Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 07:40:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153324.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_SRR1153324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 07:40:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	130,158,636
Mapped reads	126,236,035 / 96.99%
Unmapped reads	3,922,601 / 3.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	795,850 / 0.61%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	64,815,513 / 49.8%
Duplication rate	33.52%
Clipped reads	10,414,150 / 8%

2.2. ACGT Content

Number/percentage of A's	3,104,438,919 / 25.01%
Number/percentage of C's	3,102,416,273 / 24.99%
Number/percentage of T's	3,132,183,961 / 25.23%
Number/percentage of G's	3,071,748,135 / 24.75%
Number/percentage of N's	2,538,858 / 0.02%
GC Percentage	49.74%

2.3. Coverage

Mean	4.0105

Standard Deviation	31.9809

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

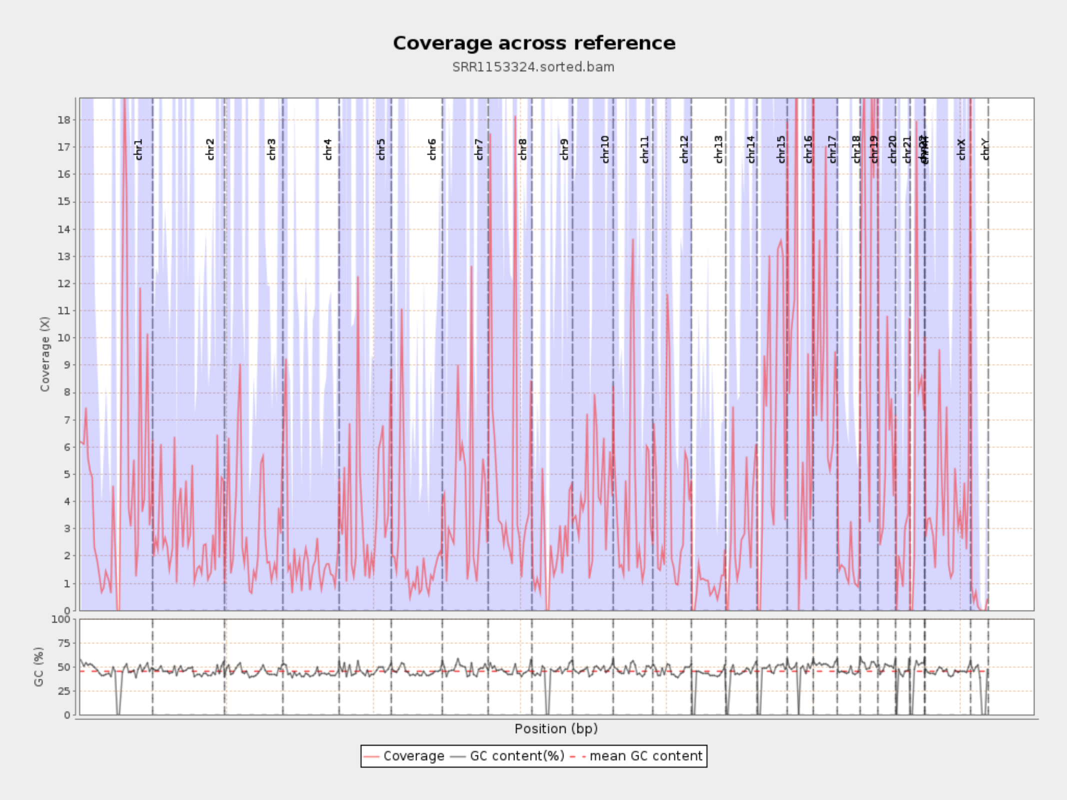
General error rate	0.41%
Mismatches	49,305,350
Insertions	726,371
Mapped reads with at least one insertion	0.57%
Deletions	933,457
Mapped reads with at least one deletion	0.73%
Homopolymer indels	45.14%

2.6. Chromosome stats

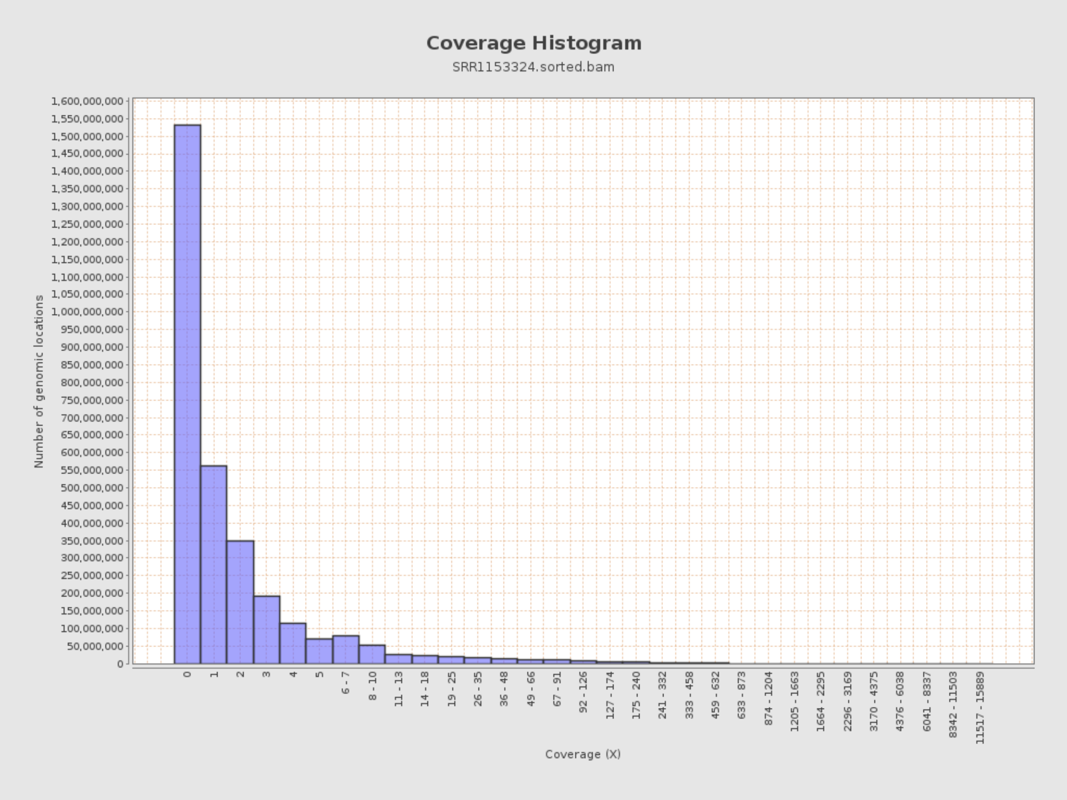
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1186360259	4.7597	31.6344
chr2	243199373	701369554	2.8839	16.555
chr3	198022430	585286658	2.9557	16.7726
chr4	191154276	387494467	2.0271	21.2484
chr5	180915260	712408113	3.9378	59.8009
chr6	171115067	349598703	2.0431	13.4376
chr7	159138663	656433872	4.1249	34.0085

chr8	146364022	745840113	5.0958	60.5789
chr9	141213431	301571104	2.1356	12.8934
chr10	135534747	583822170	4.3075	23.2229
chr11	135006516	573308050	4.2465	22.5448
chr12	133851895	517888365	3.8691	20.2496
chr13	115169878	102408338	0.8892	6.3905
chr14	107349540	321774686	2.9974	17.6298
chr15	102531392	716311780	6.9863	41.2788
chr16	90354753	714173009	7.9041	47.1751
chr17	81195210	730862763	9.0013	48.6156
chr18	78077248	120722565	1.5462	11.5299
chr19	59128983	902023919	15.2552	58.007
chr20	63025520	379906867	6.0278	29.5197
chr21	48129895	137785805	2.8628	27.9395
chr22	51304566	357578036	6.9697	40.1284
chrMT	16571	166424	10.0431	5.0476
chrX	155270560	613329883	3.9501	21.7553
chrY	59373566	16975230	0.2859	11.1914

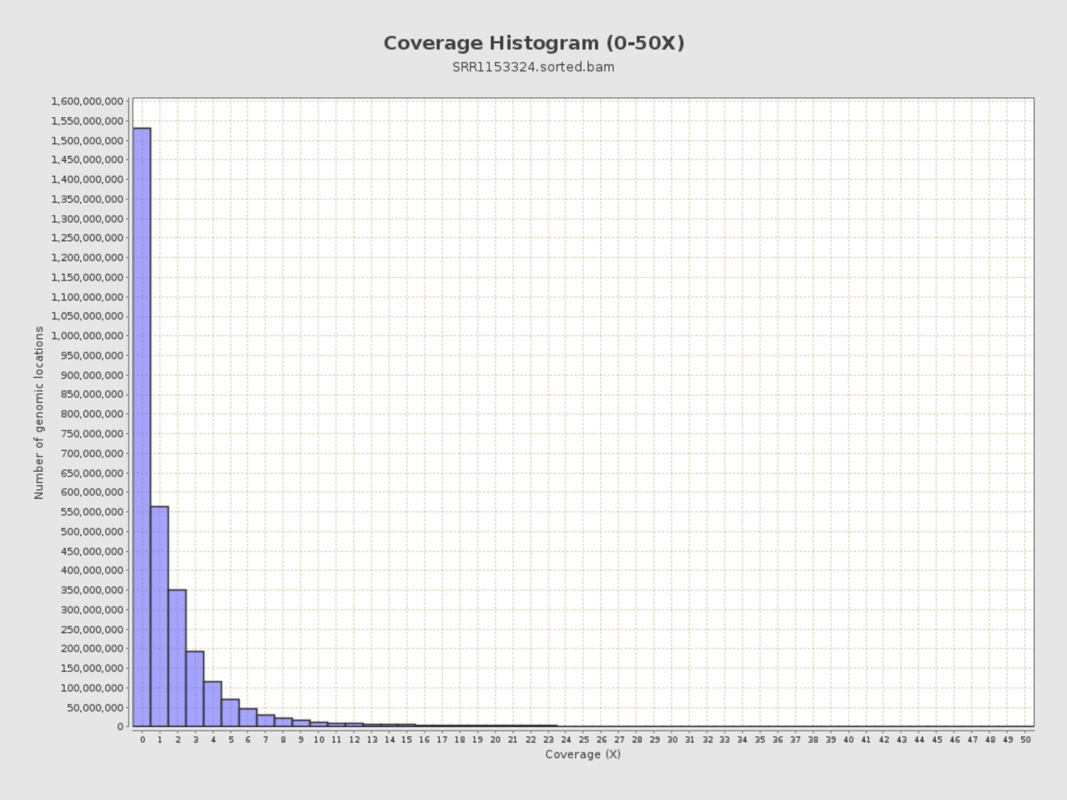
3. Results : Coverage across reference



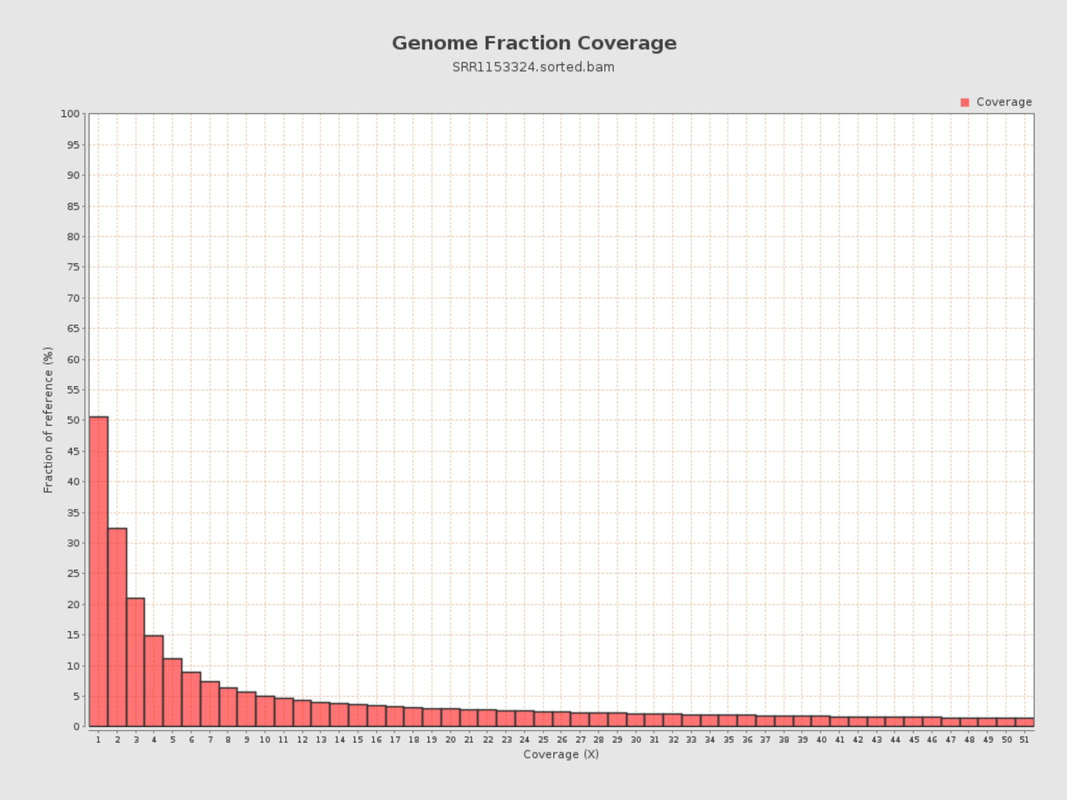
4. Results : Coverage Histogram



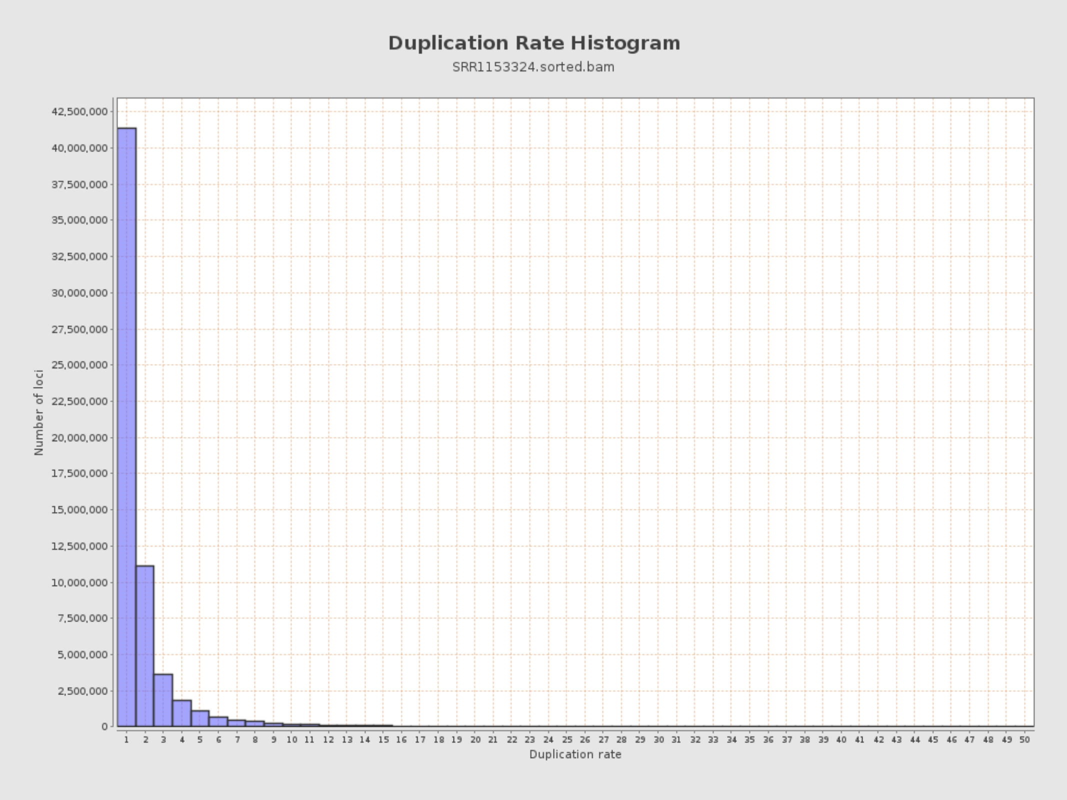
5. Results : Coverage Histogram (0-50X)



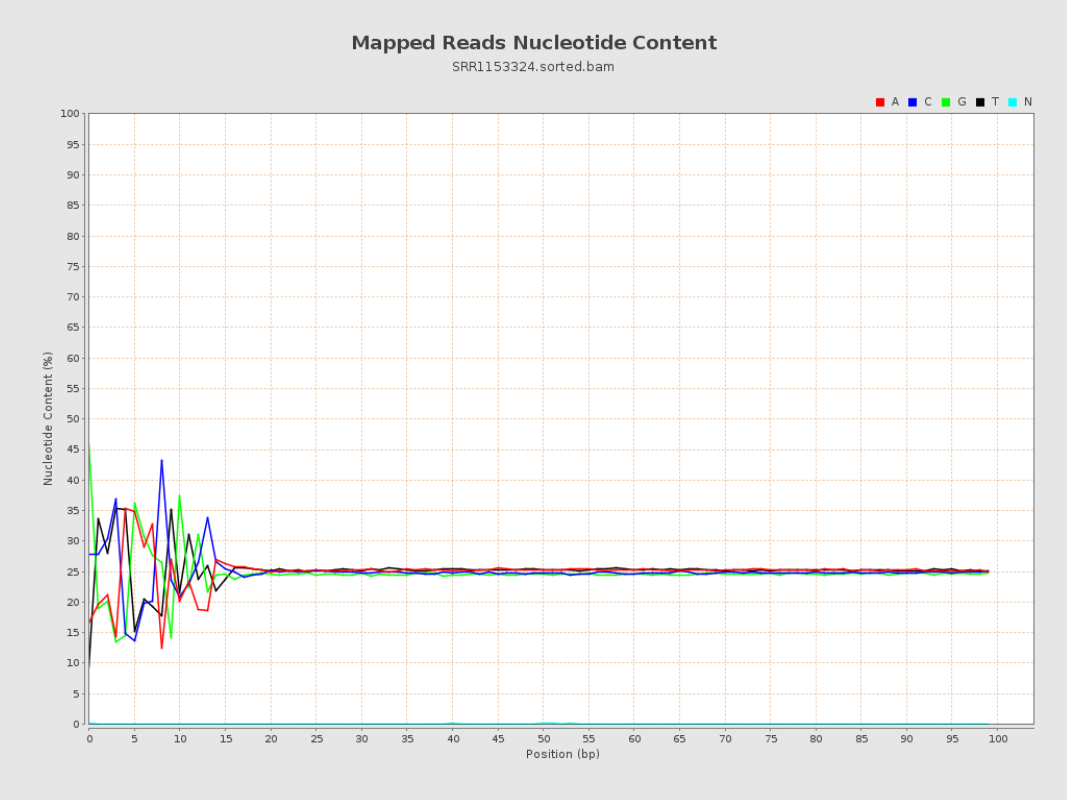
6. Results : Genome Fraction Coverage



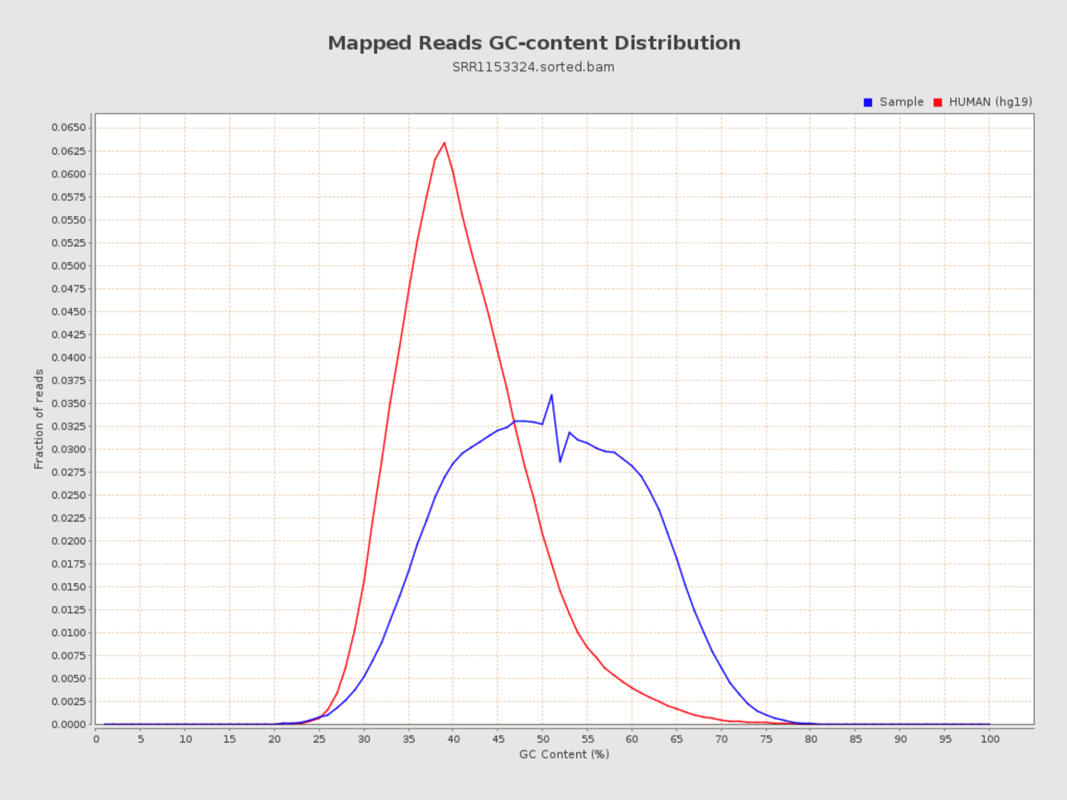
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

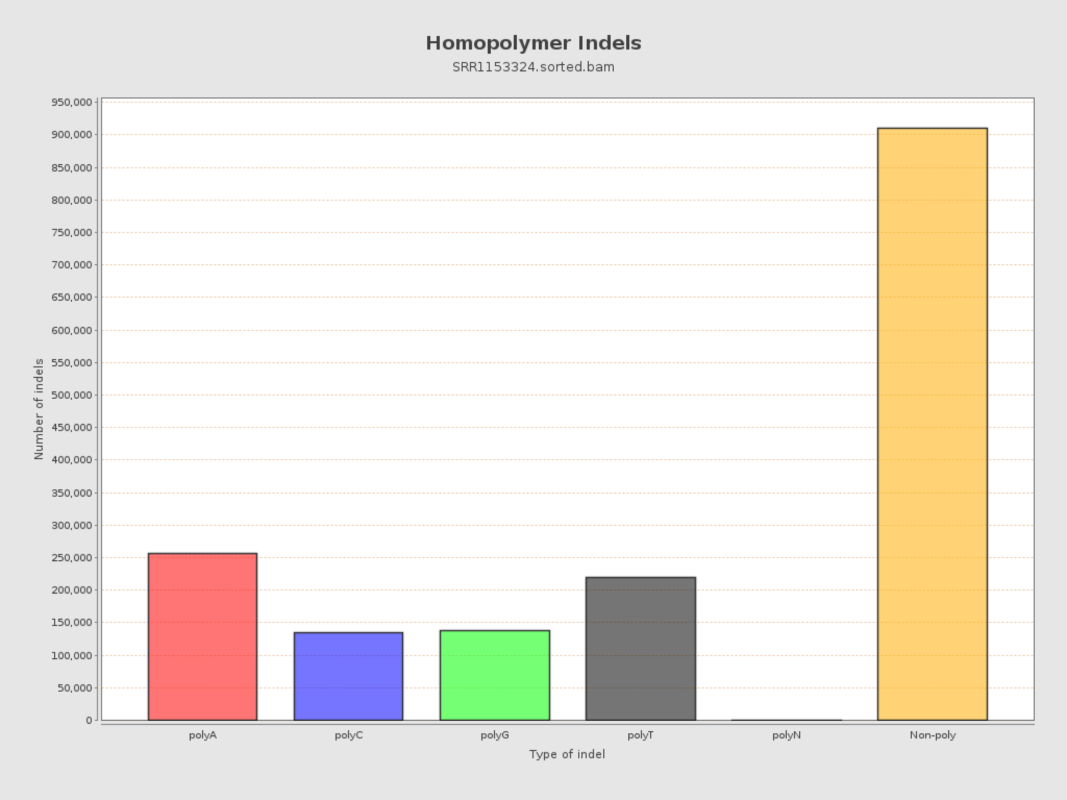


9. Results : Mapped Reads GC-content Distribution

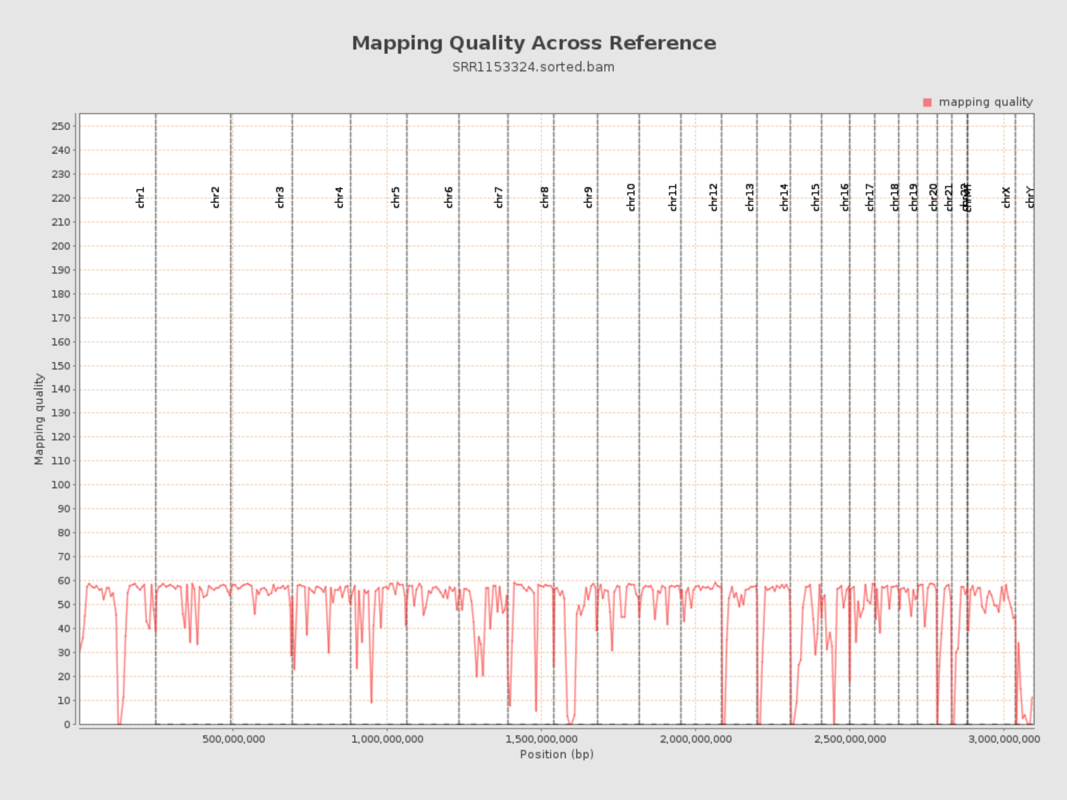


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram