Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 01:53:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153342.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_SRR1153342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 01:53:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,330,008
Mapped reads	63,536,734 / 98.77%
Unmapped reads	793,274 / 1.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	444,527 / 0.69%
Read min/max/mean length	30 / 100 / 100.28
Duplicated reads (estimated)	26,431,654 / 41.09%
Duplication rate	33.7%
Clipped reads	2,869,663 / 4.46%

2.2. ACGT Content

Number/percentage of A's	1,650,949,584 / 26.12%
Number/percentage of C's	1,506,702,612 / 23.84%
Number/percentage of T's	1,650,704,879 / 26.11%
Number/percentage of G's	1,512,401,018 / 23.93%
Number/percentage of N's	288,818 / 0%
GC Percentage	47.76%

2.3. Coverage

Mean	2.0422

Standard Deviation	20.5606

2.4. Mapping Quality

Mean Mapping Quality	48.8

2.5. Mismatches and indels

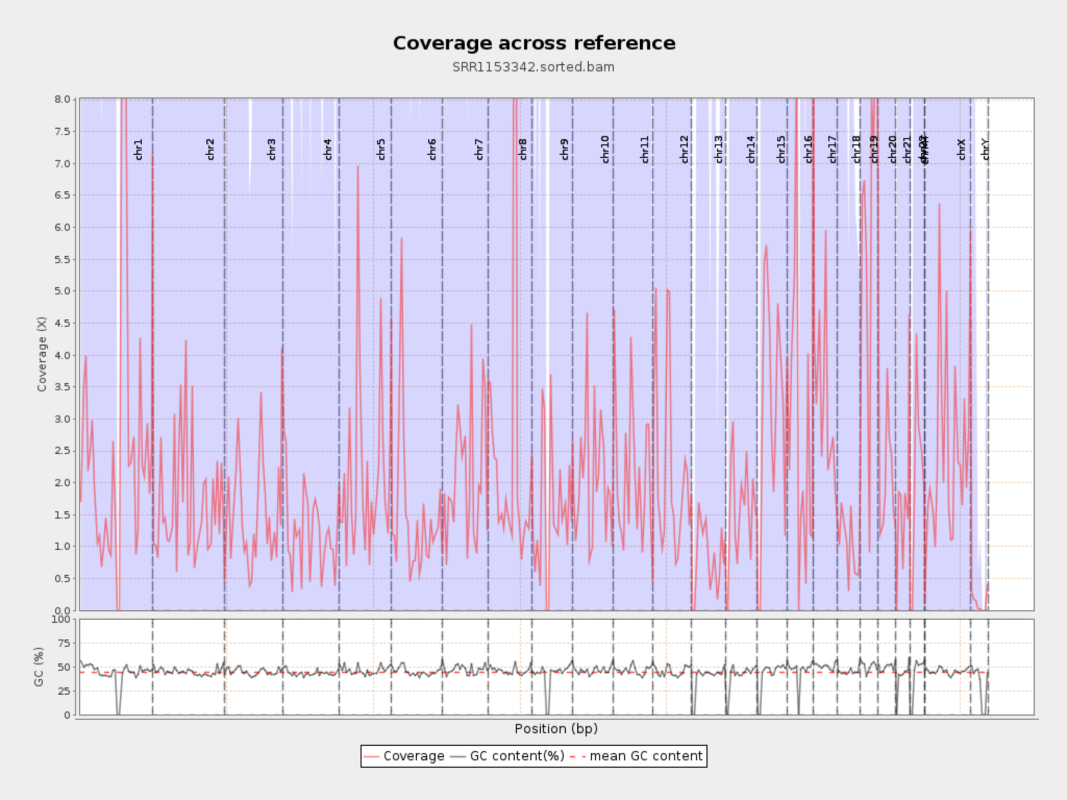
General error rate	0.32%
Mismatches	19,221,665
Insertions	545,009
Mapped reads with at least one insertion	0.85%
Deletions	386,977
Mapped reads with at least one deletion	0.6%
Homopolymer indels	47.79%

2.6. Chromosome stats

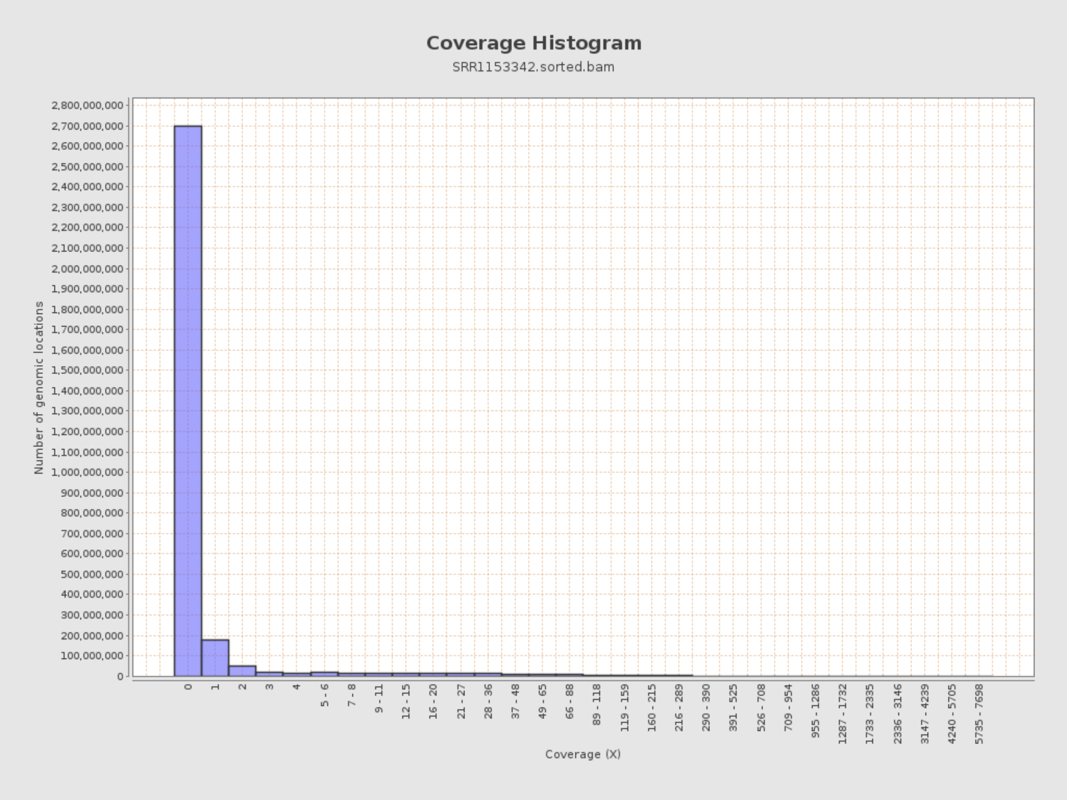
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	671093983	2.6924	22.2167
chr2	243199373	411661011	1.6927	14.4131
chr3	198022430	299237045	1.5111	12.5285
chr4	191154276	240863755	1.26	13.407
chr5	180915260	390973340	2.1611	28.5841
chr6	171115067	250379026	1.4632	12.9784
chr7	159138663	333615852	2.0964	22.3689

chr8	146364022	365487618	2.4971	45.145
chr9	141213431	217011285	1.5368	14.1942
chr10	135534747	285673069	2.1077	18.0773
chr11	135006516	293553174	2.1744	15.4822
chr12	133851895	295992088	2.2113	17.1538
chr13	115169878	94412221	0.8198	9.2529
chr14	107349540	162174707	1.5107	12.8256
chr15	102531392	314283710	3.0652	24.4985
chr16	90354753	259189308	2.8686	21.3577
chr17	81195210	260792941	3.2119	19.6165
chr18	78077248	78937129	1.011	9.3516
chr19	59128983	378397382	6.3995	34.6643
chr20	63025520	138502617	2.1976	16.315
chr21	48129895	81498300	1.6933	24.4273
chr22	51304566	107251139	2.0905	16.0789
chrMT	16571	1514	0.0914	0.3279
chrX	155270560	383417170	2.4693	20.9212
chrY	59373566	7517658	0.1266	5.9892

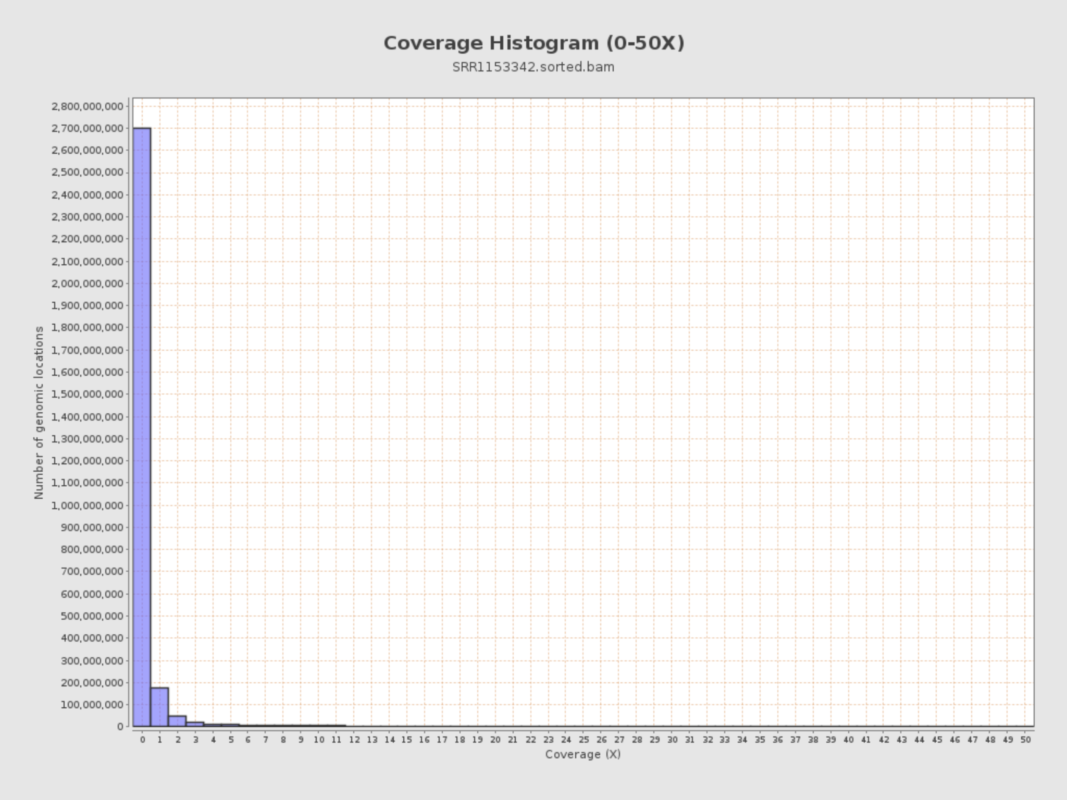
3. Results : Coverage across reference



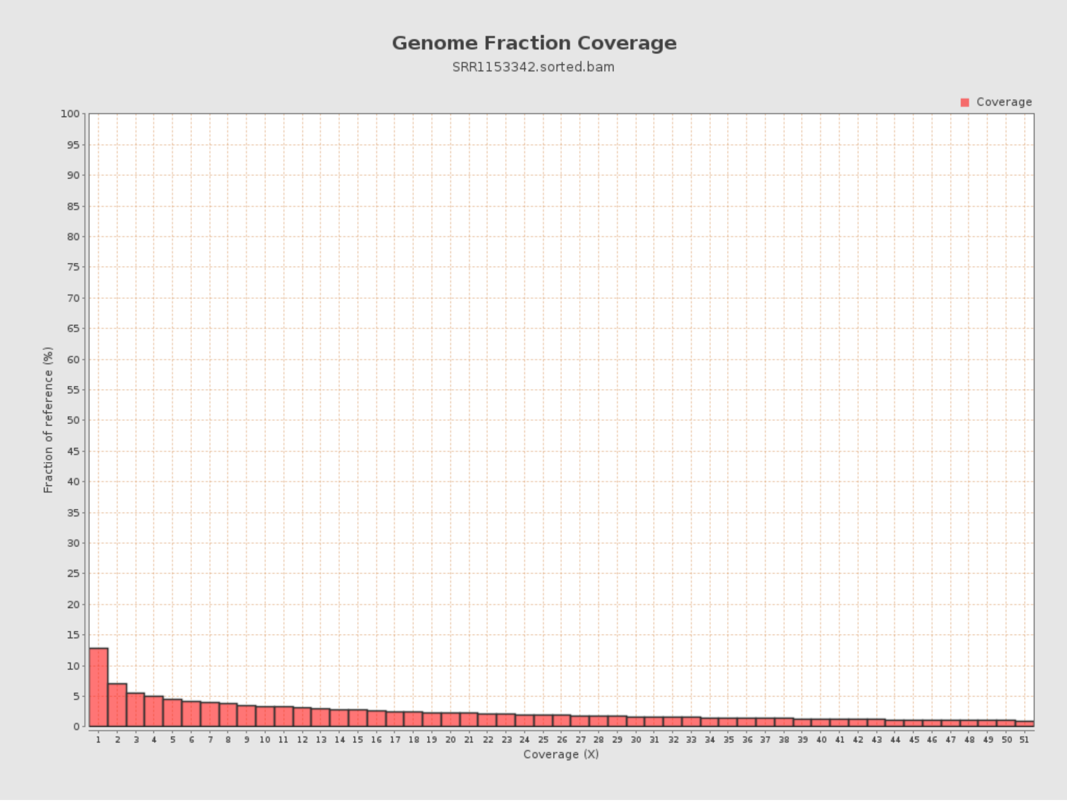
4. Results : Coverage Histogram



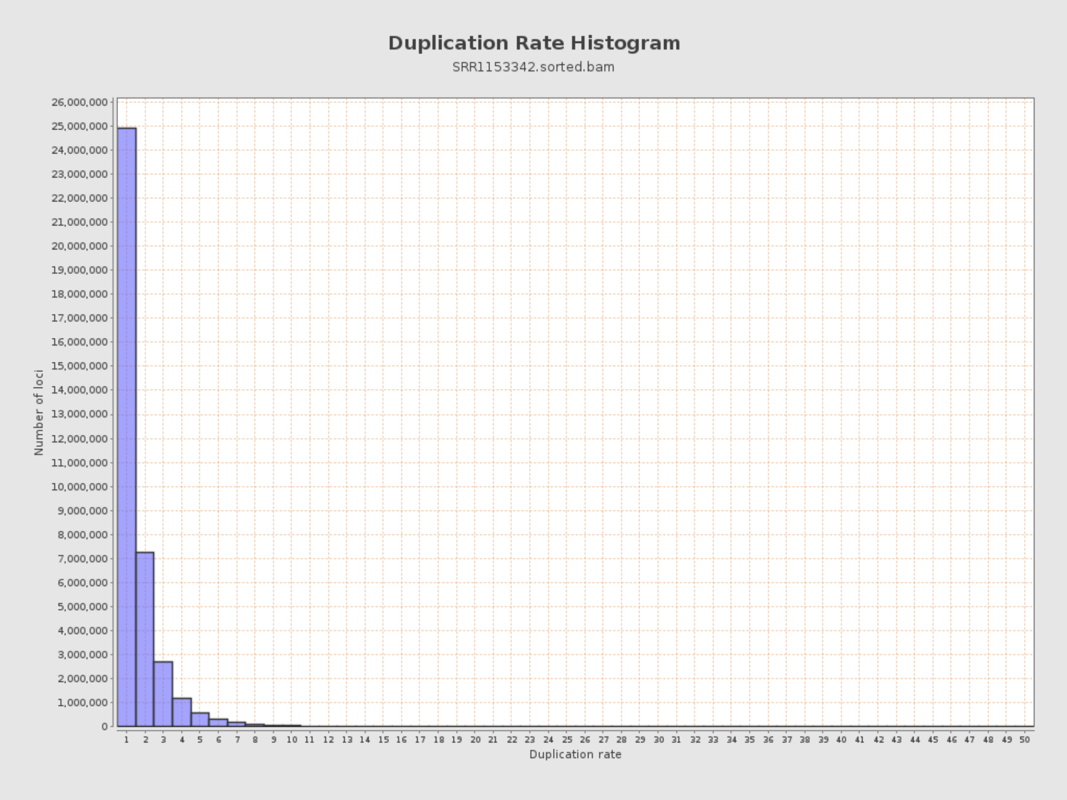
5. Results : Coverage Histogram (0-50X)



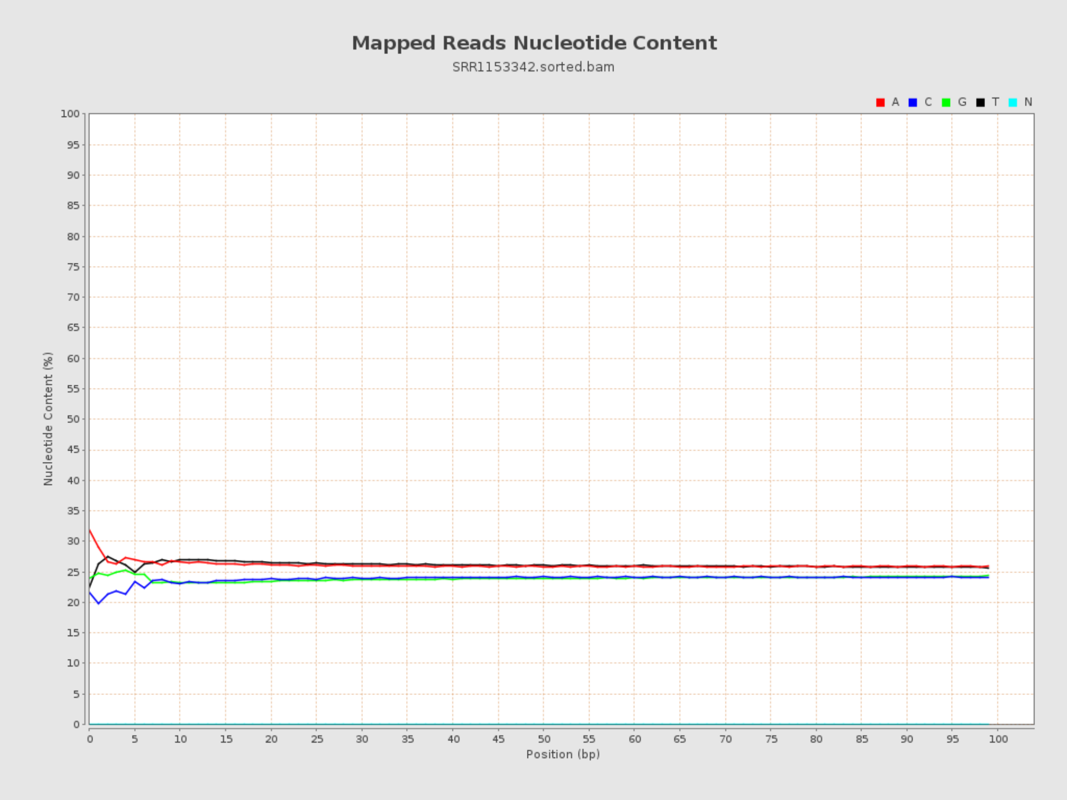
6. Results : Genome Fraction Coverage



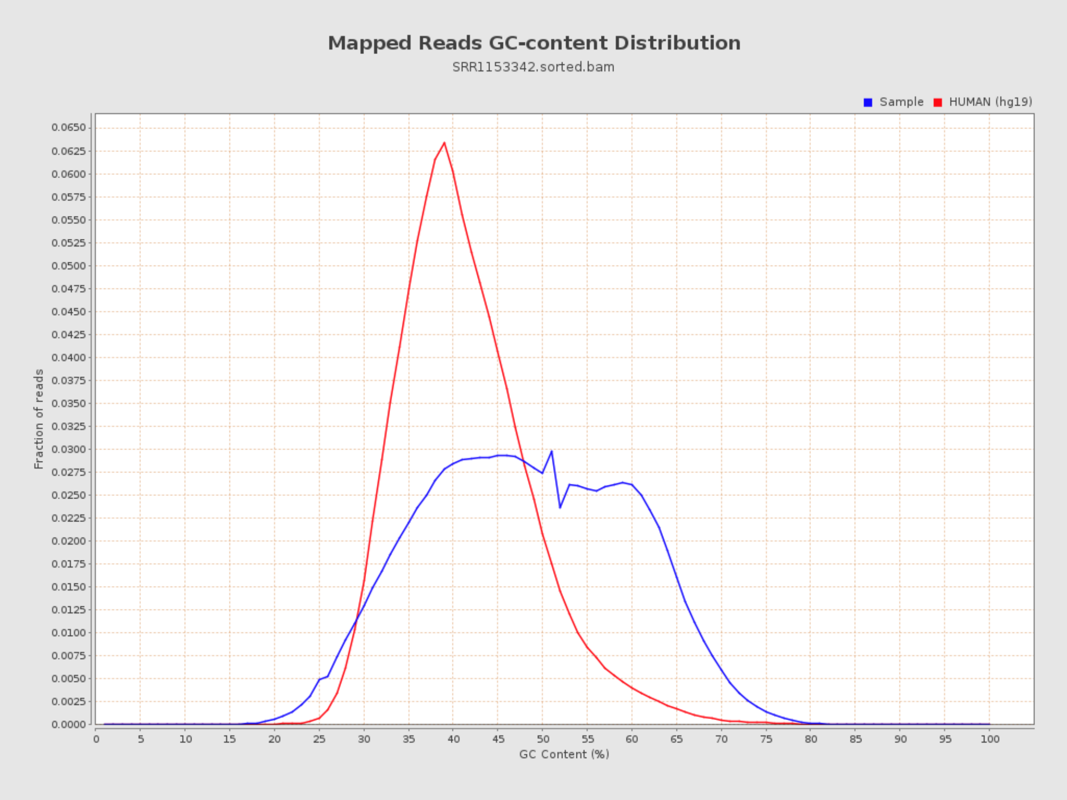
7. Results : Duplication Rate Histogram



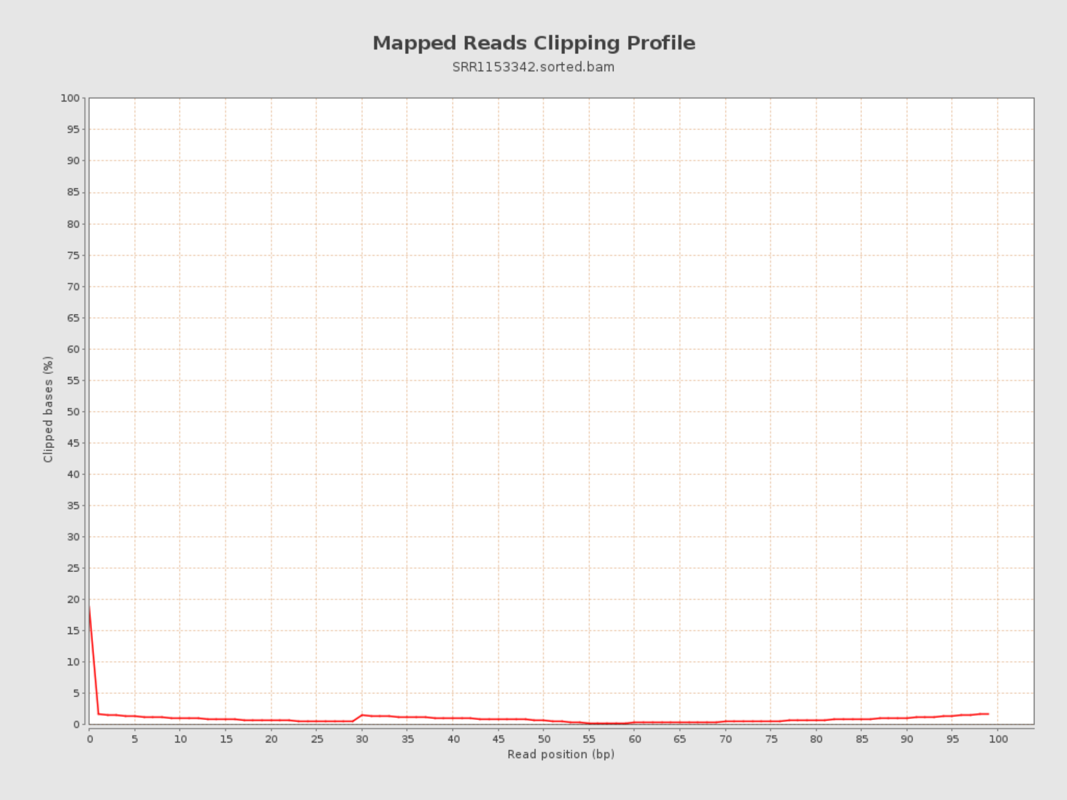
8. Results : Mapped Reads Nucleotide Content



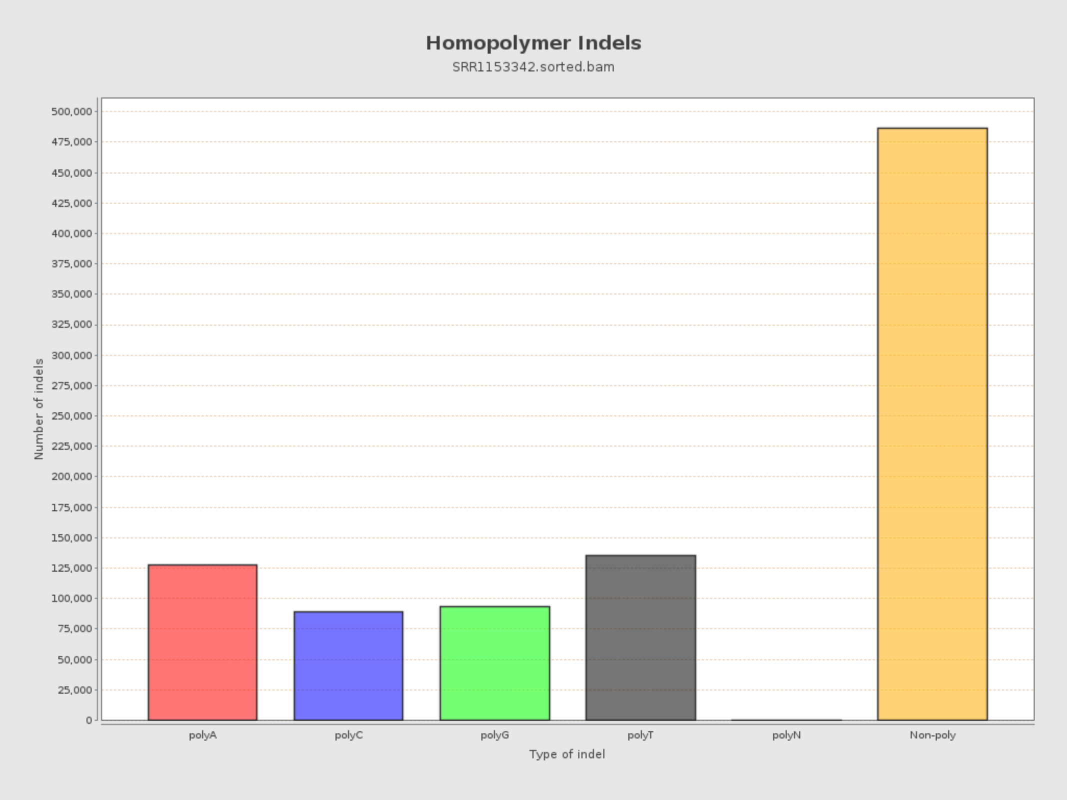
9. Results : Mapped Reads GC-content Distribution



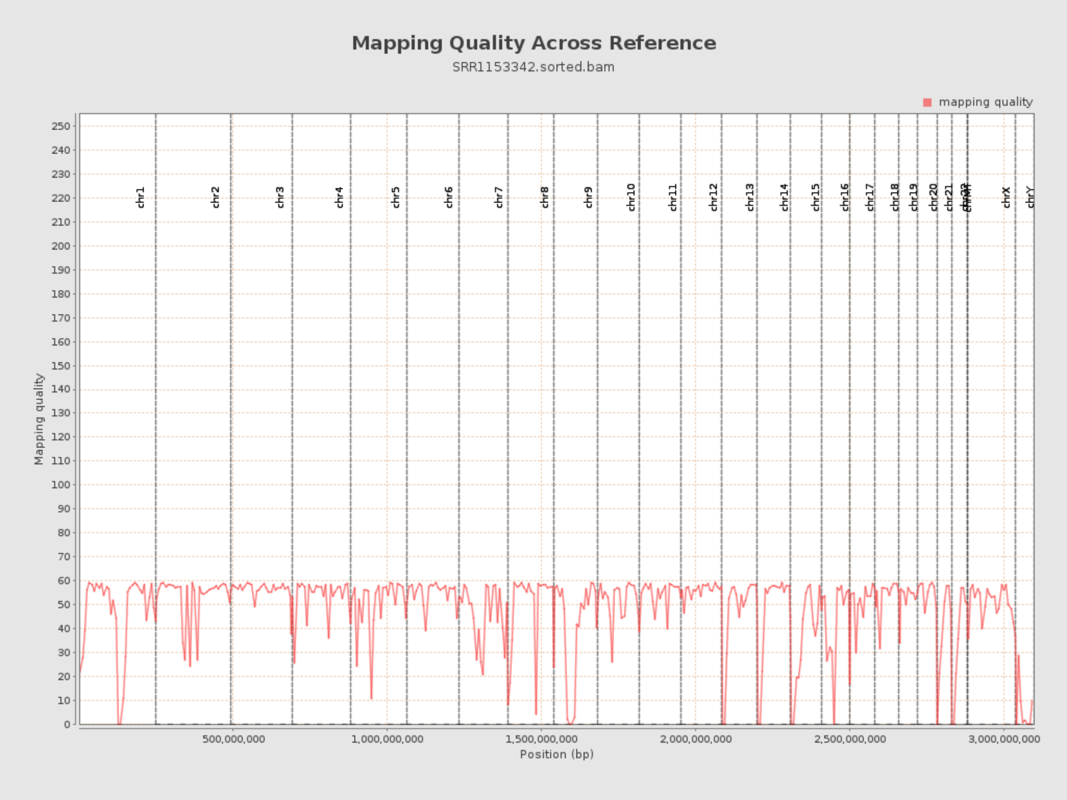
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram