## Table S9. Genes pseudogenized or deleted in the House Finch MG isolates and their status in other *Mycoplasma* genomes.

Among the 12 House Finch isolates we identified 34 genes that had been removed by a deletion, 2 that had been disrupted by a transposon insertion (including one that was deleted following this insertion) and 17 genes that had been pseudogenized by frameshift or nonsense mutations, for a total of 52 genes . We sought to evaluate if these genes were unique to the reference MG genome by evaluating if they had any homologues in any of the 20 Mollicute genomes available has determined by the Molligen Database [24]. We found that 5 of the 33 genes (15%) lost by a deletion lacked a homologue in at least one other genome, while 3 of the 17 genes lost by pseudogenization in the House Finch isolates (~18%) lacked a homologue in the other genomes. We also checked whether any of the genes that were lost in the House Finch isolates had homologues in every one of the 13 *Mycoplasma* genomes available in the database, and thus could be considered "core" genes. We found that of the 229 genes in the reference genome that had a homologue in all of the other genomes, 7 of these had been lost by a combination of 1 deletion and 3 frameshift mutations in the House Finch MG strains.

**Table S9. Genes pseudogenized or deleted in the House Finch MG isolates and their status in other *Mycoplasma* genomes.**

| Gene ID | Start | End | How Lost | No Homology to other *Mycoplasma* genomes | Homology to all other *Mycoplasma* genomes | Gene Name | Product |
|---|---|---|---|---|---|---|---|
| MGA_0625a | 5159 | 6077 | Disruptor Mutation | FALSE | FALSE | | ABC-type multidrug/protein/lipid (MdlB-like) transport system component domain protein |
| MGA_0626 | 6392 | 8294 | Disruptor Mutation | FALSE | TRUE | | ABC-type multidrug/protein/lipid (MdlB-like) transport system component |
| MGA_0641 | 14480 | 15212 | Disruptor Mutation | FALSE | FALSE | glpF | glycerol uptake facilitator protein GlpF |
| MGA_0648 | 18209 | 20462 | Disruptor Mutation | FALSE | FALSE | | conserved lipoprotein |
| MGA_0656 | 30264 | 30948 | Disruptor Mutation | TRUE | FALSE | | unique hypothetical lipoprotein |
| MGA_0686 | 50592 | 52587 | Disruptor Mutation | FALSE | TRUE | uvrB | excinuclease ABC subunit B |
| MGA_0687 | 52631 | 53789 | Disruptor Mutation | FALSE | FALSE | pstS | ABC-type phosphate transport system periplasmic phosphate binding protein |
| MGA_0801 | 124459 | 125605 | Deletion/IS Insertion | FALSE | FALSE | | Subtilisin-like serine protease domain protein |
| MGA_0802 | 125682 | 126432 | Deletion | TRUE | FALSE | | Subtilisin-like serine protease domain protein |
| MGA_0815 | 137104 | 139078 | Deletion | FALSE | FALSE | | Subtilisin-like serine protease |
| MGA_1037 | 332335 | 334084 | Disruptor Mutation | FALSE | FALSE | | conserved hypothetical membrane protein |
| MGA_1328 | 369554 | 369794 | Deletion | FALSE | TRUE | deoC_1 | Deoxyribose-phosphate aldolase domain protein |
| MGA_1081 | 369839 | 371102 | Deletion | FALSE | FALSE | | putative transposase |

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|---|---|---|---|---|---|---|---|
| MGA_1083 | 371070 | 371919 | Deletion | FALSE | FALSE | | HAD superfamily hydrolase Cof |
| MGA_1085 | 371929 | 373567 | Deletion | FALSE | FALSE | | conserved hypothetical protein |
| MGA_1087 | 373576 | 374212 | Deletion | FALSE | FALSE | | conserved hypothetical protein |
| MGA_1088 | 374241 | 374925 | Deletion | FALSE | TRUE | | ABC transporter ATPase component |
| MGA_1089 | 374908 | 376459 | Deletion | FALSE | FALSE | | ABC transporter permease domain protein |
| MGA_1091 | 376555 | 376891 | Deletion | FALSE | FALSE | | putative signal peptidase I |
| MGA_1092 | 376969 | 377530 | Deletion | FALSE | TRUE | | Elongation factor G domain protein |
| MGA_1100 | 379435 | 380476 | Deletion | FALSE | TRUE | asnS_2 | Asparaginyl-tRNA synthetase |
| MGA_1102 | 380479 | 382111 | Deletion | FALSE | FALSE | | conserved hypothetical membrane protein |
| MGA_1103 | 382094 | 384026 | Deletion | FALSE | FALSE | | predicted integral membrane methylase-domain protein |
| MGA_1347 | 384502 | 384670 | Deletion | FALSE | FALSE | | putative transposase domain protein |
| MGA_1106 | 384754 | 384946 | Deletion | TRUE | FALSE | | putative transposase domain protein |
| MGA_1107 | 384995 | 386495 | Deletion | FALSE | FALSE | | conserved hypothetical RmuC-domain protein |
| MGA_1108 | 386618 | 387119 | Deletion | FALSE | FALSE | | putative transposase domain protein |
| MGA_1109 | 387260 | 388307 | Deletion | FALSE | FALSE | | putative transposase domain protein |
| MGA_1220 | 464277 | 465489 | IS Insertion | FALSE | FALSE | arcA_1 | Arginine deiminase |
| MGA_1263 | 507145 | 507823 | Disruptor Mutation | FALSE | FALSE | beta-pgm | putative beta-phosphoglucomutase (beta-PGM) |
| MGA_1283 | 520043 | 520808 | Disruptor Mutation | FALSE | FALSE | | PTS system mannitol-specific (MtlA)-like IIB domain protein |
| MGA_1305 | 536425 | 536824 | Disruptor Mutation | FALSE | FALSE | maoC | MaoC-like dehydratase |
| MGA_0135 | 652030 | 653536 | Disruptor Mutation | FALSE | TRUE | potA | ABC-type spermidine/putrescine import ATP-binding protein potA |
| MGA_0137 | 653891 | 655376 | Disruptor Mutation | TRUE | FALSE | | unique hypothetical protein |
| MGA_1361 | 747656 | 747986 | Disruptor Mutation | FALSE | FALSE | | unique hypothetical protein |
| MGA_1354 | 876961 | 877114 | Disruptor Mutation | FALSE | FALSE | | hypothetical protein |
| MGA_0508 | 910763 | 912797 | Deletion | FALSE | FALSE | fruA | PTS system fructose-specific enzyme EIIABC component |

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|---|---|---|---|---|---|---|---|
| MGA_0512 | 912799 | 913246 | Deletion | TRUE | FALSE | | hypothetical protein |
| MGA_0514 | 913193 | 914144 | Deletion | FALSE | FALSE | manA | mannose-6-phosphate isomerase (phosphomannose isomerase) |
| MGA_0516 | 915226 | 916669 | Deletion | TRUE | FALSE | | unique hypothetical protein |
| MGA_0517 | 916577 | 917954 | Deletion | FALSE | FALSE | | Subtilisin-like serine protease domain protein |
| MGA_0518 | 917874 | 918705 | Deletion | TRUE | FALSE | | Subtilisin-like serine protease domain protein |
| MGA_0519 | 919247 | 923060 | Deletion | FALSE | FALSE | | Csn1 family CRISPR-associated protein |
| MGA_0523 | 923127 | 924054 | Deletion | FALSE | FALSE | cas1 | CRISPR-associated protein Cas1 |
| MGA_0525 | 924040 | 924370 | Deletion | FALSE | FALSE | cas2 | CRISPR-associated protein Cas2 |
| MGA_0526 | 924369 | 925134 | Deletion | FALSE | FALSE | | conserved hypothetical protein |
| MGA_0537 | 938710 | 941338 | Deletion | FALSE | FALSE | hsdM | type I restriction-modification system methyltransferase (M) subunit |
| MGA_0539 | 941547 | 942165 | Deletion | FALSE | FALSE | hsdS_1 | type I restriction-modification system specificity (S) subunit domain protein |
| MGA_0540 | 942139 | 942724 | Deletion | FALSE | FALSE | hsdS_2 | type I restriction-modification system specificity (S) subunit domain protein |
| MGA_0541 | 942734 | 945890 | Deletion | FALSE | FALSE | hsdR | type I site-specific restriction-modification system restriction (R) subunit (deoxyribonuclease) |
| MGA_0567 | 970243 | 970549 | Disruptor Mutation | TRUE | FALSE | | unique hypothetical protein |
| MGA_0586 | 987980 | 990098 | Disruptor Mutation | FALSE | FALSE | | conserved hypothetical protein |