

Interchromosomal interactions by cryoFISH

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Probes Info

Probe id	Probes name	mm9 coordinates	mm10 coordinates		
RP24-301L12	SE17B	chr17:29209678-29359671	chr17	29072733	29222726
RP23-271M12	SE17A	chr17:29418431-29611542	chr17	29281486	29474597

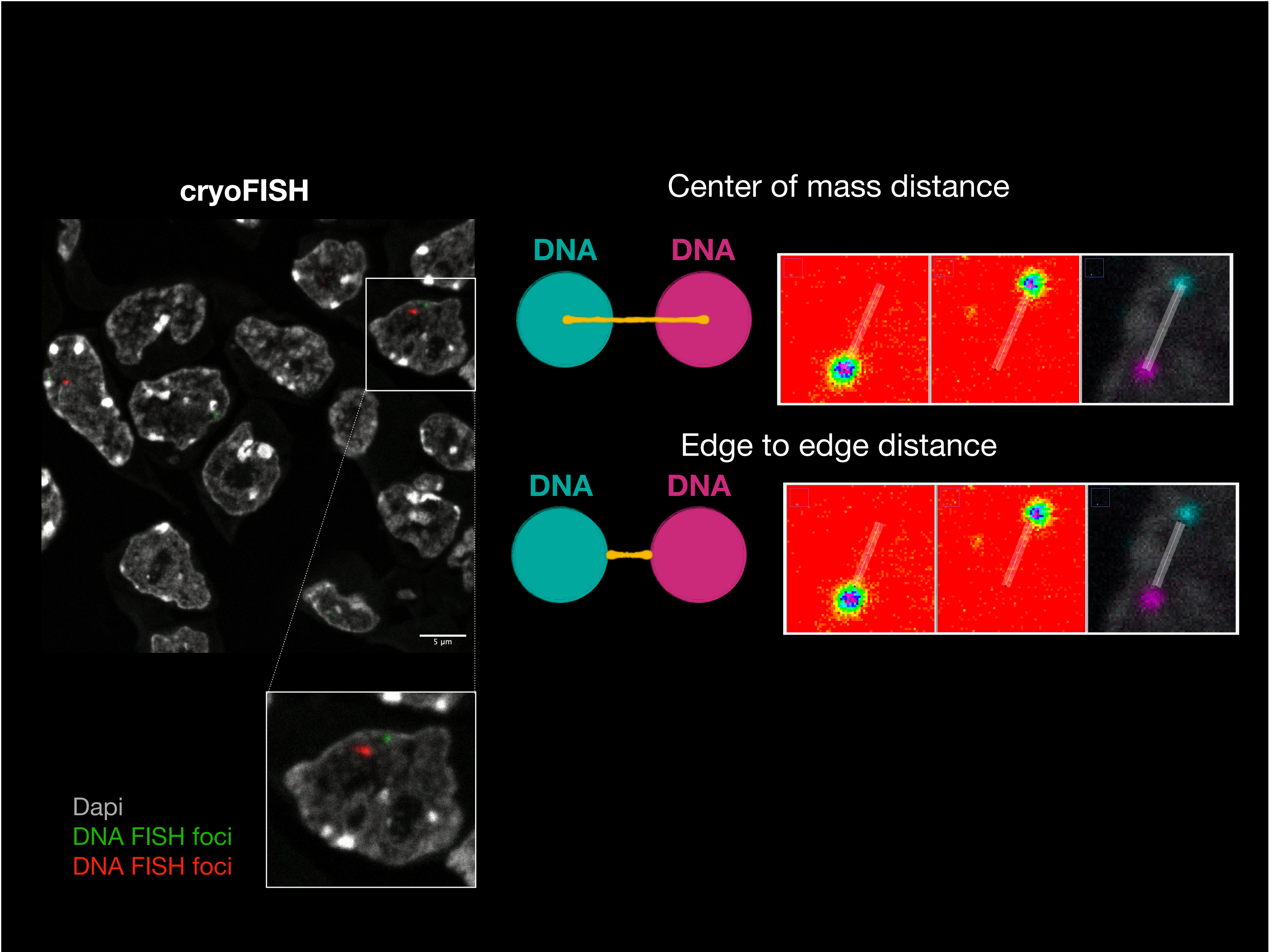
RP24-342H23	2mTAD1	chr2:118620573-118804850	chr2	118794837	118979114
RP23-360K10	2hTAD2	chr2:118852412-119047211	chr2	119026676	119221475
RP23-388F24	2hTAD3	chr2:120154144-120335204	chr2	120328408	120509468
RP23-158L6	2hTAD3A	chr2:120335831-120539128	chr2	120510095	120713392
RP23-467K21	2hTAD3-4	chr2:121247622-121428193	chr2	121421886	121602457

RP23-307O19	14mTAD1	chr14:51398359-51575185	chr14	50778684	50955510
RP23-258M10	14hTAD2	chr14:56169403-56330093	chr14	55550566	55711256
RP23-290G5	14hTAD3	chr14:56389307-56571860	chr14	55770470	55953023
RP23-67O12	14mTAD4	chr14:68272104-68540410	chr14	67654047	67922353
RP24-330L18	14SETAD5	chr14:70908979-71073229	chr14	70509172	70673422

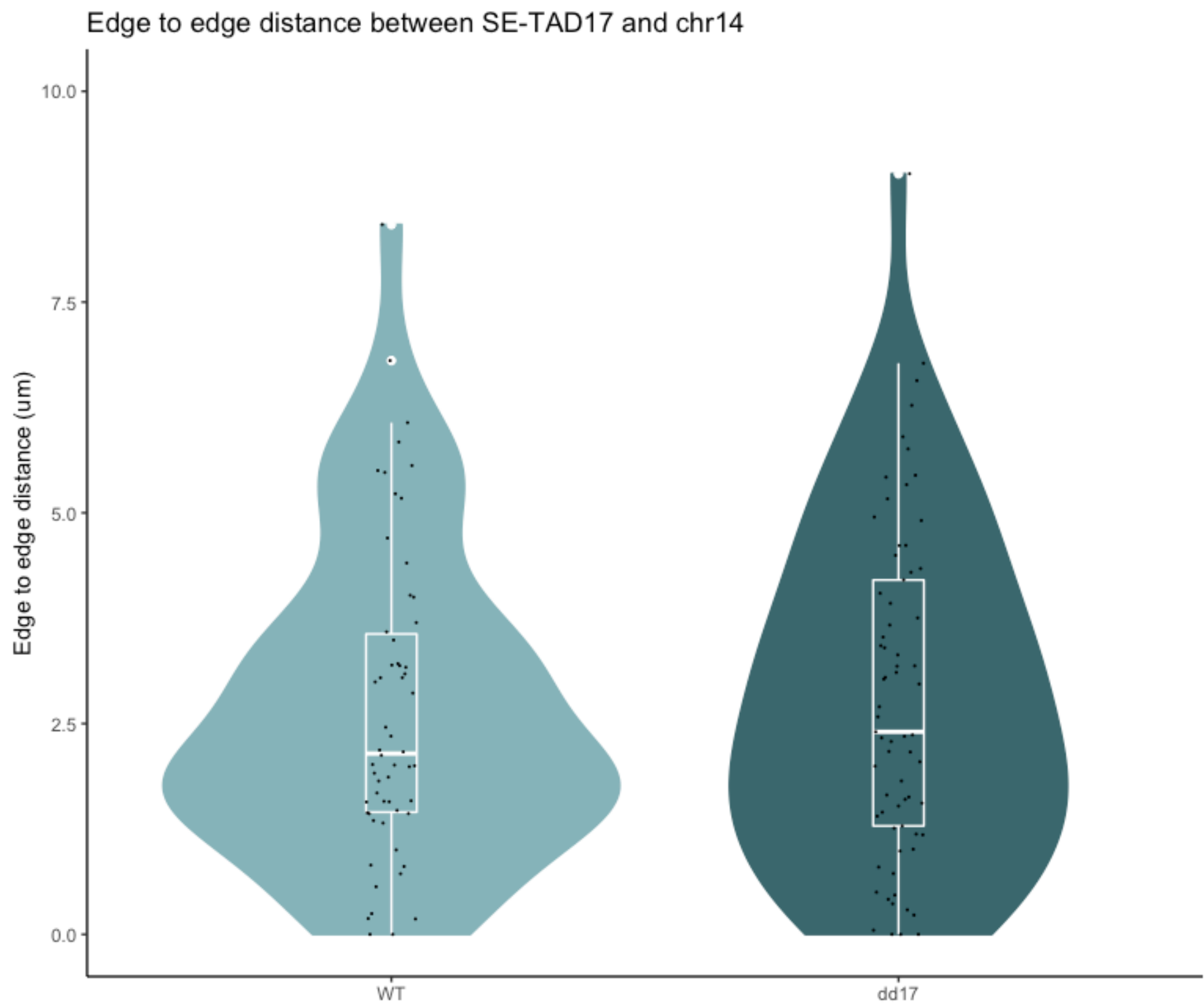
Cryosections Info

mESC 46C, cryoblock: T2T10P48/T2T10P49, 600 nm thickness

CryoFISH measurements between foci

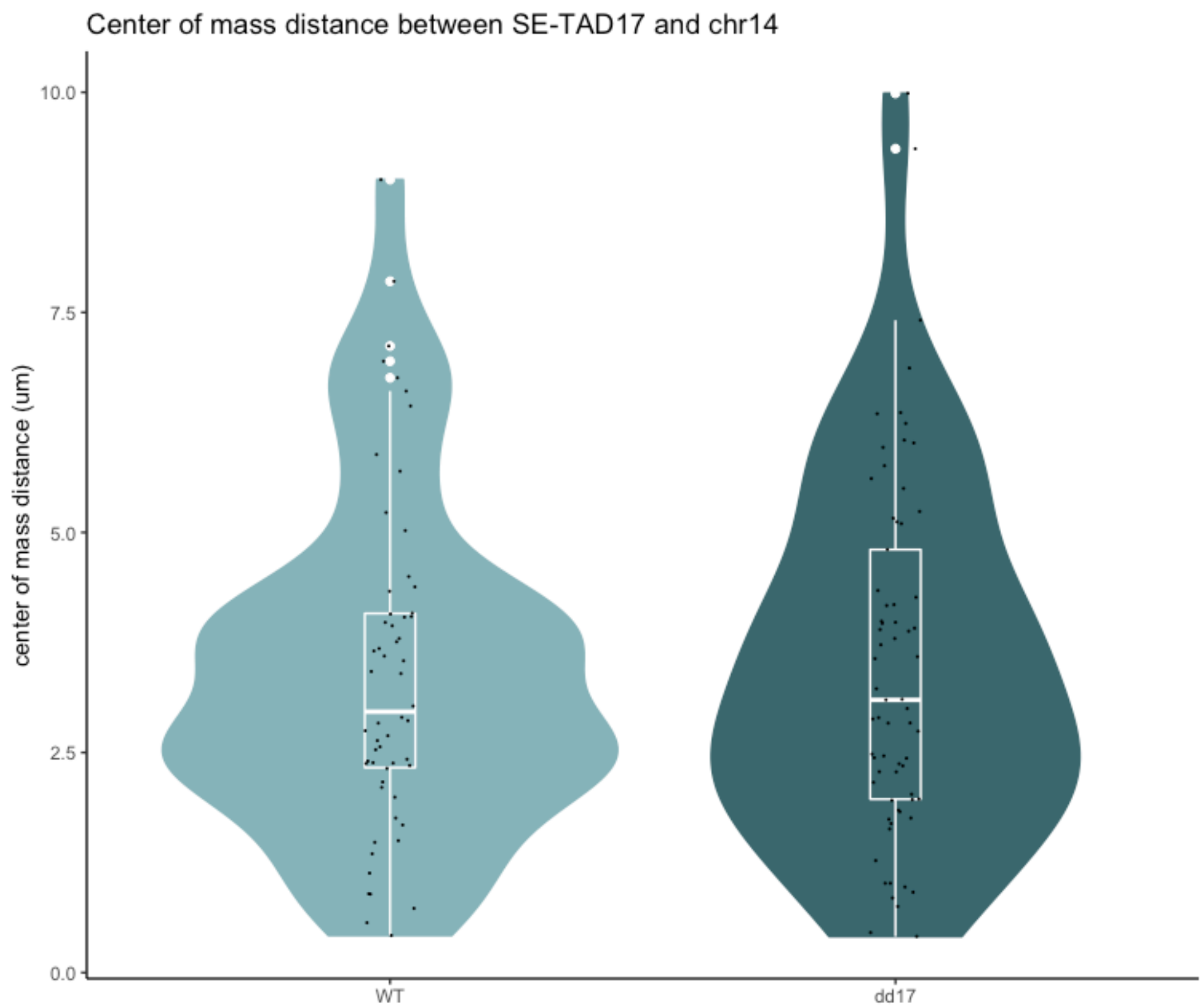


Distances between SE17A, SE17B vs 14mTAD1,14hTAD2,14hTAD3,14mTAD4,14SETAD5



Min.	1st	Qu.	Median	Mean	3rd	Qu.	Max.
0	1	450	2.144	2.	683	3	564 8. 420

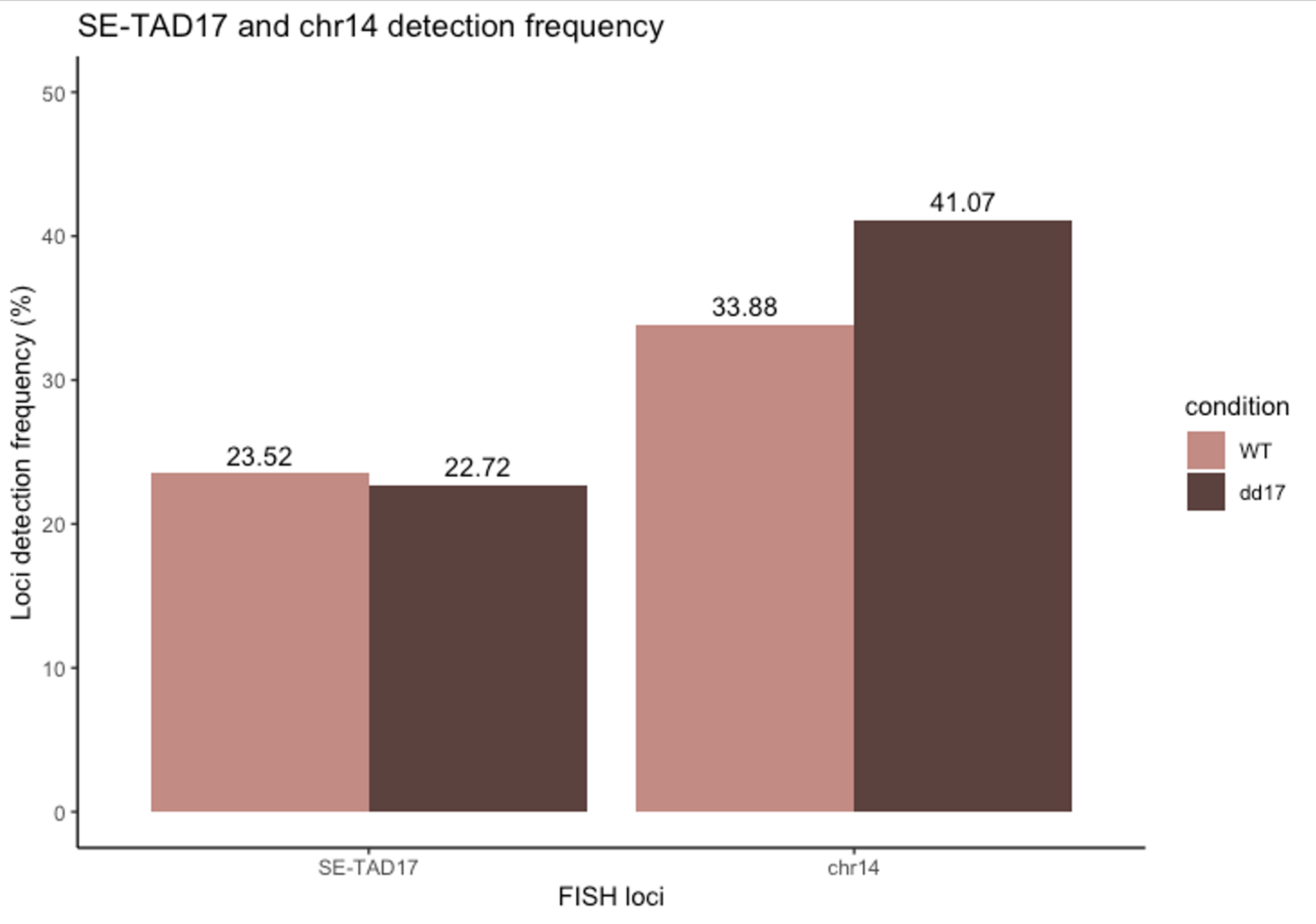
Min.	1st	Qu.	Median	Mean	3rd	Qu.	Max.
0	1	286	2.403	2.	818	4	204 9. 22



Min.	1st	Qu.	Median	Mean	3rd	Qu.	Max.
422	2	328	2.964	3	429	4	080 9 8

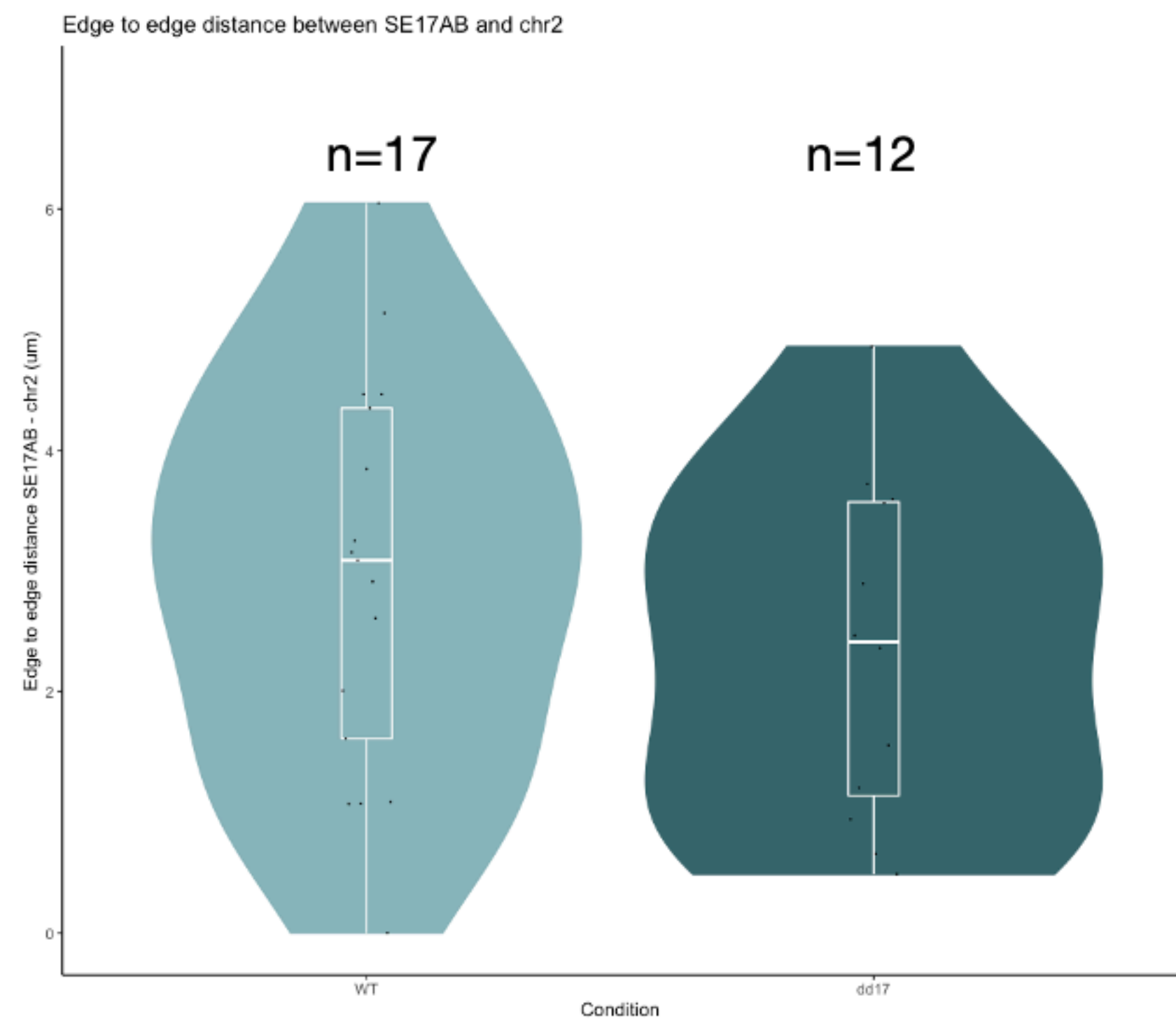
Min.	1st	Qu.	Median	Mean	3rd	Qu.	Max.
411	1	971	3.098	3	509	4	806 9 988

Detection frequency SE17A, SE17B vs 14mTAD1,14hTAD2,14hTAD3,14mTAD4,14SETAD5



cells	target	n	%
WT	SE-TAD17	275	23.52
WT	chr14	396	33.88
dd17	SE-TAD17	327	22.72
dd17	chr14	591	41.07

FISH between SE17A, SE17B vs 2mTAD1, 2hTAD2, 2hTAD3, 2hTAD3A, 2hTAD3-4



	WT	dd18
Number of cells	17	12
Median	3.088	2.413

