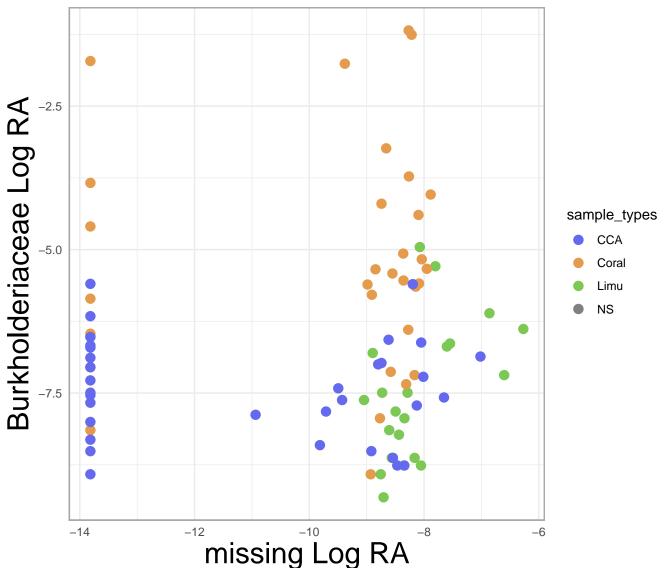
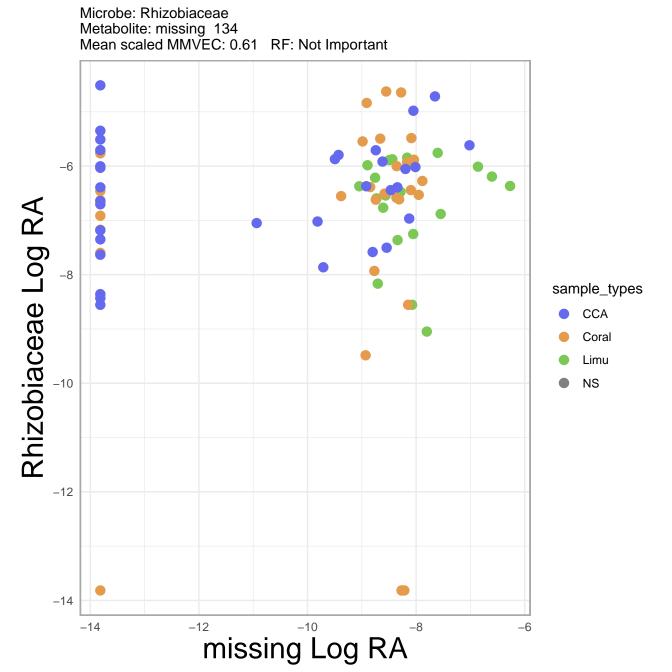
Microbe: Burkholderiaceae Metabolite: missing 134

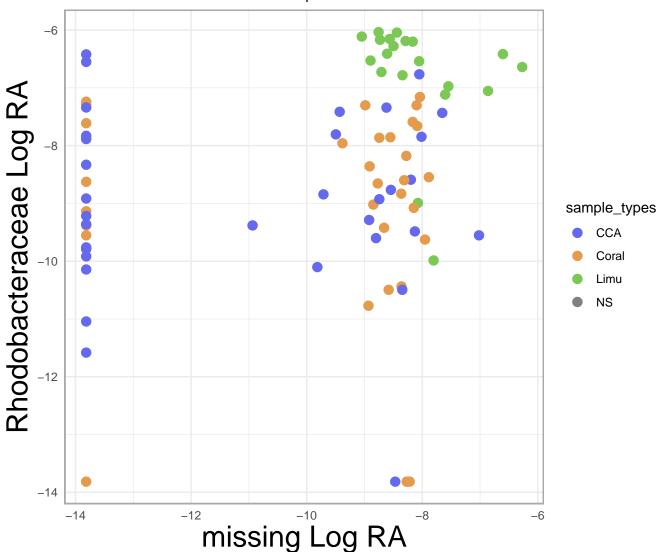
Mean scaled MMVEC: 2.61 RF: Not Important

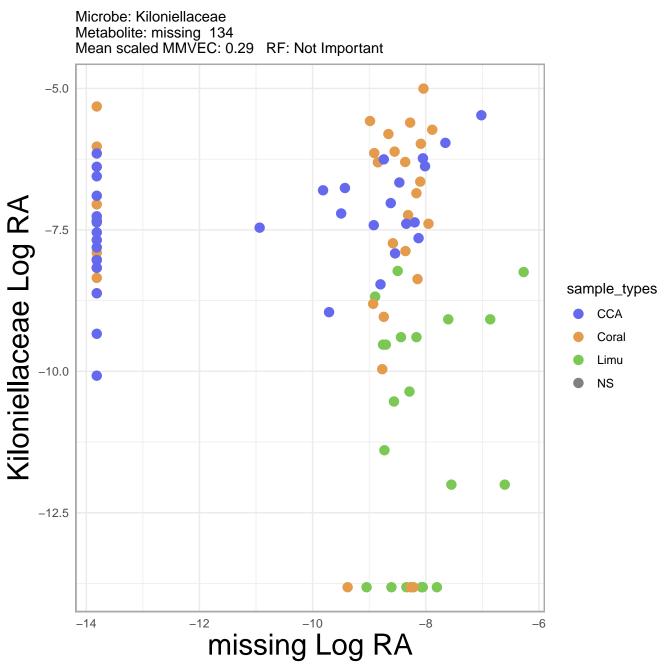




Microbe: Rhodobacteraceae Metabolite: missing 134 Mean scaled MMVEC: 1

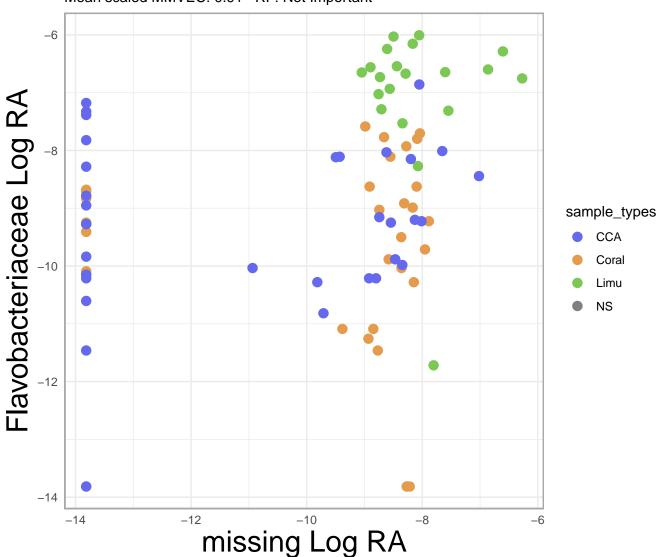
RF: Not Important





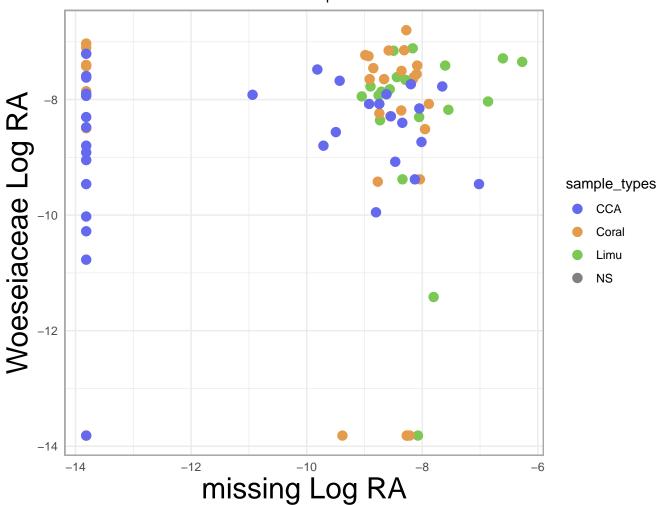
Microbe: Flavobacteriaceae Metabolite: missing 134 Mean scaled MMVEC: 0.91

RF: Not Important



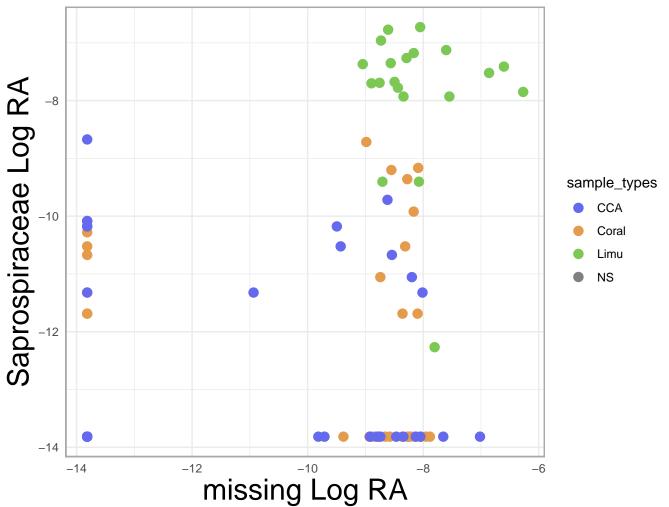
Microbe: Woeseiaceae Metabolite: missing 134

Mean scaled MMVEC: 0.17 RF: Not Important



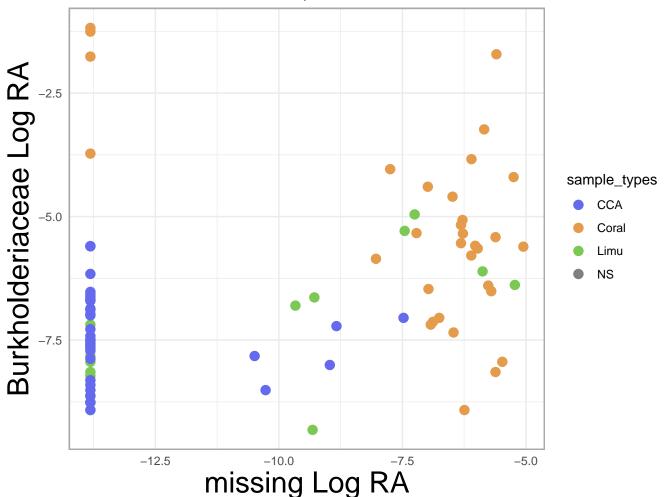
Microbe: Saprospiraceae Metabolite: missing 134

Mean scaled MMVEC: 0.97 RF: Not Important



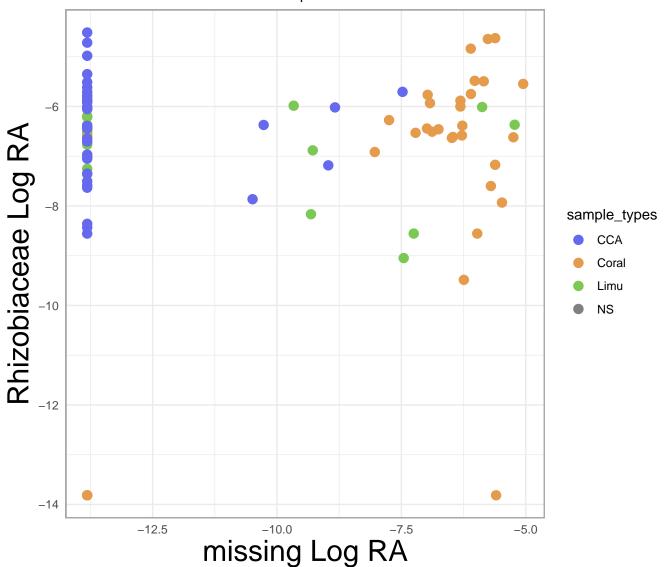
Microbe: Burkholderiaceae Metabolite: missing 15072

Mean scaled MMVEC: 2.76 RF: Important



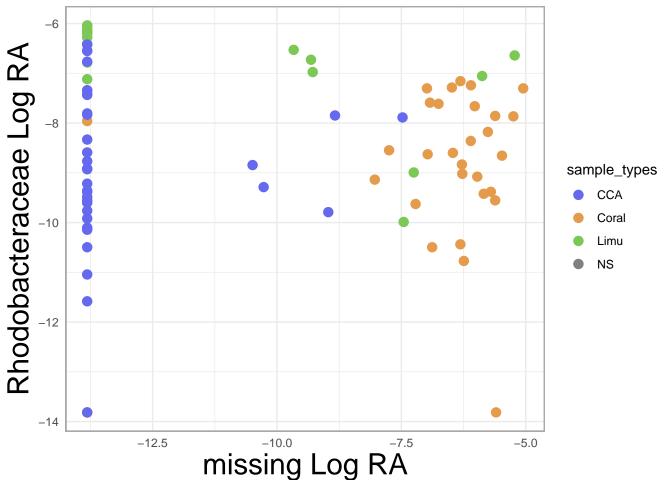
Microbe: Rhizobiaceae Metabolite: missing 15072

Mean scaled MMVEC: 0.75 RF: Important



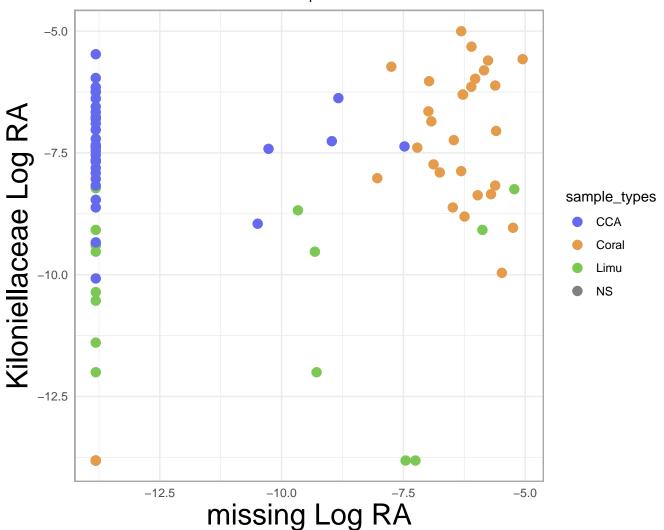
Microbe: Rhodobacteraceae Metabolite: missing 15072

Mean scaled MMVEC: -0.69 RF: Important



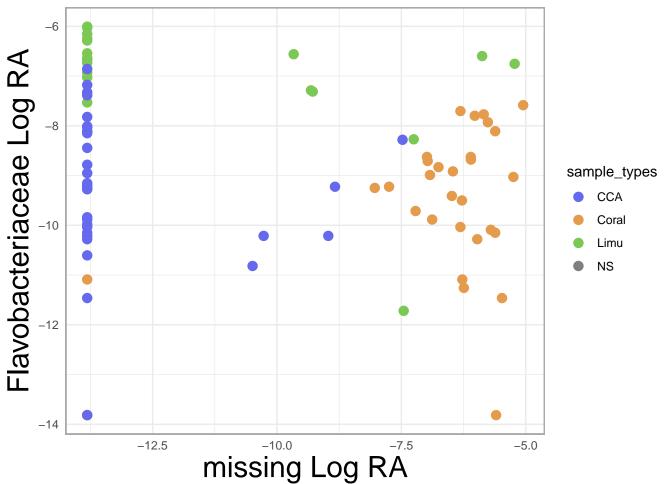
Microbe: Kiloniellaceae

Metabolite: missing 15072 Mean scaled MMVEC: 1.28 RF: Important



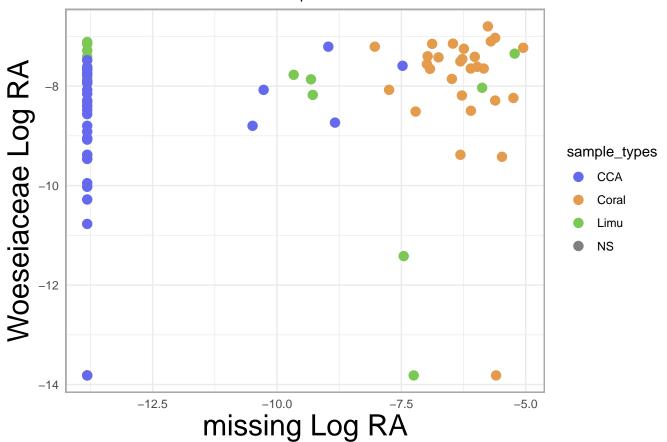
Microbe: Flavobacteriaceae Metabolite: missing 15072

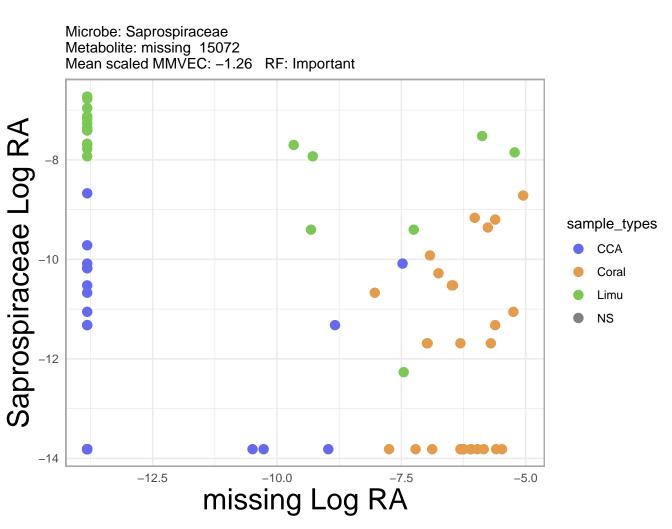
Mean scaled MMVEC: -0.68 RF: Important



Microbe: Woeseiaceae Metabolite: missing 15072

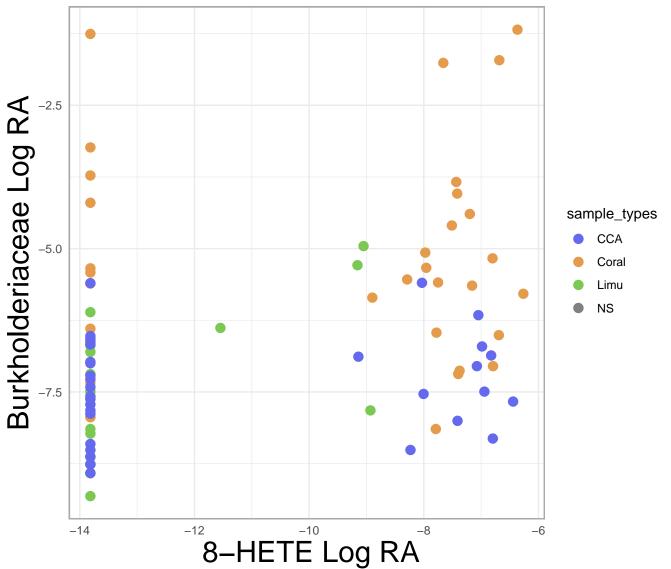
Mean scaled MMVEC: 0.34 RF: Important

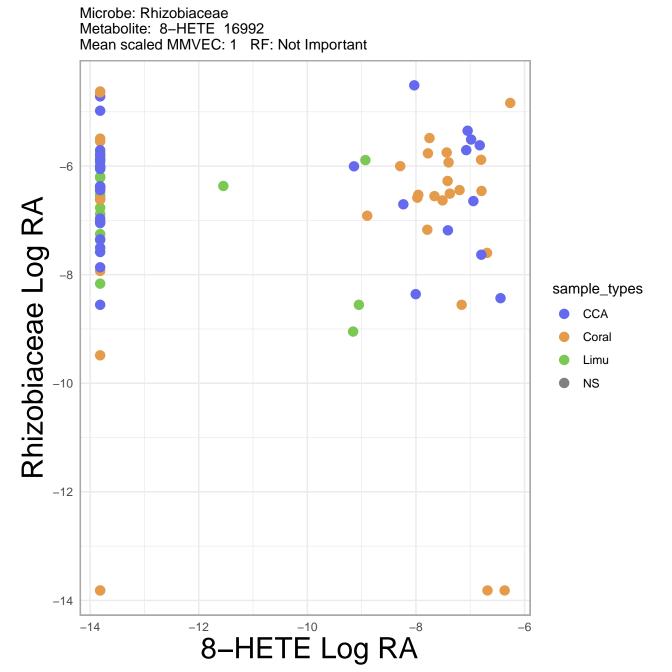




Microbe: Burkholderiaceae Metabolite: 8-HETE 16992

Mean scaled MMVEC: 3.92 RF: Not Important





Microbe: Rhodobacteraceae Metabolite: 8-HETE 16992 Mean scaled MMVEC: -0.31 RF: Not Important -6 sample\_types CCA Coral -10 Limu NS

Rhodobacteraceae Log RA

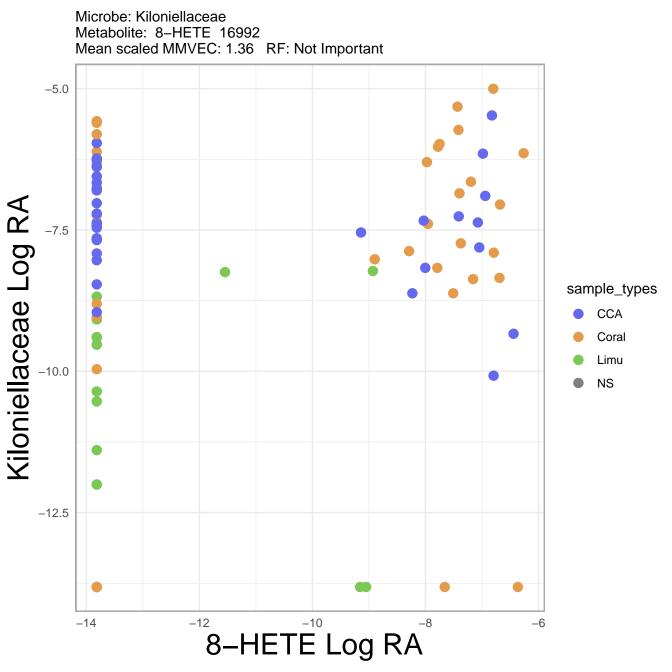
-14

-14

-12

8-HETE Log RA

-6



Microbe: Flavobacteriaceae Metabolite: 8-HETE 16992 Mean scaled MMVEC: -0.32 RF: Not Important -6 Flavobacteriaceae Log RA sample\_types CCA Coral -10 Limu NS -14

-10

8-HETE Log RA

-6

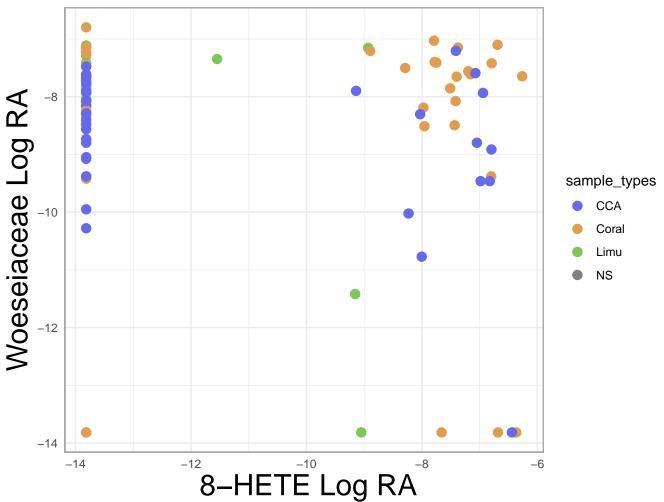
-14

-12

Microbe: Woeseiaceae

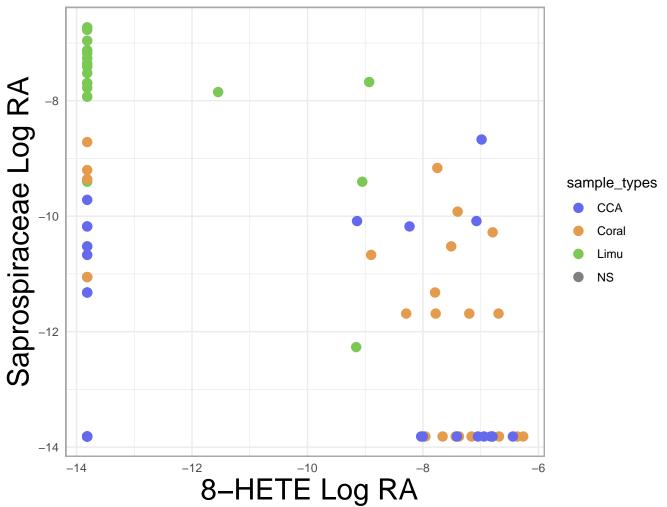
Metabolite: 8-HETE 16992

Mean scaled MMVEC: 0.33 RF: Not Important



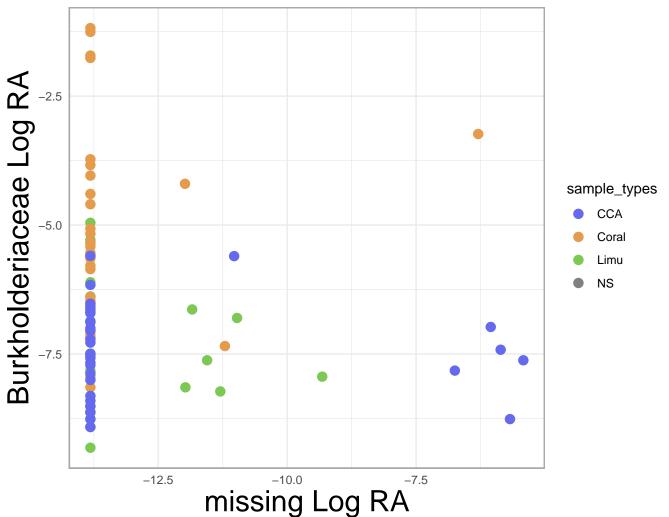
Microbe: Saprospiraceae Metabolite: 8-HETE 16992

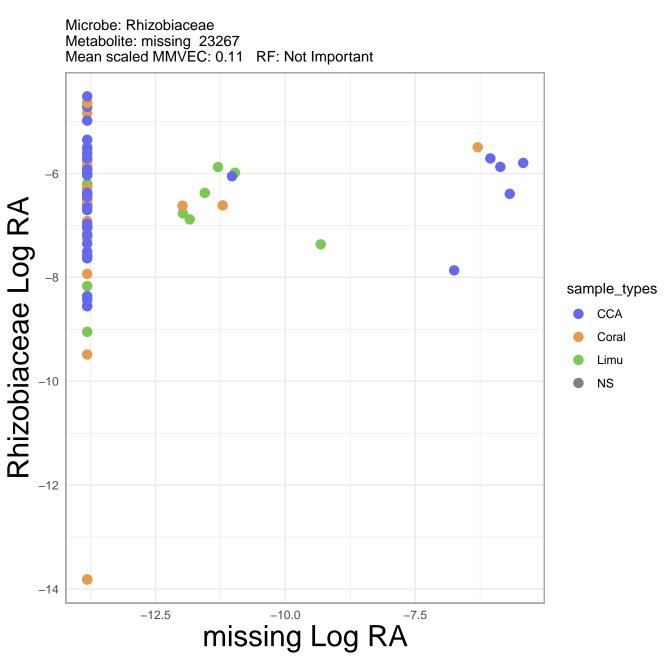
Mean scaled MMVEC: -0.86 RF: Not Important



Microbe: Burkholderiaceae Metabolite: missing 23267

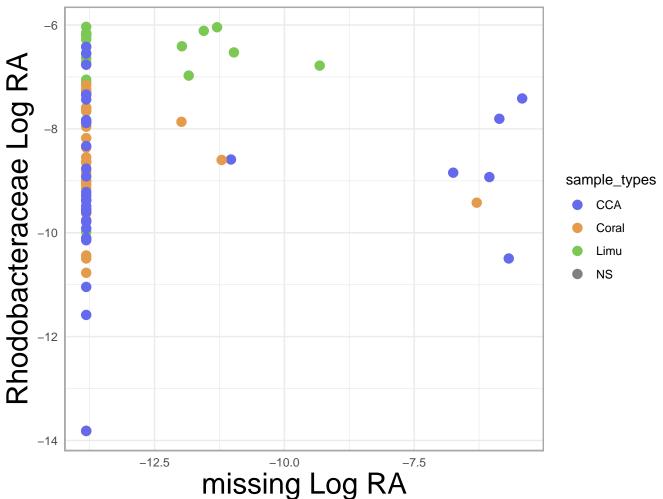
Mean scaled MMVEC: 0.56 RF: Not Important





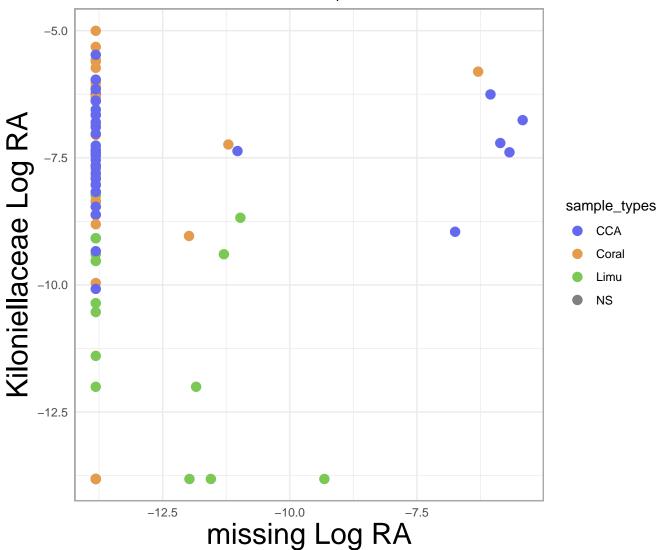
Microbe: Rhodobacteraceae Metabolite: missing 23267

Mean scaled MMVEC: -1 RF: Not Important



Microbe: Kiloniellaceae Metabolite: missing 23267

Mean scaled MMVEC: 0.43 RF: Not Important



Microbe: Flavobacteriaceae Metabolite: missing 23267 Mean scaled MMVEC: -0.89 RF: Not Important -6 Flavobacteriaceae Log RA sample\_types CCA Coral -10 Limu NS

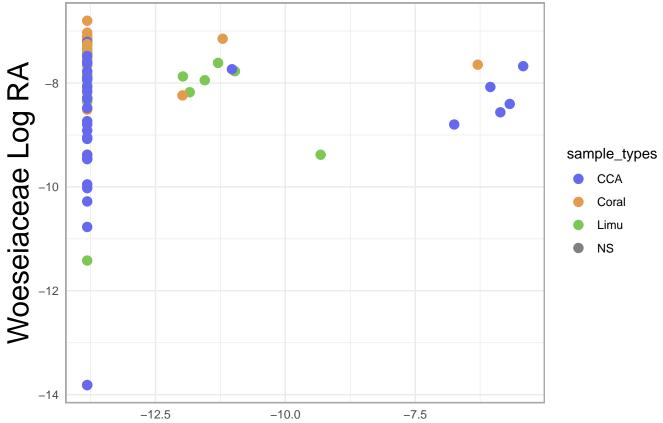
missing Log RA

-14

-12.5

Microbe: Woeseiaceae

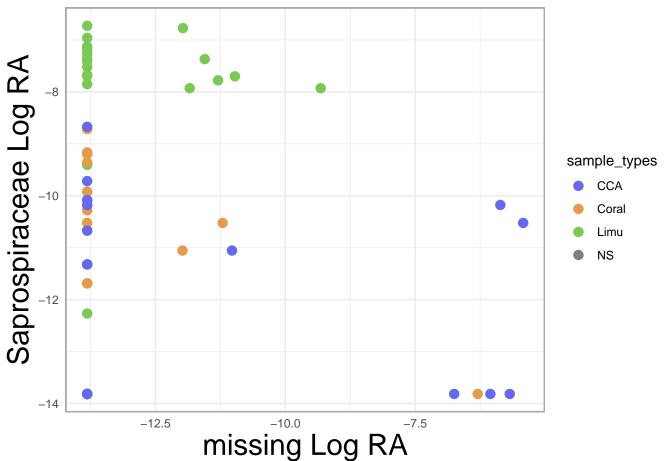
Metabolite: missing 23267 Mean scaled MMVEC: -0.24 RF: Not Important



missing Log RA

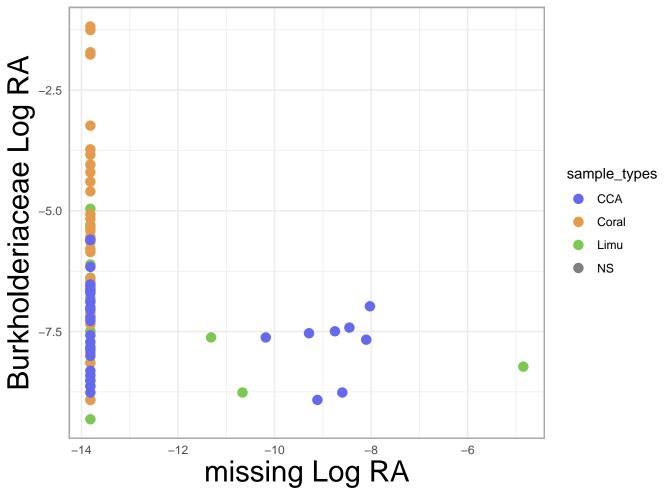
Microbe: Saprospiraceae Metabolite: missing 23267

Mean scaled MMVEC: -1.16 RF: Not Important

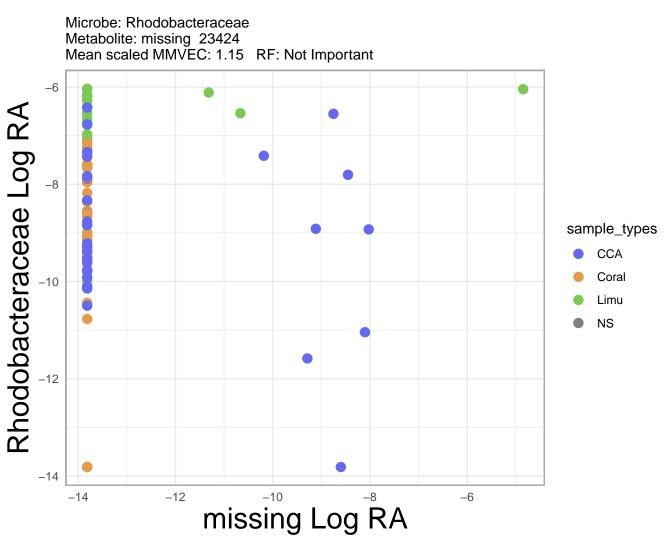


Microbe: Burkholderiaceae Metabolite: missing 23424

Mean scaled MMVEC: -0.37 RF: Not Important

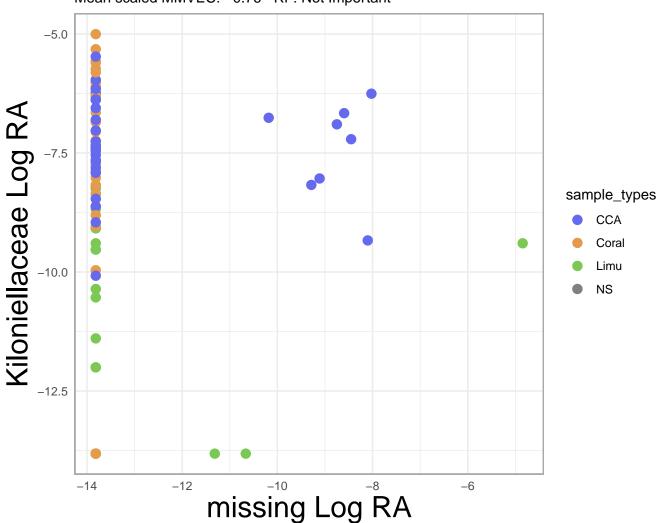


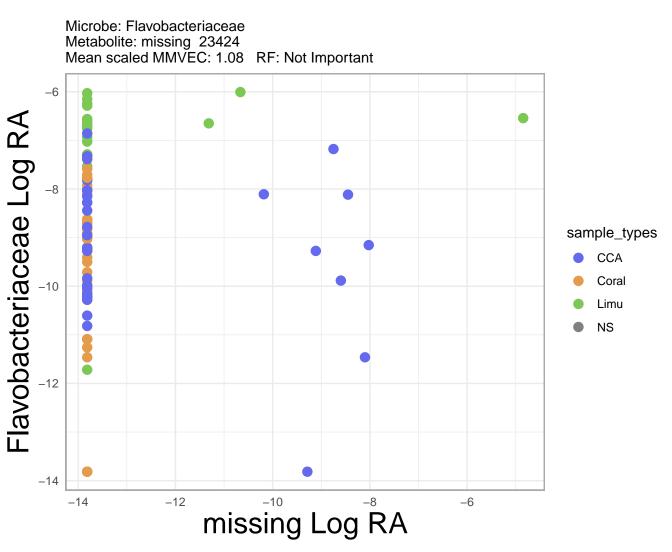




Microbe: Kiloniellaceae Metabolite: missing 23424

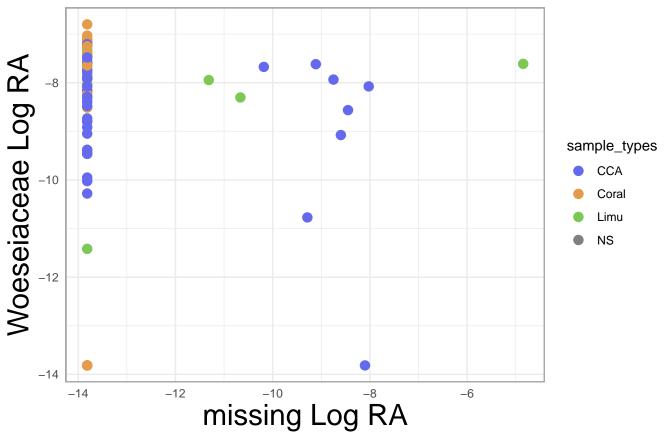
Mean scaled MMVEC: -0.76 RF: Not Important





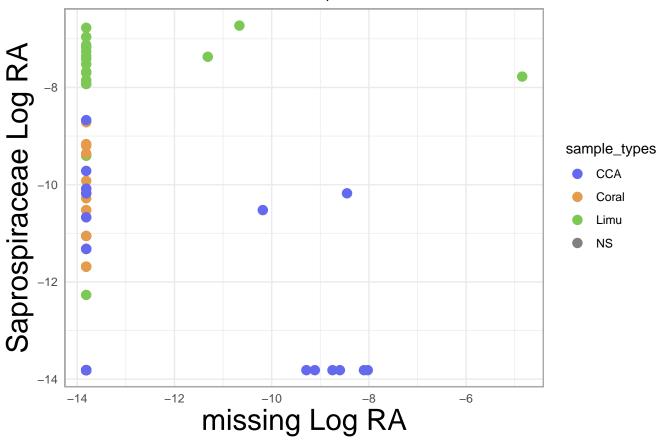
Microbe: Woeseiaceae Metabolite: missing 23424

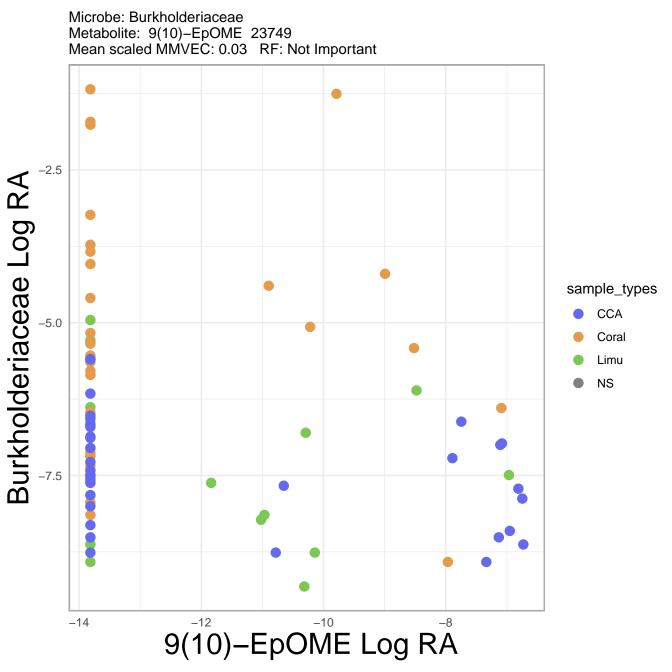
Mean scaled MMVEC: -0.15 RF: Not Important

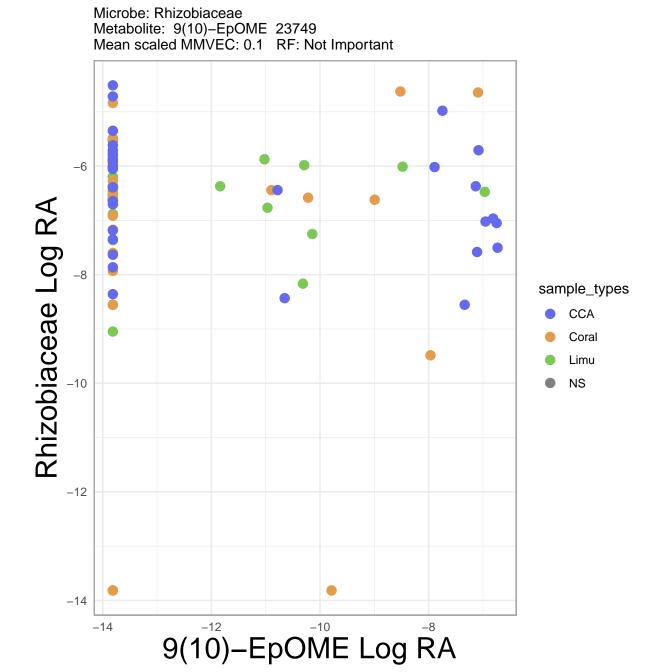


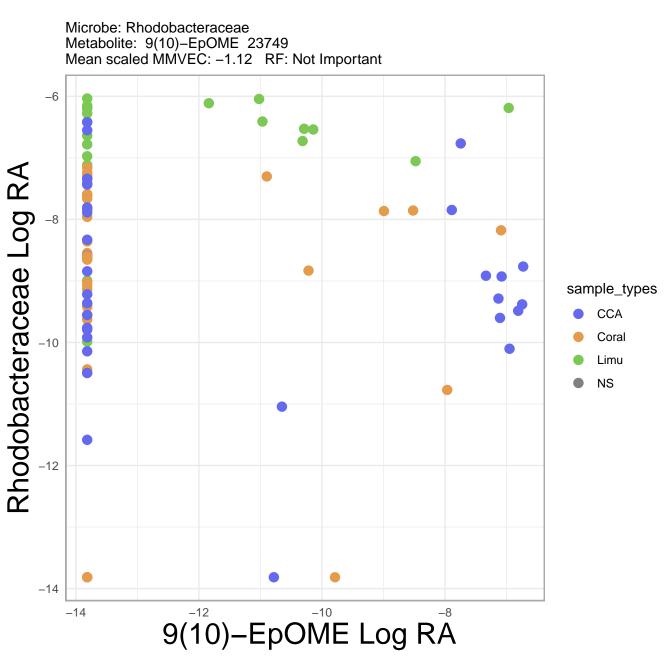
Microbe: Saprospiraceae

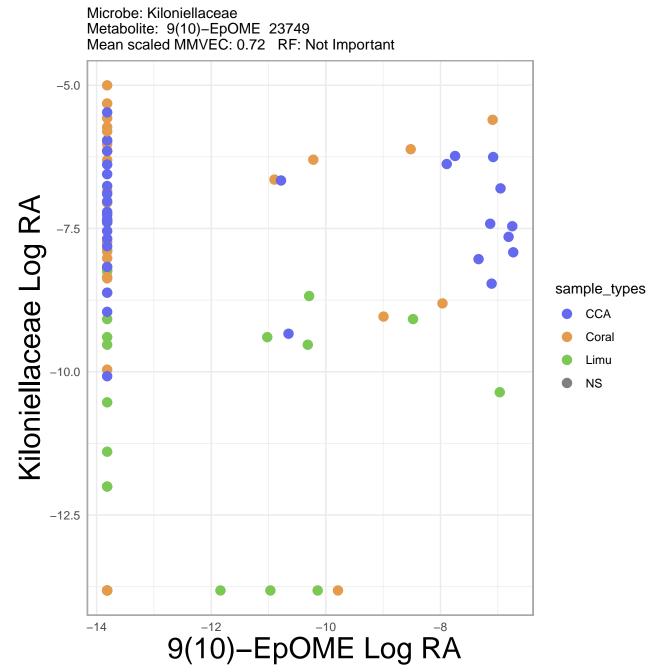
Metabolite: missing 23424 Mean scaled MMVEC: 1.55 RF: Not Important

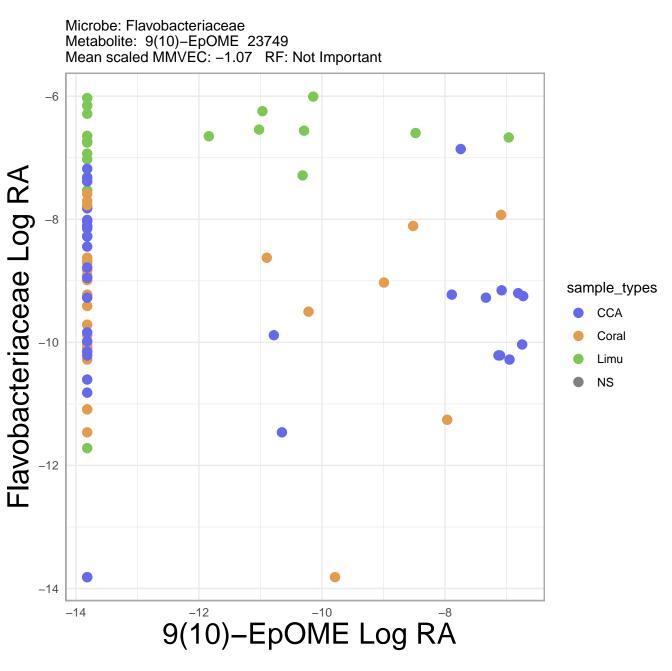








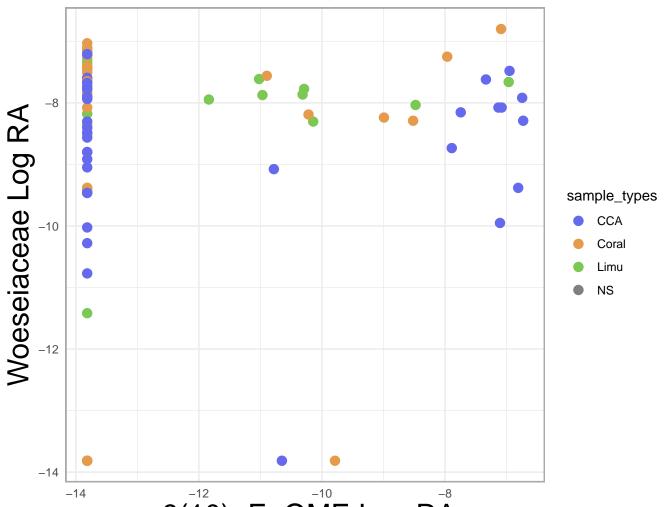




Microbe: Woeseiaceae

Metabolite: 9(10)-EpOME 23749

Mean scaled MMVEC: 0.21 RF: Not Important

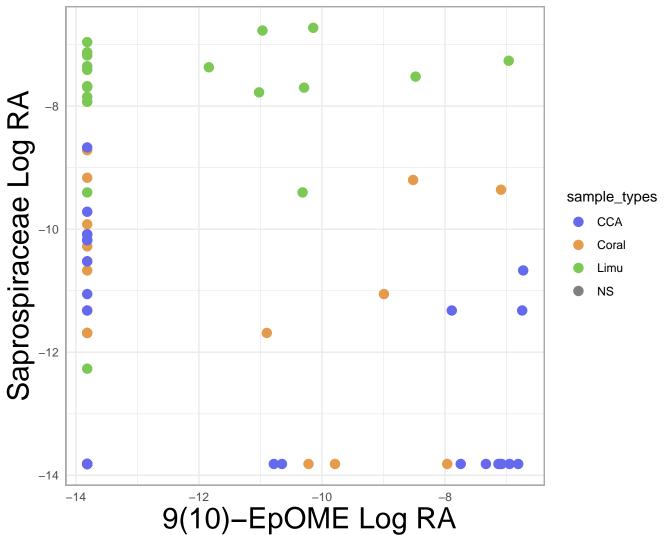


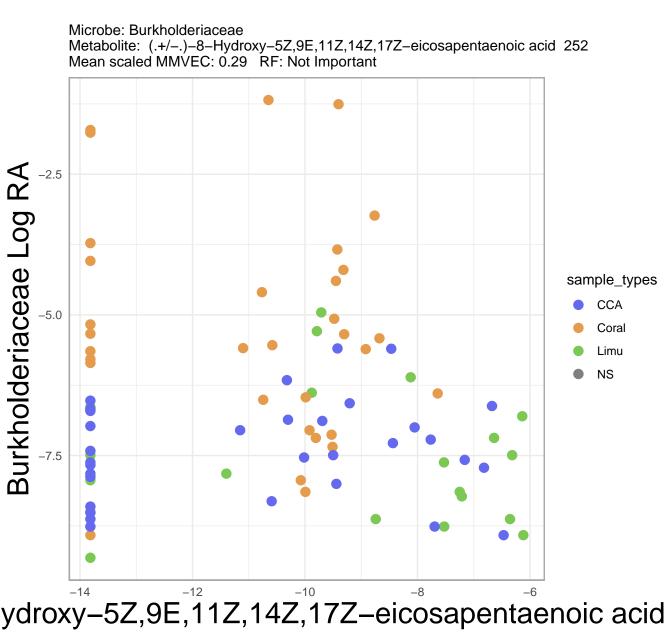
9(10)-EpOME Log RA

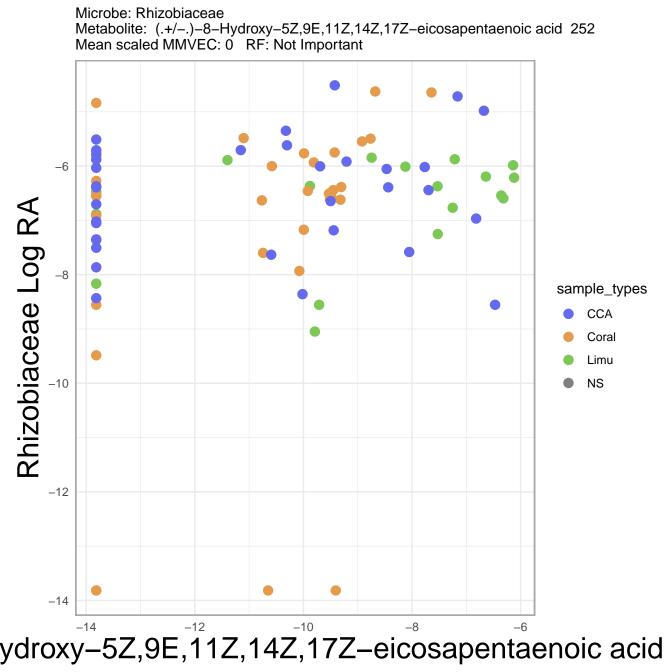
Microbe: Saprospiraceae

Metabolite: 9(10)-EpOME 23749

Mean scaled MMVEC: -1.53 RF: Not Important



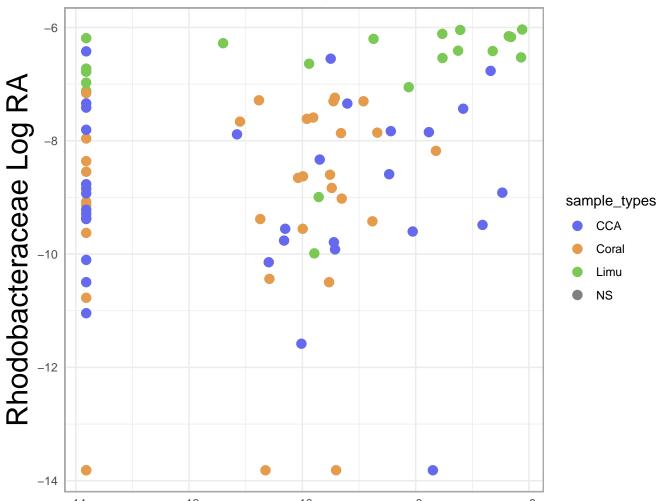




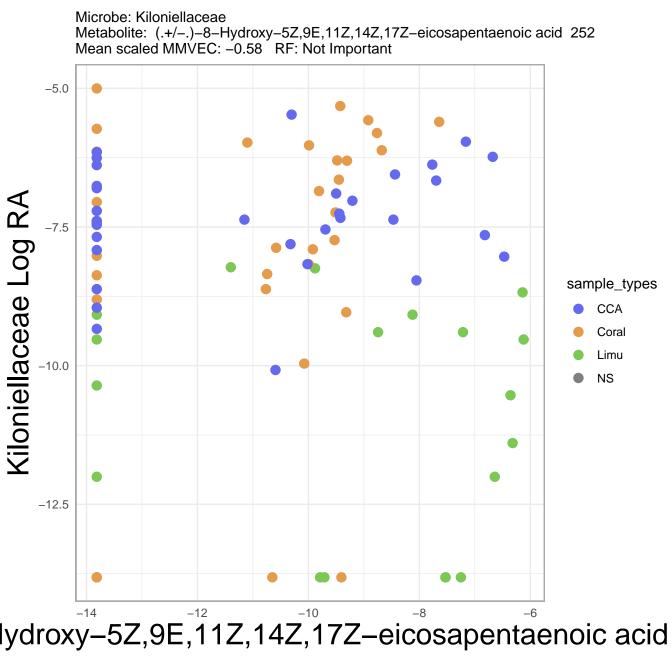
Microbe: Rhodobacteraceae

Metabolite: (.+/-.)-8-Hydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid 252

Mean scaled MMVEC: 1.18 RF: Not Important



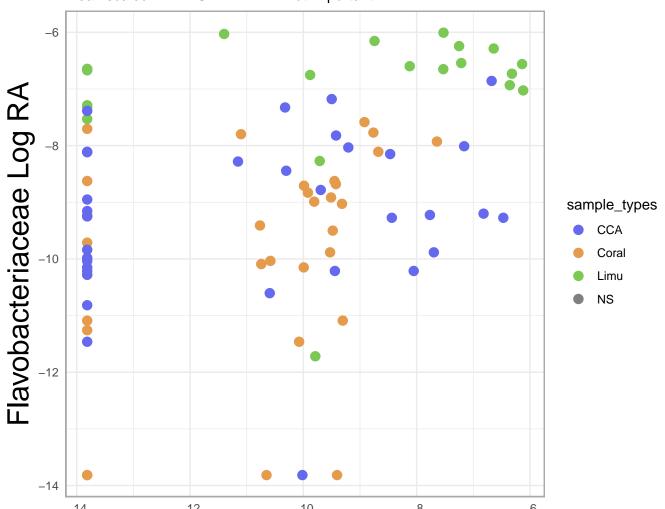
ydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid



Microbe: Flavobacteriaceae

Metabolite: (.+/-.)-8-Hydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid 252

Mean scaled MMVEC: 1.11 RF: Not Important

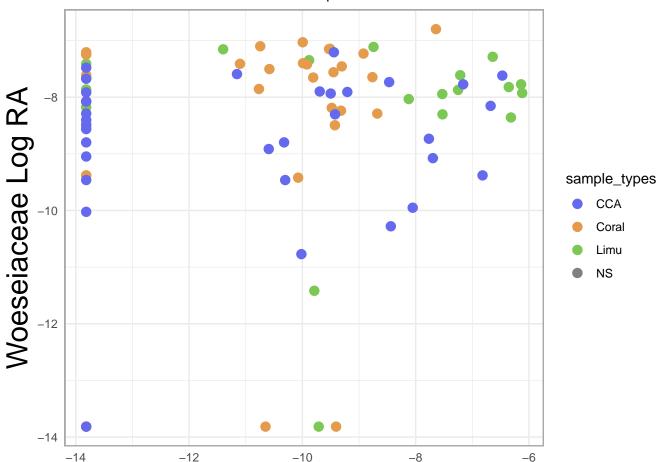


ydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid

Microbe: Woeseiaceae

 $Metabolite: \ (.+/-.)-8-Hydroxy-5Z, 9E, 11Z, 14Z, 17Z-eicosapentaenoic\ acid\ 252$ 

Mean scaled MMVEC: -0.1 RF: Not Important

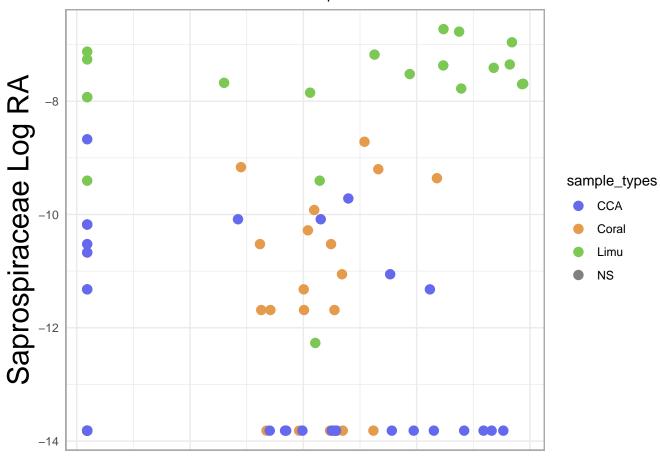


ydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid

Microbe: Saprospiraceae

Metabolite: (.+/-.)-8-Hydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid 252

Mean scaled MMVEC: 1.52 RF: Not Important



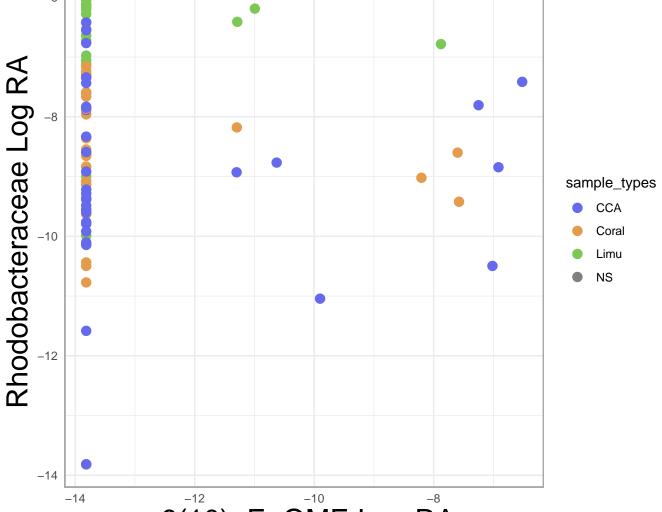
ydroxy-5Z,9E,11Z,14Z,17Z-eicosapentaenoic acid

Metabolite: 9(10)-EpOME 25651 Mean scaled MMVEC: 0.22 RF: Not Important Burkholderiaceae Log RA sample\_types CCA -5.0 Coral Limu NS -14 -10 -129(10)-EpOME Log RA

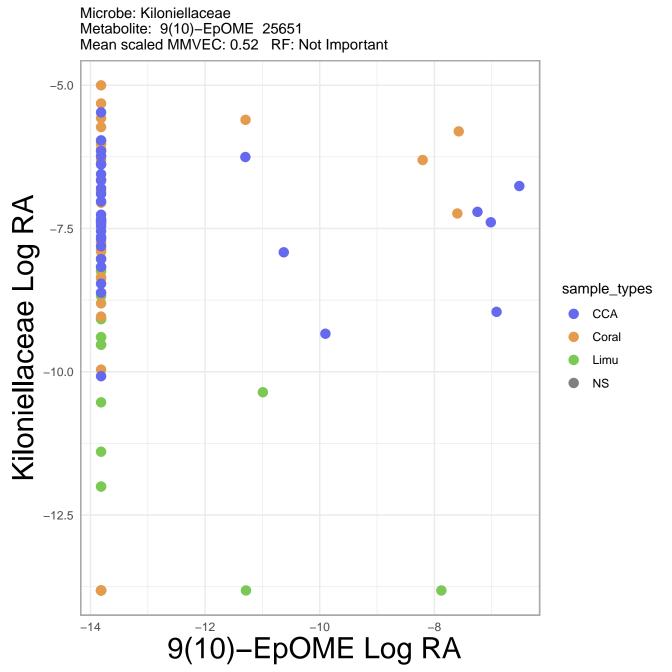
Microbe: Burkholderiaceae

Microbe: Rhizobiaceae Metabolite: 9(10)-EpOME 25651 Mean scaled MMVEC: 0.07 RF: Not Important -6 Rhizobiaceae Log RA -8 sample\_types CCA Coral Limu -10 NS -12 -149(10)–EpOME Log RA -14

Microbe: Rhodobacteraceae Metabolite: 9(10)-EpOME 25651 Mean scaled MMVEC: -1.14 RF: Not Important -6



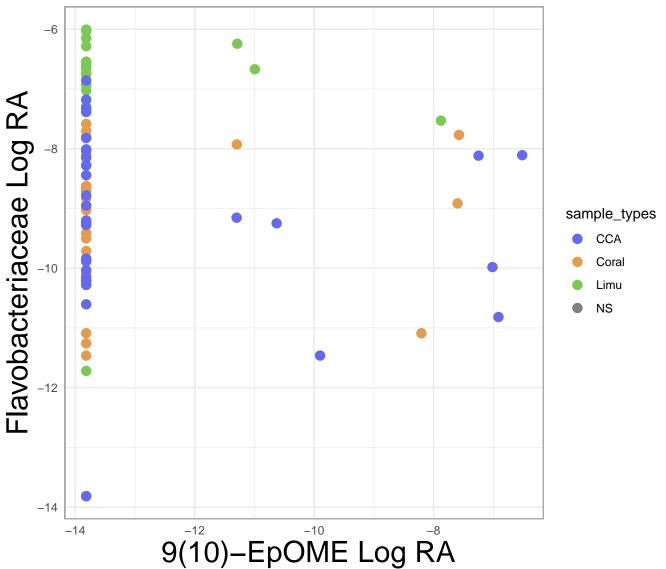
9(10)-EpOME Log RA



Microbe: Flavobacteriaceae

Metabolite: 9(10)-EpOME 25651

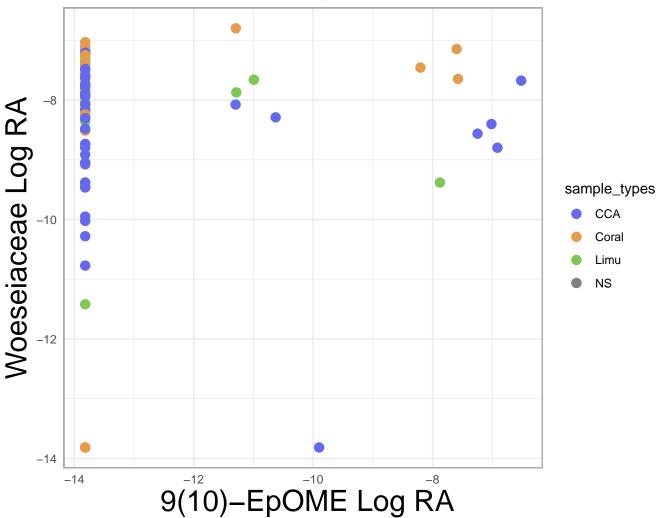
Mean scaled MMVEC: -1.04 RF: Not Important



Microbe: Woeseiaceae

Metabolite: 9(10)-EpOME 25651

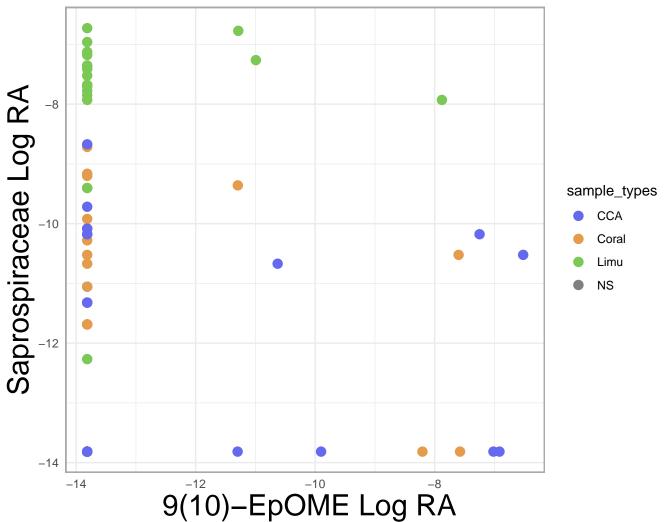
Mean scaled MMVEC: -0.1 RF: Not Important



Microbe: Saprospiraceae

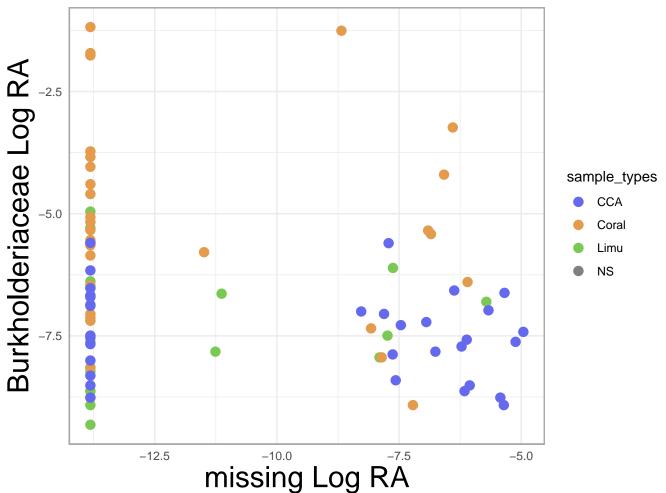
Metabolite: 9(10)-EpOME 25651

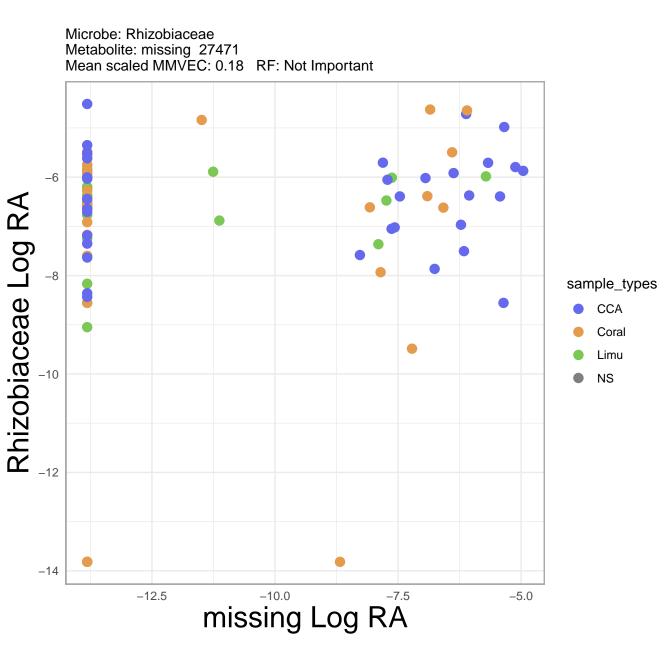
Mean scaled MMVEC: -1.39 RF: Not Important



Microbe: Burkholderiaceae Metabolite: missing 27471

Mean scaled MMVEC: 0.9 RF: Not Important





Microbe: Rhodobacteraceae Metabolite: missing 27471 Mean scaled MMVEC: -0.96 RF: Not Important Rhodobacteraceae Log RA sample\_types CCA Coral -10 Limu NS -12

missing Log RA

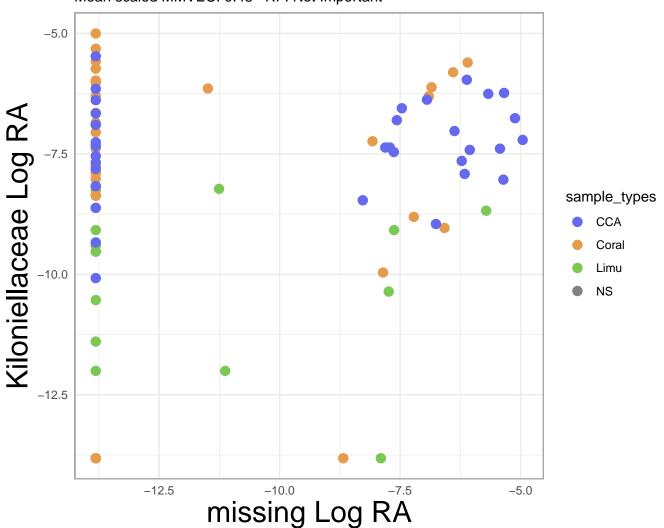
-5.0

-14

-12.5

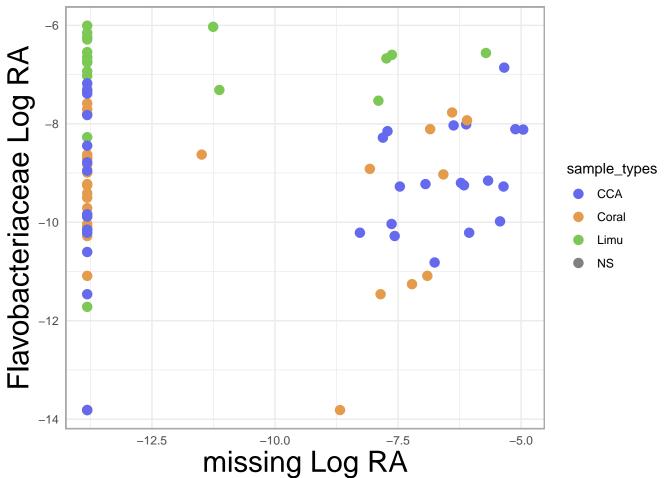
Microbe: Kiloniellaceae Metabolite: missing 27471

Mean scaled MMVEC: 0.48 RF: Not Important



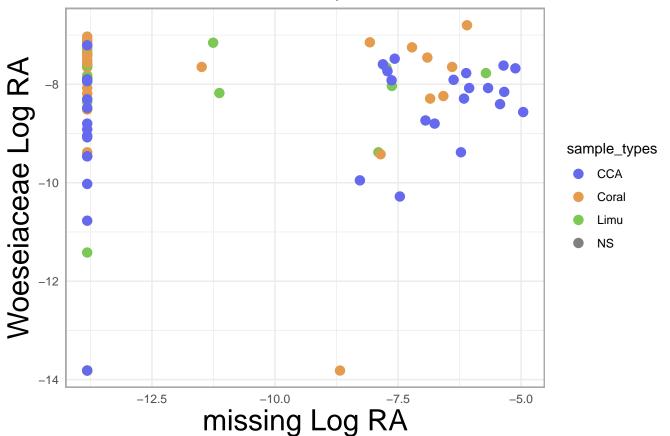
Microbe: Flavobacteriaceae Metabolite: missing 27471

Mean scaled MMVEC: -0.85 RF: Not Important



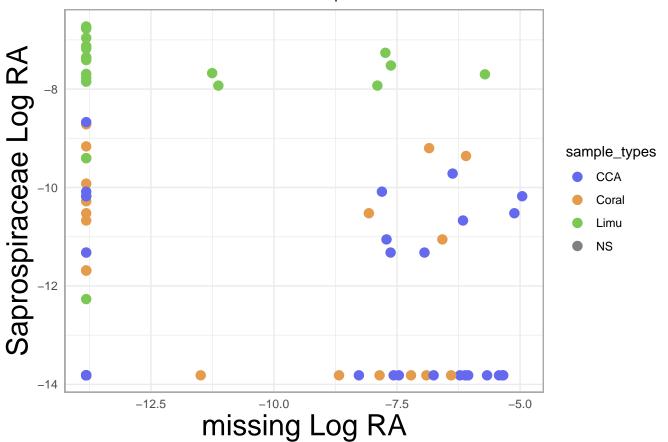
Microbe: Woeseiaceae Metabolite: missing 27471

Mean scaled MMVEC: -0.25 RF: Not Important



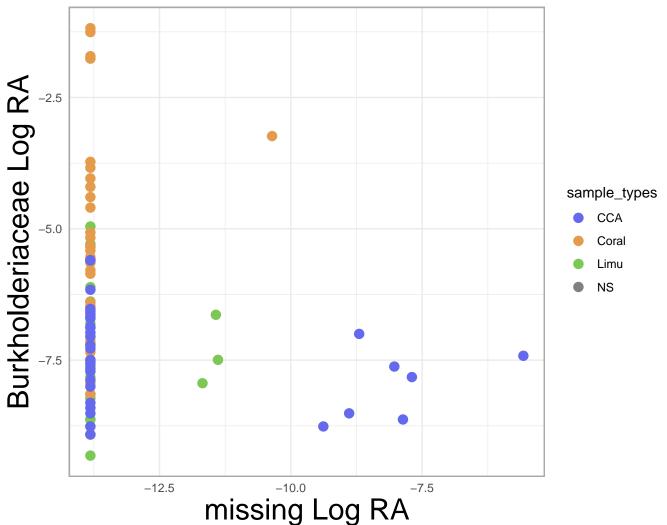
Microbe: Saprospiraceae Metabolite: missing 27471

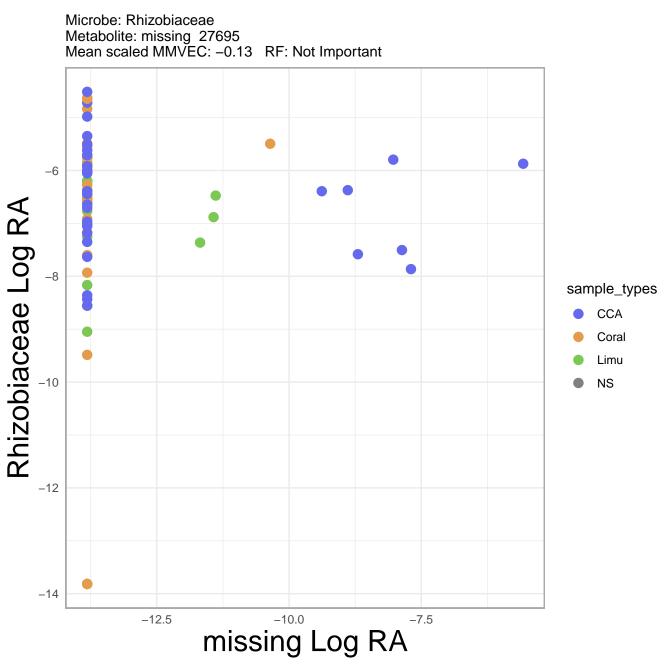
Mean scaled MMVEC: -1.13 RF: Not Important



Microbe: Burkholderiaceae Metabolite: missing 27695 Mean scaled MMVEC: -0.29

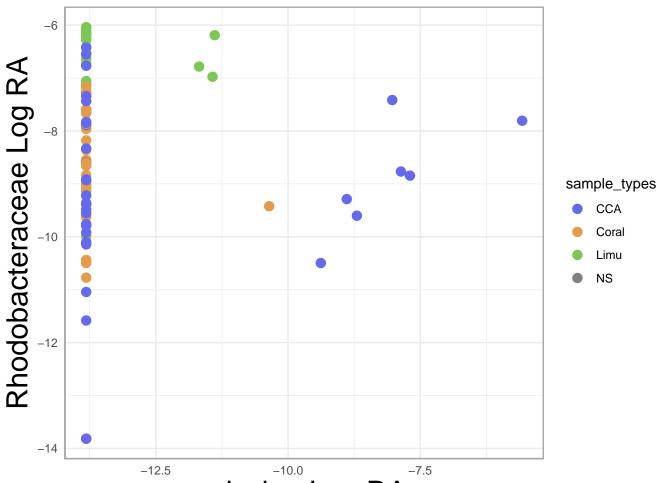
RF: Not Important





Microbe: Rhodobacteraceae Metabolite: missing 27695

Mean scaled MMVEC: -0.82 RF: Not Important



missing Log RA

Microbe: Kiloniellaceae Metabolite: missing 27695 Mean scaled MMVEC: 0.02 RF: Not Important -5.0-7.5 sample\_types CCA Coral Limu -10.0NS -12.5

Kiloniellaceae Log RA

missing Log RA

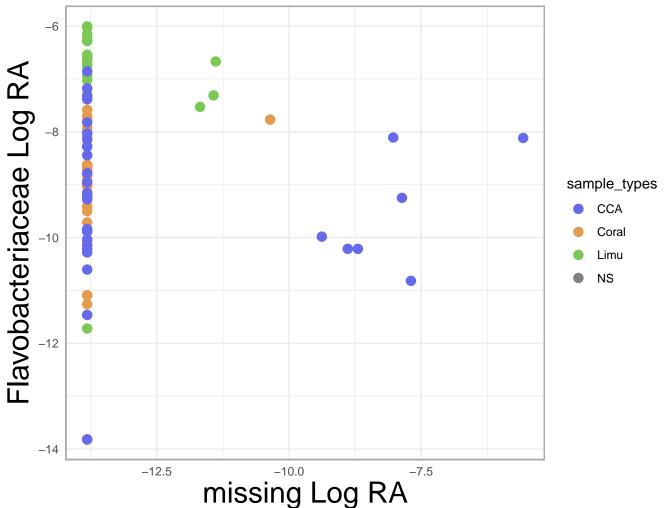
-7.5

-10.0

-12.5

Microbe: Flavobacteriaceae

Metabolite: missing 27695 Mean scaled MMVEC: -0.7 RF: Not Important



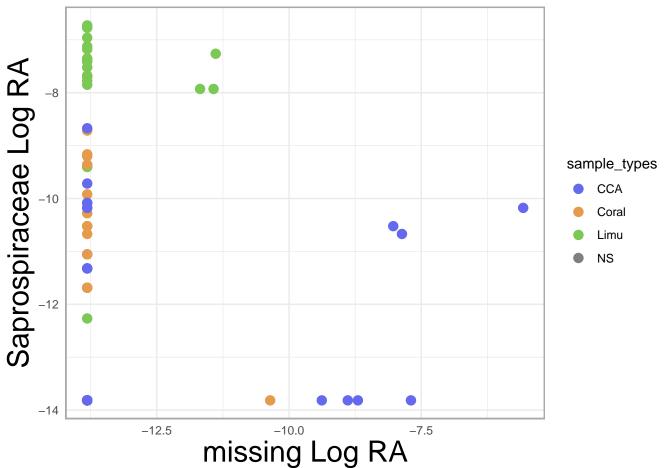
Microbe: Woeseiaceae Metabolite: missing 27695 Mean scaled MMVEC: -0.38 RF: Not Important Woeseiaceae Log RA sample\_types CCA Coral Limu NS -14 -10.0 -12.5

missing Log RA

-7.5

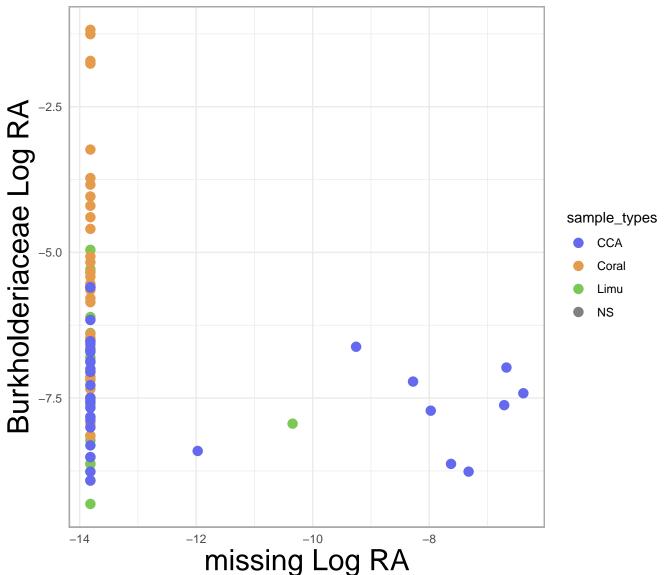
Microbe: Saprospiraceae Metabolite: missing 27695

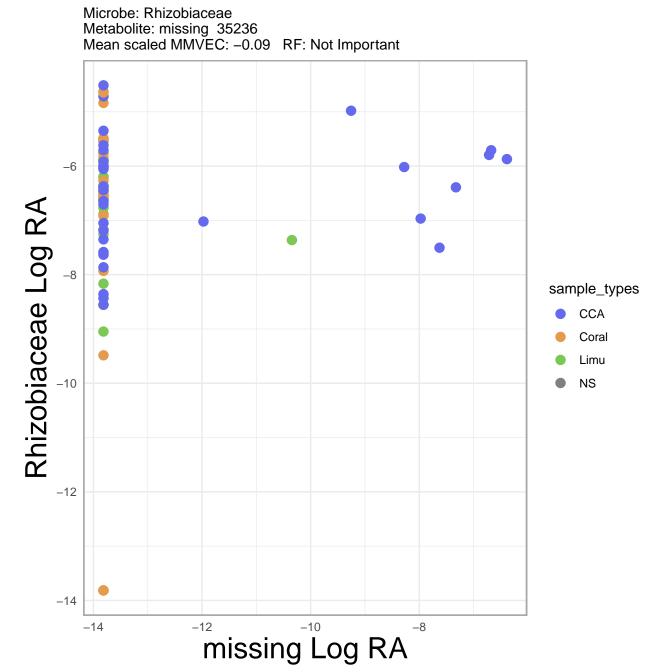
Mean scaled MMVEC: -0.79 RF: Not Important

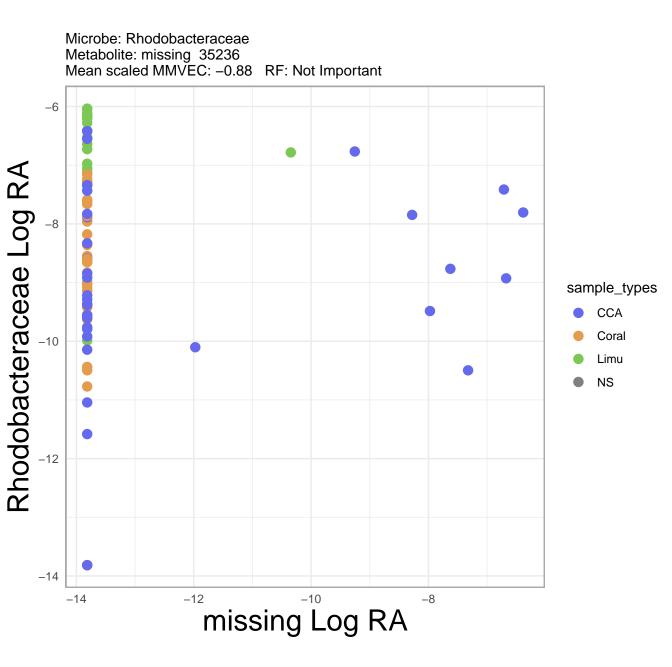


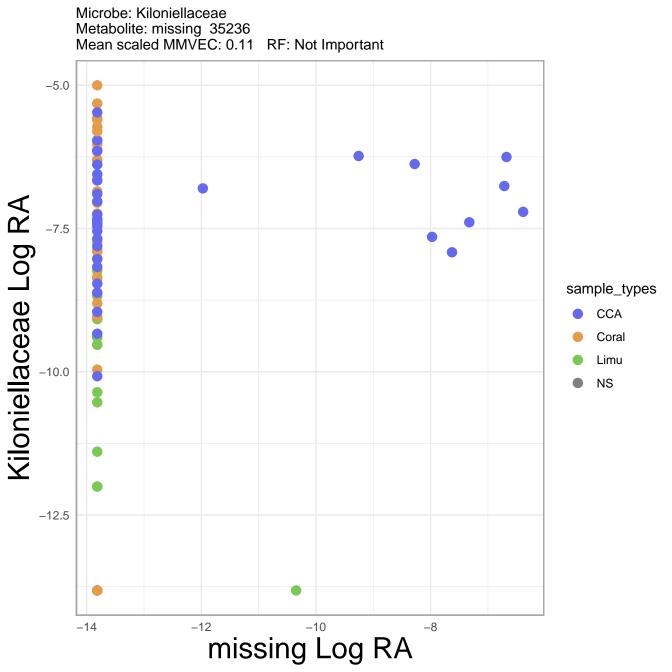
Microbe: Burkholderiaceae Metabolite: missing 35236

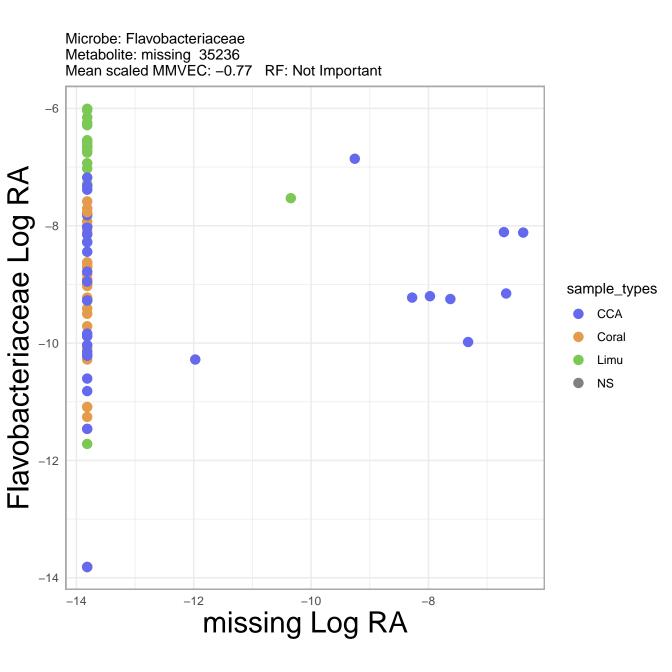
Mean scaled MMVEC: -0.18 RF: Not Important











Microbe: Woeseiaceae Metabolite: missing 35236 Mean scaled MMVEC: -0.35 RF: Not Important sample\_types CCA Coral Limu NS

missing Log RA

-8

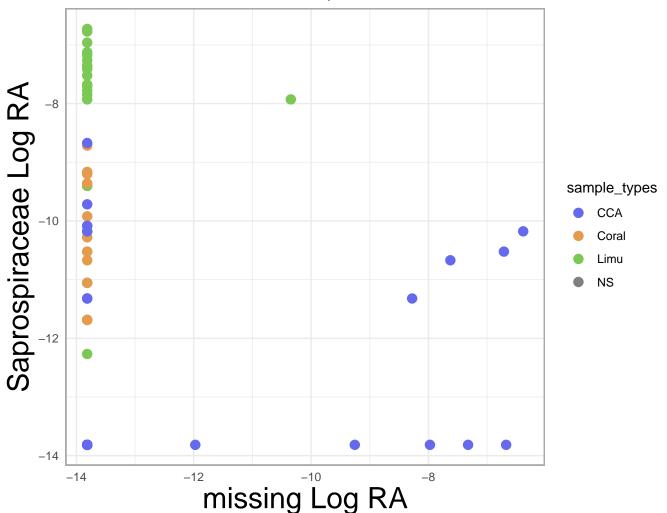
Woeseiaceae Log RA

-14

-14

Microbe: Saprospiraceae Metabolite: missing 35236

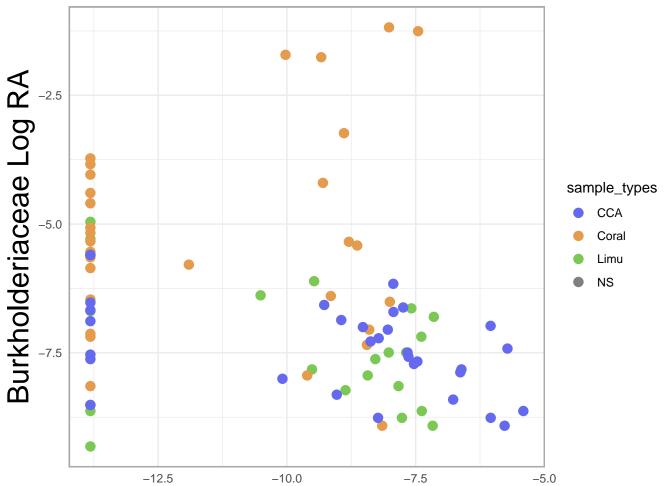
Mean scaled MMVEC: -0.9 RF: Not Important



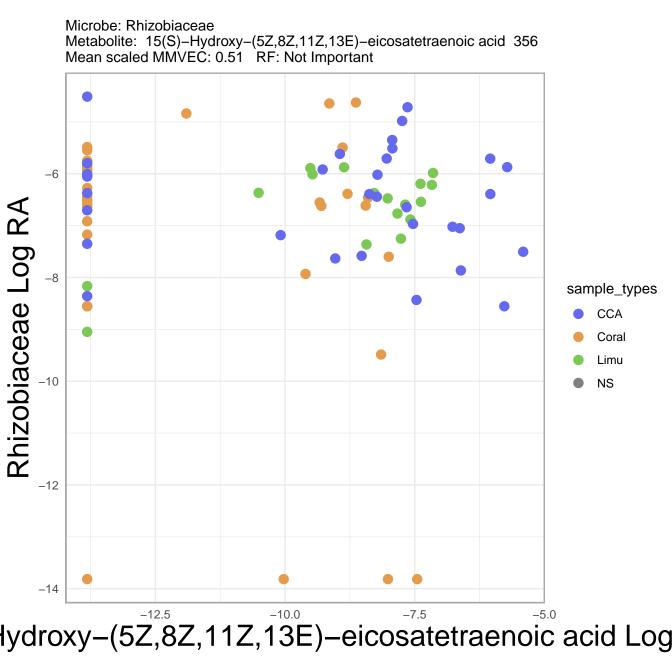
Microbe: Burkholderiaceae

Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356

Mean scaled MMVEC: 2.58 RF: Not Important



Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log



Microbe: Rhodobacteraceae Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356 Mean scaled MMVEC: -0.39 RF: Not Important sample\_types CCA Coral -10 Limu NS

Rhodobacteraceae Log RA

-14

-12.5

lydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log

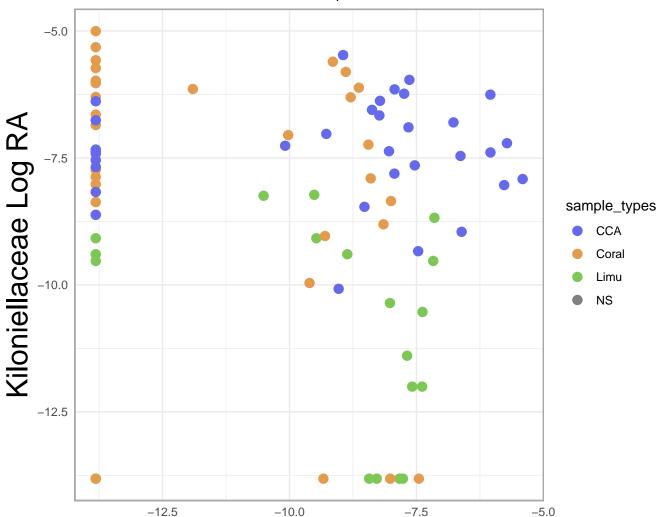
-7.5

-10.0

Microbe: Kiloniellaceae

Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356

Mean scaled MMVEC: 0.51 RF: Not Important

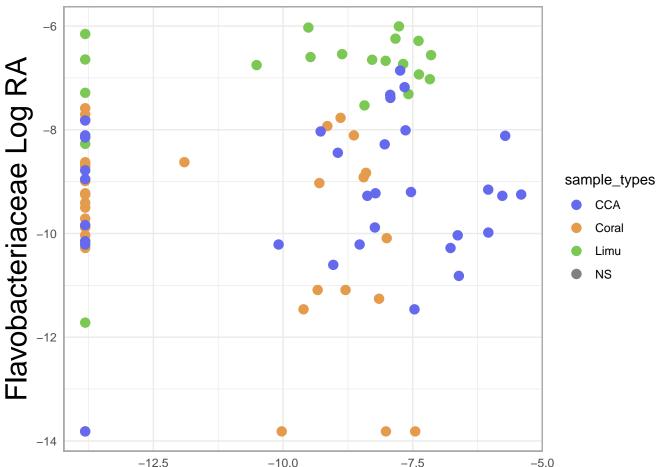


Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log

Microbe: Flavobacteriaceae

Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356

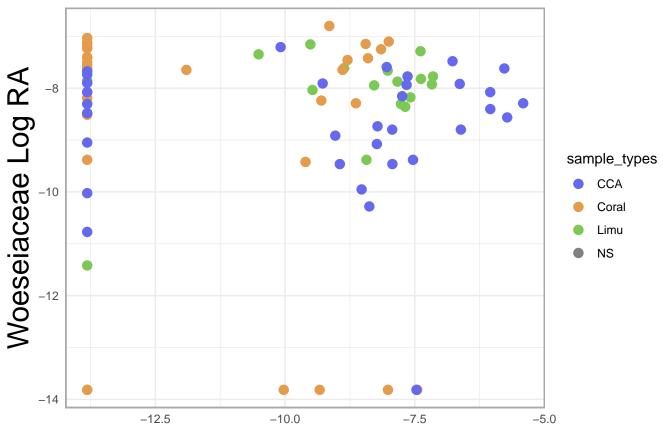
Mean scaled MMVEC: -0.3 RF: Not Important



lydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log

Microbe: Woeseiaceae

Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356 Mean scaled MMVEC: -0.38 RF: Not Important



lydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log

Microbe: Saprospiraceae Metabolite: 15(S)-Hydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid 356 Mean scaled MMVEC: -0.46 RF: Not Important sample\_types CCA Coral Limu NS

Saprospiraceae Log RA

-14

-12.5

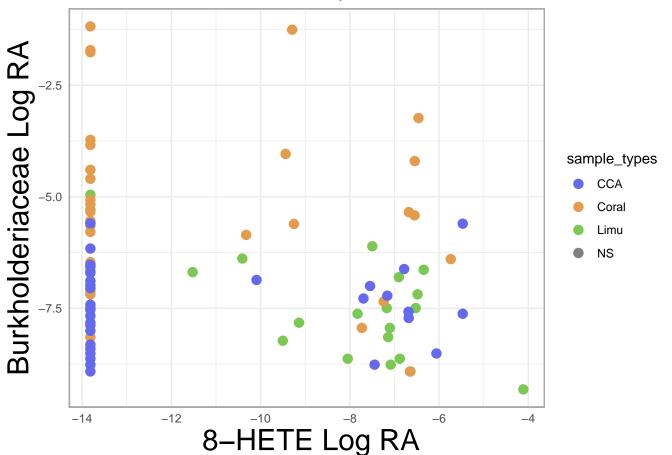
lydroxy-(5Z,8Z,11Z,13E)-eicosatetraenoic acid Log

-7.5

-10.0

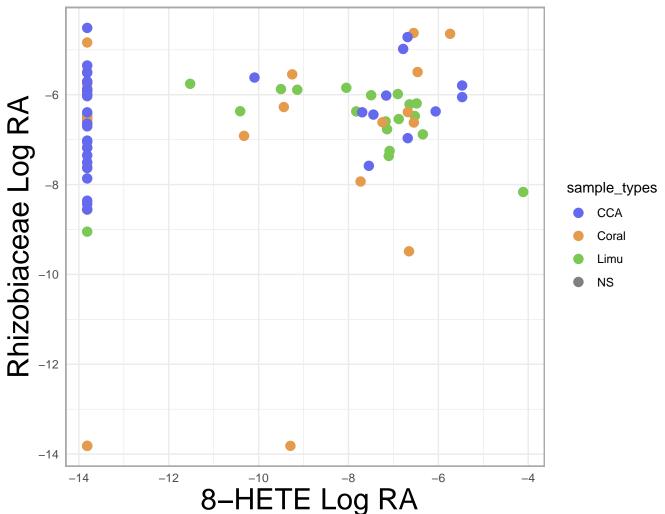
Microbe: Burkholderiaceae Metabolite: 8-HETE 363

Mean scaled MMVEC: -1.31 RF: Not Important



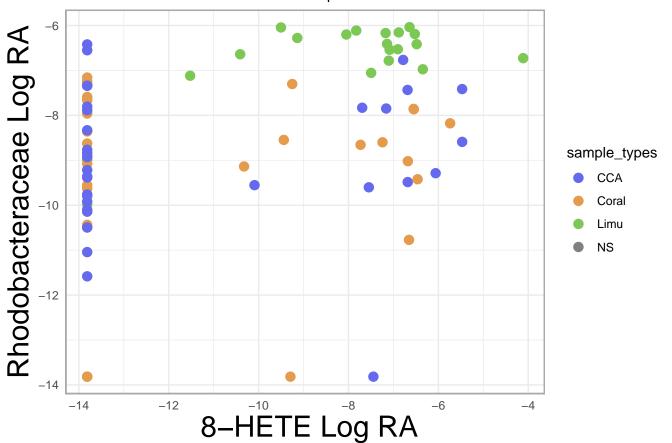
Microbe: Rhizobiaceae Metabolite: 8-HETE 363

Mean scaled MMVEC: -0.3 RF: Not Important



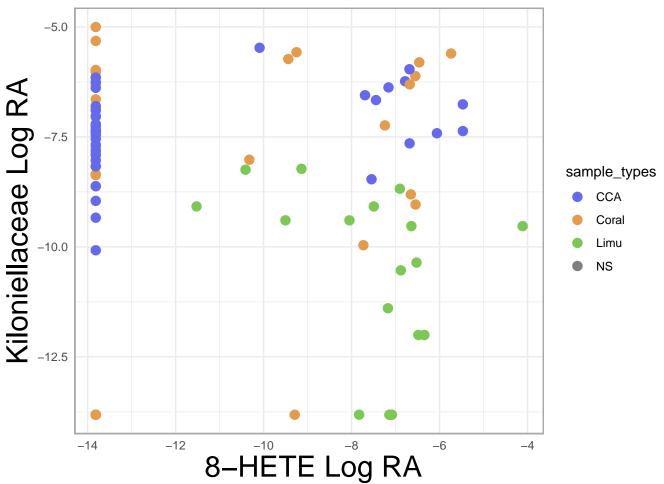
Microbe: Rhodobacteraceae Metabolite: 8-HETE 363

Mean scaled MMVEC: 1.02 RF: Not Important



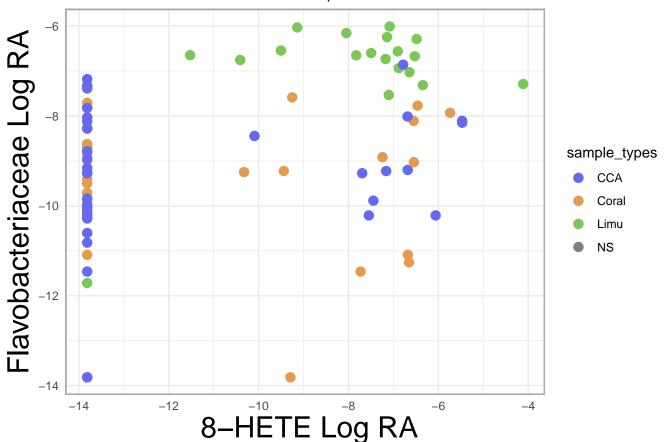
Microbe: Kiloniellaceae Metabolite: 8-HETE 363

Mean scaled MMVEC: -0.69 RF: Not Important



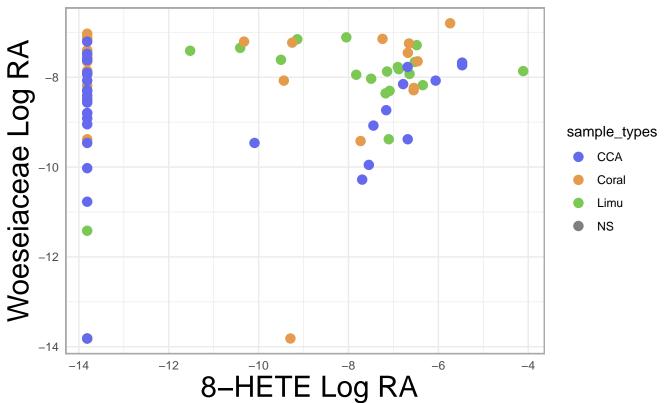
Microbe: Flavobacteriaceae Metabolite: 8-HETE 363

Mean scaled MMVEC: 0.92 RF: Not Important



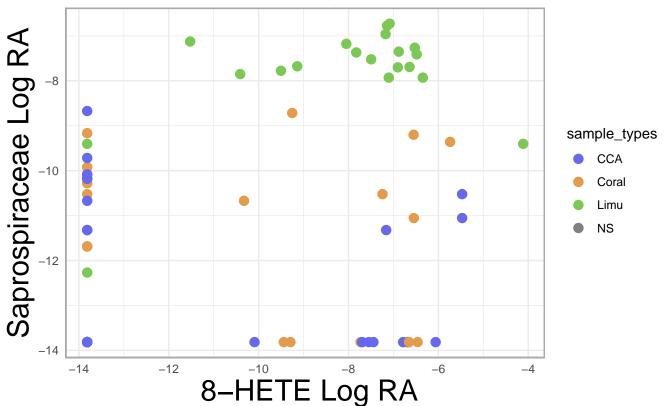
Microbe: Woeseiaceae Metabolite: 8-HETE 363

Mean scaled MMVEC: 0.15 RF: Not Important



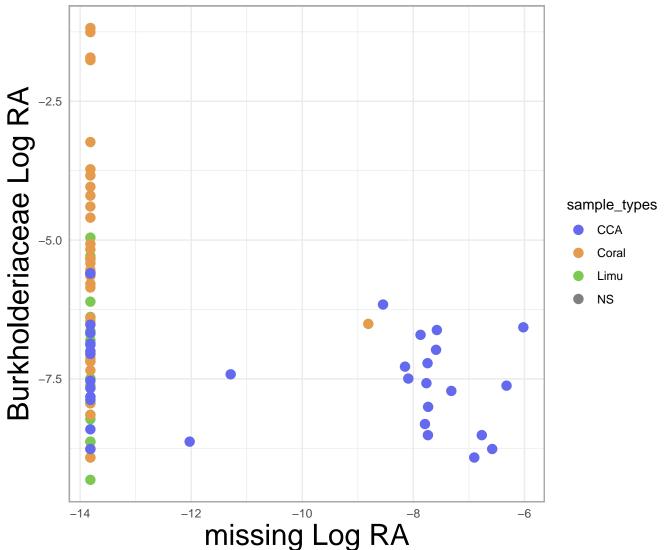
Microbe: Saprospiraceae Metabolite: 8-HETE 363

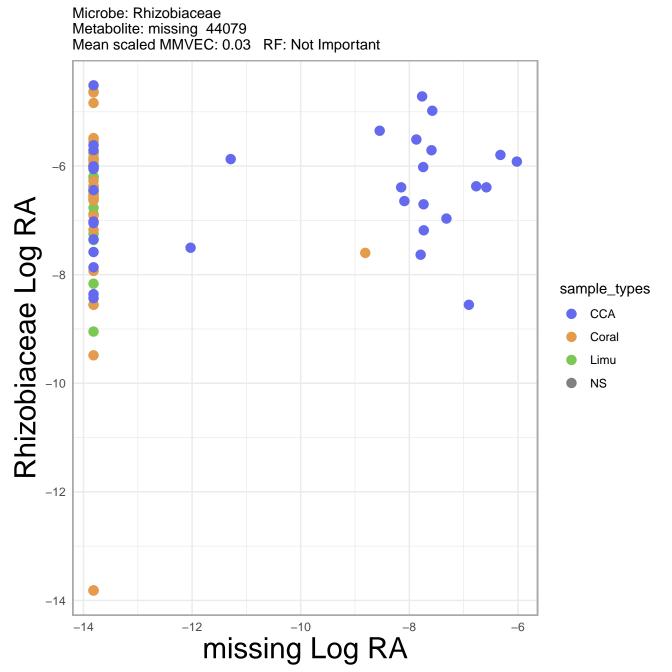
Mean scaled MMVEC: 1.29 RF: Not Important



Microbe: Burkholderiaceae Metabolite: missing 44079

Mean scaled MMVEC: 0.15 RF: Not Important





Microbe: Rhodobacteraceae Metabolite: missing 44079 Mean scaled MMVEC: -1.08 RF: Not Important -6 Rhodobacteraceae Log RA sample\_types CCA Coral -10 Limu NS

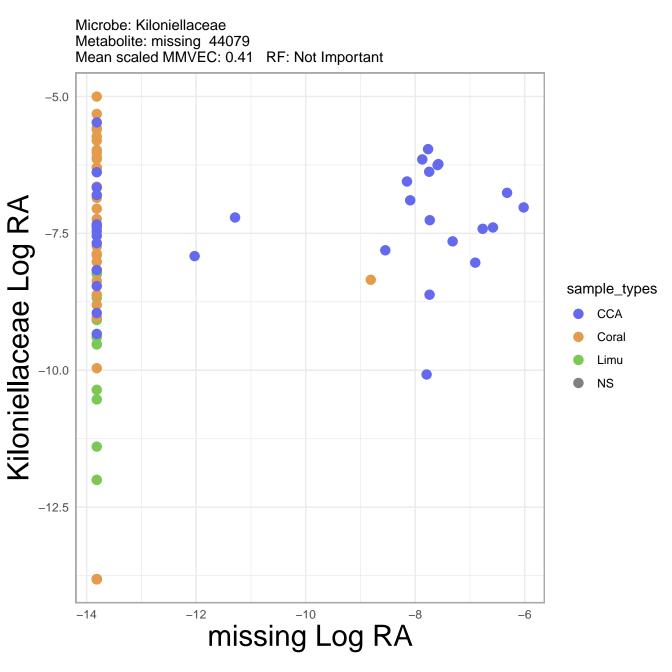
missing Log RA

-6

-12

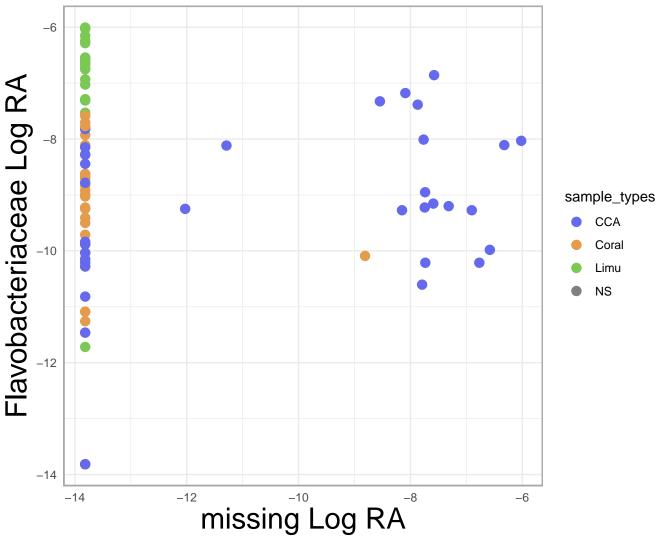
-14

-14



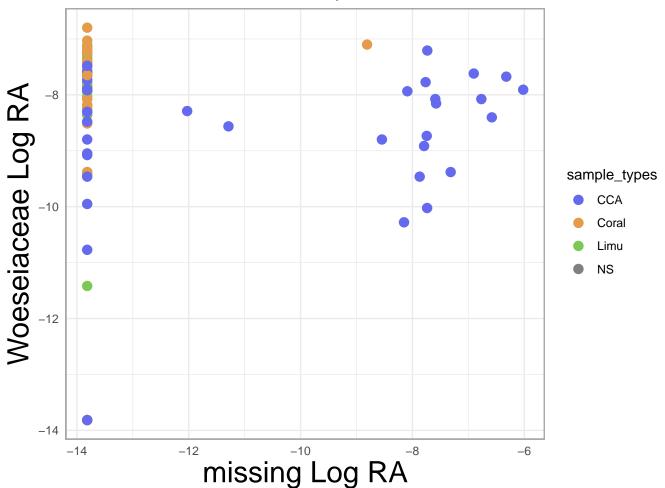
Microbe: Flavobacteriaceae Metabolite: missing 44079

Mean scaled MMVEC: -0.97 RF: Not Important



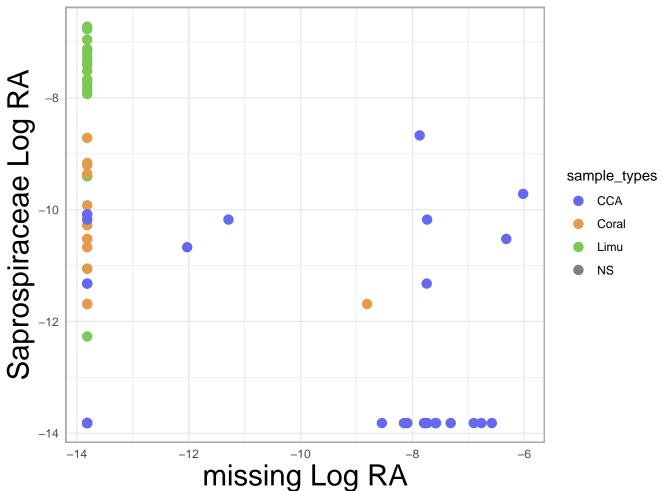
Microbe: Woeseiaceae Metabolite: missing 44079

Mean scaled MMVEC: -0.19 RF: Not Important



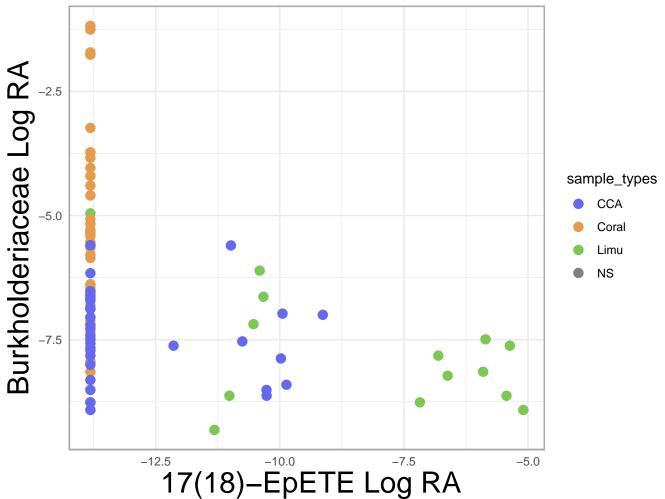
Microbe: Saprospiraceae Metabolite: missing 44079

Mean scaled MMVEC: -1.25 RF: Not Important



Microbe: Burkholderiaceae

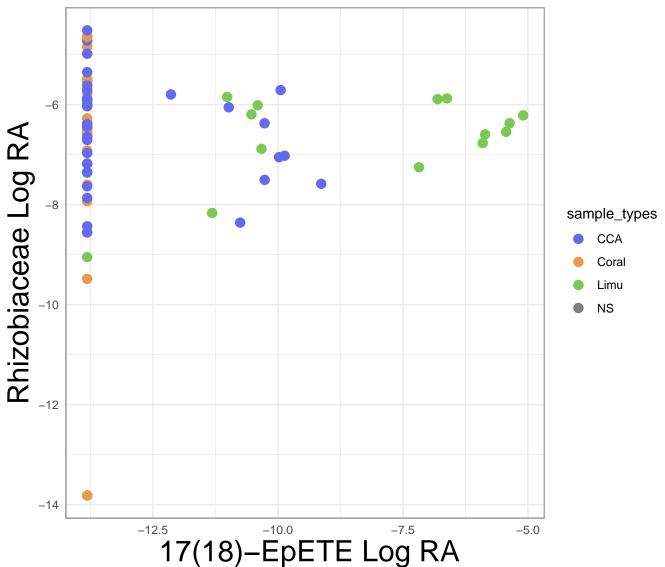
Metabolite: 17(18)-EpETE 5263 Mean scaled MMVEC: -0.21 RF: Not Important



Microbe: Rhizobiaceae

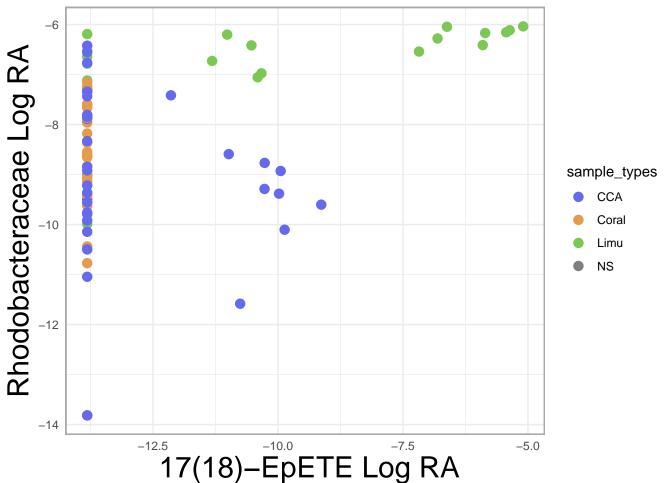
Metabolite: 17(18)-EpETE 5263

Mean scaled MMVEC: -0.14 RF: Not Important



Microbe: Rhodobacteraceae Metabolite: 17(18)-EpETE 5263

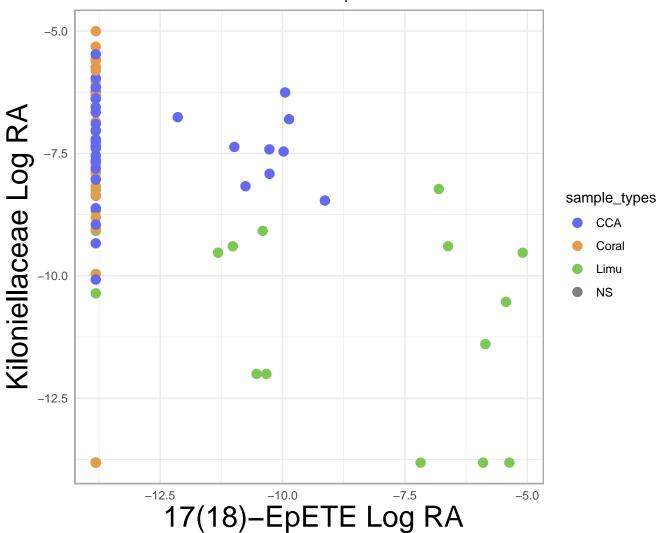
Mean scaled MMVEC: 1.14 RF: Not Important



Microbe: Kiloniellaceae

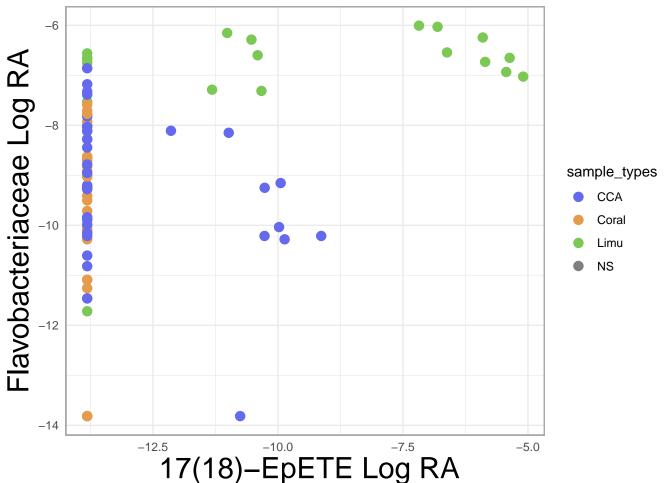
Metabolite: 17(18)-EpETE 5263

Mean scaled MMVEC: -0.74 RF: Not Important



Microbe: Flavobacteriaceae

Metabolite: 17(18)-EpETE 5263 Mean scaled MMVEC: 1.08 RF: Not Important



Microbe: Woeseiaceae Metabolite: 17(18)-EpETE 5263 Mean scaled MMVEC: -0.18 RF: Not Important Woeseiaceae Log RA sample\_types CCA -10 Coral Limu NS

17(18)-EPETE Log RA

-5.0

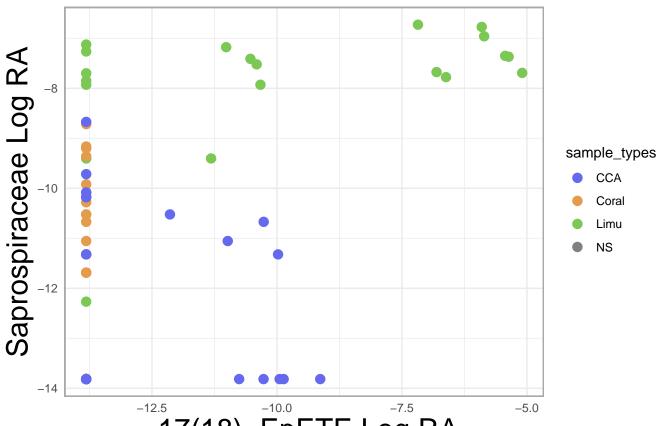
-10.0

-14

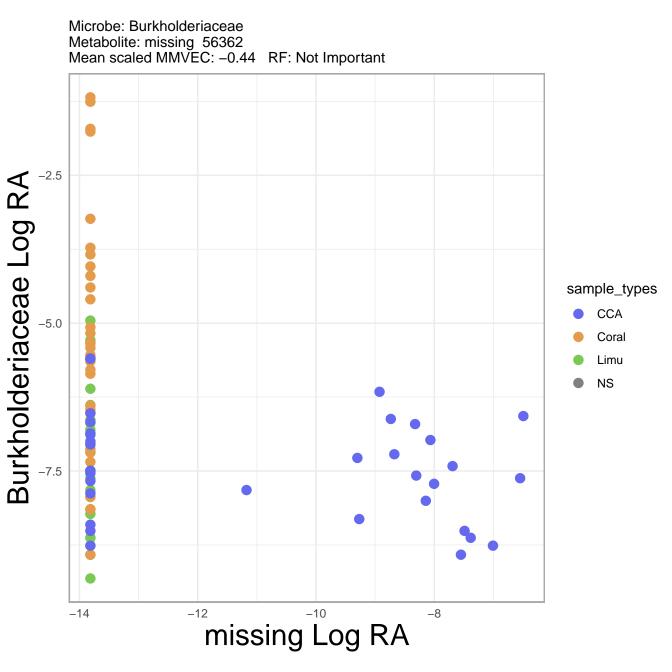
-12.5

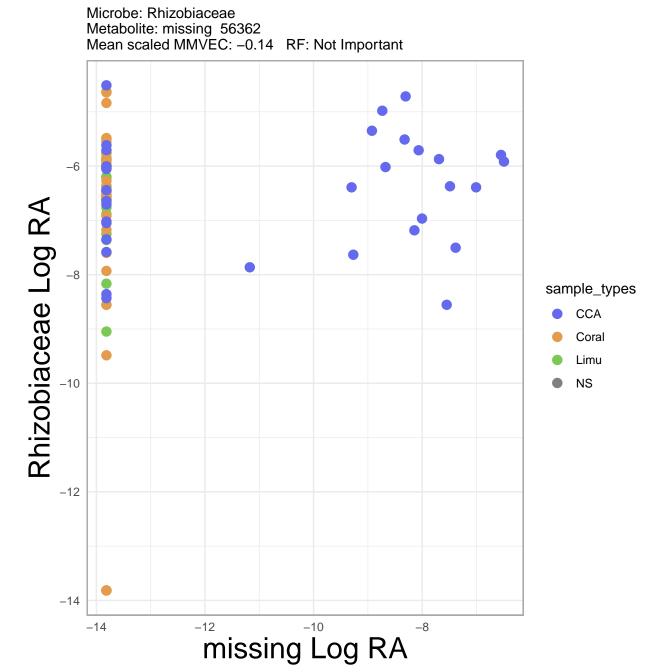
Microbe: Saprospiraceae

Metabolite: 17(18)-EpETE 5263 Mean scaled MMVEC: 1.54 RF: Not Important



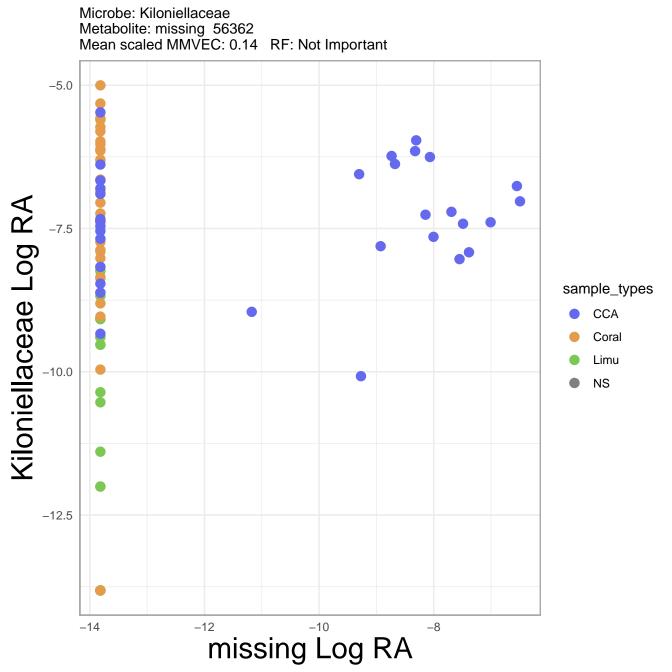
17(18)-EPETE Log RA





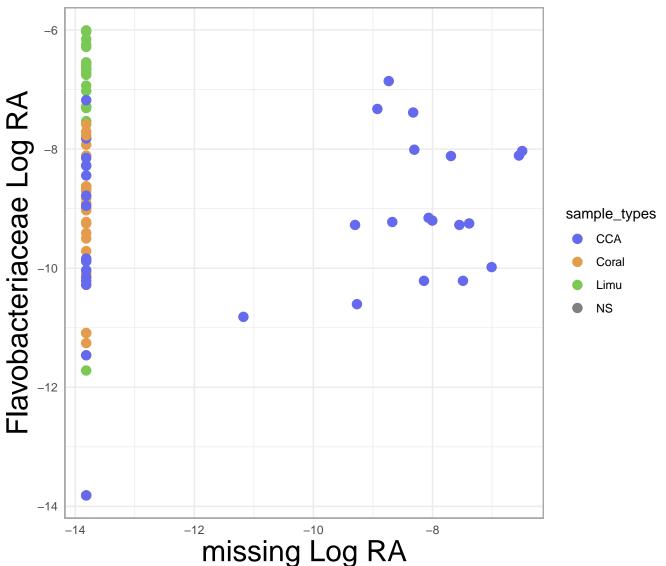
Microbe: Rhodobacteraceae Metabolite: missing 56362 Mean scaled MMVEC: -0.98 RF: Not Important -6 sample\_types CCA Coral -10 Limu NS -14-12 -10 -8 -14 missing Log RA

Rhodobacteraceae Log RA



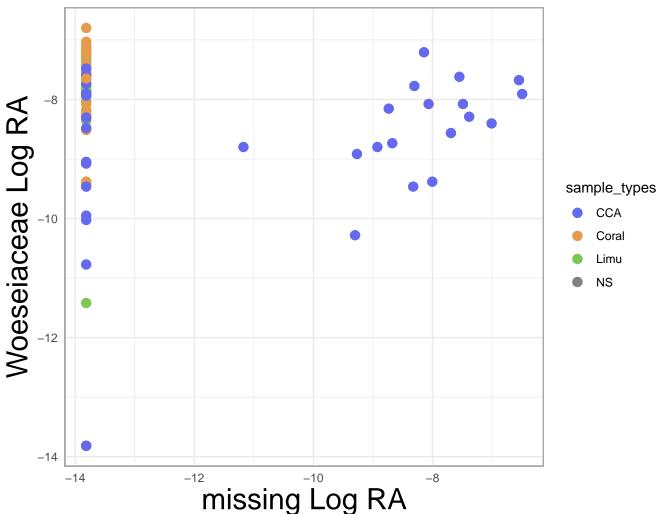
Microbe: Flavobacteriaceae Metabolite: missing 56362 Mean scaled MMVEC: –0.87





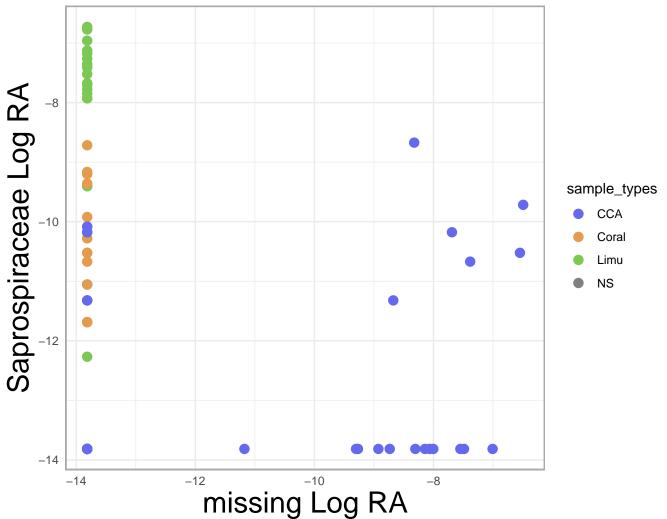
Microbe: Woeseiaceae Metabolite: missing 56362

Mean scaled MMVEC: -0.29 RF: Not Important



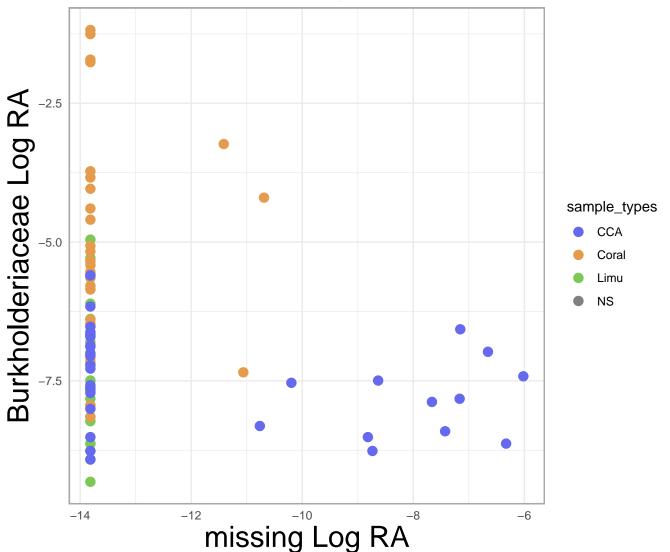
Microbe: Saprospiraceae Metabolite: missing 56362

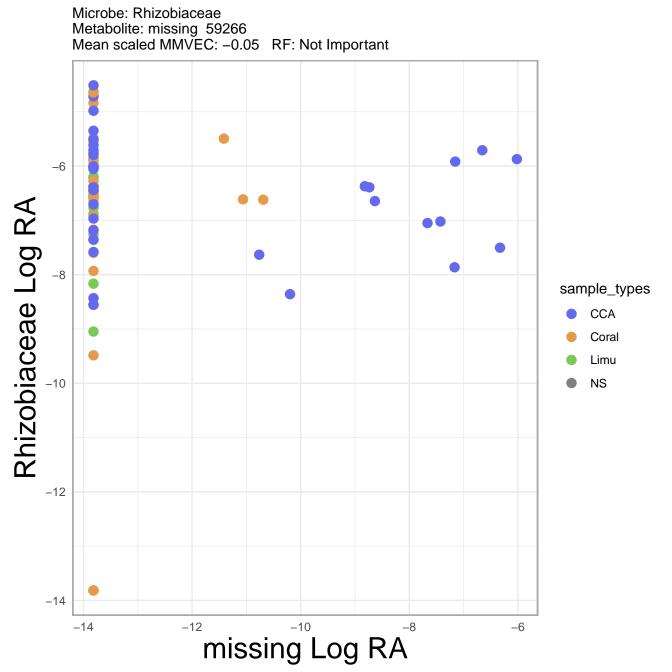
Mean scaled MMVEC: -1.03 RF: Not Important



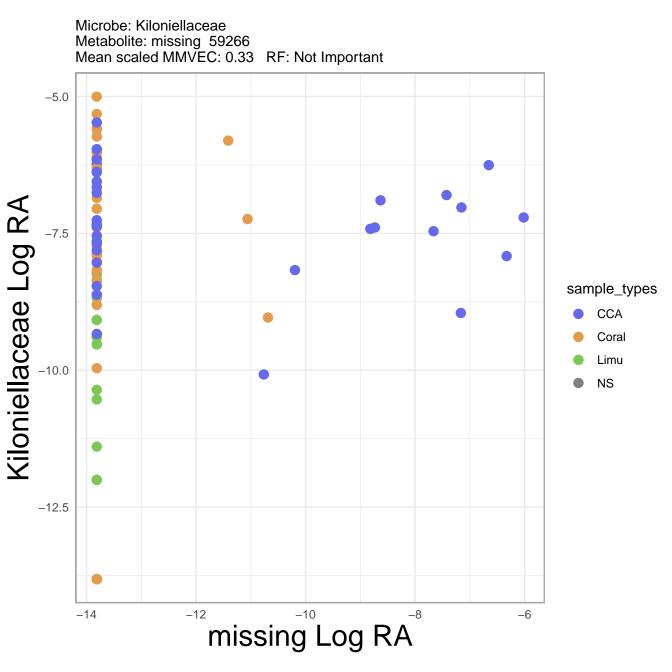
Microbe: Burkholderiaceae Metabolite: missing 59266

Mean scaled MMVEC: -0.17 RF: Not Important



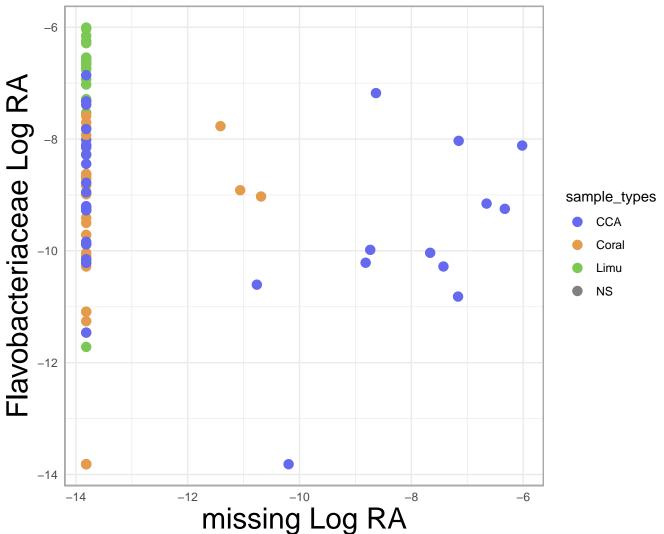


Microbe: Rhodobacteraceae Metabolite: missing 59266 Mean scaled MMVEC: -1.09 RF: Not Important -6 Rhodobacteraceae Log RA sample\_types CCA Coral -10 Limu NS -14missing Log RA -12 -6 -14



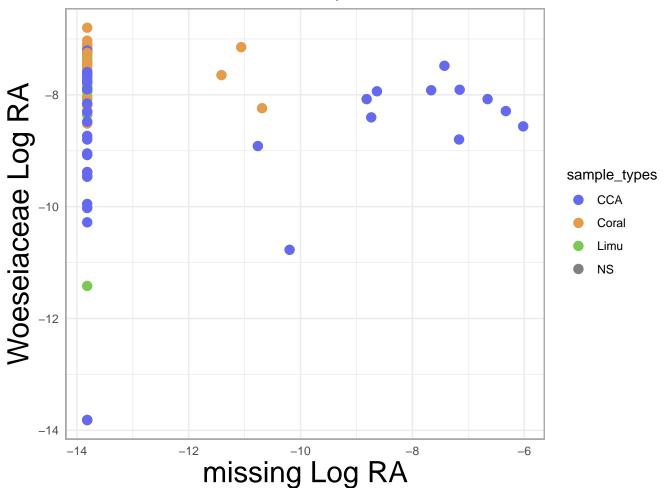
Microbe: Flavobacteriaceae Metabolite: missing 59266

Mean scaled MMVEC: -0.98 RF: Not Important



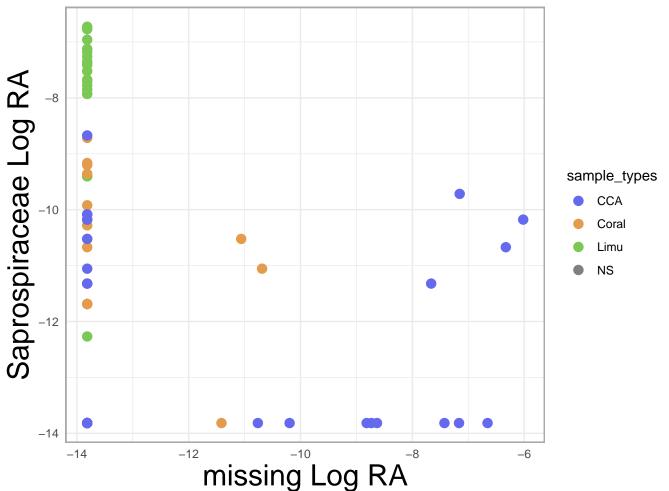
Microbe: Woeseiaceae Metabolite: missing 59266

Mean scaled MMVEC: -0.19 RF: Not Important



Microbe: Saprospiraceae Metabolite: missing 59266

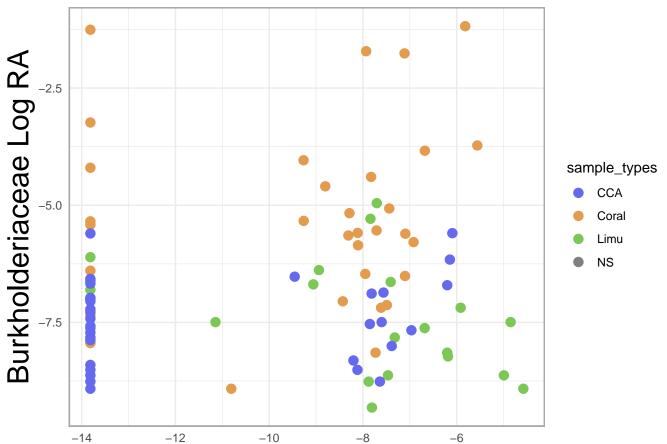
Mean scaled MMVEC: -1.25 RF: Not Important



Microbe: Burkholderiaceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: 1.44 RF: Not Important

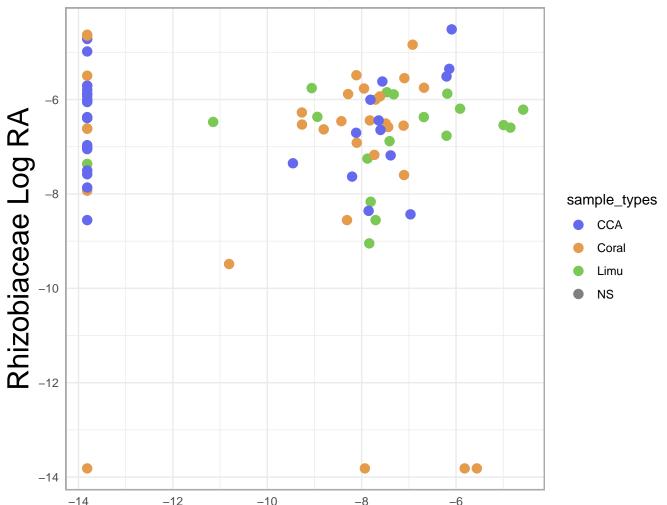


droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F

Microbe: Rhizobiaceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: 0.28 RF: Not Important

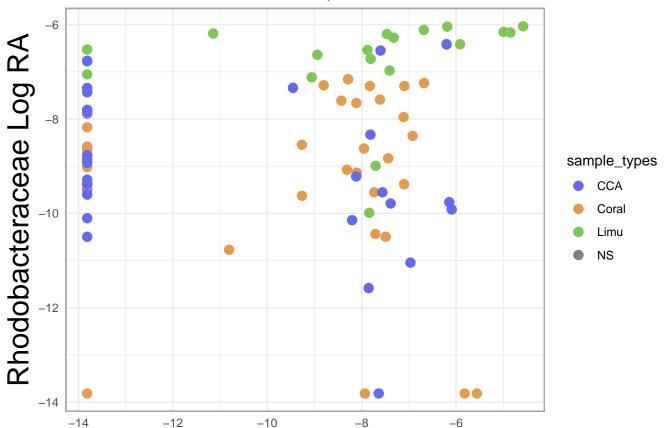


droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F

Microbe: Rhodobacteraceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: 1.17 RF: Not Important

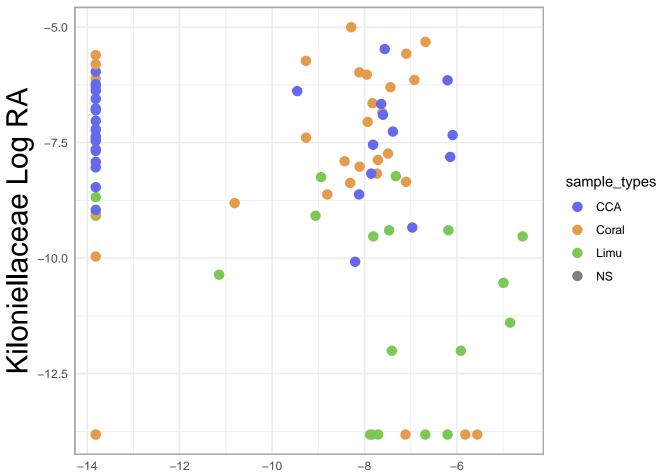


droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F

Microbe: Kiloniellaceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: -0.24 RF: Not Important

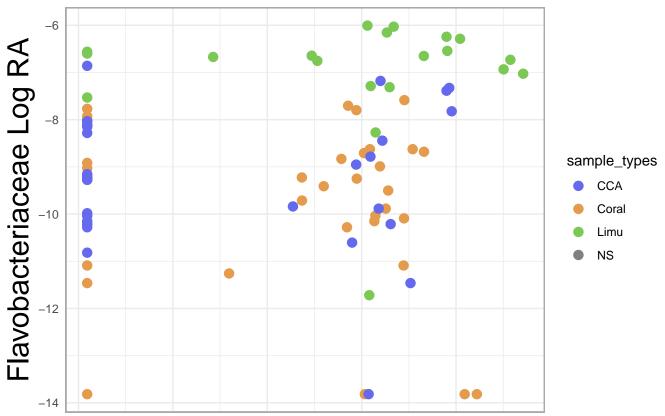


droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log I

Microbe: Flavobacteriaceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: 1.09 RF: Not Important



droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F

Microbe: Woeseiaceae Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70 Mean scaled MMVEC: -0.03 RF: Not Important Woeseiaceae Log RA sample\_types CCA Coral Limu NS -14

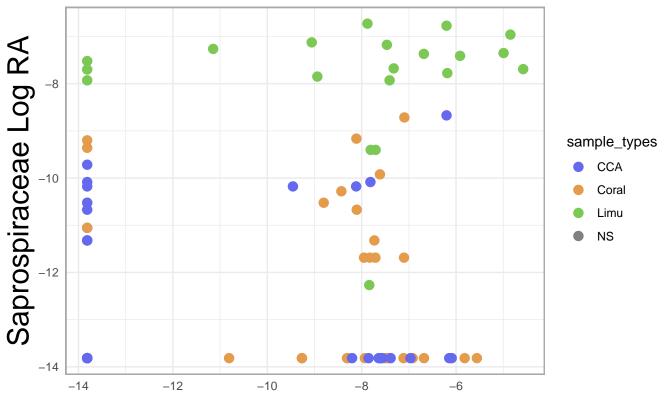
droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F

-12

Microbe: Saprospiraceae

Metabolite: 20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid 70

Mean scaled MMVEC: 1.38 RF: Not Important



droxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid Log F