

Analyzing MS-DIAL data

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BBRB 711

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Open the Area.txt file from MS-DIAL in Excel

A	B	C	D	E	F	G	H	I	J	K	L	M	N
Alignment ID	Average Rt (r)	Average Mz	Metabolite name	Adduct type	Post curation	Fill %	MS/MS assigned	Reference R ¹	Reference m	Formula	Ontology	INCHIKEY	SMILES
0	25.967	61.80658	Unknown	[M-H]-		1	FALSE	null	null	null	null	null	null
1	17.134	61.99174	Unknown	[M-H]-		0.667	TRUE	null	null	null	null	null	null
2	16.073	61.99218	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
3	13.208	61.9929	Unknown	[M-C6H10O5 adduct linker		0.167	TRUE	null	null	null	null	null	null
4	25.971	61.99305	Unknown	[M-H]-		1	TRUE	null	null	null	null	null	null
5	16.073	68.9986	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
6	20.489	68.99867	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
7	26.208	68.99916	Unknown	[M-H]-	found in high	1	TRUE	null	null	null	null	null	null
8	14.321	74.02563	w/o MS2:GL	[M-H]-	similar chr	0.333	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOQ O=C(O)CN	
9	19.987	74.02805	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOQ O=C(O)CN	
10	16.531	74.02966	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOQ O=C(O)CN	
11	17.43	74.03057	w/o MS2:GL	[M-H]-		0.167	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOQ O=C(O)CN	
12	16.202	76.02376	Unknown	[M-H]-	similar chr	0.167	FALSE	null	null	null	null	null	null
13	12.231	79.95722	Unknown	[M-H]-	found in high	0.167	FALSE	null	null	null	null	null	null
14	18.611	79.95961	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
15	15.141	79.96063	Unknown	[M-H]-		0.5	TRUE	null	null	null	null	null	null
16	17.462	79.96455	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
17	0.131	88.98872	Unknown	[M-H]-		0.333	TRUE	null	null	null	null	null	null
18	7.351	88.99012	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
19	6.49	88.99024	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
20	13.212	92.05163	Unknown	[M-C6H10O5 similar chr		0.667	TRUE	null	null	null	null	null	null
21	16.057	96.96115	w/o MS2:Ph	[M-H]-		0.333	TRUE	null	96.96962	H3O4P	Non-metal p	NBIXXVUZA O=P(O)(O)O	

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Delete the top four lines

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Alignment IC	Average Rt(r	Average Mz	Metabolite n	Adduct type	Post curatior	Fill %	MS/MS assig	Reference R	Reference m	Formula	Ontology	INCHIKEY	SMILES
2	0	25.967	61.80658	Unknown	[M-H]-		1	FALSE	null	null	null	null	null	null
3	1	17.134	61.99174	Unknown	[M-H]-		0.667	TRUE	null	null	null	null	null	null
4	2	16.073	61.99218	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
5	3	13.208	61.9929	Unknown	[M-C6H10O5 adduct linke		0.167	TRUE	null	null	null	null	null	null
6	4	25.971	61.99305	Unknown	[M-H]-		1	TRUE	null	null	null	null	null	null
7	5	16.073	68.9986	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
8	6	20.489	68.99867	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
9	7	26.208	68.99916	Unknown	[M-H]-	found in high	1	TRUE	null	null	null	null	null	null
10	8	14.321	74.02563	w/o MS2:GL	[M-H]-	similar chr	0.333	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
11	9	19.987	74.02805	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
12	10	16.531	74.02966	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
13	11	17.43	74.03057	w/o MS2:GL	[M-H]-		0.167	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
14	12	16.202	76.02376	Unknown	[M-H]-	similar chr	0.167	FALSE	null	null	null	null	null	null
15	13	12.231	79.95722	Unknown	[M-H]-	found in high	0.167	FALSE	null	null	null	null	null	null
16	14	18.611	79.95961	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
17	15	15.141	79.96063	Unknown	[M-H]-		0.5	TRUE	null	null	null	null	null	null
18	16	17.462	79.96455	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
19	17	0.131	88.98872	Unknown	[M-H]-		0.333	TRUE	null	null	null	null	null	null
20	18	7.351	88.99012	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
21	19	6.49	88.99024	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
22	20	13.212	92.05163	Unknown	[M-C6H10O5 similar chr		0.667	TRUE	null	null	null	null	null	null
23	21	16.057	96.96115	w/o MS2:Ph	[M-H]-		0.333	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
24	22	26.031	96.96125	Phosphoric a	[M-H]-		1	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
25	23	17.669	96.96135	w/o MS2:Ph	[M-H]-	found in high	0.167	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
26	24	18.241	96.96317	Phosphoric a	[M-H]-	found in high	0.167	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O

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Now highlight all the cells

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Alignment IC	Average Rt(r	Average Mz	Metabolite n	Adduct type	Post curatior	Fill %	MS/MS assig	Reference R	Reference m	Formula	Ontology	INCHIKEY	SMILES
2	0	25.967	61.80658	Unknown	[M-H]-		1	FALSE	null	null	null	null	null	null
3	1	17.134	61.99174	Unknown	[M-H]-		0.667	TRUE	null	null	null	null	null	null
4	2	16.073	61.99218	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
5	3	13.208	61.9929	Unknown	[M-C6H10O5 adduct linke		0.167	TRUE	null	null	null	null	null	null
6	4	25.971	61.99305	Unknown	[M-H]-		1	TRUE	null	null	null	null	null	null
7	5	16.073	68.9986	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
8	6	20.489	68.99867	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
9	7	26.208	68.99916	Unknown	[M-H]-	found in high	1	TRUE	null	null	null	null	null	null
10	8	14.321	74.02563	w/o MS2:GL	[M-H]-	similar chr	0.333	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
11	9	19.987	74.02805	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
12	10	16.531	74.02966	w/o MS2:GL	[M-H]-	found in high	0.167	TRUE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
13	11	17.43	74.03057	w/o MS2:GL	[M-H]-		0.167	FALSE	null	74.0242	C2H5NO2	Alpha amino	DHMQDGOO	O=C(O)CN
14	12	16.202	76.02376	Unknown	[M-H]-	similar chr	0.167	FALSE	null	null	null	null	null	null
15	13	12.231	79.95722	Unknown	[M-H]-	found in high	0.167	FALSE	null	null	null	null	null	null
16	14	18.611	79.95961	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
17	15	15.141	79.96063	Unknown	[M-H]-		0.5	TRUE	null	null	null	null	null	null
18	16	17.462	79.96455	Unknown	[M-H]-	found in high	0.333	TRUE	null	null	null	null	null	null
19	17	0.131	88.98872	Unknown	[M-H]-		0.333	TRUE	null	null	null	null	null	null
20	18	7.351	88.99012	Unknown	[M-H]-		0.167	FALSE	null	null	null	null	null	null
21	19	6.49	88.99024	Unknown	[M-H]-		0.167	TRUE	null	null	null	null	null	null
22	20	13.212	92.05163	Unknown	[M-C6H10O5 similar chr		0.667	TRUE	null	null	null	null	null	null
23	21	16.057	96.96115	w/o MS2:Ph	[M-H]-		0.333	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
24	22	26.031	96.96125	Phosphoric a	[M-H]-		1	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
25	23	17.669	96.96135	w/o MS2:Ph	[M-H]-	found in high	0.167	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O
26	24	18.241	96.96317	Phosphoric a	[M-H]-	found in high	0.167	TRUE	null	96.96962	H3O4P	Non-metal p	NBIIXVUZA	O=P(O)(O)O

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Click on <data> and <sort>

Select metabolite name

Select "My list has headers"

Add levels to sort by: My list has headers

	Column	Sort On	Order	Color/Icon
Sort by	Metabolite name	Values	A to Z	

+ - Copy

Options... Cancel OK

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Sorted by metabolite name

1	Alignment I	Average Rt(r	Average Mz	Metabolite name	Adduct type	Post curation	Fill %	MS/MS assign	Reference R'	Reference m
2	322	16.477	197.08145	(-)-Camphanic acid	[M-H]-		1	TRUE	null	197.08192
3	323	17.203	197.08147	(-)-Camphanic acid	[M-H]-		0.833	TRUE	null	197.08192
4	326	16.109	197.08331	(-)-Camphanic acid	[M-H]-	found in high	1	TRUE	null	197.08192
5	2717	12.467	375.13495	(-)-Riboflavin; LC-ESI-QTOF; MS2; CE	[M-H]-		0.167	TRUE	null	375.13101
6	105	25.663	149.01062	(R,R)-TARTARIC ACID	[M-H]-		0.333	TRUE	null	149.009
7	53	14.418	121.03027	2-Hydroxybenzaldehyde	[M-H]-	similar chr	1	TRUE	null	121.0295
8	131	11.452	160.04082	2,8-Quinolinediol	[M-H]-	found in high	1	TRUE	null	160.04041
9	150	15.215	165.05748	3-(3-Hydroxyphenyl)propionic acid	[M-H]-		0.333	TRUE	null	165.05573
10	501	14.526	217.10864	3-Hydroxysebacic acid	[M-H]-	similar chr	0.833	TRUE	null	217.10815
11	438	13.374	212.00157	3-Indoxyl sulfate; LC-ESI-QTOF; MS2; CE	[M-H]-	similar chr	1	TRUE	null	212.0023
12	261	12.12	188.03555	4-HYDROXY-2-QUINOLINECARBOXYLIC ACID	[M-H]-		1	TRUE	null	188.035
13	93	12.12	144.04584	4-Hydroxyquinoline	[M-H]-	similar chr	1	TRUE	2.933	144.04549
14	94	17.145	144.04784	4-Hydroxyquinoline	[M-H]-	similar chr	1	TRUE	2.933	144.04549
15	95	18.645	144.04805	4-Hydroxyquinoline	[M-H]-		0.5	TRUE	2.933	144.04549
16	5121	12.561	621.10785	4'-O-GlcA-7-O-GlcA Apigenin (NMR)	[M-H]-	adduct linke	0.5	TRUE	null	621.10974
17	3560	18.074	431.2114	5-hydroxy-2,2,6,6-tetramethyl-4-[2-methyl-1-[2,4,6-	[M-H]-		1	TRUE	null	431.2077
18	3490	23.751	426.96555	6:2 Fluorotelomer sulfonic acid	[M-H]-		0.833	TRUE	null	426.9679
19	121	25.48	157.03886	ALLANTOIN	[M-H]-		0.333	TRUE	null	157.03671
20	122	11.438	157.04041	ALLANTOIN	[M-H]-		0.333	TRUE	null	157.03671
21	1084	20.534	269.04648	Aloe-emodin	[M-H]-	similar chr	0.833	TRUE	5.889	269.04553
22	3734	16.341	445.07587	apigenin-7-O-glucuronide	[M-H]-	adduct linke	0.5	TRUE	null	445.07761
23	3735	15.558	445.07611	apigenin-7-O-glucuronide	[M-H]-	adduct linke	0.833	TRUE	null	445.07761
24	1082	17.634	269.04385	Apigenin; LC-ESI-QTOF; MS2; CE	[M-H]-	found in high	0.167	TRUE	null	269.04553
25	1083	18.079	269.04626	Apigenin; LC-ESI-QTOF; MS2; CF	[M-H]-	similar chr	0.5	TRUE	null	269.04553

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Open a new Excel file and copy the highlighted rows into it

Then go back the original file and scroll down to the end of the unknowns (no entries in this dataset)
Then scroll down to the very end of the file and collect metabolites beginning with X, Y and Z

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Edit the compounds in the new file

	A	B	C	D	E	F	G	H	I	J	K
88	1756	19.114	311.15079	Thymol-beta [M-H]-			0.333	TRUE	null	311.14999	C16H24O6
89	295	12.86	193.05223	trans-Ferulic [M-H]-	found in high		0.833	TRUE	4.228	193.05063	C10H10O4
90	29	20	112.98609	Trifluoroacet [M-H]-			0.167	TRUE	null	112.98559	C2HF3O2
91	30	21.705	112.98636	Trifluoroacet [M-H]-			0.333	TRUE	null	112.98559	C2HF3O2
92	31	25.769	112.98677	Trifluoroacet [M-H]-			0.5	TRUE	null	112.98559	C2HF3O2
93	32	18.316	112.98697	Trifluoroacet [M-H]-	found in high		0.333	TRUE	null	112.98559	C2HF3O2
94	33	26.191	112.98698	Trifluoroacet [M-H]-	found in high		1	TRUE	null	112.98559	C2HF3O2
95	34	15.853	112.98714	Trifluoroacet [M-H]-	found in high		0.333	TRUE	null	112.98559	C2HF3O2
96	35	22.366	112.98718	Trifluoroacet [M-H]-			0.167	TRUE	null	112.98559	C2HF3O2
97	36	19.116	112.98722	Trifluoroacet [M-H]-			0.167	TRUE	null	112.98559	C2HF3O2
98	37	15.28	112.98778	Trifluoroacet [M-H]-			0.167	TRUE	null	112.98559	C2HF3O2
99	38	20.58	112.9887	Trifluoroacet [M-H]-			0.833	TRUE	null	112.98559	C2HF3O2
100	39	17.252	112.98892	Trifluoroacet [M-H]-			1	TRUE	null	112.98559	C2HF3O2
101	40	14.959	112.98996	Trifluoroacet [M-H]-			0.167	TRUE	null	112.98559	C2HF3O2
102	41	17.957	112.9902	Trifluoroacet [M-H]-			0.333	TRUE	null	112.98559	C2HF3O2

Delete the trifluoroacetic acid

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Delete more contaminants

40	275	26.155	191.01985	CITRATE	[M-H]-		0.833	TRUE	null	
41	274	15.74	191.01971	Citric acid	[M-H]-		0.167	TRUE	null	
42	276	20.462	191.02	Citric acid	[M-H]-		0.167	TRUE	null	
43	278	14.743	191.02106	Citric acid (Not validated, isomer of 22	[M-H]-		0.333	TRUE	1.64	
44	279	6.506	191.02122	Citric acid (Not validated, isomer of 22	[M-H]-		0.667	TRUE	1.64	
45	280	7.373	191.02129	Citric acid (Not validated, isomer of 22	[M-H]-		0.167	TRUE	1.64	
46	294	21.401	193.03987	D-(+)-Galacturonic acid	[M-H]-	found in high	1	TRUE	null	
47	507	9.964	218.10304	D-PANTOTHENIC ACID	[M-H]-		0.833	TRUE	null	
48	833	17.487	249.03384	Diphenylphosphate	[M-H]-		0.5	TRUE	null	
49	218	11.453	181.05011	DL-3-(4-Hydroxyphenyl)lactic acid; LC-E	[M-H]-		0.833	TRUE	null	
50	1979	19.685	325.17944	Dodecylbenzenesulfonic acid	[M-H]-	adduct linker	0.167	TRUE	null	
51	1981	20.806	325.18381	Dodecylbenzenesulfonic acid	[M-H]-		0.667	TRUE	null	
52	1982	21.765	325.18414	Dodecylbenzenesulfonic acid	[M-H]-		0.833	TRUE	null	
53	1983	24.591	325.18436	Dodecylbenzenesulfonic acid	[M-H]-		0.5	TRUE	null	
54	1984	25.694	325.18555	Dodecylbenzenesulfonic acid	[M-H]-		1	TRUE	null	
55	1985	22.492	325.18637	Dodecylbenzenesulfonic acid	[M-H]-		0.333	TRUE	null	
56	1986	22.731	325.1864	Dodecylbenzenesulfonic acid	[M-H]-		0.667	TRUE	null	
57	1987	24.423	325.18658	Dodecylbenzenesulfonic acid	[M-H]-		0.5	TRUE	null	
58	873	14.742	253.07675	FA 9:0 + 10, sulfate; PlaSMA ID-416	[M-H]-		0.833	TRUE	4.24	
59	290	14.139	193.03535	Glucuronate	[M-H]-	adduct linker	0.667	TRUE	null	
60	73	10.066	131.03609	Glutaric acid; LC-ESI-QTOF; MS2; CE	[M-H]-		0.333	TRUE	null	

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Order by retention time and delete after 20 min

	A	B	C	D	E	F	G	H	I	J	K
65	367	18.475	201.11378	Sebacic acid; LC-ESI-QTOF; MS2; CE	[M-H]-	similar chror	1	TRUE	null	201.11324	C10H18O4
66	95	18.645	144.04805	4-Hydroxyquinoline	[M-H]-		0.5	TRUE	2.933	144.04549	C9H7NO
67	1756	19.114	311.15079	Thymol-beta-D-glucoside	[M-H]-		0.333	TRUE	null	311.14999	C16H24O6
68	3902	19.719	459.08923	oroxindin	[M-H]-	adduct linker	0.5	TRUE	null	459.09329	C22H20O11
69	276	20.462	191.02	Citric acid	[M-H]-		0.167	TRUE	null	191.01973	C6H8O7
70	1084	20.534	269.04648	Aloe-emodin	[M-H]-	similar chror	0.833	TRUE	5.889	269.04553	C15H10O5
71	294	21.401	193.03987	D-(+)-Galacturonic acid	[M-H]-	found in high	1	TRUE	null	193.03537	C6H10O7
72	1762	21.719	311.16913	Triptophenolide	[M-H]-		1	TRUE	null	311.16525	C20H24O3
73	1758	22.277	311.16809	Triptophenolide	[M-H]-		0.5	TRUE	null	311.16525	C20H24O3
74	592	22.447	227.13028	C12H20O4; PlaSMA ID-334	[M-H]-		0.5	TRUE	6.29	227.12781	C12H20O4
75	1763	22.684	311.17126	Triptophenolide	[M-H]-		0.333	TRUE	null	311.16525	C20H24O3
76	1761	22.875	311.16901	Triptophenolide	[M-H]-		0.667	TRUE	null	311.16525	C20H24O3
77	2550	23.099	362.96942	Perfluoroheptanoic acid; LC-ESI-ITFT; M	[M-H]-		0.833	TRUE	null	362.9696	C7HF13O2
78	3490	23.751	426.96555	6:2 Fluorotelomer sulfonic acid	[M-H]-		0.833	TRUE	null	426.9679	C8H5F13O3S
79	1759	23.956	311.16809	Triptophenolide	[M-H]-		0.167	TRUE	null	311.16525	C20H24O3
80	1034	24.044	265.14731	C12-AS (TENTATIVE)	[M-H]-		1	TRUE	null	265.14792	C12H26O4S
81	1534	24.072	297.15143	auraptin	[M-H]-		0.667	TRUE	null	297.1496	C19H22O3
82	1760	24.112	311.16885	Triptophenolide	[M-H]-		1	TRUE	null	311.16525	C20H24O3
83	1535	24.395	297.15158	auraptin	[M-H]-		0.333	TRUE	null	297.1496	C19H22O3
84	3270	24.617	412.96658	Perfluorooctanoic acid; LC-ESI-ITFT; MS	[M-H]-		1	TRUE	null	412.96643	C8HF15O2
85	1533	25.257	297.15125	auraptin	[M-H]-		1	TRUE	null	297.1496	C19H22O3
86	1757	25.368	311.16684	Triptophenolide	[M-H]-		1	TRUE	null	311.16525	C20H24O3
87	121	25.48	157.03886	ALLANTOIN	[M-H]-		0.333	TRUE	null	157.03671	C4H6N4O3
88	105	25.663	149.01062	(R,R)-TARTARIC ACID	[M-H]-		0.333	TRUE	null	149.009	C4H6O6
89	22	26.031	96.96125	Phosphoric acid	[M-H]-		1	TRUE	null	96.96962	H3O4P
90	275	26.155	191.01985	CITRATE	[M-H]-		0.833	TRUE	null	191.019	C6H8O7

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Now make the .csv file for Metaboanalyst

	A	B	C	D	E	F	G	H	I	J
1	Average Rt(r	Average Mz			Neg_C4	Neg_C5	Neg_C6	Neg_G4	Neg_G5	Neg_G6
2	6.506	191.02122			235848	53153	85784	123138	35588	56659
3	6.508	243.06226			19692	6511	16178	13515	7707	4292
4	7.368	243.06299			16732	3962	16253	9737	4639	2805
5	7.373	191.02129			92896	25257	44343	113153	5783	33098
6	7.76	129.02118			84099	35847	51680	58043	18988	27532
7	7.761	173.01138			213978	89710	150305	154546	50933	76814
8	8.241	173.01088			127133	26632	128326	42323	16503	19900
9	8.263	129.02121			44624	20650	43276	31488	18854	12860
10	8.809	283.06799			18749	6375	25046	20589	5816	4751
11	8.926	296.10205			34463	14379	51741	35751	13218	12828
12	9.83	310.11398			42950	17037	38915	41848	12340	13893
13	9.964	218.10304			63110	35459	4987	146302	26614	26211
14	10.066	131.03609			13679	5426	65176	41387	7318	5757
15	11.438	157.04041			73055	46932	137093	51498	26769	41104
16	11.452	160.04082			76374	44816	117040	42273	83257	42133
17	11.452	204.03236			349988	222678	540669	198630	414675	238475
18	11.453	181.05011			64747	39361	35054	46219	11776	32574
19	12.12	188.03555			175359	104729	276318	121653	217057	97967
20	12.12	144.04584			123917	64246	188987	86421	144416	60157
21	12.467	375.13495			50693	21724	47911	22717	34506	24888

Make the concatenated string in column C and copy (special) into column D

13

Added the concatenated string

	A	B	C	D	E	F	G	H	I	J
1	Average Rt(r	Average Mz	RT/MZ	RT/N	Neg_C4	Neg_C5	Neg_C6	Neg_G4	Neg_G5	Neg_G6
2	6.506	191.02122	6.51/191.02	6.51/191.02	235848	53153	85784	123138	35588	56659
3	6.508	243.06226	6.51/243.06	6.51/243.06	19692	6511	16178	13515	7707	4292
4	7.368	243.06299	7.37/243.06	7.37/243.06	16732	3962	16253	9737	4639	2805
5	7.373	191.02129	7.37/191.02	7.37/191.02	92896	25257	44343	113153	5783	33098
6	7.76	129.02118	7.76/129.02	7.76/129.02	84099	35847	51680	58043	18988	27532
7	7.761	173.01138	7.76/173.01	7.76/173.01	213978	89710	150305	154546	50933	76814
8	8.241	173.01088	8.24/173.01	8.24/173.01	127133	26632	128326	42323	16503	19900
9	8.263	129.02121	8.26/129.02	8.26/129.02	44624	20650	43276	31488	18854	12860
10	8.809	283.06799	8.81/283.06	8.81/283.06	18749	6375	25046	20589	5816	4751
11	8.926	296.10205	8.93/296.10	8.93/296.10	34463	14379	51741	35751	13218	12828
12	9.83	310.11398	9.83/310.11	9.83/310.11	42950	17037	38915	41848	12340	13893
13	9.964	218.10304	9.96/218.10	9.96/218.10	63110	35459	4987	146302	26614	26211
14	10.066	131.03609	10.07/131.03	10.07/131.03	13679	5426	65176	41387	7318	5757
15	11.438	157.04041	11.44/157.04	11.44/157.04	73055	46932	137093	51498	26769	41104
16	11.452	160.04082	11.45/160.04	11.45/160.04	76374	44816	117040	42273	83257	42133
17	11.452	204.03236	11.45/204.03	11.45/204.03	349988	222678	540669	198630	414675	238475
18	11.453	181.05011	11.45/181.05	11.45/181.05	64747	39361	35054	46219	11776	32574
19	12.12	188.03555	12.12/188.03	12.12/188.03	175359	104729	276318	121653	217057	97967
20	12.12	144.04584	12.12/144.04	12.12/144.04	123917	64246	188987	86421	144416	60157
21	12.467	375.13495	12.47/375.13	12.47/375.13	50693	21724	47911	22717	34506	24888
22	12.561	621.10785	12.56/621.11	12.56/621.11	1790	2116	1277	438935	43220	74094
23	12.586	367.10422	12.59/367.11	12.59/367.11	229088	204082	106350	147689	160699	141379

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Completed .csv file (added a line for groups)

RT/MZ	Neg_C4	Neg_C5	Neg_C6	Neg_G4	Neg_G5	Neg_G6
Group	1	1	1	2	2	2
6.51/191.02	235848	53153	85784	123138	35588	56659
6.51/243.06	19692	6511	16178	13515	7707	4292
7.37/243.06	16732	3962	16253	9737	4639	2805
7.37/191.02	92896	25257	44343	113153	5783	33098
7.76/129.02	84099	35847	51680	58043	18988	27532
7.76/173.01	213978	89710	150305	154546	50933	76814
8.24/173.01	127133	26632	128326	42323	16503	19900
8.26/129.02	44624	20650	43276	31488	18854	12860
8.81/283.06	18749	6375	25046	20589	5816	4751
8.93/296.10	34463	14379	51741	35751	13218	12828
9.83/310.11	42950	17037	38915	41848	12340	13893
9.96/218.10	63110	35459	4987	146302	26614	26211
10.07/131.0	13679	5426	65176	41387	7318	5757
11.44/157.0	73055	46932	137093	51498	26769	41104
11.45/160.0	76374	44816	117040	42273	83257	42133
11.45/204.0	349988	222678	540669	198630	414675	238475
11.45/181.0	64747	39361	35054	46219	11776	32574
12.12/188.0	175359	104729	276318	121653	217057	97967
12.12/144.0	123917	64246	188987	86421	144416	60157

Now save as a .csv file (no spaces in name!)

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Submit to Metaboanalyst

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Data Integrity Check:

1. Checking the class labels - at least three replicates are required in each class.
2. If the samples are paired, the pair labels must conform to the specified format.
3. The data (except class labels) must not contain non-numeric values.
4. The presence of missing values or features with constant values (i.e. all zeros).

Data processing information:

Checking data content ...passed.

Samples are in columns and features in rows.

The uploaded file is in comma separated values (.csv) format.

The uploaded data file contains 6 (samples) by 67 (peaks(mz/rt)) data matrix.

Samples are not paired.

2 groups were detected in samples.

Only English letters, numbers, underscore, hyphen and forward slash (/) are allowed.

Other special characters or punctuations (if any) will be stripped off.

All data values are numeric.

A total of 0 (0%) missing values were detected.

By default, missing values will be replaced by 1/5 of min positive values of their corresponding variables

Click the **Skip** button if you accept the default practice;

Or click the **Missing value imputation** to use other methods.

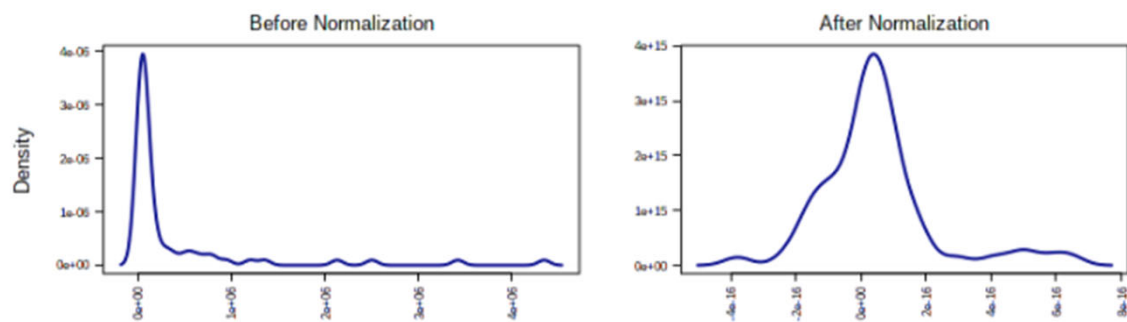
Edit Groups

Missing Values

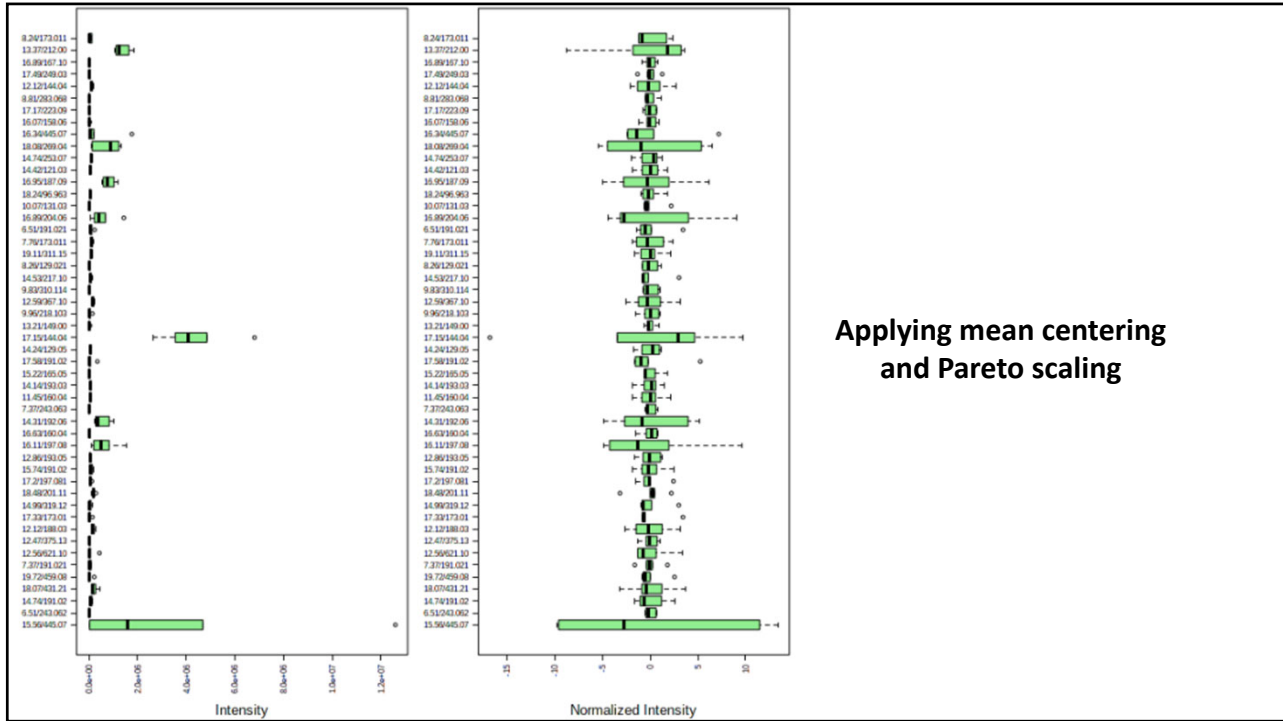
→ Proceed

17

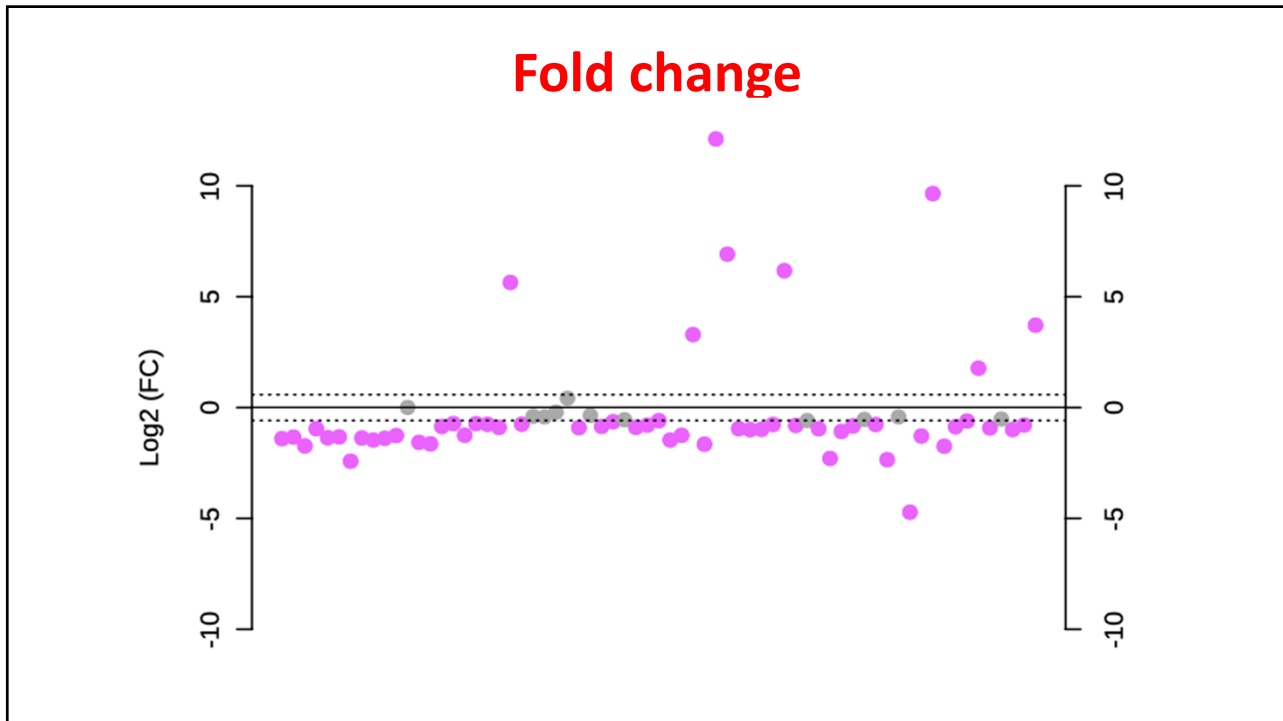
Normalizing the data



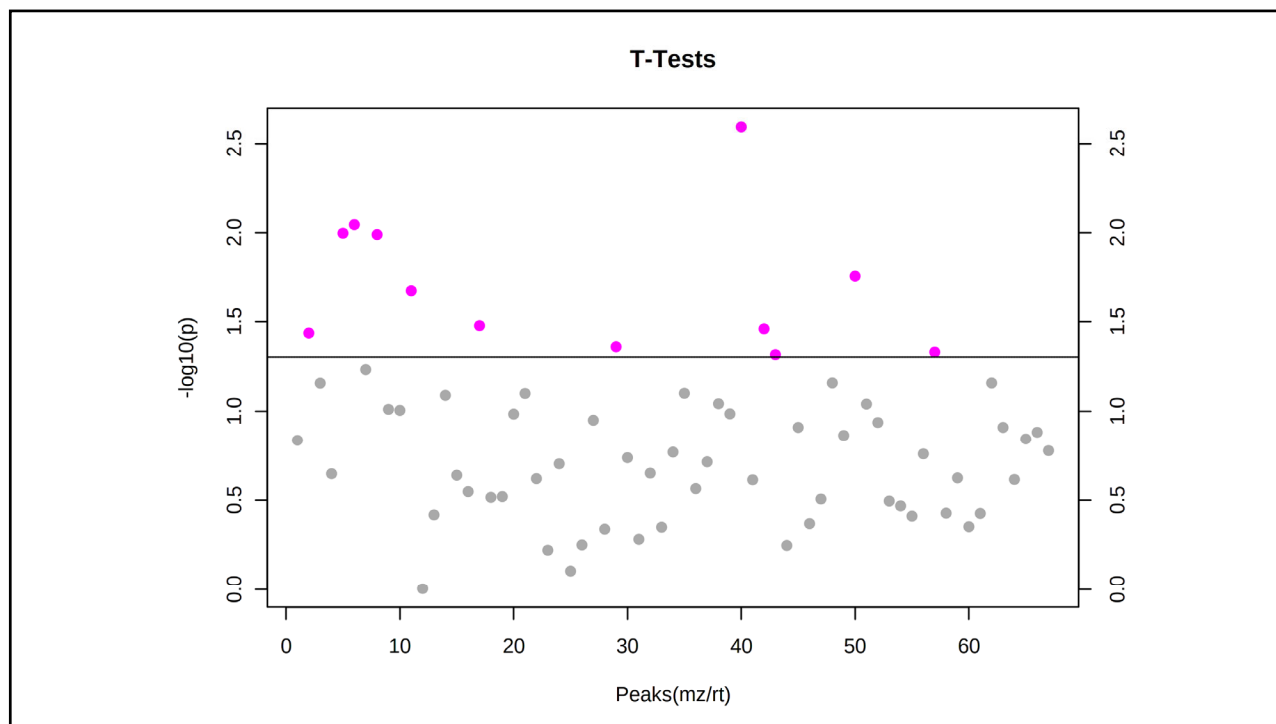
18



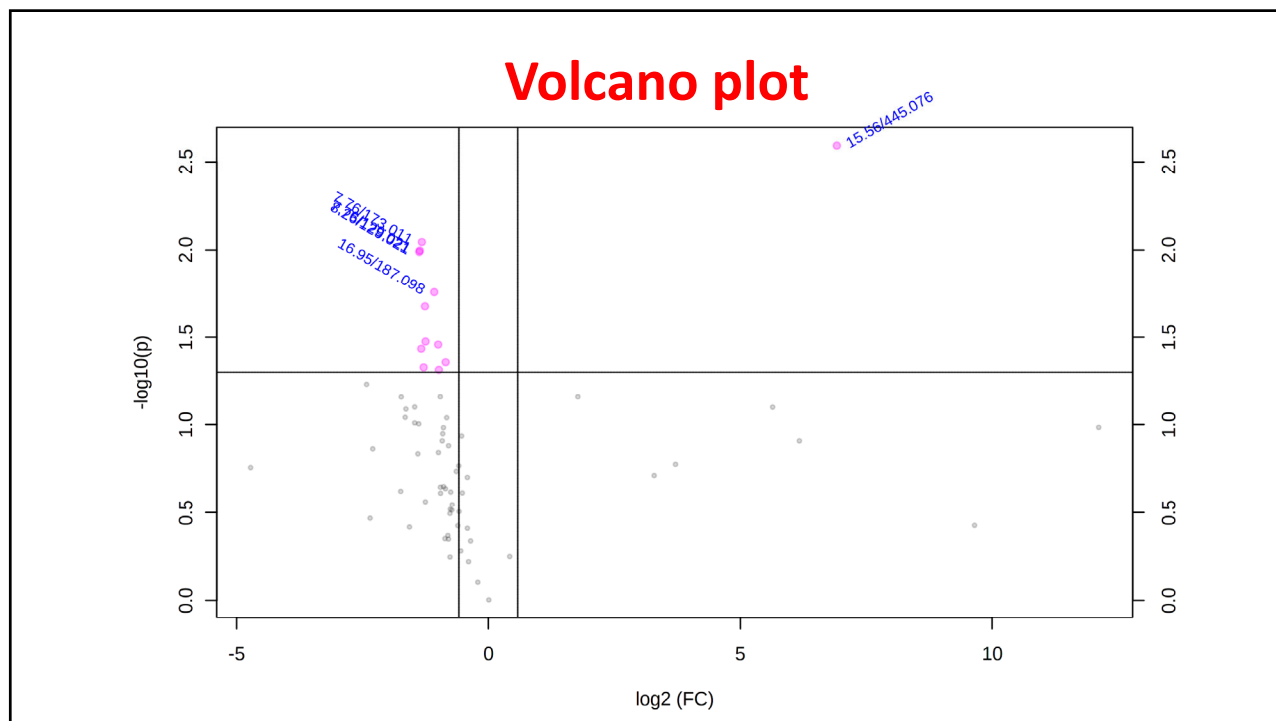
19



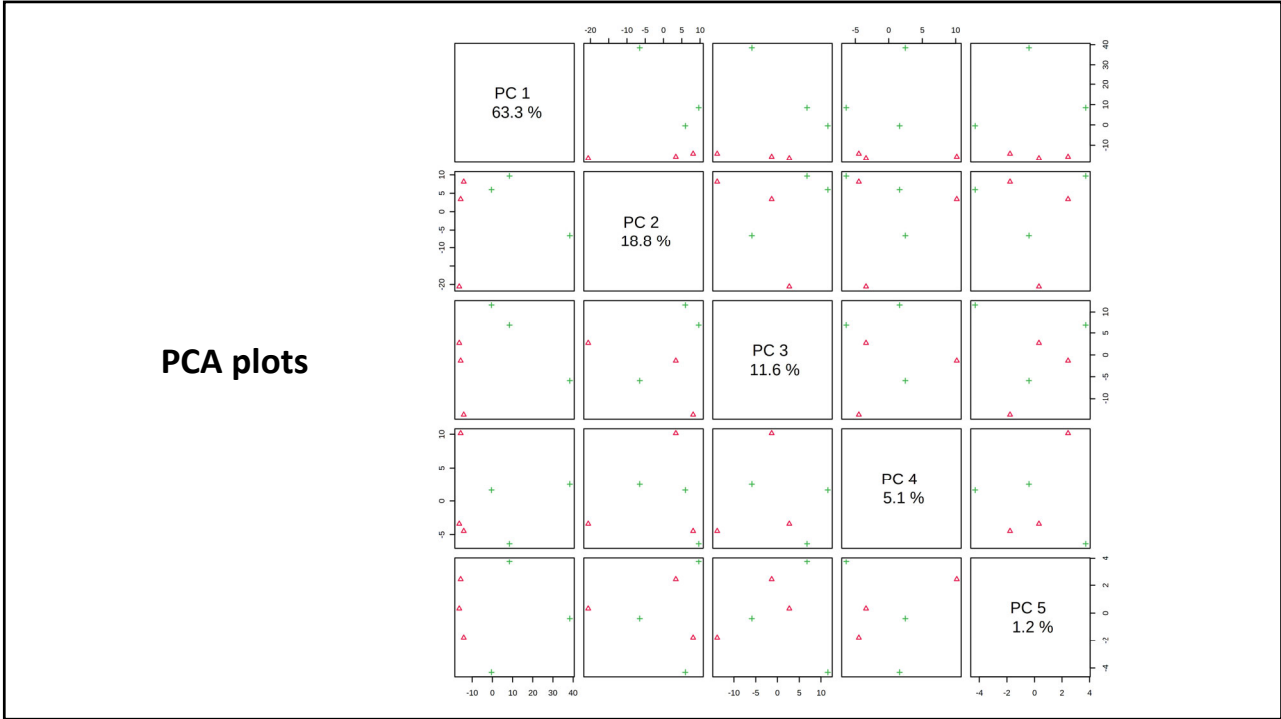
20



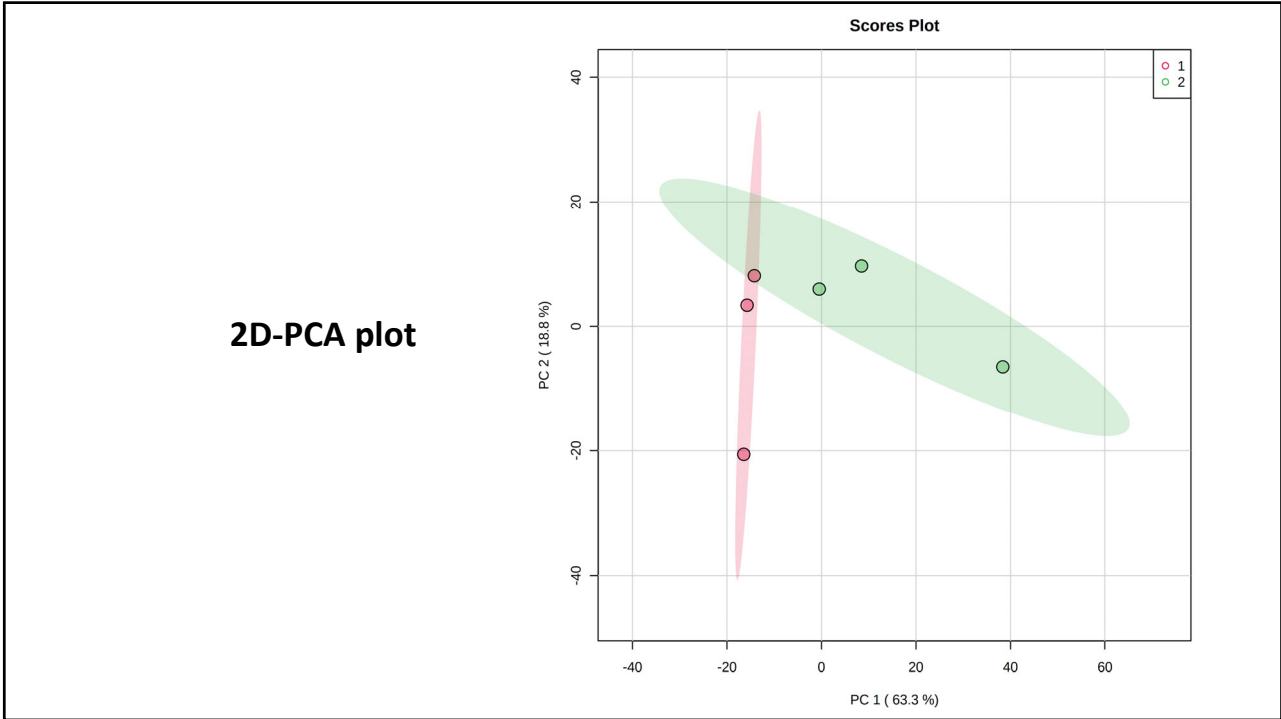
21



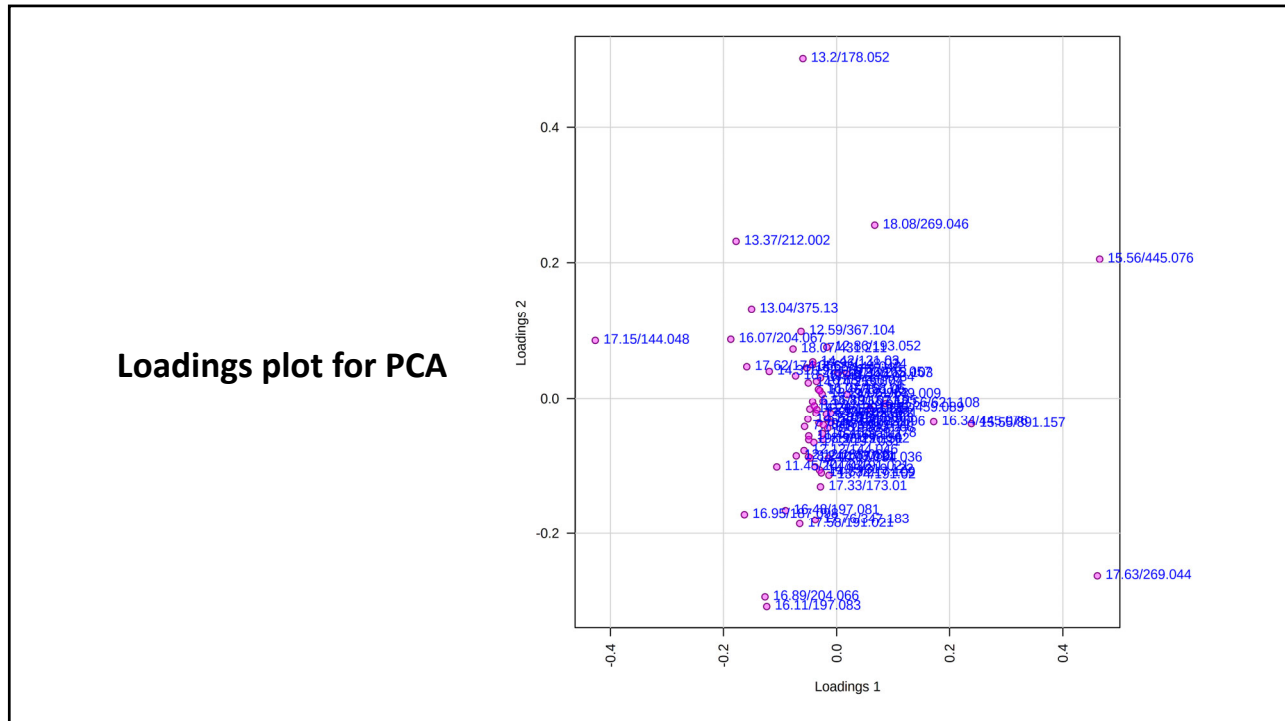
22



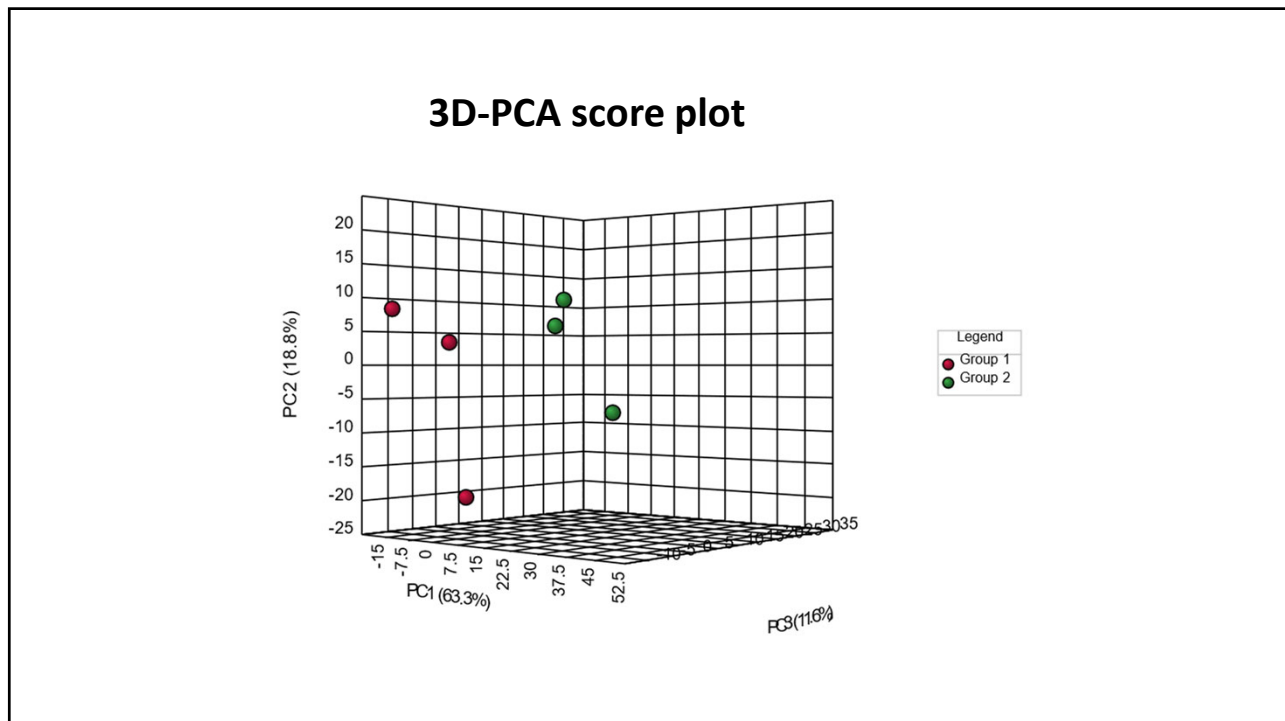
23



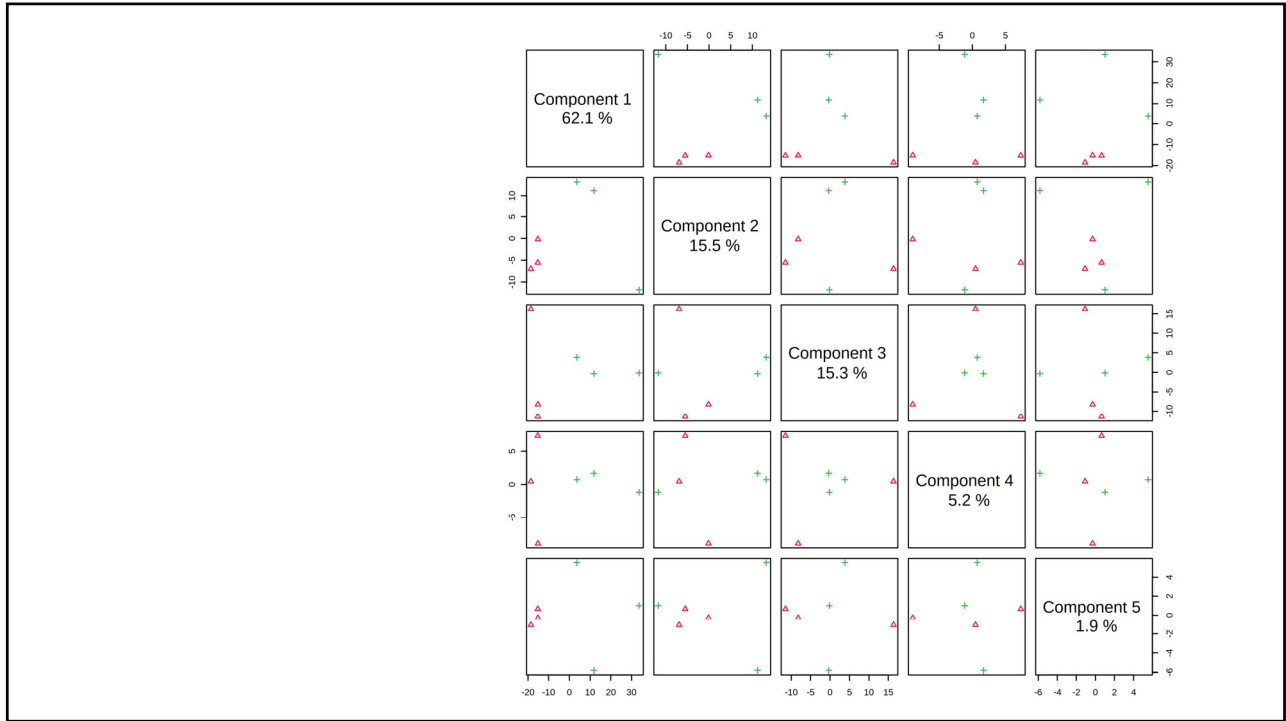
24



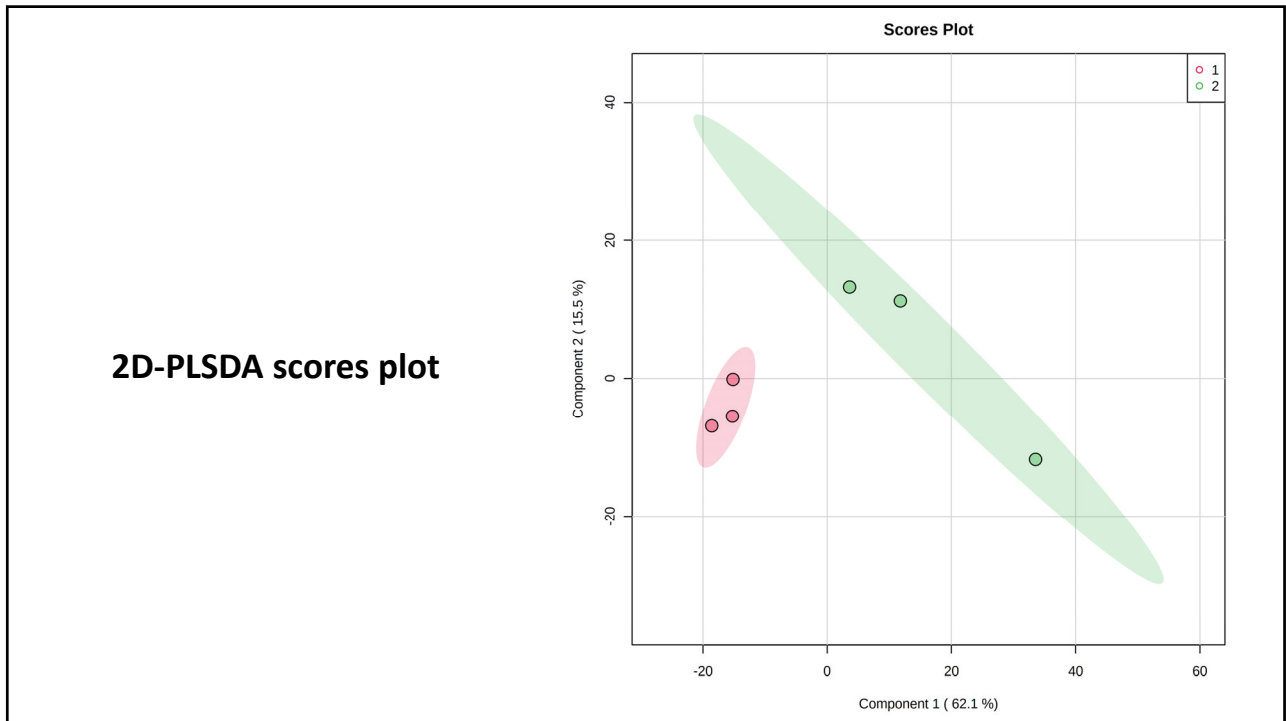
25



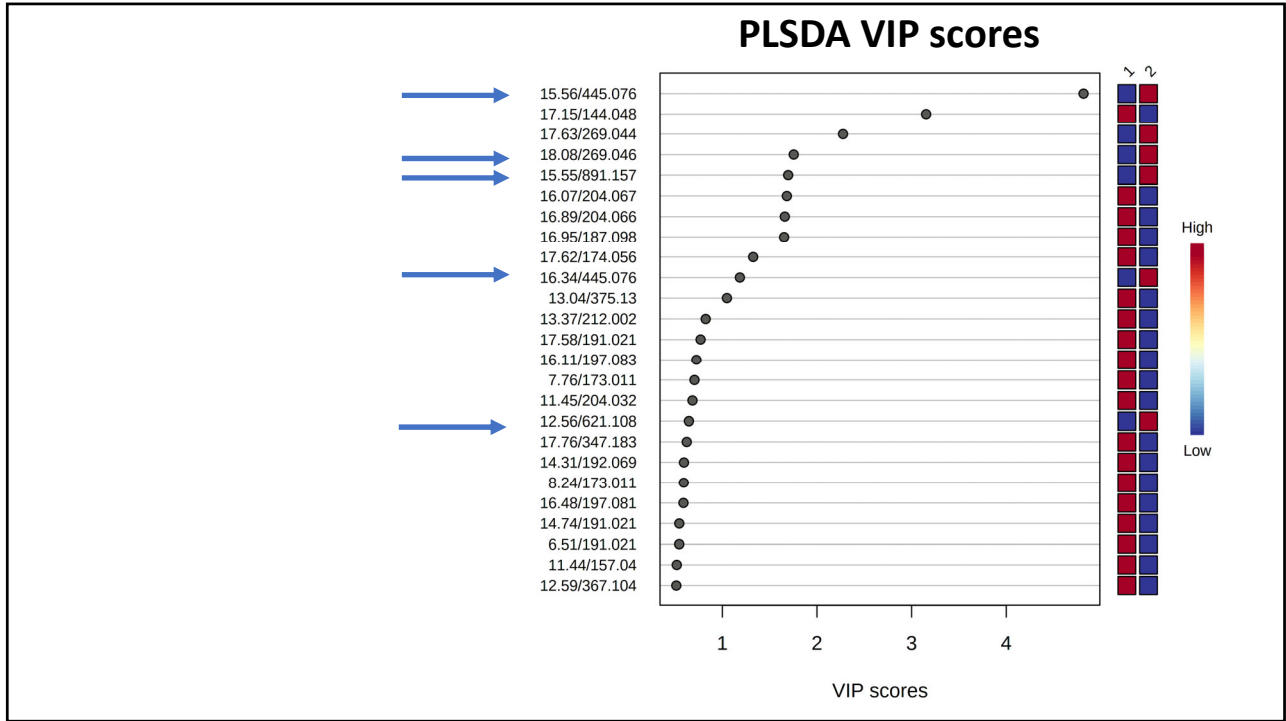
26



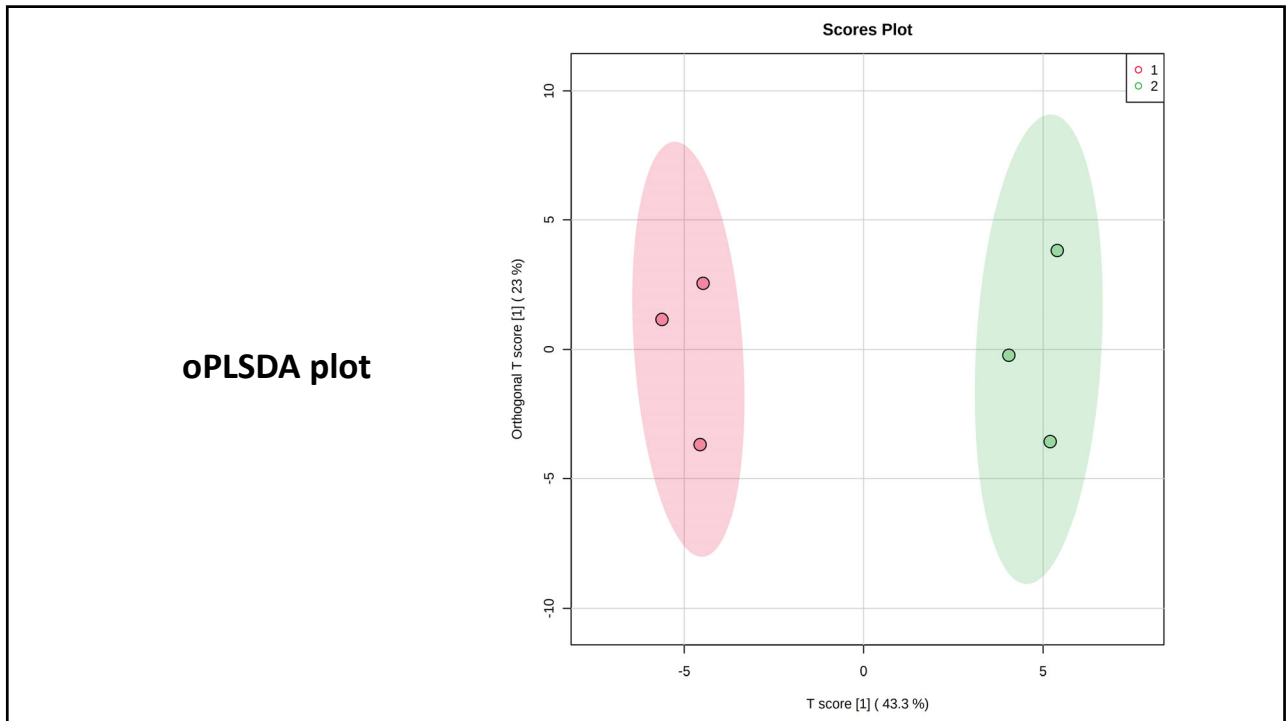
27



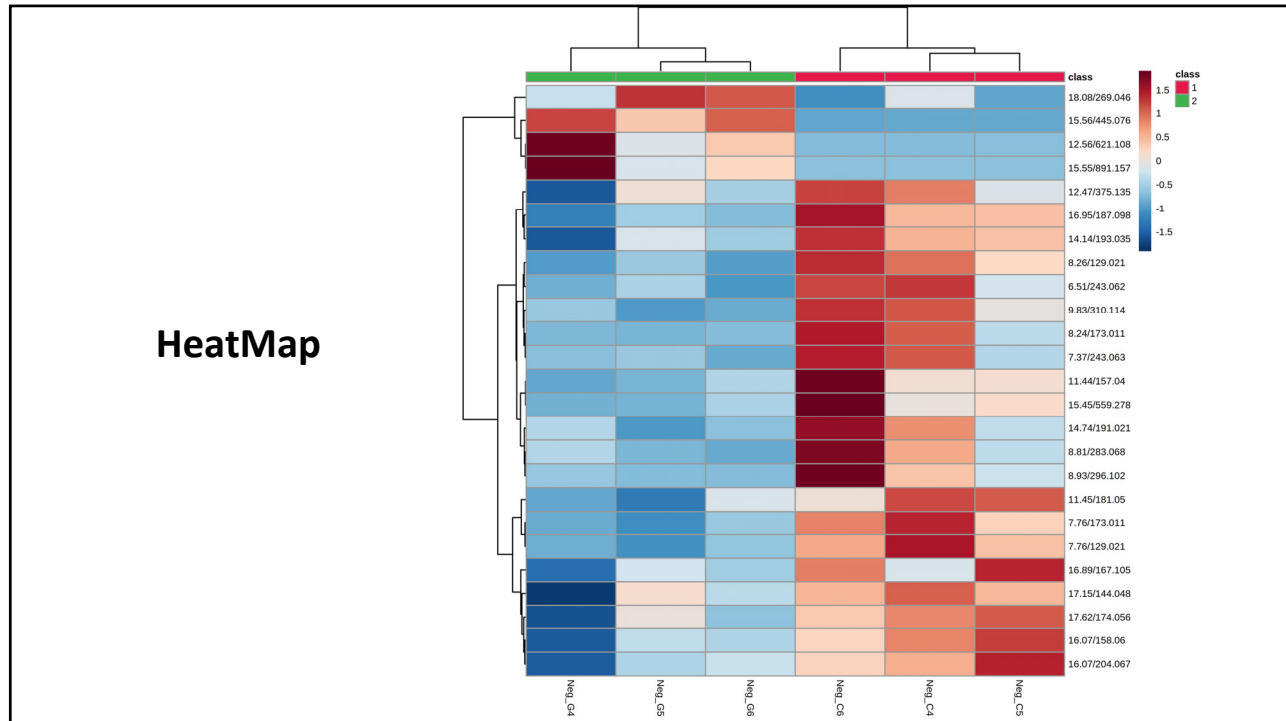
28



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30



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What did we get out of this experiment?

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