Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 11:36:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153366.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_SRR1153366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153366.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 11:36:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	111,308,230
Mapped reads	108,902,312 / 97.84%
Unmapped reads	2,405,918 / 2.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	680,264 / 0.61%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	54,802,421 / 49.23%
Duplication rate	33.18%
Clipped reads	10,979,964 / 9.86%

2.2. ACGT Content

Number/percentage of A's	2,683,004,945 / 25.18%
Number/percentage of C's	2,646,216,628 / 24.83%
Number/percentage of T's	2,706,904,375 / 25.4%
Number/percentage of G's	2,619,552,581 / 24.58%
Number/percentage of N's	1,717,108 / 0.02%
GC Percentage	49.41%

2.3. Coverage

Mean	3.4432

Standard Deviation	28.1791

2.4. Mapping Quality

Mean Mapping Quality	49.31

2.5. Mismatches and indels

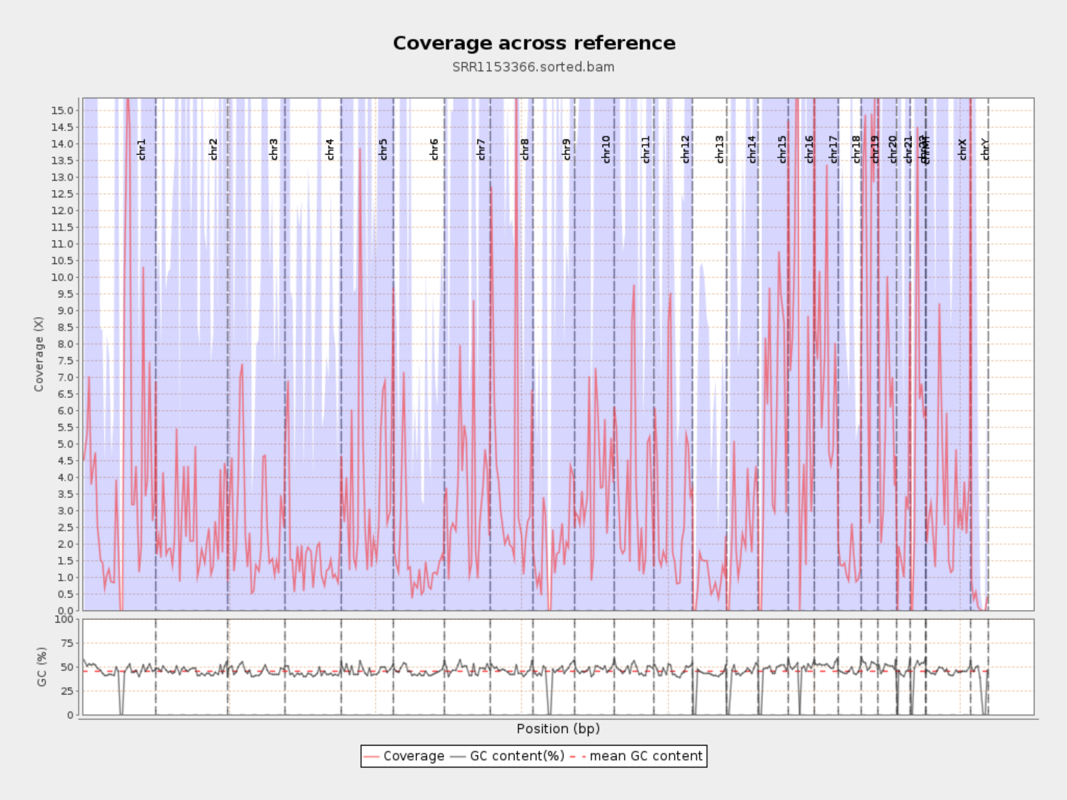
General error rate	0.4%
Mismatches	42,002,044
Insertions	608,207
Mapped reads with at least one insertion	0.55%
Deletions	777,005
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.02%

2.6. Chromosome stats

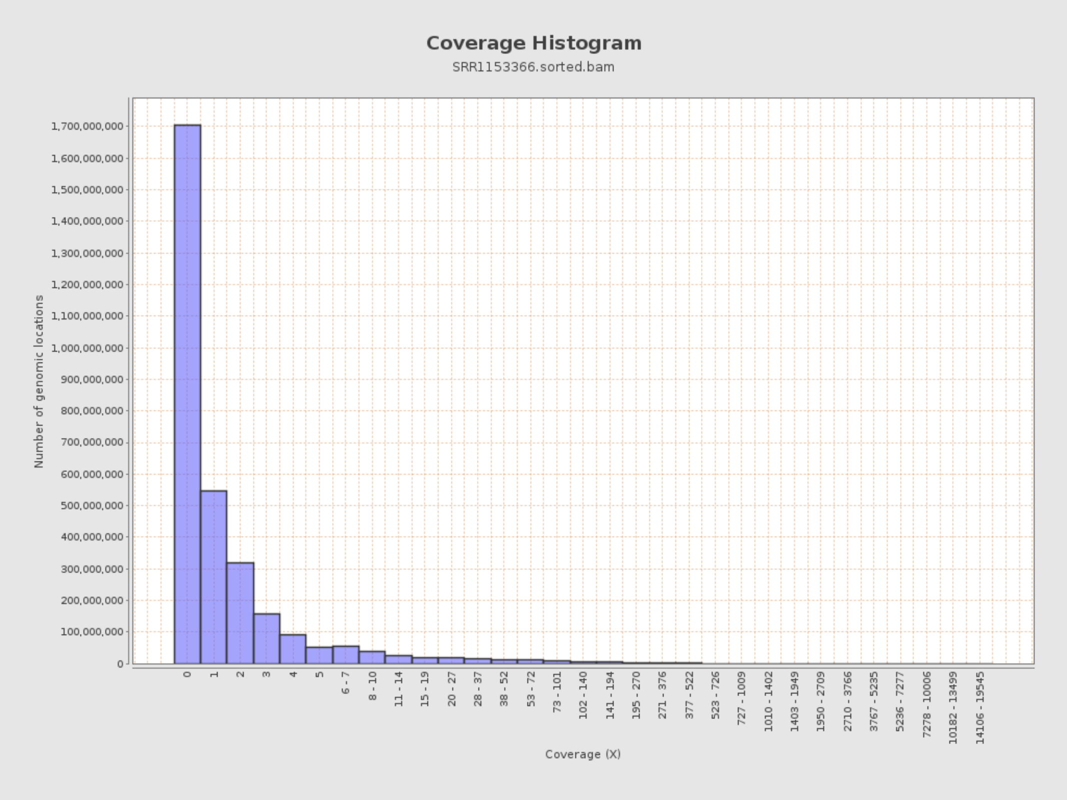
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1026498594	4.1183	26.7473
chr2	243199373	596848839	2.4542	15.5904
chr3	198022430	508255955	2.5667	15.8978
chr4	191154276	329845138	1.7255	16.1094
chr5	180915260	700660968	3.8729	56.1313
chr6	171115067	265659190	1.5525	10.8833
chr7	159138663	563674253	3.542	31.8546

chr8	146364022	609374555	4.1634	50.6719
chr9	141213431	259778913	1.8396	11.1499
chr10	135534747	521789358	3.8499	20.73
chr11	135006516	496644613	3.6787	19.178
chr12	133851895	457503737	3.418	18.5748
chr13	115169878	108413499	0.9413	6.1643
chr14	107349540	252316534	2.3504	13.6191
chr15	102531392	564536239	5.506	32.617
chr16	90354753	625799669	6.926	39.1383
chr17	81195210	595597005	7.3354	44.7869
chr18	78077248	106128585	1.3593	9.4685
chr19	59128983	746671353	12.6278	48.6945
chr20	63025520	343345302	5.4477	27.0578
chr21	48129895	132946103	2.7622	31.2915
chr22	51304566	287333644	5.6005	33.915
chrMT	16571	65283	3.9396	2.6343
chrX	155270560	544100938	3.5042	20.8551
chrY	59373566	15325321	0.2581	11.591

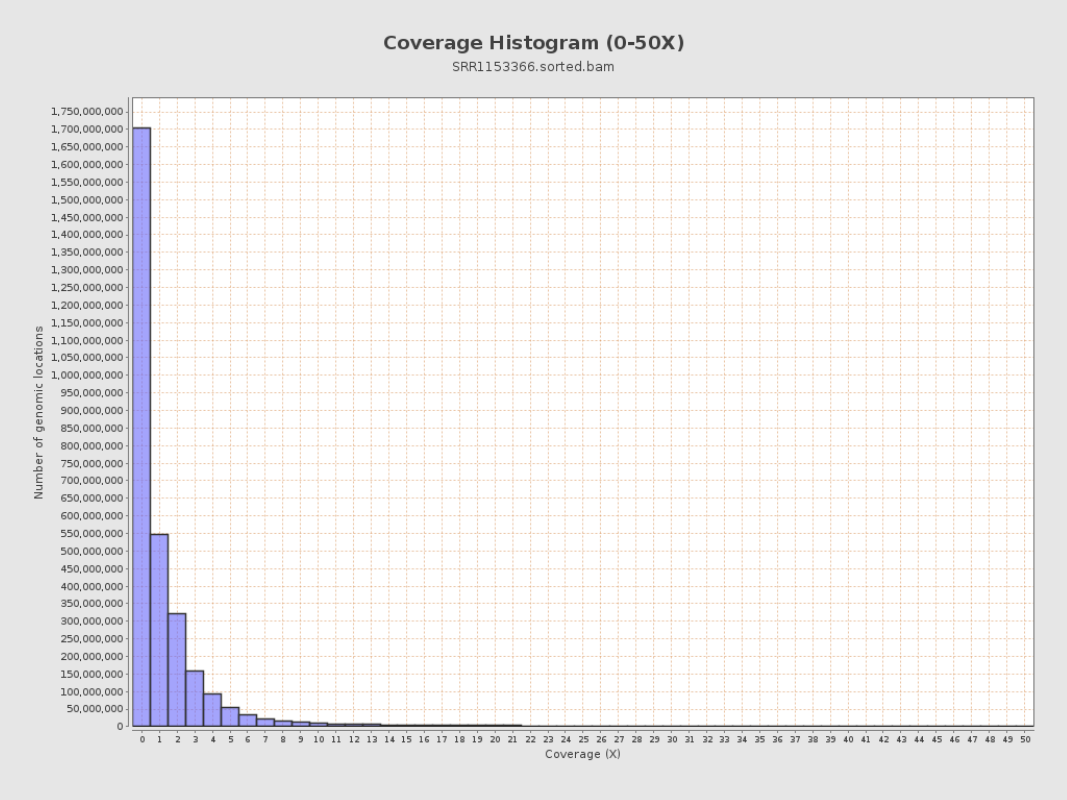
3. Results : Coverage across reference



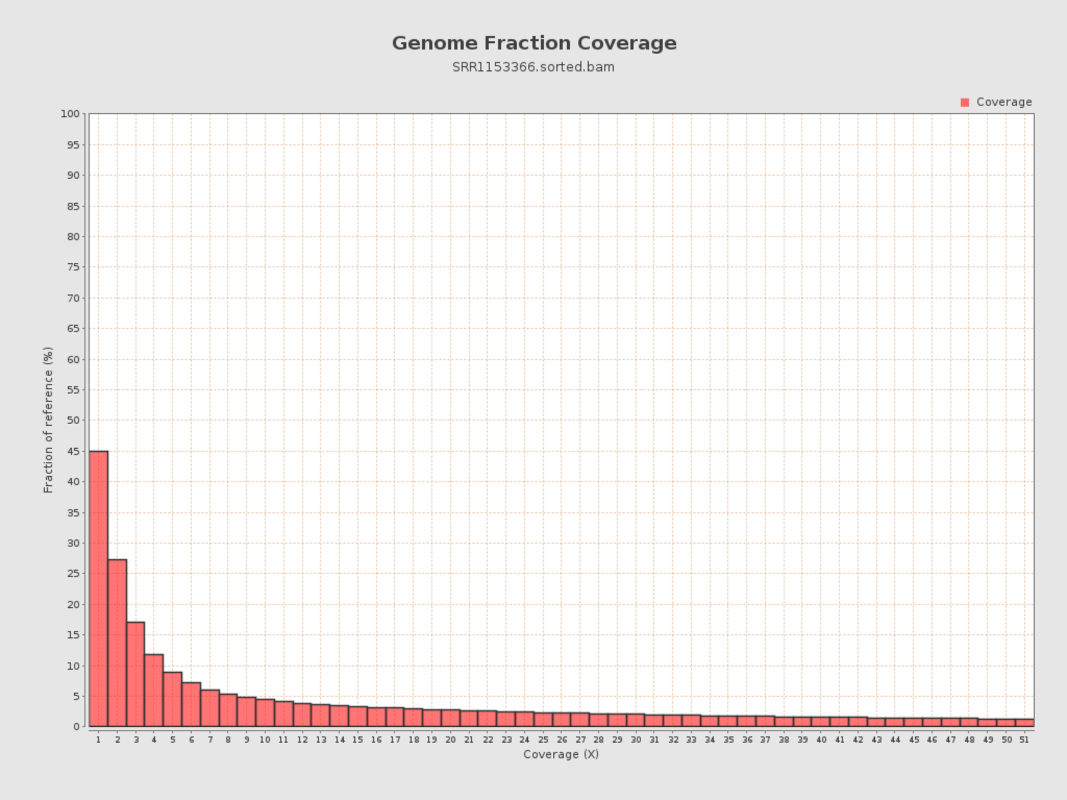
4. Results : Coverage Histogram



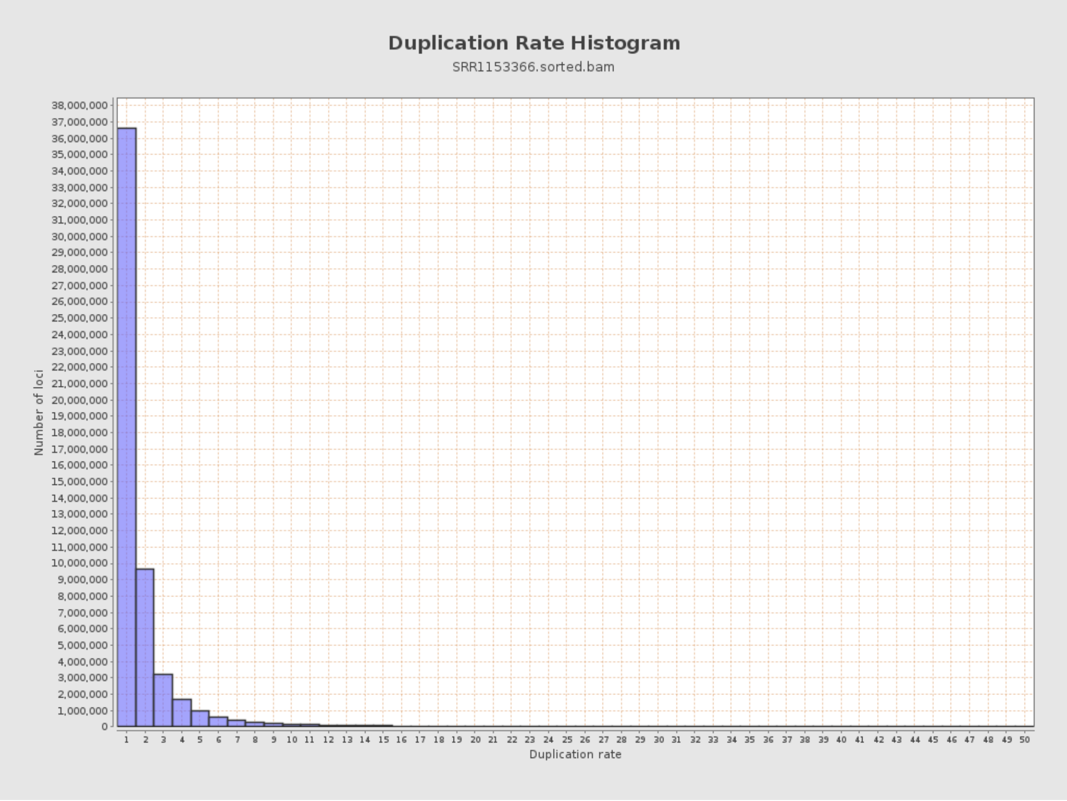
5. Results : Coverage Histogram (0-50X)



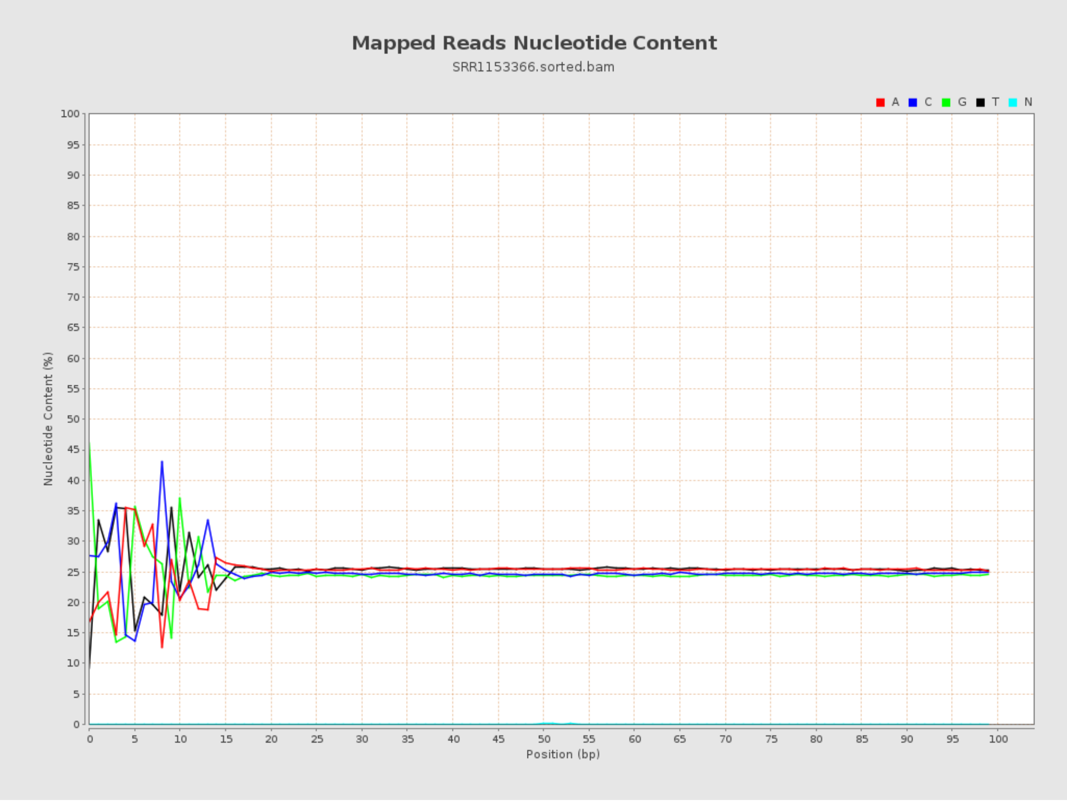
6. Results : Genome Fraction Coverage



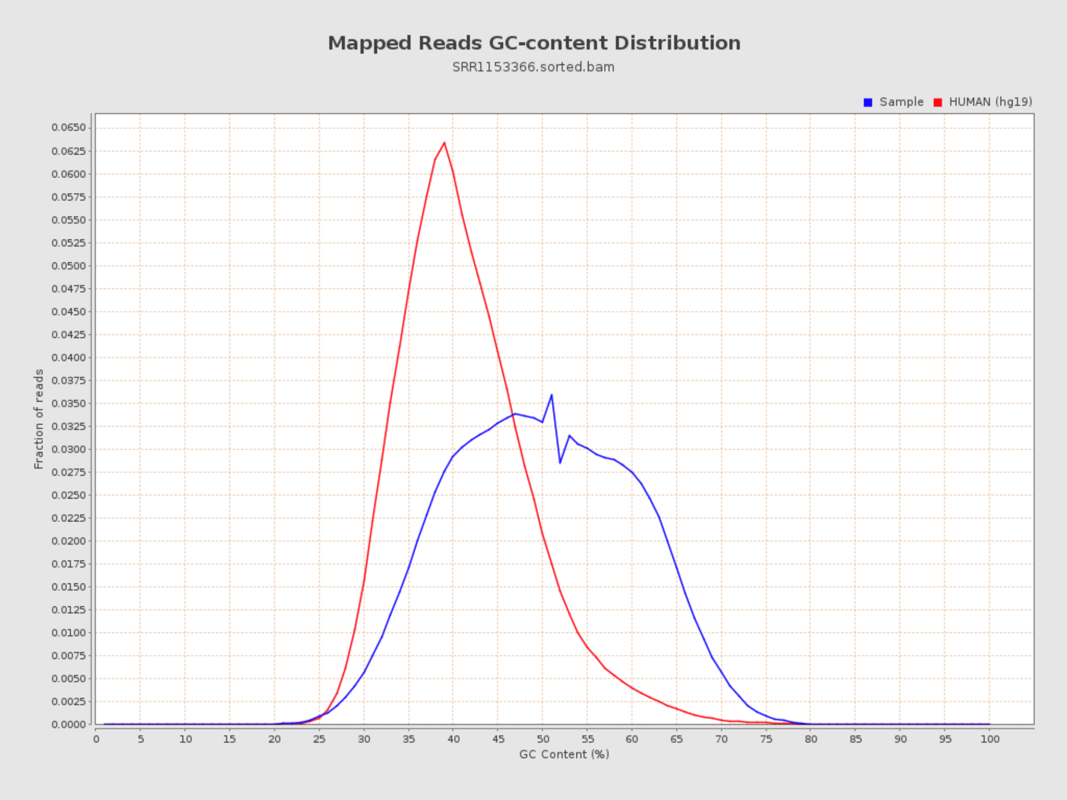
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

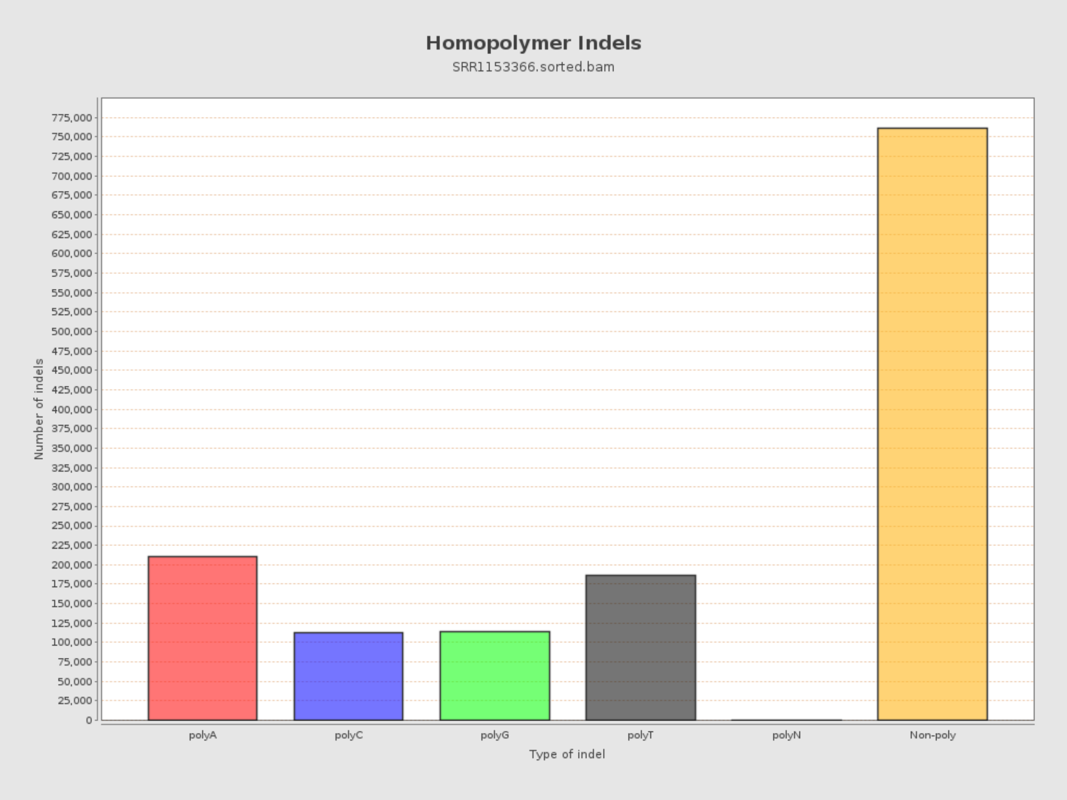


9. Results : Mapped Reads GC-content Distribution

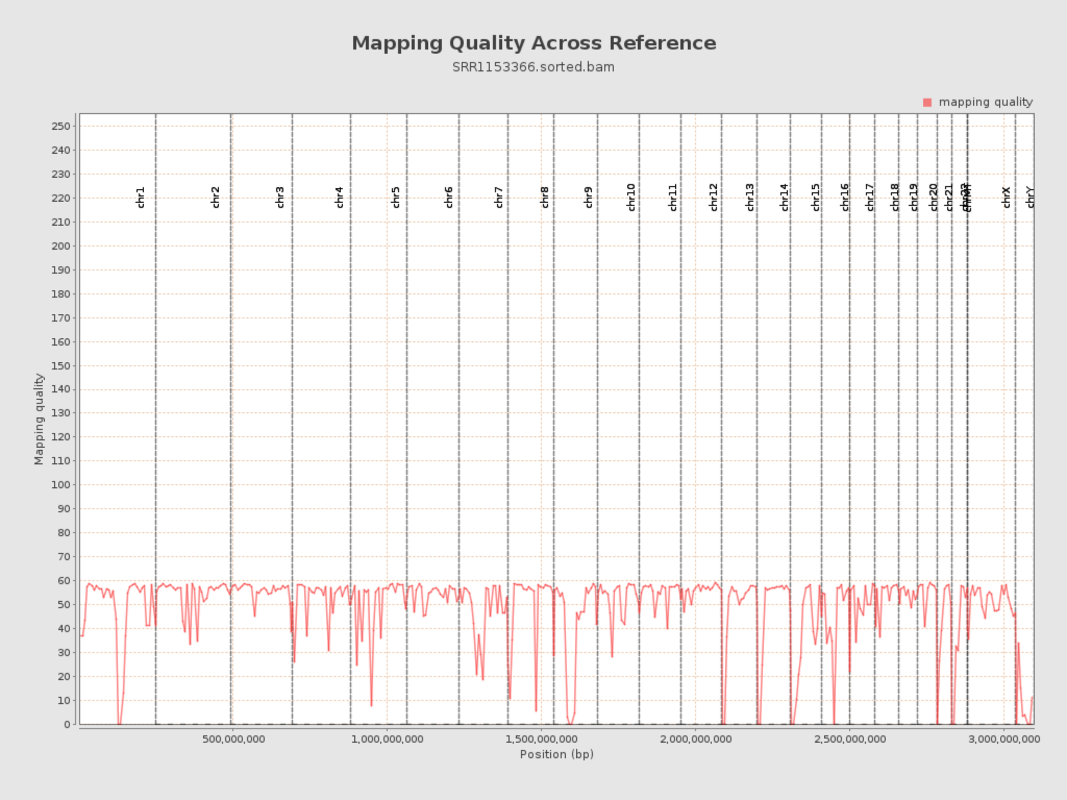


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram