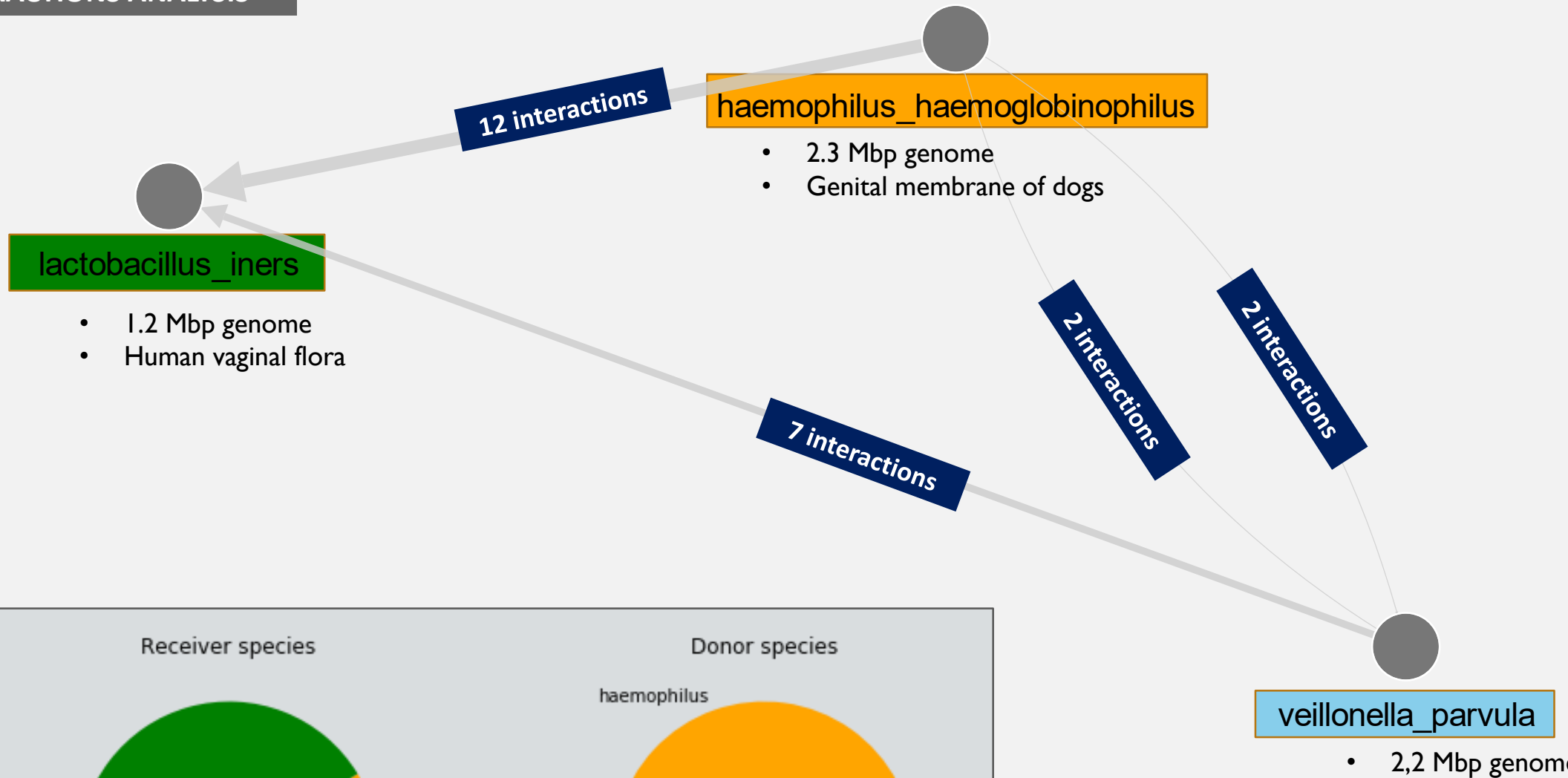
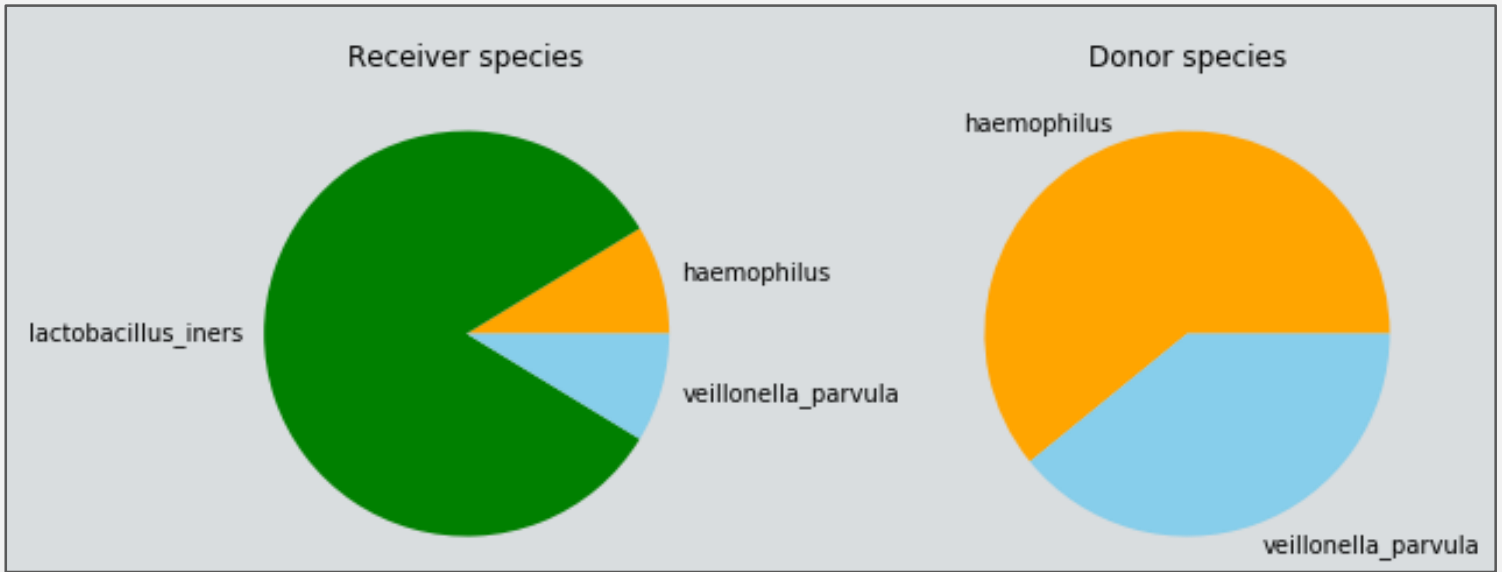
INTERACTIONS ANALYSIS





Compounds received by *lactobacillus iners*:

- Amino acids
  - L-alanine
  - L-isoleucine
  - L-leucine
  - L-lysine
  - L-serine
  - L-threonine
  - L-tryptophan
  - L-tyrosine
  - L-valine
  - L-glutamate
- Xanthosine
- Succinate

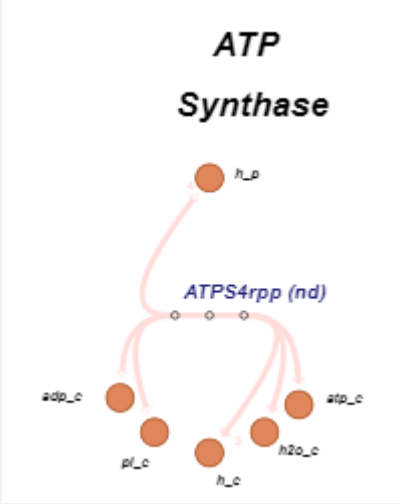
Possible explanation:

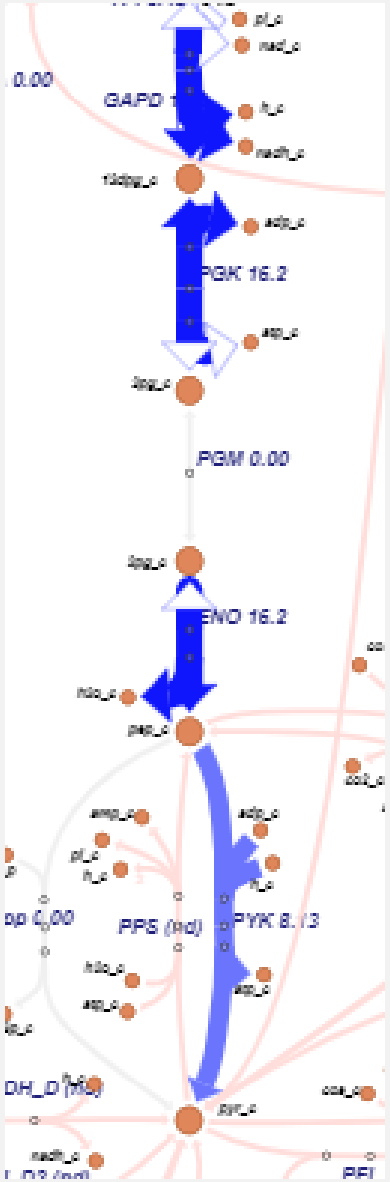
- Amino acids
  - Lacks genes for synthesize AAs
  - Required for normal growth: glutamate
  - Not required: alanine, asparagine, glutamine, glycine
- Xanthosine
  - Present in minimal medium
- Succinate
  - Not present in minimal medium
  - Incomplete citric acid cycle, only fumarate reductase

TABLE 3. *Classification of amino acid biosynthetic pathways according to the extent of genetic lesions*[a]

Class	Pathway	Growth on medium lacking each amino acid				
		L.p.	*L.c.*	*L.c.* (S1)	*L.h.*	*L.a.*
I	Alanine (1)[b]	+	+	+	+	±
	Asparagine (1)	+	+	+	+	+
	Glutamine (1)	+	+	+	+	+
	Glycine (1)	+	+	+	+	±
II	Isoleucine (5)	−(+)	−(+)	−(+)	−(+)	−(+)
	Leucine (4)	−(+)	−(+)	−(+)	−(+)	−(+)
	Lysine (7)	+	+	−(+)	−(+)	±
	Serine (3)	+	±	−(+)	±	−(+)
	Tyrosine (2)	±	−(+)	−(+)	−(+)	−(+)
III	Aspartate (1)	+	−(+)	−(+)	−(+)	−
	Cysteine (5)	+	−(+)	±	+	−
	Proline (3)	+	+	+	−(+)	−
	Phenylalanine (2)	−(+)	−(+)	±	−(+)	−
IV	Arginine (8)	±	−	−	−(+)	−
	Histidine (10)	+	+	+	−	−
	Methionine (4)	−(+)	+	−(+)	−	−
	Threonine (2)	+	+	−	−	−
	Tryptophan (5)	−(+)	−	−	−(+)	−
	Valine (4)	−	−	−	−(+)	−
V	Glutamate (1)	−	−	−	−	−

- ATP synthase not present
- Pyruvate kinase and phosphoglycerate kinase reactions produce ATP
- No evidence found…

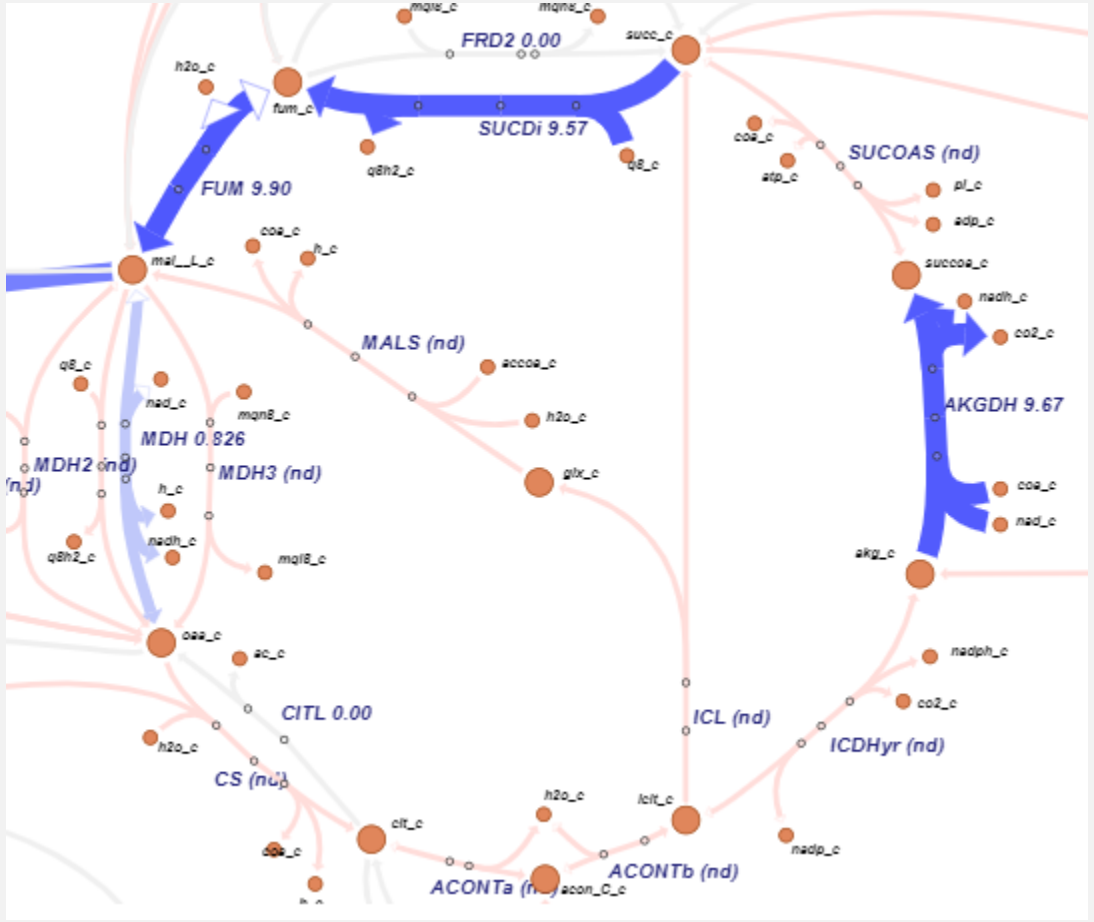




VEILLONELLA – HAEMOPHILUS INTERACTIONS ANALYSIS

- *Veillonella -> haemophilus*
  - L-asparagine
  - L-leucine
- *Haemophilus -> veillonella*
  - L-serine
    - Haemophilus has extra serine…
  - 2-oxoglutarate
    - In the minimal medium
    - Has 2-oxoglutarate dehydrogenase
    - Is probably important

[--> o]	R_AKGt2r	7.18618
[o <--]	R_AKGMAL	2.81382
[o <--]	R_ASPTA	0.82612
[o <--]	R_ALATA_L	0.22368
[o <--]	R_LEUTA	0.142243
[o <--]	R_VALTA	0.133602
[o <--]	R_SDPTA	0.111501
[o <--]	R_ACOTA	0.0933886
[o <--]	R_PHETA1	0.0584926
[o <--]	R_TYRTA	0.0436075
[--> o]	R_HSTPTr	0.029911
[--> o]	R_OHPBAT	7.04064e-05
[o -->]	R_AKGDH	-9.66725
[<-- o]	R_GLUDy	-1.99534
[o -->]	R_2S6HCCi	-3.15724e-05



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