Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 02:57:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153343.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_SRR1153343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 02:57:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,538,884
Mapped reads	50,040,083 / 99.01%
Unmapped reads	498,801 / 0.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	414,558 / 0.82%
Read min/max/mean length	30 / 100 / 100.34
Duplicated reads (estimated)	24,088,613 / 47.66%
Duplication rate	31.79%
Clipped reads	6,492,782 / 12.85%

2.2. ACGT Content

Number/percentage of A's	1,295,705,292 / 26.66%
Number/percentage of C's	1,128,487,481 / 23.22%
Number/percentage of T's	1,321,041,054 / 27.18%
Number/percentage of G's	1,113,947,400 / 22.92%
Number/percentage of N's	1,801,409 / 0.04%
GC Percentage	46.13%

2.3. Coverage

Mean	1.5705

Standard Deviation	14.3566

2.4. Mapping Quality

Mean Mapping Quality	50.22

2.5. Mismatches and indels

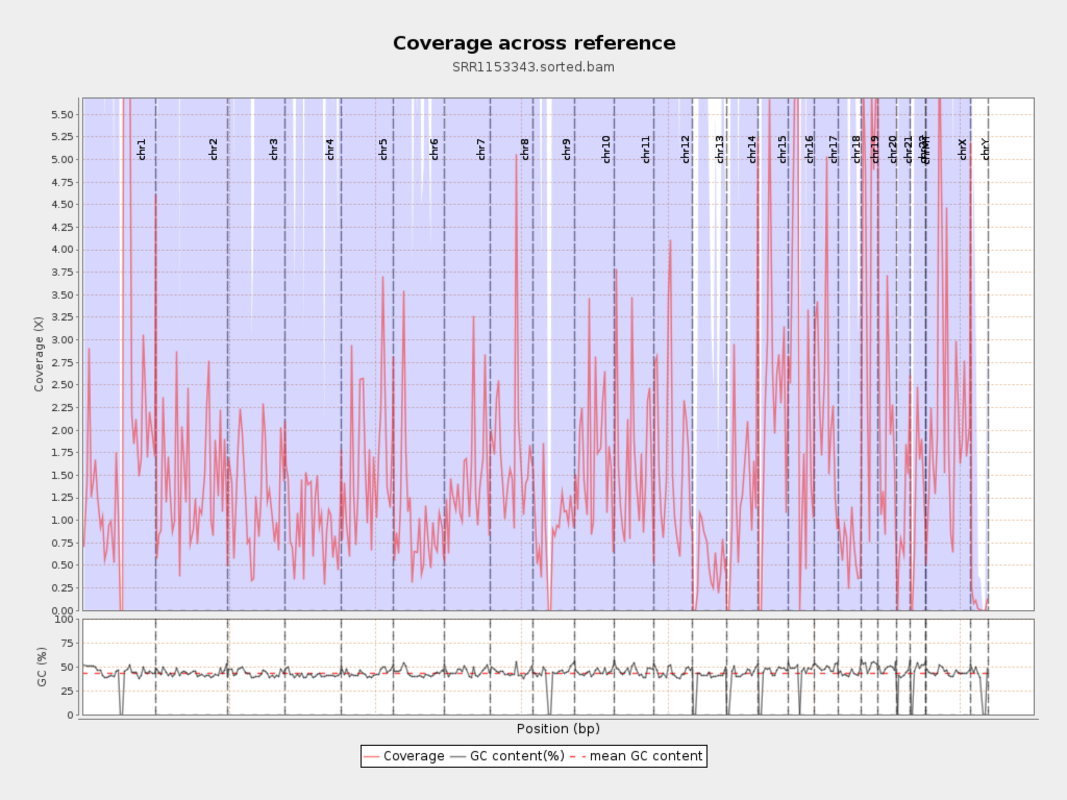
General error rate	0.31%
Mismatches	14,155,842
Insertions	523,568
Mapped reads with at least one insertion	1.03%
Deletions	410,445
Mapped reads with at least one deletion	0.81%
Homopolymer indels	49.08%

2.6. Chromosome stats

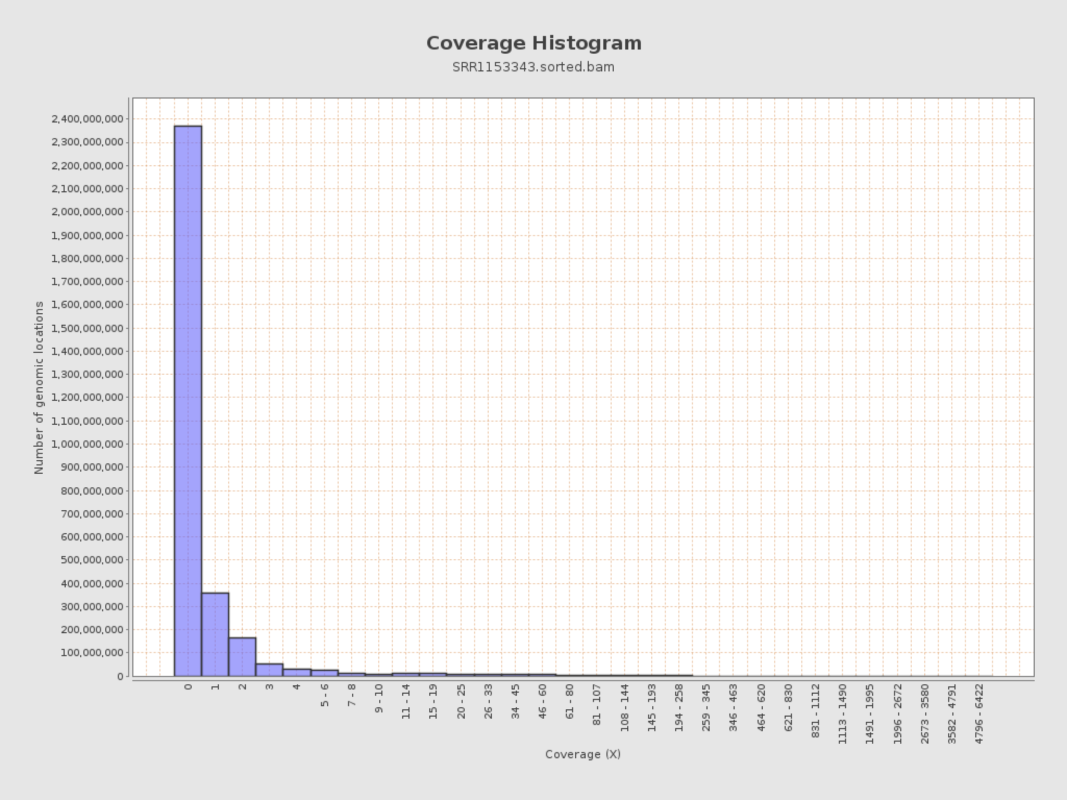
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	555120692	2.2272	24.4712
chr2	243199373	344926349	1.4183	11.1745
chr3	198022430	248037732	1.2526	9.4444
chr4	191154276	186267726	0.9744	7.74
chr5	180915260	297063093	1.642	13.5526
chr6	171115067	164092493	0.959	7.8836
chr7	159138663	226503622	1.4233	11.5519

chr8	146364022	263542835	1.8006	19.2227
chr9	141213431	123487061	0.8745	7.726
chr10	135534747	238339742	1.7585	13.0181
chr11	135006516	225108316	1.6674	12.2422
chr12	133851895	237333743	1.7731	13.086
chr13	115169878	59107641	0.5132	4.8057
chr14	107349540	137956820	1.2851	10.3821
chr15	102531392	228894146	2.2324	17.4406
chr16	90354753	232302206	2.571	20.8291
chr17	81195210	198946631	2.4502	15.9713
chr18	78077248	52645107	0.6743	5.6851
chr19	59128983	252126072	4.264	25.6814
chr20	63025520	117274933	1.8608	14.7361
chr21	48129895	53512677	1.1118	10.996
chr22	51304566	63726105	1.2421	9.3221
chrMT	16571	8399	0.5068	1.2749
chrX	155270560	351545790	2.2641	20.1389
chrY	59373566	3982276	0.0671	2.5273

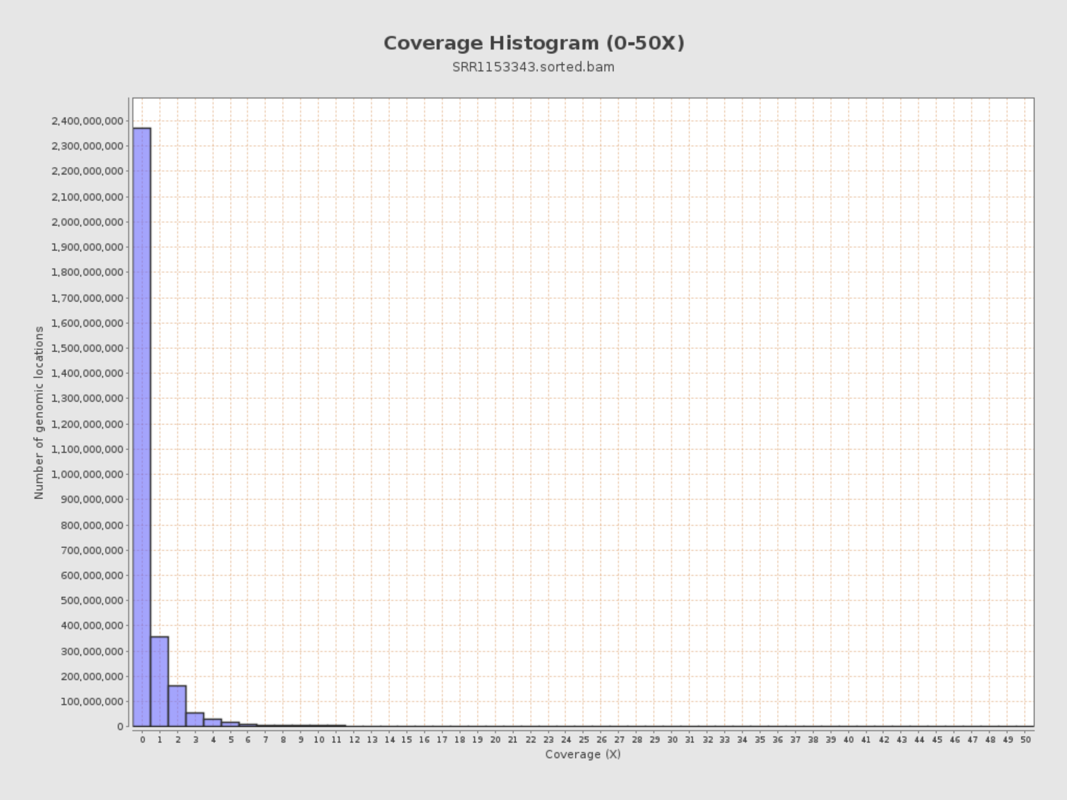
3. Results : Coverage across reference



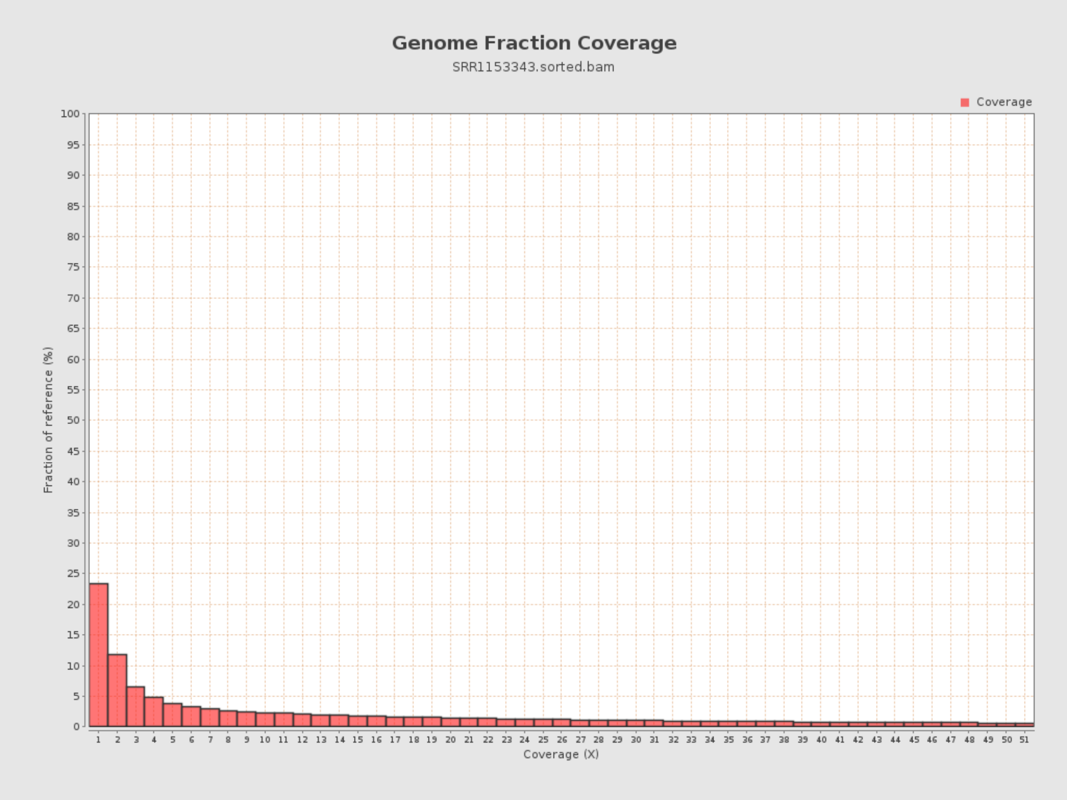
4. Results : Coverage Histogram



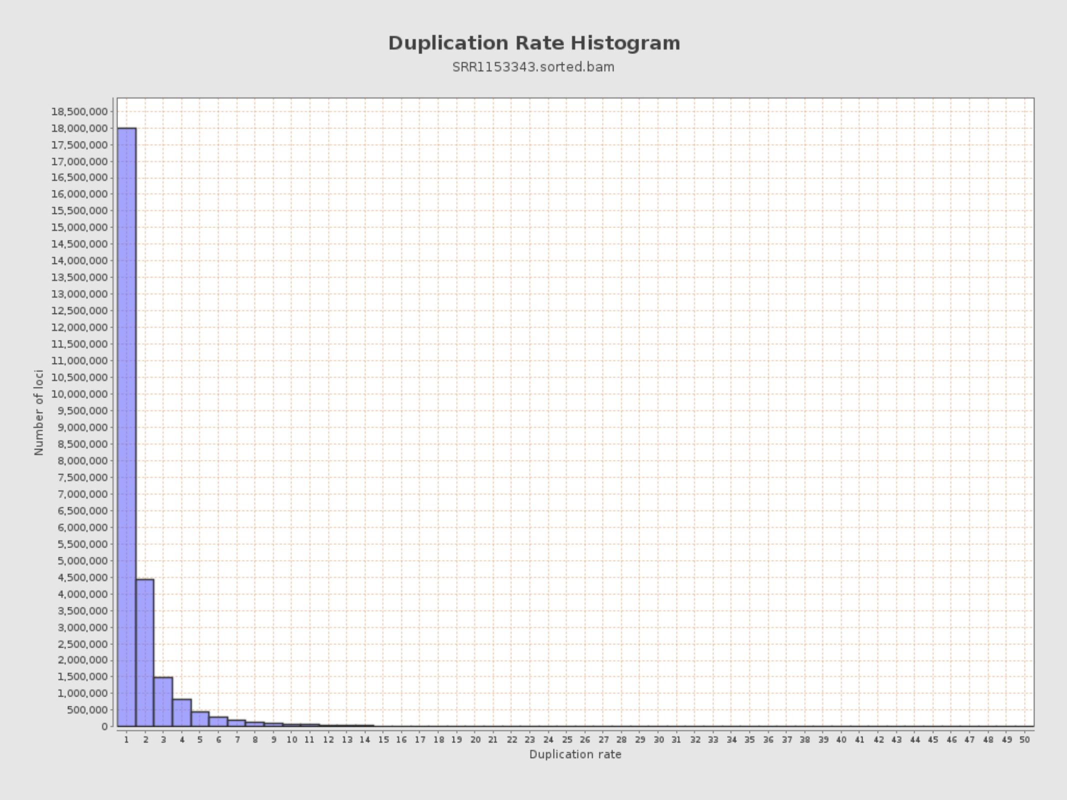
5. Results : Coverage Histogram (0-50X)



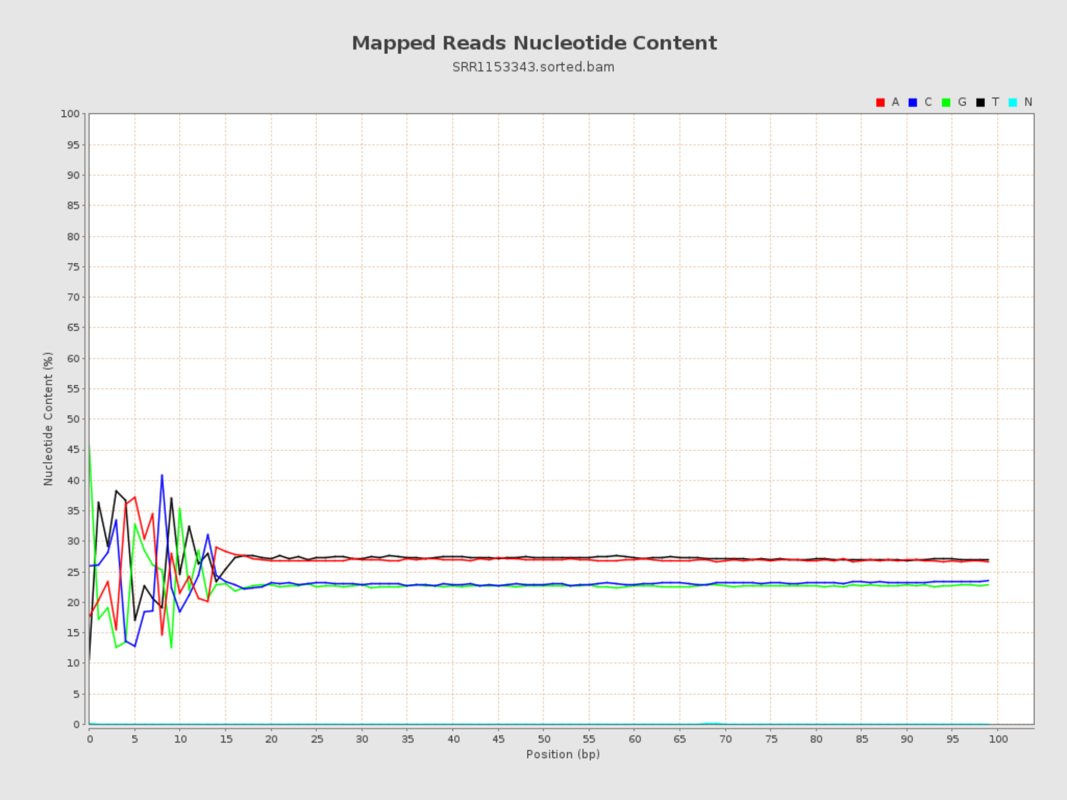
6. Results : Genome Fraction Coverage



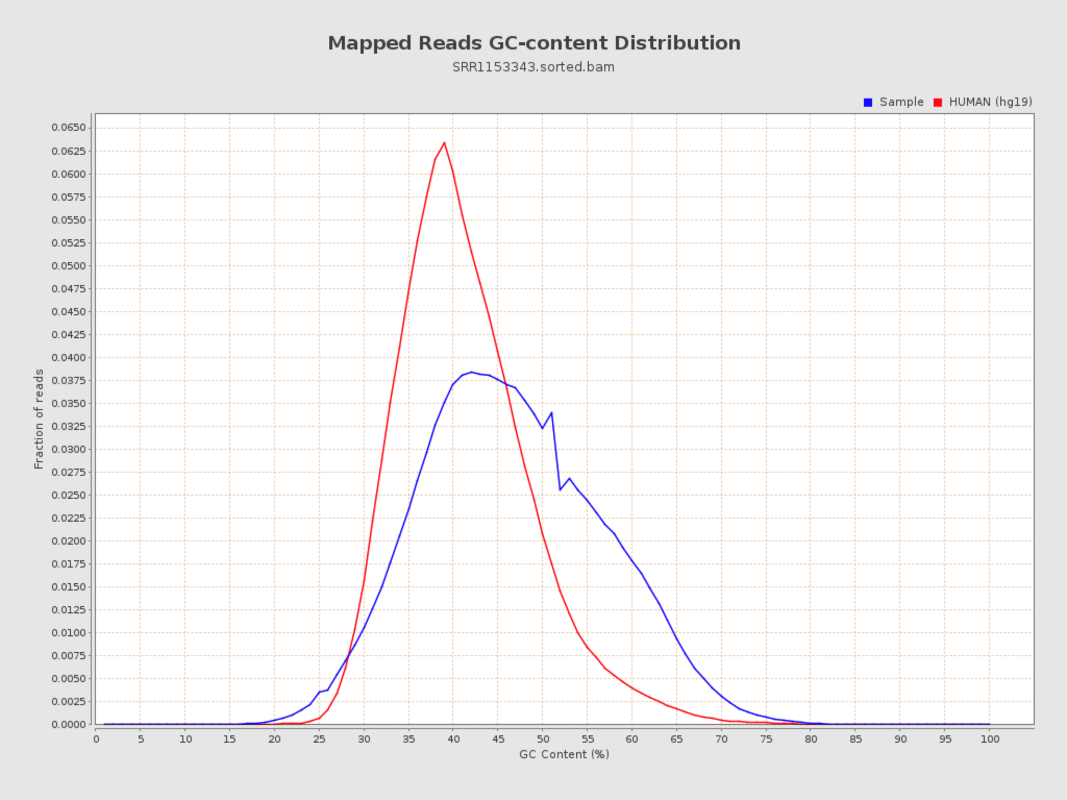
7. Results : Duplication Rate Histogram



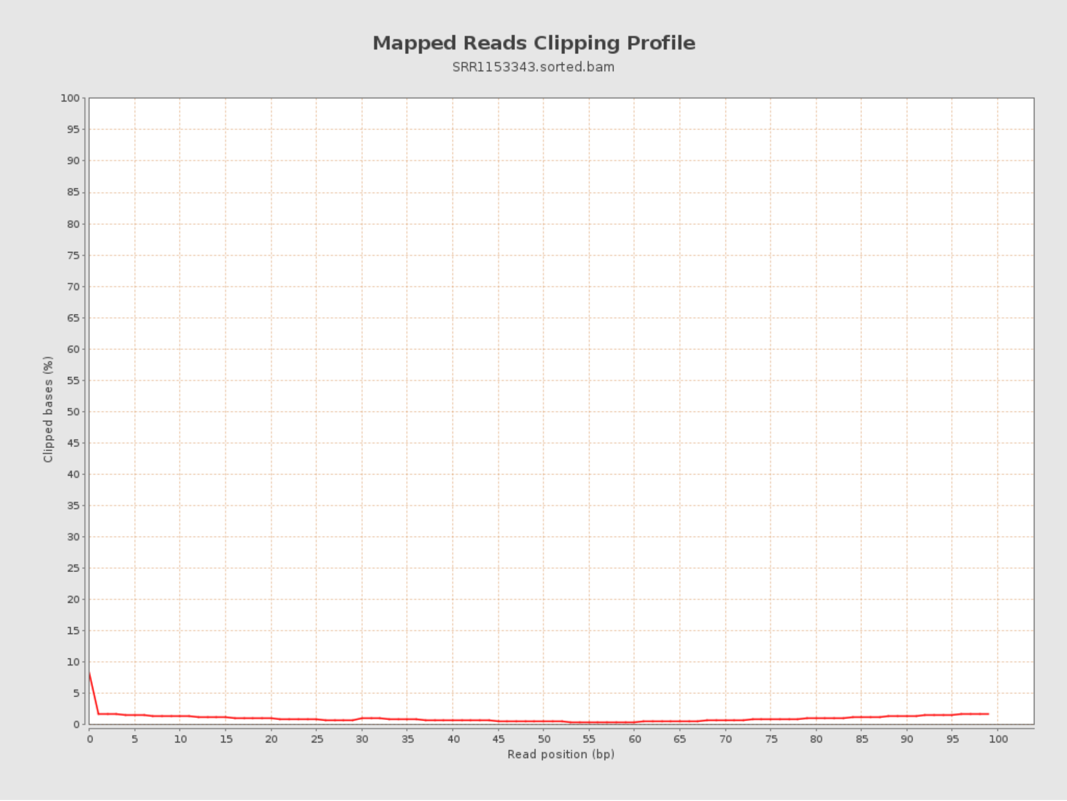
8. Results : Mapped Reads Nucleotide Content



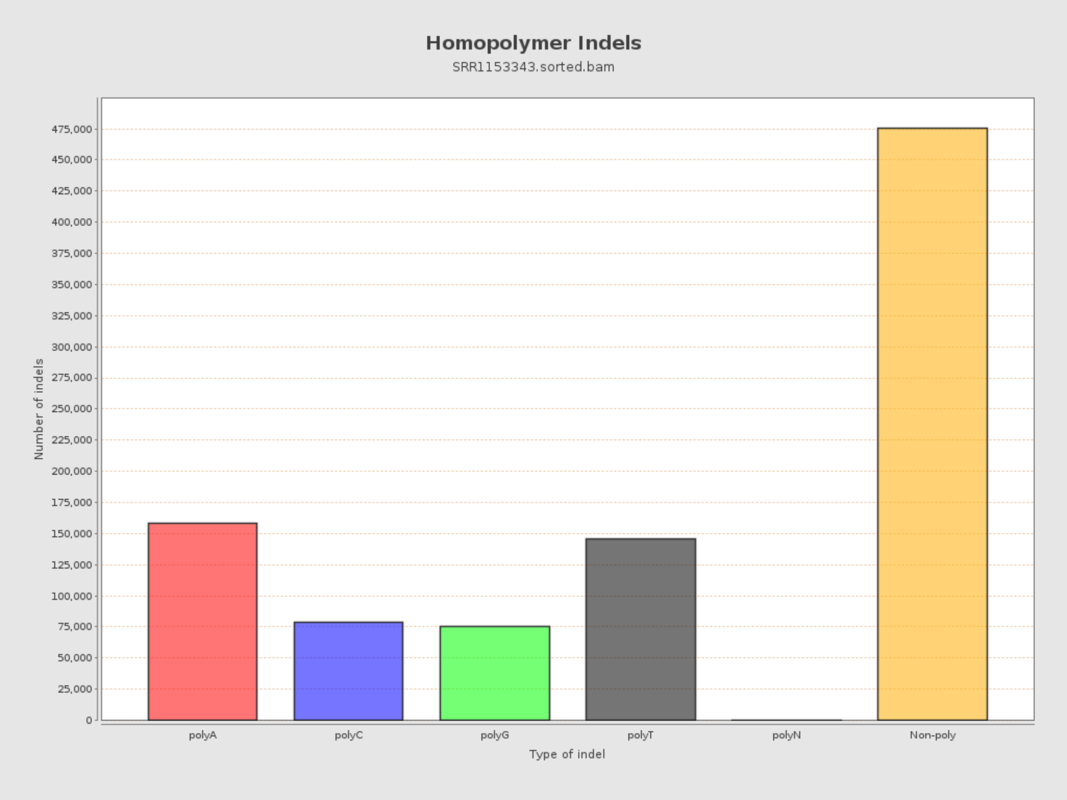
9. Results : Mapped Reads GC-content Distribution



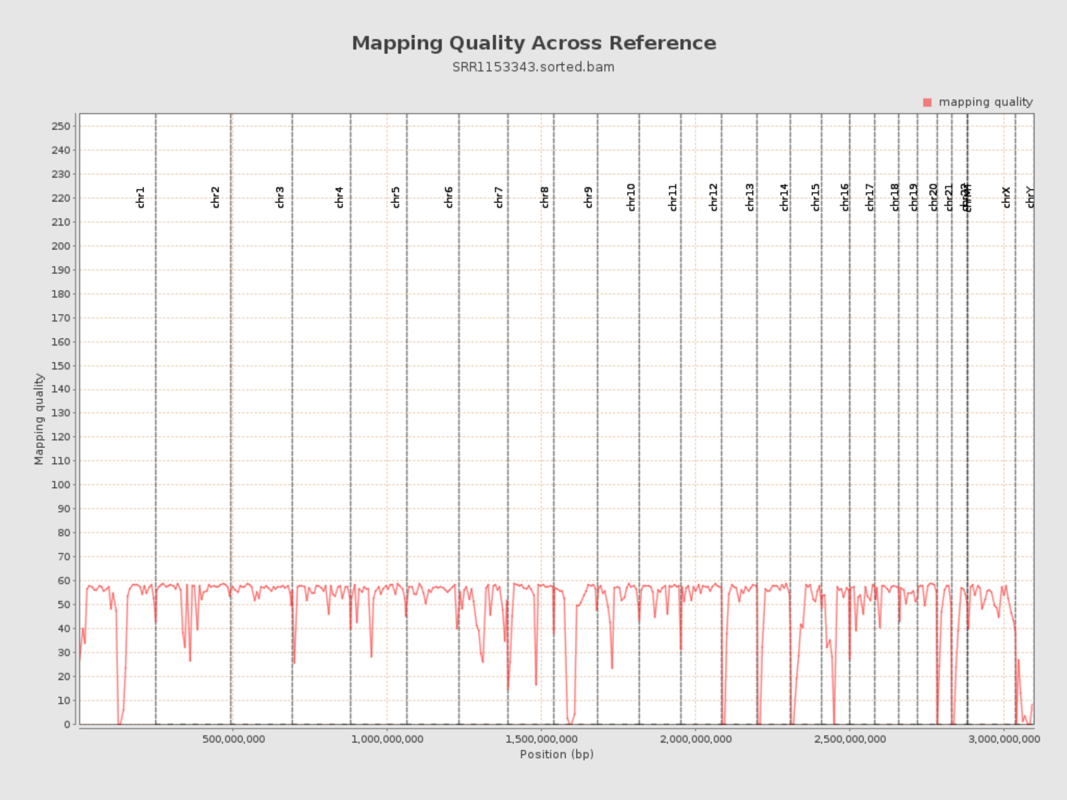
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram