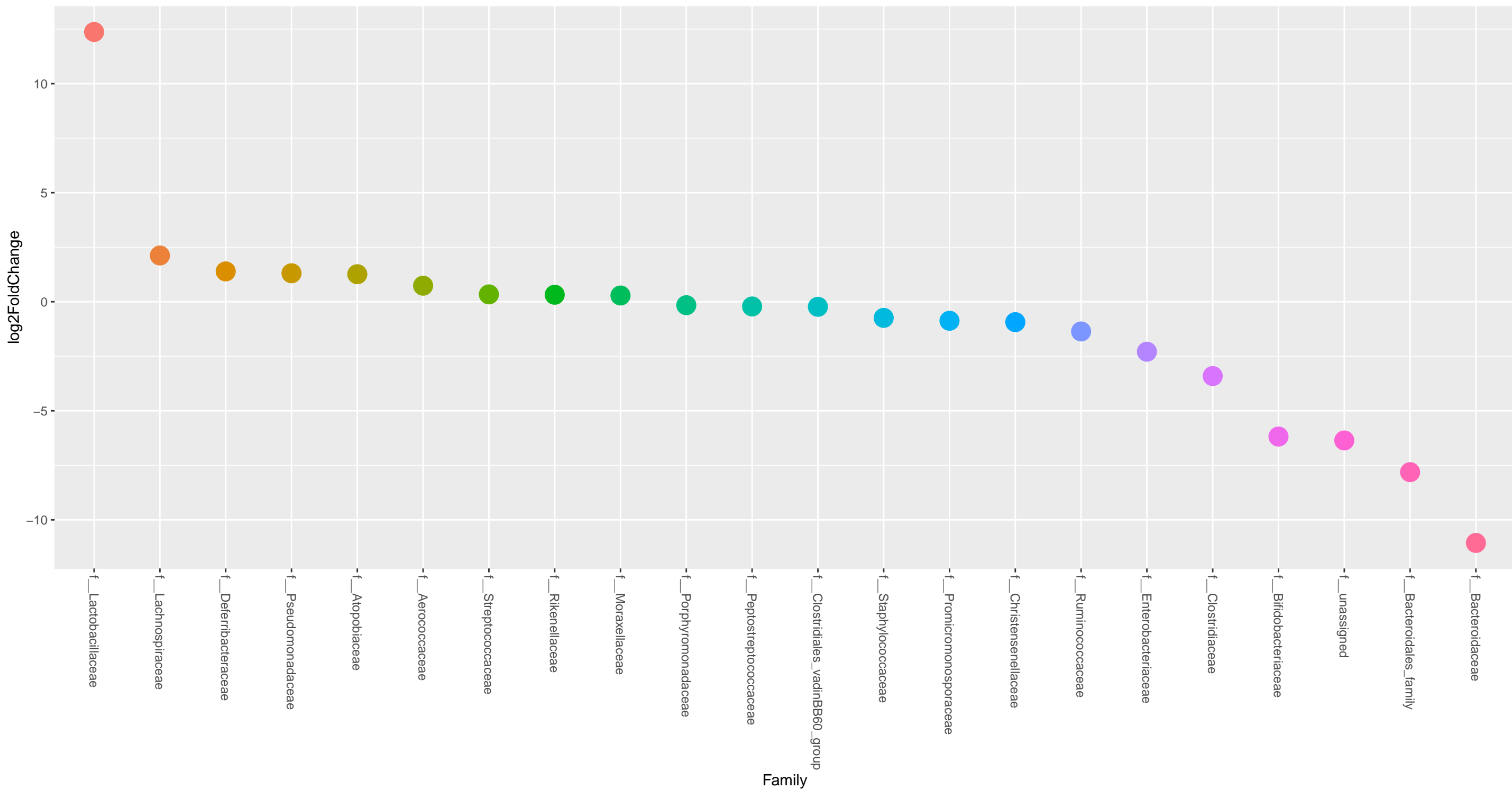


Combination sauvange_t0 VS mutant_t0



baseMean	log2FoldChange	stat	pvalue	padj	Family
1.760981e+04	2.1215570	2.72813171	6.369417e-03	2.802544e-02	f__Lachnospiraceae
6.788889e+03	-0.1566045	-0.21017108	8.335342e-01	9.237277e-01	f__Porphyromonadaceae
1.607467e+03	-11.0577457	-5.16647734	2.385471e-07	2.624018e-06	f__Bacteroidaceae
1.284460e+03	1.2638124	2.16014010	3.076183e-02	1.091047e-01	f__Atopobiaceae
1.234164e+00	-3.4058701	-1.12643397	2.599819e-01	5.283617e-01	f__Clostridiaceae
6.574587e+02	1.3931094	2.11166579	3.471513e-02	1.091047e-01	f__Deferribacteraceae
1.714740e+03	-1.3600931	-1.11656389	2.641808e-01	5.283617e-01	f__Ruminococcaceae
7.716799e+02	0.3226088	0.14995398	8.808009e-01	9.237277e-01	f__Rikenellaceae
1.582145e-01	-0.2306967	-0.07422795	9.408290e-01	9.408290e-01	f__Clostridiales_vadinBB60_group
3.837529e+02	12.3703635	5.73208405	9.920409e-09	2.182490e-07	f__Lactobacillaceae
1.321077e+02	-6.3589830	-4.57011882	4.874478e-06	2.680963e-05	f__unassigned
4.904215e+01	-7.8114478	-5.04933057	4.433610e-07	3.251314e-06	f__Bacteroidales_family
2.615084e+01	0.7377465	0.64187143	5.209567e-01	7.640698e-01	f__Aerococcaceae
1.193753e+01	-0.2149493	-0.14876374	8.817401e-01	9.237277e-01	f__Peptostreptococcaceae
1.629622e+01	0.3391571	0.65796705	5.105593e-01	7.640698e-01	f__Streptococcaceae
8.446224e+00	-6.1789650	-2.05541717	3.983873e-02	1.095565e-01	f__Bifidobacteriaceae
2.481234e+00	0.2876807	0.17930698	8.576967e-01	9.237277e-01	f__Moraxellaceae
2.483561e+00	1.3075396	0.86217856	3.885893e-01	7.124137e-01	f__Pseudomonadaceae
2.960287e+00	-0.7388743	-0.37065502	7.108945e-01	9.237277e-01	f__Staphylococcaceae
1.146256e+00	-2.2896648	-1.38804312	1.651239e-01	4.036362e-01	f__Enterobacteriaceae
7.920421e+00	-0.9334607	-0.69289336	4.883765e-01	7.640698e-01	f__Christensenellaceae
6.575919e-01	-0.8702756	-0.28554093	7.752298e-01	9.237277e-01	f__Promicromonosporaceae