Molecular fingerprints of pig male reproduction from omics data

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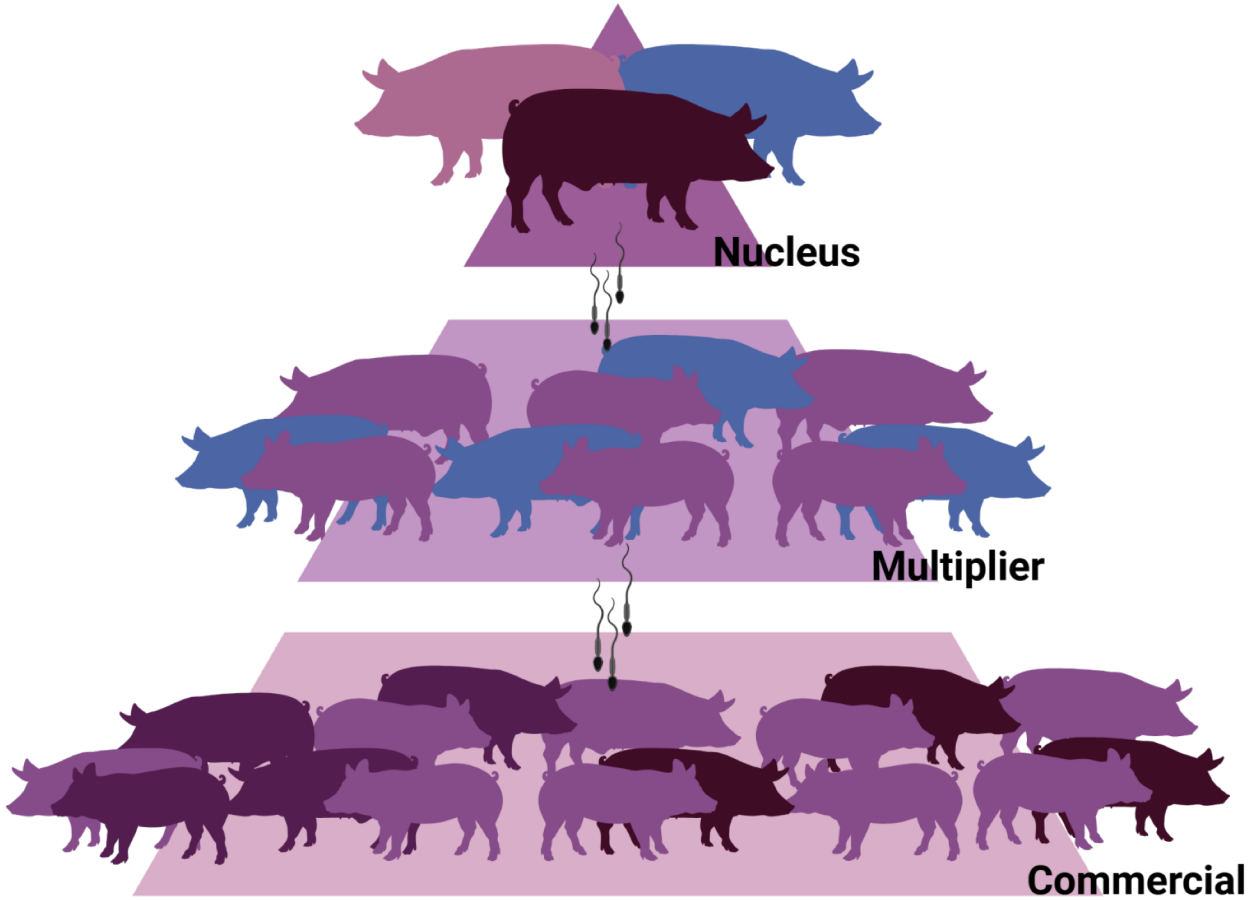

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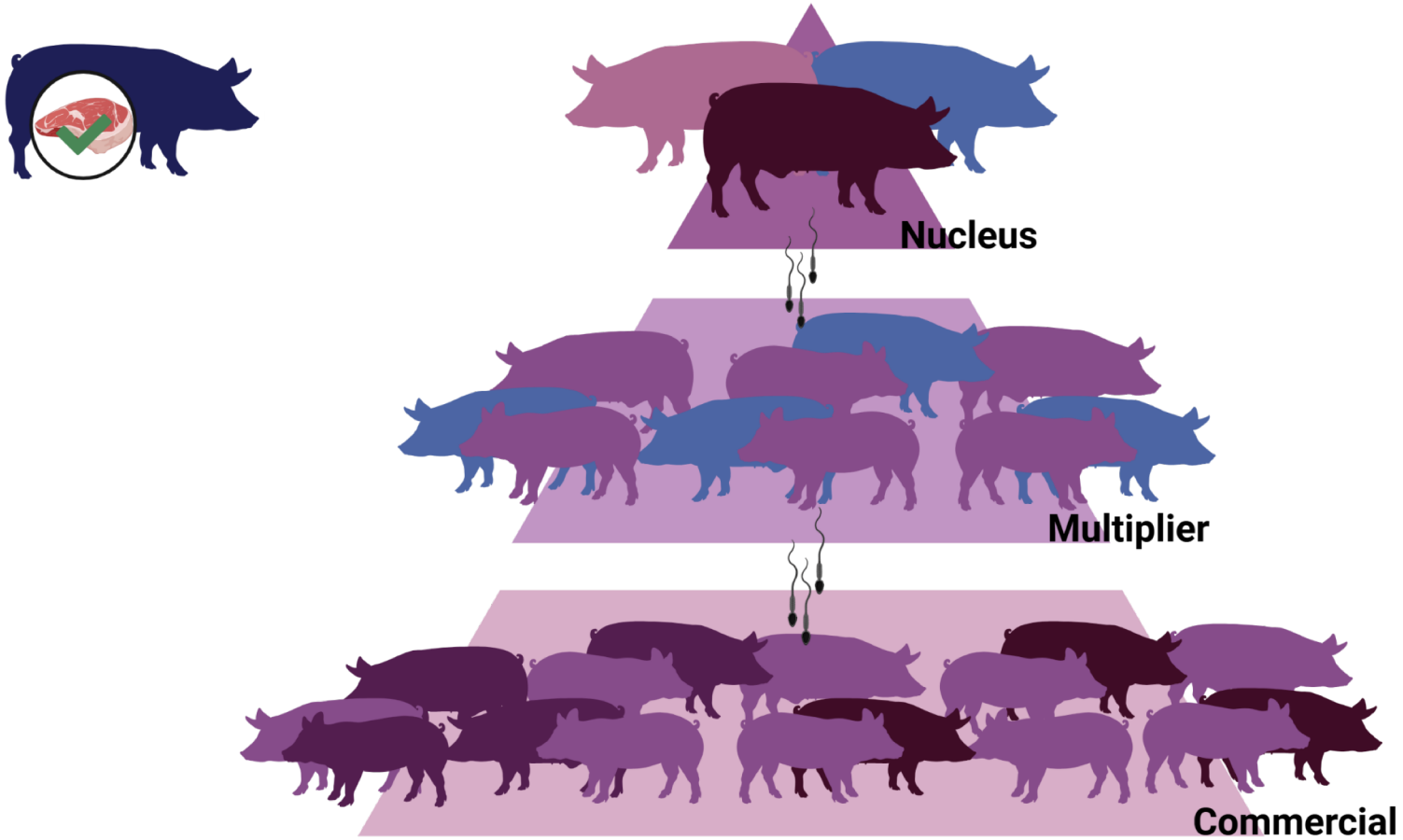

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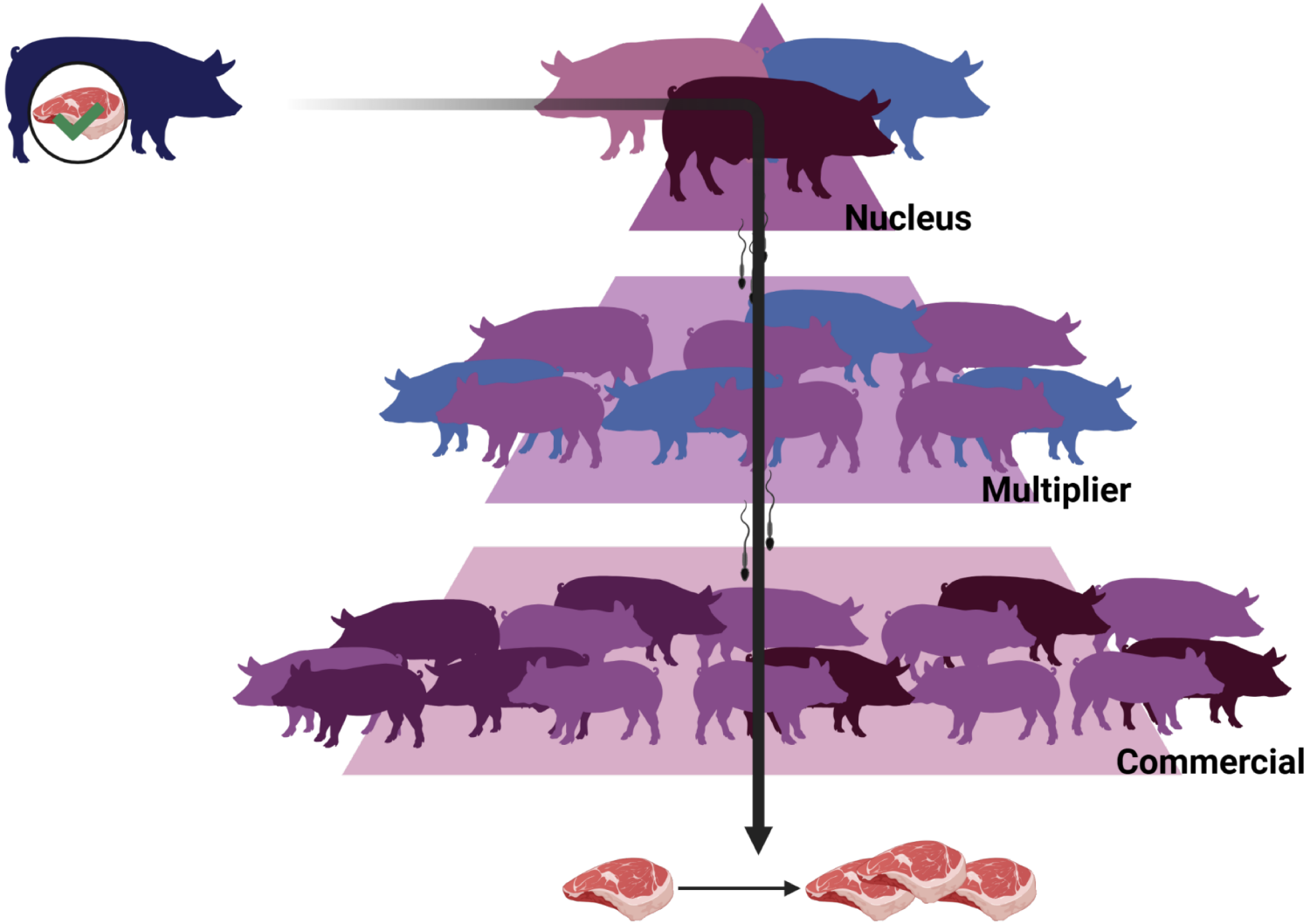

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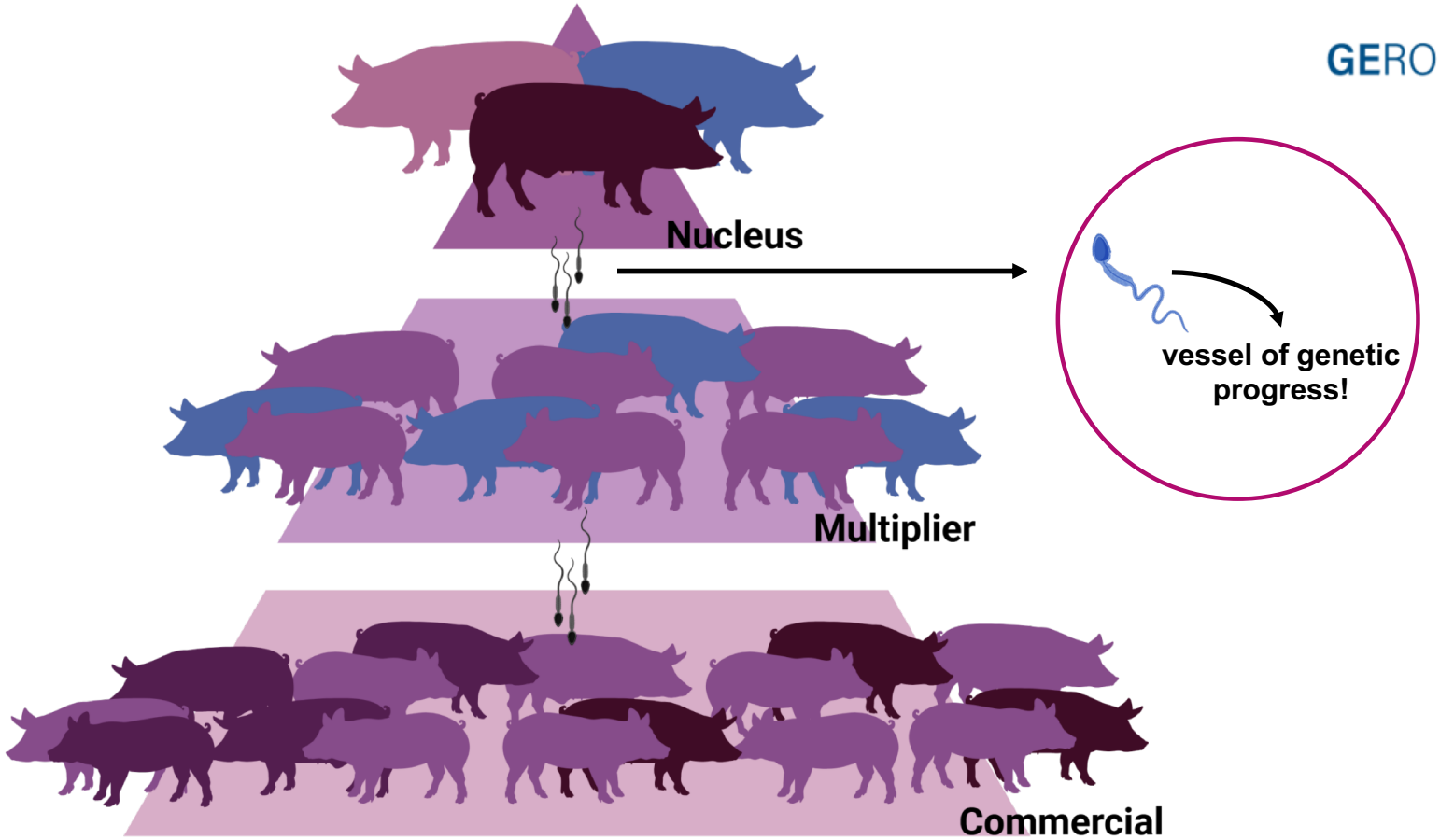

Male reproduction is key to the transfer of genetic potential for production!

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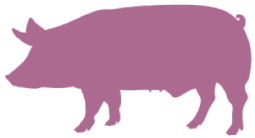
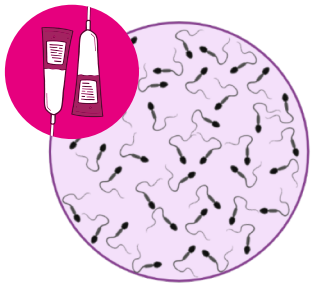
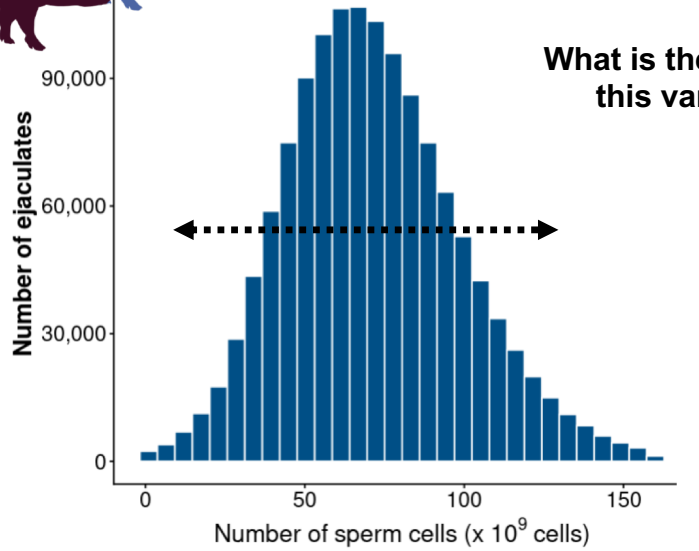




80 billion sperm cells



What is the source of this variation?

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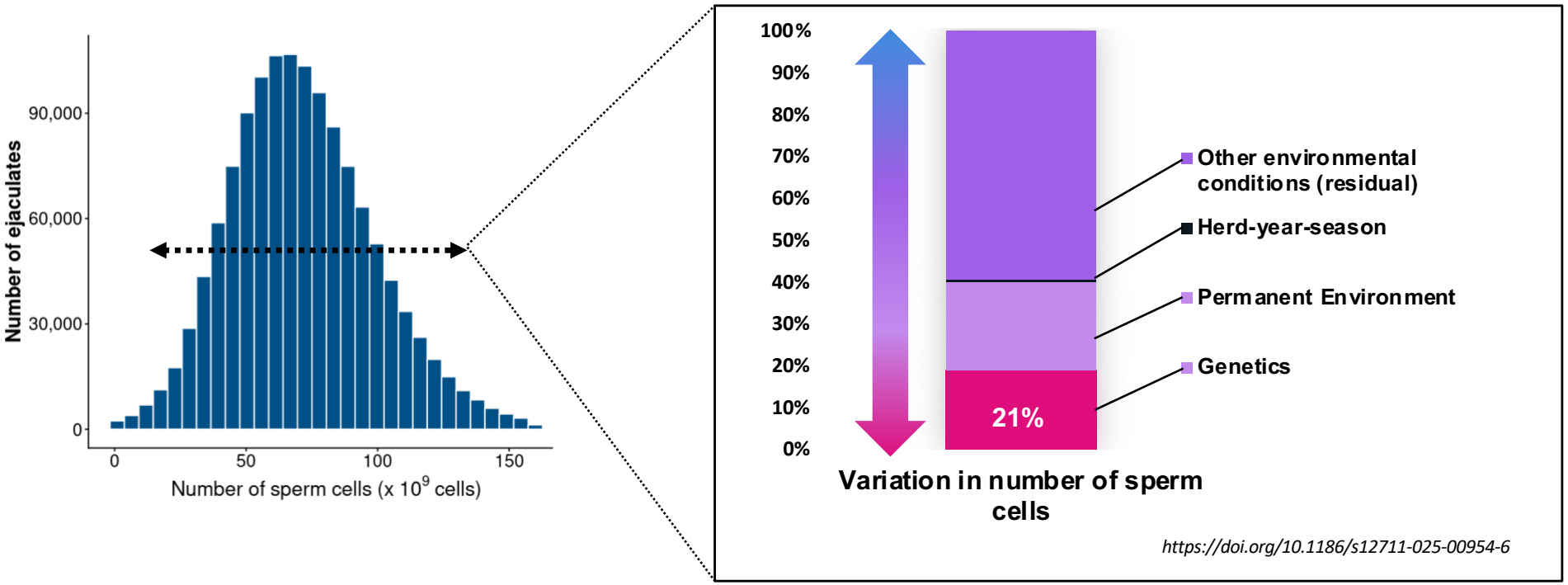
Genetics explains a small part of phenotypic differences



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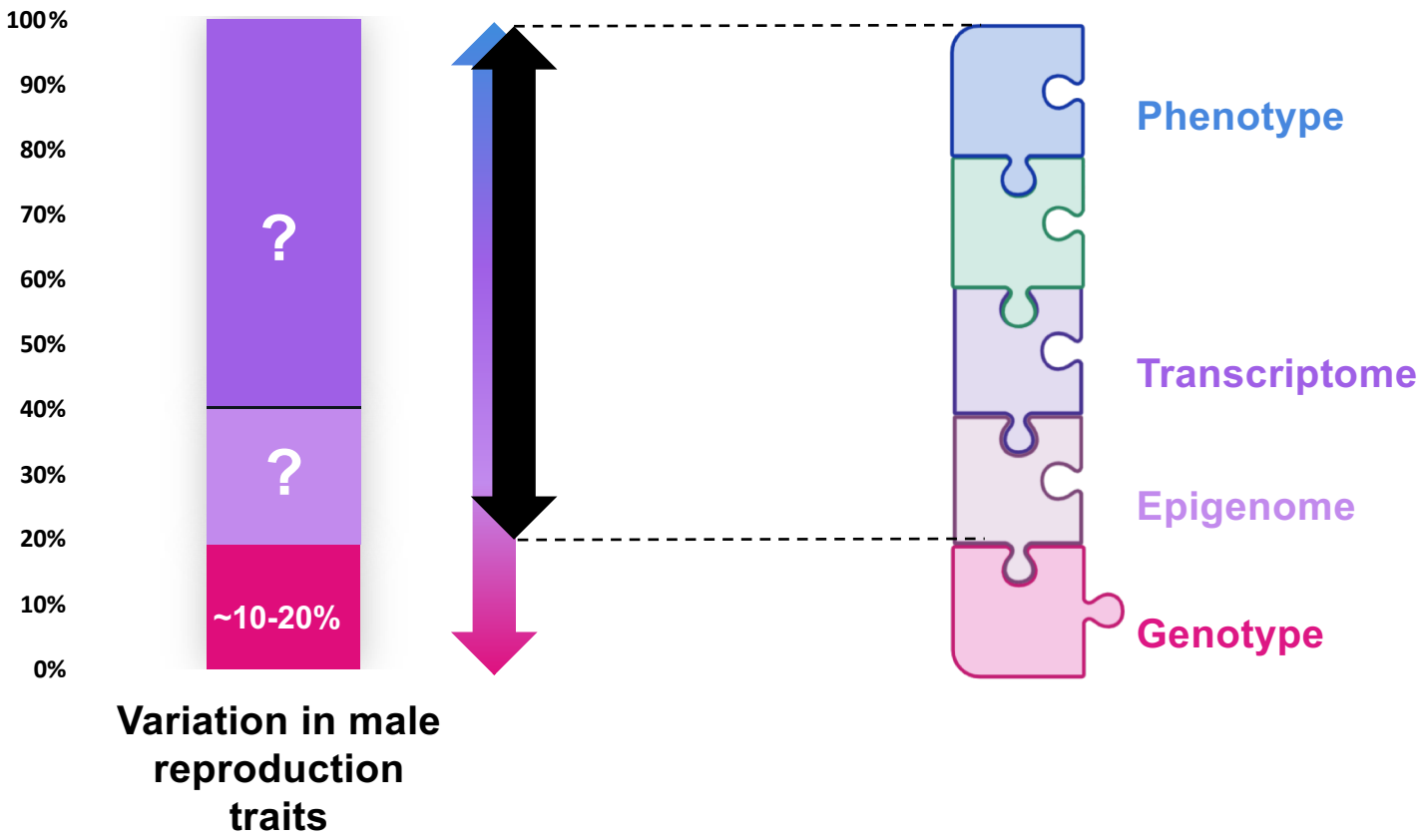
This is the gap



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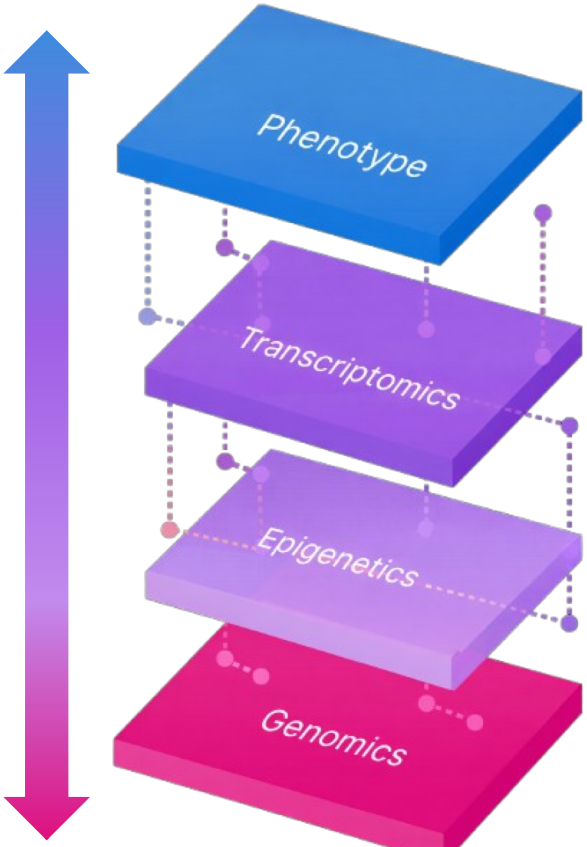
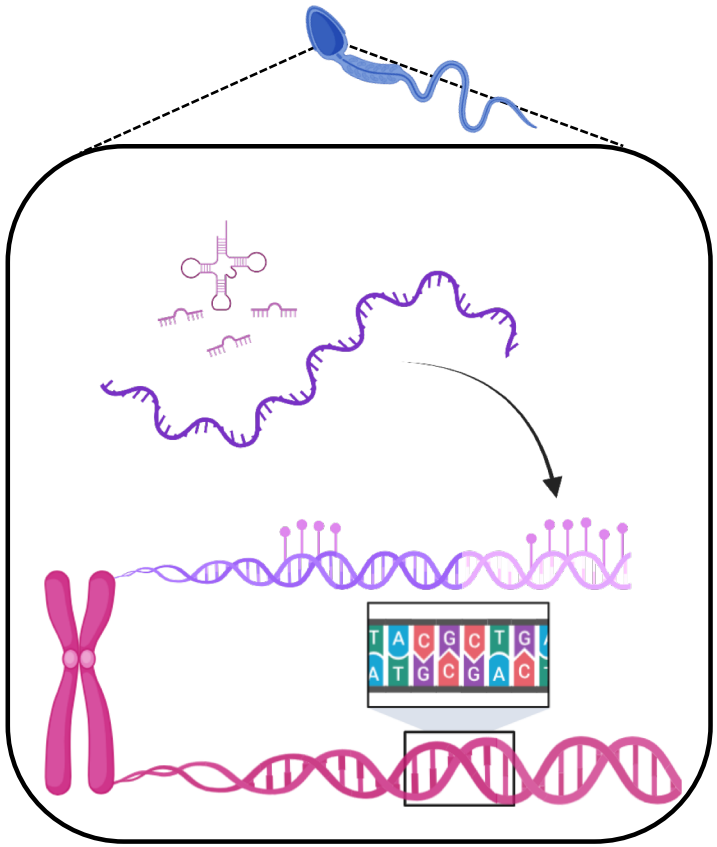
Sperm multi-omics to study pig male reproduction





Transcriptomics
The complete set of RNAs produced by the genome.

Epigenetics
Chemical modifications (e.g., DNA methylation) that affect gene function without changing the DNA sequence.

Genomics
The complete set of genes or genetic material present in a cell or organism.

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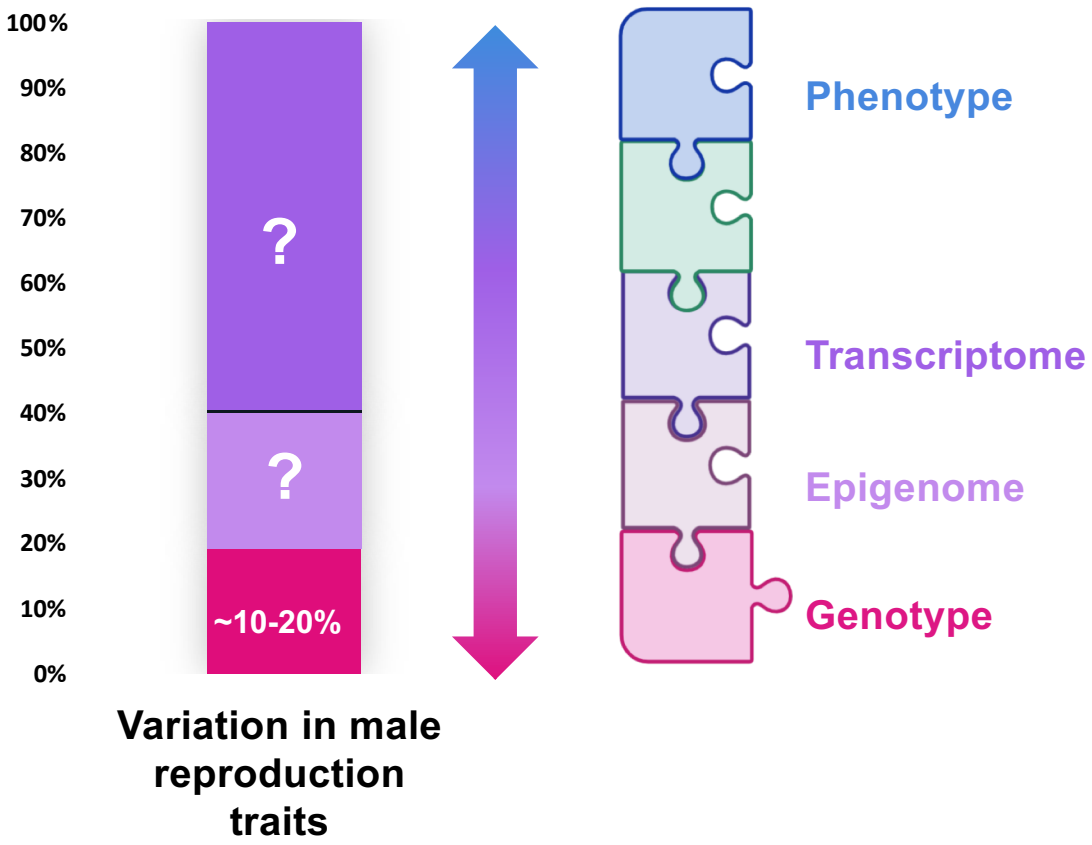
Closing the gap



- Characterize the **transcriptome** and **epigenome** layers of sperm cells.
- Detect markers affected by the environment.
- Detect **genetic** effects on the phenotype, transcriptome and epigenome of sperm cells.

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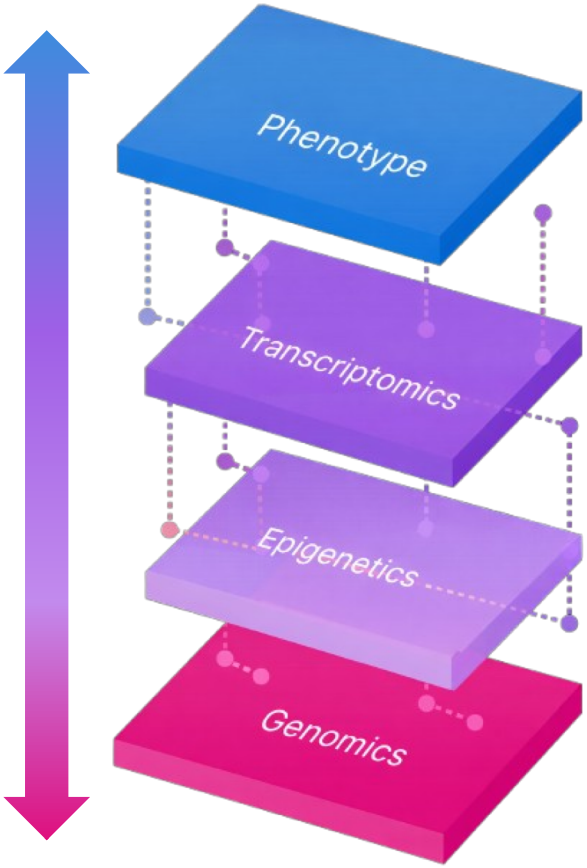

5k boars

Male reproduction
- Semen quantity, sperm motility, sperm morphology, etc.

170-182 semen samples

Coding and non-coding RNAs (lncRNA/sncRNA)
- 14,888 messenger RNAs
- 1,468 long non-coding RNAs
- 1,281 small non-coding RNAs

480 semen samples

DNA methylation
- RRBS: ~2.4 million CpG sites (215,724 CpG sites)
- ONT: ~30 million CpG sites

3k boars

Genotypes
- 660K imputed SNP
- ~24M WGS SNP

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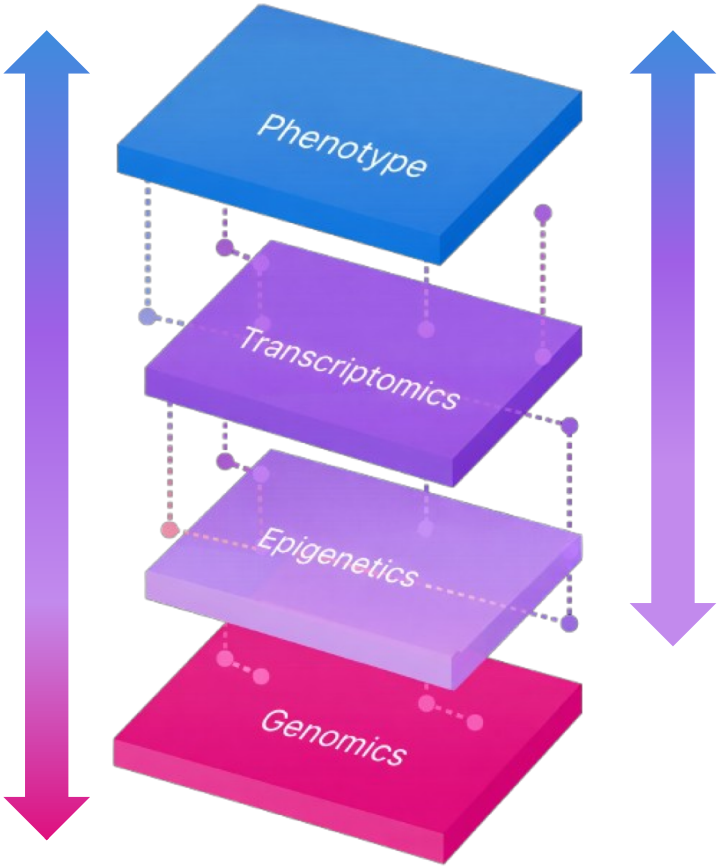
Sperm biomarkers are affected by environmental conditions



Age of the boar	Season of collection	Season of birth	Days between collection	Housing
ssc-miR-1 *PARP4* *TBX1* *SCUBE2* *HHIPL2*	*ssc-miR-106b*	*ssc-miR-421* *ssc-miR-98* *AK9* *SPAM1* *POLE2* *RCAN1*	*tRNA Tyr-GTA*	
57,672 CpG *(~26%)* *Hormone synthesis changes*	***33 CpG*** *IGF2R* *PPP2R2C* *GJB4*	***19 CpG*** *POR* *MYH9* *ATP8A2*		

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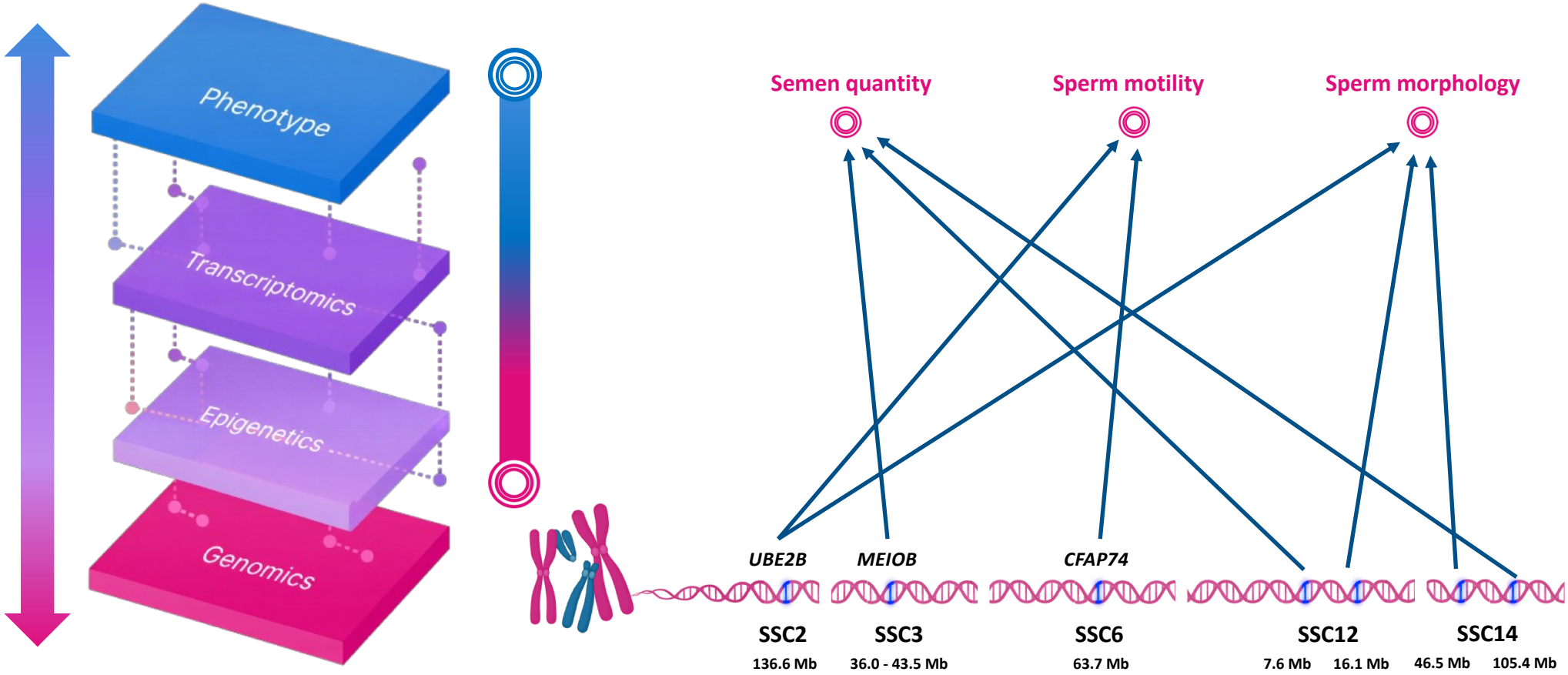
Sperm multi-omics: genetic control over pig male reproduction



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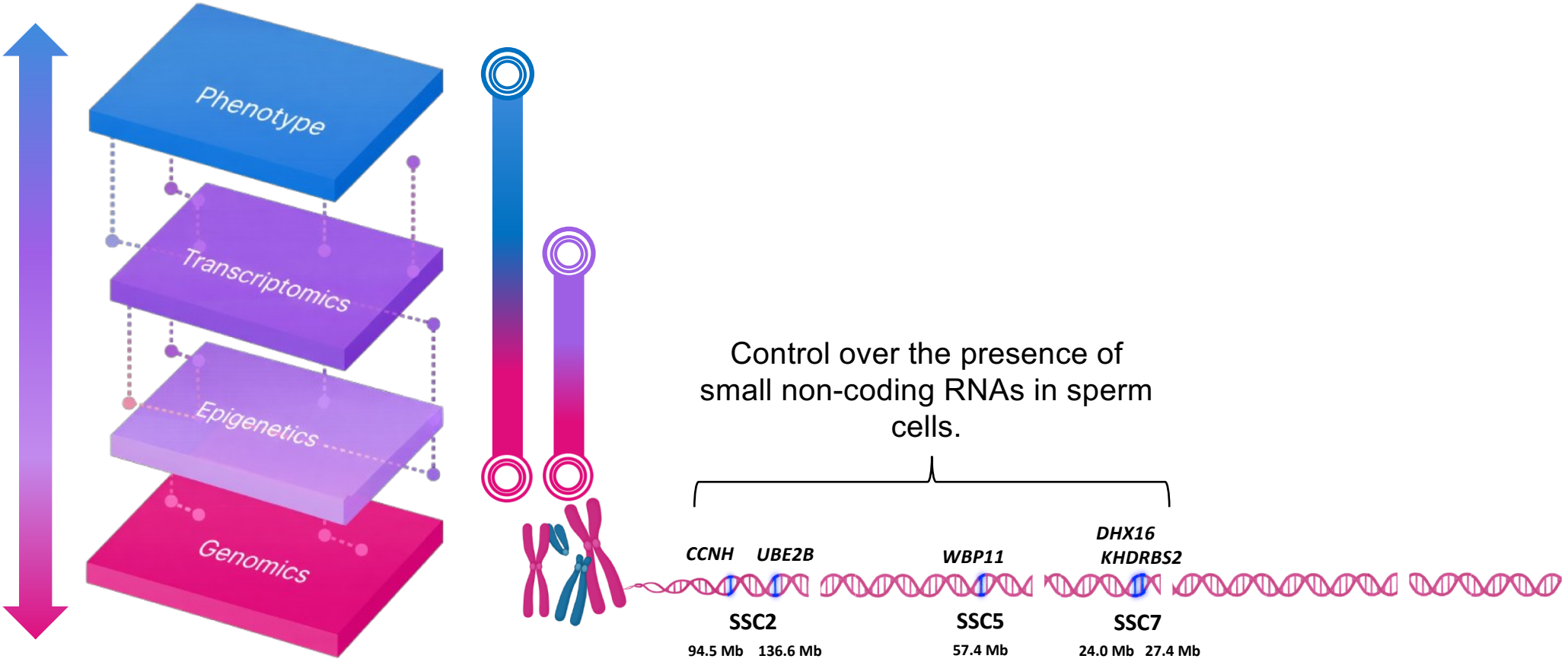
Sperm multi-omics: genetic control over the transcriptome



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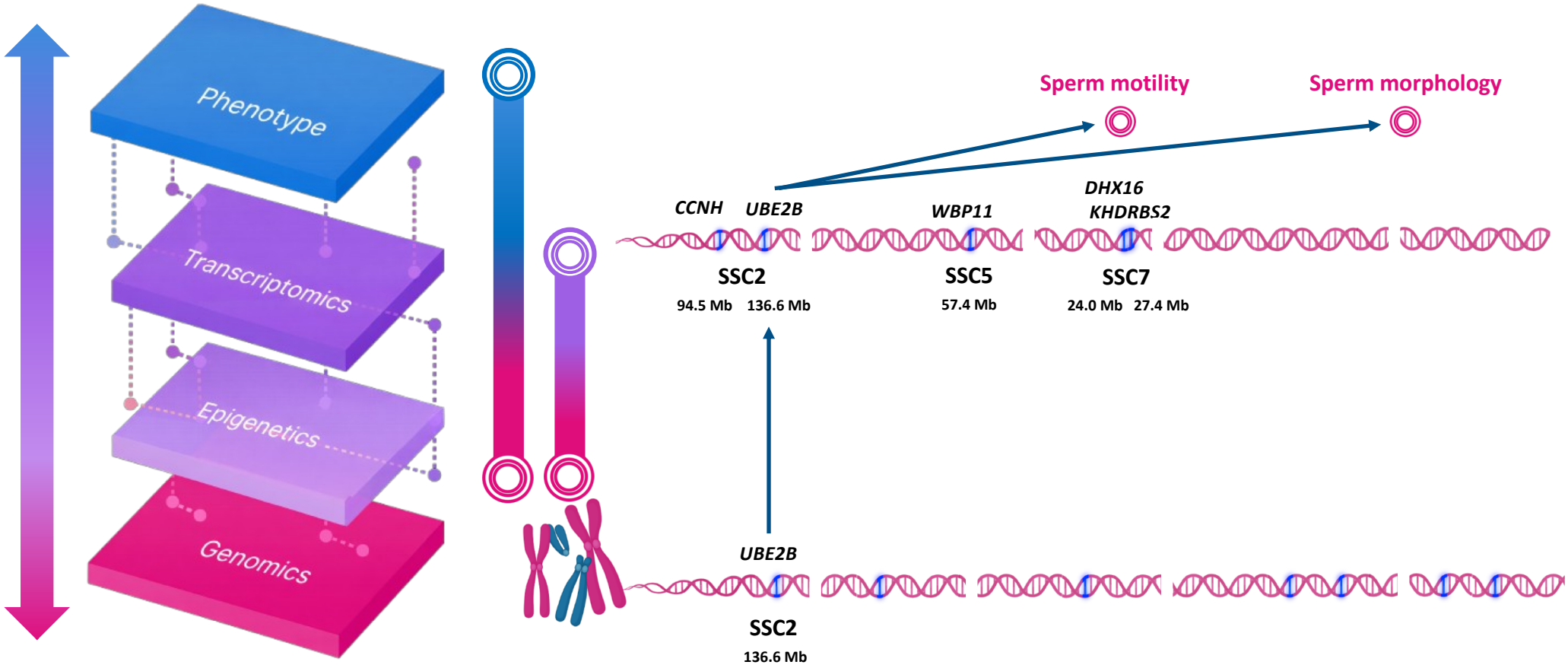
Sperm multi-omics: genetic control (via) the transcriptome



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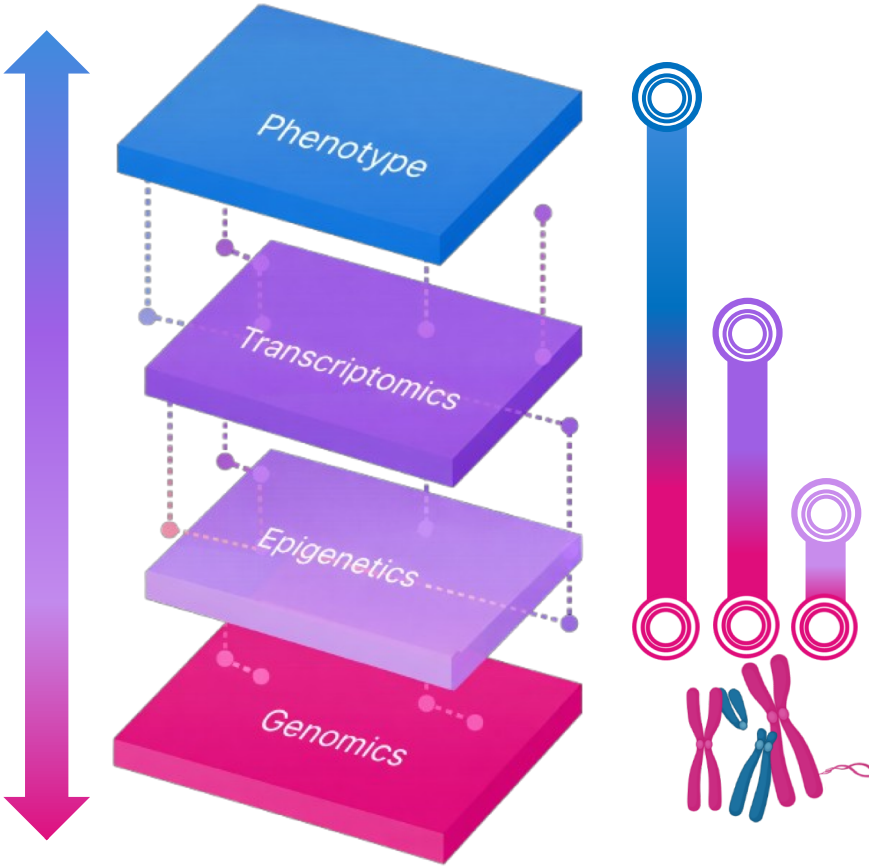
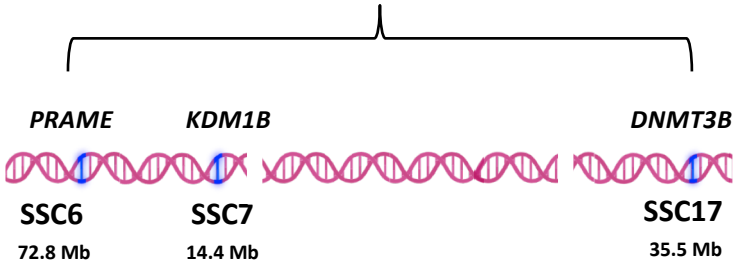
Sperm multi-omics: genetic control over the epigenome



Control over genome-wide DNA methylation in sperm cells.



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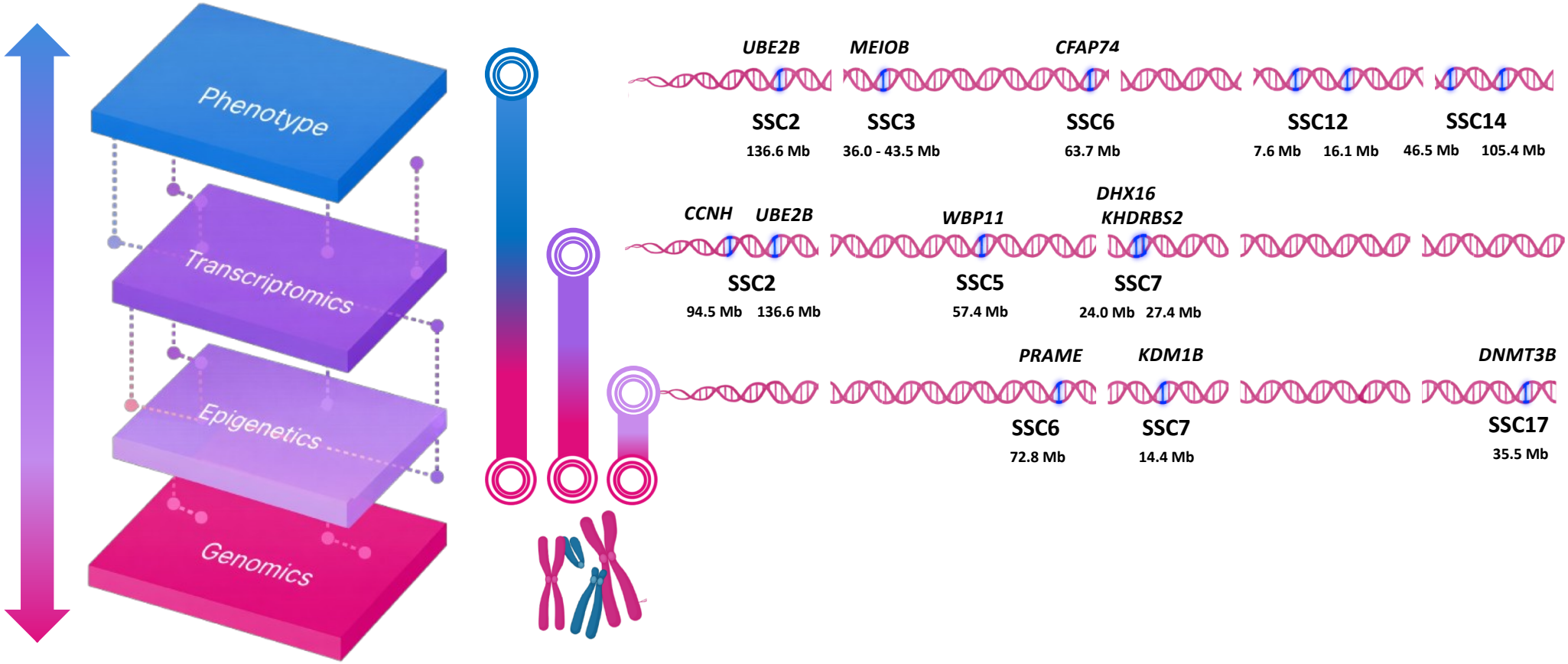
Sperm multi-omics: genetic control over the epigenome



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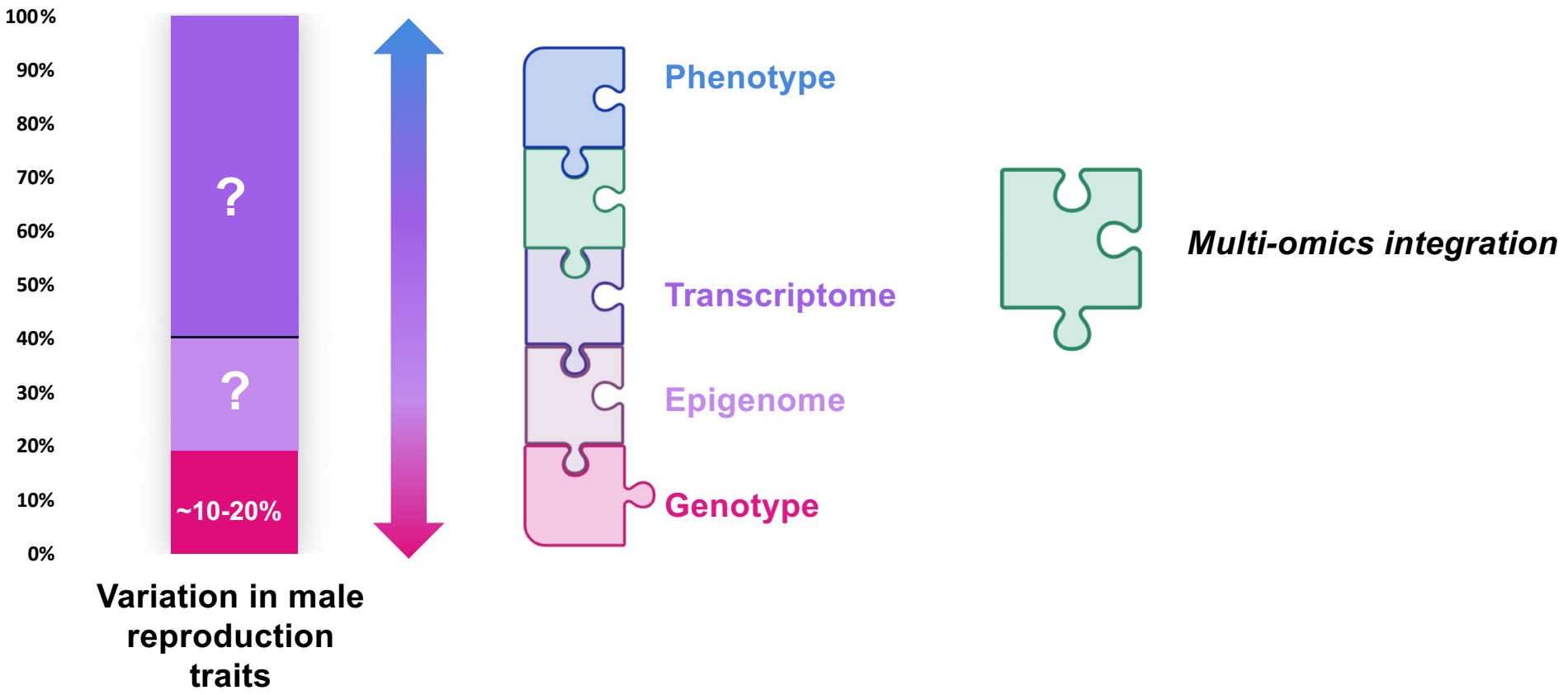

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