Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 10:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153325.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_SRR1153325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 10:22:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	171,484,808
Mapped reads	168,112,031 / 98.03%
Unmapped reads	3,372,777 / 1.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	922,476 / 0.54%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	90,807,975 / 52.95%
Duplication rate	36.52%
Clipped reads	27,326,340 / 15.94%

2.2. ACGT Content

Number/percentage of A's	4,164,763,884 / 25.74%
Number/percentage of C's	3,926,474,753 / 24.27%
Number/percentage of T's	4,221,651,174 / 26.09%
Number/percentage of G's	3,864,265,607 / 23.88%
Number/percentage of N's	4,227,139 / 0.03%
GC Percentage	48.15%

2.3. Coverage

Mean	5.2279

Standard Deviation	36.6239

2.4. Mapping Quality

Mean Mapping Quality	49.65

2.5. Mismatches and indels

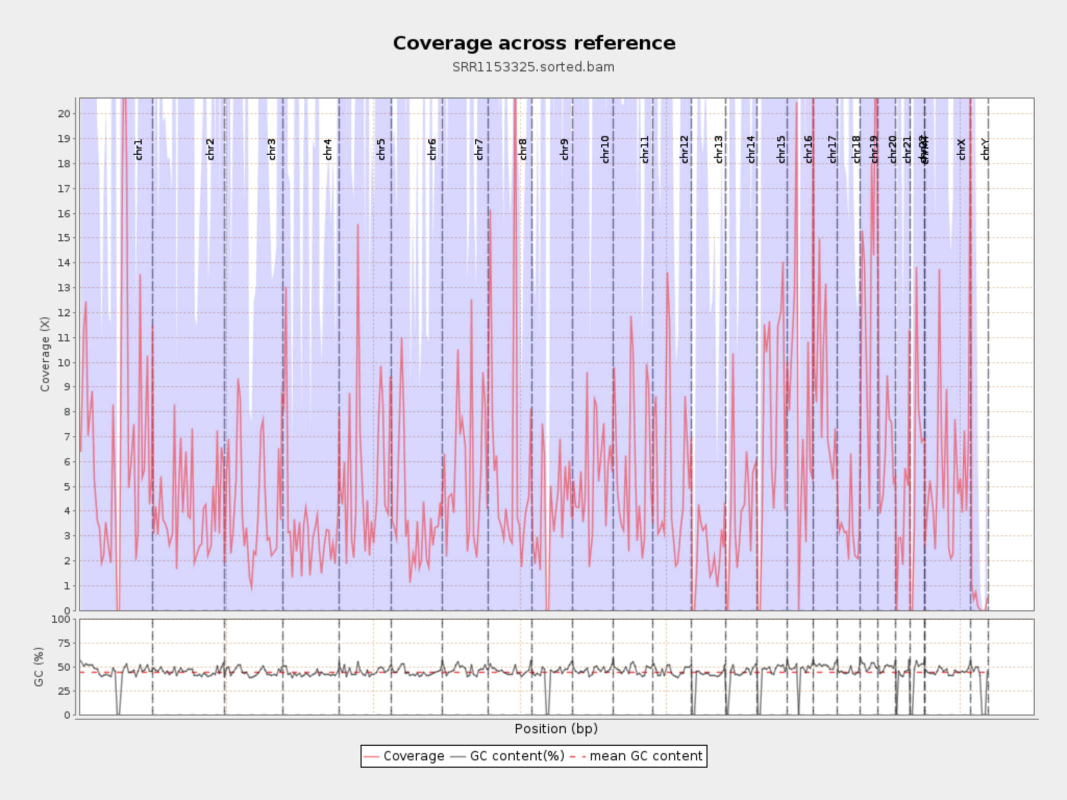
General error rate	0.38%
Mismatches	60,416,044
Insertions	904,645
Mapped reads with at least one insertion	0.53%
Deletions	1,157,528
Mapped reads with at least one deletion	0.68%
Homopolymer indels	44.38%

2.6. Chromosome stats

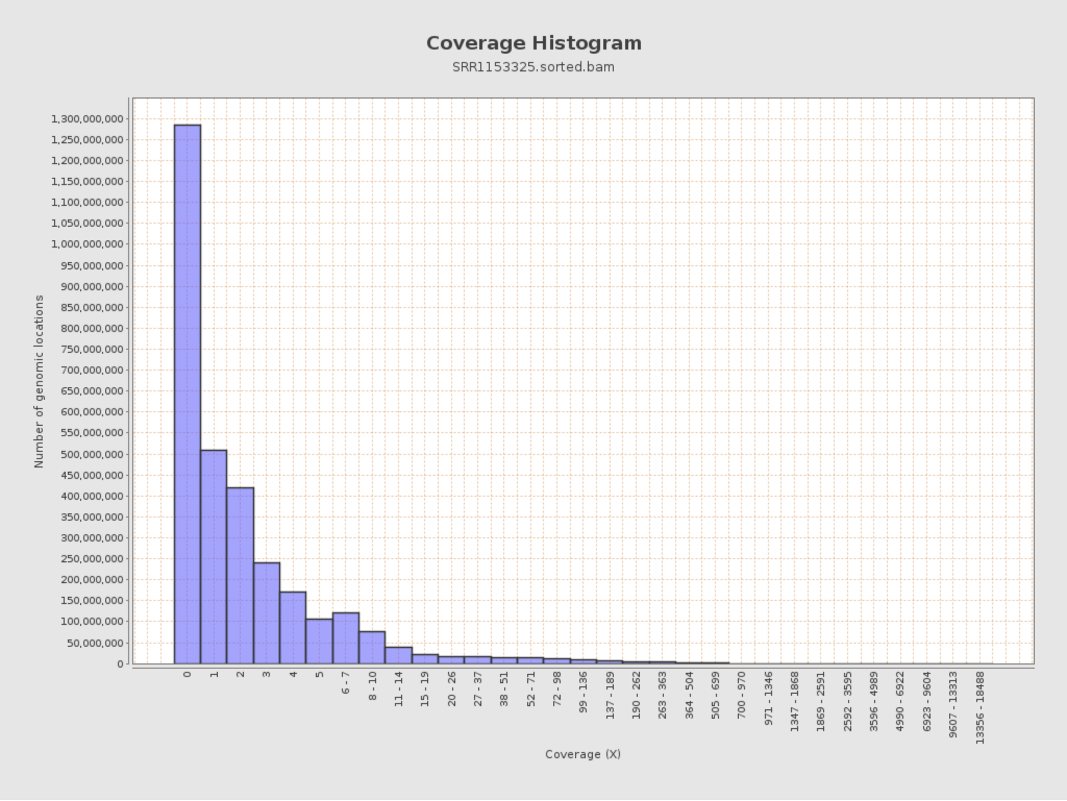
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1713468333	6.8745	41.6532
chr2	243199373	1005913943	4.1362	21.8278
chr3	198022430	824989963	4.1661	22.2097
chr4	191154276	651477248	3.4081	27.9799
chr5	180915260	994028706	5.4944	64.4762
chr6	171115067	622214051	3.6362	20.8934
chr7	159138663	911972251	5.7307	41.4672

chr8	146364022	858410808	5.8649	68.6299
chr9	141213431	548405783	3.8835	21.7173
chr10	135534747	743507436	5.4857	26.612
chr11	135006516	789236255	5.8459	27.9761
chr12	133851895	734309071	5.486	27.9027
chr13	115169878	256851347	2.2302	13.2273
chr14	107349540	434941168	4.0516	23.2468
chr15	102531392	756900261	7.3821	39.4864
chr16	90354753	731174179	8.0923	43.3418
chr17	81195210	713695022	8.7899	48.5779
chr18	78077248	250526253	3.2087	21.9912
chr19	59128983	829958064	14.0364	59.3723
chr20	63025520	412922181	6.5517	31.9198
chr21	48129895	198297234	4.12	35.0713
chr22	51304566	316081800	6.1609	32.4339
chrMT	16571	42580	2.5695	2.2838
chrX	155270560	865112368	5.5716	30.8739
chrY	59373566	19485139	0.3282	13.4344

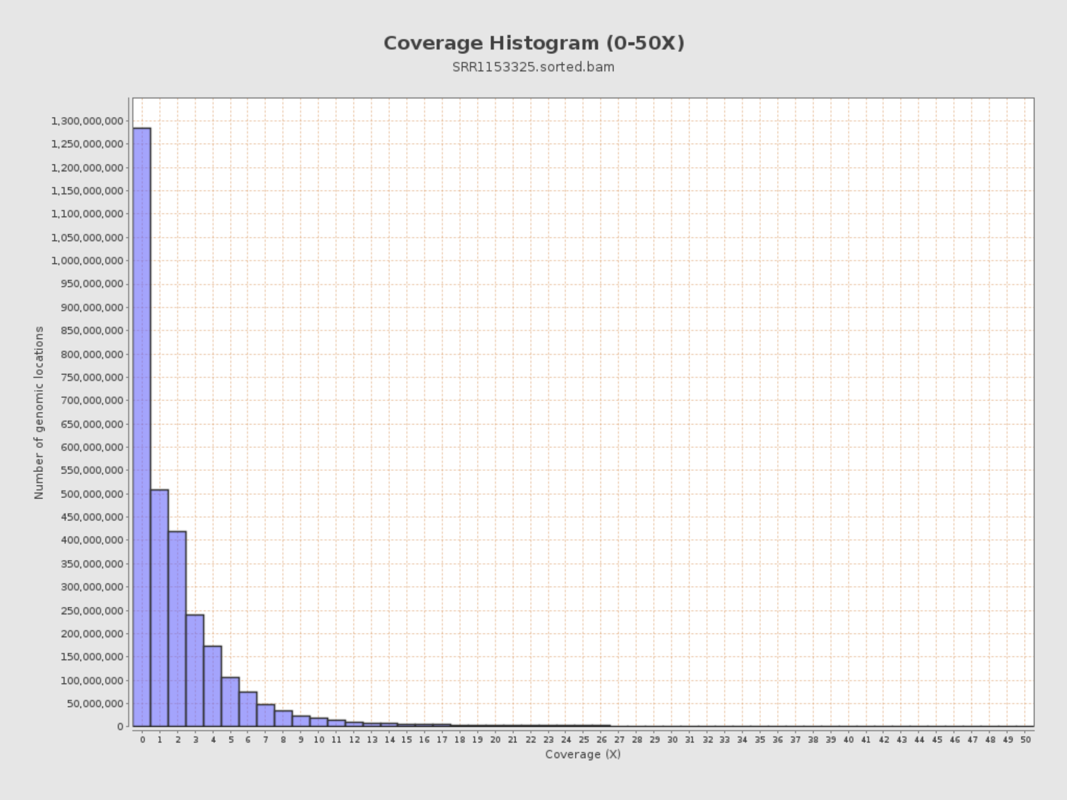
3. Results : Coverage across reference



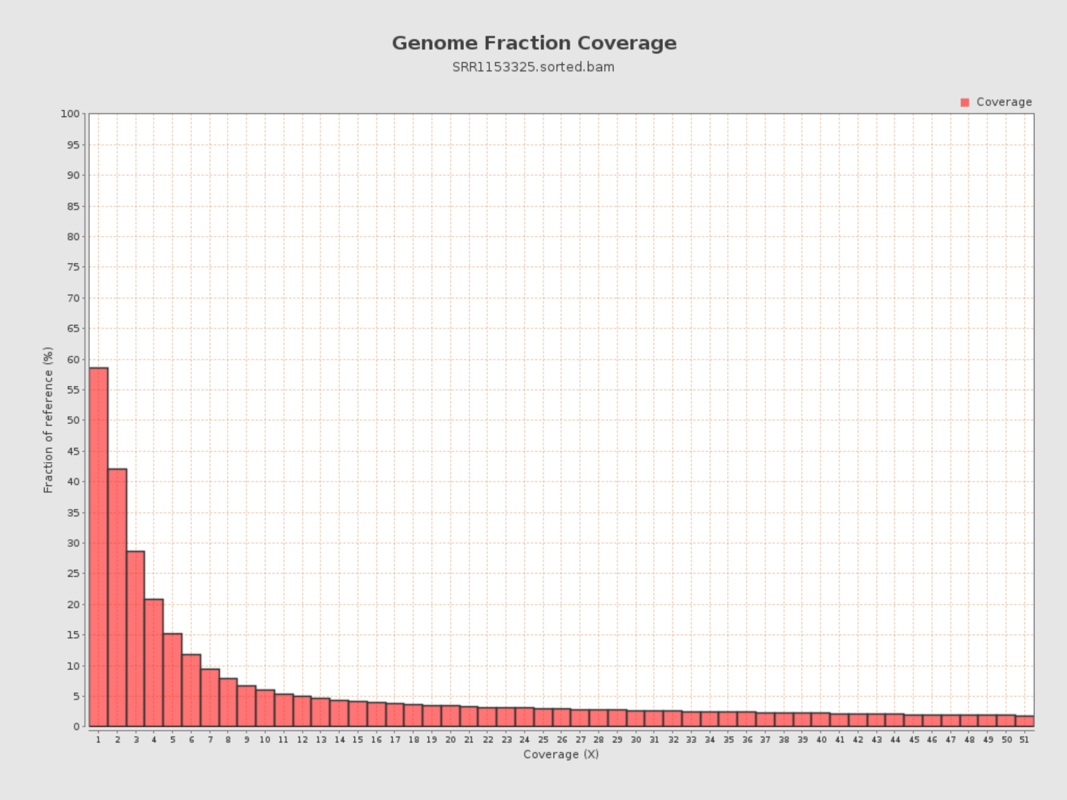
4. Results : Coverage Histogram



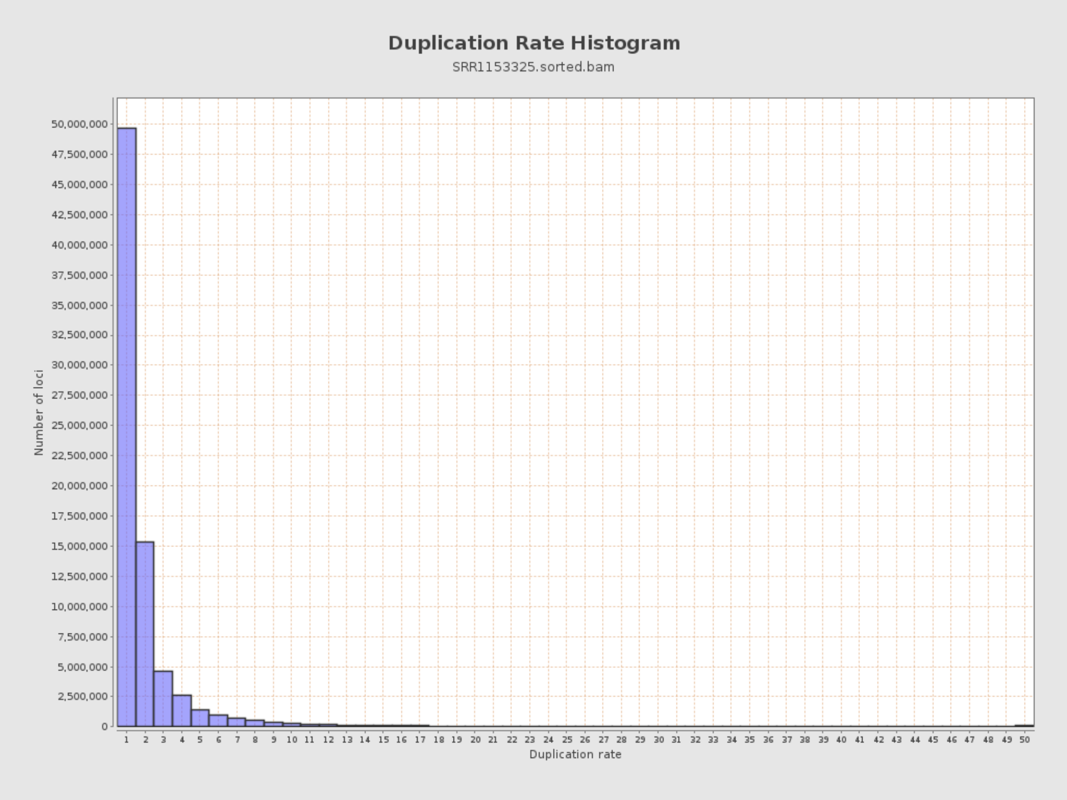
5. Results : Coverage Histogram (0-50X)



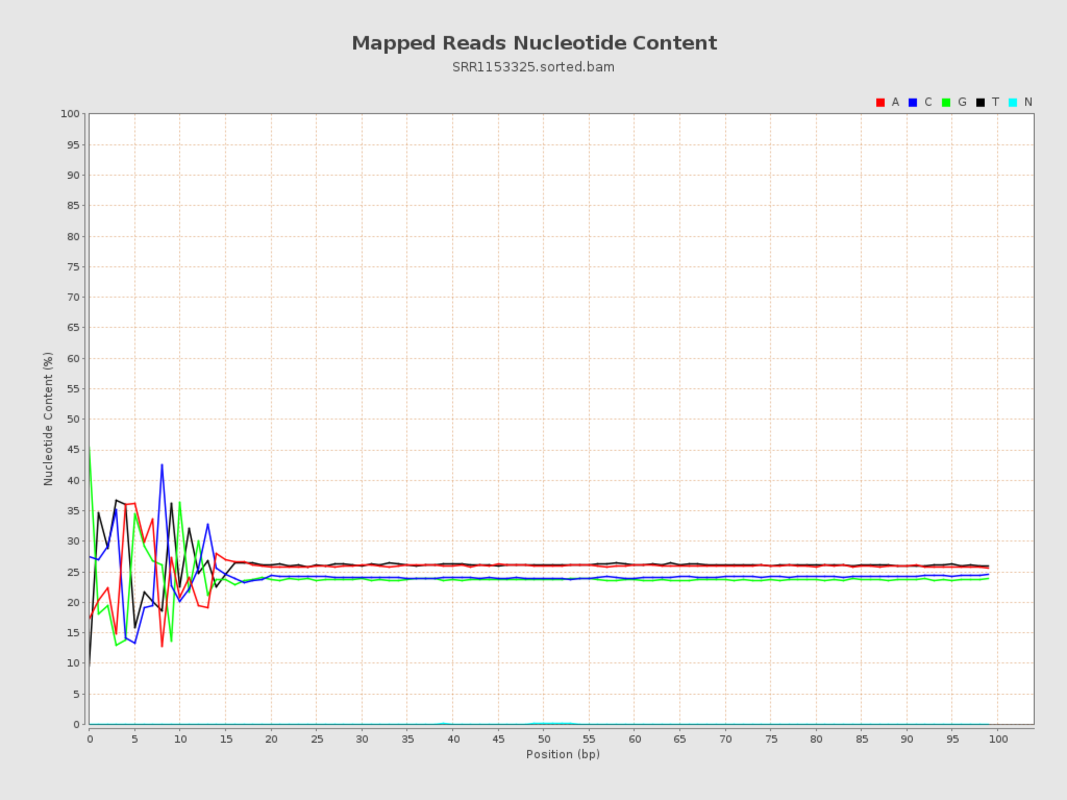
6. Results : Genome Fraction Coverage



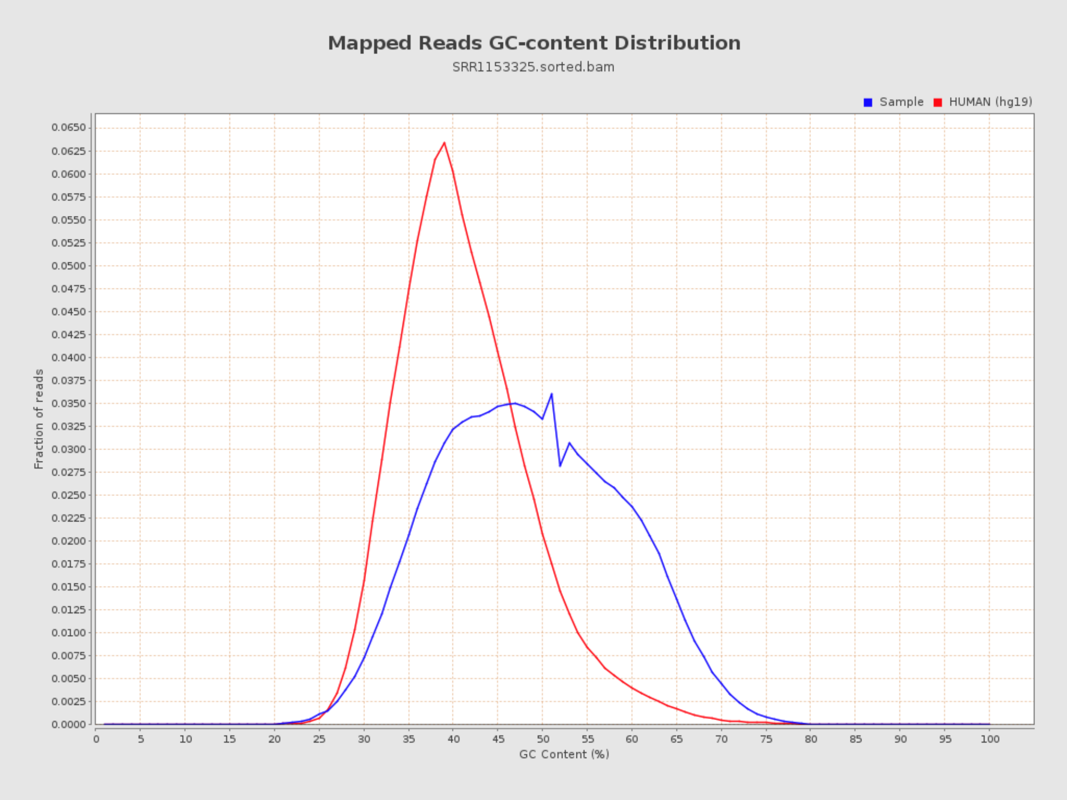
7. Results : Duplication Rate Histogram



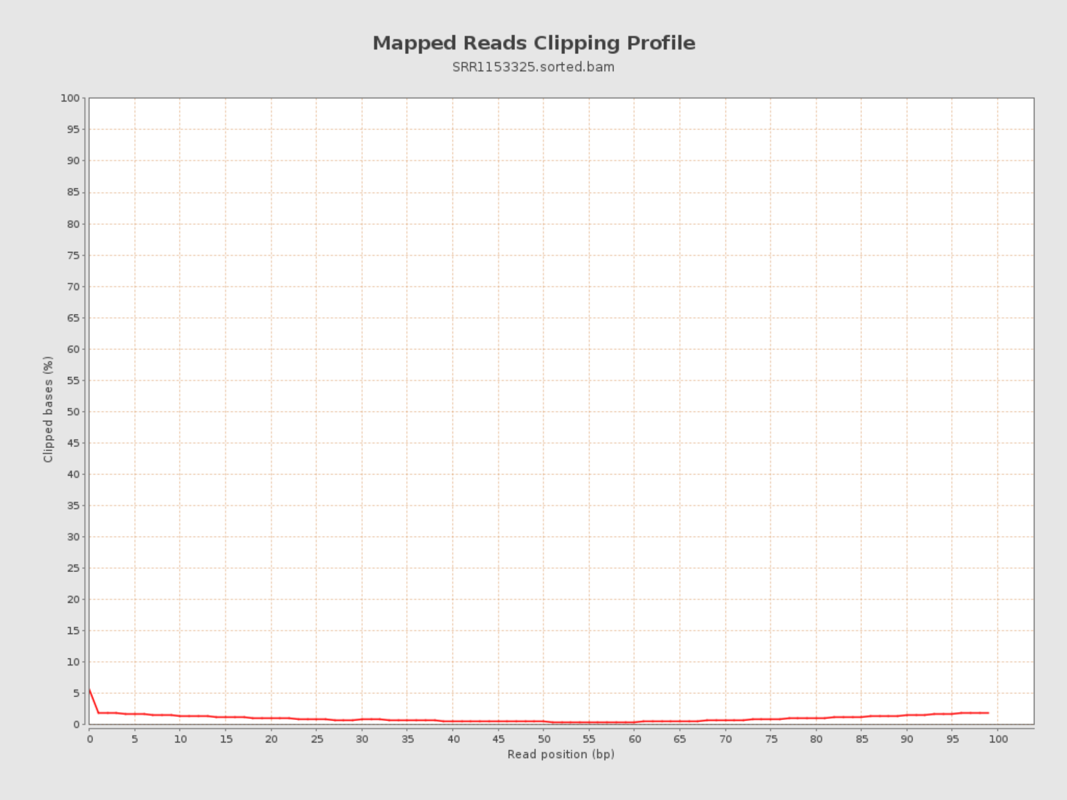
8. Results : Mapped Reads Nucleotide Content



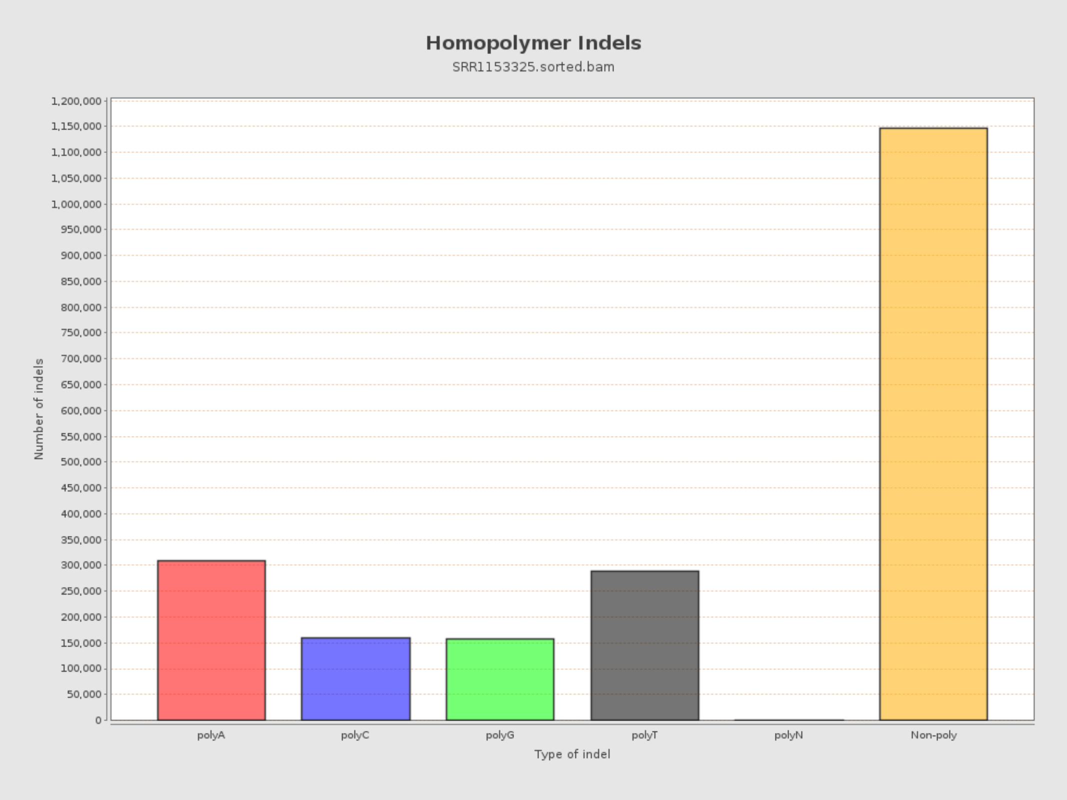
9. Results : Mapped Reads GC-content Distribution



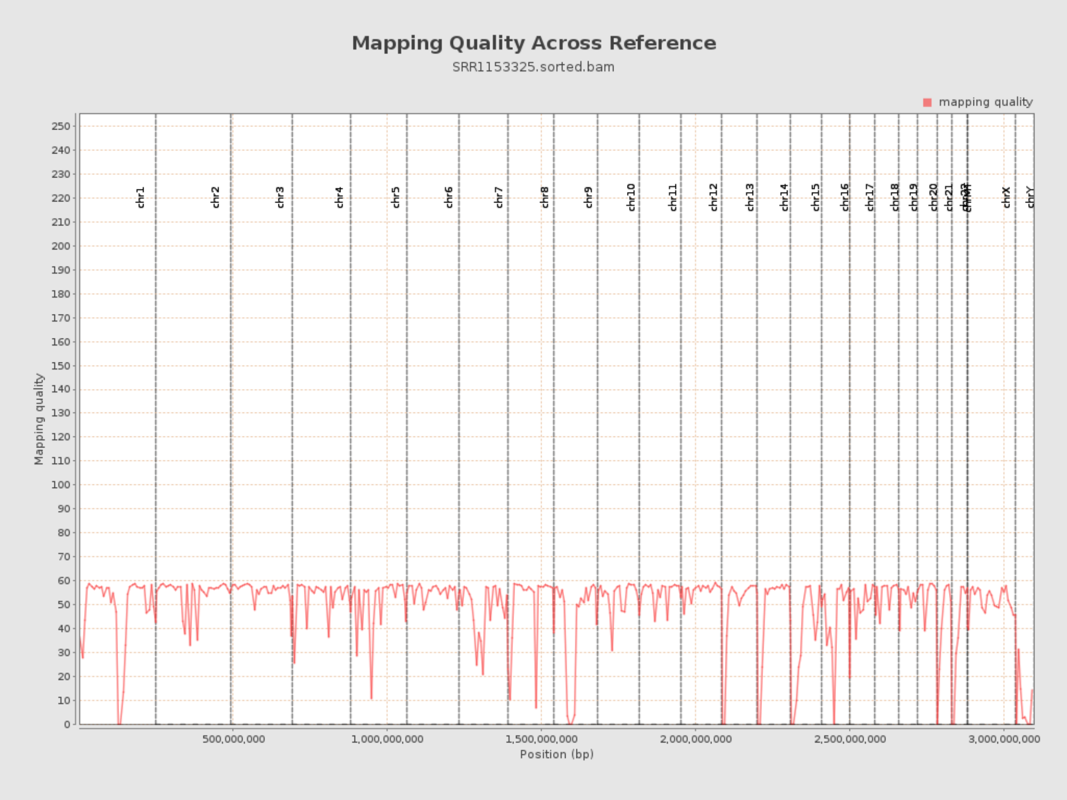
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram