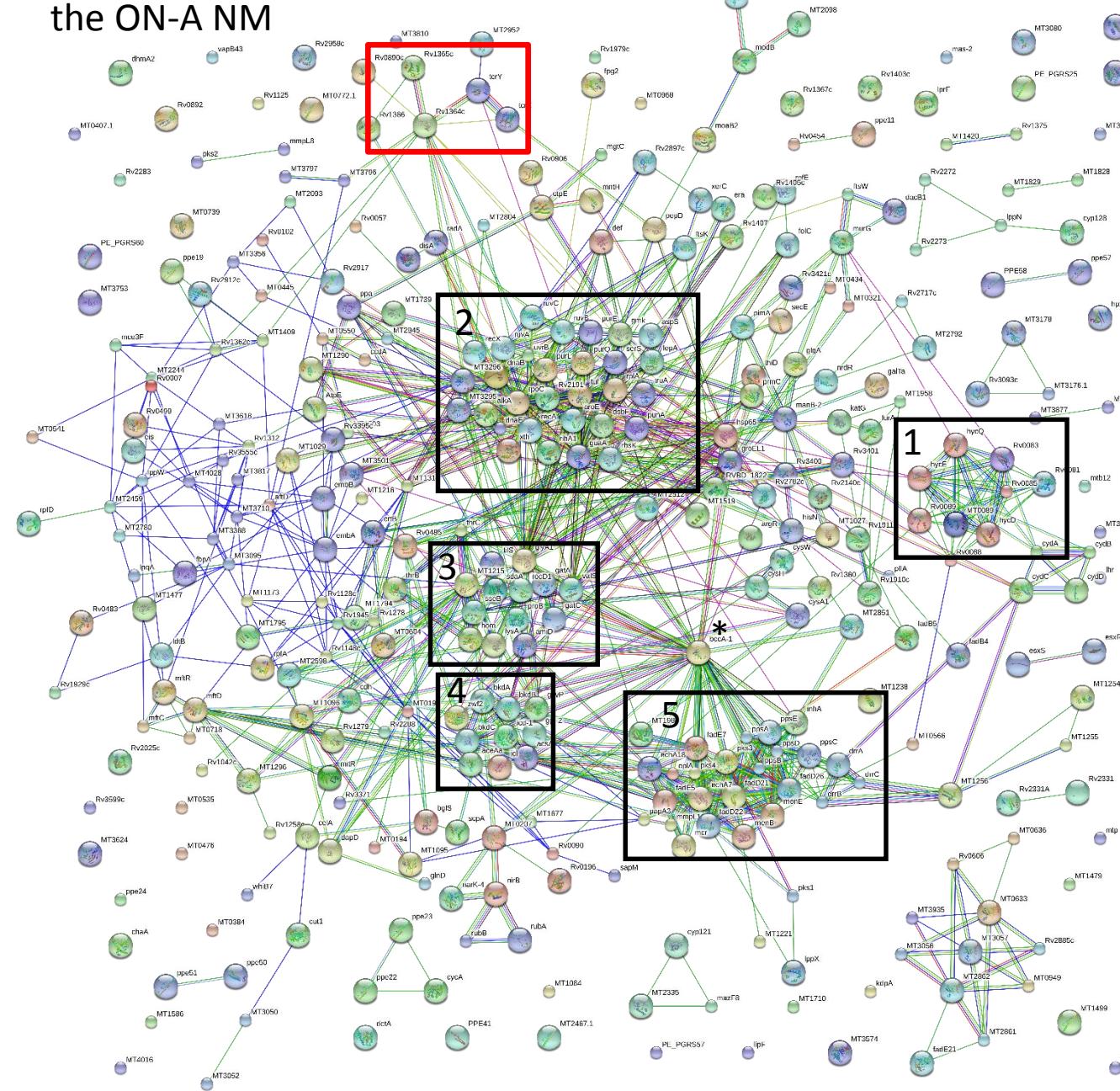


S5 Fig. STRING network of genes found up-regulated in the ON-A NM



1. Hyc operon:

Rv0081, Rv0083, Rv0084 (hycD), hycP (Rv0085), Rv0086 (hycQ), Rv0087 (hycE), Rv0088, Rv0089

2. Information Pathway:

DNA related: *recA, recX, ruvABC, dnaE2, dnaB, uvrB, MT3296 (Rv3202c), MT3295 (Rv3201c)*

Transcription: *rpoC, Rv1407*

Translation: *rplA, lepA, era*

t-RNA synthesis: *valS, serS, aspS*,

Also includes enzymes involved in nucleotide synthesis: *purE, purQ, purL, gmk, guaA*

3. Amino acid metabolism:

lysA, hom, sdaA, thrBC, proB, gcvP, gatAC, glyA1, amiD, gatA, rocD, MT1215 (Rv1178)

4. Intermediate metabolism and respiration:

bkdABC, acsA, aceAa, icl, icd-1, zwf2

5. Lipid metabolism:

PDIM synthesis and export: *ppsABCDE, drrABC, lppX, fabD26*

Menaquinone biosynthesis: *menB, menE*

Lipid degradation: *fadD21, fadE7, fadE5, mcr*

Other lipid synthesis: *fadD22, echA7, echA18, inhA, papA3, pks4, pks1*

* *bccA1* is a node for both, amino acid biosynthesis and lipid metabolism cluster.

In red box, *Rv1364-Rv1365 (RsfA)-Rv1366* (part of 15Kb deletion)