

Solutions

2.1

- $6.4 \times 10^9 / 4^8 = 6.4 \times 10^9 / 65\,536 \approx 98\,000 \checkmark$.

2.2

- Promoter: fixed position at the transcription start, assembles Pol II. Enhancer: distance- and orientation-independent, boosts via looping.

2.3

- Marks are copied through cell divisions but are reprogrammable (development, some therapies target writers/erasers).

3.1

- $6.4 \times 10^9 / 4096 \approx 1.6 \times 10^6 \checkmark$.
- Two cooperating 6-base sites: expected joint hits divide by ~ 4096 again $\rightarrow \sim 380$ – specificity returns multiplicatively.
- Consequence: most disease-relevant non-coding variants sit in regulatory logic, not code.

3.2

- Access differs: methylation compacts chromatin, silencing the allele without changing letters.
- Methylated CpG recruits repressors/compact histone marks $\rightarrow$ enhancer and promoter inaccessible.
- Diagnostics: severity modifiers live in the access layer, so assays of methylation complement sequencing.