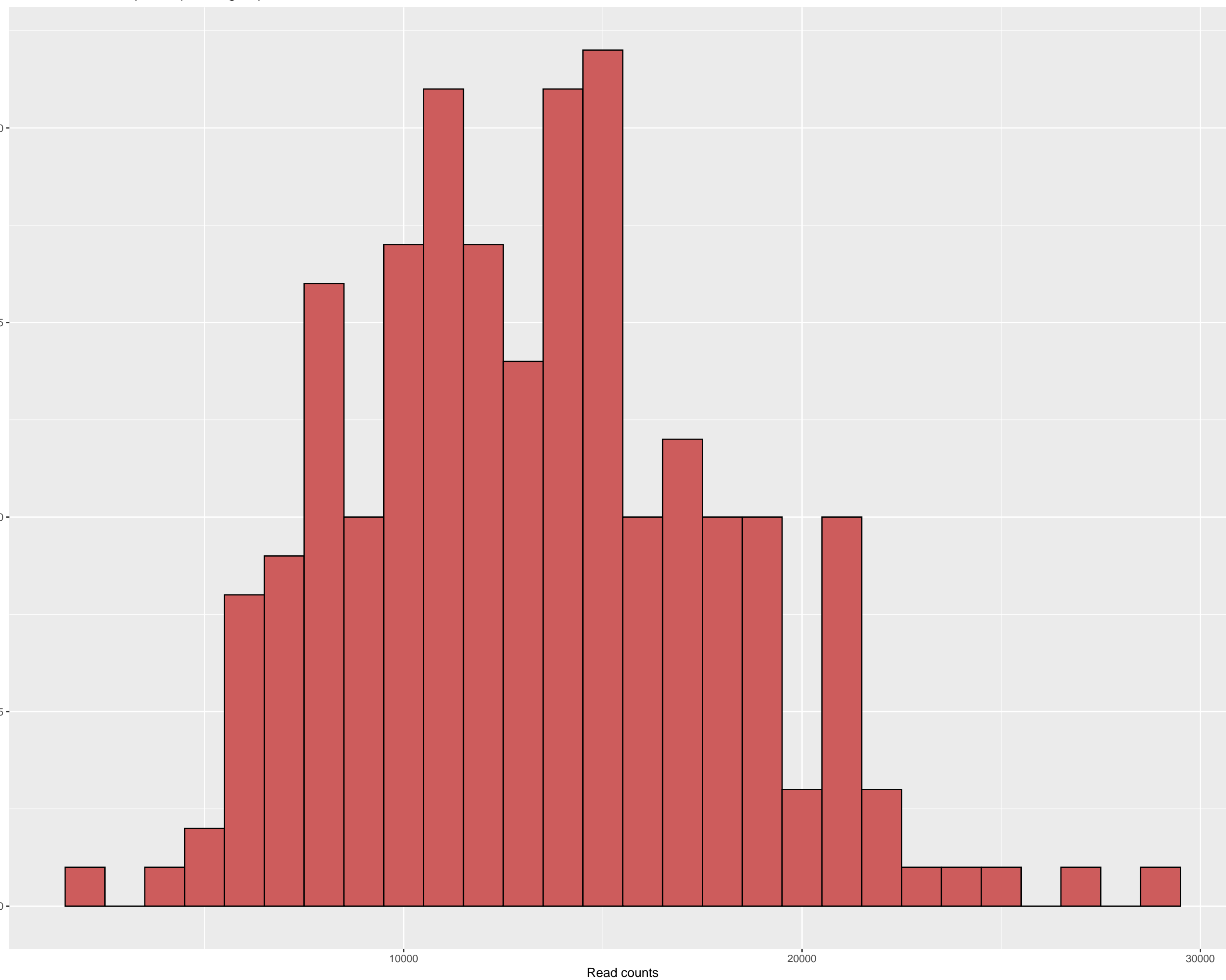
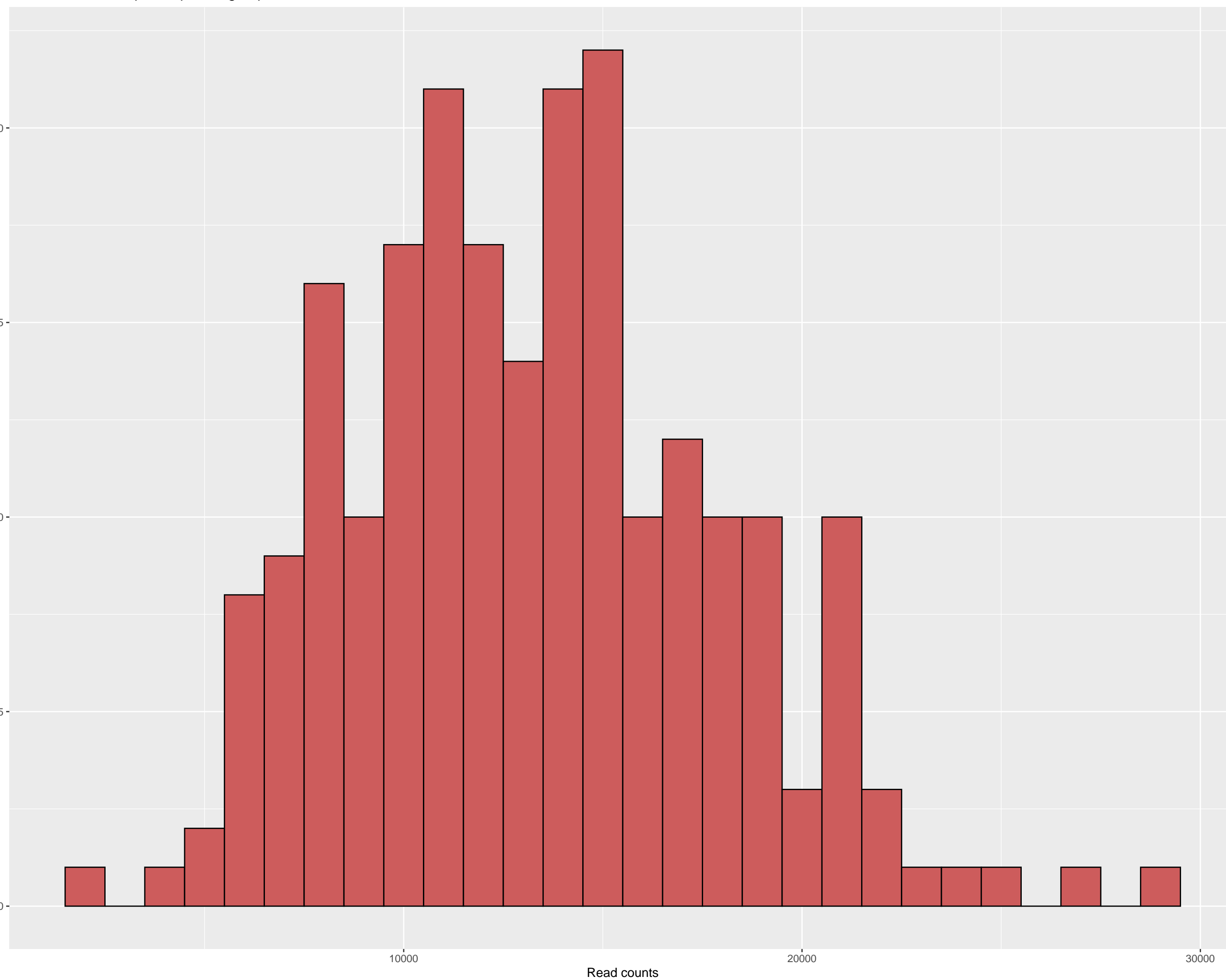


1.Explore your Data (Sequencing depths)

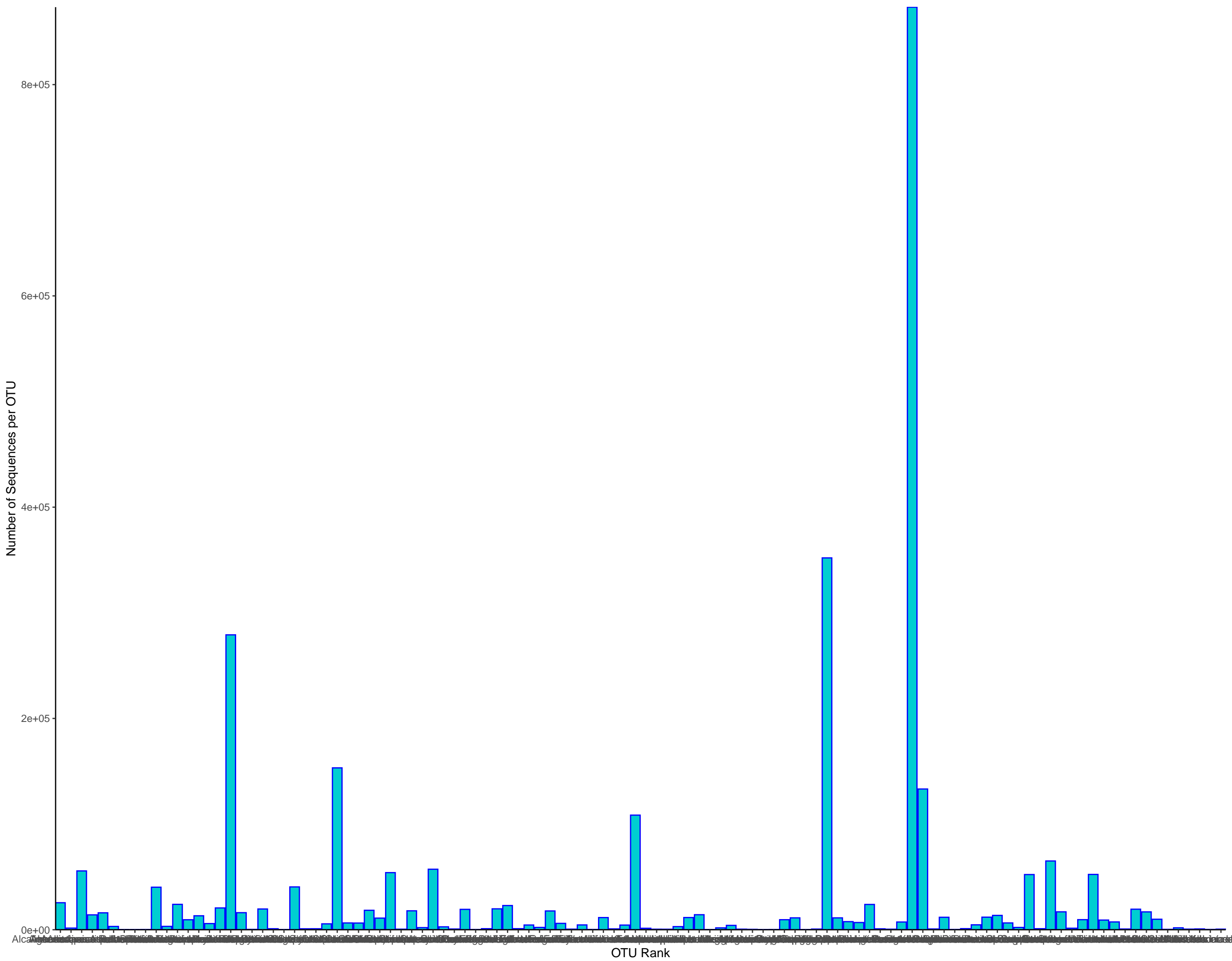
Distribution of sample sequencing depth



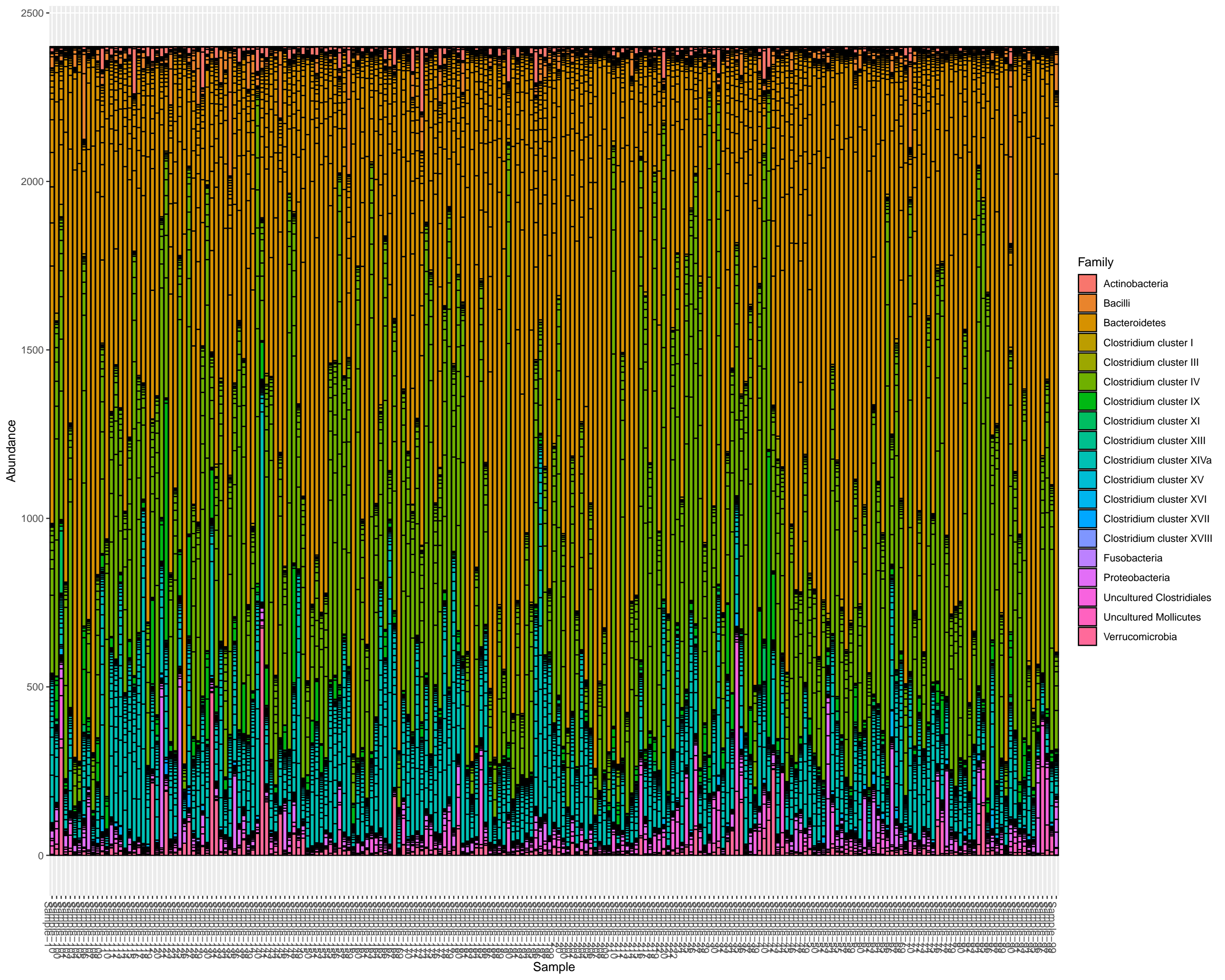
Distribution of sample sequencing depth

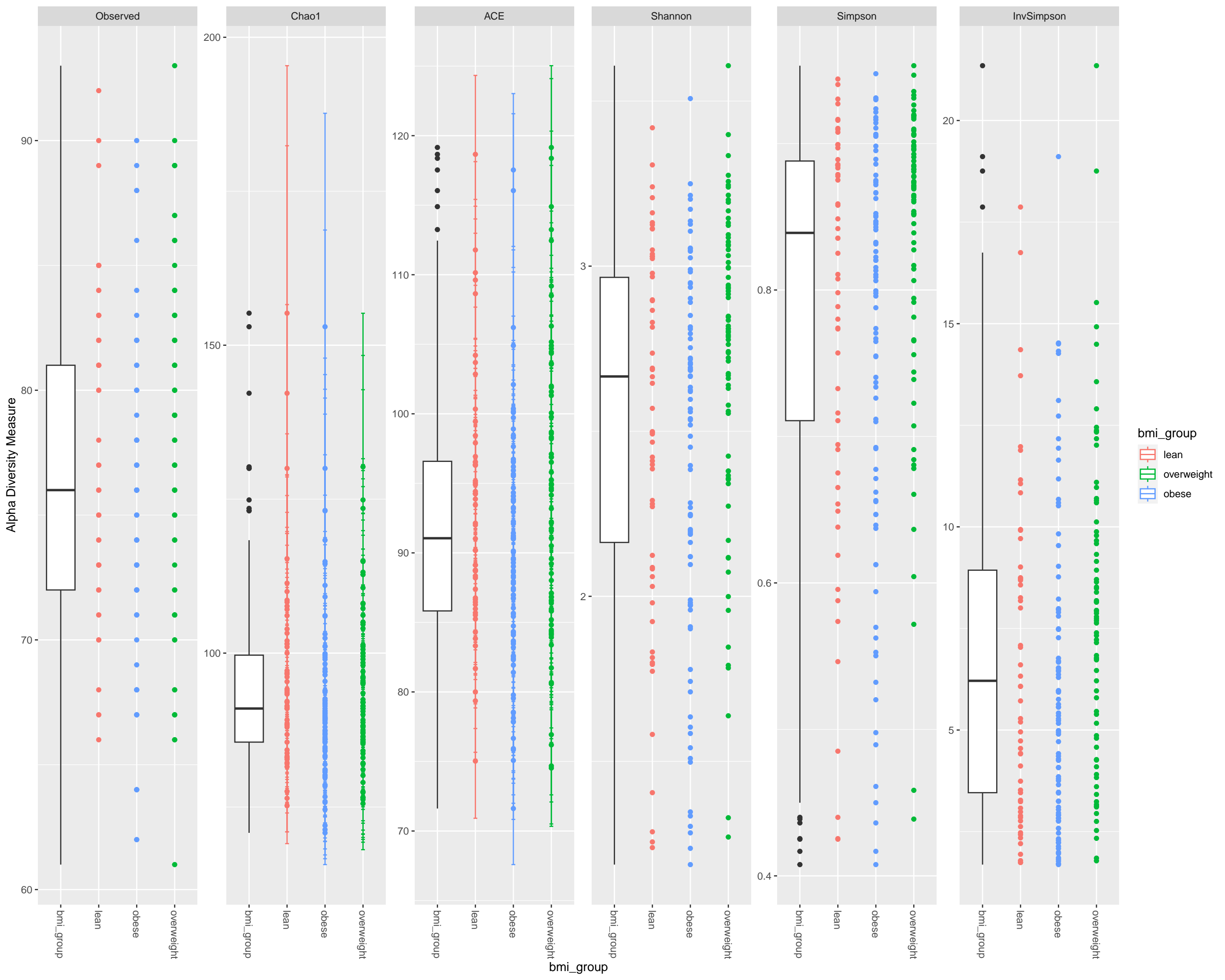


Rank Abundance Curve of the OTUs



## 2.Alpha diversity





**richness**



	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.1</i>	81	86.353	3.97	93.187	4.828	2.983	0.875	7.987	16.18
<i>Sample.2</i>	73	88	9.979	86.462	4.672	2.866	0.886	8.749	14.217
<i>Sample.3</i>	66	77.375	8.082	76.93	4.33	2.38	0.765	4.261	12.551
<i>Sample.4</i>	86	96.462	6.753	97.645	4.784	2.936	0.866	7.475	17.438
<i>Sample.5</i>	66	79	9.255	74.681	4.171	2.073	0.691	3.237	12.551
<i>Sample.6</i>	67	114.5	30.725	86.723	4.73	1.974	0.639	2.773	12.786
<i>Sample.7</i>	73	86	9.256	81.405	4.272	2.947	0.911	11.18	14.217
<i>Sample.8</i>	70	91.375	13.145	86.595	4.51	2.118	0.684	3.166	13.497
<i>Sample.9</i>	81	92.143	8.23	88.763	4.583	3.307	0.94	16.749	16.18
<i>Sample.10</i>	76	88.364	7.95	91.019	4.818	2.815	0.879	8.256	14.946
<i>Sample.11</i>	61	80.125	12.046	76.195	4.107	1.791	0.681	3.13	11.391
<i>Sample.12</i>	72	75.75	3.329	77.868	4.137	2.568	0.833	5.972	13.976
<i>Sample.13</i>	81	124.875	23.458	118.37	5.732	2.811	0.883	8.518	16.18
<i>Sample.14</i>	68	74.6	5.135	77.84	4.404	3.053	0.918	12.168	13.022
<i>Sample.15</i>	67	78.4	6.954	83.606	4.74	1.585	0.532	2.138	12.786
<i>Sample.16</i>	78	85.5	5.226	87.107	4.308	2.579	0.864	7.327	15.437
<i>Sample.17</i>	70	76.429	5.466	75.029	4.113	2.645	0.835	6.073	13.497
<i>Sample.18</i>	92	115.333	13.636	110.147	5.269	3.419	0.944	17.871	18.978
<i>Sample.19</i>	77	92	9.979	86.839	4.409	2.354	0.739	3.83	15.191
<i>Sample.20</i>	72	81.1	6.484	81.923	4.415	2.283	0.737	3.8	13.976
<i>Sample.21</i>	79	88.231	6.165	90.509	4.635	2.425	0.766	4.273	15.684
<i>Sample.22</i>	72	80.667	6.413	84.335	4.565	3.172	0.921	12.727	13.976
<i>Sample.23</i>	73	97.429	15.165	88.711	4.608	2.396	0.771	4.358	14.217
<i>Sample.24</i>	82	99	10.654	94.878	4.701	2.8	0.865	7.393	16.43
<i>Sample.25</i>	71	91	13.494	86.64	4.67	2.978	0.897	9.711	13.736
<i>Sample.26</i>	83	96.6	8.745	96.302	4.898	3.161	0.916	11.884	16.68
<i>Sample.27</i>	72	85.6	8.745	85.195	4.418	2.63	0.845	6.465	13.976
<i>Sample.28</i>	73	130	38.701	88.353	4.638	2.269	0.726	3.652	14.217
<i>Sample.29</i>	76	93.5	10.106	94.917	4.88	1.958	0.637	2.752	14.946
<i>Sample.30</i>	76	84.75	6.04	91.423	4.885	3.214	0.93	14.268	14.946

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
Sample.31	64	71.333	5.675	71.618	4.032	1.959	0.656	2.909	12.084
Sample.32	84	105	11.892	109.188	5.388	3.167	0.919	12.332	16.932
Sample.33	71	88.143	11.464	84.206	4.586	2.786	0.874	7.927	13.736
Sample.34	84	91	5.056	93.183	4.668	3.275	0.931	14.494	16.932
Sample.35	82	92	6.656	94.417	4.82	3.03	0.889	9.012	16.43
Sample.36	78	91.909	8.684	91.043	4.539	2.902	0.895	9.539	15.437
Sample.37	75	82	5.056	86.388	4.713	2.819	0.877	8.145	14.702
Sample.38	71	81.929	6.852	82.598	4.258	2.12	0.712	3.47	13.736
Sample.39	84	130	26.596	109.619	5.31	3.125	0.916	11.974	16.932
Sample.40	81	106.091	13.658	98.906	4.617	2.246	0.788	4.715	16.18
Sample.41	83	104	11.892	104.904	5.3	3.087	0.926	13.572	16.68
Sample.42	86	113.143	16.502	101.321	4.901	2.994	0.896	9.587	17.438
Sample.43	79	98.429	12.647	92.229	4.756	3.032	0.906	10.593	15.684
Sample.44	76	89.154	7.993	93.451	4.825	2.03	0.638	2.763	14.946
Sample.45	75	84.1	6.484	84.743	4.418	2.78	0.851	6.699	14.702
Sample.46	67	82.111	9.732	84.444	4.641	2.341	0.781	4.576	12.786
Sample.47	77	89.214	7.434	93.269	4.592	2.89	0.889	9.03	15.191
Sample.48	73	82.75	7.2	81.683	4.313	2.895	0.885	8.709	14.217
Sample.49	76	89.6	8.745	90.049	4.72	2.753	0.85	6.669	14.946
Sample.50	81	108.273	14.582	102.854	4.816	1.831	0.596	2.473	16.18
Sample.51	82	103.231	11.472	103.687	4.896	2.124	0.694	3.273	16.43
Sample.52	78	85.65	4.92	93.697	4.668	1.981	0.662	2.958	15.437
Sample.53	84	96.75	7.963	96.931	4.751	2.898	0.878	8.181	16.932
Sample.54	73	101.5	17.932	90.184	4.81	2.499	0.798	4.954	14.217
Sample.55	82	91.714	6.29	93.801	4.633	2.096	0.671	3.042	16.43
Sample.57	74	83.067	5.894	88.702	4.663	1.815	0.588	2.426	14.459
Sample.58	76	107.625	17.963	94.902	4.691	1.799	0.619	2.624	14.946
Sample.59	89	99.909	7.245	98.447	4.698	2.704	0.813	5.355	18.204
Sample.60	77	87.2	6.415	92.142	4.685	2.273	0.756	4.096	15.191
Sample.61	74	89.833	9.367	91.237	4.635	1.742	0.594	2.463	14.459

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.62</i>	85	91.067	4.437	93.872	4.556	2.687	0.859	7.082	17.184
<i>Sample.63</i>	83	91	5.39	95.173	4.787	2.497	0.789	4.732	16.68
<i>Sample.64</i>	81	92.143	8.23	87.392	4.365	2.29	0.733	3.741	16.18
<i>Sample.65</i>	84	103.091	11.049	100.364	4.73	2.188	0.734	3.755	16.932
<i>Sample.66</i>	80	86.5	4.881	86.821	4.367	2.713	0.832	5.964	15.931
<i>Sample.67</i>	82	89.5	5.226	92.092	4.604	2.718	0.847	6.53	16.43
<i>Sample.68</i>	89	112.75	14.287	104.691	4.972	3.095	0.896	9.66	18.204
<i>Sample.69</i>	74	83.231	6.165	85.693	4.379	1.773	0.574	2.346	14.459
<i>Sample.70</i>	84	105	11.892	103.568	5.05	2.669	0.827	5.793	16.932
<i>Sample.71</i>	82	101.091	11.049	99.724	4.916	2.452	0.774	4.419	16.43
<i>Sample.72</i>	76	89.6	8.745	88.239	4.471	1.973	0.612	2.58	14.946
<i>Sample.73</i>	78	86.75	6.04	91.158	4.876	2.796	0.878	8.223	15.437
<i>Sample.74</i>	68	77.545	6.566	80.006	4.345	2.28	0.773	4.413	13.022
<i>Sample.75</i>	85	93.571	5.748	96.532	4.799	2.968	0.886	8.734	17.184
<i>Sample.76</i>	83	106	12.761	102.101	4.924	2.485	0.832	5.963	16.68
<i>Sample.77</i>	74	104.667	16.94	97.104	4.825	2.116	0.723	3.606	14.459
<i>Sample.78</i>	76	97	12.2	94.67	4.804	2.195	0.755	4.081	14.946
<i>Sample.79</i>	72	82.2	6.415	85.532	4.316	1.794	0.649	2.849	13.976
<i>Sample.80</i>	80	91.333	7.298	94.272	4.803	2.691	0.858	7.036	15.931
<i>Sample.81</i>	77	90.636	7.259	106.204	5.582	1.509	0.52	2.084	15.191
<i>Sample.82</i>	73	96.75	14.286	88.754	4.57	2.06	0.711	3.458	14.217
<i>Sample.83</i>	80	93.333	8.848	92.004	4.742	2.569	0.78	4.548	15.931
<i>Sample.84</i>	83	95.364	7.95	95.035	4.702	2.665	0.842	6.326	16.68
<i>Sample.85</i>	76	101.091	13.658	100.173	5.106	1.902	0.692	3.252	14.946
<i>Sample.86</i>	78	102.429	15.165	94.074	4.856	2.596	0.815	5.417	15.437
<i>Sample.87</i>	77	96.125	12.047	90.183	4.552	2.422	0.835	6.076	15.191
<i>Sample.88</i>	73	76.667	3.145	79.547	4.115	1.974	0.647	2.831	14.217
<i>Sample.89</i>	67	84.273	10.233	84.314	4.432	1.256	0.425	1.739	12.786
<i>Sample.90</i>	81	94.154	7.993	96.537	4.797	2.41	0.774	4.425	16.18
<i>Sample.91</i>	77	111.364	17.515	108.638	5.371	1.924	0.691	3.237	15.191

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.92</i>	81	123.167	24.737	100.091	4.824	2.384	0.809	5.231	16.18
<i>Sample.93</i>	80	91.4	6.955	94.326	4.506	1.778	0.57	2.324	15.931
<i>Sample.94</i>	72	142.2	40.189	97.906	4.781	1.405	0.485	1.942	13.976
<i>Sample.95</i>	71	90.25	10.868	92.243	5.016	1.635	0.562	2.285	13.736
<i>Sample.96</i>	70	97.143	16.501	89.12	4.672	2.399	0.808	5.197	13.497
<i>Sample.97</i>	73	101.5	17.932	89.122	4.684	2.492	0.825	5.717	14.217
<i>Sample.98</i>	72	93.857	13.88	85.66	4.468	2.244	0.765	4.252	13.976
<i>Sample.99</i>	77	87.462	6.752	88.614	4.372	1.989	0.637	2.757	15.191
<i>Sample.100</i>	90	107.1	10.41	104.206	5.03	3.24	0.93	14.36	18.461
<i>Sample.101</i>	74	101.083	14.157	101.995	5.113	1.846	0.66	2.945	14.459
<i>Sample.102</i>	82	101	11.29	98.434	4.83	2.467	0.811	5.282	16.43
<i>Sample.103</i>	68	75.556	4.982	80.676	4.04	1.329	0.458	1.846	13.022
<i>Sample.104</i>	72	103.909	16.51	100.341	5.016	1.287	0.44	1.786	13.976
<i>Sample.105</i>	78	89.143	8.23	85.812	4.493	3.074	0.92	12.45	15.437
<i>Sample.106</i>	73	90.1	10.41	87.462	4.422	1.972	0.647	2.83	14.217
<i>Sample.107</i>	71	82.053	6.448	88.346	4.491	1.239	0.425	1.74	13.736
<i>Sample.108</i>	72	81.545	6.566	83.317	4.467	2.386	0.757	4.115	13.976
<i>Sample.109</i>	89	123.5	19.274	113.247	5.153	3.398	0.947	18.756	18.204
<i>Sample.110</i>	81	107.25	15.47	104.349	5.222	2.847	0.86	7.151	16.18
<i>Sample.111</i>	79	106.143	16.501	101.588	5.074	3.145	0.919	12.374	15.684
<i>Sample.112</i>	77	83	4.699	88.704	4.777	3.036	0.875	8.004	15.191
<i>Sample.113</i>	68	88	13.494	85.433	4.743	2.538	0.796	4.899	13.022
<i>Sample.114</i>	73	84.143	8.23	83.927	4.613	2.915	0.871	7.737	14.217
<i>Sample.115</i>	76	99.333	13.635	96.583	4.84	2.816	0.874	7.958	14.946
<i>Sample.116</i>	78	108.6	20.008	94.235	4.87	3.132	0.91	11.157	15.437
<i>Sample.117</i>	76	88	7.96	91.591	4.886	3.05	0.909	10.97	14.946
<i>Sample.118</i>	67	91.429	15.164	83.837	4.491	1.98	0.654	2.889	12.786
<i>Sample.119</i>	76	82	4.699	84.328	4.544	3.065	0.917	12.01	14.946
<i>Sample.120</i>	82	92.462	6.752	94.938	4.746	2.722	0.862	7.221	16.43
<i>Sample.121</i>	81	90.545	6.566	91.744	4.705	2.846	0.873	7.874	16.18

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.122</i>	82	86.789	3.605	92.139	4.631	2.736	0.849	6.604	16.43
<i>Sample.123</i>	75	85.5	7.206	85.611	4.518	2.536	0.82	5.565	14.702
<i>Sample.124</i>	82	90	5.249	96.894	4.926	2.639	0.852	6.756	16.43
<i>Sample.125</i>	64	83.125	12.046	78.506	4.177	1.541	0.55	2.223	12.084
<i>Sample.126</i>	85	155.2	40.191	118.658	5.675	3.029	0.899	9.915	17.184
<i>Sample.127</i>	78	87.429	7.256	86.034	4.578	3.137	0.916	11.935	15.437
<i>Sample.128</i>	79	86	5.056	88.018	4.465	2.905	0.898	9.786	15.684
<i>Sample.129</i>	75	110	25.609	86.282	4.569	3.113	0.908	10.838	14.702
<i>Sample.130</i>	78	101.333	13.635	98.313	4.995	2.933	0.907	10.698	15.437
<i>Sample.131</i>	75	86.375	8.083	85.827	4.606	2.803	0.852	6.777	14.702
<i>Sample.132</i>	79	96.1	10.41	100.057	5.148	2.936	0.882	8.487	15.684
<i>Sample.133</i>	76	85.545	6.566	85.977	4.406	2.272	0.716	3.521	14.946
<i>Sample.134</i>	82	99	10.654	96.194	4.835	2.99	0.906	10.591	16.43
<i>Sample.135</i>	86	92	4.535	94.513	4.803	3.131	0.906	10.647	17.438
<i>Sample.136</i>	74	86	7.959	86.962	4.624	2.721	0.845	6.446	14.459
<i>Sample.137</i>	81	106.091	13.658	111.781	6.351	2.83	0.883	8.57	16.18
<i>Sample.138</i>	90	115	13.299	114.897	5.431	2.66	0.806	5.166	18.461
<i>Sample.139</i>	85	102	10.992	99.446	5.093	3.023	0.885	8.686	17.184
<i>Sample.140</i>	81	95.25	8.653	96.879	5.117	2.675	0.851	6.726	16.18
<i>Sample.141</i>	87	108	11.892	106.308	5.088	2.836	0.869	7.633	17.692
<i>Sample.142</i>	76	83	5.056	85.963	4.526	2.791	0.888	8.934	14.946
<i>Sample.143</i>	75	88.6	8.745	88.201	4.598	2.087	0.665	2.986	14.702
<i>Sample.144</i>	74	84.462	6.752	89.53	4.804	2.693	0.873	7.897	14.459
<i>Sample.145</i>	76	88.75	7.963	89.569	4.528	2.357	0.744	3.906	14.946
<i>Sample.146</i>	72	78.6	5.135	79.783	4.345	2.633	0.846	6.477	13.976
<i>Sample.147</i>	89	93.875	3.768	96.364	4.723	3.114	0.899	9.935	18.204
<i>Sample.148</i>	76	89.333	8.848	90.138	4.776	3.045	0.905	10.518	14.946
<i>Sample.149</i>	76	91	8.655	99.764	5.081	2.738	0.87	7.69	14.946
<i>Sample.150</i>	69	90.375	13.145	91.053	4.956	2.199	0.71	3.449	13.259
<i>Sample.151</i>	76	95.429	12.647	91.08	4.86	2.666	0.82	5.562	14.946

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.152</i>	74	89.3	9.562	89.022	4.623	2.12	0.678	3.101	14.459
<i>Sample.153</i>	68	70.812	2.607	75.073	4.239	2.163	0.692	3.244	13.022
<i>Sample.154</i>	76	91	10.334	87.828	4.781	3.025	0.898	9.827	14.946
<i>Sample.155</i>	74	87	9.256	86.74	4.687	3.047	0.906	10.678	14.459
<i>Sample.156</i>	76	83.333	5.675	82.393	4.351	2.95	0.886	8.769	14.946
<i>Sample.157</i>	79	96.143	11.465	95.797	4.874	3.257	0.919	12.346	15.684
<i>Sample.158</i>	71	76.6	5.345	74.527	4.192	3.201	0.936	15.52	13.736
<i>Sample.159</i>	71	85.882	8.21	94.654	4.955	1.638	0.572	2.335	13.736
<i>Sample.160</i>	73	86	9.256	83.465	4.442	2.81	0.867	7.492	14.217
<i>Sample.161</i>	64	87.333	13.634	84.251	4.483	1.711	0.612	2.581	12.084
<i>Sample.162</i>	80	97	10.654	92.941	4.637	2.624	0.843	6.365	15.931
<i>Sample.163</i>	76	90.615	8.645	95.529	4.832	2.567	0.81	5.276	14.946
<i>Sample.164</i>	87	100.6	8.745	101.914	5.102	3.335	0.923	12.905	17.692
<i>Sample.165</i>	80	110.6	20.009	95.227	4.928	2.943	0.885	8.705	15.931
<i>Sample.166</i>	70	87	10.654	86.535	4.707	2.741	0.884	8.643	13.497
<i>Sample.167</i>	77	88.667	8	87.95	4.528	3.203	0.931	14.502	15.191
<i>Sample.168</i>	68	79.769	7.361	82.539	4.239	1.284	0.436	1.773	13.022
<i>Sample.169</i>	73	80.8	5.793	83.201	4.585	3.106	0.924	13.11	14.217
<i>Sample.170</i>	76	86.909	7.244	89.528	4.73	3.127	0.931	14.525	14.946
<i>Sample.171</i>	79	98	11.612	98.207	4.862	2.996	0.881	8.391	15.684
<i>Sample.172</i>	83	95	7.96	96.522	4.894	3.215	0.918	12.17	16.68
<i>Sample.173</i>	79	92.333	8.848	94.088	4.923	3.055	0.914	11.642	15.684
<i>Sample.174</i>	88	123.1	18.314	116.05	5.528	2.62	0.822	5.632	17.947
<i>Sample.175</i>	86	114.875	16.696	108.496	5.239	2.924	0.839	6.211	17.438
<i>Sample.176</i>	85	95.5	7.206	95.255	4.776	3.193	0.933	14.924	17.184
<i>Sample.177</i>	75	80	4.132	84.099	4.572	3.25	0.93	14.324	14.702
<i>Sample.178</i>	82	93.667	8	91.002	4.535	2.688	0.806	5.164	16.43
<i>Sample.179</i>	77	92	10.334	89.221	4.66	3.123	0.901	10.121	15.191
<i>Sample.180</i>	72	91.429	12.646	83.379	4.282	2.81	0.893	9.323	13.976
<i>Sample.181</i>	67	76.231	6.165	84.111	4.901	2.379	0.814	5.386	12.786

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.182</i>	67	86.091	11.048	83.665	4.253	1.237	0.417	1.715	12.786
<i>Sample.183</i>	67	80.2	10.216	75.927	4.341	2.559	0.826	5.756	12.786
<i>Sample.184</i>	90	153	34.661	117.532	5.495	2.851	0.862	7.271	18.461
<i>Sample.185</i>	82	97	9.979	94.962	4.862	3.011	0.878	8.185	16.43
<i>Sample.186</i>	83	130.25	24.937	119.152	5.88	2.561	0.817	5.458	16.68
<i>Sample.187</i>	70	118.333	24.514	104.903	5.294	1.188	0.408	1.688	13.497
<i>Sample.188</i>	82	109.143	16.502	96.524	4.785	2.684	0.831	5.932	16.43
<i>Sample.189</i>	77	100	12.761	104.454	5.346	2.169	0.707	3.416	15.191
<i>Sample.190</i>	76	92.235	8.756	98.297	5.12	1.498	0.498	1.991	14.946
<i>Sample.191</i>	80	93.909	8.684	95.662	4.925	2.707	0.847	6.524	15.931
<i>Sample.192</i>	72	81.1	6.484	81.73	4.316	2.366	0.792	4.798	13.976
<i>Sample.193</i>	74	99.667	14.701	93.849	4.752	2.202	0.74	3.852	14.459
<i>Sample.194</i>	77	88.667	8	87.804	4.577	2.668	0.841	6.293	15.191
<i>Sample.195</i>	93	99.5	4.723	103.623	5.061	3.607	0.953	21.349	19.237
<i>Sample.196</i>	88	92.583	3.821	95.584	4.941	3.508	0.948	19.112	17.947
<i>Sample.197</i>	89	108.091	11.049	112.452	5.407	3.245	0.899	9.88	18.204
<i>Sample.198</i>	76	89.333	8.848	87.34	4.544	2.534	0.799	4.987	14.946
<i>Sample.199</i>	83	100	10.992	98.688	5.009	3.062	0.891	9.15	16.68
<i>Sample.200</i>	62	75.909	8.683	78.543	4.332	1.604	0.553	2.235	11.621
<i>Sample.201</i>	75	82.091	5.293	88.524	4.85	2.966	0.877	8.156	14.702
<i>Sample.202</i>	72	85.6	8.745	86.979	4.664	2.248	0.754	4.073	13.976
<i>Sample.203</i>	82	95.909	8.684	105.166	5.299	3.239	0.91	11.097	16.43
<i>Sample.204</i>	71	84.125	9.009	82.314	4.437	2.19	0.767	4.288	13.736
<i>Sample.205</i>	80	92	7.96	94.154	4.932	2.848	0.854	6.834	15.931
<i>Sample.206</i>	62	81	11.611	76.663	4.062	1.303	0.461	1.855	11.621
<i>Sample.207</i>	66	75.231	6.165	79.358	4.2	1.582	0.546	2.204	12.551
<i>Sample.208</i>	68	85.273	10.233	87.089	4.696	1.783	0.604	2.527	13.022
<i>Sample.209</i>	72	114.857	23.947	95.927	4.769	1.347	0.45	1.818	13.976
<i>Sample.210</i>	67	76.5	5.856	84.825	4.791	1.271	0.439	1.782	12.786
<i>Sample.211</i>	77	89	7.96	89.296	4.633	2.685	0.852	6.767	15.191

	Observed	Chao1	se.chao1	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher
<i>Sample.212</i>	64	72	5.39	75.845	3.849	1.335	0.49	1.959	12.084
<i>Sample.213</i>	71	77.5	4.723	80.579	4.221	1.999	0.678	3.107	13.736
<i>Sample.214</i>	75	88.333	8.848	85.244	4.353	2.083	0.675	3.078	14.702
<i>Sample.215</i>	83	100	10.654	96.302	4.803	3.049	0.91	11.062	16.68
<i>Sample.216</i>	74	83.714	6.29	91.061	4.901	2.763	0.874	7.945	14.459
<i>Sample.217</i>	72	81	7.613	78.123	4.337	2.519	0.798	4.946	13.976
<i>Sample.218</i>	77	87.5	7.206	86.813	4.448	2.554	0.794	4.862	15.191
<i>Sample.219</i>	76	111	21.208	96.735	5.029	2.703	0.872	7.803	14.946
<i>Sample.220</i>	72	98.25	15.469	89.608	4.555	1.908	0.656	2.903	13.976
<i>Sample.221</i>	82	95.154	7.993	98.579	4.906	2.777	0.872	7.786	16.43
<i>Sample.222</i>	74	83.75	7.2	86.761	4.639	3.207	0.927	13.72	14.459



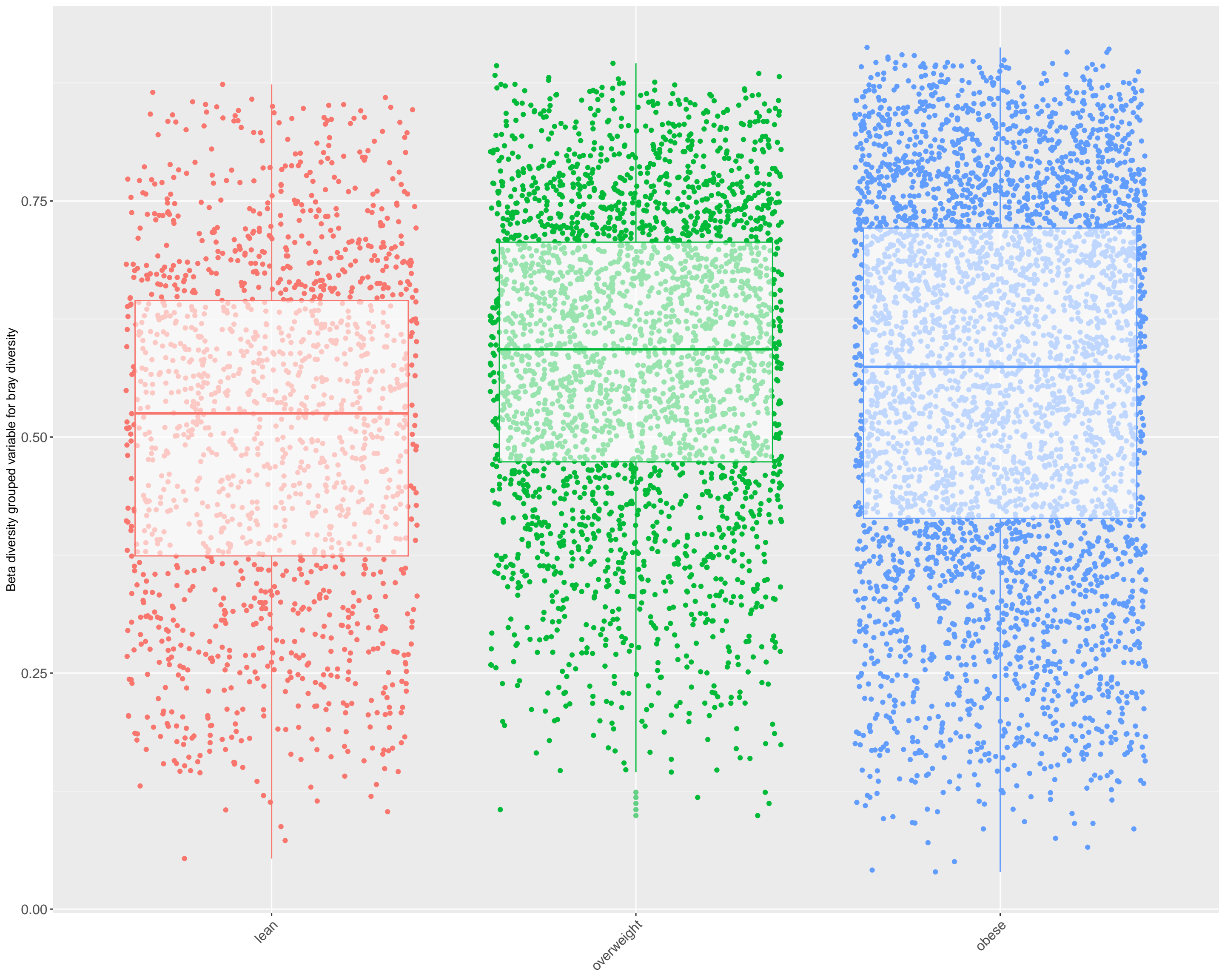
Test whether the observed number of OTUs differs significantly between the variable using Wilcoxon rank–sum test

	bmi_group_lean	bmi_group_overweight
bmi_group_overweight	0.647215274368327	NA
bmi_group_obese	0.0604640306081627	0.00647708901884598

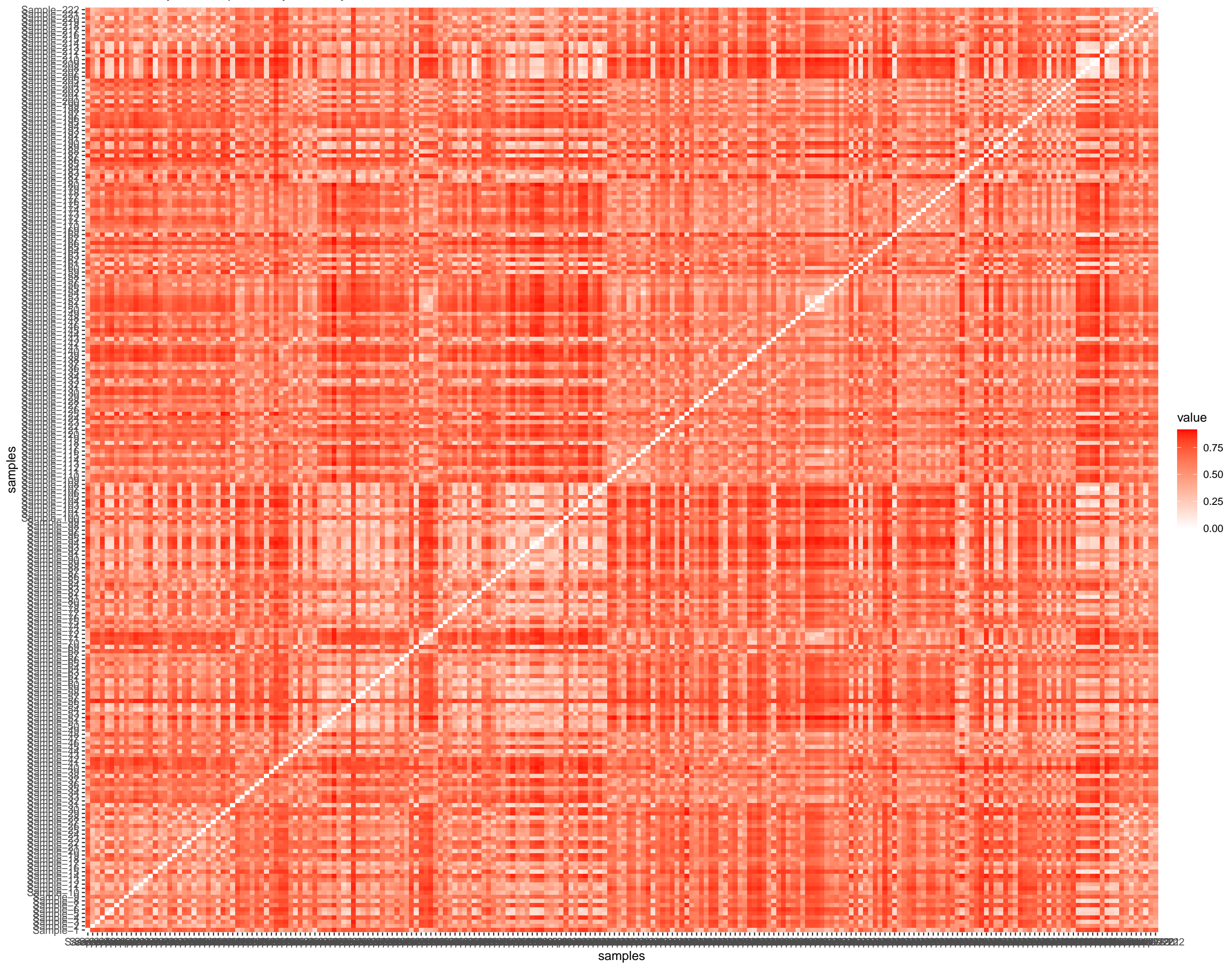
Test whether the Shannon indexes of OTUs differs significantly between the variable using Wilcoxon rank–sum test

	bmi_group_lean	bmi_group_overweight
<i>bmi_group_overweight</i>	0.070480417788966	NA
<i>bmi_group_obese</i>	0.379872175221919	0.000526948234327374

### 3.Beta diversity

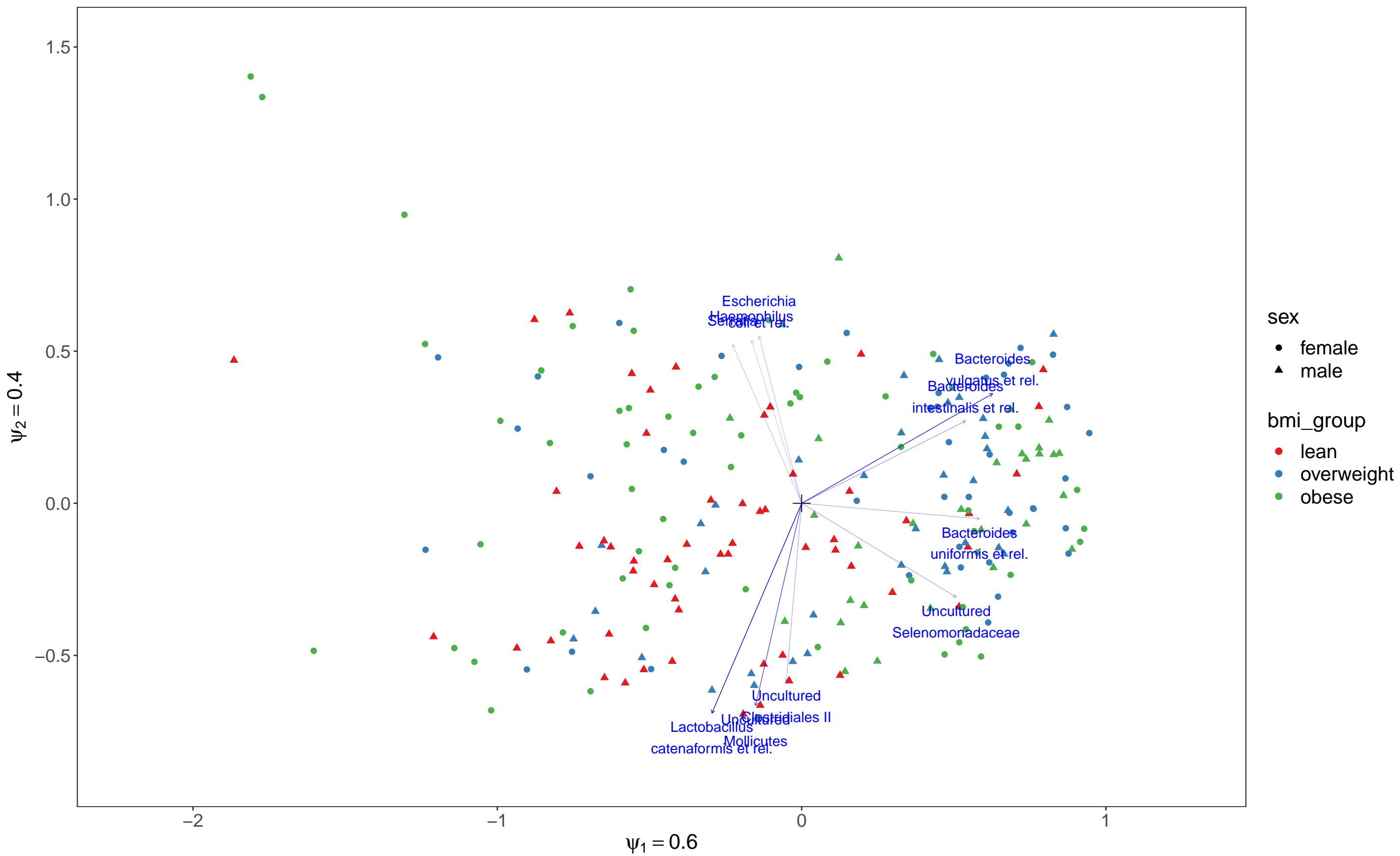


Beta diversity heatmap for bray diversity

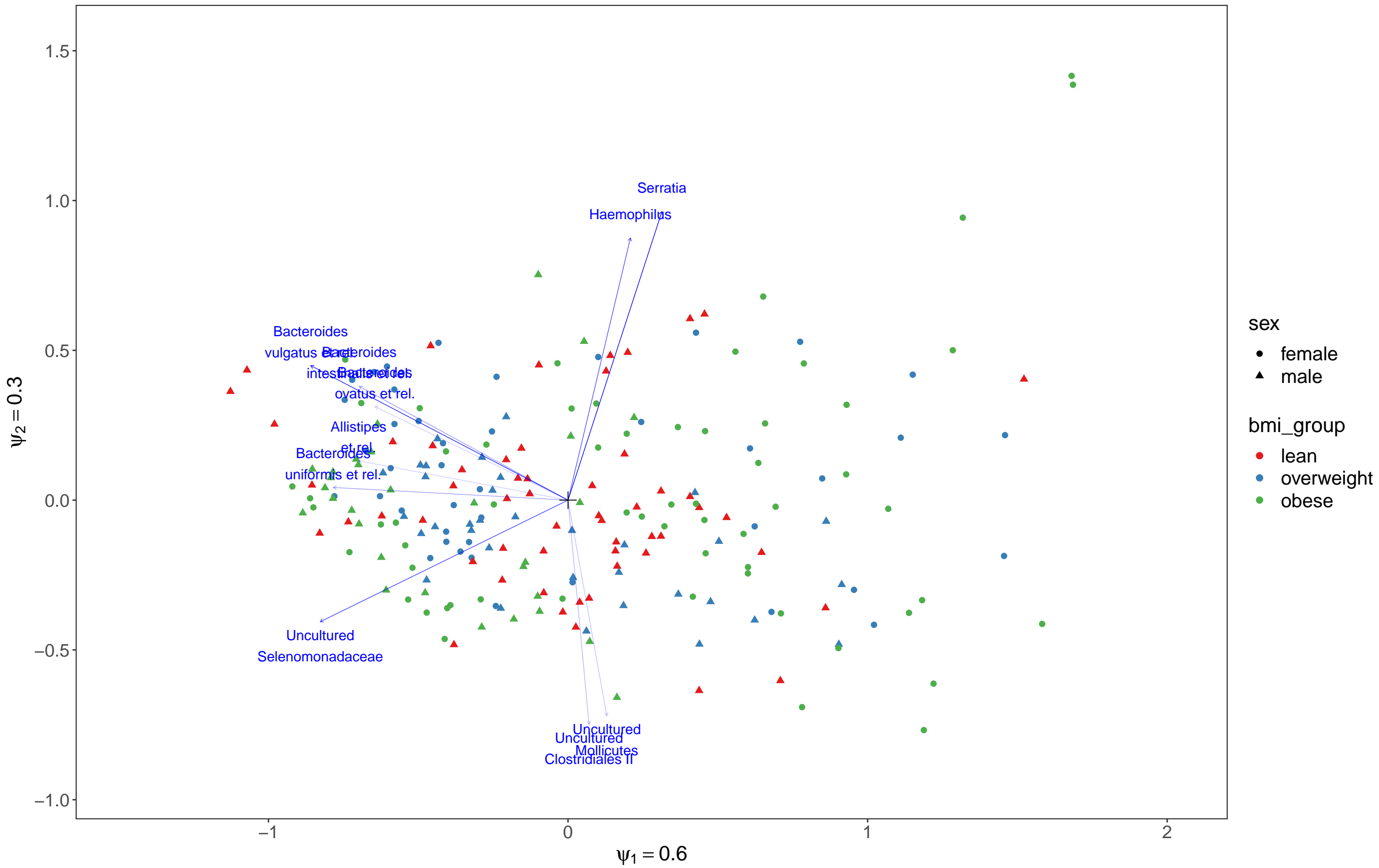


## 4. Ordination techniques

**Fit Unconstrained RCM**

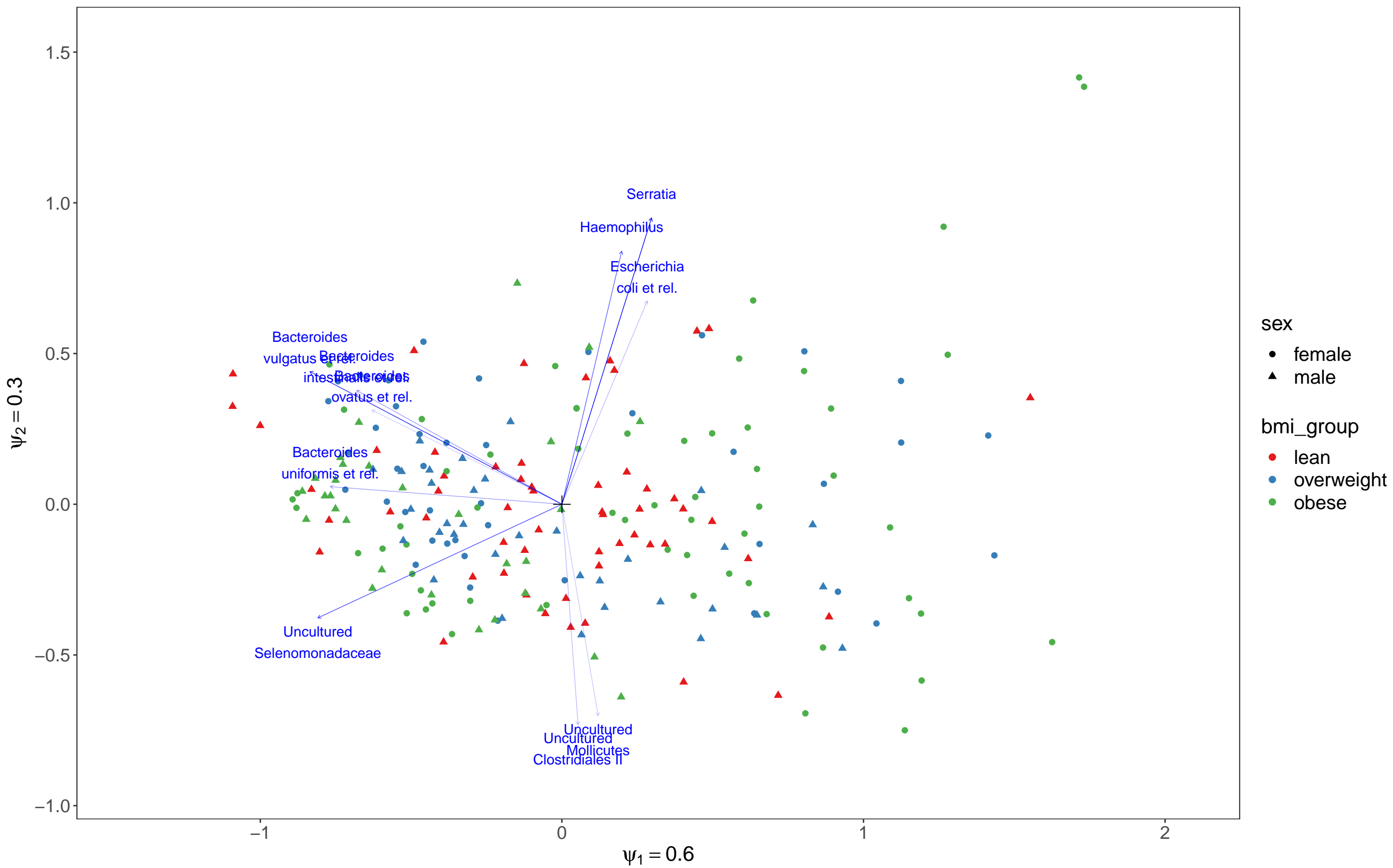


**Total confounders RCM**

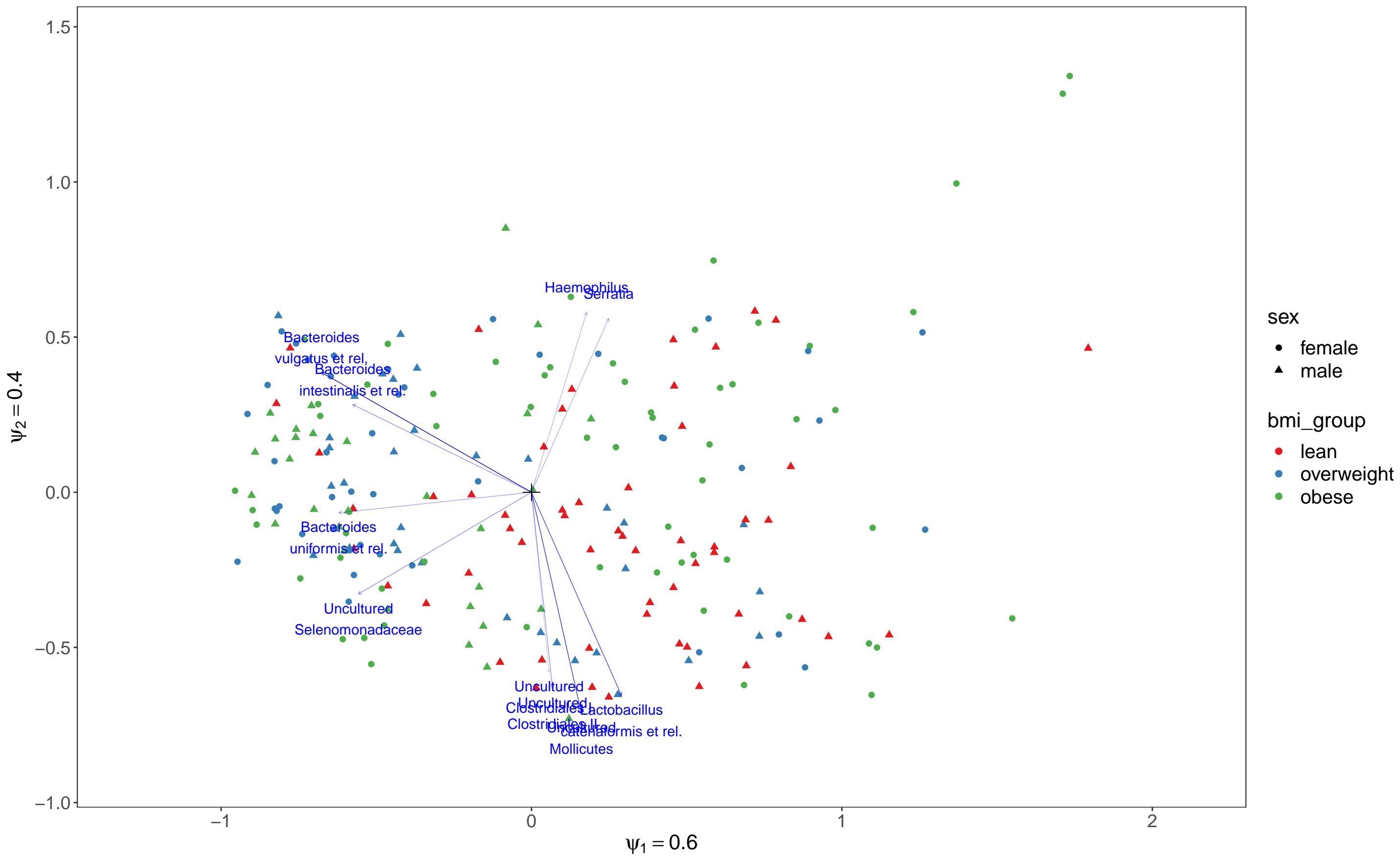




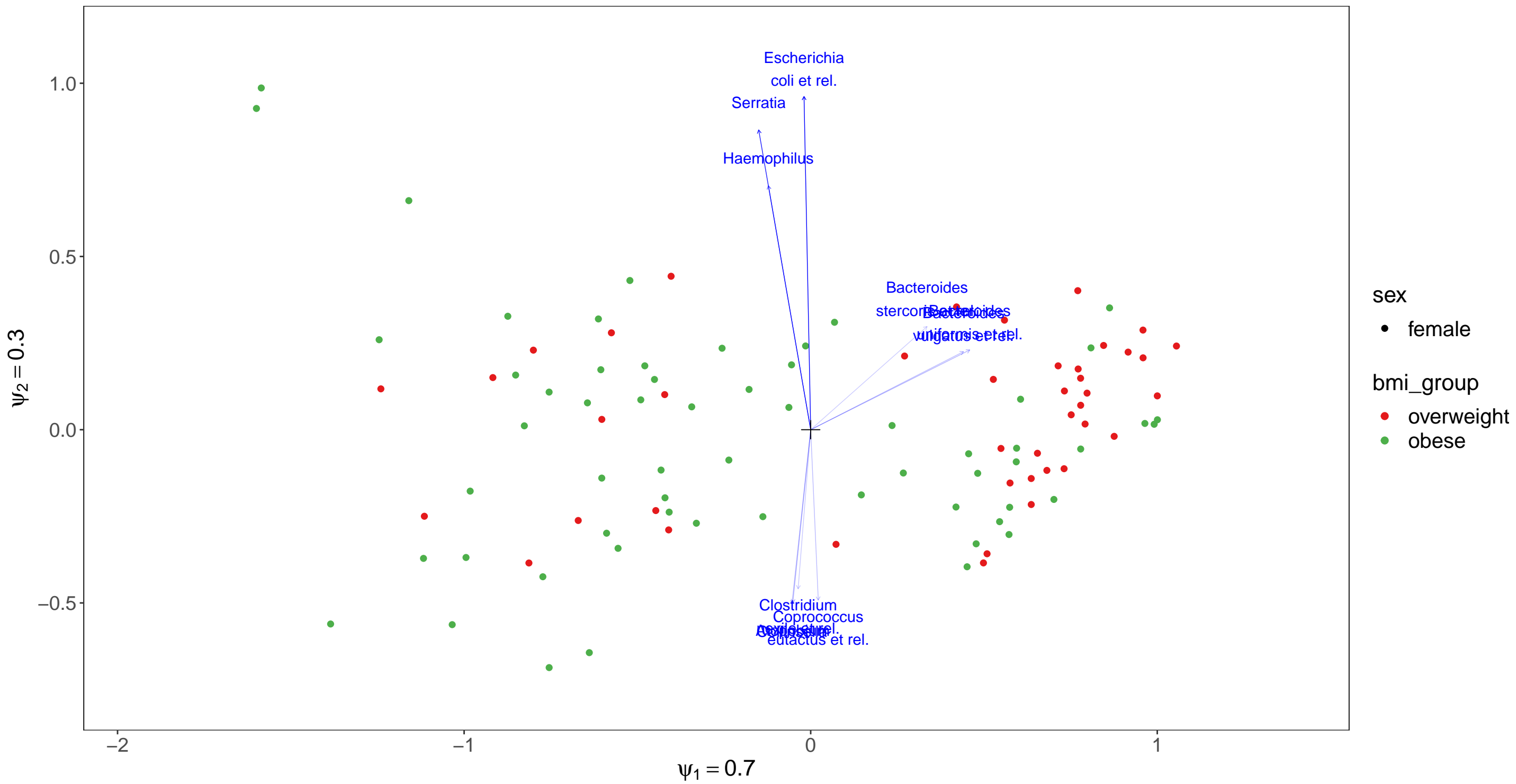
**RCM for confounder bmi\_group**



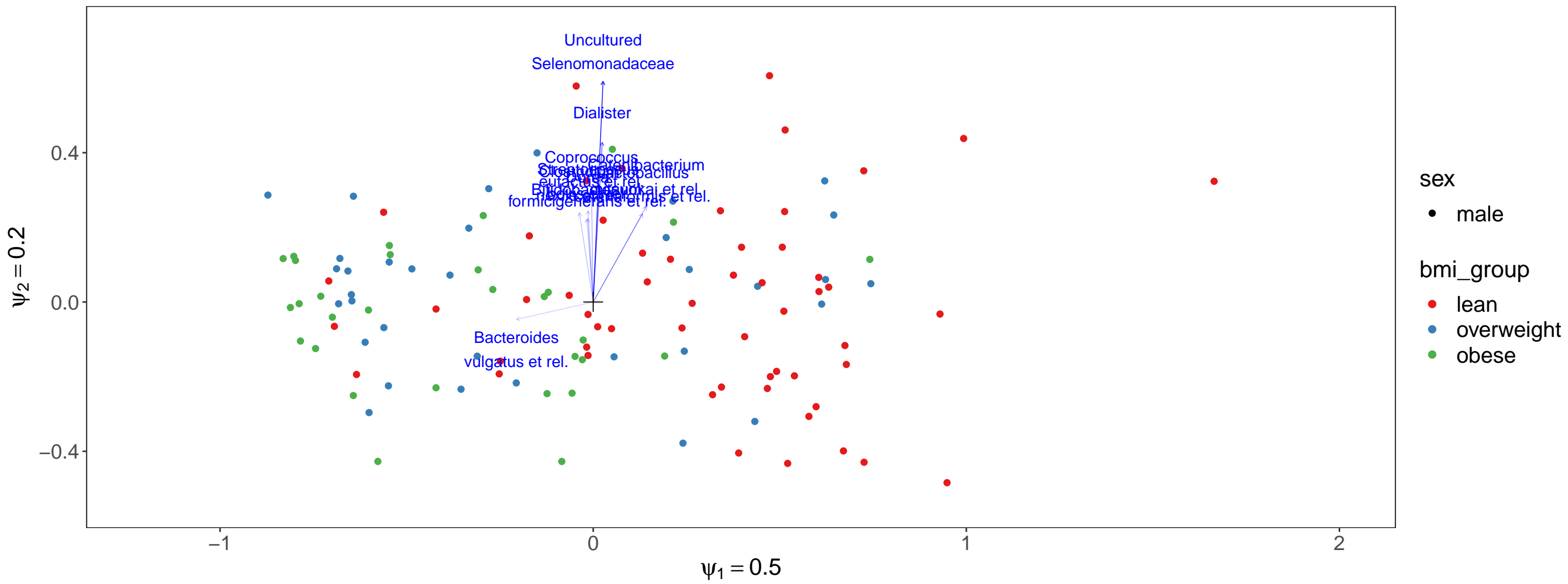
**RCM for confounder timepoint.within.group**

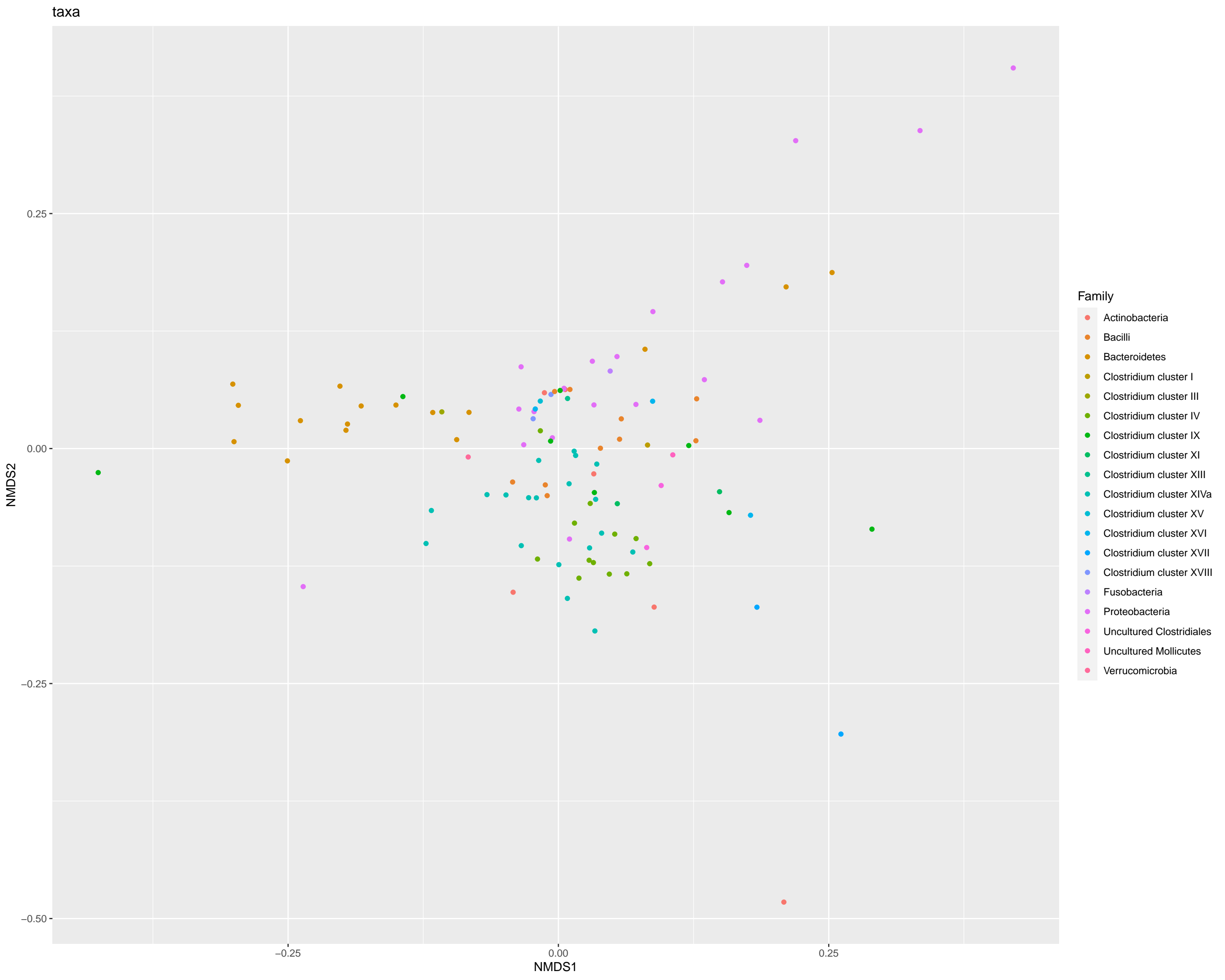


**RCM split sex to female**



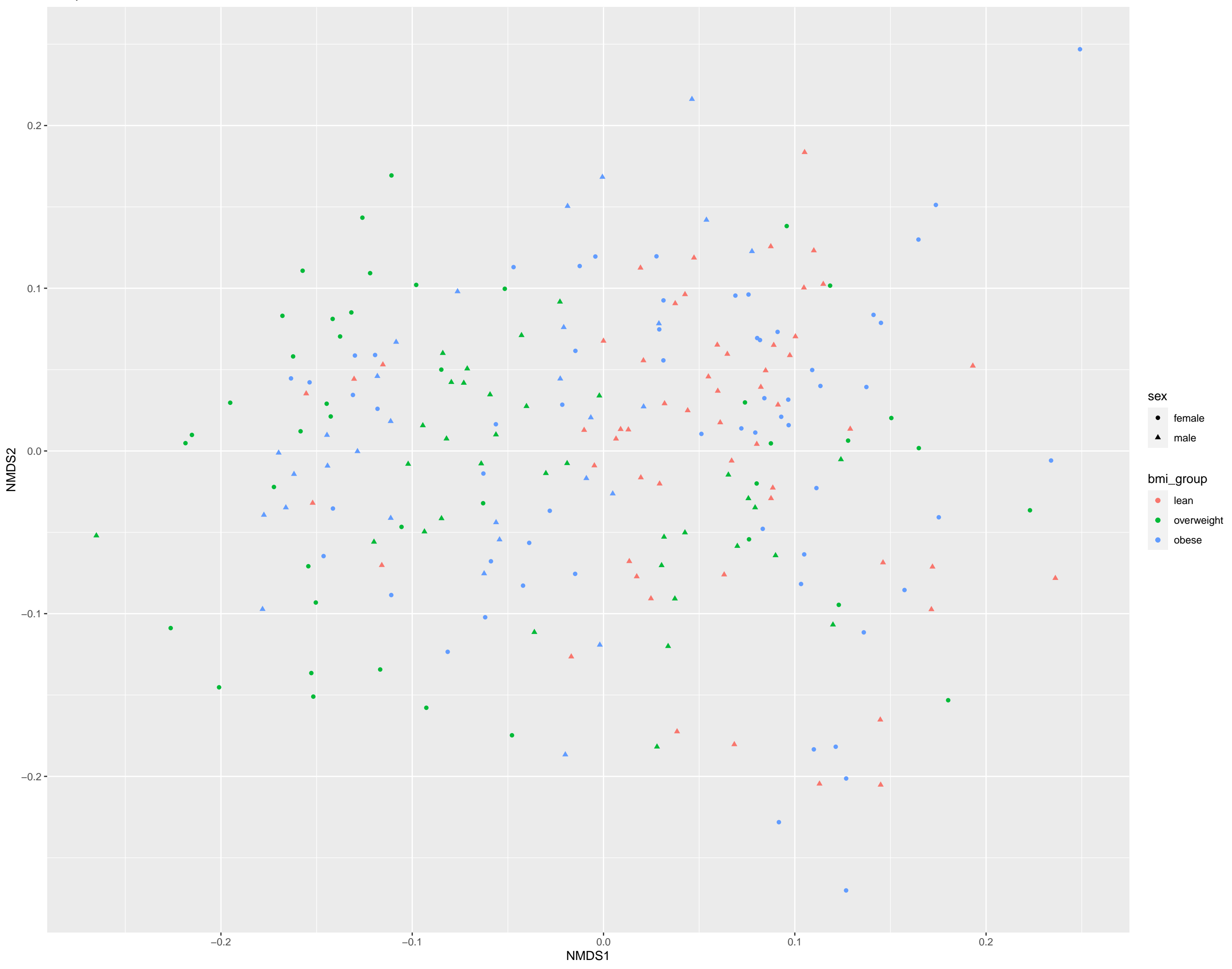
**RCM split sex to male**

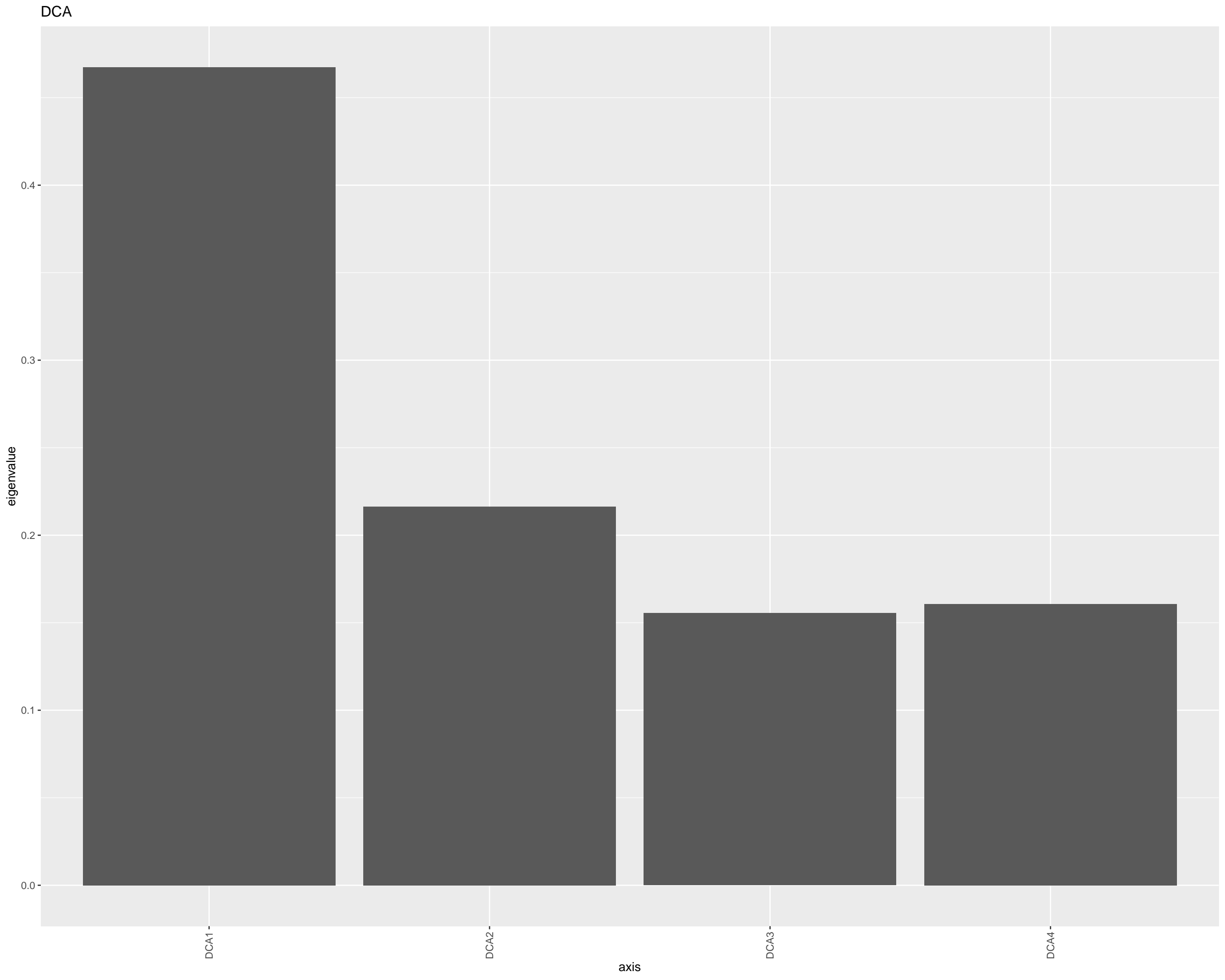






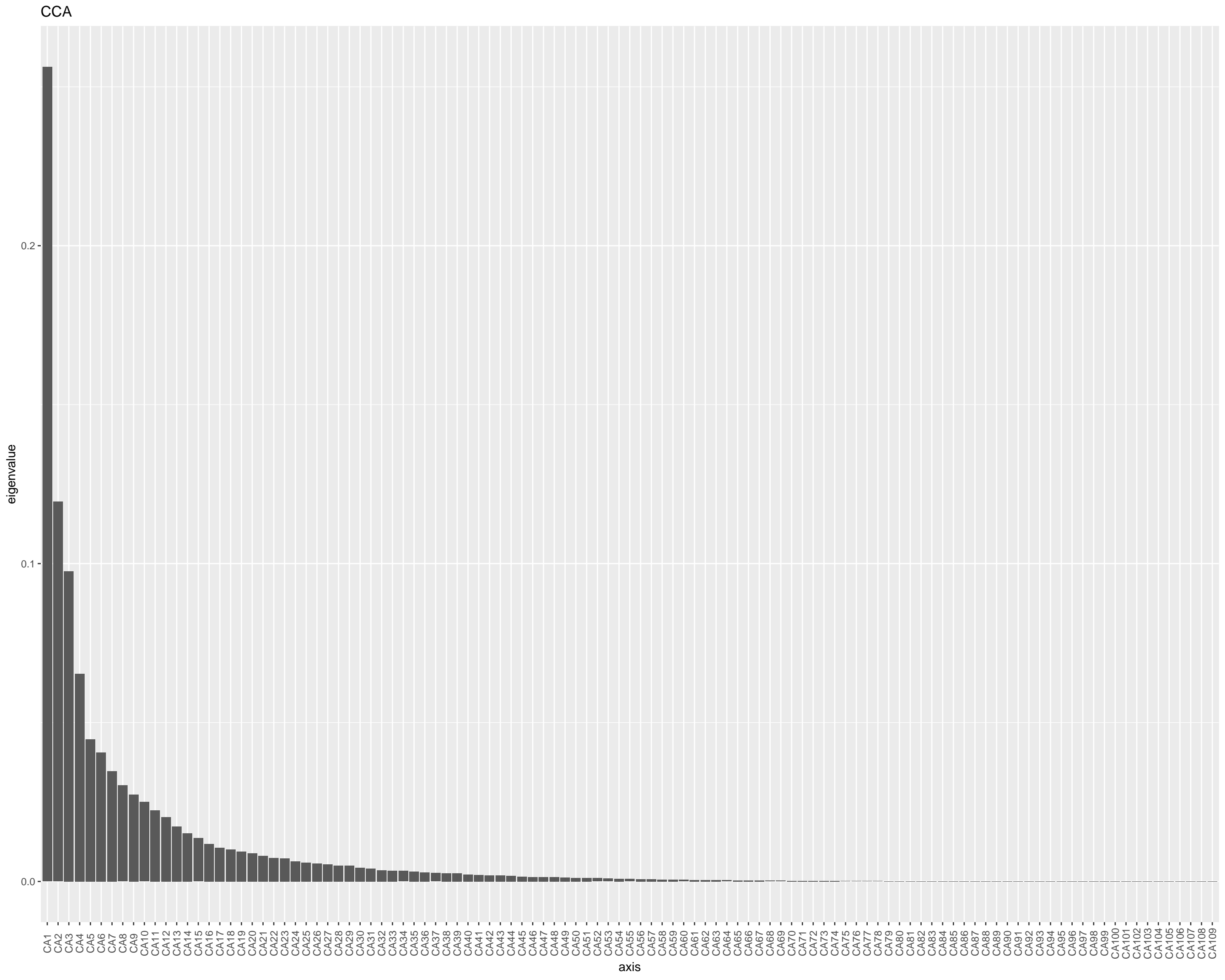
samples

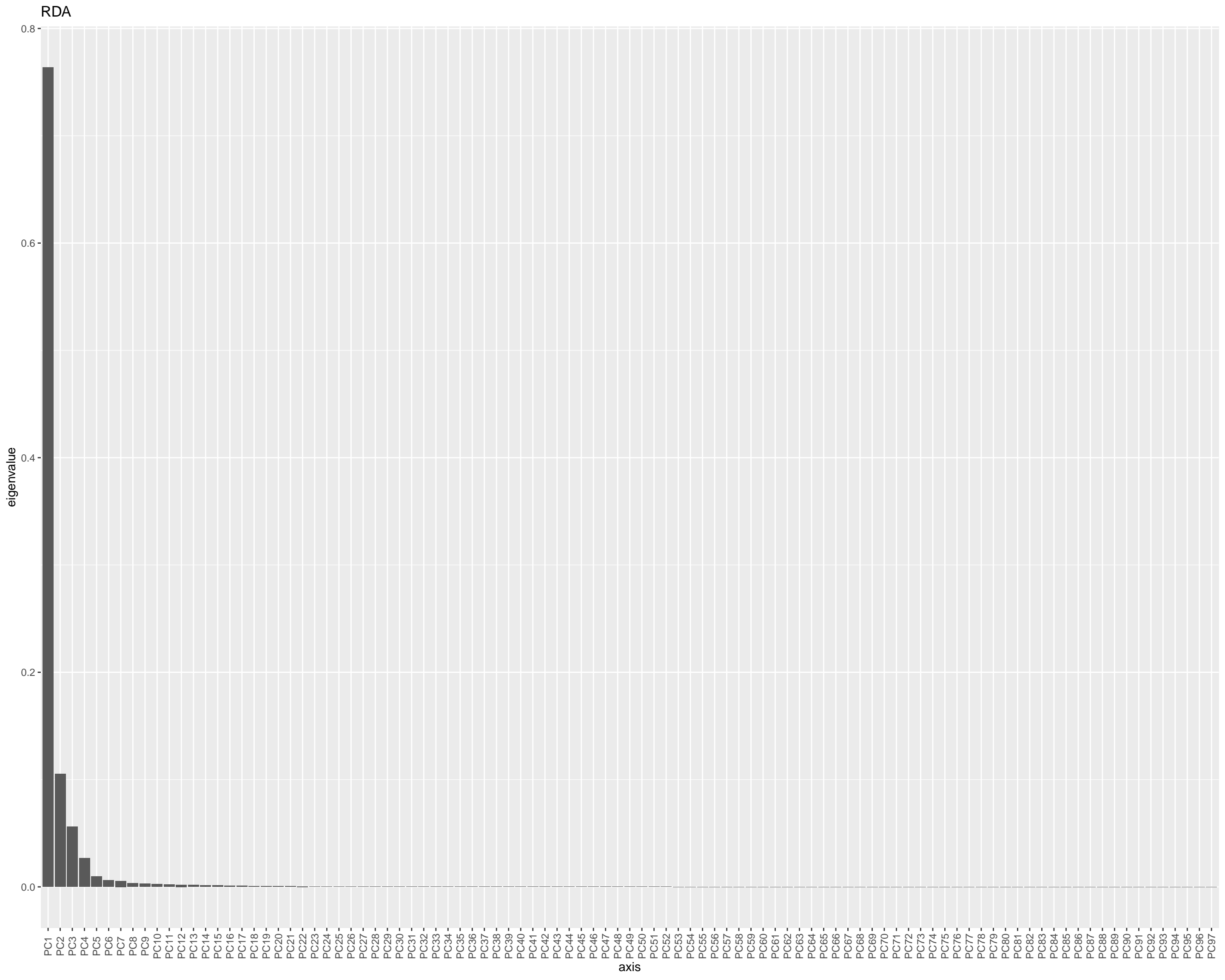




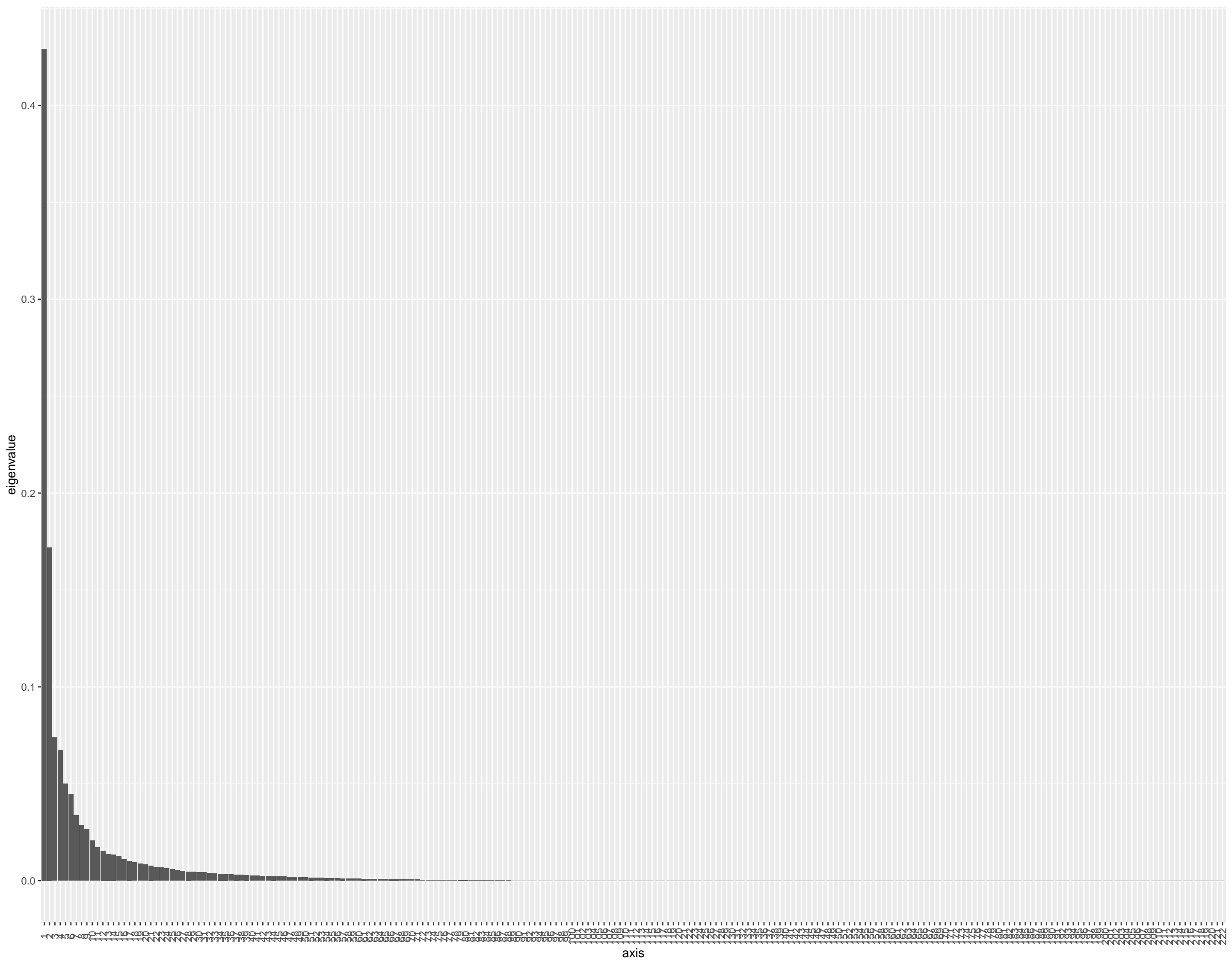


CCA

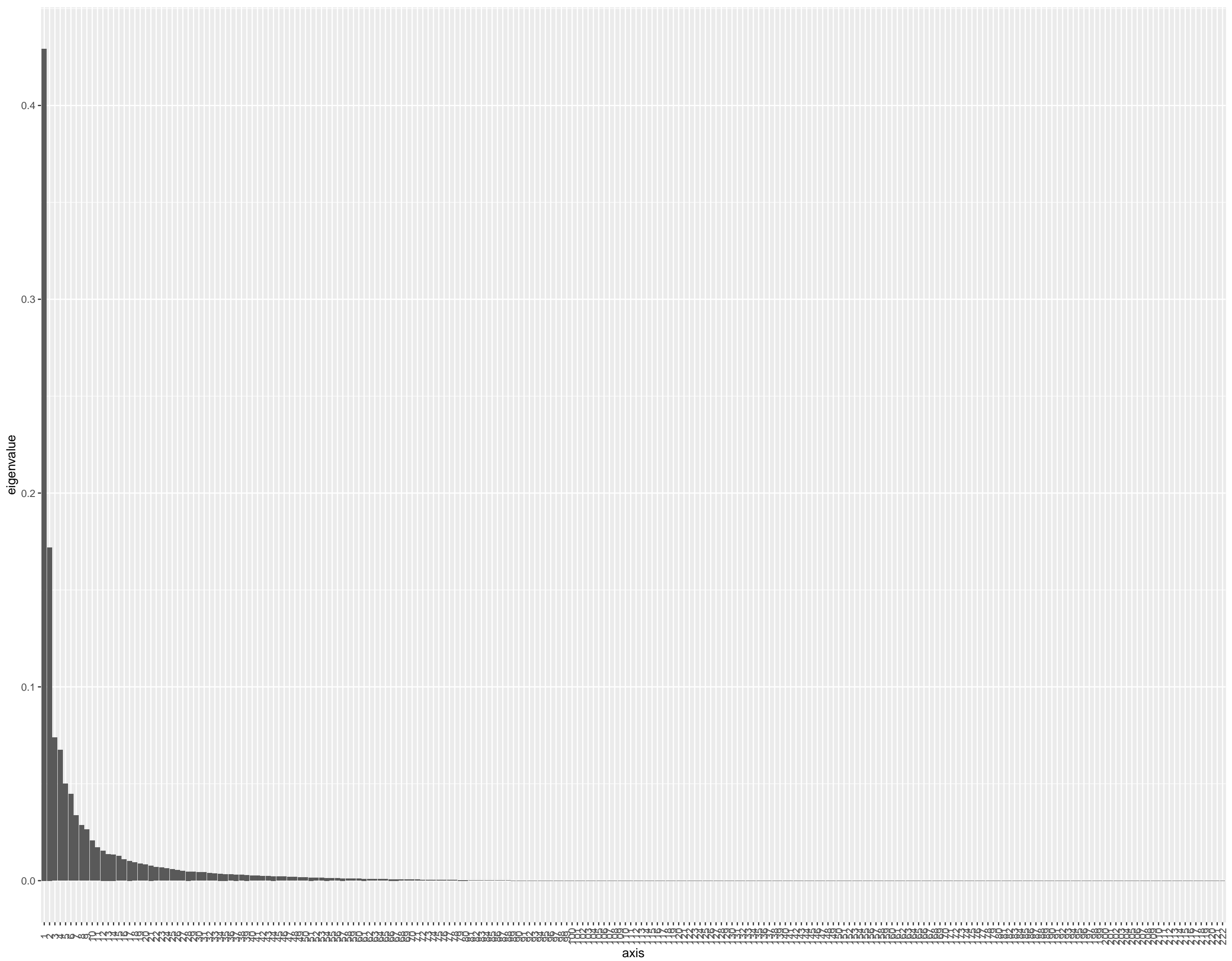




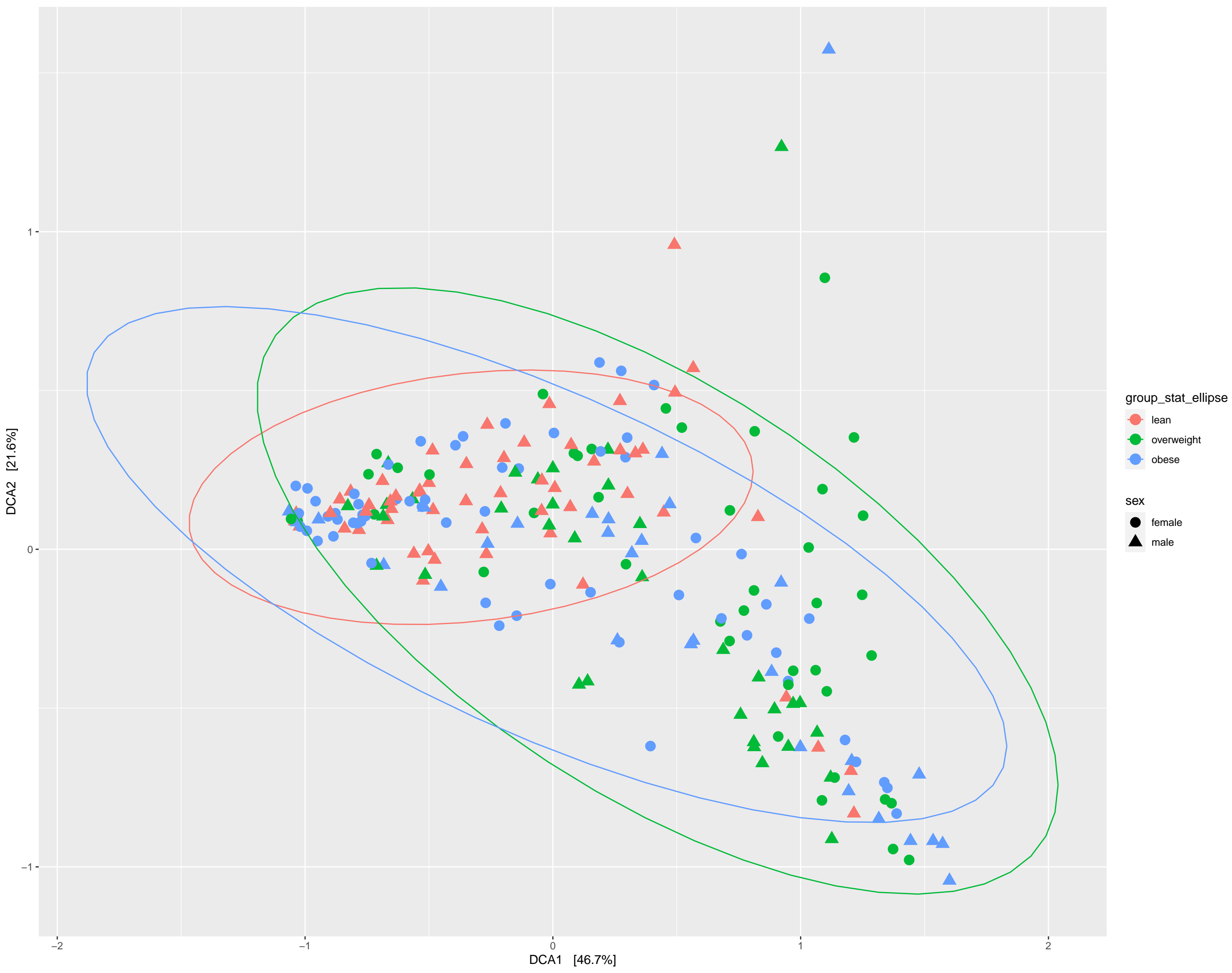
MDS



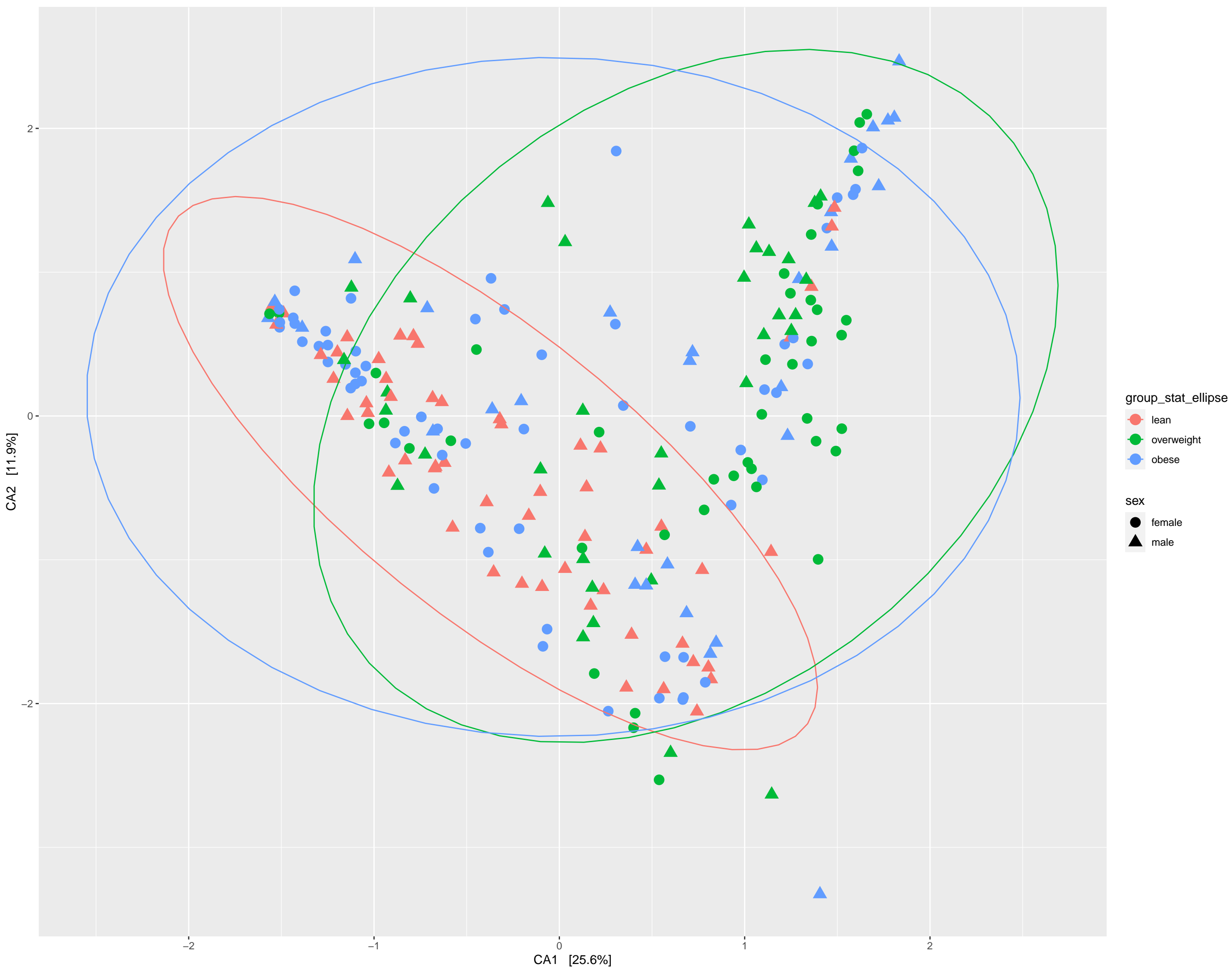
PCoA



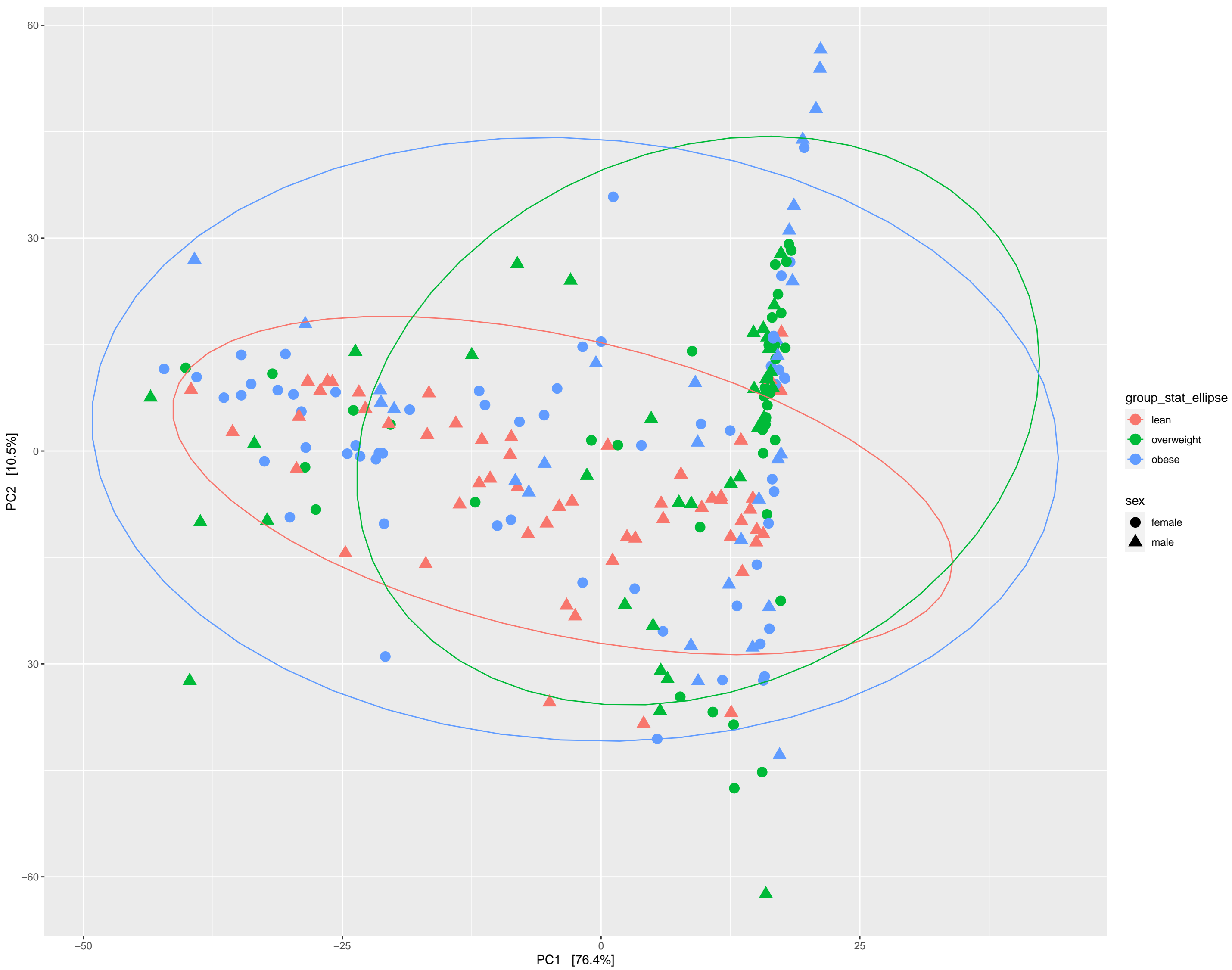
DCA



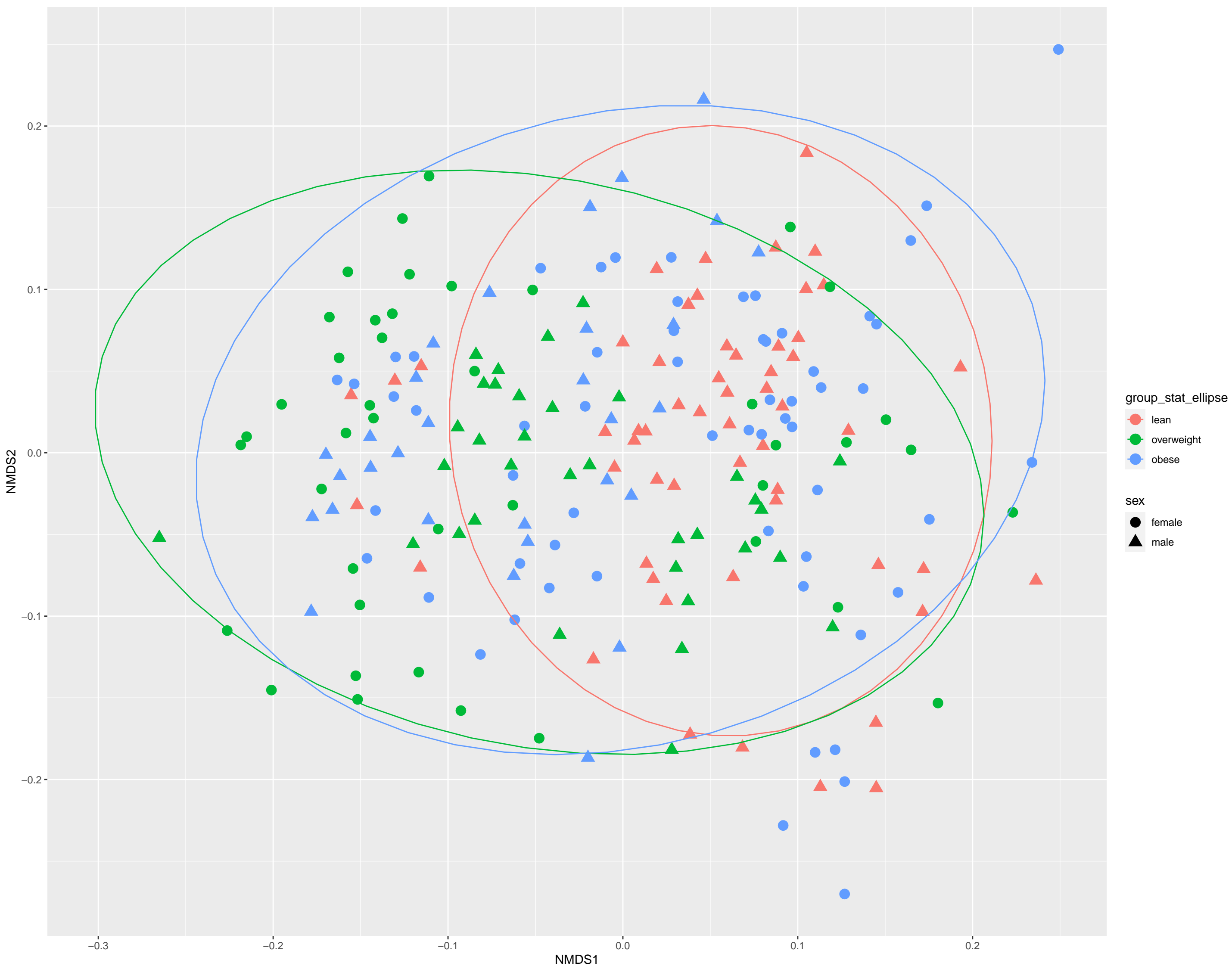
CCA



RDA

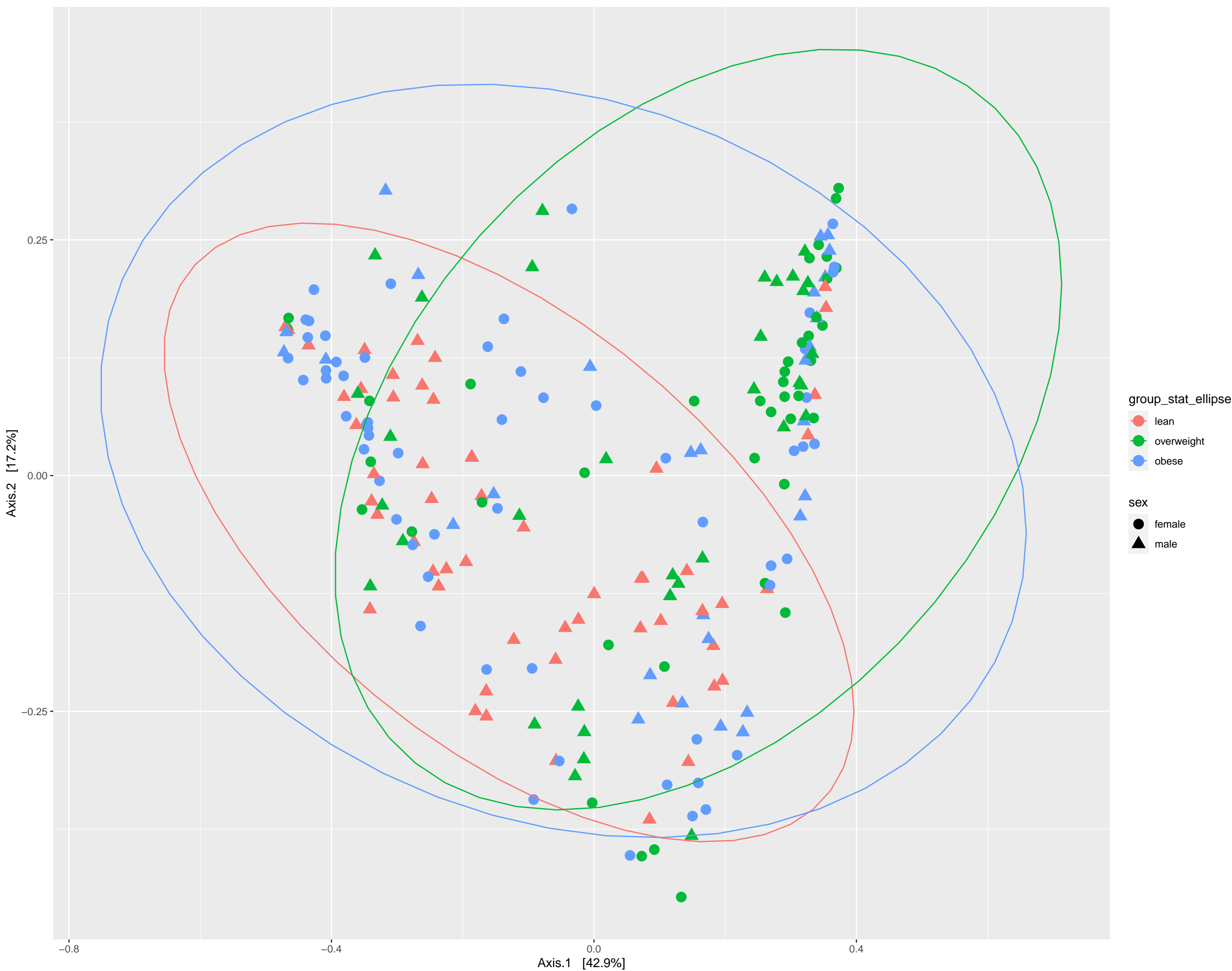


NMDS

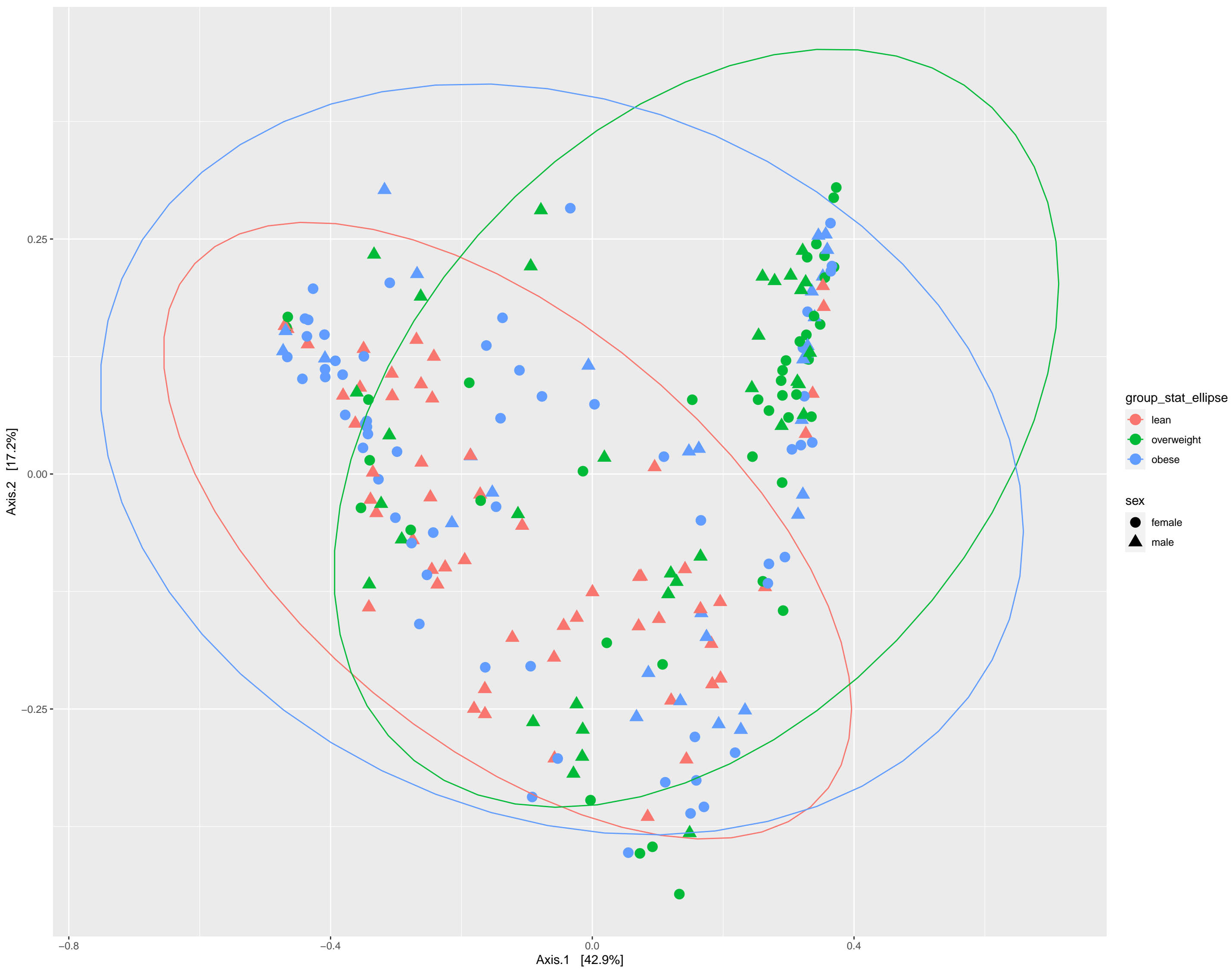




MDS



PCoA



5.Null hypothesis

Permutational Multivariate Analysis of Variance Using Distance Matrices–PERMANOVA

	Df	SumOfSqs	R2	F	Pr(>F)
<i>bmi_group</i>	2	2.30296034271684	0.0584228224870496	6.77894757411653	1e−04
<i>timepoint.within.group</i>	1	0.167346077978897	0.00424533155274884	0.985193073724105	0.3775
<i>bmi_group:timepoint.within.group</i>	2	0.258522041044655	0.00655833582228501	0.760980261139823	0.6438
<i>Residual</i>	216	36.6900192535909	0.930773510137917	NA	NA
<i>Total</i>	221	39.4188477153313	1	NA	NA

pairwise.adonis2 for obese\_vs\_lean

	obese_vs_lean.Df	obese_vs_lean.SumOfSqs	obese_vs_lean.R2	obese_vs_lean.F	obese_vs_lean.Pr..F.
bmi_group	1	0.658835470259135	0.0272344071634611	4.00864856708681	0.009
timepoint.within.group	1	0.067584165987248	0.00279373952585719	0.411212180236712	0.832
bmi_group:timepoint.within.group	1	0.126672713606196	0.00523629405911425	0.770733232815701	0.55
Residual	142	23.3381986999139	0.964735559251568	NA	NA
Total	145	24.1912910497665	1	NA	NA

pairwise.adonis2 for obese\_vs\_overweight

	obese_vs_overweight.Df	obese_vs_overweight.SumOfSqs	obese_vs_overweight.R2	obese_vs_overweight.F	obese_vs_overweight.Pr..F.
bmi_group	1	0.94244137059091	0.0312732524162163	5.28311487899947	0.003
timepoint.within.group	1	0.117845438533519	0.00391049274826261	0.660615088817976	0.613
bmi_group:timepoint.within.group	1	0.176647494188051	0.00586173511352889	0.990246220088703	0.398
Residual	162	28.8987662643144	0.958954519721992	NA	NA
Total	165	30.1357005676269	1	NA	NA

pairwise.adonis2 for lean\_vs\_overweight

	lean_vs_overweight.Df	lean_vs_overweight.SumOfSqs	lean_vs_overweight.R2	lean_vs_overweight.F	lean_vs_overweight.Pr..F.
bmi_group	1	1.95925719626678	0.0834958753164913	11.8613275696489	0.001
timepoint.within.group	1	0.290486777039481	0.0123794097900944	1.75860465062071	0.093
bmi_group:timepoint.within.group	1	0.0724996486925957	0.00308965134299914	0.438912299756204	0.866
Residual	128	21.1430735429534	0.901035063550415	NA	NA
Total	131	23.4653171649523	1	NA	NA

6. metaGEENOME results global & local



## The global result

	chi2	df	pval	AdjPvalue
<i>Alcaligenes faecalis et rel.</i>	0.59	3	0.899	0.924
<i>Allistipes et rel.</i>	7.99	3	0.046	0.231
<i>Anaerostipes caccae et rel.</i>	10.22	3	0.017	0.186
<i>Anaerotruncus colihominis et rel.</i>	1.64	3	0.651	0.715
<i>Anaerovorax odorimutans et rel.</i>	4.65	3	0.199	0.368
<i>Aquabacterium</i>	5.35	3	0.148	0.34
<i>Atopobium</i>	0.72	3	0.869	0.91
<i>Bacillus</i>	4.96	3	0.175	0.344
<i>Bacteroides fragilis et rel.</i>	3.18	3	0.365	0.466
<i>Bacteroides intestinalis et rel.</i>	18.01	3	0	0.044
<i>Bacteroides ovatus et rel.</i>	7.53	3	0.057	0.245
<i>Bacteroides plebeius et rel.</i>	8.01	3	0.046	0.231
<i>Bacteroides splachnicus et rel.</i>	2.3	3	0.512	0.59
<i>Bacteroides stercoris et rel.</i>	16.17	3	0.001	0.056
<i>Bacteroides uniformis et rel.</i>	10.8	3	0.013	0.179
<i>Bacteroides vulgatus et rel.</i>	14.65	3	0.002	0.078
<i>Bifidobacterium</i>	9.63	3	0.022	0.188
<i>Bilophila et rel.</i>	2.28	3	0.516	0.59
<i>Bryantella formatexigens et rel.</i>	4.42	3	0.22	0.369
<i>Bulleidia moorei et rel.</i>	3.57	3	0.311	0.437
<i>Burkholderia</i>	2.05	3	0.562	0.63
<i>Butyrivibrio crossotus et rel.</i>	3.8	3	0.284	0.42
<i>Campylobacter</i>	4.4	3	0.221	0.369
<i>Catenibacterium mitsuokai et rel.</i>	4.2	3	0.241	0.382
<i>Clostridium (sensu stricto)</i>	5.67	3	0.129	0.331
<i>Clostridium cellulosi et rel.</i>	3.28	3	0.351	0.46
<i>Clostridium colinum et rel.</i>	4.39	3	0.223	0.369
<i>Clostridium difficile et rel.</i>	6.53	3	0.088	0.322
<i>Clostridium leptum et rel.</i>	1.54	3	0.673	0.732
<i>Clostridium nexile et rel.</i>	5.97	3	0.113	0.331

	chi2	df	pval	AdjPvalue
<i>Clostridium orbiscindens</i> et rel.	0.8	3	0.849	0.898
<i>Clostridium ramosum</i> et rel.	4.53	3	0.21	0.369
<i>Clostridium sphenoides</i> et rel.	5.31	3	0.15	0.34
<i>Clostridium stercorearium</i> et rel.	6.29	3	0.098	0.322
<i>Clostridium symbiosum</i> et rel.	9.4	3	0.024	0.193
<i>Collinsella</i>	2.58	3	0.462	0.545
<i>Coprobacillus cateniformis</i> et rel.	5.47	3	0.14	0.331
<i>Coprococcus eutactus</i> et rel.	2.96	3	0.397	0.49
<i>Corynebacterium</i>	4.62	3	0.202	0.368
<i>Desulfovibrio</i> et rel.	0.55	3	0.909	0.925
<i>Dialister</i>	3.81	3	0.283	0.42
<i>Dorea formicigenerans</i> et rel.	3.63	3	0.304	0.437
<i>Eggerthella lenta</i> et rel.	4.26	3	0.235	0.378
<i>Enterobacter aerogenes</i> et rel.	10.02	3	0.018	0.186
<i>Enterococcus</i>	4.01	3	0.261	0.406
<i>Escherichia coli</i> et rel.	0.47	3	0.926	0.935
<i>Eubacterium bifforme</i> et rel.	5.56	3	0.135	0.331
<i>Eubacterium cylindroides</i> et rel.	2.08	3	0.557	0.63
<i>Eubacterium hallii</i> et rel.	5.02	3	0.17	0.344
<i>Eubacterium limosum</i> et rel.	3.24	3	0.356	0.46
<i>Eubacterium rectale</i> et rel.	12.84	3	0.005	0.111
<i>Eubacterium siraeum</i> et rel.	3.26	3	0.353	0.46
<i>Eubacterium ventriosum</i> et rel.	8.68	3	0.034	0.231
<i>Faecalibacterium prausnitzii</i> et rel.	8.37	3	0.039	0.231
<i>Fusobacteria</i>	5.76	3	0.124	0.331
<i>Haemophilus</i>	5.68	3	0.128	0.331
<i>Helicobacter</i>	4.42	3	0.22	0.369
<i>Klebsiella pneumoniae</i> et rel.	7.82	3	0.05	0.231
<i>Lachnobacillus bovis</i> et rel.	7.89	3	0.048	0.231
<i>Lachnospira pectinoschiza</i> et rel.	13.92	3	0.003	0.083

	chi2	df	pval	AdjPvalue
<i>Lactobacillus cateniformis et rel.</i>	6.53	3	0.089	0.322
<i>Lactobacillus gasseri et rel.</i>	5.23	3	0.156	0.34
<i>Lactobacillus plantarum et rel.</i>	5.56	3	0.135	0.331
<i>Lactobacillus salivarius et rel.</i>	9.73	3	0.021	0.188
<i>Lactococcus</i>	5.79	3	0.122	0.331
<i>Leminorella</i>	4.62	3	0.202	0.368
<i>Megamonas hypermegale et rel.</i>	4.58	3	0.205	0.368
<i>Megasphaera elsdenii et rel.</i>	1.77	3	0.621	0.689
<i>Mitsuokella multiacida et rel.</i>	3.59	3	0.309	0.437
<i>Moraxellaceae</i>	8.25	3	0.041	0.231
<i>Oceanospirillum</i>	5.1	3	0.165	0.344
<i>Oscillospira guillermontii et rel.</i>	4.95	3	0.175	0.344
<i>Outgrouping clostridium cluster XIVa</i>	7.97	3	0.047	0.231
<i>Oxalobacter formigenes et rel.</i>	0.42	3	0.936	0.936
<i>Papillibacter cinnamivorans et rel.</i>	3.67	3	0.299	0.437
<i>Parabacteroides distasonis et rel.</i>	7.51	3	0.057	0.245
<i>Peptococcus niger et rel.</i>	3.25	3	0.355	0.46
<i>Peptostreptococcus micros et rel.</i>	6.17	3	0.104	0.329
<i>Phascolarctobacterium faecium et rel.</i>	2.73	3	0.435	0.52
<i>Prevotella melaninogenica et rel.</i>	12.11	3	0.007	0.111
<i>Prevotella oralis et rel.</i>	6.97	3	0.073	0.299
<i>Prevotella ruminicola et rel.</i>	3.11	3	0.375	0.473
<i>Prevotella tannerae et rel.</i>	6.47	3	0.091	0.322
<i>Propionibacterium</i>	4.61	3	0.203	0.368
<i>Proteus et rel.</i>	5.27	3	0.153	0.34
<i>Roseburia intestinalis et rel.</i>	12.37	3	0.006	0.111
<i>Ruminococcus bromii et rel.</i>	0.64	3	0.886	0.92
<i>Ruminococcus callidus et rel.</i>	2.99	3	0.394	0.49
<i>Ruminococcus gnavus et rel.</i>	6	3	0.112	0.331
<i>Ruminococcus lactaris et rel.</i>	3.33	3	0.343	0.46

	chi2	df	pval	AdjPvalue
<i>Ruminococcus obeum</i> et rel.	4.28	3	0.233	0.378
<i>Serratia</i>	8.93	3	0.03	0.224
<i>Sporobacter termitidis</i> et rel.	3.35	3	0.341	0.46
<i>Streptococcus bovis</i> et rel.	4.93	3	0.177	0.344
<i>Streptococcus intermedius</i> et rel.	2.88	3	0.41	0.501
<i>Streptococcus mitis</i> et rel.	5.71	3	0.127	0.331
<i>Subdoligranulum variable</i> at rel.	10.1	3	0.018	0.186
<i>Sutterella wadsworthia</i> et rel.	5.48	3	0.14	0.331
<i>Tannerella</i> et rel.	3.91	3	0.272	0.413
Uncultured Bacteroidetes	2.77	3	0.428	0.517
Uncultured Clostridiales I	2.42	3	0.49	0.572
Uncultured Clostridiales II	5.61	3	0.132	0.331
Uncultured Mollicutes	5.02	3	0.171	0.344
Uncultured Selenomonadaceae	3.55	3	0.315	0.437
<i>Veillonella</i>	6.65	3	0.084	0.322
<i>Vibrio</i>	3.98	3	0.263	0.406
<i>Weissella</i> et rel.	7.94	3	0.047	0.231
<i>Xanthomonadaceae</i>	6.38	3	0.095	0.322
<i>Yersinia</i> et rel.	6.29	3	0.098	0.322
_group2	0.04	1	0.848	0.898
_group3	0.11	1	0.745	0.803

## The local result

	estimate	std_err	wald	pval	AdjPvalue
<i>Akkermansia</i>	1.12	0.235	4.756	0	0
<i>Alcaligenes faecalis et rel.</i>	−1.597	0.157	−10.155	0	0
<i>Allistipes et rel.</i>	1.678	0.177	9.465	0	0
<i>Anaerostipes caccae et rel.</i>	0.753	0.161	4.681	0	0
<i>Anaerotruncus colihominis et rel.</i>	1.113	0.172	6.462	0	0
<i>Anaerovorax odorimutans et rel.</i>	−0.039	0.091	−0.427	0.67	0.966
<i>Aquabacterium</i>	−0.274	0.141	−1.942	0.052	0.292
<i>Atopobium</i>	−0.278	0.154	−1.802	0.072	0.387
<i>Bacillus</i>	−2.486	0.062	−40.158	0	0
<i>Bacteroides fragilis et rel.</i>	1.461	0.234	6.239	0	0
<i>Bacteroides intestinalis et rel.</i>	−1.619	0.168	−9.637	0	0
<i>Bacteroides ovatus et rel.</i>	0.89	0.162	5.489	0	0
<i>Bacteroides plebeius et rel.</i>	0.263	0.14	1.87	0.062	0.335
<i>Bacteroides splachnicus et rel.</i>	0.777	0.096	8.057	0	0
<i>Bacteroides stercoris et rel.</i>	−0.44	0.091	−4.861	0	0
<i>Bacteroides uniformis et rel.</i>	0.02	0.309	0.066	0.947	0.991
<i>Bacteroides vulgatus et rel.</i>	2.524	0.223	11.334	0	0
<i>Bifidobacterium</i>	0.945	0.141	6.7	0	0
<i>Bilophila et rel.</i>	−2.392	0.091	−26.232	0	0
<i>Bryantella formatexigens et rel.</i>	1.269	0.112	11.38	0	0
<i>Bulleidia moorei et rel.</i>	−1.501	0.073	−20.594	0	0
<i>Burkholderia</i>	−1.182	0.248	−4.774	0	0
<i>Butyrivibrio crossotus et rel.</i>	2.076	0.11	18.886	0	0
<i>Campylobacter</i>	−1.197	0.061	−19.589	0	0
<i>Catenibacterium mitsuokai et rel.</i>	−1.279	0.184	−6.949	0	0
<i>Clostridium (sensu stricto)</i>	0.624	0.111	5.634	0	0
<i>Clostridium cellulosi et rel.</i>	2.888	0.218	13.249	0	0
<i>Clostridium colinum et rel.</i>	0.338	0.167	2.026	0.043	0.248
<i>Clostridium difficile et rel.</i>	0.529	0.157	3.377	0.001	0.005
<i>Clostridium leptum et rel.</i>	1.499	0.152	9.871	0	0

	estimate	std_err	wald	pval	AdjPvalue
<i>Clostridium nexile</i> et rel.	0.836	0.14	5.955	0	0
<i>Clostridium orbiscindens</i> et rel.	2.585	0.142	18.189	0	0
<i>Clostridium ramosum</i> et rel.	-1.747	0.053	-33.08	0	0
<i>Clostridium sphenoides</i> et rel.	1.495	0.1	14.876	0	0
<i>Clostridium stercorearium</i> et rel.	-0.995	0.096	-10.42	0	0
<i>Clostridium symbiosum</i> et rel.	2.379	0.131	18.176	0	0
<i>Collinsella</i>	-0.605	0.146	-4.138	0	0
<i>Coprobacillus cateniformis</i> et rel.	-1.47	0.084	-17.398	0	0
<i>Coprococcus eutactus</i> et rel.	1.42	0.175	8.115	0	0
<i>Corynebacterium</i>	-2.558	0.05	-51.355	0	0
<i>Desulfovibrio</i> et rel.	-1.283	0.073	-17.482	0	0
<i>Dialister</i>	-0.356	0.251	-1.417	0.156	0.666
<i>Dorea formicigenerans</i> et rel.	1.68	0.134	12.526	0	0
<i>Eggerthella lenta</i> et rel.	-1.147	0.06	-19.177	0	0
<i>Enterobacter aerogenes</i> et rel.	-0.163	0.139	-1.172	0.241	0.86
<i>Enterococcus</i>	-0.783	0.228	-3.438	0.001	0.005
<i>Escherichia coli</i> et rel.	0.281	0.139	2.024	0.043	0.248
<i>Eubacterium bifforme</i> et rel.	0.495	0.202	2.451	0.014	0.097
<i>Eubacterium cylindroides</i> et rel.	-1.736	0.076	-22.747	0	0
<i>Eubacterium hallii</i> et rel.	0.09	0.146	0.617	0.538	0.939
<i>Eubacterium limosum</i> et rel.	-2.534	0.062	-40.799	0	0
<i>Eubacterium rectale</i> et rel.	0.873	0.13	6.729	0	0
<i>Eubacterium siraeum</i> et rel.	-1.646	0.097	-17.003	0	0
<i>Eubacterium ventriosum</i> et rel.	0.031	0.123	0.251	0.802	0.966
<i>Faecalibacterium prausnitzii</i> et rel.	3.077	0.164	18.784	0	0
<i>Fusobacteria</i>	-0.985	0.064	-15.481	0	0
<i>Haemophilus</i>	-1.273	0.22	-5.793	0	0
<i>Helicobacter</i>	-1.85	0.056	-32.982	0	0
<i>Klebsiella pneumoniae</i> et rel.	-0.666	0.141	-4.723	0	0
<i>Lachnobacillus bovis</i> et rel.	0.7	0.137	5.096	0	0



	estimate	std_err	wald	pval	AdjPvalue
<i>Lachnospira pectinoschiza</i> et rel.	1.117	0.094	11.895	0	0
<i>Lactobacillus catenaformis</i> et rel.	−0.507	0.189	−2.689	0.007	0.052
<i>Lactobacillus gasseri</i> et rel.	−0.519	0.06	−8.705	0	0
<i>Lactobacillus plantarum</i> et rel.	−0.065	0.082	−0.783	0.434	0.931
<i>Lactobacillus salivarius</i> et rel.	−2.187	0.132	−16.539	0	0
<i>Lactococcus</i>	−2.357	0.091	−25.928	0	0
<i>Leminorella</i>	−0.502	0.16	−3.126	0.002	0.013
<i>Megamonas hypermegale</i> et rel.	−2.558	0.05	−51.355	0	0
<i>Megasphaera elsdenii</i> et rel.	0.306	0.258	1.184	0.236	0.853
<i>Mitsuokella multiacida</i> et rel.	−0.524	0.382	−1.374	0.17	0.713
<i>Moraxellaceae</i>	−0.595	0.188	−3.162	0.002	0.012
<i>Oceanospirillum</i>	−2.247	0.084	−26.588	0	0
<i>Oscillospira guillermundii</i> et rel.	4.266	0.184	23.161	0	0
Outgrouping clostridium cluster XIVa	0.997	0.131	7.622	0	0
<i>Oxalobacter formigenes</i> et rel.	0.409	0.187	2.18	0.029	0.178
<i>Papillibacter cinnamivorans</i> et rel.	0.604	0.118	5.1	0	0
<i>Parabacteroides distasonis</i> et rel.	1.026	0.154	6.646	0	0
<i>Peptococcus niger</i> et rel.	−1.338	0.098	−13.694	0	0
<i>Peptostreptococcus micros</i> et rel.	−1.775	0.058	−30.649	0	0
<i>Phascolarctobacterium faecium</i> et rel.	−0.133	0.119	−1.118	0.264	0.877
<i>Prevotella melaninogenica</i> et rel.	5.168	0.339	15.252	0	0
<i>Prevotella oralis</i> et rel.	3.463	0.269	12.891	0	0
<i>Prevotella ruminicola</i> et rel.	−1.866	0.128	−14.613	0	0
<i>Prevotella tannerae</i> et rel.	0.372	0.155	2.397	0.016	0.11
<i>Propionibacterium</i>	−2.51	0.066	−38.258	0	0
<i>Proteus</i> et rel.	−1.052	0.068	−15.519	0	0
<i>Roseburia intestinalis</i> et rel.	−0.183	0.121	−1.51	0.131	0.607
<i>Ruminococcus bromii</i> et rel.	0.973	0.211	4.615	0	0
<i>Ruminococcus callidus</i> et rel.	1.041	0.136	7.683	0	0
<i>Ruminococcus gnavus</i> et rel.	0.388	0.109	3.554	0	0.003

	estimate	std_err	wald	pval	AdjPvalue
<i>Ruminococcus lactaris</i> et rel.	-0.682	0.143	-4.773	0	0
<i>Ruminococcus obeum</i> et rel.	2.511	0.115	21.832	0	0
<i>Serratia</i>	-1.108	0.214	-5.17	0	0
<i>Sporobacter termitidis</i> et rel.	2.598	0.135	19.231	0	0
<i>Streptococcus bovis</i> et rel.	0.811	0.208	3.908	0	0.001
<i>Streptococcus intermedius</i> et rel.	-1.218	0.147	-8.294	0	0
<i>Streptococcus mitis</i> et rel.	0.434	0.2	2.169	0.03	0.181
<i>Subdoligranulum variable</i> at rel.	2.169	0.139	15.618	0	0
<i>Sutterella wadsworthia</i> et rel.	0.396	0.149	2.647	0.008	0.057
<i>Tannerella</i> et rel.	0.439	0.093	4.718	0	0
Uncultured Bacteroidetes	-1.592	0.196	-8.105	0	0
Uncultured Clostridiales I	1.329	0.158	8.401	0	0
Uncultured Clostridiales II	1.452	0.146	9.93	0	0
Uncultured Mollicutes	0.687	0.181	3.8	0	0.001
Uncultured Selenomonadaceae	-0.143	0.097	-1.469	0.142	0.641
<i>Veillonella</i>	-1.04	0.158	-6.583	0	0
<i>Vibrio</i>	-1.558	0.071	-21.909	0	0
<i>Weissella</i> et rel.	-1.777	0.266	-6.689	0	0
Xanthomonadaceae	-1.685	0.204	-8.261	0	0
<i>Yersinia</i> et rel.	-1.865	0.09	-20.765	0	0
<i>bmi_groupoverweight</i>	0.046	0.296	0.155	0.877	0.966
<i>bmi_groupobese</i>	-0.35	0.304	-1.15	0.25	0.862
<i>timepoint.within.group2</i>	0.201	0.325	0.618	0.537	0.939
<i>Alcaligenes faecalis</i> et rel.: <i>bmi_groupoverweight</i>	-0.004	0.374	-0.012	0.99	0.997
<i>Allistipes</i> et rel.: <i>bmi_groupoverweight</i>	0.659	0.386	1.706	0.088	0.45
<i>Anaerostipes caccae</i> et rel.: <i>bmi_groupoverweight</i>	0.313	0.363	0.864	0.387	0.931
<i>Anaerotruncus colihominis</i> et rel.: <i>bmi_groupoverweight</i>	-0.313	0.381	-0.822	0.411	0.931
<i>Anaerovorax odorimutans</i> et rel.: <i>bmi_groupoverweight</i>	-0.299	0.319	-0.937	0.349	0.931
<i>Aquabacterium</i> : <i>bmi_groupoverweight</i>	-0.065	0.351	-0.184	0.854	0.966
<i>Atopobium</i> : <i>bmi_groupoverweight</i>	-0.101	0.365	-0.276	0.782	0.966

	estimate	std_err	wald	pval	AdjPvalue
<i>Bacillus:bmi_groupoverweight</i>	-0.284	0.304	-0.933	0.351	0.931
<i>Bacteroides fragilis et rel.:bmi_groupoverweight</i>	0.698	0.412	1.694	0.09	0.455
<i>Bacteroides intestinalis et rel.:bmi_groupoverweight</i>	1.242	0.409	3.037	0.002	0.018
<i>Bacteroides ovatus et rel.:bmi_groupoverweight</i>	0.847	0.377	2.249	0.024	0.157
<i>Bacteroides plebeius et rel.:bmi_groupoverweight</i>	0.689	0.35	1.97	0.049	0.275
<i>Bacteroides splachnicus et rel.:bmi_groupoverweight</i>	0.174	0.328	0.53	0.596	0.962
<i>Bacteroides stercoris et rel.:bmi_groupoverweight</i>	0.873	0.351	2.488	0.013	0.088
<i>Bacteroides uniformis et rel.:bmi_groupoverweight</i>	1.463	0.501	2.918	0.004	0.025
<i>Bacteroides vulgatus et rel.:bmi_groupoverweight</i>	1.382	0.434	3.181	0.002	0.011
<i>Bifidobacterium:bmi_groupoverweight</i>	0.088	0.365	0.242	0.809	0.966
<i>Bilophila et rel.:bmi_groupoverweight</i>	-0.056	0.317	-0.178	0.859	0.966
<i>Bryantella formatexigens et rel.:bmi_groupoverweight</i>	0.226	0.346	0.653	0.514	0.939
<i>Bulleidia moorei et rel.:bmi_groupoverweight</i>	-0.343	0.316	-1.086	0.278	0.889
<i>Burkholderia:bmi_groupoverweight</i>	-0.325	0.438	-0.741	0.459	0.931
<i>Butyrivibrio crossotus et rel.:bmi_groupoverweight</i>	-0.005	0.343	-0.015	0.988	0.997
<i>Campylobacter:bmi_groupoverweight</i>	-0.184	0.304	-0.605	0.545	0.944
<i>Catenibacterium mitsuokai et rel.:bmi_groupoverweight</i>	0.054	0.394	0.136	0.892	0.967
<i>Clostridium (sensu stricto):bmi_groupoverweight</i>	-0.471	0.322	-1.461	0.144	0.644
<i>Clostridium cellulosi et rel.:bmi_groupoverweight</i>	-0.092	0.446	-0.207	0.836	0.966
<i>Clostridium colinum et rel.:bmi_groupoverweight</i>	-0.288	0.373	-0.771	0.44	0.931
<i>Clostridium difficile et rel.:bmi_groupoverweight</i>	-0.62	0.347	-1.789	0.074	0.393
<i>Clostridium leptum et rel.:bmi_groupoverweight</i>	-0.251	0.351	-0.715	0.474	0.931
<i>Clostridium nexile et rel.:bmi_groupoverweight</i>	-0.044	0.349	-0.125	0.9	0.969
<i>Clostridium orbiscindens et rel.:bmi_groupoverweight</i>	0.076	0.342	0.221	0.825	0.966
<i>Clostridium ramosum et rel.:bmi_groupoverweight</i>	-0.23	0.304	-0.756	0.45	0.931
<i>Clostridium sphenoides et rel.:bmi_groupoverweight</i>	0.062	0.328	0.189	0.85	0.966
<i>Clostridium stercorarium et rel.:bmi_groupoverweight</i>	0.136	0.349	0.389	0.697	0.966
<i>Clostridium symbiosum et rel.:bmi_groupoverweight</i>	0.405	0.342	1.185	0.236	0.853
<i>Collinsella:bmi_groupoverweight</i>	-0.015	0.356	-0.042	0.967	0.997
<i>Coprobacillus cateniformis et rel.:bmi_groupoverweight</i>	-0.335	0.318	-1.053	0.292	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Coprococcus eutactus</i> et rel.:bmi_groupoverweight	-0.066	0.378	-0.175	0.862	0.966
<i>Corynebacterium</i> :bmi_groupoverweight	-0.212	0.302	-0.703	0.482	0.931
<i>Desulfovibrio</i> et rel.:bmi_groupoverweight	-0.069	0.326	-0.211	0.833	0.966
<i>Dialister</i> :bmi_groupoverweight	0.111	0.474	0.235	0.814	0.966
<i>Dorea formicigenerans</i> et rel.:bmi_groupoverweight	0.113	0.339	0.334	0.739	0.966
<i>Eggerthella lenta</i> et rel.:bmi_groupoverweight	-0.188	0.305	-0.617	0.537	0.939
<i>Enterobacter aerogenes</i> et rel.:bmi_groupoverweight	-0.511	0.336	-1.522	0.128	0.603
<i>Enterococcus</i> :bmi_groupoverweight	-0.434	0.389	-1.114	0.265	0.877
<i>Escherichia coli</i> et rel.:bmi_groupoverweight	0.122	0.401	0.305	0.761	0.966
<i>Eubacterium bifforme</i> et rel.:bmi_groupoverweight	-0.837	0.409	-2.046	0.041	0.243
<i>Eubacterium cylindroides</i> et rel.:bmi_groupoverweight	-0.047	0.313	-0.151	0.88	0.966
<i>Eubacterium hallii</i> et rel.:bmi_groupoverweight	0.073	0.352	0.208	0.835	0.966
<i>Eubacterium limosum</i> et rel.:bmi_groupoverweight	0.049	0.312	0.156	0.876	0.966
<i>Eubacterium rectale</i> et rel.:bmi_groupoverweight	0.144	0.357	0.402	0.688	0.966
<i>Eubacterium siraeum</i> et rel.:bmi_groupoverweight	0.084	0.323	0.26	0.795	0.966
<i>Eubacterium ventriosum</i> et rel.:bmi_groupoverweight	0.021	0.338	0.064	0.949	0.991
<i>Faecalibacterium prausnitzii</i> et rel.:bmi_groupoverweight	0.169	0.362	0.466	0.641	0.966
<i>Fusobacteria</i> :bmi_groupoverweight	-0.192	0.306	-0.627	0.53	0.939
<i>Haemophilus</i> :bmi_groupoverweight	0.471	0.414	1.138	0.255	0.862
<i>Helicobacter</i> :bmi_groupoverweight	-0.172	0.304	-0.565	0.572	0.948
<i>Klebsiella pneumoniae</i> et rel.:bmi_groupoverweight	-0.554	0.34	-1.628	0.104	0.514
<i>Lachnobacillus bovis</i> et rel.:bmi_groupoverweight	0.052	0.349	0.149	0.882	0.966
<i>Lachnospira pectinoschiza</i> et rel.:bmi_groupoverweight	-0.037	0.325	-0.115	0.908	0.974
<i>Lactobacillus catenaformis</i> et rel.:bmi_groupoverweight	0.312	0.366	0.851	0.395	0.931
<i>Lactobacillus gasseri</i> et rel.:bmi_groupoverweight	-0.235	0.307	-0.764	0.445	0.931
<i>Lactobacillus plantarum</i> et rel.:bmi_groupoverweight	-0.262	0.31	-0.848	0.397	0.931
<i>Lactobacillus salivarius</i> et rel.:bmi_groupoverweight	-0.298	0.35	-0.851	0.395	0.931
<i>Lactococcus</i> :bmi_groupoverweight	-0.271	0.318	-0.851	0.394	0.931
<i>Leminorella</i> :bmi_groupoverweight	-0.359	0.391	-0.918	0.359	0.931
<i>Megamonas hypermegale</i> et rel.:bmi_groupoverweight	-0.183	0.303	-0.602	0.547	0.945

	estimate	std_err	wald	pval	AdjPvalue
<i>Megasphaera elsdenii</i> et rel.:bmi_groupoverweight	−0.505	0.441	−1.145	0.252	0.862
<i>Mitsuokella multiacida</i> et rel.:bmi_groupoverweight	−0.654	0.571	−1.146	0.252	0.862
<i>Moraxellaceae</i> :bmi_groupoverweight	0.095	0.386	0.247	0.805	0.966
<i>Oceanospirillum</i> :bmi_groupoverweight	−0.101	0.316	−0.319	0.75	0.966
<i>Oscillospira guillermundii</i> et rel.:bmi_groupoverweight	−0.321	0.379	−0.846	0.397	0.931
Outgrouping clostridium cluster XIVa:bmi_groupoverweight	−0.178	0.343	−0.518	0.604	0.966
<i>Oxalobacter formigenes</i> et rel.:bmi_groupoverweight	−0.098	0.381	−0.257	0.797	0.966
<i>Papillibacter cinnamivorans</i> et rel.:bmi_groupoverweight	−0.112	0.341	−0.328	0.743	0.966
<i>Parabacteroides distasonis</i> et rel.:bmi_groupoverweight	0.88	0.375	2.35	0.019	0.123
<i>Peptococcus niger</i> et rel.:bmi_groupoverweight	−0.255	0.327	−0.779	0.436	0.931
<i>Peptostreptococcus micros</i> et rel.:bmi_groupoverweight	−0.269	0.304	−0.886	0.376	0.931
<i>Phascolarctobacterium faecium</i> et rel.:bmi_groupoverweight	0.274	0.371	0.737	0.461	0.931
<i>Prevotella melaninogenica</i> et rel.:bmi_groupoverweight	−1.993	0.601	−3.316	0.001	0.007
<i>Prevotella oralis</i> et rel.:bmi_groupoverweight	−1.263	0.497	−2.543	0.011	0.076
<i>Prevotella ruminicola</i> et rel.:bmi_groupoverweight	0.032	0.35	0.091	0.928	0.986
<i>Prevotella tannerae</i> et rel.:bmi_groupoverweight	0.659	0.371	1.777	0.076	0.396
<i>Propionibacterium</i> :bmi_groupoverweight	−0.167	0.307	−0.542	0.588	0.951
<i>Proteus</i> et rel.:bmi_groupoverweight	−0.289	0.306	−0.944	0.345	0.931
<i>Roseburia intestinalis</i> et rel.:bmi_groupoverweight	0.464	0.345	1.345	0.179	0.737
<i>Ruminococcus bromii</i> et rel.:bmi_groupoverweight	−0.288	0.402	−0.717	0.473	0.931
<i>Ruminococcus callidus</i> et rel.:bmi_groupoverweight	−0.246	0.346	−0.709	0.478	0.931
<i>Ruminococcus gnavus</i> et rel.:bmi_groupoverweight	0.273	0.336	0.813	0.416	0.931
<i>Ruminococcus lactaris</i> et rel.:bmi_groupoverweight	−0.399	0.35	−1.14	0.254	0.862
<i>Ruminococcus obeum</i> et rel.:bmi_groupoverweight	0.172	0.34	0.507	0.612	0.966
<i>Serratia</i> :bmi_groupoverweight	0.591	0.399	1.483	0.138	0.629
<i>Sporobacter termitidis</i> et rel.:bmi_groupoverweight	−0.305	0.36	−0.846	0.397	0.931
<i>Streptococcus bovis</i> et rel.:bmi_groupoverweight	0.306	0.411	0.744	0.457	0.931
<i>Streptococcus intermedius</i> et rel.:bmi_groupoverweight	0.067	0.359	0.188	0.851	0.966
<i>Streptococcus mitis</i> et rel.:bmi_groupoverweight	0.252	0.392	0.643	0.52	0.939
<i>Subdoligranulum variable</i> et rel.:bmi_groupoverweight	0.251	0.35	0.716	0.474	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Sutterella wadsworthia</i> et rel.:bmi_groupoverweight	0.289	0.365	0.792	0.429	0.931
<i>Tannerella</i> et rel.:bmi_groupoverweight	0.369	0.322	1.146	0.252	0.862
Uncultured <i>Bacteroidetes</i> :bmi_groupoverweight	-0.438	0.376	-1.164	0.245	0.862
Uncultured <i>Clostridiales I</i> :bmi_groupoverweight	-0.428	0.386	-1.109	0.267	0.877
Uncultured <i>Clostridiales II</i> :bmi_groupoverweight	-0.631	0.355	-1.777	0.076	0.396
Uncultured <i>Mollicutes</i> :bmi_groupoverweight	-0.683	0.389	-1.756	0.079	0.41
Uncultured <i>Selenomonadaceae</i> :bmi_groupoverweight	-0.396	0.344	-1.151	0.25	0.862
<i>Veillonella</i> :bmi_groupoverweight	-0.46	0.359	-1.28	0.2	0.765
<i>Vibrio</i> :bmi_groupoverweight	-0.351	0.307	-1.142	0.253	0.862
<i>Weissella</i> et rel.:bmi_groupoverweight	-0.732	0.41	-1.788	0.074	0.393
<i>Xanthomonadaceae</i> :bmi_groupoverweight	-0.062	0.413	-0.15	0.881	0.966
<i>Yersinia</i> et rel.:bmi_groupoverweight	-0.256	0.312	-0.82	0.412	0.931
<i>Alcaligenes faecalis</i> et rel.:bmi_groupobese	0.158	0.372	0.425	0.671	0.966
<i>Allistipes</i> et rel.:bmi_groupobese	0.755	0.402	1.879	0.06	0.332
<i>Anaerostipes caccae</i> et rel.:bmi_groupobese	0.863	0.38	2.268	0.023	0.151
<i>Anaerotruncus colihominis</i> et rel.:bmi_groupobese	-0.004	0.362	-0.012	0.99	0.997
<i>Anaerovorax odorimutans</i> et rel.:bmi_groupobese	0.286	0.332	0.86	0.39	0.931
<i>Aquabacterium</i> :bmi_groupobese	0.497	0.342	1.456	0.145	0.644
<i>Atopobium</i> :bmi_groupobese	0.155	0.395	0.391	0.696	0.966
<i>Bacillus</i> :bmi_groupobese	0.225	0.312	0.72	0.472	0.931
<i>Bacteroides fragilis</i> et rel.:bmi_groupobese	0.382	0.43	0.888	0.375	0.931
<i>Bacteroides intestinalis</i> et rel.:bmi_groupobese	0.758	0.381	1.992	0.046	0.264
<i>Bacteroides ovatus</i> et rel.:bmi_groupobese	0.6	0.395	1.519	0.129	0.603
<i>Bacteroides plebeius</i> et rel.:bmi_groupobese	0.624	0.368	1.694	0.09	0.455
<i>Bacteroides splachnicus</i> et rel.:bmi_groupobese	0.493	0.347	1.42	0.156	0.666
<i>Bacteroides stercoris</i> et rel.:bmi_groupobese	0.823	0.337	2.442	0.015	0.098
<i>Bacteroides uniformis</i> et rel.:bmi_groupobese	0.658	0.507	1.297	0.195	0.76
<i>Bacteroides vulgatus</i> et rel.:bmi_groupobese	1.194	0.454	2.632	0.009	0.06
<i>Bifidobacterium</i> :bmi_groupobese	0.541	0.375	1.443	0.149	0.647
<i>Bilophila</i> et rel.:bmi_groupobese	0.235	0.323	0.726	0.468	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Bryantella formatexigens et rel.:bmi_groupobese</i>	0.549	0.356	1.542	0.123	0.584
<i>Bulleidia moorei et rel.:bmi_groupobese</i>	0.201	0.328	0.611	0.541	0.94
<i>Burkholderia:bmi_groupobese</i>	-0.014	0.444	-0.031	0.975	0.997
<i>Butyrivibrio crossotus et rel.:bmi_groupobese</i>	0.456	0.334	1.366	0.172	0.718
<i>Campylobacter:bmi_groupobese</i>	0.302	0.312	0.966	0.334	0.931
<i>Catenibacterium mitsuokai et rel.:bmi_groupobese</i>	0.384	0.382	1.006	0.314	0.931
<i>Clostridium (sensu stricto):bmi_groupobese</i>	0.156	0.331	0.471	0.637	0.966
<i>Clostridium cellulosi et rel.:bmi_groupobese</i>	0.536	0.416	1.287	0.198	0.765
<i>Clostridium colinum et rel.:bmi_groupobese</i>	0.374	0.373	1.003	0.316	0.931
<i>Clostridium difficile et rel.:bmi_groupobese</i>	0.096	0.362	0.266	0.79	0.966
<i>Clostridium leptum et rel.:bmi_groupobese</i>	0.098	0.359	0.272	0.786	0.966
<i>Clostridium nexile et rel.:bmi_groupobese</i>	0.589	0.371	1.588	0.112	0.549
<i>Clostridium orbiscindens et rel.:bmi_groupobese</i>	0.215	0.369	0.584	0.559	0.948
<i>Clostridium ramosum et rel.:bmi_groupobese</i>	0.301	0.312	0.966	0.334	0.931
<i>Clostridium sphenoides et rel.:bmi_groupobese</i>	0.465	0.331	1.405	0.16	0.677
<i>Clostridium stercorarium et rel.:bmi_groupobese</i>	0.512	0.358	1.431	0.152	0.658
<i>Clostridium symbiosum et rel.:bmi_groupobese</i>	0.689	0.345	1.996	0.046	0.263
<i>Collinsella:bmi_groupobese</i>	0.362	0.365	0.992	0.321	0.931
<i>Coprobacillus cateniformis et rel.:bmi_groupobese</i>	0.284	0.322	0.883	0.377	0.931
<i>Coprococcus eutactus et rel.:bmi_groupobese</i>	0.288	0.382	0.752	0.452	0.931
<i>Corynebacterium:bmi_groupobese</i>	0.287	0.31	0.925	0.355	0.931
<i>Desulfovibrio et rel.:bmi_groupobese</i>	0.127	0.318	0.398	0.691	0.966
<i>Dialister:bmi_groupobese</i>	0.656	0.452	1.452	0.146	0.644
<i>Dorea formicigenerans et rel.:bmi_groupobese</i>	0.454	0.348	1.308	0.191	0.75
<i>Eggerthella lenta et rel.:bmi_groupobese</i>	0.329	0.314	1.047	0.295	0.931
<i>Enterobacter aerogenes et rel.:bmi_groupobese</i>	0.463	0.364	1.27	0.204	0.765
<i>Enterococcus:bmi_groupobese</i>	-0.011	0.388	-0.028	0.978	0.997
<i>Escherichia coli et rel.:bmi_groupobese</i>	0.231	0.358	0.647	0.518	0.939
<i>Eubacterium bifforme et rel.:bmi_groupobese</i>	-0.476	0.406	-1.173	0.241	0.86
<i>Eubacterium cylindroides et rel.:bmi_groupobese</i>	0.203	0.316	0.642	0.52	0.939

	estimate	std_err	wald	pval	AdjPvalue
<i>Eubacterium hallii</i> et rel.:bmi_groupobese	0.431	0.35	1.229	0.219	0.813
<i>Eubacterium limosum</i> et rel.:bmi_groupobese	0.283	0.312	0.905	0.366	0.931
<i>Eubacterium rectale</i> et rel.:bmi_groupobese	0.766	0.349	2.194	0.028	0.174
<i>Eubacterium siraeum</i> et rel.:bmi_groupobese	0.425	0.324	1.309	0.191	0.75
<i>Eubacterium ventriosum</i> et rel.:bmi_groupobese	0.535	0.34	1.574	0.116	0.561
<i>Faecalibacterium prausnitzii</i> et rel.:bmi_groupobese	0.595	0.385	1.544	0.123	0.584
<i>Fusobacteria</i> :bmi_groupobese	0.424	0.319	1.327	0.184	0.742
<i>Haemophilus</i> :bmi_groupobese	0.839	0.435	1.928	0.054	0.298
<i>Helicobacter</i> :bmi_groupobese	0.3	0.312	0.961	0.337	0.931
<i>Klebsiella pneumoniae</i> et rel.:bmi_groupobese	0.295	0.367	0.804	0.421	0.931
<i>Lachnobacillus bovis</i> et rel.:bmi_groupobese	0.755	0.347	2.176	0.03	0.179
<i>Lachnospira pectinoschiza</i> et rel.:bmi_groupobese	0.78	0.331	2.357	0.018	0.121
<i>Lactobacillus catenaformis</i> et rel.:bmi_groupobese	0.352	0.38	0.926	0.355	0.931
<i>Lactobacillus gasseri</i> et rel.:bmi_groupobese	0.298	0.313	0.951	0.342	0.931
<i>Lactobacillus plantarum</i> et rel.:bmi_groupobese	0.302	0.328	0.919	0.358	0.931
<i>Lactobacillus salivarius</i> et rel.:bmi_groupobese	0.461	0.35	1.315	0.188	0.75
<i>Lactococcus</i> :bmi_groupobese	0.338	0.334	1.011	0.312	0.931
<i>Leminorella</i> :bmi_groupobese	0.354	0.368	0.962	0.336	0.931
<i>Megamonas hypermegale</i> et rel.:bmi_groupobese	0.303	0.311	0.976	0.329	0.931
<i>Megasphaera elsdenii</i> et rel.:bmi_groupobese	-0.125	0.435	-0.287	0.774	0.966
<i>Mitsuokella multiacida</i> et rel.:bmi_groupobese	0.231	0.551	0.419	0.675	0.966
<i>Moraxellaceae</i> :bmi_groupobese	0.542	0.373	1.454	0.146	0.644
<i>Oceanospirillum</i> :bmi_groupobese	0.48	0.332	1.445	0.148	0.647
<i>Oscillospira guillermundii</i> et rel.:bmi_groupobese	0.386	0.384	1.006	0.315	0.931
<i>Outgrouping clostridium cluster XIVa</i> :bmi_groupobese	0.55	0.346	1.591	0.112	0.549
<i>Oxalobacter formigenes</i> et rel.:bmi_groupobese	-0.045	0.396	-0.113	0.91	0.974
<i>Papillibacter cinnamivorans</i> et rel.:bmi_groupobese	0.215	0.34	0.633	0.527	0.939
<i>Parabacteroides distasonis</i> et rel.:bmi_groupobese	0.567	0.378	1.499	0.134	0.614
<i>Peptococcus niger</i> et rel.:bmi_groupobese	0.209	0.329	0.634	0.526	0.939
<i>Peptostreptococcus micros</i> et rel.:bmi_groupobese	0.301	0.312	0.964	0.335	0.931



	estimate	std_err	wald	pval	AdjPvalue
<i>Phascolarctobacterium faecium</i> et rel.:bmi_groupobese	0.445	0.348	1.282	0.2	0.765
<i>Prevotella melaninogenica</i> et rel.:bmi_groupobese	-0.661	0.583	-1.135	0.256	0.862
<i>Prevotella oralis</i> et rel.:bmi_groupobese	-0.577	0.521	-1.107	0.268	0.877
<i>Prevotella ruminicola</i> et rel.:bmi_groupobese	0.45	0.354	1.274	0.203	0.765
<i>Prevotella tannerae</i> et rel.:bmi_groupobese	0.775	0.38	2.038	0.042	0.245
<i>Propionibacterium</i> :bmi_groupobese	0.325	0.314	1.036	0.3	0.931
<i>Proteus</i> et rel.:bmi_groupobese	0.296	0.318	0.932	0.352	0.931
<i>Roseburia intestinalis</i> et rel.:bmi_groupobese	0.76	0.341	2.232	0.026	0.161
<i>Ruminococcus bromii</i> et rel.:bmi_groupobese	-0.114	0.399	-0.287	0.774	0.966
<i>Ruminococcus callidus</i> et rel.:bmi_groupobese	0.262	0.349	0.75	0.453	0.931
<i>Ruminococcus gnavus</i> et rel.:bmi_groupobese	0.428	0.335	1.277	0.202	0.765
<i>Ruminococcus lactaris</i> et rel.:bmi_groupobese	0.118	0.348	0.339	0.735	0.966
<i>Ruminococcus obeum</i> et rel.:bmi_groupobese	0.32	0.344	0.93	0.352	0.931
<i>Serratia</i> :bmi_groupobese	0.983	0.438	2.246	0.025	0.157
<i>Sporobacter termitidis</i> et rel.:bmi_groupobese	0.3	0.357	0.842	0.4	0.931
<i>Streptococcus bovis</i> et rel.:bmi_groupobese	0.171	0.402	0.425	0.671	0.966
<i>Streptococcus intermedius</i> et rel.:bmi_groupobese	0.198	0.352	0.562	0.574	0.948
<i>Streptococcus mitis</i> et rel.:bmi_groupobese	0.307	0.388	0.792	0.428	0.931
<i>Subdoligranulum variable</i> et rel.:bmi_groupobese	0.818	0.367	2.229	0.026	0.161
<i>Sutterella wadsworthia</i> et rel.:bmi_groupobese	0.622	0.368	1.689	0.091	0.456
<i>Tannerella</i> et rel.:bmi_groupobese	0.46	0.341	1.347	0.178	0.737
Uncultured <i>Bacteroidetes</i> :bmi_groupobese	0.061	0.397	0.153	0.878	0.966
Uncultured <i>Clostridiales I</i> :bmi_groupobese	-0.013	0.36	-0.035	0.972	0.997
Uncultured <i>Clostridiales II</i> :bmi_groupobese	-0.08	0.35	-0.229	0.819	0.966
Uncultured <i>Mollicutes</i> :bmi_groupobese	-0.086	0.383	-0.224	0.823	0.966
Uncultured <i>Selenomonadaceae</i> :bmi_groupobese	0.194	0.354	0.547	0.584	0.951
<i>Veillonella</i> :bmi_groupobese	0.261	0.361	0.721	0.471	0.931
<i>Vibrio</i> :bmi_groupobese	0.175	0.315	0.555	0.579	0.949
<i>Weissella</i> et rel.:bmi_groupobese	-0.076	0.418	-0.18	0.857	0.966
<i>Xanthomonadaceae</i> :bmi_groupobese	0.407	0.442	0.922	0.356	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Yersinia et rel.:bmi_groupobese</i>	0.439	0.331	1.328	0.184	0.742
<i>Alcaligenes faecalis et rel.:timepoint.within.group2</i>	-0.111	0.386	-0.288	0.774	0.966
<i>Allistipes et rel.:timepoint.within.group2</i>	-0.12	0.405	-0.295	0.768	0.966
<i>Anaerostipes caccae et rel.:timepoint.within.group2</i>	-0.246	0.39	-0.631	0.528	0.939
<i>Anaerotruncus colihominis et rel.:timepoint.within.group2</i>	0.139	0.414	0.337	0.736	0.966
<i>Anaerovorax odorimutans et rel.:timepoint.within.group2</i>	-0.232	0.342	-0.679	0.497	0.938
<i>Aquabacterium:timepoint.within.group2</i>	-0.121	0.365	-0.332	0.74	0.966
<i>Atopobium:timepoint.within.group2</i>	-0.142	0.39	-0.364	0.716	0.966
<i>Bacillus:timepoint.within.group2</i>	-0.333	0.335	-0.995	0.32	0.931
<i>Bacteroides fragilis et rel.:timepoint.within.group2</i>	0.253	0.45	0.563	0.573	0.948
<i>Bacteroides intestinalis et rel.:timepoint.within.group2</i>	-0.259	0.401	-0.647	0.517	0.939
<i>Bacteroides ovatus et rel.:timepoint.within.group2</i>	0.027	0.403	0.067	0.947	0.991
<i>Bacteroides plebeius et rel.:timepoint.within.group2</i>	-0.085	0.381	-0.224	0.823	0.966
<i>Bacteroides splachnicus et rel.:timepoint.within.group2</i>	0.111	0.355	0.313	0.754	0.966
<i>Bacteroides stercoris et rel.:timepoint.within.group2</i>	-0.219	0.353	-0.621	0.534	0.939
<i>Bacteroides uniformis et rel.:timepoint.within.group2</i>	0.228	0.525	0.435	0.664	0.966
<i>Bacteroides vulgatus et rel.:timepoint.within.group2</i>	0.218	0.464	0.47	0.638	0.966
<i>Bifidobacterium:timepoint.within.group2</i>	-0.593	0.381	-1.556	0.12	0.576
<i>Bilophila et rel.:timepoint.within.group2</i>	-0.216	0.345	-0.627	0.531	0.939
<i>Bryantella formatexigens et rel.:timepoint.within.group2</i>	-0.152	0.37	-0.411	0.681	0.966
<i>Bulleidia moorei et rel.:timepoint.within.group2</i>	-0.024	0.359	-0.067	0.946	0.991
<i>Burkholderia:timepoint.within.group2</i>	-0.549	0.479	-1.147	0.252	0.862
<i>Butyrivibrio crossotus et rel.:timepoint.within.group2</i>	-0.088	0.359	-0.245	0.807	0.966
<i>Campylobacter:timepoint.within.group2</i>	-0.238	0.335	-0.711	0.477	0.931
<i>Catenibacterium mitsuokai et rel.:timepoint.within.group2</i>	-0.418	0.434	-0.962	0.336	0.931
<i>Clostridium (sensu stricto):timepoint.within.group2</i>	-0.281	0.354	-0.795	0.427	0.931
<i>Clostridium cellulosi et rel.:timepoint.within.group2</i>	-0.049	0.471	-0.103	0.918	0.98
<i>Clostridium colinum et rel.:timepoint.within.group2</i>	-0.17	0.394	-0.431	0.666	0.966
<i>Clostridium difficile et rel.:timepoint.within.group2</i>	-0.217	0.383	-0.566	0.572	0.948
<i>Clostridium leptum et rel.:timepoint.within.group2</i>	-0.202	0.399	-0.506	0.613	0.966

	estimate	std_err	wald	pval	AdjPvalue
<i>Clostridium nexile</i> et rel.:timepoint.within.group2	-0.274	0.404	-0.678	0.498	0.938
<i>Clostridium orbiscindens</i> et rel.:timepoint.within.group2	-0.095	0.38	-0.25	0.803	0.966
<i>Clostridium ramosum</i> et rel.:timepoint.within.group2	-0.199	0.334	-0.595	0.551	0.948
<i>Clostridium sphenoides</i> et rel.:timepoint.within.group2	-0.247	0.351	-0.705	0.481	0.931
<i>Clostridium stercorearium</i> et rel.:timepoint.within.group2	-0.347	0.348	-0.996	0.319	0.931
<i>Clostridium symbiosum</i> et rel.:timepoint.within.group2	-0.228	0.363	-0.629	0.529	0.939
<i>Collinsella</i> :timepoint.within.group2	-0.183	0.389	-0.472	0.637	0.966
<i>Coprobacillus cateniformis</i> et rel.:timepoint.within.group2	-0.24	0.344	-0.697	0.486	0.931
<i>Coprococcus eutactus</i> et rel.:timepoint.within.group2	-0.333	0.398	-0.836	0.403	0.931
<i>Corynebacterium</i> :timepoint.within.group2	-0.261	0.333	-0.785	0.432	0.931
<i>Desulfovibrio</i> et rel.:timepoint.within.group2	-0.054	0.343	-0.156	0.876	0.966
<i>Dialister</i> :timepoint.within.group2	-0.151	0.496	-0.304	0.761	0.966
<i>Dorea formicigenerans</i> et rel.:timepoint.within.group2	-0.164	0.383	-0.429	0.668	0.966
<i>Eggerthella lenta</i> et rel.:timepoint.within.group2	-0.163	0.336	-0.485	0.628	0.966
<i>Enterobacter aerogenes</i> et rel.:timepoint.within.group2	-0.089	0.382	-0.234	0.815	0.966
<i>Enterococcus</i> :timepoint.within.group2	-0.534	0.408	-1.309	0.191	0.75
<i>Escherichia coli</i> et rel.:timepoint.within.group2	0.055	0.422	0.129	0.897	0.968
<i>Eubacterium bifforme</i> et rel.:timepoint.within.group2	-0.08	0.432	-0.185	0.854	0.966
<i>Eubacterium cylindroides</i> et rel.:timepoint.within.group2	-0.228	0.341	-0.668	0.504	0.939
<i>Eubacterium hallii</i> et rel.:timepoint.within.group2	-0.327	0.386	-0.846	0.398	0.931
<i>Eubacterium limosum</i> et rel.:timepoint.within.group2	-0.259	0.336	-0.772	0.44	0.931
<i>Eubacterium rectale</i> et rel.:timepoint.within.group2	-0.408	0.368	-1.108	0.268	0.877
<i>Eubacterium siraeum</i> et rel.:timepoint.within.group2	-0.088	0.352	-0.25	0.802	0.966
<i>Eubacterium ventriosum</i> et rel.:timepoint.within.group2	-0.393	0.358	-1.099	0.272	0.883
<i>Faecalibacterium prausnitzii</i> et rel.:timepoint.within.group2	-0.493	0.401	-1.229	0.219	0.813
<i>Fusobacteria</i> :timepoint.within.group2	-0.162	0.339	-0.476	0.634	0.966
<i>Haemophilus</i> :timepoint.within.group2	-0.035	0.451	-0.079	0.938	0.991
<i>Helicobacter</i> :timepoint.within.group2	-0.26	0.334	-0.779	0.436	0.931
<i>Klebsiella pneumoniae</i> et rel.:timepoint.within.group2	-0.033	0.389	-0.085	0.932	0.987
<i>Lachnobacillus bovis</i> et rel.:timepoint.within.group2	0.025	0.383	0.067	0.947	0.991

	estimate	std_err	wald	pval	AdjPvalue
<i>Lachnospira pectinoschiza</i> et rel.:timepoint.within.group2	-0.342	0.354	-0.968	0.333	0.931
<i>Lactobacillus catenaformis</i> et rel.:timepoint.within.group2	-0.613	0.458	-1.34	0.18	0.739
<i>Lactobacillus gasseri</i> et rel.:timepoint.within.group2	-0.292	0.333	-0.876	0.381	0.931
<i>Lactobacillus plantarum</i> et rel.:timepoint.within.group2	-0.34	0.339	-1.002	0.316	0.931
<i>Lactobacillus salivarius</i> et rel.:timepoint.within.group2	-0.479	0.359	-1.333	0.183	0.742
<i>Lactococcus</i> :timepoint.within.group2	-0.318	0.341	-0.933	0.351	0.931
<i>Leminorella</i> :timepoint.within.group2	-0.199	0.394	-0.504	0.614	0.966
<i>Megamonas hypermegale</i> et rel.:timepoint.within.group2	-0.261	0.333	-0.785	0.432	0.931
<i>Megasphaera elsdenii</i> et rel.:timepoint.within.group2	-0.375	0.485	-0.774	0.439	0.931
<i>Mitsuokella multiacida</i> et rel.:timepoint.within.group2	-0.025	0.639	-0.039	0.969	0.997
<i>Moraxellaceae</i> :timepoint.within.group2	-0.565	0.444	-1.27	0.204	0.765
<i>Oceanospirillum</i> :timepoint.within.group2	-0.136	0.347	-0.39	0.696	0.966
<i>Oscillospira guillermundii</i> et rel.:timepoint.within.group2	0.23	0.398	0.577	0.564	0.948
Outgrouping clostridium cluster XIVa:timepoint.within.group2	-0.252	0.367	-0.687	0.492	0.936
<i>Oxalobacter formigenes</i> et rel.:timepoint.within.group2	0.138	0.418	0.331	0.741	0.966
<i>Papillibacter cinnamivorans</i> et rel.:timepoint.within.group2	-0.397	0.359	-1.107	0.268	0.877
<i>Parabacteroides distasonis</i> et rel.:timepoint.within.group2	0.062	0.407	0.152	0.879	0.966
<i>Peptococcus niger</i> et rel.:timepoint.within.group2	-0.257	0.356	-0.722	0.47	0.931
<i>Peptostreptococcus micros</i> et rel.:timepoint.within.group2	-0.336	0.334	-1.004	0.315	0.931
<i>Phascolarctobacterium faecium</i> et rel.:timepoint.within.group2	-0.052	0.374	-0.14	0.888	0.967
<i>Prevotella melaninogenica</i> et rel.:timepoint.within.group2	-0.423	0.572	-0.74	0.459	0.931
<i>Prevotella oralis</i> et rel.:timepoint.within.group2	-0.355	0.492	-0.721	0.471	0.931
<i>Prevotella ruminicola</i> et rel.:timepoint.within.group2	-0.097	0.371	-0.261	0.794	0.966
<i>Prevotella tannerae</i> et rel.:timepoint.within.group2	0.096	0.397	0.243	0.808	0.966
<i>Propionibacterium</i> :timepoint.within.group2	-0.243	0.337	-0.719	0.472	0.931
<i>Proteus</i> et rel.:timepoint.within.group2	-0.238	0.341	-0.698	0.485	0.931
<i>Roseburia intestinalis</i> et rel.:timepoint.within.group2	-0.304	0.362	-0.839	0.402	0.931
<i>Ruminococcus bromii</i> et rel.:timepoint.within.group2	-0.256	0.443	-0.578	0.564	0.948
<i>Ruminococcus callidus</i> et rel.:timepoint.within.group2	-0.154	0.389	-0.395	0.693	0.966
<i>Ruminococcus gnavus</i> et rel.:timepoint.within.group2	-0.317	0.357	-0.888	0.375	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Ruminococcus lactaris</i> et rel.:timepoint.within.group2	0.062	0.418	0.147	0.883	0.966
<i>Ruminococcus obeum</i> et rel.:timepoint.within.group2	-0.345	0.363	-0.951	0.342	0.931
<i>Serratia</i> :timepoint.within.group2	-0.15	0.451	-0.331	0.74	0.966
<i>Sporobacter termitidis</i> et rel.:timepoint.within.group2	-0.021	0.372	-0.057	0.955	0.991
<i>Streptococcus bovis</i> et rel.:timepoint.within.group2	-0.521	0.429	-1.213	0.225	0.826
<i>Streptococcus intermedius</i> et rel.:timepoint.within.group2	-0.357	0.377	-0.948	0.343	0.931
<i>Streptococcus mitis</i> et rel.:timepoint.within.group2	-0.521	0.426	-1.223	0.222	0.817
<i>Subdoligranulum variable</i> at rel.:timepoint.within.group2	-0.268	0.378	-0.709	0.478	0.931
<i>Sutterella wadsworthia</i> et rel.:timepoint.within.group2	-0.143	0.38	-0.376	0.707	0.966
<i>Tannerella</i> et rel.:timepoint.within.group2	-0.082	0.354	-0.233	0.816	0.966
Uncultured <i>Bacteroidetes</i> :timepoint.within.group2	-0.278	0.41	-0.679	0.497	0.938
Uncultured <i>Clostridiales I</i> :timepoint.within.group2	0.138	0.422	0.327	0.744	0.966
Uncultured <i>Clostridiales II</i> :timepoint.within.group2	0.077	0.391	0.196	0.845	0.966
Uncultured <i>Mollicutes</i> :timepoint.within.group2	0.077	0.45	0.171	0.864	0.966
Uncultured <i>Selenomonadaceae</i> :timepoint.within.group2	-0.258	0.367	-0.703	0.482	0.931
<i>Veillonella</i> :timepoint.within.group2	-0.431	0.396	-1.089	0.276	0.889
<i>Vibrio</i> :timepoint.within.group2	-0.129	0.338	-0.381	0.703	0.966
<i>Weissella</i> et rel.:timepoint.within.group2	-0.755	0.43	-1.754	0.08	0.41
<i>Xanthomonadaceae</i> :timepoint.within.group2	-0.629	0.417	-1.508	0.132	0.607
<i>Yersinia</i> et rel.:timepoint.within.group2	-0.094	0.345	-0.272	0.786	0.966
<i>bmi_groupoverweight</i> :timepoint.within.group2	0.083	0.433	0.192	0.848	0.966
<i>bmi_groupobese</i> :timepoint.within.group2	0.154	0.472	0.325	0.745	0.966
<i>Alcaligenes faecalis</i> et rel.: <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.01	0.531	-0.019	0.985	0.997
<i>Allistipes</i> et rel.: <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.265	0.552	-0.479	0.632	0.966
<i>Anaerostipes caccae</i> et rel.: <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.319	0.512	-0.622	0.534	0.939
<i>naerotruncus colihominis</i> et rel.: <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.241	0.561	-0.43	0.667	0.966
<i>naerovorax odorimutans</i> et rel.: <i>bmi_groupoverweight</i> :timepoint.within.group2	0.004	0.459	0.008	0.993	0.997
<i>Aquabacterium</i> : <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.189	0.5	-0.378	0.705	0.966
<i>Atopobium</i> : <i>bmi_groupoverweight</i> :timepoint.within.group2	-0.296	0.533	-0.554	0.579	0.949
<i>Bacillus</i> : <i>bmi_groupoverweight</i> :timepoint.within.group2	0.137	0.444	0.309	0.757	0.966

	estimate	std_err	wald	pval	AdjPvalue
<i>Bacteroides fragilis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.448	0.589	-0.761	0.447	0.931
<i>Bacteroides intestinalis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.087	0.592	-0.147	0.883	0.966
<i>Bacteroides ovatus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.367	0.56	-0.656	0.512	0.939
<i>Bacteroides plebeius</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.248	0.511	-0.486	0.627	0.966
<i>Bacteroides splachnicus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.357	0.482	-0.741	0.458	0.931
<i>Bacteroides stercoris</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.123	0.516	-0.238	0.812	0.966
<i>Bacteroides uniformis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.466	0.71	-0.656	0.512	0.939
<i>Bacteroides vulgatus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.512	0.643	-0.796	0.426	0.931
<i>Bifidobacterium</i> :bmi_groupoverweight:timepoint.within.group2	0.302	0.522	0.578	0.563	0.948
<i>Bilophila</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.006	0.462	-0.013	0.99	0.997
<i>Bryantella formatexigens</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.505	0.504	-1.001	0.317	0.931
<i>Bulleidia moorei</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.23	0.473	-0.486	0.627	0.966
<i>Burkholderia</i> :bmi_groupoverweight:timepoint.within.group2	0.551	0.628	0.877	0.38	0.931
<i>Butyrivibrio crossotus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.101	0.5	-0.202	0.84	0.966
<i>Campylobacter</i> :bmi_groupoverweight:timepoint.within.group2	0.067	0.443	0.151	0.88	0.966
<i>Lactobacillus mitsuokai</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.287	0.589	0.487	0.626	0.966
<i>Clostridium (sensu stricto)</i> :bmi_groupoverweight:timepoint.within.group2	0.175	0.468	0.373	0.709	0.966
<i>Clostridium cellulosi</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.075	0.66	0.114	0.909	0.974
<i>Clostridium colinum</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.324	0.529	-0.611	0.541	0.94
<i>Clostridium difficile</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.03	0.5	0.059	0.953	0.991
<i>Clostridium leptum</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.021	0.518	0.041	0.968	0.997
<i>Clostridium nexile</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.411	0.523	-0.785	0.432	0.931
<i>Clostridium orbiscindens</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.456	0.495	-0.921	0.357	0.931
<i>Clostridium ramosum</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.044	0.445	0.1	0.92	0.981
<i>Clostridium sphenoides</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.284	0.479	-0.594	0.553	0.948
<i>Clostridium stercorearium</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.106	0.51	0.208	0.835	0.966
<i>Clostridium symbiosum</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.303	0.489	-0.619	0.536	0.939
<i>Collinsella</i> :bmi_groupoverweight:timepoint.within.group2	-0.302	0.514	-0.587	0.558	0.948
<i>Coprotherobacter acetivorans</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.02	0.46	-0.044	0.965	0.997
<i>Coprococcus eutactus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.544	0.523	-1.041	0.298	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Corynebacterium:bmi_groupoverweight:timepoint.within.group2</i>	0.065	0.442	0.148	0.883	0.966
<i>Desulfovibrio et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.159	0.478	-0.333	0.739	0.966
<i>Dialister:bmi_groupoverweight:timepoint.within.group2</i>	0.047	0.699	0.068	0.946	0.991
<i>Dorea formicigenerans et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.489	0.498	-0.982	0.326	0.931
<i>Eggerthella lenta et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.092	0.445	-0.206	0.837	0.966
<i>Enterobacter aerogenes et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.153	0.491	-0.312	0.755	0.966
<i>Enterococcus:bmi_groupoverweight:timepoint.within.group2</i>	0.244	0.521	0.468	0.64	0.966
<i>Escherichia coli et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.231	0.626	-0.37	0.712	0.966
<i>Eubacterium bifforme et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.462	0.584	-0.791	0.429	0.931
<i>Eubacterium cylindroides et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.054	0.455	-0.118	0.906	0.974
<i>Eubacterium hallii et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.447	0.507	-0.882	0.378	0.931
<i>Eubacterium limosum et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.101	0.454	-0.223	0.824	0.966
<i>Eubacterium rectale et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.354	0.508	-0.696	0.486	0.931
<i>Eubacterium siraeum et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.009	0.474	-0.019	0.985	0.997
<i>Eubacterium ventriosum et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.188	0.481	-0.392	0.695	0.966
<i>Lactobacillus reuteri et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.246	0.535	-0.461	0.645	0.966
<i>Fusobacteria:bmi_groupoverweight:timepoint.within.group2</i>	-0.038	0.448	-0.086	0.931	0.987
<i>Haemophilus:bmi_groupoverweight:timepoint.within.group2</i>	-0.133	0.591	-0.225	0.822	0.966
<i>Helicobacter:bmi_groupoverweight:timepoint.within.group2</i>	0.084	0.443	0.19	0.849	0.966
<i>Klebsiella pneumoniae et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.175	0.5	-0.35	0.726	0.966
<i>Lachnobacillus bovis et rel.:bmi_groupoverweight:timepoint.within.group2</i>	-0.32	0.517	-0.62	0.535	0.939
<i>Lachnospira pectinoschiza et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.047	0.489	0.097	0.923	0.982
<i>Lactobacillus cateniformis et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.297	0.563	0.527	0.598	0.963
<i>Lactobacillus gasseri et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.057	0.444	0.129	0.897	0.968
<i>Lactobacillus plantarum et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.11	0.451	0.245	0.806	0.966
<i>Lactobacillus salivarius et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.198	0.487	0.406	0.685	0.966
<i>Lactococcus:bmi_groupoverweight:timepoint.within.group2</i>	0.075	0.455	0.165	0.869	0.966
<i>Leminorella:bmi_groupoverweight:timepoint.within.group2</i>	0.28	0.549	0.509	0.611	0.966
<i>Megamonas hypermegale et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.109	0.443	0.245	0.806	0.966
<i>Megasphaera elsdenii et rel.:bmi_groupoverweight:timepoint.within.group2</i>	0.563	0.648	0.869	0.385	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Mitsuokella multiacida</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.276	0.838	0.329	0.742	0.966
<i>Moraxellaceae</i> :bmi_groupoverweight:timepoint.within.group2	0.398	0.571	0.698	0.485	0.931
<i>Oceanospirillum</i> :bmi_groupoverweight:timepoint.within.group2	-0.115	0.46	-0.25	0.803	0.966
<i>Oscillospira guillermundii</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.405	0.548	-0.739	0.46	0.931
<i>Outgrouping clostridium cluster XIVa</i> :bmi_groupoverweight:timepoint.within.group2	-0.164	0.491	-0.335	0.737	0.966
<i>Oxalobacter formigenes</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.24	0.544	-0.442	0.658	0.966
<i>Papillibacter cinnamivorans</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.358	0.48	-0.746	0.455	0.931
<i>Parabacteroides distasonis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.396	0.552	-0.717	0.474	0.931
<i>Peptococcus niger</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.103	0.472	-0.219	0.827	0.966
<i>Peptostreptococcus micros</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.19	0.444	0.427	0.669	0.966
<i>Parascolarctobacterium faecium</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.093	0.547	0.171	0.865	0.966
<i>Prevotella melaninogenica</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.458	0.815	0.561	0.575	0.948
<i>Prevotella oralis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.159	0.68	0.233	0.816	0.966
<i>Prevotella ruminicola</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.086	0.5	-0.172	0.863	0.966
<i>Prevotella tannerae</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.468	0.538	-0.87	0.384	0.931
<i>Propionibacterium</i> :bmi_groupoverweight:timepoint.within.group2	0.063	0.448	0.14	0.889	0.967
<i>Proteus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.105	0.449	0.234	0.815	0.966
<i>Roseburia intestinalis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.286	0.499	-0.573	0.566	0.948
<i>Ruminococcus bromii</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.174	0.58	-0.301	0.764	0.966
<i>Ruminococcus callidus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.033	0.523	0.062	0.95	0.991
<i>Ruminococcus gnavus</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.414	0.484	-0.855	0.393	0.931
<i>Ruminococcus lactaris</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.461	0.534	-0.863	0.388	0.931
<i>Ruminococcus obeum</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.328	0.488	-0.672	0.502	0.939
<i>Serratia</i> :bmi_groupoverweight:timepoint.within.group2	-0.078	0.578	-0.136	0.892	0.967
<i>Sporobacter termitidis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.099	0.523	-0.189	0.85	0.966
<i>Streptococcus bovis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.003	0.577	-0.005	0.996	0.997
<i>Streptococcus intermedius</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.158	0.509	0.31	0.756	0.966
<i>Streptococcus mitis</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.305	0.558	0.546	0.585	0.951
<i>Subdoligranulum variable</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.144	0.502	-0.287	0.774	0.966
<i>Sutterella wadsworthia</i> et rel.:bmi_groupoverweight:timepoint.within.group2	-0.231	0.519	-0.445	0.656	0.966



	estimate	std_err	wald	pval	AdjPvalue
<i>Tannerella</i> et rel.:bmi_groupoverweight:timepoint.within.group2	−0.208	0.473	−0.44	0.66	0.966
<i>Uncultured Bacteroidetes</i> :bmi_groupoverweight:timepoint.within.group2	0.252	0.531	0.476	0.634	0.966
<i>Uncultured Clostridiales I</i> :bmi_groupoverweight:timepoint.within.group2	−0.557	0.56	−0.994	0.32	0.931
<i>Uncultured Clostridiales II</i> :bmi_groupoverweight:timepoint.within.group2	−0.149	0.52	−0.287	0.774	0.966
<i>Uncultured Mollicutes</i> :bmi_groupoverweight:timepoint.within.group2	−0.514	0.576	−0.893	0.372	0.931
<i>Uncultured Selenomonadaceae</i> :bmi_groupoverweight:timepoint.within.group2	0.204	0.503	0.406	0.685	0.966
<i>Veillonella</i> :bmi_groupoverweight:timepoint.within.group2	0.348	0.524	0.663	0.507	0.939
<i>Vibrio</i> :bmi_groupoverweight:timepoint.within.group2	0.013	0.448	0.03	0.976	0.997
<i>Weissella</i> et rel.:bmi_groupoverweight:timepoint.within.group2	0.487	0.532	0.915	0.36	0.931
<i>Xanthomonadaceae</i> :bmi_groupoverweight:timepoint.within.group2	0.53	0.58	0.913	0.361	0.931
<i>Yersinia</i> et rel.:bmi_groupoverweight:timepoint.within.group2	−0.138	0.452	−0.306	0.759	0.966
<i>Alcaligenes faecalis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.019	0.576	0.033	0.974	0.997
<i>Allistipes</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.036	0.594	−0.061	0.952	0.991
<i>Anaerostipes caccae</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.331	0.58	−0.571	0.568	0.948
<i>Anaerotruncus colihominis</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.303	0.557	−0.544	0.586	0.951
<i>Anaerovorax odorimutans</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.232	0.509	−0.455	0.649	0.966
<i>Aquabacterium</i> :bmi_groupobese:timepoint.within.group2	−0.295	0.508	−0.58	0.562	0.948
<i>Atopobium</i> :bmi_groupobese:timepoint.within.group2	0.042	0.613	0.068	0.946	0.991
<i>Bacillus</i> :bmi_groupobese:timepoint.within.group2	0.003	0.481	0.006	0.995	0.997
<i>Bacteroides fragilis</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.428	0.633	−0.677	0.499	0.938
<i>Bacteroides intestinalis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.372	0.564	0.659	0.51	0.939
<i>Bacteroides ovatus</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.153	0.614	−0.25	0.803	0.966
<i>Bacteroides plebeius</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.097	0.565	−0.172	0.864	0.966
<i>Bacteroides splachnicus</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.218	0.543	−0.401	0.688	0.966
<i>Bacteroides stercoris</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.186	0.515	−0.36	0.719	0.966
<i>Bacteroides uniformis</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.54	0.726	−0.744	0.457	0.931
<i>Bacteroides vulgatus</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.417	0.676	−0.617	0.537	0.939
<i>Bifidobacterium</i> :bmi_groupobese:timepoint.within.group2	0.102	0.57	0.178	0.858	0.966
<i>Bilophila</i> et rel.:bmi_groupobese:timepoint.within.group2	0.083	0.495	0.168	0.866	0.966
<i>Bryantella formatexigens</i> et rel.:bmi_groupobese:timepoint.within.group2	−0.464	0.556	−0.835	0.404	0.931

	estimate	std_err	wald	pval	AdjPvalue
<i>Bulleidia moorei</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.227	0.523	-0.434	0.664	0.966
<i>Burkholderia</i> :bmi_groupobese:timepoint.within.group2	0.544	0.678	0.802	0.422	0.931
<i>Butyrivibrio crossotus</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.001	0.514	-0.002	0.998	0.998
<i>Campylobacter</i> :bmi_groupobese:timepoint.within.group2	-0.109	0.481	-0.226	0.821	0.966
<i>Lactobacillus mitsuokai</i> et rel.:bmi_groupobese:timepoint.within.group2	0.106	0.572	0.185	0.853	0.966
<i>Clostridium (sensu stricto)</i> :bmi_groupobese:timepoint.within.group2	-0.107	0.501	-0.214	0.831	0.966
<i>Clostridium cellulosi</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.266	0.612	-0.435	0.664	0.966
<i>Clostridium colinum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.326	0.555	-0.587	0.557	0.948
<i>Clostridium difficile</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.237	0.538	-0.44	0.66	0.966
<i>Clostridium leptum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.102	0.548	-0.187	0.852	0.966
<i>Clostridium nexile</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.437	0.591	-0.74	0.459	0.931
<i>Clostridium orbiscindens</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.469	0.568	-0.826	0.409	0.931
<i>Clostridium ramosum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.172	0.481	-0.358	0.721	0.966
<i>Clostridium sphenoides</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.452	0.509	-0.888	0.375	0.931
<i>Clostridium stercorarium</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.331	0.567	-0.584	0.559	0.948
<i>Clostridium symbiosum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.465	0.519	-0.895	0.371	0.931
<i>Collinsella</i> :bmi_groupobese:timepoint.within.group2	-0.382	0.545	-0.701	0.484	0.931
<i>Coprotherobacter cateniformis</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.222	0.49	-0.453	0.65	0.966
<i>Coprococcus eutactus</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.136	0.575	-0.237	0.812	0.966
<i>Corynebacterium</i> :bmi_groupobese:timepoint.within.group2	-0.098	0.48	-0.204	0.838	0.966
<i>Desulfovibrio</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.276	0.491	-0.561	0.575	0.948
<i>Dialister</i> :bmi_groupobese:timepoint.within.group2	-0.649	0.652	-0.996	0.319	0.931
<i>Dorea formicigenerans</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.444	0.538	-0.824	0.41	0.931
<i>Eggerthella lenta</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.244	0.485	-0.504	0.614	0.966
<i>Enterobacter aerogenes</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.442	0.533	-0.829	0.407	0.931
<i>Enterococcus</i> :bmi_groupobese:timepoint.within.group2	0.076	0.538	0.142	0.887	0.967
<i>Escherichia coli</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.401	0.563	-0.712	0.476	0.931
<i>Eubacterium bifforme</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.3	0.609	-0.492	0.623	0.966
<i>Eubacterium cylindroides</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.12	0.485	-0.248	0.804	0.966
<i>Eubacterium hallii</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.244	0.532	-0.458	0.647	0.966

	estimate	std_err	wald	pval	AdjPvalue
<i>Eubacterium limosum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.09	0.482	-0.187	0.852	0.966
<i>Eubacterium rectale</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.386	0.526	-0.734	0.463	0.931
<i>Eubacterium siraeum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.26	0.5	-0.521	0.603	0.966
<i>Eubacterium ventriosum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.117	0.515	-0.227	0.82	0.966
<i>Faecalibacterium prausnitzii</i> et rel.:bmi_groupobese:timepoint.within.group2	0.222	0.603	0.368	0.713	0.966
<i>Fusobacteria</i> :bmi_groupobese:timepoint.within.group2	-0.172	0.49	-0.35	0.726	0.966
<i>Haemophilus</i> :bmi_groupobese:timepoint.within.group2	-0.015	0.66	-0.022	0.982	0.997
<i>Helicobacter</i> :bmi_groupobese:timepoint.within.group2	-0.076	0.481	-0.159	0.874	0.966
<i>Klebsiella pneumoniae</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.427	0.538	-0.795	0.427	0.931
<i>Lachnobacillus bovis</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.578	0.528	-1.093	0.274	0.887
<i>Lachnospira pectinoschiza</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.406	0.509	-0.798	0.425	0.931
<i>Lactobacillus cateniformis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.215	0.589	0.365	0.715	0.966
<i>Lactobacillus gasseri</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.104	0.481	-0.217	0.828	0.966
<i>Lactobacillus plantarum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.084	0.489	-0.172	0.864	0.966
<i>Lactobacillus salivarius</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.006	0.517	-0.011	0.991	0.997
<i>Lactococcus</i> :bmi_groupobese:timepoint.within.group2	-0.193	0.494	-0.391	0.696	0.966
<i>Leminorella</i> :bmi_groupobese:timepoint.within.group2	-0.031	0.537	-0.058	0.954	0.991
<i>Megamonas hypermegale</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.098	0.48	-0.204	0.838	0.966
<i>Megasphaera elsdenii</i> et rel.:bmi_groupobese:timepoint.within.group2	0.004	0.619	0.007	0.994	0.997
<i>Mitsuokella multiacida</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.351	0.773	-0.454	0.65	0.966
<i>Moraxellaceae</i> :bmi_groupobese:timepoint.within.group2	0.169	0.574	0.294	0.768	0.966
<i>Oceanospirillum</i> :bmi_groupobese:timepoint.within.group2	-0.192	0.508	-0.378	0.705	0.966
<i>Oscillospira guillermondii</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.567	0.548	-1.035	0.301	0.931
<i>Outgrouping clostridium cluster XIVa</i> :bmi_groupobese:timepoint.within.group2	-0.413	0.52	-0.794	0.427	0.931
<i>Oxalobacter formigenes</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.228	0.6	-0.38	0.704	0.966
<i>Papillibacter cinnamivorans</i> et rel.:bmi_groupobese:timepoint.within.group2	0.168	0.51	0.33	0.742	0.966
<i>Parabacteroides distasonis</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.162	0.586	-0.276	0.782	0.966
<i>Peptococcus niger</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.203	0.503	-0.403	0.687	0.966
<i>Peptostreptococcus micros</i> et rel.:bmi_groupobese:timepoint.within.group2	0.024	0.482	0.05	0.96	0.995
<i>hascolarctobacterium faecium</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.228	0.521	-0.437	0.662	0.966

	estimate	std_err	wald	pval	AdjPvalue
<i>Prevotella melaninogenica</i> et rel.:bmi_groupobese:timepoint.within.group2	0.531	0.835	0.637	0.524	0.939
<i>Prevotella oralis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.531	0.767	0.693	0.489	0.932
<i>Prevotella ruminicola</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.07	0.527	-0.132	0.895	0.968
<i>Prevotella tannerae</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.377	0.587	-0.643	0.521	0.939
<i>Propionibacterium</i> :bmi_groupobese:timepoint.within.group2	-0.082	0.483	-0.169	0.866	0.966
<i>Proteus</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.128	0.487	-0.262	0.793	0.966
<i>Roseburia intestinalis</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.364	0.518	-0.702	0.483	0.931
<i>Ruminococcus bromii</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.022	0.6	-0.036	0.971	0.997
<i>Ruminococcus callidus</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.185	0.535	-0.346	0.73	0.966
<i>Ruminococcus gnavus</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.35	0.503	-0.696	0.487	0.931
<i>Ruminococcus lactaris</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.551	0.553	-0.996	0.319	0.931
<i>Ruminococcus obeum</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.164	0.522	-0.313	0.754	0.966
<i>Serratia</i> :bmi_groupobese:timepoint.within.group2	-0.221	0.676	-0.327	0.744	0.966
<i>Sporobacter termitidis</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.114	0.534	-0.213	0.831	0.966
<i>Streptococcus bovis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.233	0.602	0.386	0.699	0.966
<i>Streptococcus intermedius</i> et rel.:bmi_groupobese:timepoint.within.group2	0.133	0.532	0.25	0.802	0.966
<i>Streptococcus mitis</i> et rel.:bmi_groupobese:timepoint.within.group2	0.208	0.58	0.358	0.72	0.966
<i>Subdoligranulum variable</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.395	0.553	-0.714	0.475	0.931
<i>Sutterella wadsworthia</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.077	0.537	-0.144	0.885	0.967
<i>Tannerella</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.107	0.533	-0.2	0.841	0.966
Uncultured Bacteroidetes:bmi_groupobese:timepoint.within.group2	0.286	0.597	0.479	0.632	0.966
Uncultured Clostridiales I:bmi_groupobese:timepoint.within.group2	-0.457	0.561	-0.815	0.415	0.931
Uncultured Clostridiales II:bmi_groupobese:timepoint.within.group2	-0.252	0.531	-0.475	0.635	0.966
Uncultured Mollicutes:bmi_groupobese:timepoint.within.group2	-0.696	0.587	-1.186	0.236	0.853
Uncultured Selenomonadaceae:bmi_groupobese:timepoint.within.group2	0.31	0.557	0.556	0.578	0.949
<i>Veillonella</i> :bmi_groupobese:timepoint.within.group2	0.114	0.549	0.207	0.836	0.966
<i>Vibrio</i> :bmi_groupobese:timepoint.within.group2	-0.251	0.484	-0.518	0.605	0.966
<i>Weissella</i> et rel.:bmi_groupobese:timepoint.within.group2	0.305	0.562	0.542	0.588	0.951
<i>Xanthomonadaceae</i> :bmi_groupobese:timepoint.within.group2	0.346	0.692	0.5	0.617	0.966
<i>Yersinia</i> et rel.:bmi_groupobese:timepoint.within.group2	-0.447	0.497	-0.899	0.369	0.931