Analysis of ChIP-seq data using RepeatExplorer
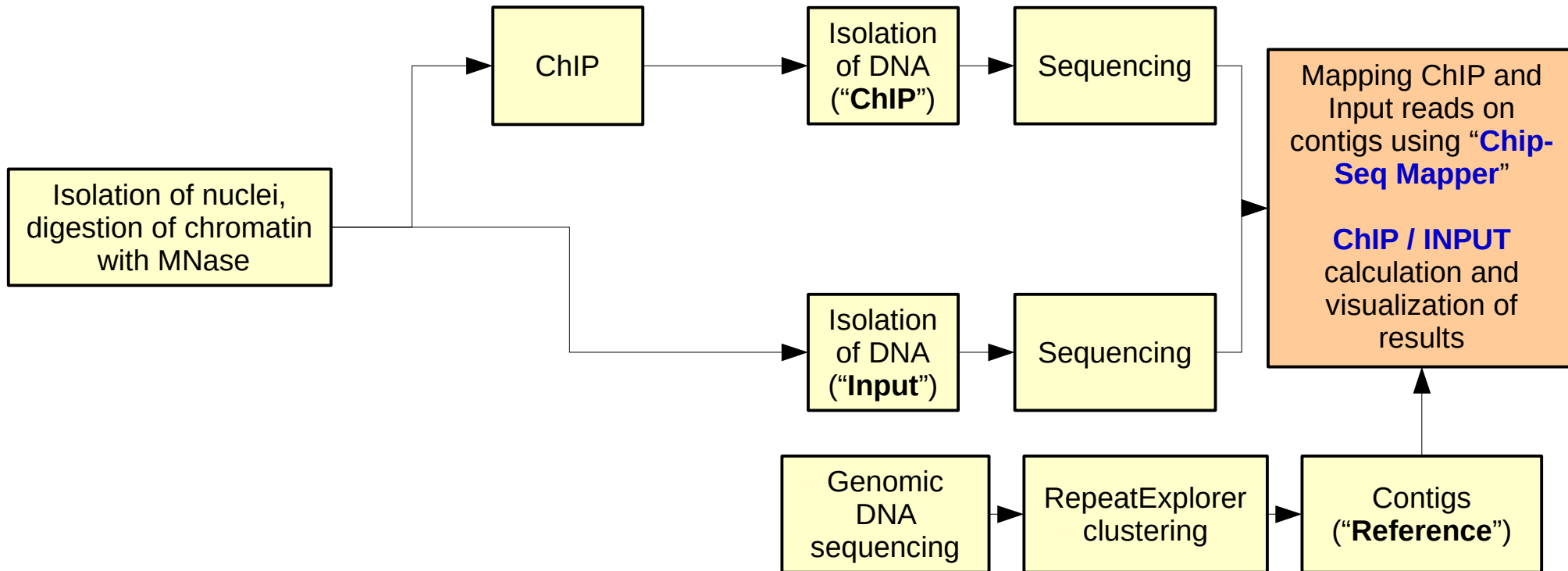
Pavel Neumann
May, 2019

BILOGICKÉ CENTRUM AVČR
ÚSTAV MOLEKULÁRNÍ BIOLOGIE ROSTLIN
České Budějovice

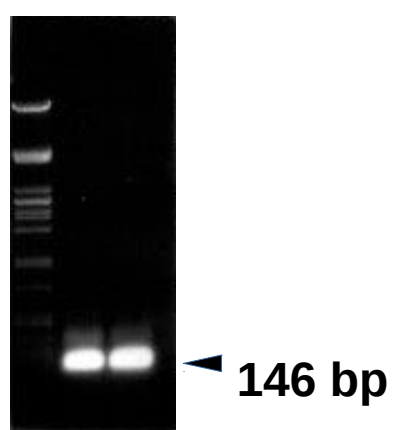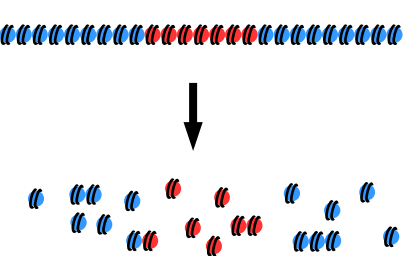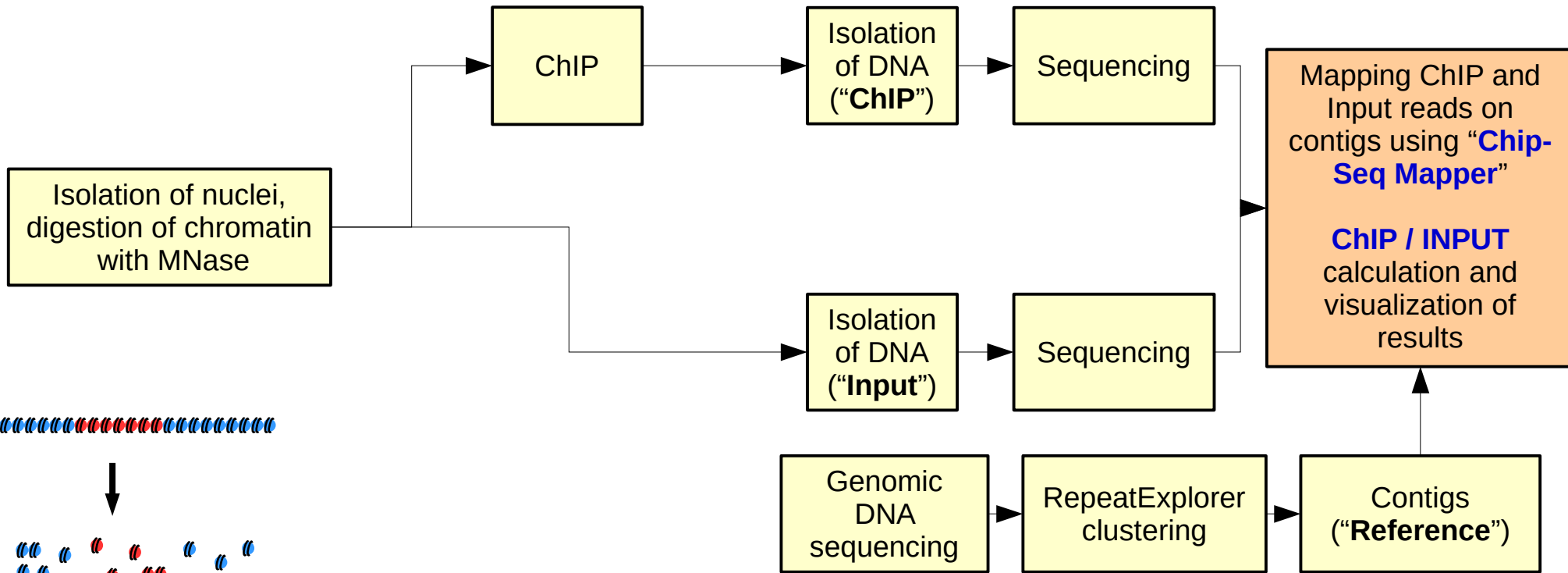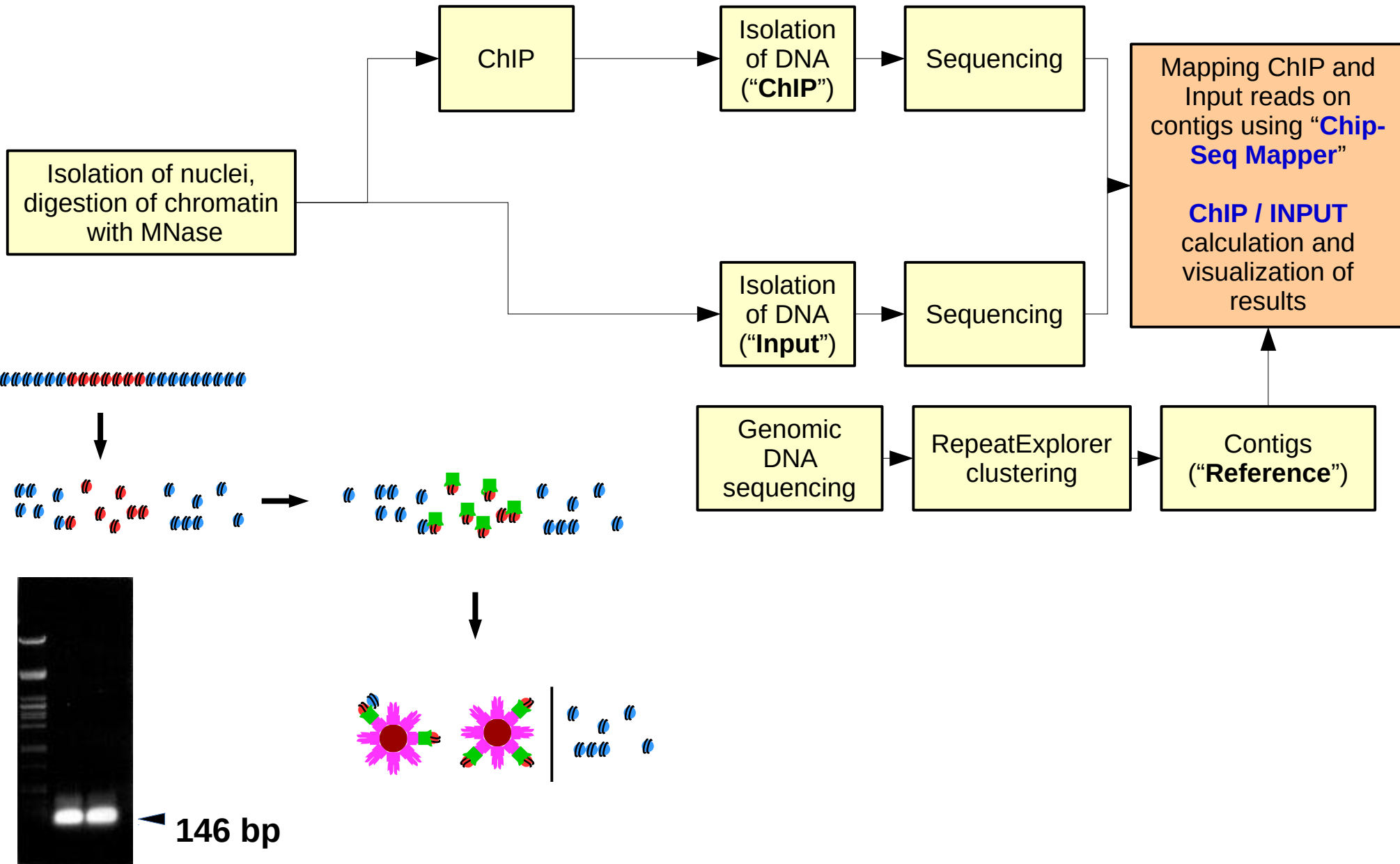# Experimental design

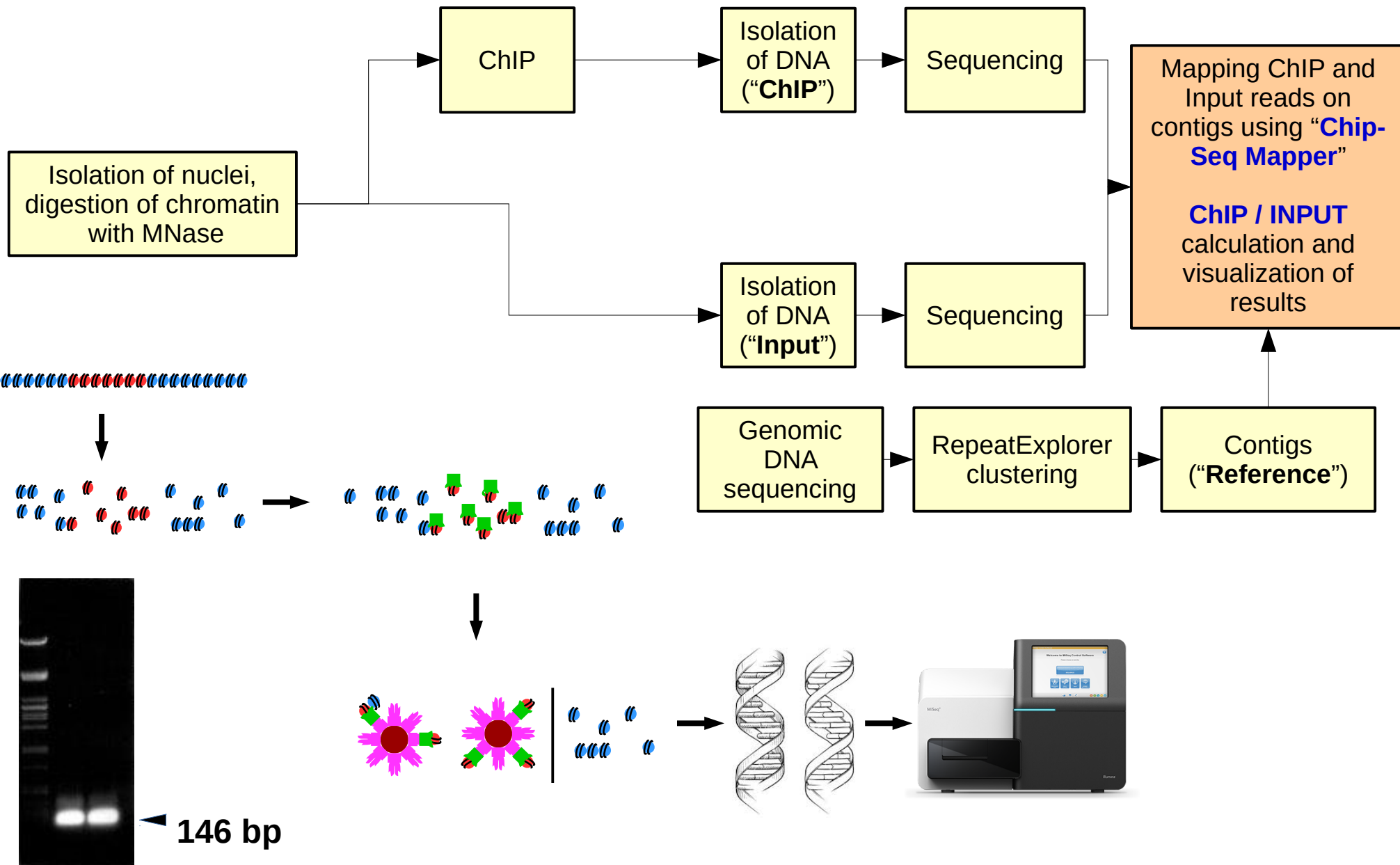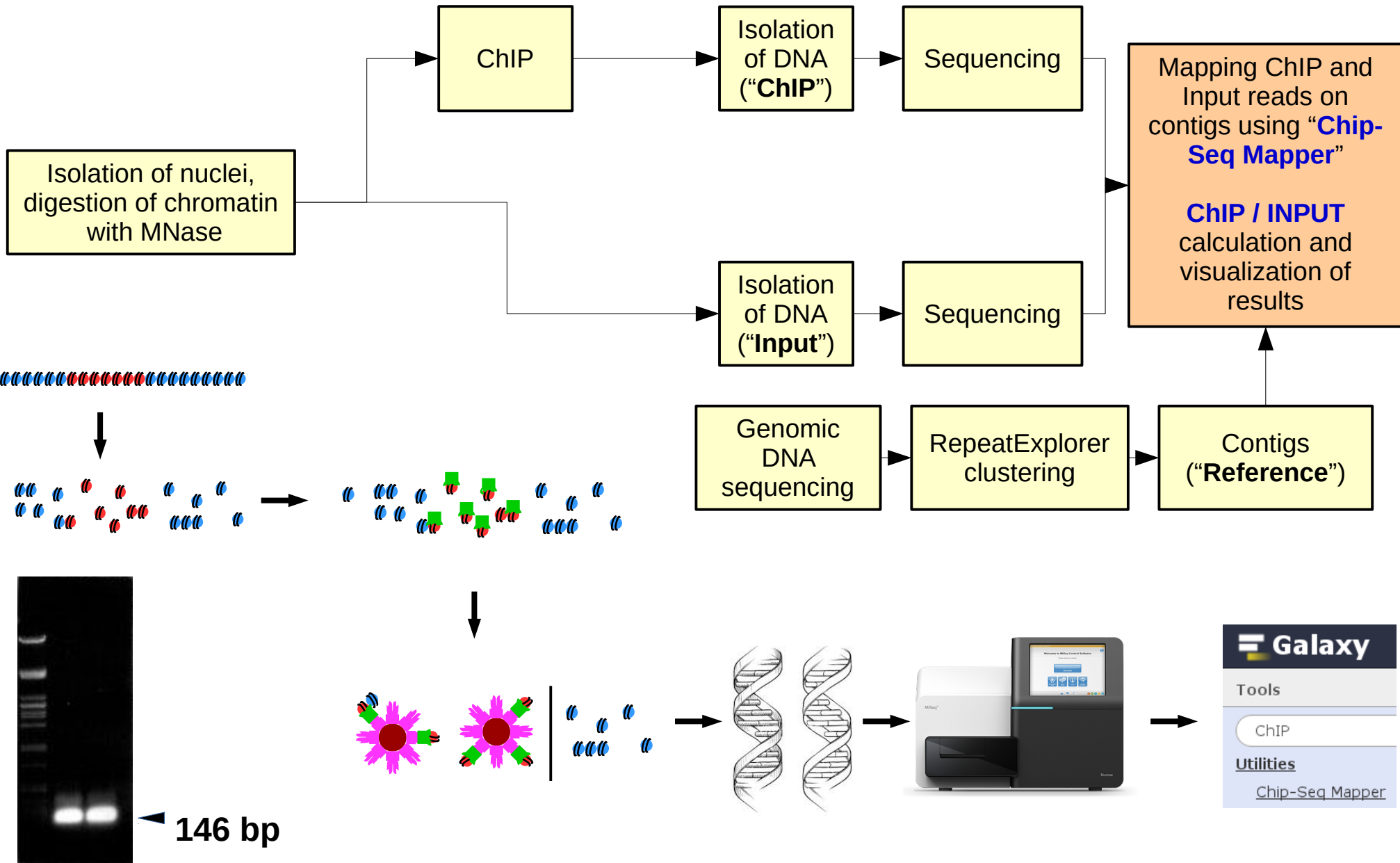# Experimental design

Experimental design
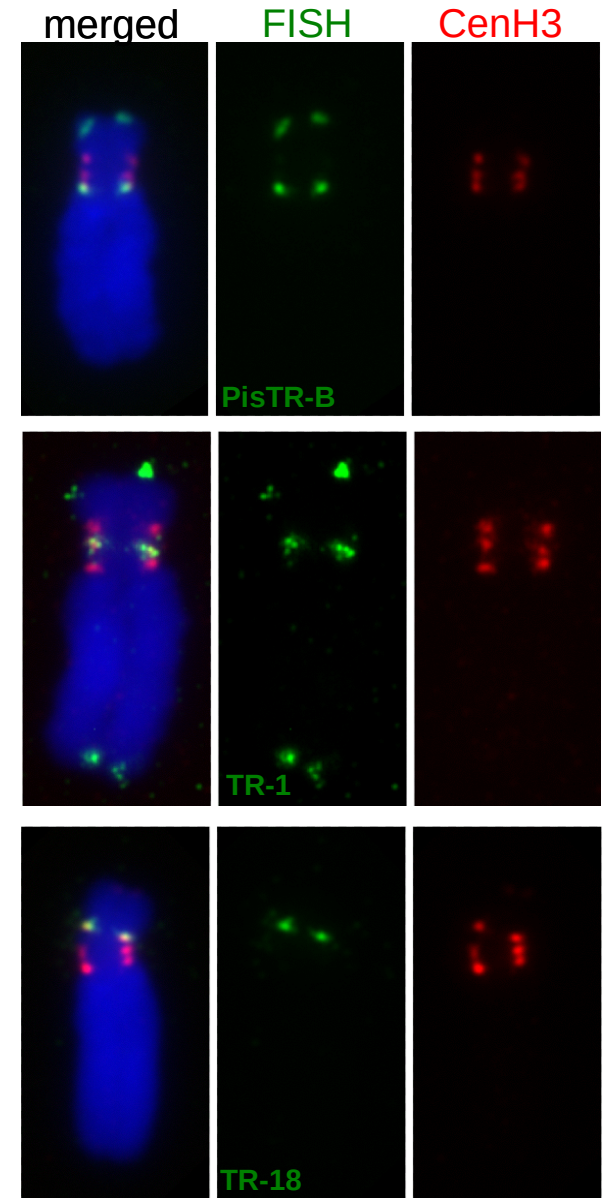
Experimental design

Experimental design

Verification of the ChIP results using Immuno-FISH detection

Basic characteristics of identified satellites

Family	Monomer [bp]	Copy number per 1C	Genome proportion [Mbp]	AT content	ChIP/input ratio	Localization on chromosomes						
						1	2	3	4	5	6	7
PisTR-B	50	1180000	59.09	0.72	**20.5**	T	T	**C**	**C**, T	C,P	T	T
TR-1	867	1050	0.91	0.67	**52.4**	C	-	**C**,T	**C**	-	-	-
TR-6	245	2000	0.49	0.76	**58.7**	-	-	-	-	**C?**	-	-
TR-7	164	35500	5.82	0.73	**53.6**	C	-	-	-	-	-	-
TR-10	659	650	0.43	0.74	**76.3**	-	-	-	**C, P**	-	-	-
TR-11	510	8700	4.44	0.76	**79.1**	C	C	-	-	**C**	**C**	**C**
TR-12	120	2400	0.29	0.69	**5.4**	I	P, I	I	C, I,t	I	I	I
TR-18	1644	350	0.57	0.74	**79.1**	-	-	**C**	-	-	-	-
TR-19	2094	690	1.45	0.77	**65.3**	C	-	-	-	**C**	-	-
TR-20	867	310	0.27	0.76	**40.9**	-	-	-	-	-	-	**C**
TR-21	642	370	0.24	0.73	**44.0**	-	-	-	-	-	**C**	-
TR-22	881	190	0.17	0.76	**102.9**	-	-	-	-	-	**C**	-
TR-23	1813	50	0.09	0.69	**25.3**	-	-	-	-	-	**C**	-
TR-2	440	98000	43.22	0.65	**0.6**	-	P	-	-	P	P	-
TR-3	82	30000	2.48	0.79	**0.3**	-	-	P	I	-	-	-
TR-4	172	50000	8.61	0.67	**0.6**	-	-	-	-	-	P	-
TR-5	54	120000	6.51	0.65	**1.1**	-	P	-	-	-	-	-
TR-9	189	2000	0.37	0.79	**0.4**	T	T	-	-	-	-	T
TR-17	191	2700	0.52	0.74	**0.5**	-	-	-	-	-	-	I

Localization: C = centromeric
P = pericentromeric
I = intercalary
T = (sub)telomeric

merged   FISH   CenH3

PisTR-B

TR-1

TR-18

Chr. 3