Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 06:17:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153313.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_SRR1153313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 06:17:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	183,203,526
Mapped reads	177,189,650 / 96.72%
Unmapped reads	6,013,876 / 3.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,062,290 / 0.58%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	115,665,973 / 63.14%
Duplication rate	52.91%
Clipped reads	14,651,448 / 8%

2.2. ACGT Content

Number/percentage of A's	4,006,275,702 / 22.91%
Number/percentage of C's	4,737,197,452 / 27.09%
Number/percentage of T's	4,028,958,512 / 23.04%
Number/percentage of G's	4,694,214,602 / 26.84%
Number/percentage of N's	20,320,707 / 0.12%
GC Percentage	53.93%

2.3. Coverage

Mean	5.6494

Standard Deviation	63.4686

2.4. Mapping Quality

Mean Mapping Quality	48.6

2.5. Mismatches and indels

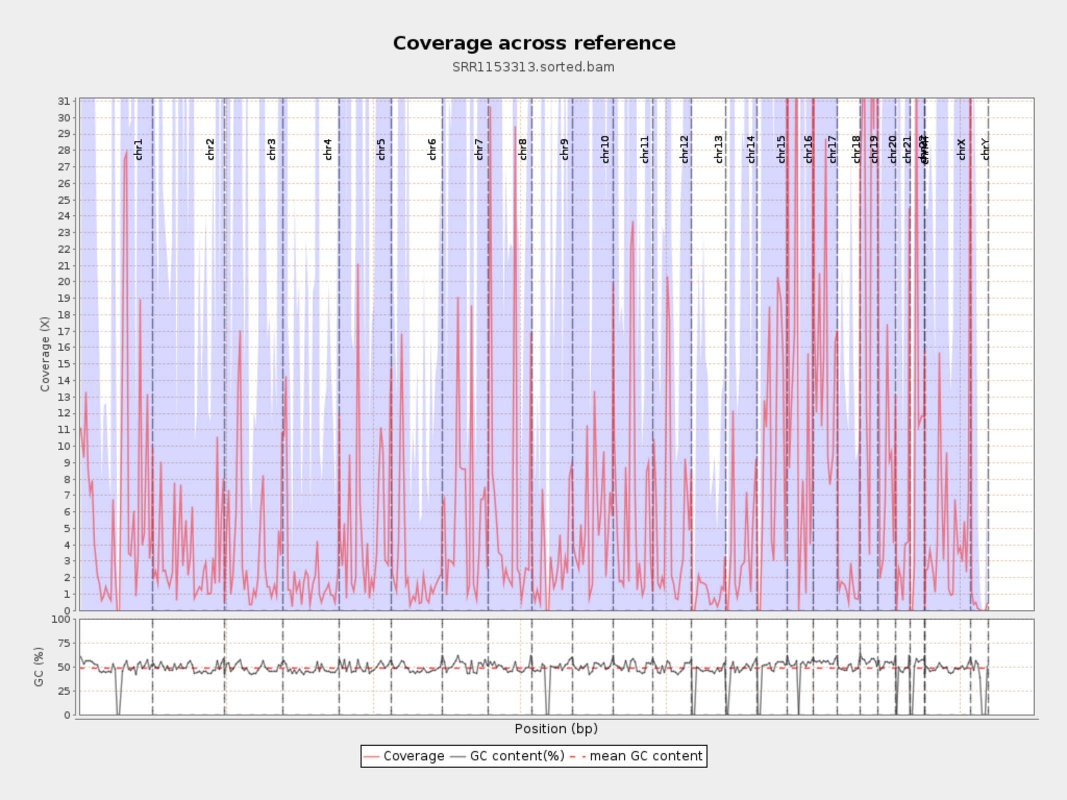
General error rate	0.64%
Mismatches	111,340,558
Insertions	712,397
Mapped reads with at least one insertion	0.39%
Deletions	791,678
Mapped reads with at least one deletion	0.44%
Homopolymer indels	41.43%

2.6. Chromosome stats

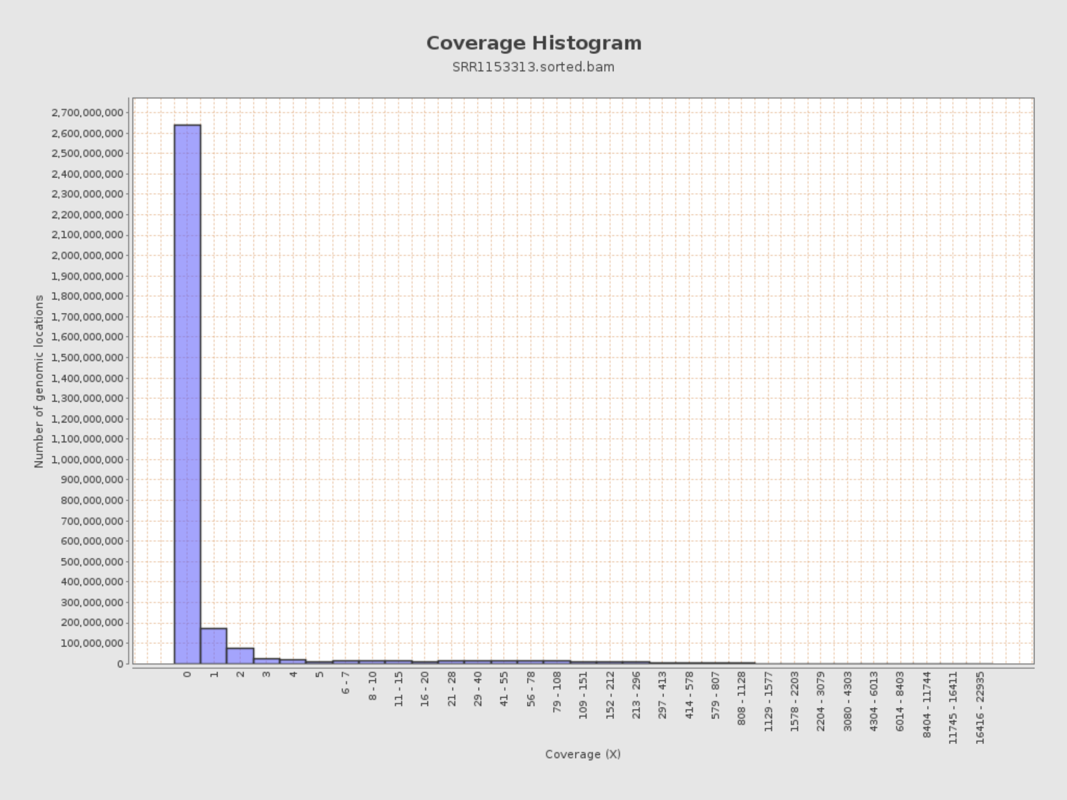
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1678360686	6.7336	57.1791
chr2	243199373	817161593	3.36	31.9808
chr3	198022430	750684735	3.7909	36.7709
chr4	191154276	429697247	2.2479	40.9396
chr5	180915260	956575255	5.2874	104.1264
chr6	171115067	418646273	2.4466	25.3047
chr7	159138663	954245100	5.9963	88.8228

chr8	146364022	964913941	6.5926	110.4846
chr9	141213431	417410928	2.9559	26.5324
chr10	135534747	731304365	5.3957	47.2863
chr11	135006516	908587619	6.73	54.1192
chr12	133851895	746284892	5.5755	43.4434
chr13	115169878	114802839	0.9968	12.0422
chr14	107349540	404236880	3.7656	35.6647
chr15	102531392	959878189	9.3618	72.3472
chr16	90354753	1162114801	12.8617	96.0217
chr17	81195210	1211768943	14.9241	93.889
chr18	78077248	108778640	1.3932	14.322
chr19	59128983	1635617719	27.6619	128.0202
chr20	63025520	517978106	8.2185	60.7937
chr21	48129895	224018971	4.6545	92.6759
chr22	51304566	583791868	11.3789	89.0733
chrMT	16571	3274	0.1976	0.5411
chrX	155270560	775274912	4.9931	44.229
chrY	59373566	16758426	0.2823	16.5398

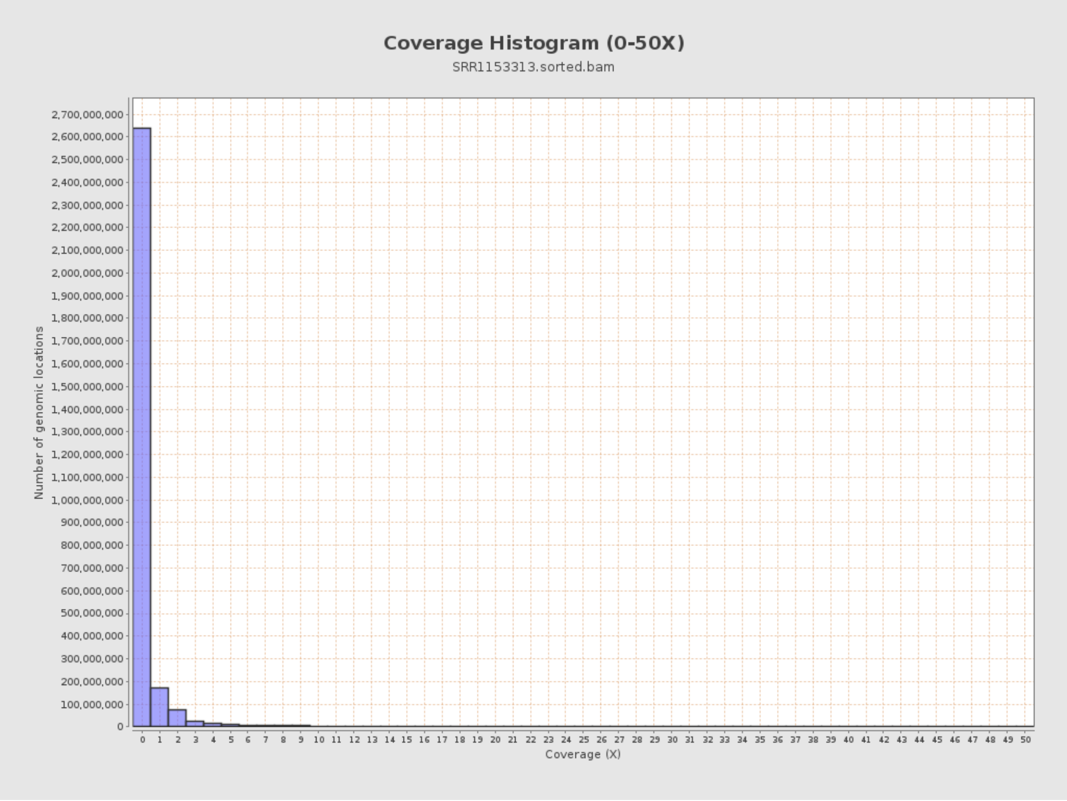
3. Results : Coverage across reference



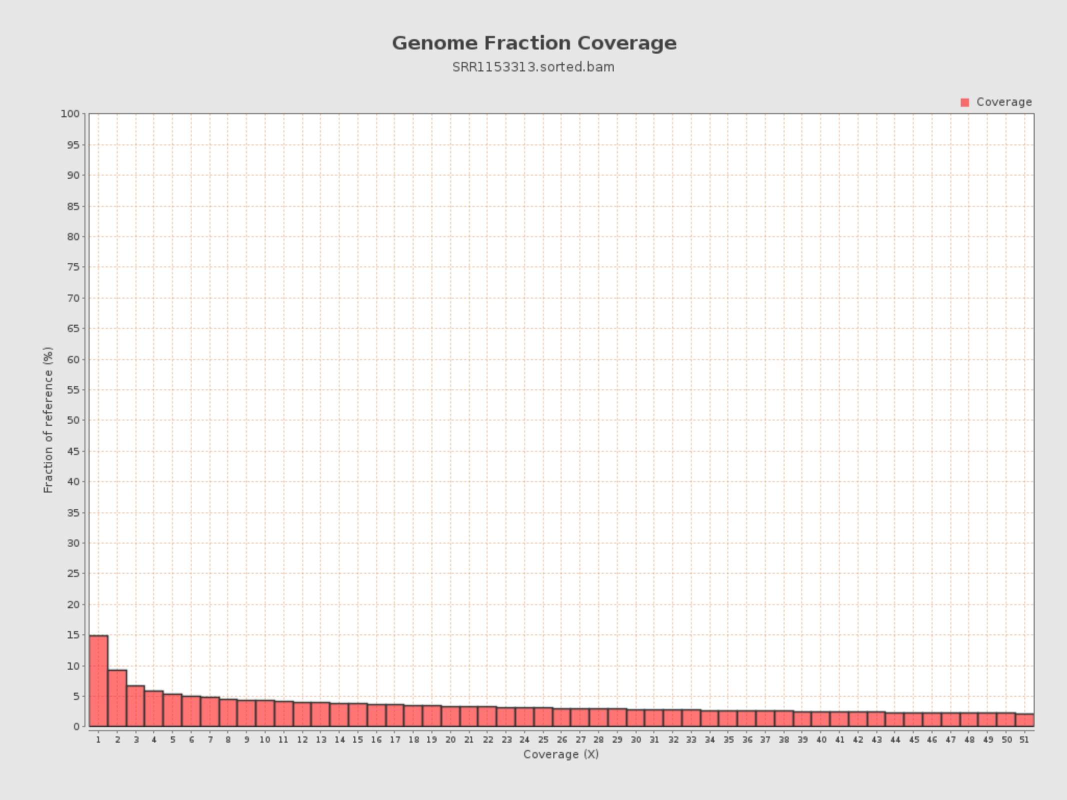
4. Results : Coverage Histogram



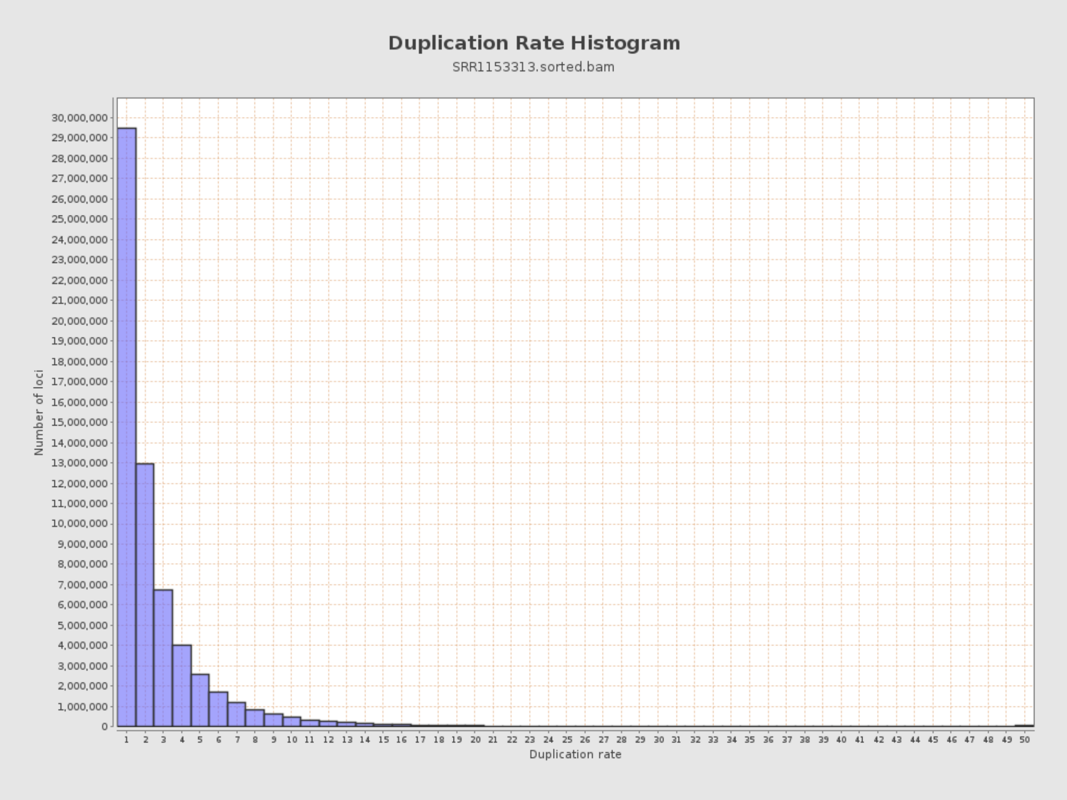
5. Results : Coverage Histogram (0-50X)



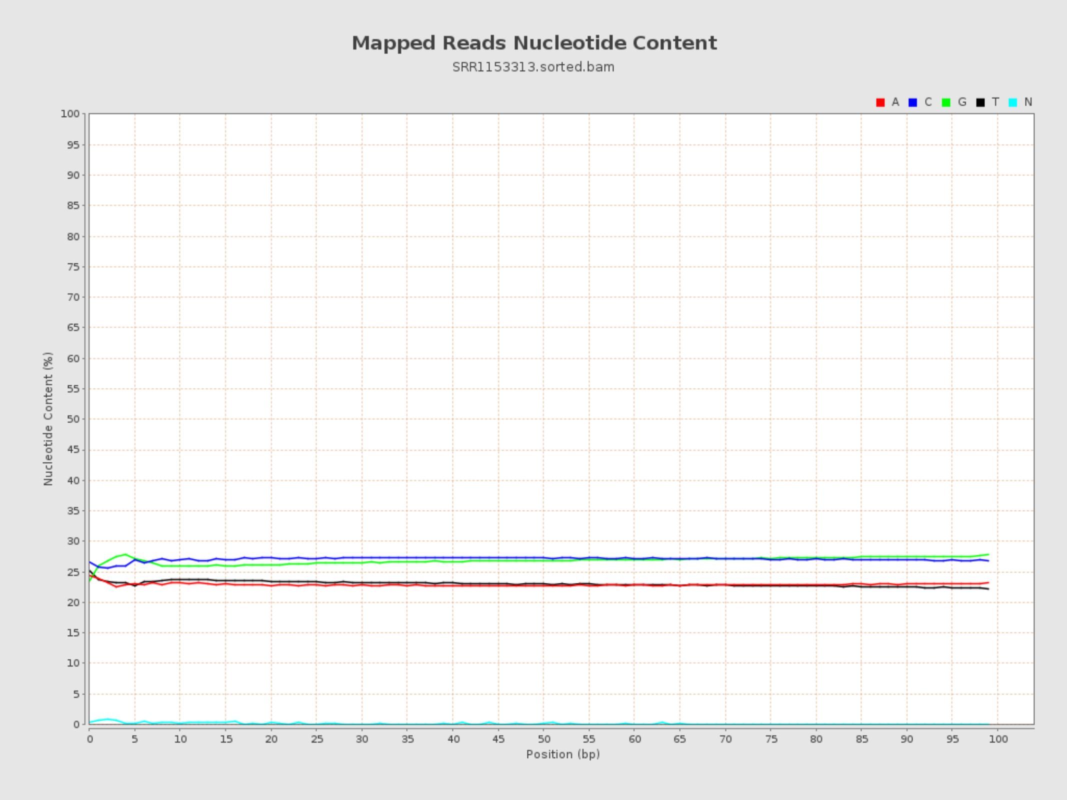
6. Results : Genome Fraction Coverage



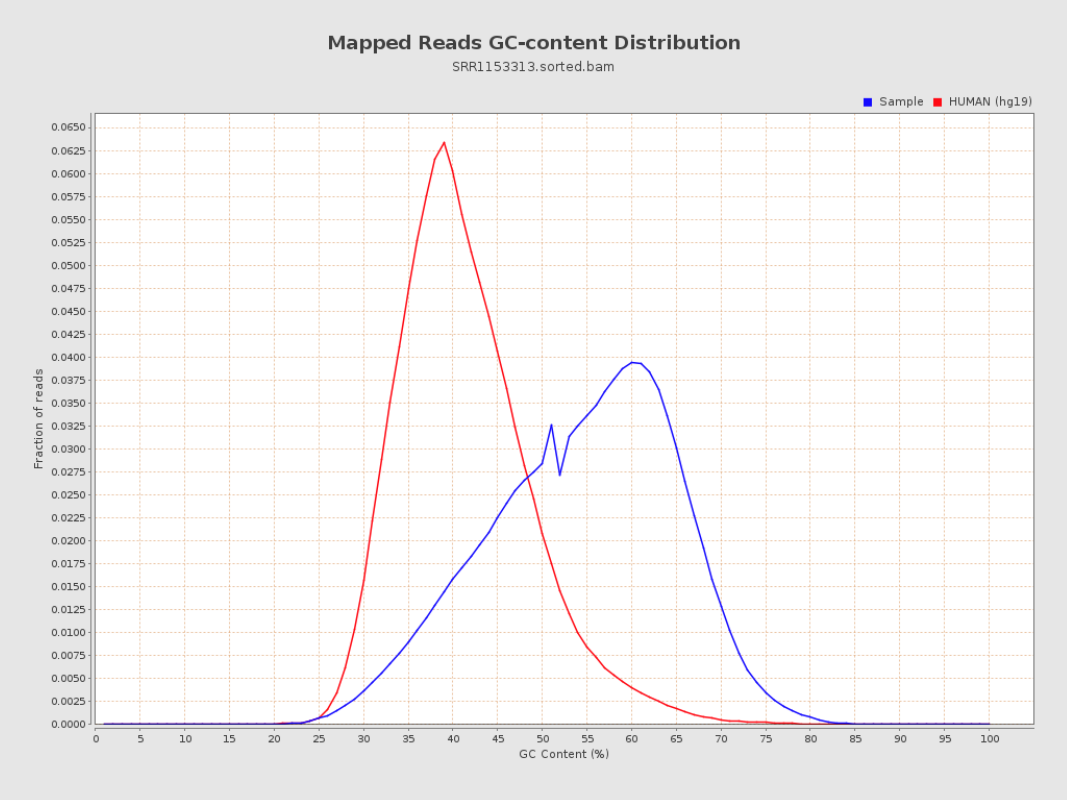
7. Results : Duplication Rate Histogram



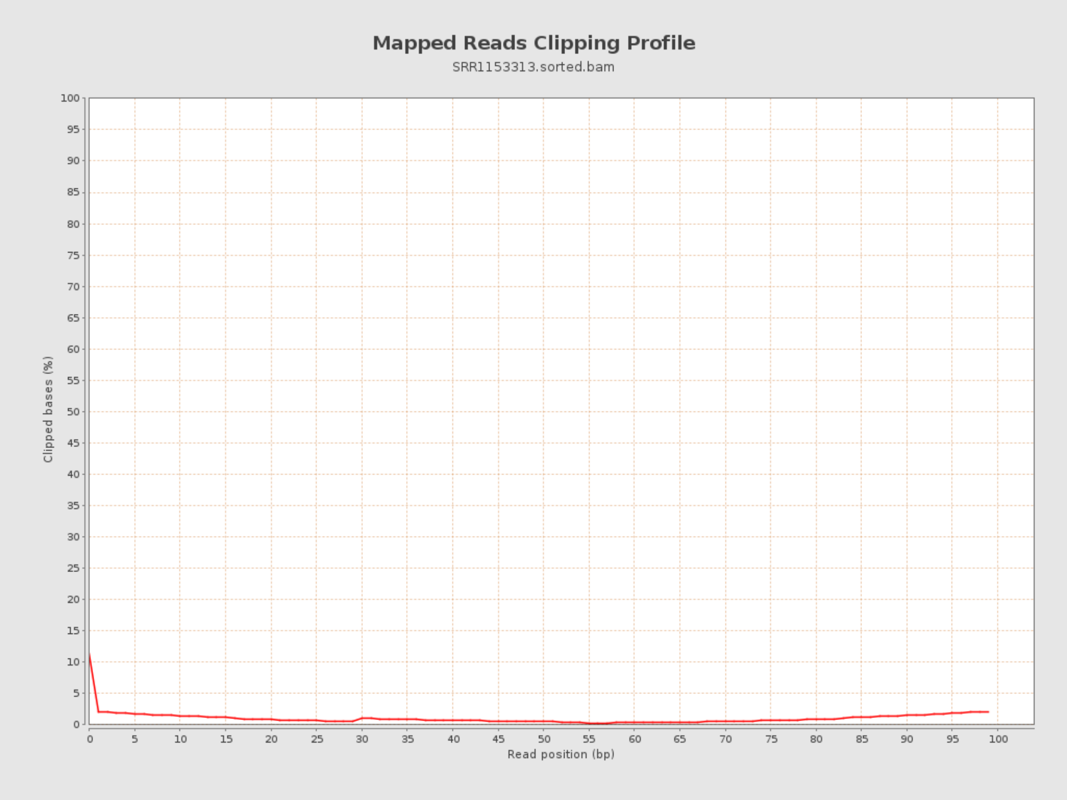
8. Results : Mapped Reads Nucleotide Content



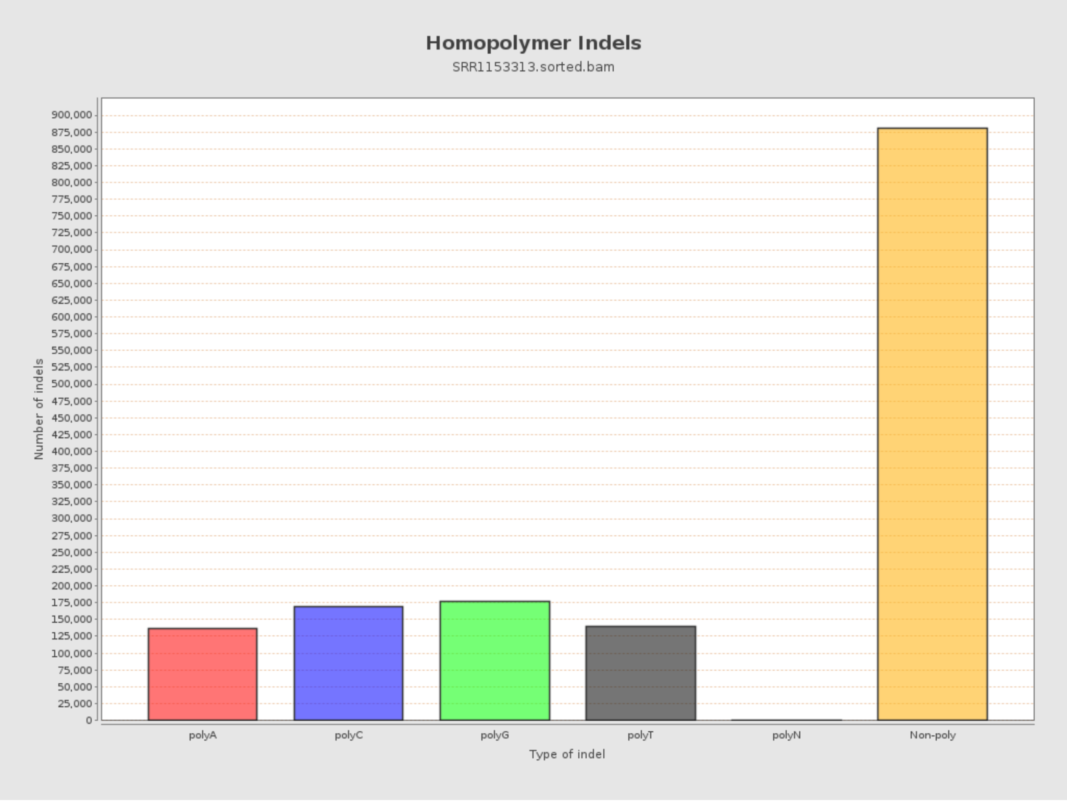
9. Results : Mapped Reads GC-content Distribution



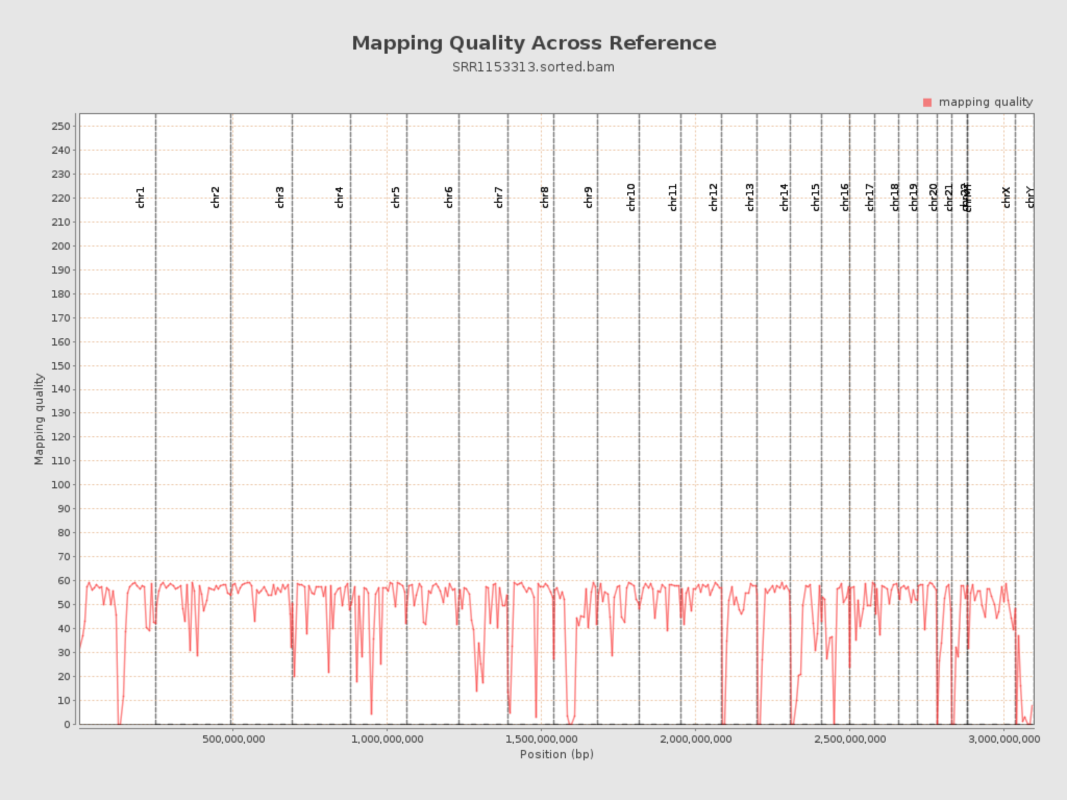
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram