

BIOLOGY IS LARGELY SOLVED.
DNA IS THE SOURCE CODE
FOR OUR BODIES. NOW THAT
GENE SEQUENCING IS EASY,
WE JUST HAVE TO READ IT.

IT'S NOT JUST "SOURCE
CODE." THERE'S A TON
OF FEEDBACK AND
EXTERNAL PROCESSING.



BUT EVEN IF IT WERE, DNA IS THE
RESULT OF THE MOST AGGRESSIVE
OPTIMIZATION PROCESS IN THE
UNIVERSE, RUNNING IN PARALLEL
AT EVERY LEVEL, IN EVERY LIVING
THING, FOR FOUR BILLION YEARS.

IT'S STILL JUST CODE.



OK, TRY OPENING GOOGLE.COM
AND CLICKING "VIEW SOURCE."

OK, I-... OH MY GOD.

THAT'S JUST A FEW YEARS OF
OPTIMIZATION BY GOOGLE DEVS.
DNA IS THOUSANDS OF TIMES
LONGER AND WAY, WAY WORSE.

WOW, BIOLOGY
IS IMPOSSIBLE.



<https://xkcd.com/1605/>

The evolution of gene expression in the term placenta of viviparous mammals

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Function and Evolution of Placenta

- Placenta functions in the transfer of nutrients, oxygen, and waste between mother and offspring
- Placenta is highly variable structure and form in mammals, even though major function is conserved
- Placenta likely arose before the origin of therian mammals
- Form relatively well characterized, but diversity of molecular environment of the placenta is only recently being understood
- Possible role of evolutionary interplay between maternal and fetal strategies

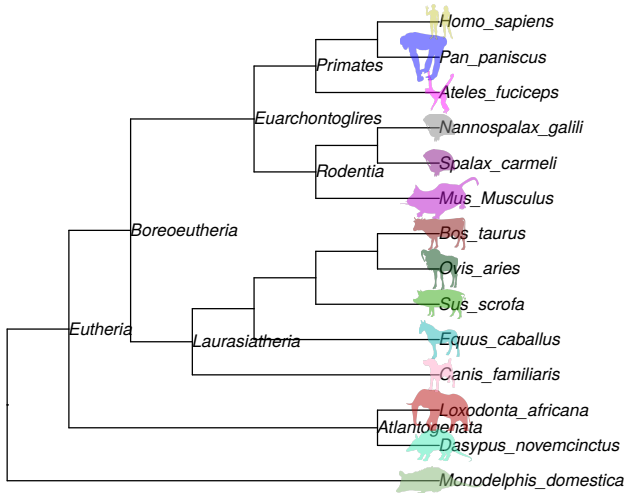
Impacts on Human Health?

- Humans possess a deeply invasive trophoblast layer that can penetrate the myometrium of the uterus¹.
- Defects in placental growth can lead to pre-eclampsia, which can cause hypertension, proteinuria, and mortality of mother and/or infant².
- Pre-eclampsia has been seen in *Pan troglodytes*³, and *Gorilla gorilla*⁴
- Far higher incidence in *Homo sapiens*, with as many as 4% of pregnancies United States affected².

Overall Hypotheses

- Gene expression patterns correlate with placenta morphology
- Altered expression of genes correlates with invasiveness, and therefore pre-eclampsia
- Maternal/Fetal evolutionary strategies will be reflected in gene expression patterns

Species Studied



Variation in Gestational Periods and Litter Size

Species	Gestation (days)	Litter Size	Source
<i>Ateles fusciceps</i>	224	1	Ernest [5]
<i>Bos taurus</i>	278	1	Kiltie [6]
<i>Canis familiaris</i>	61	4	Kiltie [6]
<i>Dasypus novemcinctus</i>	150	4	Smith & Doughty [7]
<i>Equus caballus</i>	336	1	Kiltie [6]
<i>Loxodonta africana</i>	644	1	Ernest [5]
<i>Homo sapiens</i>	270	1.1	Kiltie [6]
<i>Monodelphis domestica</i>	15	7.1	Harder <i>et al.</i> [8]
<i>Mus musculus</i>	20	6.1	Kiltie [6]
<i>Nannospalax galili</i>	28-42	4	Nevo [9]
<i>Ovis aries</i>	151	1.35	Kiltie [6]
<i>Pan paniscus</i>	223	1	Ernest [5]
<i>Spalax carmeli</i>	28-42	4	Nevo [9]
<i>Sus scrofa</i>	114	5.8	Kiltie [6]

Variations in Placenta Morphology

Species	Interhemal Membrane	Pattern
<i>A. fusciceps</i>	hemochorial	trabecular
<i>B. taurus</i>	epitheliochorial	villous
<i>C. familiaris</i>	endotheliochorial	labyrinthine
<i>D. novemcinctus</i>	hemochorial	trabecular
<i>E. caballus</i>	epitheliochorial	villous
<i>L. africana</i>	endotheliochorial	labyrinthine
<i>H. sapiens</i>	hemochorial	villous
<i>M. domestica</i>	epitheliochorial	choriovitelline
<i>M. musculus</i>	hemotrichorial	labyrinthine
<i>N. galili</i>	hemotrichorial	labyrinthine
<i>O. aries</i>	epitheliochorial	villous
<i>P. paniscus</i>	hemochorial	villous
<i>S. carmeli</i>	hemotrichorial	labyrinthine
<i>S. scrofa</i>	epitheliochorial	diffuse

Collection of Placental Tissue

- Collected from 8 mammalian species
- Only fetal portion was sampled
- Sequenced using GAll with an insert size of 230 bp
- Four additional species and additional *M. musculus* and *H. sapiens* samples were obtained from SRA

Assembly, Alignment, Annotation and Quantification

- QC Using FASTQC v0.11.2
- Transcriptomes without suitable reference (*A. fusciceps*, *N. galili*, *S. carmeli*)
 - assembled using Trinity
 - annotated using Diamond against *H. sapiens* or *M. musculus*
- Aligned to the reference (or assembled genome) using STAR
- Expression values were quantified using Cufflinks

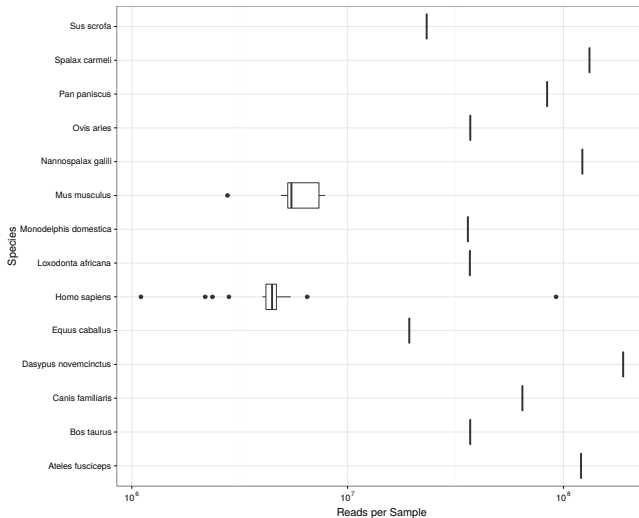
Additional Methods

All of the code used to produce every analysis presented in this poster is available at

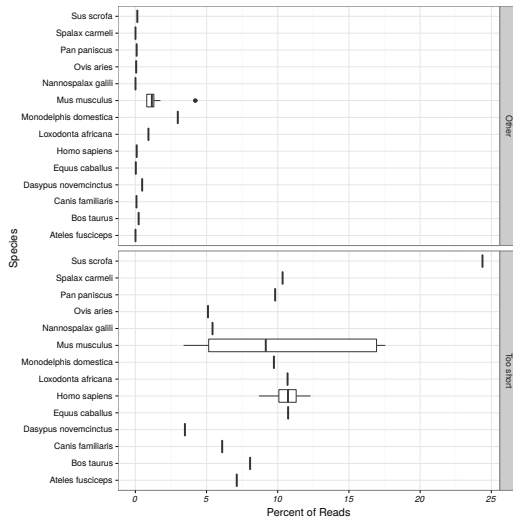
<https://github.com/uiuc-cgm/placenta-viviparous.git>.

All of the sequences used are or will be deposited in SRA.

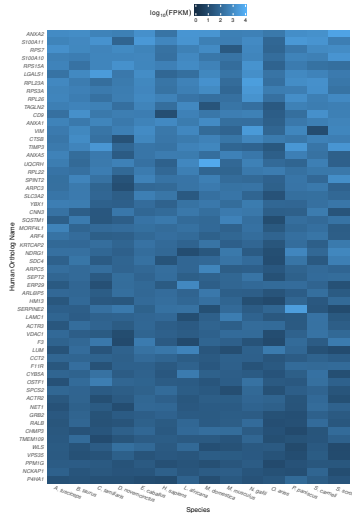
Transcriptome Mapping Statistics: Reads



Transcriptome Mapping Statistics: Unmapped



Core Placenta Transcriptome

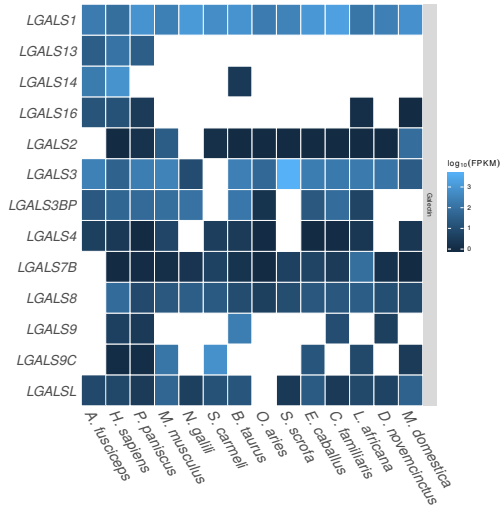


Core placenta transcriptome

- Gene is core to the placenta transcriptome if a 1:1 ortholog is expressed with FPKM ≥ 10 in all species studied and was not a human housekeeping gene according to Eisenberg & Levanon [10].
- Multiple components of annexin complexes are included in the core transcriptome, including *ANXA2*, *ANXA1*, *S100A11*, *S100A10*.
- *ANXA1* is involved in resolution of inflammation by inhibiting phospholipase A2 activity and signaling via formyl peptide receptor family
- hypothesized to be important for the maintenance of the anti-inflammatory during pregnancy¹¹.
- *ANXA2* interacts with *S100A10*, *S100A6*, *S100A11*, and *S100A4*¹², and there is evidence for its interaction with *S100P* as well
- *ANXA2* involved in cell-cell interaction as well as vesicle trafficking and von Willibrand Factor secretion.
- *TIMP3* has been implicated in pre-eclampsia^{13,14}.

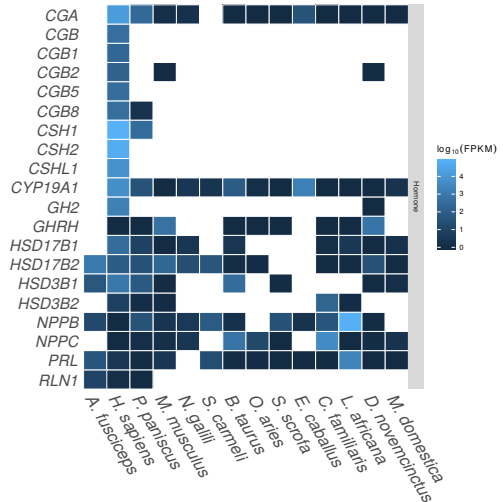
Galectin Expression

- Galectins are major regulators of pregnancy in fetal and maternal tissues¹⁵
- *LGALS1* expressed everywhere
- Primate expansion of *LGALS13* and *LGALS14*
- Likely present in ancestral placenta of therian mammals as it is expressed even in *M. domestica*



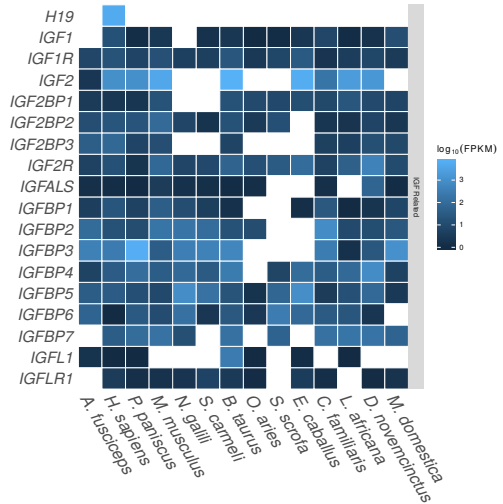
Hormone Expression

- *H. sapiens* specific high expression of *CGA*
- *H. sapiens* expansion of *CGB*
- Vasodilation-involved proteins (*NPPB* & *NPPC*) highly-expressed in *L. africana* and *C. familiaris*, but not expressed elsewhere
- *PRL* highly expressed in *L. africana*



IGF Related

- *IGF2* is highly expressed in most clades
- *IGF2* promotes the growth and division of cells; highly active during fetal development
- *IGF2* binding partners are also highly expressed (*IGFBP3*, *IGFBP5*)

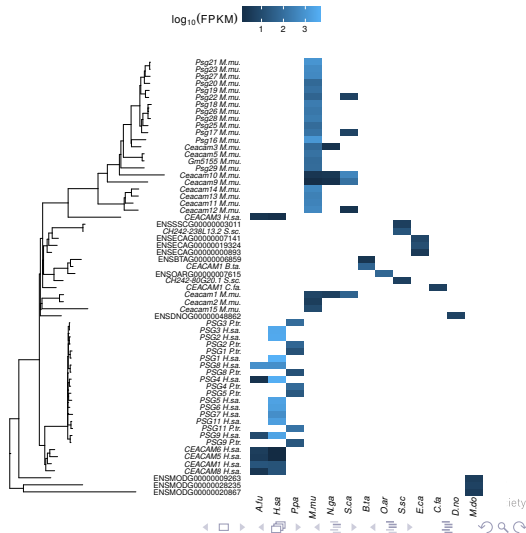


Primate Placenta Transcriptome

Human Symbol	Human Name	p (t-test)	FDR	Fold Change
<i>FSTL1</i>	folliculin like 1	1.06×10^{-6}	0.0011	3.45
<i>GNB2L1</i>	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	1.84×10^{-3}	0.65	2.04
<i>CORO1B</i>	coronin, actin binding protein, 1B	3.17×10^{-3}	0.65	-3.94
<i>ATP1B1</i>	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	3.39×10^{-3}	0.65	-4.77
<i>ACTR3</i>	ARP3 actin-related protein 3 homolog (yeast)	6.05×10^{-3}	0.65	-2.36

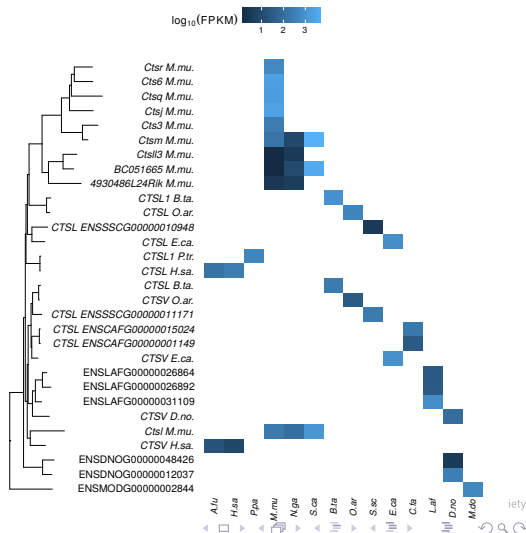
Pregnancy-Specific Glycoprotein Expansion

- 11 highly expressed *PSG* genes in *H. sapiens* and some expression in *A. fusciceps* and *P. paniscus*
- M. musculus* specific expansion and high expression of *PSG* as well
- No other species have high expression of *PSG* or *CEACAM*



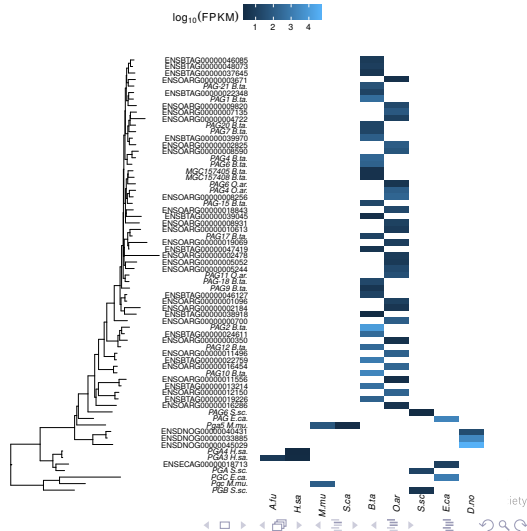
Cathepsin-L expansion

- Cathepsins are highly expressed in many placentas
- Expanded in *M. musculus* and *N. galili* and possibly also *S. carmeli* to a lesser degree
- Intracellular protease which degrades collagen, elastin, and in IGF1R



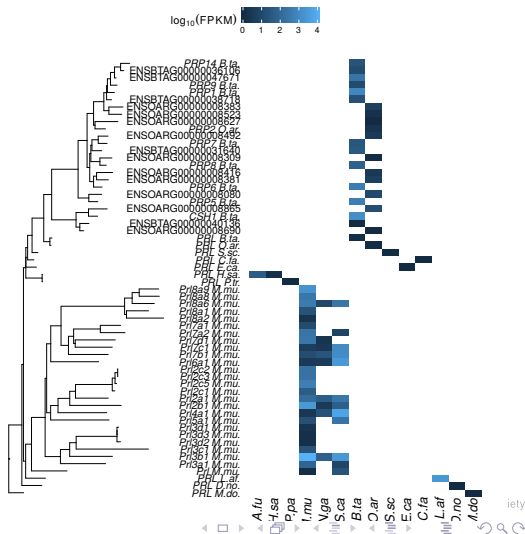
Pregnancy associated glycoprotein

- Massive expansion in ruminants (*B. taurus* and *O. aries*)
- 28 members of this family have FPKM ≥ 1 in *B. taurus*
- *PAG2* = 9730 FPKM
- *PAG10* = 2146 FPKM



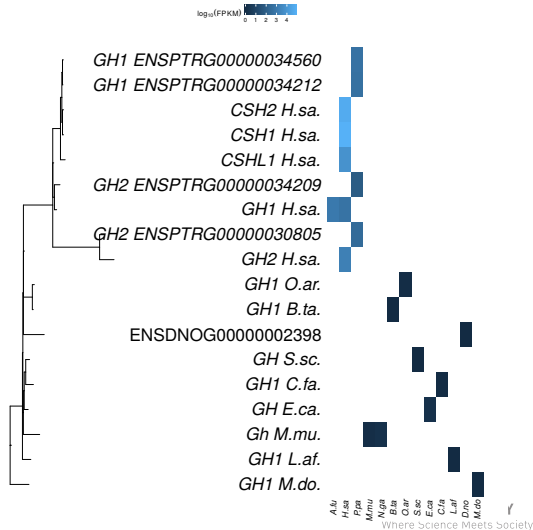
Prolactin

- *L. africana* is only analyzed mammal with high prolactin expression (*PRL*) in the placenta
- However, *M. musculus*, *S. carmeli*, and *B. taurus* have duplications of *PRL* with expression



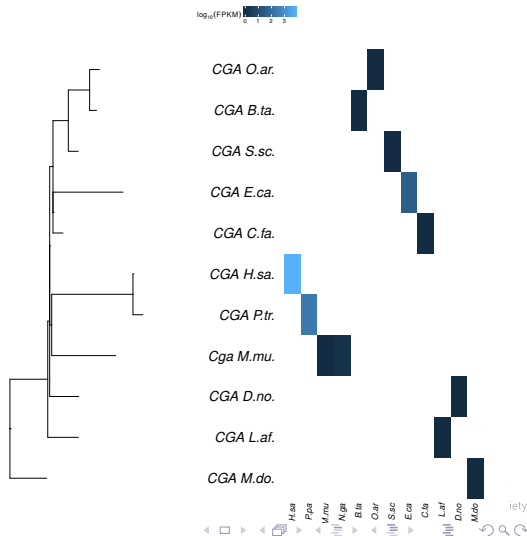
Growth Hormone (GH) family

The GH family has expanded in anthropoid primates, resulting in approximately 5 genes in *H. sapiens* (*GH1*, *GH2*, *CSH1*, *CSH2*, *CSHL1*) and at least three in *P. paniscus* (two *GH2* and *GH1*; owing to the similarity between the two *GH1* in *Pan troglodytes* we cannot reliably distinguish transcripts between the two).



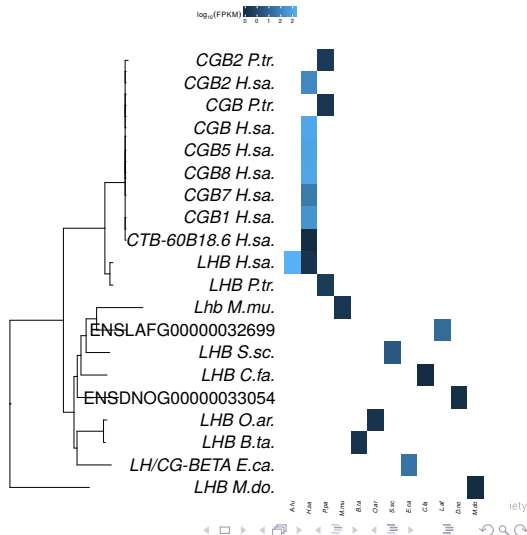
CGA

- *CGA* codes for the alpha subunit of multiple hormones as well as numerous chorionic gonadotropins with variable beta subunits¹⁶.
- Chorionic gonadotropins prevent the regression of the corpus luteum¹⁷.
- *CGA* only expressed in the placentas of *H. sapiens* and *P. paniscus*



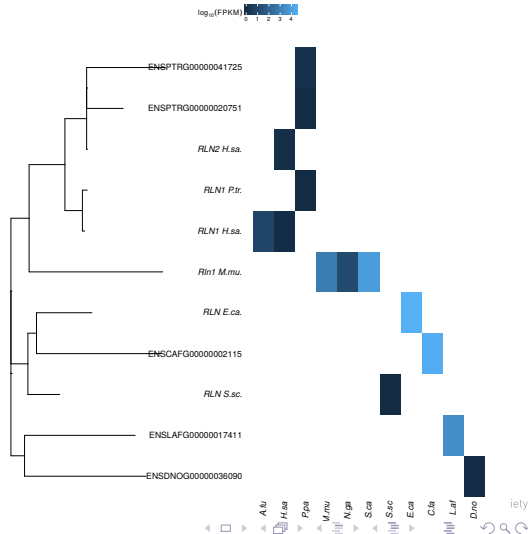
CGB

- *CGB* is highly expressed in *H. sapiens*
- Some expansion of *CGB* in *P. paniscus*, but not highly expressed
- High expression of *LHB* in *A. fusciceps*
 - May be indicative of expansion
 - Would have to examine assembled transcripts to tell



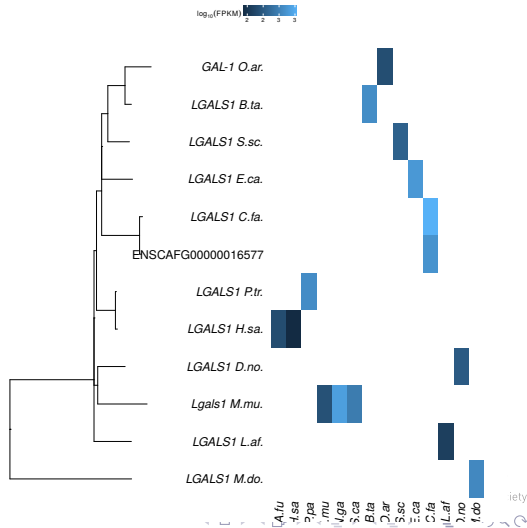
Relaxin

- *RLN* increasing maternal blood flow, widening the pubic bone and relaxing uterine musculature in preparation for labor
- We show that the placenta is a source of *RLN* in *C. familiaris*, *L. africana*, *M. musculus*, *S. carmeli*, and *E. caballus*.

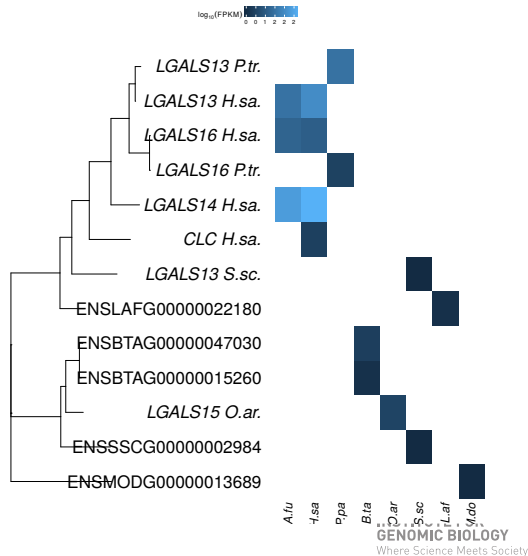


Galectins

- Galectins are major regulators of pregnancy in fetal and maternal tissues
- *LGALS1* mediates maternal-fetal immune tolerance
- substantial expression of galectins in the *M. domestica*
- consistent with ancestral placenta may have maternal-fetal immune tolerance mediated by galectins



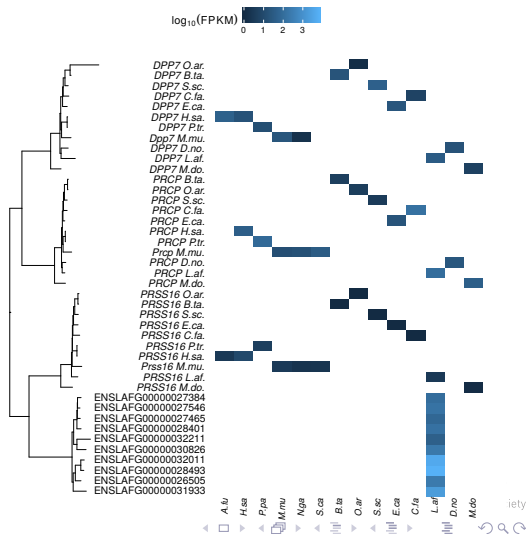
- Evolution of new lineage-specific galectins has occurred in both primates and ruminants, with the genes *LGALS13*, *LGALS14*, and *LGALS16* recognized as being placenta-specific in *H. sapiens* and regulating immune responses by inducing apoptosis of maternal T-cells¹⁸



- The *M. domestica* placenta shows expression of genes that either do not exist in eutherians or are not found in the term eutherian placenta
- The existence of embryonic forms of hemoglobin in fetal tissues at term, as evidenced by the expression of *HBE* and *HBZ* is a feature of marsupials that is generally due to their very short gestation periods.
- Embryonic hemoglobins in marsupials have a lower affinity for oxygen and allow for a lower rate of oxygen uptake from maternal tissues¹⁹.
- One novel uncharacterized gene that shows high expression (*LOC10001195*) is not found in eutherians; Ensembl gene trees reveal that homologs of this gene exist in other amniotes such as birds and turtles, but are not present in eutherian mammals.
- *WFDC2* is a member of the whey acidic protein (WAP) family and involved in innate immunity.

PRSS16

- *PRSS16*, a thymus-specific serine protease that regulates the presentation of self-peptides in CD4⁺ T-lymphocytes²⁰.
- Possibly involved in the mediation of maternal-fetal immune tolerance in *L. africana*



Conclusion

- Sequenced placentas of 14 species
- lineage-specific expansions of gene families and differential gene expression
- Identified common expression patterns of the mammalian expression
- Still much more to learn about the changes in placenta expression during placentation
- Many clades are only represented by a single species; need to have more information to make stronger inferences about evolution of placenta expression
- Lots to learn about what is actually driving the changes in expression

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