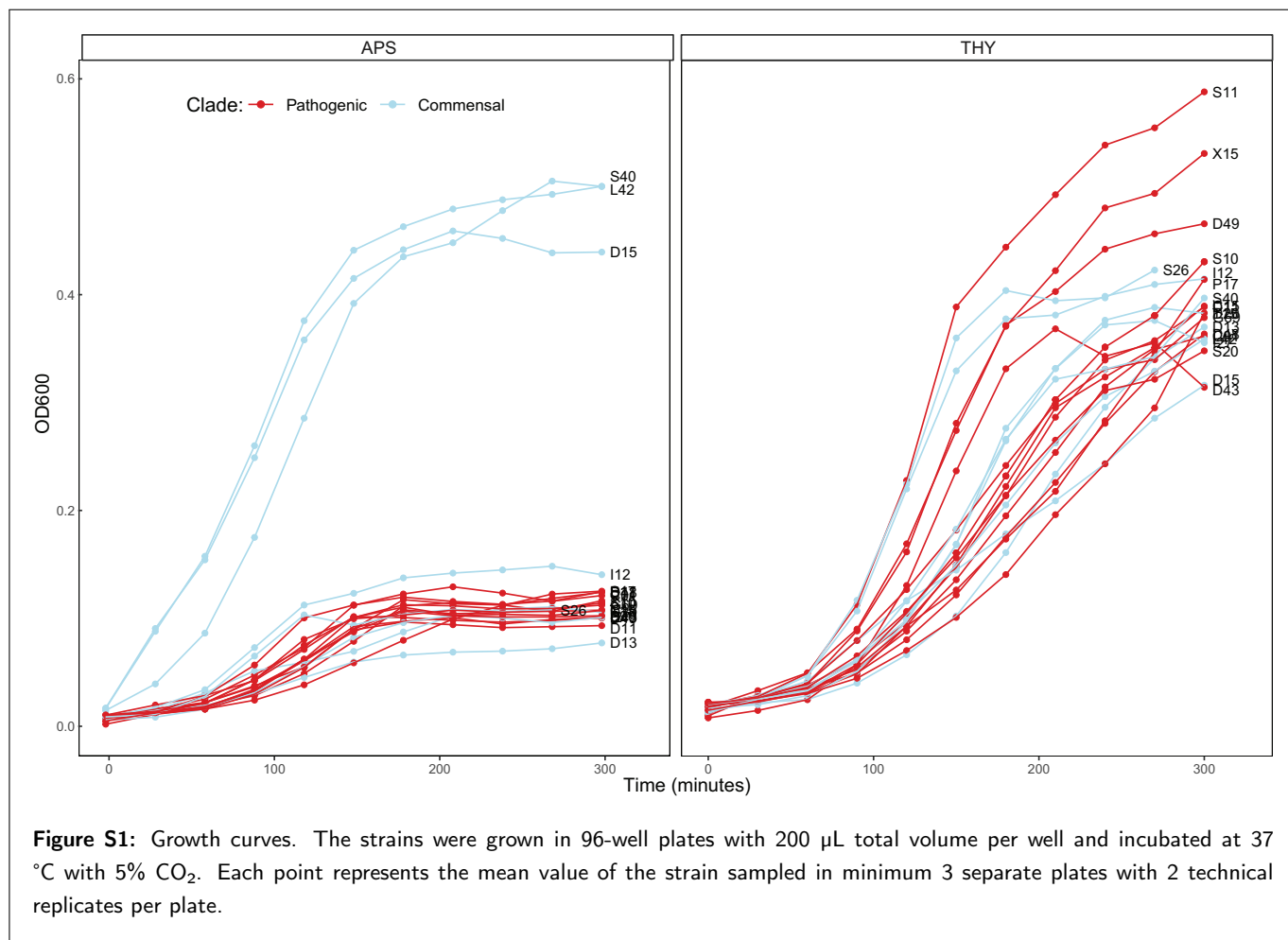
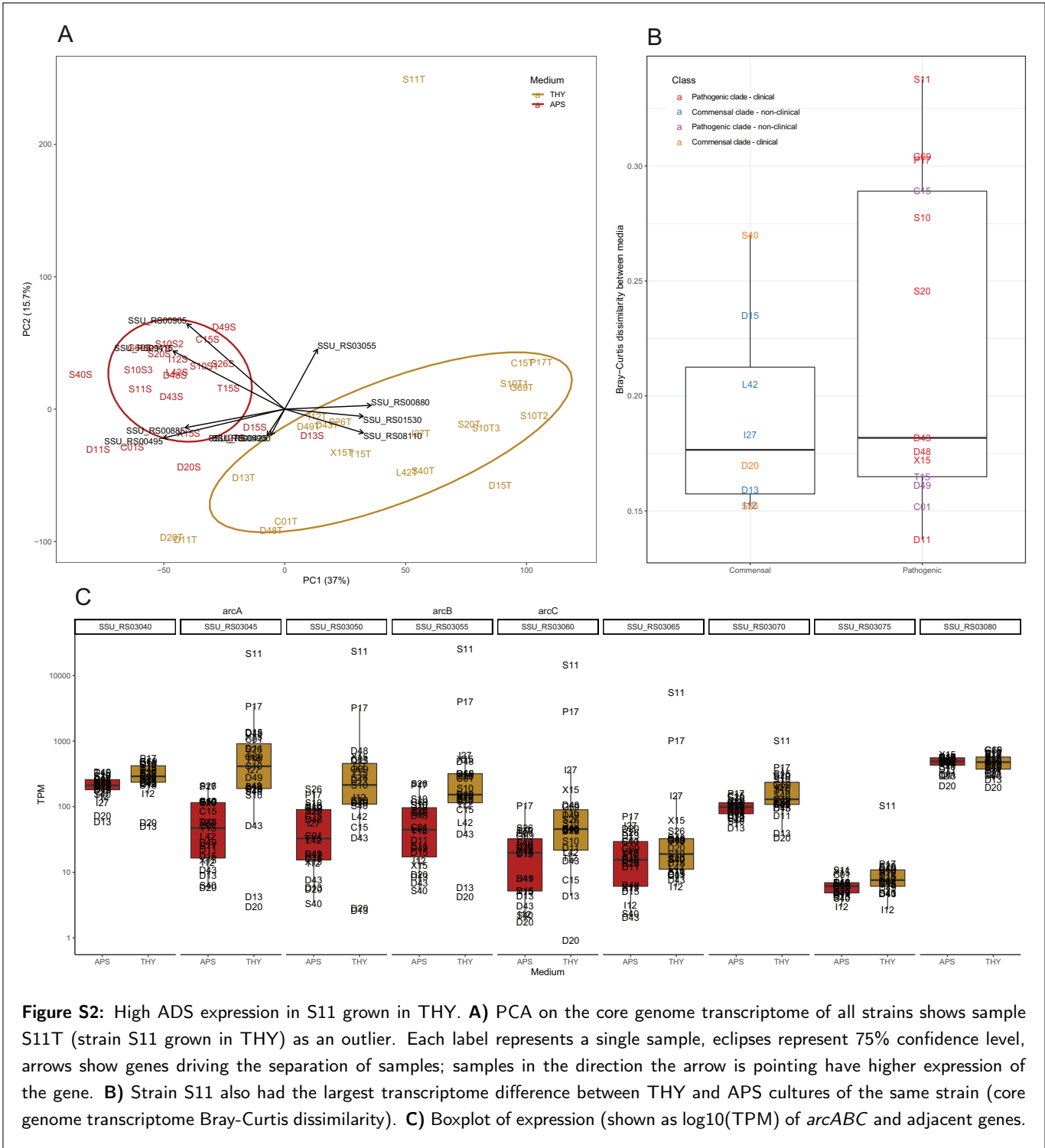
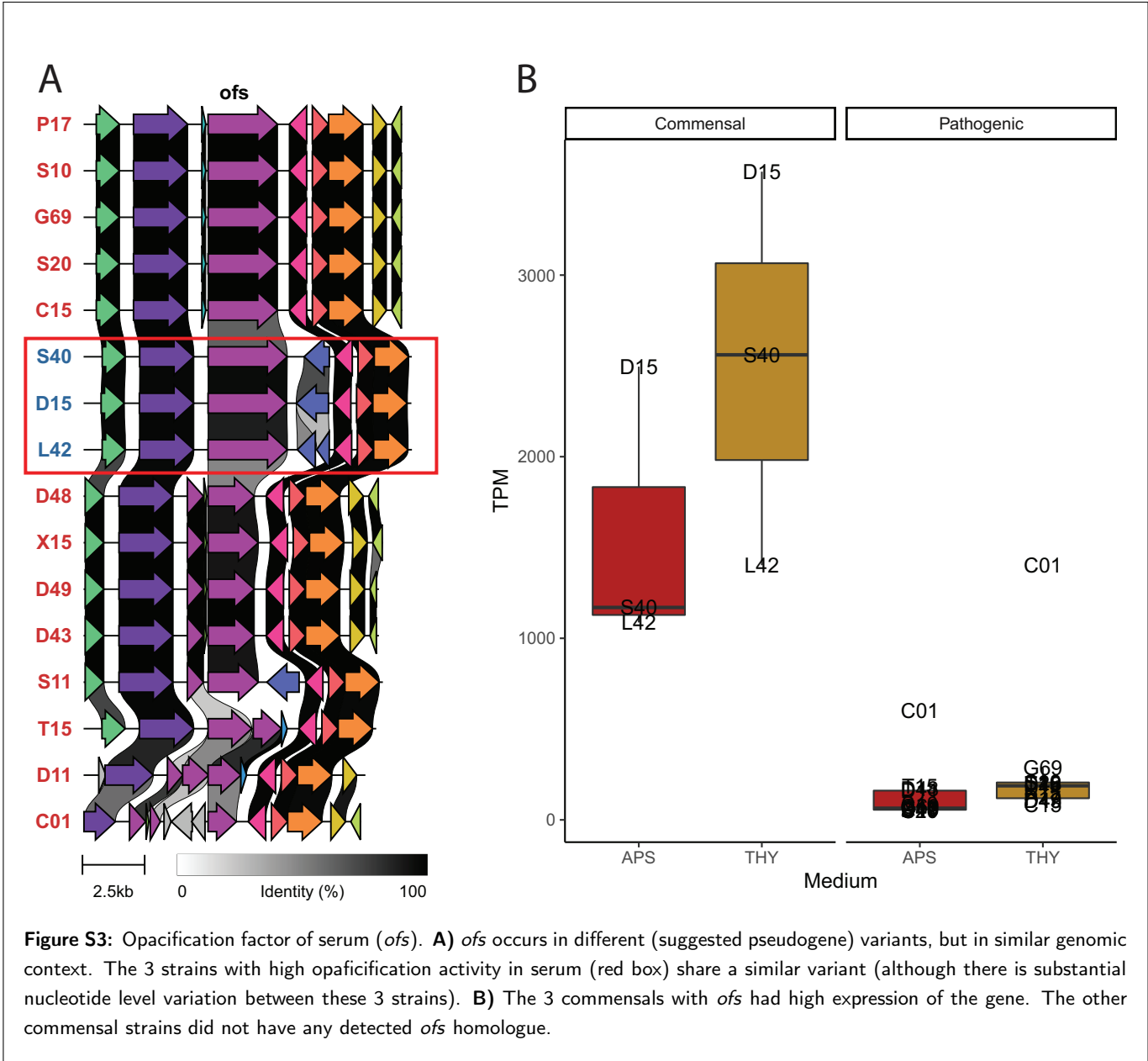


Supplementary figures

Transcriptomics in serum and culture medium reveal shared and differential gene regulation in pathogenic and commensal *Streptococcus suis*







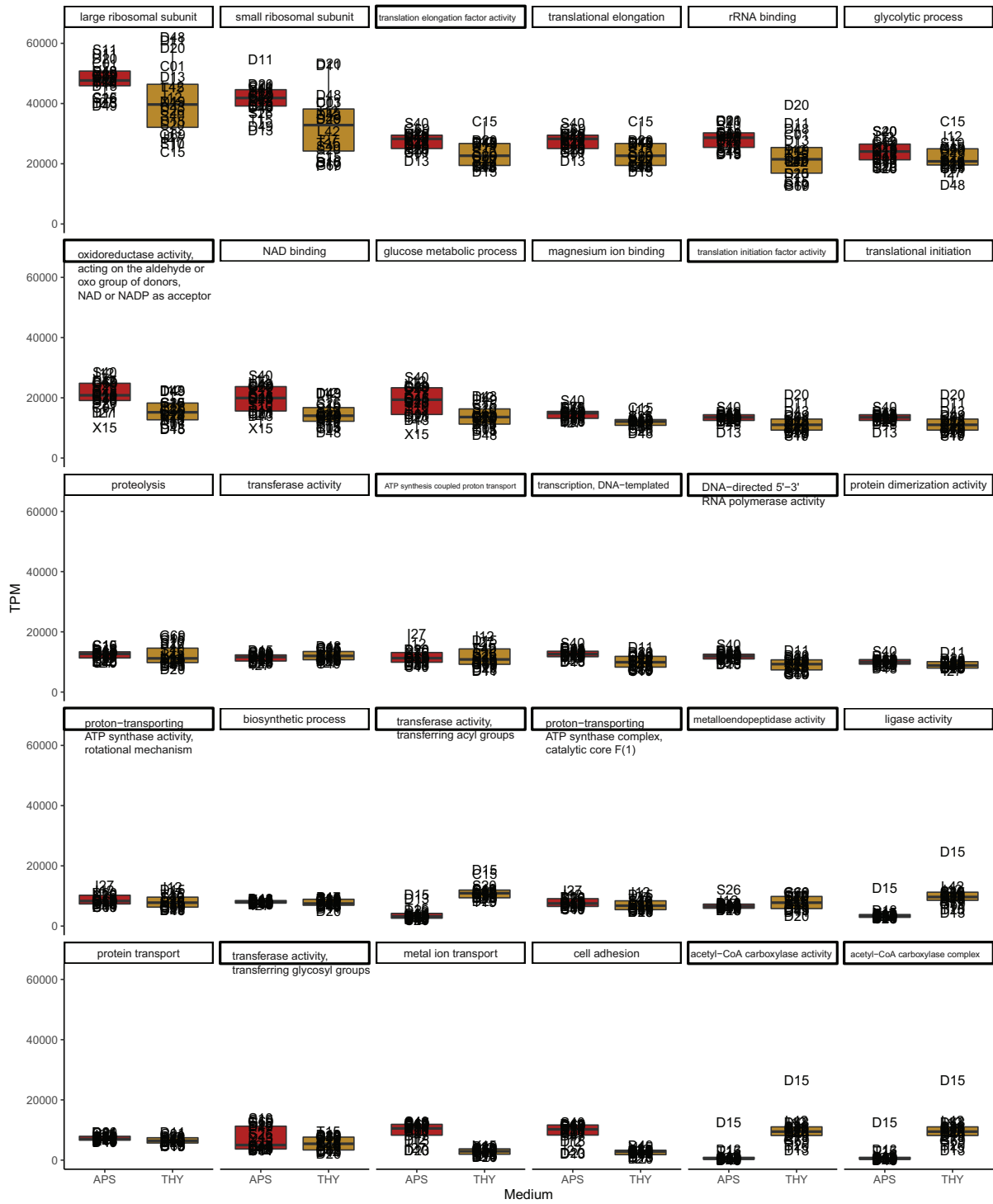
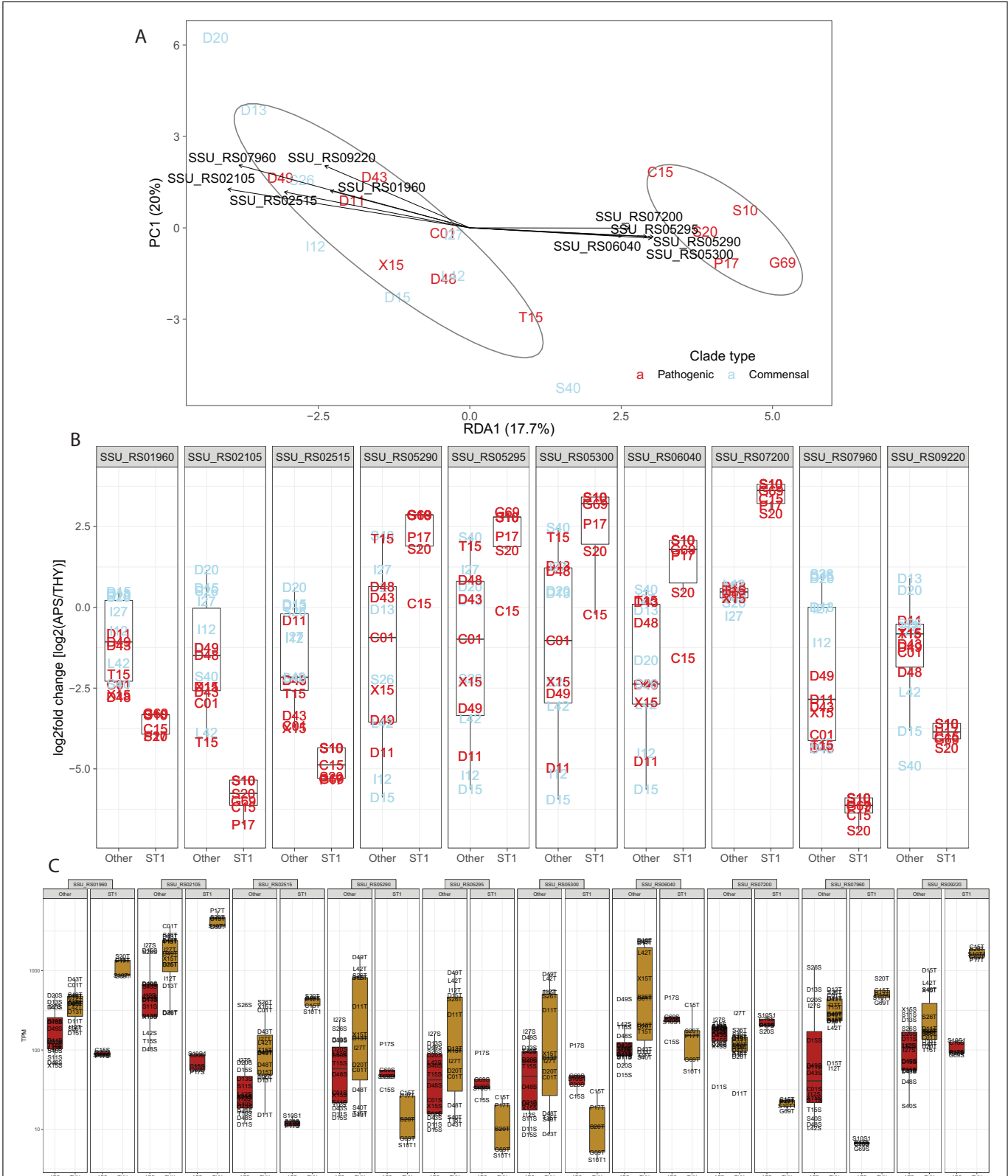
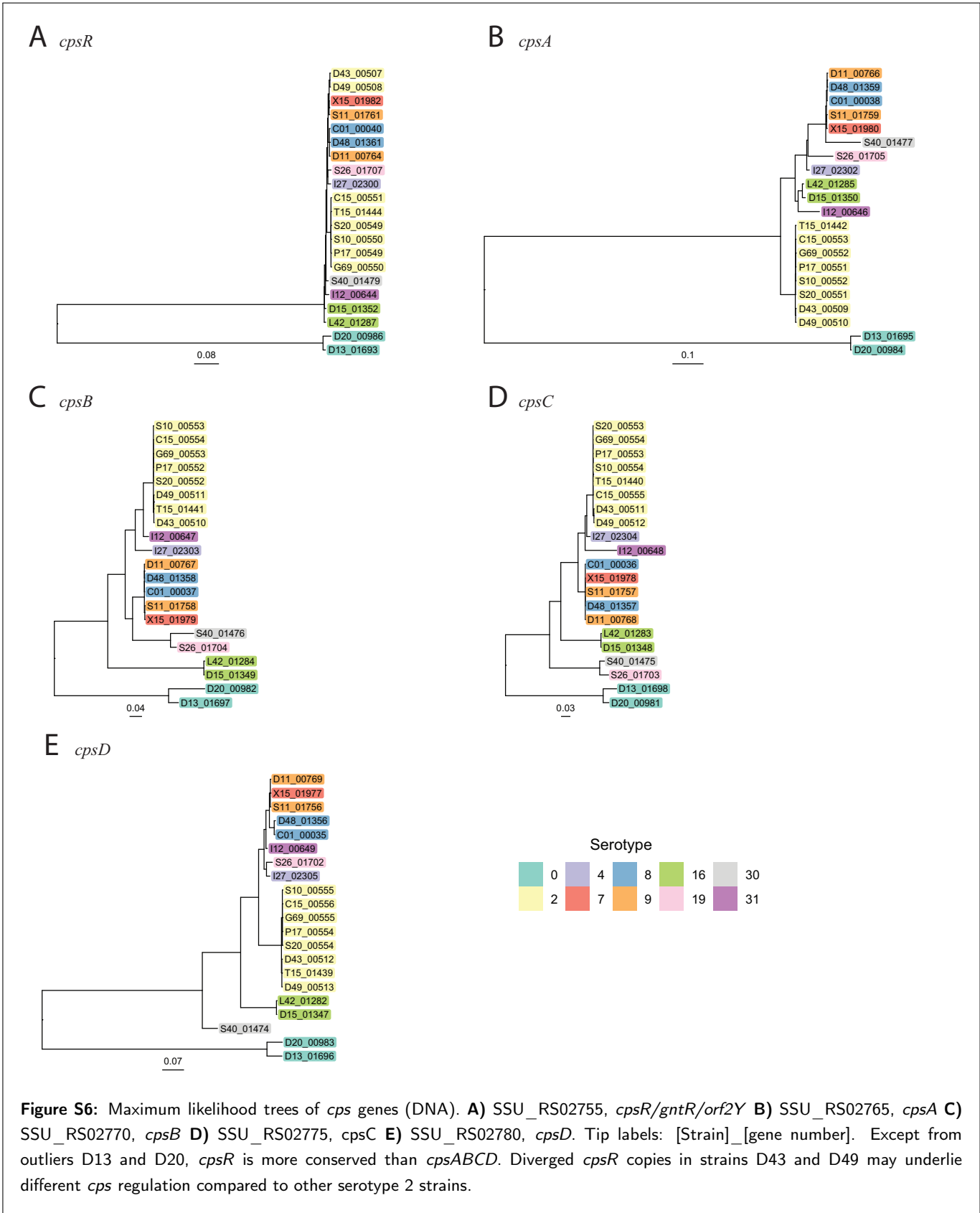


Figure S4: Boxplots showing expression of the overall most expressed GO terms in APS vs THY.





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C15 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
G69 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
P17 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
S10 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
S20 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
T15 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
S40 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
I12 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 87
D15 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
L42 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
S26 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
D43 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
D49 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
X15 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
I27 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
C01 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
D11 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
D48 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
S11 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 88
D13 .. MKKYVDTGHRKRKRSRYHCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC KSGRNYYYHGASSVSMDYHVYTKKDVTAGSAYT 86
D20 MSKYRVDVDRDYKRGKRSYCSKDTVKAMKYNKYAVKSGYYDRDDHTVNTDYDRC HSGRNYYYHAGTTSVMDYHVYSR KDV TAGSAYS 89
consensus *****!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*

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C15 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
G69 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
P17 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
S10 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
S20 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
T15 MT. AGKNTYSRMRHG YTRNDG... DSTGKKYTRHNGSTYDATKTA V KAKYDVYDDYADDSSHSHYD T DNRVYKSTTARGA . SNRD KHKS 173
S40 MT. AGKNTY SRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNR Y TKHKS 173
I12 MT. AGKNTYSRMRHG YTRDDG... N STGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD TN H VYKSTTARGA SNRD TKHKS 173
D15 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
L42 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
S26 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNR H D TKHKS 175
D43 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
D49 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
X15 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
I27 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
C01 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
D11 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
D48 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
S11 MT. AGKNTYSRMRHG YTRDDG... DSTGKKYTRHNGSTYDATKTA V KAKY DVYDDYADDSSHSHYD T DNRVYKSTTARGA SNRD TKHKS 174
D13 MD. GDR THSTYTRM R C YTR SMG D DR D K T G T K Y TR H N G . T S Y DR K T M R V A K R V Y V D D Y A . D D G N R H Y D K N D V Y Y K S S T A R G A V S D A G . Y K G 172
D20 D. GDR THSTYTRM R C YTR SMG. D DR D K T G T K Y TR H N G . T S Y DR K T M R V A K R V Y V D D Y A . D D G N R H Y D K N D V Y Y K S S T A R G A . V S N A T Y K G 173
consensus ** * * * * * ! * ! ! * ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! * *

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C15 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
G69 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
P17 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
S10 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
S20 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
T15 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
S40 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKGSSHM GKCY YSGKADDADKVRYN ... 240
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D15 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG S N H M GKCY YSGKADDADK T R Y N ... 241
L42 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG S N H M GKCY YSGKADDADK V R Y N ... 241
S26 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG . S SHM K C Y Y S G K A D D A D K V R Y S R M N 244
D43 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG . S SHM K C Y Y S G K A D D A D K V R Y N ... 240
D49 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG . S SHM K C Y Y S G K A D D A D K V R Y N ... 240
X15 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG . S SHM K C Y Y S G K A D D A D K V R Y N ... 240
I27 DYDTNMKASYDNGMARNTHHH YHAWNKKDCKYAN YRSKGSVTSKG . S SHM K C Y Y S G K A D D A D K V R Y N ... 240
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D11 DYDTNMKASYDNGMARNT H H Y H A W N K K D C K Y A N Y R S K G S V T S K G . S S H M K C Y Y S G K A D D A D K V R Y N ... 239
D48 DYDTNMKASYDNGMARNT H H Y H A W N K K D C K Y A N Y R S K G S V T S K G . S S H M K C Y Y S G K A D D A D K V R Y N ... 239
S11 DYDTNMKASYDNGMARNT H H Y H A W N K K D C K Y A N Y R S K G S V T S K G . S S H M K C Y Y S G K A D D A D K V R Y N ... 240
D13 DYDTNMKASYDNGMARNT R S N V D K K Y A Y V V R D D N R T A R G R H R N G . . . . . T A Y R H H D T K S T Y K D 231
D20 DYDTNMKASYDNGMARNT R S N V N K K Y A Y V V R D D N R T A R G R Y R N G . . . . . T A Y R H H D T K S T Y K D 232
consensus !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

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 non-conserved
 ≥ 50% conserved

Figure S7: Multiple sequence alignment of *cpsR* (SSU_RS02755) protein sequences. Strains D43 and D49 do not share sequence similarity with other serotype 2 strain, except from a R/S SNP in position 17.

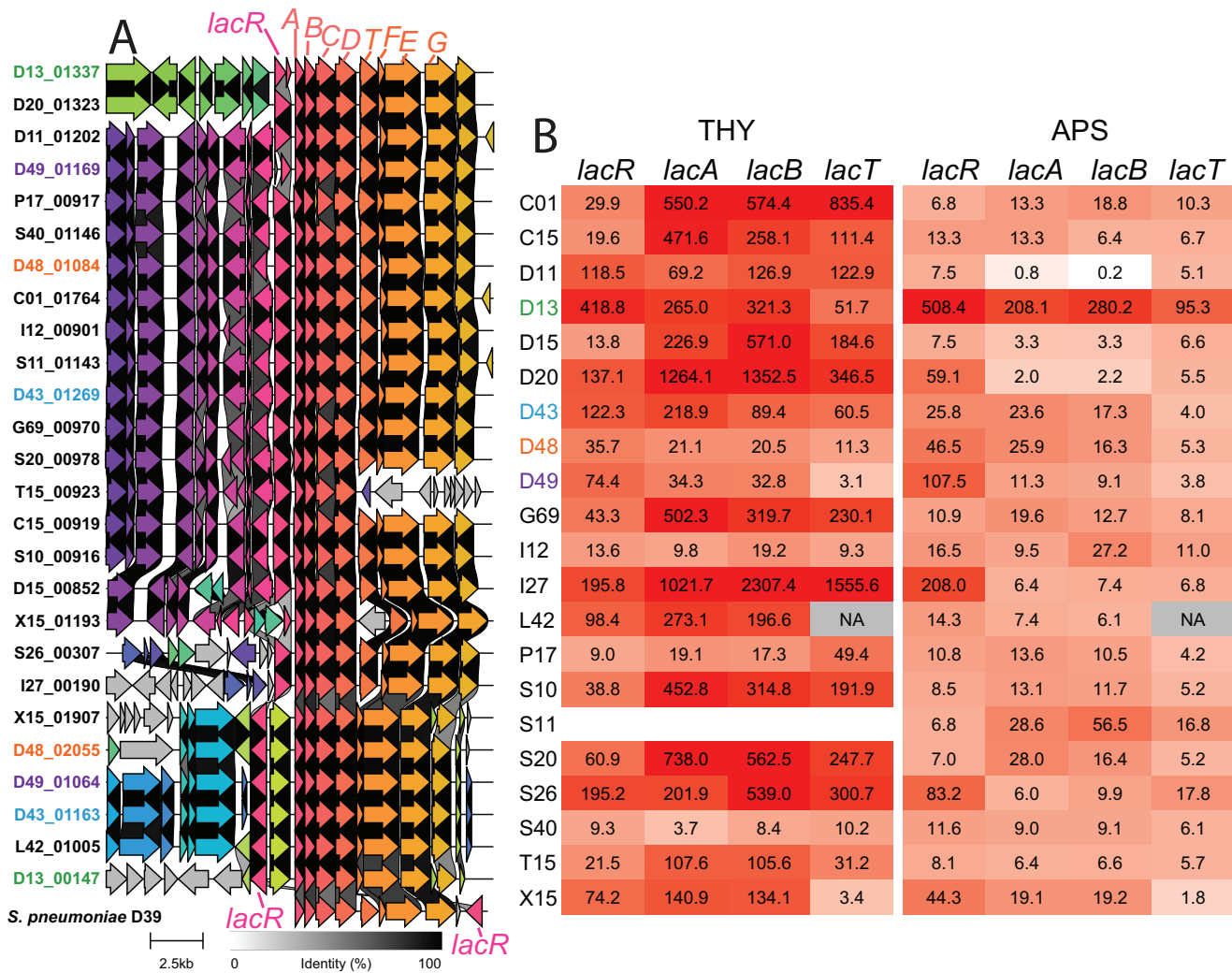


Figure S8: Divergent *lac* gene cluster expression in strain D13. **A)** Several variants of the *lac* gene cluster are carried by the strains, and these may occur alone or two (at different locations) in the same genome. D13 has 2 *lac* gene clusters, which both feature inverted or pseudogene *lacR* copies (although other strains sharing the inverted variant had expressino as expected). Genomes with several copies highlighted in color. Annotation based on Afzal et. al. 2014 (<https://doi.org/10.1128/AEM.01370-14>) and *S. pneumoniae* D39 assembly CP000410.2. **B)** *lacR* is highly expressed in D13, but *lacA* and *lacB* (and *lacT*) are nonetheless highly expressed in both media. P1/7 has unexpectedly low *lac* expression compared to other ST1 strains.

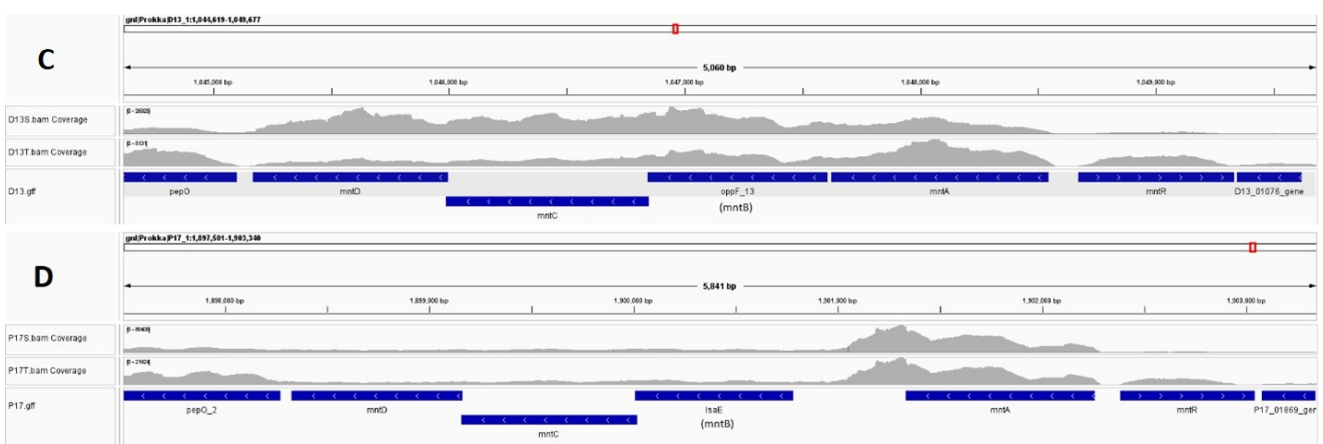
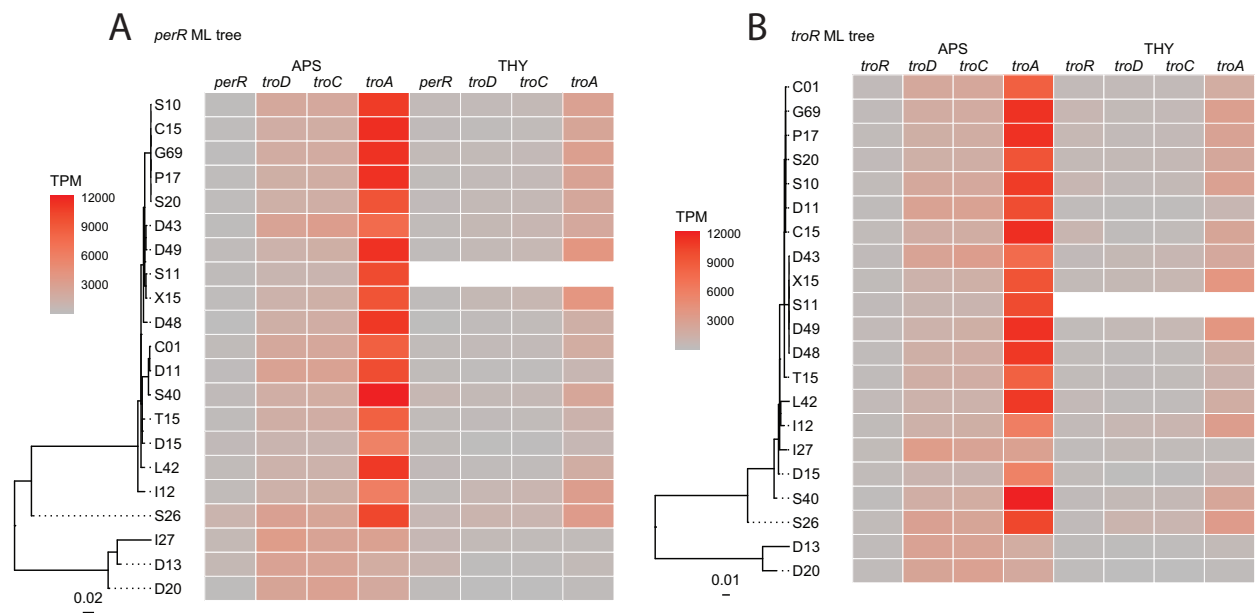


Figure S9: Gene expression of the *tro/mnt* gene cluster. A) ML tree of *perR* with *tro* expression heatmap. B) ML tree of *troR* with *tro* expression heatmap. C) Raw RNA-seq coverage of the *tro* gene cluster in strain D13 (visualized in IGV, <https://igv.org>). D) Raw RNA-seq coverage of the *tro* gene cluster in strain P17.