Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:29:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549017.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_SRR1549017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,313,285
Mapped reads	8,103,695 / 87.01%
Unmapped reads	1,209,590 / 12.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	416,822 / 4.48%
Duplication rate	4.12%
Clipped reads	640,534 / 6.88%

2.2. ACGT Content

Number/percentage of A's	93,518,132 / 29.17%
Number/percentage of C's	66,126,127 / 20.62%
Number/percentage of T's	94,484,992 / 29.47%
Number/percentage of G's	66,470,864 / 20.73%
Number/percentage of N's	11,826 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.1036
Standard Deviation	1.2665

2.4. Mapping Quality

Mean Mapping Quality	43.48

2.5. Mismatches and indels

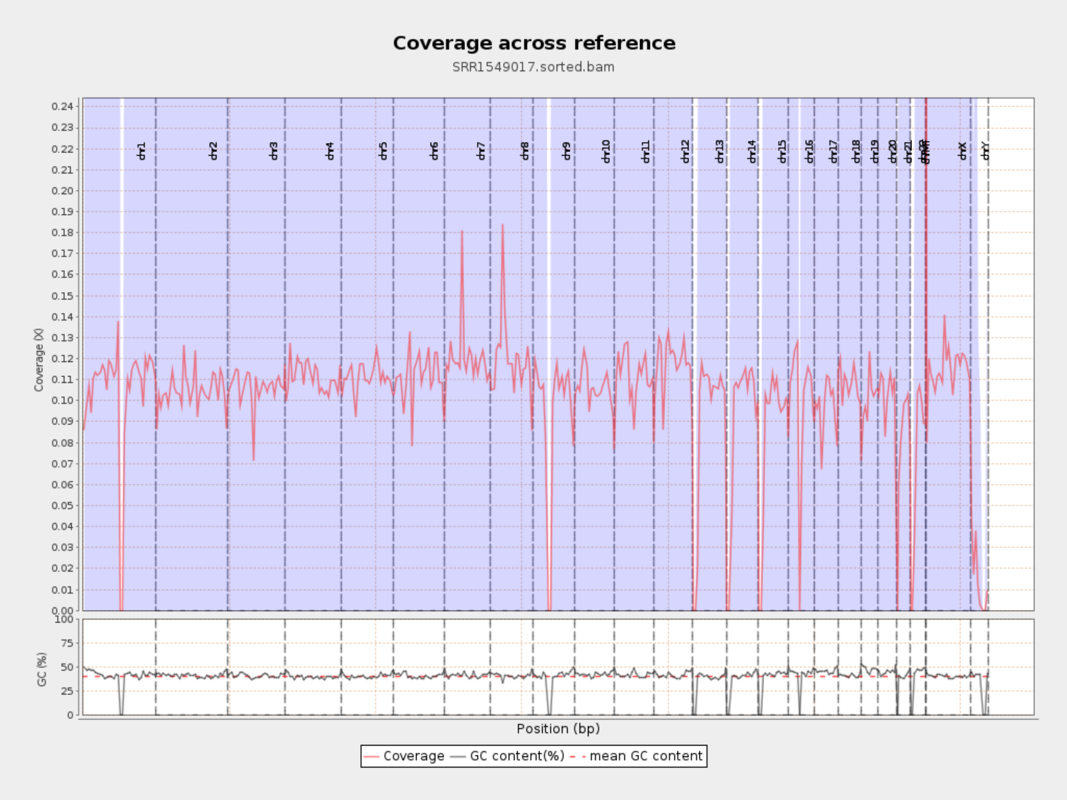
General error rate	0.25%
Mismatches	791,975
Insertions	10,628
Mapped reads with at least one insertion	0.13%
Deletions	26,098
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.1%

2.6. Chromosome stats

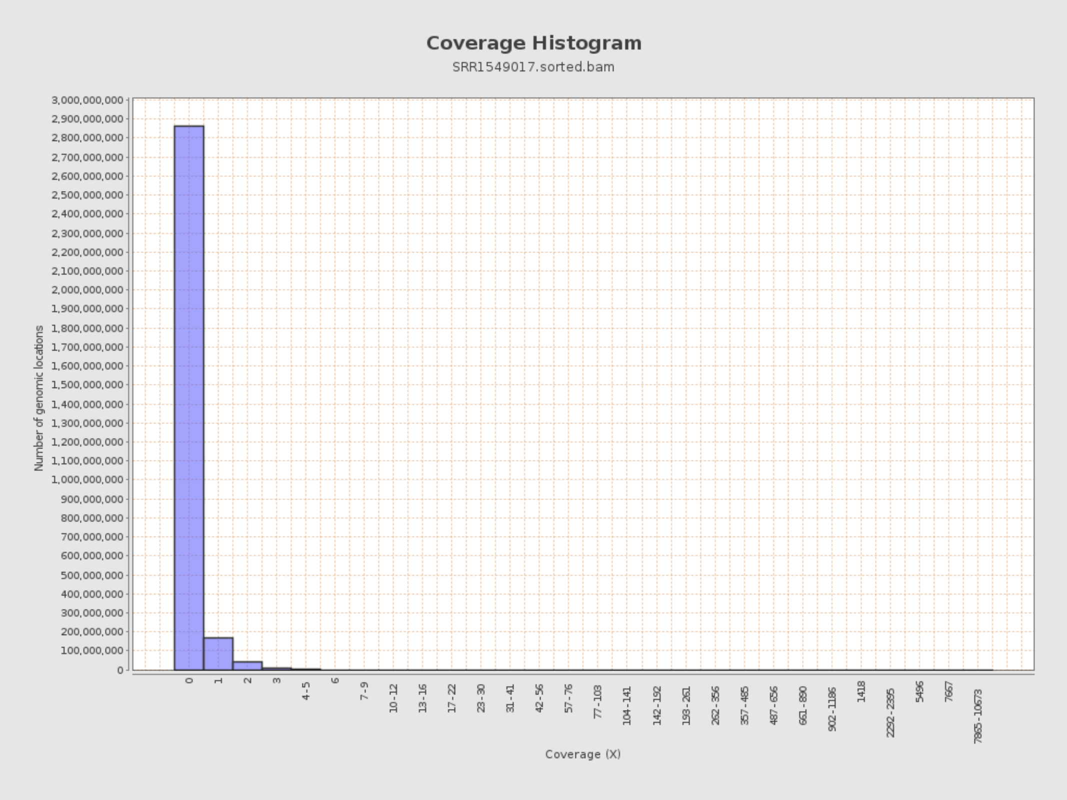
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25986113	0.1043	1.0032
chr2	243199373	25551632	0.1051	0.5548
chr3	198022430	21028728	0.1062	0.4283
chr4	191154276	21237391	0.1111	0.4512
chr5	180915260	20011524	0.1106	0.4416
chr6	171115067	19154221	0.1119	0.4825
chr7	159138663	19106055	0.1201	0.9716
chr8	146364022	17598095	0.1202	5.1637

chr9	141213431	13263096	0.0939	0.5203
chr10	135534747	14471196	0.1068	0.5217
chr11	135006516	15067182	0.1116	0.7318
chr12	133851895	15862677	0.1185	0.4637
chr13	115169878	10386071	0.0902	0.3916
chr14	107349540	9692136	0.0903	0.4311
chr15	102531392	8523121	0.0831	0.3761
chr16	90354753	8811021	0.0975	0.4269
chr17	81195210	7935149	0.0977	0.4485
chr18	78077248	8484267	0.1087	0.8412
chr19	59128983	5976606	0.1011	0.8691
chr20	63025520	6478485	0.1028	0.433
chr21	48129895	3810807	0.0792	0.4009
chr22	51304566	3517212	0.0686	0.4656
chrMT	16571	17236	1.0401	1.5238
chrX	155270560	17838508	0.1149	0.517
chrY	59373566	837682	0.0141	0.1999

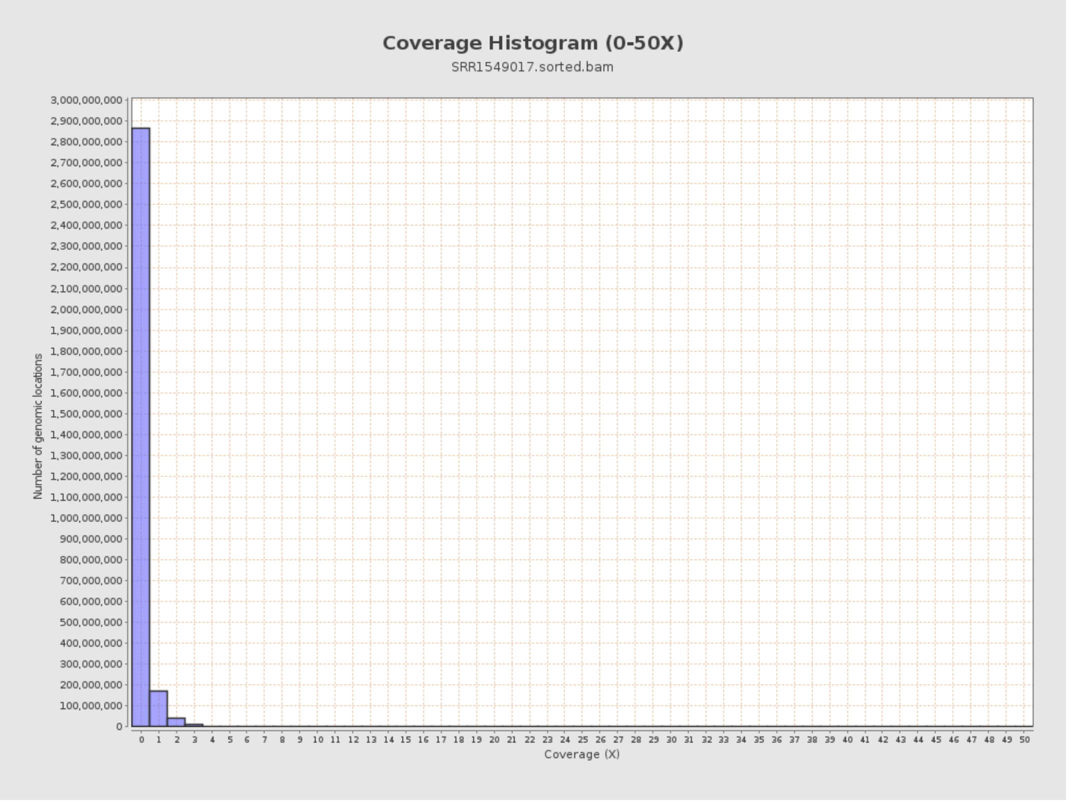
3. Results : Coverage across reference



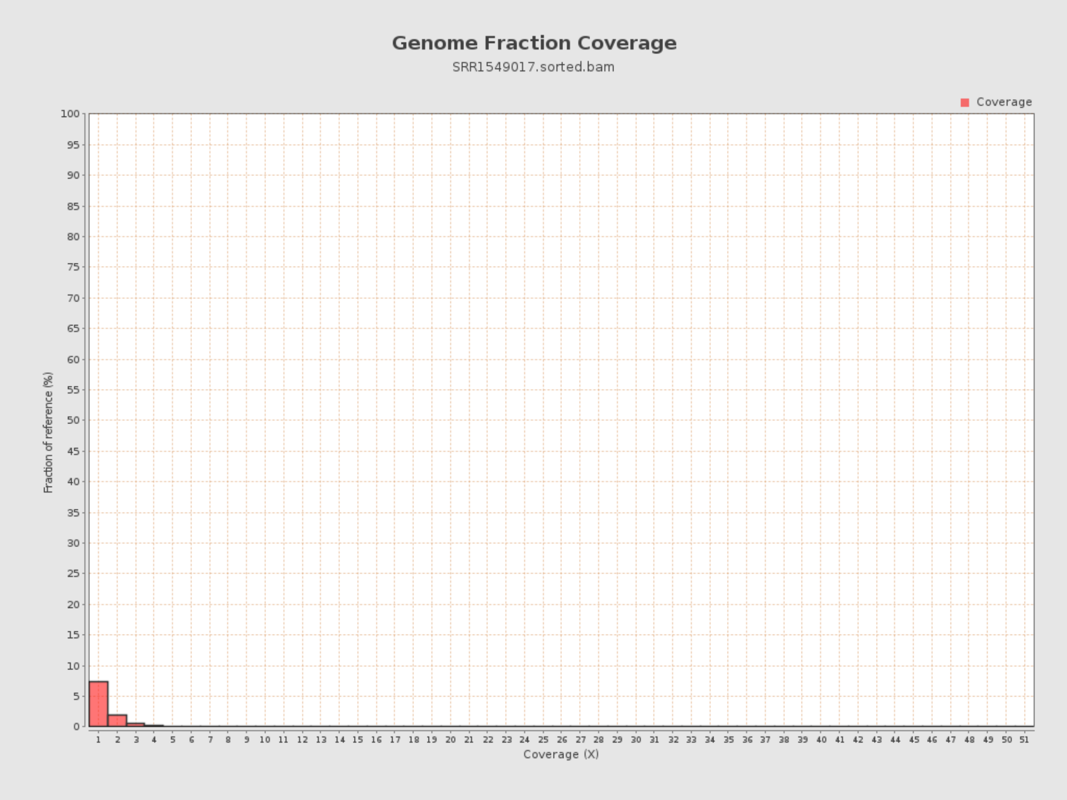
4. Results : Coverage Histogram



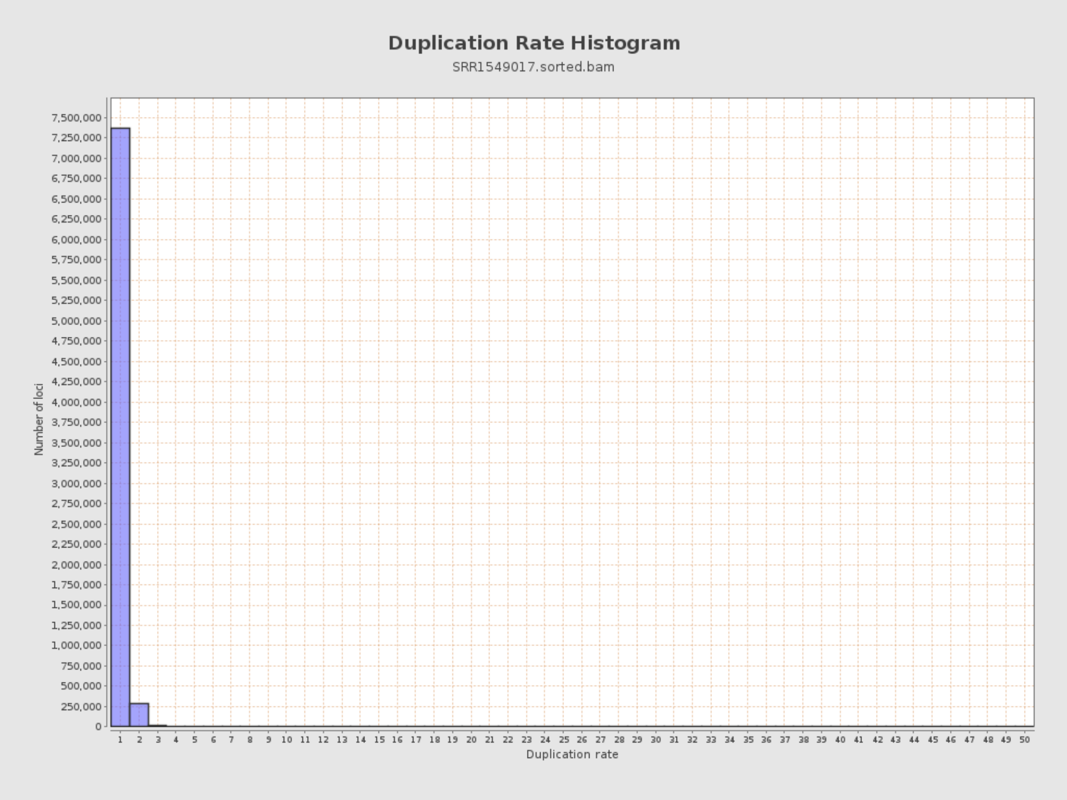
5. Results : Coverage Histogram (0-50X)



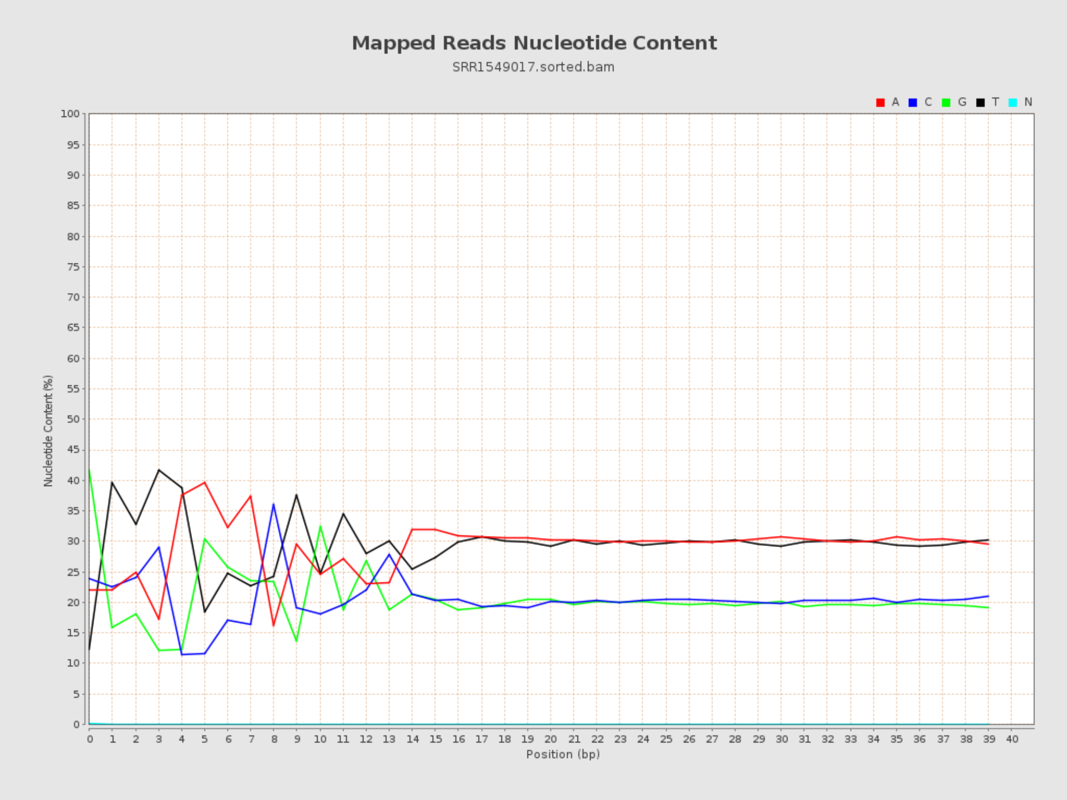
6. Results : Genome Fraction Coverage



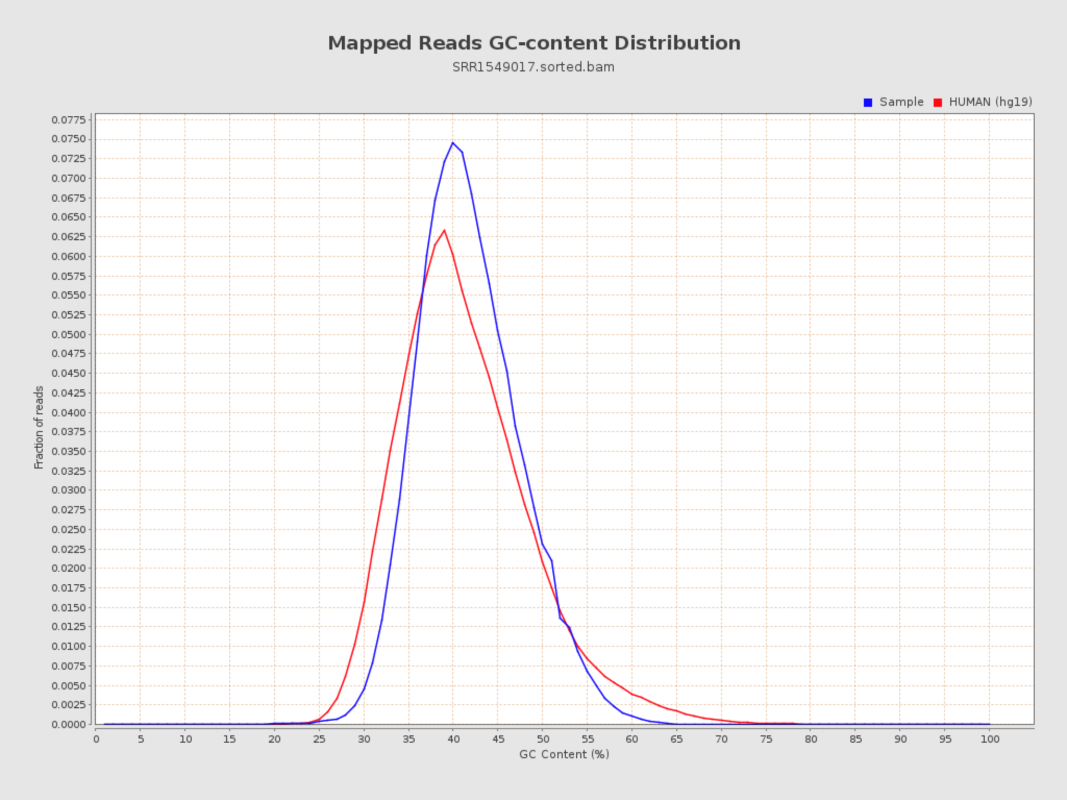
7. Results : Duplication Rate Histogram



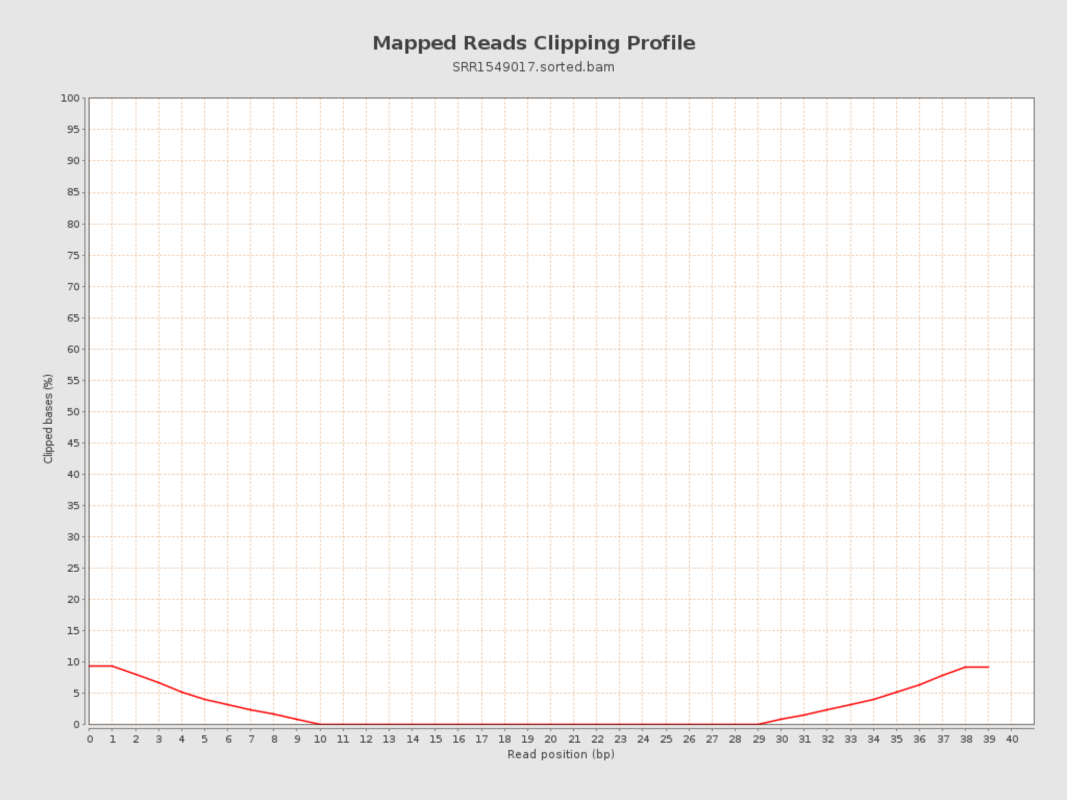
8. Results : Mapped Reads Nucleotide Content



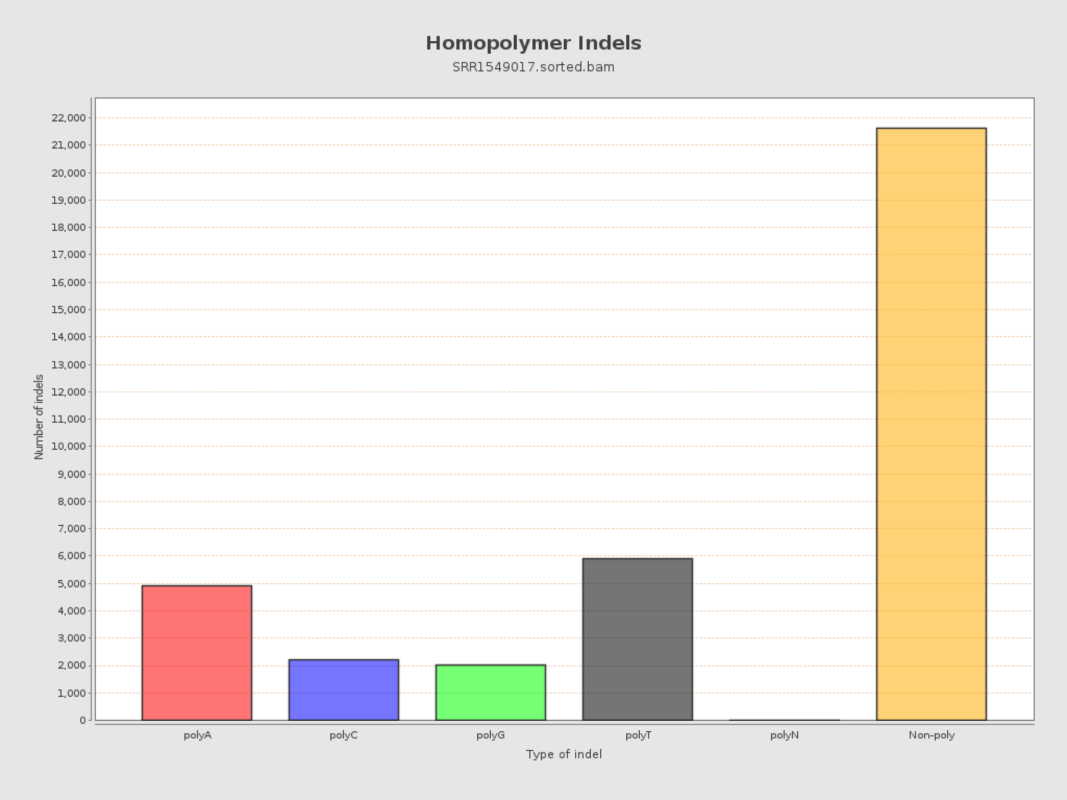
9. Results : Mapped Reads GC-content Distribution



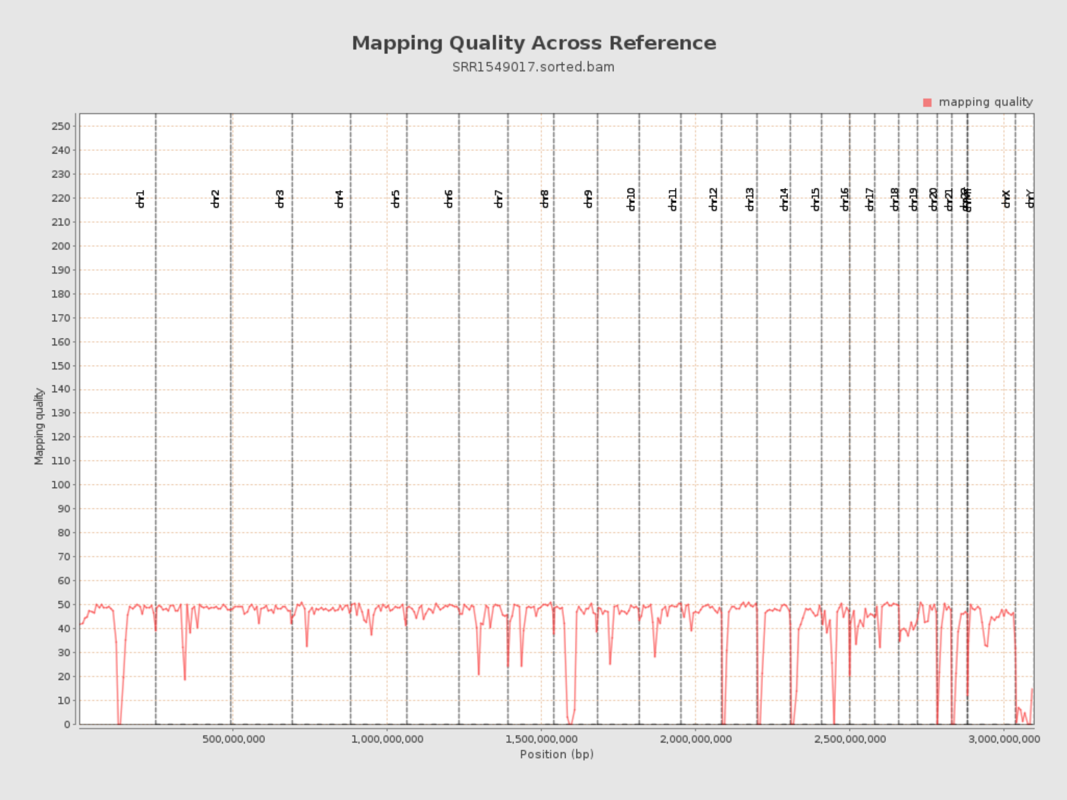
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram