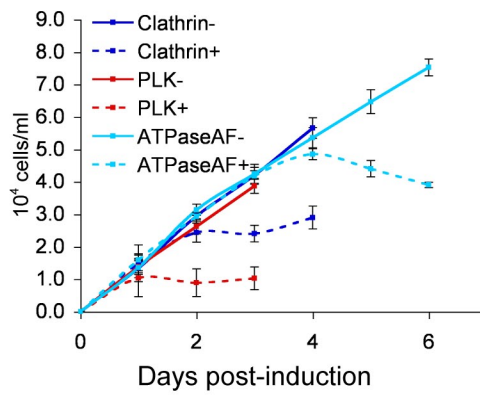
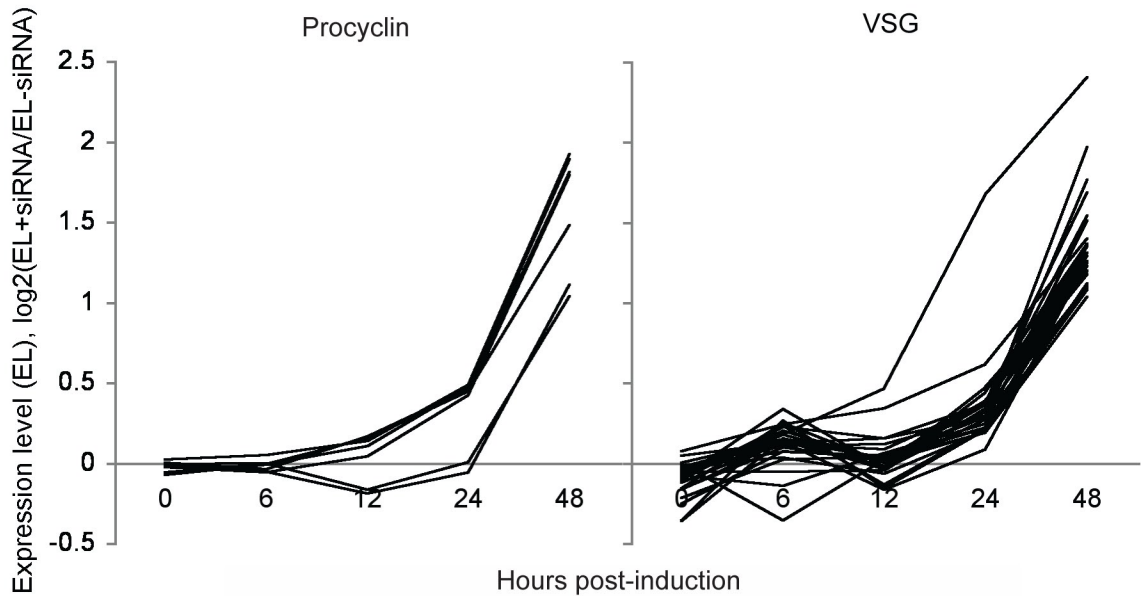


A**B****C**

VSG 2

VSG 2 sequencing 45 TGCAAATCCC **CATGCAAAATGGCATAACGATGCGGAAAAACA** AAGTGCACATTGGATAAG
VSG 2 241 TGCAAATCCC **CATGCAAAATGGCATAACGATGCGGAAAAACA** AAGTGCACATTGGATAAG
Tb11.57.0084oligo 1 -----GCAAATTTGGTTGAAGAAGAAGGTGGCAAA--AAGCAAGTGCACATTGGATGCA

VSG 2 sequencing 105 GAGGAGGCCAAAAAAGGTAGCAGATGAGACTGCAAAAGATGGGAAAACTGGAAACACAAAC
VSG 2 301 GAGGAGGCCAAAAAAGGTAGCAGATGAGACTGCAAAAGATGGGAAAACTGGAAACACAAAC
Tb11.57.0084oligo 51 AAAGCAGCTA-----

VSG 21

VSG 21 241 CAAAGTTGATACTGAGAAAAAGATGACAAATCGTTTTCTAGCAATGTGAGAGTGTCTGT
VSG 21 sequencing 108 CAAAGTTGATACTGAGAAAAAGATGACAAATCGTTTTCTAGCAATGTGAGAGTGTCTGT
Tb09.244.0640oligo 1 -----AGCAATGTGAGAGTGTCTGT

VSG 21 301 TCCTCAGGTATTTGCTGCGTTAGTTTTGGCTGCAATTCCTAAGAATTCTGAC
VSG 21 sequencing 168 TCCTCAGGTATTTGCTGCGTTAGTTTTGGCTGCAATTCCTAAGAATTCT---
Tb09.244.0640oligo 21 TCCTCACGTTGTTTCTGCAATTTGCTGCC-TTGCCTTTTCTAA-----

VSG 16

VSG 16 61 ATCAGAGAAGTCAACTTCCGAAGCAGACGTAACGTGCGAAAAAGAAAGGAACAGGAGATAA
VSG 16 sequencing 1 -----CTTCCGAN-CANACGTAACGTGCGAAA-GAAAGGAACAGGAGATAA
Tb927.4.5530oligo 1 -----GCA

VSG 16 121 CTGCAAAGATGGATGTAAAGAAGTCGAAGAAGGTGGAAAAAAGAAGTGCCTAAAGGATCC
VSG 16 sequencing 45 CTGCAAAGATGGATGTAAAGAAGTCGAAGAAGGTGGAAAAAAGAAGTGCCTAAAGGATCC
Tb927.4.5530oligo 3 TGGCAAAGATGGCTGCAAAAGAAATCAGTGAAACGGCCAAAAGAAGTGCCTAGTGGAT--

VSG 17

VSG 17 241 TAAAACAAACACCA**CAGGAAGTAATTCTCTTGTGATTAAAAAGCGCCCTCTTTTGCTTGC**
VSG 17 sequencing 142 TAAAACAAACACCA**CAGGAAGTAATTCTCTTGTGATTAAAAAGCGCCCTCTTTTGCTTGC**
Tb09.244.1790oligo 1 -----GGAGCAGTTGTTATTTCTGCTGTGATTAA---TGCCCTCTTTTGCTTGC

VSG 17 301 ATTTTTGATTCTAGCATAACTTTCCCCCTC-----
VSG 17 sequencing 202 ATTTTTGATTCTAGCATAACTTTCCCCCTCATATTTCCCTCTTTTTAAATTTTCCTTG
Tb09.244.1790oligo 48 ATTTTTGATTCTA-----