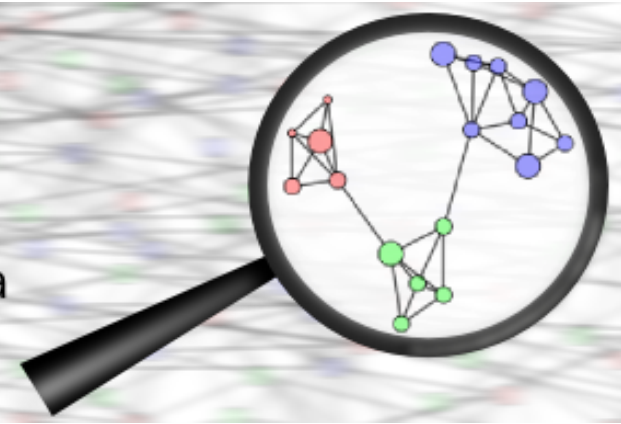


RepeatExplorer

Discover repeats in your next generation sequencing data



Analysis of ChIP-seq data using RepeatExplorer

Pavel Neumann

May, 2017

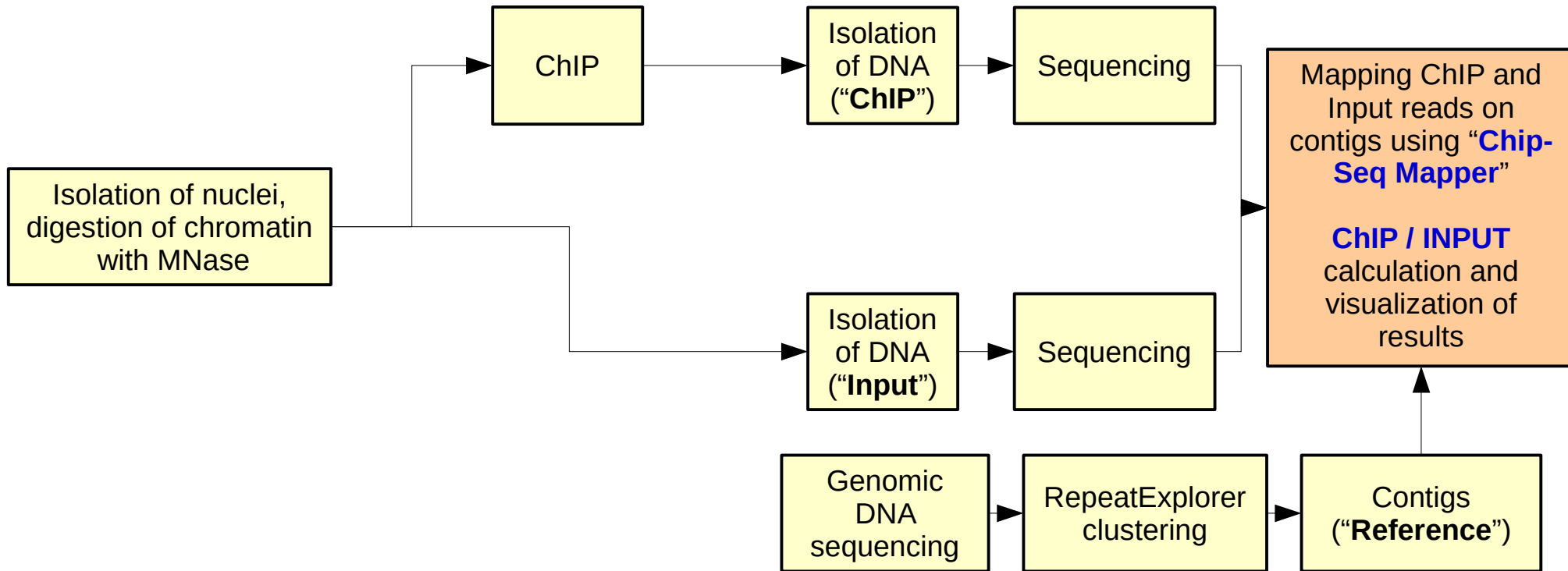


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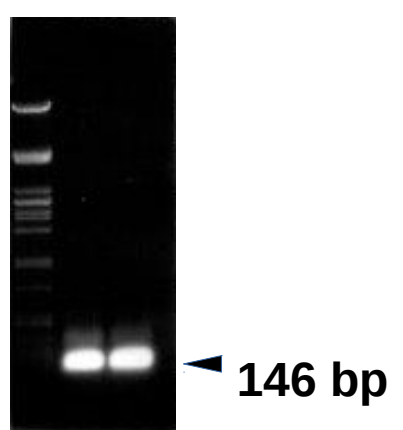
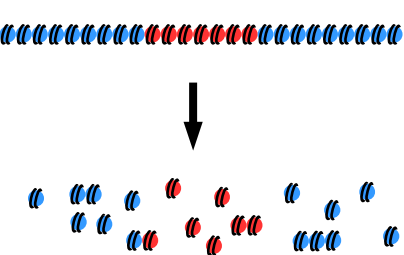
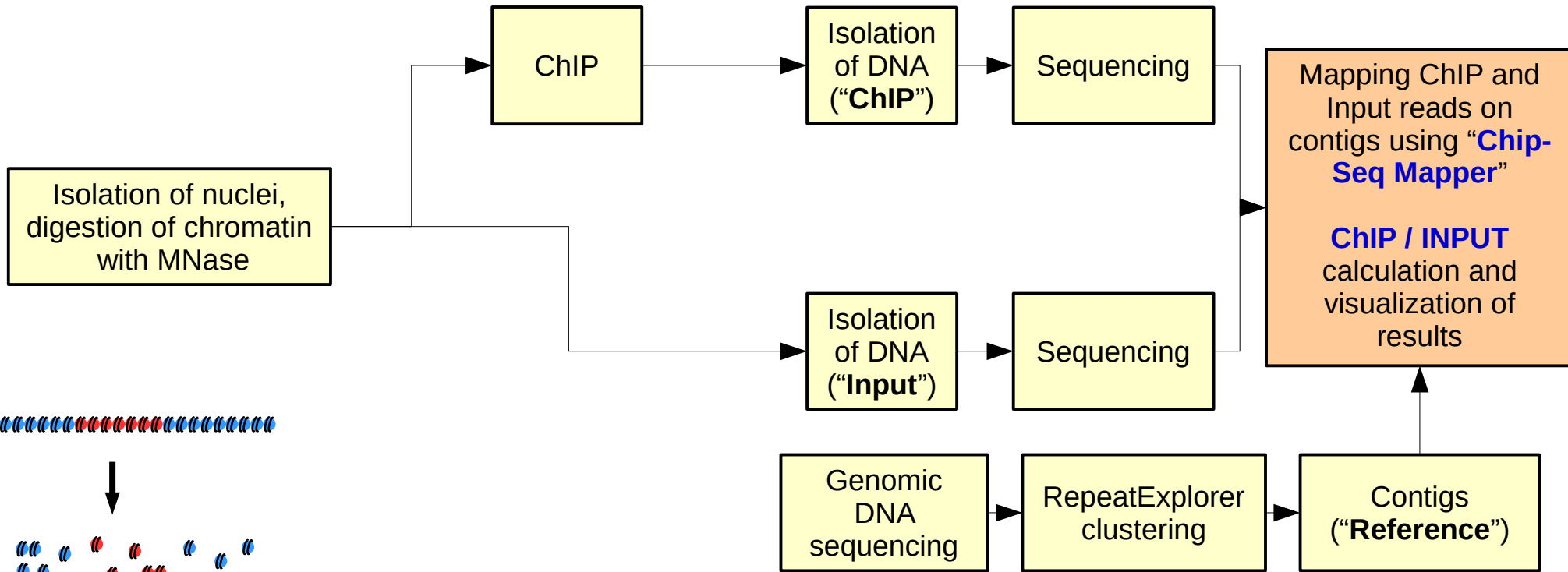
*BILOGICKÉ CENTRUM AVČR
ÚSTAV MOLEKULÁRNÍ BIOLOGIE ROSTLIN
České Budějovice*



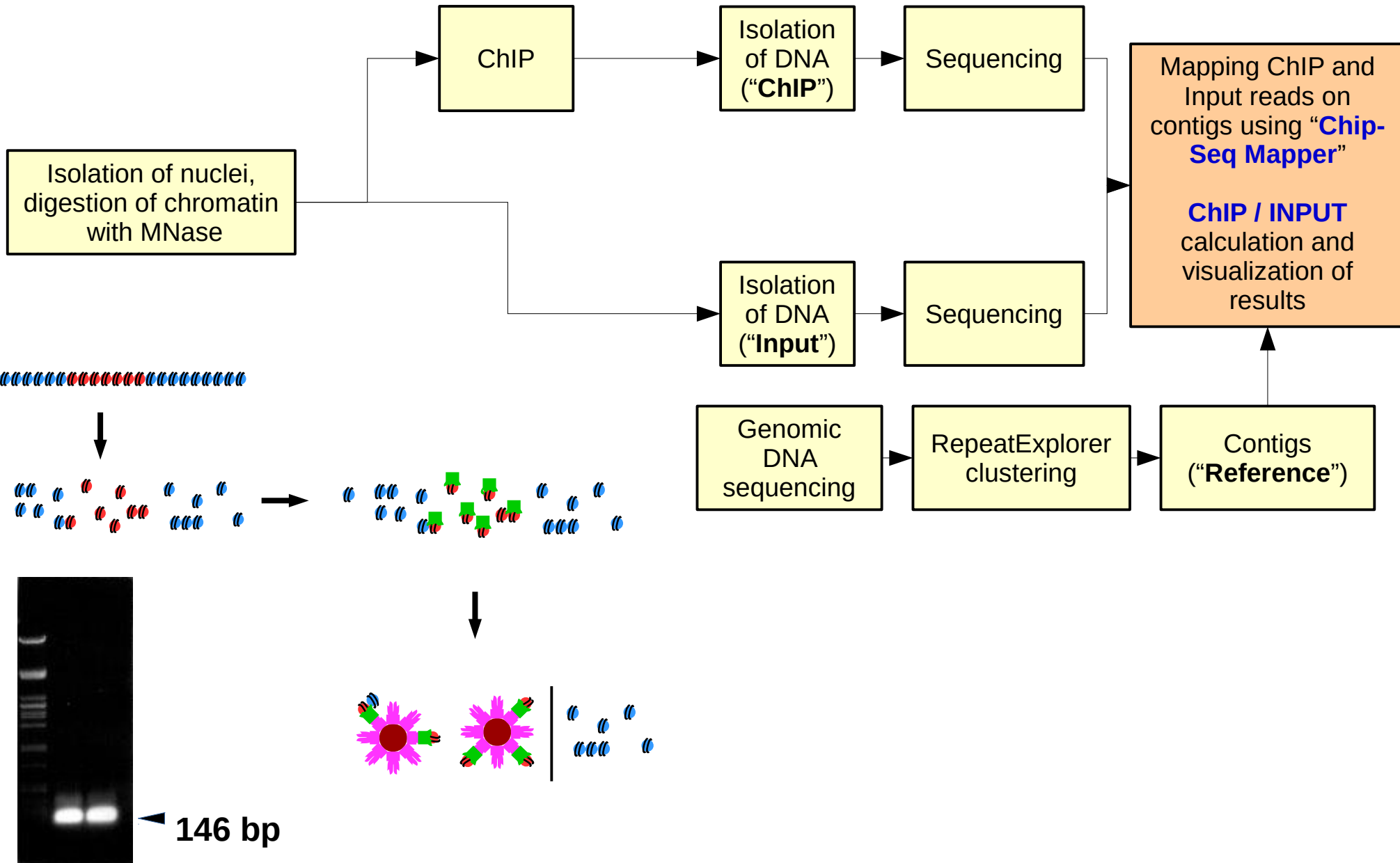
Experimental design



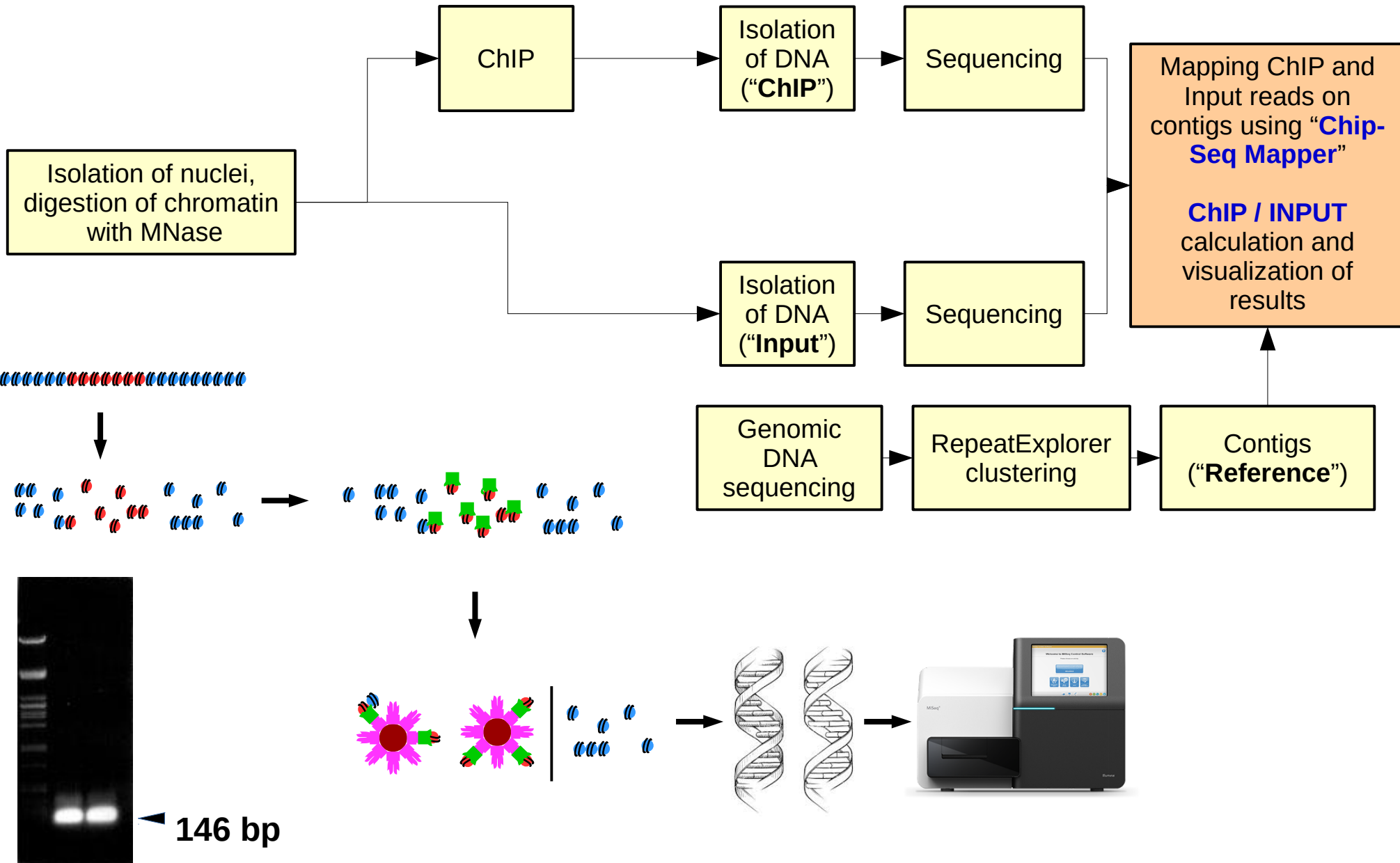
Experimental design



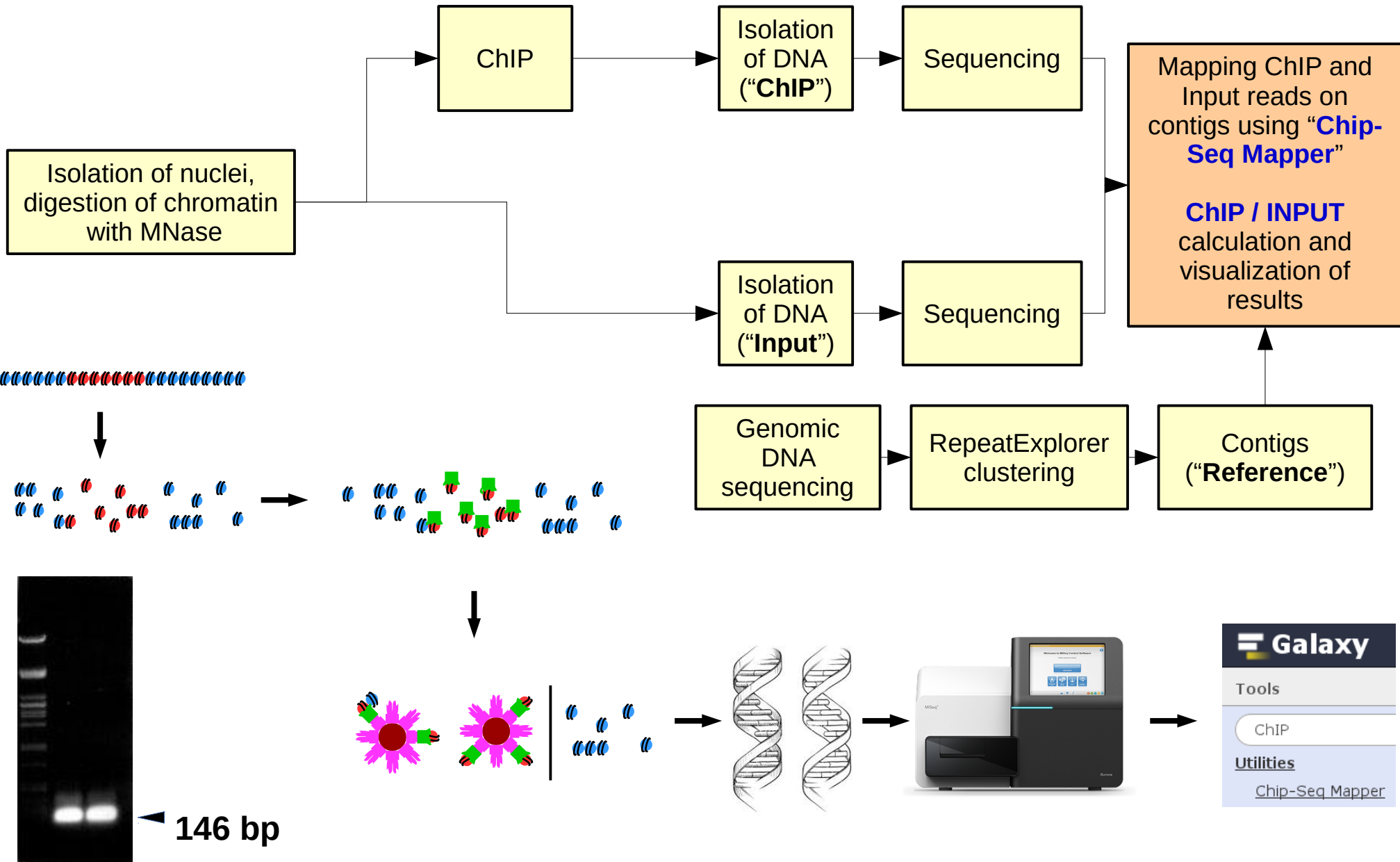
Experimental design



Experimental design



Experimental design

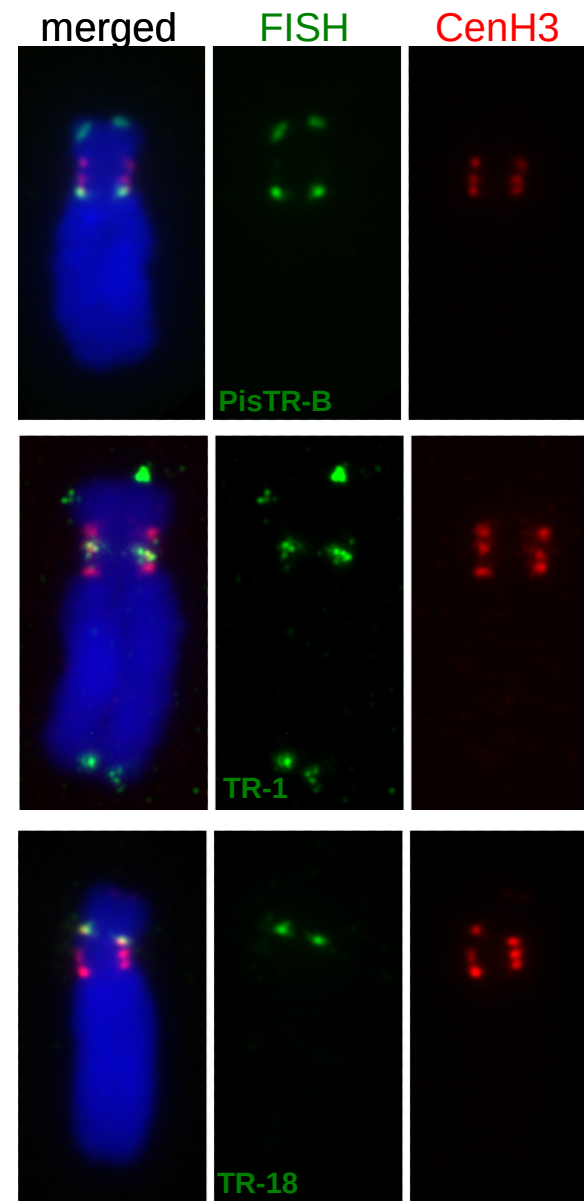


Verification of the ChIP results using Immuno-FISH

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



Chr. 3