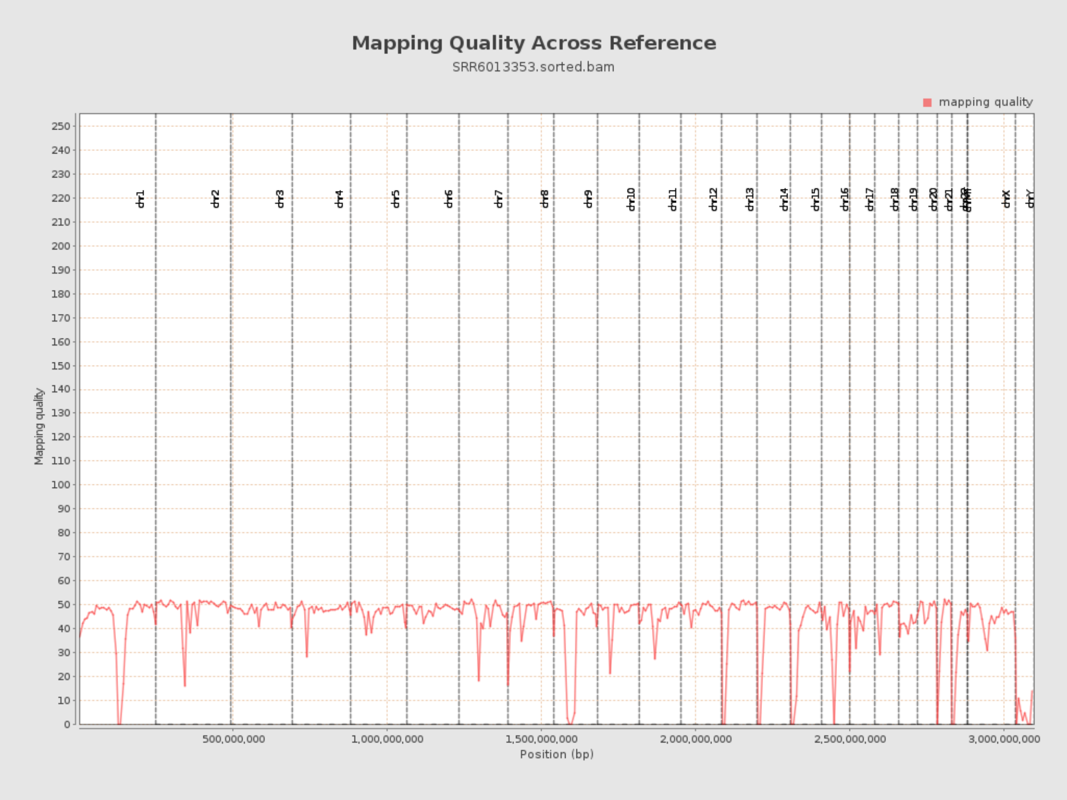
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram