Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 03:57:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153344.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_SRR1153344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 03:57:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,201,886
Mapped reads	62,415,556 / 98.76%
Unmapped reads	786,330 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	432,109 / 0.68%
Read min/max/mean length	30 / 100 / 100.28
Duplicated reads (estimated)	26,480,591 / 41.9%
Duplication rate	34.95%
Clipped reads	2,935,897 / 4.65%

2.2. ACGT Content

Number/percentage of A's	1,643,025,406 / 26.46%
Number/percentage of C's	1,457,297,464 / 23.47%
Number/percentage of T's	1,644,392,640 / 26.49%
Number/percentage of G's	1,463,497,993 / 23.57%
Number/percentage of N's	286,680 / 0%
GC Percentage	47.05%

2.3. Coverage

Mean	2.0058

Standard Deviation	19.9574

2.4. Mapping Quality

Mean Mapping Quality	49

2.5. Mismatches and indels

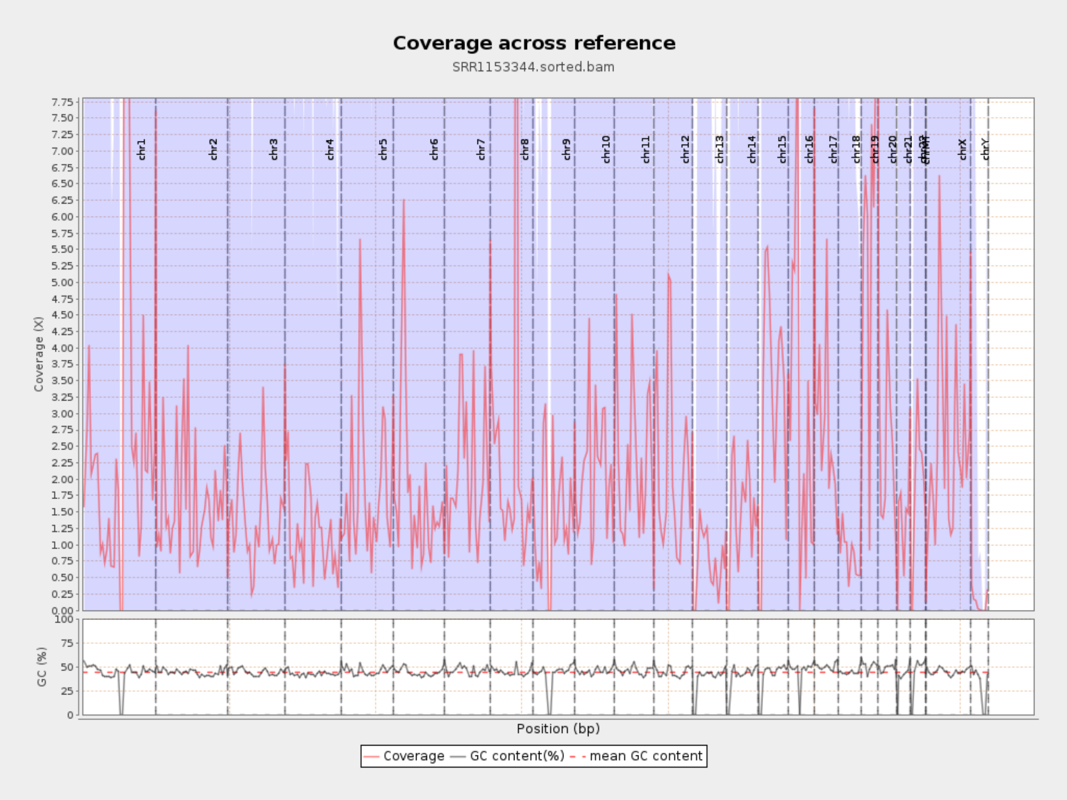
General error rate	0.31%
Mismatches	18,680,782
Insertions	546,913
Mapped reads with at least one insertion	0.87%
Deletions	389,760
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.1%

2.6. Chromosome stats

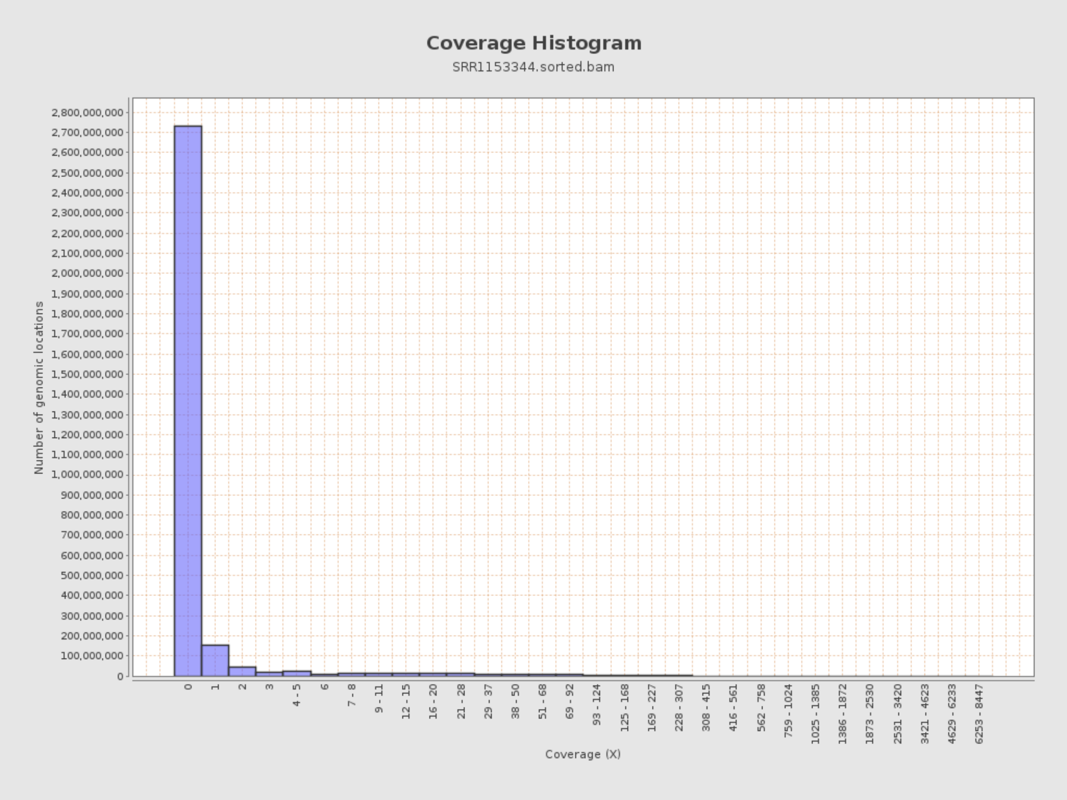
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	673350892	2.7015	23.7194
chr2	243199373	406683803	1.6722	13.8269
chr3	198022430	277400313	1.4009	12.0267
chr4	191154276	225024923	1.1772	12.1168
chr5	180915260	332826748	1.8397	24.0879
chr6	171115067	300171224	1.7542	14.3332
chr7	159138663	335648899	2.1092	22.0921

chr8	146364022	374347051	2.5576	44.5069
chr9	141213431	191580810	1.3567	12.3011
chr10	135534747	285491079	2.1064	16.3983
chr11	135006516	312285252	2.3131	16.2308
chr12	133851895	300033378	2.2415	16.1277
chr13	115169878	83912144	0.7286	7.5072
chr14	107349540	157507517	1.4672	12.293
chr15	102531392	321960000	3.1401	27.1104
chr16	90354753	264962665	2.9325	22.1575
chr17	81195210	230333615	2.8368	17.0751
chr18	78077248	67992199	0.8708	8.8841
chr19	59128983	353708049	5.982	31.7804
chr20	63025520	151592420	2.4053	17.7269
chr21	48129895	69242201	1.4387	17.5618
chr22	51304566	95311285	1.8578	14.909
chrMT	16571	2035	0.1228	0.3731
chrX	155270560	390698703	2.5162	21.4731
chrY	59373566	7282202	0.1227	5.3941

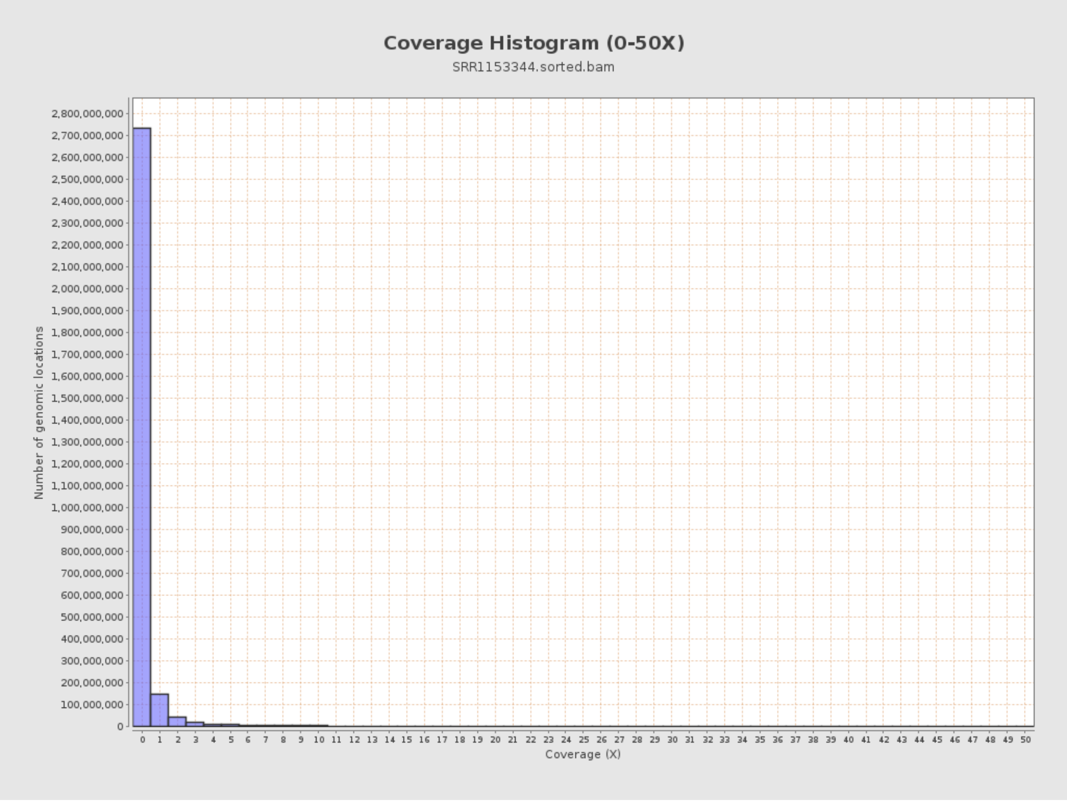
3. Results : Coverage across reference



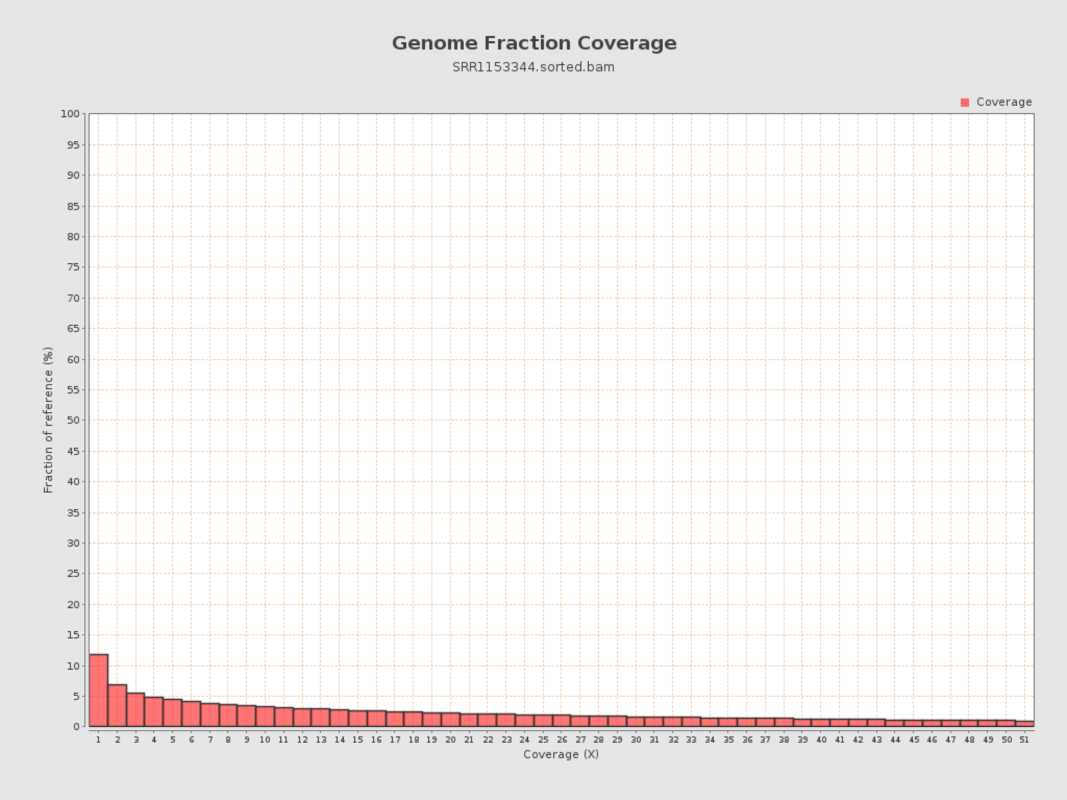
4. Results : Coverage Histogram



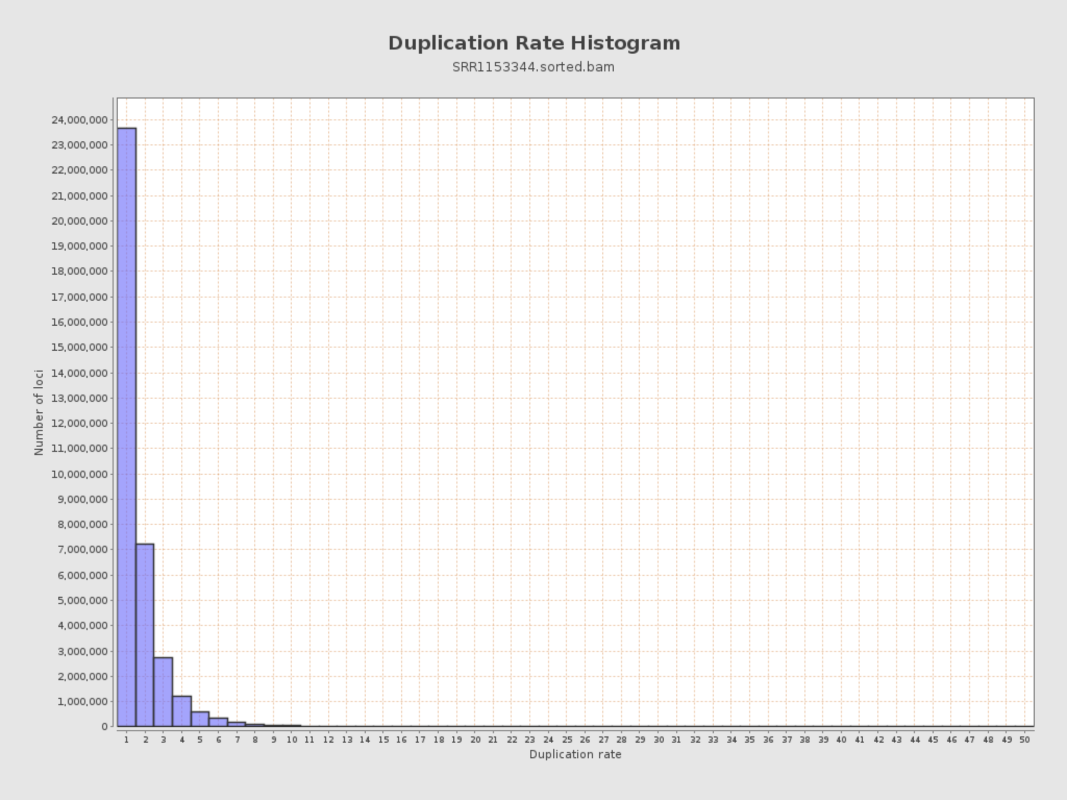
5. Results : Coverage Histogram (0-50X)



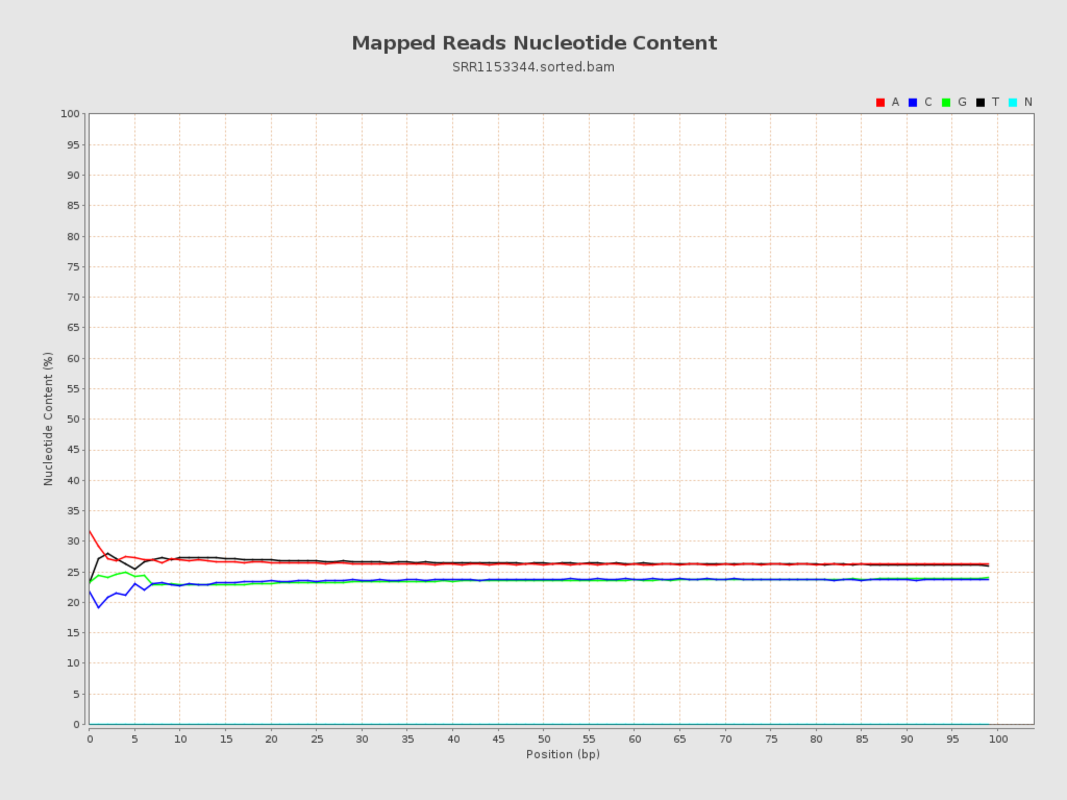
6. Results : Genome Fraction Coverage



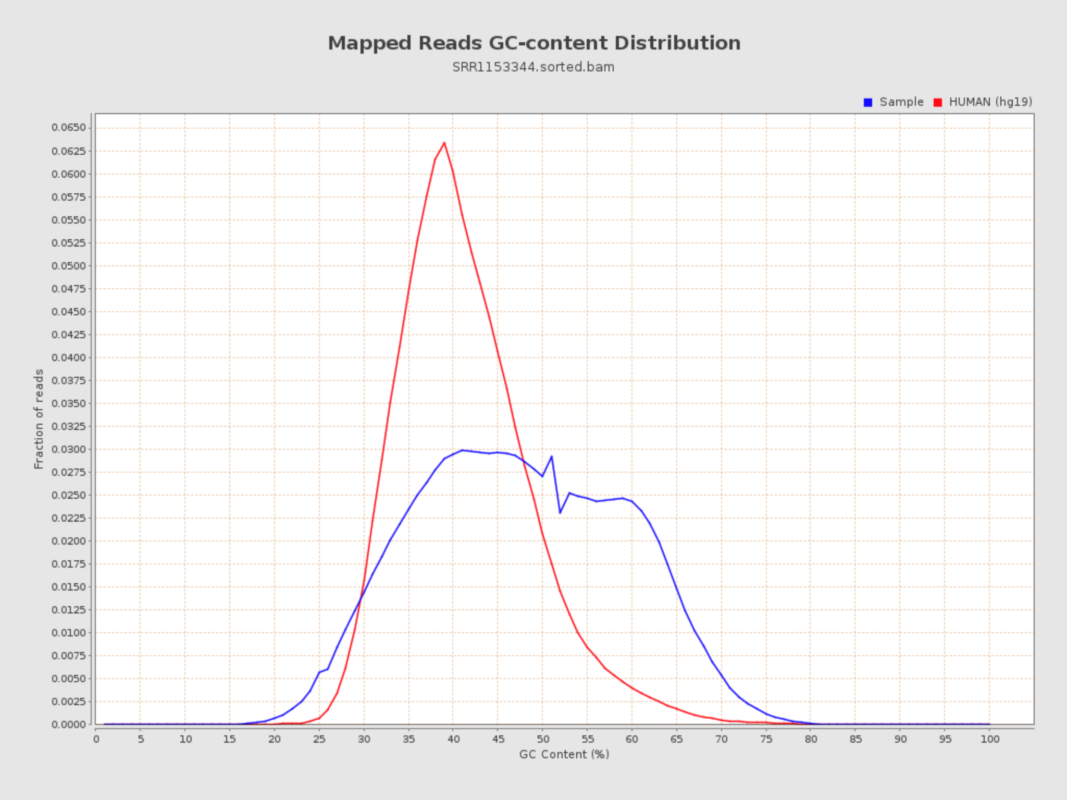
7. Results : Duplication Rate Histogram



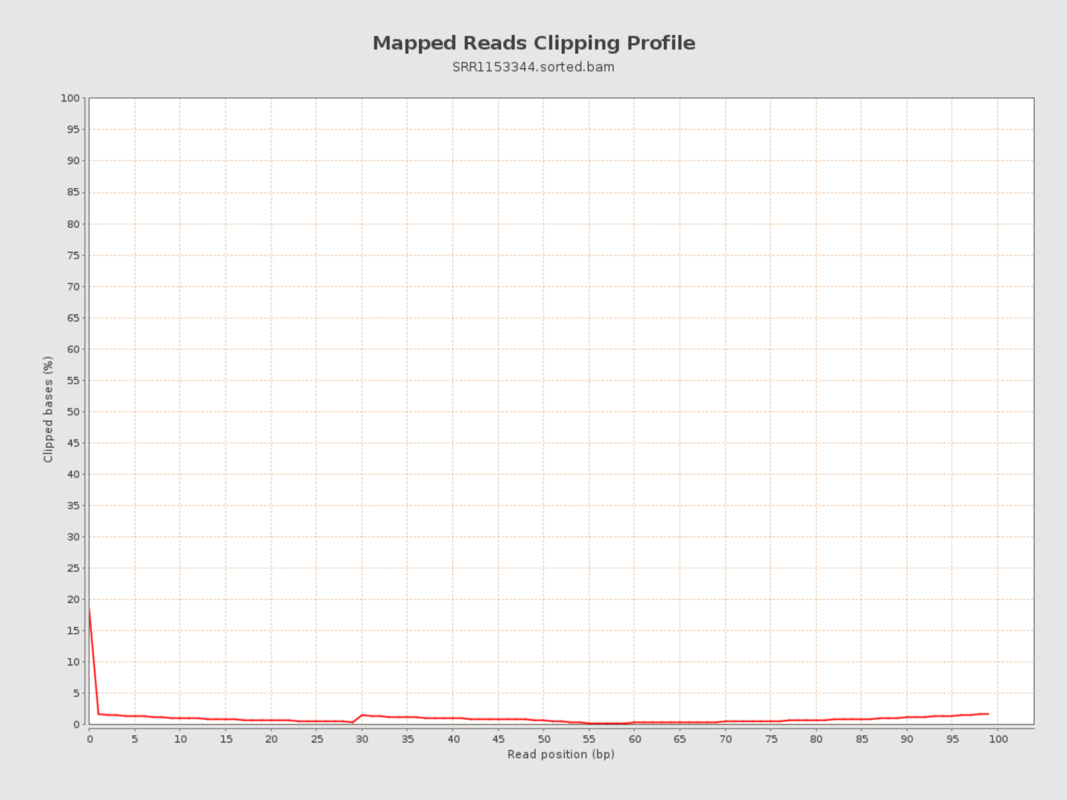
8. Results : Mapped Reads Nucleotide Content



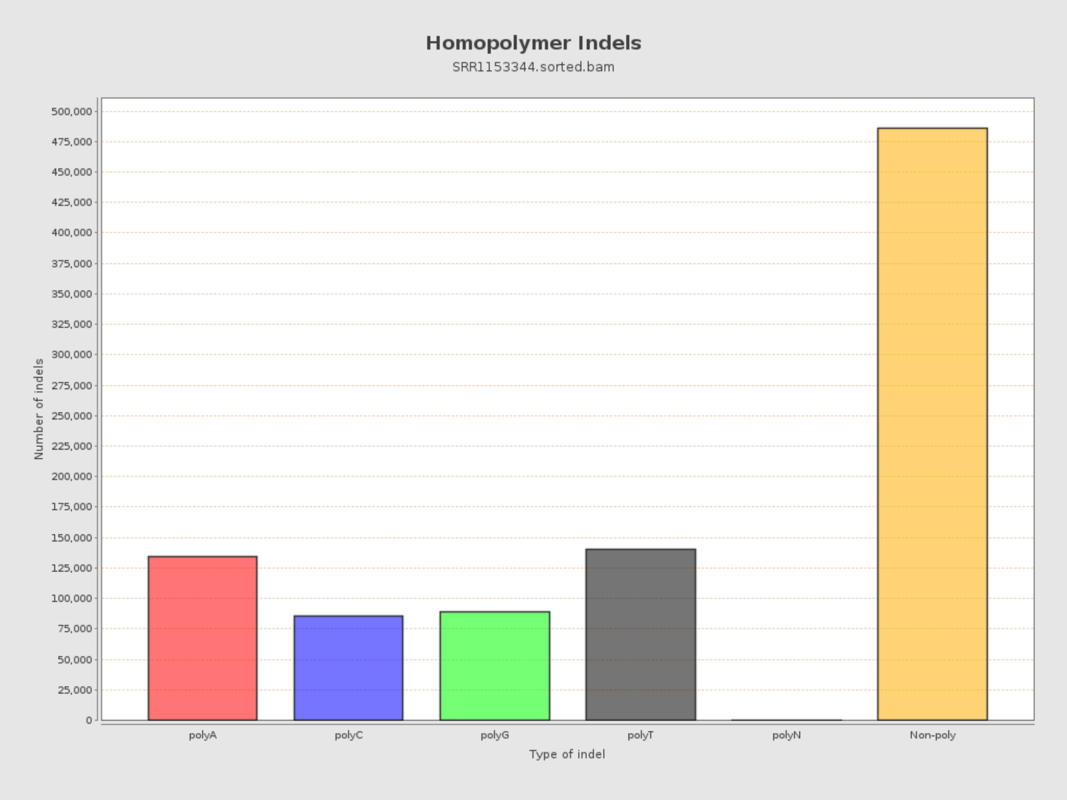
9. Results : Mapped Reads GC-content Distribution



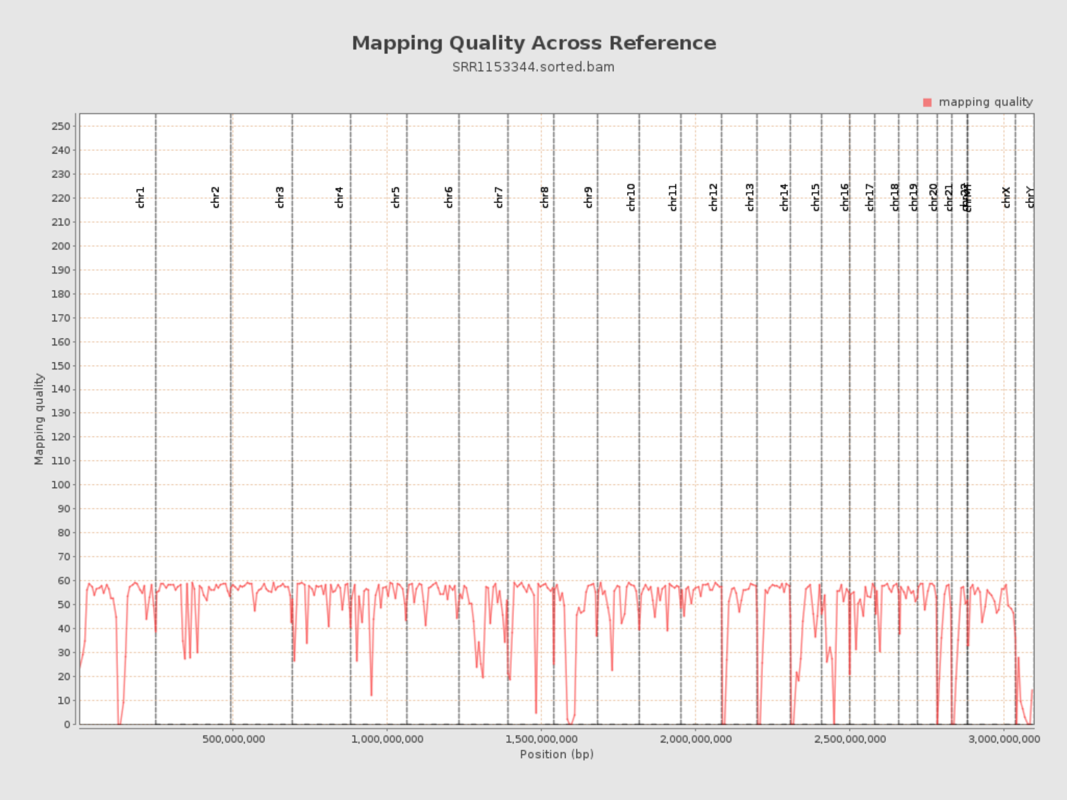
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram