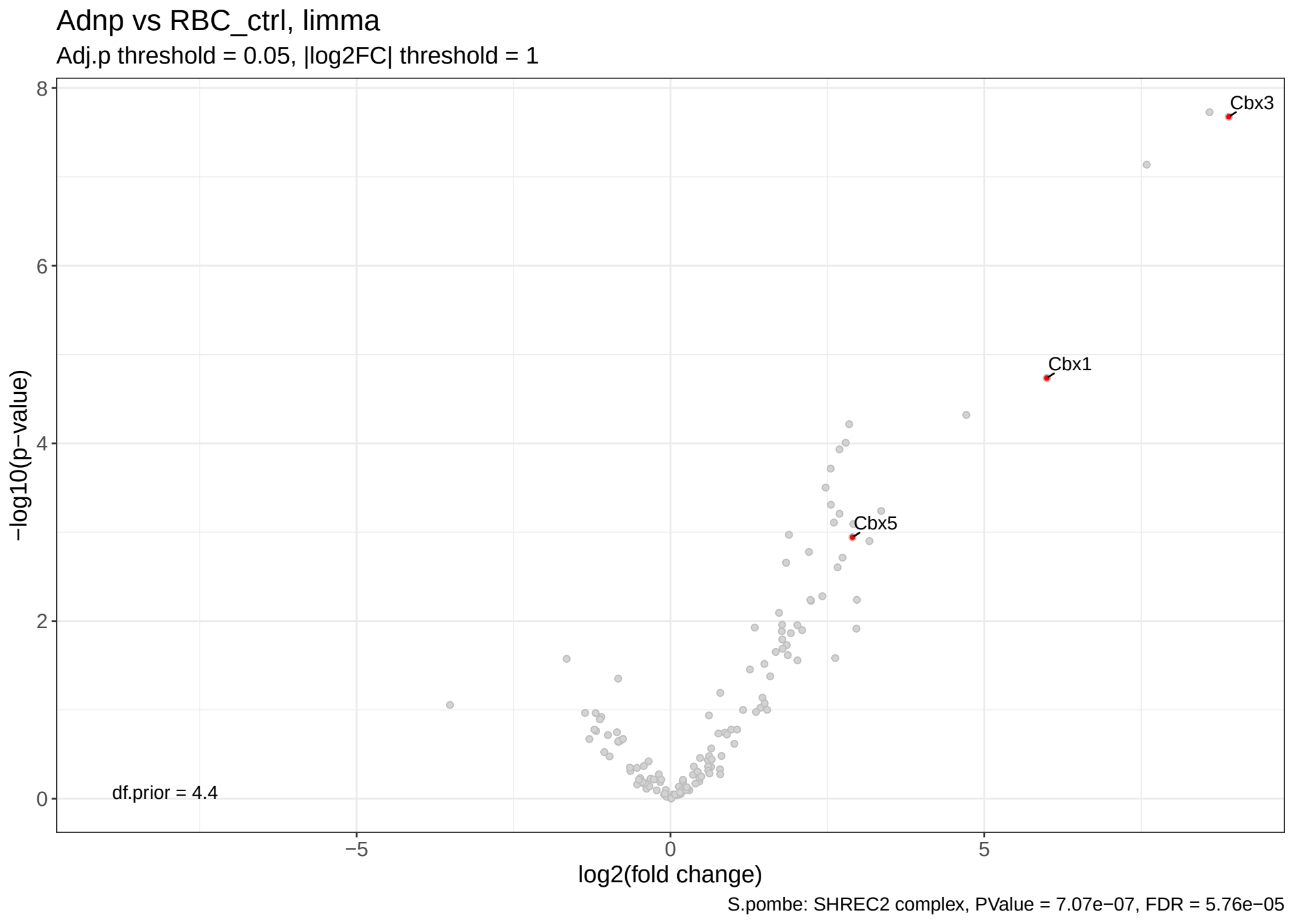
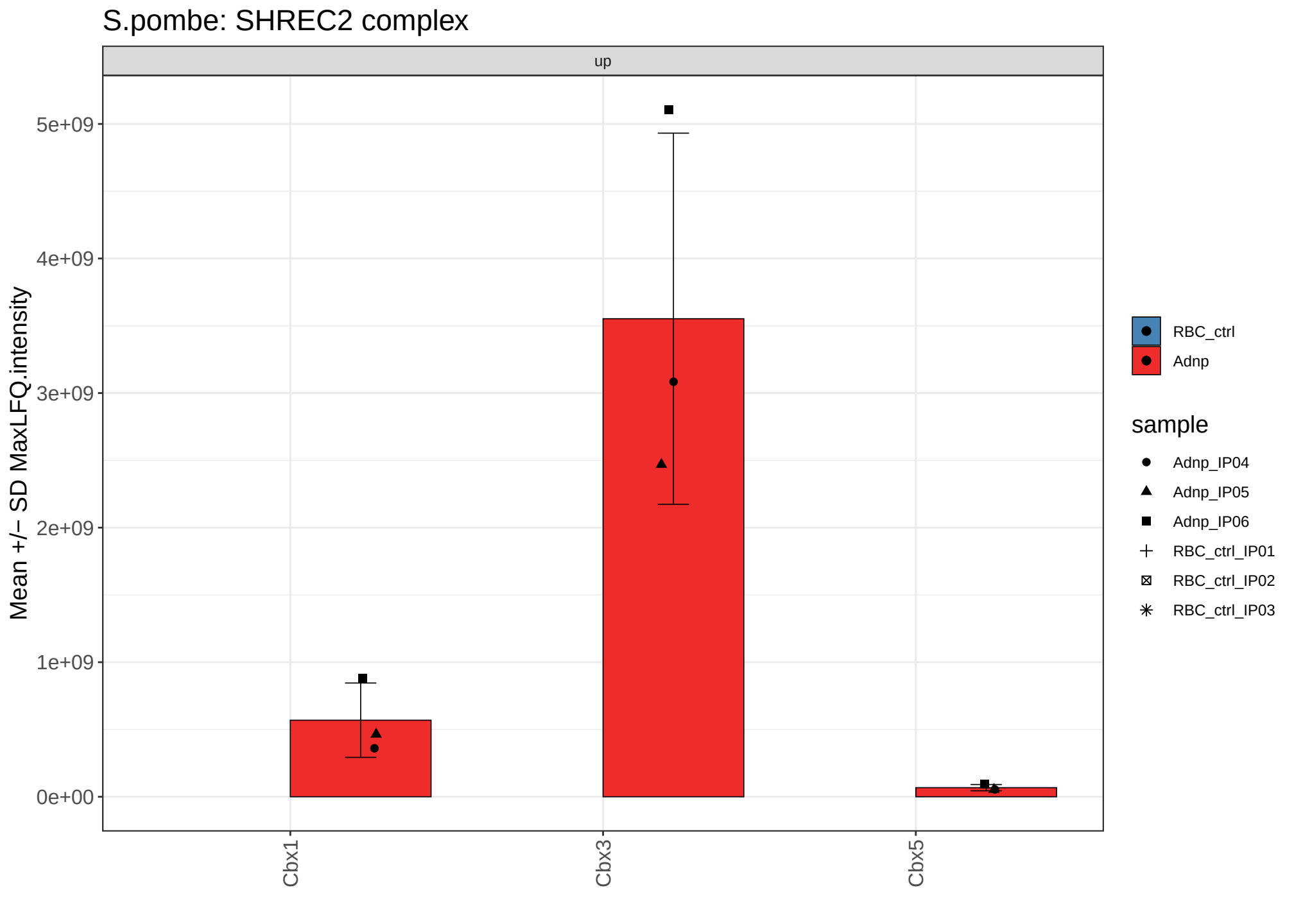
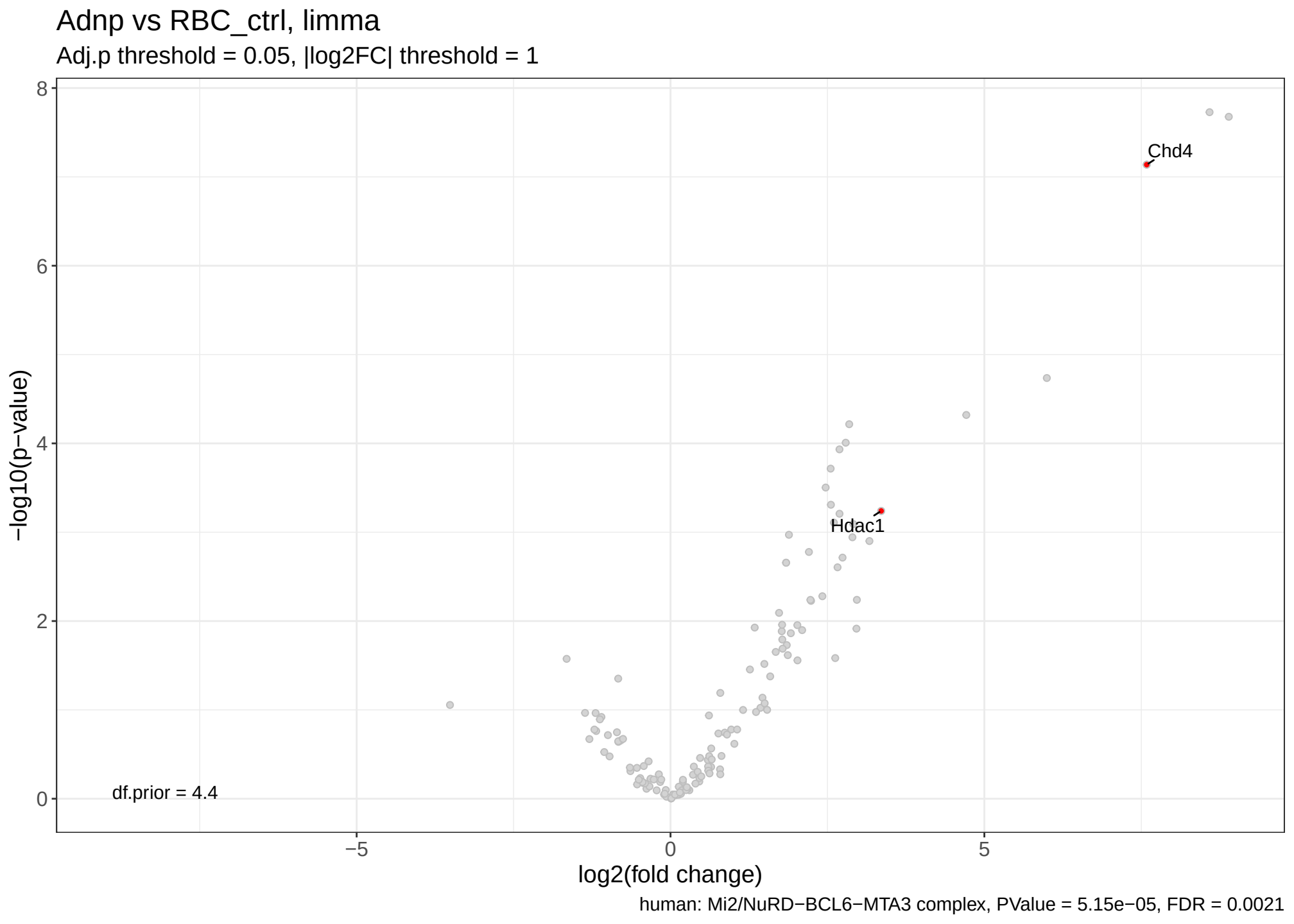
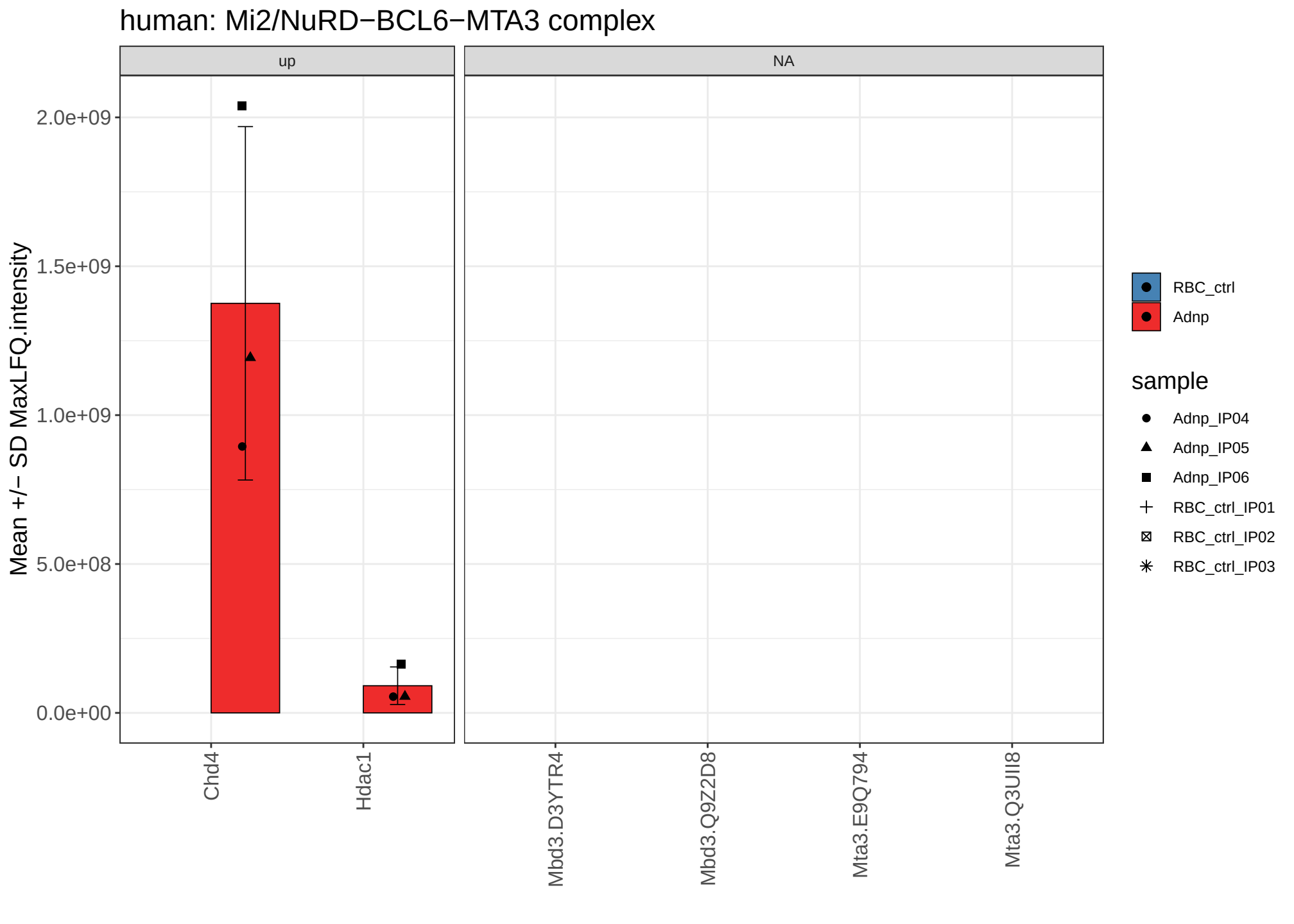
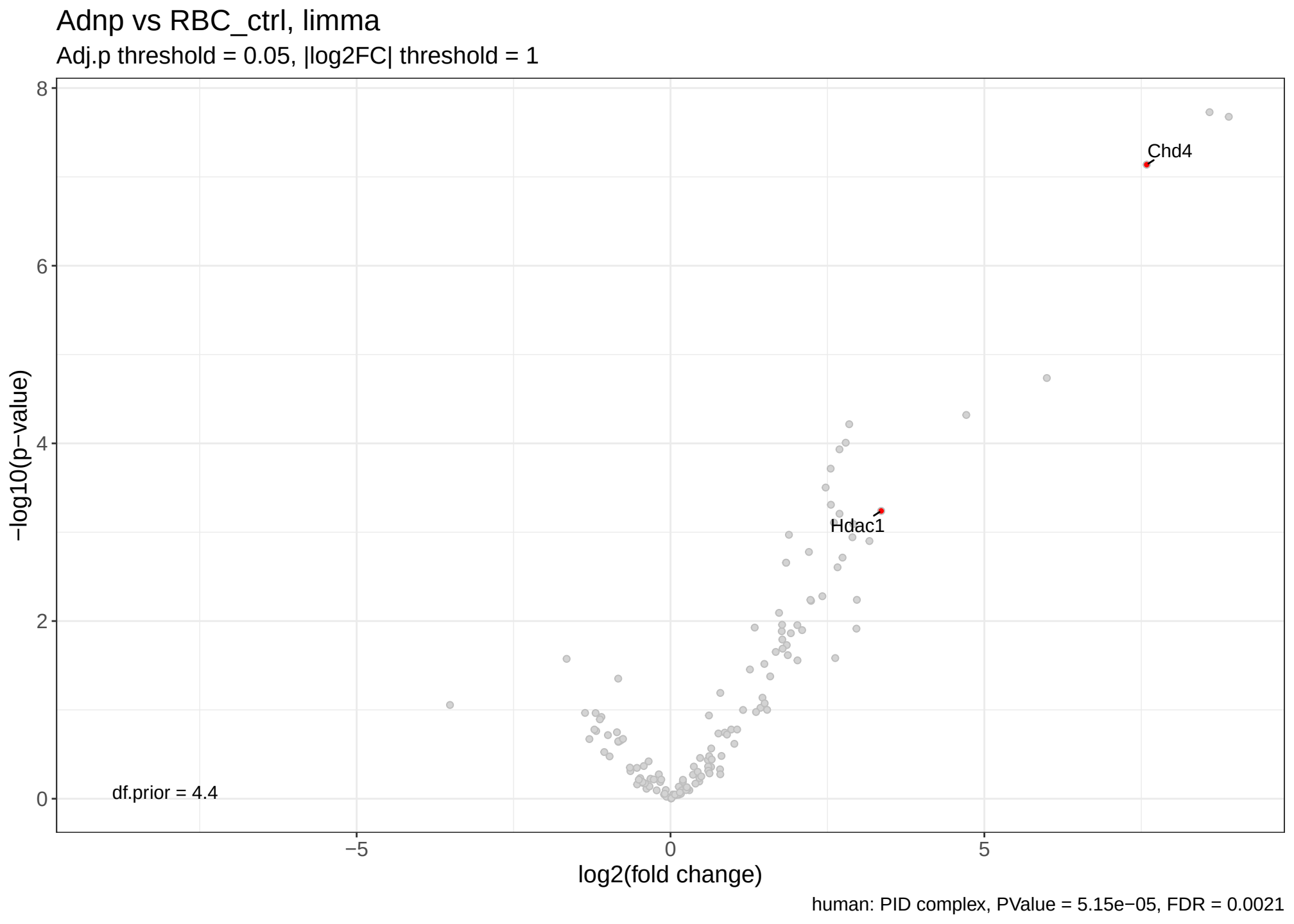
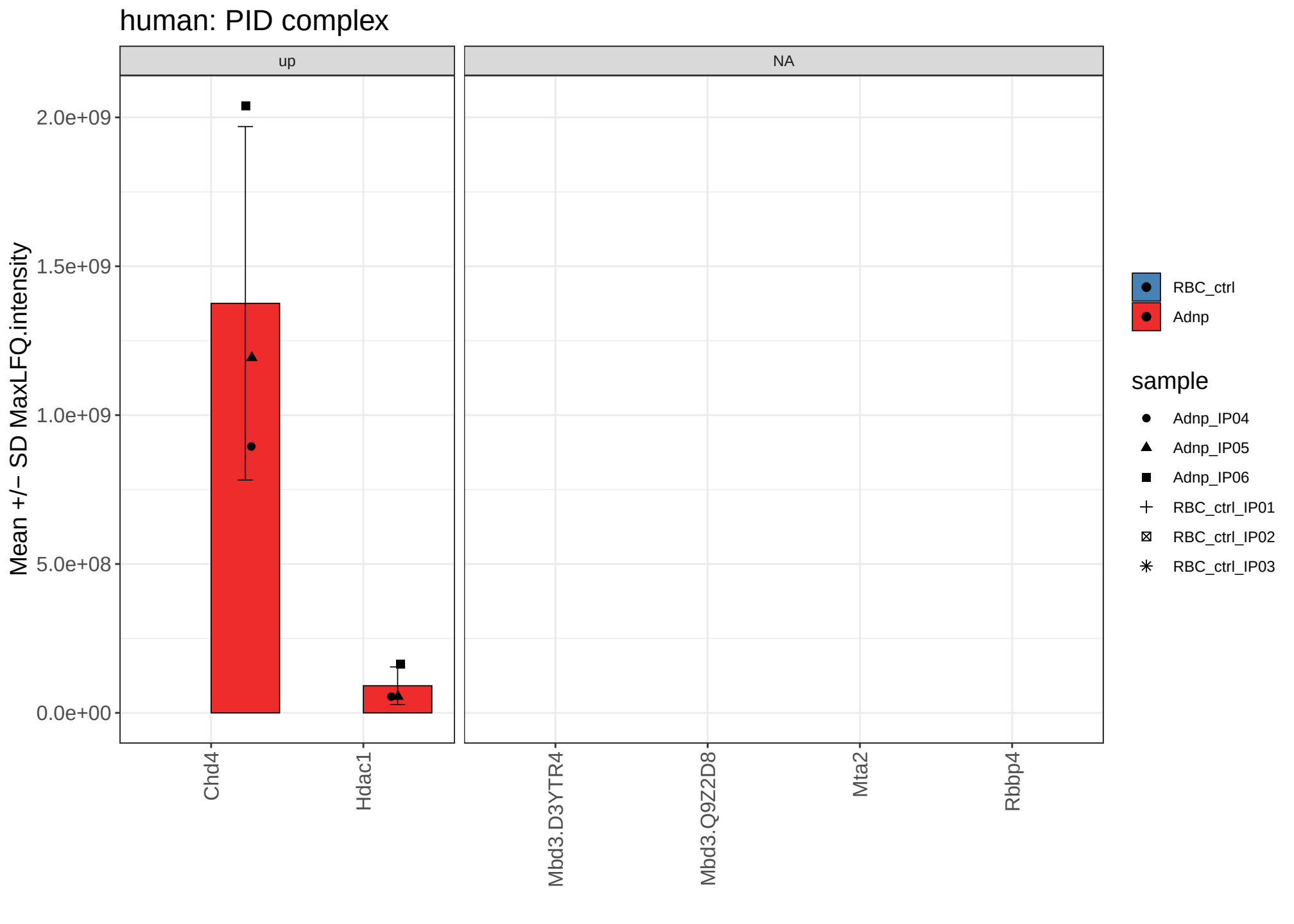

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Cbx3
Cbx1
Cbx5
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
S.pombe: SHREC2 complex, PValue = 7.07e−07, FDR = 5.76e−05

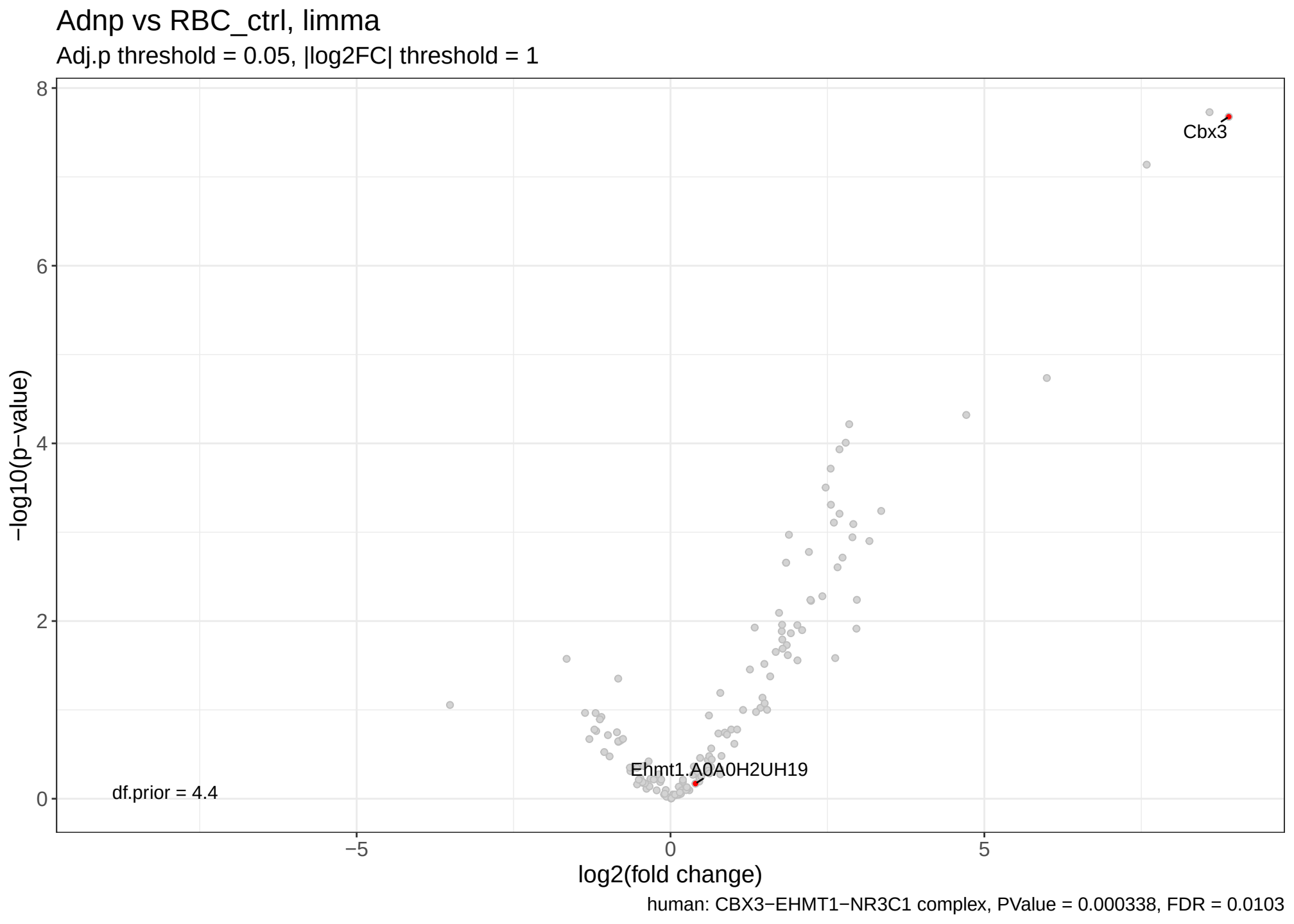

S.pombe: SHREC2 complex
up
Mean +/− SD MaxLFQ.intensity
5e+09
4e+09
3e+09
2e+09
1e+09
0e+00
Cbx1
Cbx3
Cbx5
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

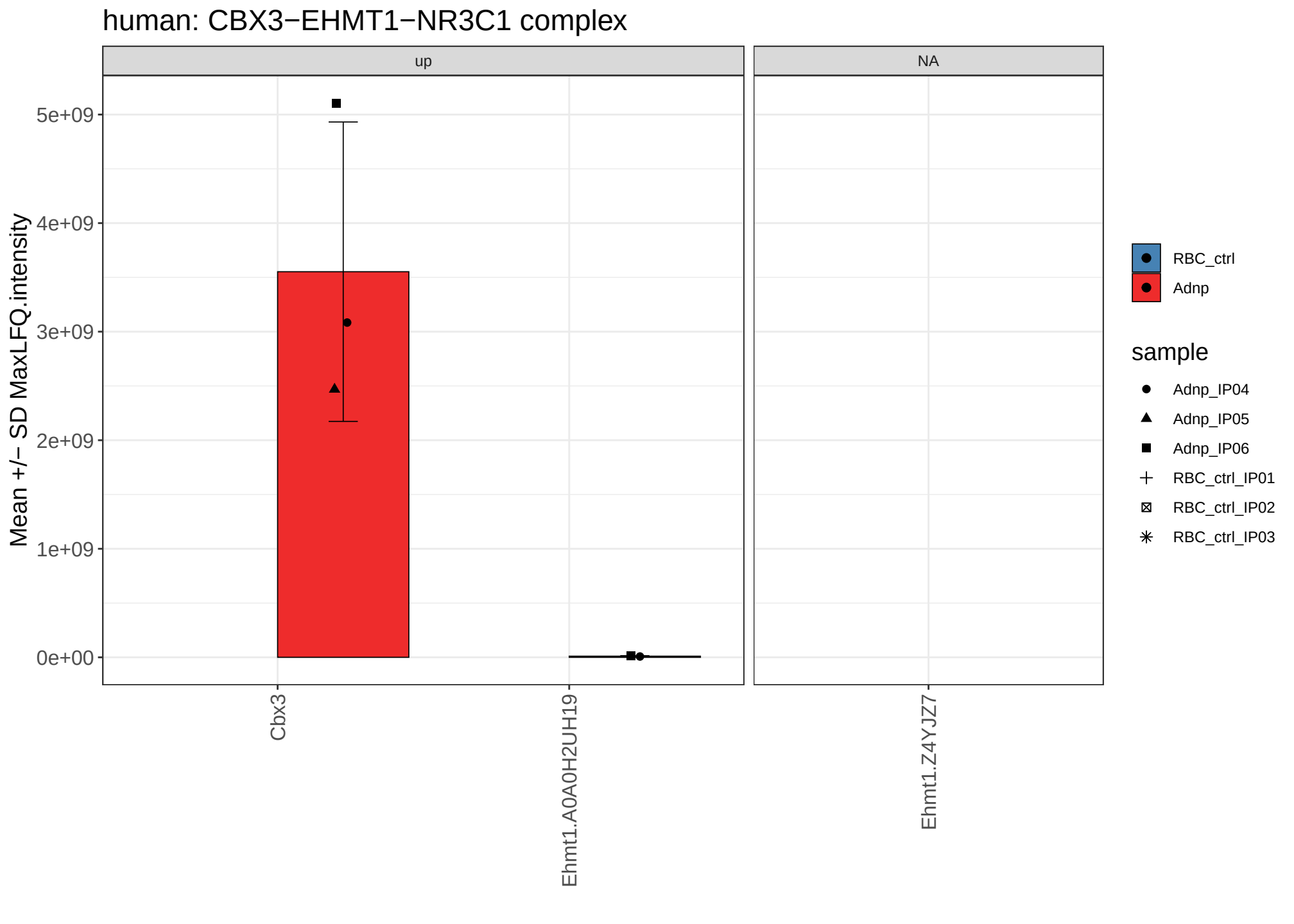

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac1
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
human: Mi2/NuRD−BCL6−MTA3 complex, PValue = 5.15e−05, FDR = 0.0021

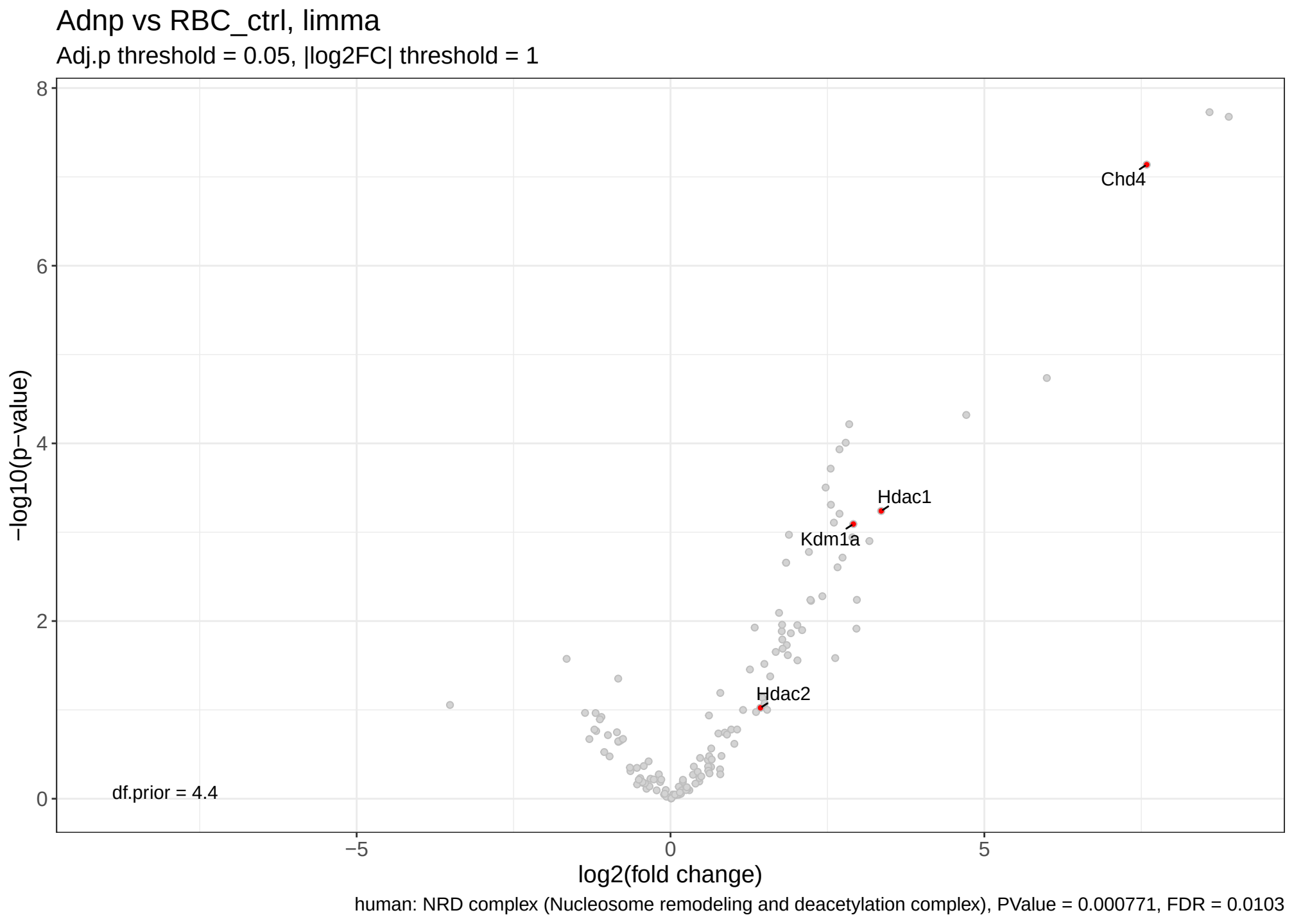

human: Mi2/NuRD−BCL6−MTA3 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta3.E9Q794
Mta3.Q3UII8
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

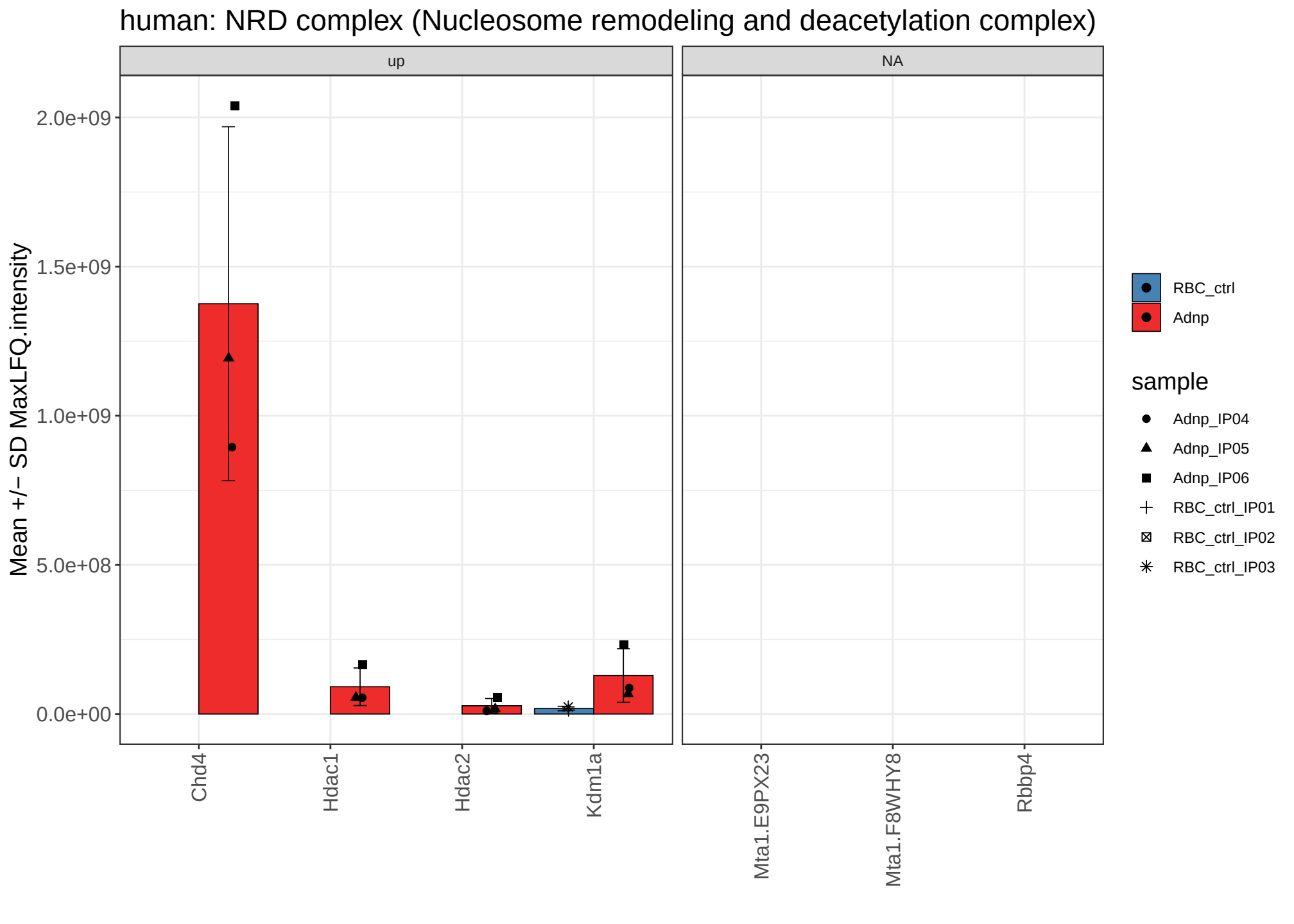

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac1
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
human: PID complex, PValue = 5.15e−05, FDR = 0.0021

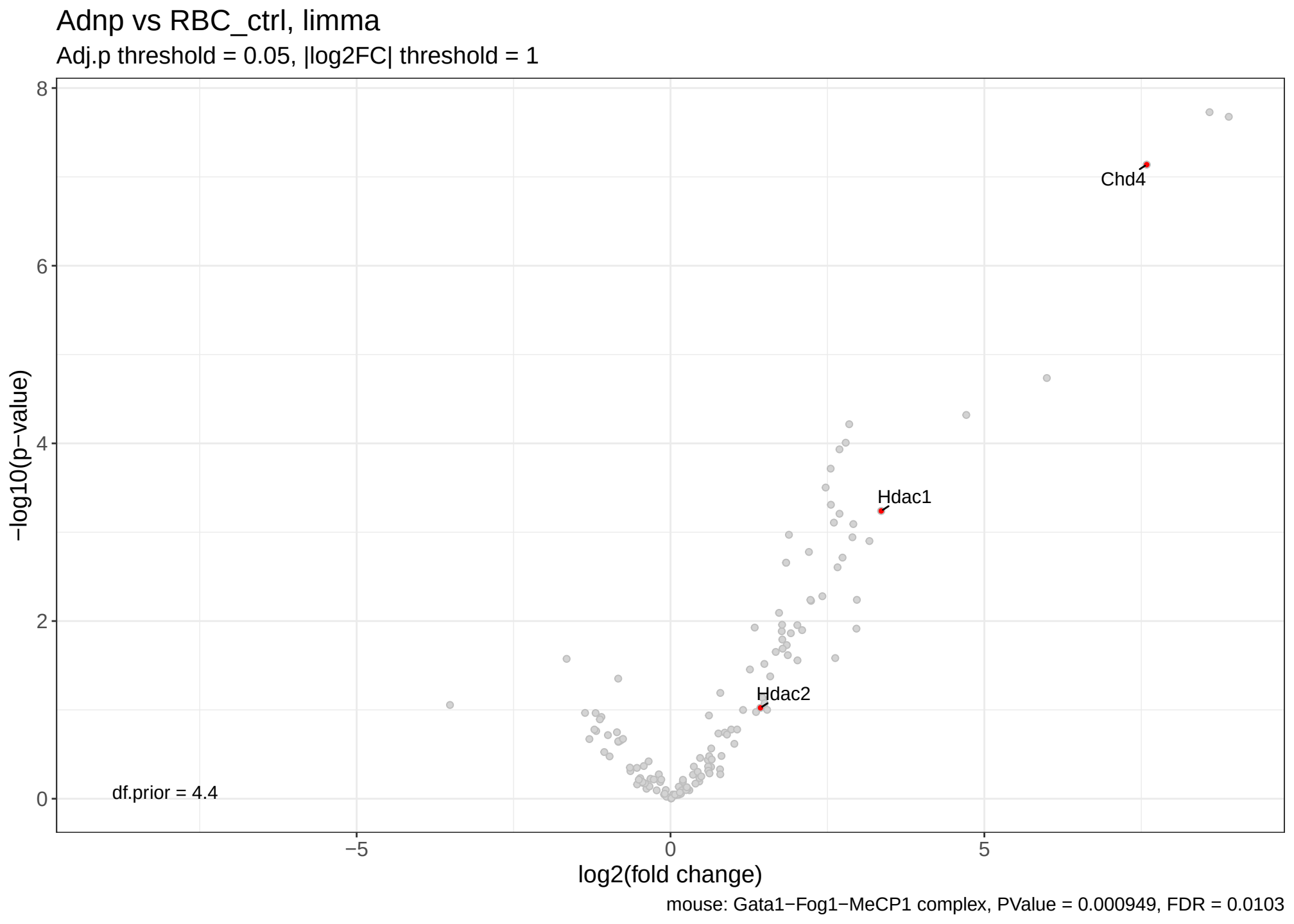

human: PID complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

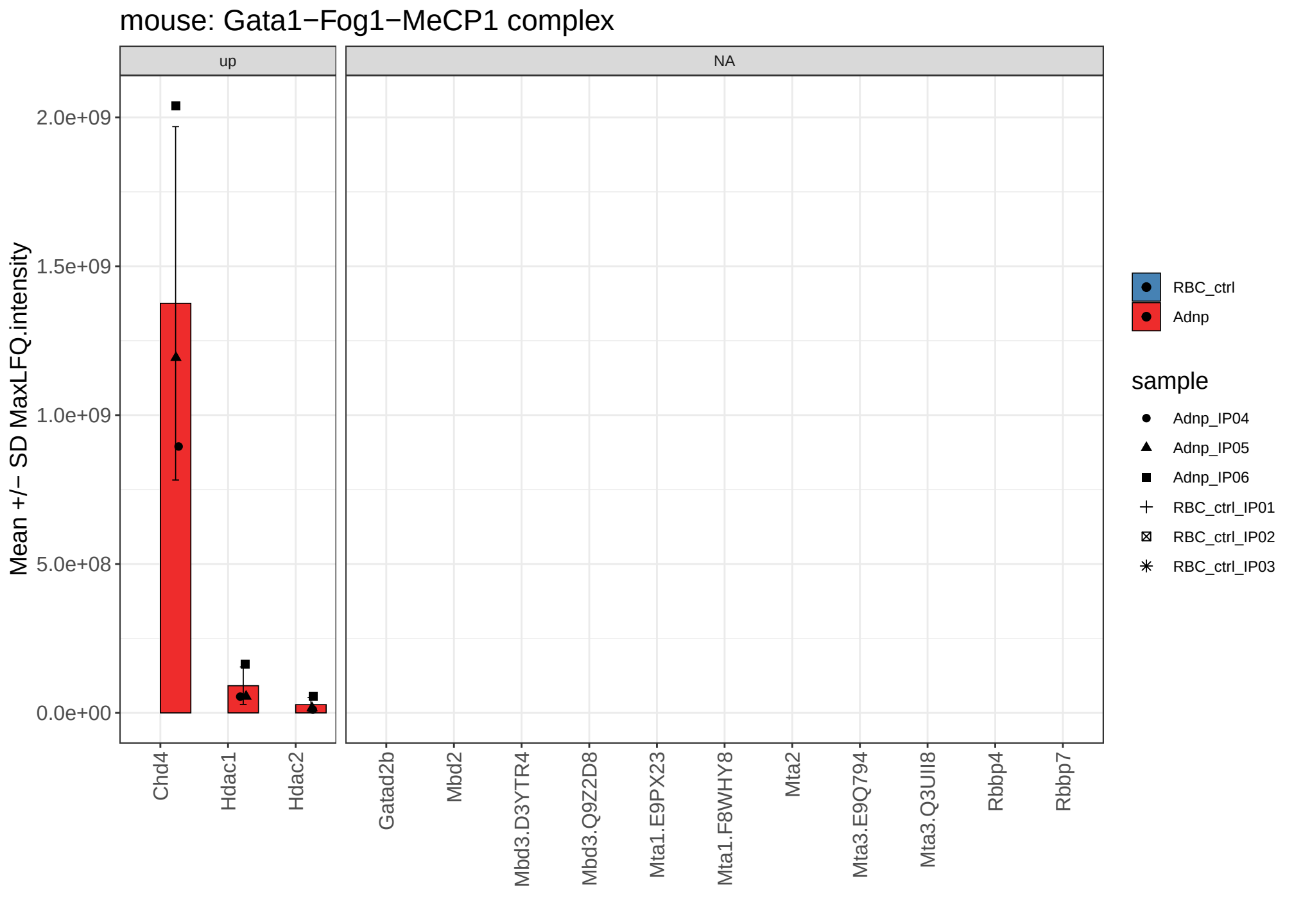

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Cbx3
Ehmt1.A0A0H2UH19
df.prior = 4.4
human: CBX3−EHMT1−NR3C1 complex, PValue = 0.000338, FDR = 0.0103

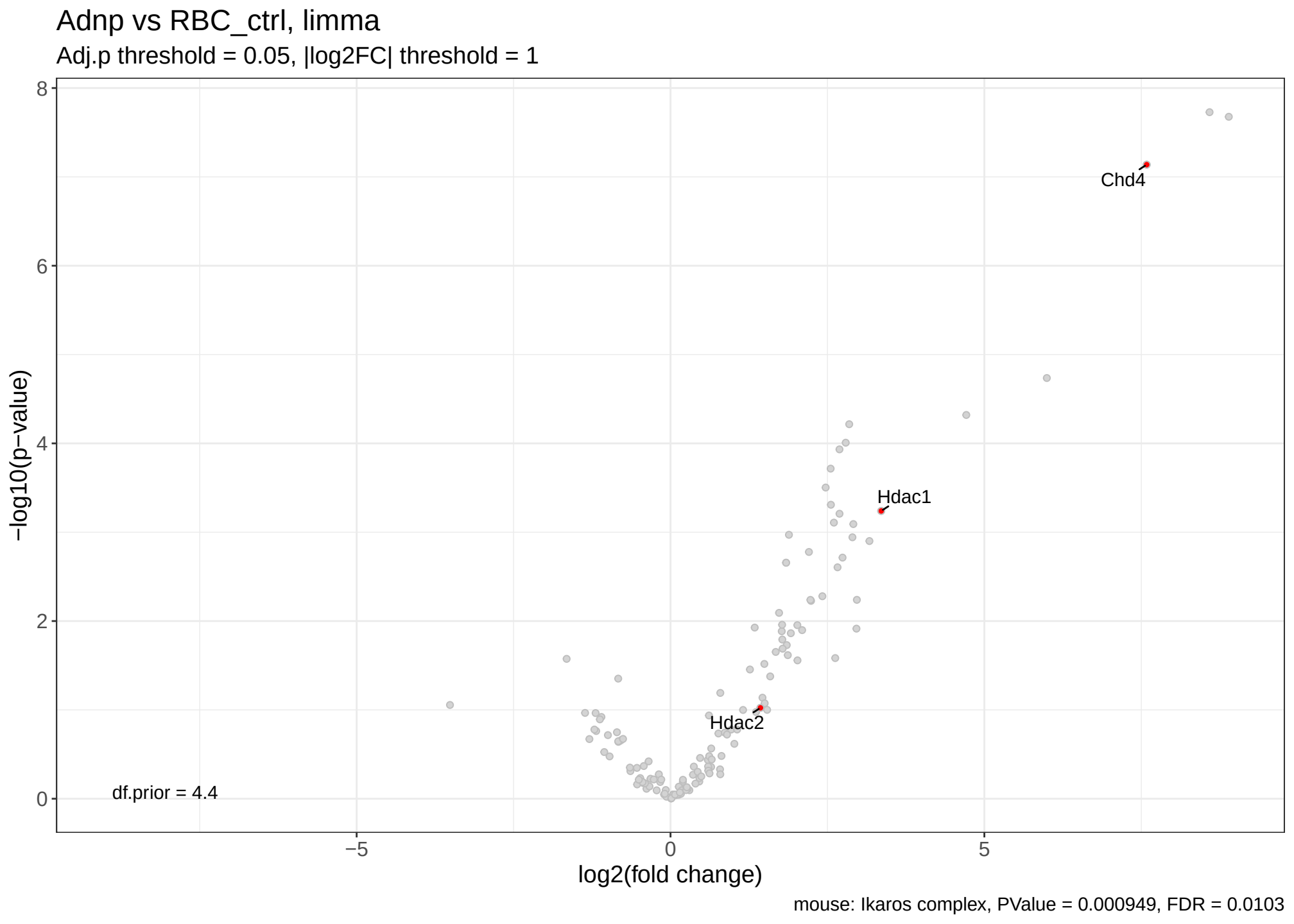

human: CBX3−EHMT1−NR3C1 complex
up
NA
Mean +/− SD MaxLFQ.intensity
5e+09
4e+09
3e+09
2e+09
1e+09
0e+00
Cbx3
Ehmt1.A0A0H2UH19
Ehmt1.Z4YJZ7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

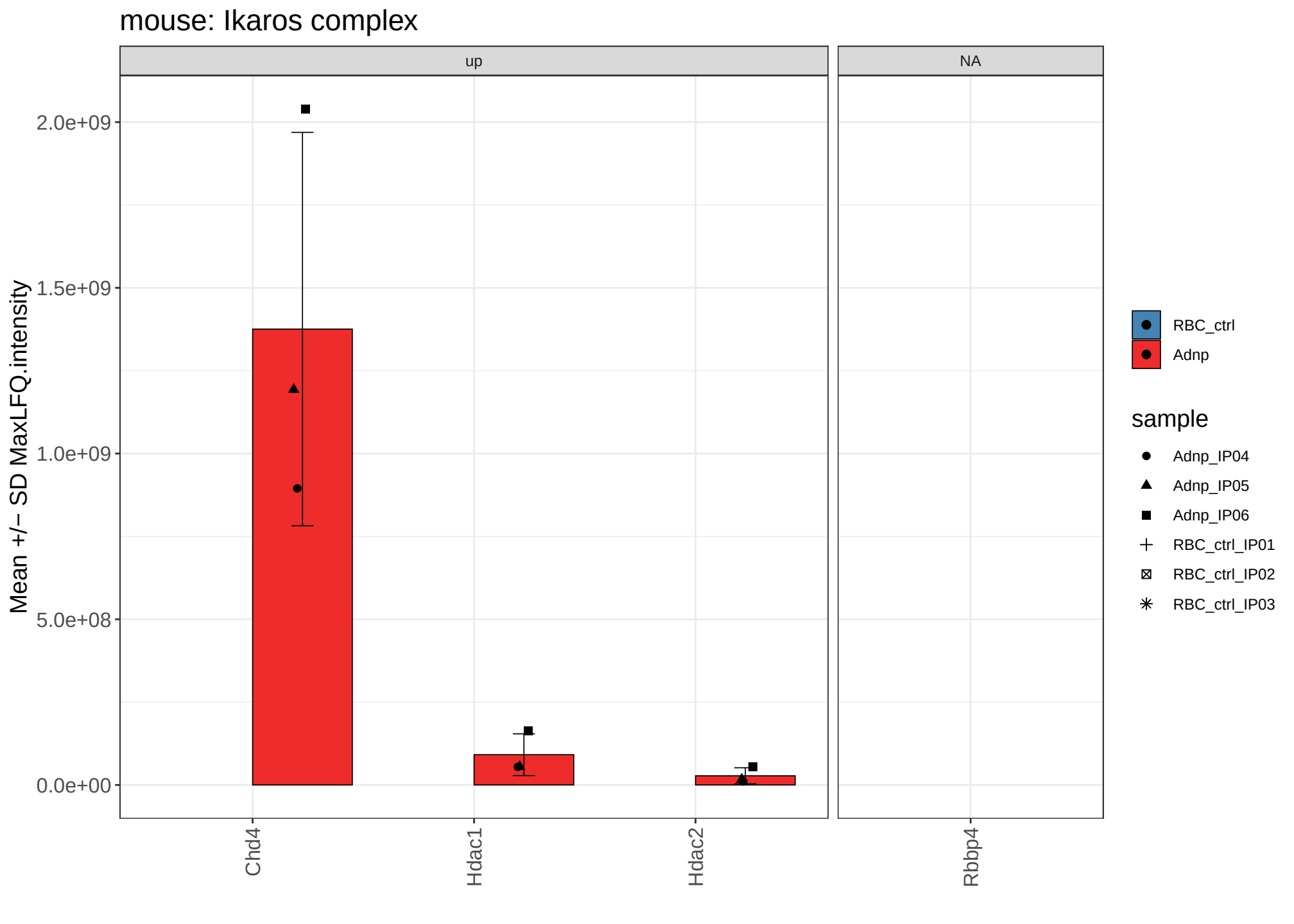

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Kdm1a
Hdac2
df.prior = 4.4
human: NRD complex (Nucleosome remodeling and deacetylation complex), PValue = 0.000771, FDR = 0.0103

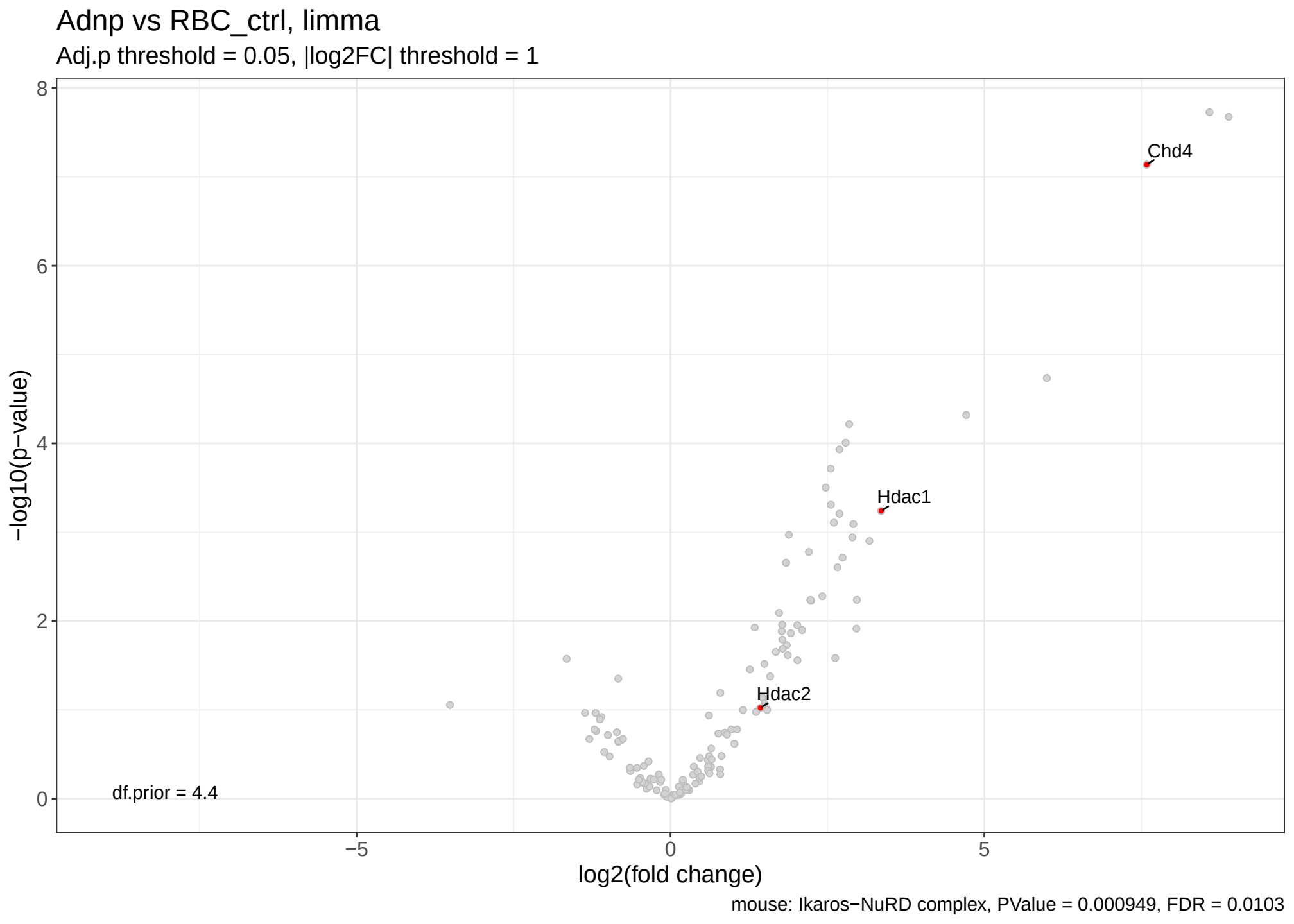

human: NRD complex (Nucleosome remodeling and deacetylation complex)
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Kdm1a
Mta1.E9PX23
Mta1.F8WHY8
Rbbp4
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

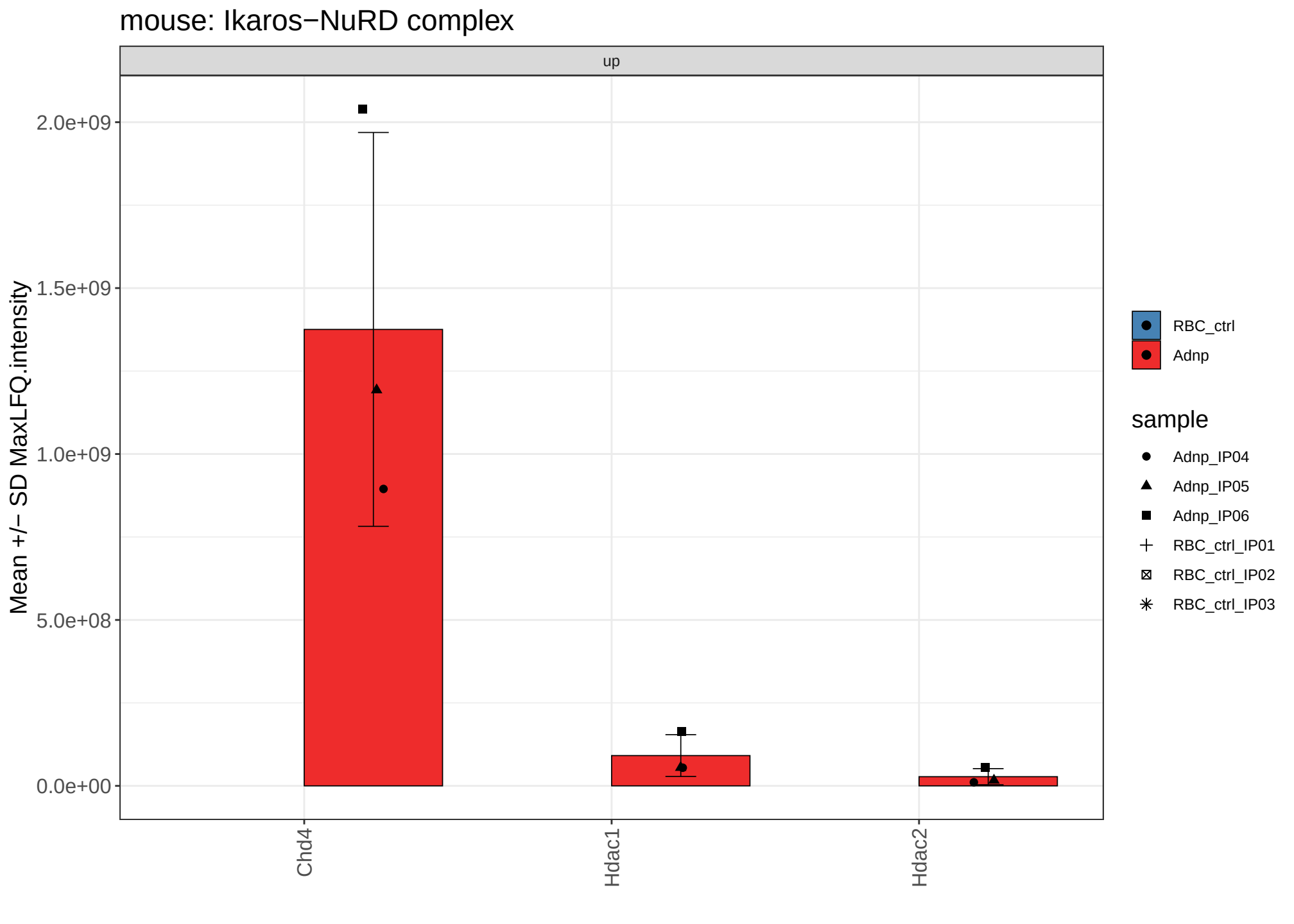

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Hdac2
df.prior = 4.4
mouse: Gata1−Fog1−MeCP1 complex, PValue = 0.000949, FDR = 0.0103

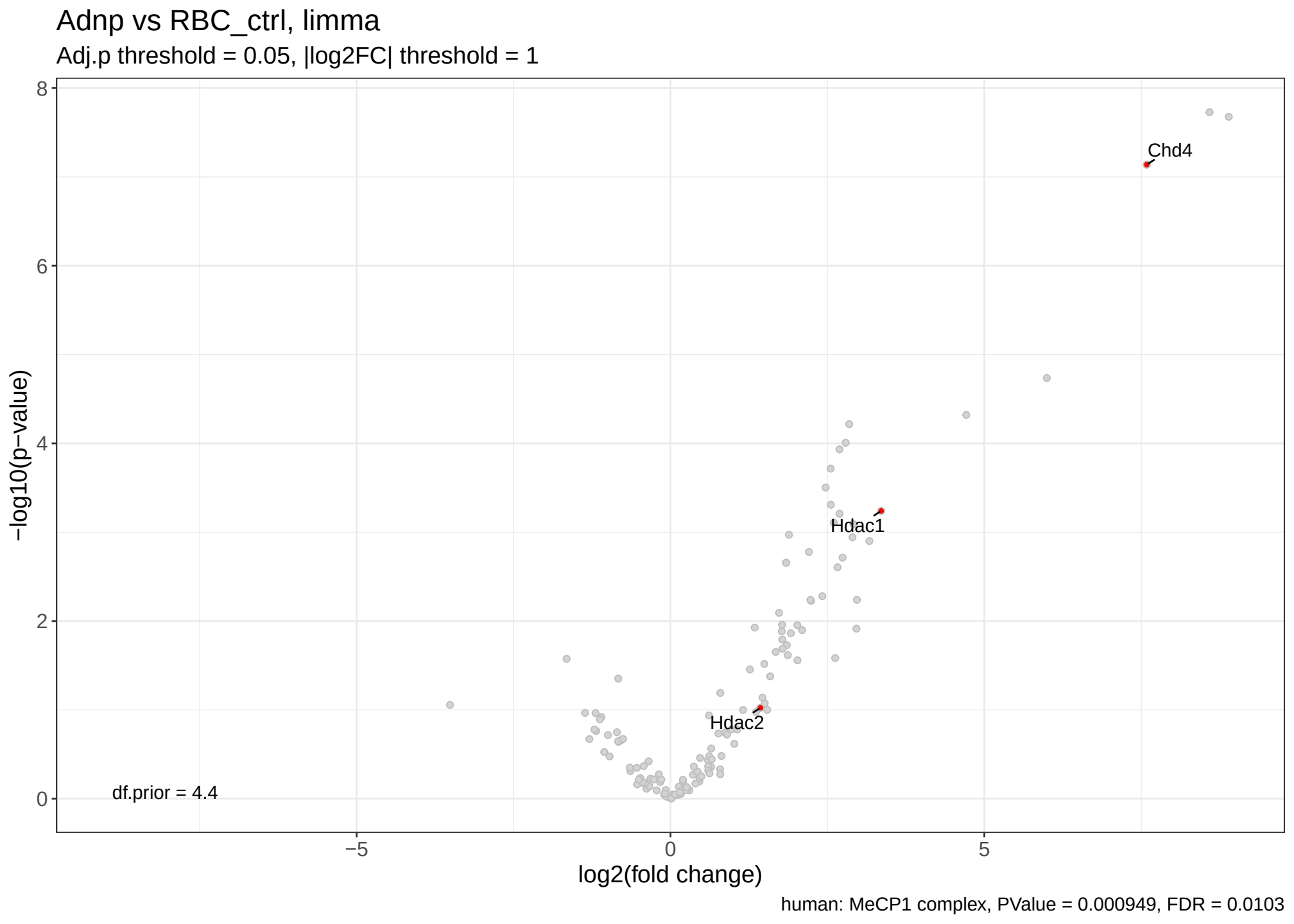

mouse: Gata1−Fog1−MeCP1 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Gatad2b
Mbd2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta1.E9PX23
Mta1.F8WHY8
Mta2
Mta3.E9Q794
Mta3.Q3UII8
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

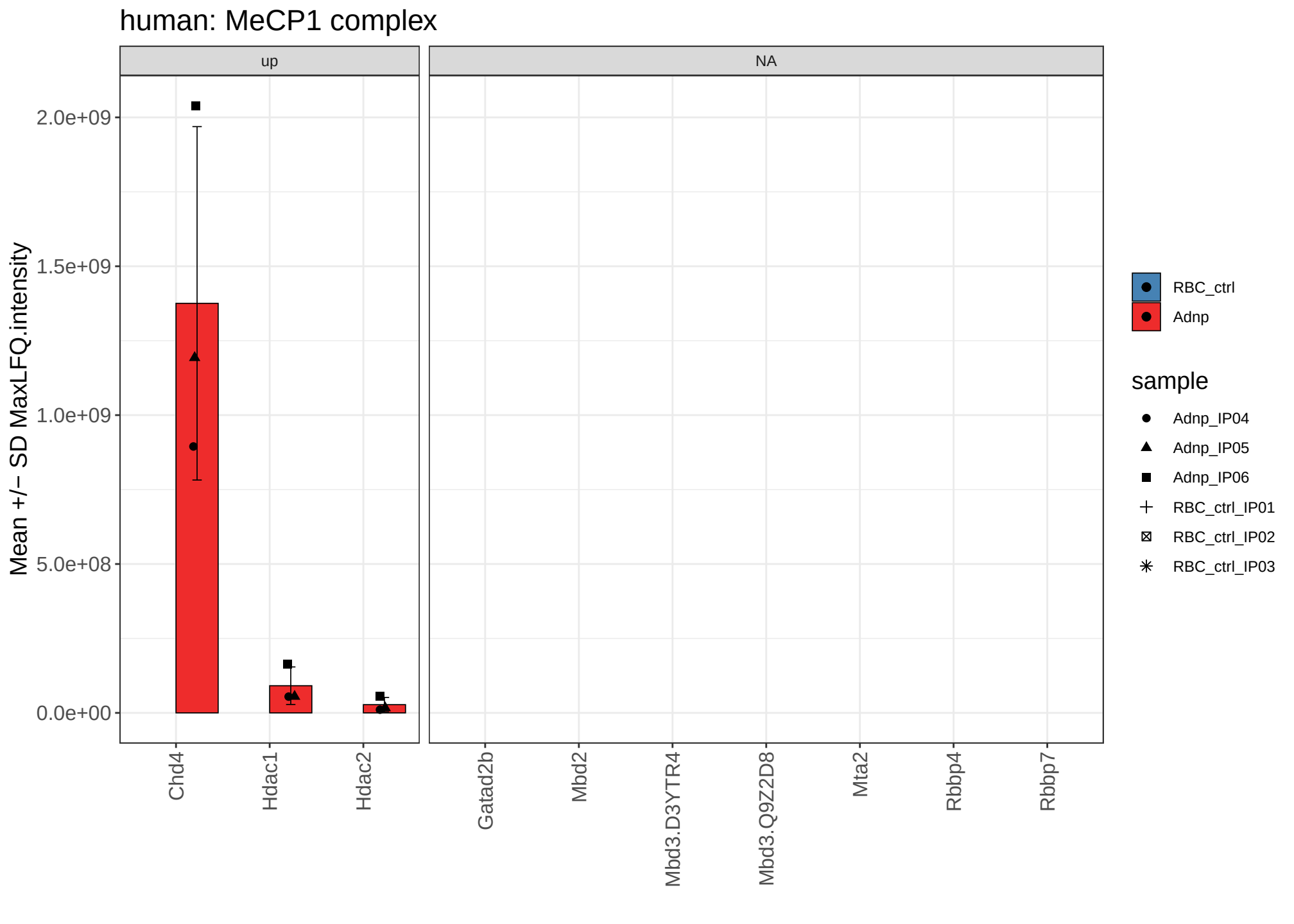

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Hdac2
df.prior = 4.4
mouse: Ikaros complex, PValue = 0.000949, FDR = 0.0103

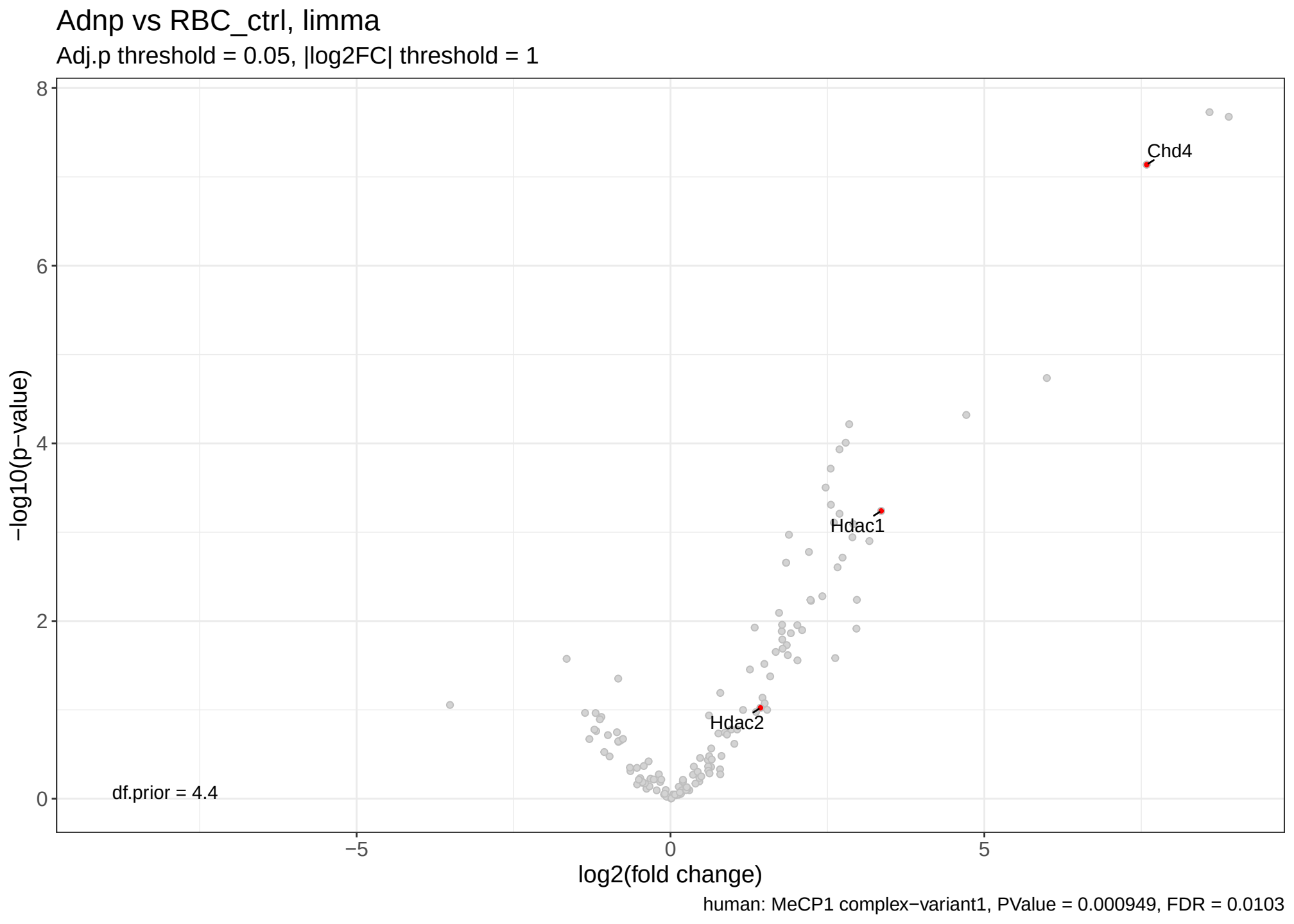

mouse: Ikaros complex
up
NA
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Mean +/− SD MaxLFQ.intensity
Chd4
Hdac1
Hdac2
Rbbp4
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

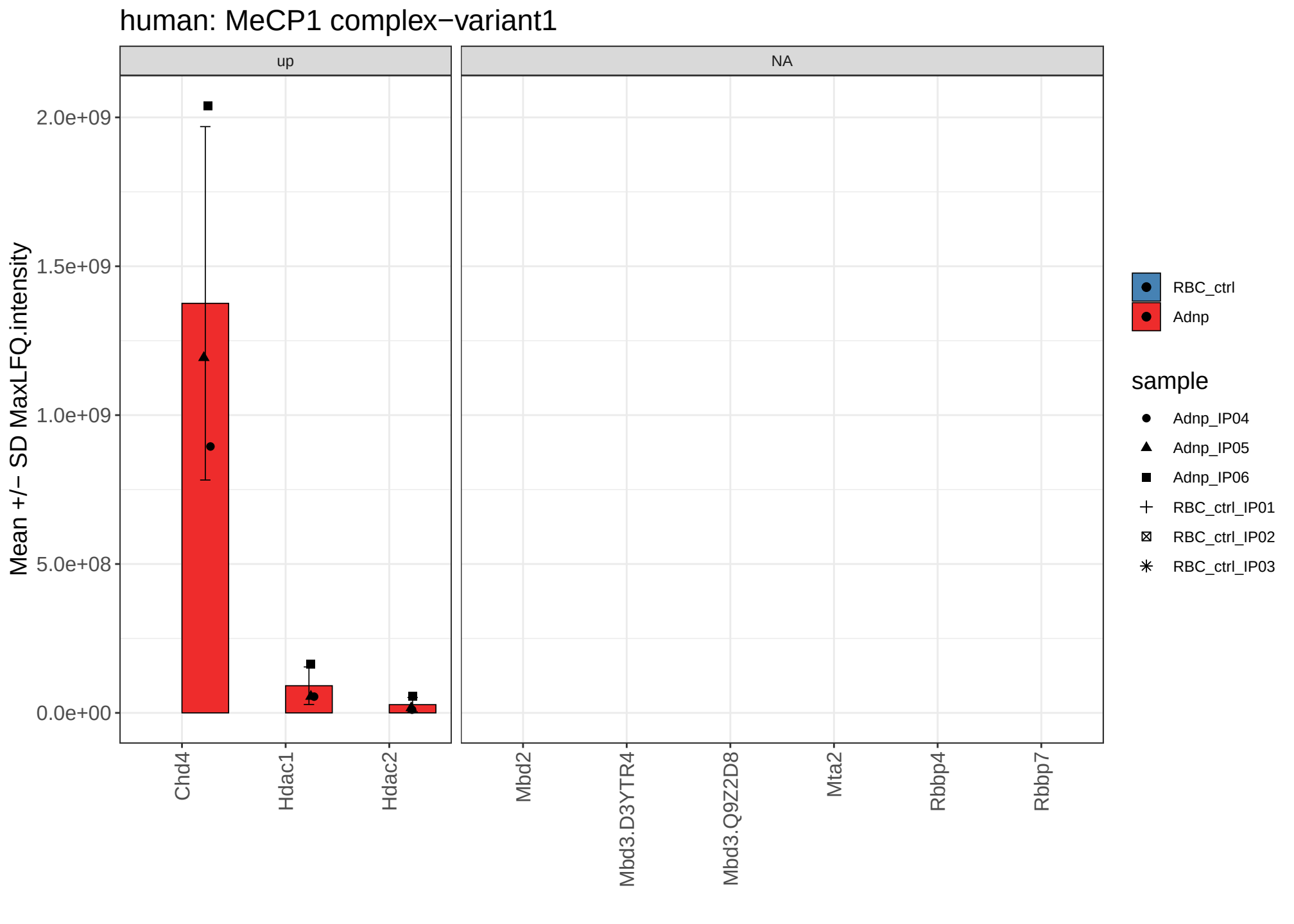

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac1
Hdac2
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
mouse: Ikaros−NuRD complex, PValue = 0.000949, FDR = 0.0103

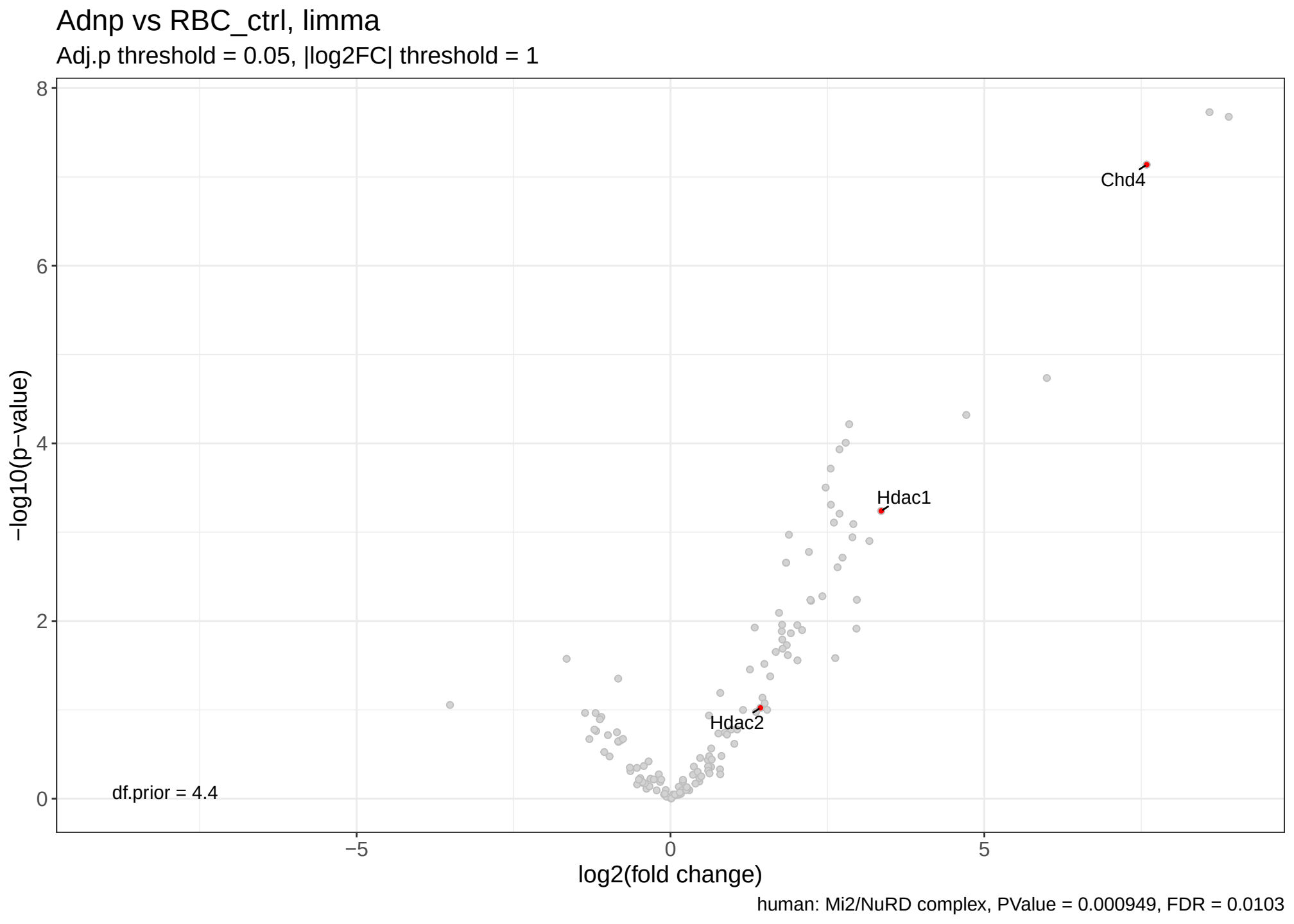

mouse: Ikaros−NuRD complex
up
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

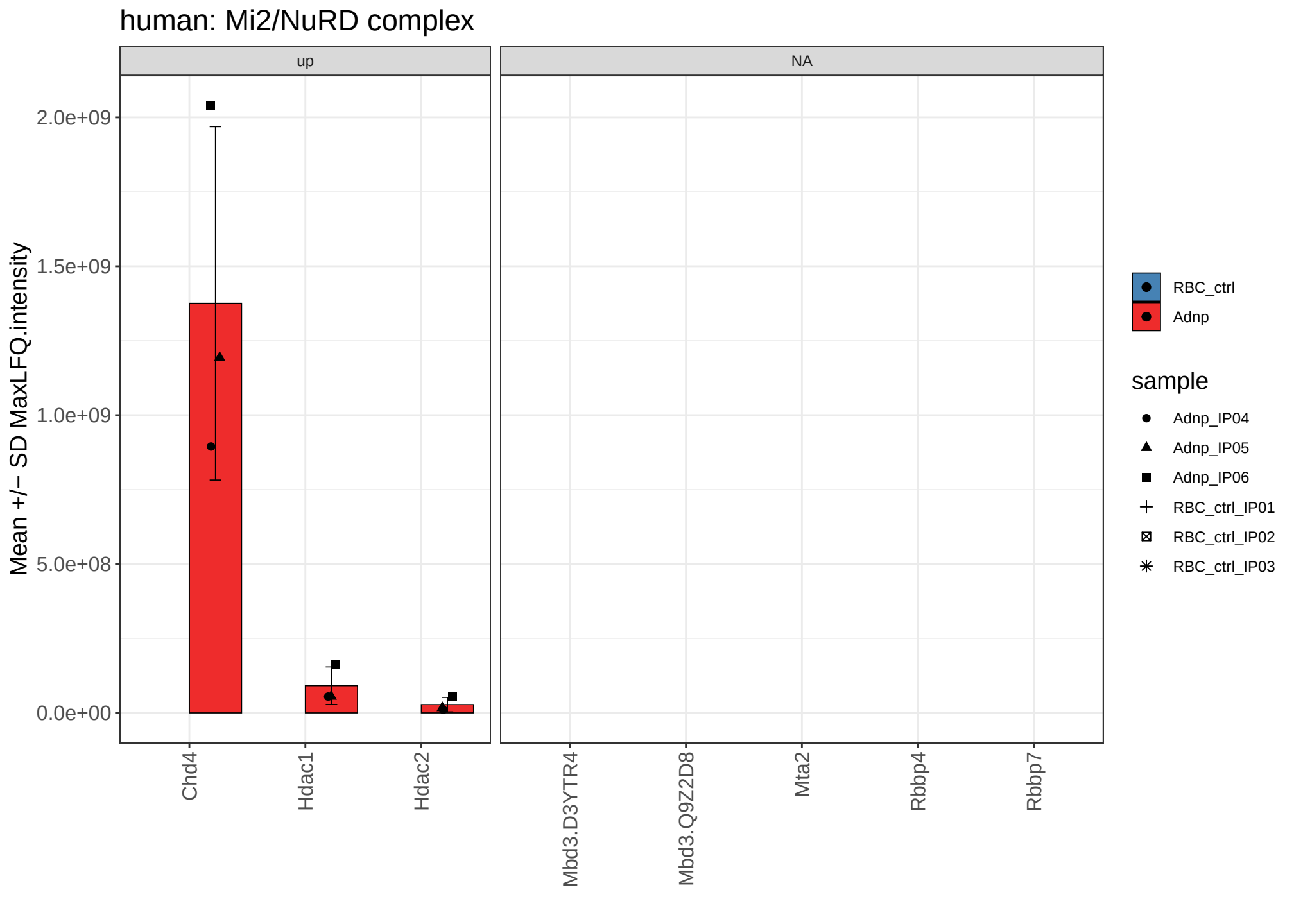

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Hdac2
df.prior = 4.4
human: MeCP1 complex, PValue = 0.000949, FDR = 0.0103

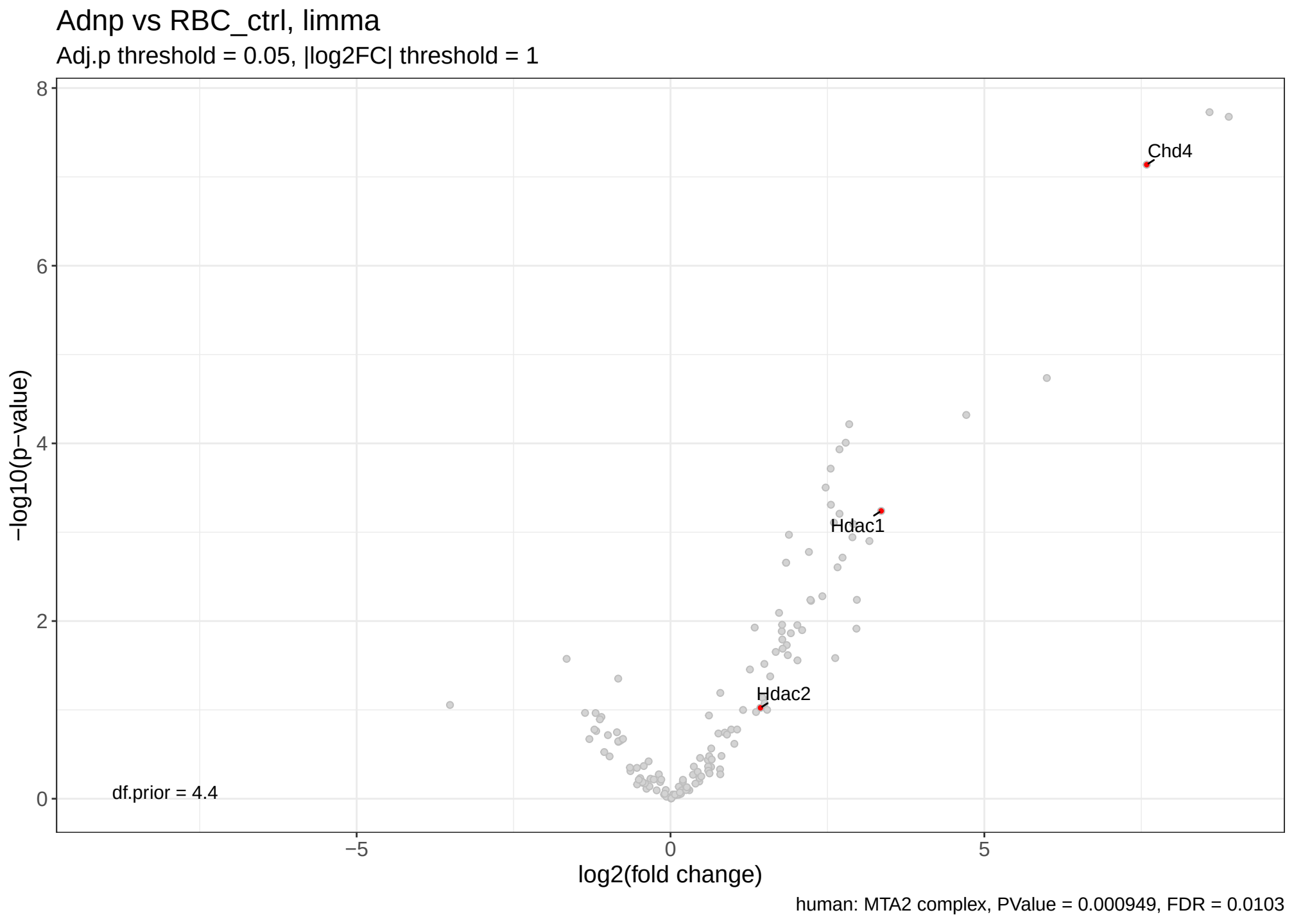

human: MeCP1 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Gatad2b
Mbd2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

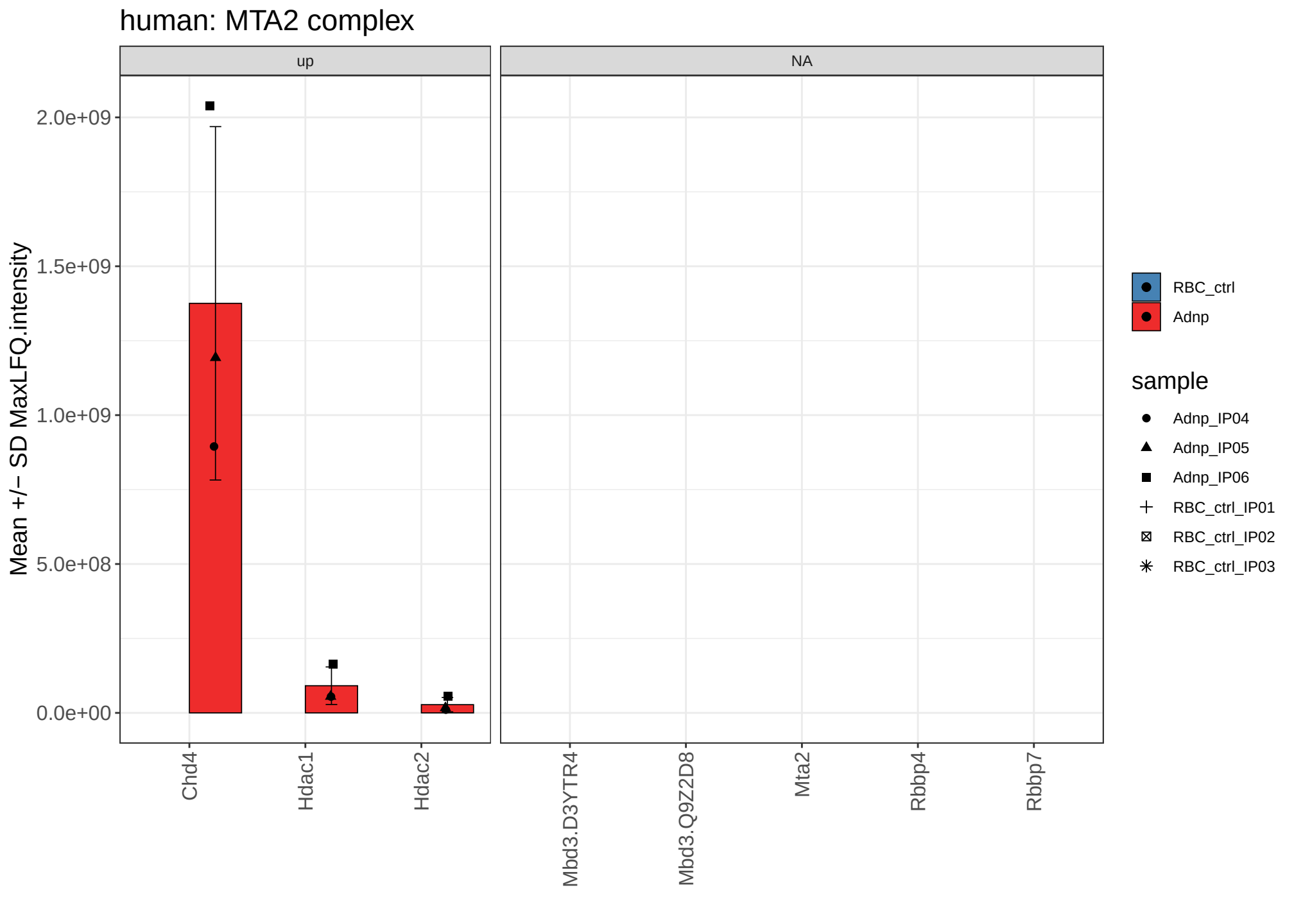

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac1
Hdac2
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
human: MeCP1 complex−variant1, PValue = 0.000949, FDR = 0.0103

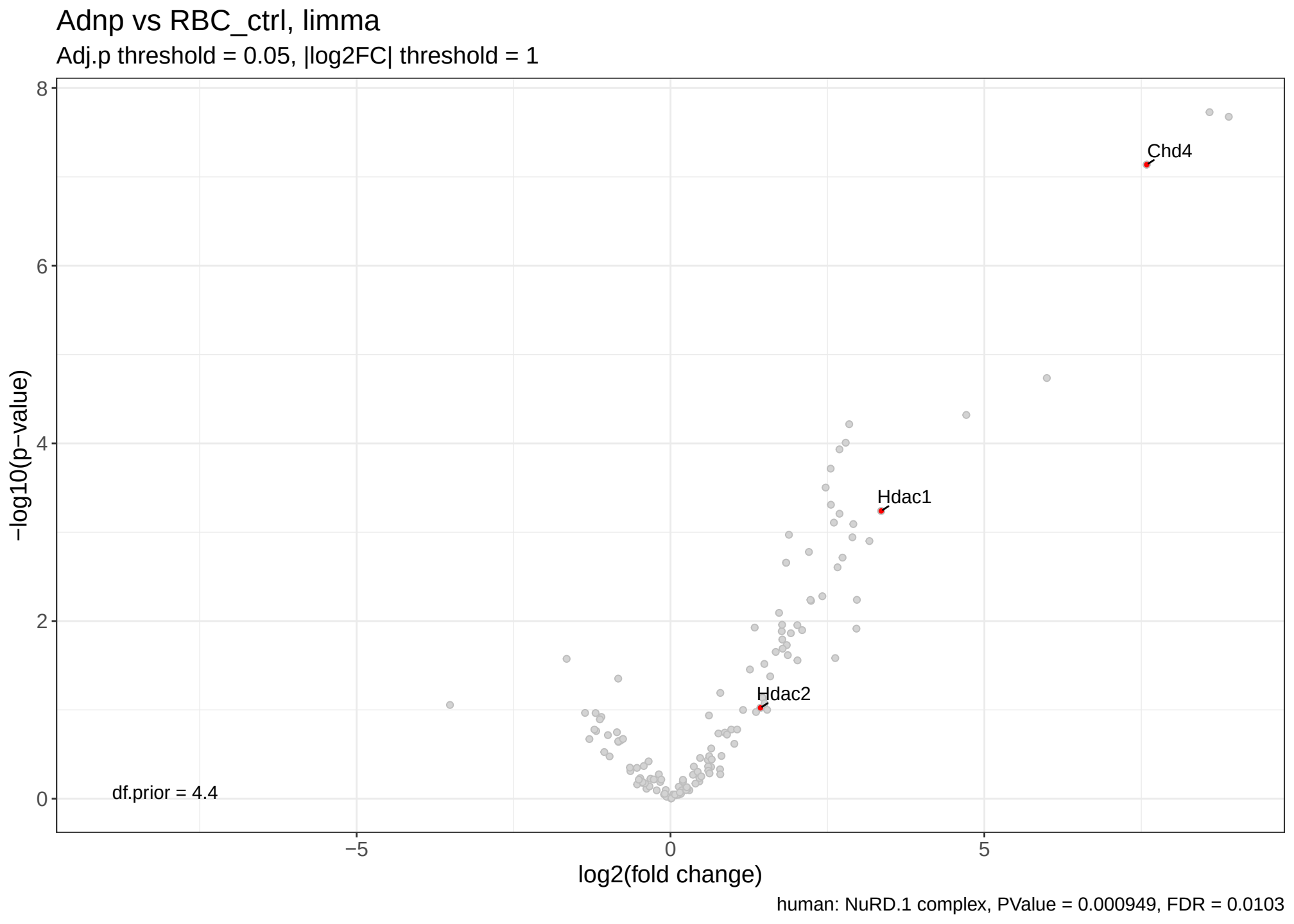

human: MeCP1 complex−variant1
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Mbd2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

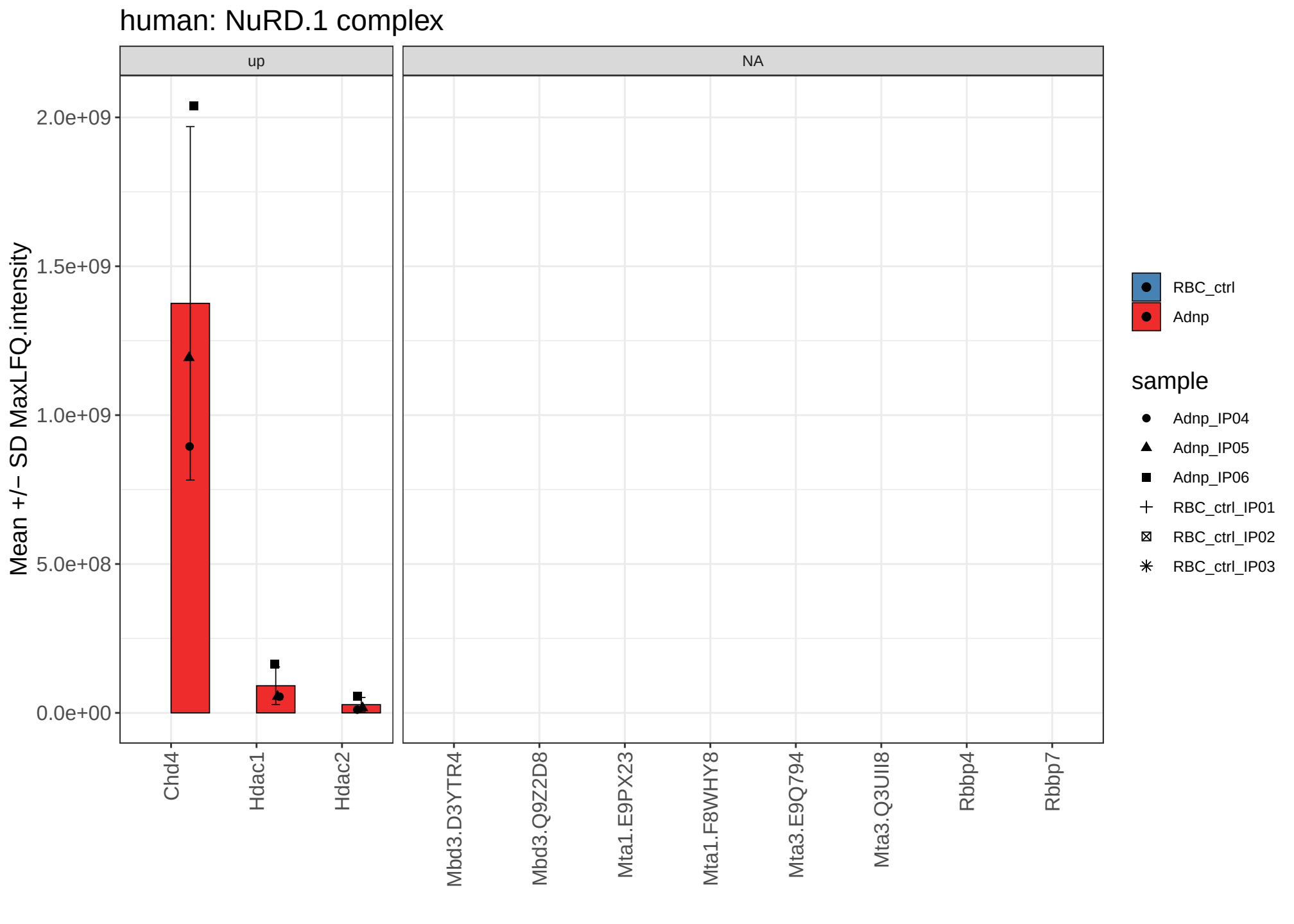

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Hdac2
df.prior = 4.4
human: Mi2/NuRD complex, PValue = 0.000949, FDR = 0.0103

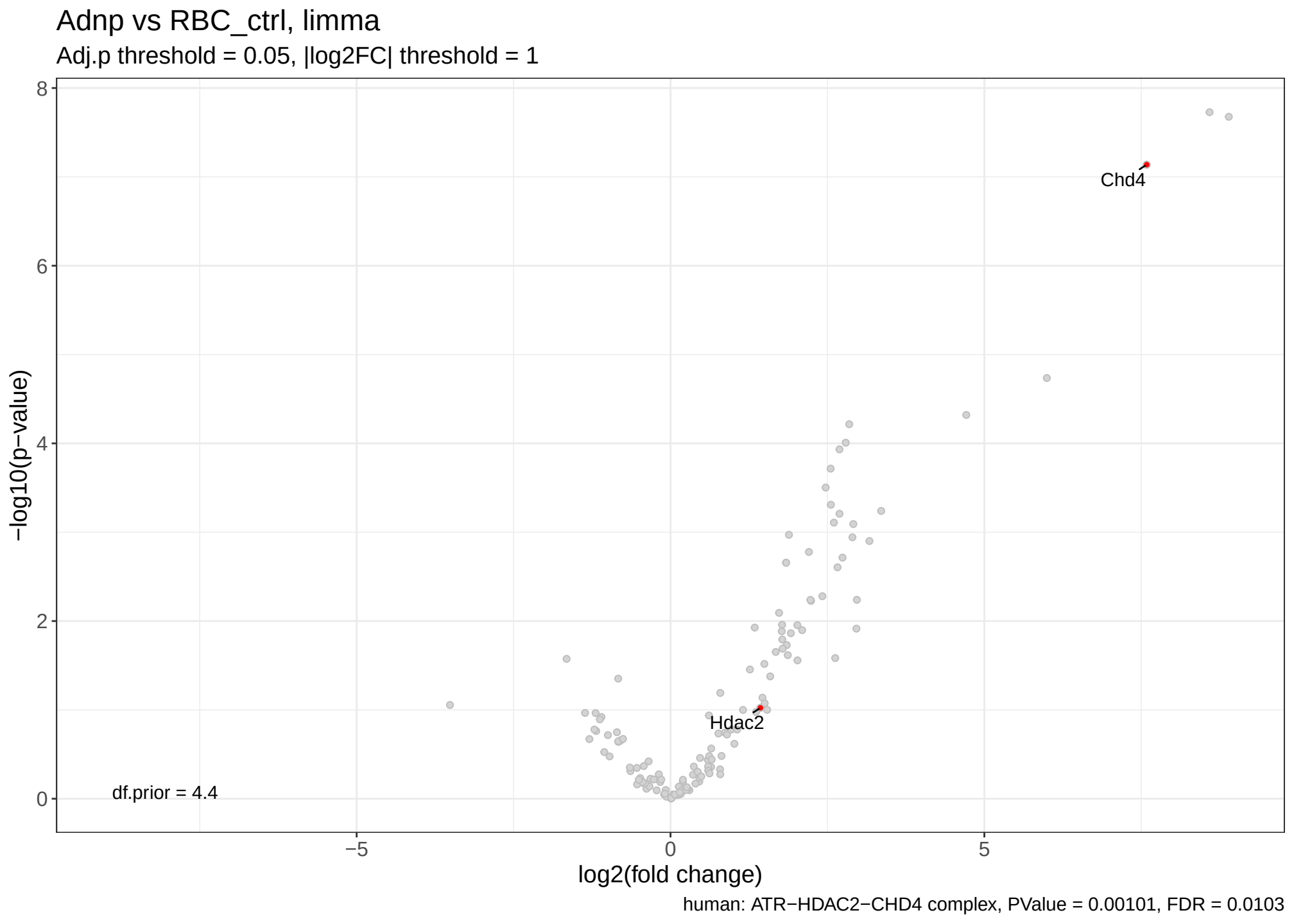

human: Mi2/NuRD complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

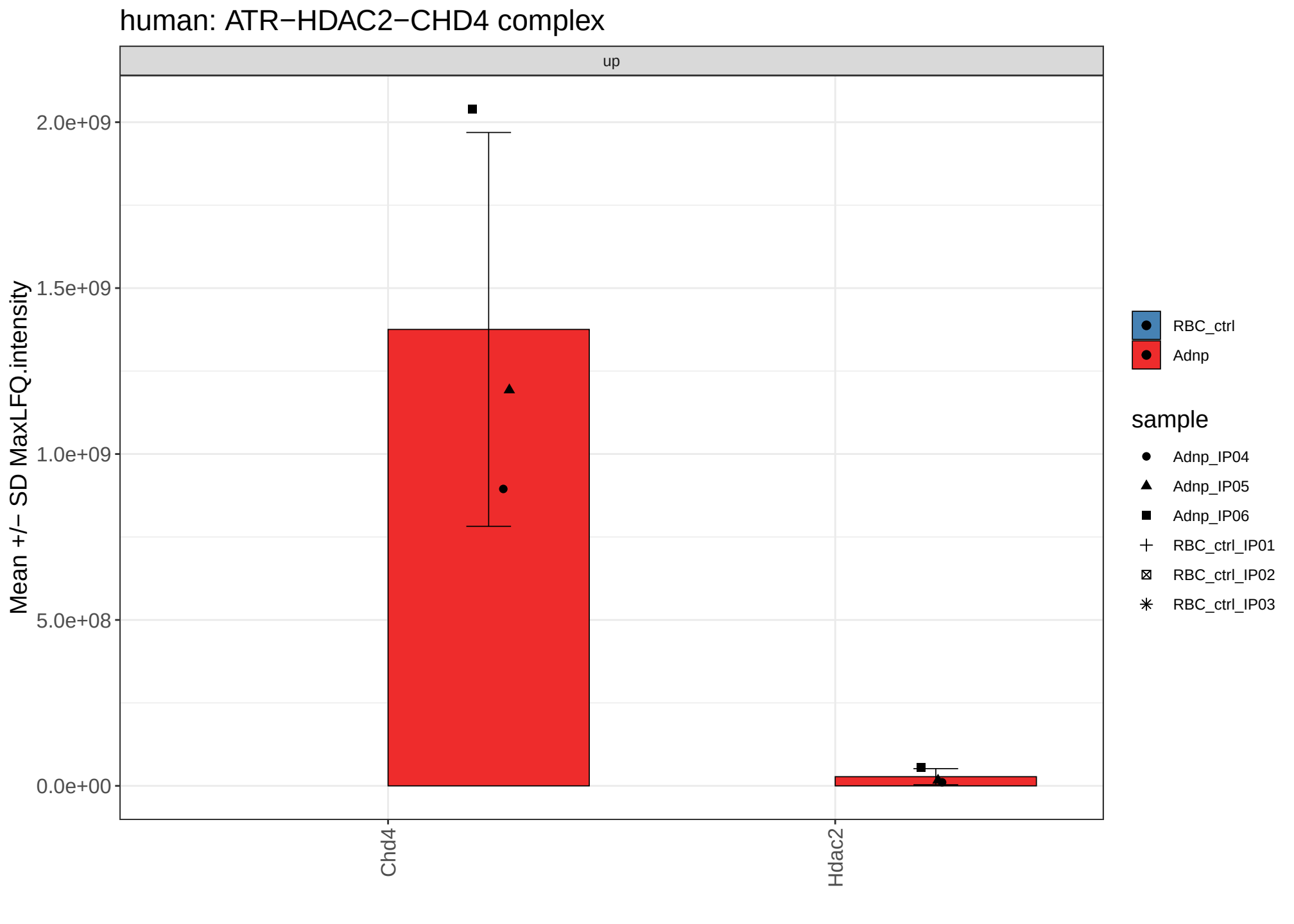

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac1
Hdac2
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
human: MTA2 complex, PValue = 0.000949, FDR = 0.0103

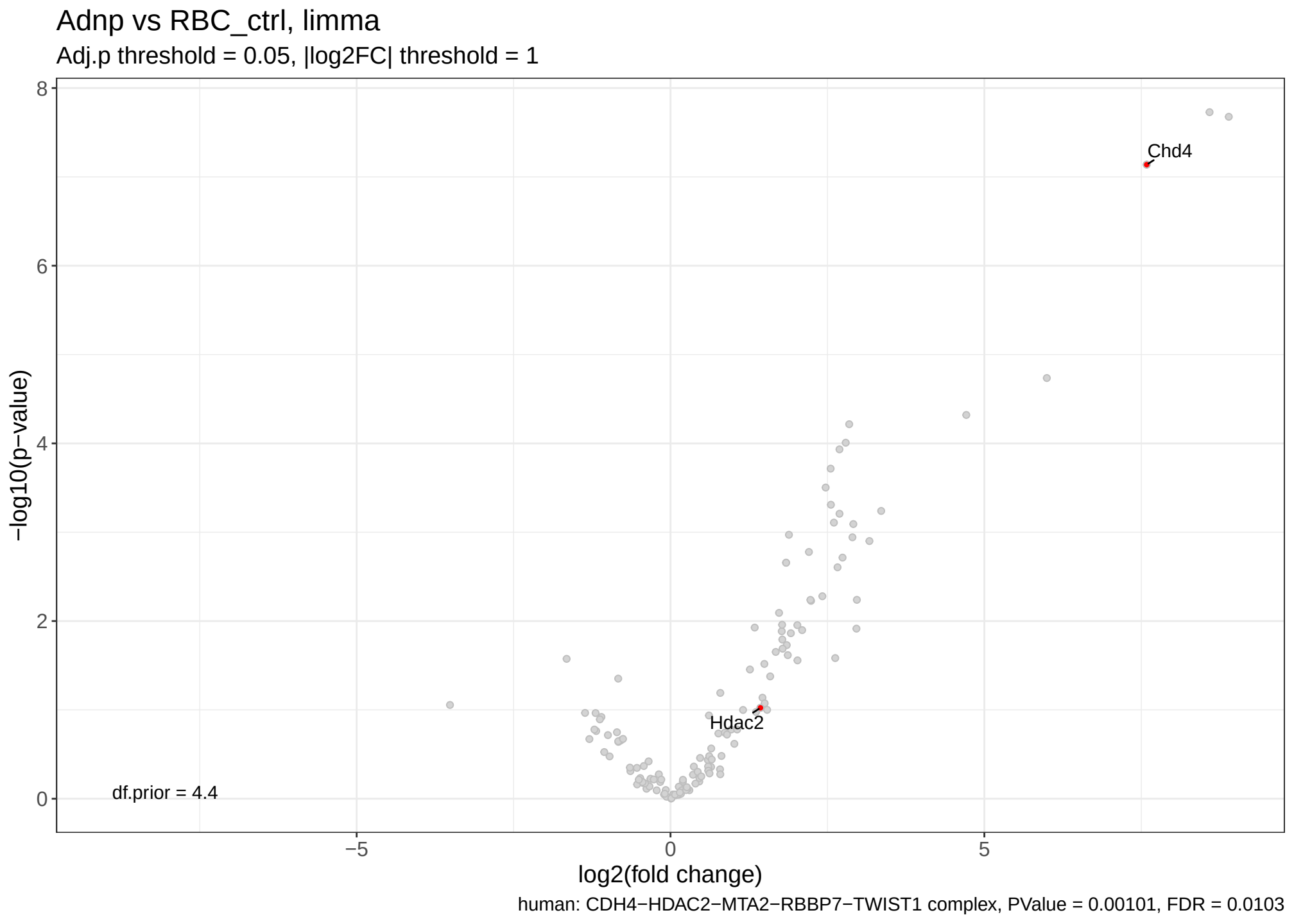

human: MTA2 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

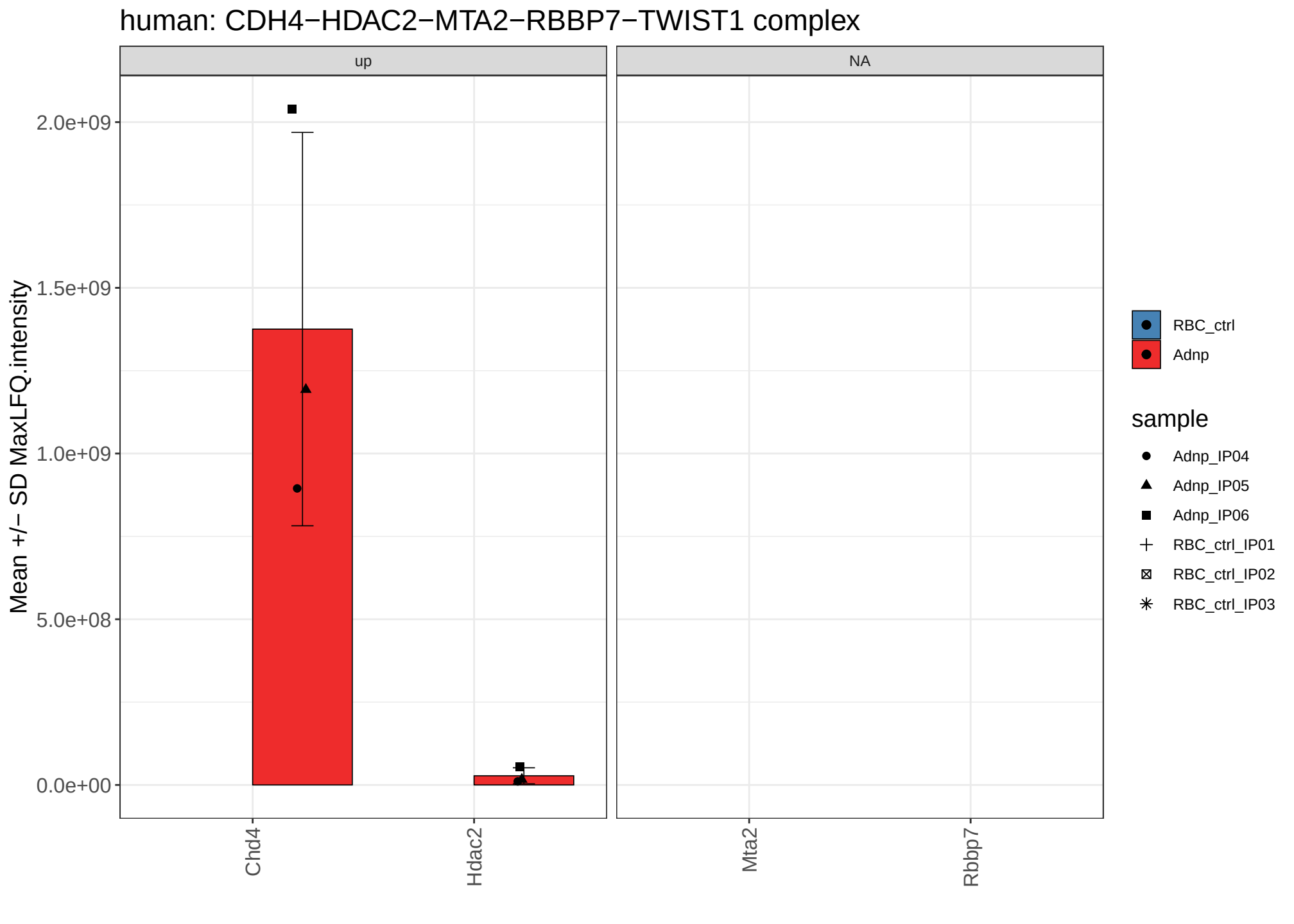

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Hdac2
df.prior = 4.4
human: NuRD.1 complex, PValue = 0.000949, FDR = 0.0103

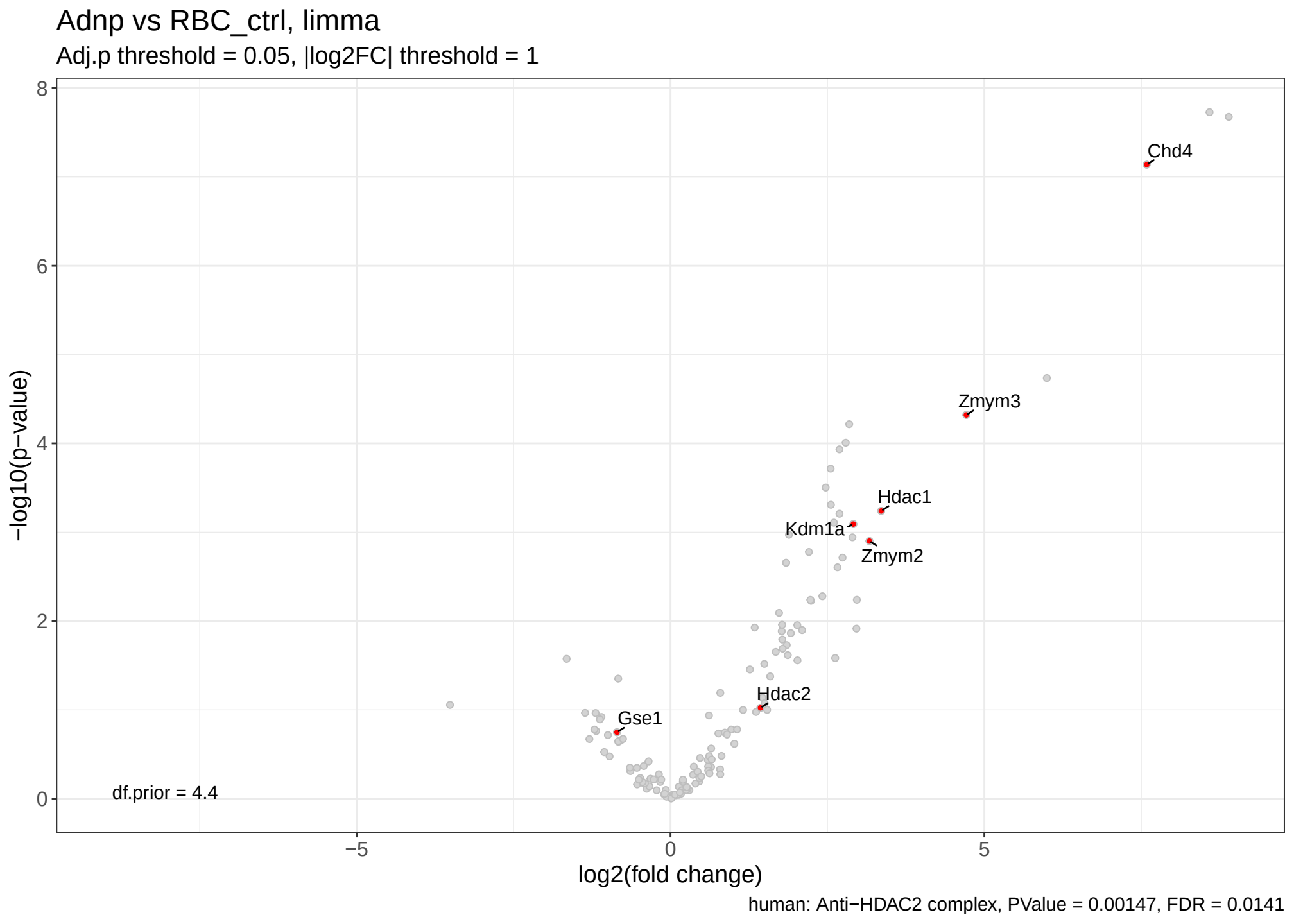

human: NuRD.1 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac1
Hdac2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta1.E9PX23
Mta1.F8WHY8
Mta3.E9Q794
Mta3.Q3UII8
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

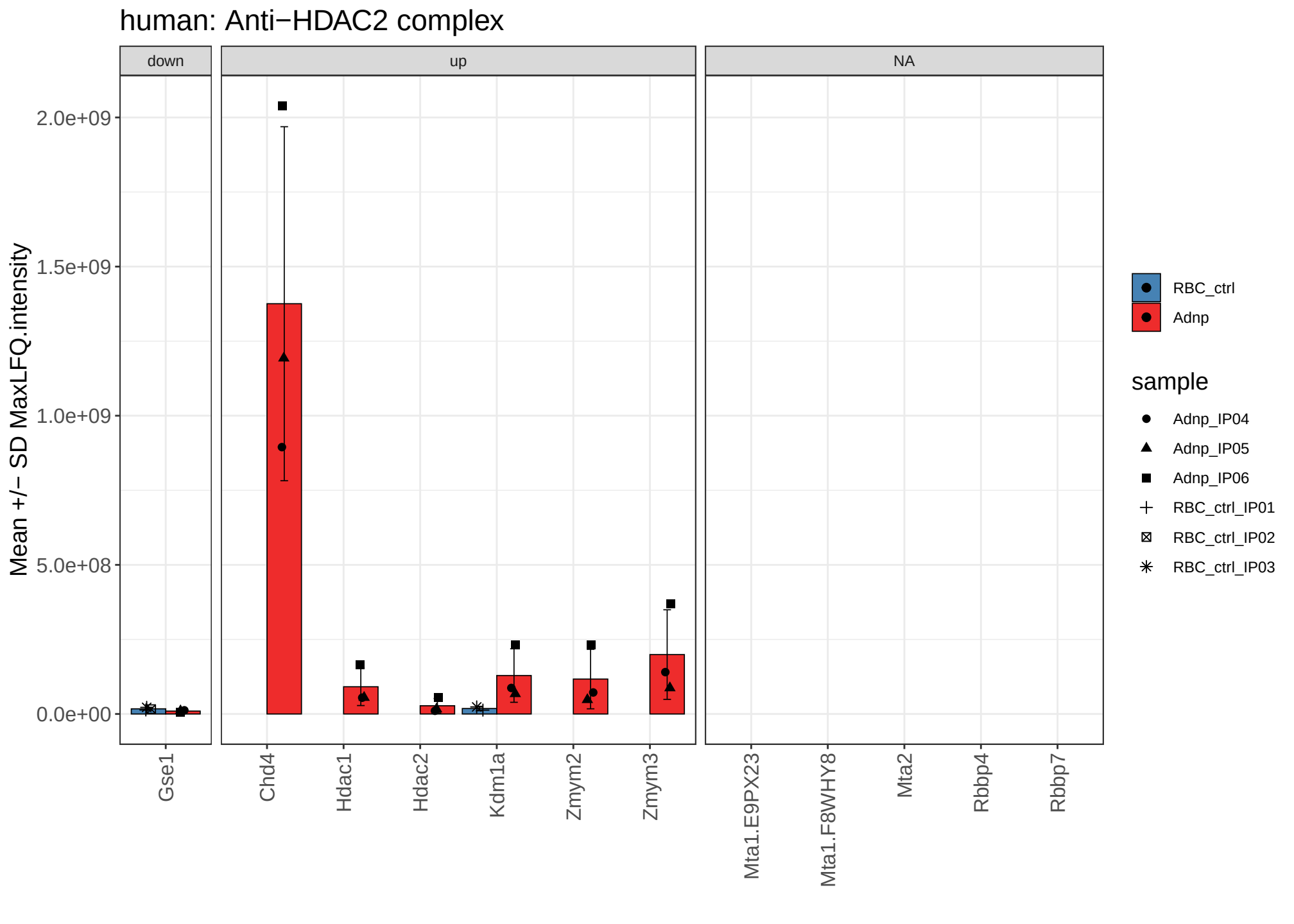

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac2
df.prior = 4.4
human: ATR−HDAC2−CHD4 complex, PValue = 0.00101, FDR = 0.0103

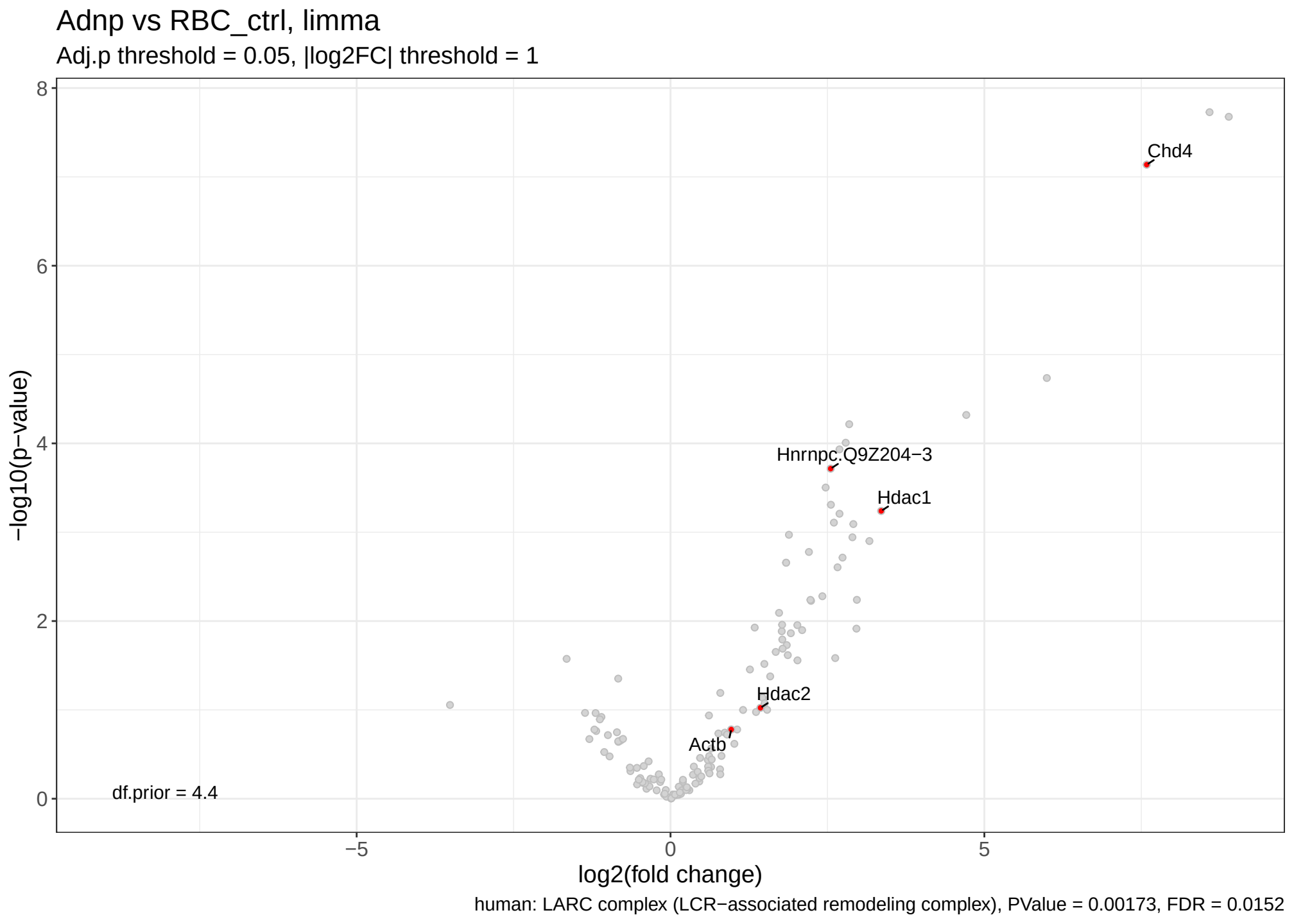

human: ATR−HDAC2−CHD4 complex
up
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac2
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

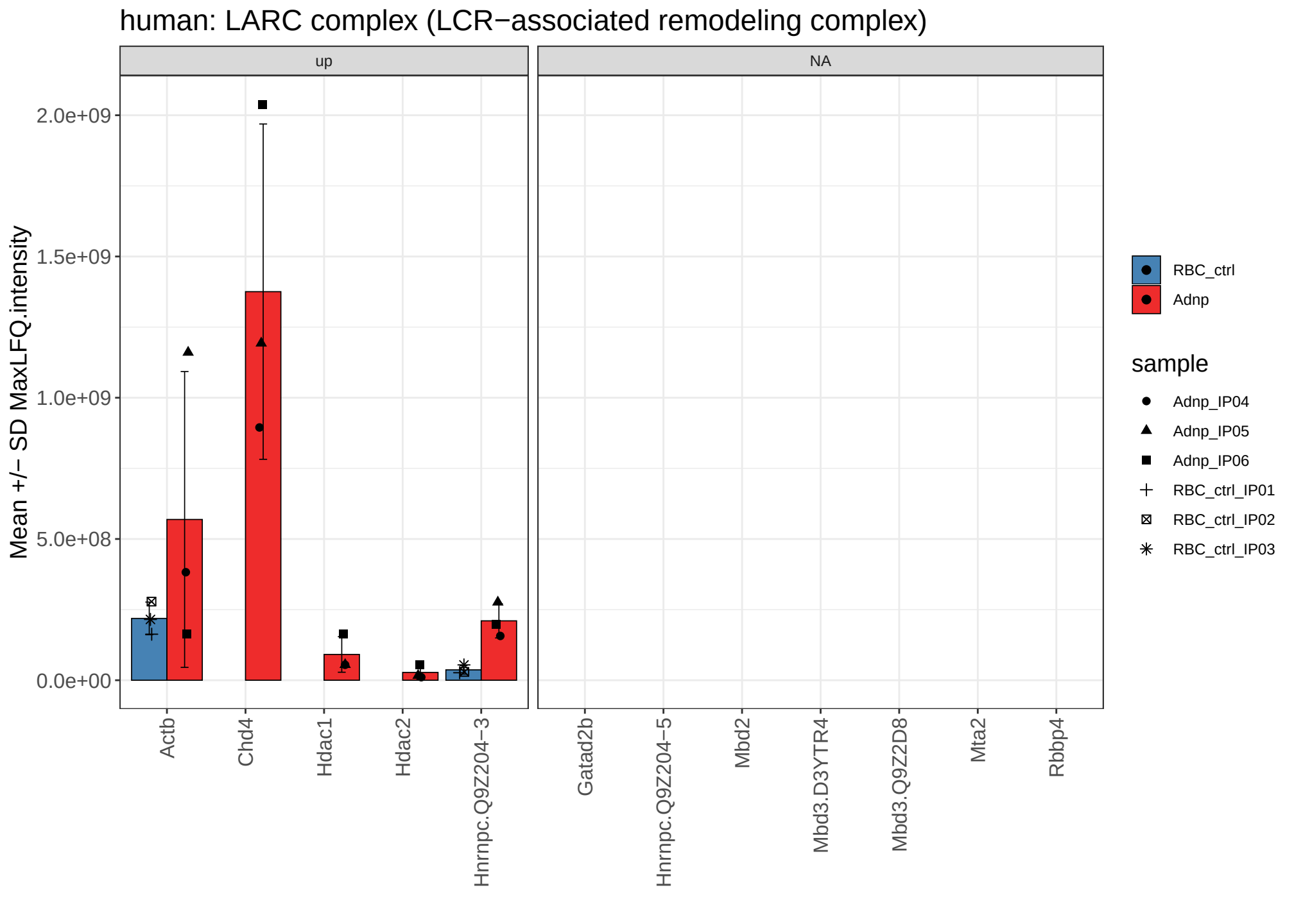

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
Chd4
Hdac2
df.prior = 4.4
−log10(p−value)
log2(fold change)
8
6
4
2
0
−5
0
5
human: CDH4−HDAC2−MTA2−RBBP7−TWIST1 complex, PValue = 0.00101, FDR = 0.0103

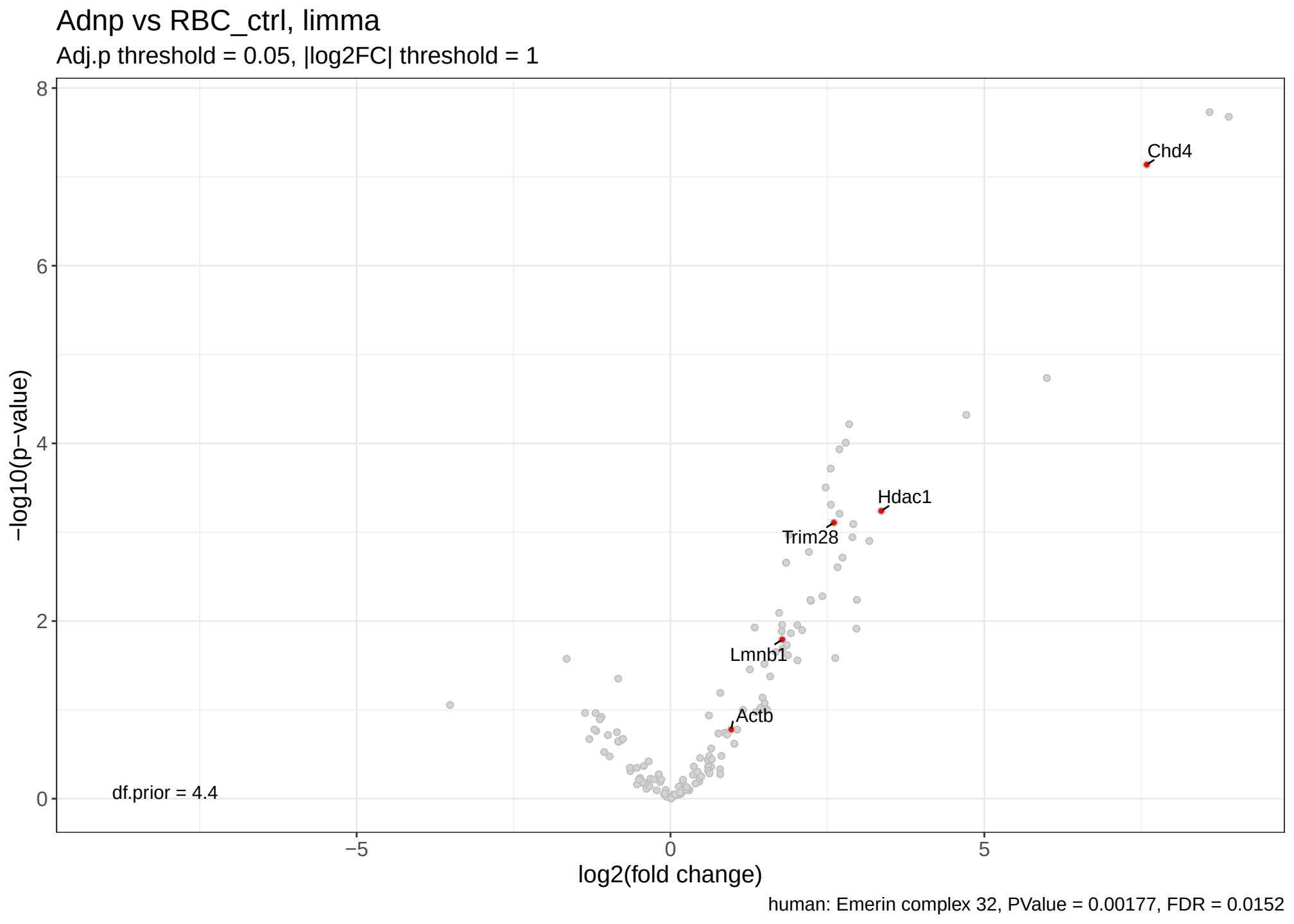

human: CDH4−HDAC2−MTA2−RBBP7−TWIST1 complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Chd4
Hdac2
Mta2
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

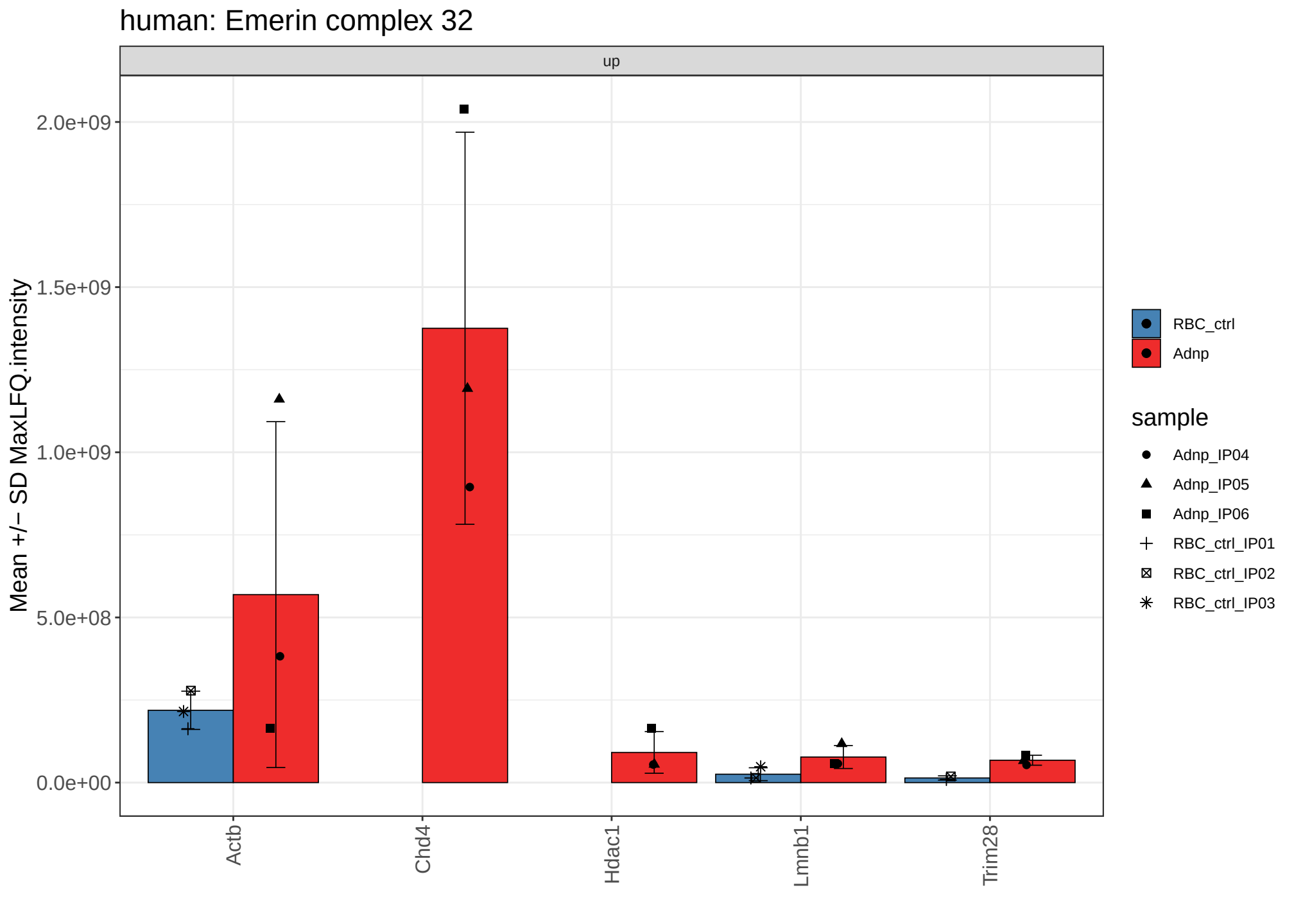

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Zmym3
Hdac1
Kdm1a
Zmym2
Hdac2
Gse1
df.prior = 4.4
human: Anti−HDAC2 complex, PValue = 0.00147, FDR = 0.0141

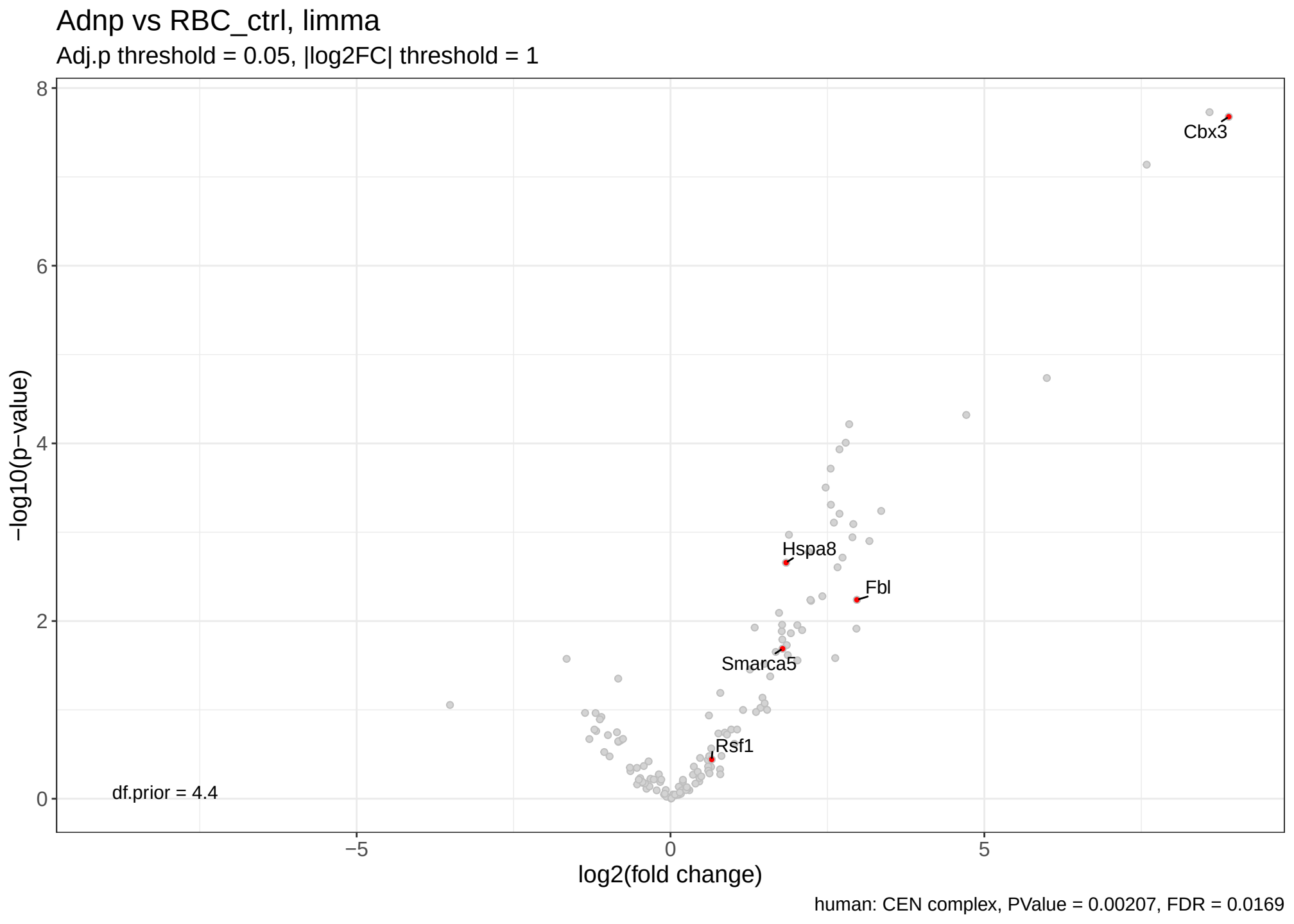

human: Anti−HDAC2 complex
down
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Gse1
Chd4
Hdac1
Hdac2
Kdm1a
Zmym2
Zmym3
Mta1.E9PX23
Mta1.F8WHY8
Mta2
Rbbp4
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

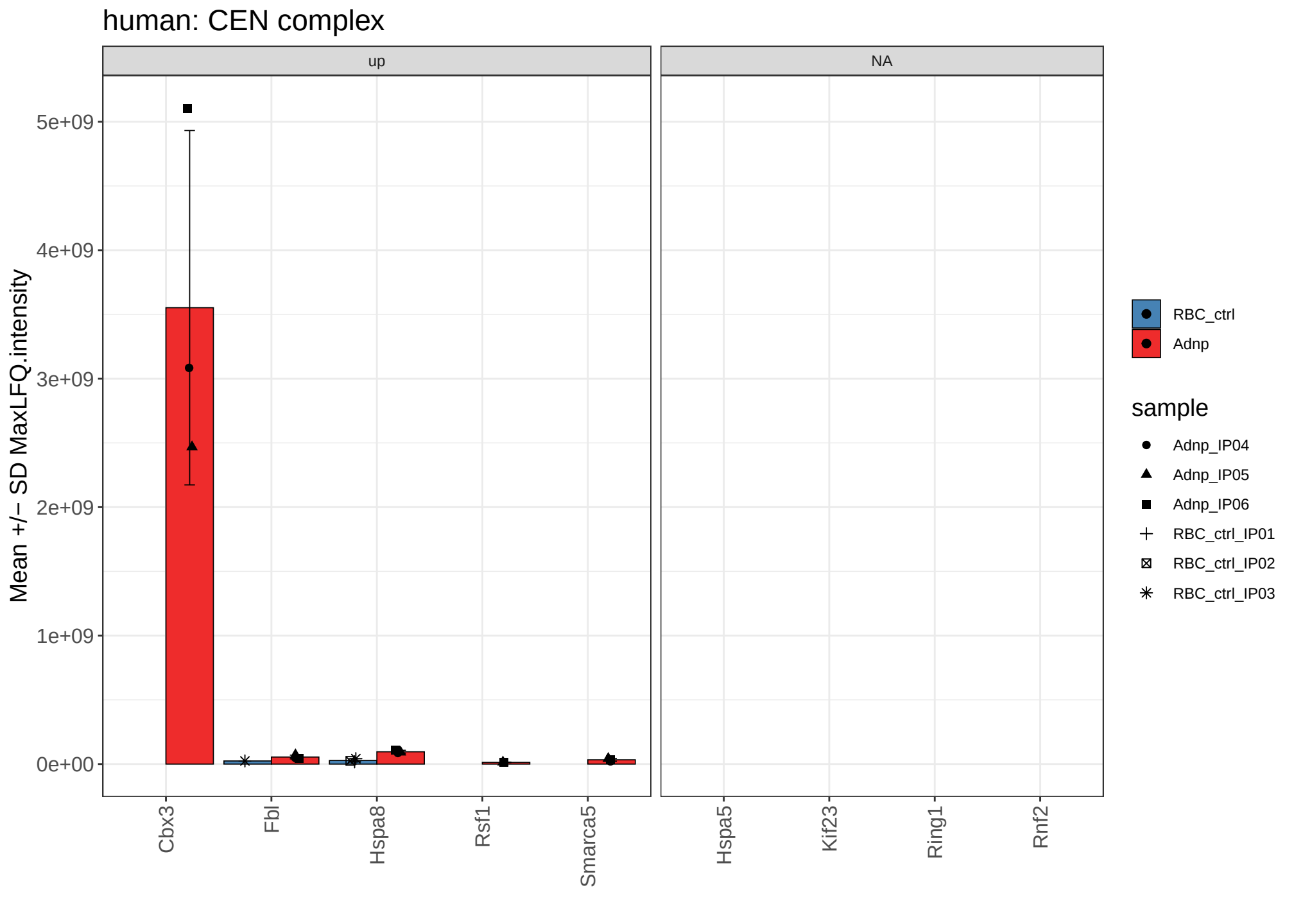

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hnrnpc.Q9Z204−3
Hdac1
Hdac2
Actb
df.prior = 4.4
human: LARC complex (LCR−associated remodeling complex), PValue = 0.00173, FDR = 0.0152

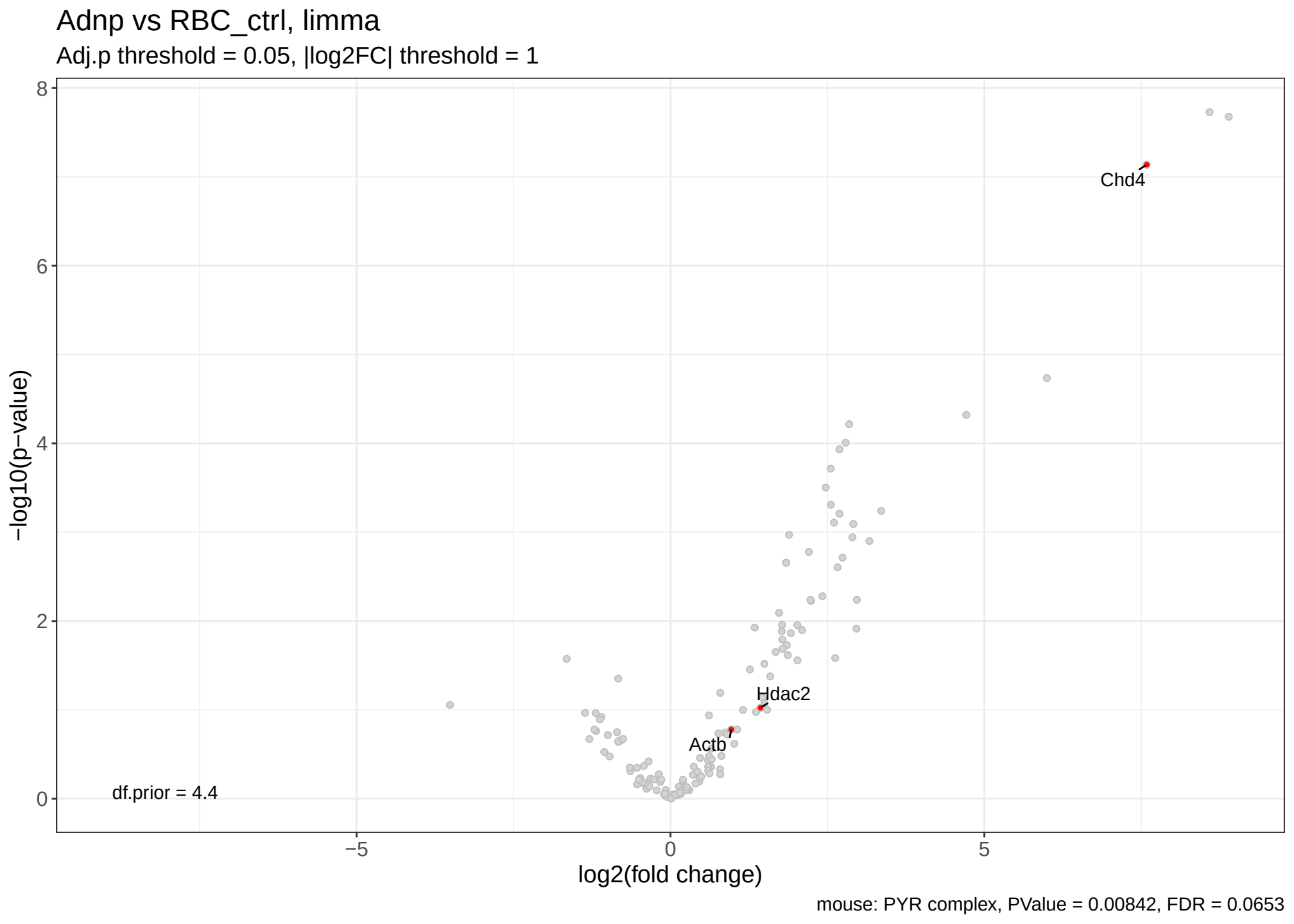

human: LARC complex (LCR−associated remodeling complex)
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Actb
Chd4
Hdac1
Hdac2
Hnrnpc.Q9Z204−3
Gatad2b
Hnrnpc.Q9Z204−5
Mbd2
Mbd3.D3YTR4
Mbd3.Q9Z2D8
Mta2
Rbbp4
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03

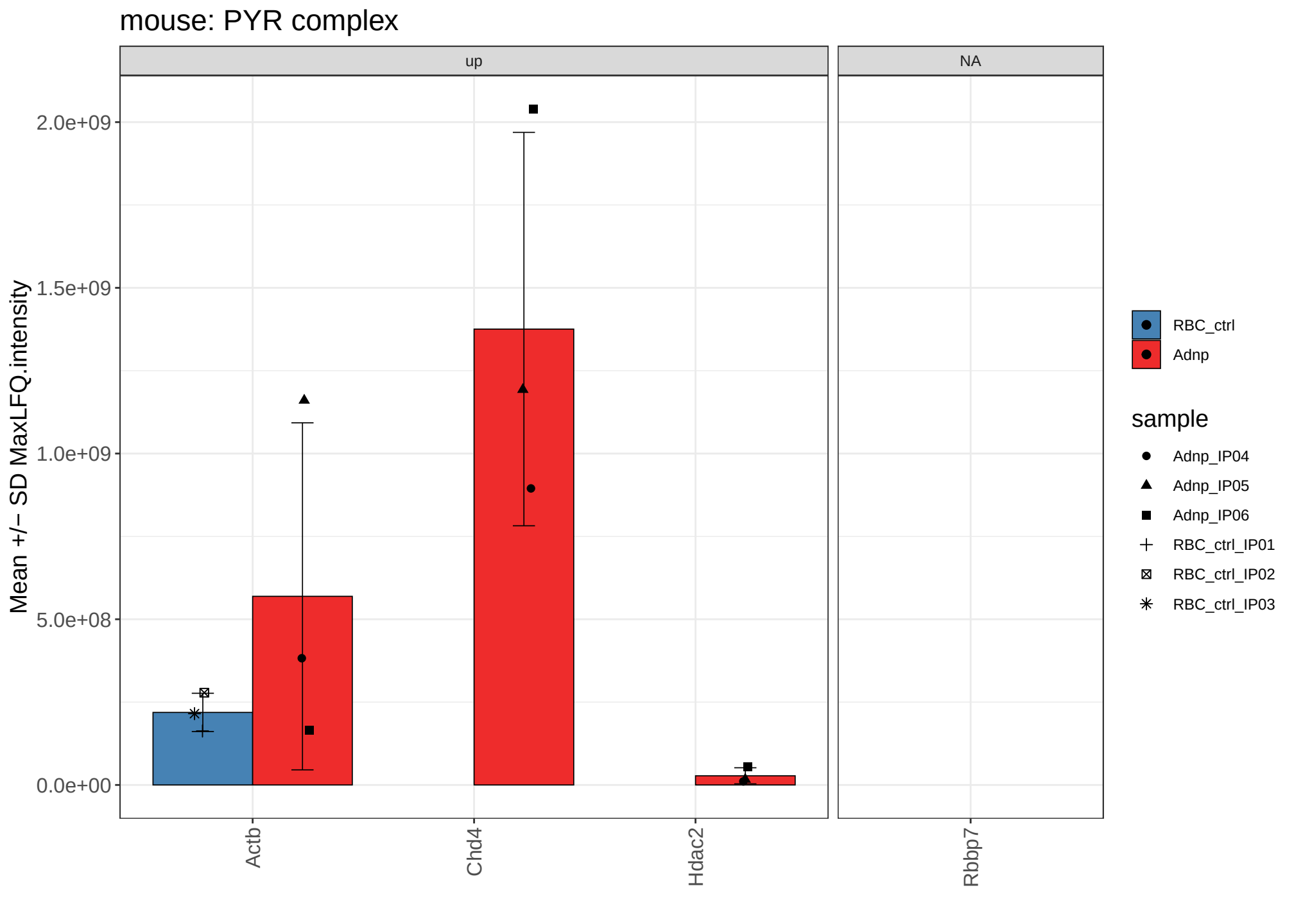

Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac1
Trim28
Lmnb1
Actb
df.prior = 4.4
human: Emerin complex 32, PValue = 0.00177, FDR = 0.0152


human: Emerin complex 32
up
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Actb
Chd4
Hdac1
Lmnb1
Trim28
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03


Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Cbx3
Hspa8
Fbl
Smarca5
Rsf1
df.prior = 4.4
human: CEN complex, PValue = 0.00207, FDR = 0.0169


human: CEN complex
up
NA
Mean +/− SD MaxLFQ.intensity
5e+09
4e+09
3e+09
2e+09
1e+09
0e+00
Cbx3
Fbl
Hspa8
Rsf1
Smarca5
Hspa5
Kif23
Ring1
Rnf2
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03


Adnp vs RBC_ctrl, limma
Adj.p threshold = 0.05, |log2FC| threshold = 1
−log10(p−value)
log2(fold change)
Chd4
Hdac2
Actb
df.prior = 4.4
mouse: PYR complex, PValue = 0.00842, FDR = 0.0653


mouse: PYR complex
up
NA
Mean +/− SD MaxLFQ.intensity
2.0e+09
1.5e+09
1.0e+09
5.0e+08
0.0e+00
Actb
Chd4
Hdac2
Rbbp7
RBC_ctrl
Adnp
sample
Adnp_IP04
Adnp_IP05
Adnp_IP06
RBC_ctrl_IP01
RBC_ctrl_IP02
RBC_ctrl_IP03