Résultats des top gènes les plus différentiellement exprimés :
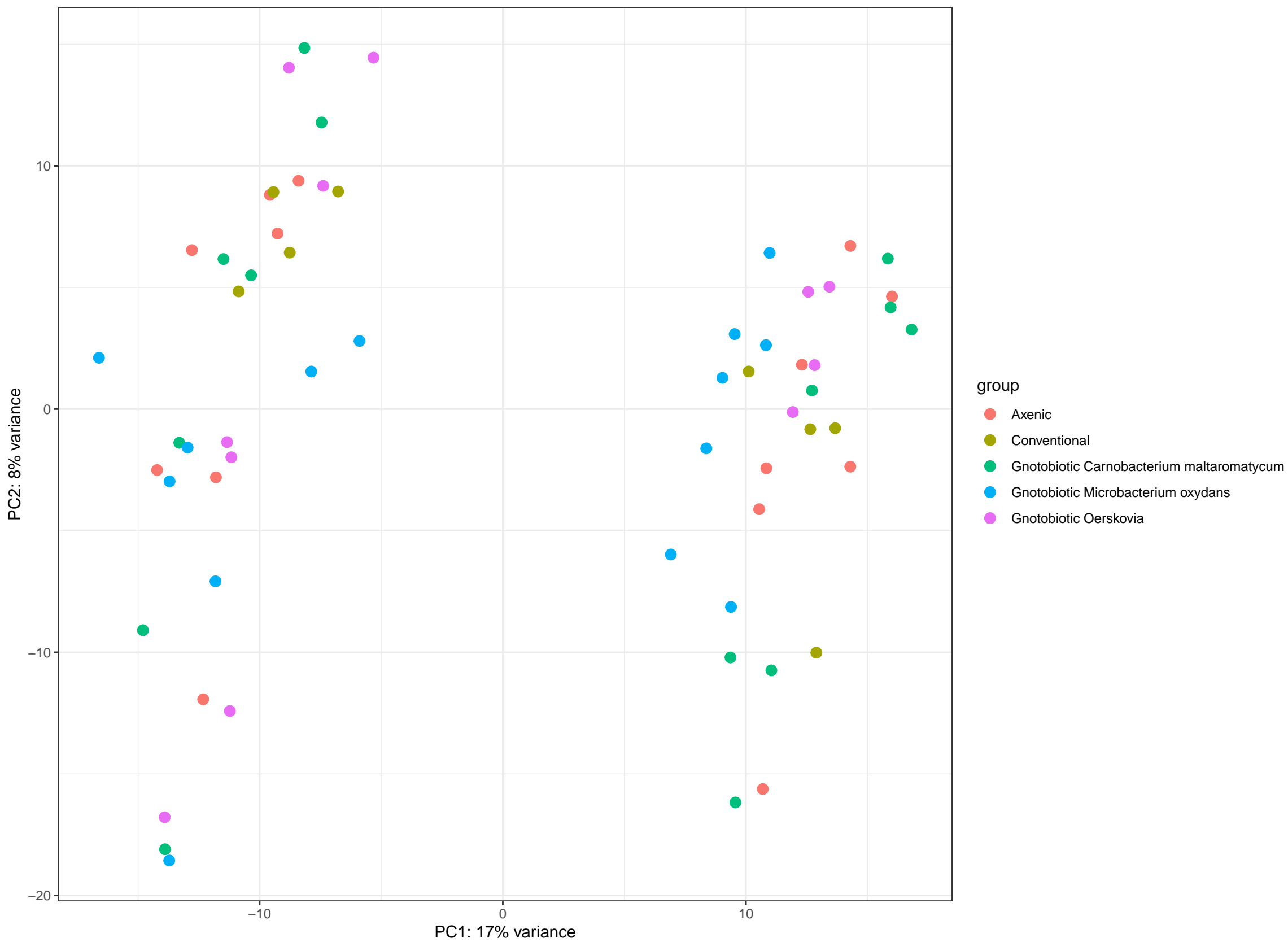
	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
LOC115265203	24.0088644599641	3.80295532385681	0.287907461612389	13.208950204204	7.79033162412505e−40	9.87814049939057e−37
LOC115265311	7.38343079886589	1.85614835124234	0.304753854010567	6.09064767127763	1.12454797929628e−09	7.12963418873842e−07
LOC109425568	21.7287944118527	2.46872763579915	0.442488406988152	5.5791916732979	2.41638856365151e−08	1.02132689957004e−05
LOC109420013	21.8575981951835	1.50306863851617	0.273891784156938	5.48781937049605	4.06925853738694e−08	1.28995495635166e−05
LOC109433105	9.22951392533371	1.26431802327566	0.316566121357697	3.99385132512988	6.50086355905037e−05	0.0164861899857517
LOC109420719	7.85772004508062	−1.48352021996949	0.376238032610108	−3.94303629985981	8.04564719046168e−05	0.0170031343958423
LOC109404815	7.11614673553505	1.79404624554839	0.461943025408486	3.88369592540542	0.000102880557610676	0.0186360781500482

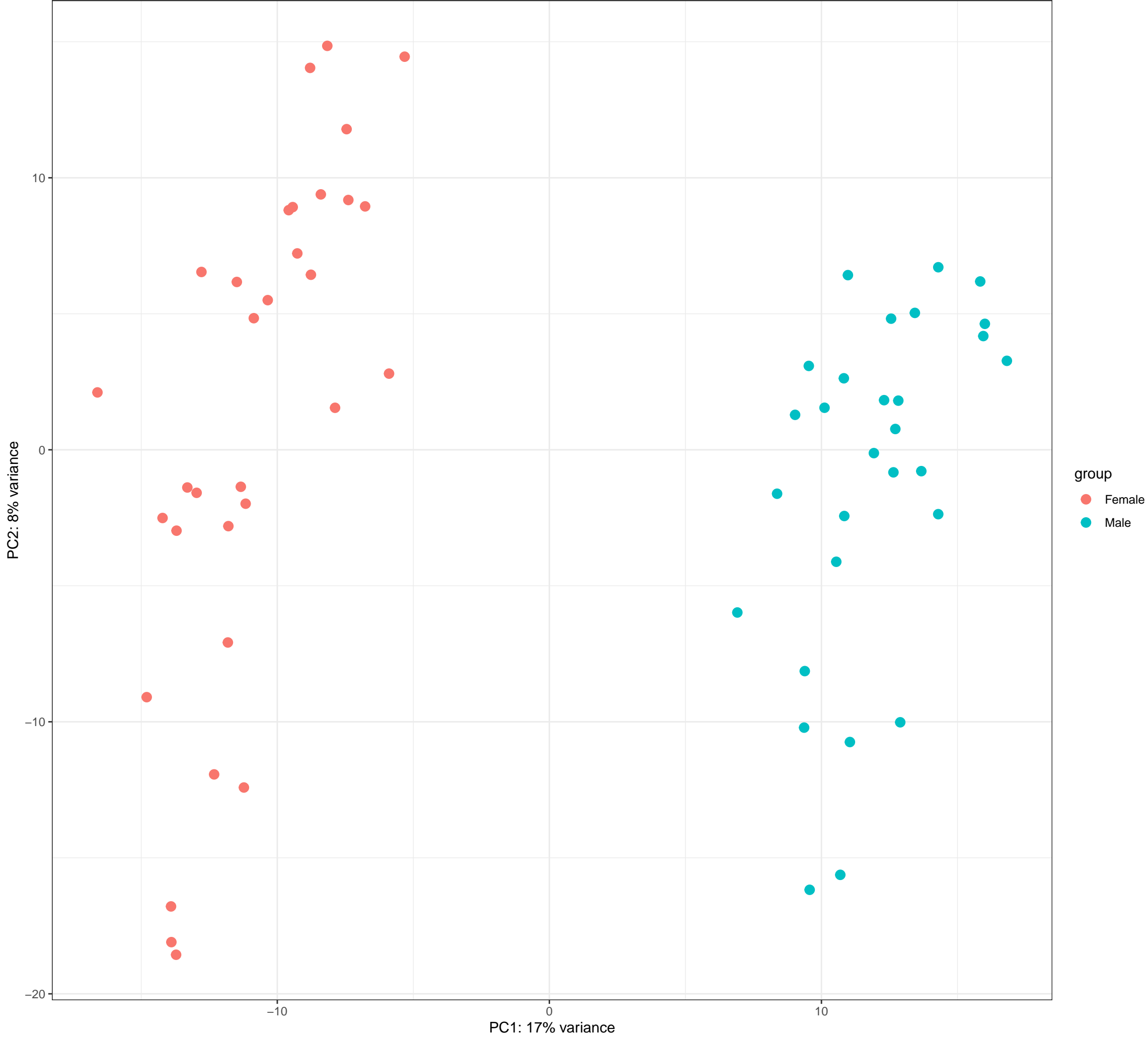**rlog transformed read counts**
distance: Pearson correlation

Height
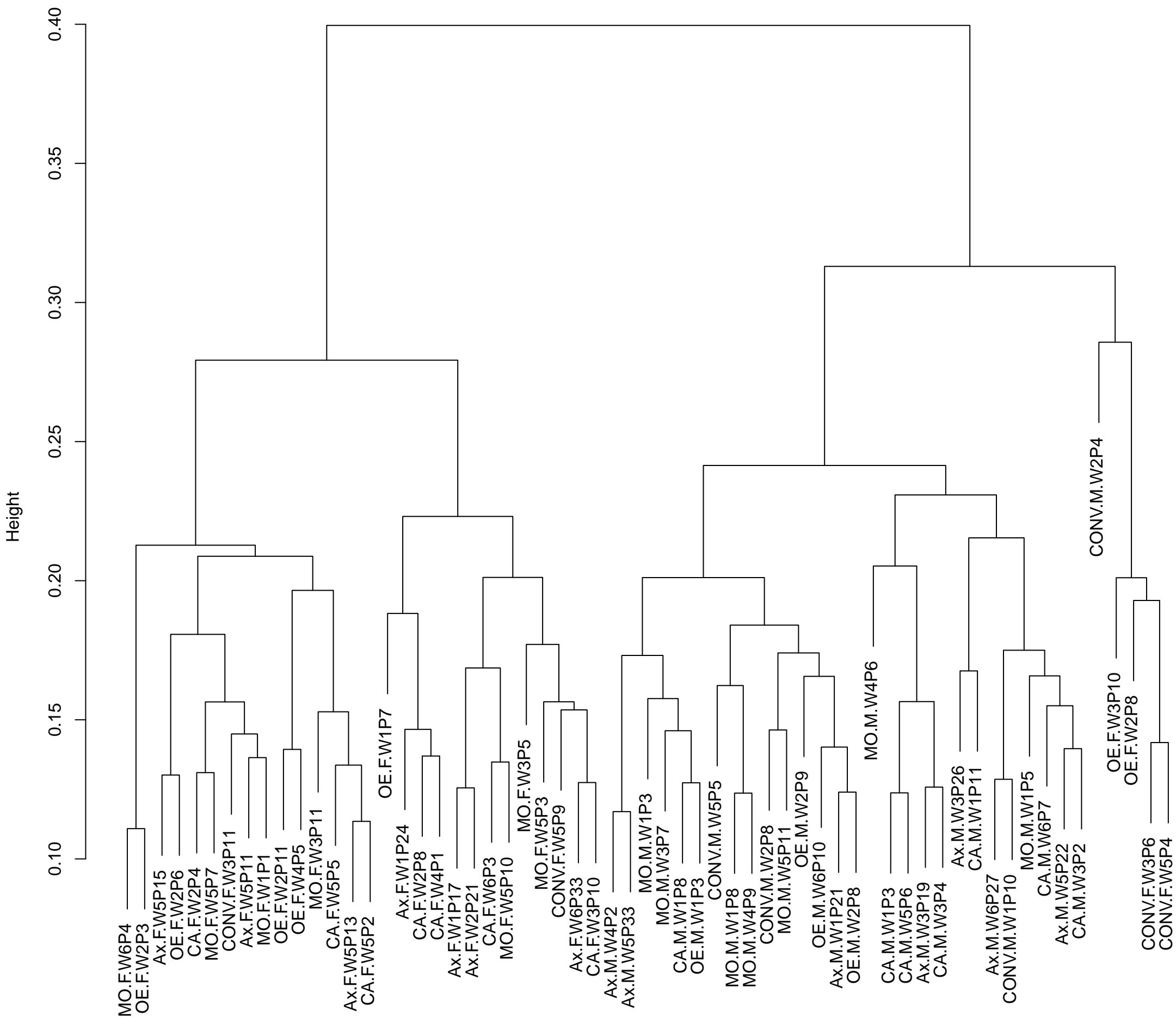
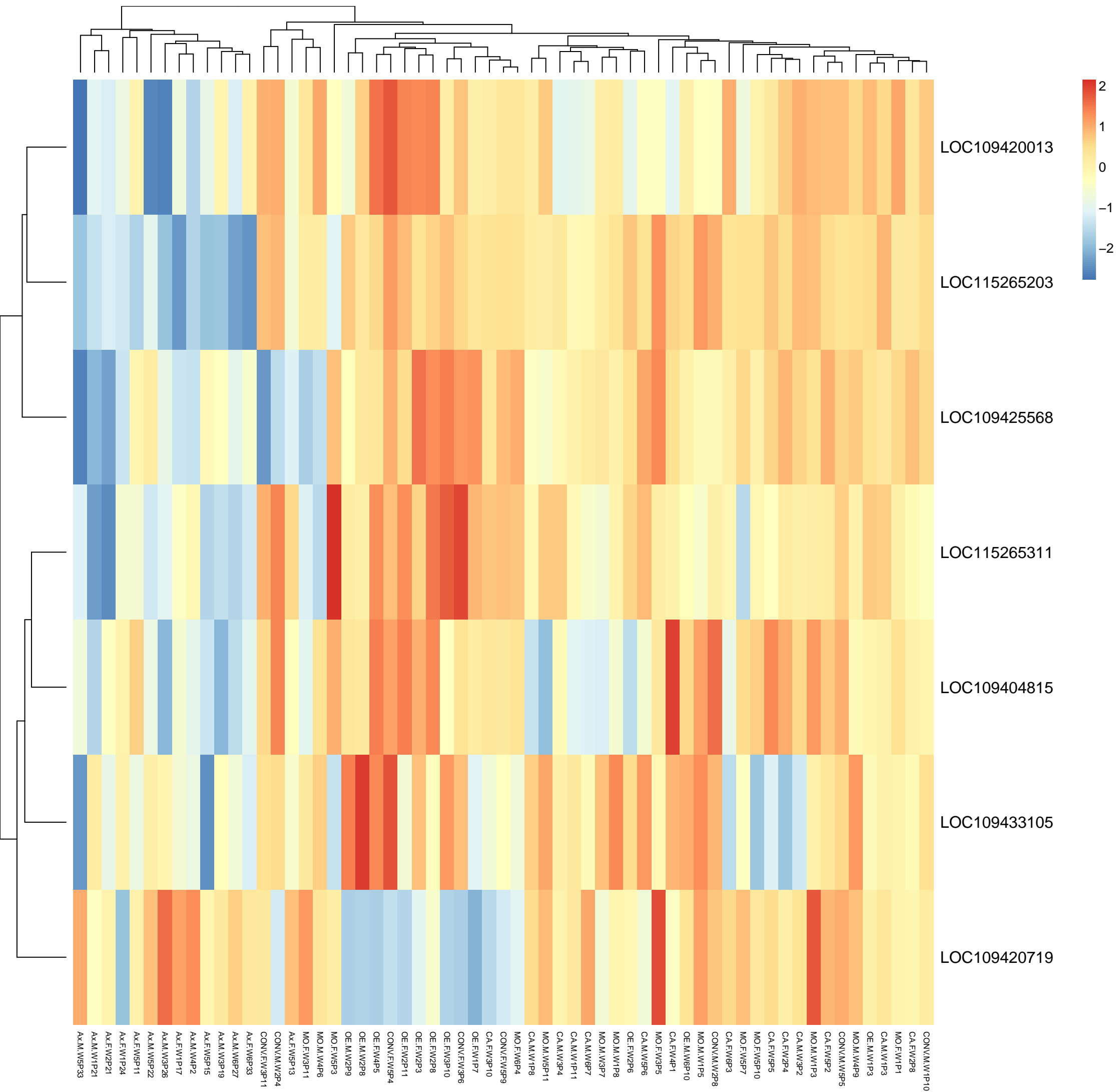distance.m_rlog
hclust (*, "complete")

By modality

Rows (top to bottom): LOC109420013, LOC115265203, LOC109425568, LOC115265311, LOC109404815, LOC109433105, LOC109420719

Columns (left to right): Ax.M.W5P33, Ax.M.W1P21, Ax.F.W2P21, Ax.F.W1P24, Ax.F.W5P11, Ax.M.W5P22, Ax.M.W3P26, Ax.F.W1P17, Ax.M.W4P2, Ax.F.W5P15, Ax.M.W3P19, Ax.M.W6P27, Ax.F.W6P33, CONV.M.W3P11, CONV.M.W2P4, Ax.F.W5P13, MO.F.W3P11, MO.M.W4P6, MO.F.W5P3, OE.M.W2P9, OE.M.W2P8, OE.F.W4P5, CONV.F.W5P4, OE.F.W2P11, OE.F.W2P3, OE.F.W2P8, OE.F.W3P10, CONV.F.W3P6, OE.F.W1P7, CA.F.W3P10, CONV.F.W5P9, MO.F.W6P4, CA.M.W1P8, MO.M.W5P11, CA.M.W3P4, CA.M.W1P11, CA.M.W6P7, MO.M.W3P7, MO.M.W1P8, OE.F.W2P6, CA.M.W5P6, MO.F.W3P5, CA.F.W4P1, OE.M.W6P10, MO.M.W1P5, CONV.M.W2P8, CA.F.W6P3, MO.F.W5P7, MO.F.W5P10, CA.F.W5P5, CA.F.W2P4, CA.M.W3P2, MO.M.W1P3, CA.F.W5P2, CONV.M.W5P5, MO.M.W4P9, OE.M.W1P3, CA.M.W1P3, MO.F.W1P1, MO.F.W1P10, CA.F.W2P8, CONV.M.W1P10
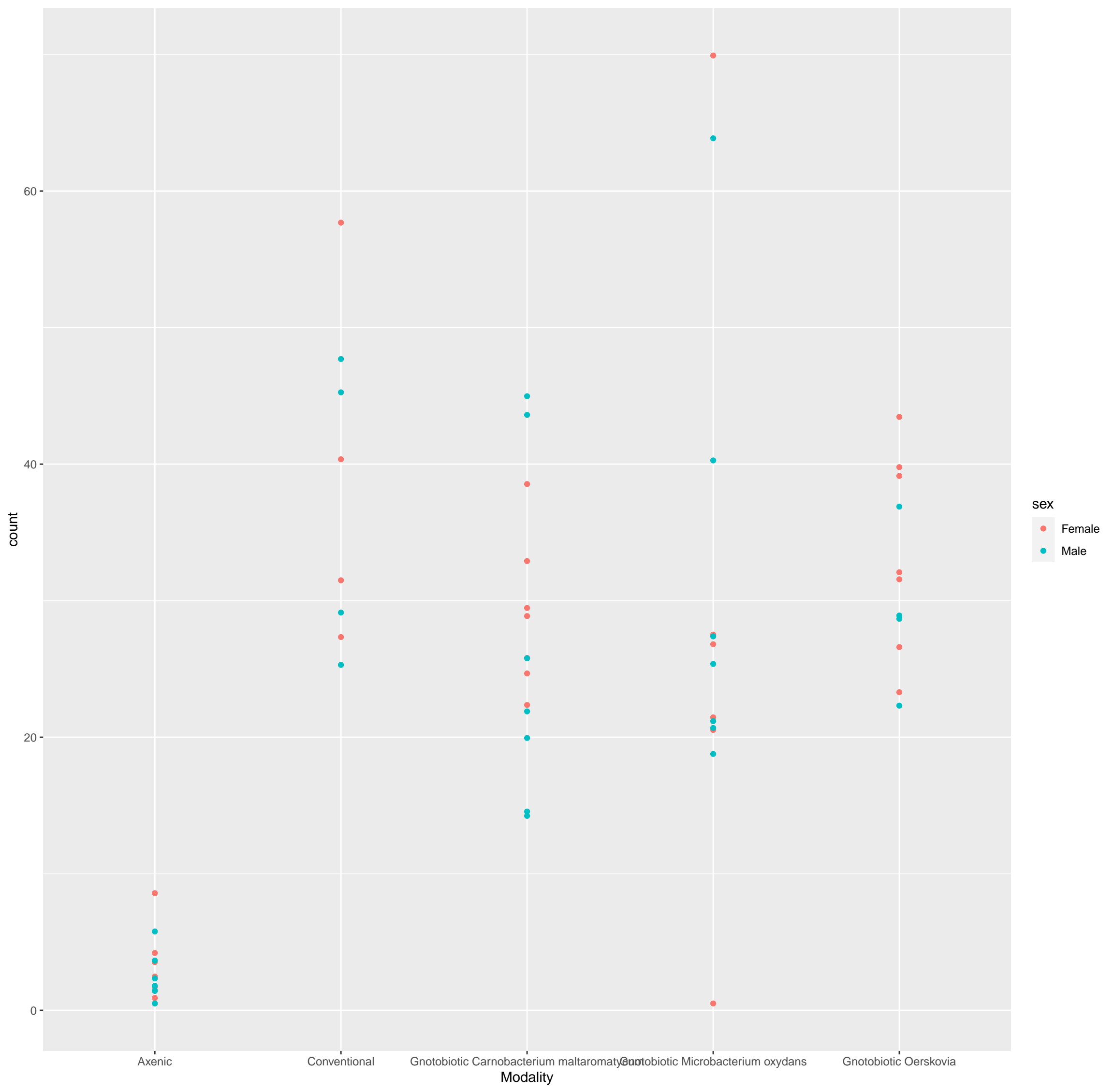
By sex

MA plot: group1 vs group2 (padj < 0.05)

Average log−expression

Expression log-ratio (this sample vs others)

+ 2 fold

−2 fold