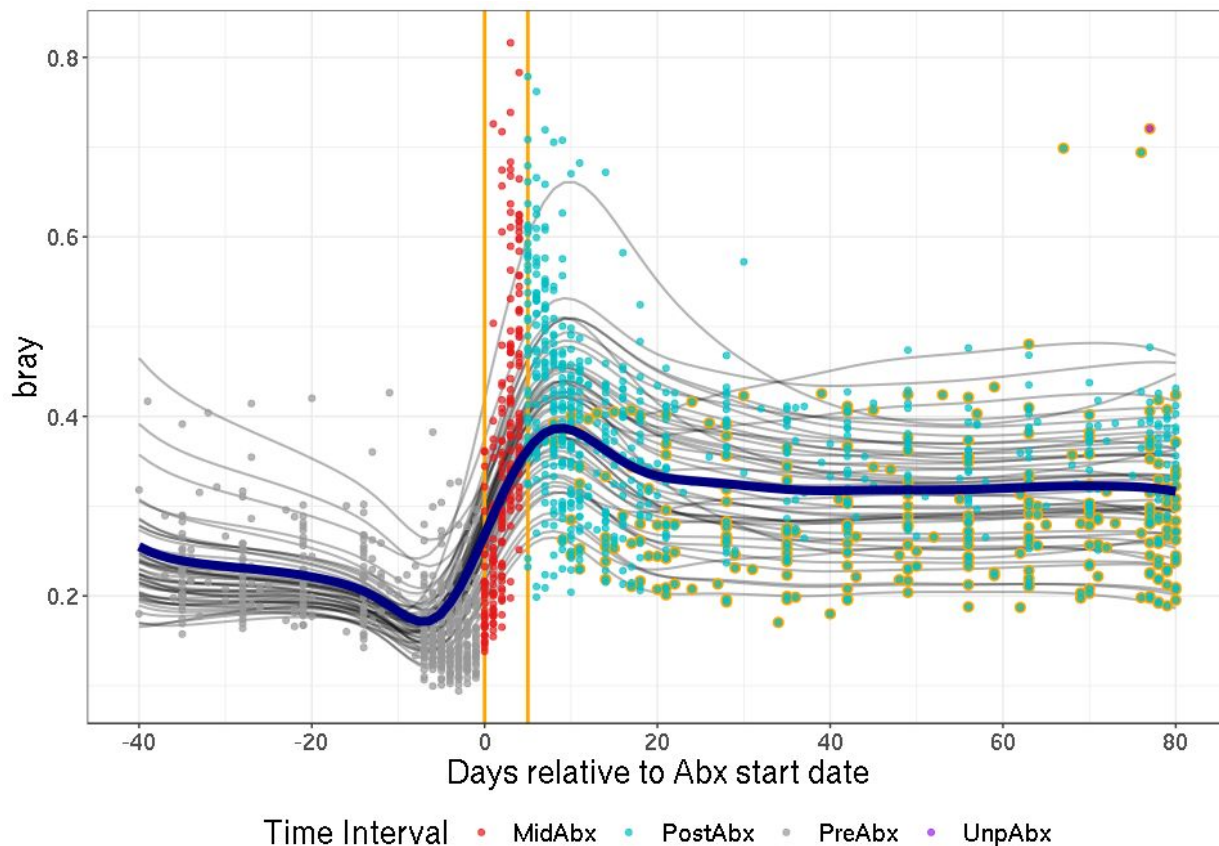


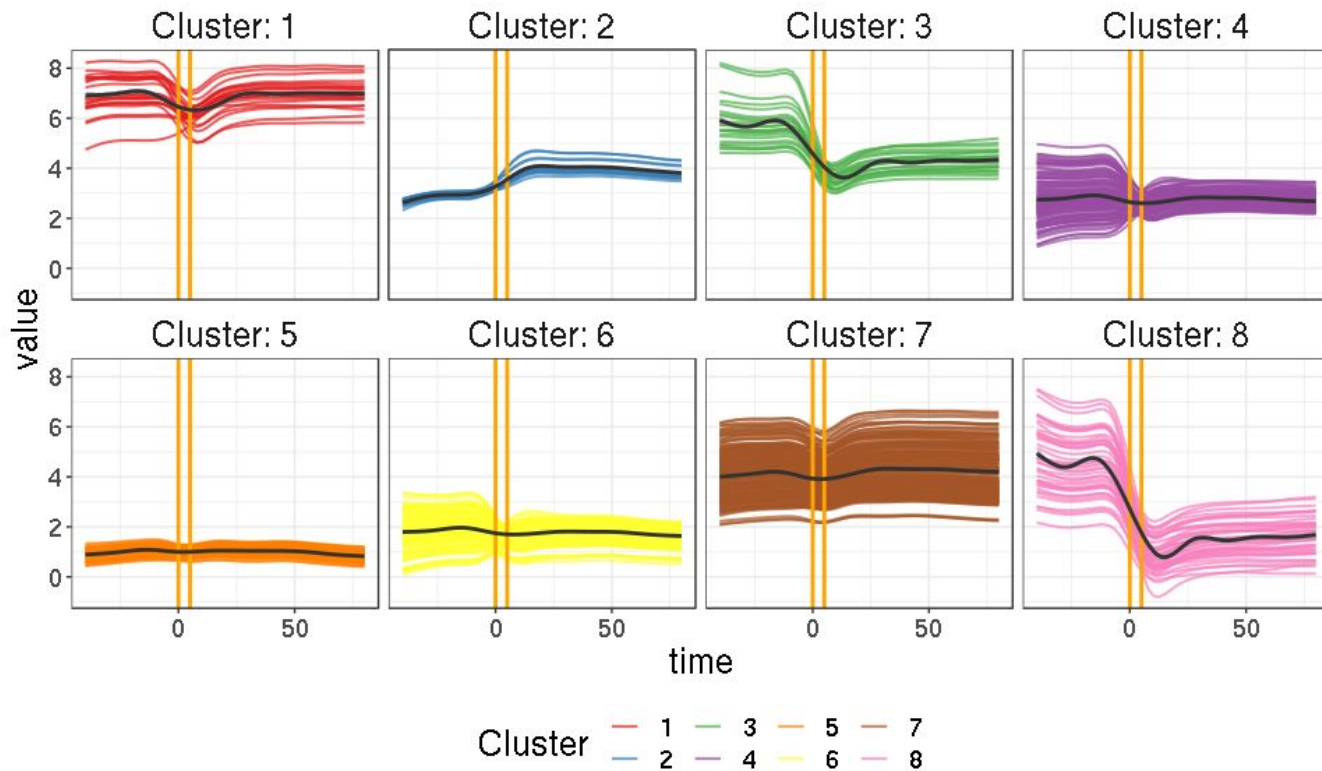
Bacterial response to Cipro

Functional analysis for smoothing and clustering
temporal patterns

Overall Subjects' response to Abx



- The overall microbiome shift in microbial composition measured as the average Bray-Curtis distance to 7 daily samples right before Abx
- Yellow borders around cyan data points after perturbation indicate “approximated” stabilization
- In this visualization we use 45 subjects with who received Abx only or other perturbation and Abx.
- Temporal data was limited to the period [-40, 80] days w.r.t. Abx start date

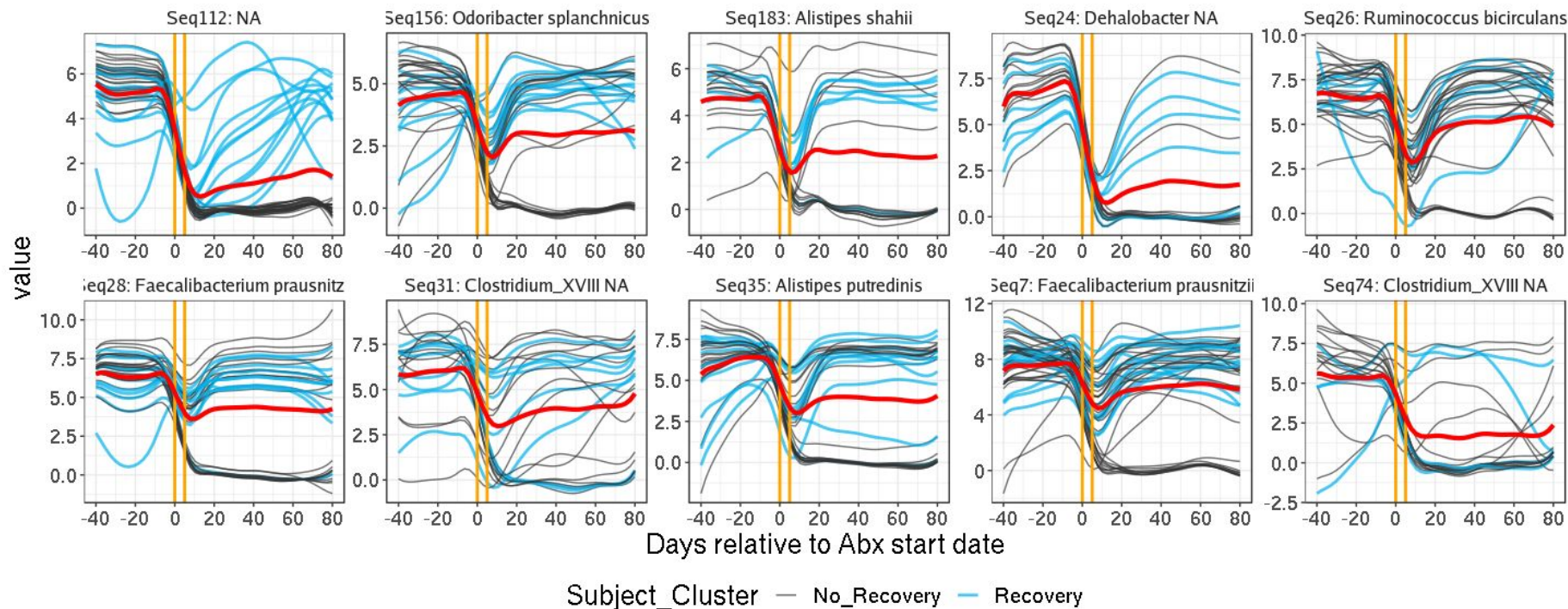


Clusters of microbes' response to Abx

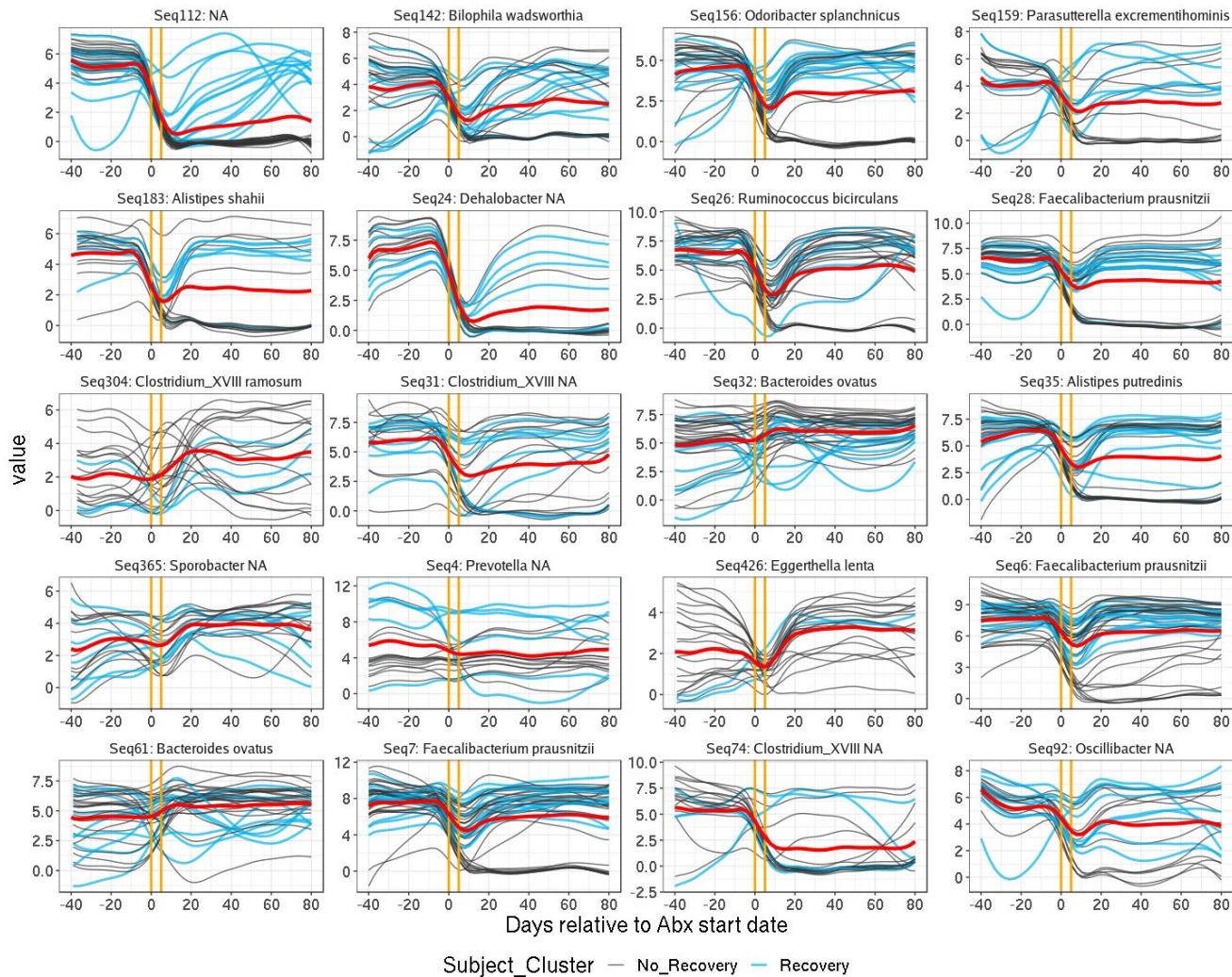
Top genera in clusters indicated below; more detailed ASV identities in CSV file

Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Bacteroides	Roseburia	Ruminococcus	Clostridium_XIVa	Clostridium_IV	Clostridium_IV	Blautia	Ruminococcus
Faecalibacterium	Blautia	Parabacteroides	Blautia	Sporobacter	Clostridium_XIVa	Bacteroides	Coprococcus
Gemmiger	Clostridium_IV	Faecalibacterium	Oscillibacter	Blautia	Blautia	Roseburia	Dehalobacter
Fusicatenibacter	Anaerostipes	Oscillibacter	Clostridium_IV	Clostridium_XIVb	Sporobacter	Clostridium_XIVa	Clostridium_XVIII
Blautia	Clostridium_XIVa	Alistipes	Bacteroides	Ruminococcus2	Oscillibacter	Sporobacter	Ethanoligenens

Subject differences in recovery: Specific ASVs



In blue are the subjects whose abundances of Seq 112 recovered, i.e. a minority (12 subj out of 36 (1/3))
These subjects seem to also more or less in recover the abundances of other bacterial sequences.



Same as
on the
previous
slide but
20 species