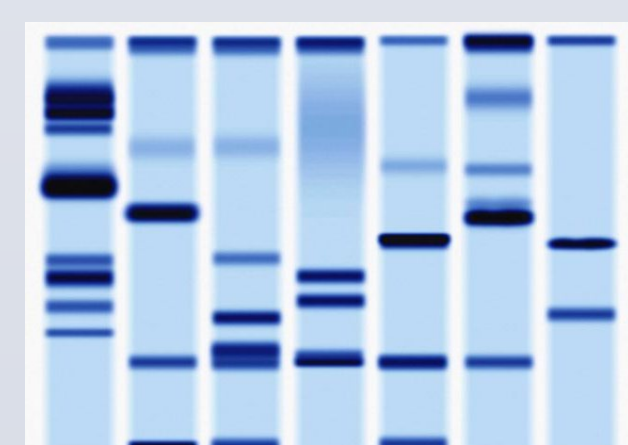
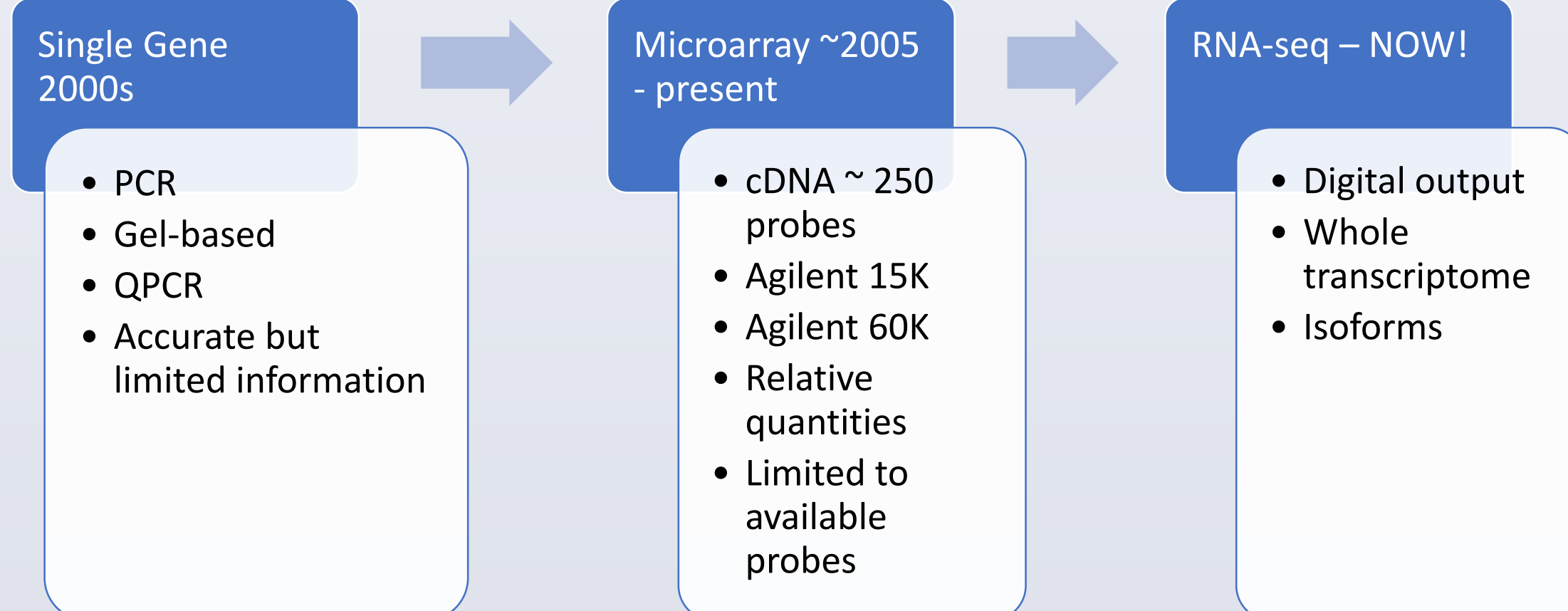
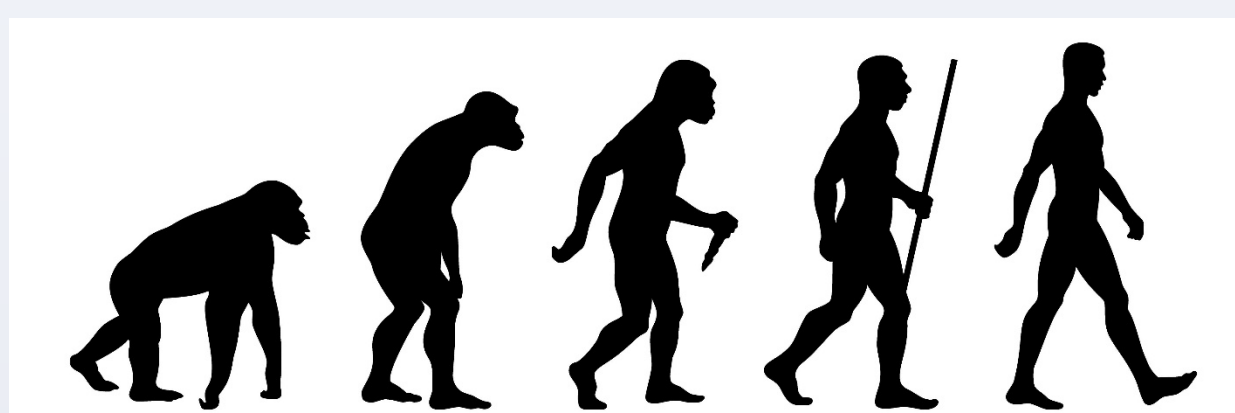


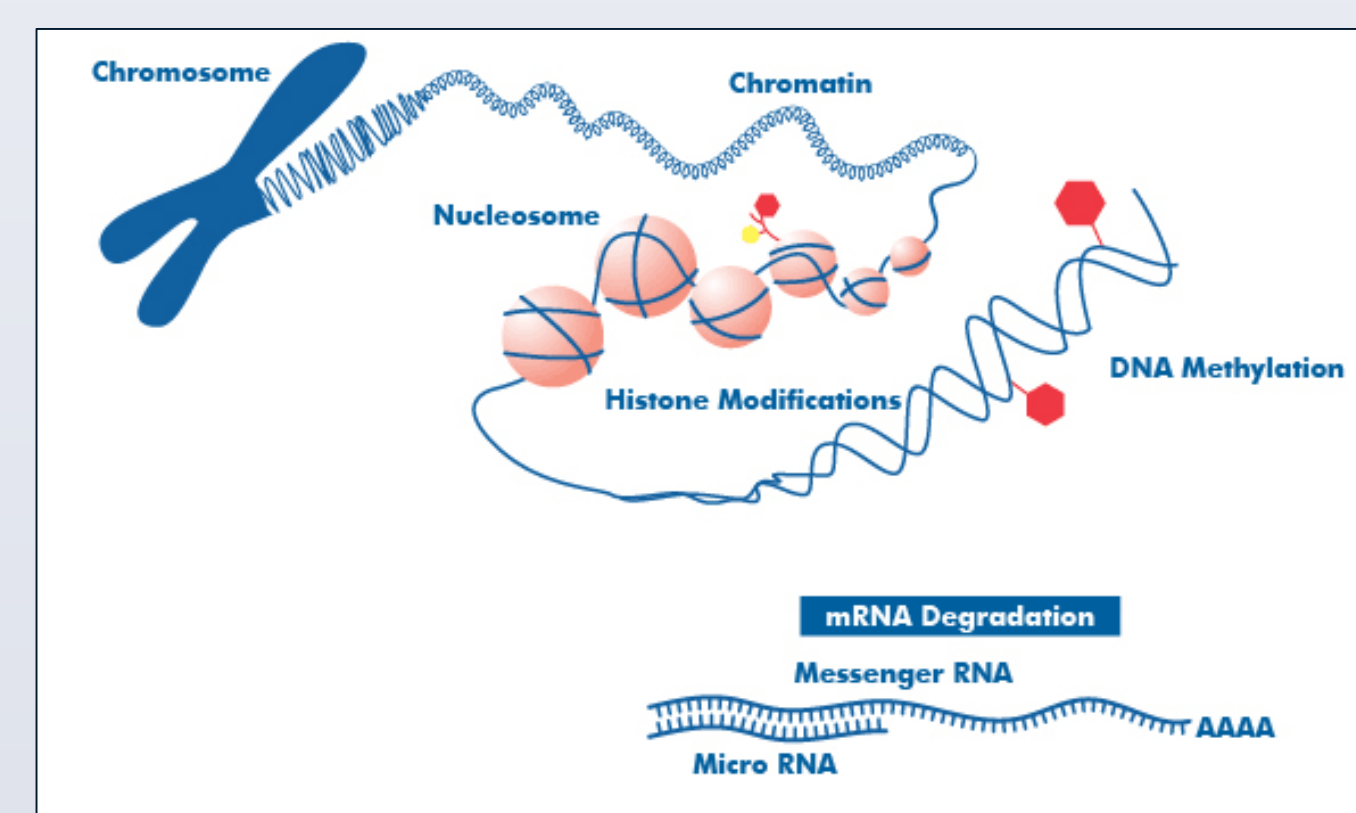
Evolution of Omics-based biomarkers



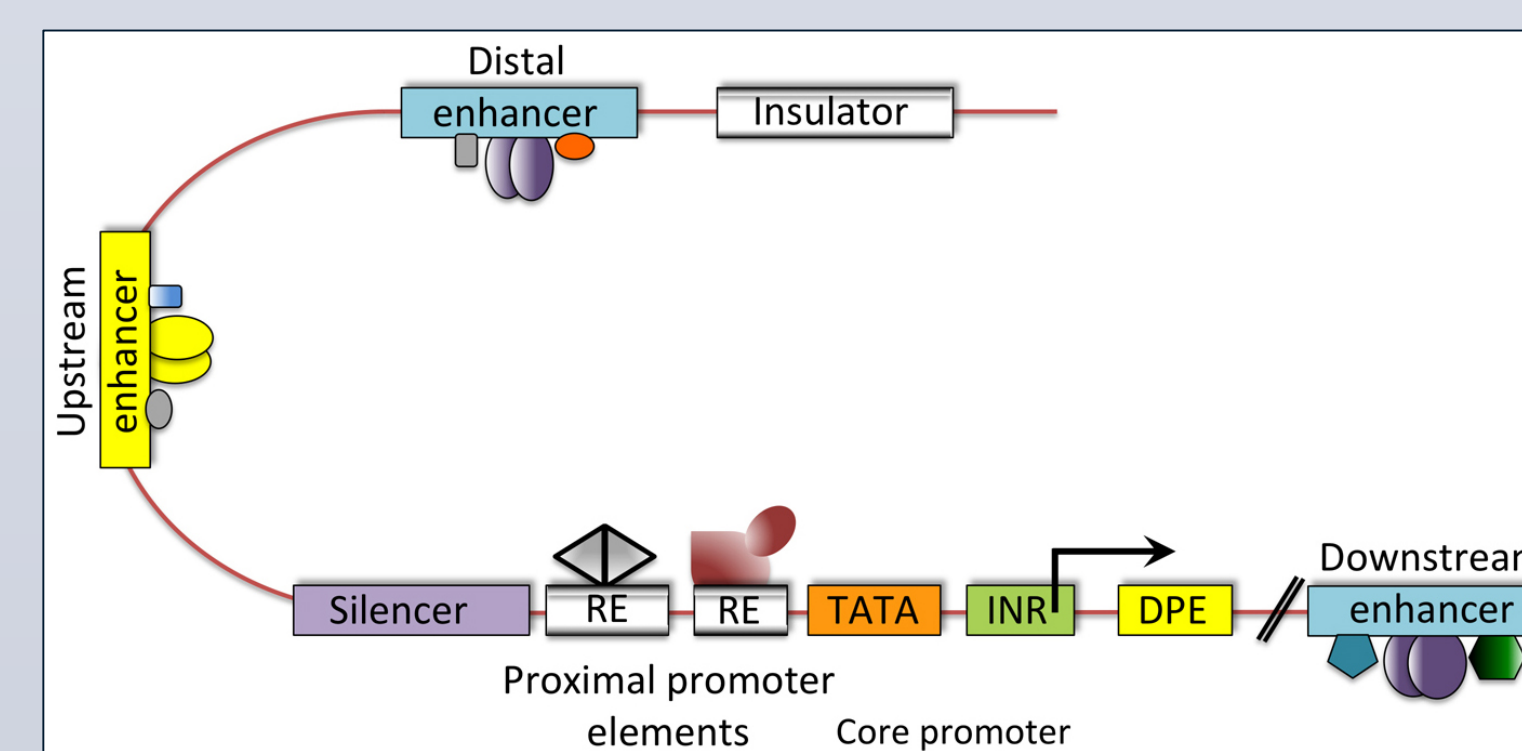
Information

Benefits of Next Generation Sequencing

- Opens the door to unexplored cellular functions
- Epigenetics – Non-sequenced based adaptation
 - Whole genome bisulfite sequencing
 - Reduced representation bisulfite sequencing
 - miRNA-seq
 - ChIP-seq
- Genome – Individual variability, cross-species extrapolation
 - Single nucleotide polymorphisms
 - Cis-element discovery and mapping

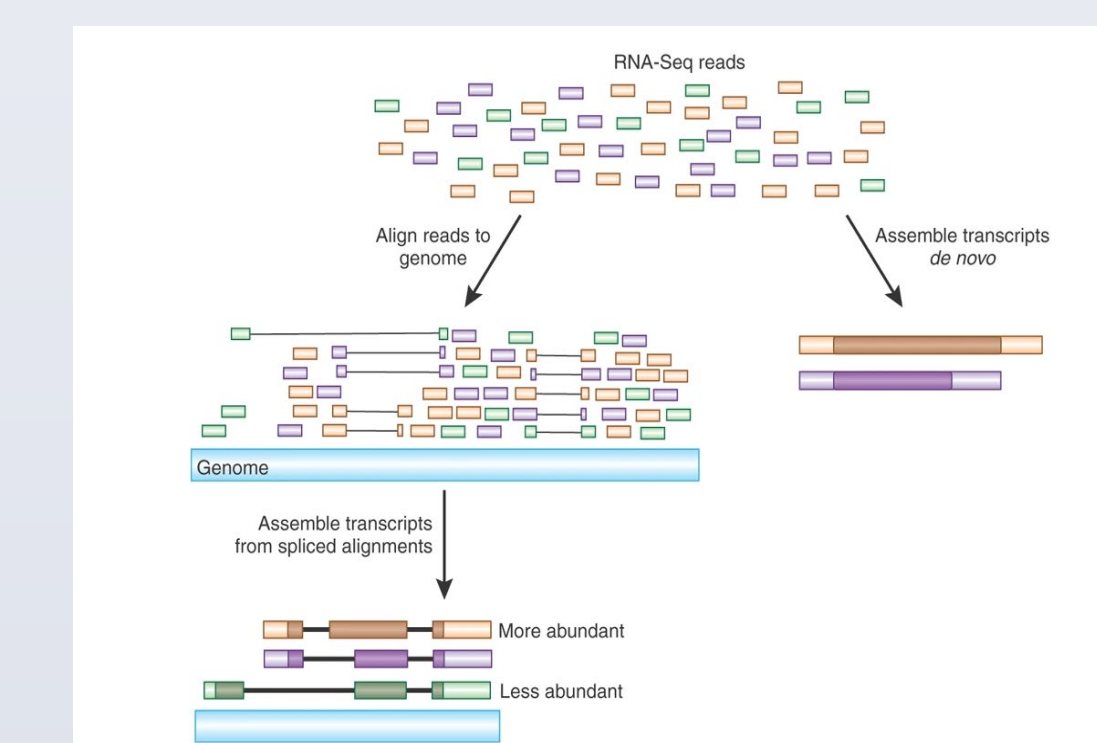


<p>Individual 1</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p> <p>Individual 2</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p> <p>Individual 3</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p>	<p>Individual 4</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p> <p>Individual 5</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p> <p>Individual 6</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy1 ...GCTATAAGGATAGCTTACAG...</p> <p>Chr 2 ...CGATATTCCATCGAATGTC...</p> <p>copy2 ...GCTATAAGGATAGCTTACAG...</p>
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Benefits of having the fathead minnow genome

- Alignment to reference genome
- Computationally faster
 - Requires lower sequence coverage
 - i.e. cheaper
 - Less fragmented FHM
 - Can serve as reference to related species



FHM Genome v. 1

- N50 scaffold = 15,414
- N50 contig = 1,668
- Benchmark of universal single copy orthologues (BUSCO)
 - Measure of functional completeness
 - %Complete BUSCOs = 1%

FHM Genome v. 2

- N50 scaffold = 13,503,935
- N50 contig = 300,151
- BUSCO
 - %Complete BUSCOs = 95%

Conclusions

Highly contiguous and complete
Annotated – mRNA and ncRNAs
Enables use of NGS technologies
Used to identify optimal age and duration of exposure for FHM
Immediately available for limited use
Fluxetine
Public release soon

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