Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 23:17:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153336.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_SRR1153336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 23:17:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,492,272
Mapped reads	63,864,279 / 99.03%
Unmapped reads	627,993 / 0.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	311,640 / 0.48%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	45,136,449 / 69.99%
Duplication rate	60.89%
Clipped reads	6,587,823 / 10.21%

2.2. ACGT Content

Number/percentage of A's	1,644,015,552 / 26.29%
Number/percentage of C's	1,472,342,942 / 23.54%
Number/percentage of T's	1,688,686,463 / 27%
Number/percentage of G's	1,447,087,235 / 23.14%
Number/percentage of N's	2,114,146 / 0.03%
GC Percentage	46.68%

2.3. Coverage

Mean	2.0206

Standard Deviation	21.6018

2.4. Mapping Quality

Mean Mapping Quality	50.59

2.5. Mismatches and indels

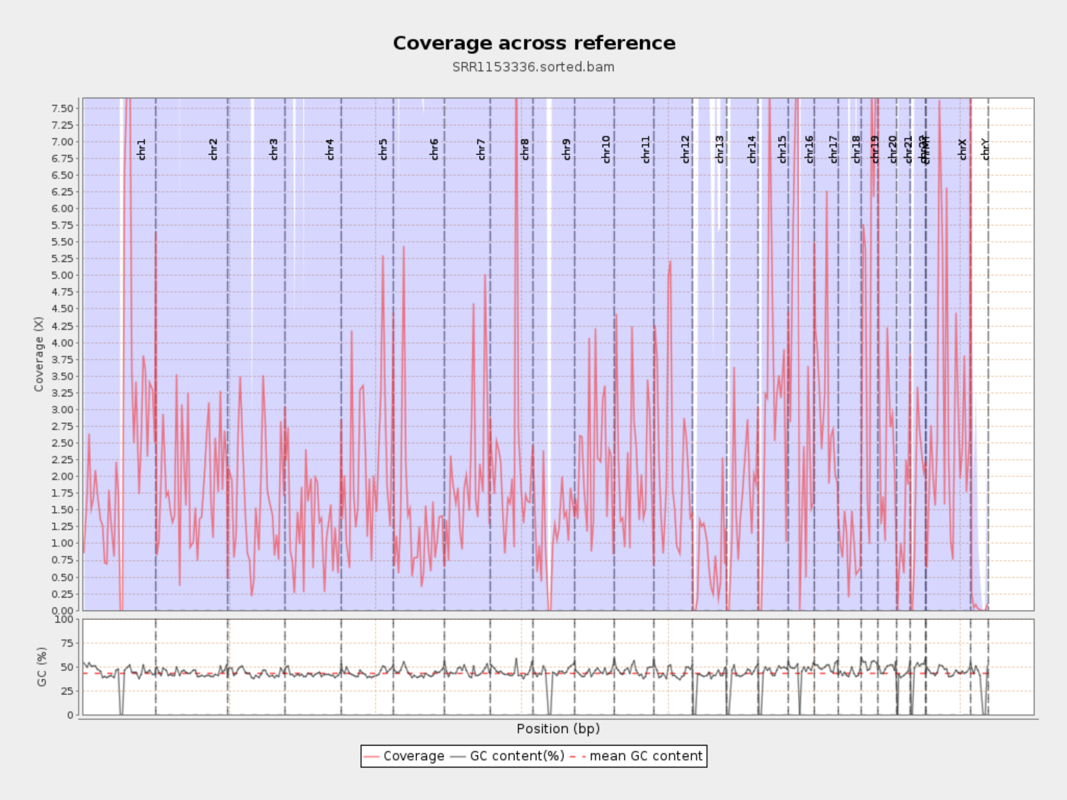
General error rate	0.31%
Mismatches	18,639,914
Insertions	413,134
Mapped reads with at least one insertion	0.64%
Deletions	381,018
Mapped reads with at least one deletion	0.59%
Homopolymer indels	49.7%

2.6. Chromosome stats

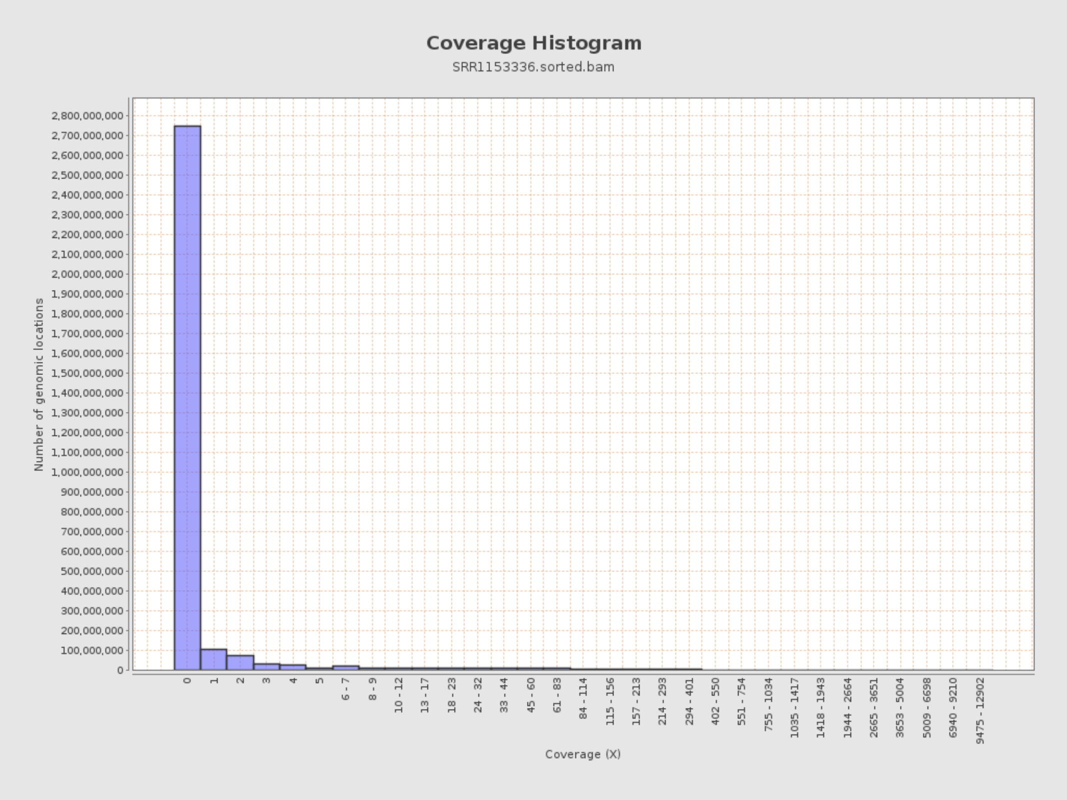
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	632194074	2.5364	23.4609
chr2	243199373	459471167	1.8893	17.7853
chr3	198022430	325705931	1.6448	16.0041
chr4	191154276	250600265	1.311	14.9726
chr5	180915260	402479032	2.2247	22.5654
chr6	171115067	216839633	1.2672	13.4728
chr7	159138663	321155927	2.0181	24.9566

chr8	146364022	323921715	2.2131	37.0762
chr9	141213431	162146382	1.1482	12.1097
chr10	135534747	303322195	2.238	20.7391
chr11	135006516	291806947	2.1614	19.3809
chr12	133851895	314409677	2.3489	20.8701
chr13	115169878	85513752	0.7425	11.7115
chr14	107349540	175063947	1.6308	15.5783
chr15	102531392	296010300	2.887	24.9363
chr16	90354753	291917378	3.2308	30.1476
chr17	81195210	257673138	3.1735	22.4299
chr18	78077248	72350628	0.9267	10.5909
chr19	59128983	307178836	5.1951	34.058
chr20	63025520	149574186	2.3732	21.1067
chr21	48129895	66704064	1.3859	15.7972
chr22	51304566	91232716	1.7783	17.9409
chrMT	16571	12236	0.7384	2.437
chrX	155270560	454391618	2.9265	32.154
chrY	59373566	3333226	0.0561	2.1733

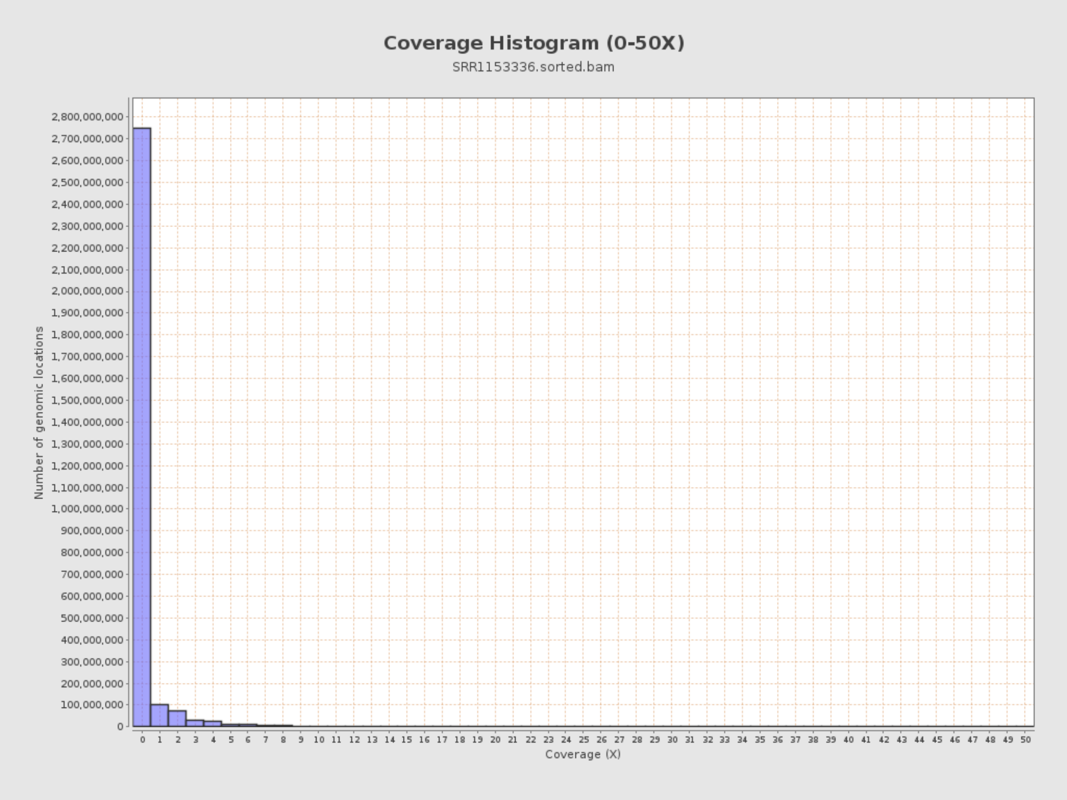
3. Results : Coverage across reference



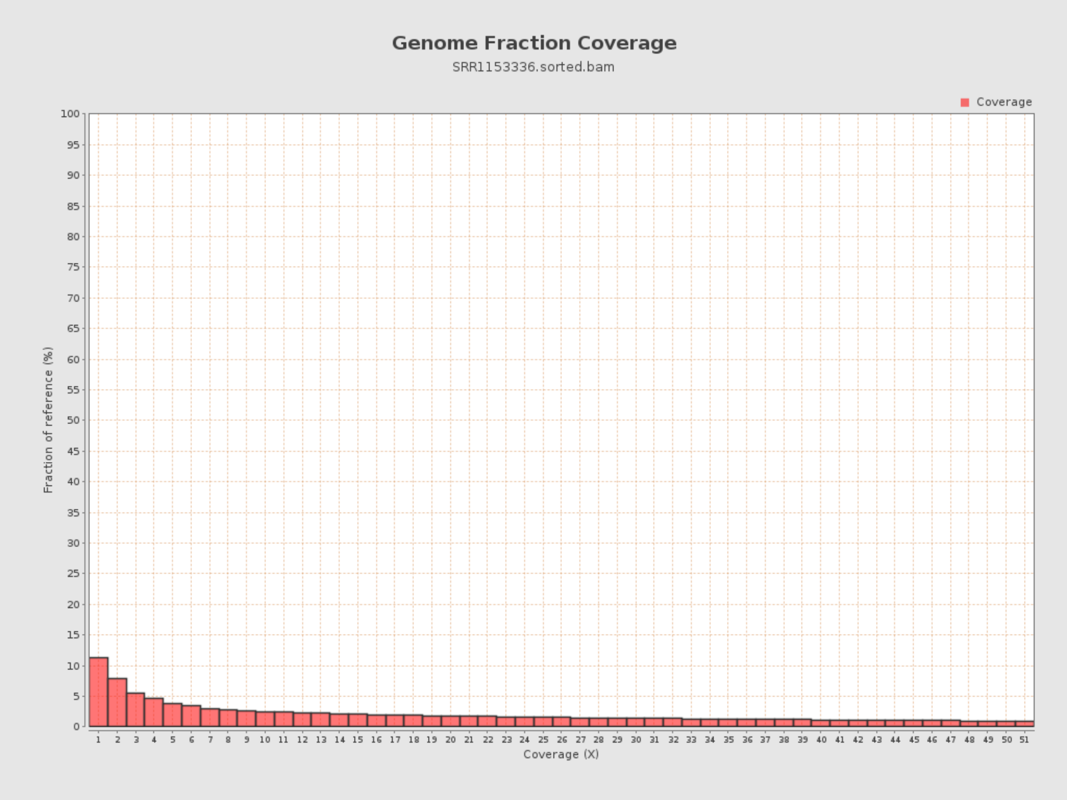
4. Results : Coverage Histogram



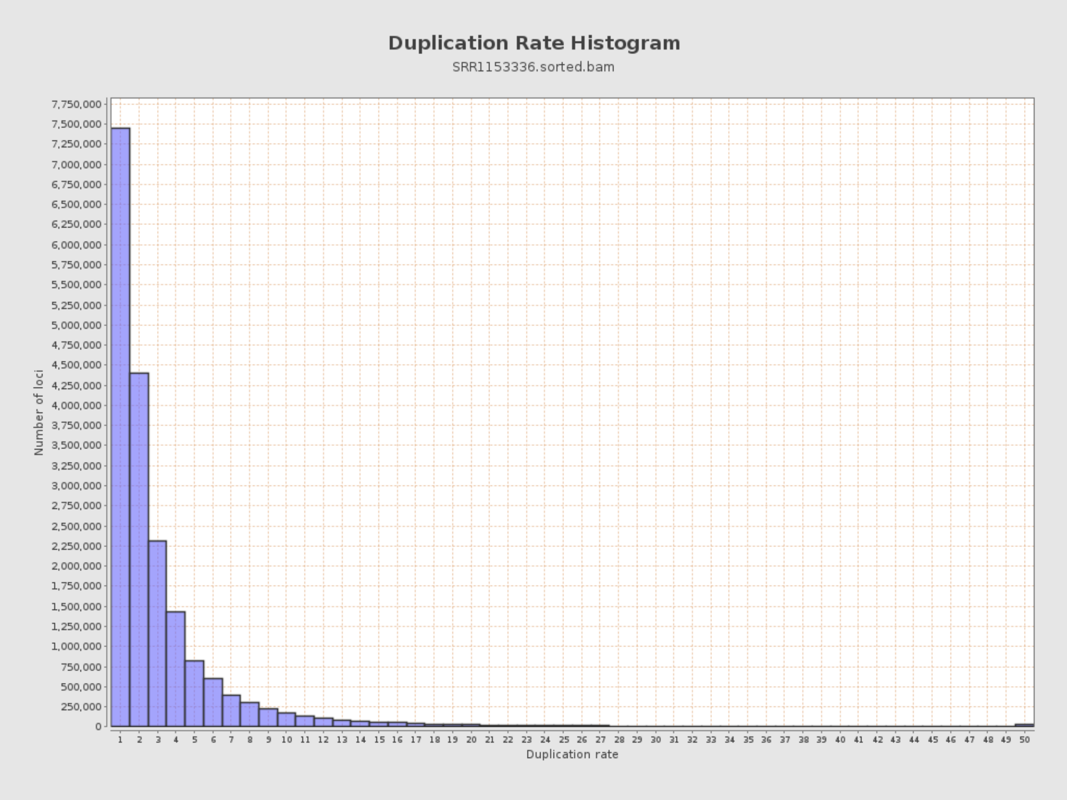
5. Results : Coverage Histogram (0-50X)



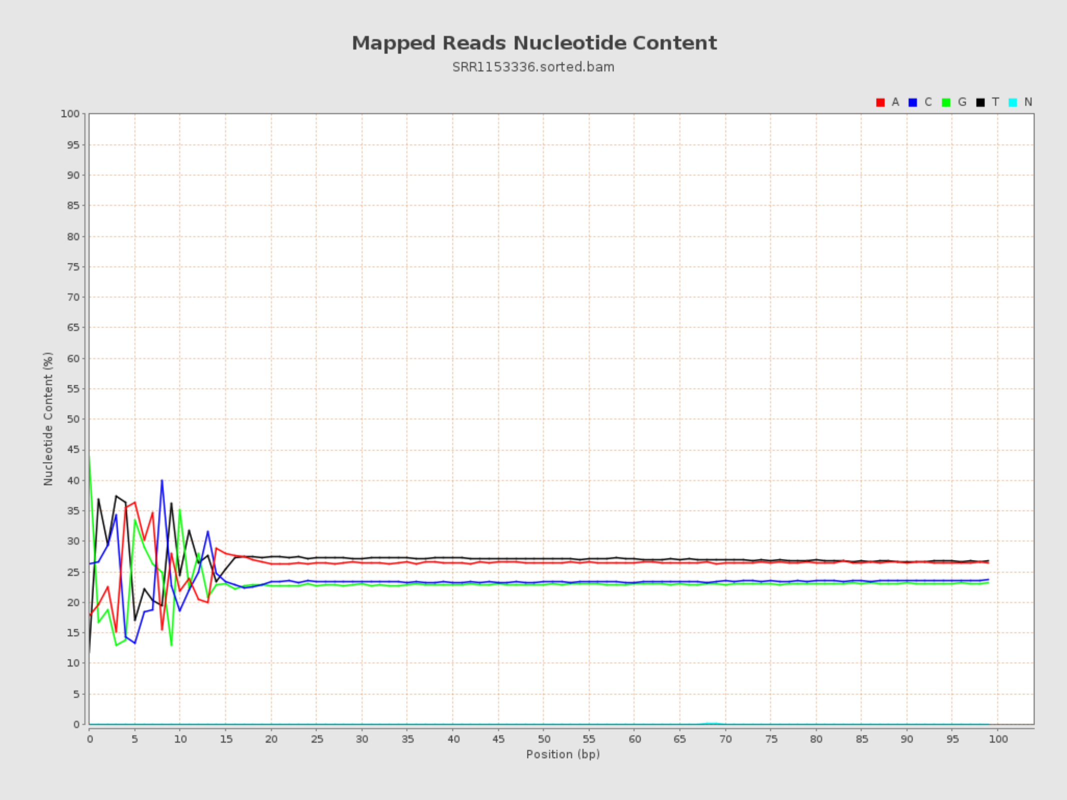
6. Results : Genome Fraction Coverage



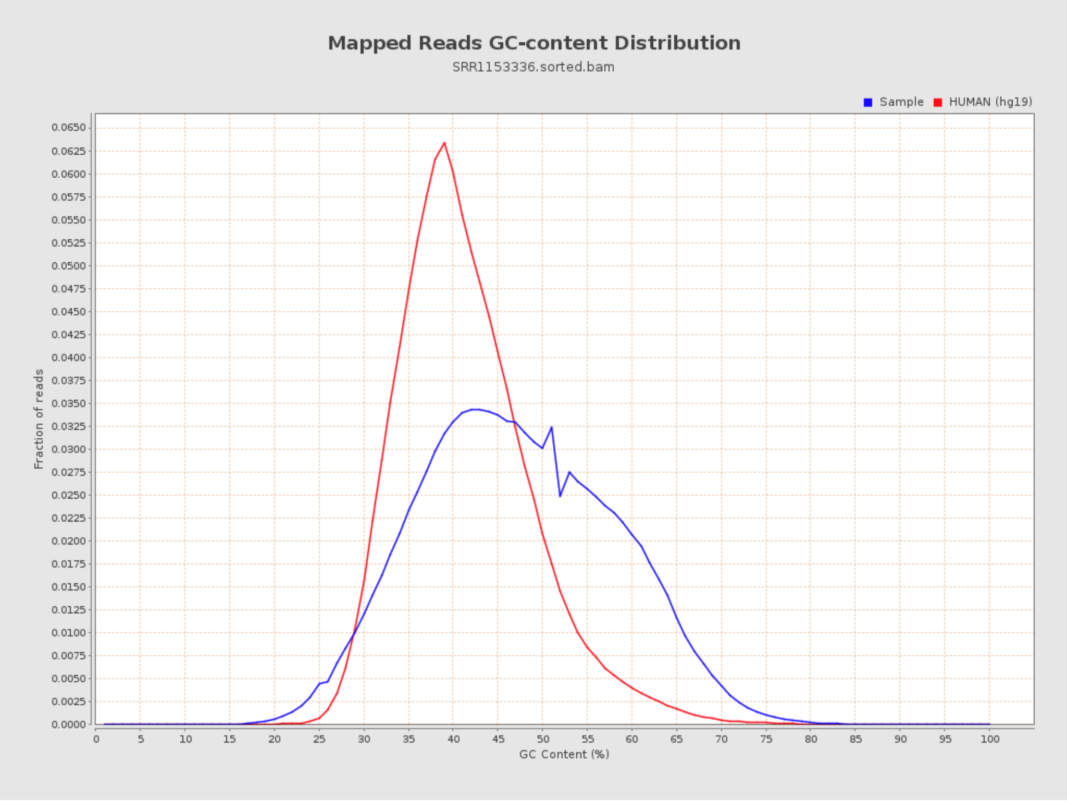
7. Results : Duplication Rate Histogram



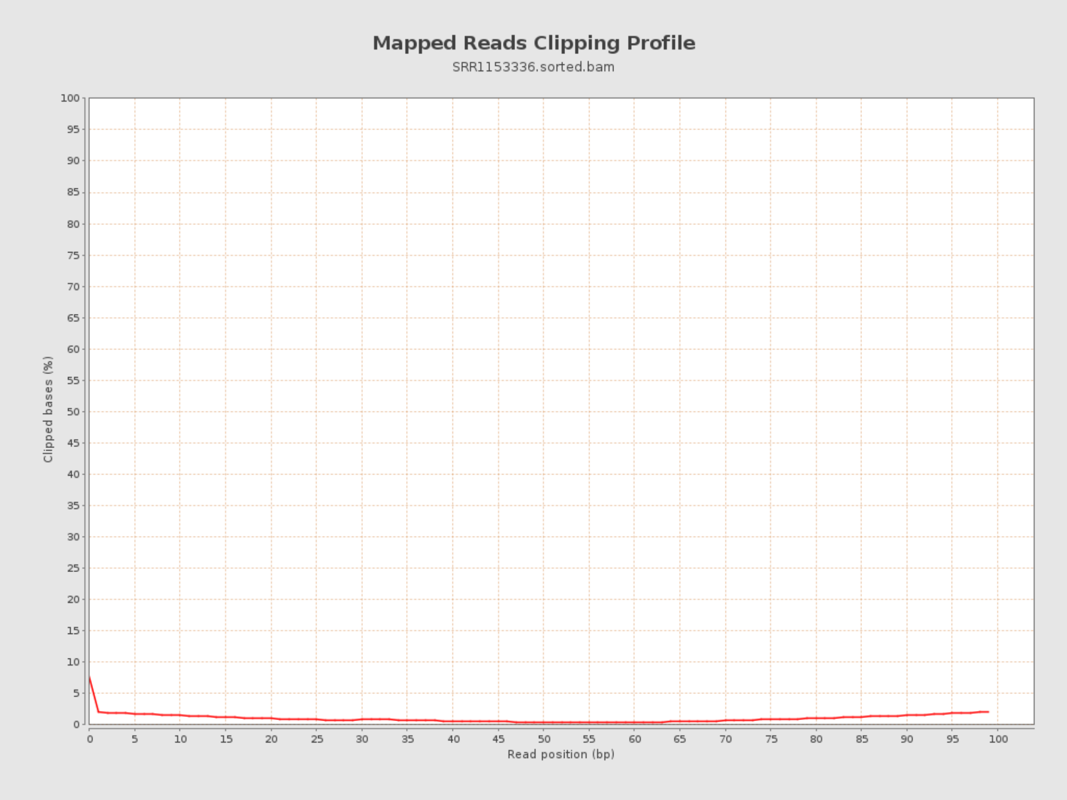
8. Results : Mapped Reads Nucleotide Content



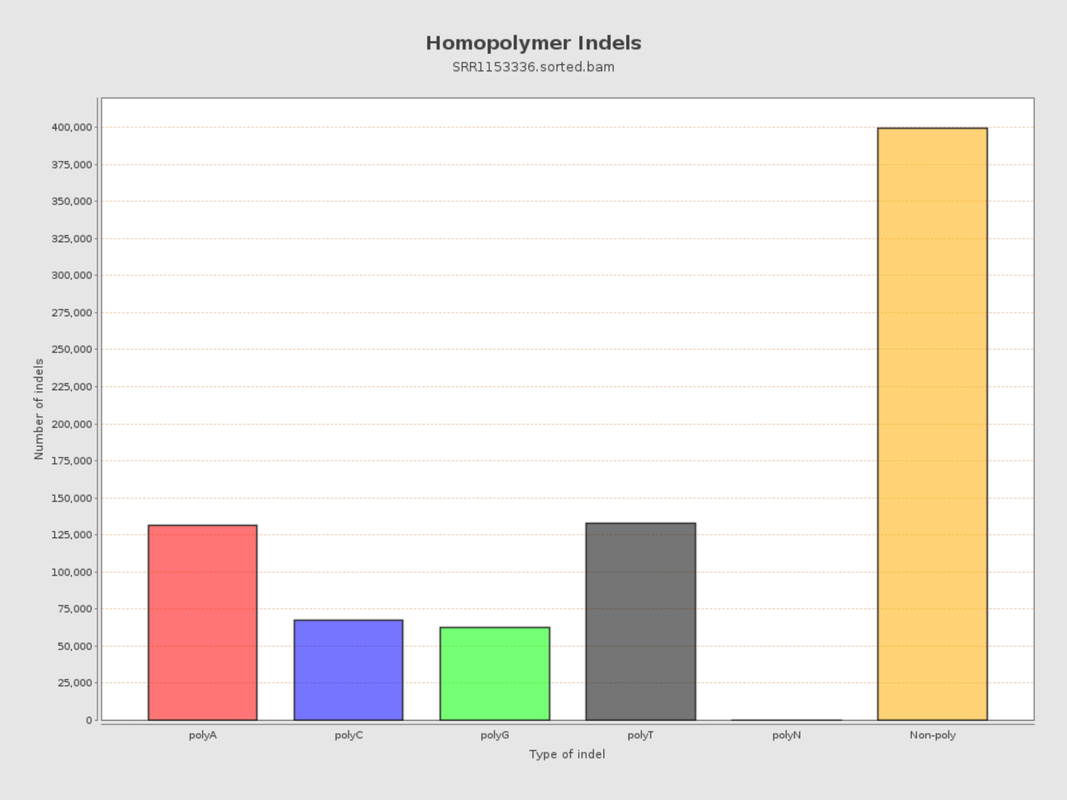
9. Results : Mapped Reads GC-content Distribution



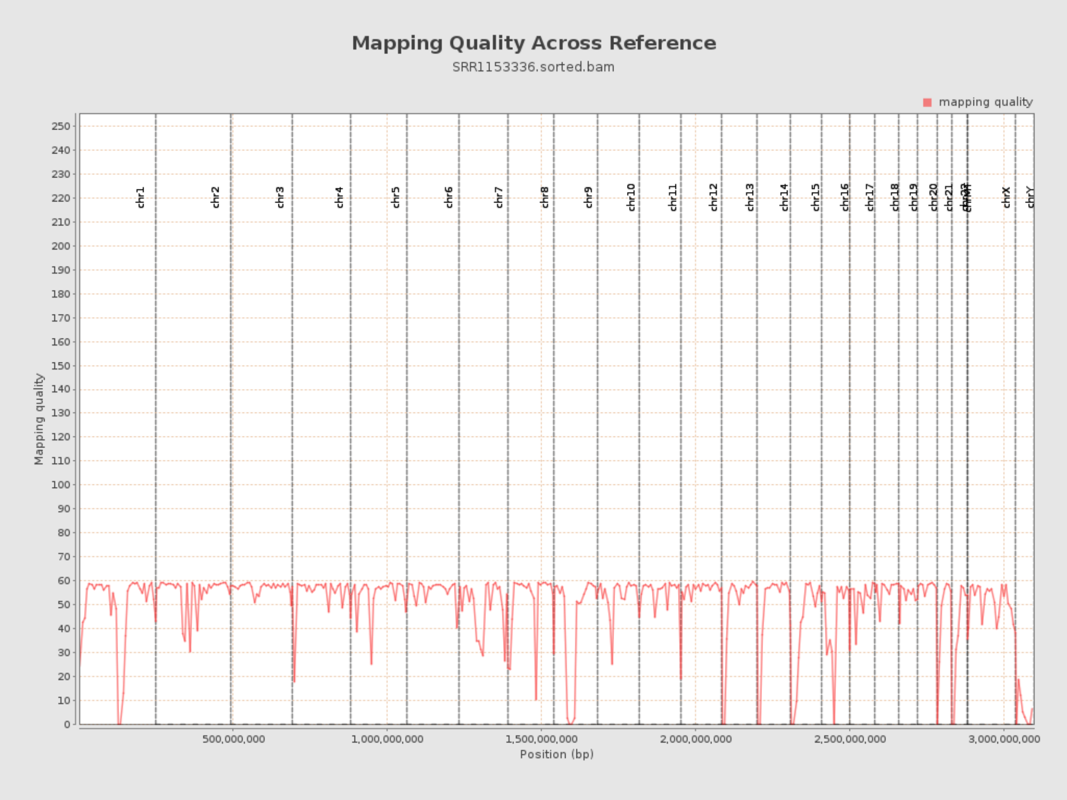
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram