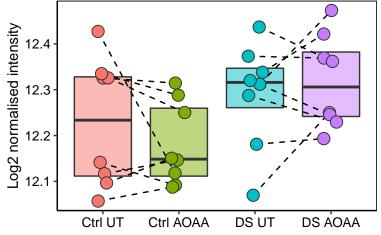
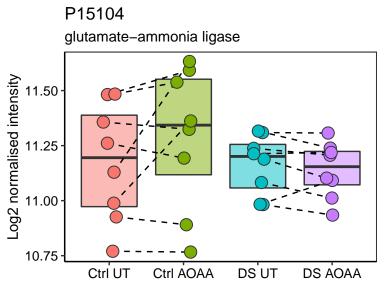
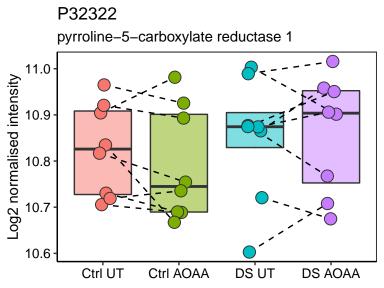
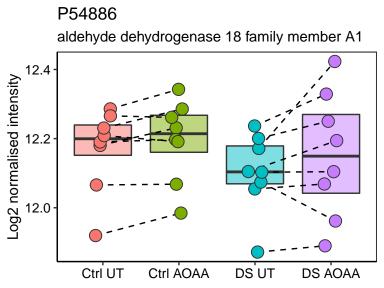


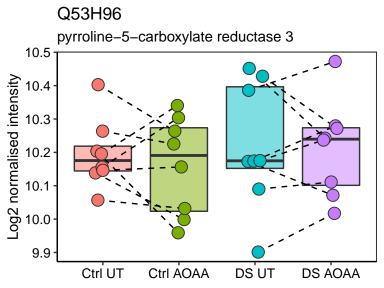
P04181 ornithine aminotransferase

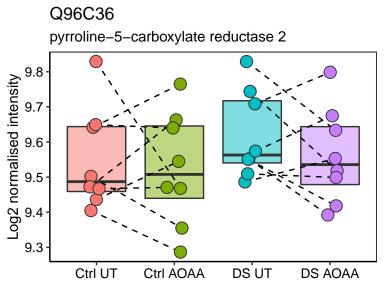


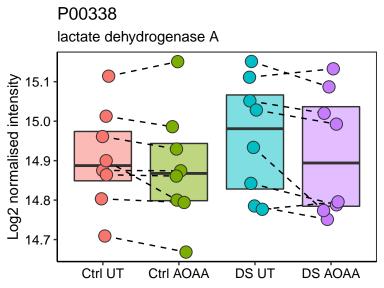


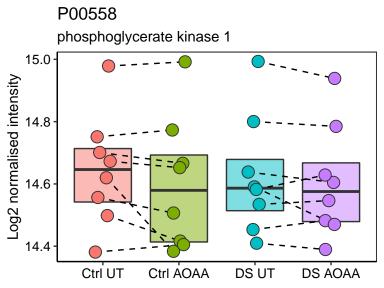




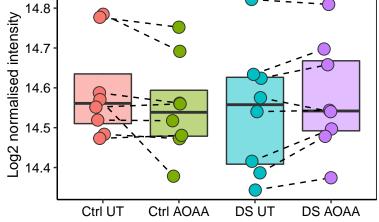








P04075
aldolase, fructose–bisphosphate A



P04406 glyceraldehyde-3-phosphate dehydrogenase 15.7 -15.6 -15.5 15.4 -15.3

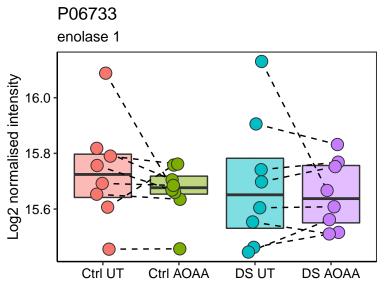
Ctrl AOAA

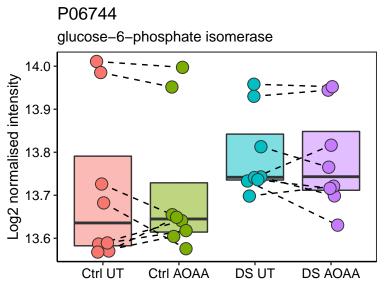
DS UT

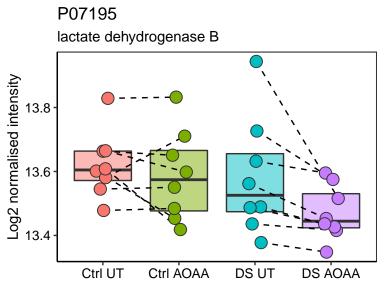
DS AOAA

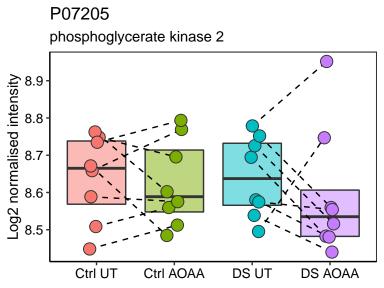
Ctrl UT

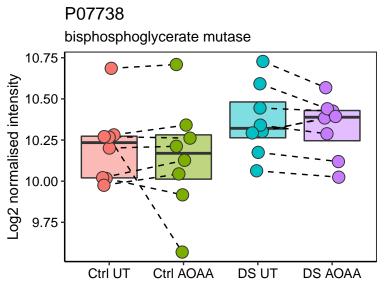
-og2 normalised intensity

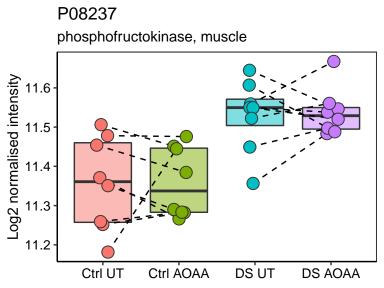


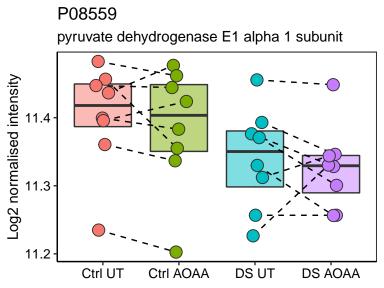


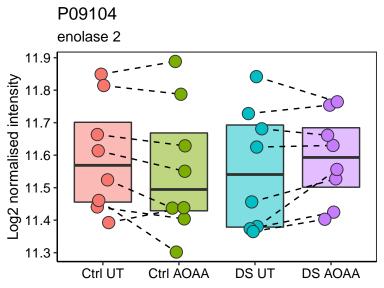


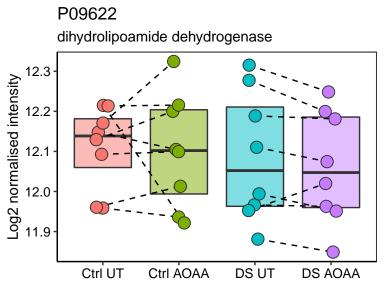




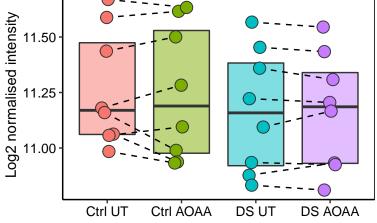


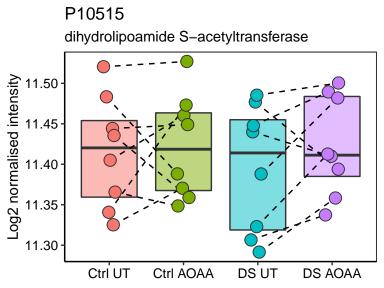






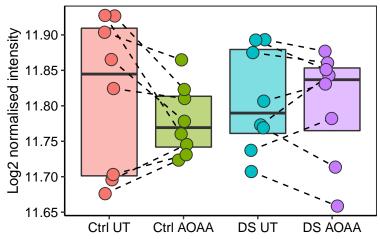
P09972 aldolase, fructose-bisphosphate C

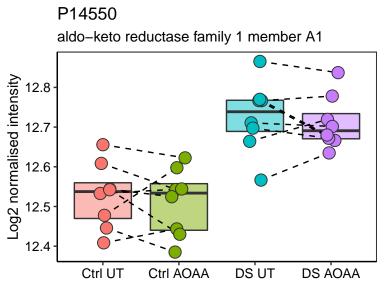


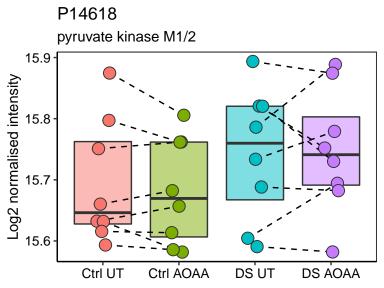


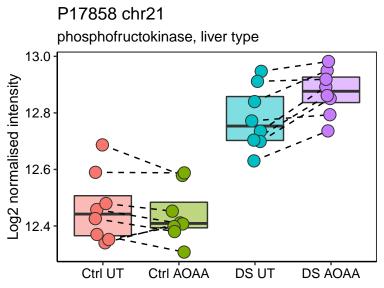
P11177

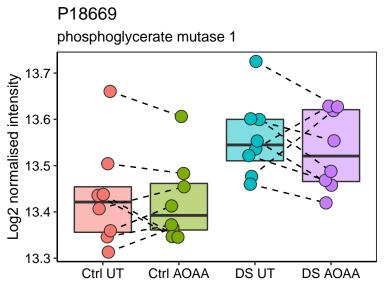
pyruvate dehydrogenase E1 beta subunit

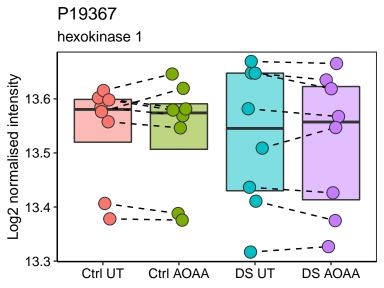


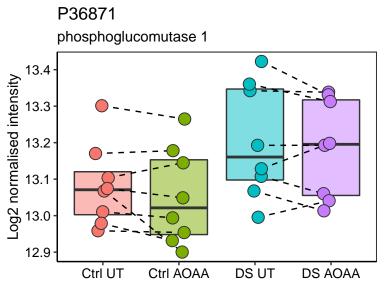


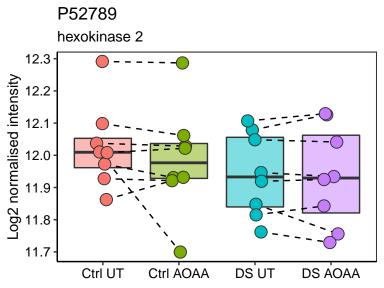


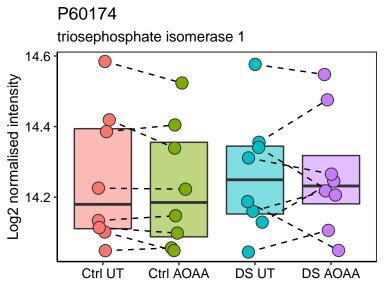


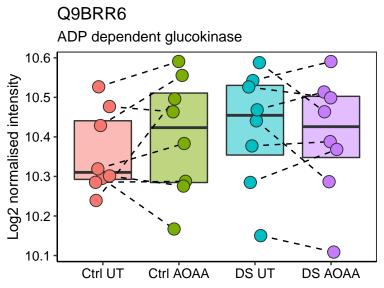


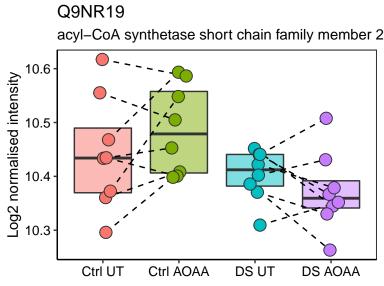


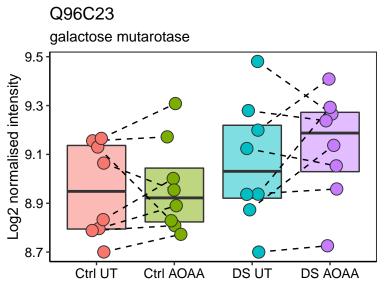


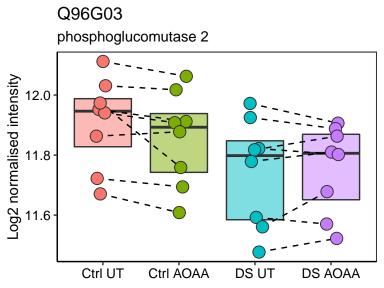


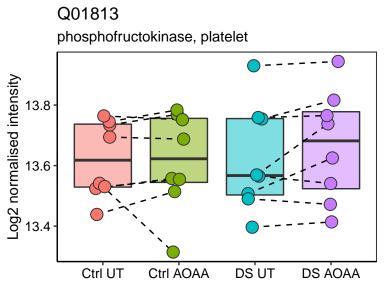


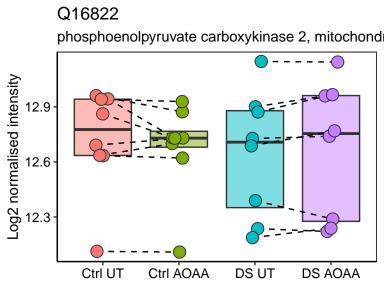


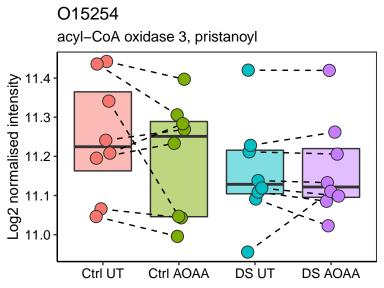


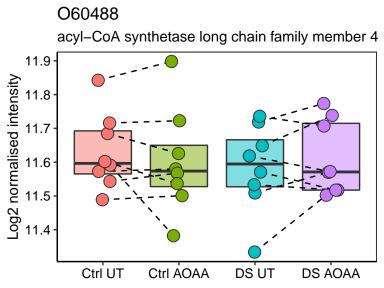


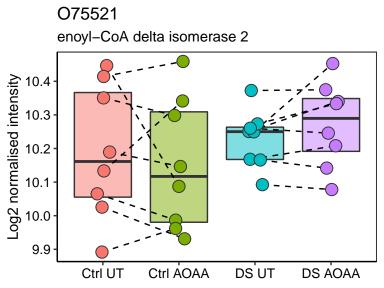


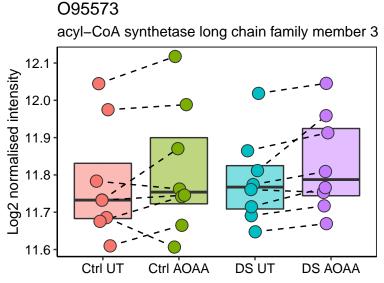




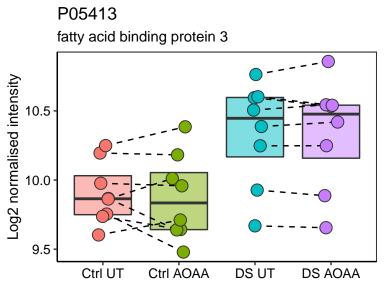


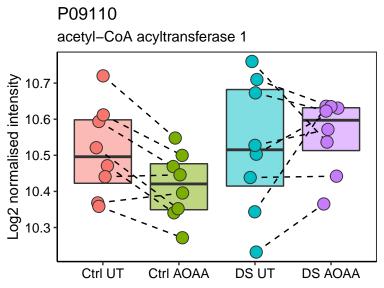


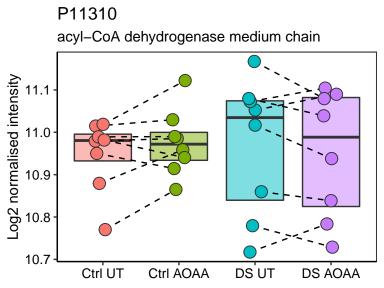


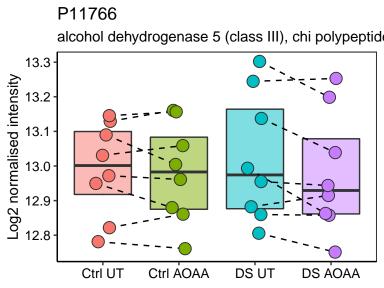


P05091 aldehyde dehydrogenase 2 family member 12.0 11.6 -11.2 Ctrl AOAA Ctrl UT DS UT DS AOAA

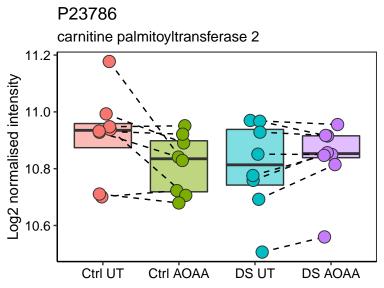


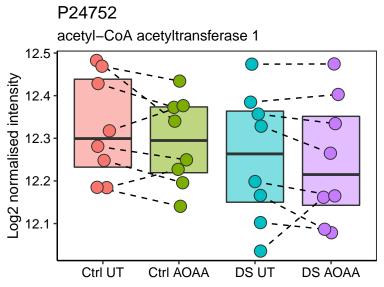


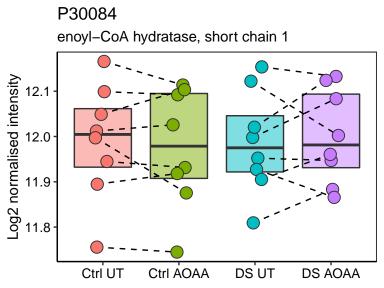


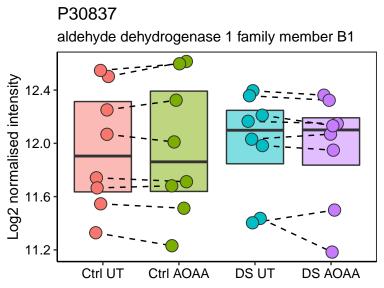


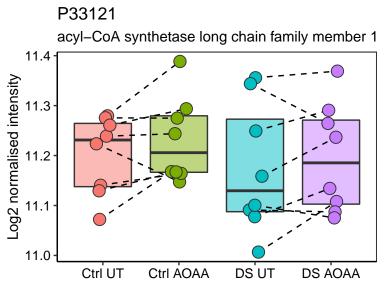
P16219 acyl-CoA dehydrogenase short chain -og2 normalised intensity 5.4 5.0 4.6 Ctrl UT Ctrl AOAA DS UT DS AOAA

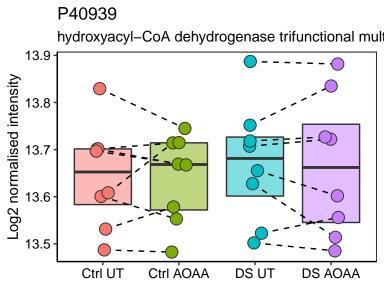


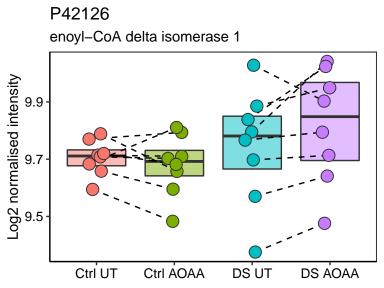




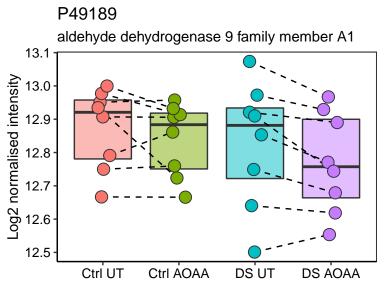




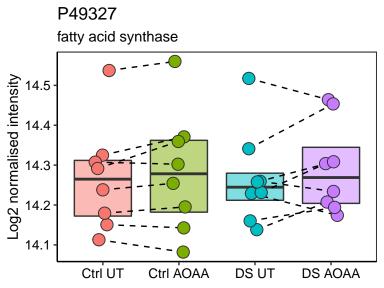


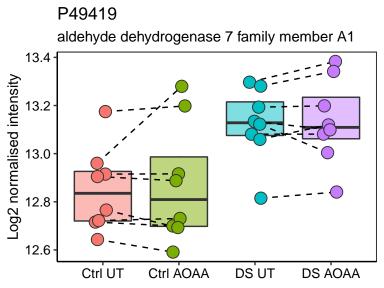


P42765 acetyl-CoA acyltransferase 2 Log2 normalised intensity 12.6 12.4 -12.2 Ctrl AOAA DS AOAA Ctrl UT DS UT



P45954 acyl-CoA dehydrogenase short/branched chain Log2 normalised intensity
6
6
7
7 9.2 Ctrl AOAA DS UT DS AOAA Ctrl UT





P49748 acyl-CoA dehydrogenase very long chain 13.4 Log2 normalised intensity 13.0-12.11 12.9 Ctrl UT Ctrl AOAA DS UT DS AOAA

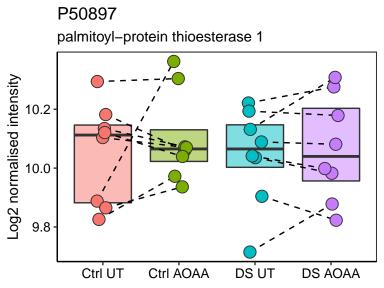
P51648 aldehyde dehydrogenase 3 family member A2 Log2 normalised intensity
8.0
7.1
7.

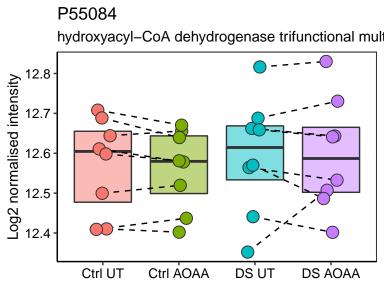
Ctrl AOAA

DS UT

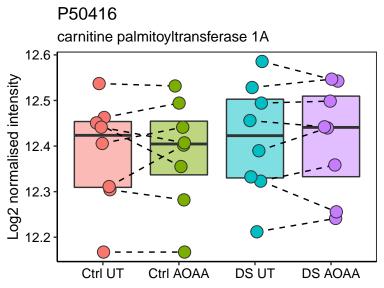
Ctrl UT

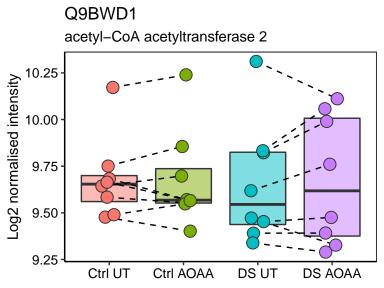
DS AOAA

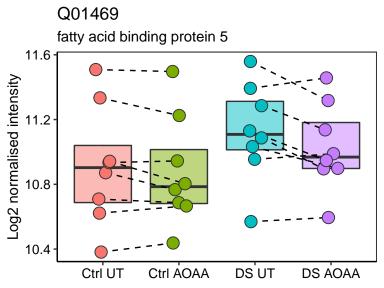


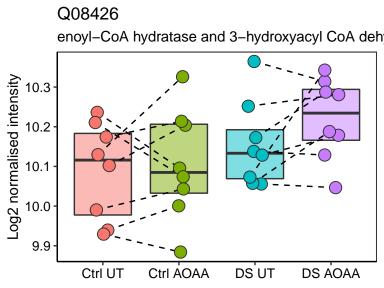


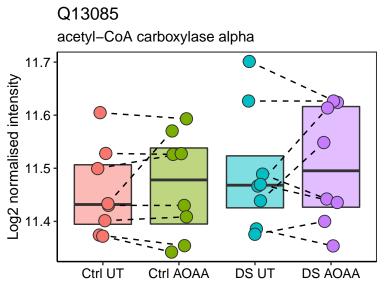
Q9BV79 mitochondrial trans-2-enoyl-CoA reductase -og2 normalised intensity Ctrl UT DS UT Ctrl AOAA DS AOAA

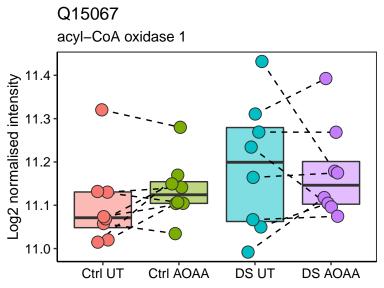






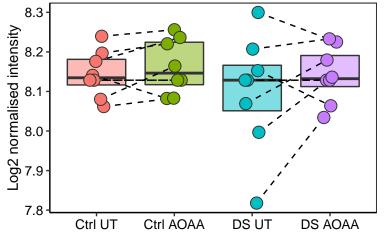


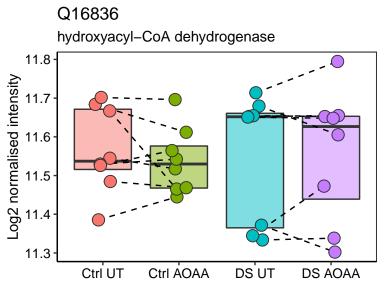


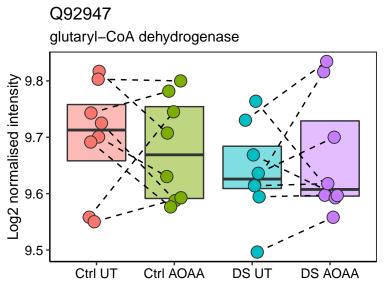


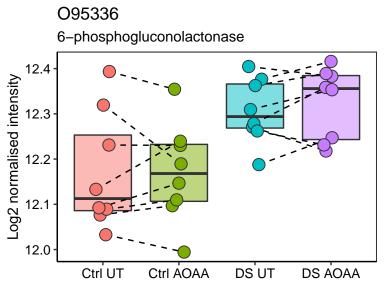
Q9NWU1

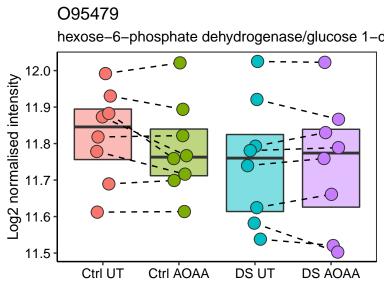
3-oxoacyl-ACP synthase, mitochondrial

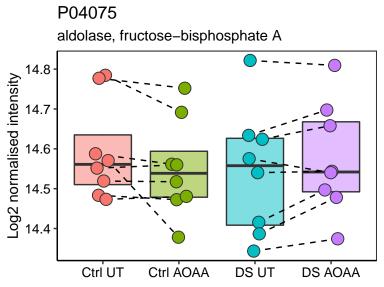


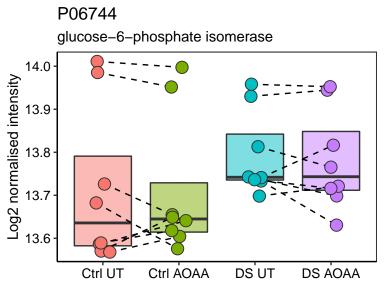


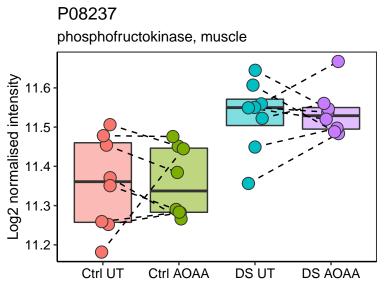




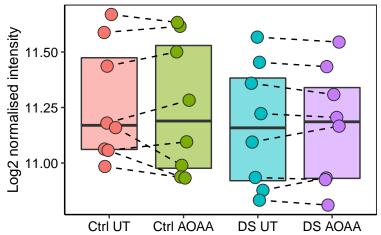


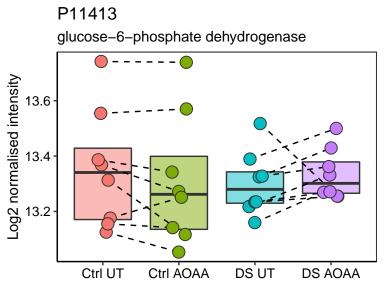


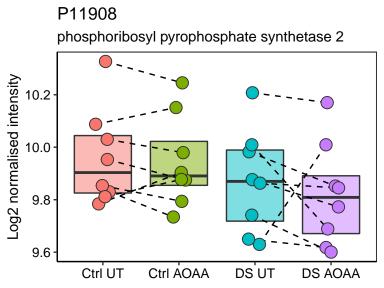


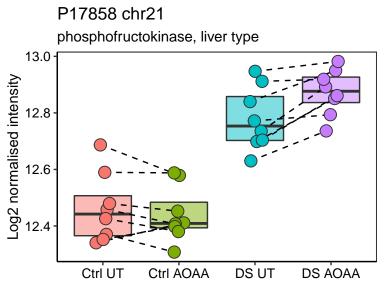


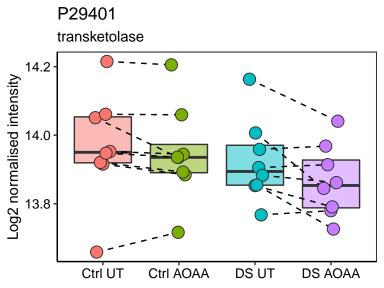
P09972 aldolase, fructose–bisphosphate C

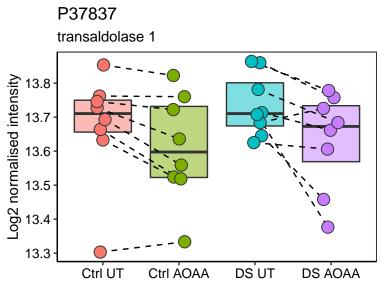


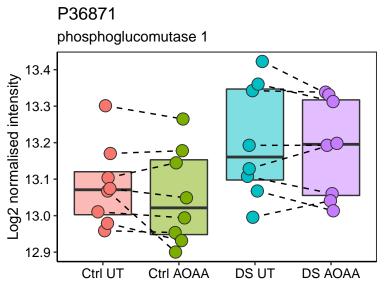




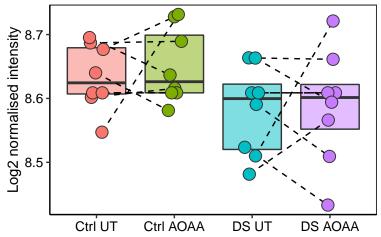


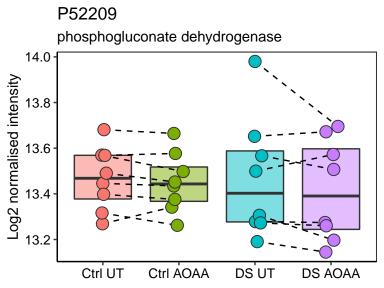




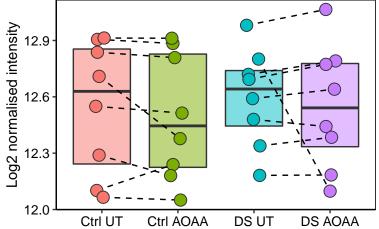


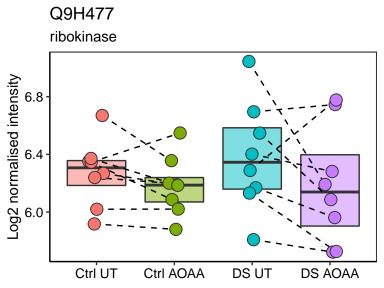
P49247
ribose 5–phosphate isomerase A

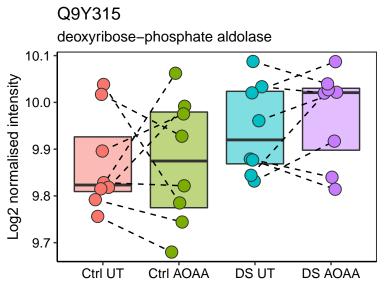




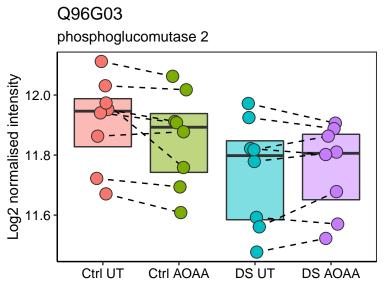
P60891
phosphoribosyl pyrophosphate synthetase 1

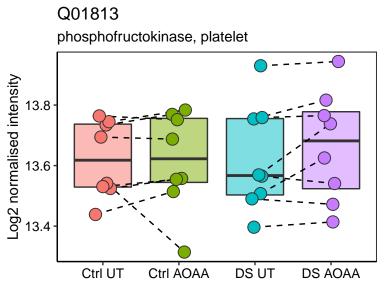


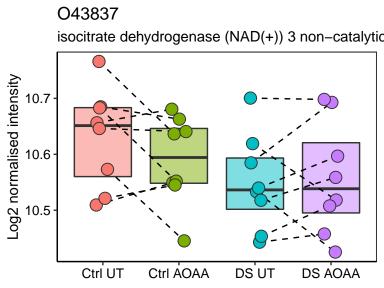


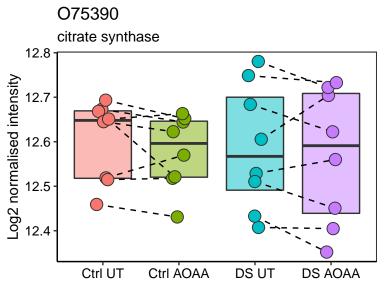


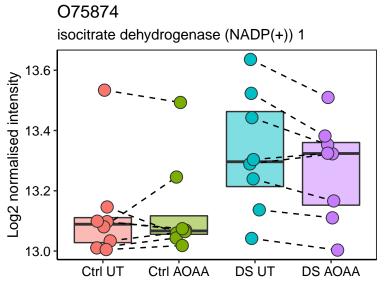
Q96AT9 ribulose-5-phosphate-3-epimerase 9.0 Log2 normalised intensity 8.9 8.8 8.7 8.6 Ctrl UT Ctrl AOAA DS UT DS AOAA

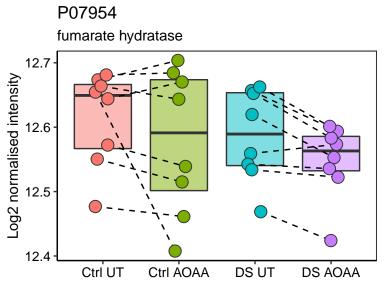


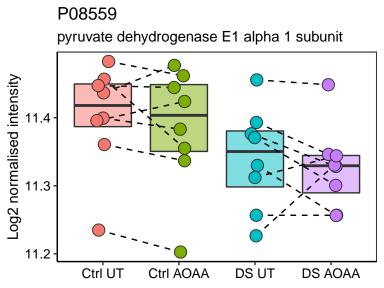


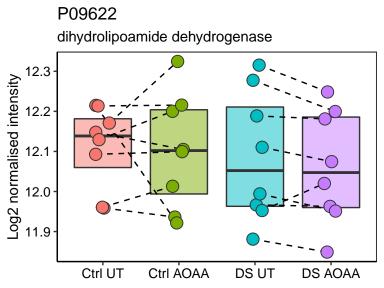


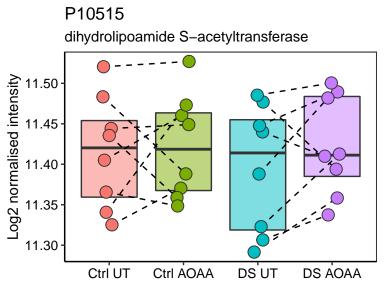




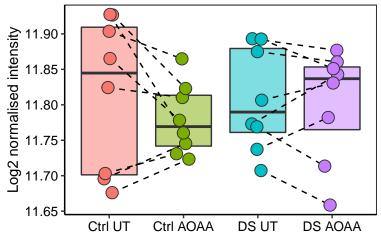


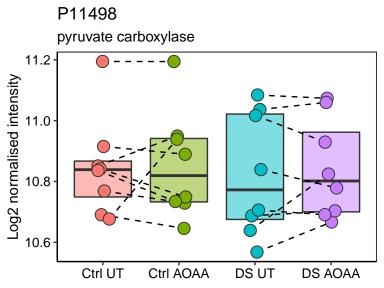


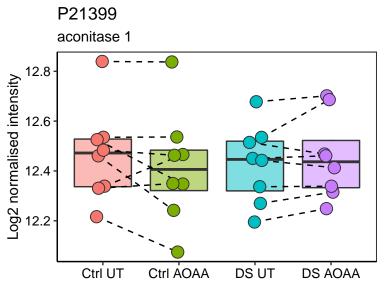




P11177
pyruvate dehydrogenase E1 beta subunit







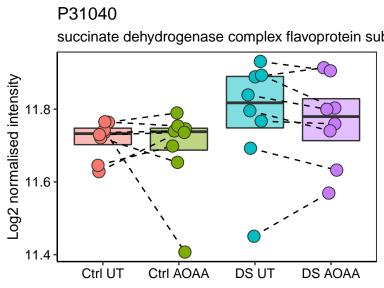
P21912 succinate dehydrogenase complex iron sulfur subu og2 normalised intensity 11.5 -11.4 -11.3 11.2

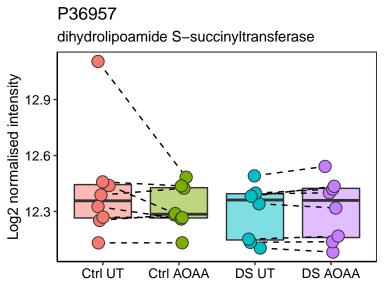
Ctrl AOAA

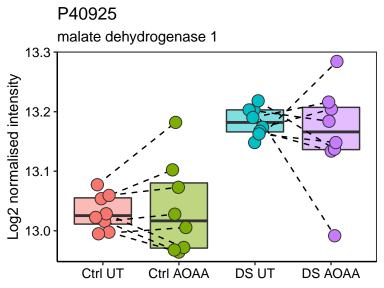
DS UT

DS AOAA

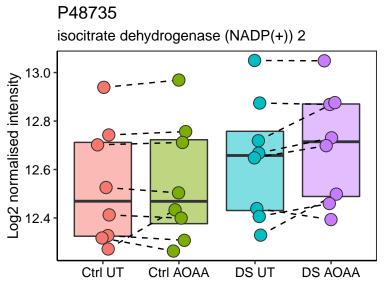
Ctrl UT

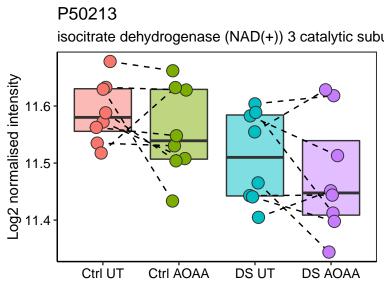


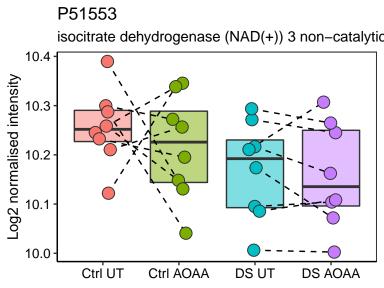


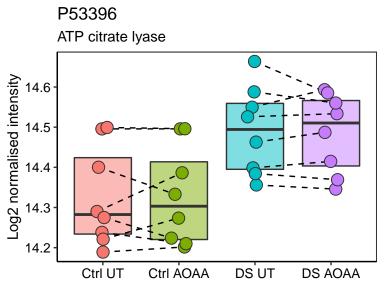


P40926 malate dehydrogenase 2 Log2 normalised intensity 13.9 13.8 -13.7 -13.6 -Ctrl UT Ctrl AOAA DS UT DS AOAA

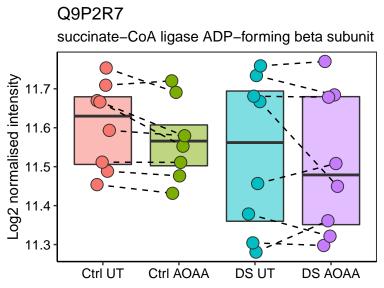


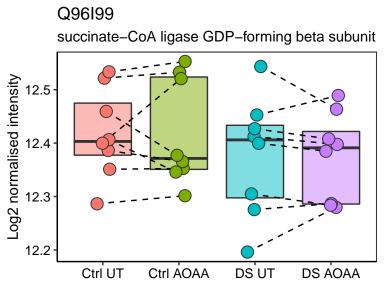


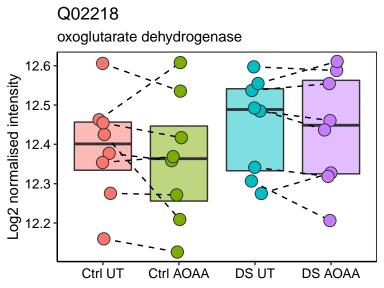


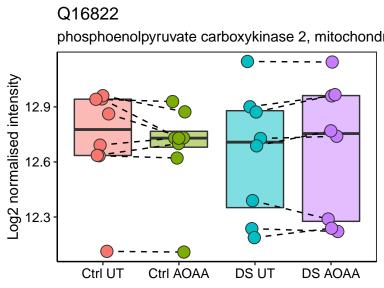


P53597 succinate-CoA ligase alpha subunit 11.2 Log2 normalised intensity 11.1 11.0 10.9 10.8 Ctrl AOAA DS AOAA Ctrl UT DS UT









Q99643 succinate dehydrogenase complex subunit C 7.4 -0g2 normalised intensity 2.2 2.1 2.0 7.2 6.9 Ctrl UT Ctrl AOAA DS UT DS AOAA

