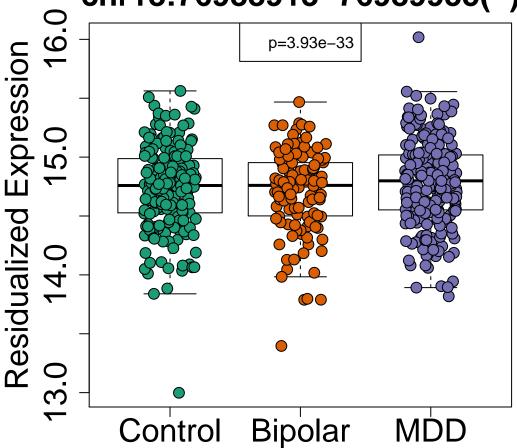
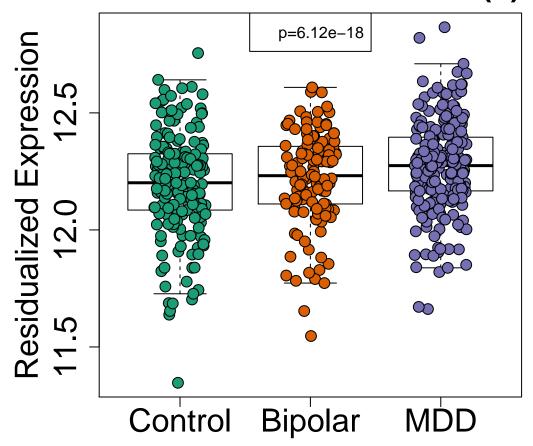
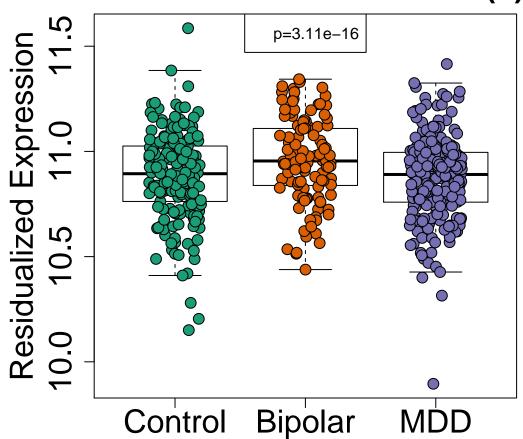
MBP, InGen chr18:76988913-76989955(-)



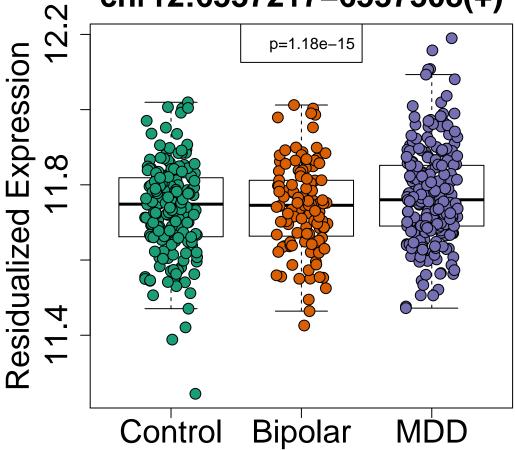
TMSB10, InGen chr2:84905719-84906002(+)



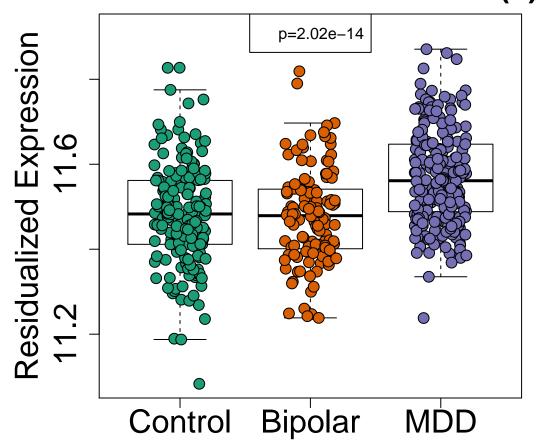
TUBA1B, InGen chr12:49129723-49131297(-)



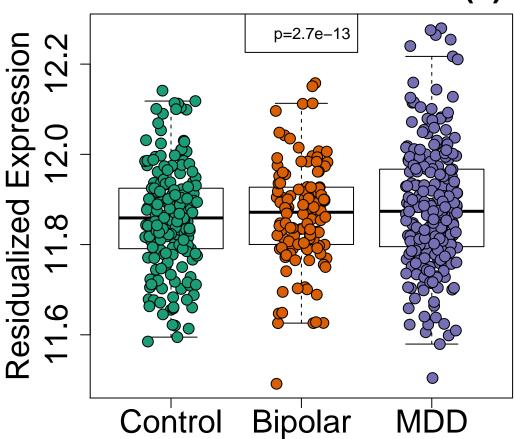
GAPDH, InGen chr12:6537217-6537308(+)



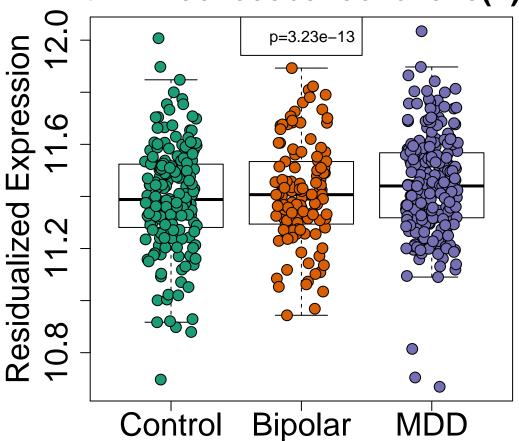
RPL31, InGen chr2:101002809-101004157(+)



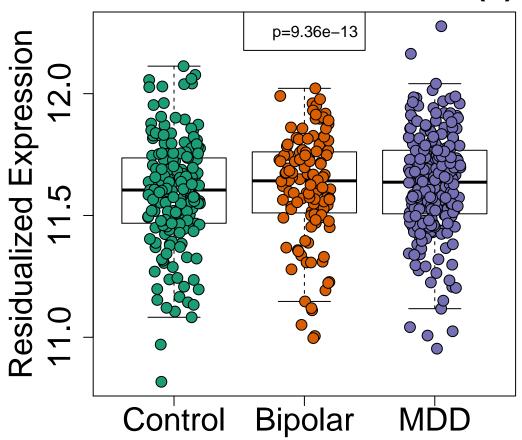
GAPDH, InGen chr12:6537391-6537583(+)



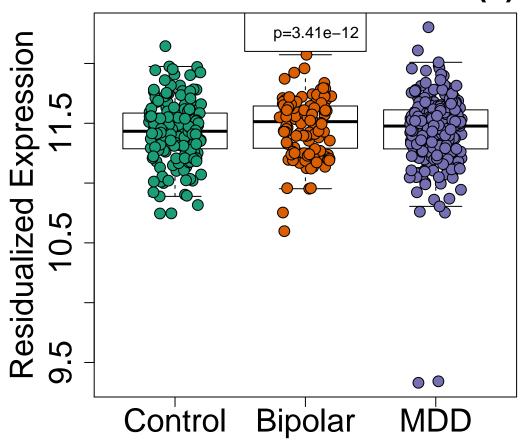
CALM1, InGen chr14:90403969-90404378(+)



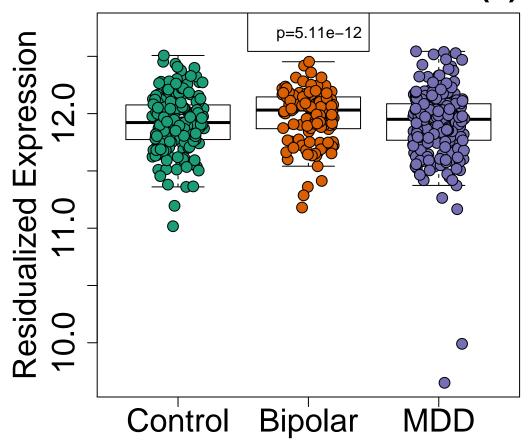
TMSB10, InGen chr2:84906118-84906388(+)



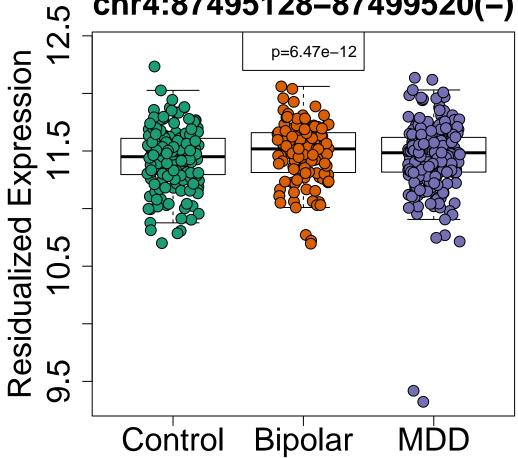
SPARCL1, InGen chr4:87494599-87494980(-)



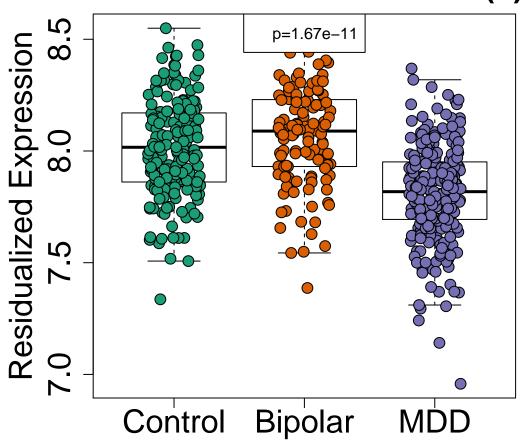
SPARCL1, InGen chr4:87480521-87482423(-)



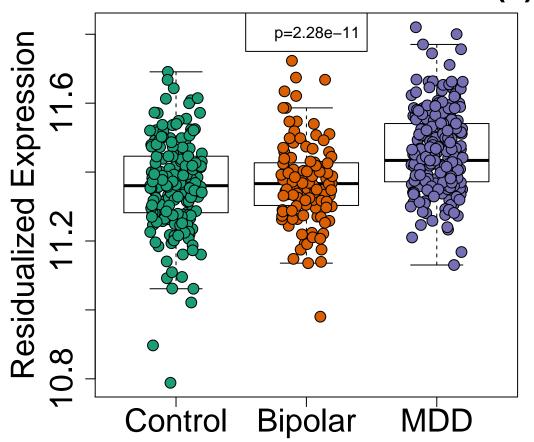
SPARCL1, InGen chr4:87495128-87499520(-)



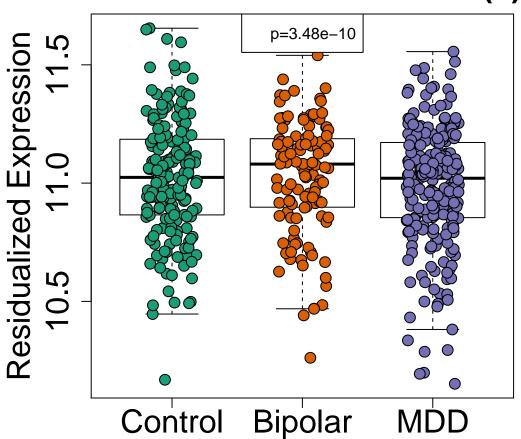
FUS, InGen chr16:31184003-31184208(+)



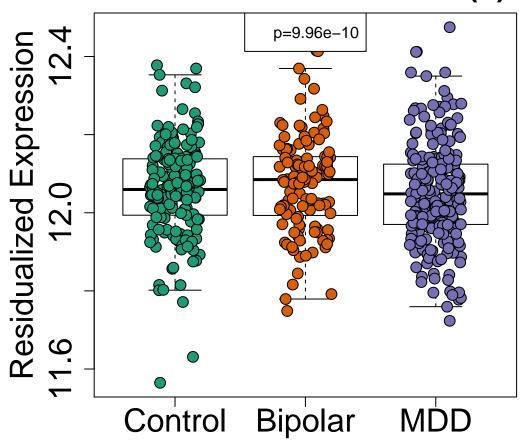
RPL31, InGen chr2:101002316-101002701(+)



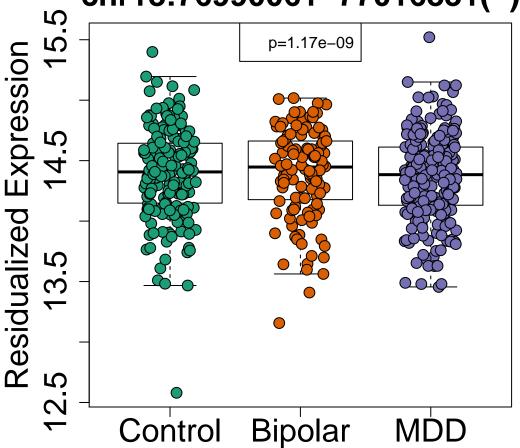
SLC1A2, InGen chr11:35306243-35312197(-)



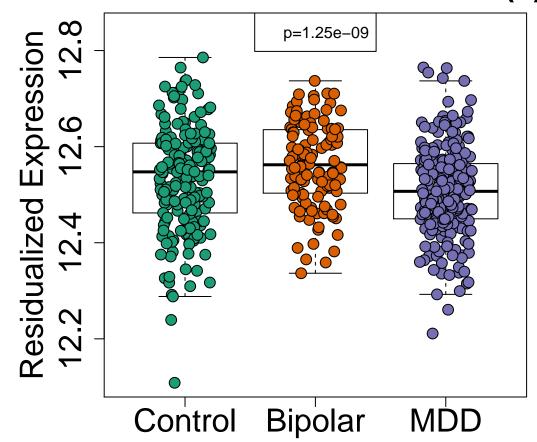
GAPDH, InGen chr12:6536594-6536683(+)



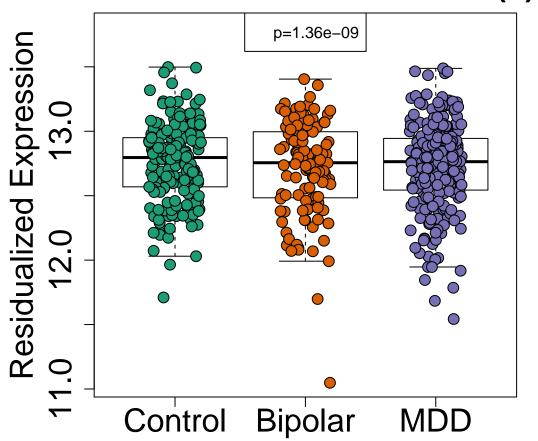
MBP, InGen chr18:76990061-77016831(-)



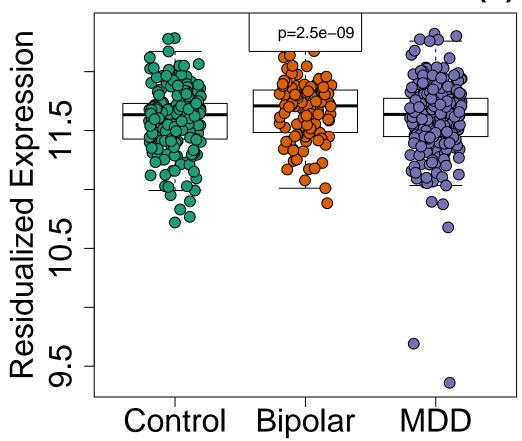
RPL37A, InGen chr2:216500032-216501340(+)



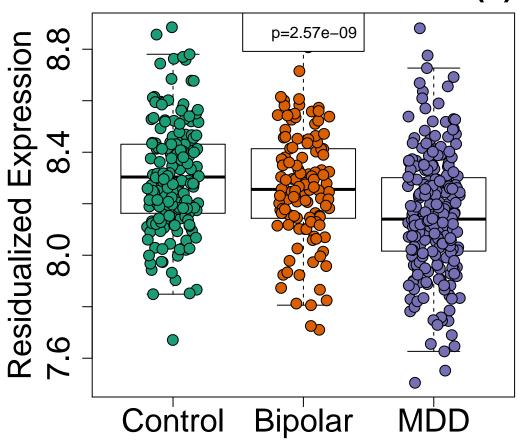
PLP1, InGen chrX:103786727-103787797(+)



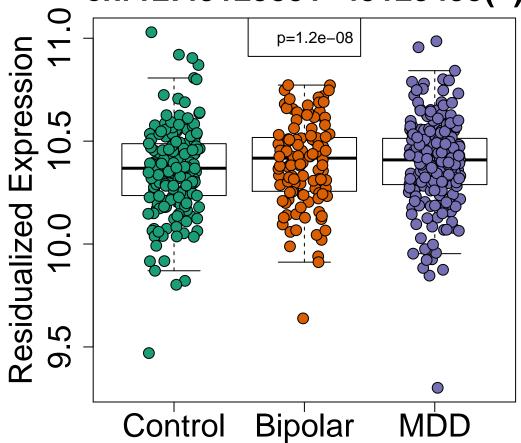
SPARCL1, InGen chr4:87491691-87493581(-)



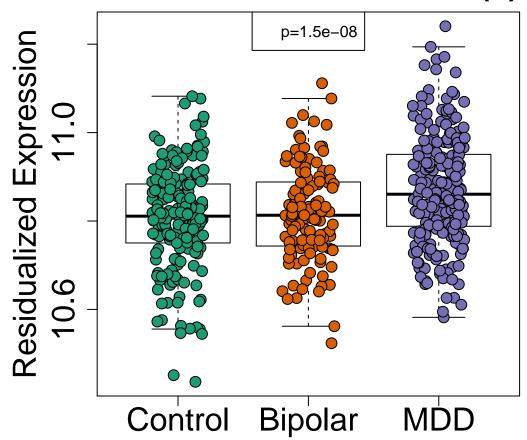
AGTPBP1, InGen chr9:85677583-85678334(-)



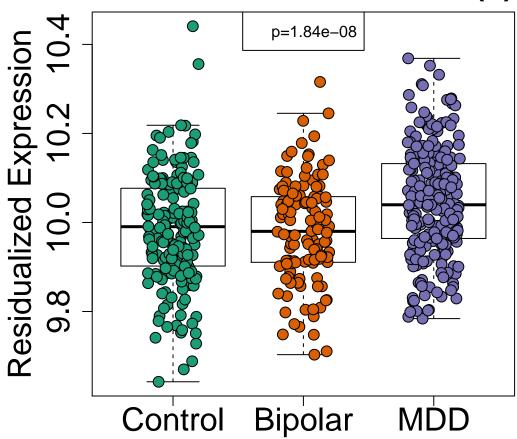
TUBA1B, InGen chr12:49129391-49129499(-)



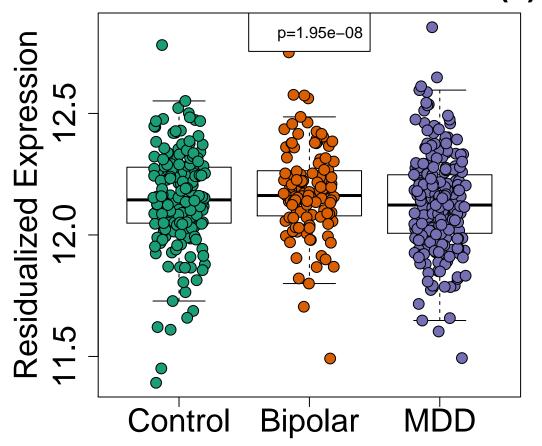
RPL7, InGen chr8:73291253-73291551(-)



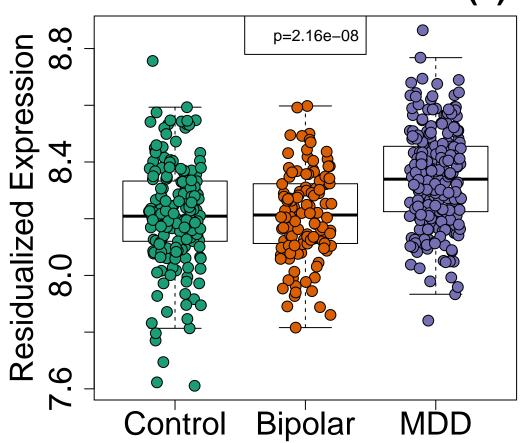
RPL7, InGen chr8:73291662-73291772(-)



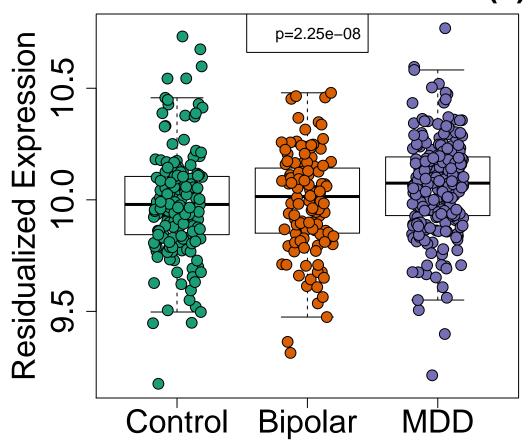
CPE, InGen chr4:165495678-165497511(+)



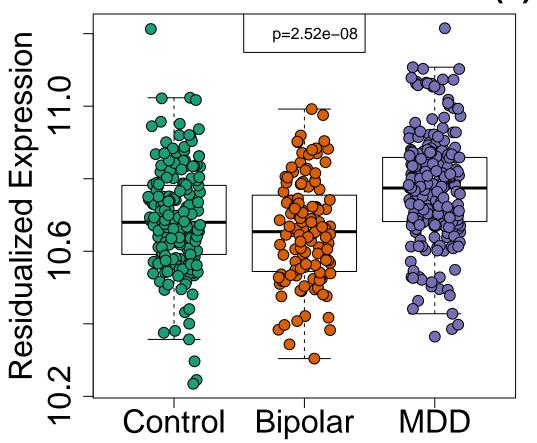
OAZ1, InGen chr19:2269745-2271384(+)



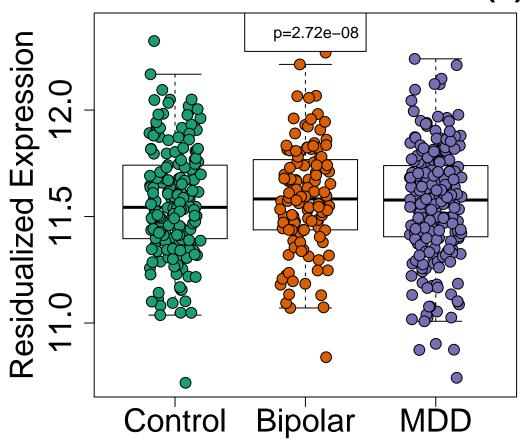
TUBA1B, InGen chr12:49128939-49129241(-)



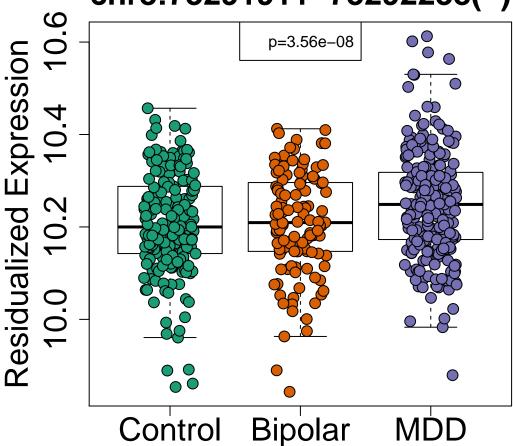
EIF4A2, InGen chr3:186787265-186787494(+)



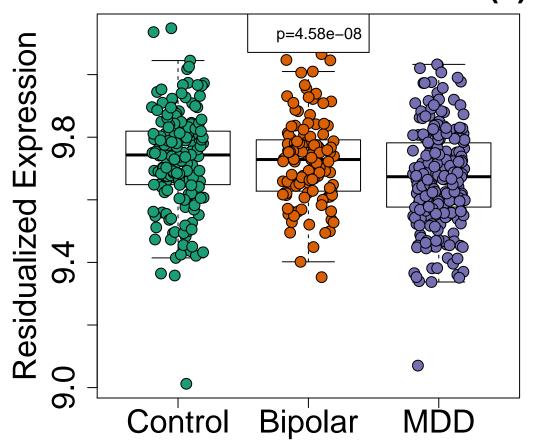
SLC1A2, InGen chr11:35301646-35306073(-)



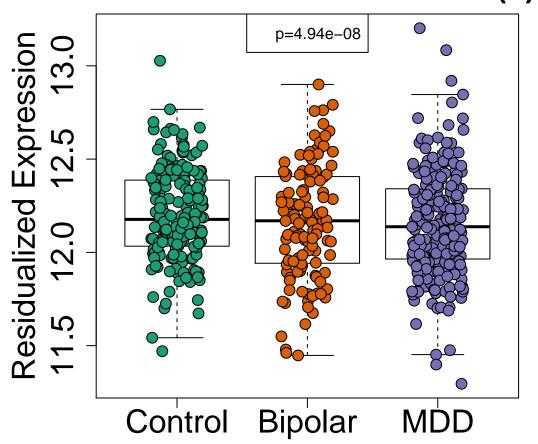
RPL7, InGen chr8:73291911-73292238(-)



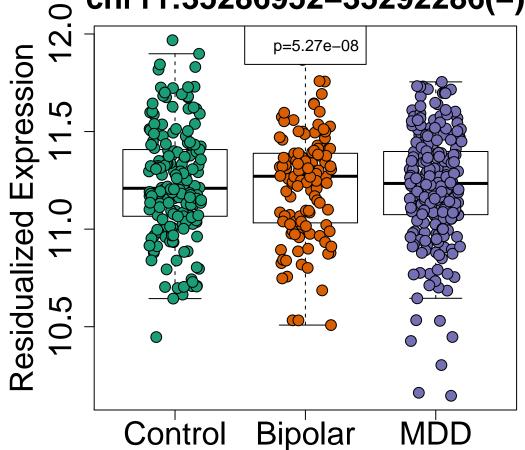
RPS29, InGen chr14:49583676-49585949(-)



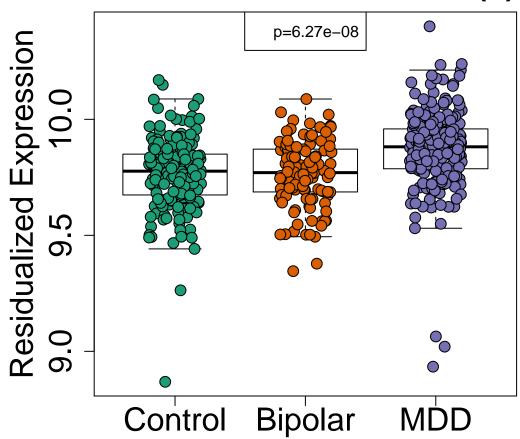
GLUL, InGen chr1:182384724-182385356(-)



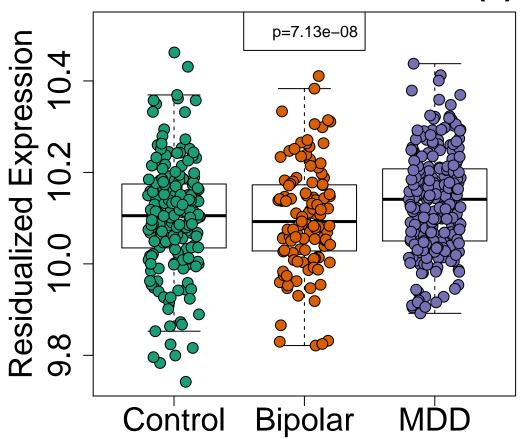
SLC1A2, InGen chr11:35286952-35292286(-)



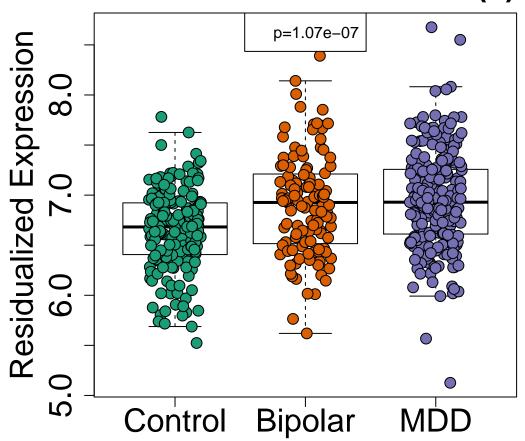
RPL7, InGen chr8:73292798-73293598(-)



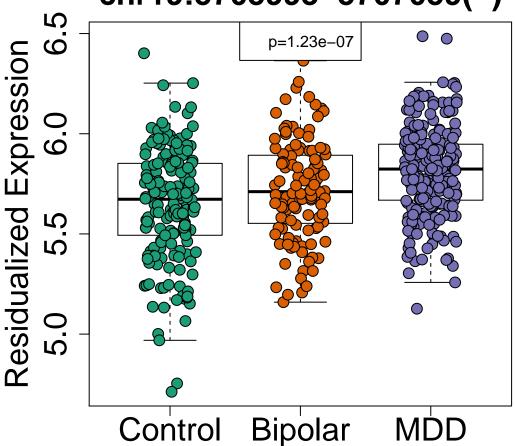
RPL7, InGen chr8:73292406-73292688(-)



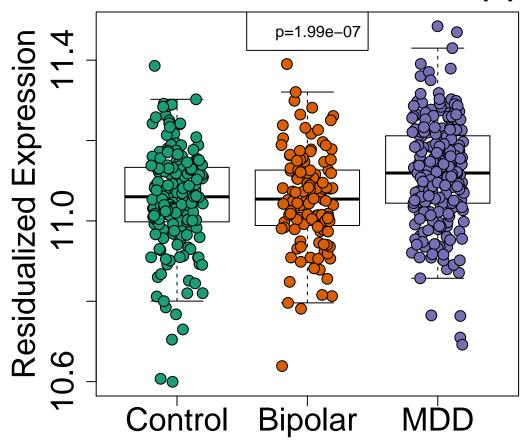
ARRDC3, InGen chr5:91373839-91374113(-)



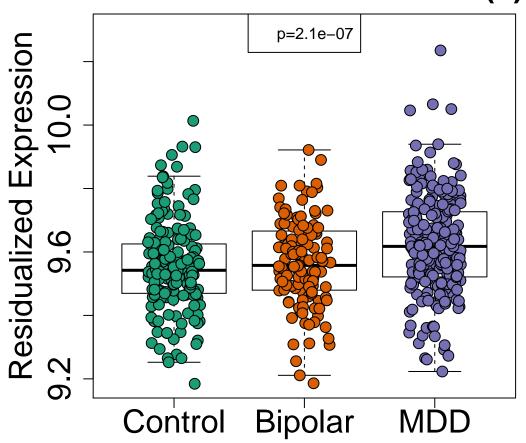
LONP1, InGen chr19:5705993-5707059(-)



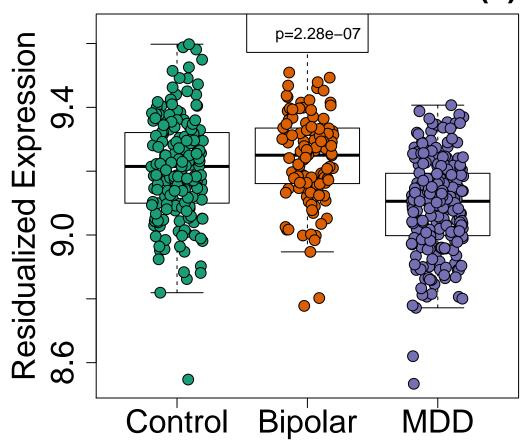
HSP90AB1, InGen chr6:44247196-44248629(+)



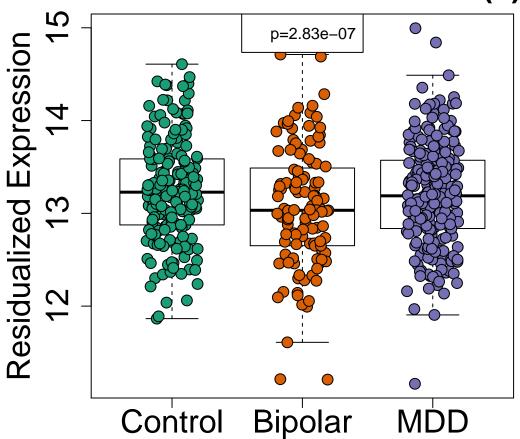
TMBIM6, InGen chr12:49761780-49762872(+)



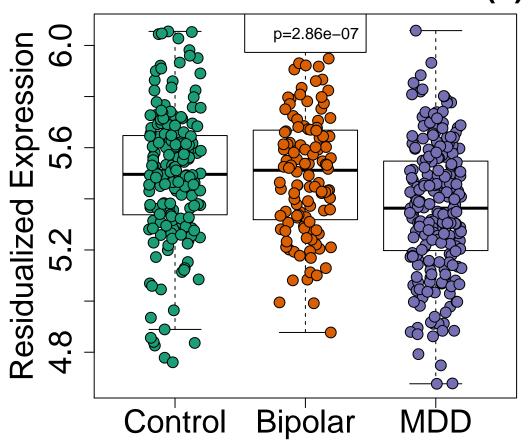
HNRNPA2B1, InGen chr7:26197733-26200571(-)



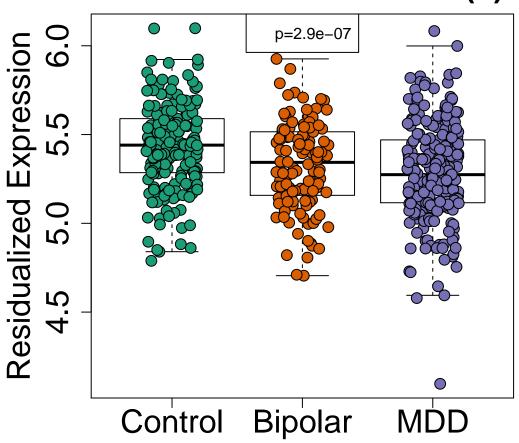
GFAP, InGen chr17:44911457-44911671(-)



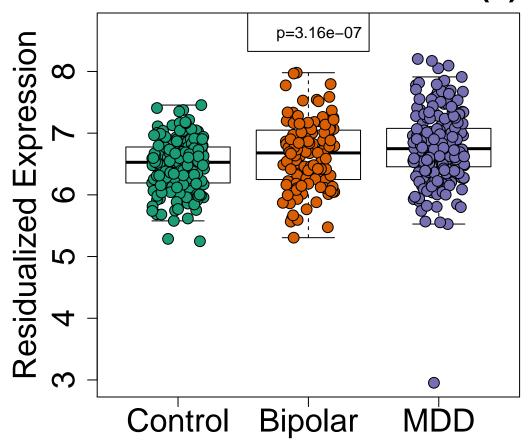
LRP1, InGen chr12:57200536-57200698(+)



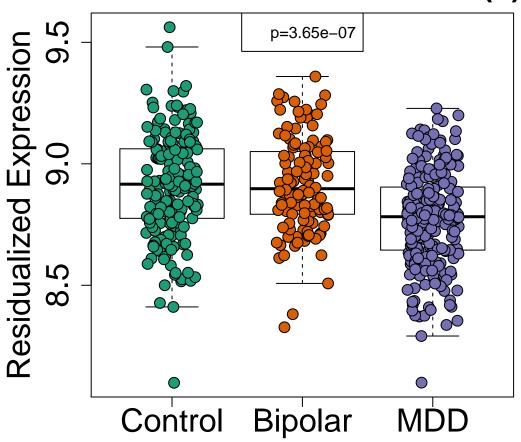
ERC1, InGen chr12:1116034-1141619(+)



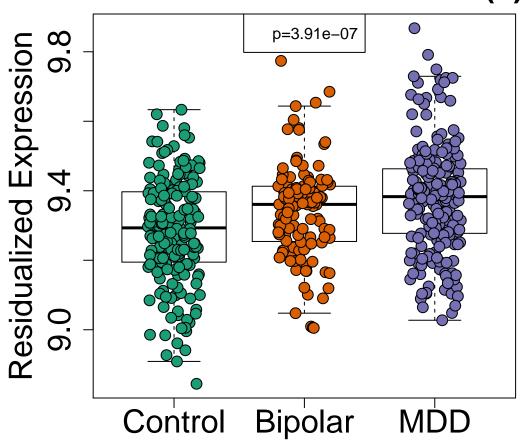
ARRDC3, InGen chr5:91378776-91382812(-)



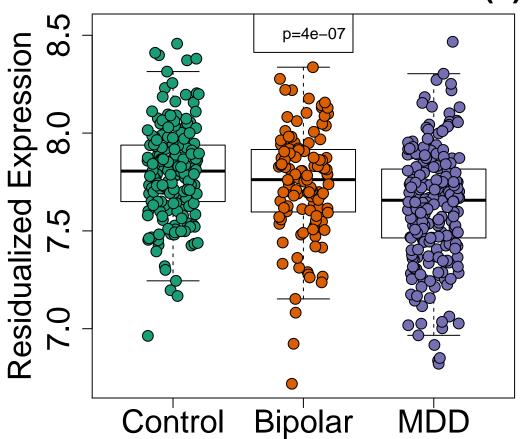
FUS, InGen chr16:31182423-31182512(+)



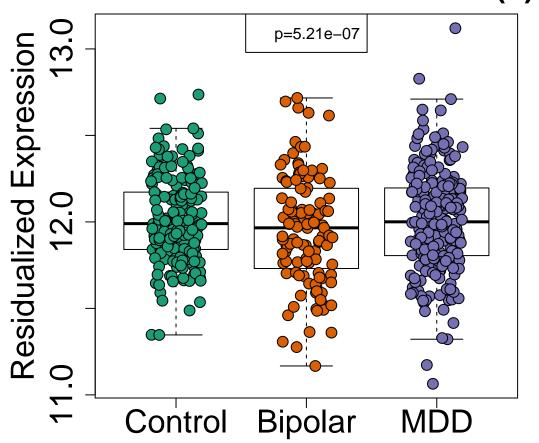
NEDD8-MDP1, InGen chr14:24217224-24218132(-)



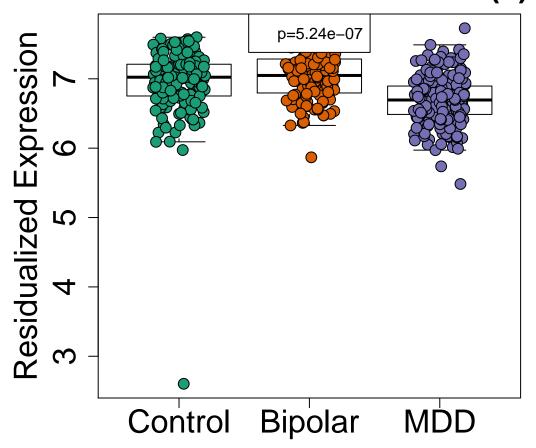
SRSF6, InGen chr20:43460242-43460514(+)



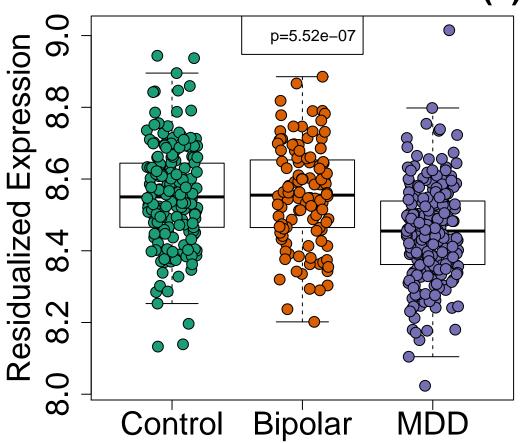
GLUL, InGen chr1:182385888-182386255(-)



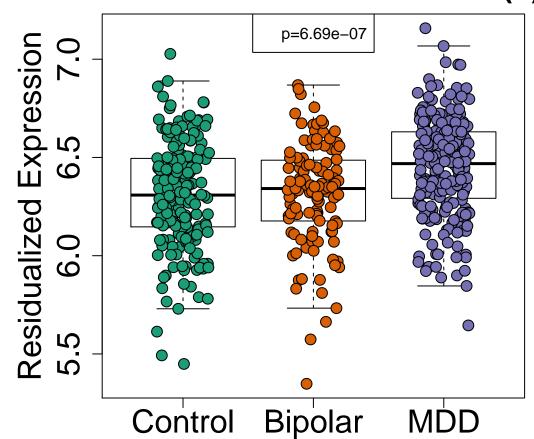
FUS, InGen chr16:31191111-31191398(+)



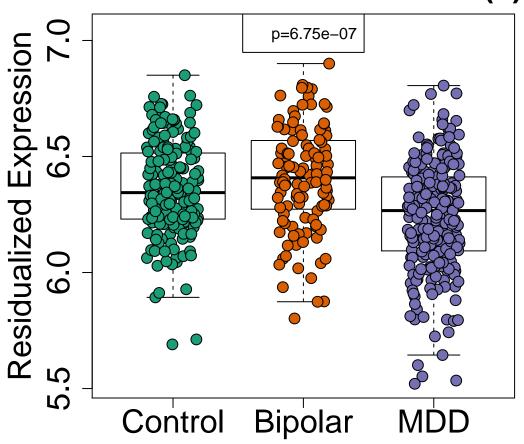
ATXN10, InGen chr22:45700379-45702688(+)



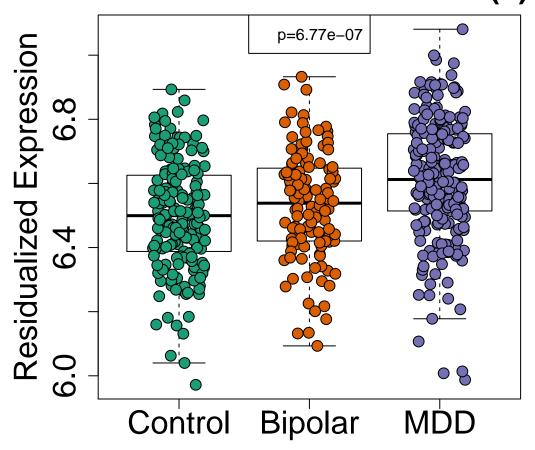
FDPS, InGen chr1:155312396-155317940(+)



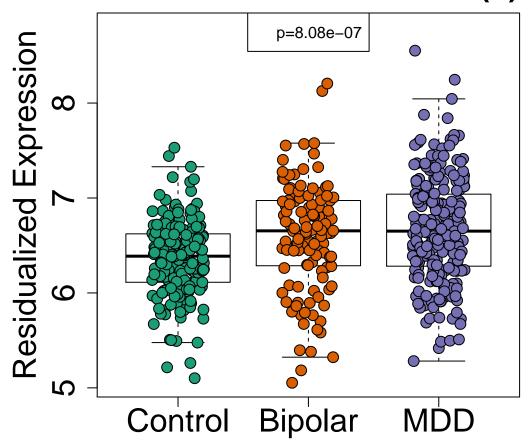
GLG1, InGen chr16:74459790-74462093(-)



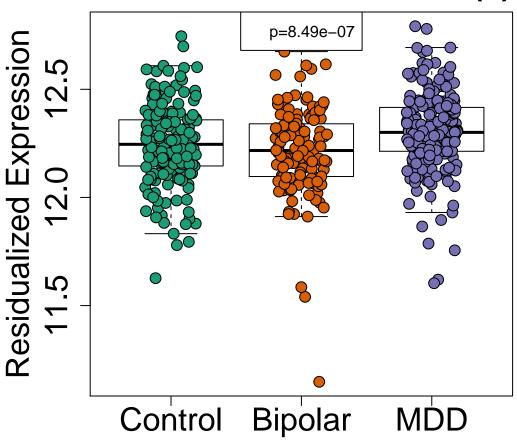
AMFR, InGen chr16:56364106-56367443(-)



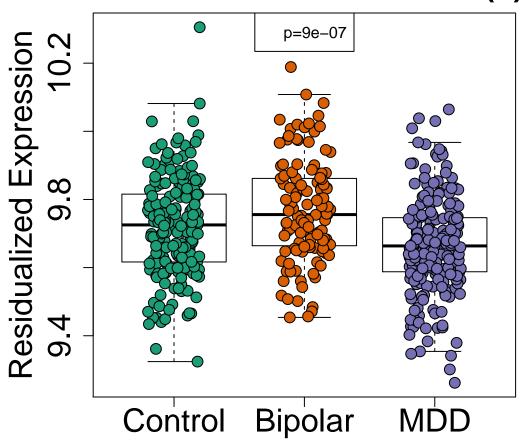
ARRDC3, InGen chr5:91376769-91378693(-)



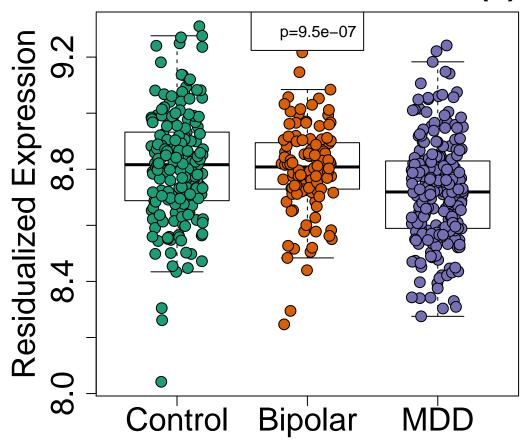
CALM2, InGen chr2:47161859-47162285(-)



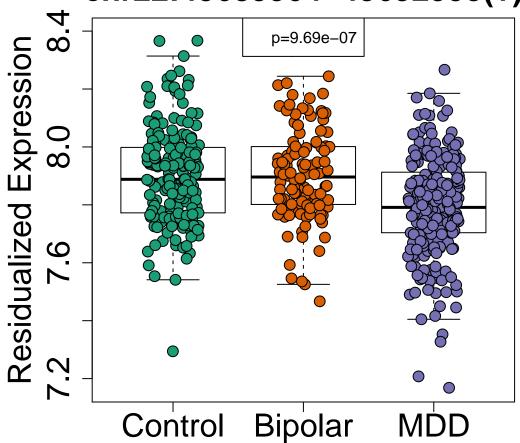
PSAP, InGen chr10:71831921-71834371(-)



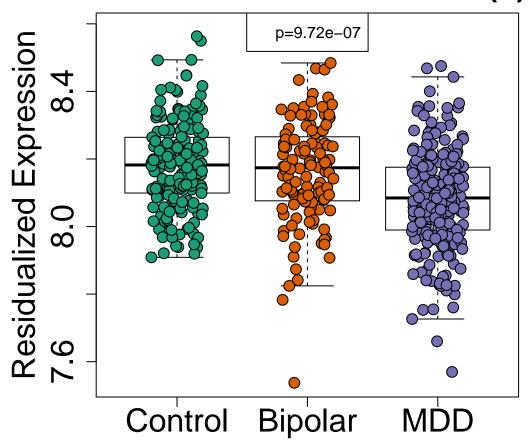
DST, InGen chr6:56487274-56489489(-)



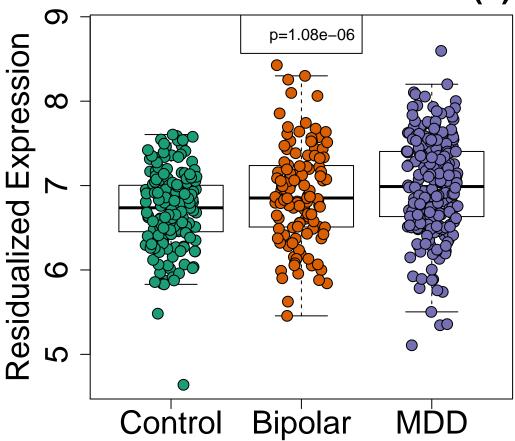
ATXN10, InGen chr22:45689904-45692995(+)



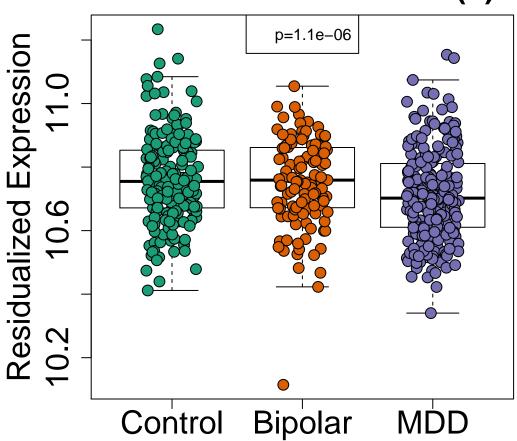
ATXN10, InGen chr22:45693079-45700281(+)



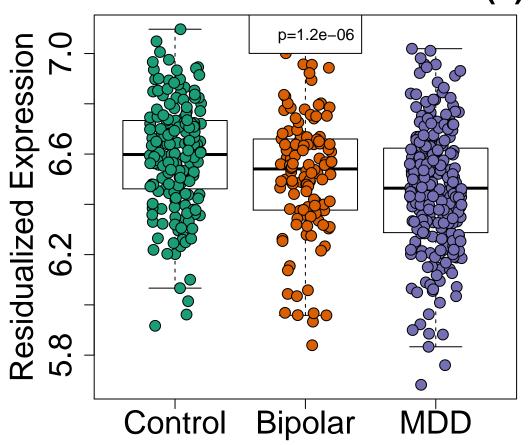
ARRDC3, InGen chr5:91375179-91375510(-)



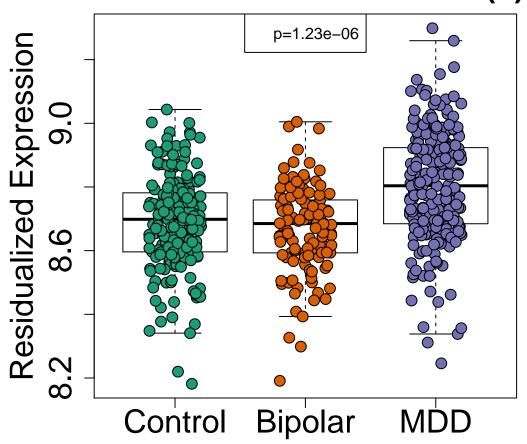
ACTB, InGen chr7:5528186-5528280(-)



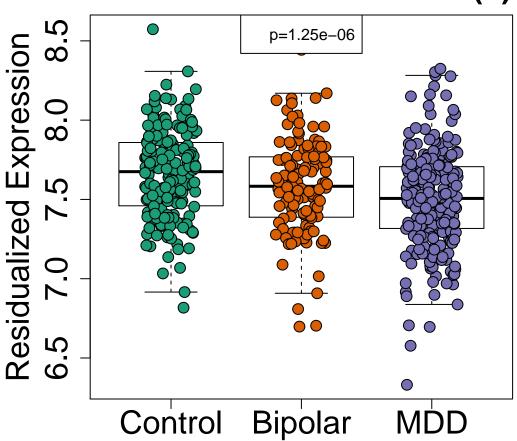
RBM25, InGen chr14:73111156-73111527(+)



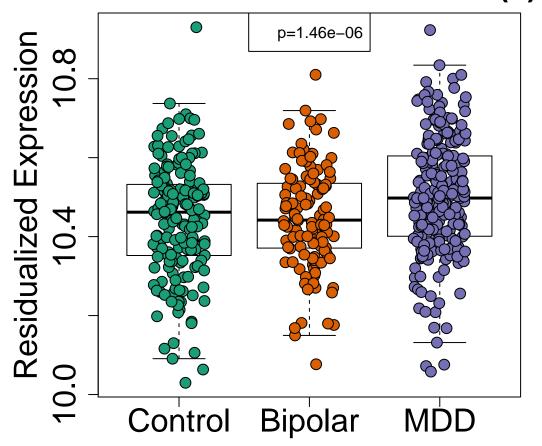
SNRPD2, InGen chr19:45688567-45691886(-)



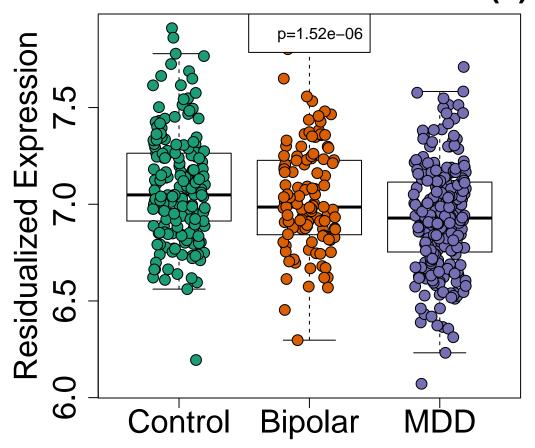
MACF1, InGen chr1:39340718-39340803(+)



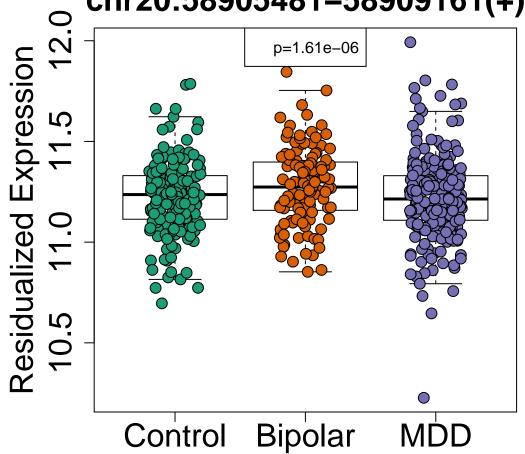
EIF4A2, InGen chr3:186787585-186787802(+)



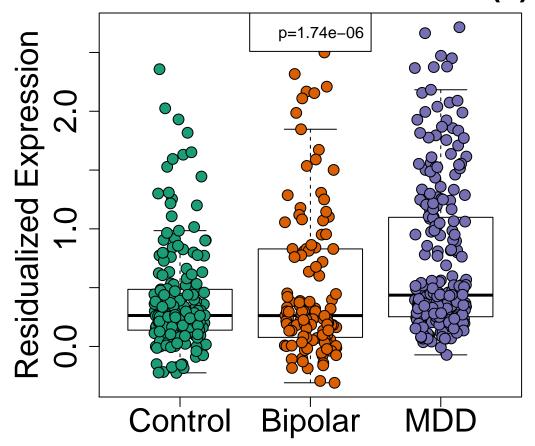
CCDC82, InGen chr11:96383474-96383961(-)



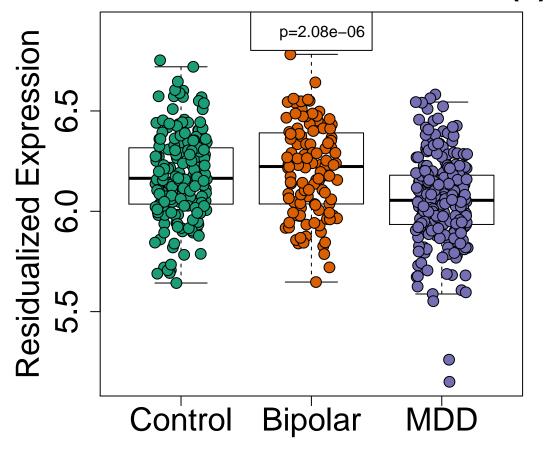
GNAS, InGen chr20:58905481-58909161(+)



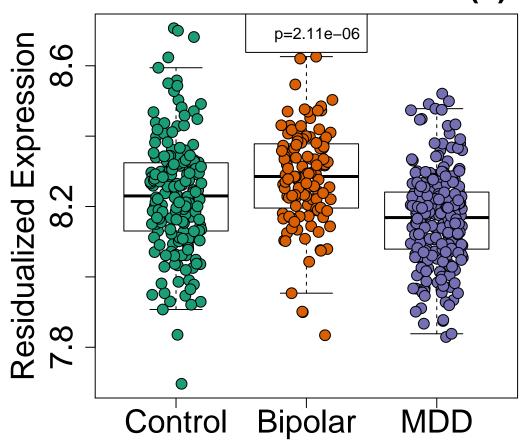
SLC26A11, AltStartEnd chr17:80227961-80230874(+)



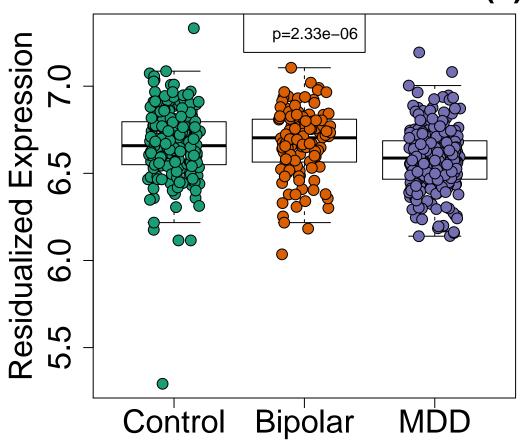
ARHGEF7, InGen chr13:111244295-111267547(+)



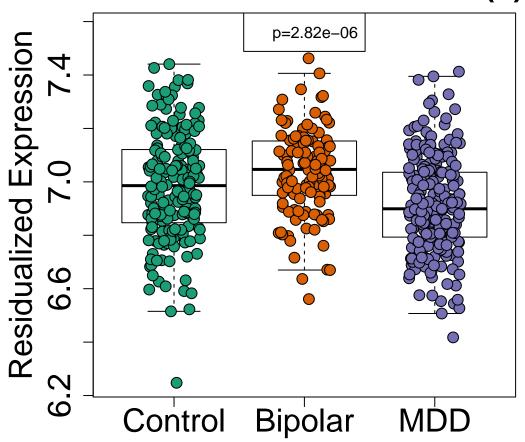
TCEB2, InGen chr16:2772103-2775450(-)



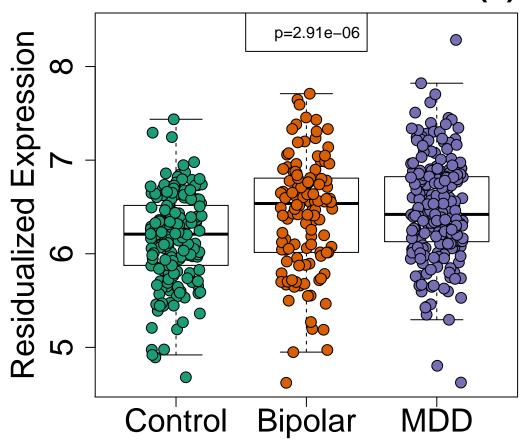
DNAJC5, InGen chr20:63928453-63929311(+)



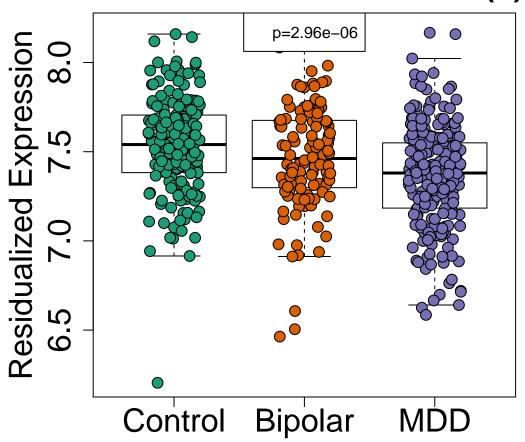
LRP1, InGen chr12:57198344-57198464(+)



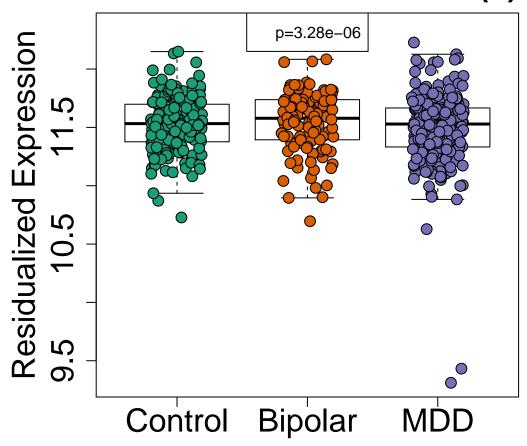
ARRDC3, InGen chr5:91374277-91374921(-)



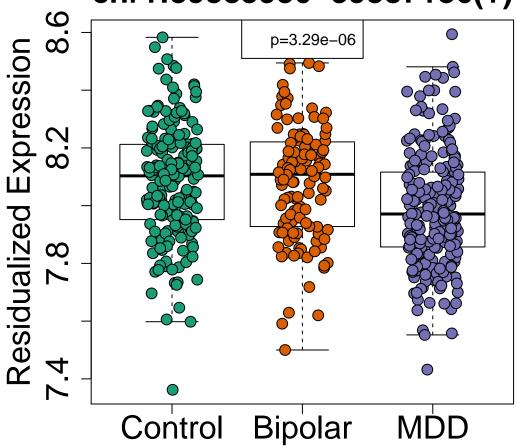
SRSF6, InGen chr20:43460599-43460702(+)



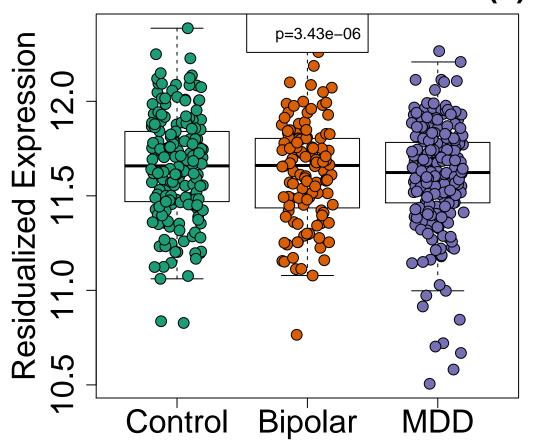
SPARCL1, InGen chr4:87490394-87490759(-)



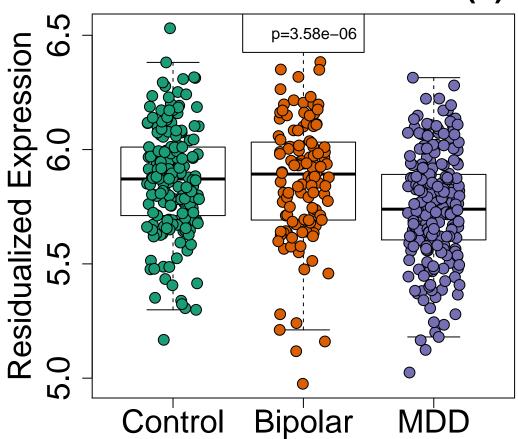
MACF1, InGen chr1:39385930-39387186(+)



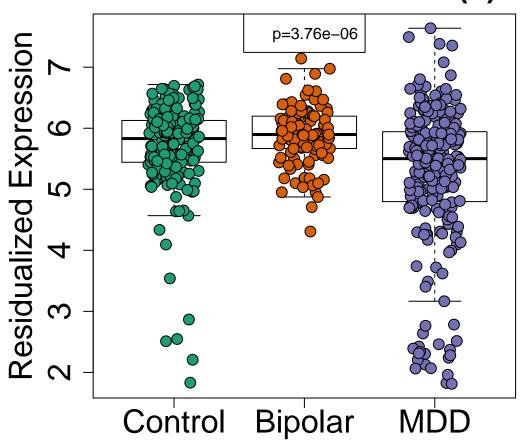
SLC1A2, InGen chr11:35260966-35265526(-)



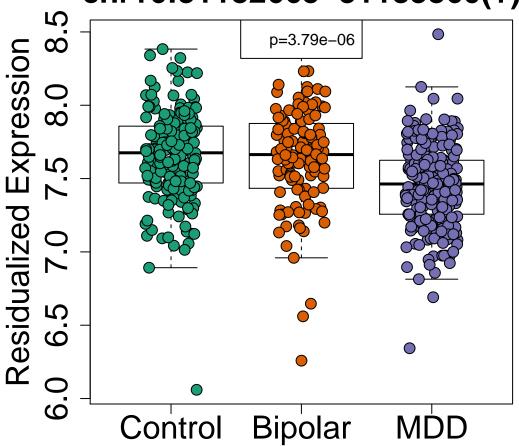
WDR37, InGen chr10:1078004-1080010(+)



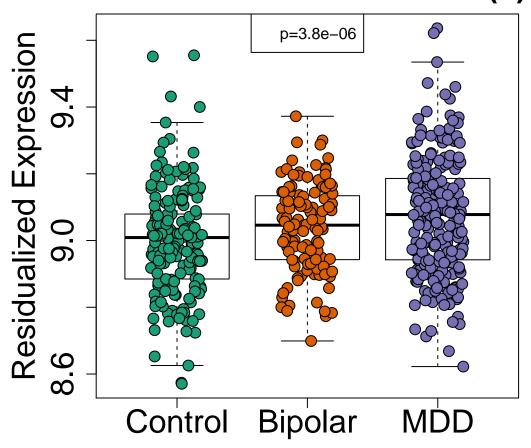
KDM4C, InGen chr9:7128237-7165237(+)



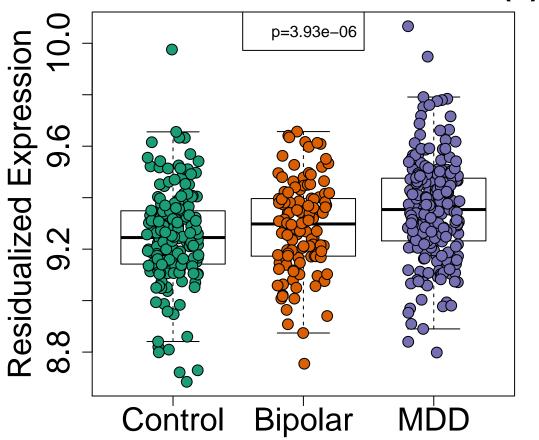
FUS, InGen chr16:31182665-31183860(+)



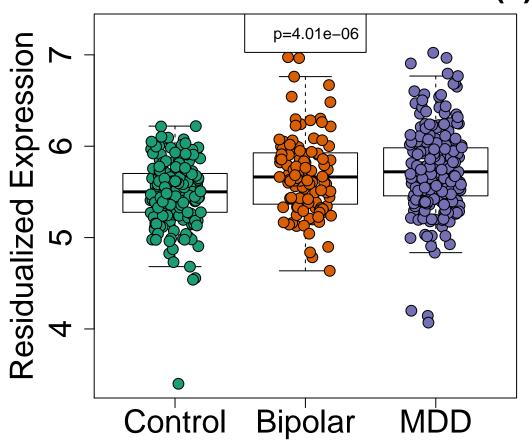
NEDD8-MDP1, InGen chr14:24218432-24232249(-)



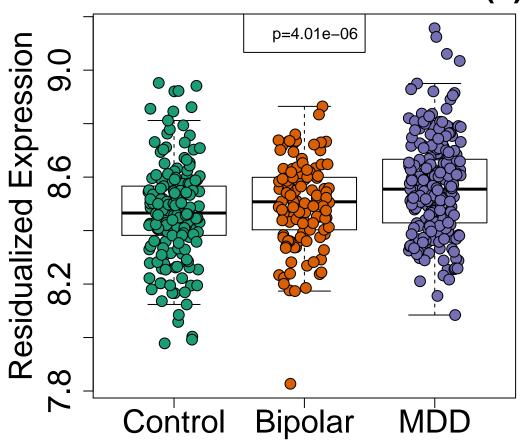
HSP90B1, InGen chr12:103932943-103933955(+)



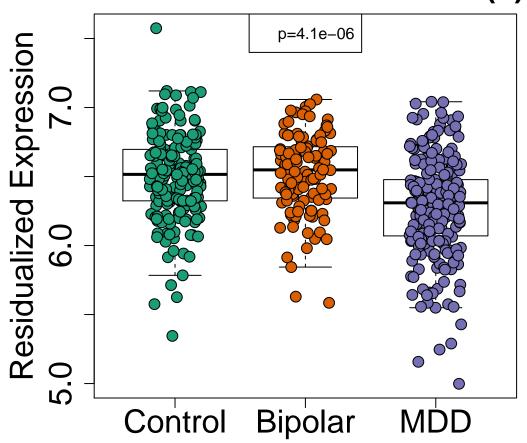
HMGB2, InGen chr4:173332239-173332820(-)



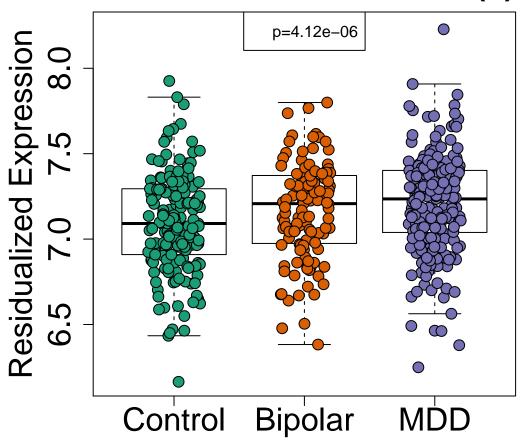
NEDD8-MDP1, InGen chr14:24218216-24218383(-)



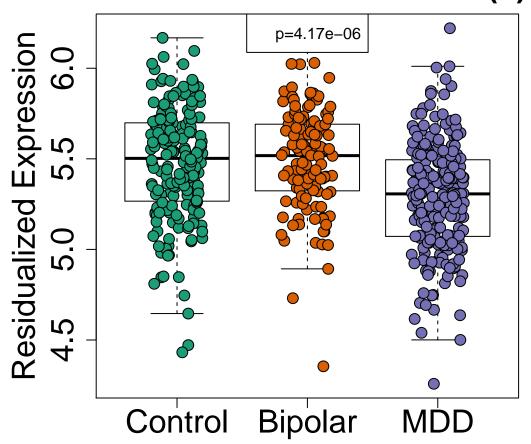
FUS, InGen chr16:31186837-31188324(+)



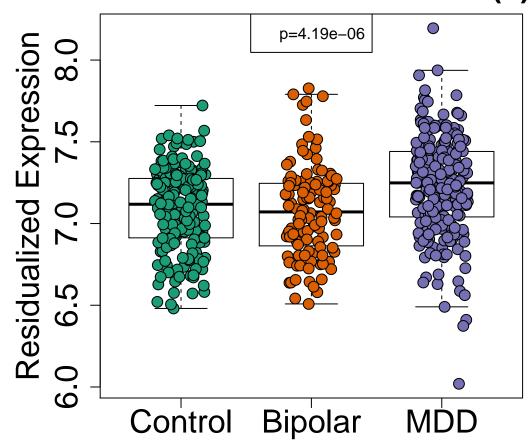
HMGCS1, InGen chr5:43298976-43313355(-)



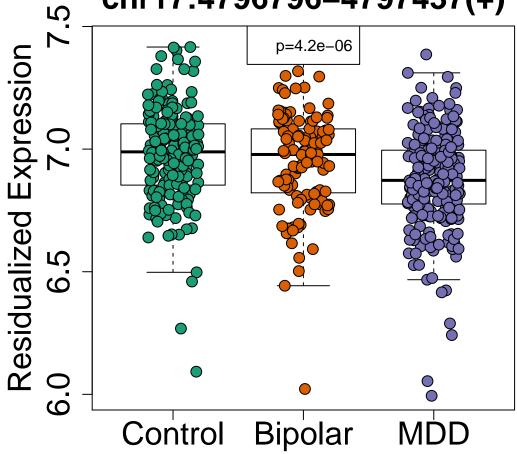
CHD8, InGen chr14:21403213-21403452(-)



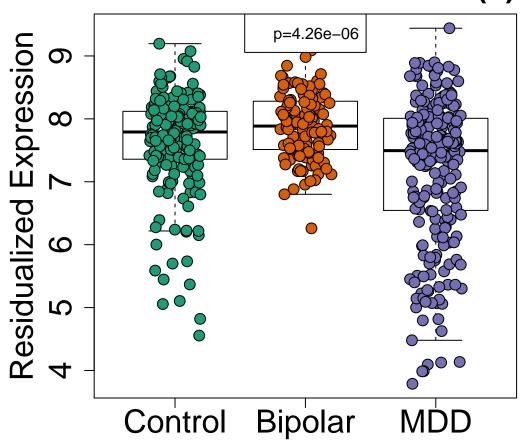
EIF4G2, InGen chr11:10807382-10808704(-)



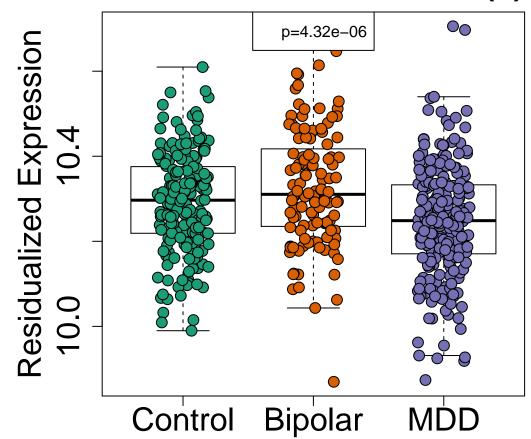
PSMB6, InGen chr17:4796796-4797437(+)



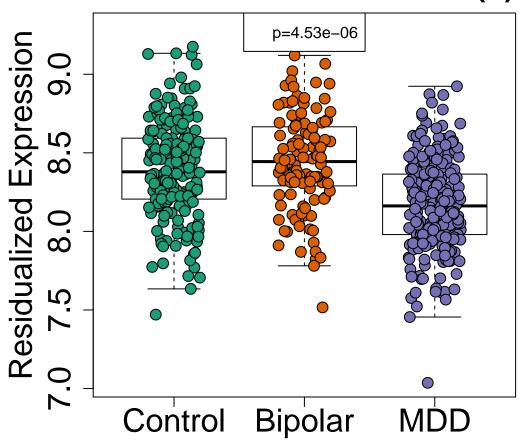
ITGB8, InGen chr7:20380832-20381726(+)



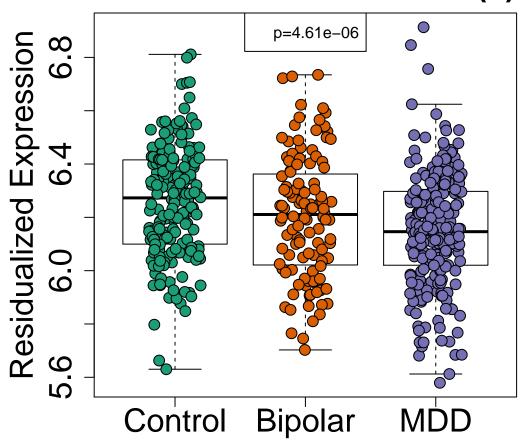
RPS10, InGen chr6:34417548-34418368(-)



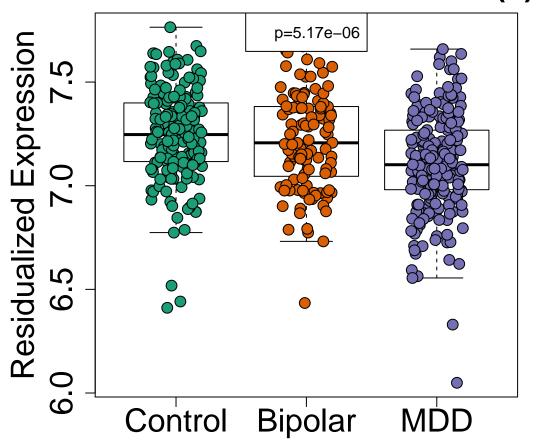
QDPR, InGen chr4:17501860-17504378(-)



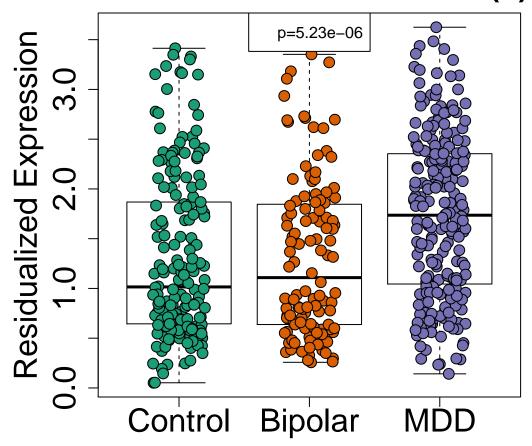
PCM1, InGen chr8:18006398-18009546(+)



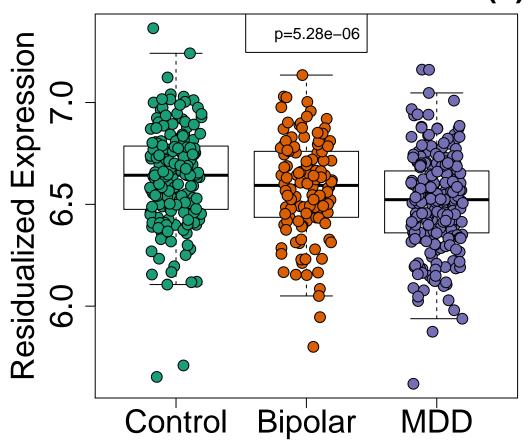
OPA1, InGen chr3:193635523-193637194(+)



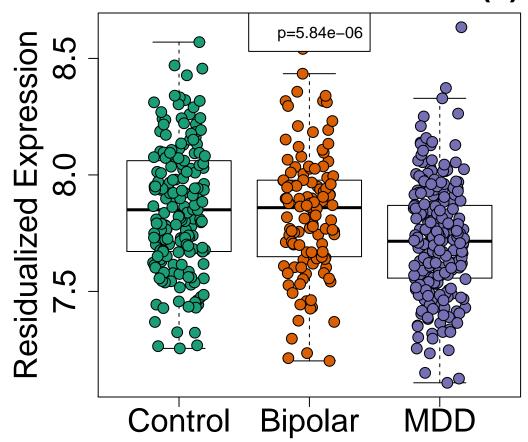
DNA2-SLC25A16, ExonSkip chr10:68470164-68487143(-)



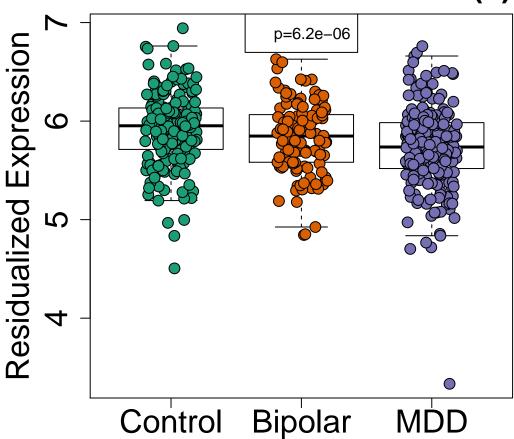
CPNE6, InGen chr14:24074366-24074530(+)



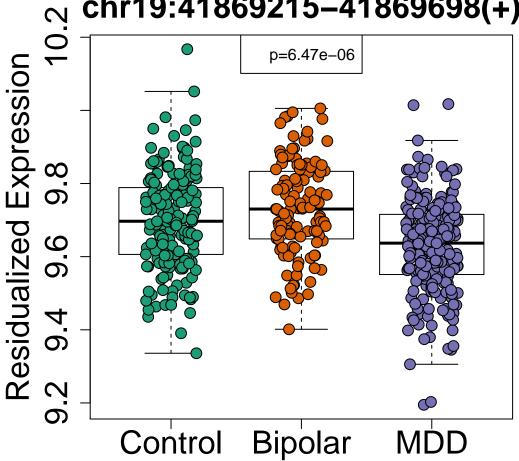
ARAP2, InGen chr4:36187572-36193577(-)



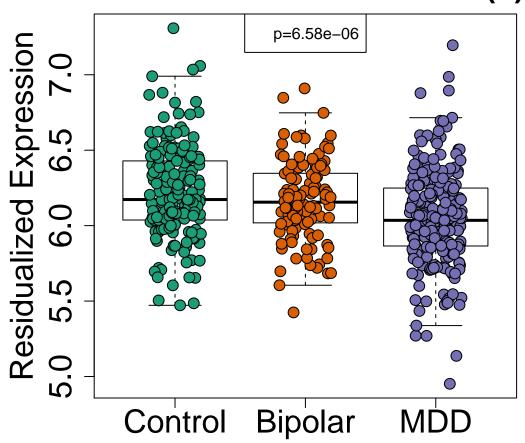
CACNA2D1, InGen chr7:81964109-81964206(-)



RPS19, InGen chr19:41869215-41869698(+)



PRKCA, InGen chr17:66774068-66786866(+)



HSP90AA1, InGen chr14:102081822-102082110(-)

