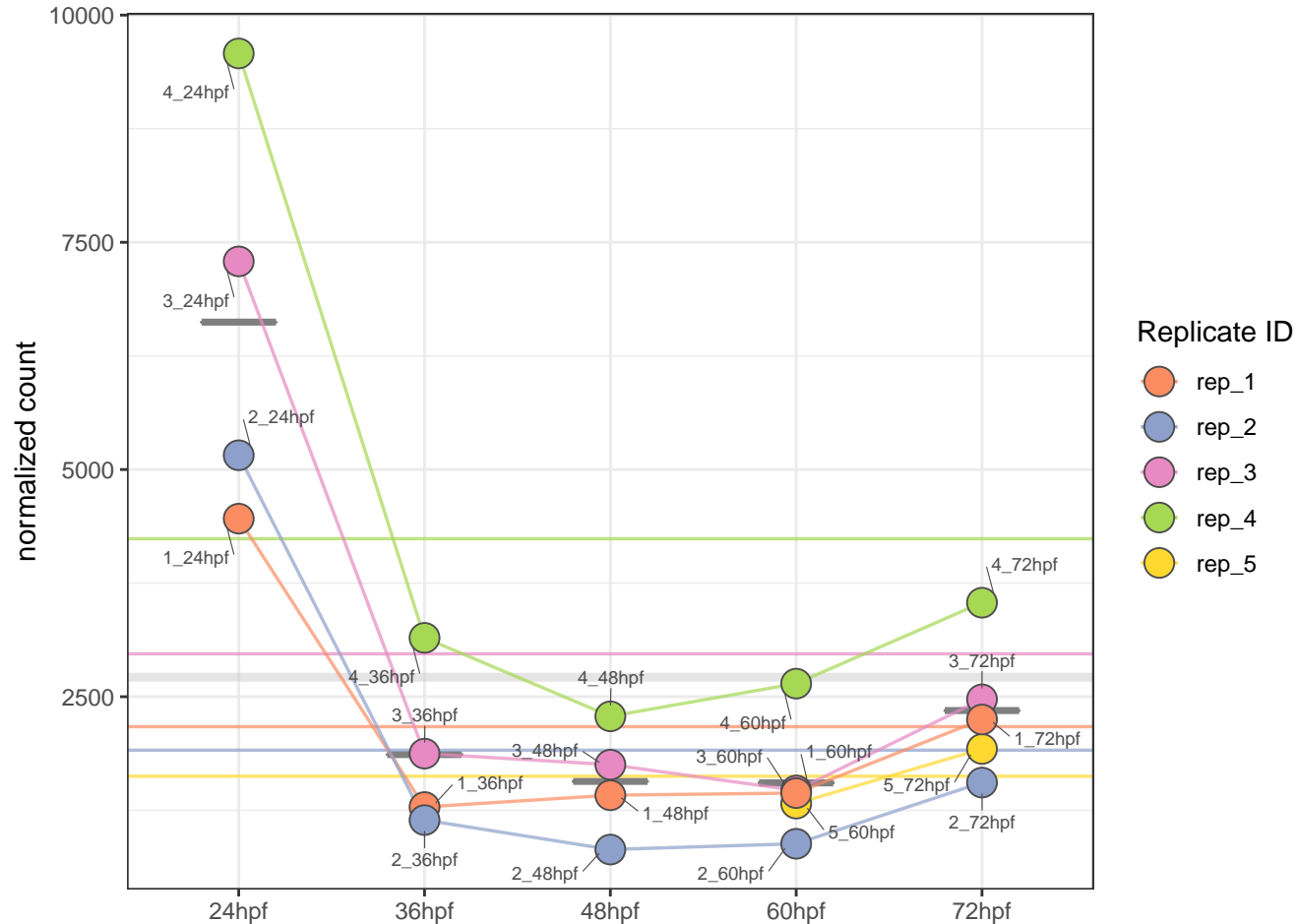Gene: si:ch211−220i18.4, ENSDARG00000030262, chromosome 23, protein_coding
P−value = 9.5e−20
Adjusted p−value = 3.2e−15
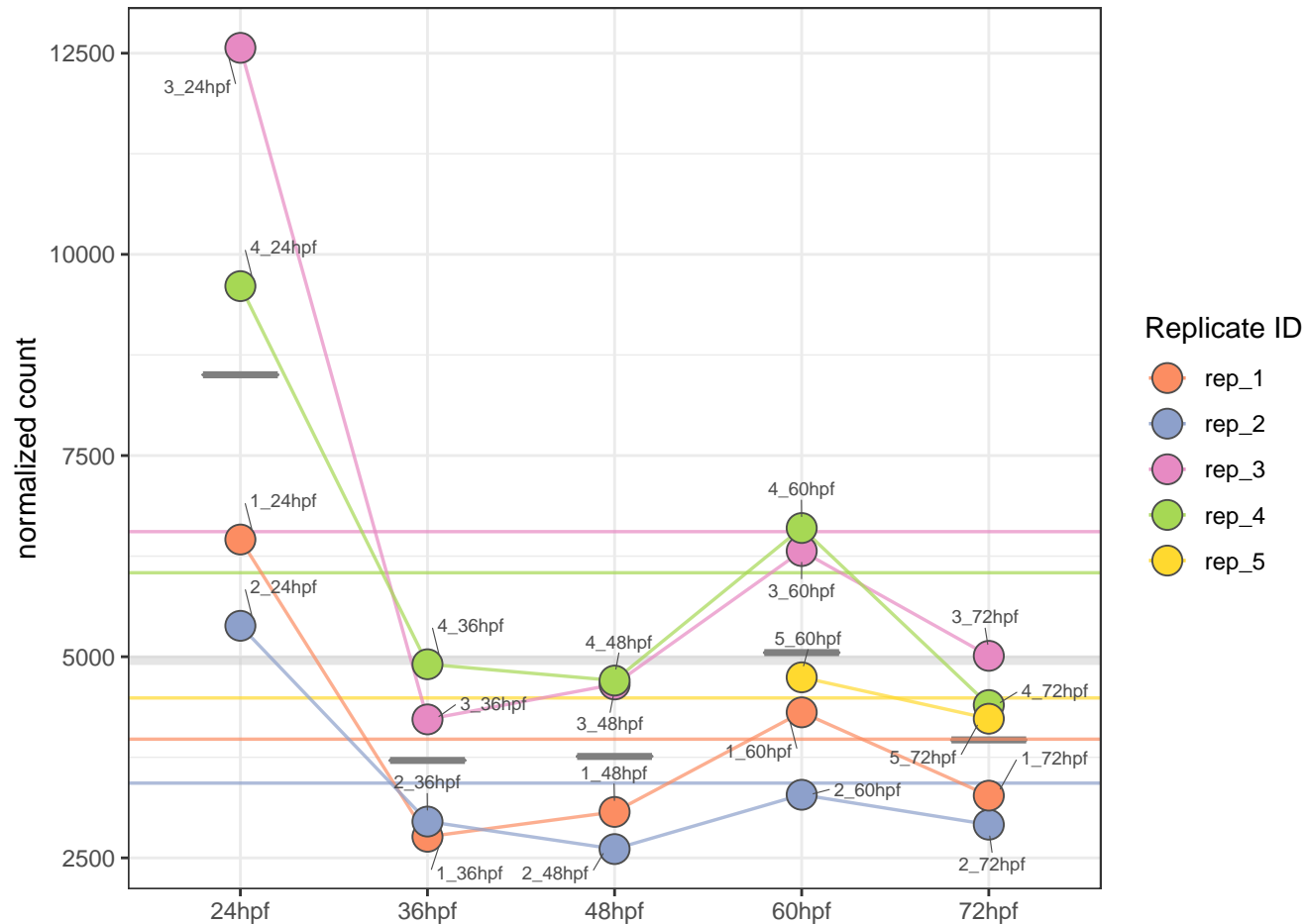Log2 fold−change (rep_5 / rep_1) = −0.02
Overall mean normalized counts = 2714.11

Gene: impdh2, ENSDARG00000006900, chromosome 8, protein_coding
P−value = 4e−19
Adjusted p−value = 6.7e−15
Log2 fold−change (rep_5 / rep_1) = 0.32
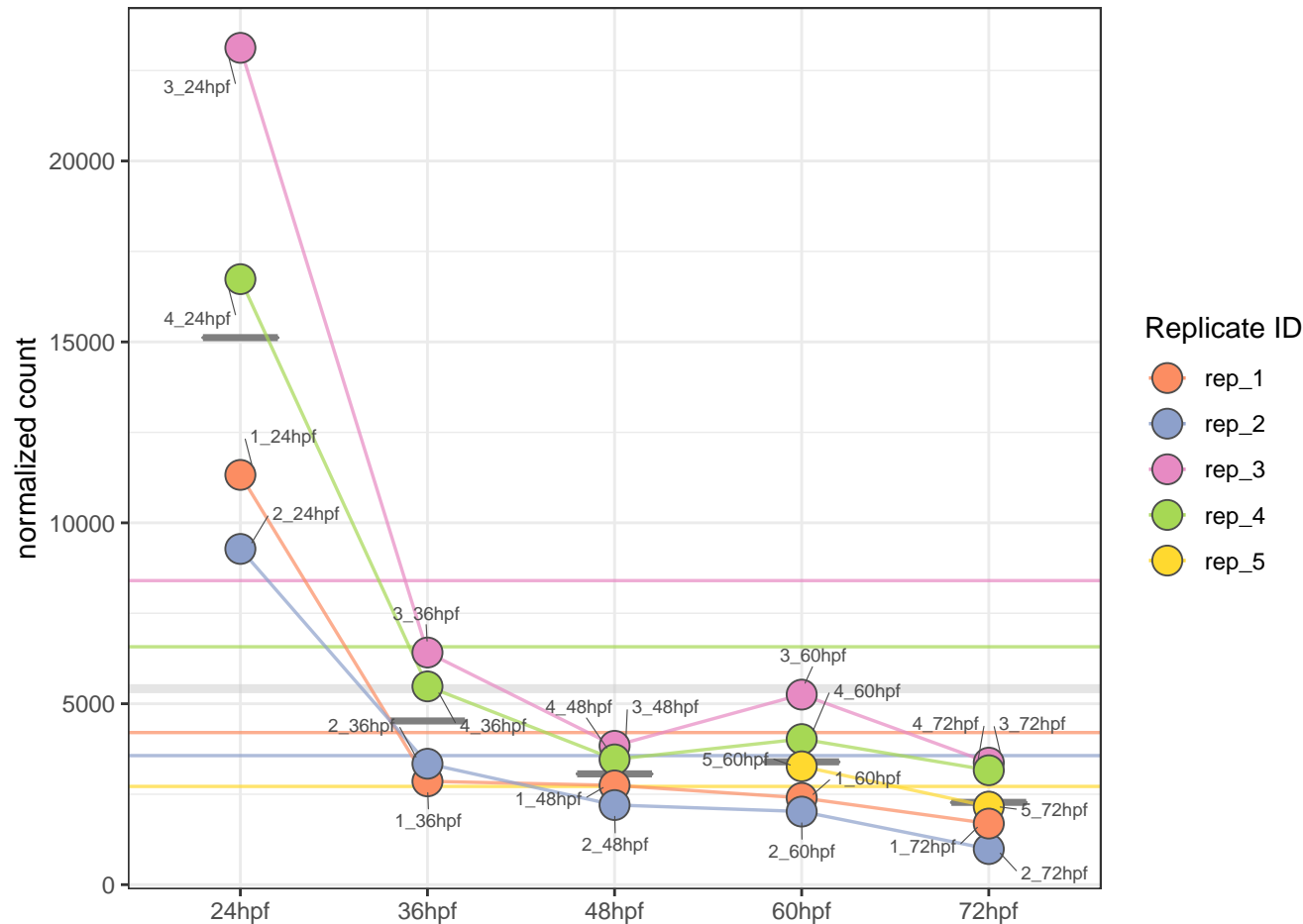Overall mean normalized counts = 4953.95

Gene: nkx2.7, ENSDARG00000021232, chromosome 8, protein_coding
P−value = 2.3e−18
Adjusted p−value = 2.6e−14
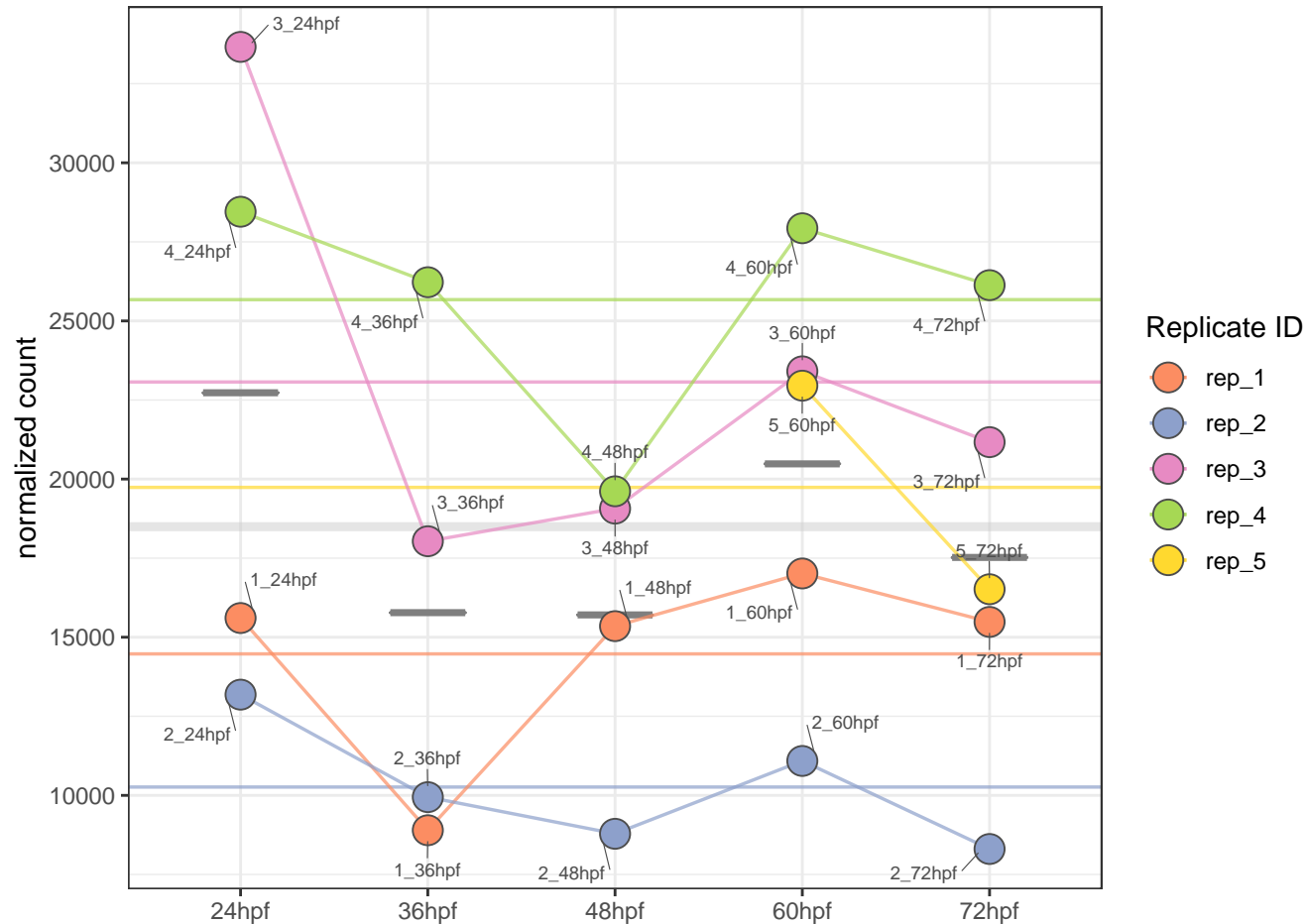Log2 fold−change (rep_5 / rep_1) = 0.39
Overall mean normalized counts = 5416.48

Gene: usp28, ENSDARG00000008880, chromosome 21, protein_coding
P−value = 7.1e−18
Adjusted p−value = 5.9e−14
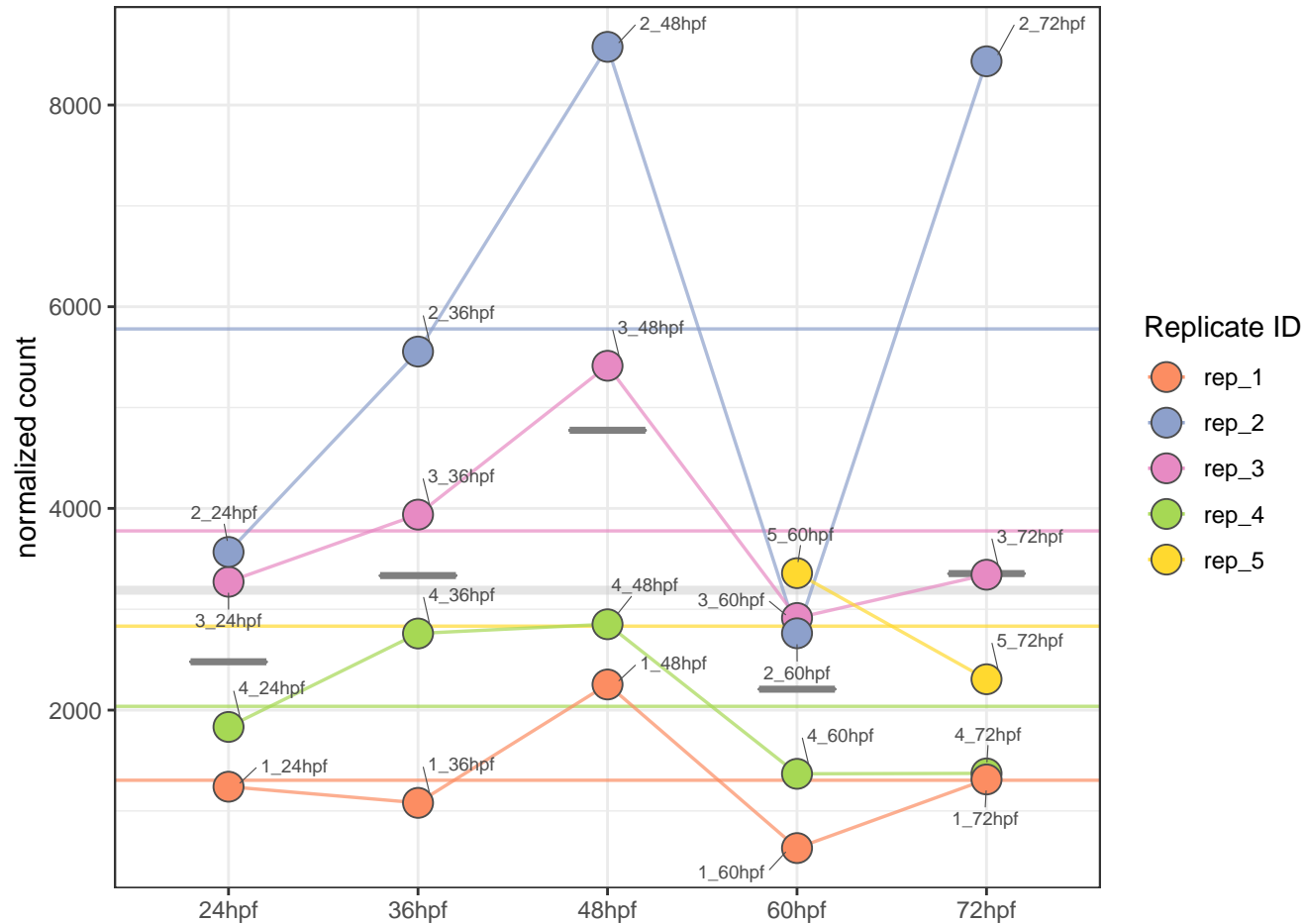Log2 fold−change (rep_5 / rep_1) = 0.40
Overall mean normalized counts = 18493.69

Gene: BX548073.2, ENSDARG00000092457, chromosome 5, processed_transcript
P−value = 1.1e−17
Adjusted p−value = 6.4e−14
Log2 fold−change (rep_5 / rep_1) = 1.57
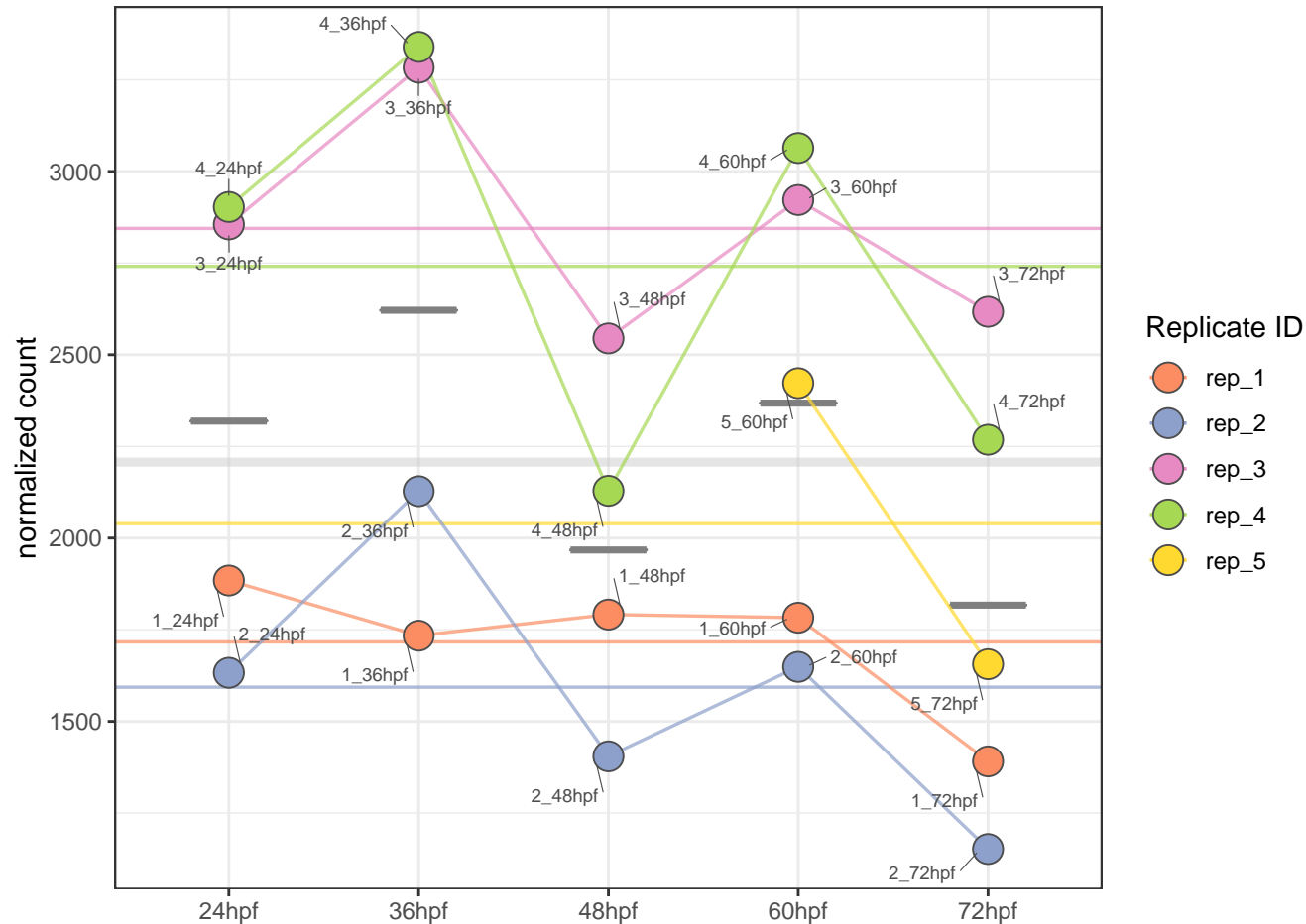Overall mean normalized counts = 3188.92

Gene: dhrs3b, ENSDARG00000044803, chromosome 11, protein_coding
P−value = 1.1e−17
Adjusted p−value = 6.4e−14
Log2 fold−change (rep_5 / rep_1) = 0.32
Overall mean normalized counts = 2207.11

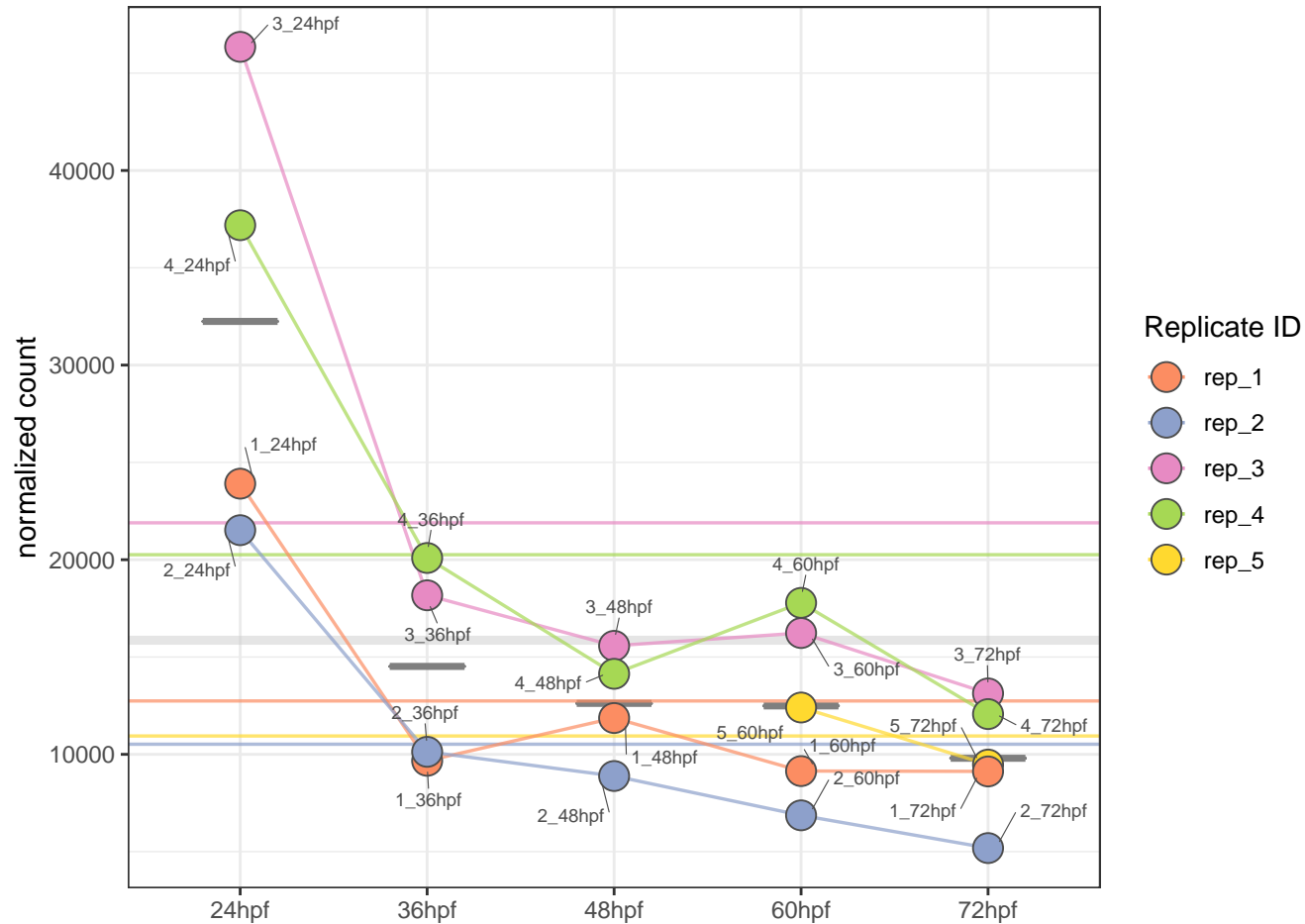Gene: prkag2a, ENSDARG00000012625, chromosome 24, protein_coding
P−value = 1.7e−17
Adjusted p−value = 8.2e−14
Log2 fold−change (rep_5 / rep_1) = 0.31
Overall mean normalized counts = 15861.73
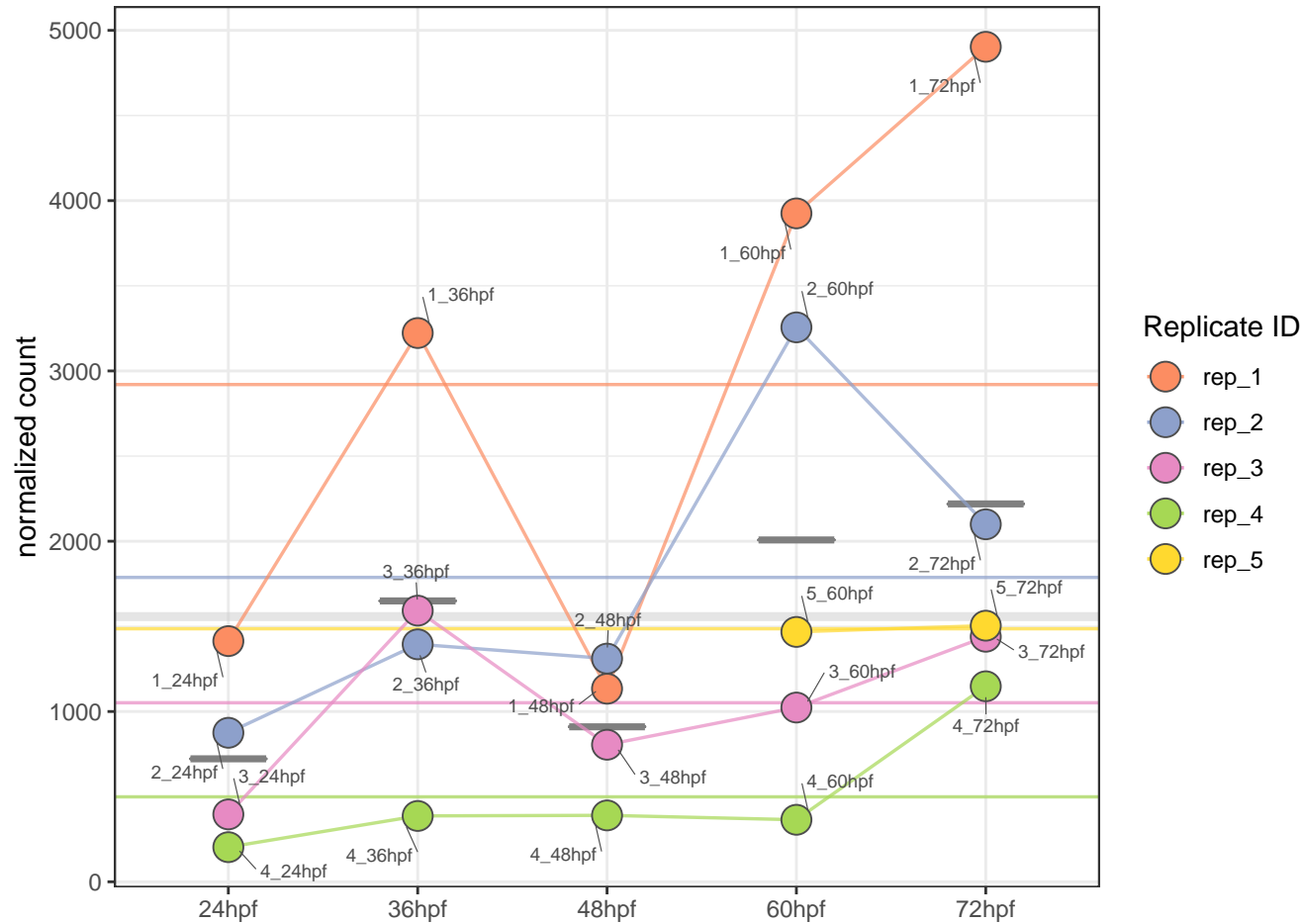
Gene: abcb5, ENSDARG00000021787, chromosome 16, protein_coding
P−value = 2.8e−17
Adjusted p−value = 1.2e−13
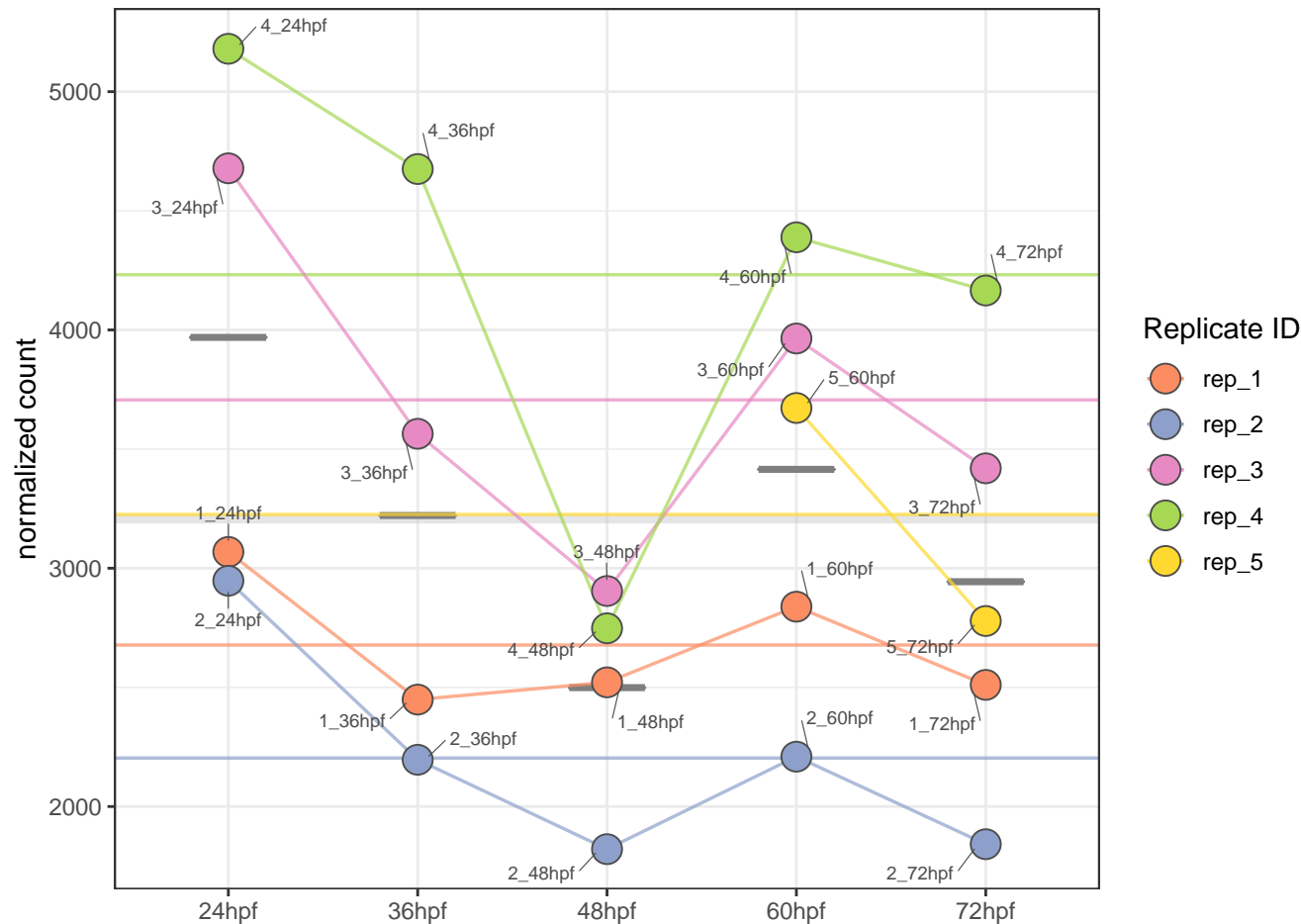Log2 fold−change (rep_5 / rep_1) = −1.43
Overall mean normalized counts = 1557.30

Gene: wwc3, ENSDARG00000061654, chromosome 6, protein_coding
P−value = 5e−17
Adjusted p−value = 1.9e−13
Log2 fold−change (rep_5 / rep_1) = 0.27
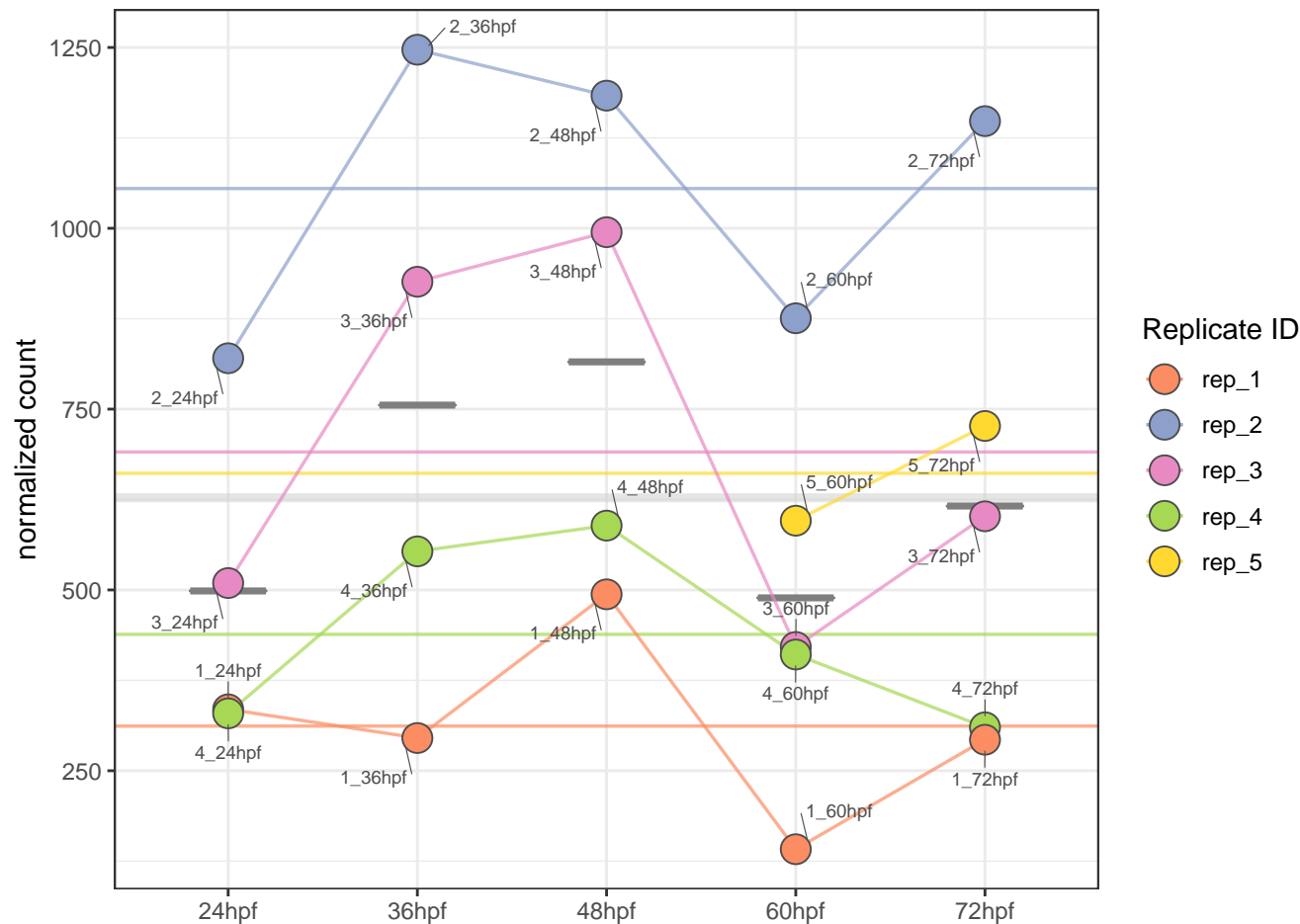Overall mean normalized counts = 3206.75

Gene: BX323087.2, ENSDARG00000117463, chromosome 23, lincRNA
P−value = 7.5e−17
Adjusted p−value = 2.5e−13
Log2 fold−change (rep_5 / rep_1) = 1.42
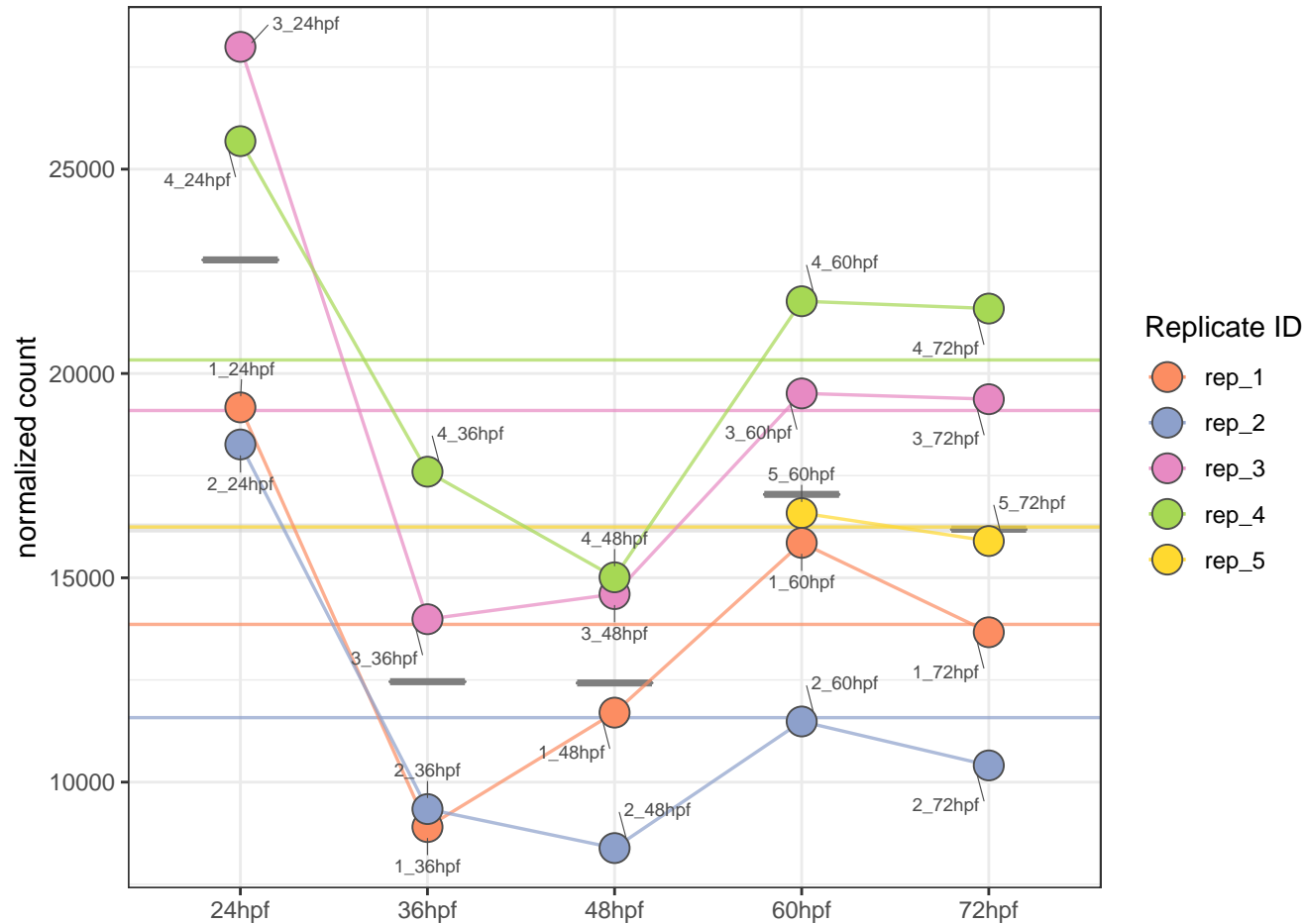Overall mean normalized counts = 627.39

Gene: itgb1b, ENSDARG00000104484, chromosome 2, protein_coding
P−value = 1.3e−16
Adjusted p−value = 3.8e−13
Log2 fold−change (rep_5 / rep_1) = 0.20
Overall mean normalized counts = 16218.43

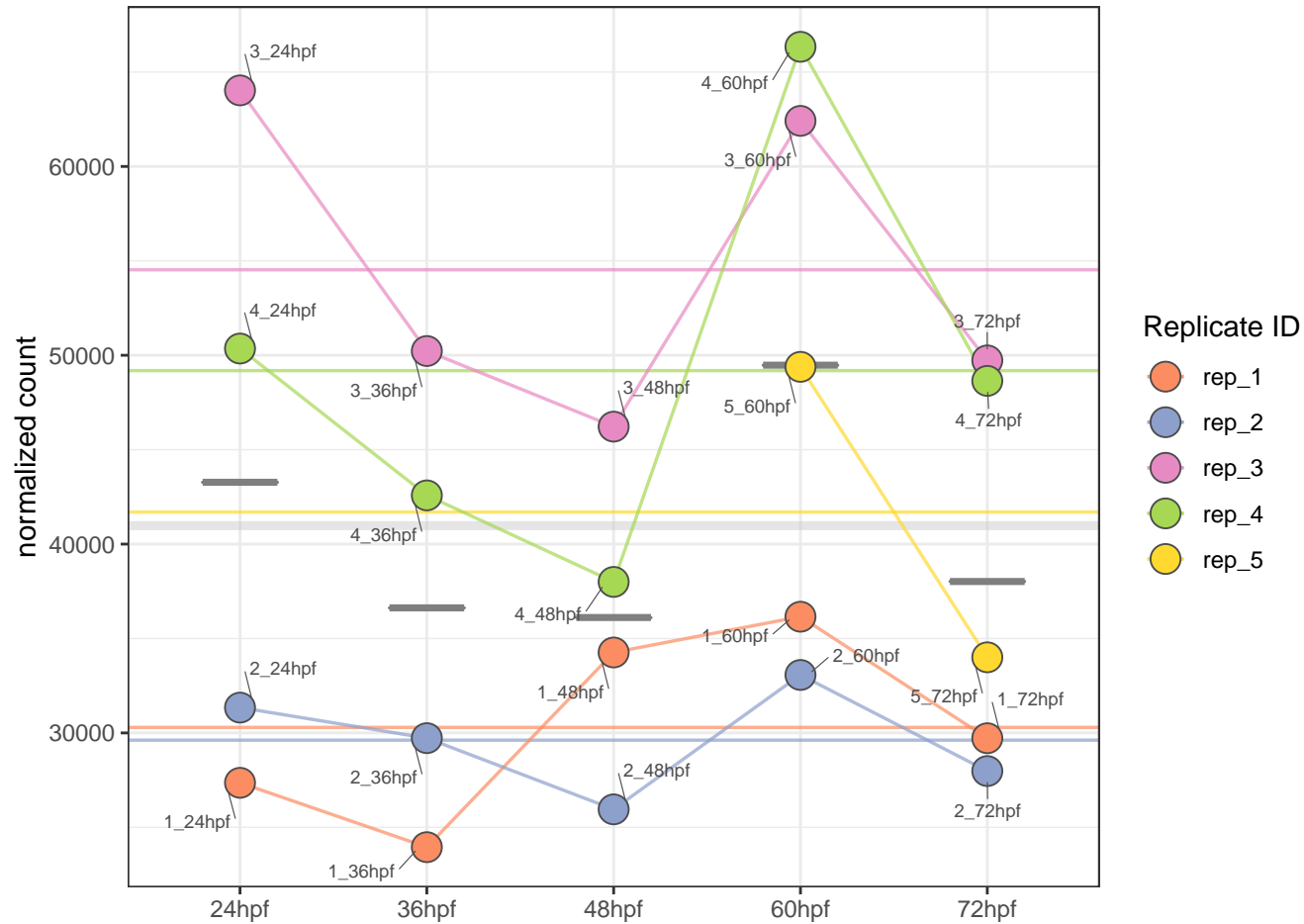Gene: atp1b1a, ENSDARG00000013144, chromosome 6, protein_coding
P−value = 1.9e−16
Adjusted p−value = 5.3e−13
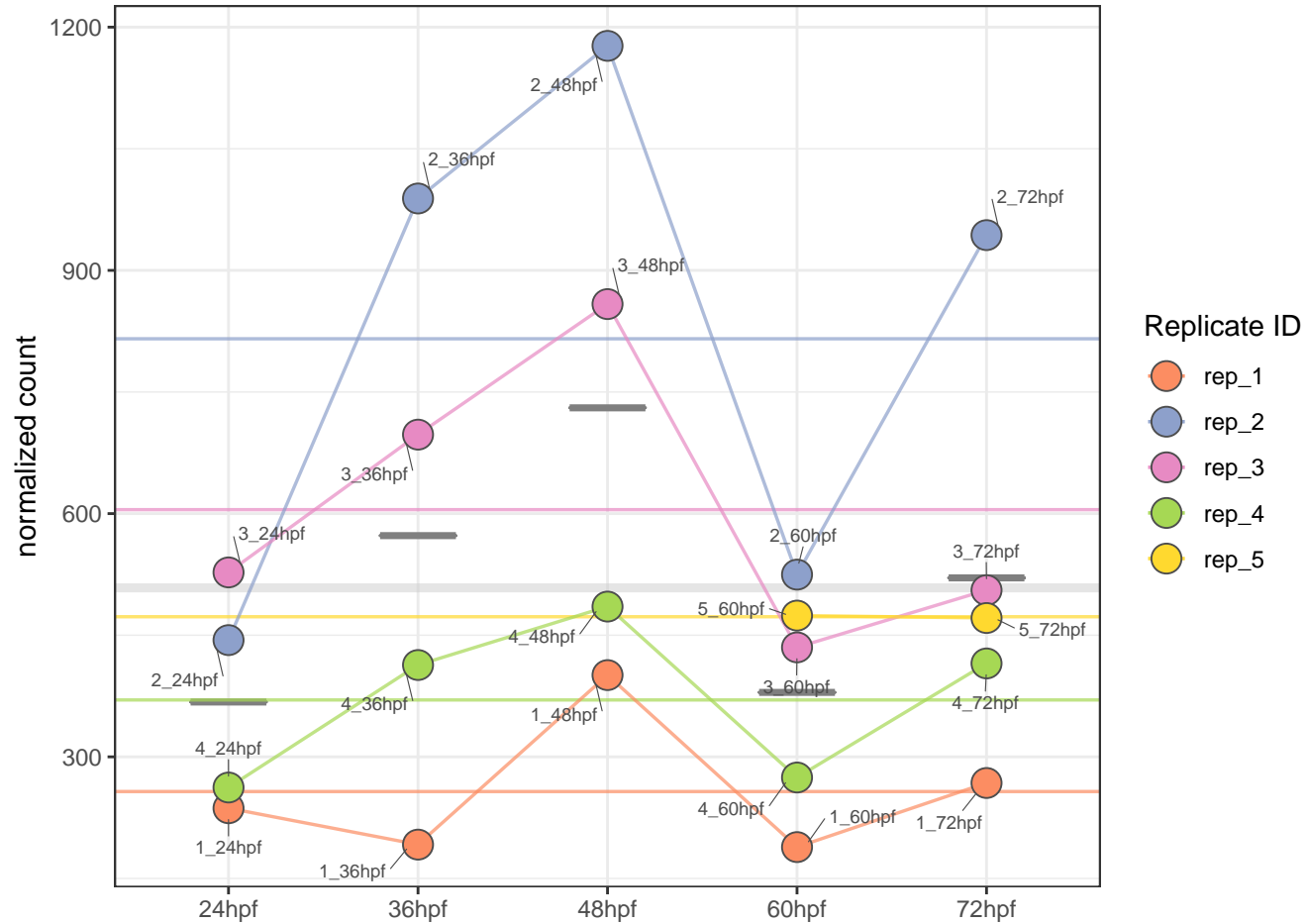Log2 fold−change (rep_5 / rep_1) = 0.33
Overall mean normalized counts = 40977.18

Gene: BX936303.1, ENSDARG00000103105, chromosome 4, processed_transcript
P−value = 2.6e−16
Adjusted p−value = 6.6e−13
Log2 fold−change (rep_5 / rep_1) = 1.10
Overall mean normalized counts = 508.40
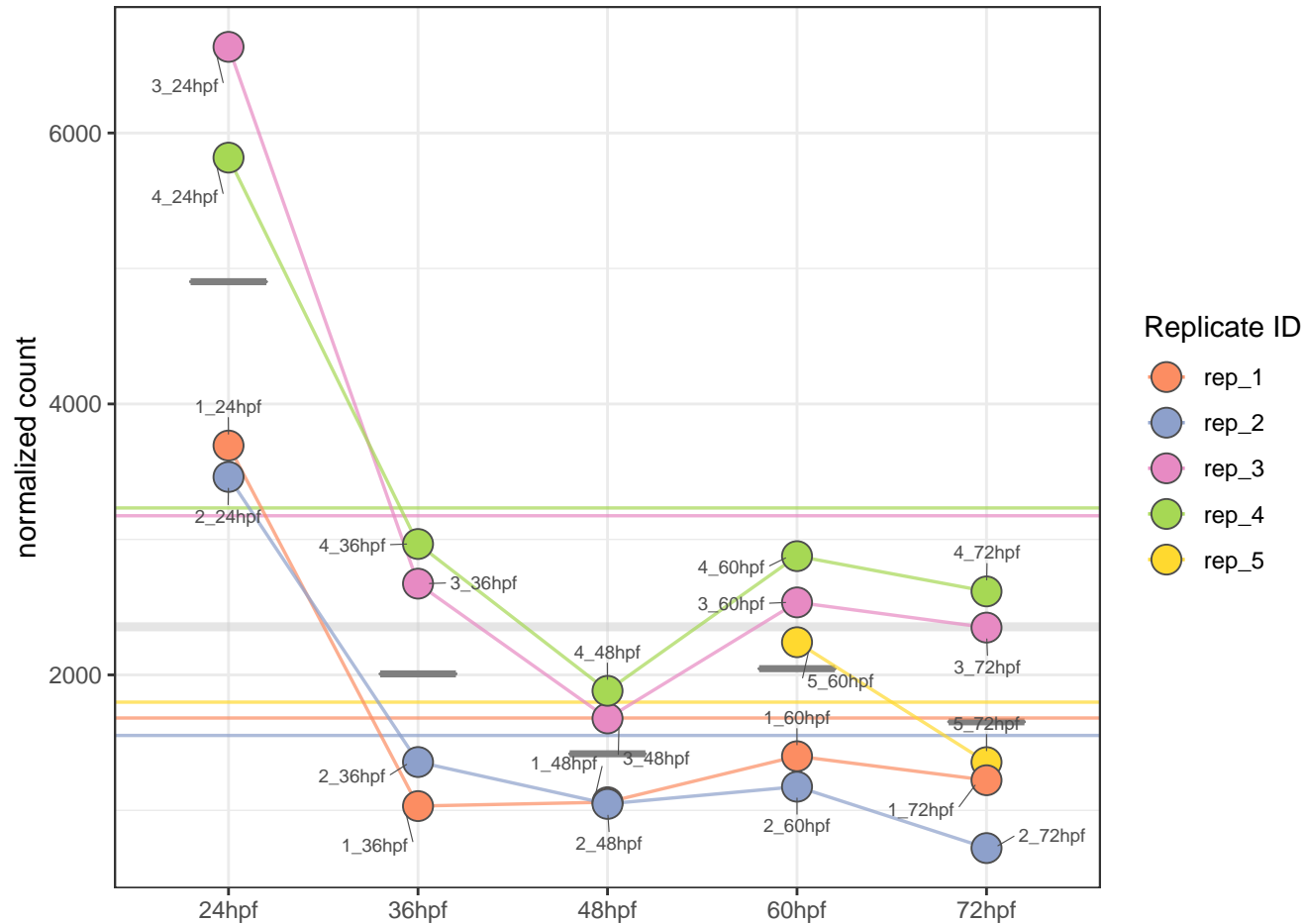
Gene: cx36.7, ENSDARG00000017927, chromosome 7, protein_coding
P−value = 3.2e−16
Adjusted p−value = 7.6e−13
Log2 fold−change (rep_5 / rep_1) = 0.50
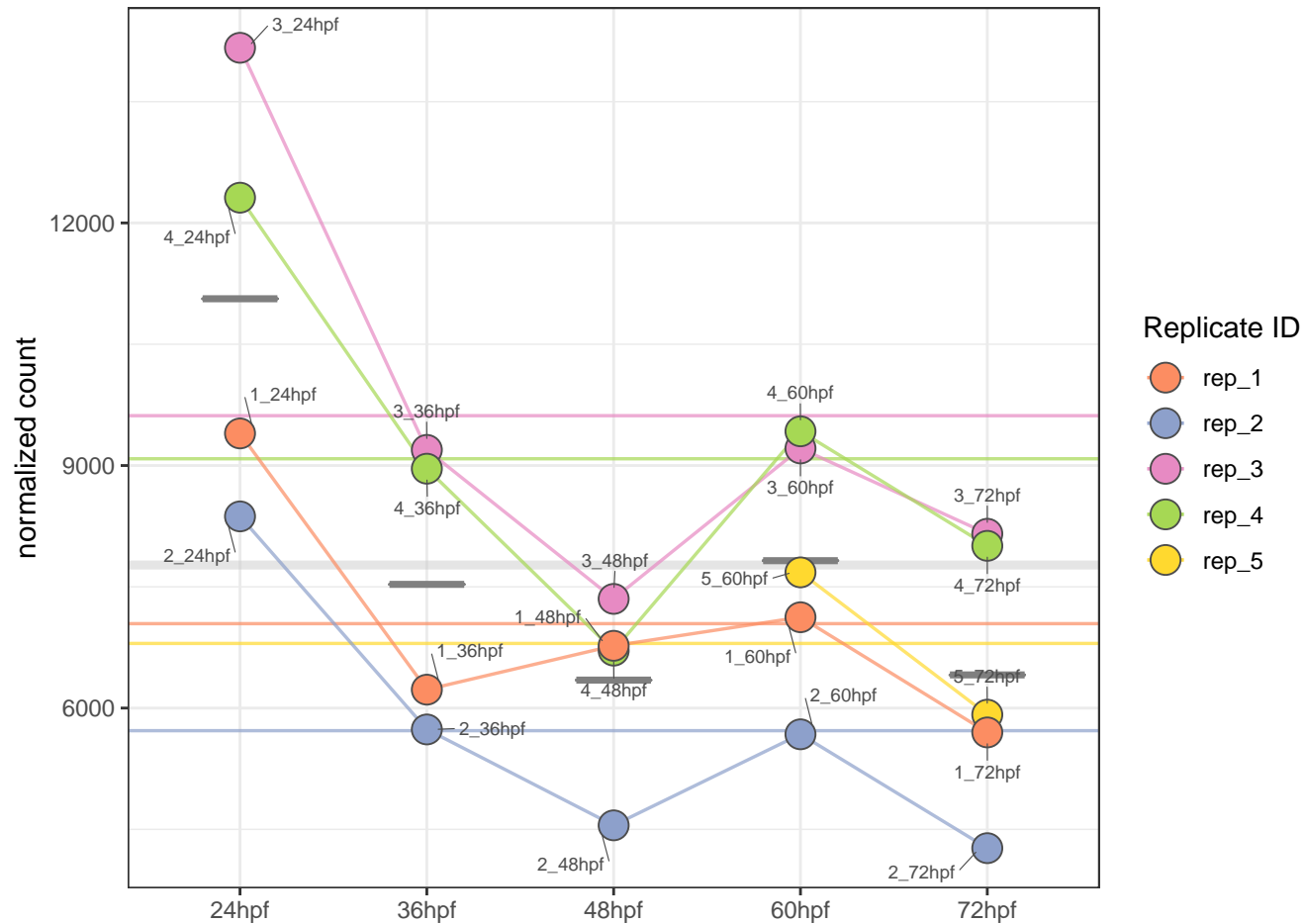Overall mean normalized counts = 2354.93

Gene: bmpr1ab, ENSDARG00000105045, chromosome 12, protein_coding
P−value = 4.7e−16
Adjusted p−value = 1e−12
Log2 fold−change (rep_5 / rep_1) = 0.07
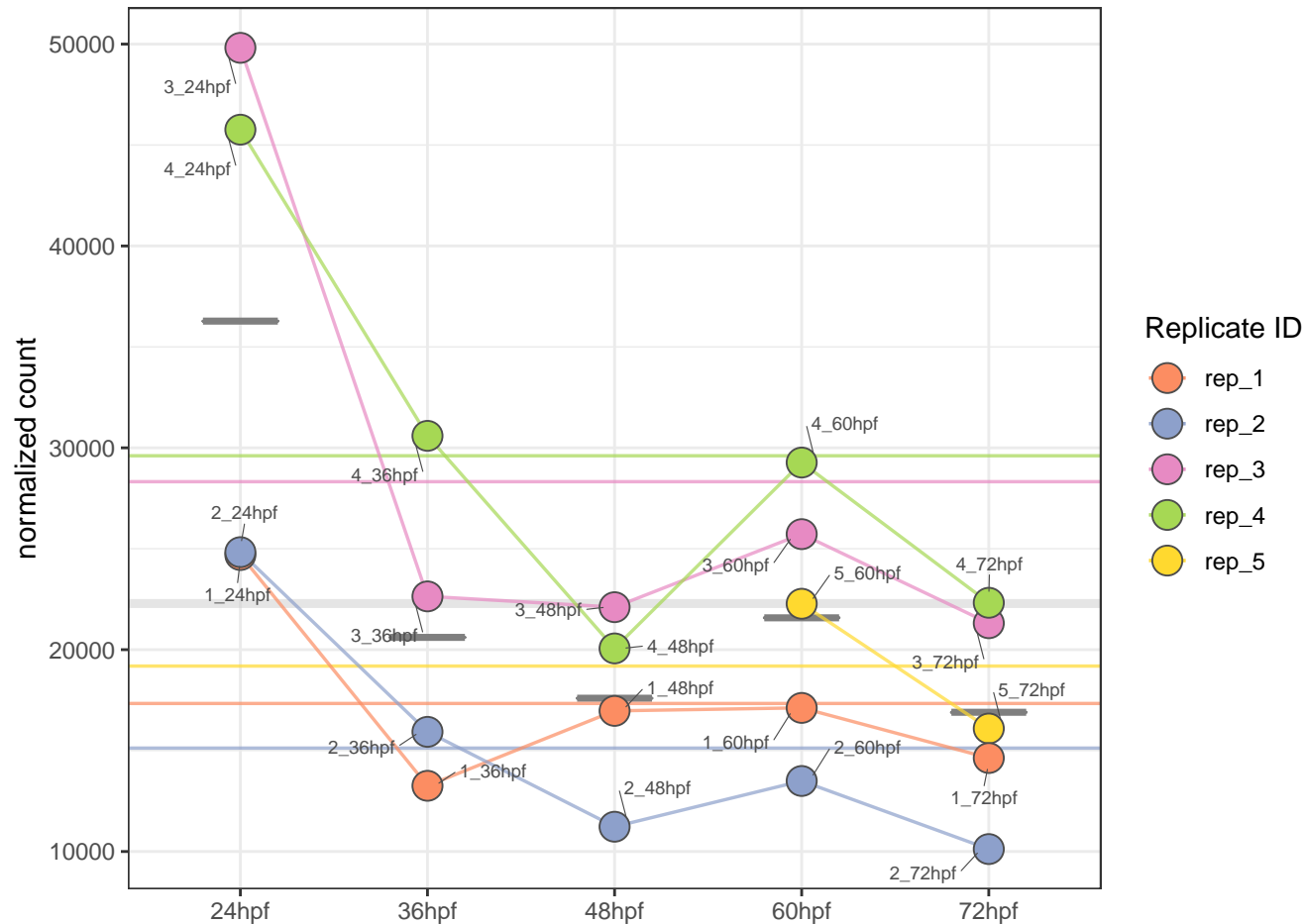Overall mean normalized counts = 7769.08

Gene: hk1, ENSDARG00000039452, chromosome 13, protein_coding
P−value = 6.4e−16
Adjusted p−value = 1.3e−12
Log2 fold−change (rep_5 / rep_1) = 0.34
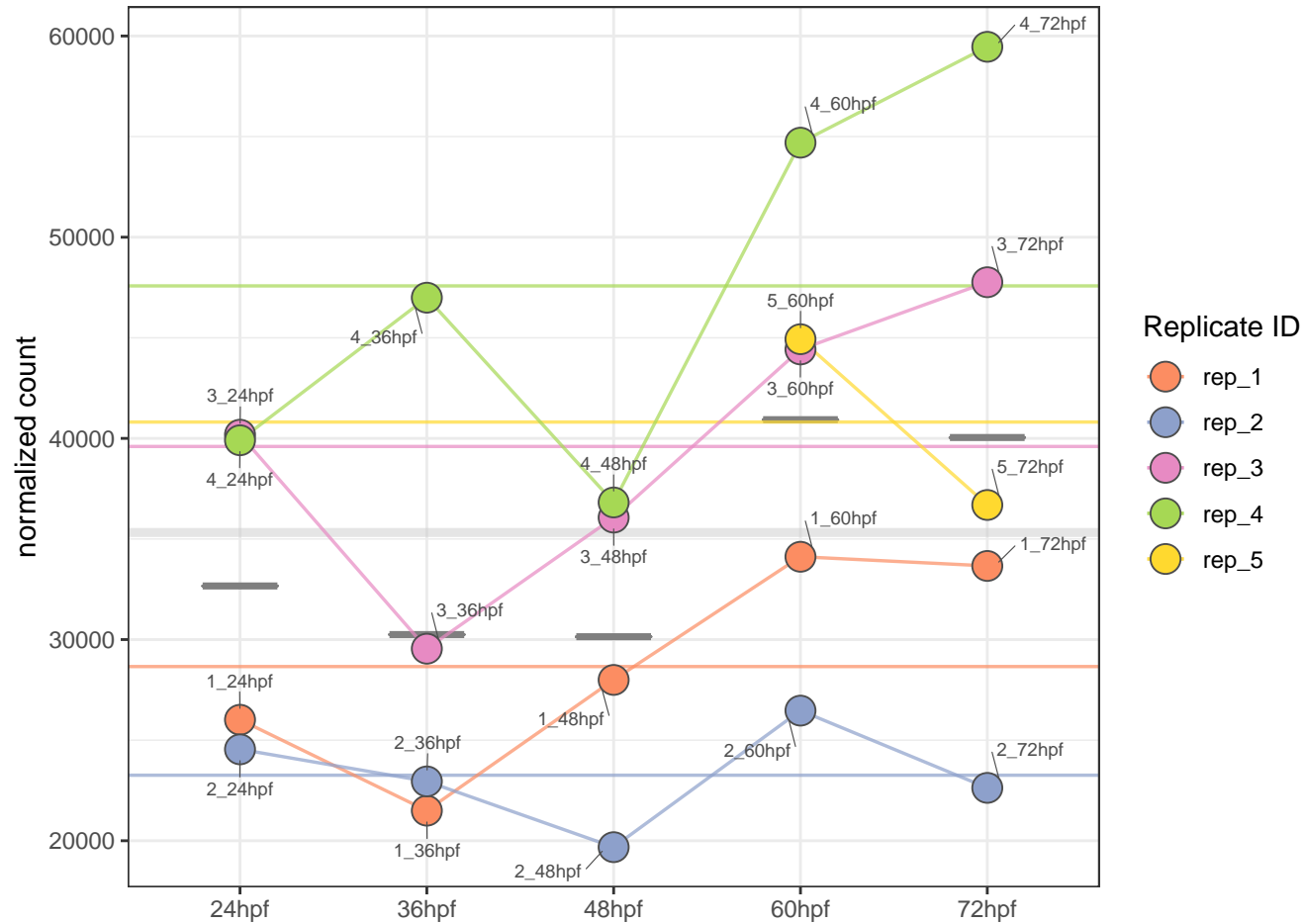Overall mean normalized counts = 22286.31

Gene: clic4, ENSDARG00000022995, chromosome 17, protein_coding
P−value = 1e−15
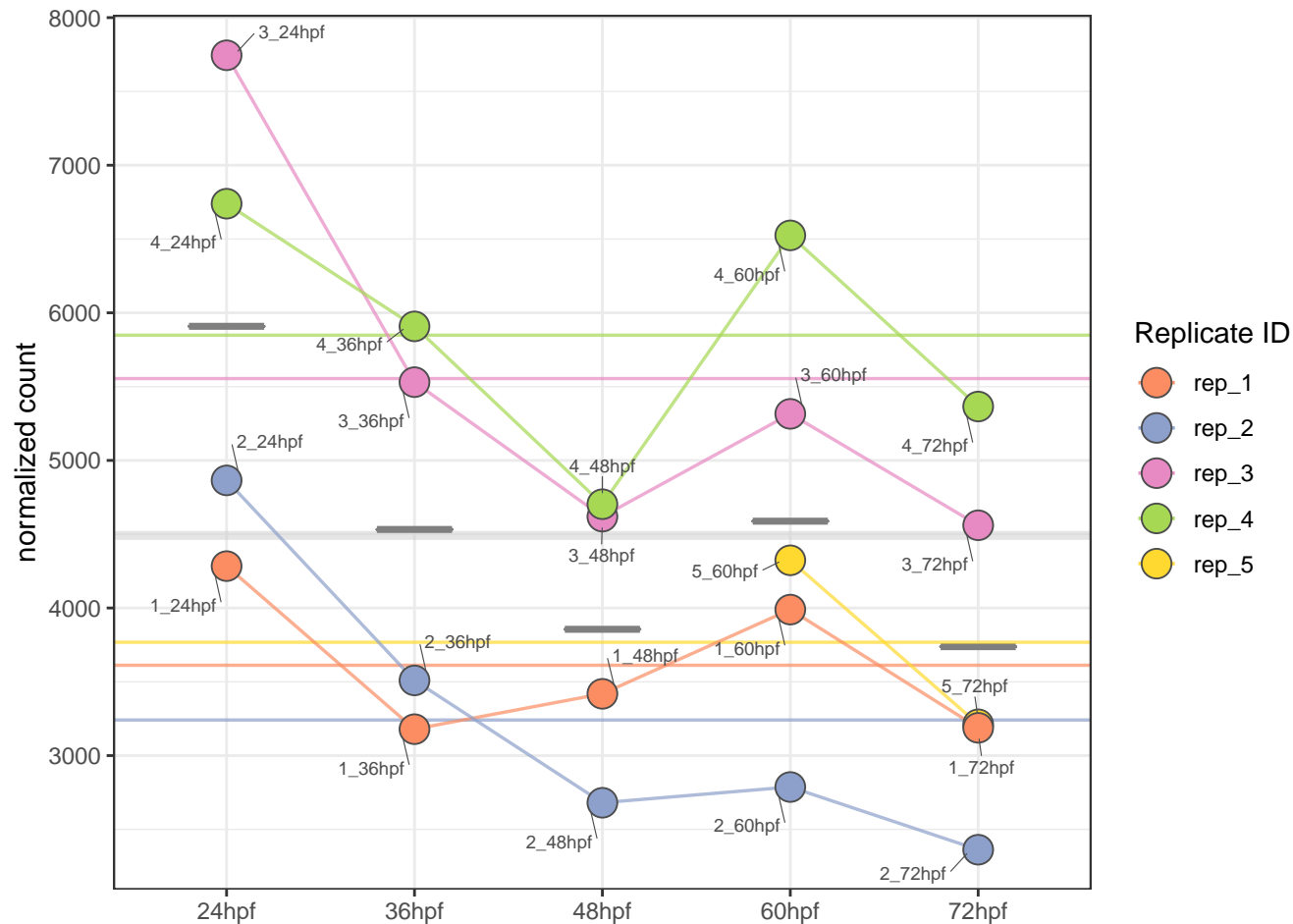Adjusted p−value = 2e−12
Log2 fold−change (rep_5 / rep_1) = 0.31
Overall mean normalized counts = 35322.28

Gene: si:ch211−74m13.1, ENSDARG00000094952, chromosome 3, protein_coding
P−value = 1.5e−15
Adjusted p−value = 2.7e−12
Log2 fold−change (rep_5 / rep_1) = 0.15
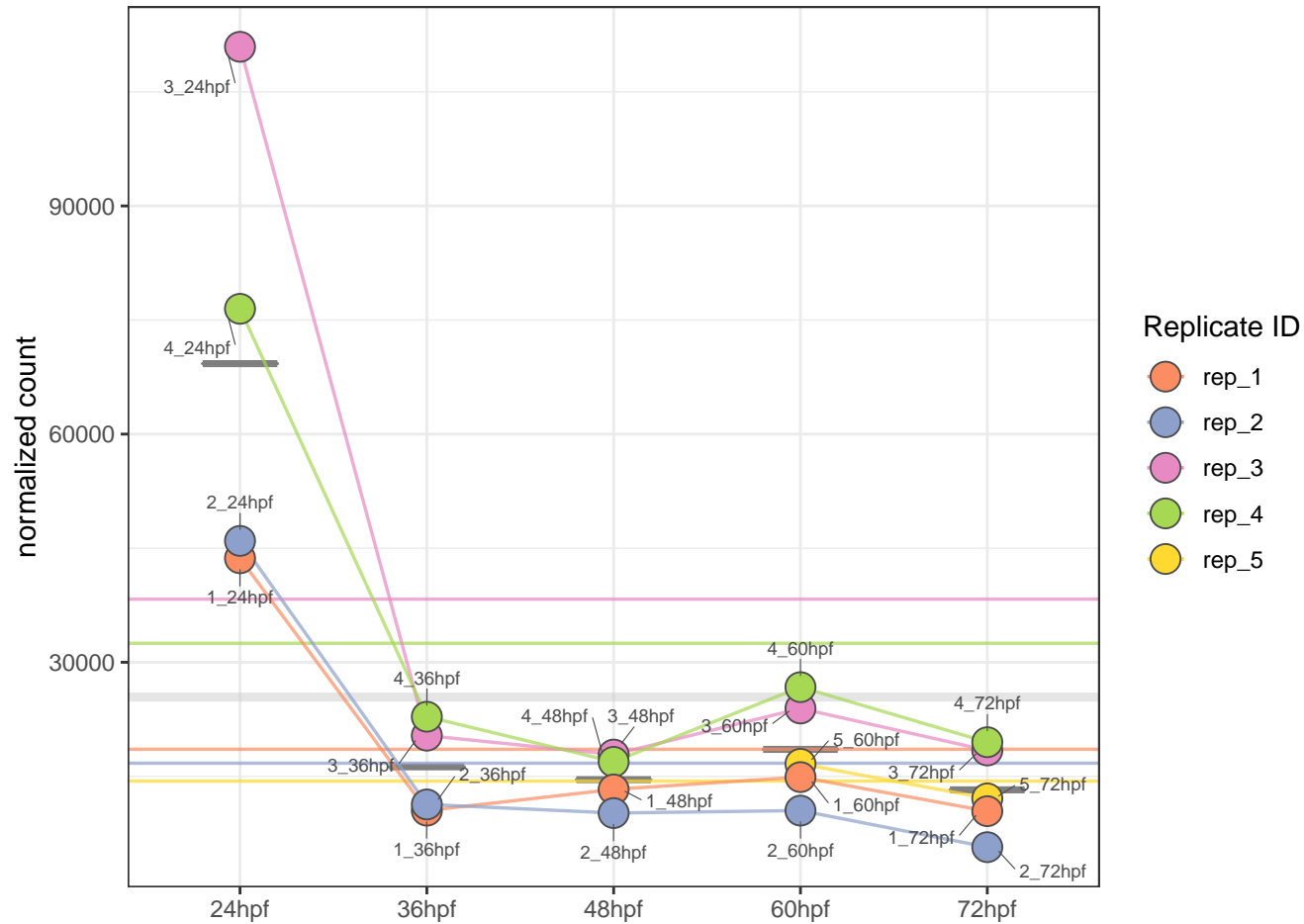Overall mean normalized counts = 4491.62

Gene: unc45b, ENSDARG00000008433, chromosome 8, protein_coding
P−value = 1.6e−15
Adjusted p−value = 2.7e−12
Log2 fold−change (rep_5 / rep_1) = 0.28
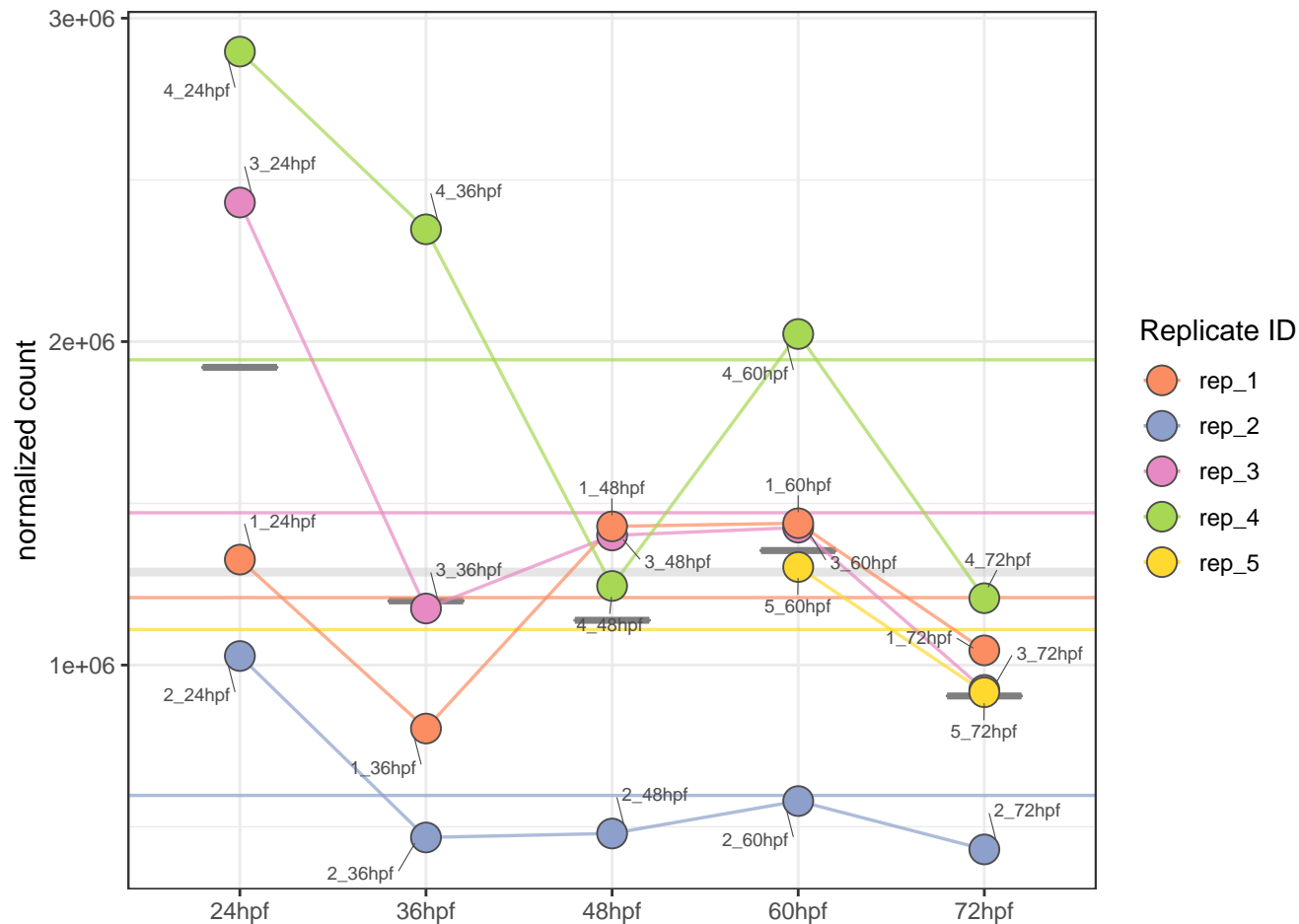Overall mean normalized counts = 25421.79

Gene: ttn.2, ENSDARG00000028213, chromosome 9, protein_coding
P−value = 1.6e−15
Adjusted p−value = 2.7e−12
Log2 fold−change (rep_5 / rep_1) = 0.02
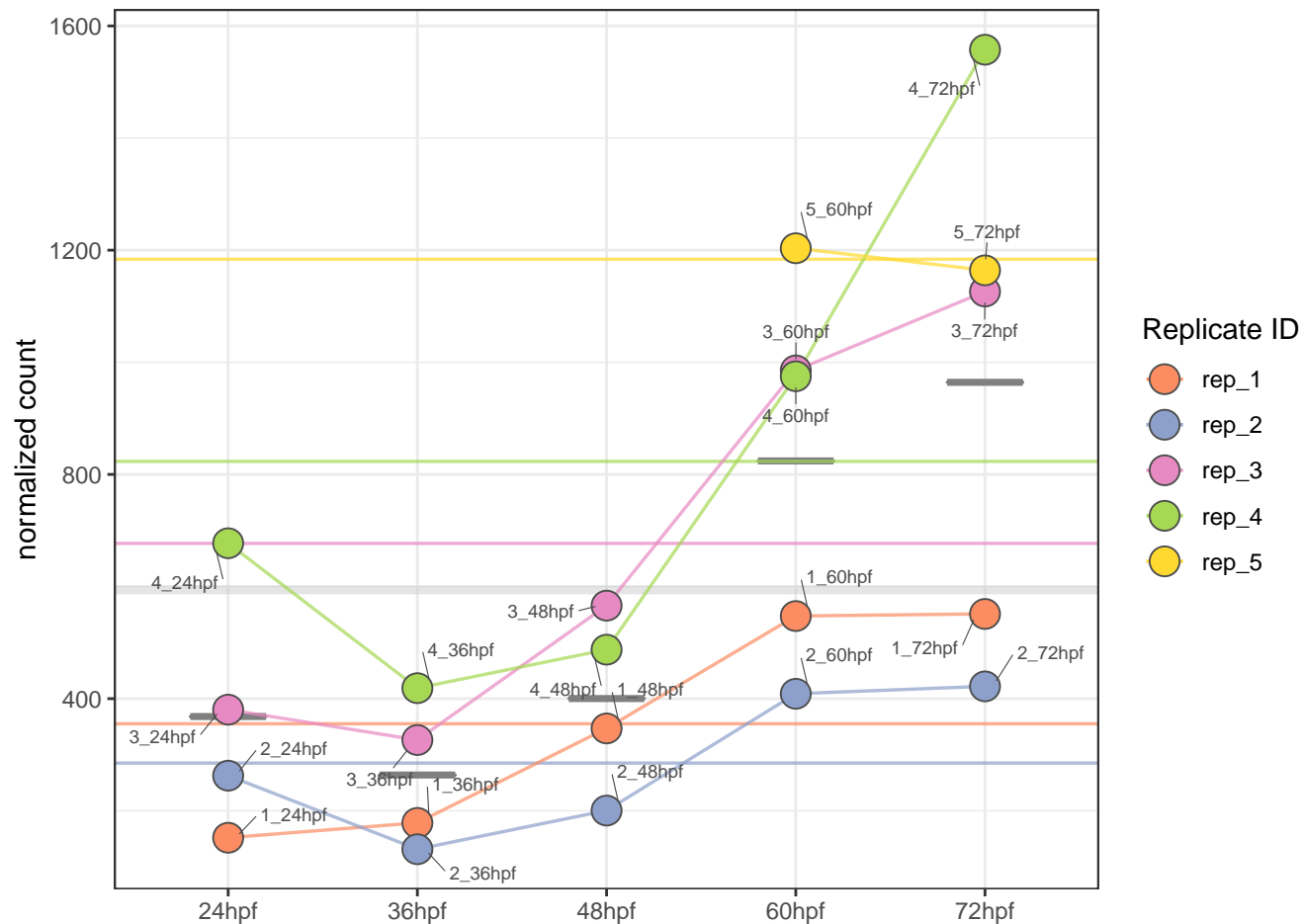Overall mean normalized counts = 1287347.33

Gene: NC_002333.13, ENSDARG00000081938, chromosome MT, Mt_tRNA
P−value = 7.1e−15
Adjusted p−value = 1.1e−11
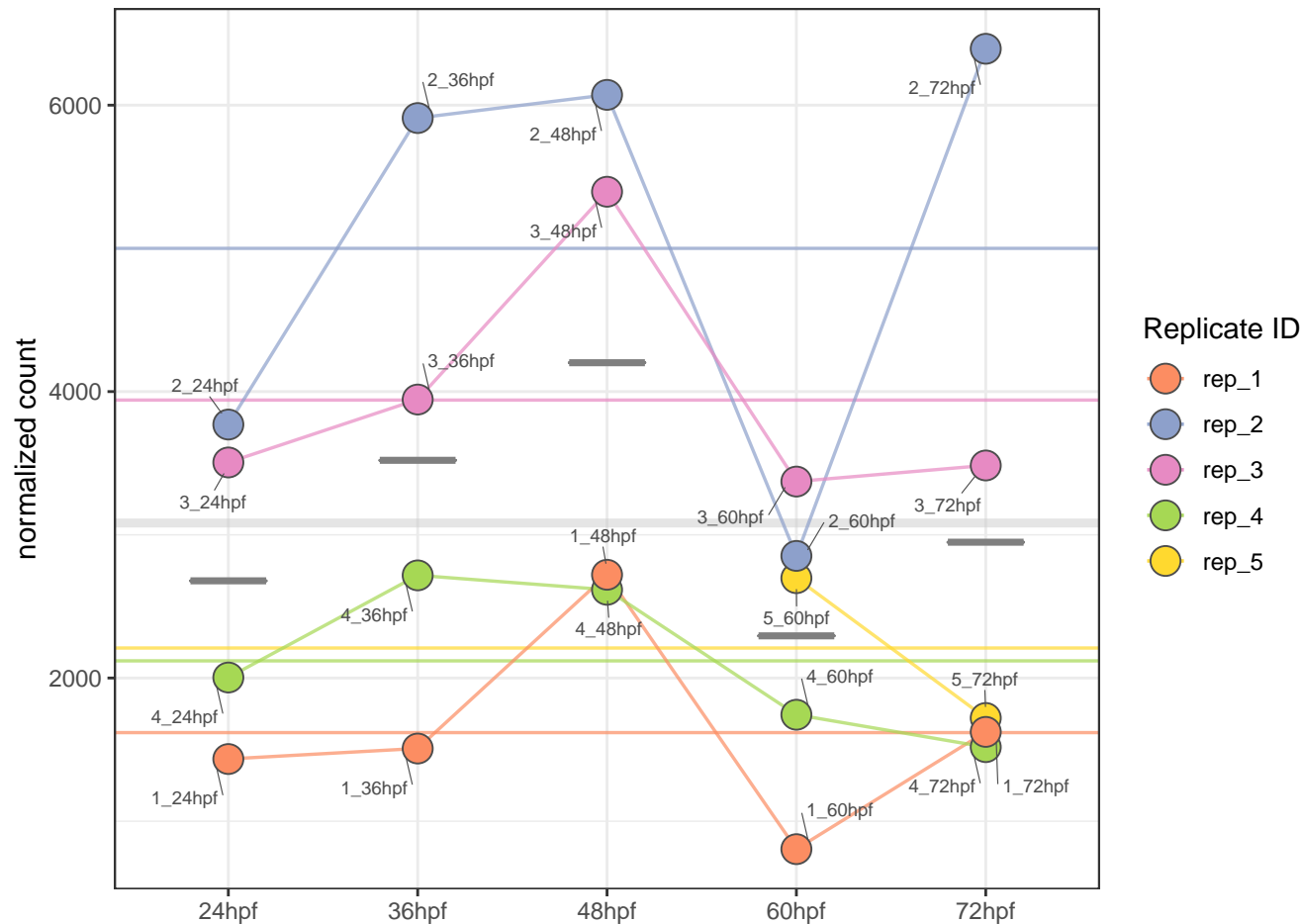Log2 fold−change (rep_5 / rep_1) = 1.15
Overall mean normalized counts = 594.14

Gene: BX547930.2, ENSDARG00000096513, chromosome 20, lincRNA
P−value = 1e−14
Adjusted p−value = 1.6e−11
Log2 fold−change (rep_5 / rep_1) = 0.81
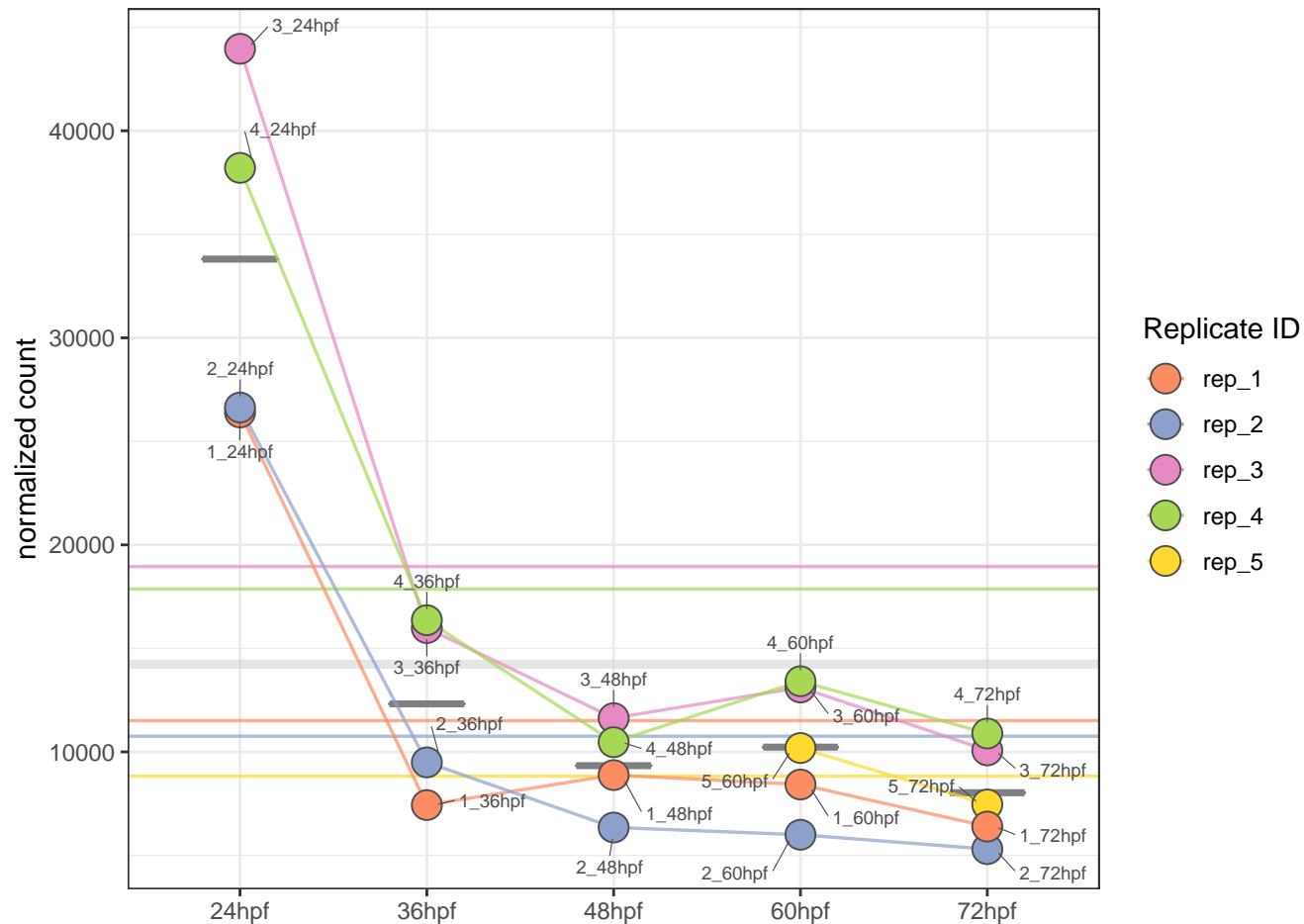Overall mean normalized counts = 3082.54

Gene: rbm24a, ENSDARG00000102995, chromosome 19, protein_coding
P−value = 1.1e−14
Adjusted p−value = 1.7e−11
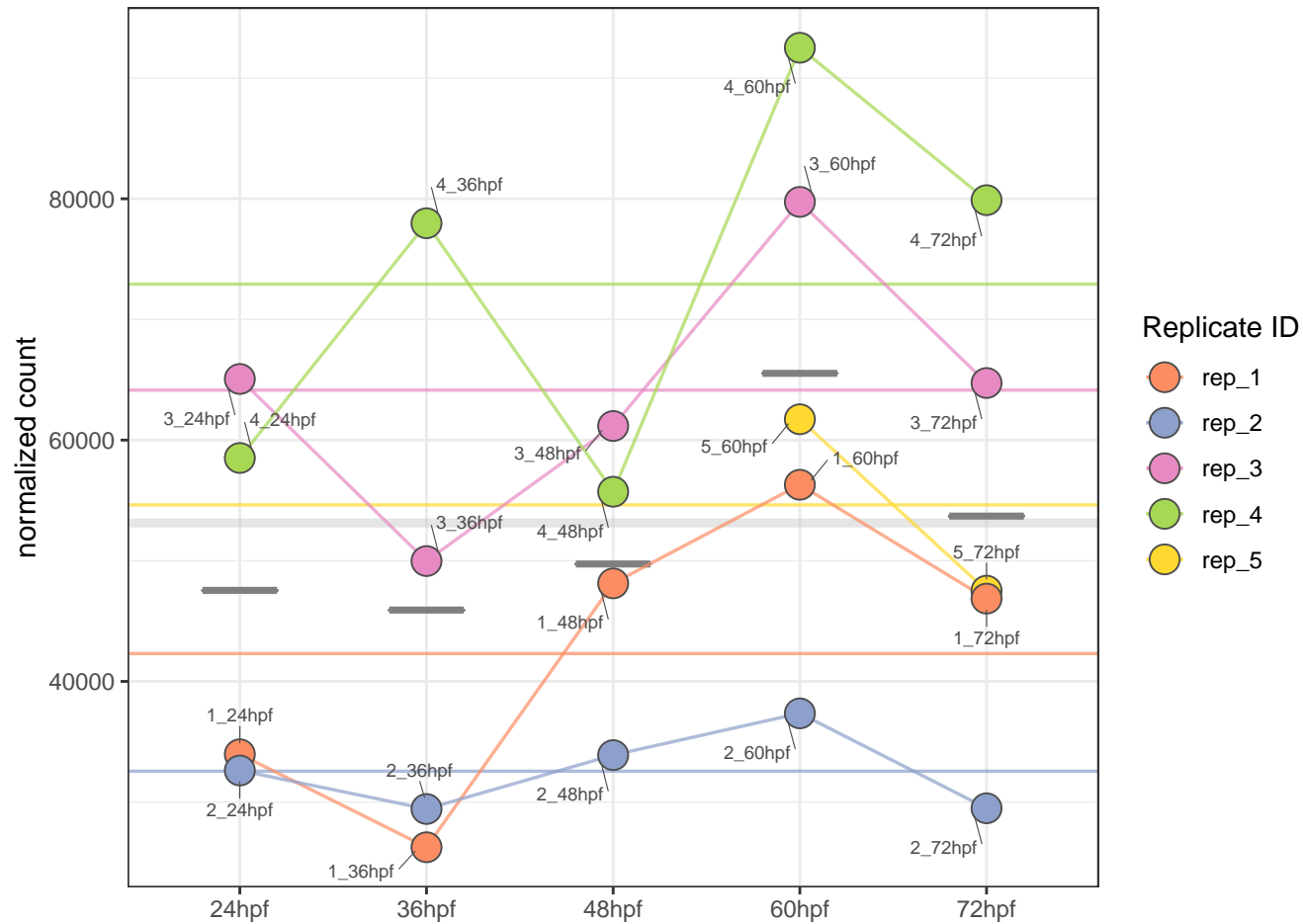Log2 fold−change (rep_5 / rep_1) = 0.29
Overall mean normalized counts = 14232.44

Gene: myh7ba, ENSDARG00000076075, chromosome 11, protein_coding
P−value = 1.5e−14
Adjusted p−value = 2.1e−11
Log2 fold−change (rep_5 / rep_1) = 0.20
Overall mean normalized counts = 53132.80

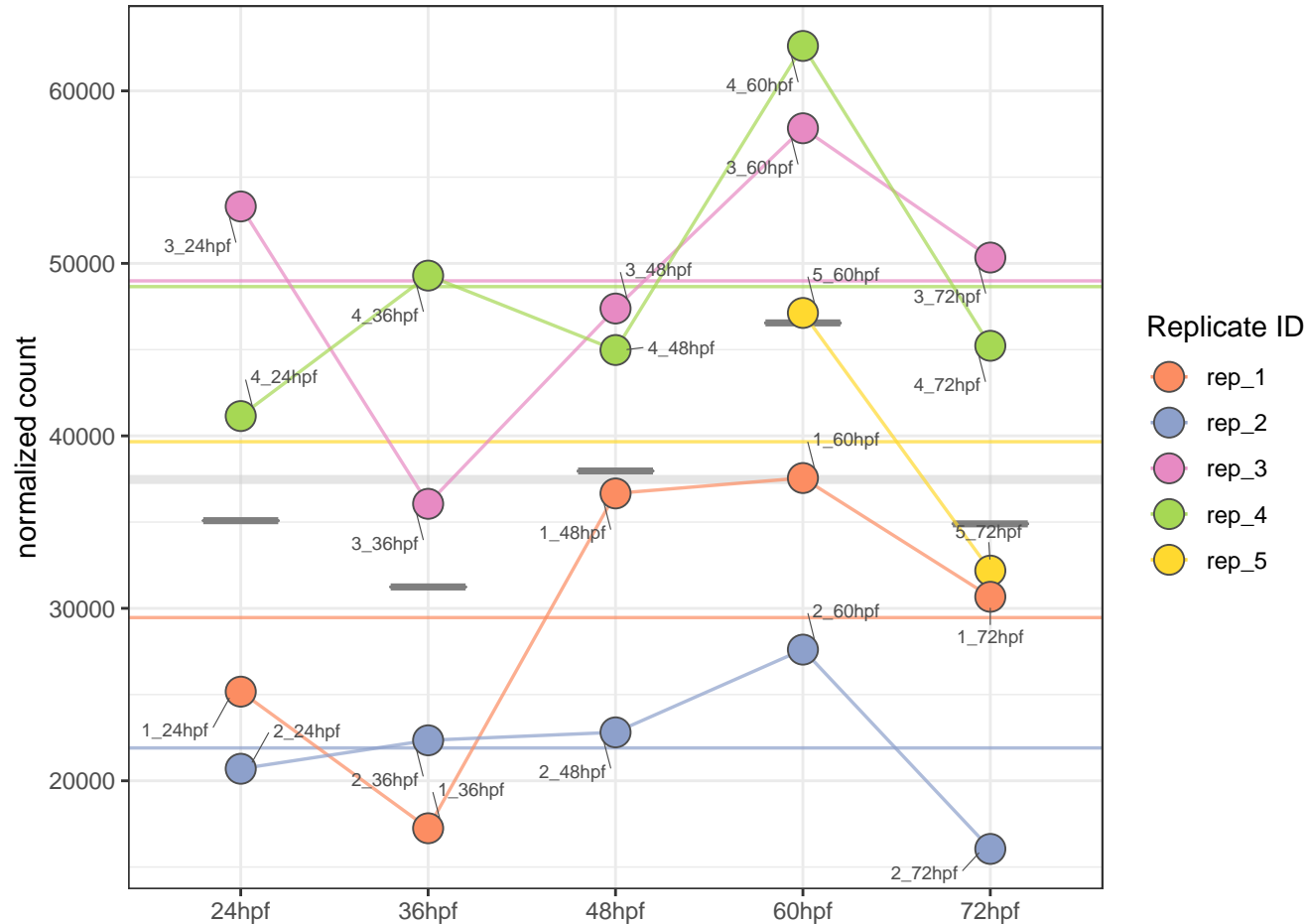Gene: desma, ENSDARG00000058656, chromosome 9, protein_coding
P−value = 1.6e−14
Adjusted p−value = 2.1e−11
Log2 fold−change (rep_5 / rep_1) = 0.31
Overall mean normalized counts = 37471.01

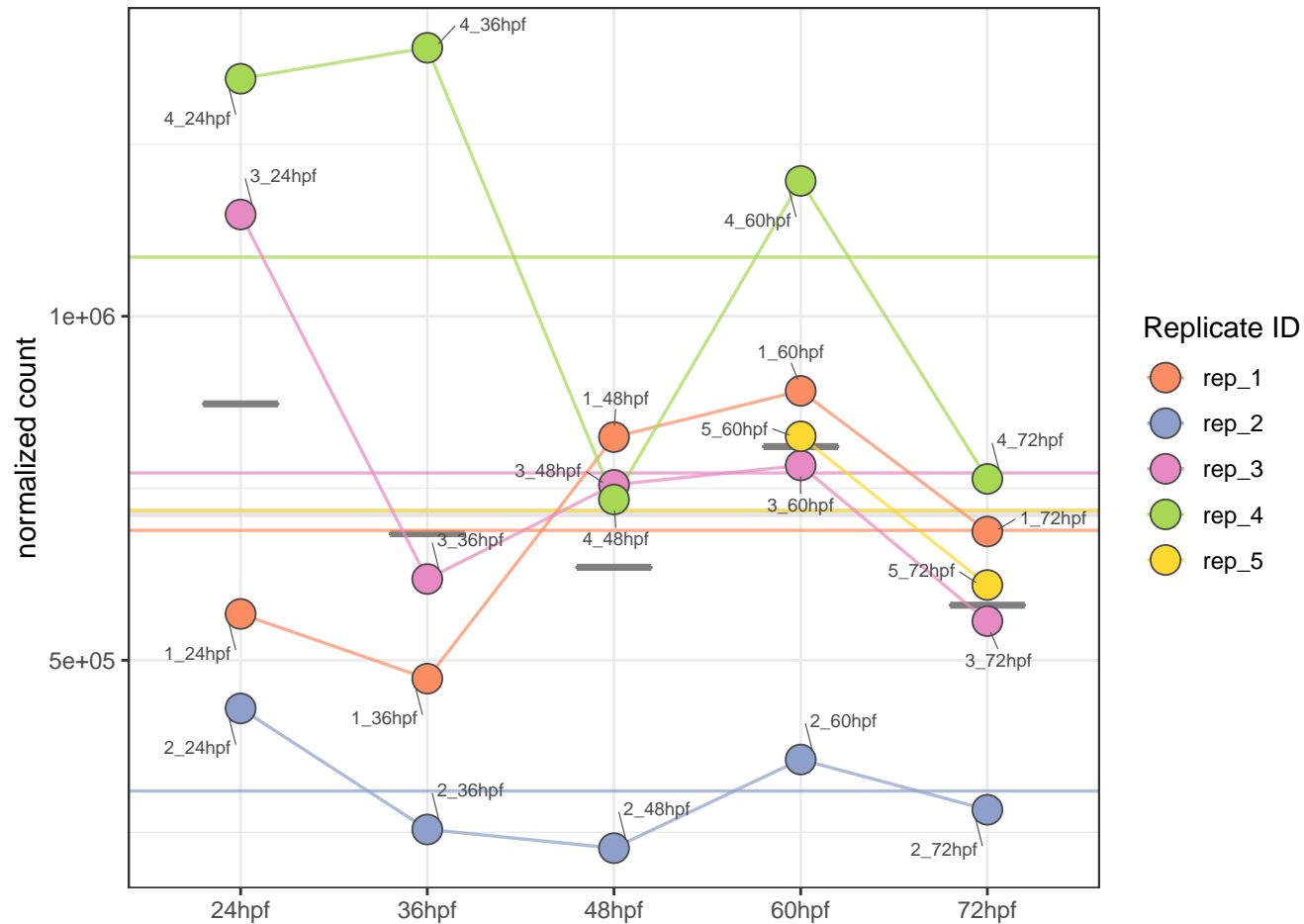Gene: ttn.1, ENSDARG00000000563, chromosome 9, protein_coding
P−value = 1.9e−14
Adjusted p−value = 2.4e−11
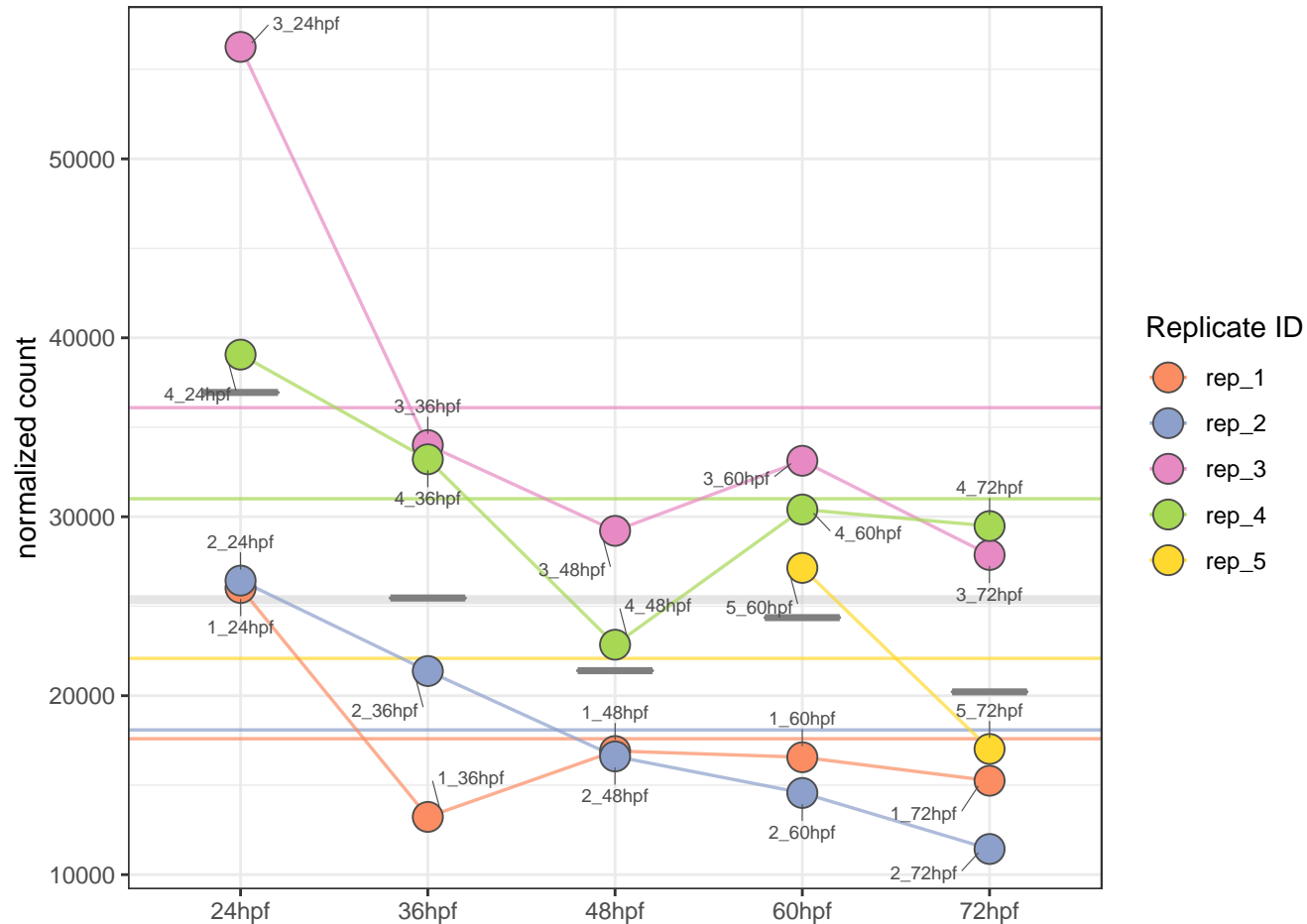Log2 fold−change (rep_5 / rep_1) = 0.05
Overall mean normalized counts = 714544.38

Gene: bves, ENSDARG00000058548, chromosome 16, protein_coding
P−value = 2.5e−14
Adjusted p−value = 3.1e−11
Log2 fold−change (rep_5 / rep_1) = 0.52
Overall mean normalized counts = 25367.57

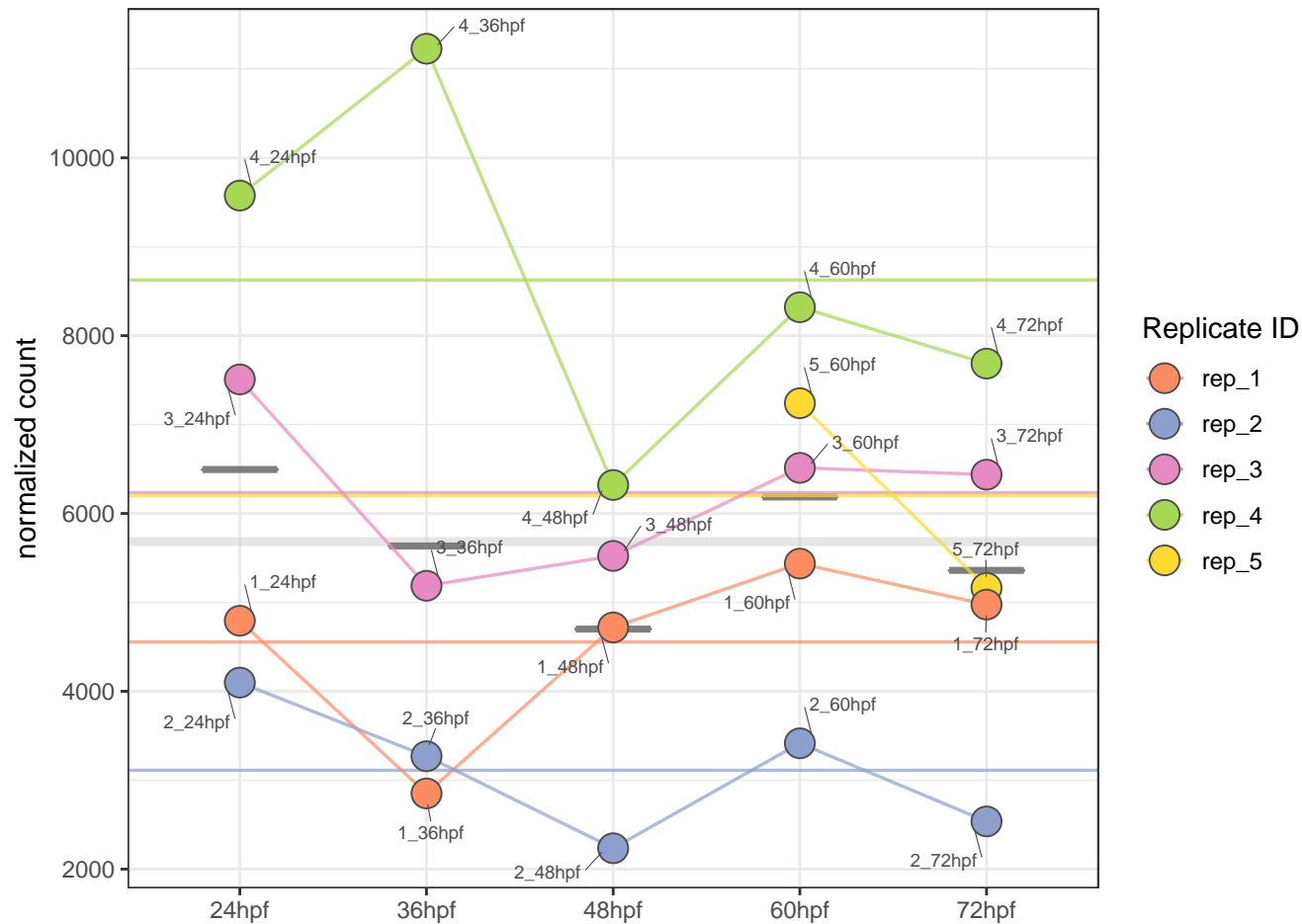Gene: usp13, ENSDARG00000110301, chromosome CHR_ALT_CTG6_1_25, protein_
P−value = 2.6e−14
Adjusted p−value = 3.2e−11
Log2 fold−change (rep_5 / rep_1) = 0.40
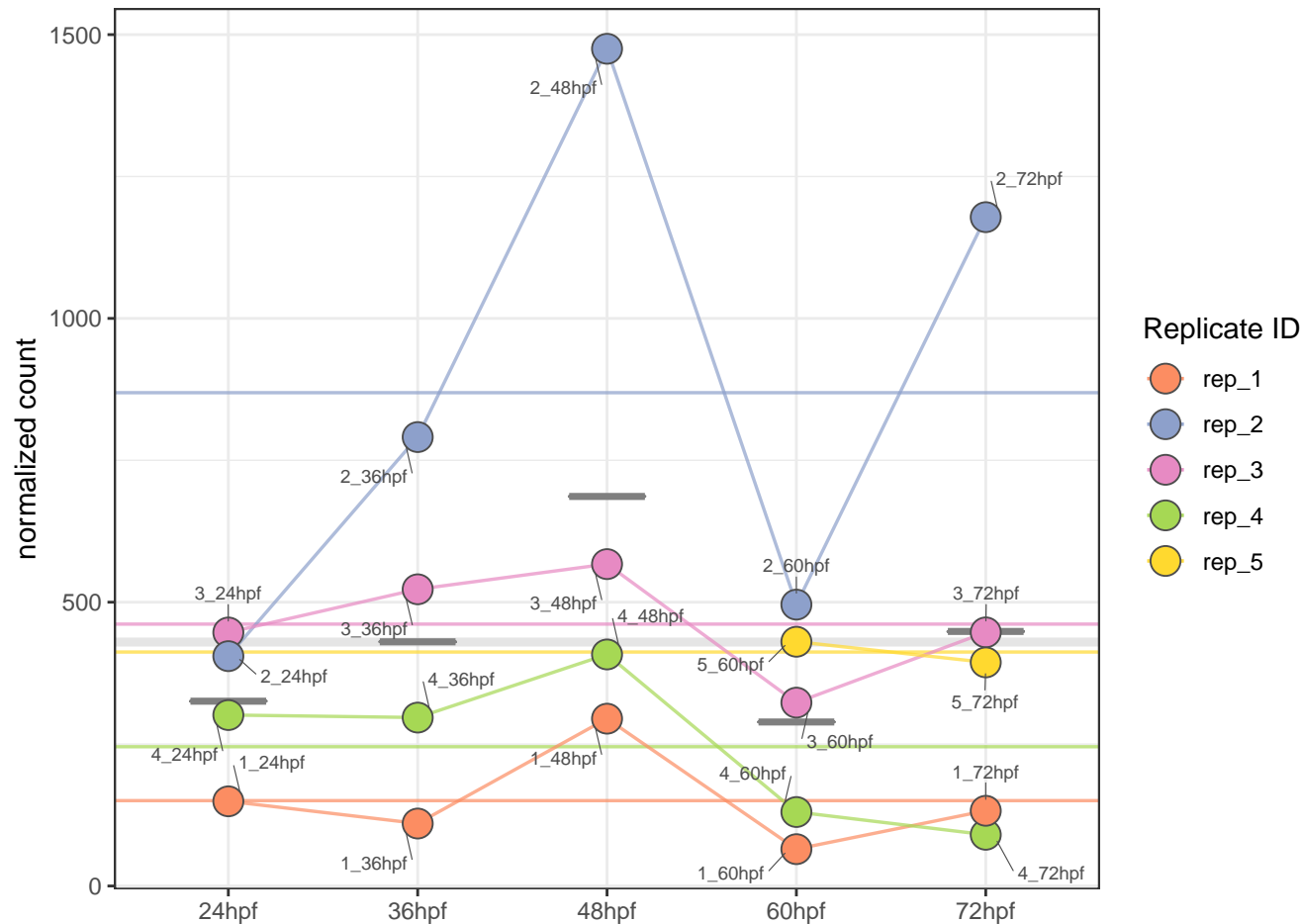Overall mean normalized counts = 5683.53

Gene: BX927341.6, ENSDARG00000117651, chromosome 6, lincRNA
P−value = 3e−14
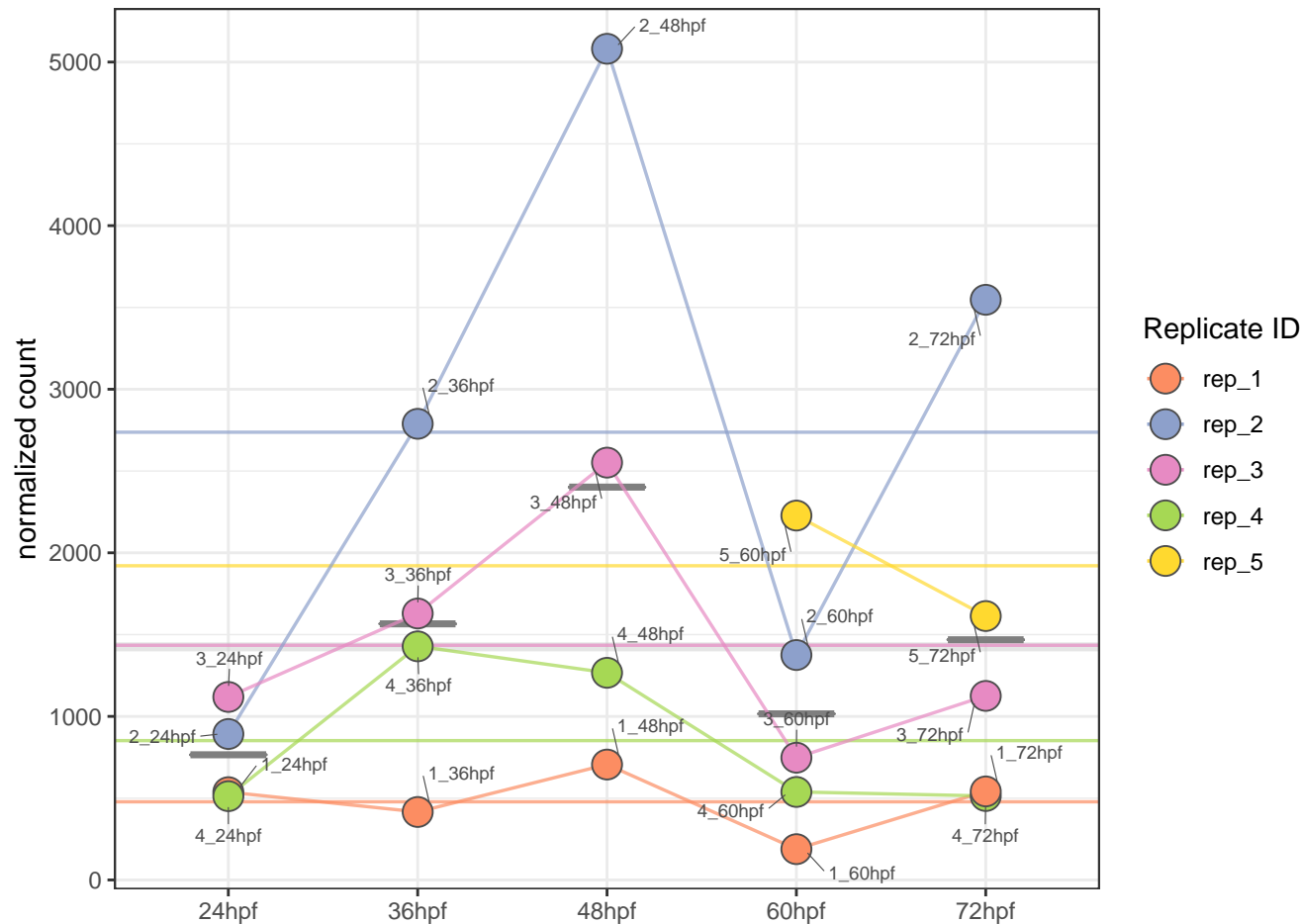Adjusted p−value = 3.4e−11
Log2 fold−change (rep_5 / rep_1) = 2.05
Overall mean normalized counts = 429.80

Gene: si:ch73−338o16.4, ENSDARG00000092778, chromosome 3, protein_coding
P−value = 3e−14
Adjusted p−value = 3.4e−11
Log2 fold−change (rep_5 / rep_1) = 2.53
Overall mean normalized counts = 1425.02

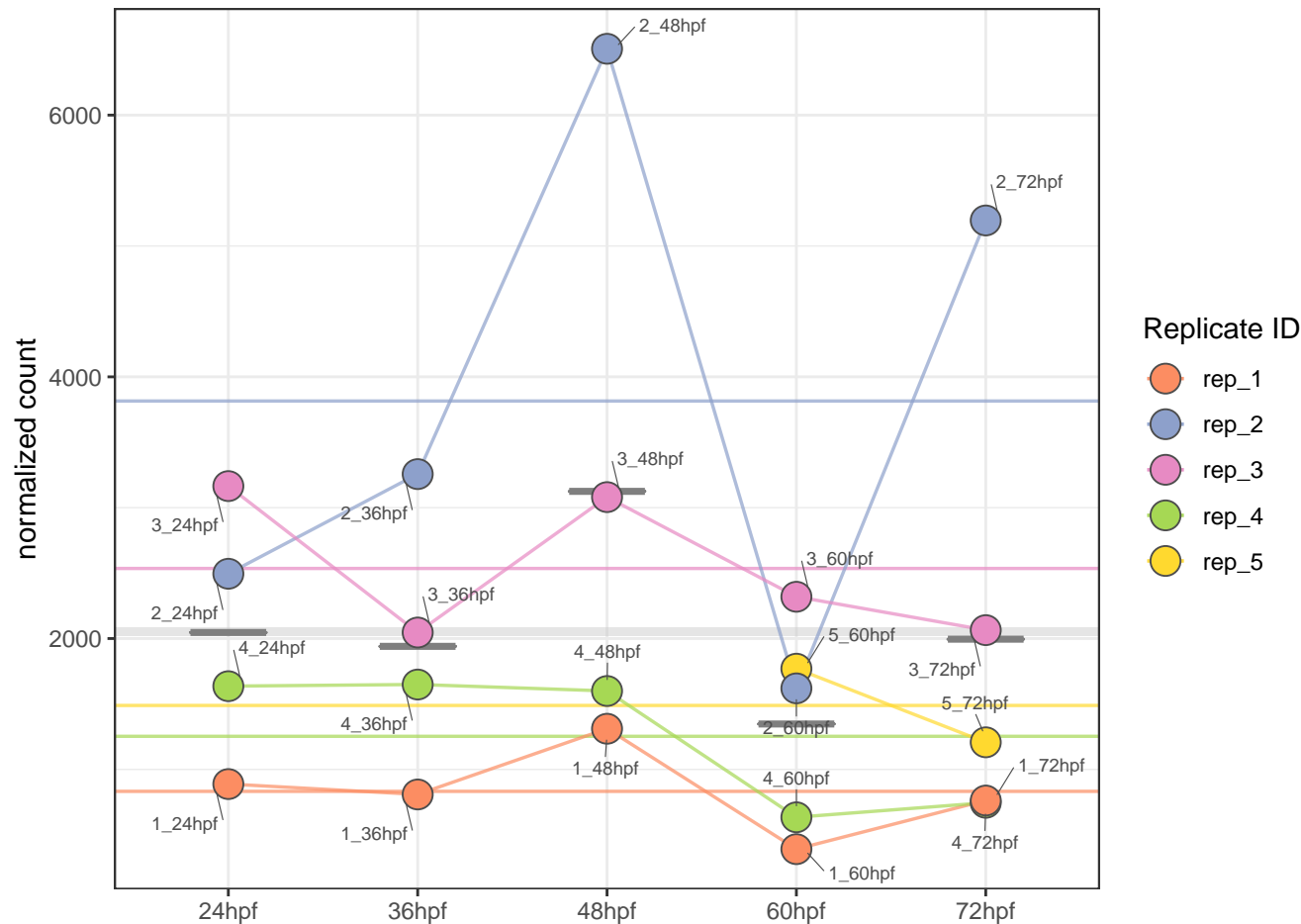Gene: BX000985.1, ENSDARG00000099469, chromosome 15, lincRNA
P−value = 3.2e−14
Adjusted p−value = 3.5e−11
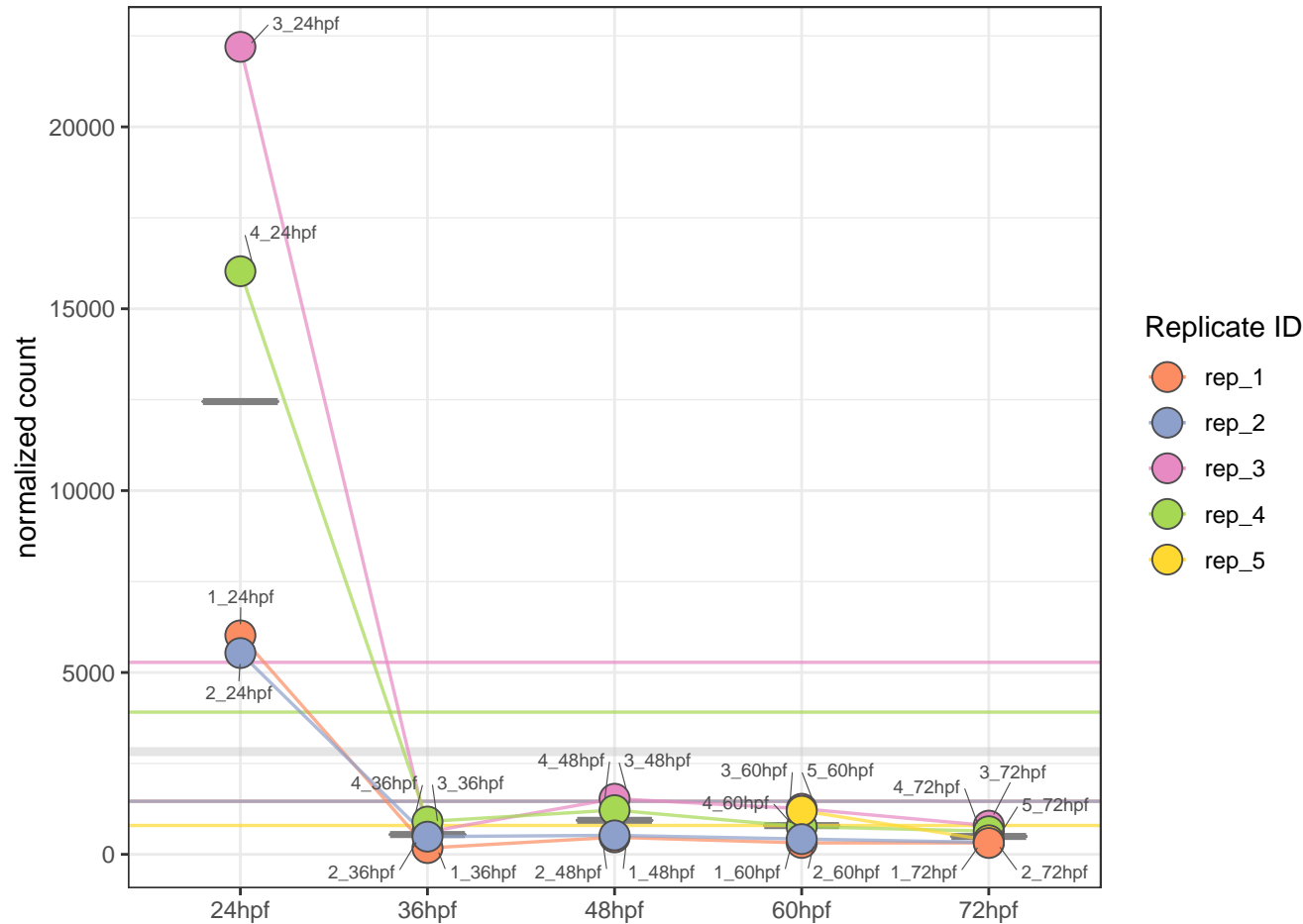Log2 fold−change (rep_5 / rep_1) = 1.38
Overall mean normalized counts = 2052.65

Gene: hsp70l, ENSDARG00000055723, chromosome 8, protein_coding
P−value = 3.5e−14
Adjusted p−value = 3.7e−11
Log2 fold−change (rep_5 / rep_1) = 1.33
Overall mean normalized counts = 2824.39

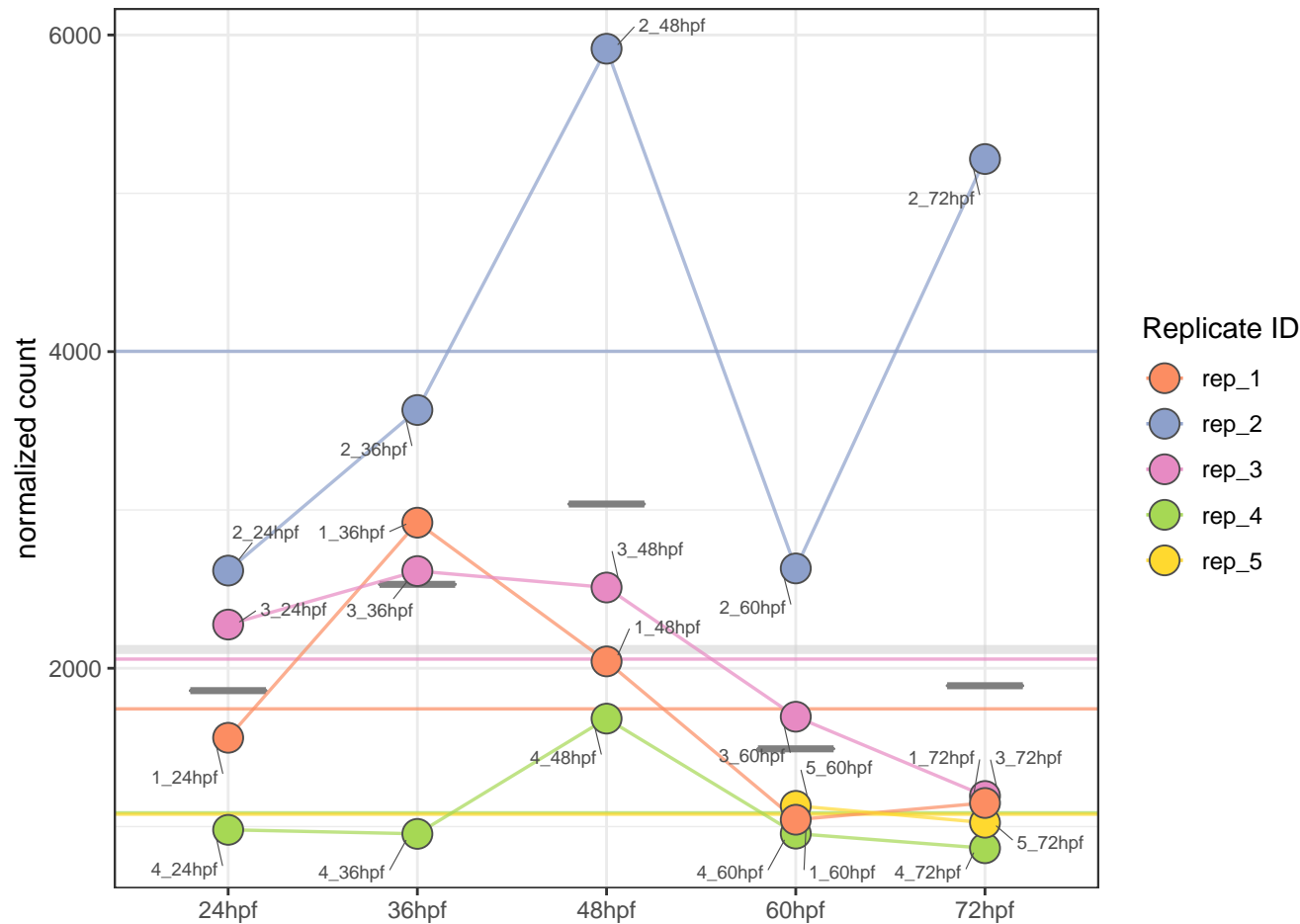Gene: CR855320.3, ENSDARG00000107486, chromosome 1, protein_coding
P−value = 3.8e−14
Adjusted p−value = 3.9e−11
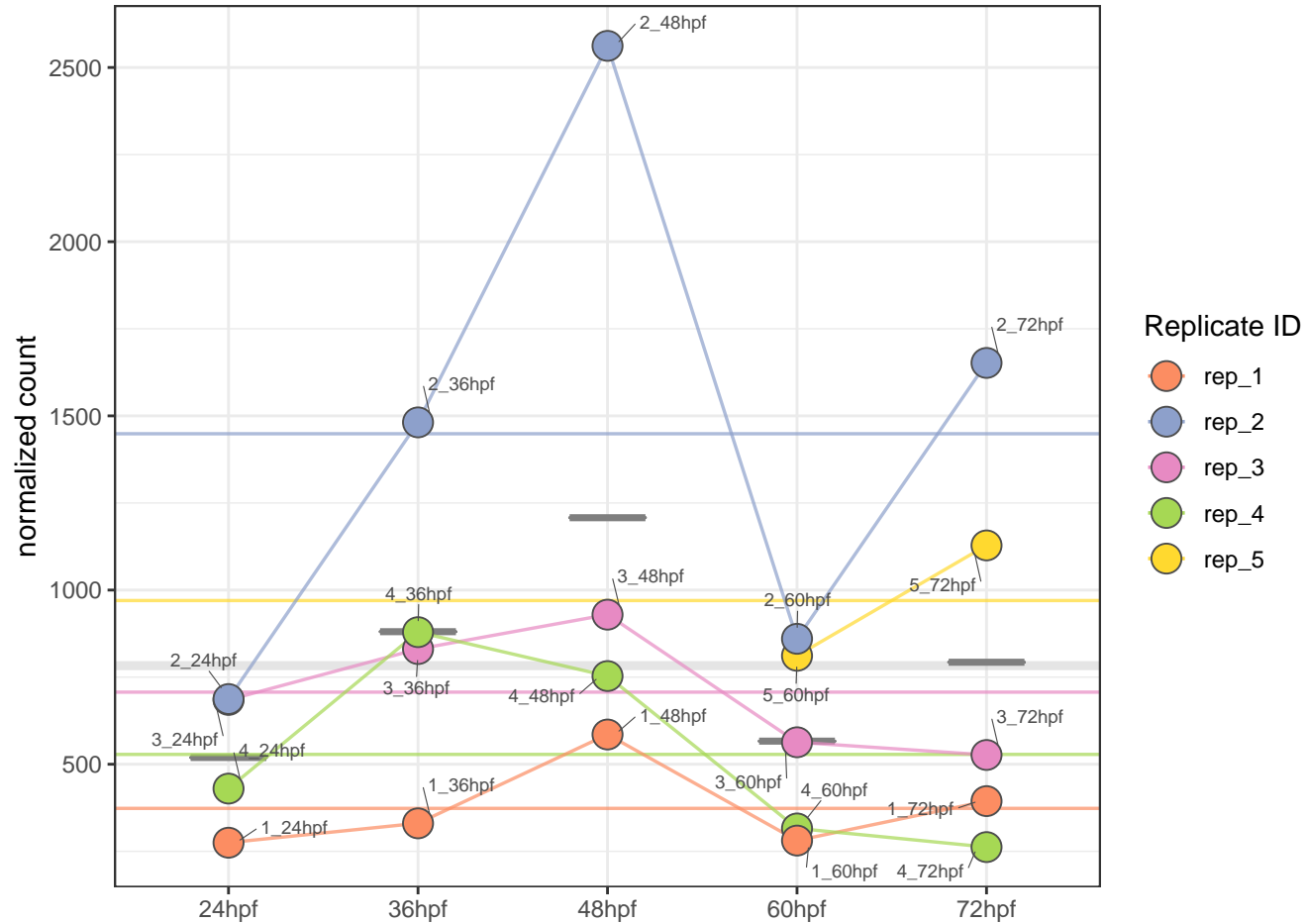Log2 fold−change (rep_5 / rep_1) = −0.31
Overall mean normalized counts = 2118.54

Gene: si:ch211−171h4.7, ENSDARG00000088408, chromosome 19, protein_coding
P−value = 4e−14
Adjusted p−value = 4e−11
Log2 fold−change (rep_5 / rep_1) = 1.72
Overall mean normalized counts = 782.99

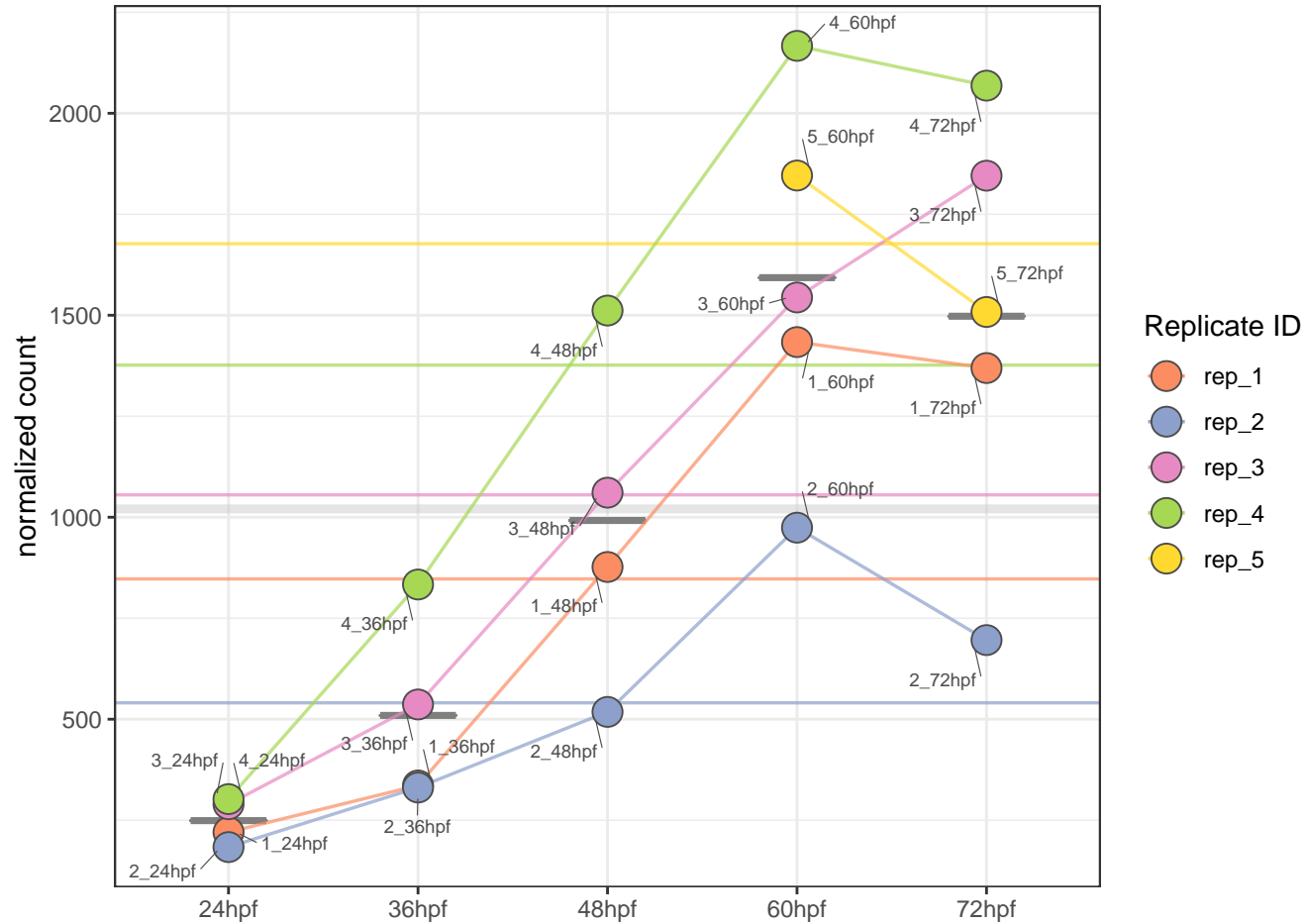Gene: RERG, ENSDARG00000104632, chromosome 4, protein_coding
P−value = 4.5e−14
Adjusted p−value = 4.3e−11
Log2 fold−change (rep_5 / rep_1) = 0.37
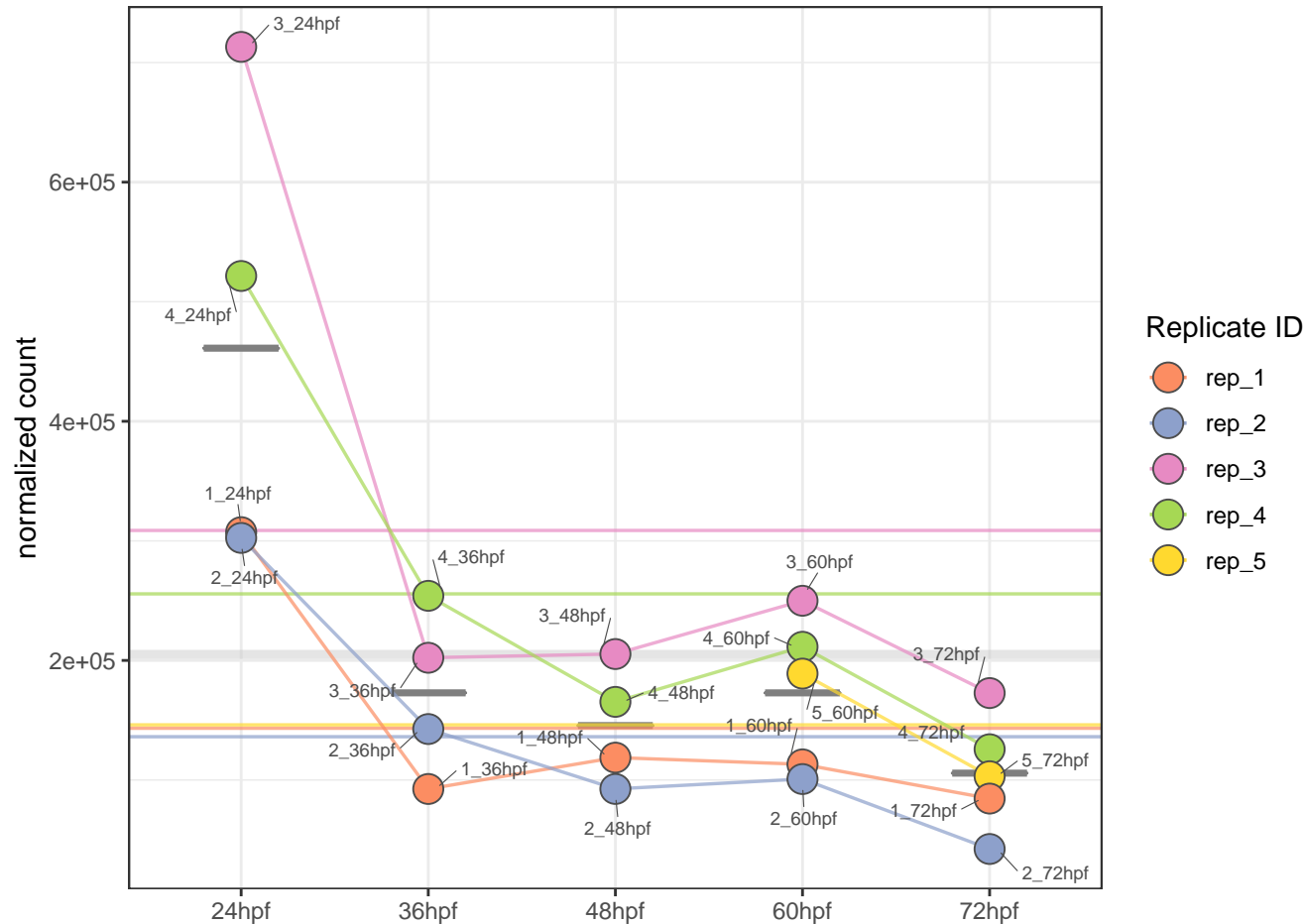Overall mean normalized counts = 1020.63

Gene: acta1b, ENSDARG00000055618, chromosome 13, protein_coding
P−value = 6.5e−14
Adjusted p−value = 6e−11
Log2 fold−change (rep_5 / rep_1) = 0.61
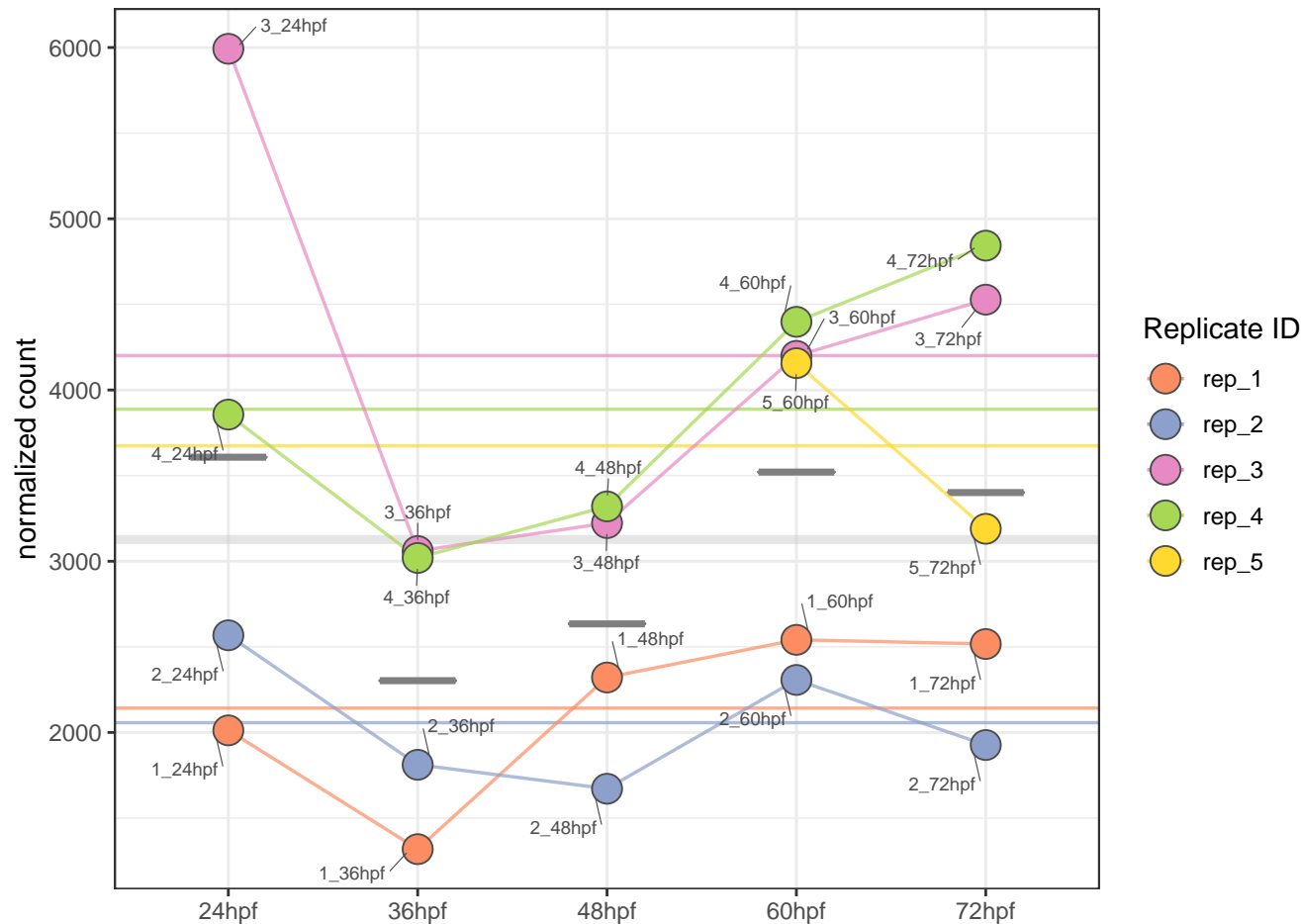Overall mean normalized counts = 205058.79

Gene: zgc:110182, ENSDARG00000040280, chromosome 16, protein_coding
P−value = 7e−14
Adjusted p−value = 6.4e−11
Log2 fold−change (rep_5 / rep_1) = 0.62
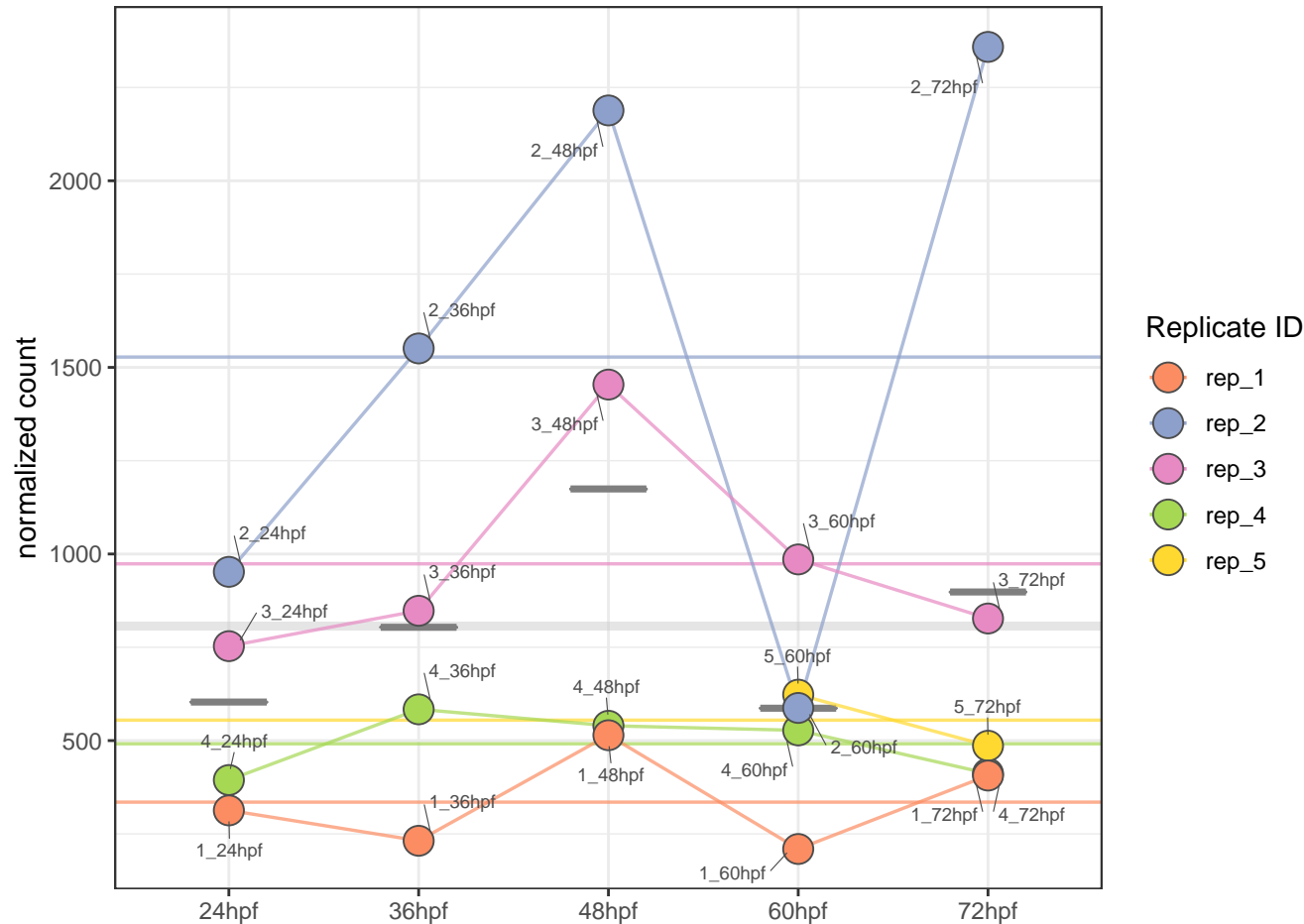Overall mean normalized counts = 3126.65

Gene: sdr42e1, ENSDARG00000098838, chromosome 18, protein_coding
P−value = 9.6e−14
Adjusted p−value = 8.5e−11
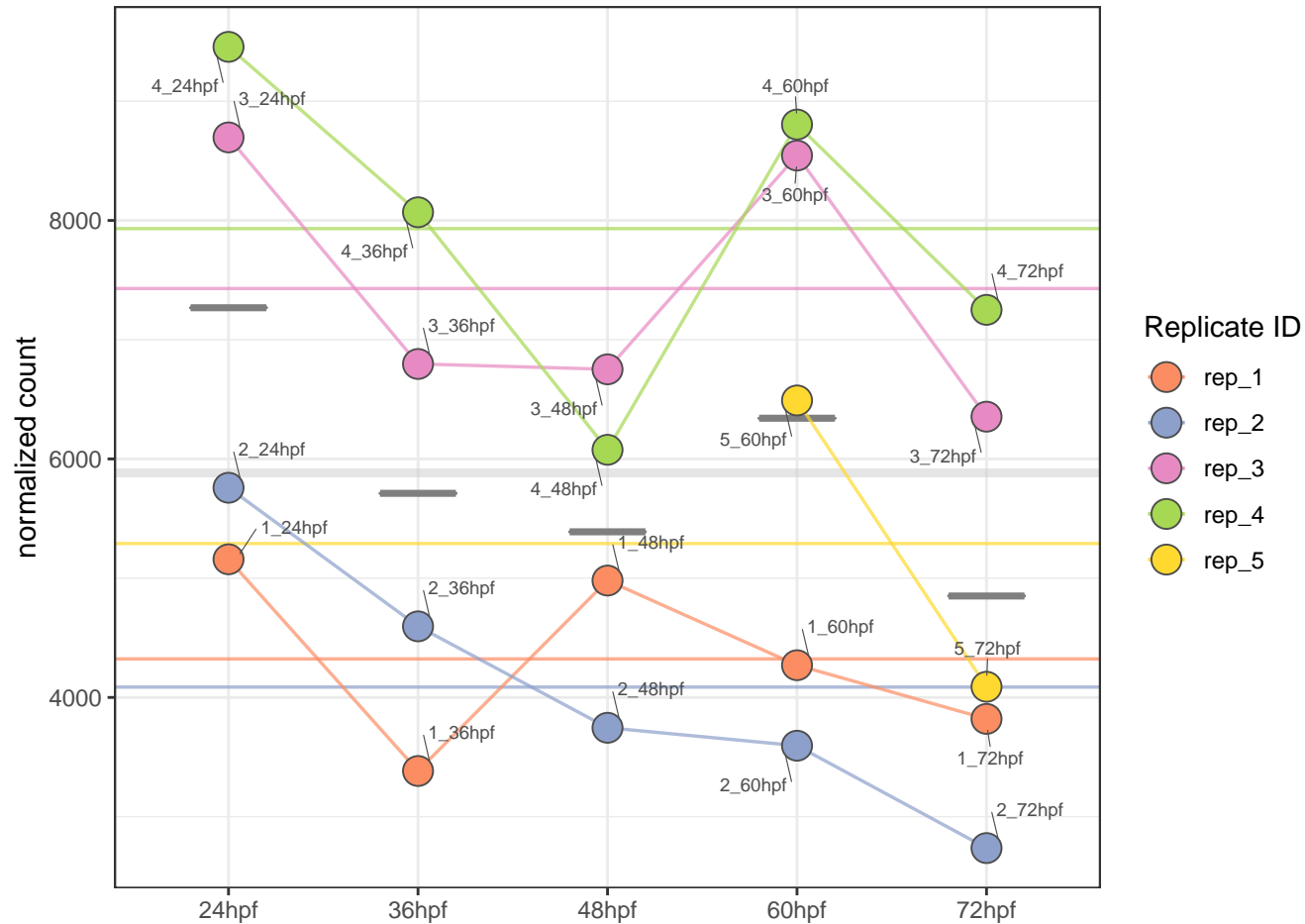Log2 fold−change (rep_5 / rep_1) = 0.88
Overall mean normalized counts = 806.79

Gene: prob1, ENSDARG00000086705, chromosome 21, protein_coding
P−value = 1.1e−13
Adjusted p−value = 9.9e−11
Log2 fold−change (rep_5 / rep_1) = 0.36
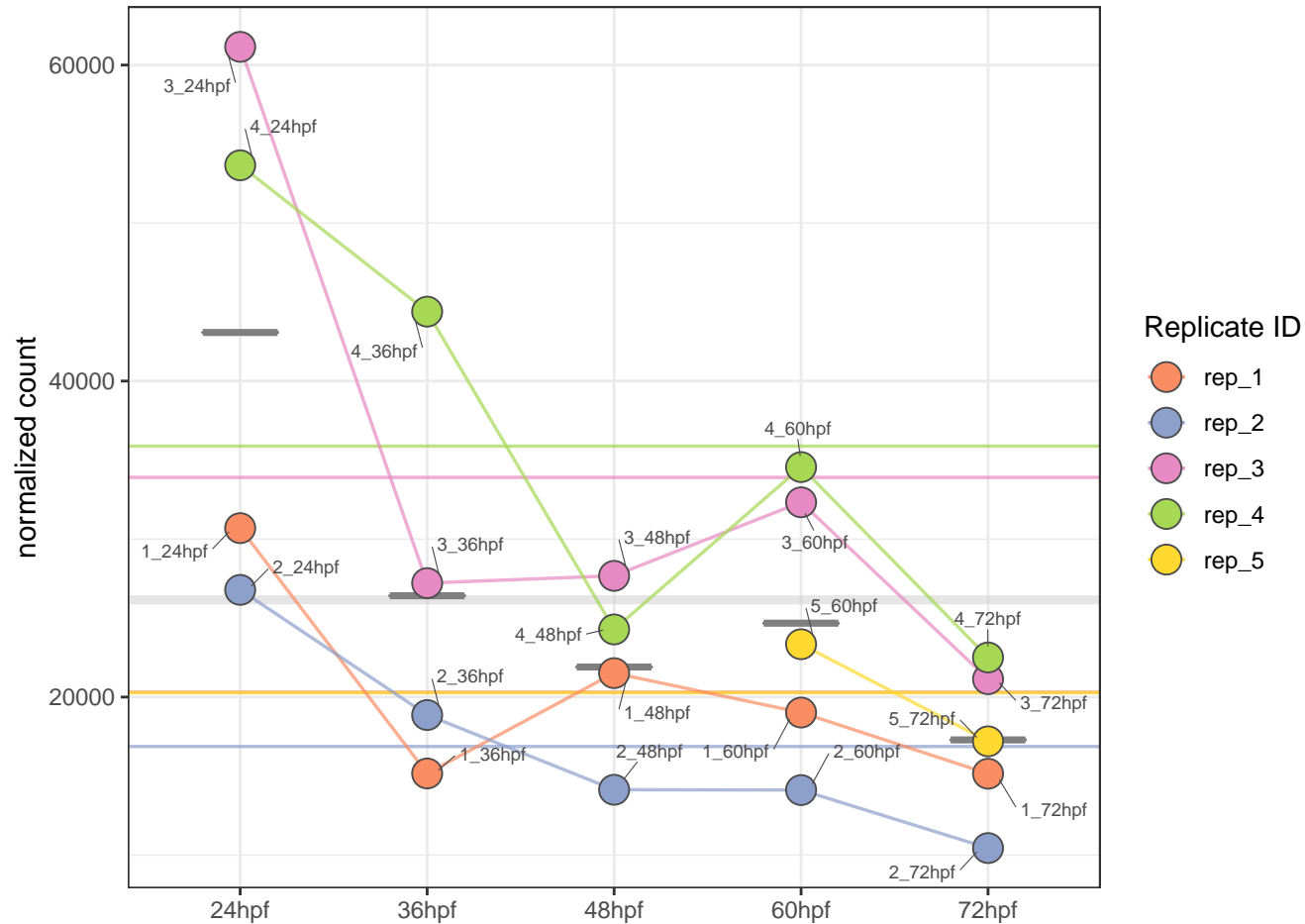Overall mean normalized counts = 5883.32

Gene: xirp1, ENSDARG00000030722, chromosome 2, protein_coding
P−value = 1.2e−13
Adjusted p−value = 1e−10
Log2 fold−change (rep_5 / rep_1) = 0.31
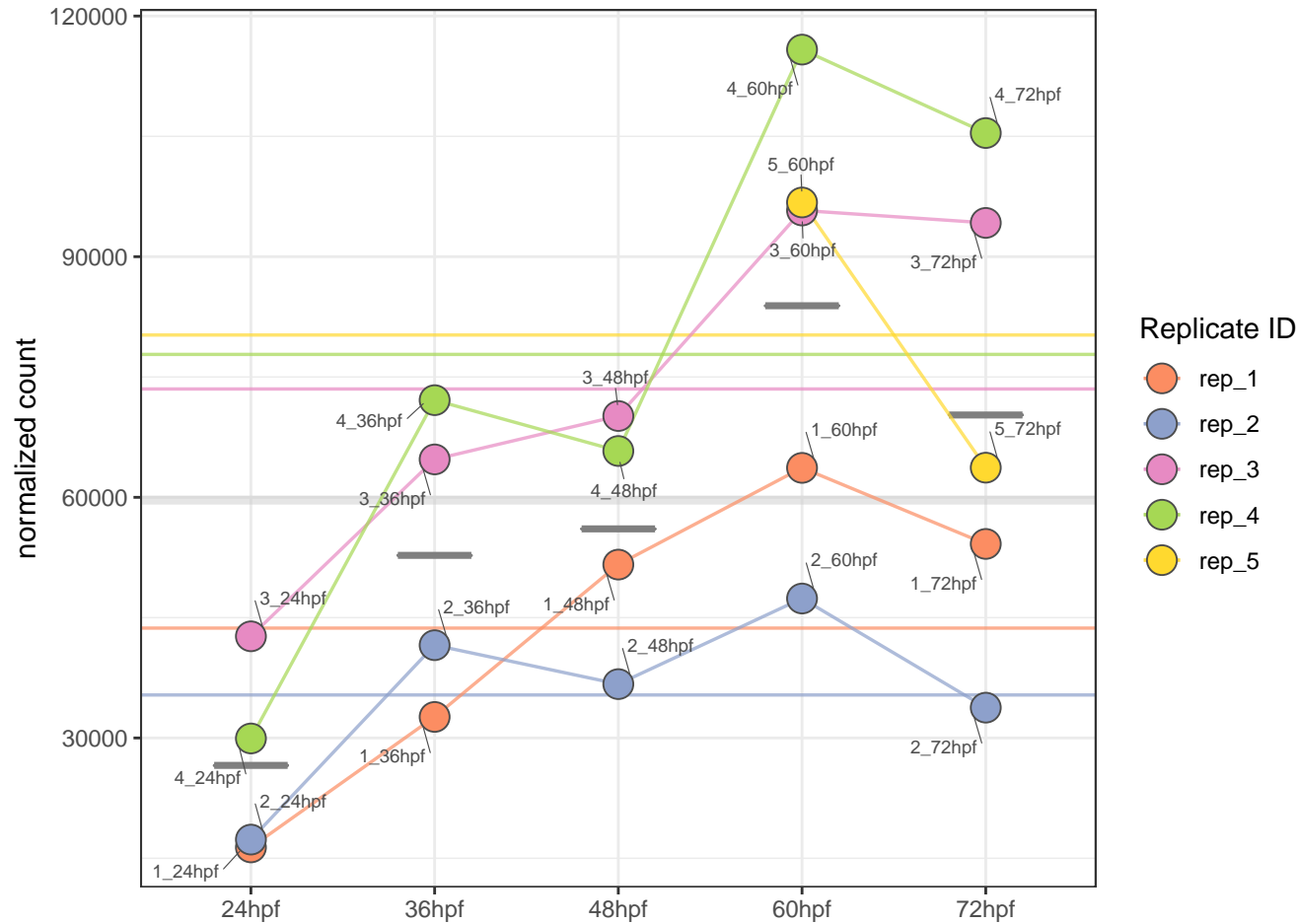Overall mean normalized counts = 26154.26

Gene: ckma, ENSDARG00000035327, chromosome 5, protein_coding
P−value = 1.3e−13
Adjusted p−value = 1e−10
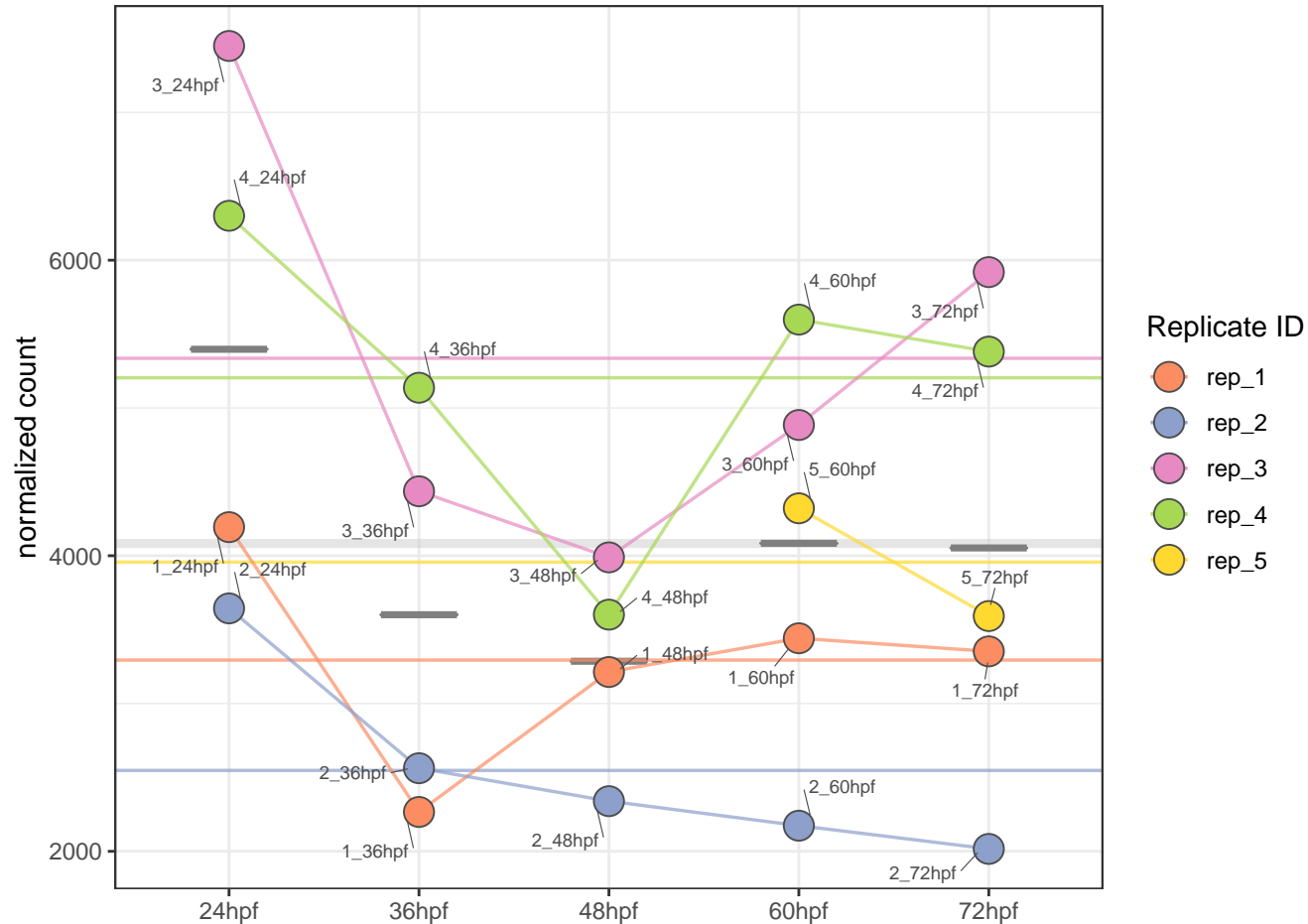Log2 fold−change (rep_5 / rep_1) = 0.51
Overall mean normalized counts = 59653.85

Gene: dub, ENSDARG00000059774, chromosome 21, protein_coding
P−value = 1.3e−13
Adjusted p−value = 1.1e−10
Log2 fold−change (rep_5 / rep_1) = 0.29
Overall mean normalized counts = 4082.80

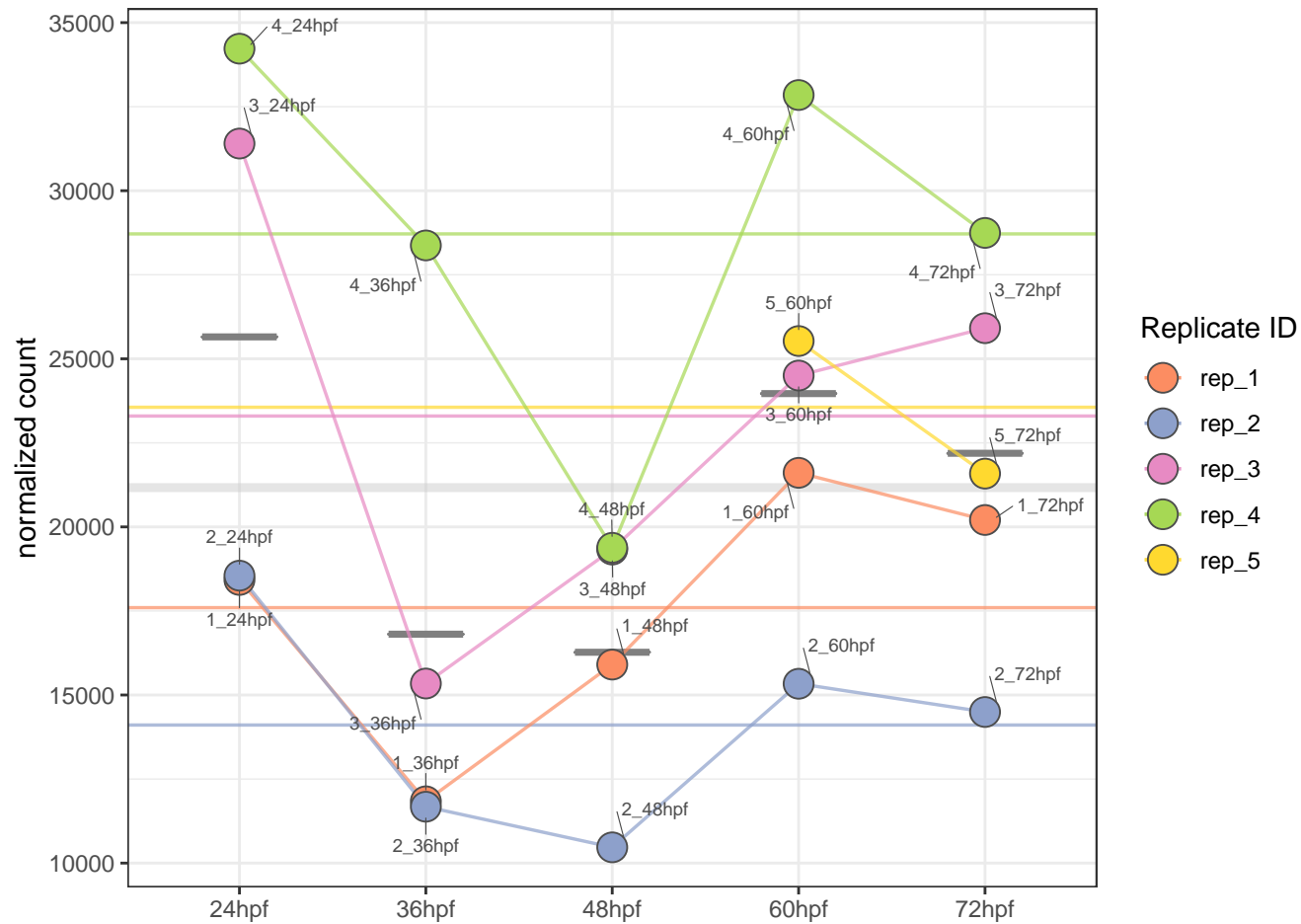Gene: znf106a, ENSDARG00000016651, chromosome 17, protein_coding
P−value = 1.6e−13
Adjusted p−value = 1.2e−10
Log2 fold−change (rep_5 / rep_1) = 0.28
Overall mean normalized counts = 21168.42
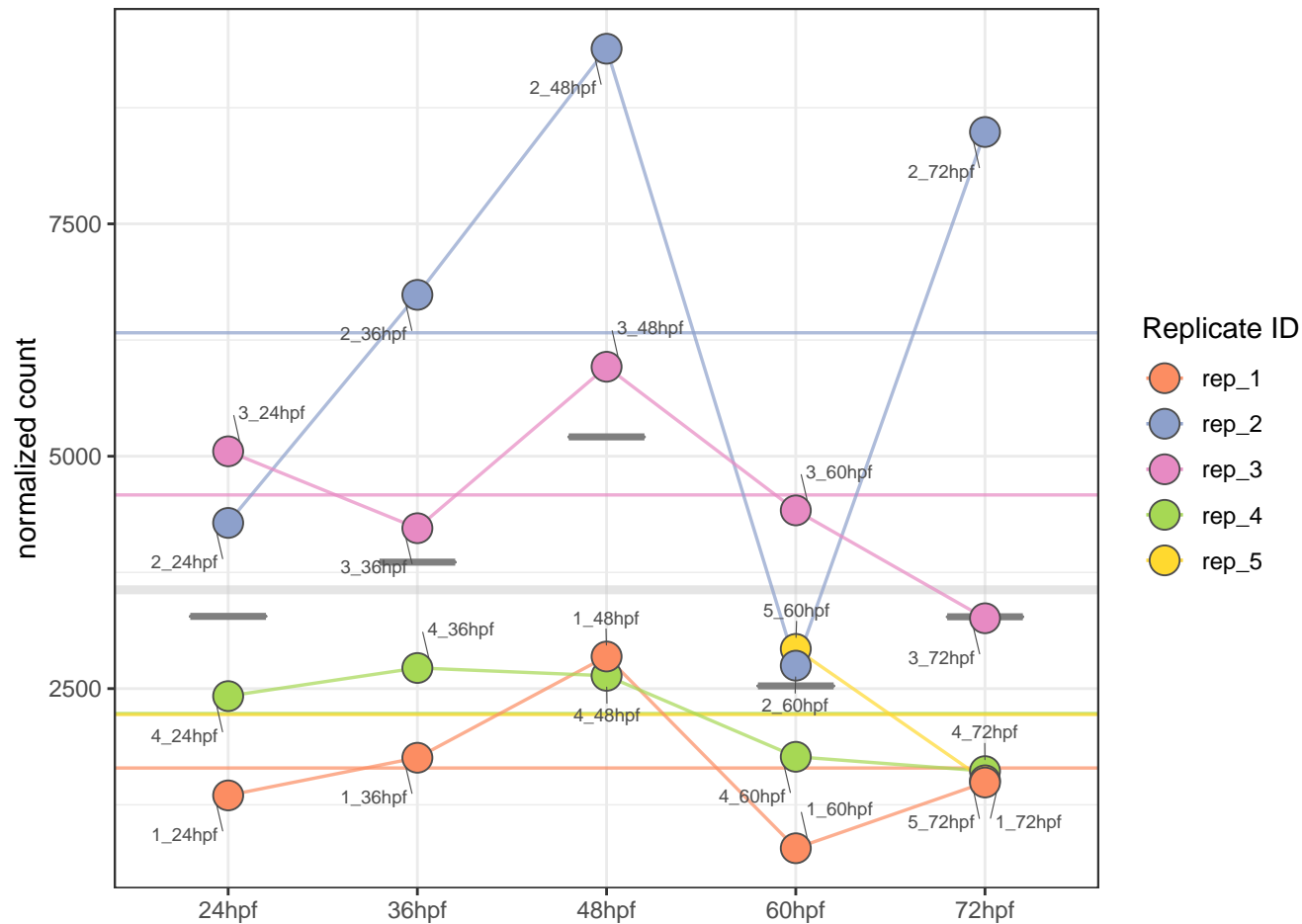
Gene: si:ch211−218m3.13, ENSDARG00000053779, chromosome 21, protein_coding
P−value = 1.8e−13
Adjusted p−value = 1.4e−10
Log2 fold−change (rep_5 / rep_1) = 0.87
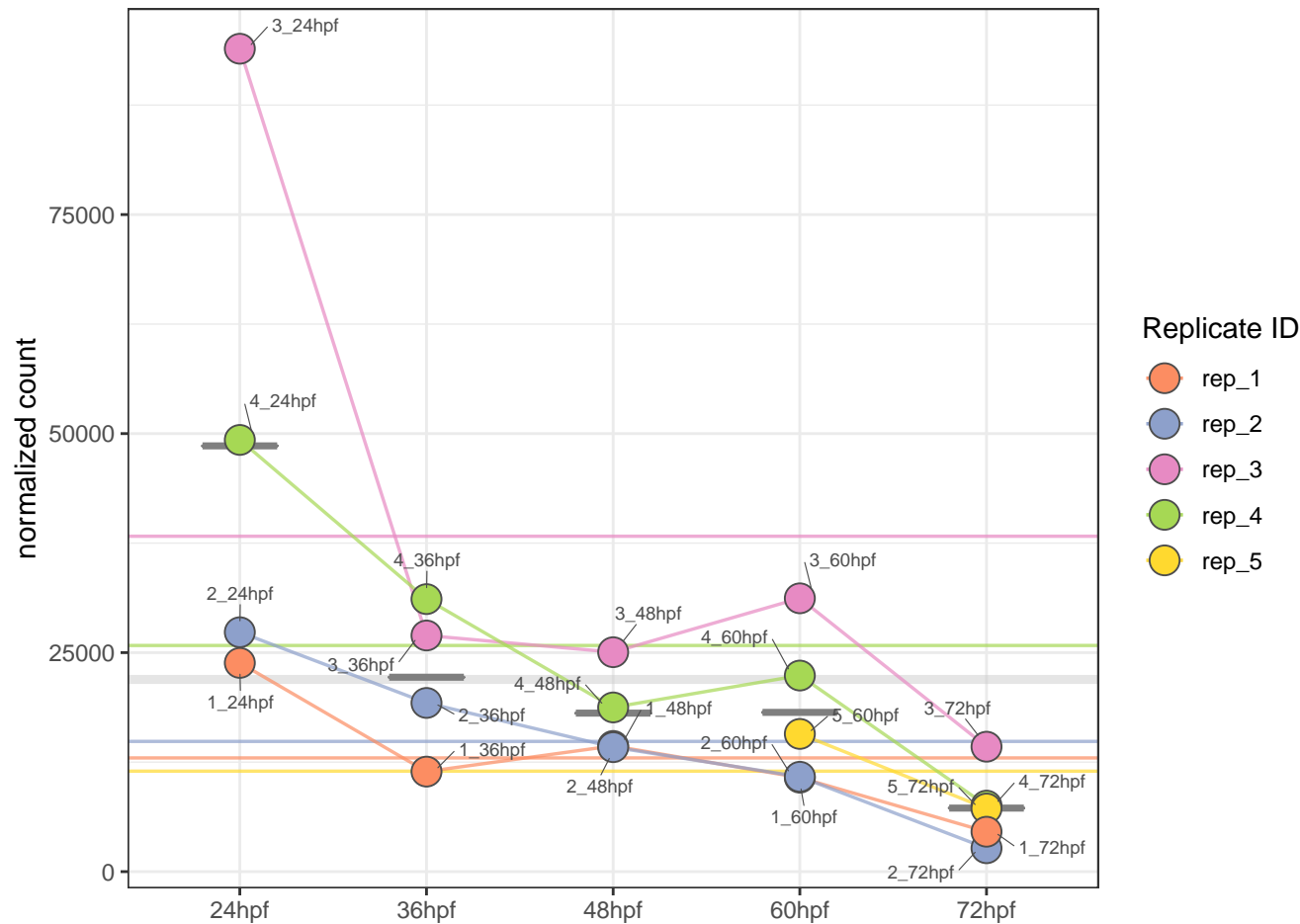Overall mean normalized counts = 3563.29

Gene: zgc:86709, ENSDARG00000057911, chromosome 20, protein_coding
P−value = 2.4e−13
Adjusted p−value = 1.8e−10
Log2 fold−change (rep_5 / rep_1) = 0.67
Overall mean normalized counts = 21939.77
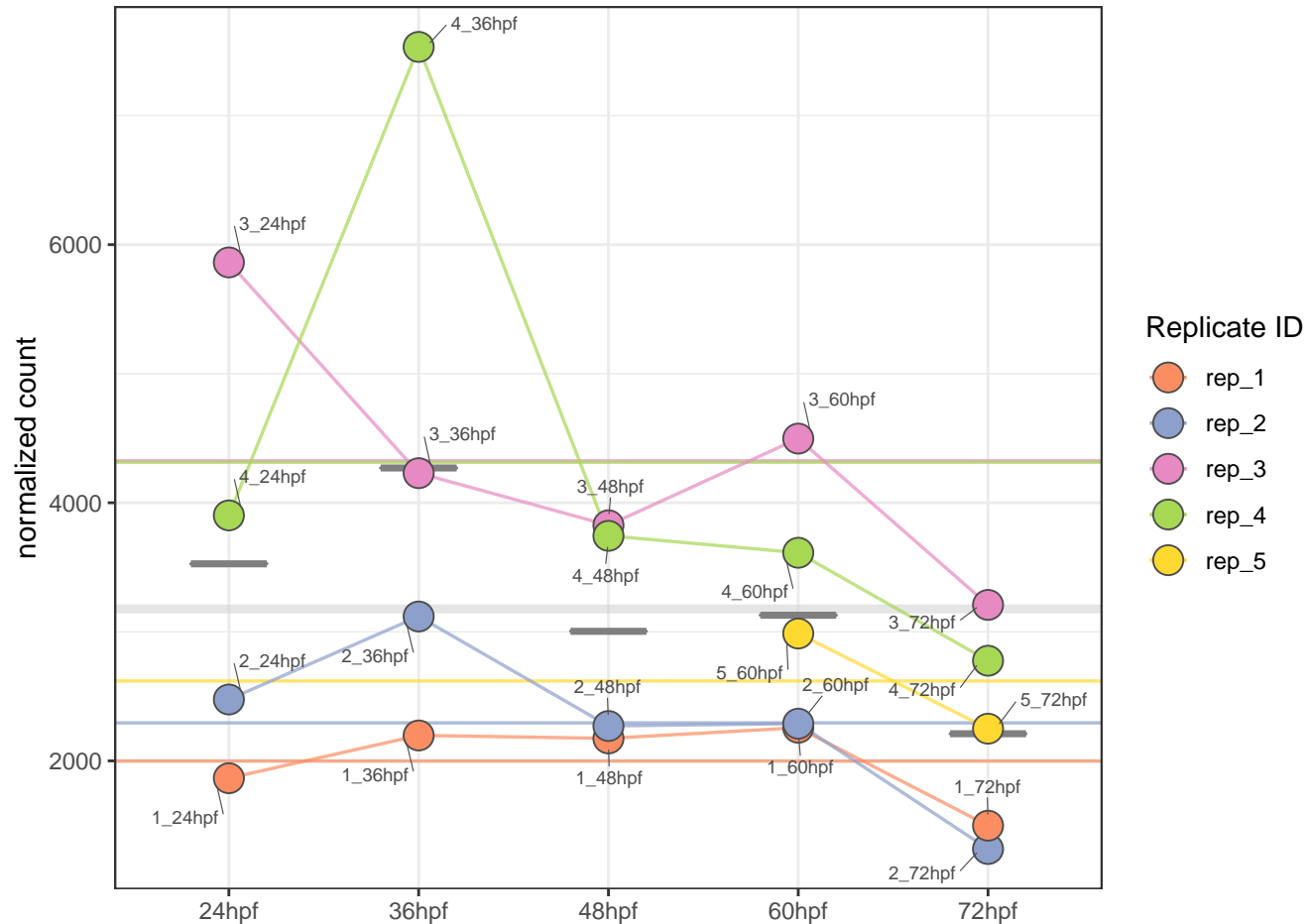
Gene: flt1, ENSDARG00000019371, chromosome 24, protein_coding
P−value = 2.4e−13
Adjusted p−value = 1.8e−10
Log2 fold−change (rep_5 / rep_1) = 0.63
Overall mean normalized counts = 3177.16

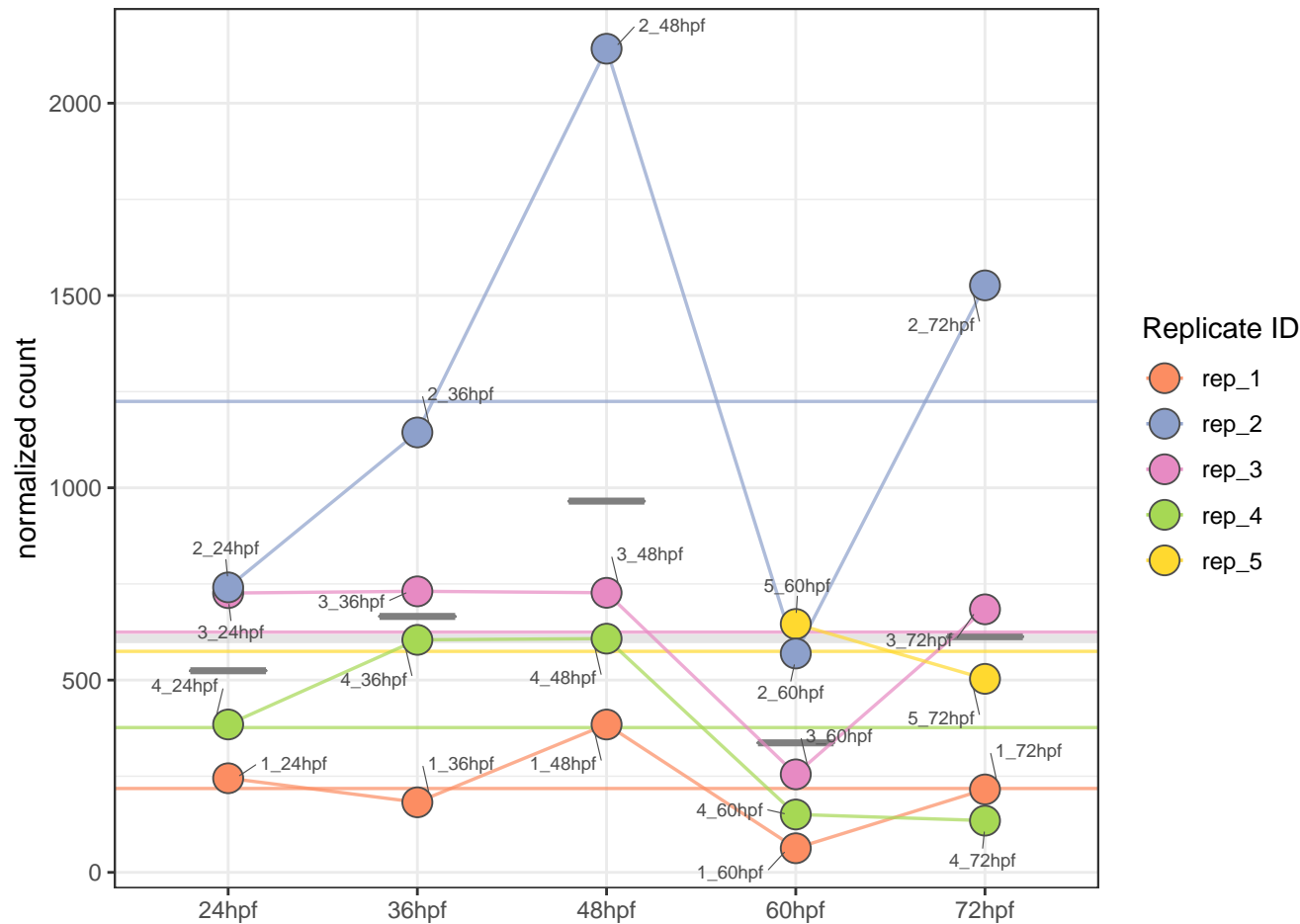Gene: CU695222.2, ENSDARG00000117426, chromosome 17, lincRNA
P−value = 2.6e−13
Adjusted p−value = 1.8e−10
Log2 fold−change (rep_5 / rep_1) = 2.29
Overall mean normalized counts = 607.67

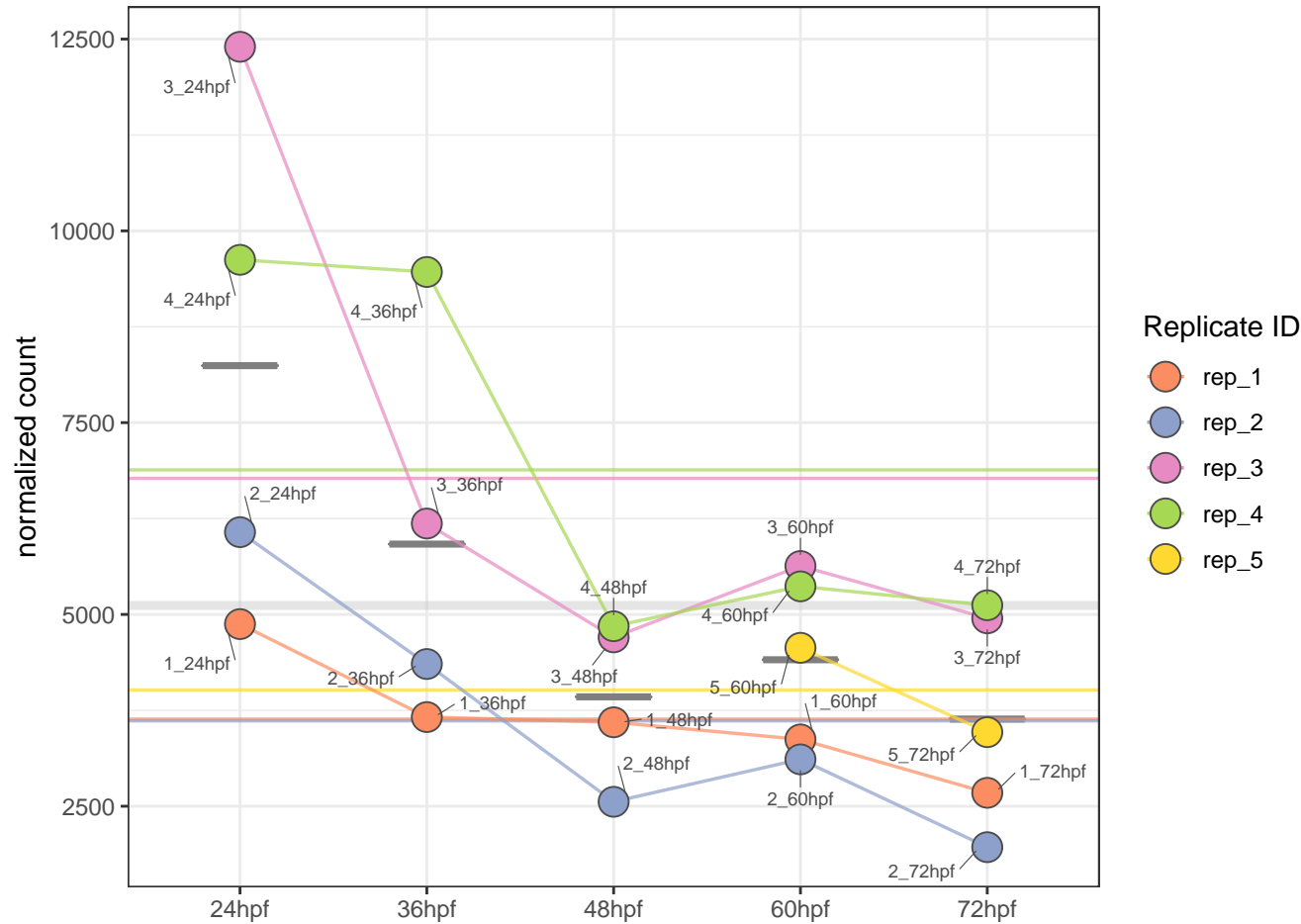Gene: ugt1b1, ENSDARG00000097491, chromosome 11, protein_coding
P−value = 2.7e−13
Adjusted p−value = 1.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.46
Overall mean normalized counts = 5116.71

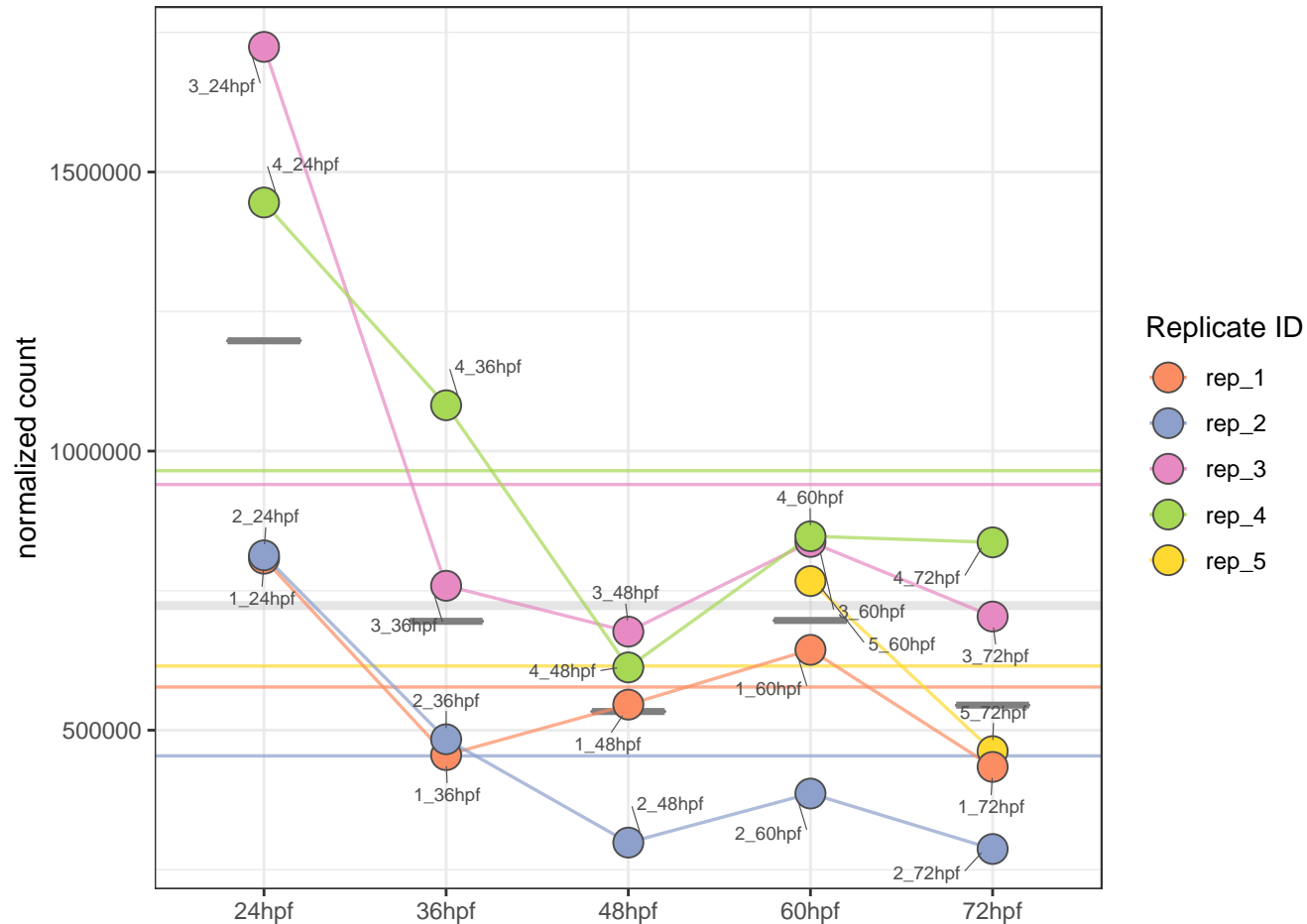Gene: myh7, ENSDARG00000079564, chromosome 2, protein_coding
P−value = 2.8e−13
Adjusted p−value = 1.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.27
Overall mean normalized counts = 723279.63

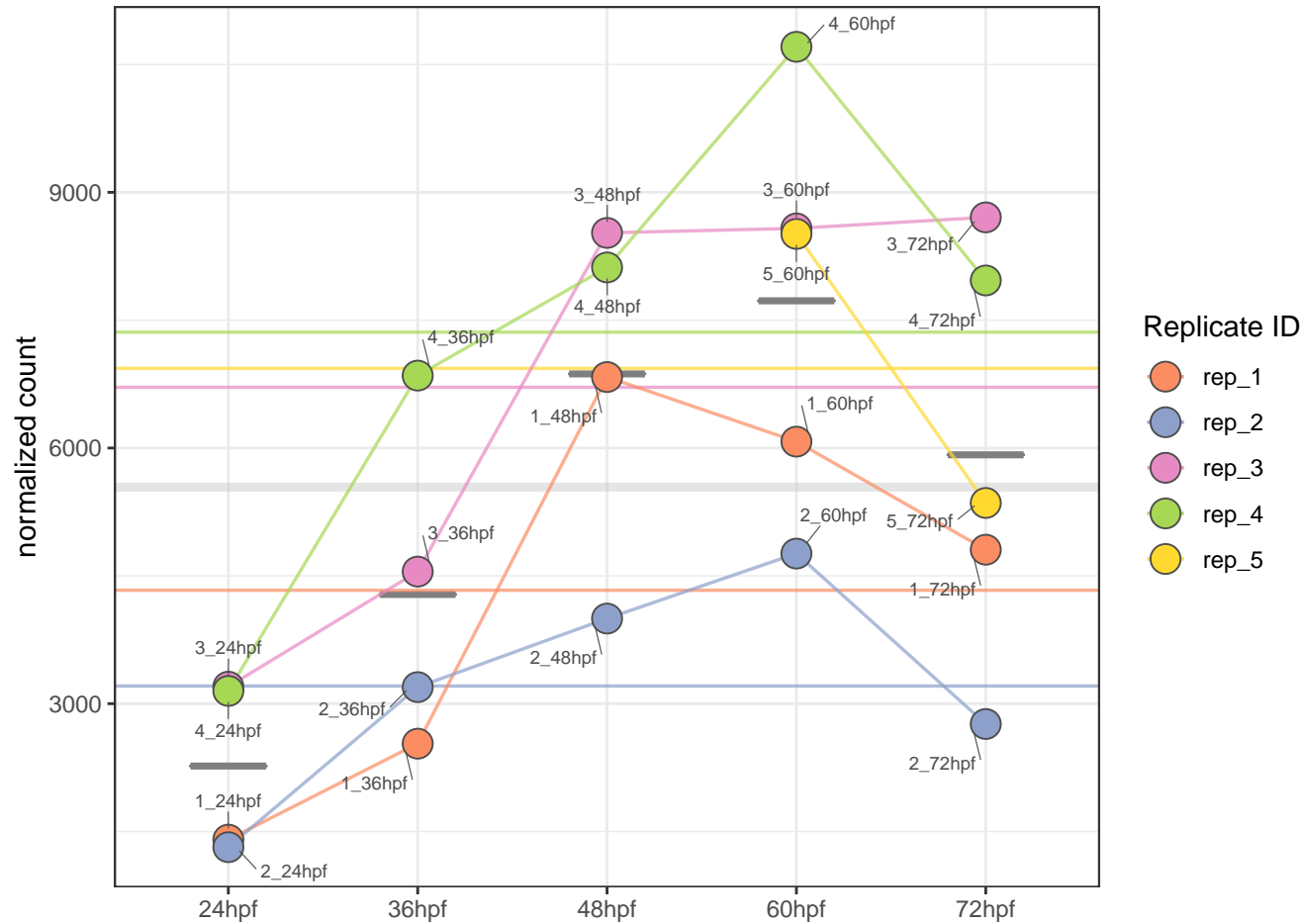Gene: fhl1a, ENSDARG00000115132, chromosome CHR_ALT_CTG14_1_25, protein_
P−value = 2.8e−13
Adjusted p−value = 1.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.41
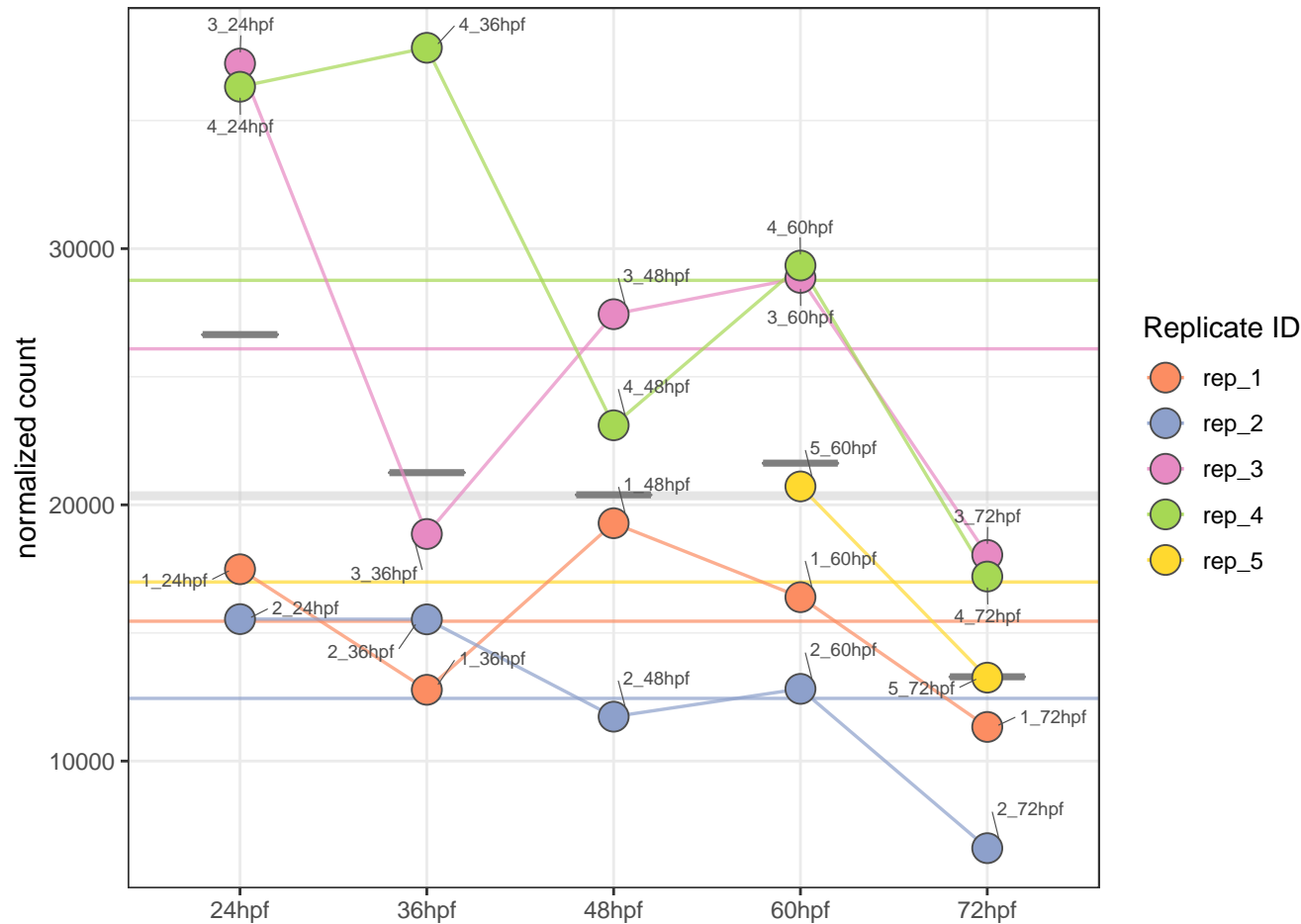Overall mean normalized counts = 5541.49

Gene: obsl1a, ENSDARG00000003684, chromosome 6, protein_coding
P−value = 3.1e−13
Adjusted p−value = 2e−10
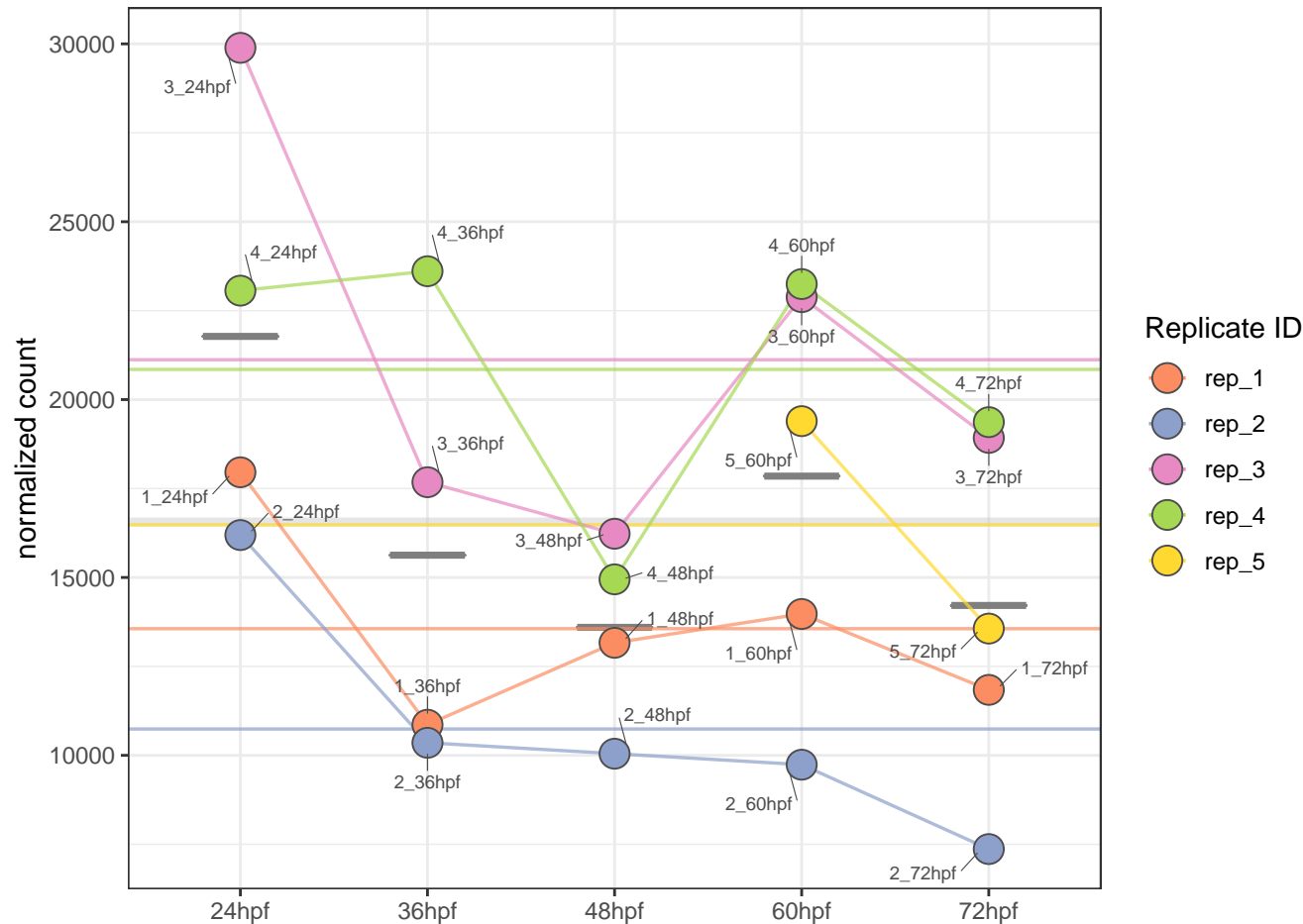Log2 fold−change (rep_5 / rep_1) = 0.36
Overall mean normalized counts = 20353.43

Gene: ppp1r13ba, ENSDARG00000004377, chromosome 17, protein_coding
P−value = 3.1e−13
Adjusted p−value = 2e−10
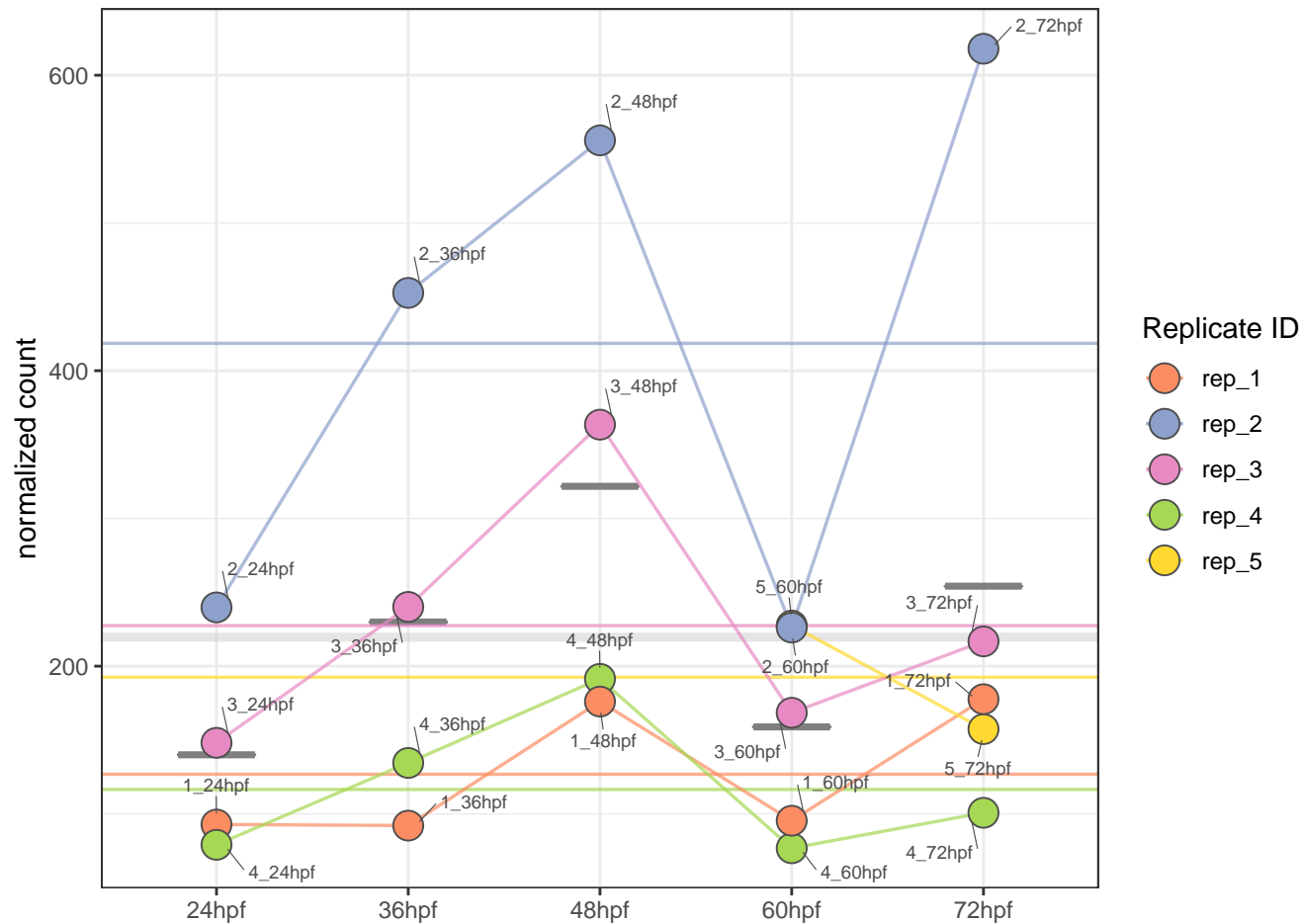Log2 fold−change (rep_5 / rep_1) = 0.35
Overall mean normalized counts = 16559.66

Gene: BX001023.1, ENSDARG00000098673, chromosome 5, processed_transcript
P−value = 3.6e−13
Adjusted p−value = 2.3e−10
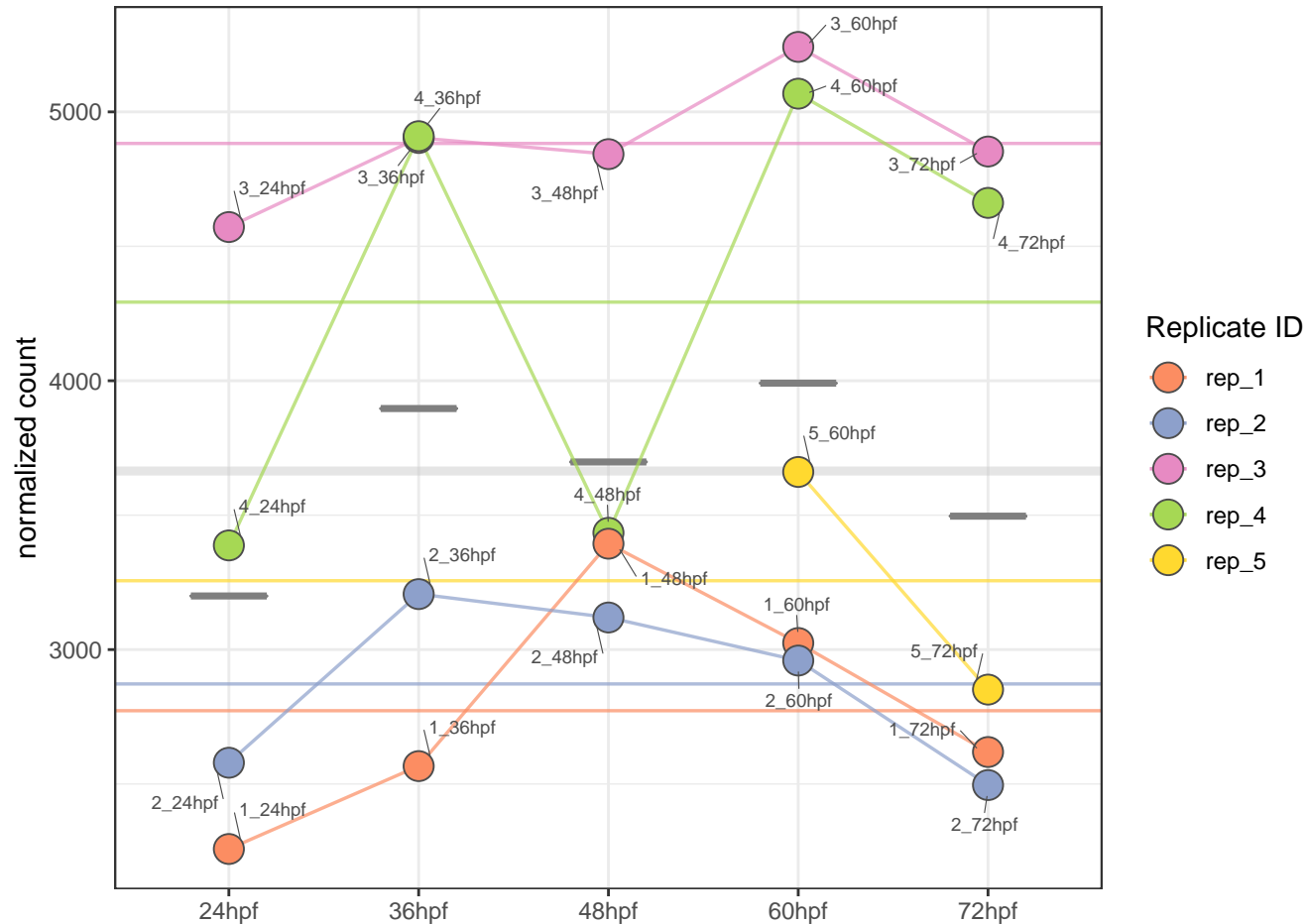Log2 fold−change (rep_5 / rep_1) = 0.81
Overall mean normalized counts = 219.62

Gene: prss23, ENSDARG00000055786, chromosome 14, protein_coding
P−value = 4.7e−13
Adjusted p−value = 2.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.18
Overall mean normalized counts = 3664.16

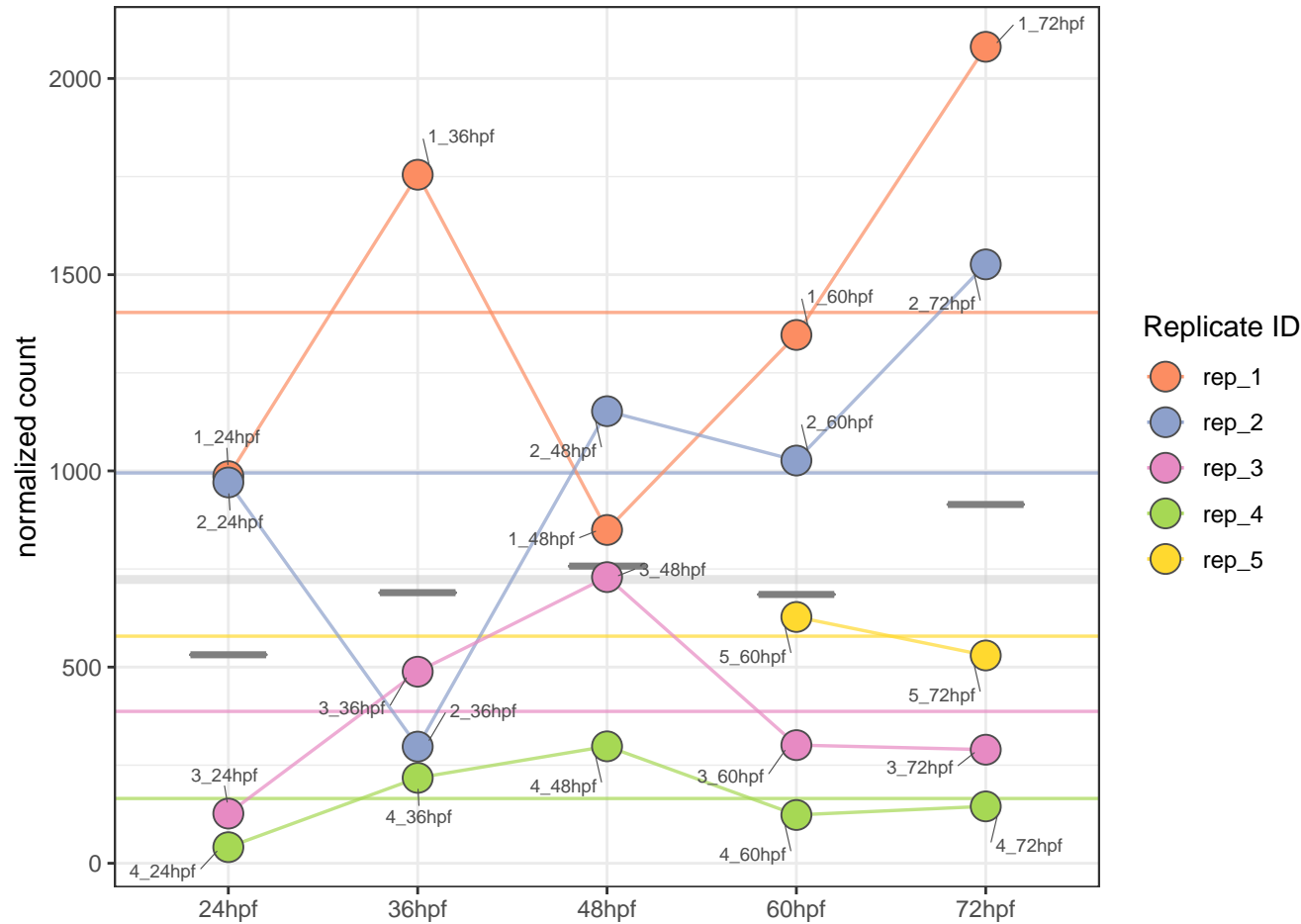Gene: atp1b1b, ENSDARG00000076833, chromosome 1, protein_coding
P−value = 4.8e−13
Adjusted p−value = 2.9e−10
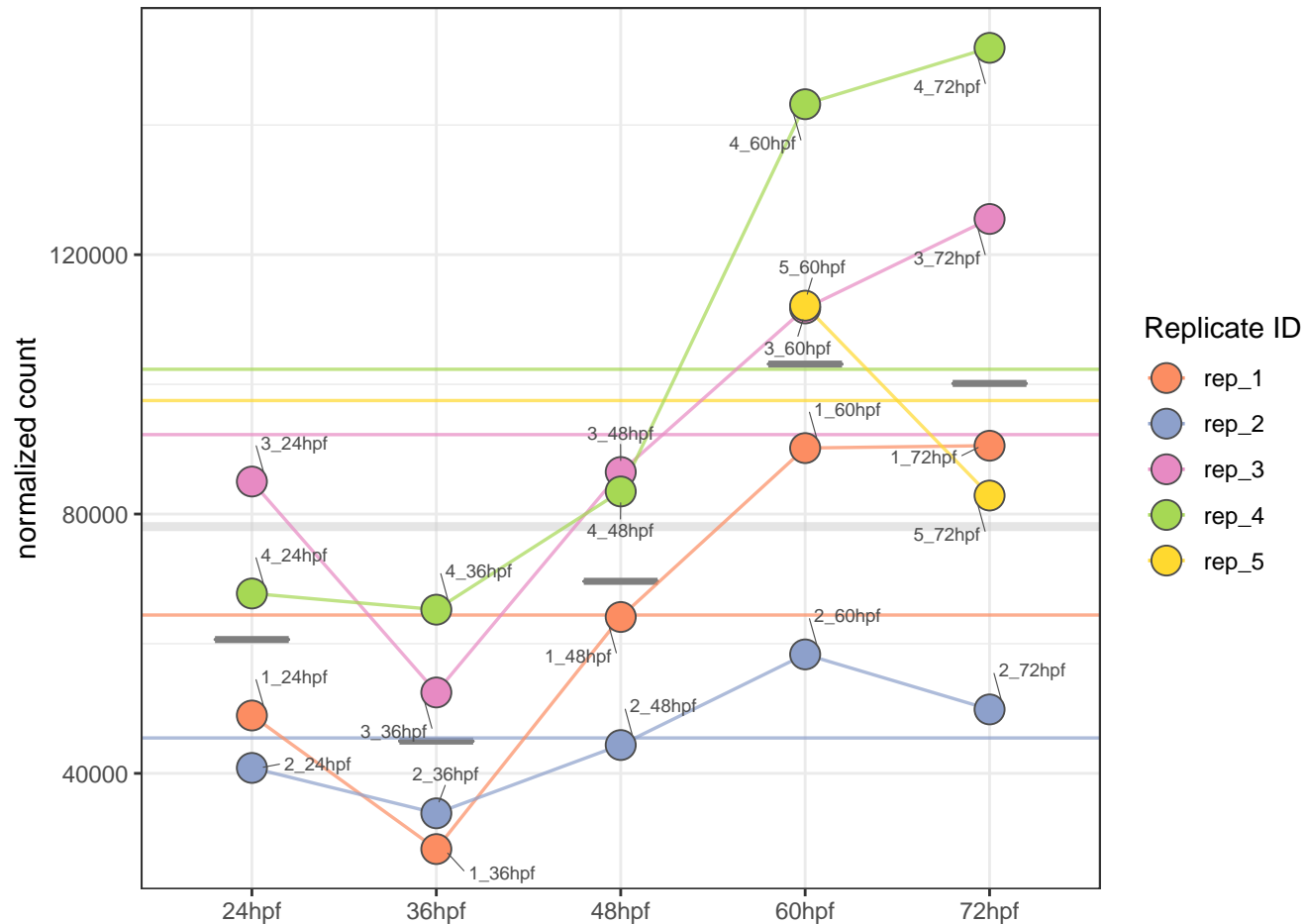Log2 fold−change (rep_5 / rep_1) = −1.35
Overall mean normalized counts = 723.20

Gene: actn2b, ENSDARG00000071090, chromosome 17, protein_coding
P−value = 5.5e−13
Adjusted p−value = 3.3e−10
Log2 fold−change (rep_5 / rep_1) = 0.22
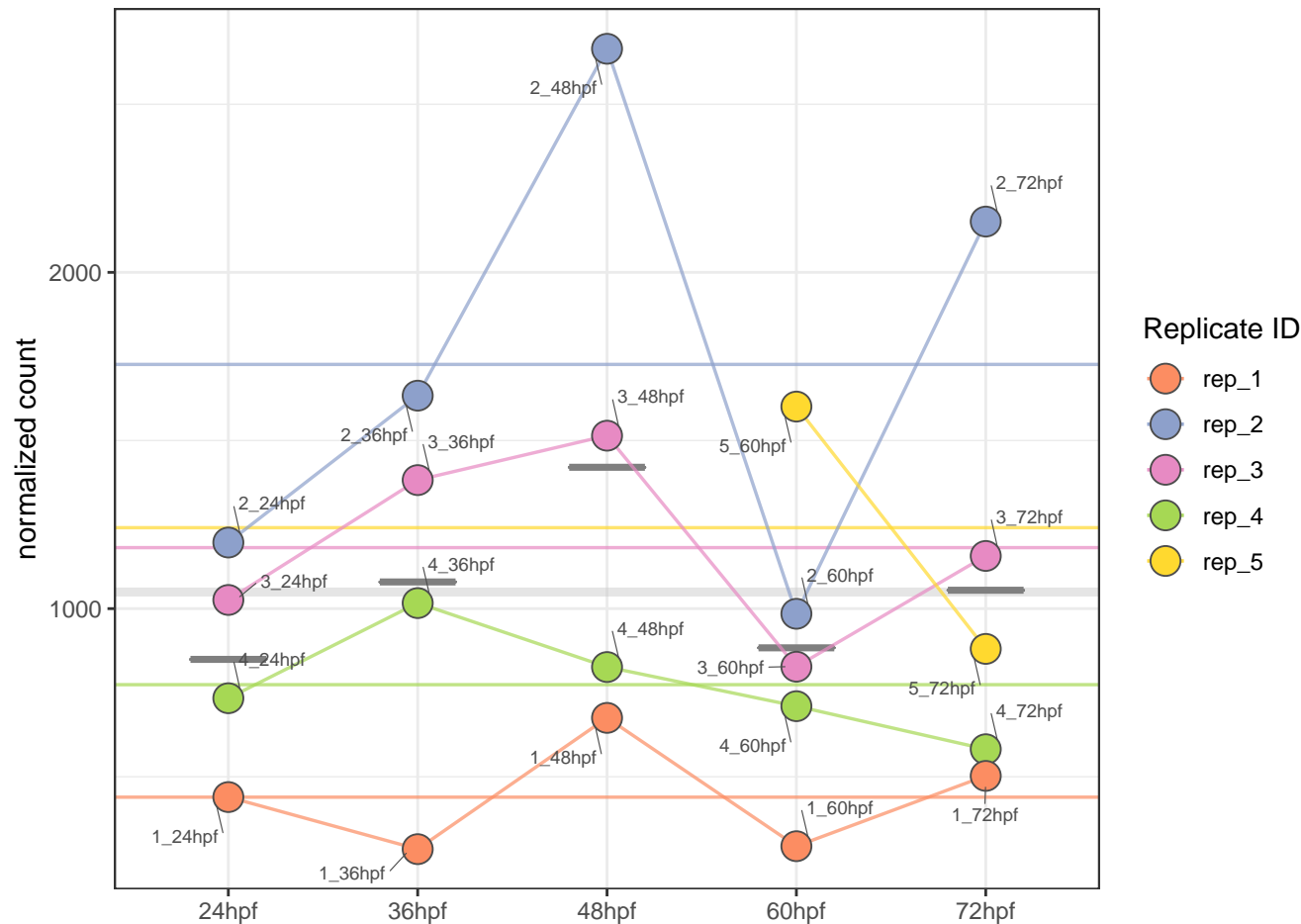Overall mean normalized counts = 78059.89

Gene: CU915770.2, ENSDARG00000117672, chromosome 5, lincRNA
P−value = 6.1e−13
Adjusted p−value = 3.6e−10
Log2 fold−change (rep_5 / rep_1) = 1.76
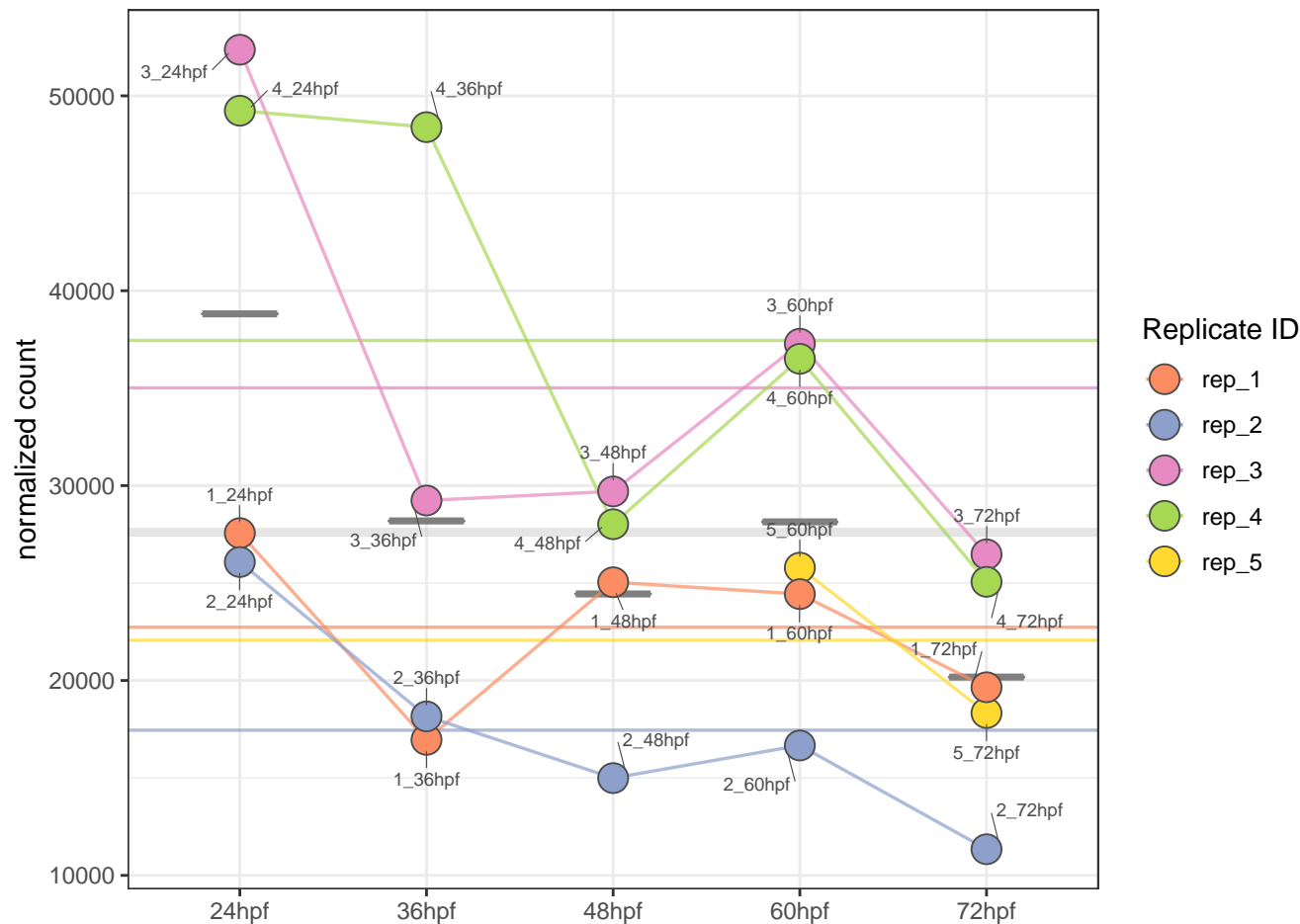Overall mean normalized counts = 1049.33

Gene: palm2akap2, ENSDARG00000069608, chromosome 10, protein_coding
P−value = 6.5e−13
Adjusted p−value = 3.8e−10
Log2 fold−change (rep_5 / rep_1) = 0.11
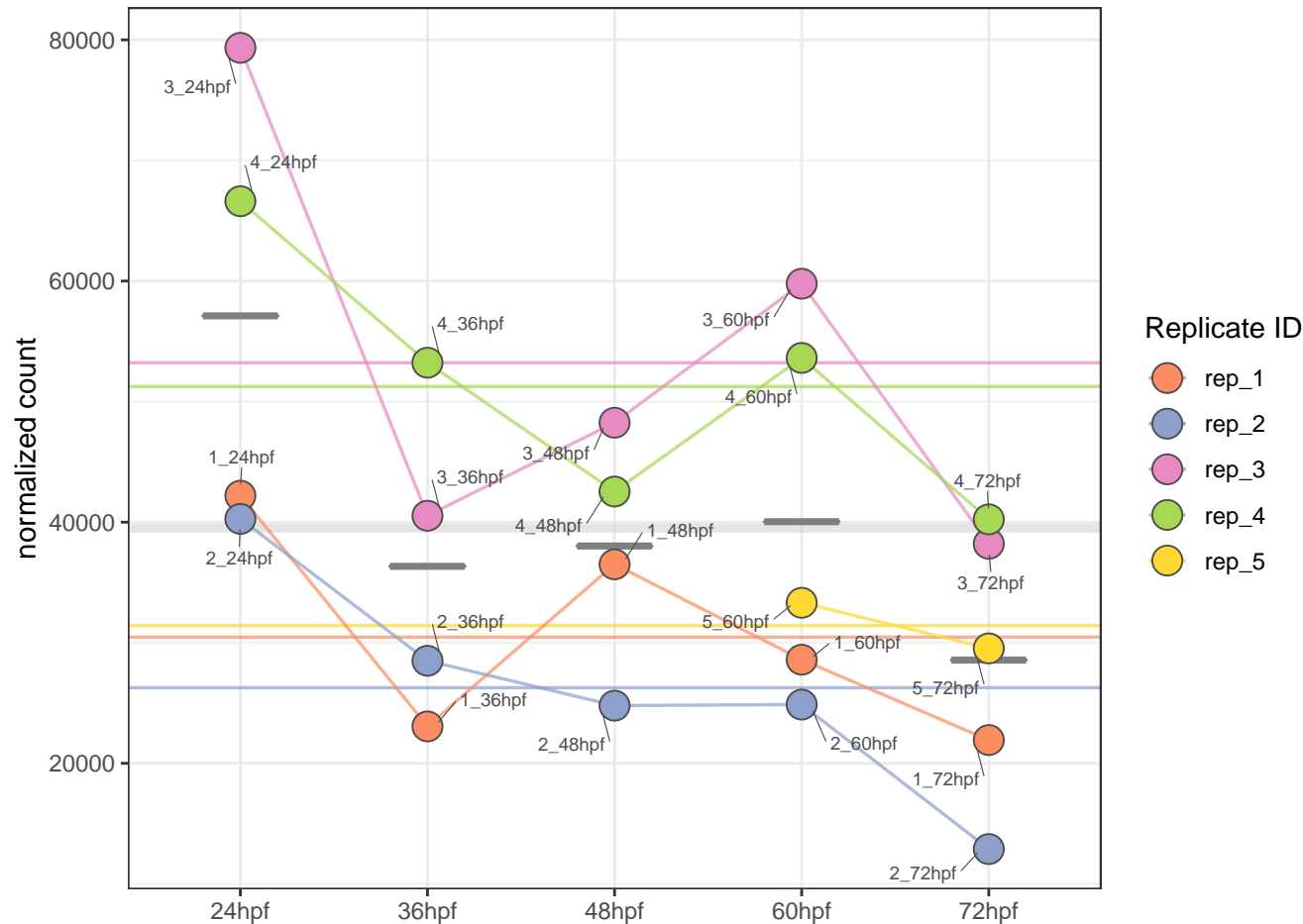Overall mean normalized counts = 27606.18

Gene: alcama, ENSDARG00000026531, chromosome 10, protein_coding
P−value = 7e−13
Adjusted p−value = 4e−10
Log2 fold−change (rep_5 / rep_1) = 0.32
Overall mean normalized counts = 39497.70

Gene: gata6, ENSDARG00000103589, chromosome 2, protein_coding
P−value = 7.2e−13
Adjusted p−value = 4e−10
Log2 fold−change (rep_5 / rep_1) = 0.51
Overall mean normalized counts = 11904.37

Gene: klhl31, ENSDARG00000039066, chromosome 13, protein_coding
P−value = 7.6e−13
Adjusted p−value = 4.2e−10
Log2 fold−change (rep_5 / rep_1) = 0.20
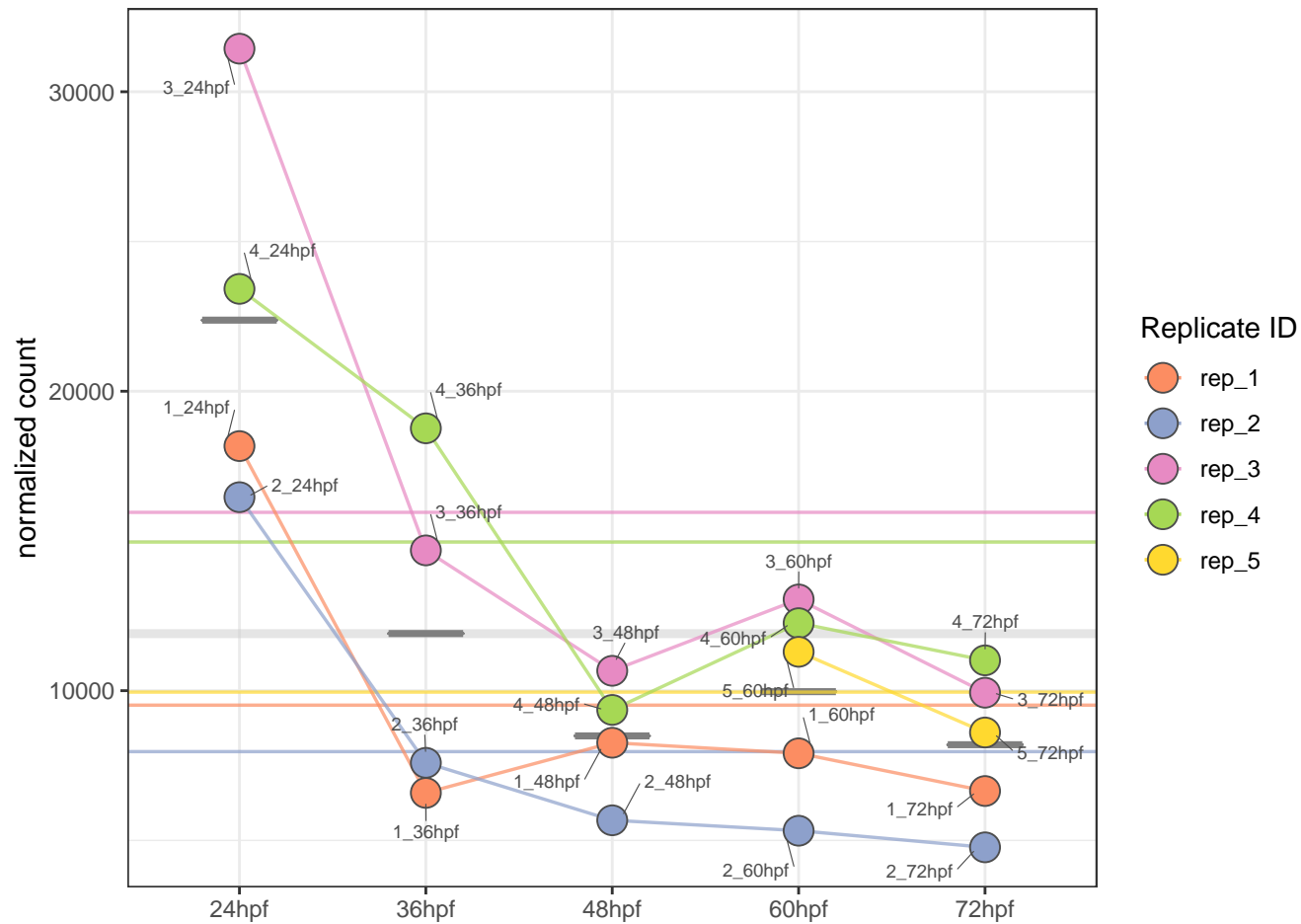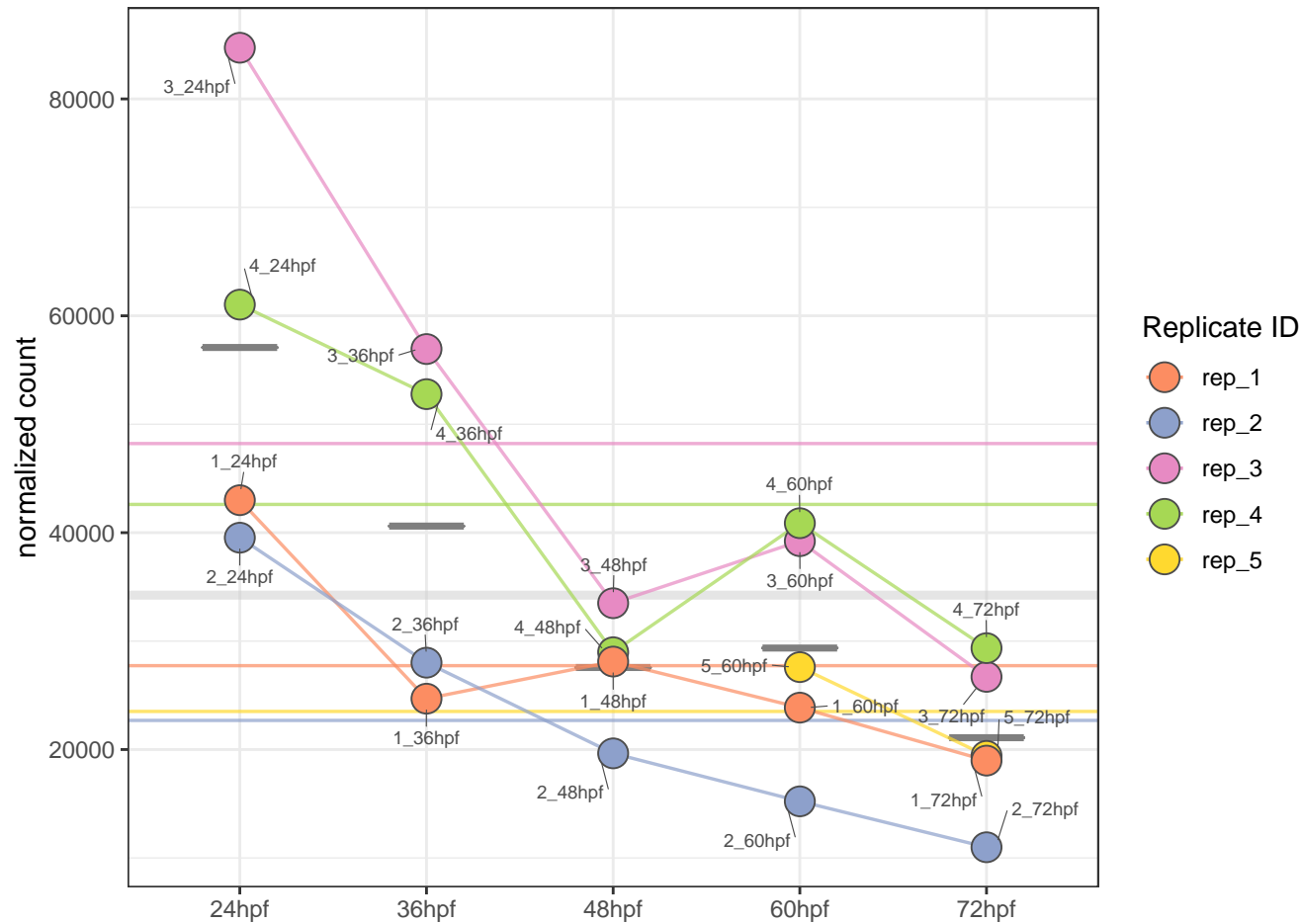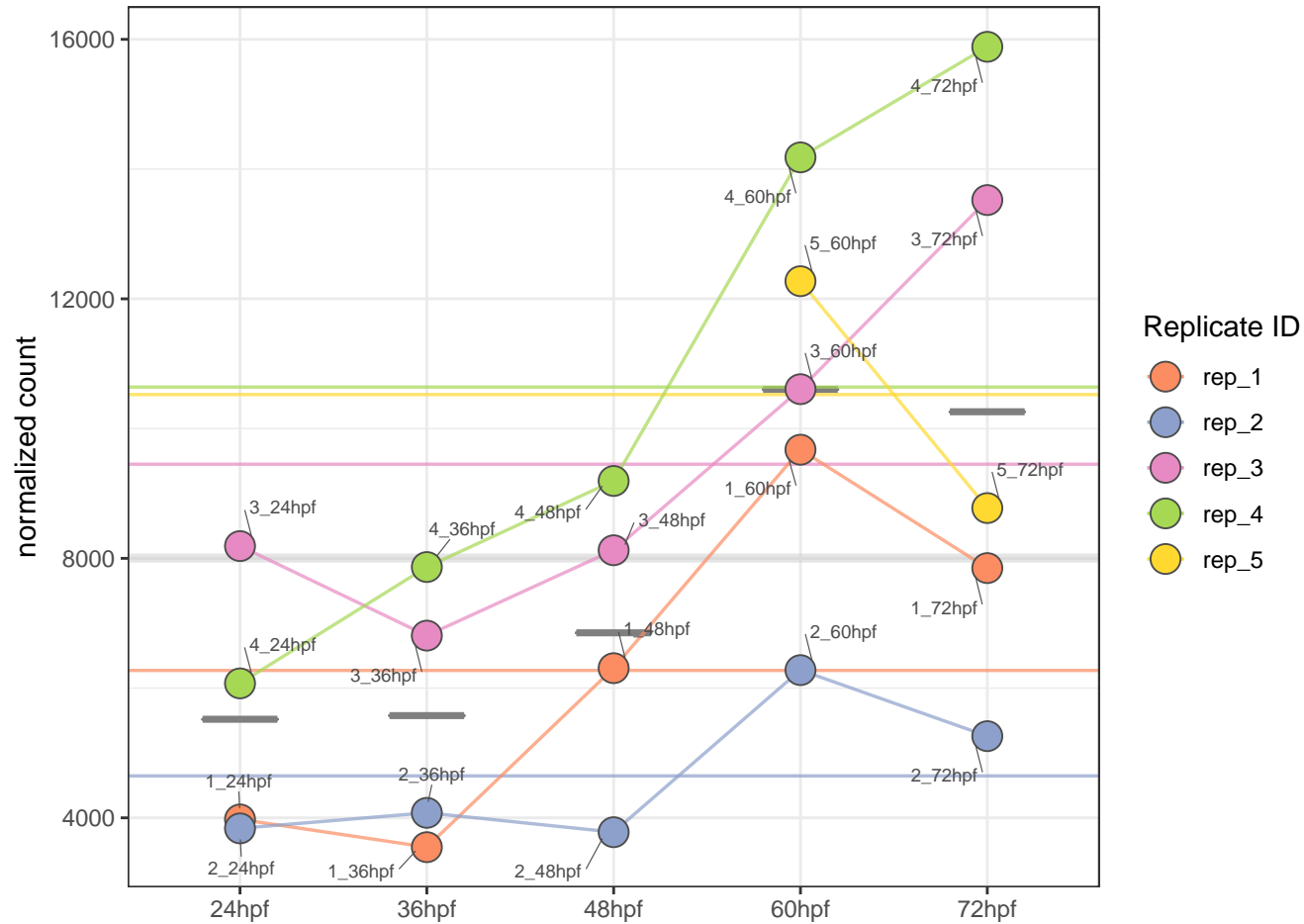Overall mean normalized counts = 34239.26

Gene: anxa6, ENSDARG00000013335, chromosome 14, protein_coding
P−value = 7.9e−13
Adjusted p−value = 4.3e−10
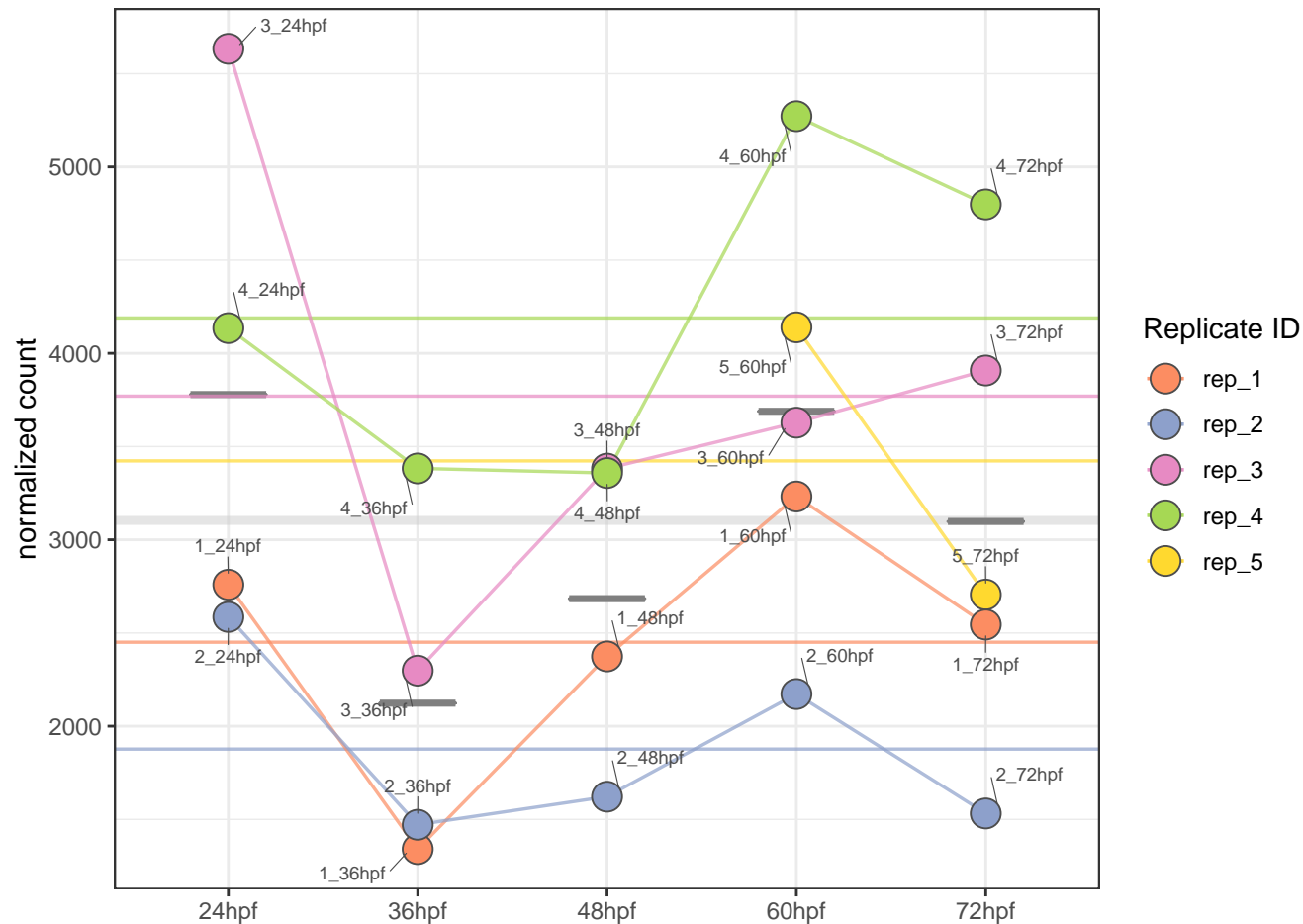Log2 fold−change (rep_5 / rep_1) = 0.36
Overall mean normalized counts = 8004.50

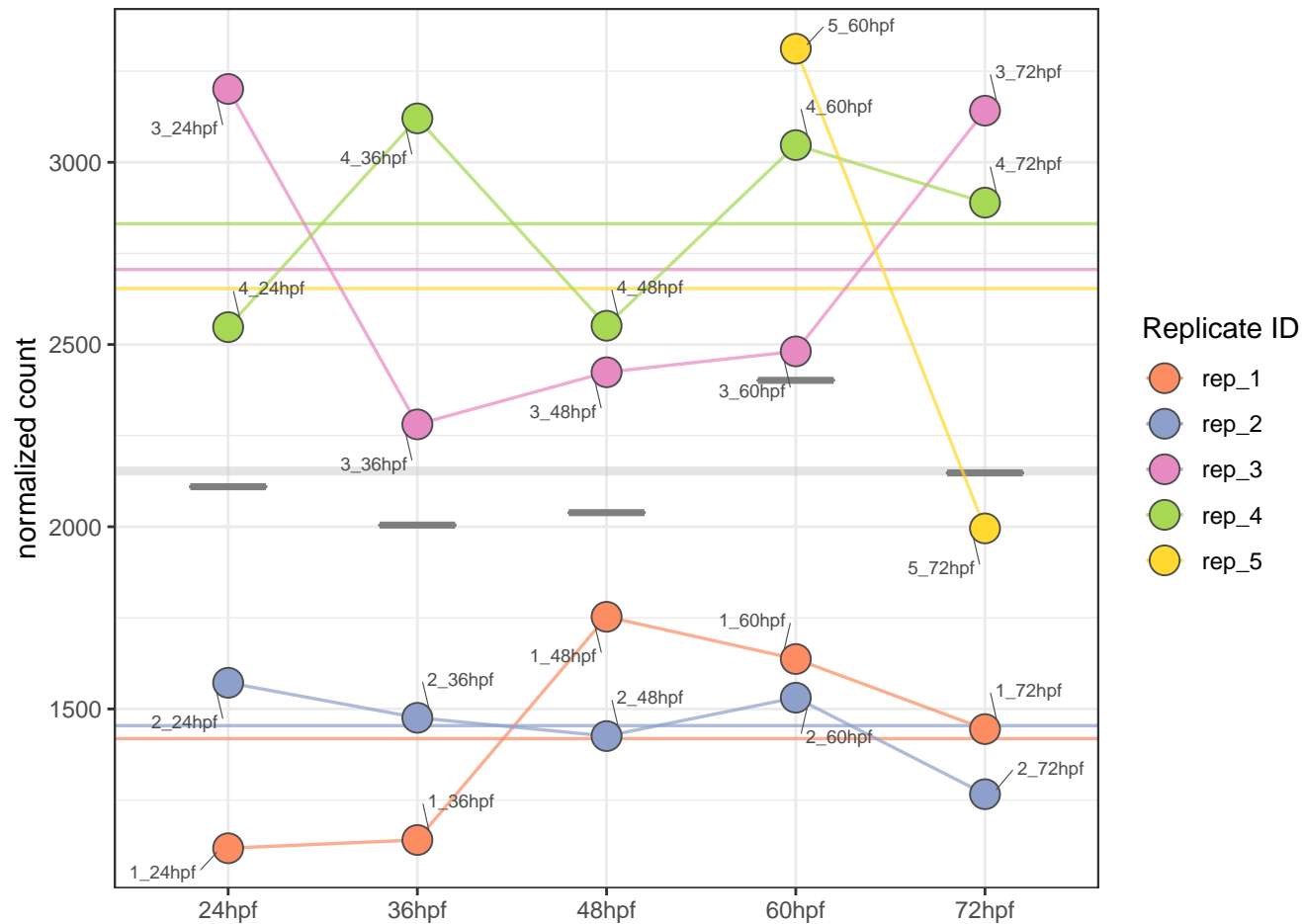Gene: hif1aa, ENSDARG00000006181, chromosome 13, protein_coding
P−value = 8.1e−13
Adjusted p−value = 4.3e−10
Log2 fold−change (rep_5 / rep_1) = 0.35
Overall mean normalized counts = 3103.71

Gene: si:dkeyp−97a10.2, ENSDARG00000098129, chromosome 16, protein_coding
P−value = 9.4e−13
Adjusted p−value = 4.9e−10
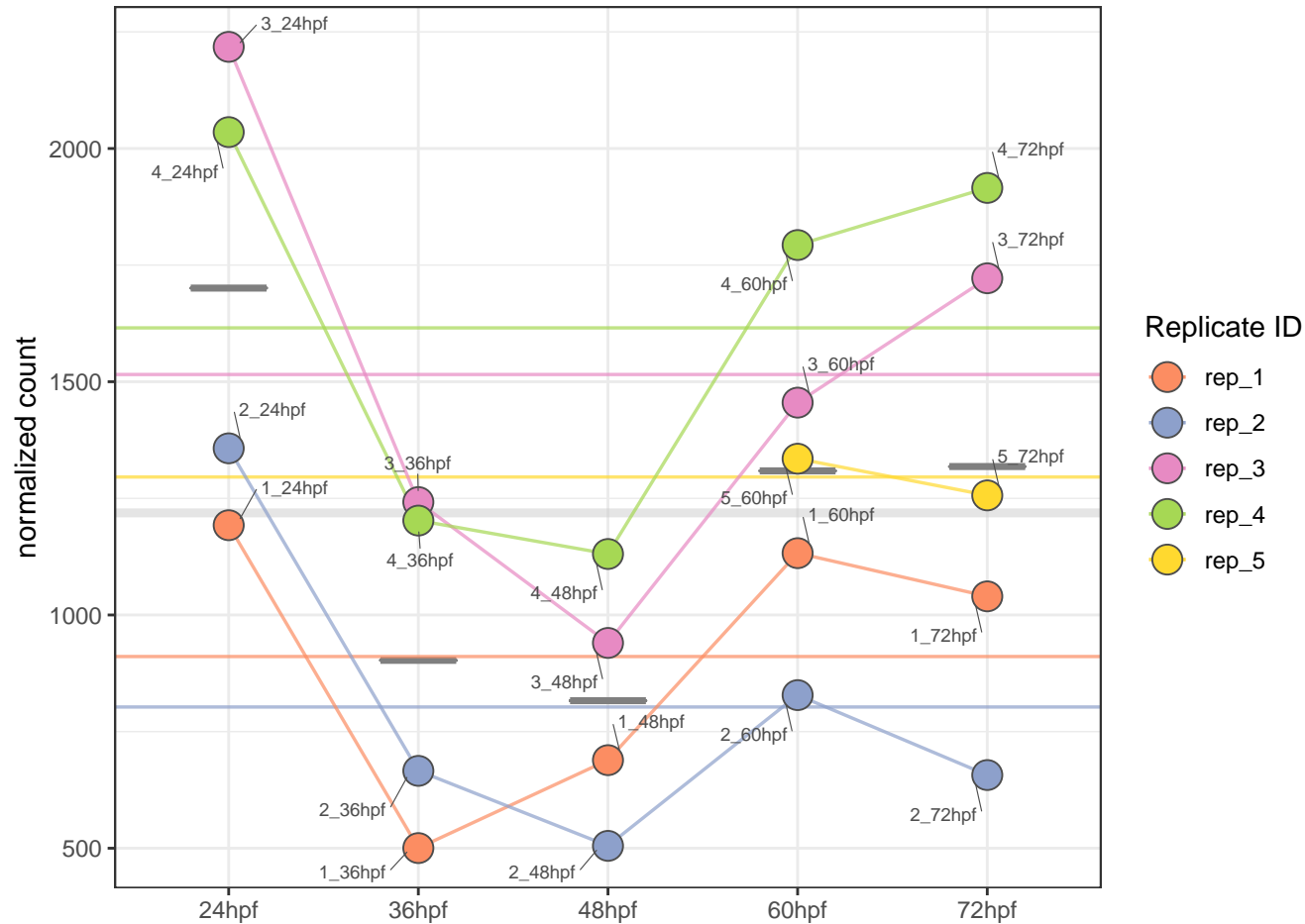Log2 fold−change (rep_5 / rep_1) = 0.84
Overall mean normalized counts = 2152.61

Gene: rassf9, ENSDARG00000074721, chromosome 18, protein_coding
P−value = 9.7e−13
Adjusted p−value = 5e−10
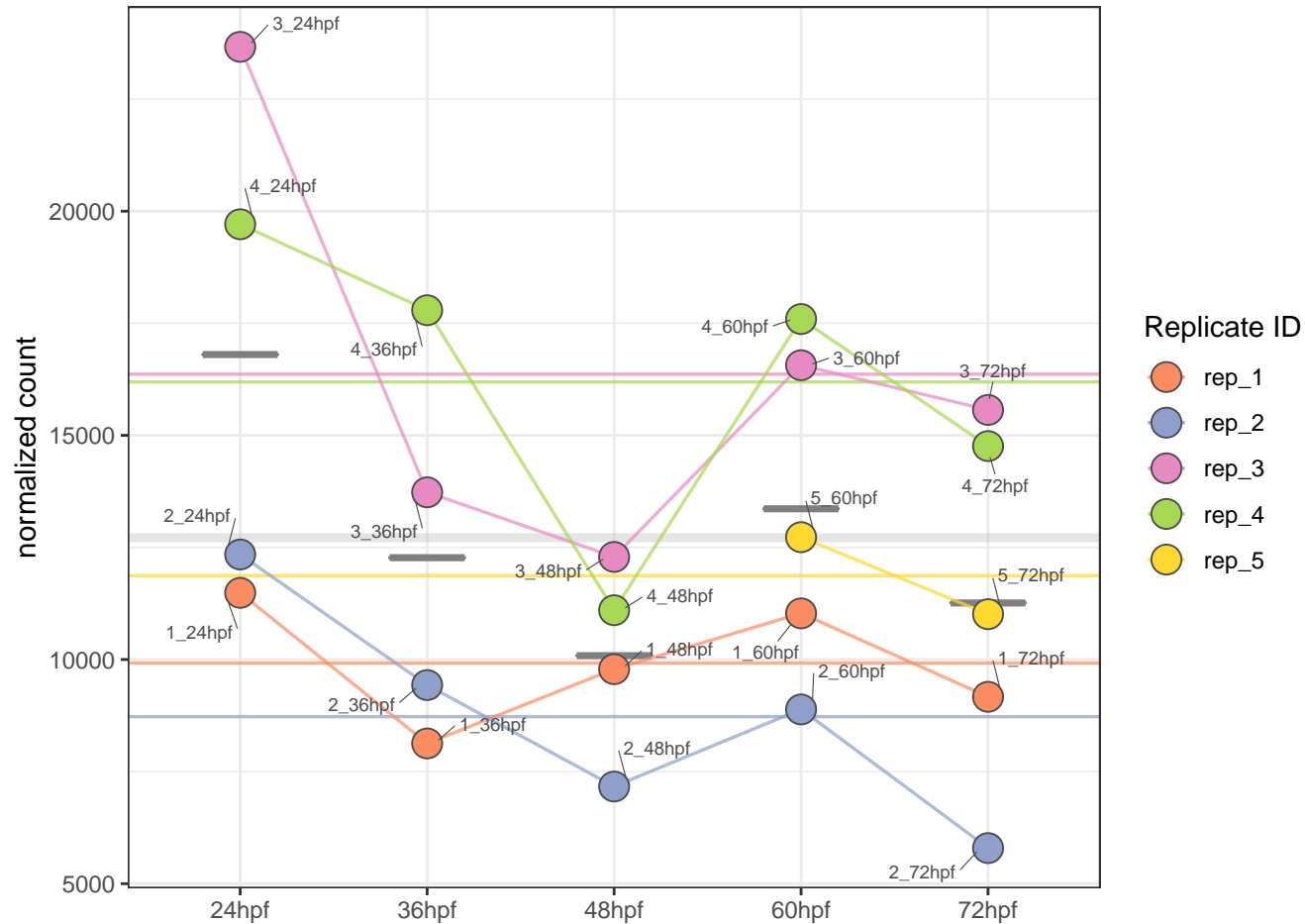Log2 fold−change (rep_5 / rep_1) = 0.40
Overall mean normalized counts = 1218.87

Gene: smad6b, ENSDARG00000031763, chromosome 18, protein_coding
P−value = 1.1e−12
Adjusted p−value = 5.6e−10
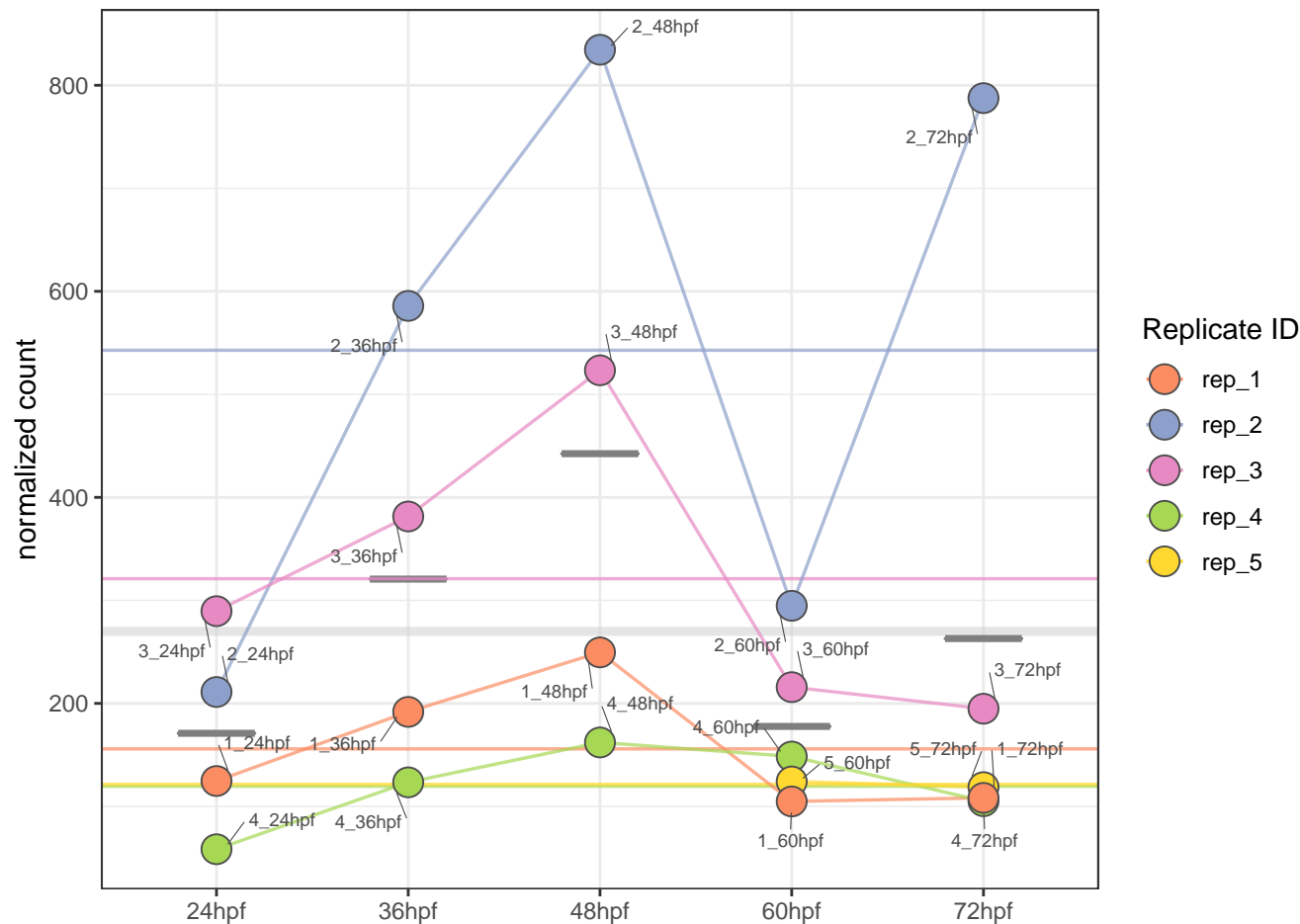Log2 fold−change (rep_5 / rep_1) = 0.30
Overall mean normalized counts = 12716.10

Gene: BX936284.1, ENSDARG00000104512, chromosome 3, lincRNA
P−value = 1.1e−12
Adjusted p−value = 5.6e−10
Log2 fold−change (rep_5 / rep_1) = −0.11
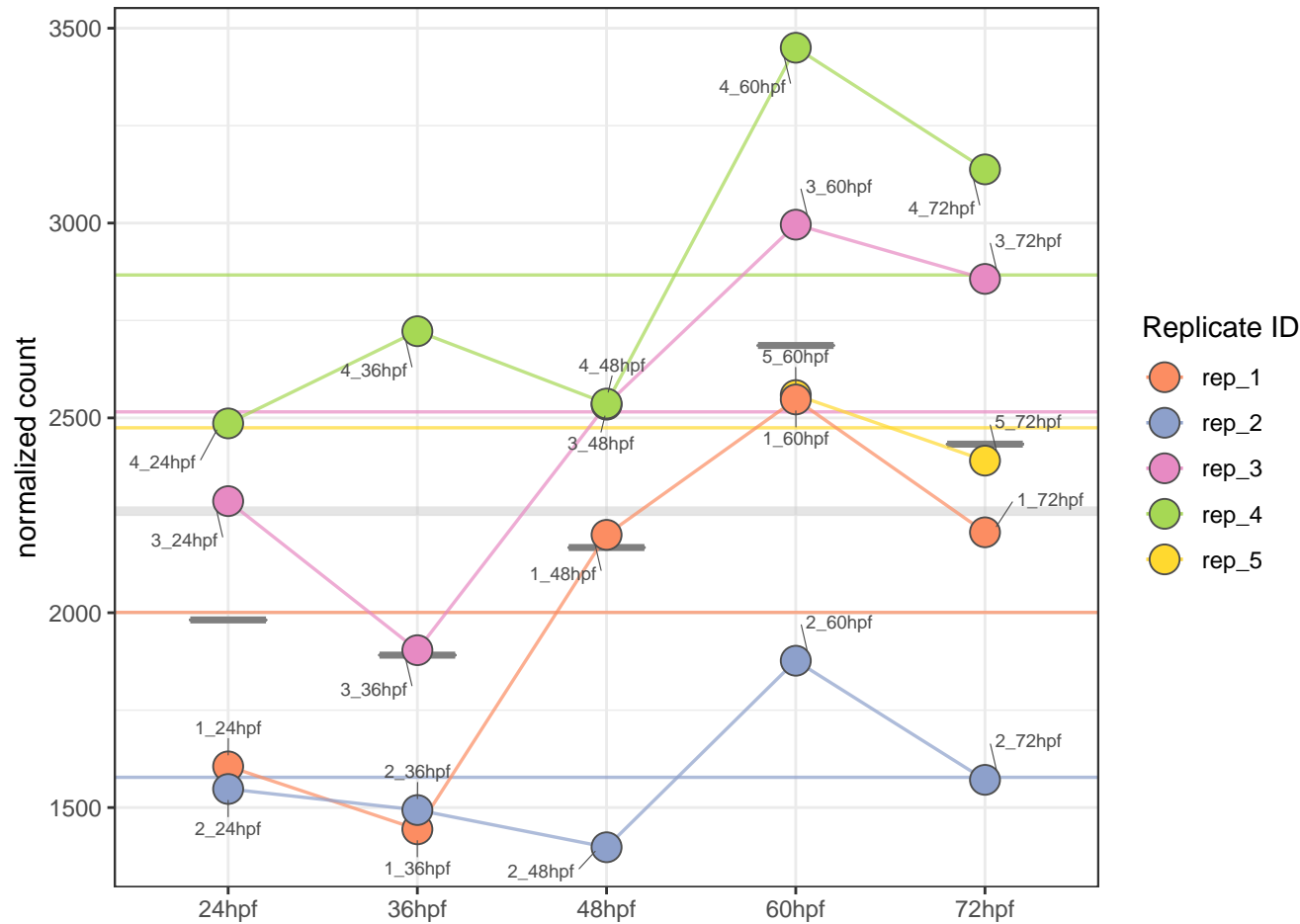Overall mean normalized counts = 269.97

Gene: phactr2, ENSDARG00000027172, chromosome 13, protein_coding
P−value = 1.2e−12
Adjusted p−value = 5.8e−10
Log2 fold−change (rep_5 / rep_1) = 0.12
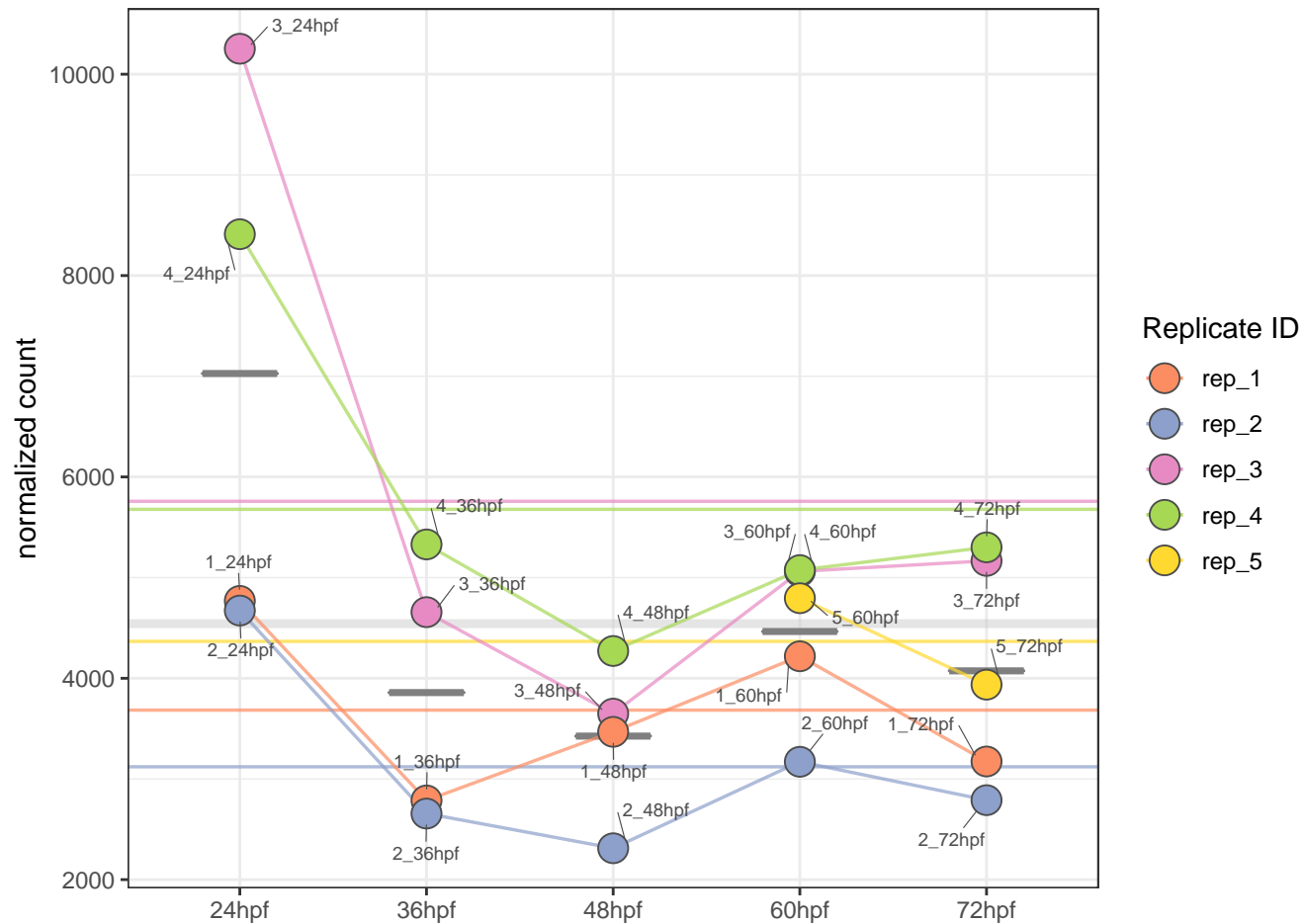Overall mean normalized counts = 2261.50

Gene: mmrn2b, ENSDARG00000073711, chromosome 12, protein_coding
P−value = 1.2e−12
Adjusted p−value = 5.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.30
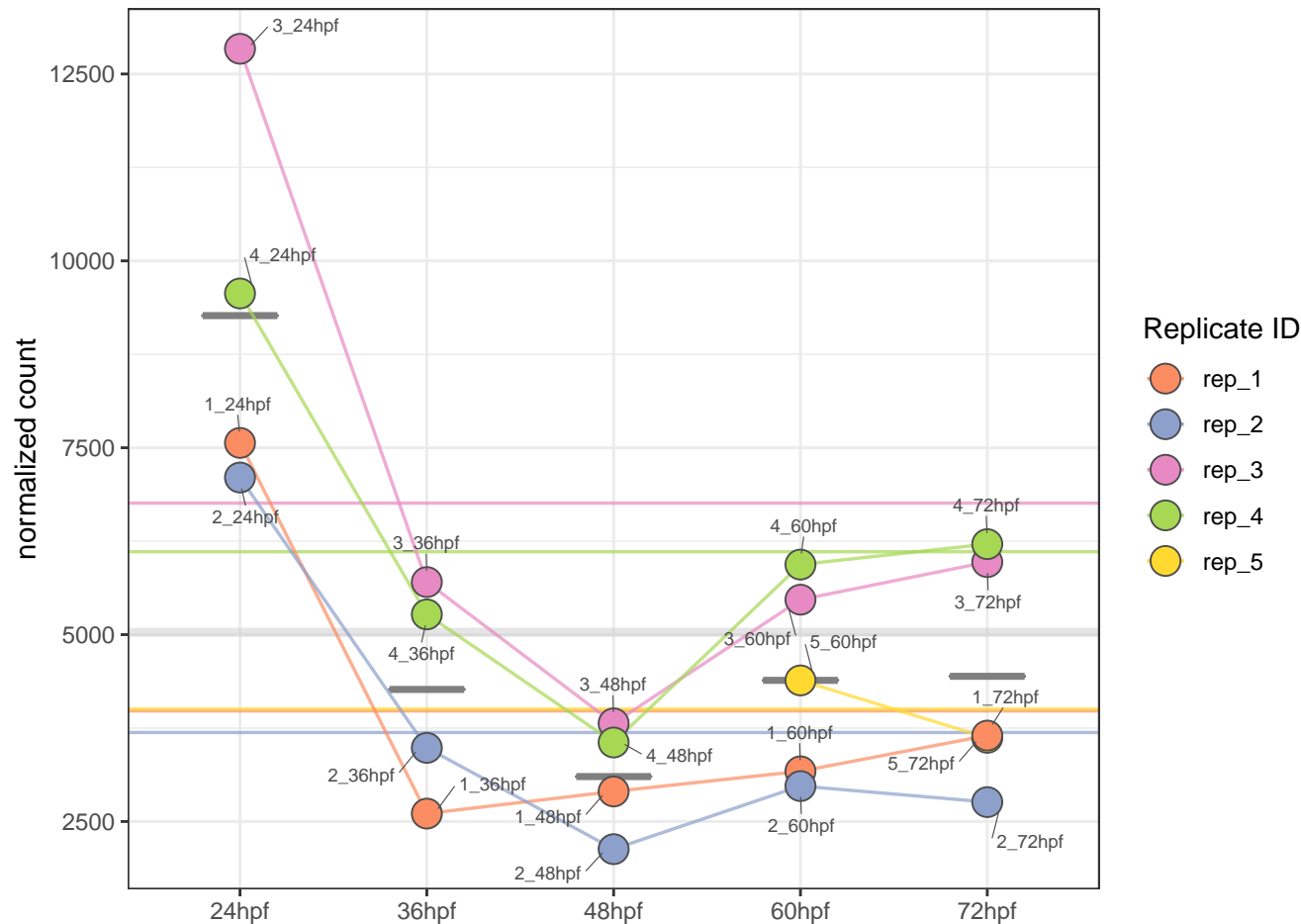Overall mean normalized counts = 4542.42

Gene: tmem38a, ENSDARG00000024047, chromosome 11, protein_coding
P−value = 1.3e−12
Adjusted p−value = 6e−10
Log2 fold−change (rep_5 / rep_1) = 0.21
Overall mean normalized counts = 5031.92

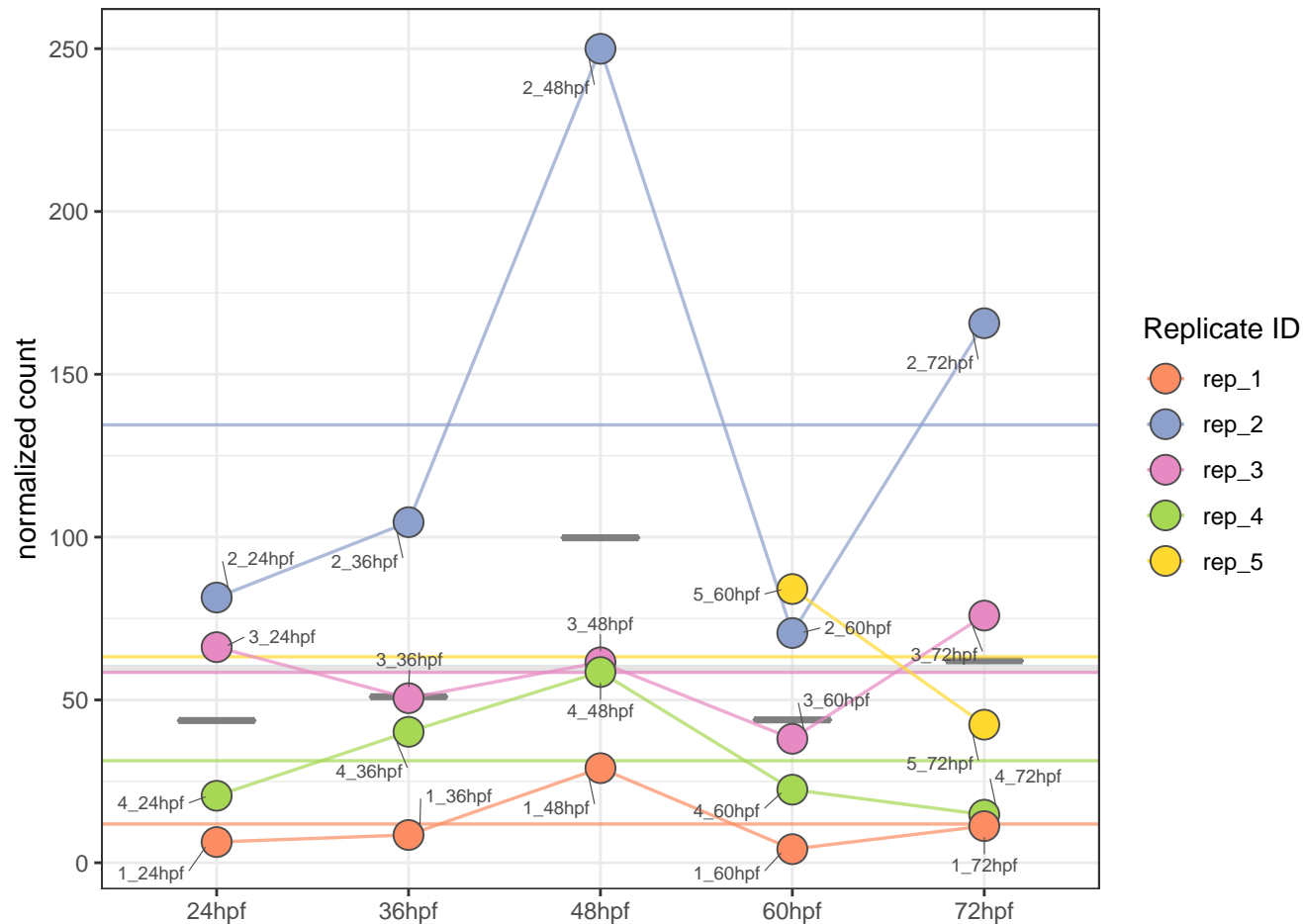Gene: igfn1.2, ENSDARG00000075926, chromosome 6, protein_coding
P−value = 1.3e−12
Adjusted p−value = 6e−10
Log2 fold−change (rep_5 / rep_1) = 2.99
Overall mean normalized counts = 59.42

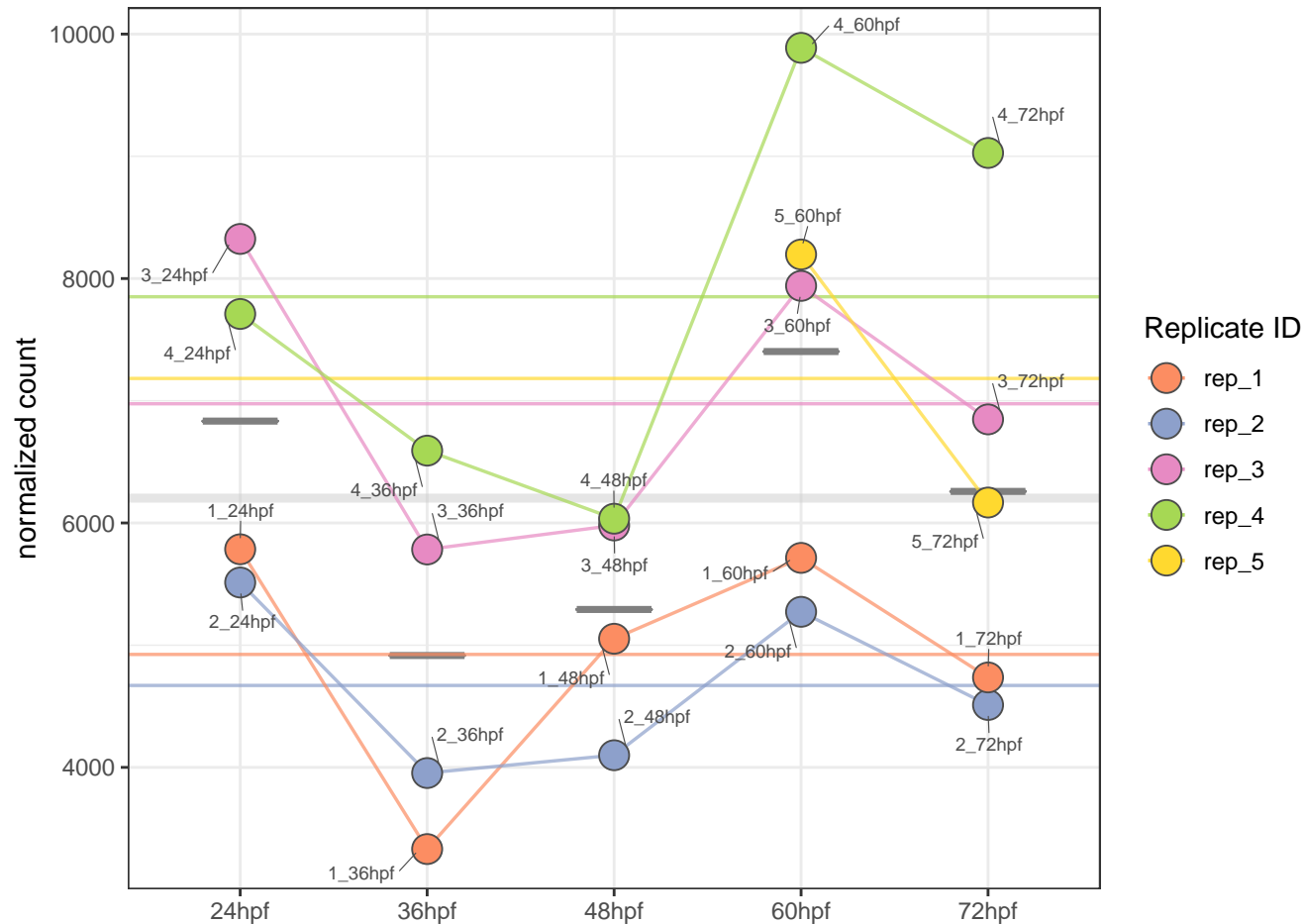Gene: fmnl3, ENSDARG00000004372, chromosome 23, protein_coding
P−value = 1.3e−12
Adjusted p−value = 6.2e−10
Log2 fold−change (rep_5 / rep_1) = 0.41
Overall mean normalized counts = 6203.12
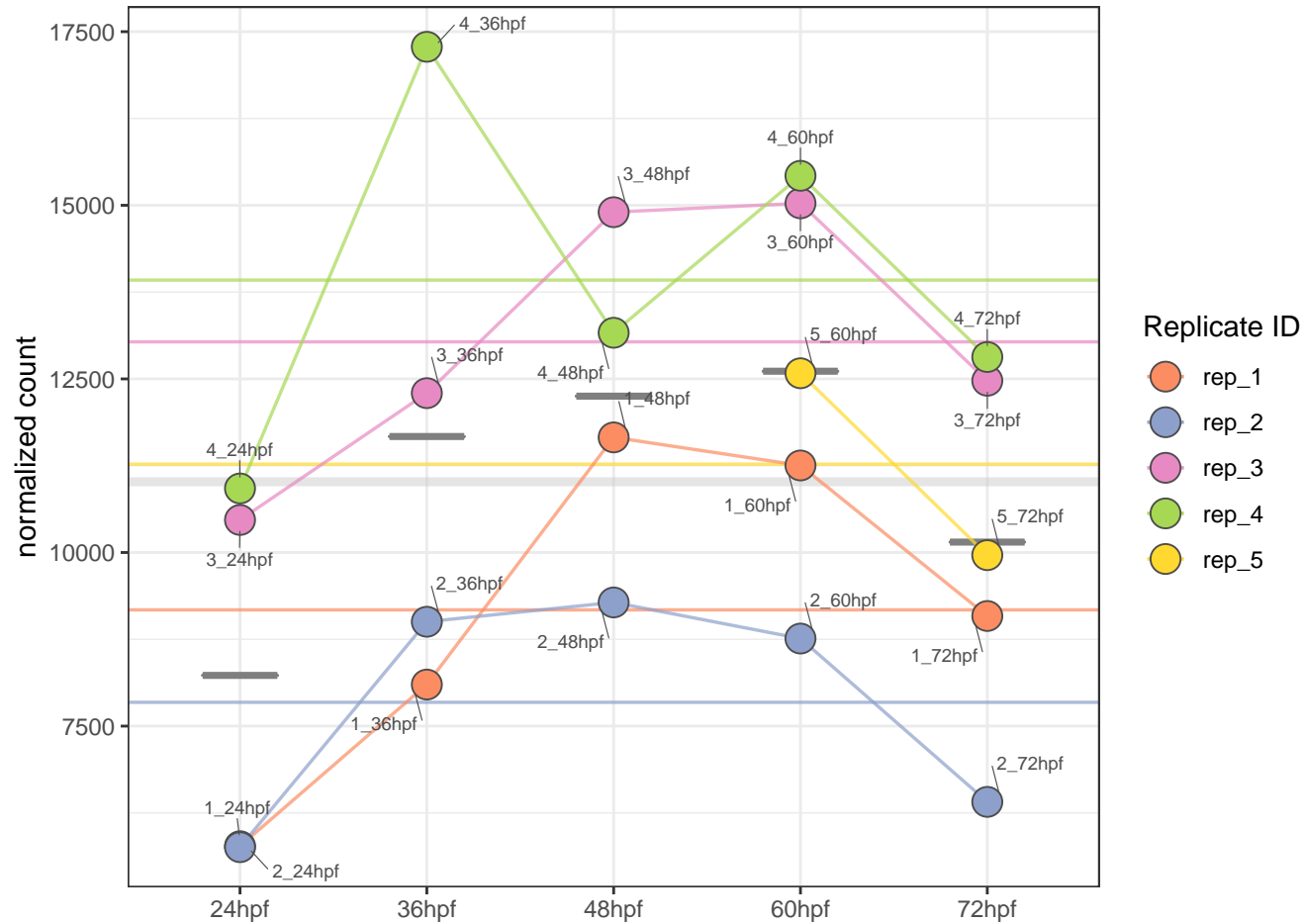
Gene: mgat4a, ENSDARG00000063330, chromosome 9, protein_coding
P−value = 1.4e−12
Adjusted p−value = 6.2e−10
Log2 fold−change (rep_5 / rep_1) = 0.26
Overall mean normalized counts = 11018.62

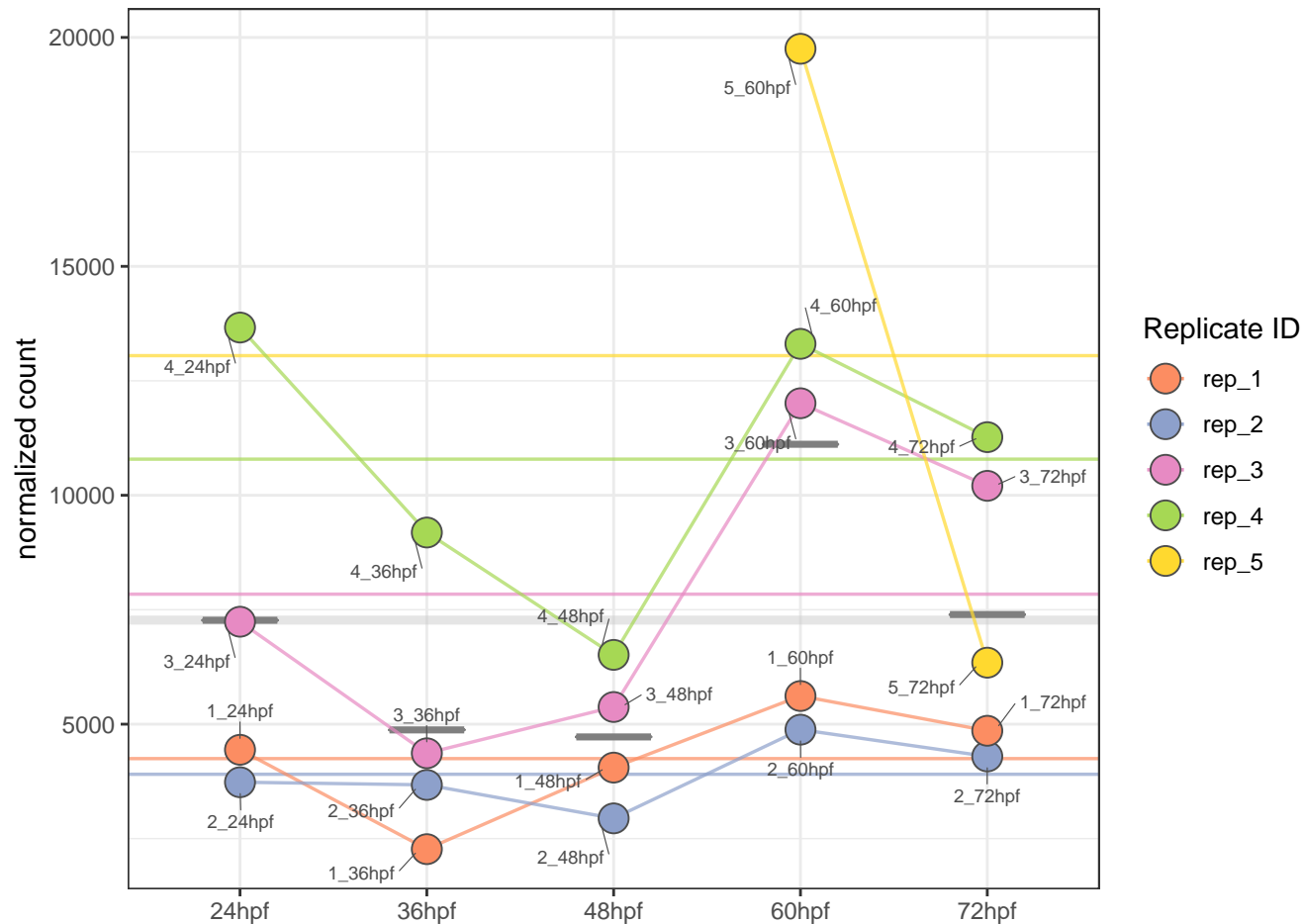Gene: klf2a, ENSDARG00000042667, chromosome 22, protein_coding
P−value = 1.4e−12
Adjusted p−value = 6.2e−10
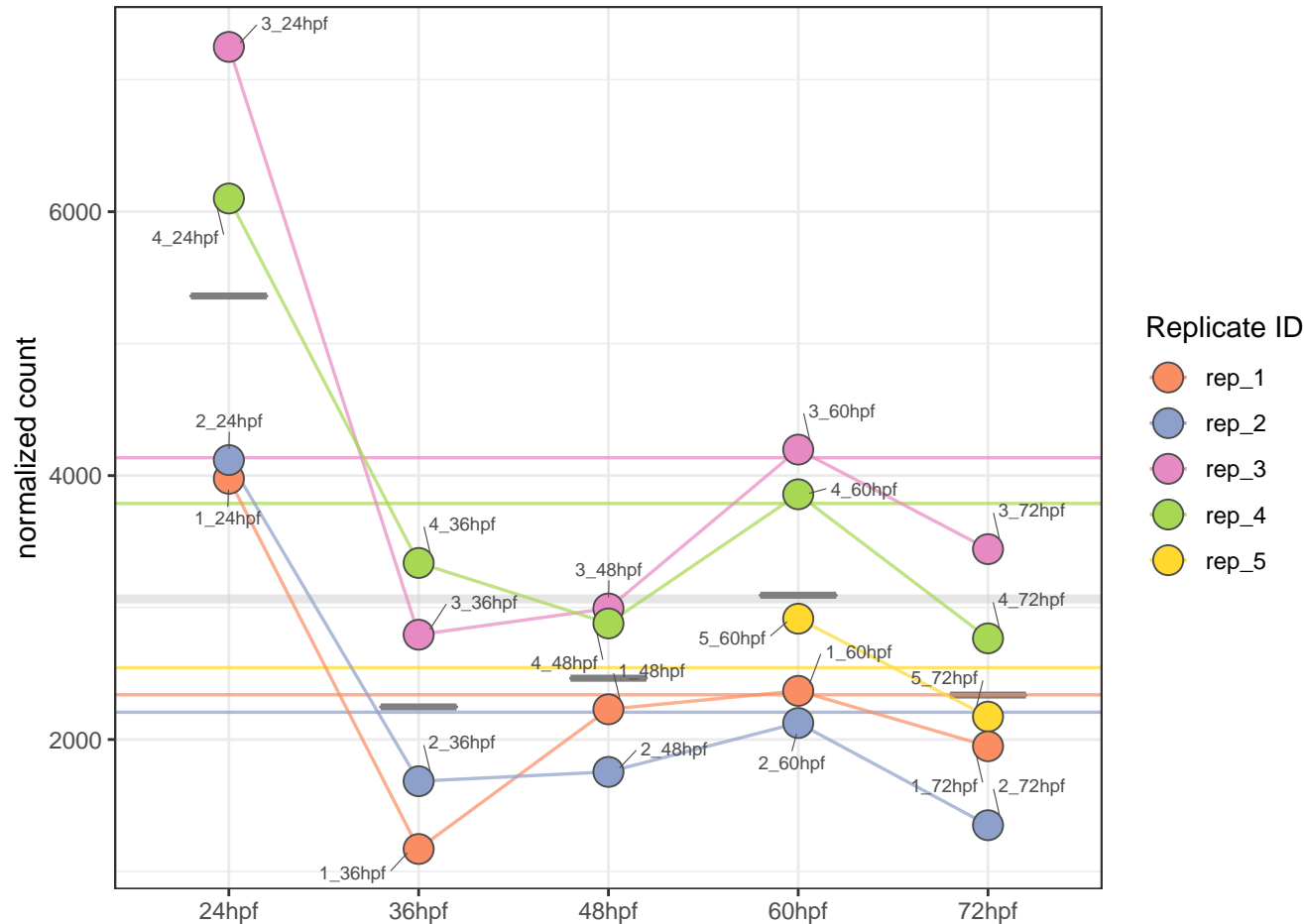Log2 fold−change (rep_5 / rep_1) = 1.19
Overall mean normalized counts = 7273.06

Gene: klhl40a, ENSDARG00000039052, chromosome 2, protein_coding
P−value = 1.4e−12
Adjusted p−value = 6.4e−10
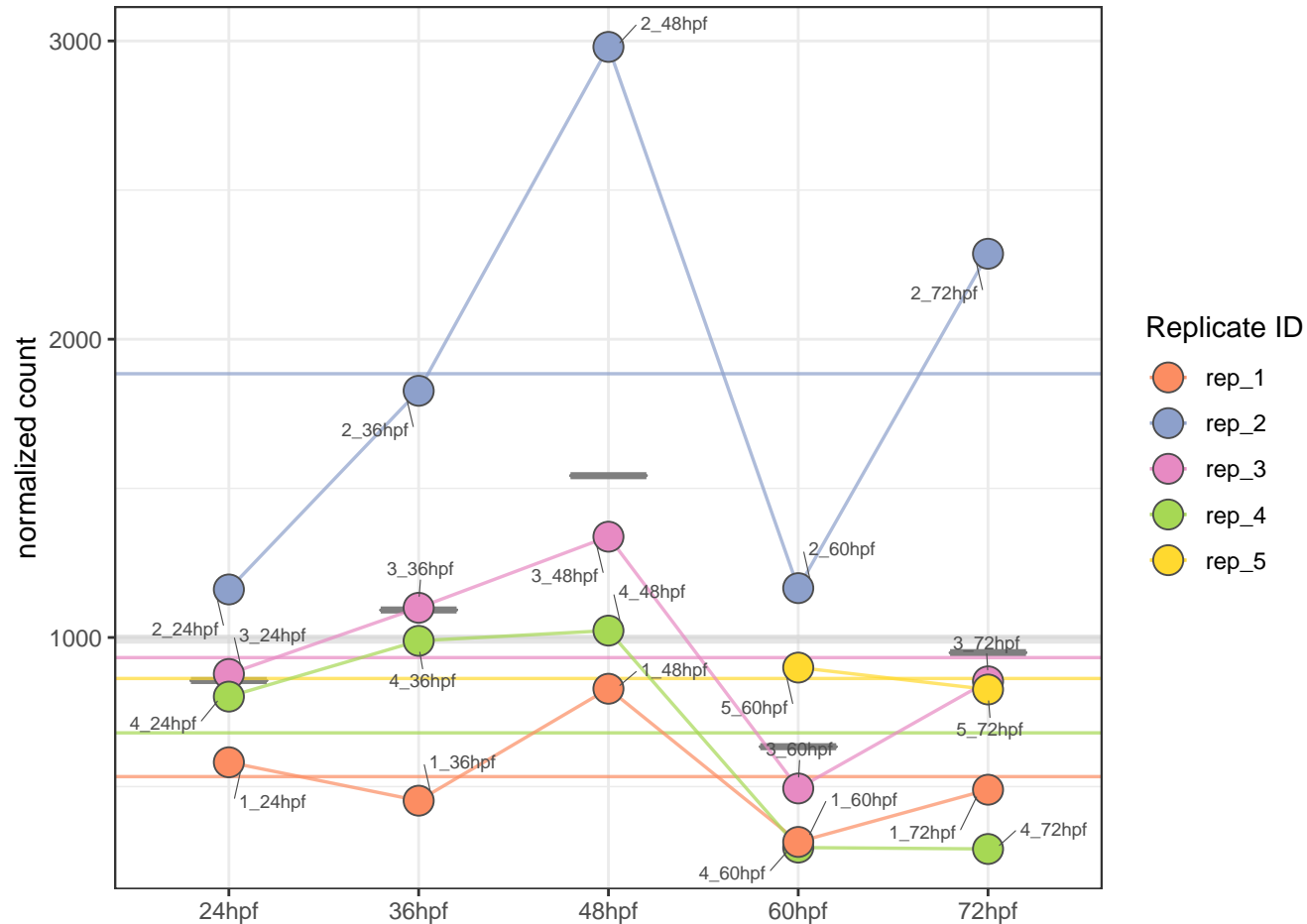Log2 fold−change (rep_5 / rep_1) = 0.31
Overall mean normalized counts = 3065.47

Gene: BX640512.1, ENSDARG00000093326, chromosome 5, processed_transcript
P−value = 1.5e−12
Adjusted p−value = 6.4e−10
Log2 fold−change (rep_5 / rep_1) = 1.25
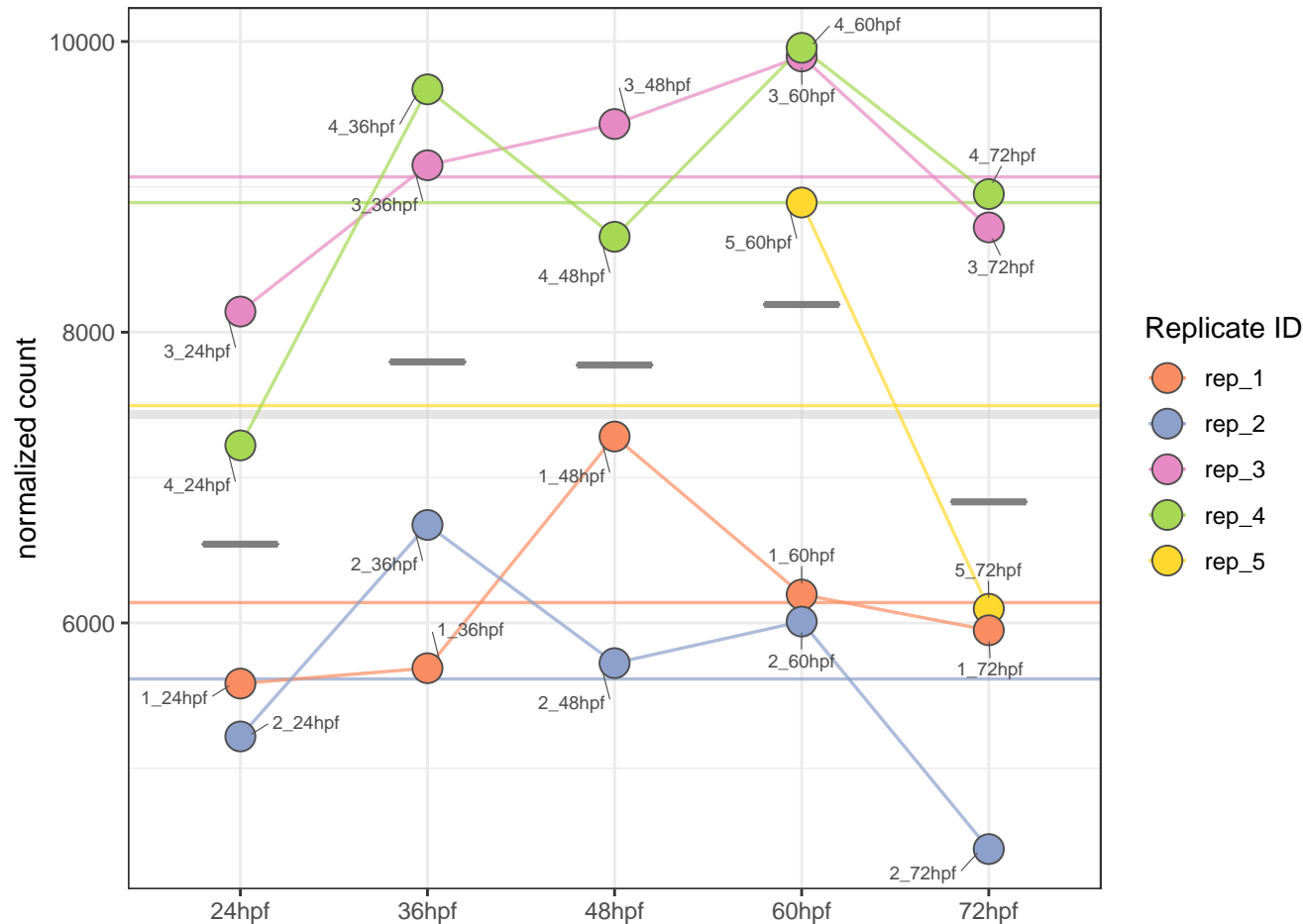Overall mean normalized counts = 994.38

Gene: capn1a, ENSDARG00000052702, chromosome 13, protein_coding
P−value = 1.7e−12
Adjusted p−value = 7.3e−10
Log2 fold−change (rep_5 / rep_1) = 0.26
Overall mean normalized counts = 7434.81

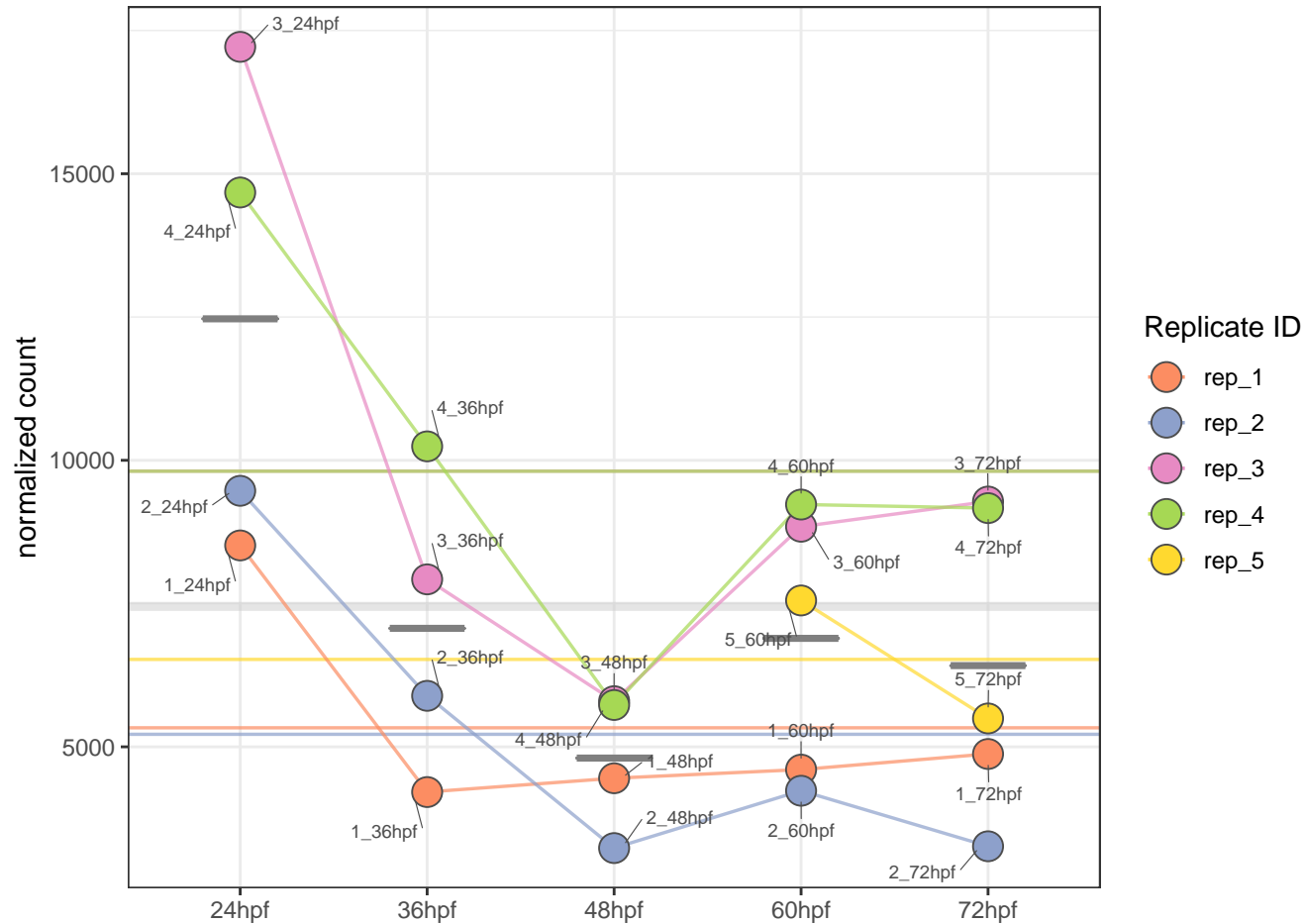Gene: smad6a, ENSDARG00000053209, chromosome 7, protein_coding
P−value = 1.8e−12
Adjusted p−value = 7.6e−10
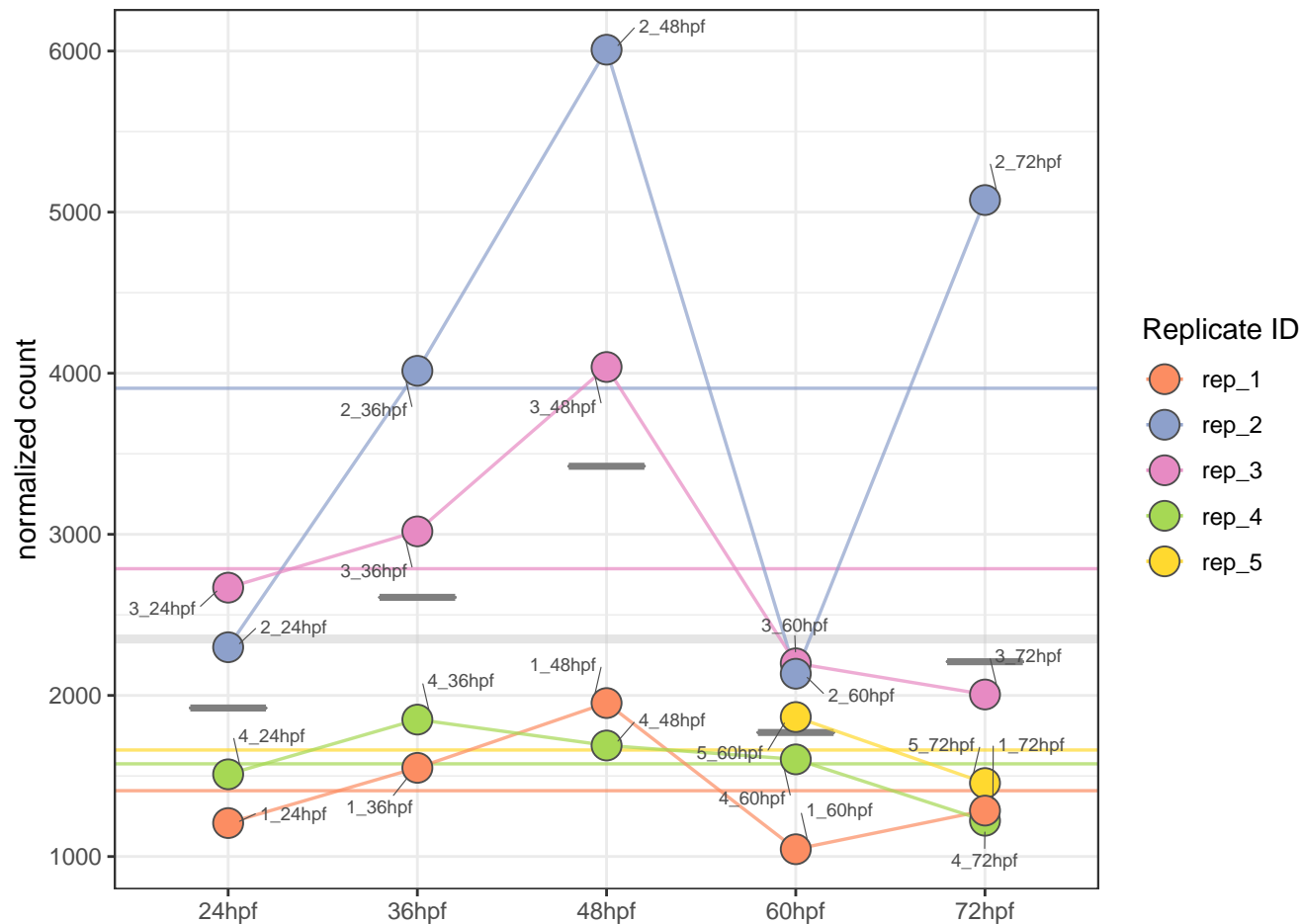Log2 fold−change (rep_5 / rep_1) = 0.45
Overall mean normalized counts = 7450.29

Gene: CT573234.1, ENSDARG00000114332, chromosome 4, protein_coding
P−value = 1.8e−12
Adjusted p−value = 7.6e−10
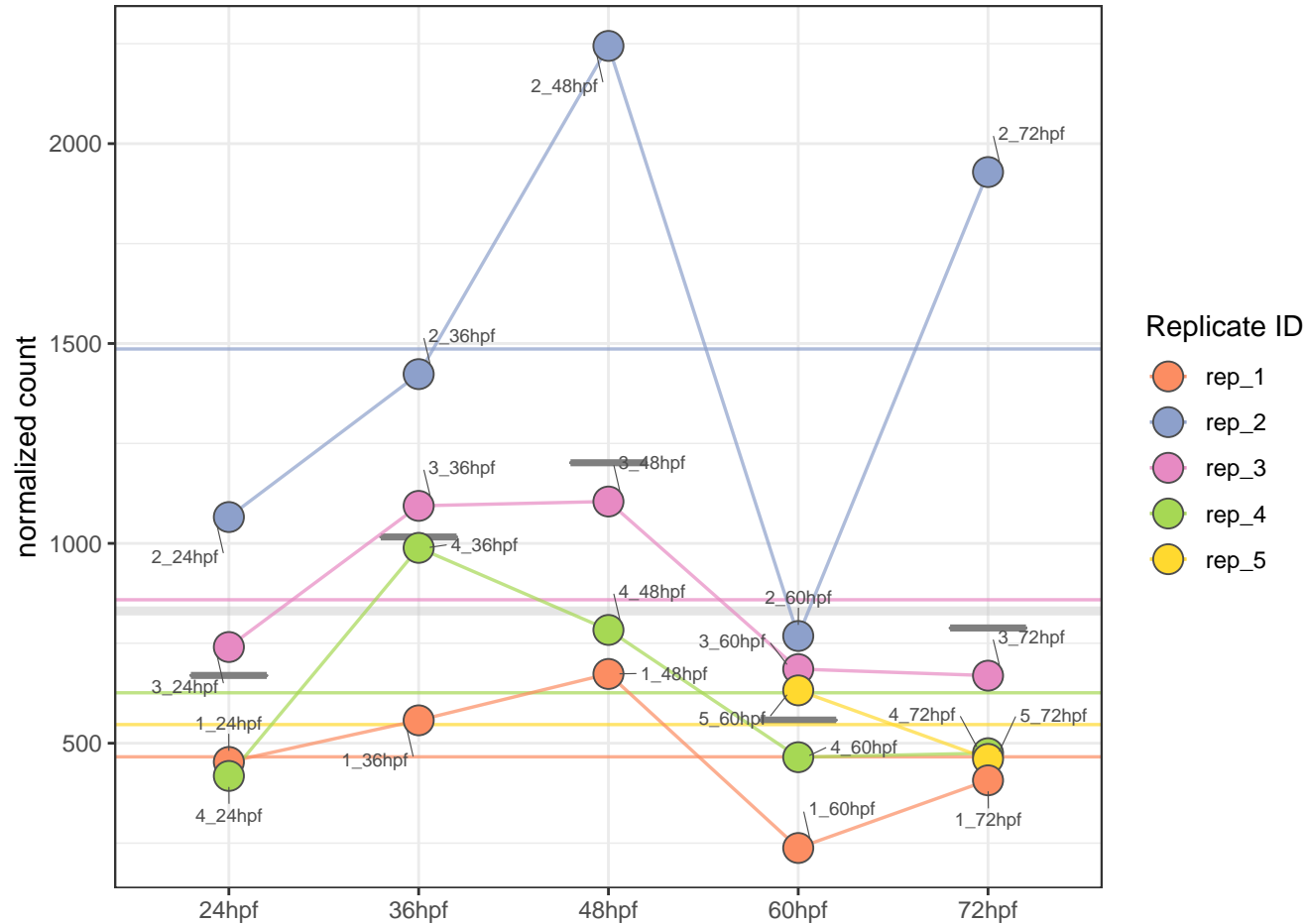Log2 fold−change (rep_5 / rep_1) = 0.49
Overall mean normalized counts = 2350.37

Gene: BX649434.3, ENSDARG00000105157, chromosome 3, protein_coding
P−value = 1.8e−12
Adjusted p−value = 7.6e−10
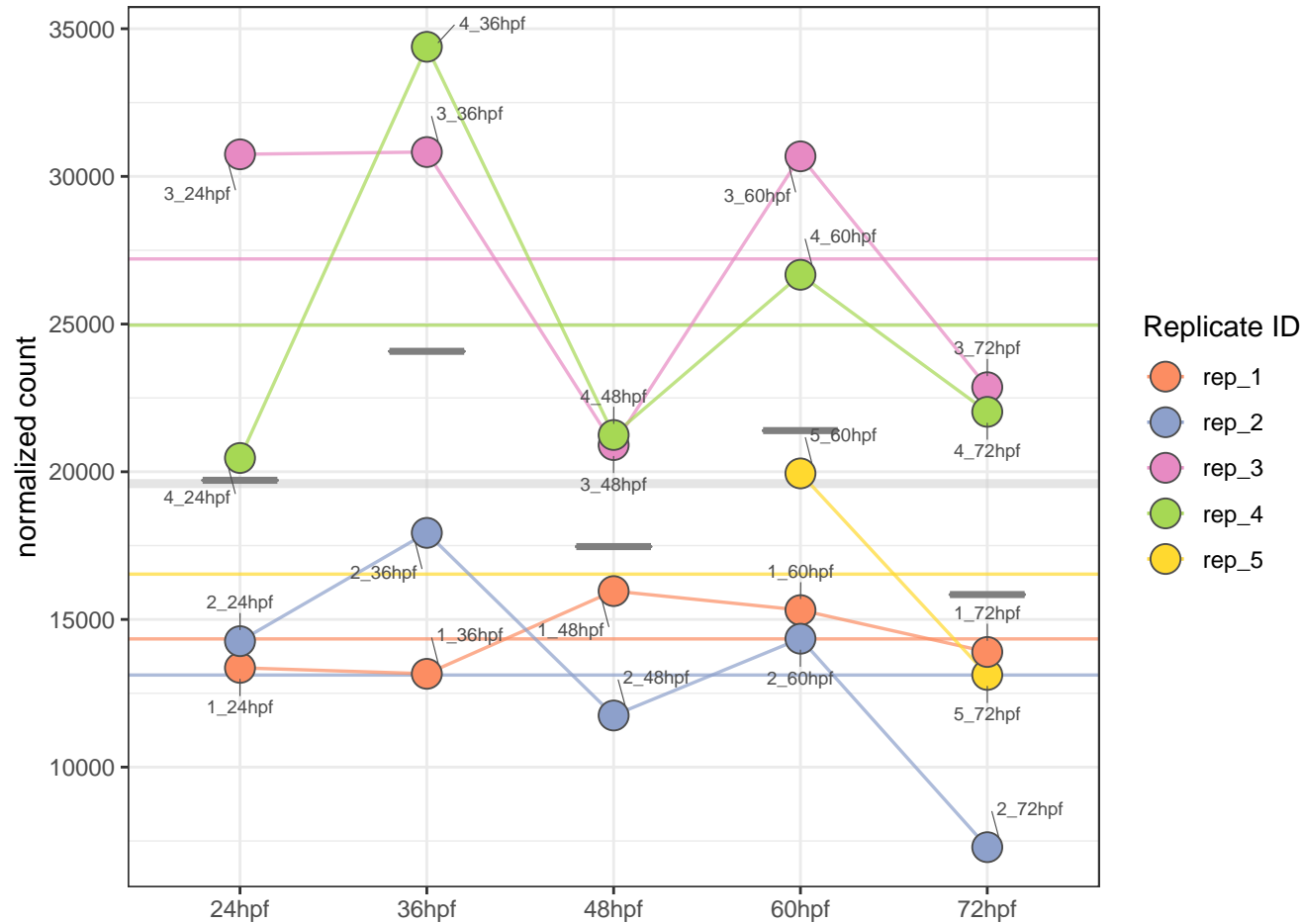Log2 fold−change (rep_5 / rep_1) = 0.64
Overall mean normalized counts = 830.91

Gene: plcd1a, ENSDARG00000059123, chromosome 24, protein_coding
P−value = 1.8e−12
Adjusted p−value = 7.6e−10
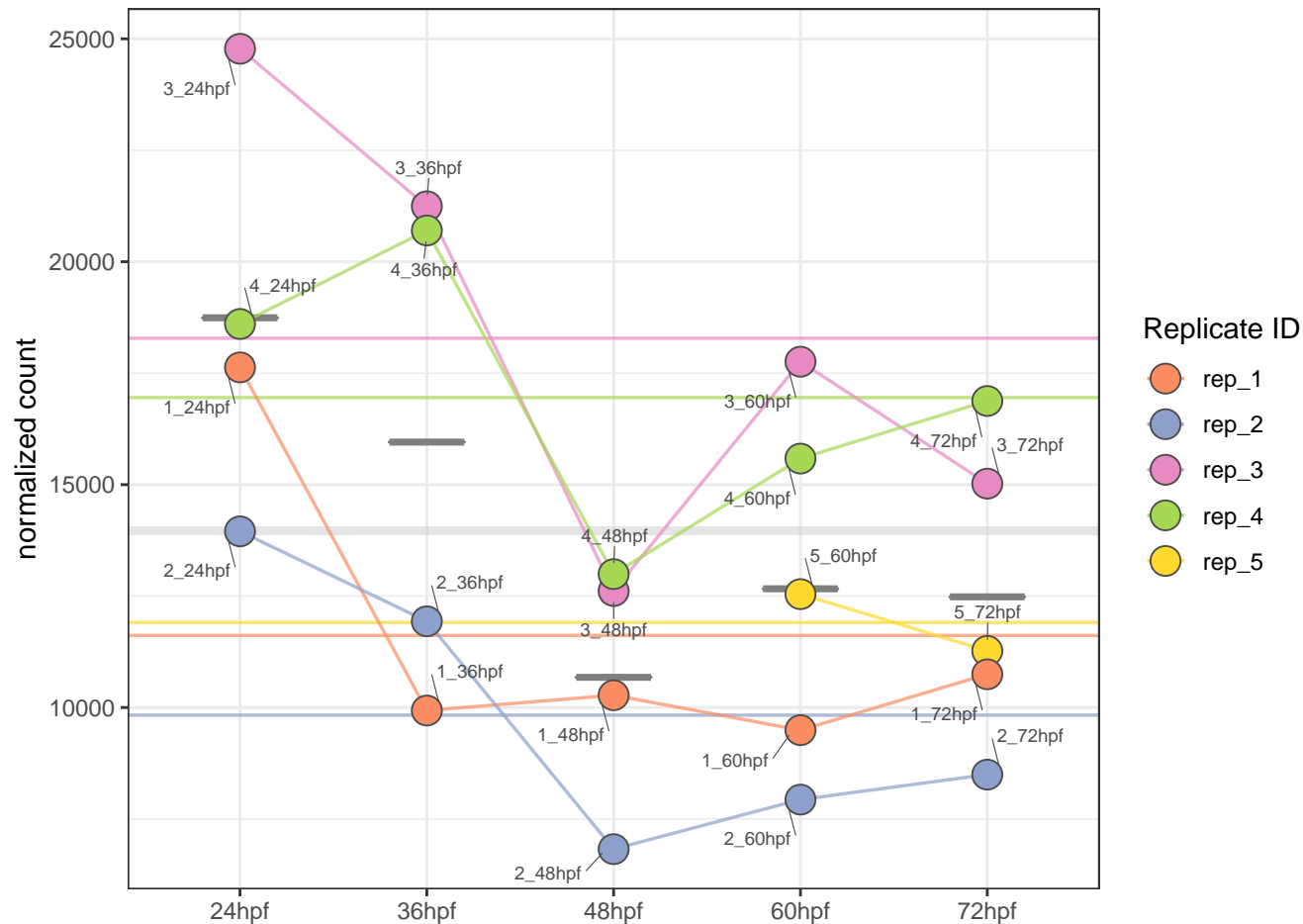Log2 fold−change (rep_5 / rep_1) = 0.23
Overall mean normalized counts = 19599.96

Gene: tuba8l2, ENSDARG00000031164, chromosome 1, protein_coding
P−value = 1.9e−12
Adjusted p−value = 7.9e−10
Log2 fold−change (rep_5 / rep_1) = 0.20
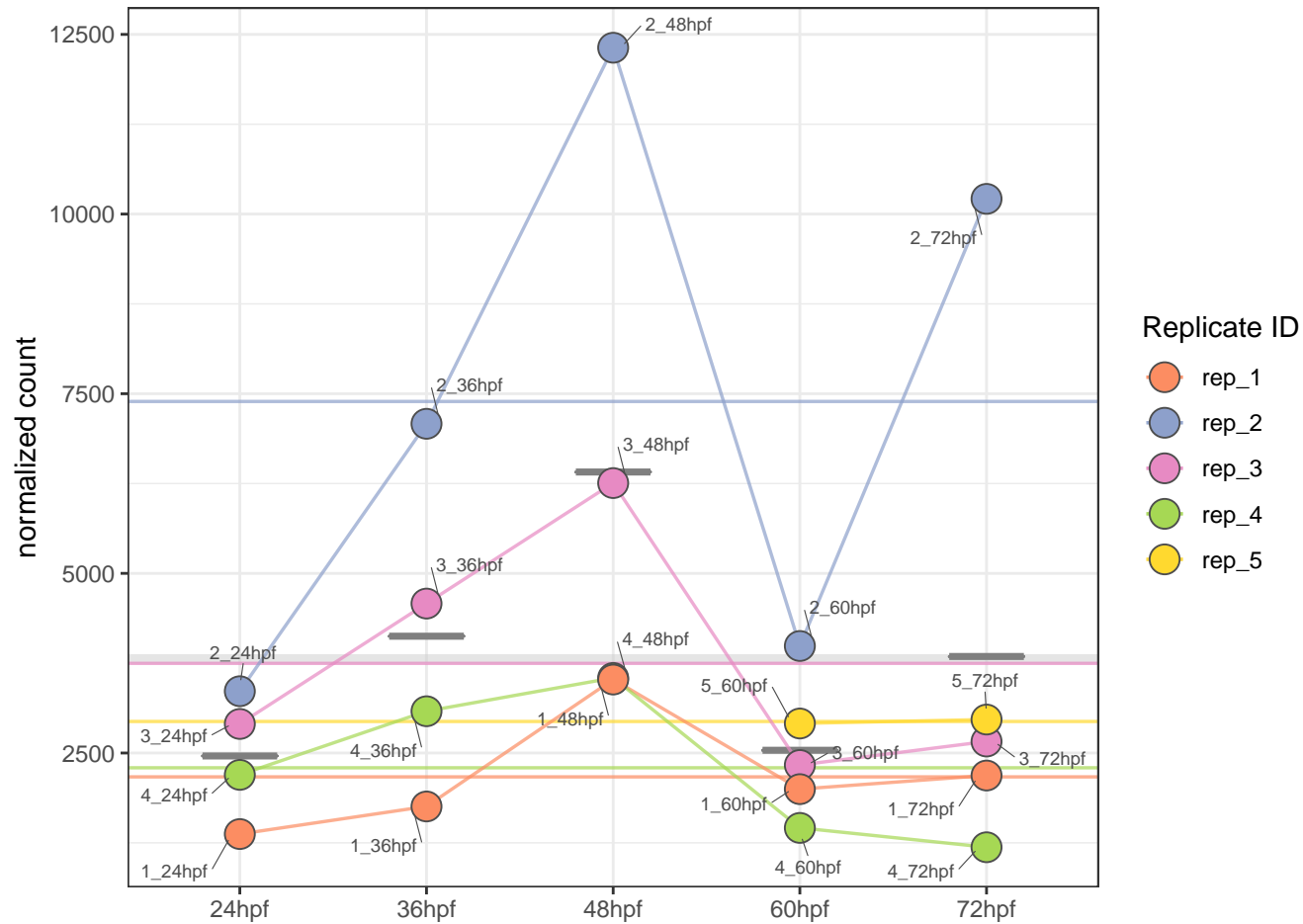Overall mean normalized counts = 13965.11

Gene: kcnq2b, ENSDARG00000091130, chromosome 6, protein_coding
P−value = 2e−12
Adjusted p−value = 8e−10
Log2 fold−change (rep_5 / rep_1) = 0.77
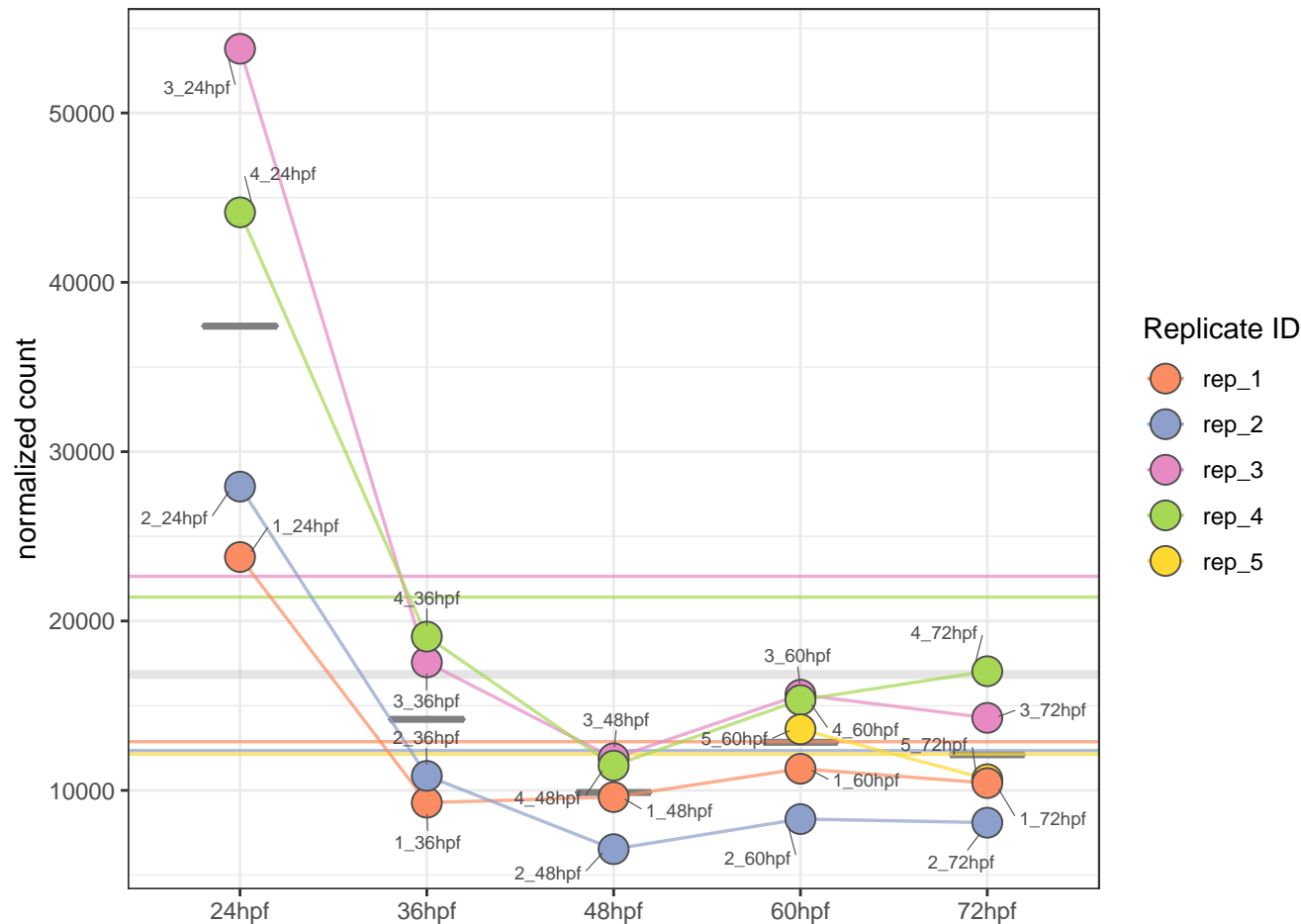Overall mean normalized counts = 3812.95

Gene: kdrl, ENSDARG00000105215, chromosome 14, protein_coding
P−value = 2.3e−12
Adjusted p−value = 9.1e−10
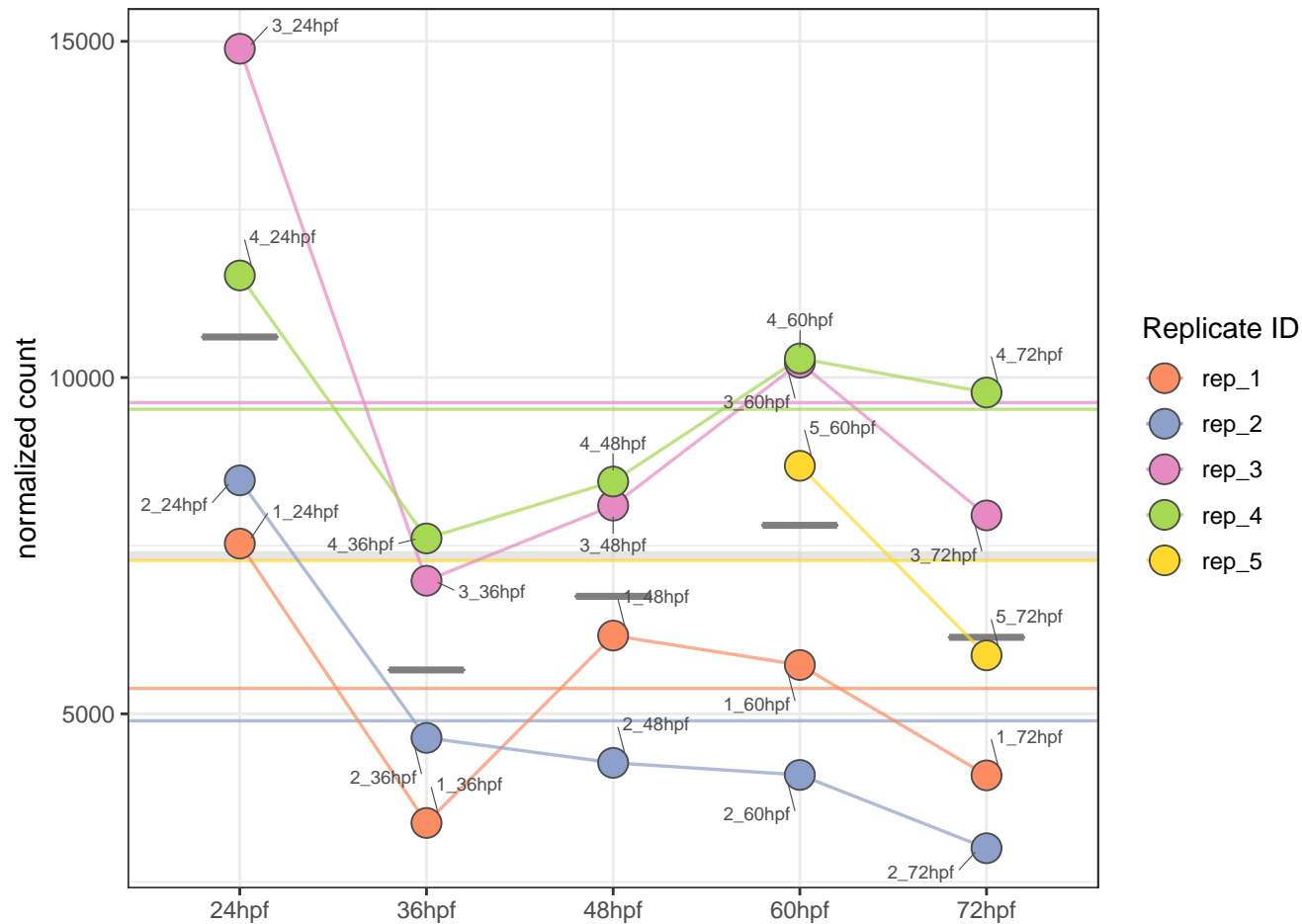Log2 fold−change (rep_5 / rep_1) = 0.27
Overall mean normalized counts = 16847.46

Gene: tmem88a, ENSDARG00000056920, chromosome 10, protein_coding
P−value = 2.5e−12
Adjusted p−value = 9.9e−10
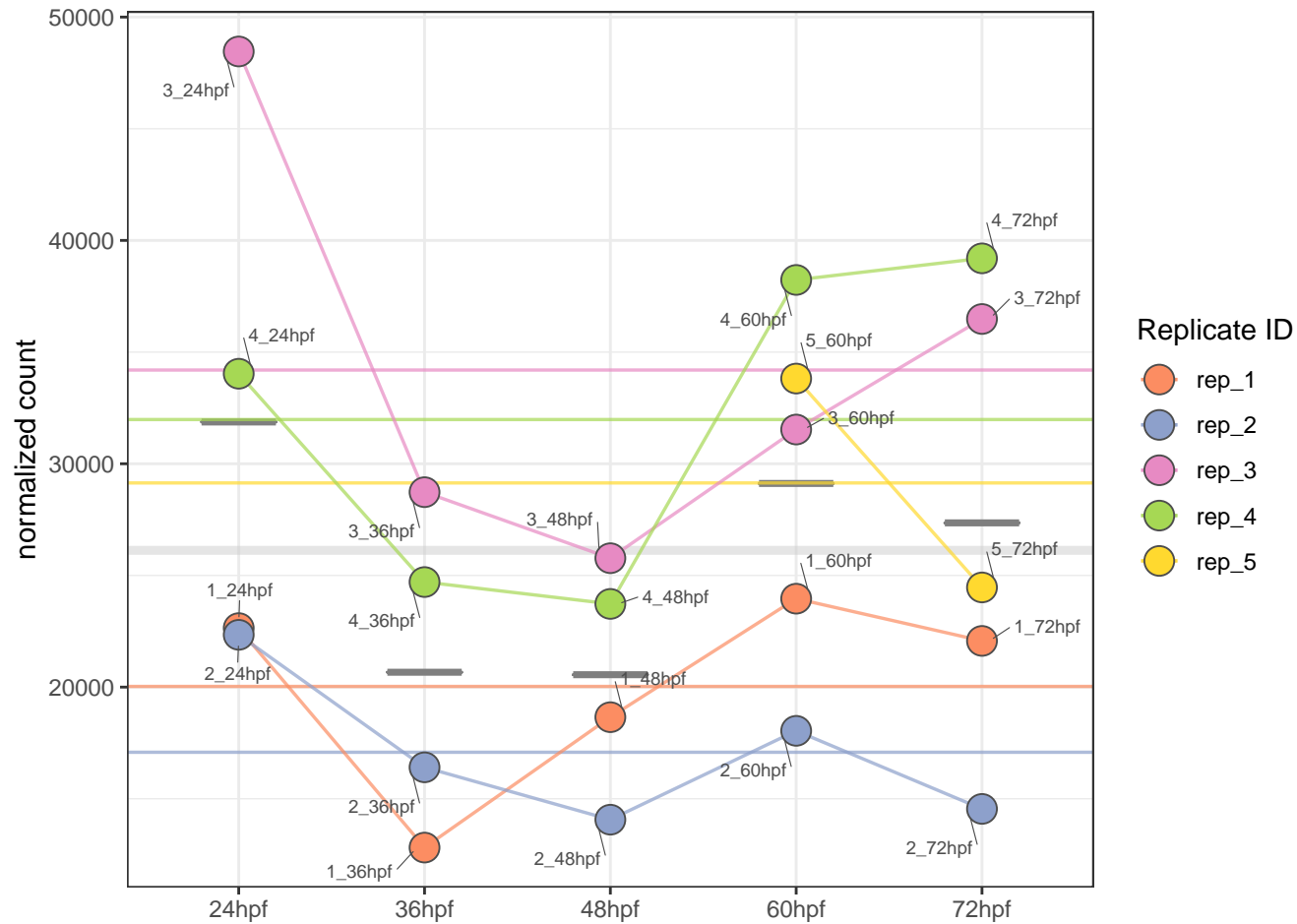Log2 fold−change (rep_5 / rep_1) = 0.57
Overall mean normalized counts = 7350.79

Gene: casq2, ENSDARG00000008982, chromosome 9, protein_coding
P−value = 2.6e−12
Adjusted p−value = 1e−09
Log2 fold−change (rep_5 / rep_1) = 0.43
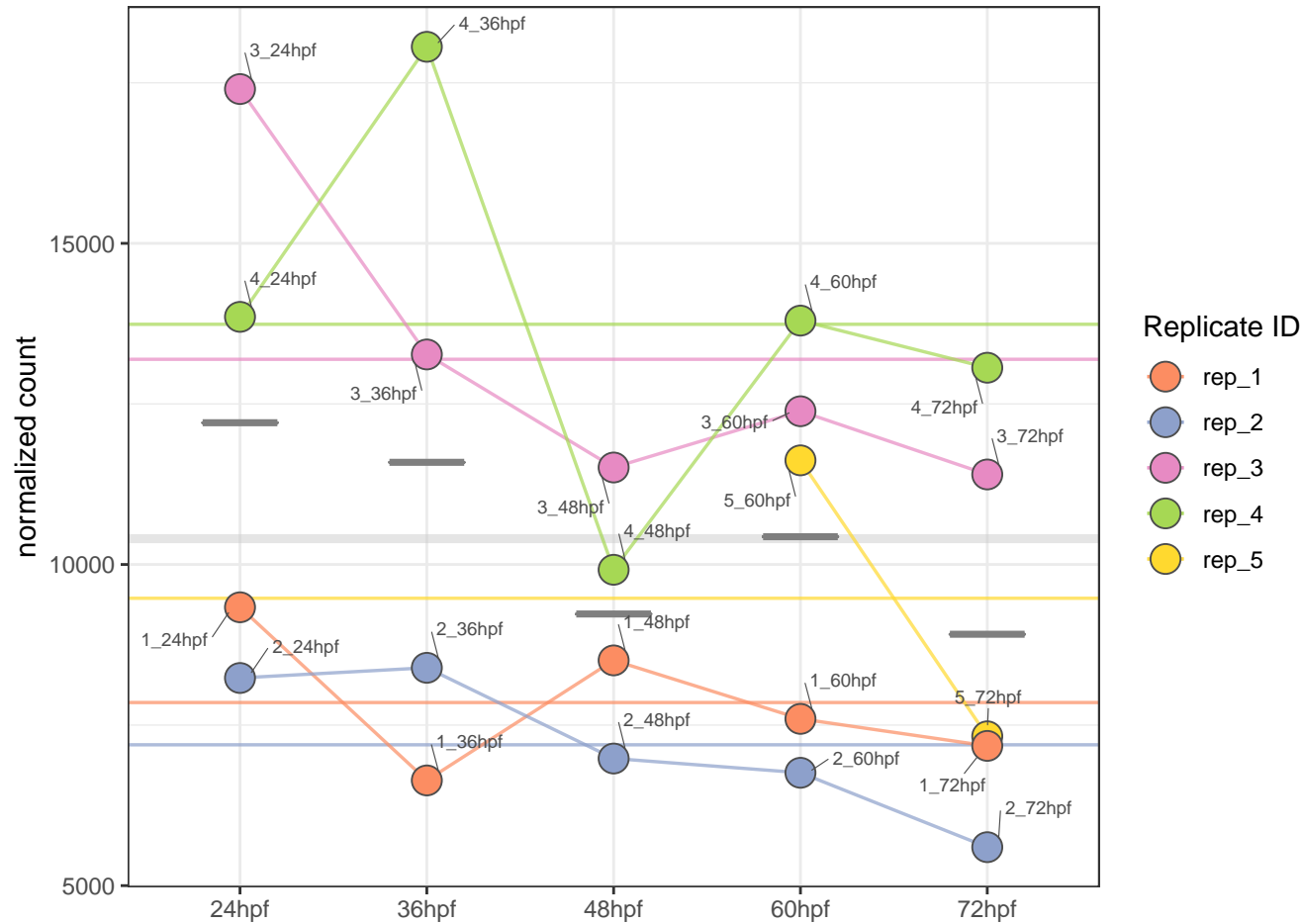Overall mean normalized counts = 26124.09

Gene: mylk2, ENSDARG00000031698, chromosome 23, protein_coding
P−value = 2.7e−12
Adjusted p−value = 1e−09
Log2 fold−change (rep_5 / rep_1) = 0.36
Overall mean normalized counts = 10401.83

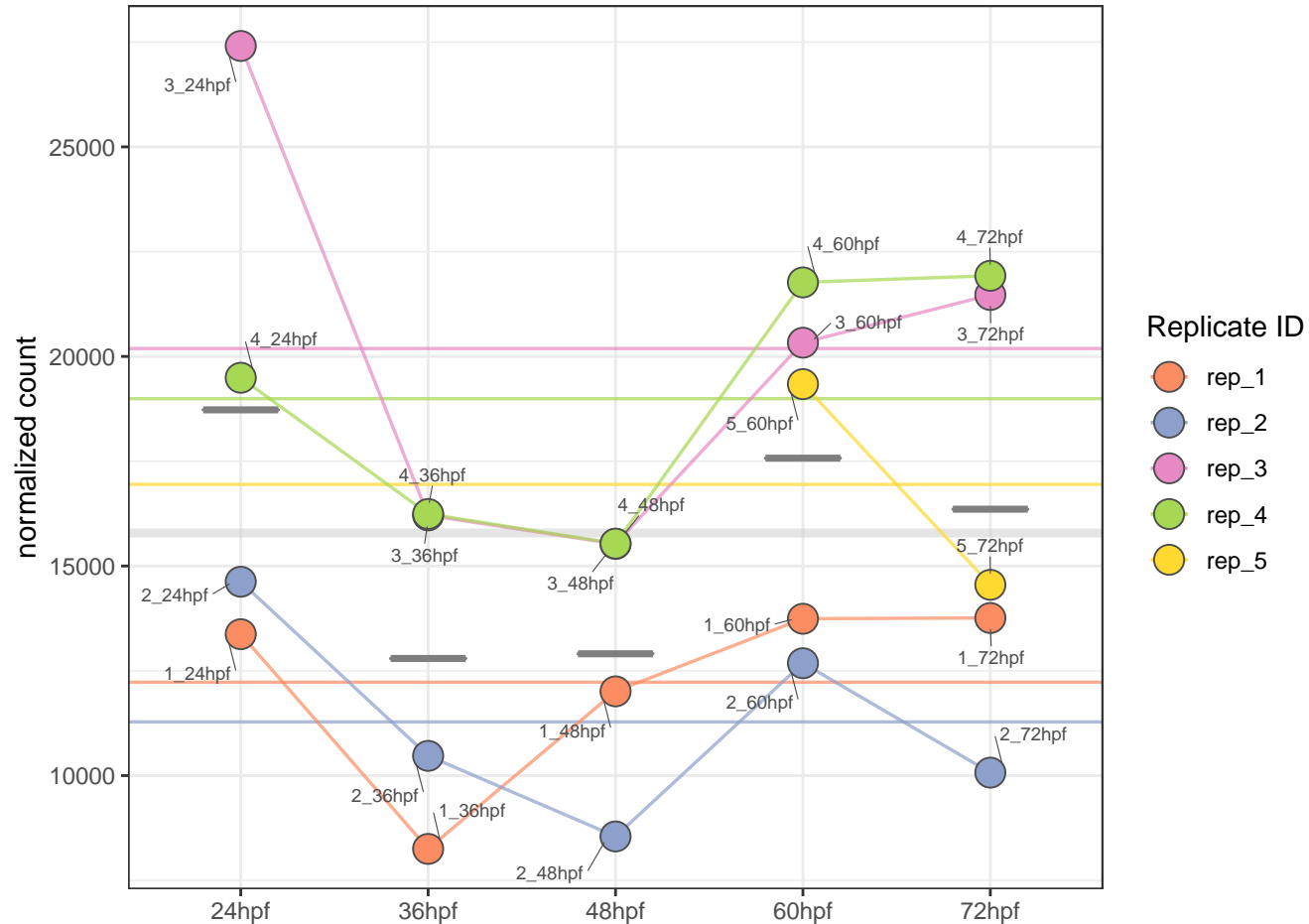Gene: si:ch211−156j16.1, ENSDARG00000092035, chromosome 8, protein_coding
P−value = 2.8e−12
Adjusted p−value = 1.1e−09
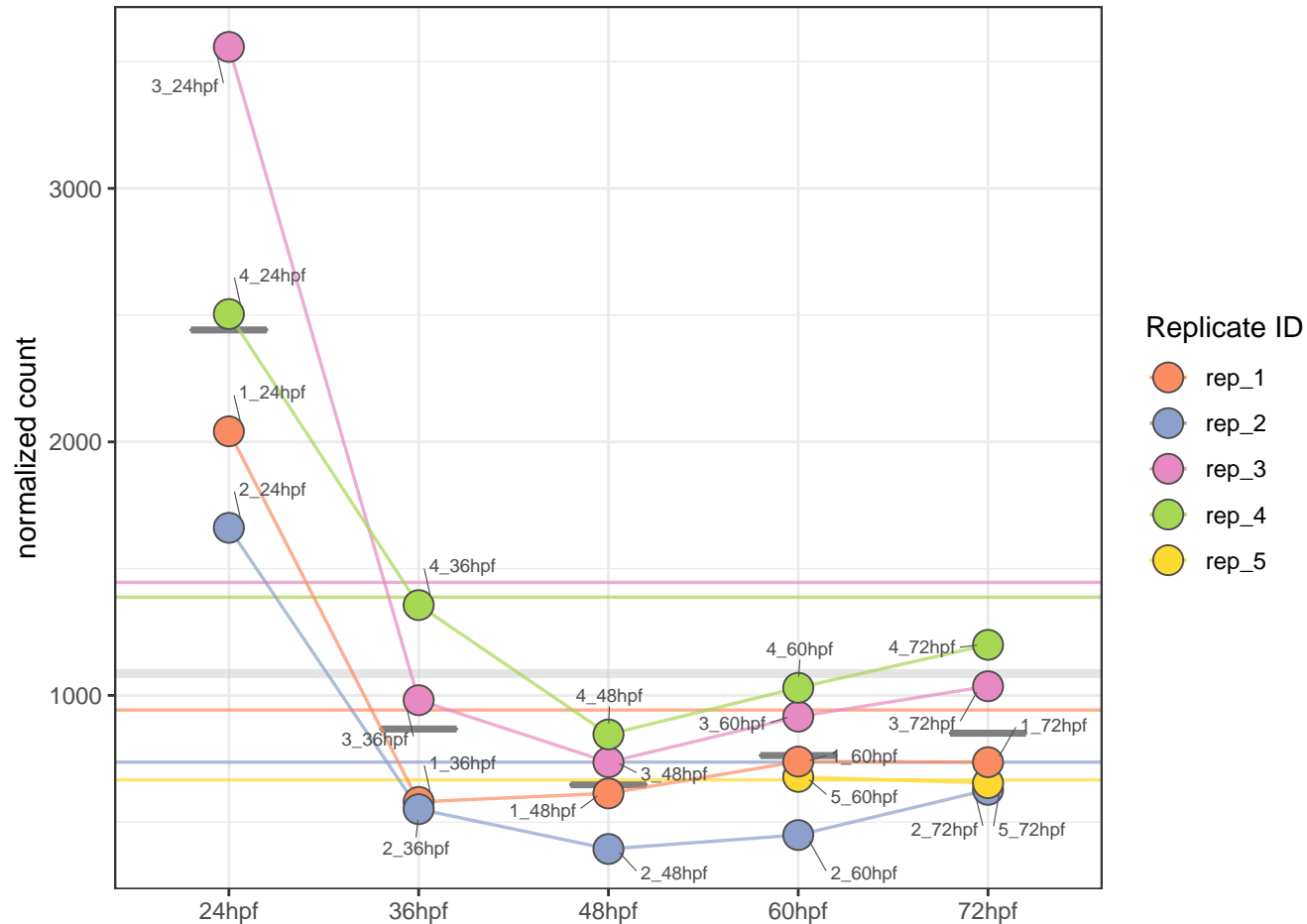Log2 fold−change (rep_5 / rep_1) = 0.35
Overall mean normalized counts = 15788.40

Gene: tbx5b, ENSDARG00000092060, chromosome 5, protein_coding
P−value = 2.9e−12
Adjusted p−value = 1.1e−09
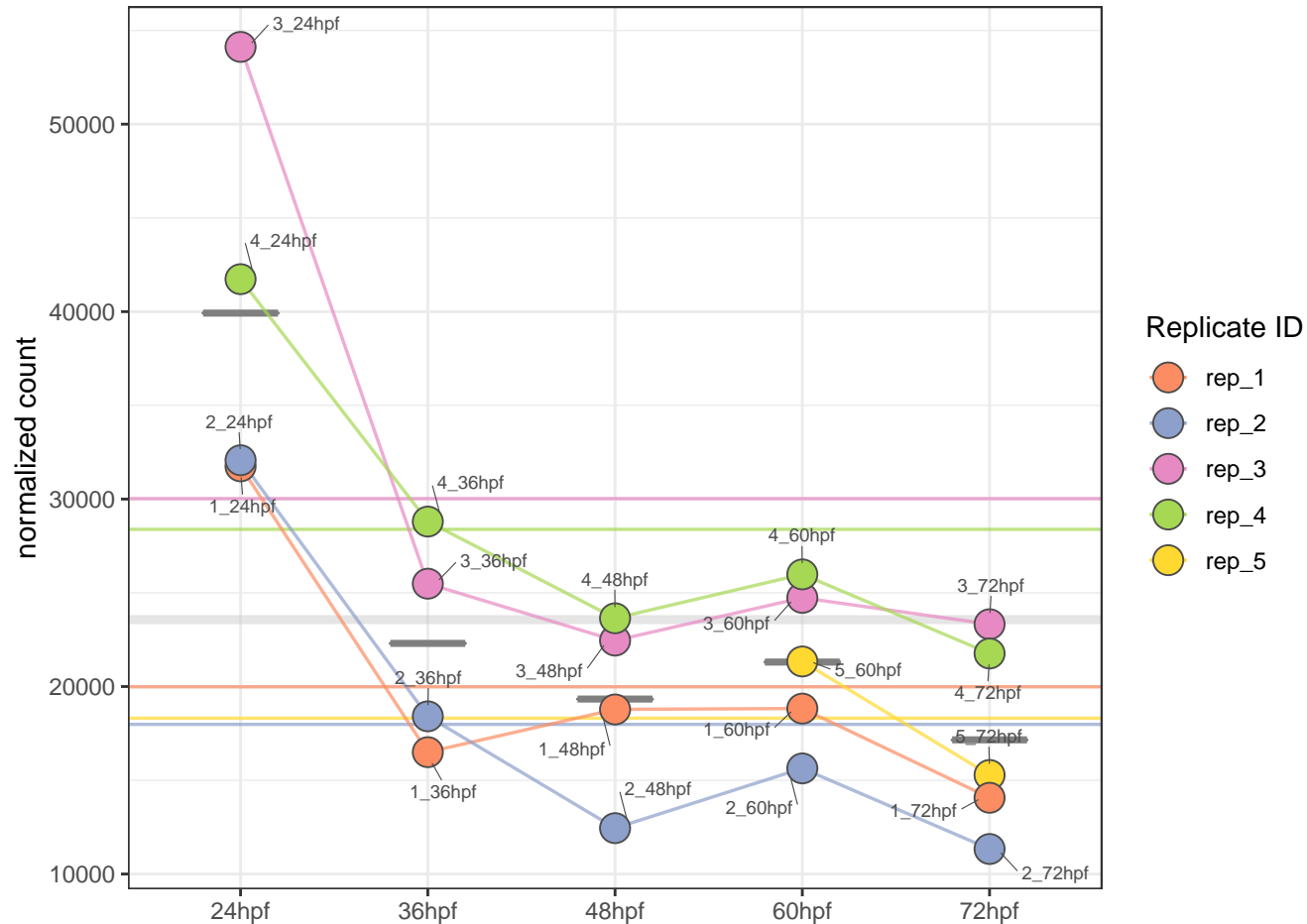Log2 fold−change (rep_5 / rep_1) = −0.08
Overall mean normalized counts = 1086.17

Gene: bcam, ENSDARG00000090190, chromosome 16, protein_coding
P−value = 2.9e−12
Adjusted p−value = 1.1e−09
Log2 fold−change (rep_5 / rep_1) = 0.16
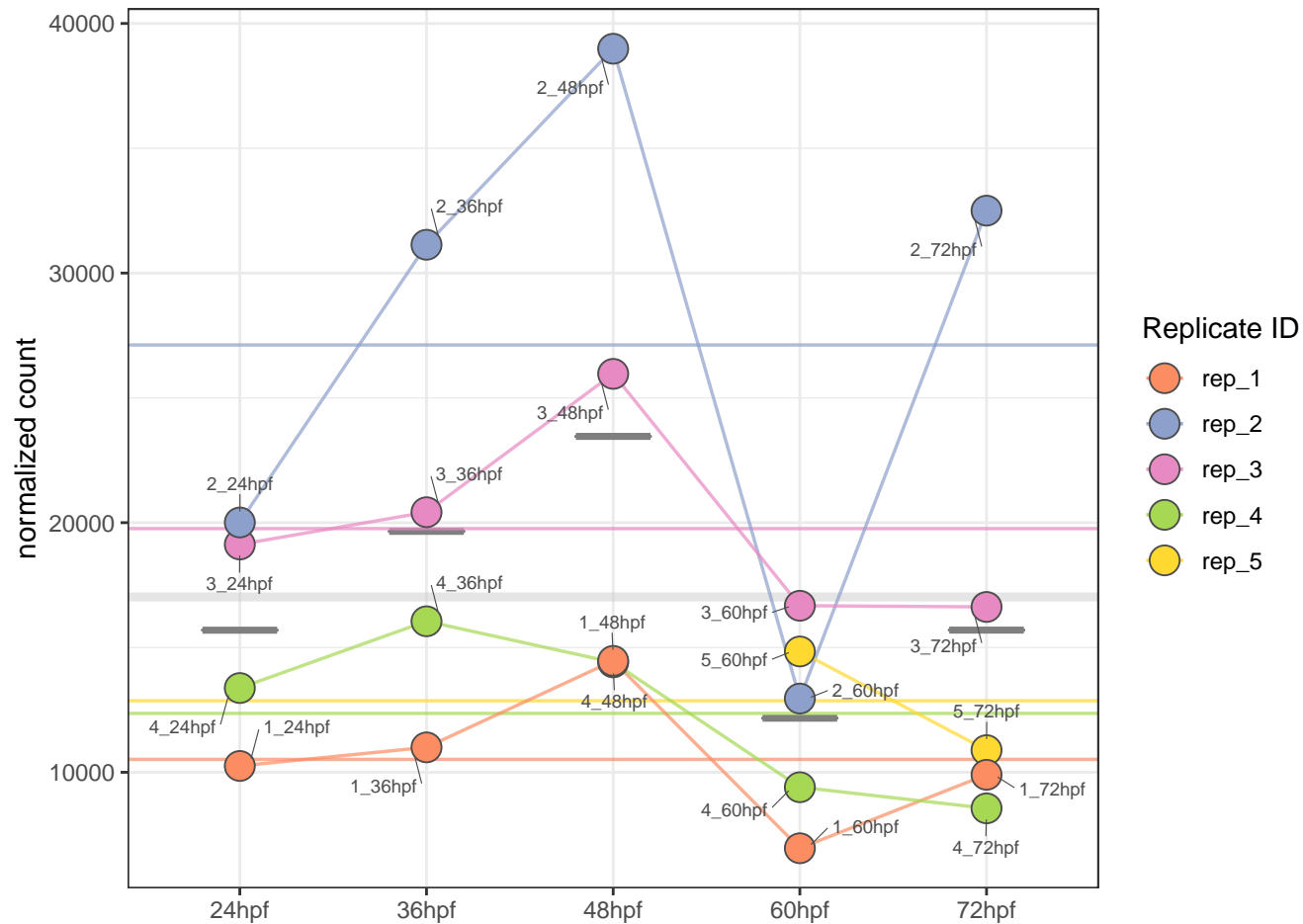Overall mean normalized counts = 23570.09

Gene: kdm2bb, ENSDARG00000046010, chromosome 10, protein_coding
P−value = 3e−12
Adjusted p−value = 1.1e−09
Log2 fold−change (rep_5 / rep_1) = 0.65
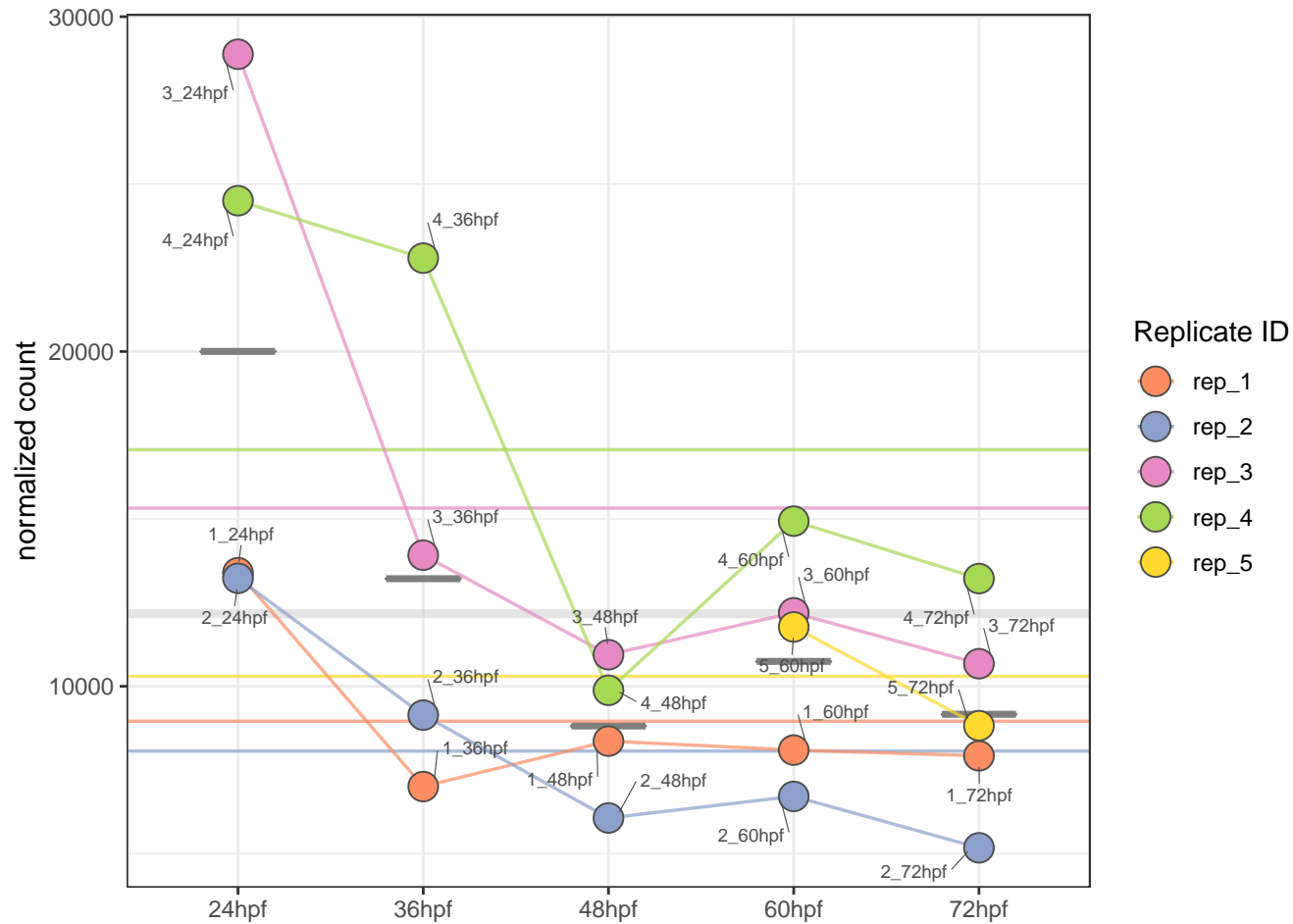Overall mean normalized counts = 17023.77

Gene: ccdc141, ENSDARG00000095675, chromosome 9, protein_coding
P−value = 3.1e−12
Adjusted p−value = 1.1e−09
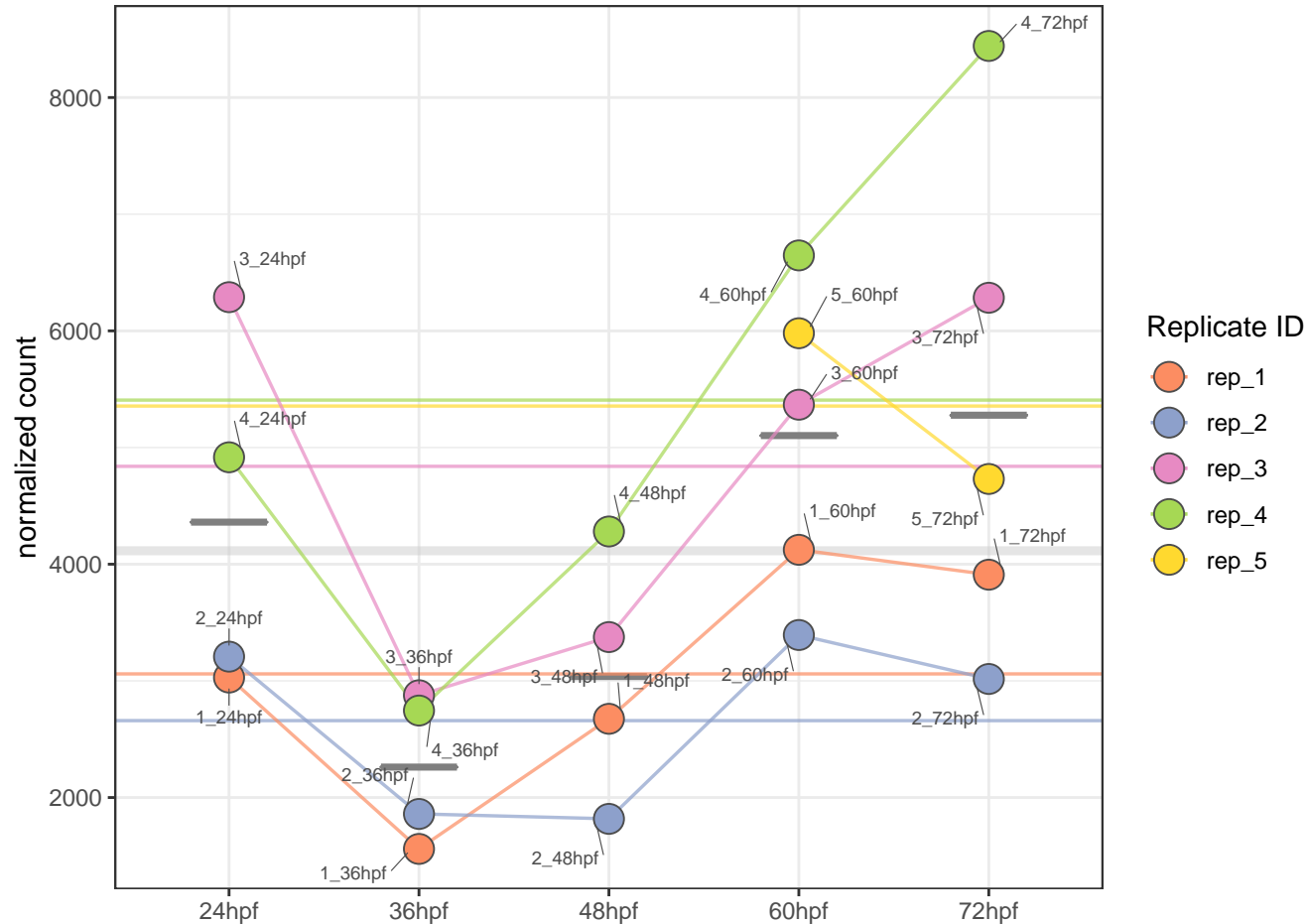Log2 fold−change (rep_5 / rep_1) = 0.46
Overall mean normalized counts = 12166.51

Gene: aplnra, ENSDARG00000002172, chromosome 8, protein_coding
P−value = 3.2e−12
Adjusted p−value = 1.2e−09
Log2 fold−change (rep_5 / rep_1) = 0.46
Overall mean normalized counts = 4115.19
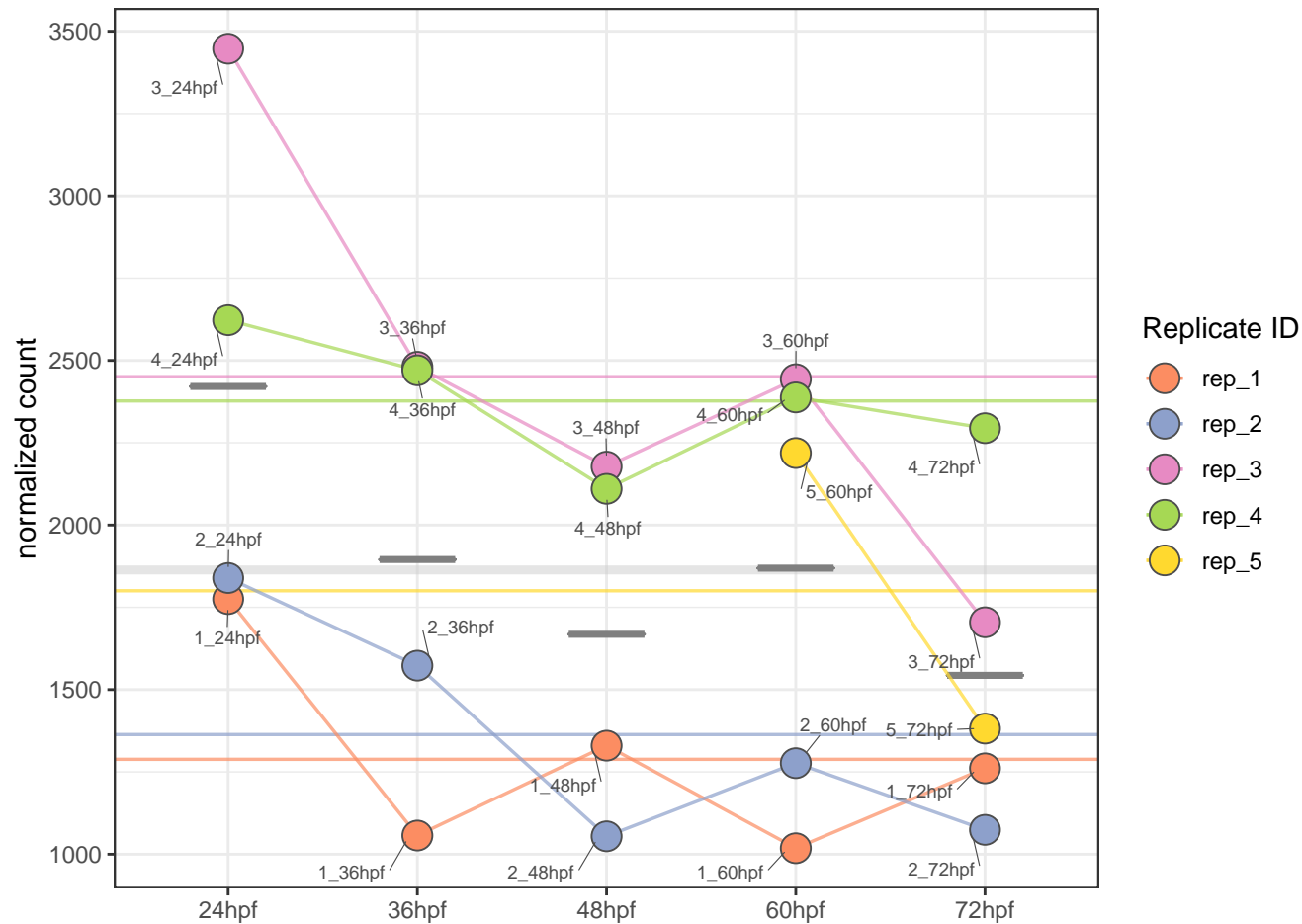
Gene: dusp22b, ENSDARG00000039850, chromosome 2, protein_coding
P−value = 3.3e−12
Adjusted p−value = 1.2e−09
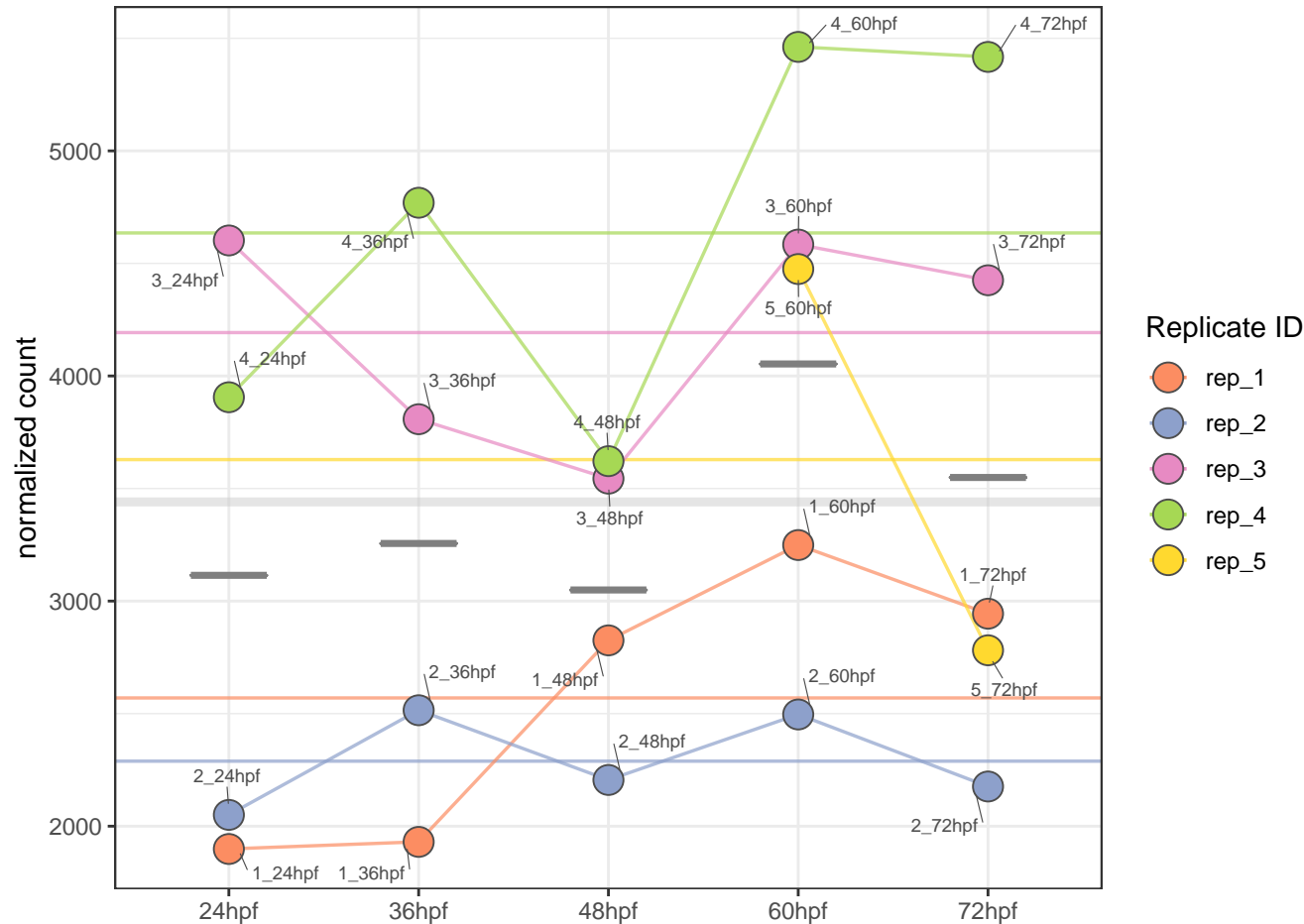Log2 fold−change (rep_5 / rep_1) = 0.62
Overall mean normalized counts = 1863.59

Gene: rapgef3, ENSDARG00000079291, chromosome 23, protein_coding
P−value = 4e−12
Adjusted p−value = 1.4e−09
Log2 fold−change (rep_5 / rep_1) = 0.32
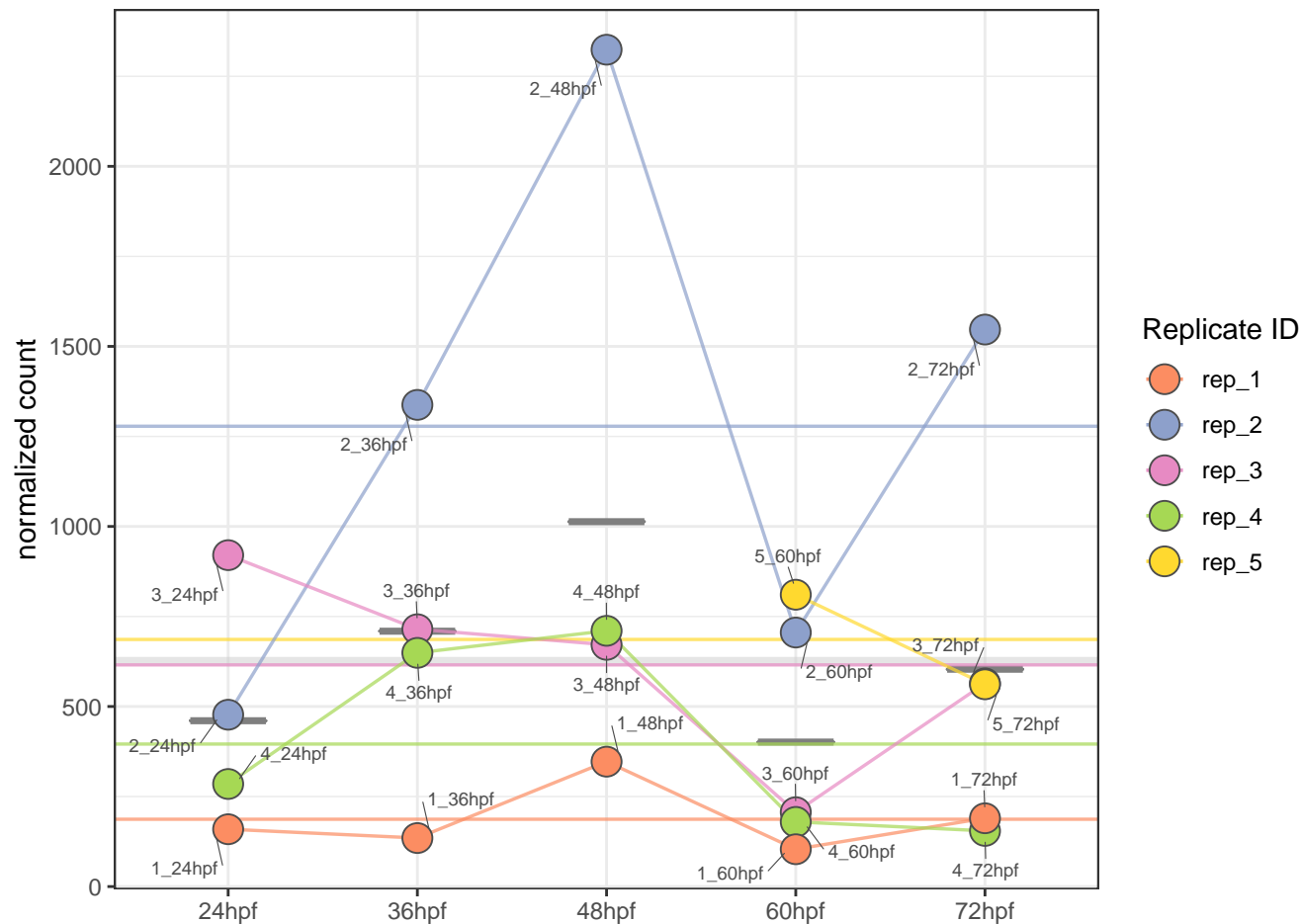Overall mean normalized counts = 3440.48

Gene: CABZ01094390.1, ENSDARG00000117598, chromosome 13, lincRNA
P−value = 4.1e−12
Adjusted p−value = 1.4e−09
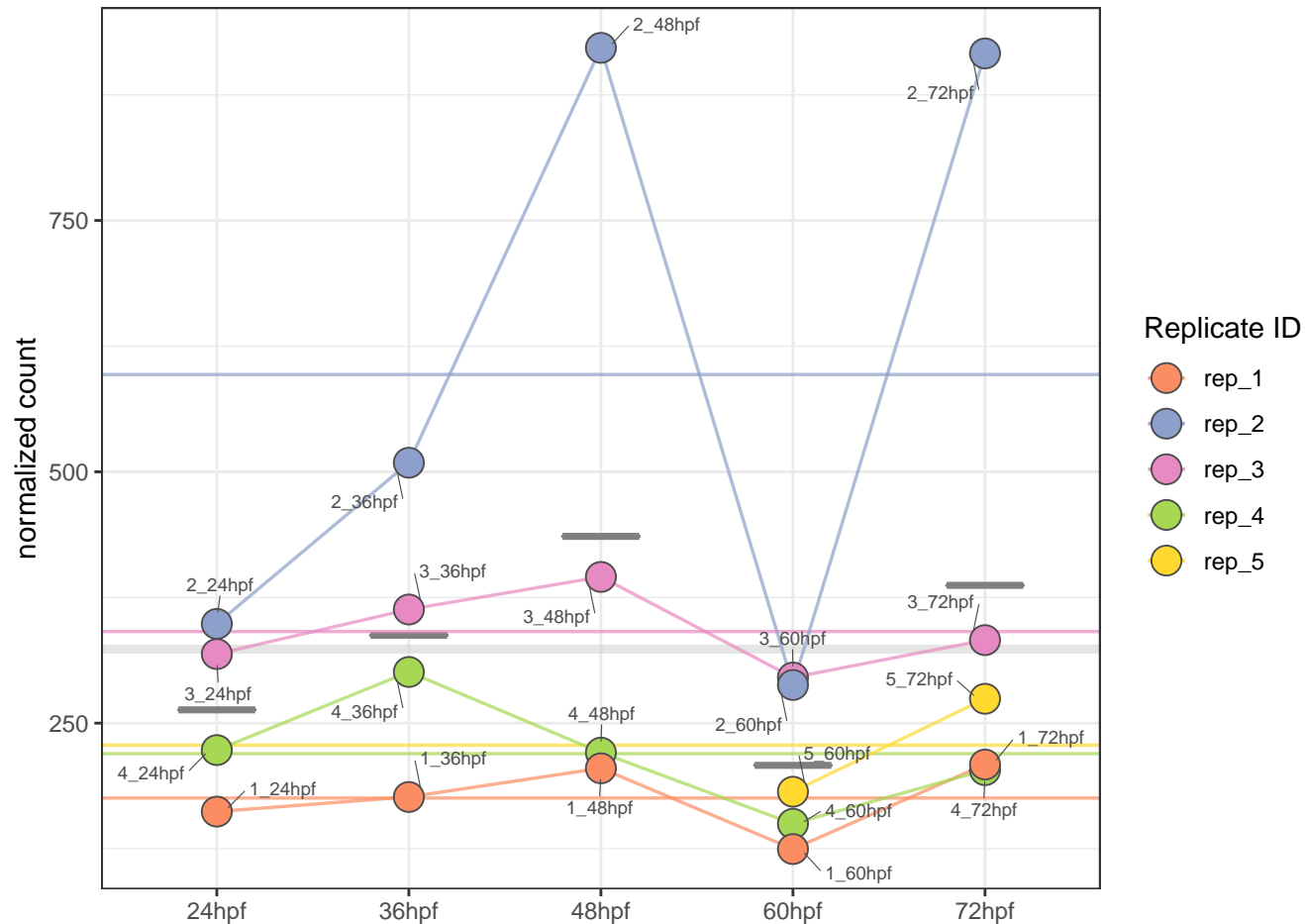Log2 fold−change (rep_5 / rep_1) = 2.56
Overall mean normalized counts = 625.23

Gene: tnfsf14, ENSDARG00000111357, chromosome 3, protein_coding
P−value = 4.3e−12
Adjusted p−value = 1.5e−09
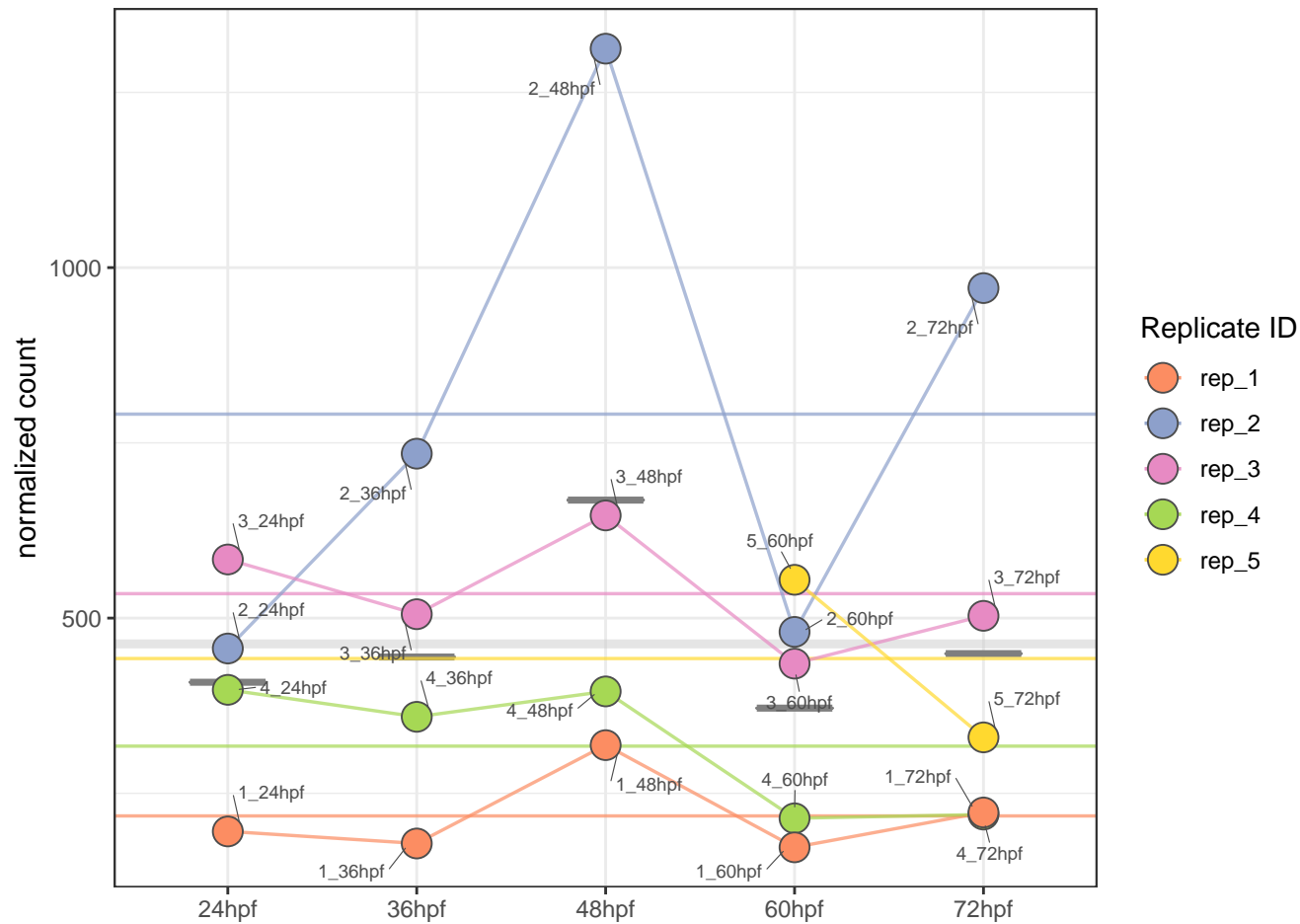Log2 fold−change (rep_5 / rep_1) = 0.51
Overall mean normalized counts = 323.70

Gene: pimr138, ENSDARG00000041550, chromosome 20, protein_coding
P−value = 5.1e−12
Adjusted p−value = 1.8e−09
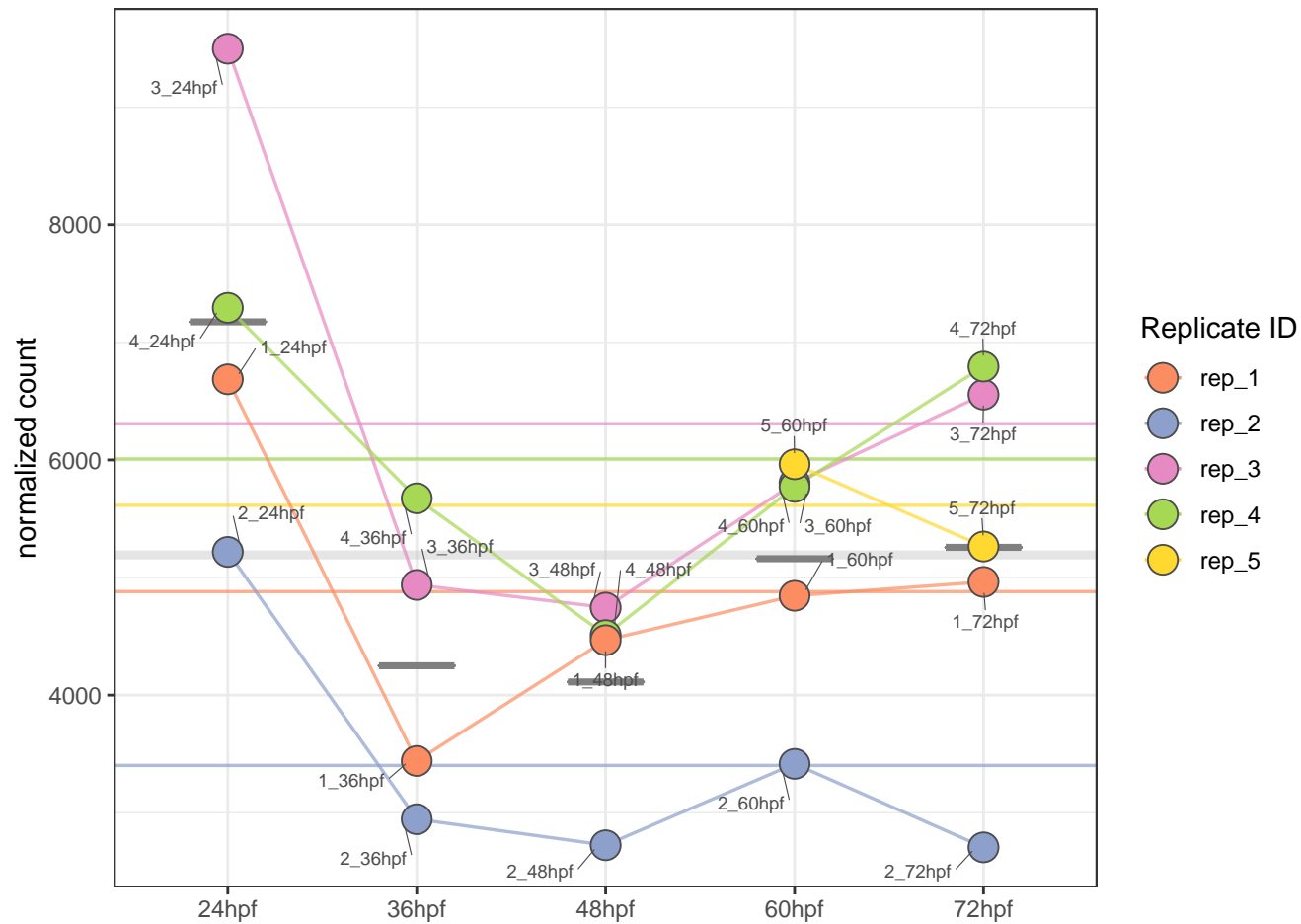Log2 fold−change (rep_5 / rep_1) = 1.30
Overall mean normalized counts = 463.15

Gene: irf2bp2b, ENSDARG00000098635, chromosome 11, protein_coding
P−value = 5.8e−12
Adjusted p−value = 2e−09
Log2 fold−change (rep_5 / rep_1) = 0.22
Overall mean normalized counts = 5192.10

Gene: klhl30, ENSDARG00000076094, chromosome 6, protein_coding
P−value = 6.4e−12
Adjusted p−value = 2.2e−09
Log2 fold−change (rep_5 / rep_1) = 0.19
Overall mean normalized counts = 889.79