

The influence of 5',8-cyclo-2'-deoxypurines on the mitochondrial repair of clustered DNA damage in xrs5 cells. The preliminary study.

Supplementary Materials

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Table S1. The sequences of double-stranded substrate oligonucleotides containing 2'-deoxyuridine (dU) and 5',8-cyclo-2'-deoxyadenosine (cdA) or 5',8-cyclo-2'-deoxyguanosine (cdG).

Oligonucleotide		Sequence
ScdA / RcdA	Control 1	* 5' -CTCTTGT CAGGAATATTGTC U CTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAGAGATACGAGGGTGGTTTCCG-5'
	Control 2	* 5' -GCCTTTGGTGGGAGCATAG X GACAATATTCCTGACAAGAG-3' 3' -CGGAAACCACCCTCGTATCTCTGTTATAAGGACTGTTCTC-5'
	dU -7	* 5' -CTCTTGT CAGGA U ATTGTCTCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU -4	* 5' -CTCTTGT CAGGAATAT U GTCTCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU -1	* 5' -CTCTTGT CAGGAATATTGT U TCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU 0	* 5' -CTCTTGT CAGGAATATTGTC U CTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU +1	* 5' -CTCTTGT CAGGAATATTGTCT U TATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU +4	* 5' -CTCTTGT CAGGAATATTGTCTCTA U GCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
	dU +7	* 5' -CTCTTGT CAGGAATATTGTCTCTATGC U CCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG X GATACGAGGGTGGTTTCCG-5'
ScdG / RcdG	Control 1	* 5' -CTCTTGT CAGGAATATTGTC U CTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAGAGATACGAGGGTGGTTTCCG-5'
	Control 2	* 5' -GCCTTTGGTGGGAGCATAG Y GACAATATTCCTGACAAGAG-3' 3' -CGGAAACCACCCTCGTATCTCTGTTATAAGGACTGTTCTC-5'
	dU -7	* 5' -CTCTTGT CAGGA U ATTGTCCCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU -4	* 5' -CTCTTGT CAGGAATAT U GTCCCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU -1	* 5' -CTCTTGT CAGGAATATTGT U CCTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU 0	* 5' -CTCTTGT CAGGAATATTGTC U CTATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU +1	* 5' -CTCTTGT CAGGAATATTGTCC U TATGCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU +4	* 5' -CTCTTGT CAGGAATATTGTCCCTA U GCTCCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'
	dU +7	* 5' -CTCTTGT CAGGAATATTGTCCCTATGC U CCCACCAAAGGC-3' 3' -GAGAACAGTCCTTATAACAG Y GATACGAGGGTGGTTTCCG-5'

U – represents dU as an AP site (after treatment with UDG); X – represents (5'S)-5',8-cyclo-2'-deoxyadenosine (ScdA) or (5'R)-5',8-cyclo-2'-deoxyadenosine (RcdA); Y – represents (5'S)-5',8-cyclo-2'-deoxyguanosine (ScdG) or (5'R)-5',8-cyclo-2'-deoxyguanosine (RcdG); * – represents the 5'-end-labeled strand with [γ -³²P]ATP

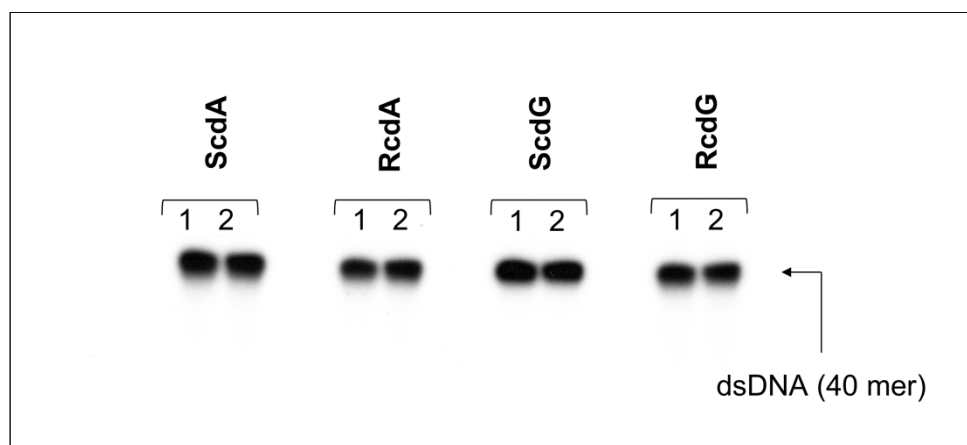


Figure S1. The stability of „matrix” oligonucleotides (Control 2) after treatment with 20 μ g of mitochondrial extracts (ME). Each lane number corresponds with different assay time: lane 1 - 0 min; lane 2 - 6 h.

Table S2. Endonuclease activity – Control 1. Raw numerical data of densitometry.

		Time [h]			
		0	0,5	3	6
Strand	Data set	Endonuclease activity [%]			
Control 1	1.	1,39	85,92	75,75	72,41
	2.	0,94	82,68	76,83	71,90
	3.	0,31	77,43	73,06	69,80
	4.	0,76	84,68	69,47	59,11
	5.	2,67	70,72	59,86	55,64
	6.	2,42	72,21	62,02	52,42
	7.	1,41	87,65	61,08	51,19
	8.	0,09	74,09	63,99	54,96
	9.	0,00	99,06	83,54	53,02
	Avg	1,35	71,92	63,98	55,75
	SD	1,66	21,93	13,23	11,42

Table S3. Polymerase activity – Control 1. Raw numerical data of densitometry.

		Time [h]			
		0	0,5	3	6
Strand	Data set	Polymerase activity [%]			
Control 1	1.	0,00	0,65	12,74	19,65
	2.	0,00	2,07	10,48	19,27
	3.	0,00	0,93	11,08	18,72
	4.	0,04	11,23	26,32	37,15
	5.	0,00	12,05	29,14	34,96
	6.	0,58	6,65	33,60	44,75
	7.	0,00	6,83	35,72	46,86
	8.	0,00	4,75	33,87	44,15
	9.	0,00	0,00	16,28	46,54
	Avg	0,18	5,88	21,65	35,16
	SD	0,47	5,06	10,36	10,53

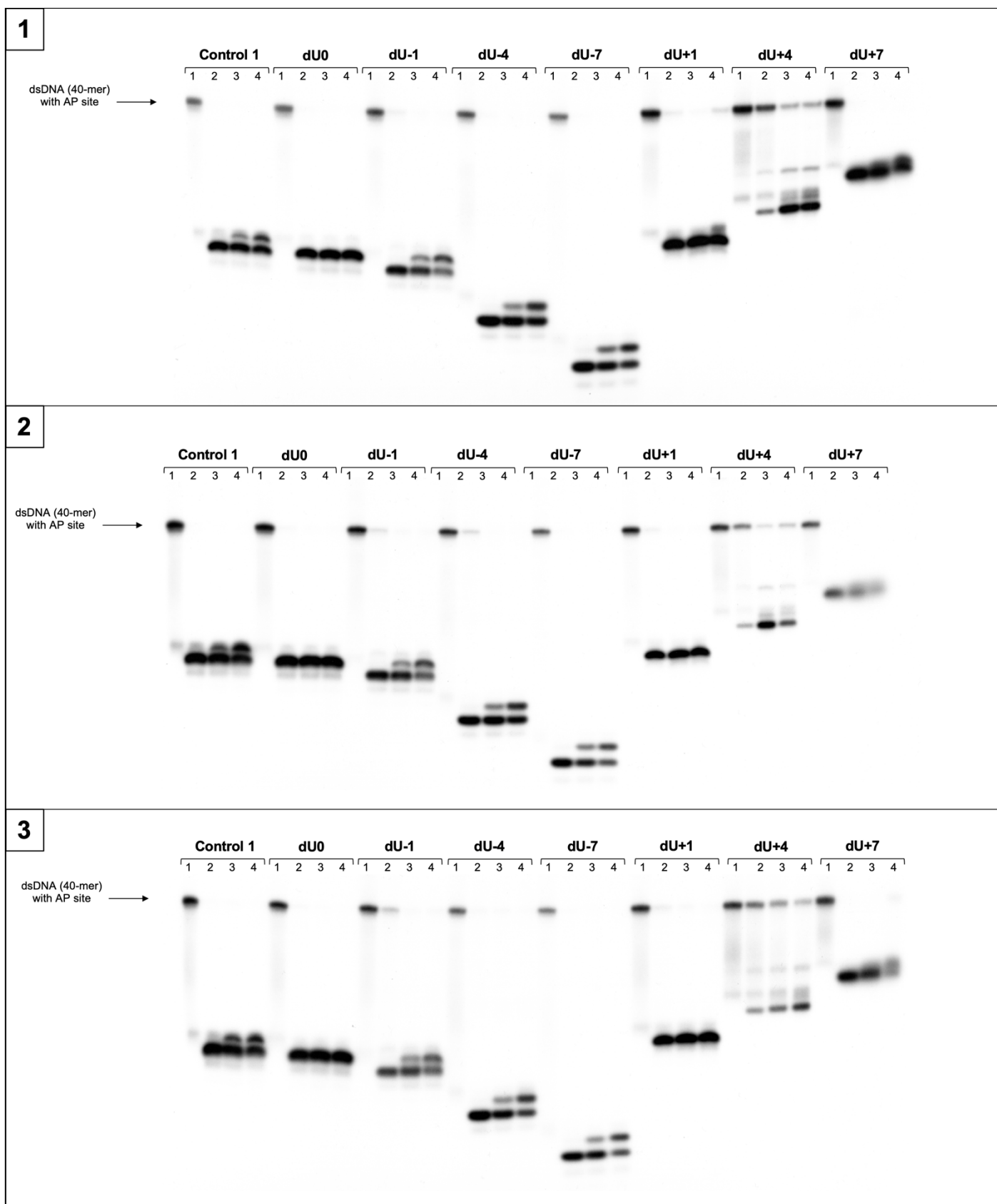


Figure S2. The autoradiograms of denaturing PAGE presenting dsDNA containing clustered damage with AP site in one strand and **ScdA** in the opposing strand. Each lane number indicates different assay time: lane 1 - 0 min; lane 2 - 30 min; lane 3 - 3h; lane 4 - 6h. Three experimental replications are presented.

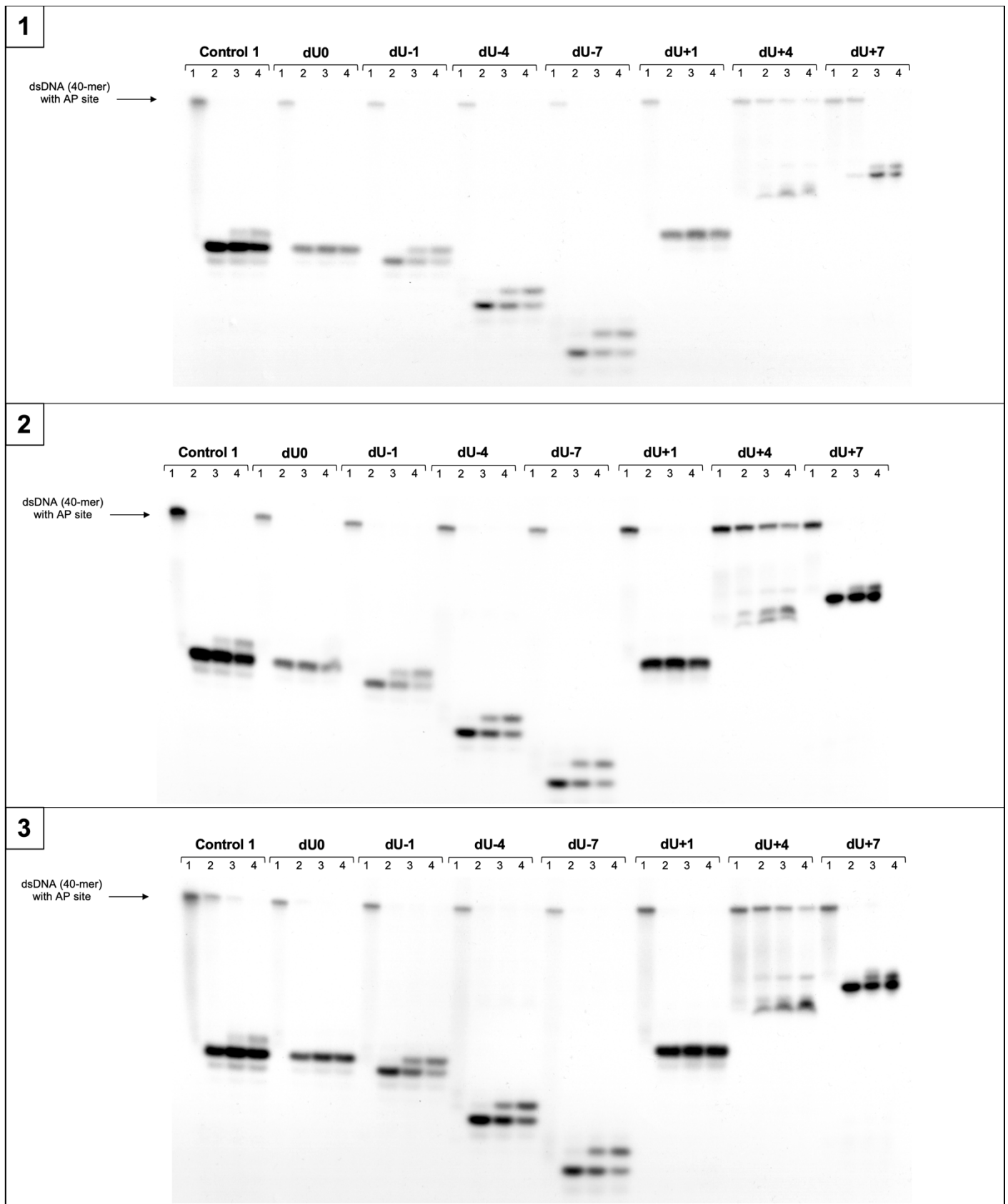


Figure S3. The autoradiograms of denaturing PAGE presenting dsDNA containing clustered damage with AP site in one strand and **RcdA** in the opposing strand. Each lane number indicates different assay time: lane 1 - 0 min; lane 2 - 30 min; lane 3 - 3h; lane 4 - 6h. Three experimental replications are presented.

Table S4. Endonuclease activity – ScdA and RcdA. Raw numerical data of densitometry obtained from Quantity One software.

RcdA		Time [h]				ScdA		Time [h]			
		0	0,5	3	6			0	0,5	3	6
Strand	Data set	Endonuclease activity [%]				Strand	Data set	Endonuclease activity [%]			
dU0	1.	7,61	86,52	89,54	90,68	dU0	1.	2,41	88,36	87,17	86,87
	2.	4,81	98,53	96,19	99,53		2.	1,44	77,19	77,40	75,55
	3.	3,20	91,53	88,33	87,08		3.	2,14	79,23	77,70	77,85
	Avg	5,21	92,19	91,36	92,43		Avg	2,00	81,60	80,76	80,09
	SD	2,23	6,03	4,23	6,41		SD	0,50	5,95	5,56	5,98
dU-1	1.	0,00	87,13	62,86	45,04	dU-1	1.	3,56	88,02	65,01	45,92
	2.	3,74	99,08	63,51	41,13		2.	1,05	80,86	64,94	47,48
	3.	3,22	81,02	56,42	38,95		3.	2,88	71,05	60,36	45,25
	Avg	2,32	89,08	60,93	41,71		Avg	2,49	79,98	63,44	46,22
	SD	2,02	9,19	3,92	3,09		SD	1,30	8,52	2,66	1,14
dU-4	1.	0,73	95,03	57,62	51,65	dU-4	1.	0,67	89,55	70,80	54,20
	2.	0,00	93,20	67,45	42,47		2.	3,06	87,27	70,39	53,73
	3.	0,74	82,65	64,73	45,40		3.	2,71	88,65	67,32	46,49
	Avg	0,49	90,29	63,27	46,51		Avg	2,15	88,49	69,51	51,47
	SD	0,43	6,68	5,07	4,69		SD	1,29	1,15	1,90	4,32
dU-7	1.	0,00	95,96	63,85	36,73	dU-7	1.	0,00	90,35	64,23	49,59
	2.	0,00	91,19	51,46	37,67		2.	0,96	96,02	68,46	47,22
	3.	4,12	84,93	57,76	37,93		3.	0,91	90,48	70,07	45,66
	Avg	1,37	90,69	57,69	37,44		Avg	0,62	92,28	67,59	47,49
	SD	2,38	5,53	6,20	0,63		SD	0,54	3,23	3,01	1,98
dU+1	1.	0,00	92,47	93,24	93,30	dU+1	1.	0,78	81,26	80,73	67,58
	2.	0,31	92,08	89,43	90,11		2.	0,52	90,49	88,68	87,66
	3.	2,83	86,40	80,96	83,67		3.	1,79	83,76	81,79	82,84
	Avg	1,05	90,32	87,88	89,03		Avg	1,03	85,17	83,73	79,36
	SD	1,55	3,40	6,28	4,91		SD	0,67	4,77	4,32	10,48
dU+4	1.	0,00	25,71	61,62	73,62	dU+4	1.	1,27	32,49	65,11	57,37
	2.	7,21	40,17	69,62	56,70		2.	0,10	31,21	82,32	67,64
	3.	2,19	29,95	48,10	62,93		3.	0,91	33,91	48,46	59,19
	Avg	3,13	31,94	59,78	64,41		Avg	0,76	32,53	65,30	61,40
	SD	3,69	7,44	10,88	8,56		SD	0,60	1,35	16,93	5,48
dU+7	1.	0,34	87,41	80,41	72,03	dU+7	1.	0,59	80,00	64,00	59,18
	2.	2,91	26,95*	79,84	60,60		2.	0,44	87,73	74,19	74,76
	3.	1,68	78,77	66,97	63,10		3.	0,64	76,63	72,02	57,54
	Avg	1,64	83,09	75,74	65,24		Avg	0,56	81,45	70,07	63,82
	SD	1,29	6,11	7,60	6,01		SD	0,10	5,69	5,37	9,50

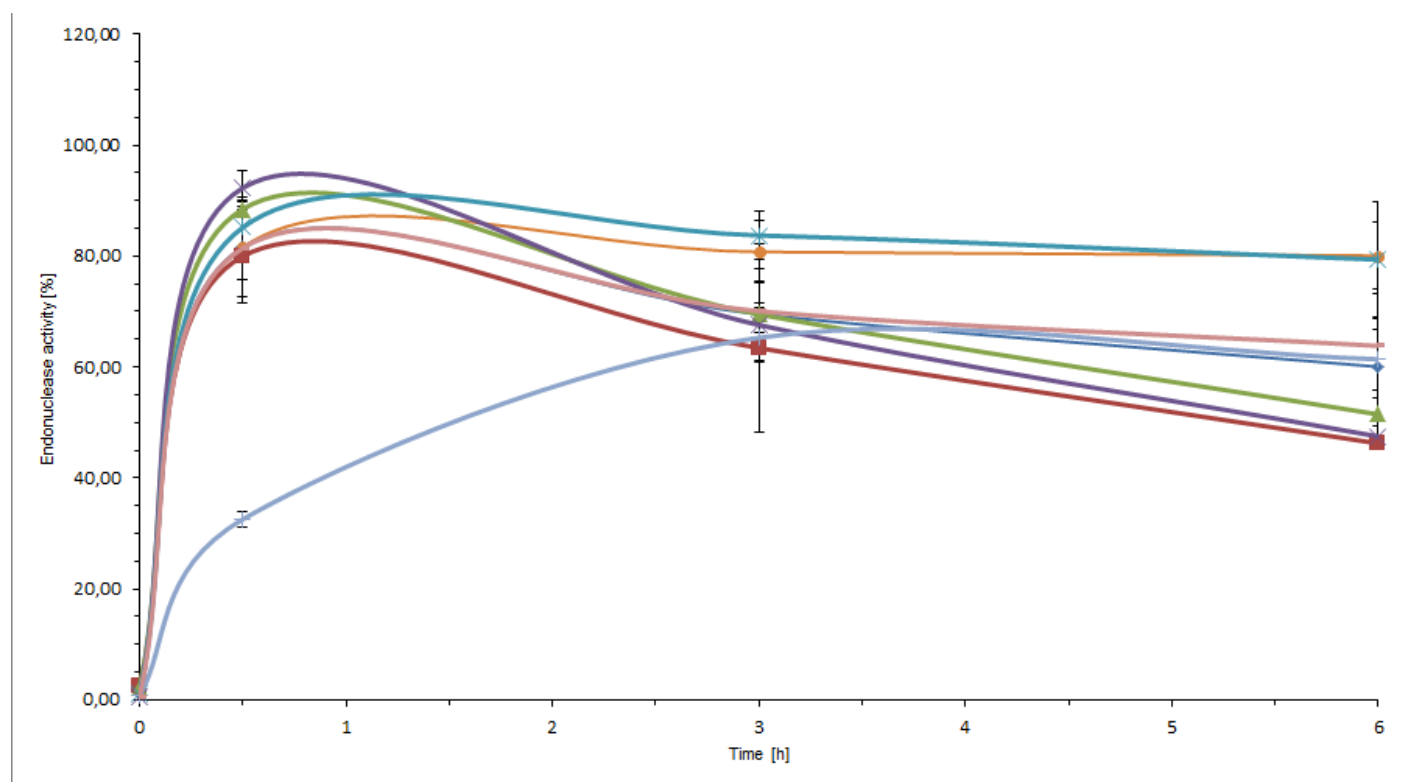
* Rejected values

Table S5. Polymerase activity – ScdA and RcdA. Raw numerical data of densitometry obtained from Quantity One software.

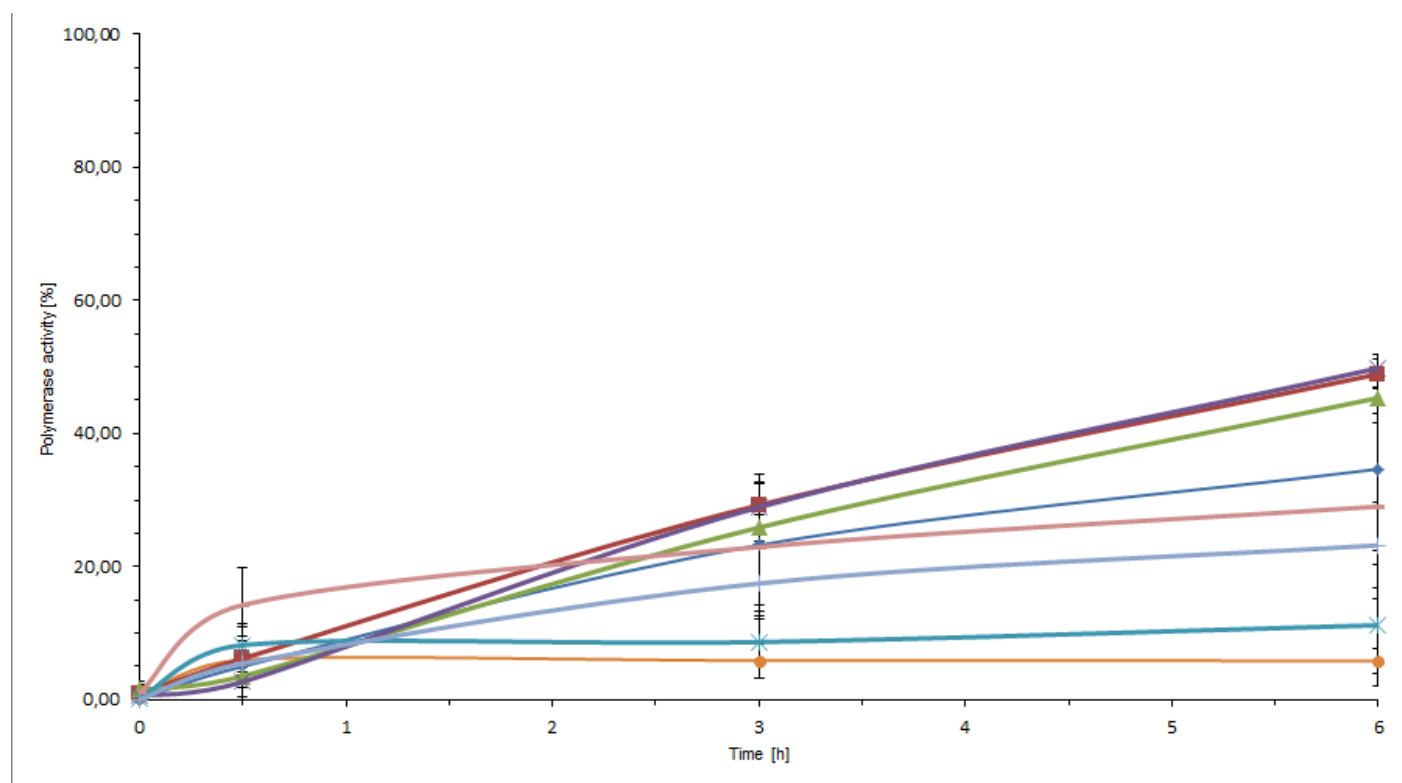
RcdA		Time [h]				ScdA		Time [h]			
		0	0,5	3	6			0	0,5	3	6
Strand	Data set	Polymerase activity [%]				Strand	Data set	Polymerase activity [%]			
dU0	1.	0,00	0,00	0,35	0,21	dU0	1.	0,32	2,87	2,90	3,66
	2.	0,00	0,00	0,00	0,00		2.	1,54	8,52	7,47	7,15
	3.	3,12*	0,00	1,31	2,91		3.	0,13	6,68	7,33	6,79
	Avg	0,00	0,00	0,55	1,04		Avg	0,66	6,02	5,90	5,87
	SD	0,00	0,00	0,68	1,62		SD	0,77	2,88	2,60	1,92
dU-1	1.	0,00	3,73	30,12	49,29	dU-1	1.	0,42	4,56	30,46	50,70
	2.	0,00	0,00	36,19	57,94		2.	0,86	5,70	25,38	46,47
	3.	0,00	6,30	34,10	52,86		3.	1,11	8,38	31,89	49,70
	Avg	0,00	3,34	33,47	53,36		Avg	0,80	6,21	29,24	48,95
	SD	0,00	3,17	3,08	4,35		SD	0,35	1,96	3,42	2,21
dU-4	1.	0,00	1,55	38,17	45,40	dU-4	1.	0,90	2,70	24,24	42,55
	2.	0,00	0,00	27,19	54,04		2.	0,66	3,00	25,33	43,93
	3.	0,00	7,10	27,82	48,87		3.	2,97	4,98	28,10	49,66
	Avg	0,00	2,88	31,06	49,43		Avg	1,51	3,56	25,89	45,38
	SD	0,00	3,74	6,17	4,35		SD	1,27	1,24	1,99	3,77
dU-7	1.	0,00	0,00	32,73	58,42	dU-7	1.	0,01	3,33	31,98	47,54
	2.	0,00	5,12	45,94	58,37		2.	0,00	1,60	29,74	51,25
	3.	0,00	6,34	33,68	54,37		3.	1,75	3,22	25,10	50,76
	Avg	0,00	3,82	37,45	57,05		Avg	0,59	2,72	28,94	49,85
	SD	0,00	3,36	7,37	2,32		SD	1,01	0,97	3,51	2,02
dU+1	1.	0,00	0,00	0,00	0,00	dU+1	1.	0,33	10,39	11,30	21,02
	2.	0,00	0,00	0,42	0,39		2.	0,00	5,03	2,41	3,04
	3.	0,00	2,67	1,89	1,15		3.	0,00	9,27	12,35	9,56
	Avg	0,00	0,89	0,77	0,51		Avg	0,11	8,23	8,69	11,21
	SD	0,00	1,54	1,00	0,58		SD	0,19	2,83	5,46	9,10
dU+4	1.	8,18*	4,33	4,30	4,54	dU+4	1.	0,02	0,13	22,57	29,00
	2.	0,66	12,15	14,27	28,59		2.	0,02	4,48	12,01	16,42
	3.	0,41	19,59	24,36	19,79		3.	0,10	11,82	17,86	24,27
	Avg	0,54	12,02	14,31	17,64		Avg	0,05	5,48	17,48	23,23
	SD	0,18	7,63	10,03	12,17		SD	0,04	5,91	5,29	6,35
dU+7	1.	2,41	1,25	14,82	22,23	dU+7	1.	0,26	18,49	33,96	39,46
	2.	1,98	5,72	17,34	37,97		2.	0,32	8,08	16,15	13,24
	3.	0,46	14,64	25,45	32,31		3.	2,46	16,21	18,78	34,44
	Avg	1,62	7,20	19,20	30,84		Avg	1,02	14,26	22,97	29,05
	SD	1,03	6,82	5,55	7,97		SD	1,25	5,47	9,61	13,92

* Rejected values

A.



B.



C.

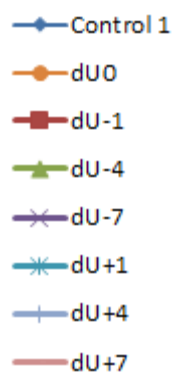
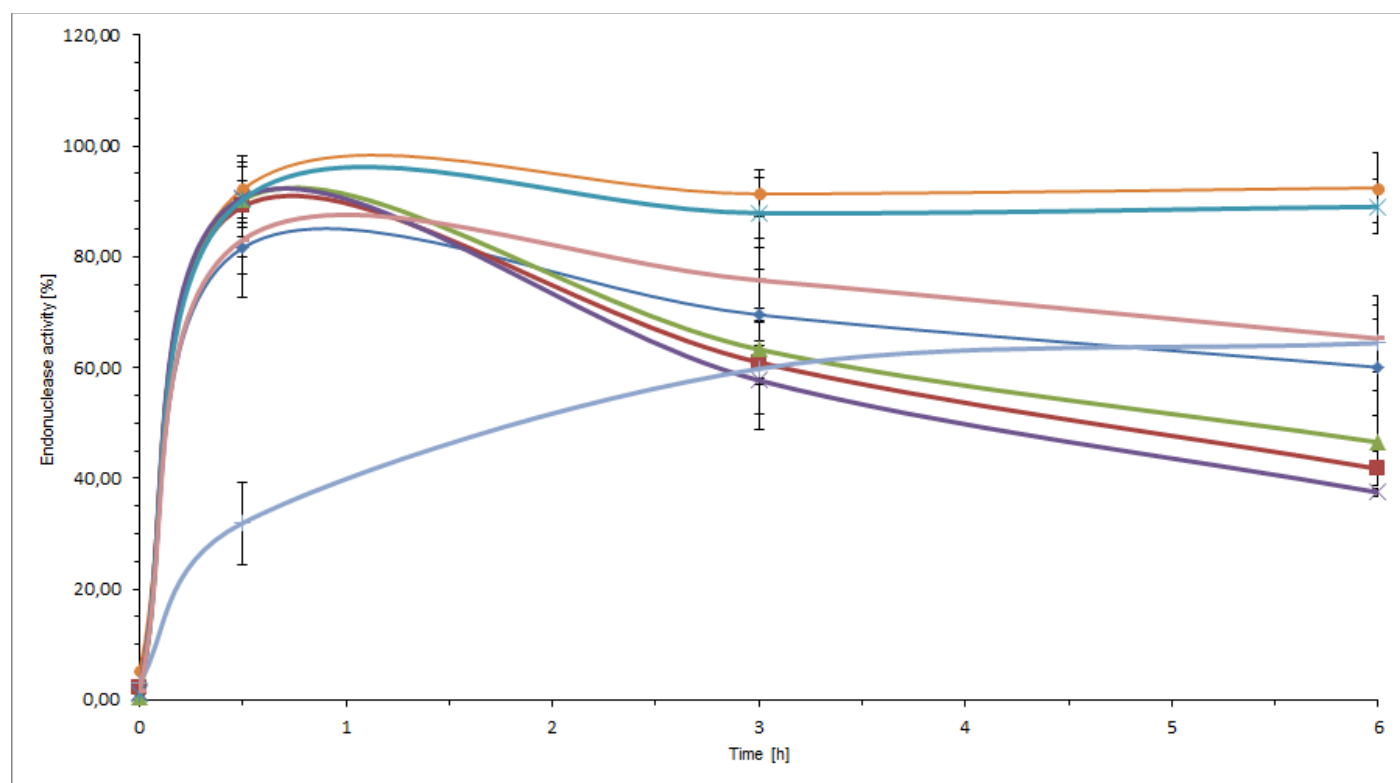
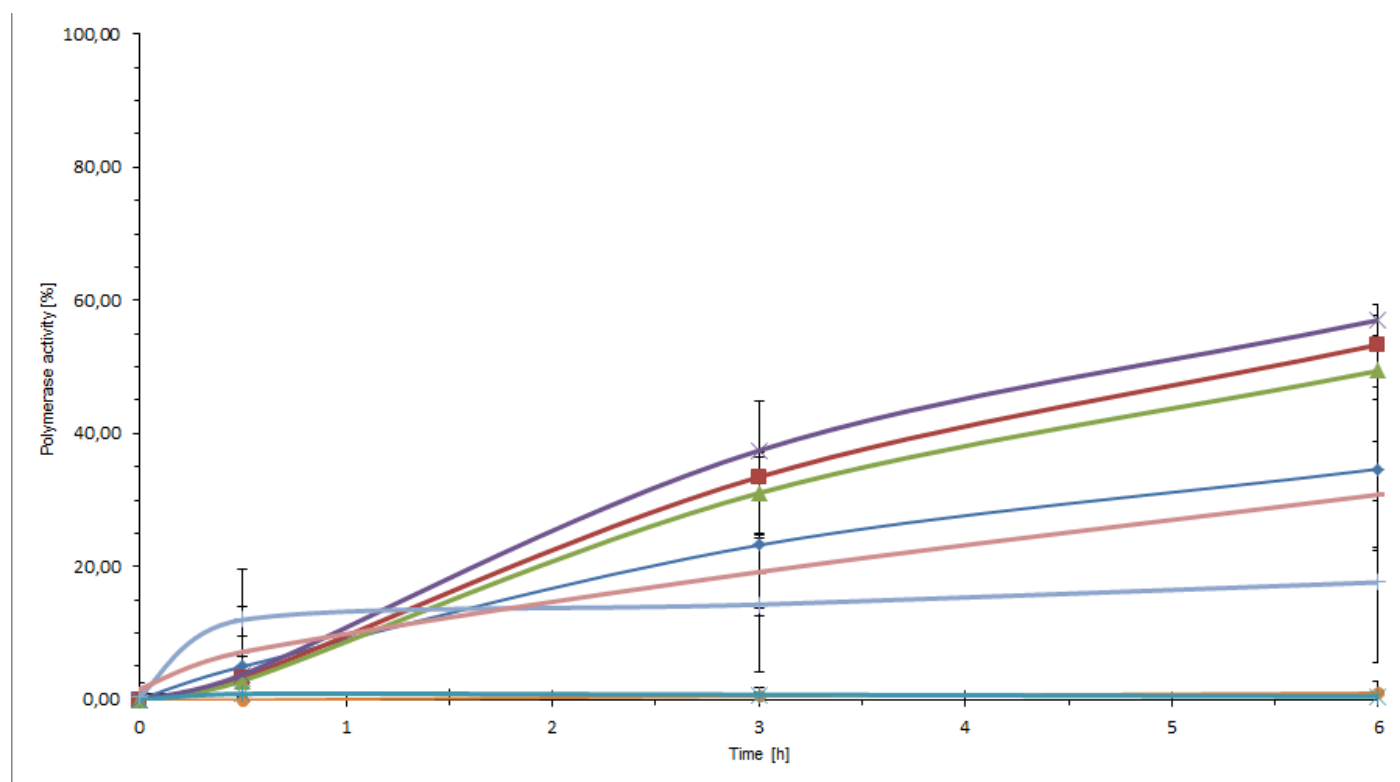


Figure S4. Graphical representation of the results for ScdA. (A) endonuclease activity +SD, (B) polymerase activity + SD; (C) figure legend.

A.



B.



C.

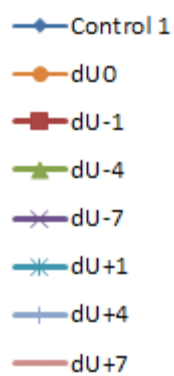
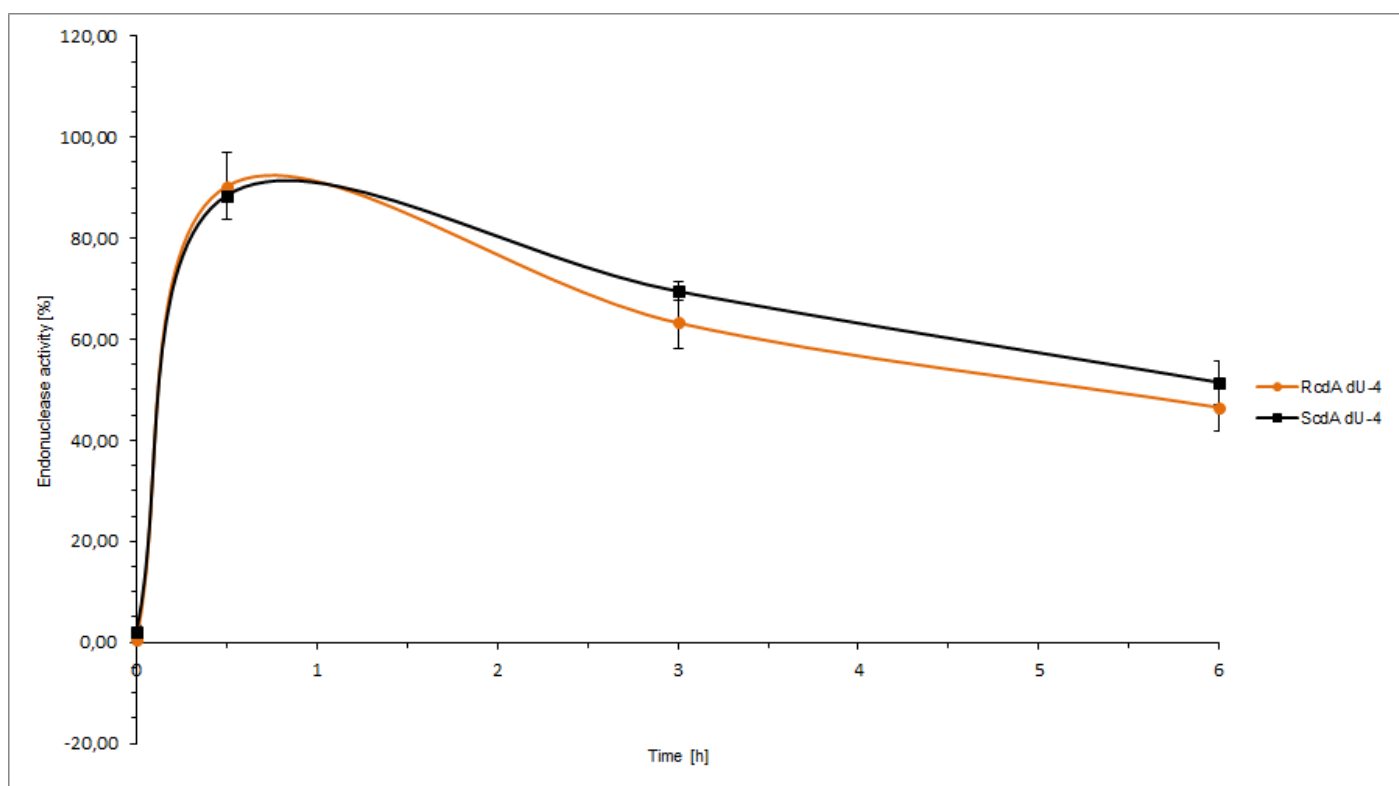
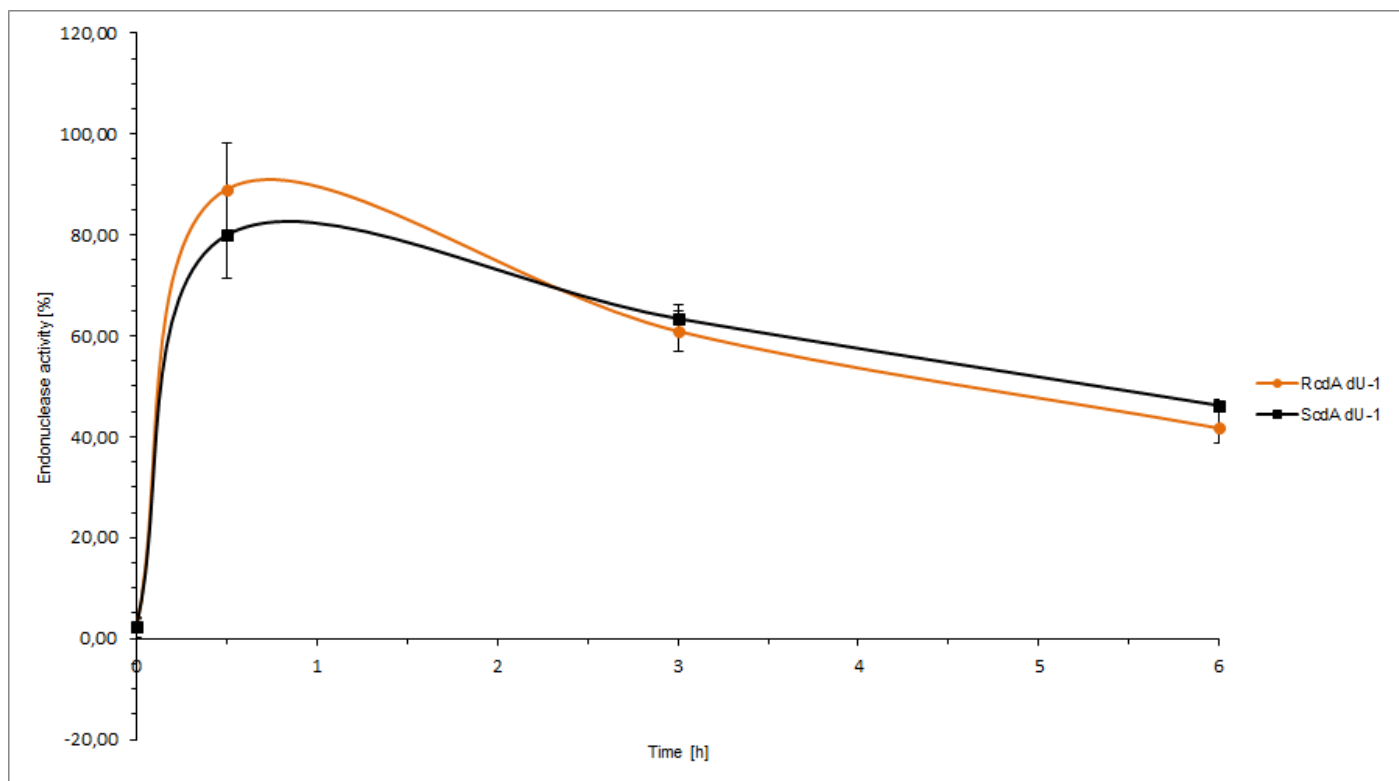
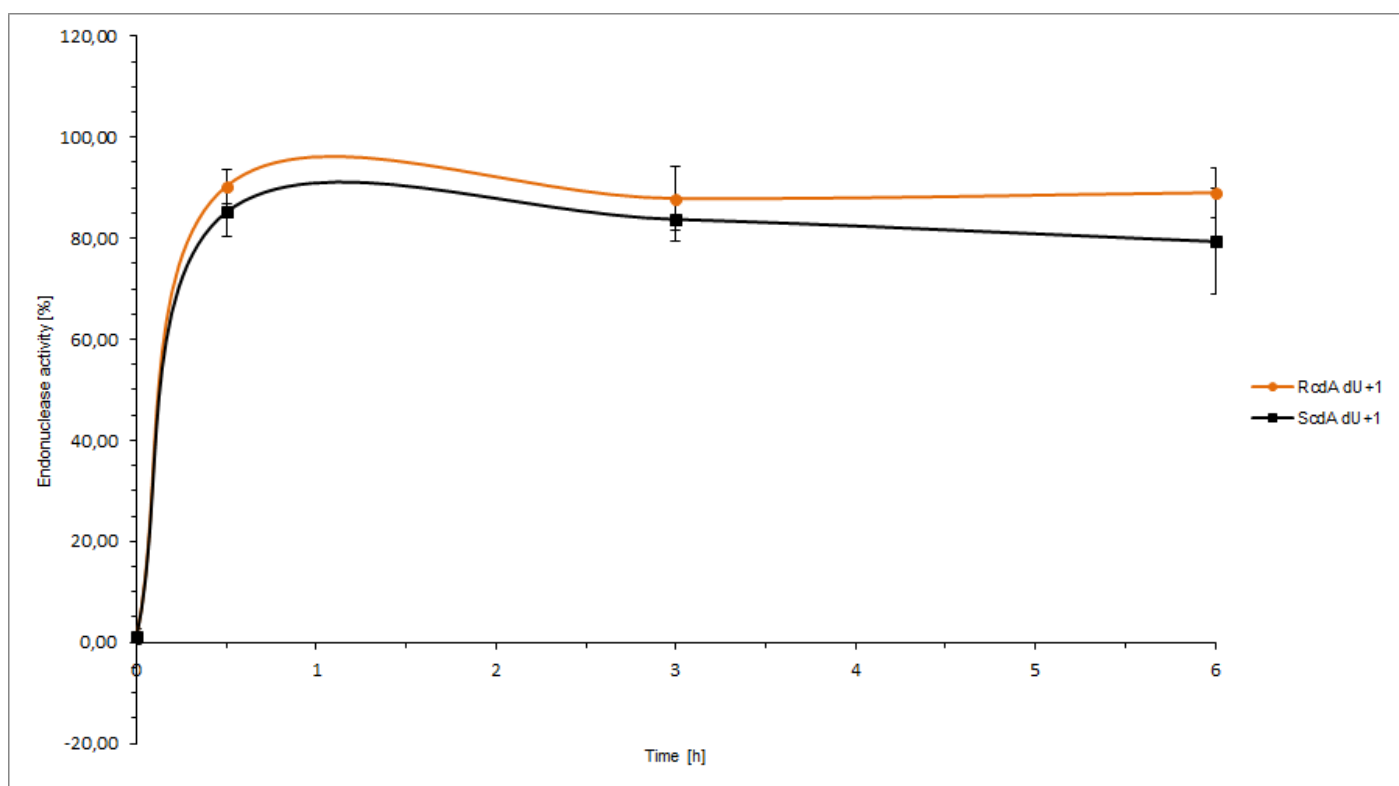
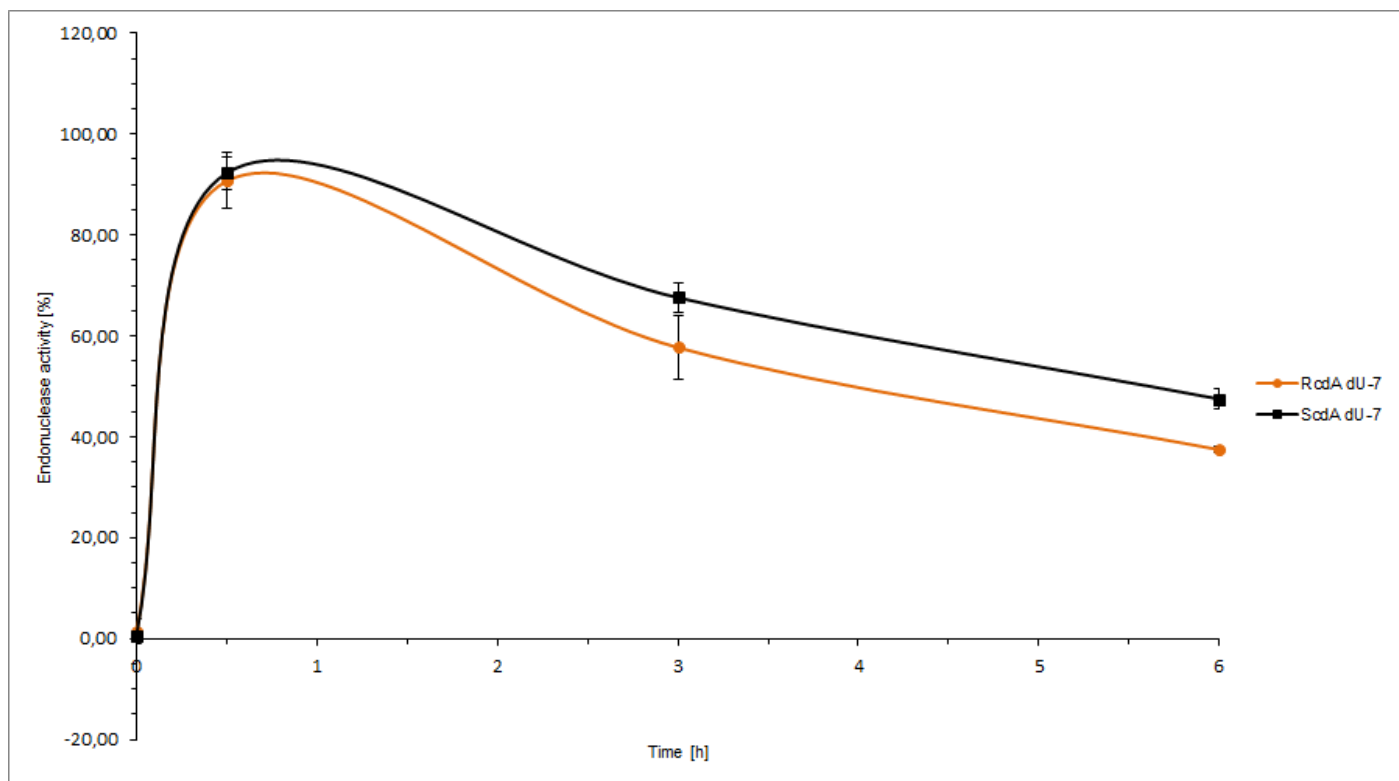
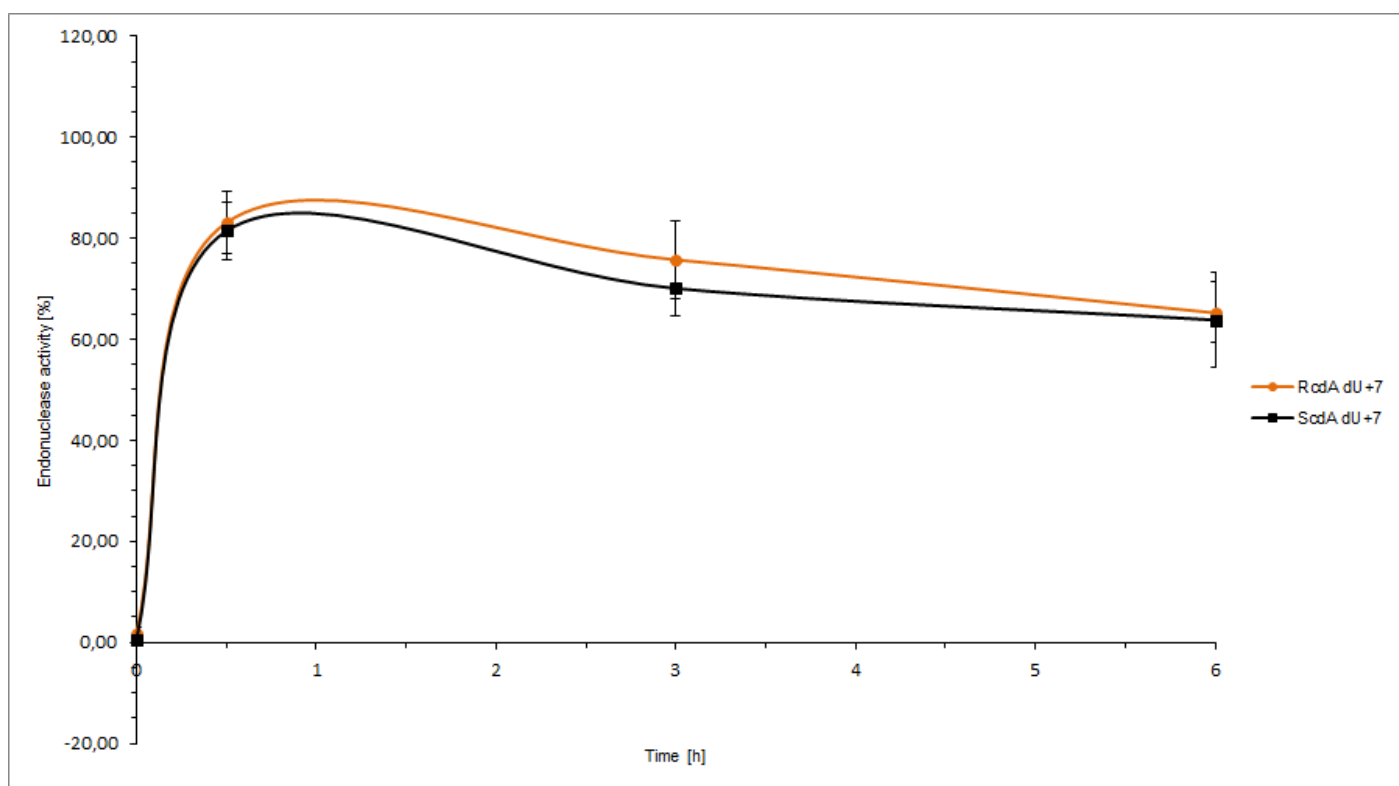
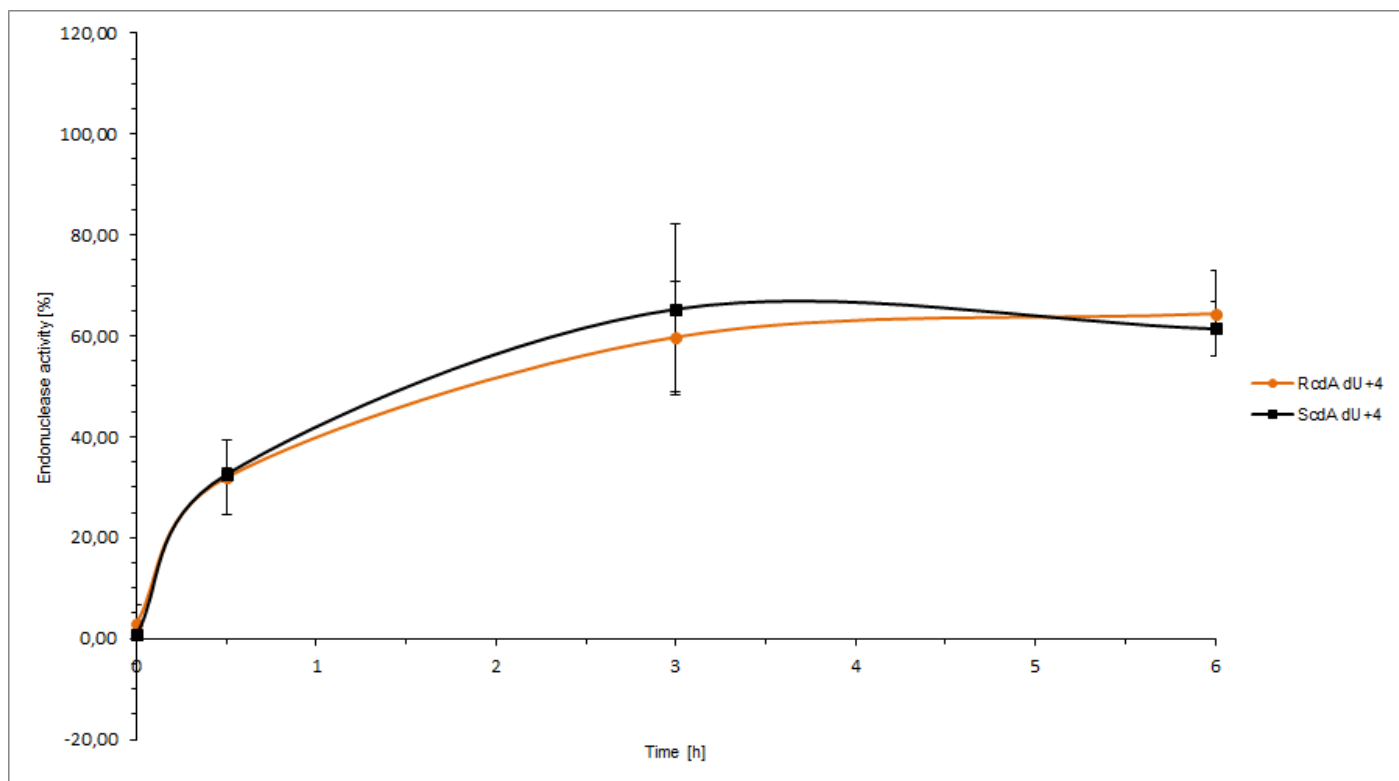


Figure S5. Graphical representation of the results for RcdA. (A) endonuclease activity +SD, (B) polymerase activity + SD; (C) figure legend.







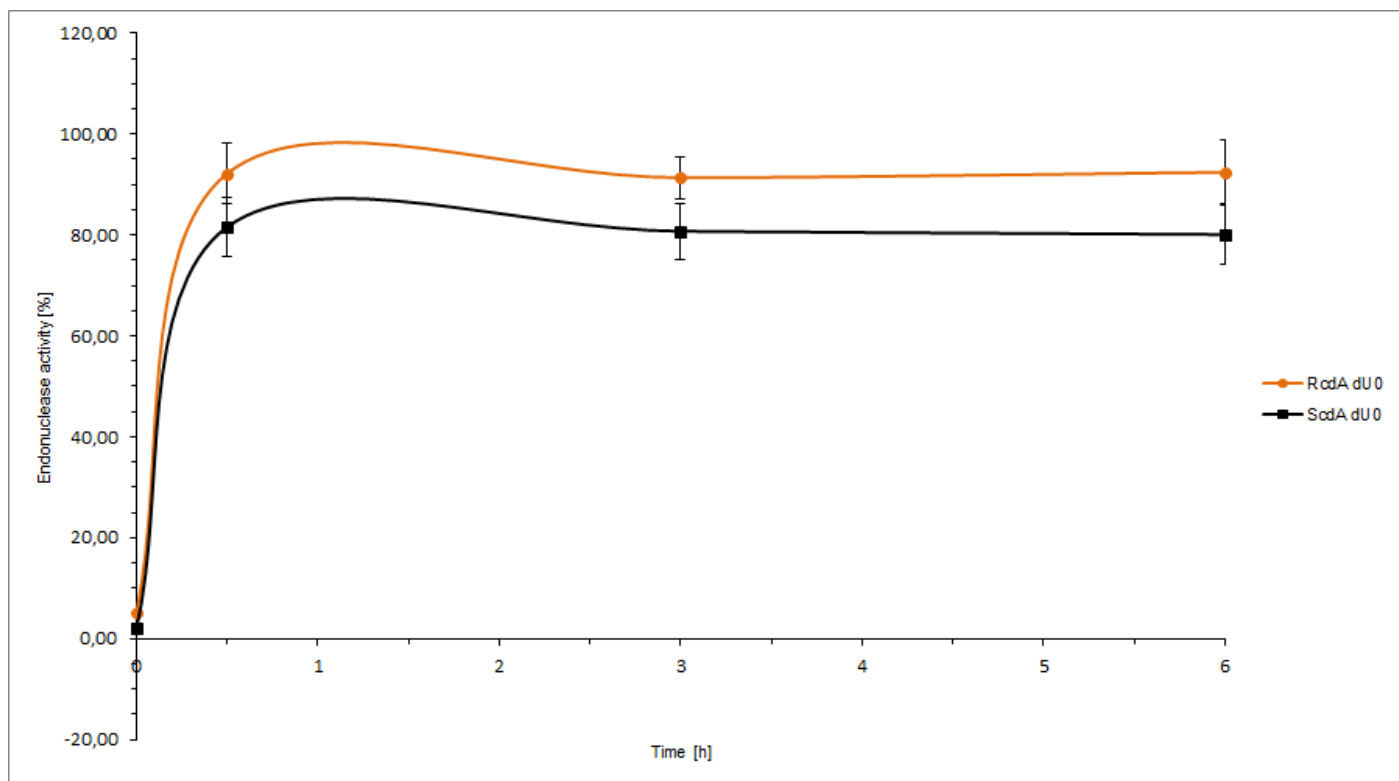
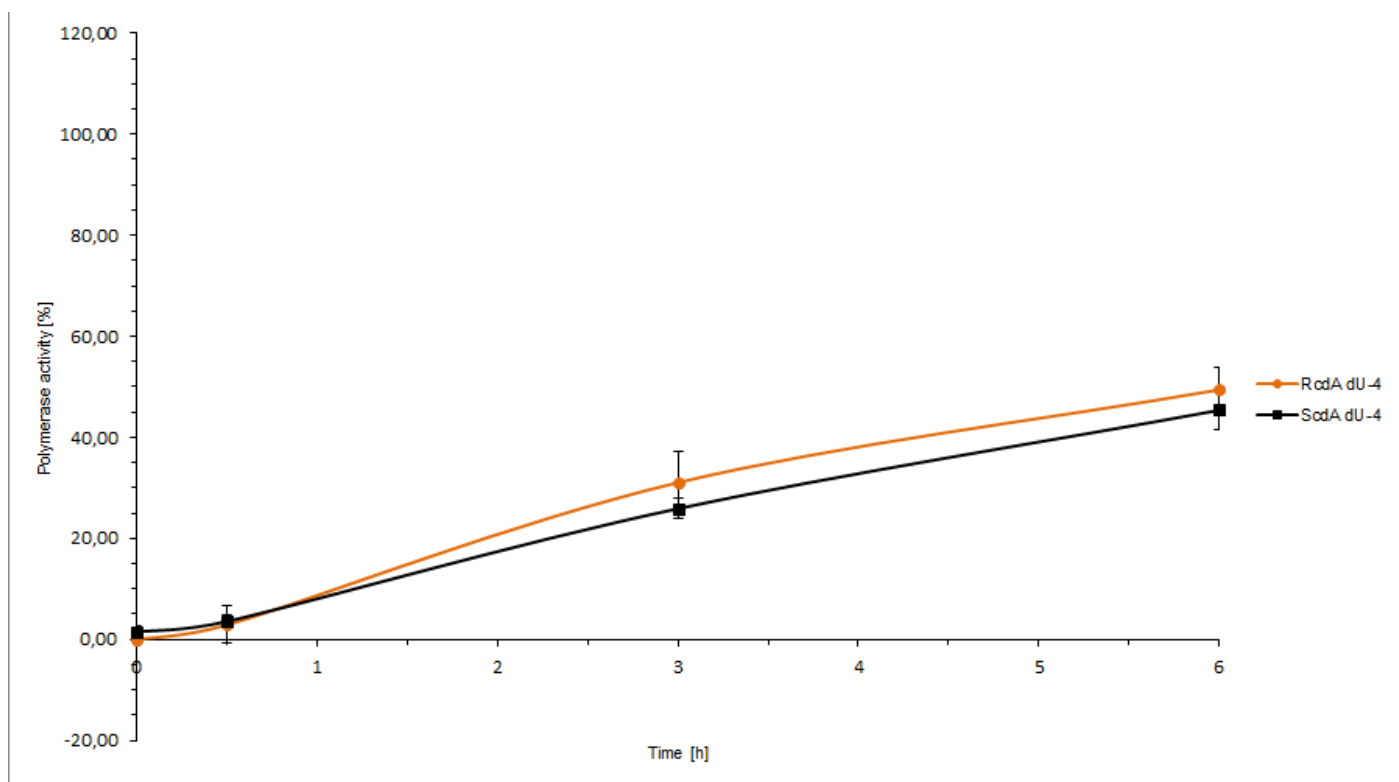
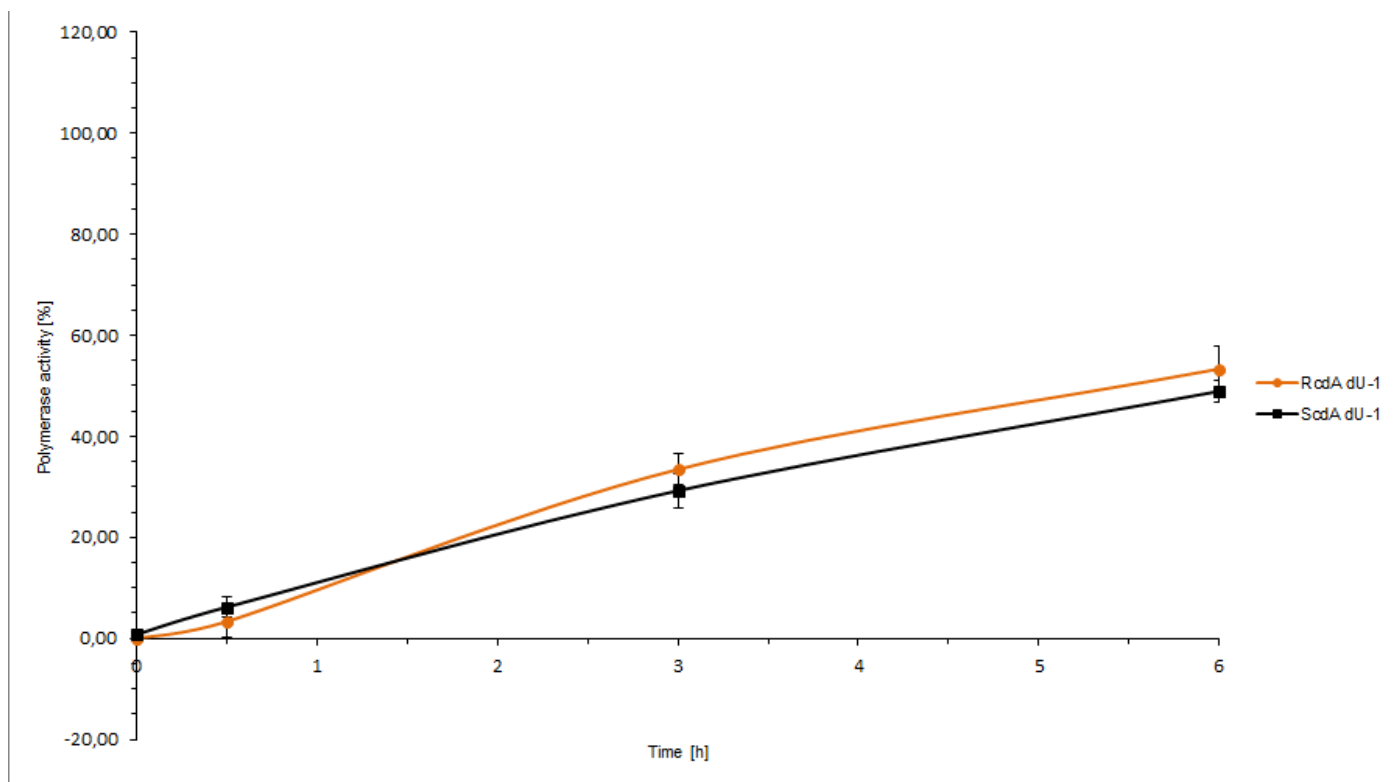
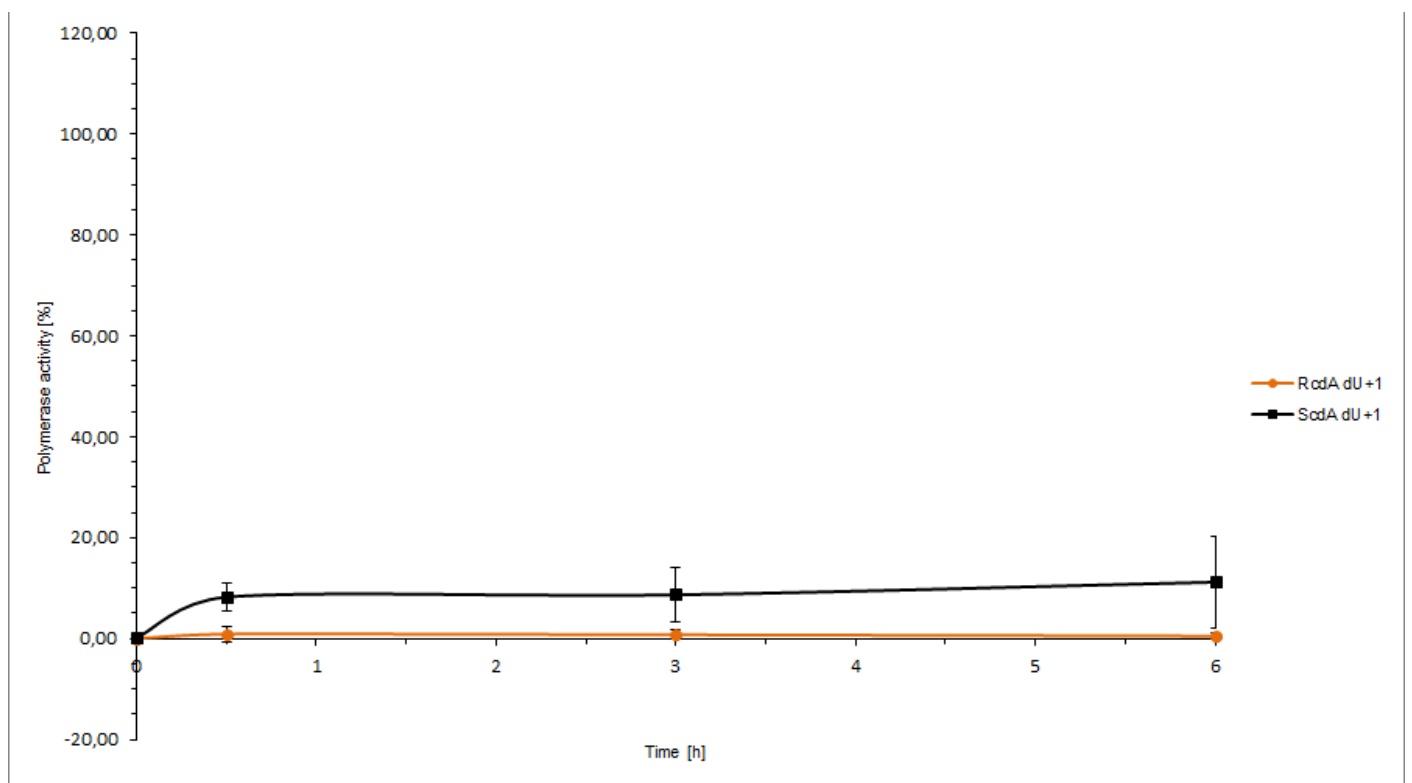
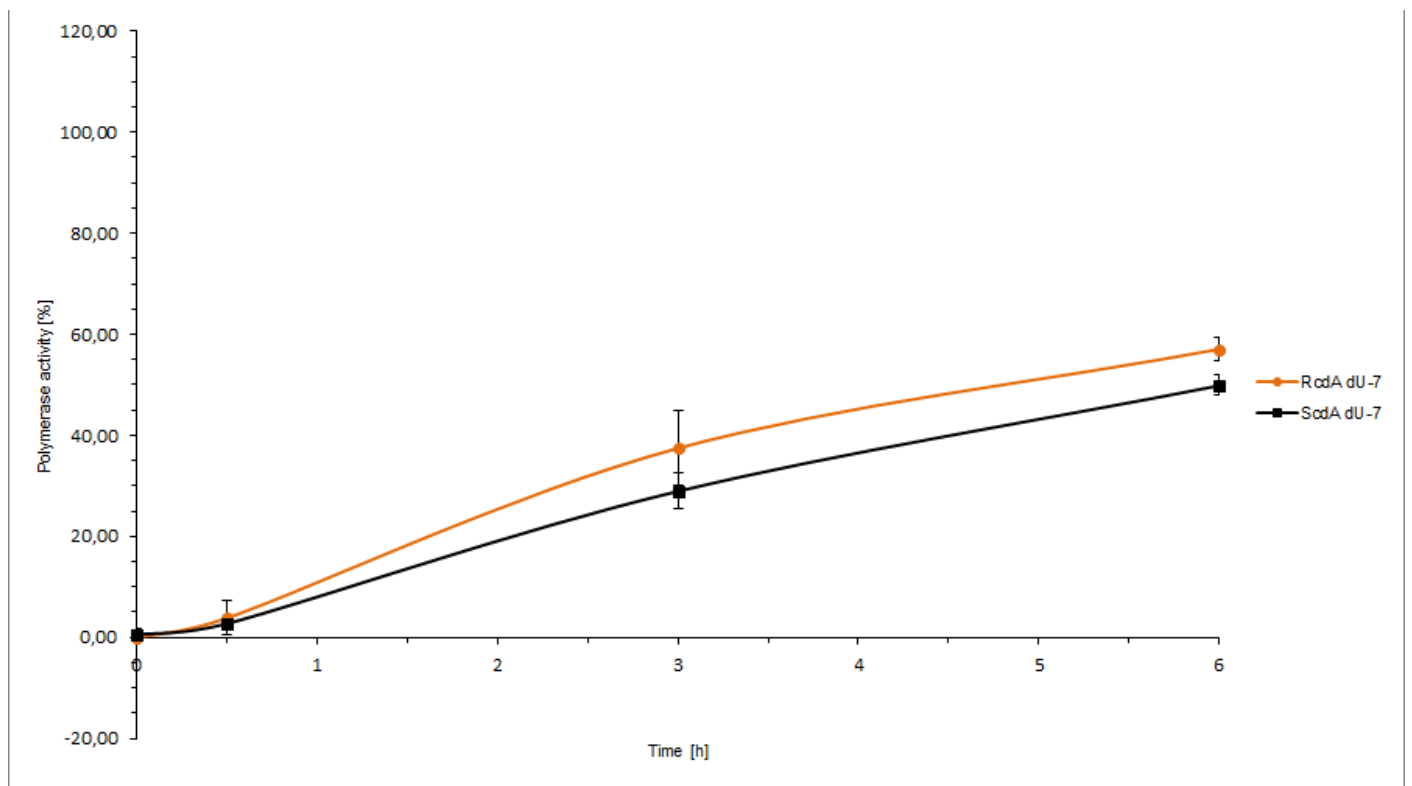
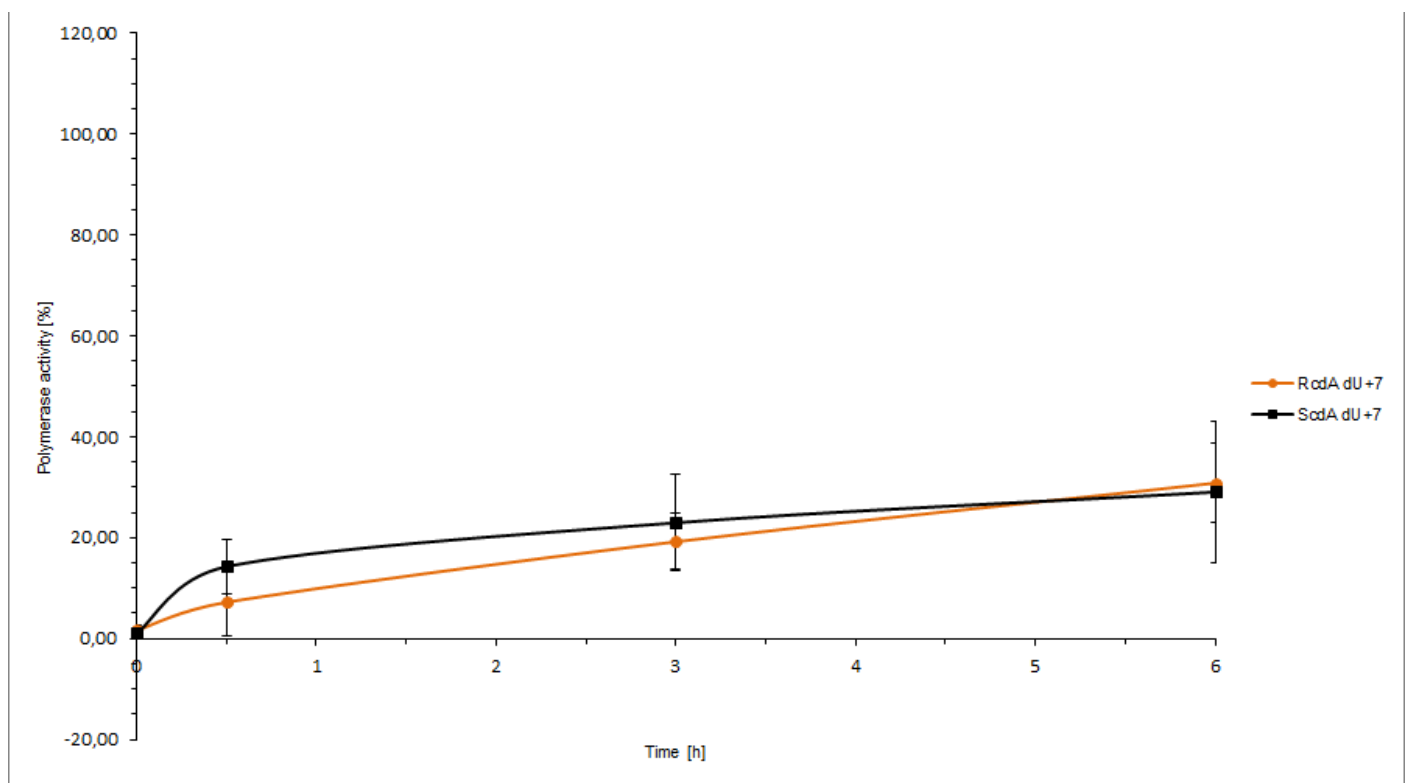
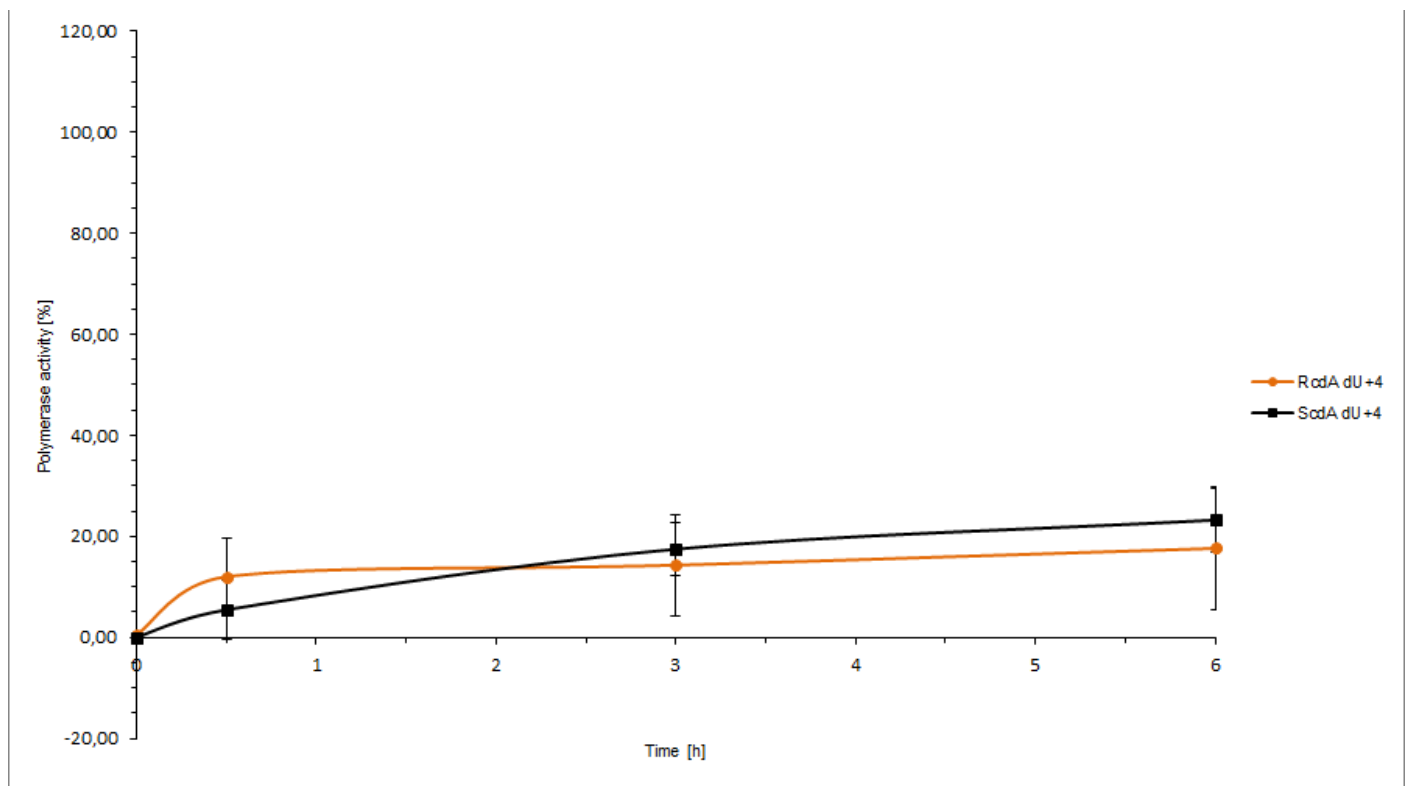


Figure S6. Endonuclease activity [%] of ScdA vs. RcdA – comparison of individual strands.







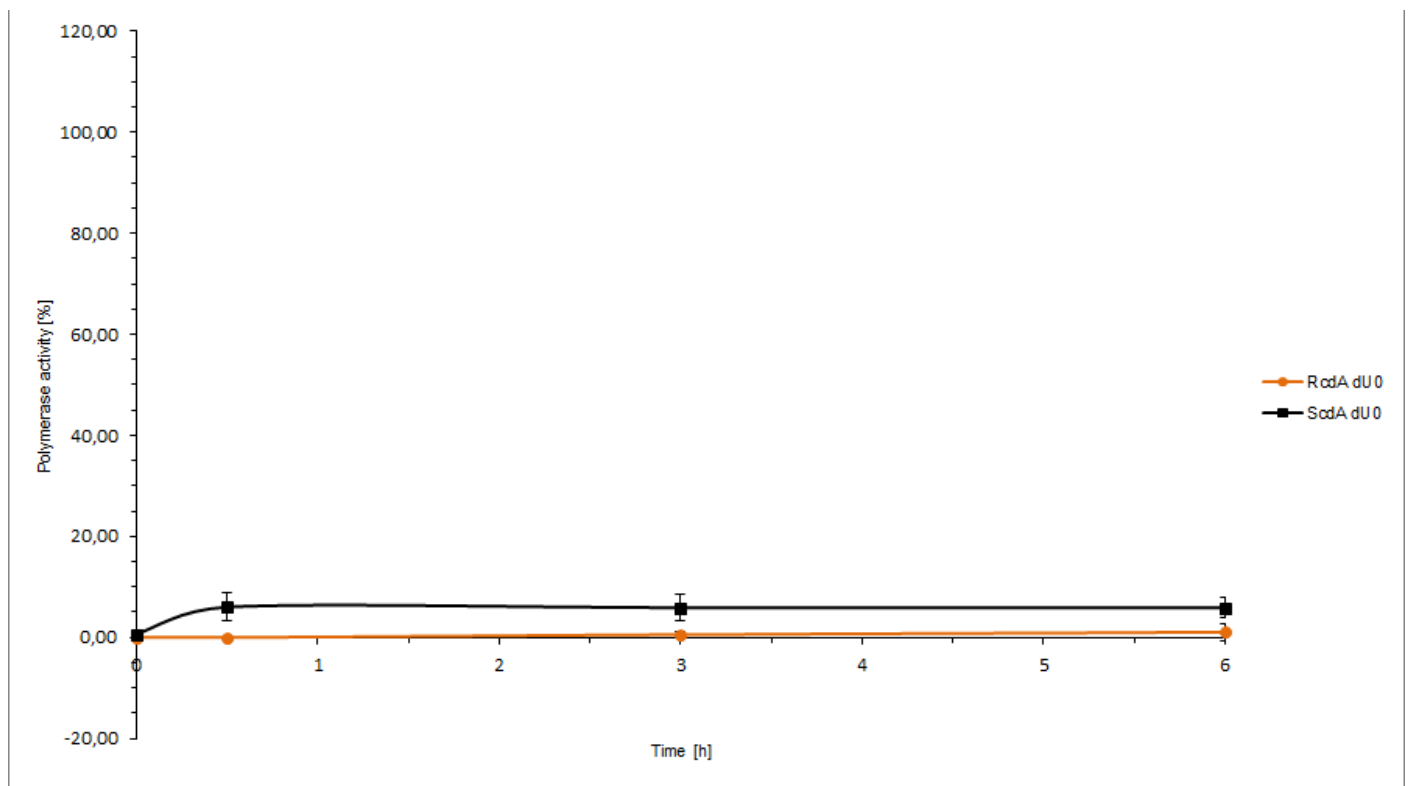


Figure S7. Polymerase activity [%] of ScdA vs. RcdA – comparison of individual strands.

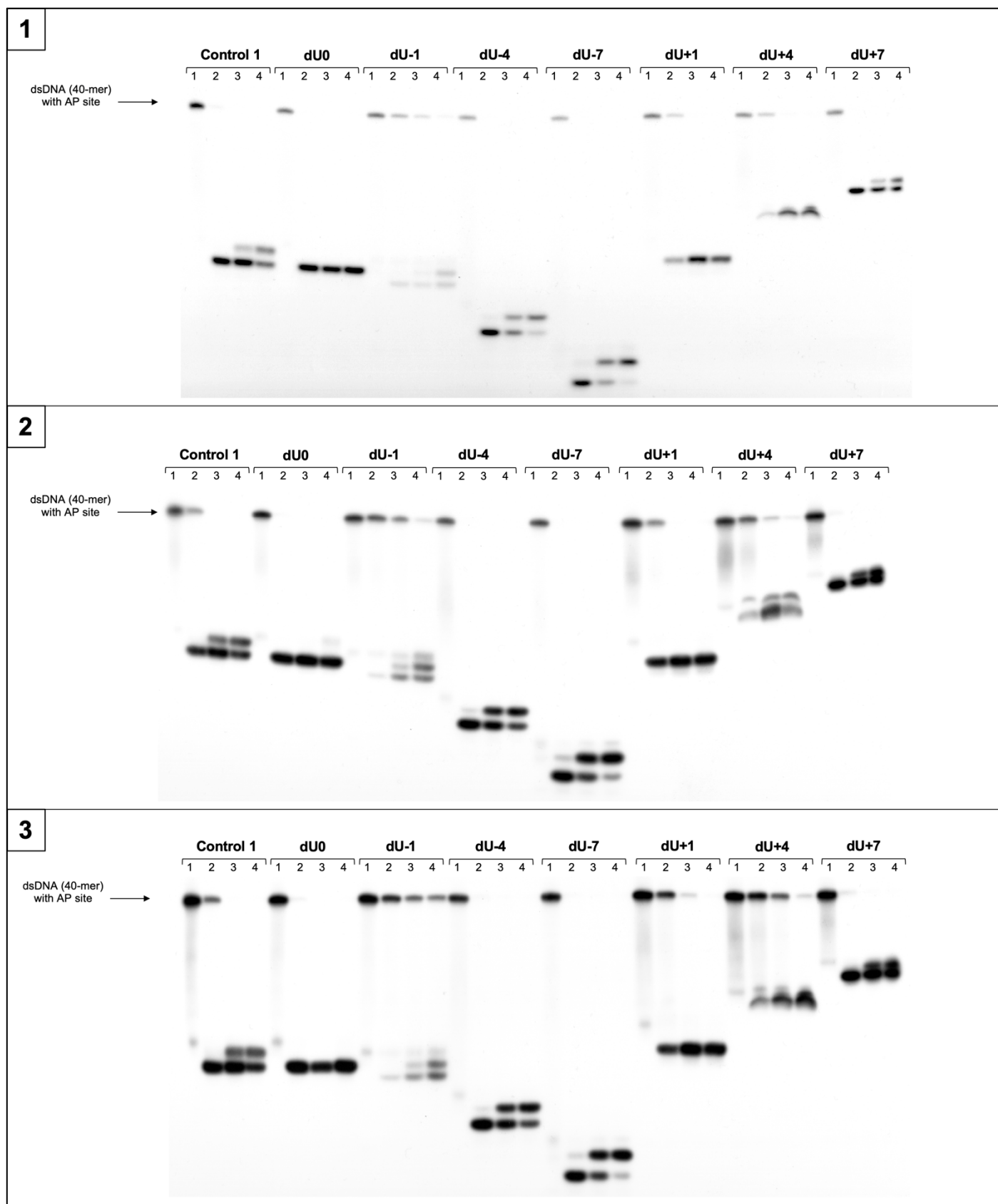


Figure S8. The autoradiograms of denaturing PAGE presenting repair of dsDNA containing clustered damage with AP site in one strand and **ScdG** in the opposing strand. Each number indicates different assay time: lane 1 - 0 min; lane 2 - 30 min; lane 3 - 3h; lane 4 - 6h. Three experimental replications are presented.

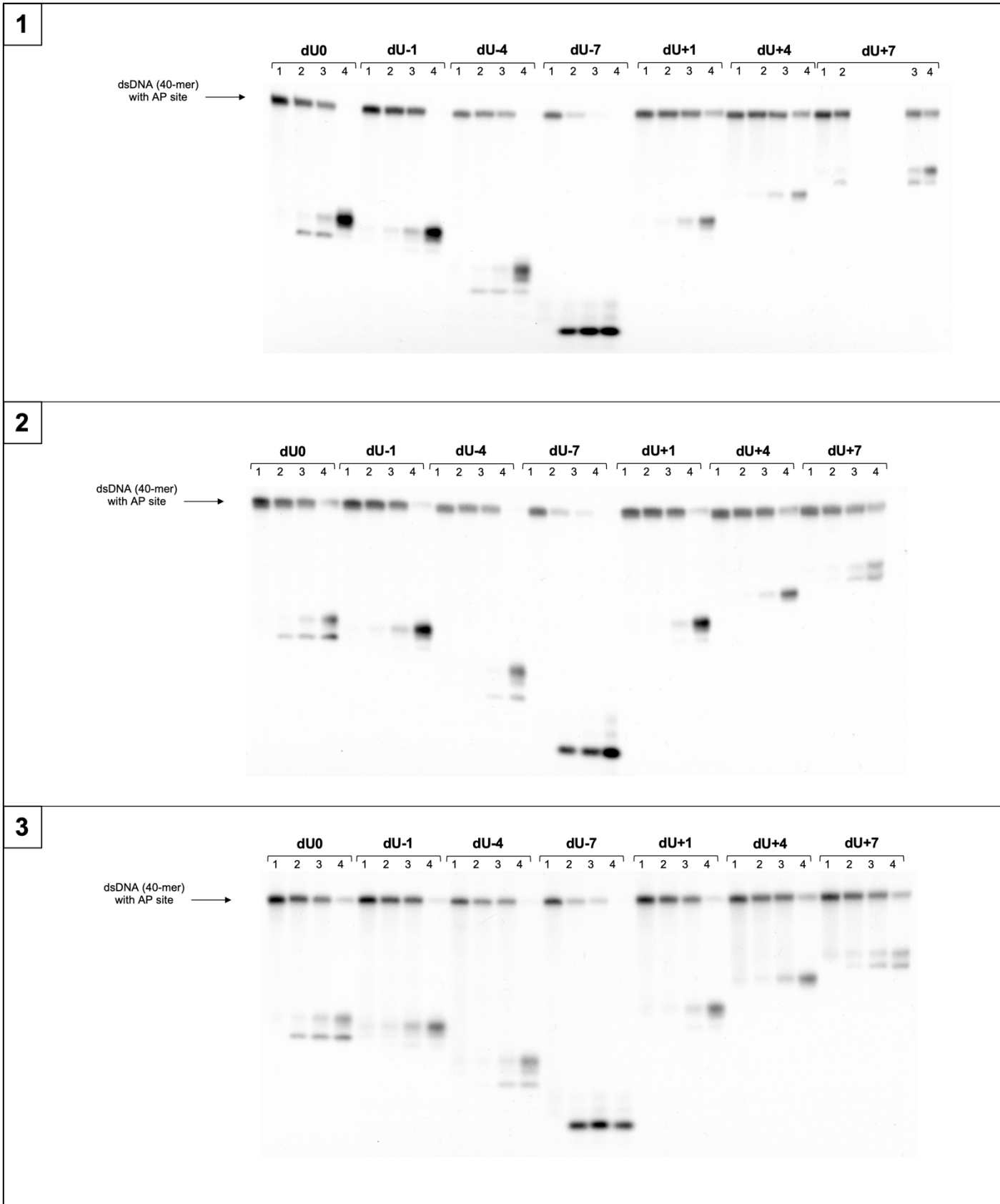


Figure S9. The autoradiograms of denaturing PAGE presenting repair of dsDNA containing clustered damage with AP site in one strand and **RcdG** in the opposing strand. Each number indicates different assay time: lane 1 - 0 min; lane 2 - 30 min; lane 3 - 3h; lane 4 - 6h. Three experimental replications are presented.

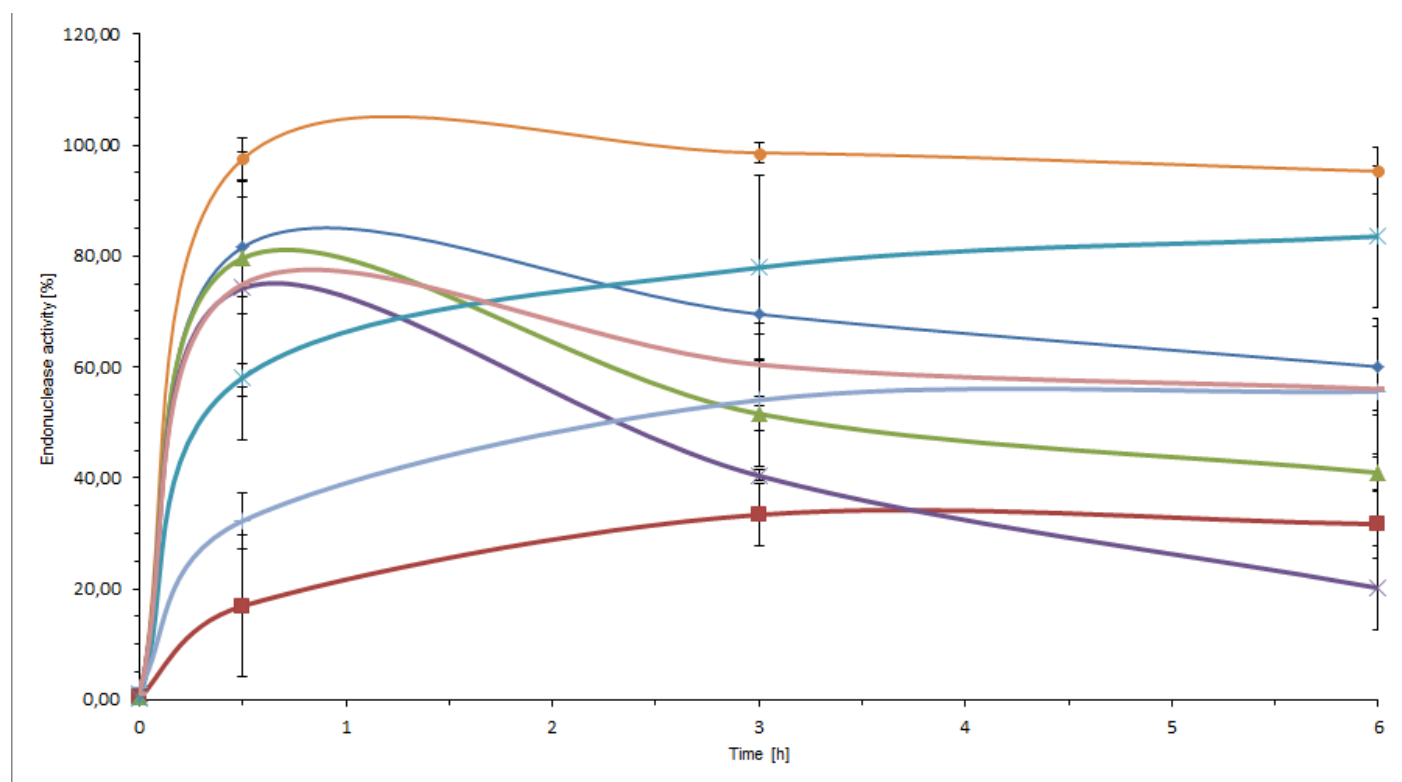
Table S6. Endonuclease activity – ScdG and RcdG. Raw numerical data of densitometry obtained from Quantity One software.

RcdG		Time [h]				ScdG		Time [h]			
		0	0,5	3	6			0	0,5	3	6
Strand	Data set	Endonuclease activity [%]				Strand	Data set	Endonuclease activity [%]			
dU0	1.	1,34	3,52	20,80	80,18	dU0	1.	0,92	99,54	99,53	94,41
	2.	0,15	11,18	19,91	34,40		2.	0,61	93,19	96,39	91,56
	3.	0,29	16,50	26,36	38,06		3.	0,00	99,82	99,91	99,87
	Avg	0,59	10,40	22,36	50,88		Avg	0,51	97,51	98,61	95,28
	SD	0,65	6,52	3,49	25,44		SD	0,47	3,75	1,93	4,22
dU-1	1.	0,00	6,45	24,32	74,24	dU-1	1.	0,00	8,07	38,34	33,08
	2.	2,20	5,31	23,15	82,50		2.	0,00	11,18	34,38	36,89
	3.	0,33	3,20	6,32	9,06		3.	1,15	31,47	27,36	25,02
	Avg	0,84	4,99	17,93	55,27		Avg	0,38	16,91	33,36	31,66
	SD	1,19	1,65	10,07	40,23		SD	0,66	12,71	5,56	6,06
dU-4	1.	0,00	0,00	7,57	63,04	dU-4	1.	0,00	89,74	52,47	38,80
	2.	0,55	0,97	6,30	78,72		2.	0,00	91,49	54,07	39,32
	3.	0,00	2,24	18,02	23,49		3.	1,24	57,67	48,13	44,72
	Avg	0,18	1,07	10,63	55,08		Avg	0,41	79,63	51,56	40,95
	SD	0,32	1,12	6,43	28,46		SD	0,71	19,04	3,07	3,28
dU-7	1.	2,53	73,82	81,68	77,08	dU-7	1.	0,28	79,48	39,88	18,78
	2.	0,00	82,62	93,85	87,47		2.	1,87	90,66	41,51	13,46
	3.	0,00	77,19	84,31	94,72		3.	0,72	52,53	39,74	28,23
	Avg	0,84	77,88	86,61	86,42		Avg	0,96	74,22	40,38	20,16
	SD	1,46	4,44	6,41	8,86		SD	0,82	19,60	0,98	7,48
dU+1	1.	1,43	3,17	18,68	58,64	dU+1	1.	0,00	69,95	86,05	85,67
	2.	0,60	1,19	13,39	82,12		2.	0,00	57,01	88,82	95,16
	3.	0,13	4,81	19,43	74,05		3.	0,49	47,27	58,87	69,80
	Avg	0,72	3,06	17,17	71,60		Avg	0,16	58,08	77,91	83,54
	SD	0,66	1,81	3,29	11,93		SD	0,28	11,38	16,55	12,81
dU+4	1.	1,19	2,64	13,43	45,41	dU+4	1.	1,07	27,69	66,03	56,93
	2.	0,89	1,77	10,91	66,59		2.	2,90	31,21	53,65	66,57
	3.	0,33	7,52	22,42	61,76		3.	2,24	37,85	42,39	43,19
	Avg	0,80	3,98	15,58	57,92		Avg	2,07	32,25	54,02	55,56
	SD	0,44	3,10	6,05	11,10		SD	0,93	5,16	11,83	11,75
dU+7	1.	0,45	10,43	19,35	13,91	dU+7	1.	2,27	86,81	63,04	54,57
	2.	1,27	2,84	16,54	30,64		2.	0,21	84,48	66,20	60,46
	3.	1,47	5,89	19,34	32,14		3.	1,08	53,61	52,08	53,08
	Avg	1,06	6,39	18,41	25,56		Avg	1,18	74,96	60,44	56,04
	SD	0,54	3,82	1,62	10,12		SD	1,03	18,53	7,41	3,90

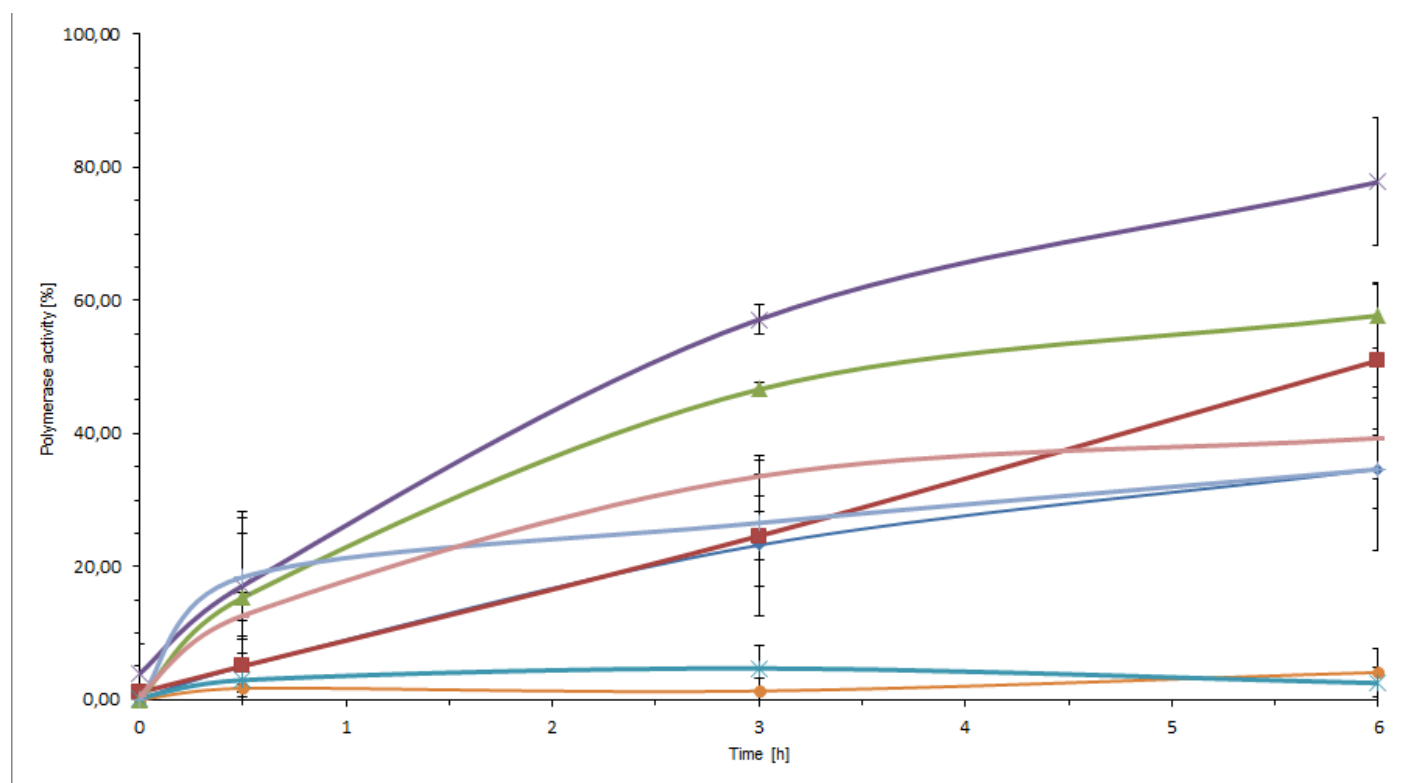
Table S7. Polymerase activity – ScdG and RcdG. Raw numerical data of densitometry obtained from Quantity One software.

RcdG		Time [h]				ScdG		Time [h]			
		0	0,5	3	6			0	0,5	3	6
Strand	Data set	Polymerase activity [%]				Strand	Data set	Polymerase activity [%]			
dU0	1.	0,54	0,47	0,71	12,18	dU0	1.	0,00	0,11	0,39	5,48
	2.	1,13	2,33	12,25	47,64		2.	0,00	5,08	3,60	6,88
	3.	2,08	5,22	17,95	44,40		3.	0,00	0,00	0,00	0,00
	Avg	1,25	2,67	10,30	34,74		Avg	0,00	1,73	1,33	4,12
	SD	0,78	2,39	8,78	19,60		SD	0,00	2,90	1,97	3,64
dU-1	1.	0,00	0,00	0,00	2,69	dU-1	1.	1,41	5,04	28,71	61,81
	2.	0,62	0,71	1,09	3,69		2.	1,94	1,16	21,72	39,25
	3.	1,15	11,76	29,72	81,46		3.	0,00	8,99	23,41	51,96
	Avg	0,59	4,16	10,27	29,28		Avg	1,11	5,06	24,61	51,01
	SD	0,58	6,60	16,86	45,19		SD	1,00	3,92	3,64	11,31
dU-4	1.	0,00	0,00	0,00	0,60	dU-4	1.	0,00	9,70	47,47	61,13
	2.	0,00	0,00	0,00	0,13		2.	0,00	6,09	45,34	60,05
	3.	0,00	5,34	17,32	72,03		3.	0,00	30,25	47,09	52,01
	Avg	0,00	1,78	5,77	24,25		Avg	0,00	15,35	46,64	57,73
	SD	0,00	3,08	10,00	41,37		SD	0,00	13,03	1,13	4,98
dU-7	1.	0,00	9,40	12,05	18,83	dU-7	1.	2,50	17,11	58,97	81,01
	2.	0,00	0,00	0,36	11,33		2.	0,34	6,89	57,65	85,37
	3.	1,36	0,83	4,27	4,20		3.	8,89	27,44	54,82	67,03
	Avg	0,45	3,41	5,56	11,45		Avg	3,91	17,15	57,15	77,80
	SD	0,78	5,20	5,95	7,32		SD	4,45	10,28	2,12	9,58
dU+1	1.	0,33	0,31	0,84	5,83	dU+1	1.	0,81	2,73	2,16	2,07
	2.	0,25	0,20	0,42	2,48		2.	0,00	1,29	3,45	0,33
	3.	2,22	1,69	2,09	4,62		3.	0,00	4,89	8,57	5,15
	Avg	0,93	0,73	1,12	4,31		Avg	0,27	2,97	4,73	2,51
	SD	1,11	0,83	0,87	1,70		SD	0,47	1,81	3,39	2,44
dU+4	1.	1,07	0,77	0,90	1,07	dU+4	1.	0,00	14,91	24,25	37,13
	2.	1,03	0,97	0,77	1,87		2.	0,05	14,51	18,46	27,86
	3.	0,44	4,30	5,06	4,35		3.	0,00	25,93	36,99	38,93
	Avg	0,85	2,01	2,24	2,43		Avg	0,02	18,45	26,57	34,64
	SD	0,35	1,98	2,44	1,71		SD	0,03	6,48	9,48	5,94
dU+7	1.	2,72	3,97	15,31	47,85	dU+7	1.	0,00	11,11	36,85	45,40
	2.	1,64	3,18	10,41	36,39		2.	0,04	10,19	32,92	39,18
	3.	1,35	9,93	15,28	33,45		3.	1,93	16,69	30,97	33,33
	Avg	1,90	5,69	13,66	39,23		Avg	0,66	12,66	33,58	39,30
	SD	0,72	3,69	2,82	7,61		SD	1,10	3,52	3,00	6,03

A.



B.



C.

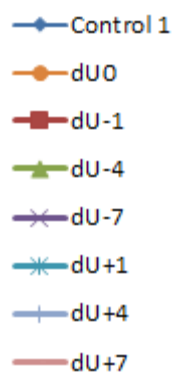
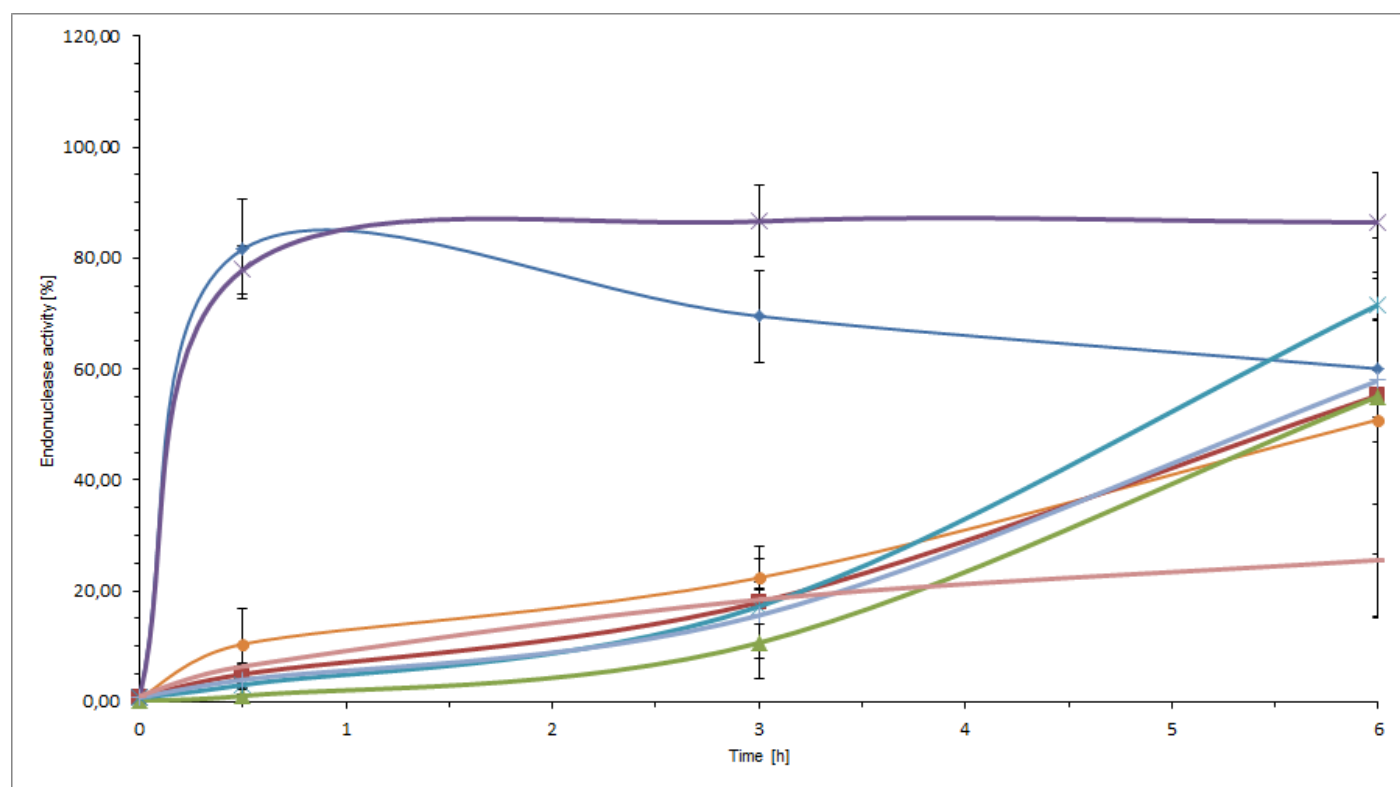
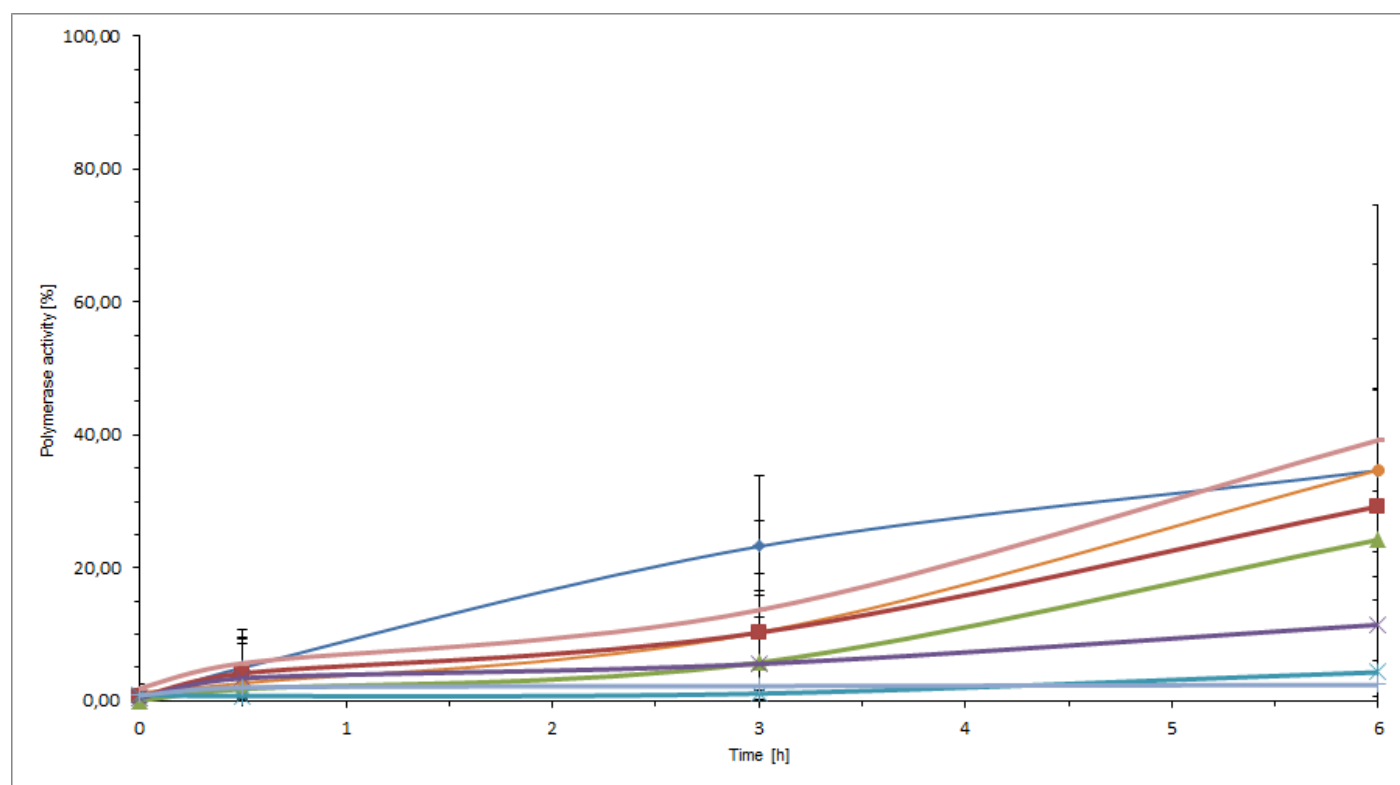


Figure S10. Graphical representation of the results for ScdG. (A) endonuclease activity +SD, (B) polymerase activity + SD; (C) figure legend.

A.



B.



C.

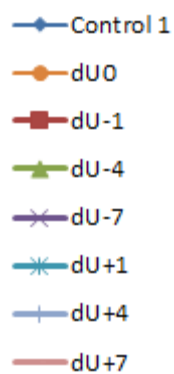
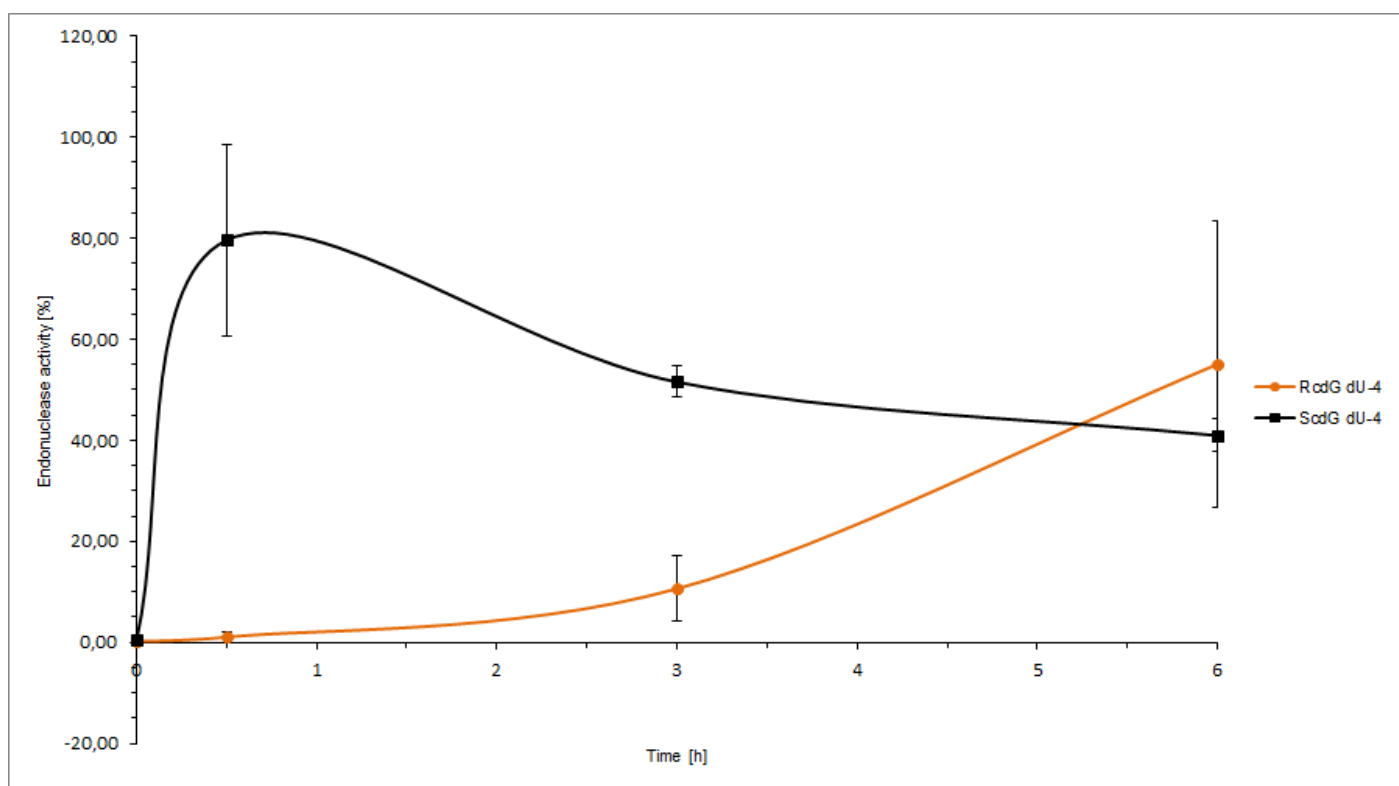
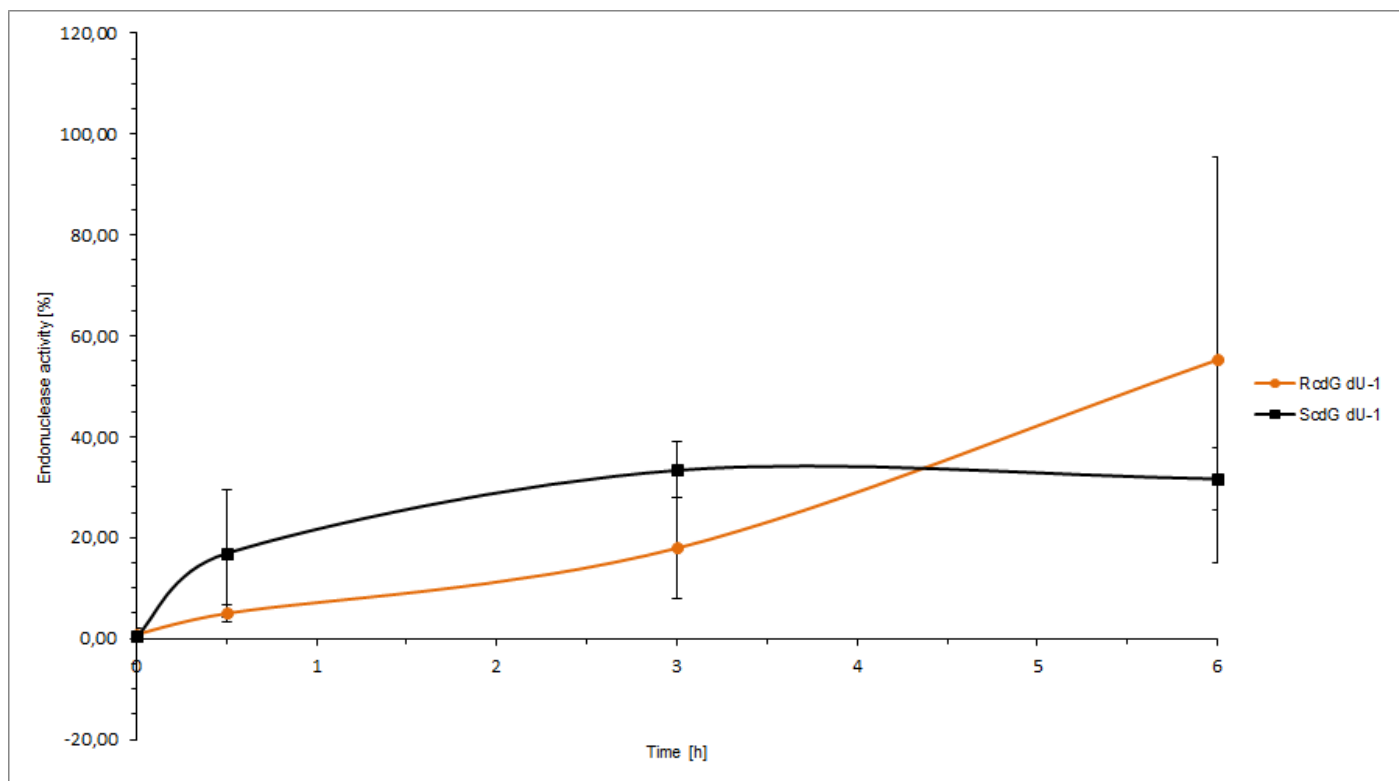
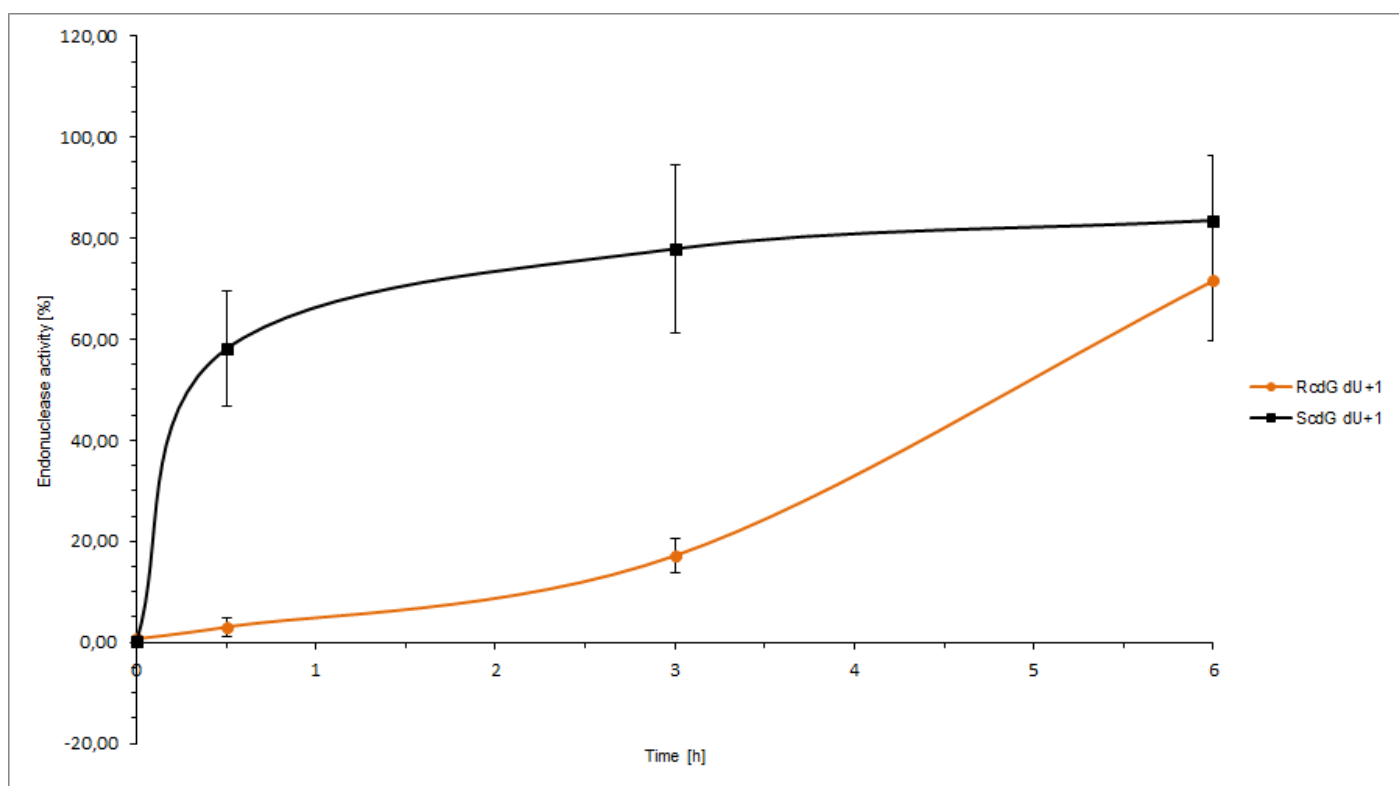
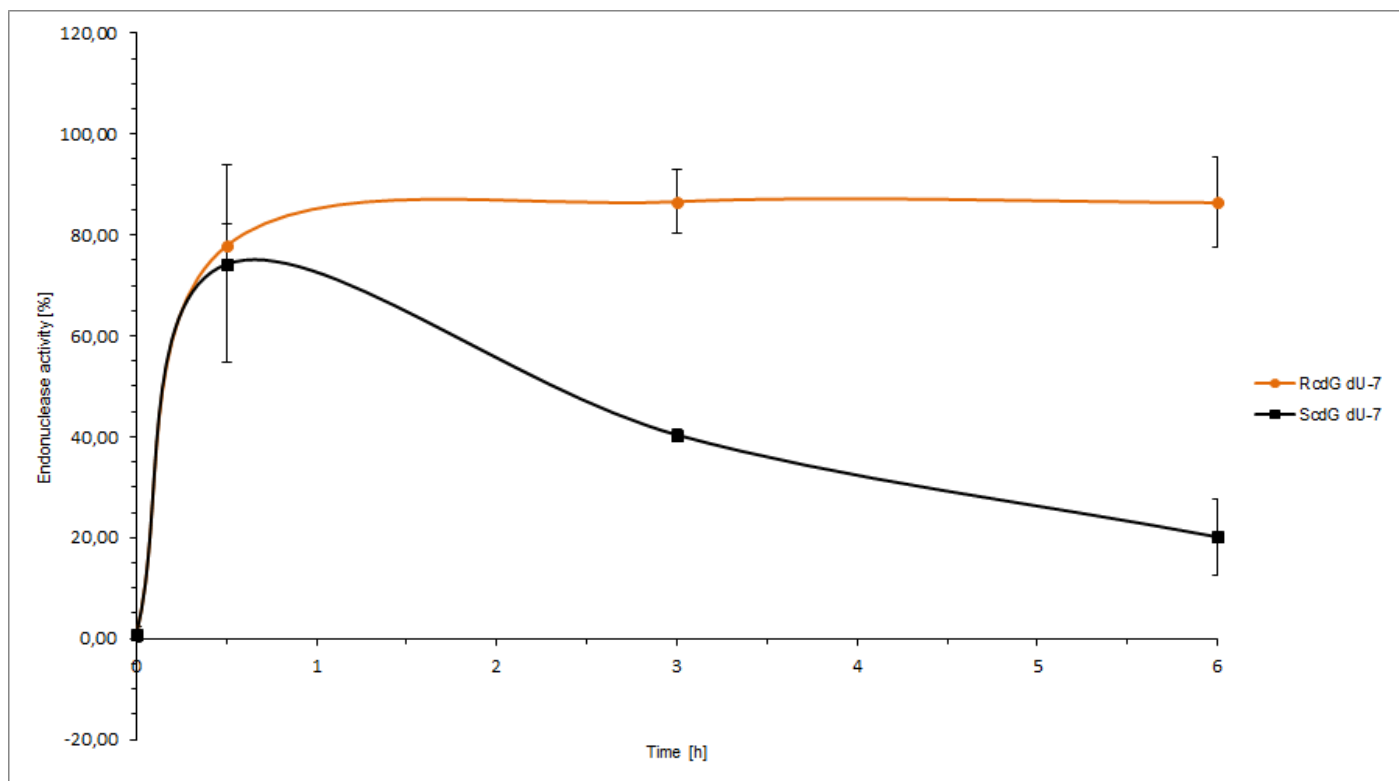
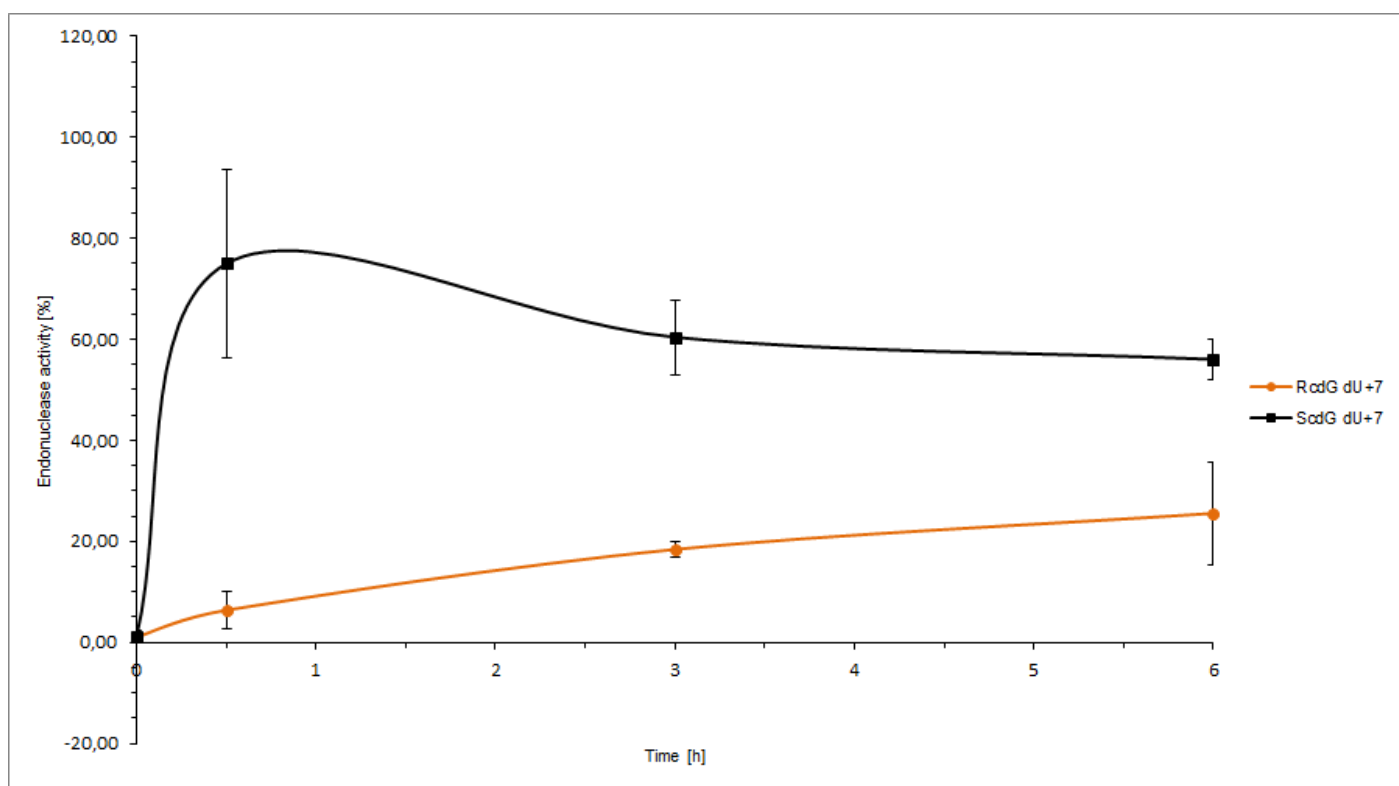
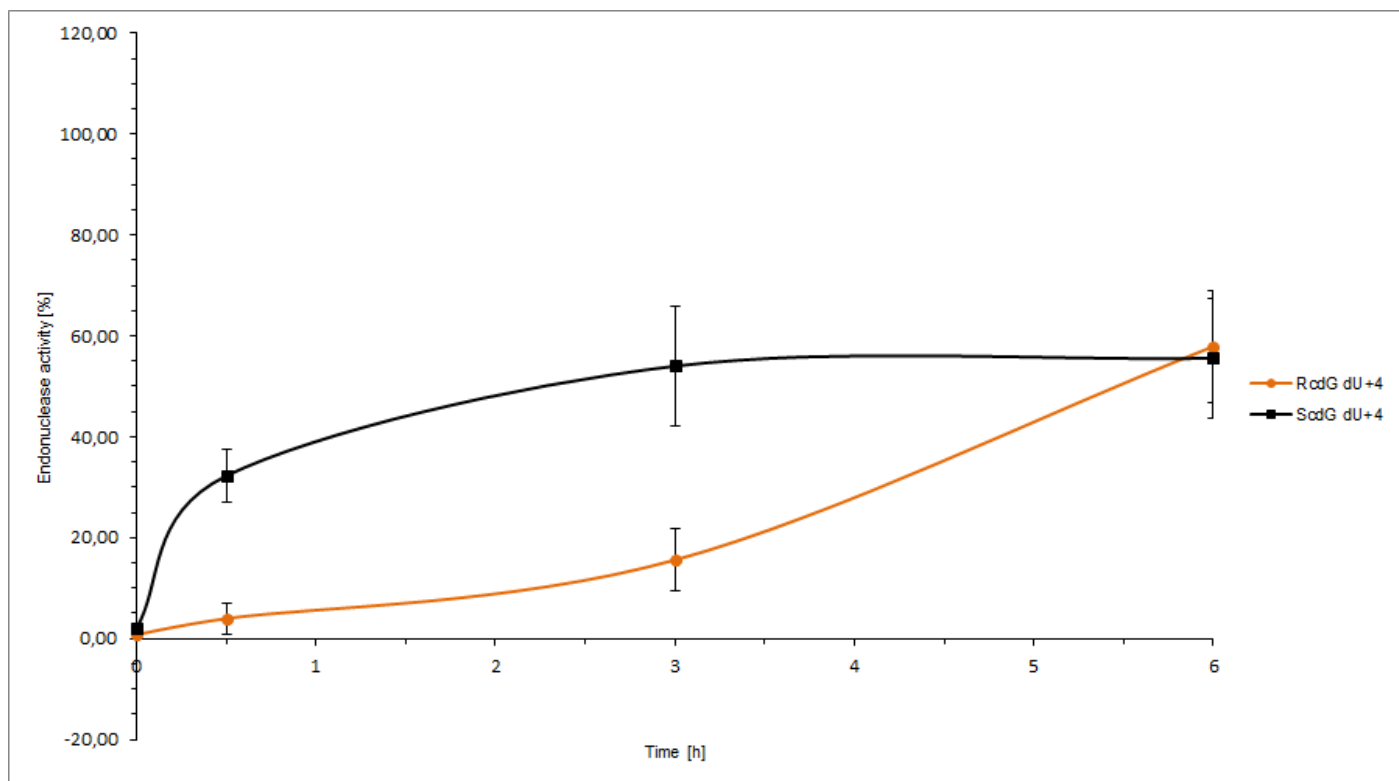


Figure S11. Graphical representation of the results for RcdG. (A) endonuclease activity +SD, (B) polymerase activity +SD; (C) figure legend.







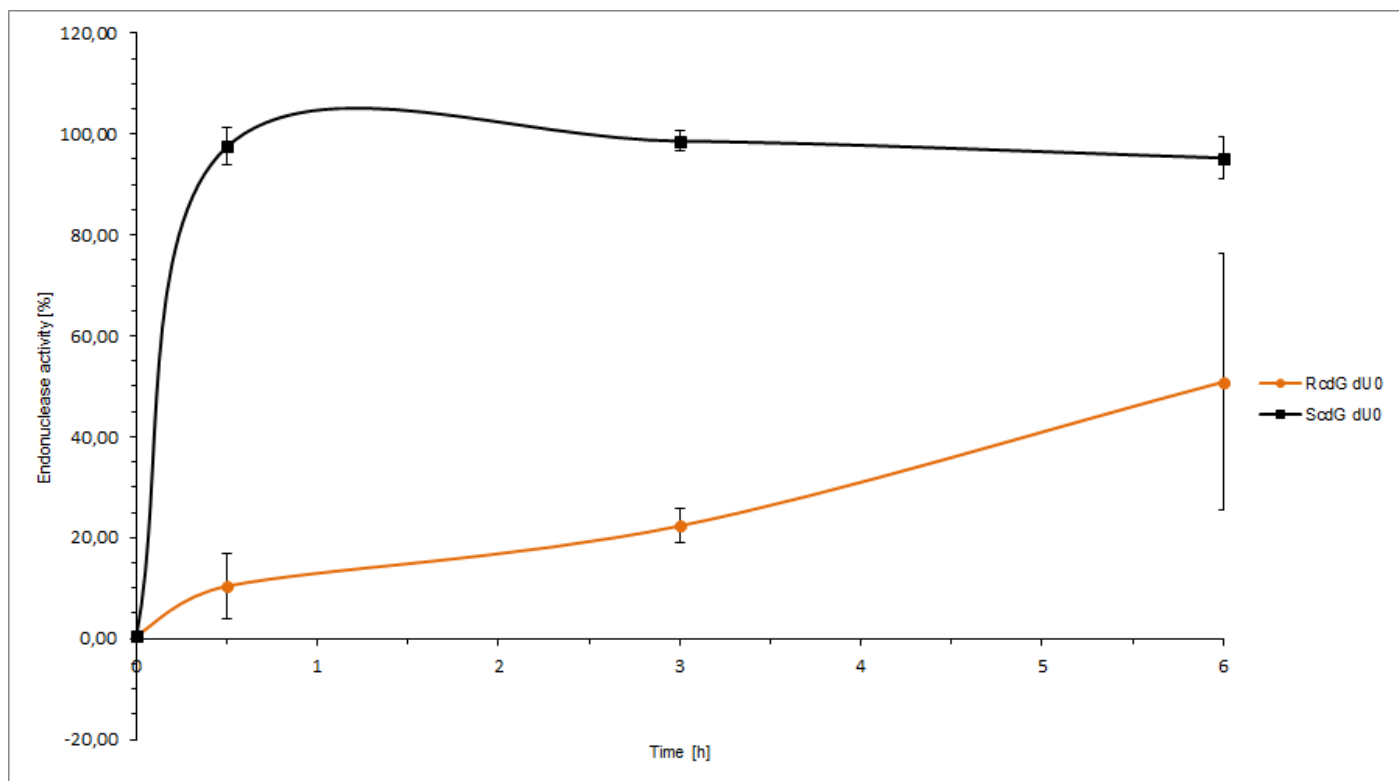
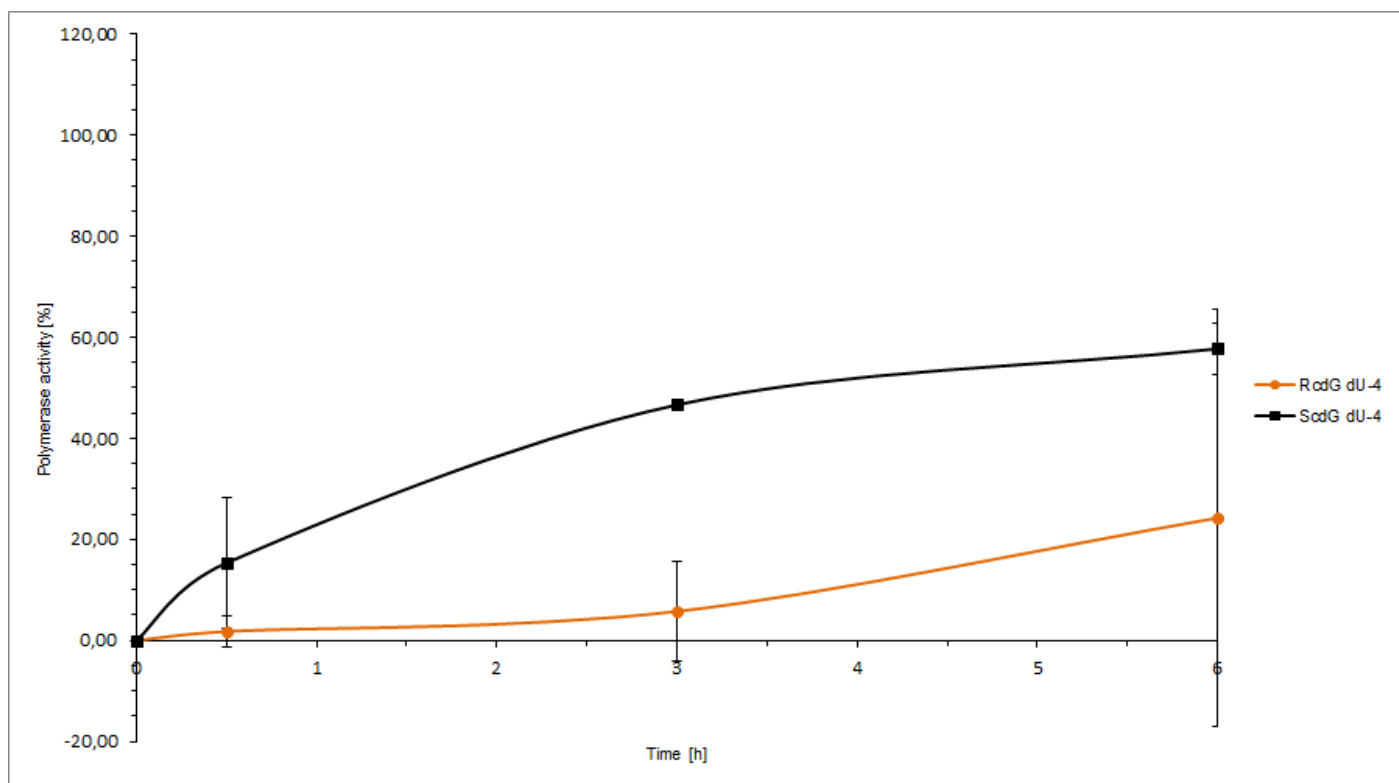
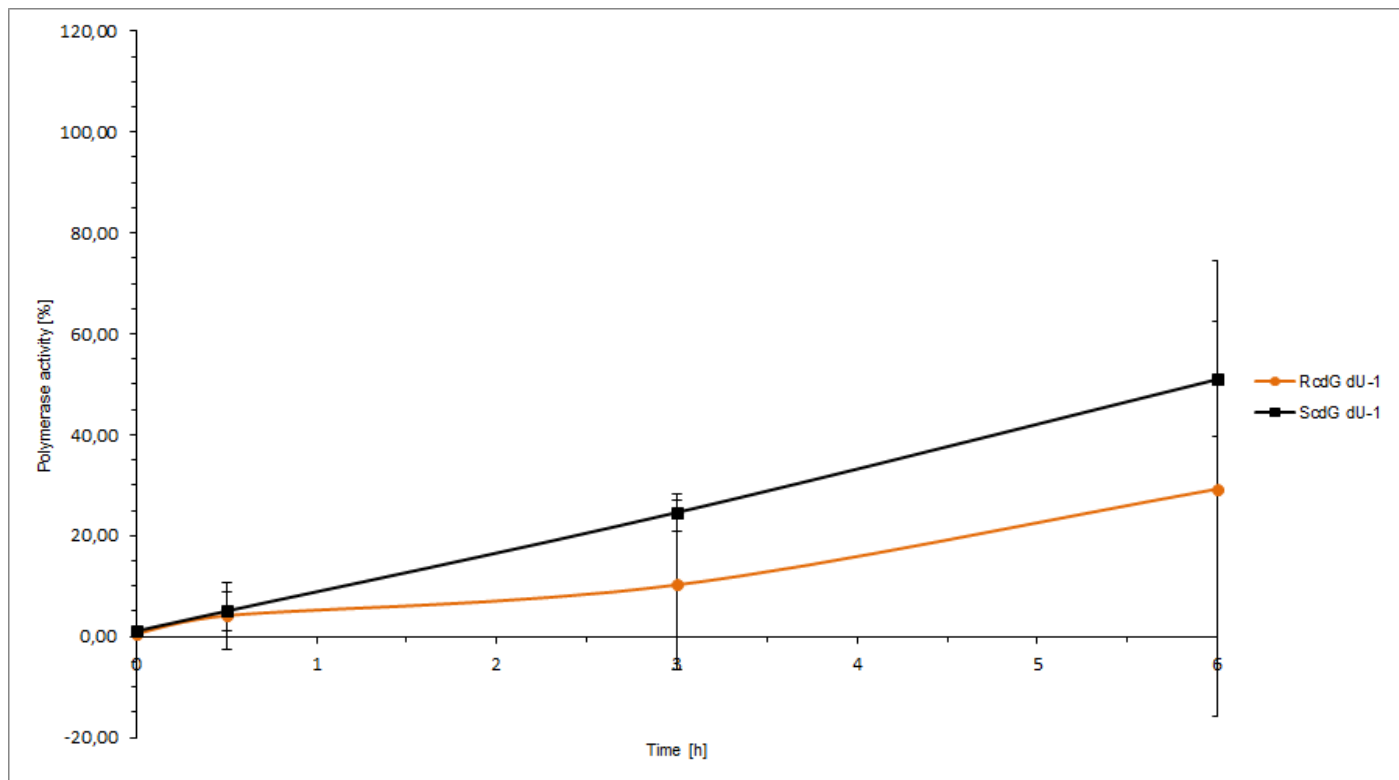
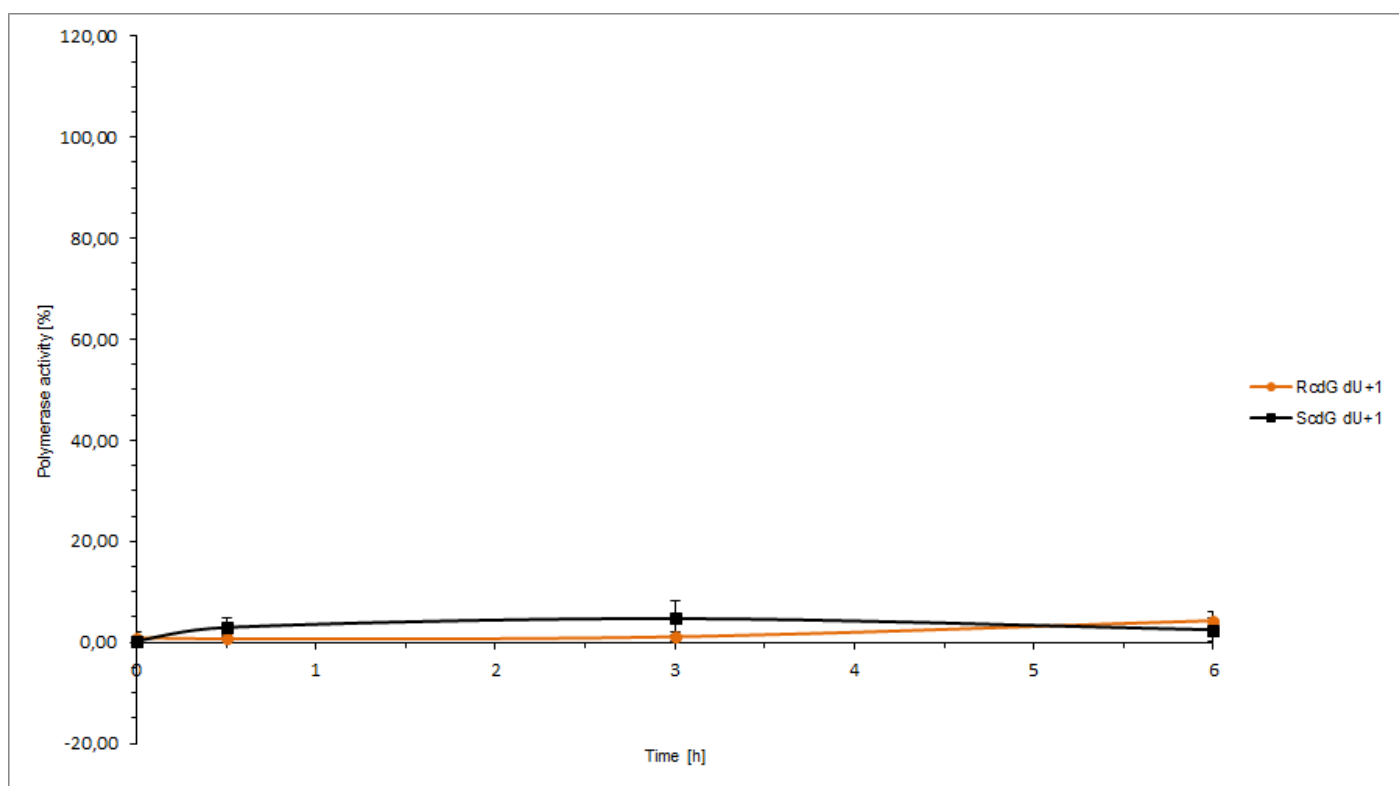
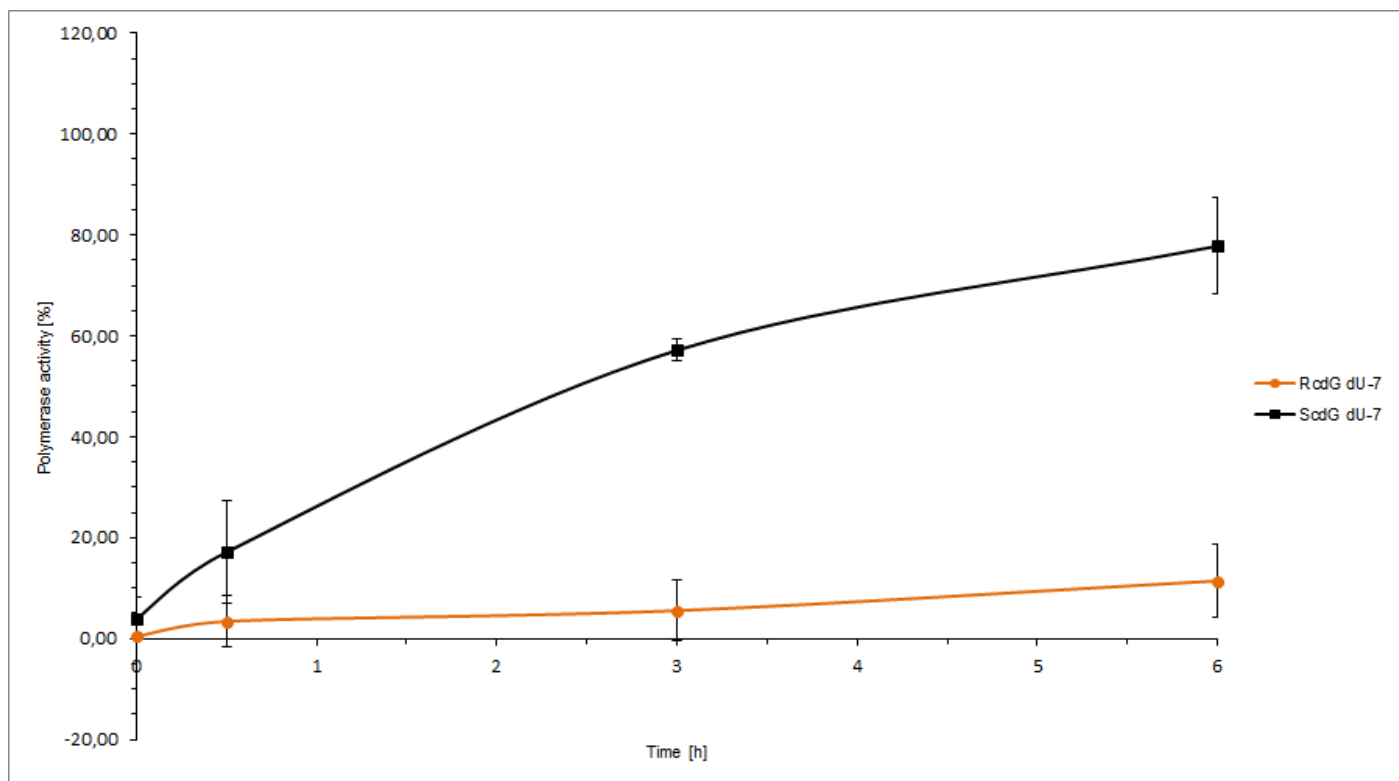
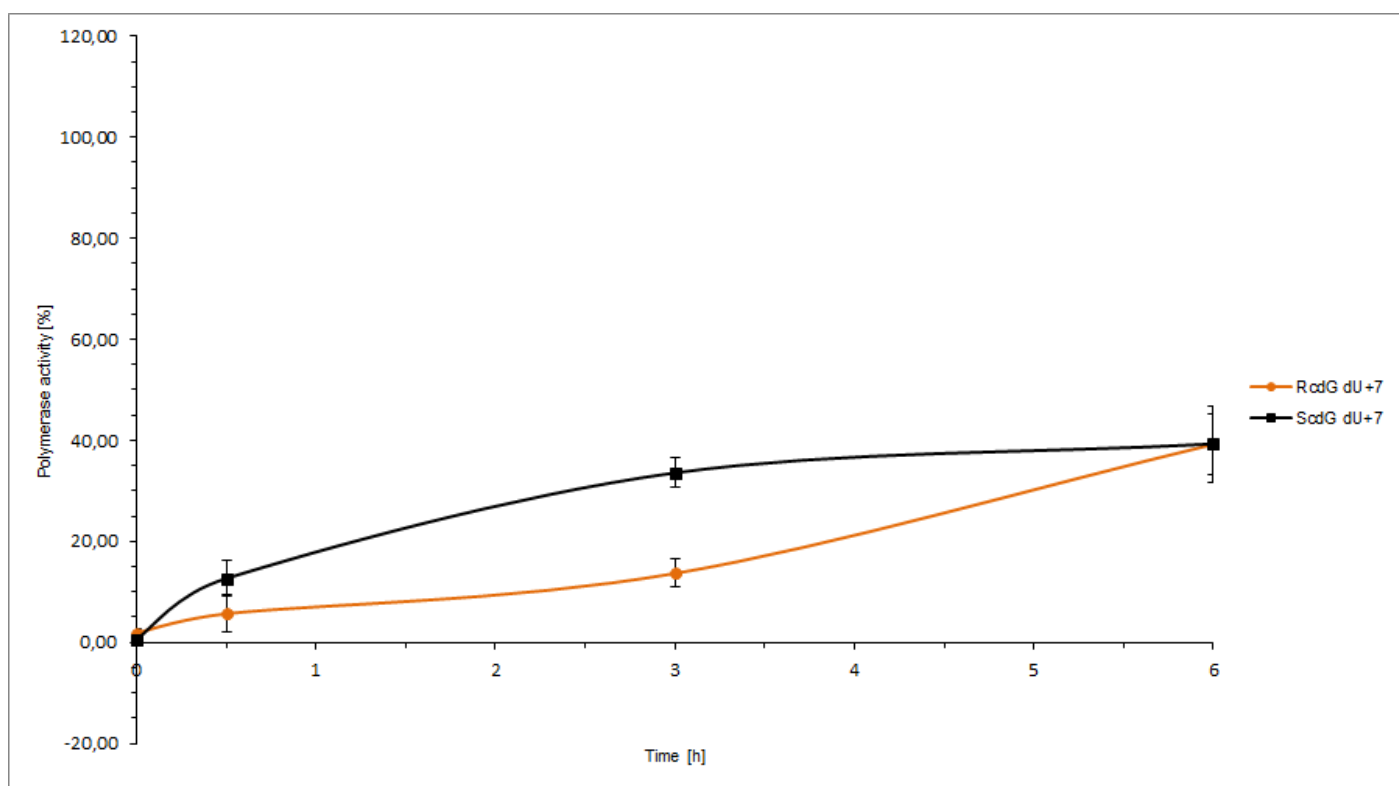
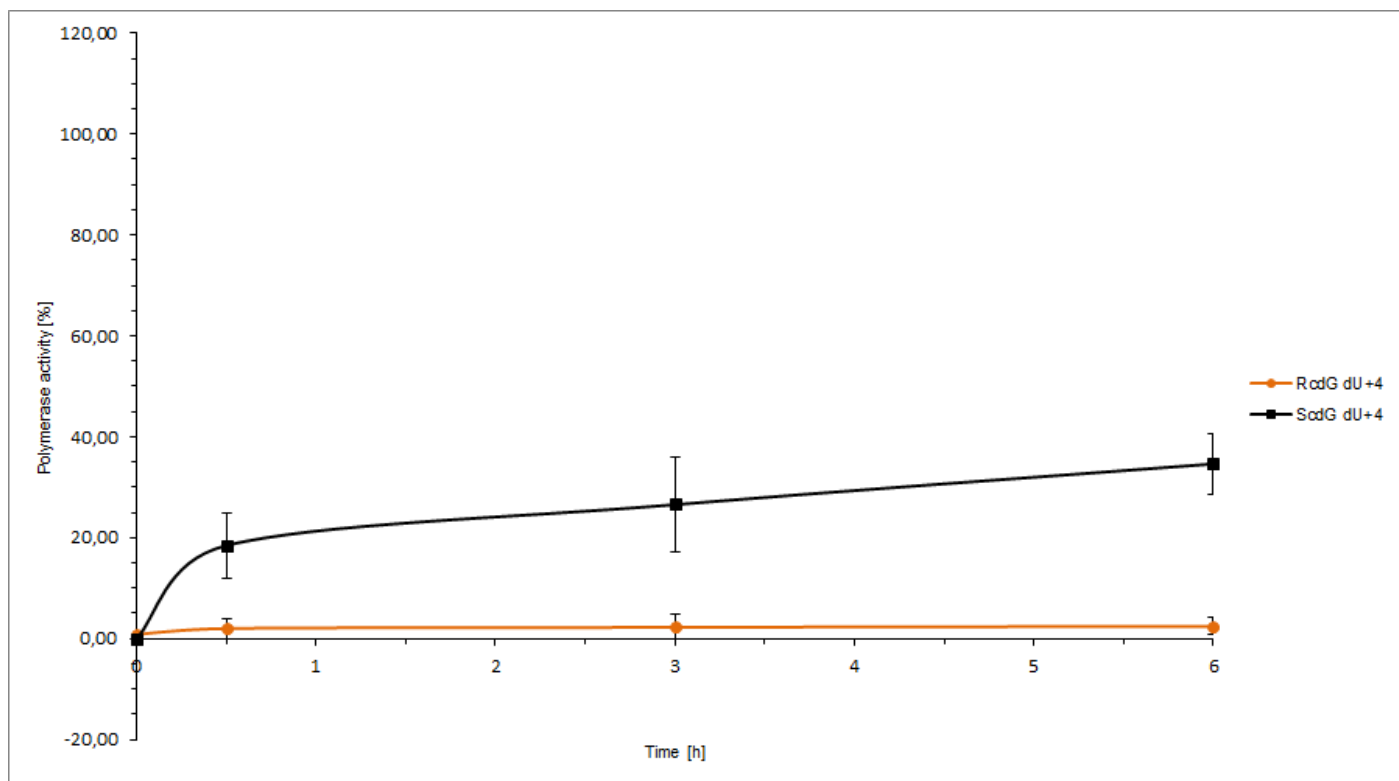


Figure S12. Endonuclease activity [%] of ScdG vs. RcdG – comparison of individual strands.







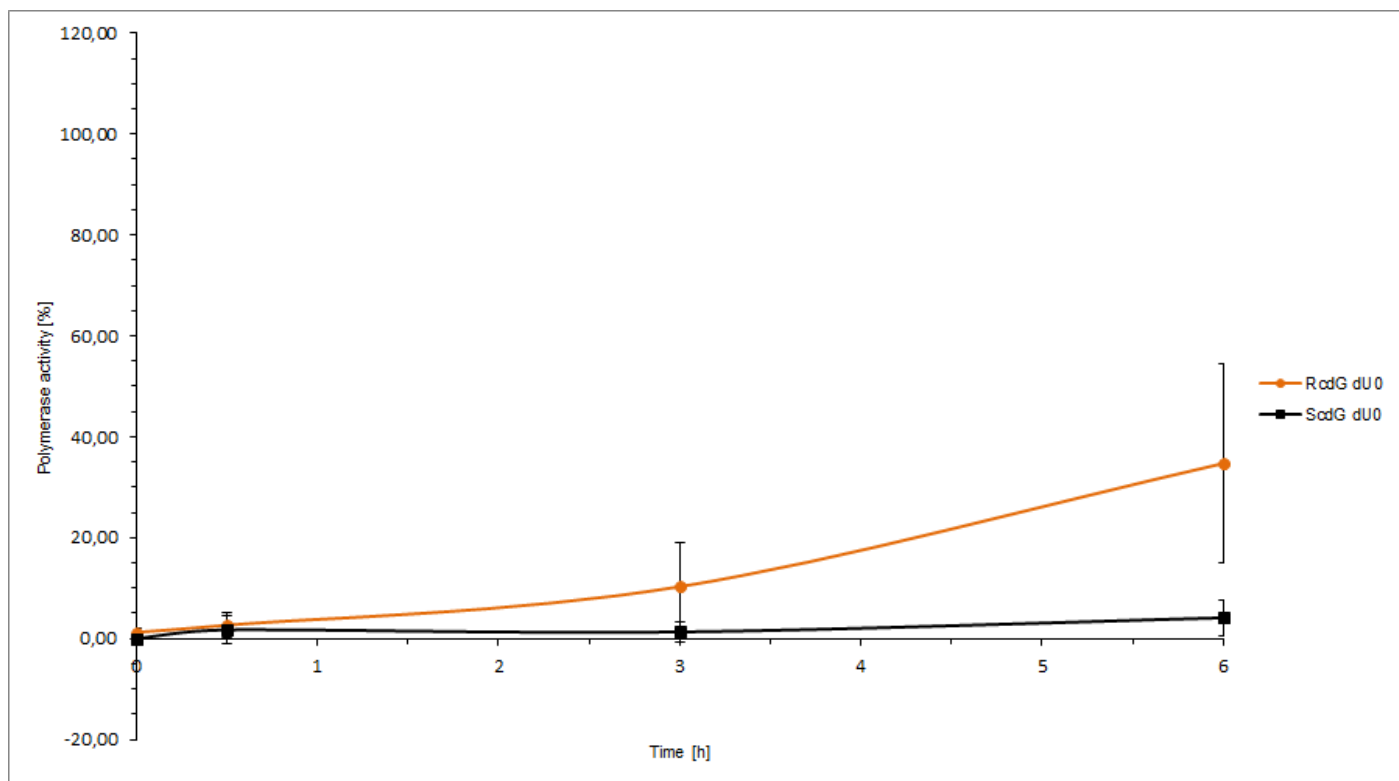


Figure S13. Polymerase activity [%] of ScdG vs. RcdG – comparison of individual strands.

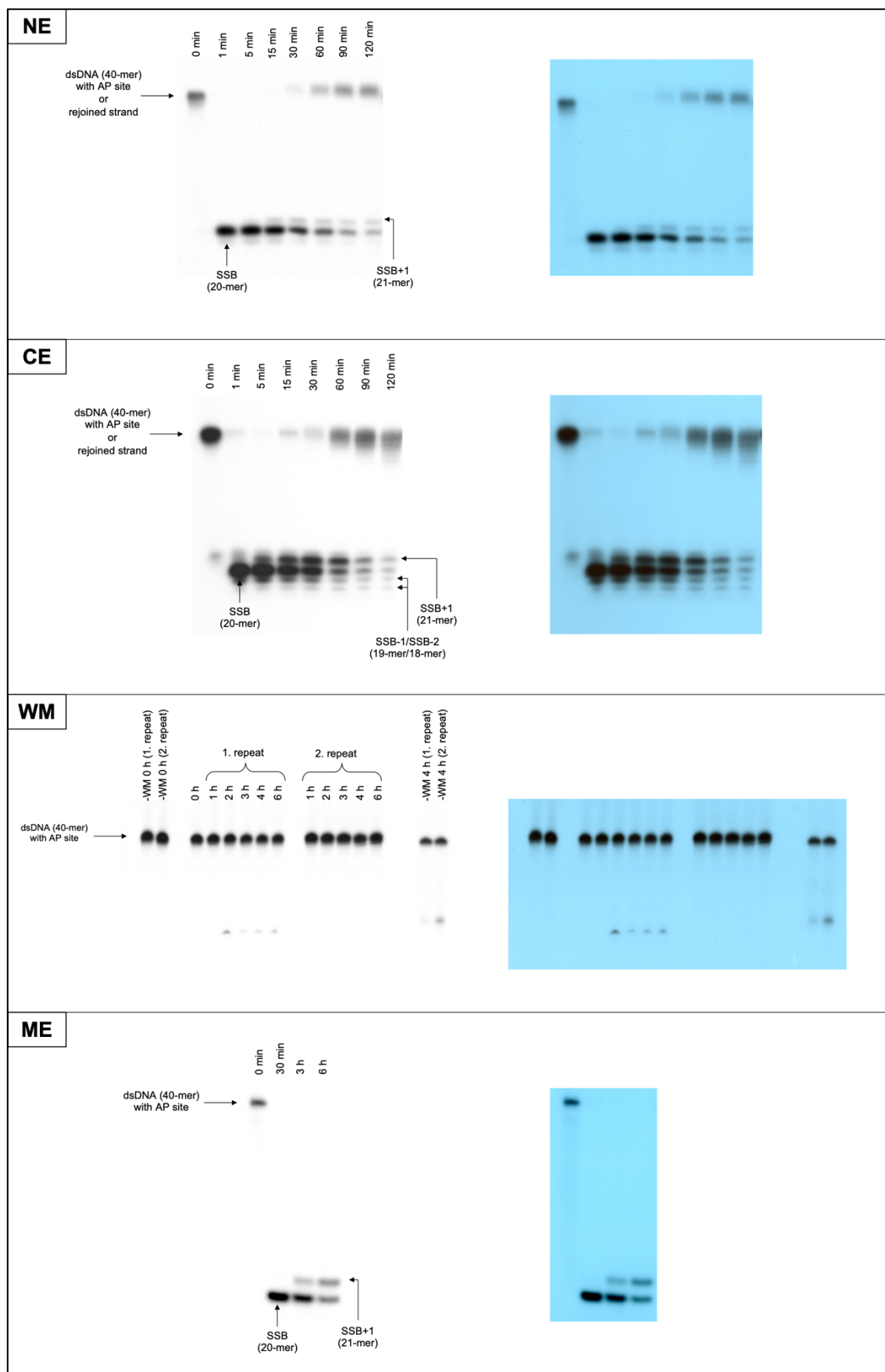


Figure S14. Functional activity test of mitochondrial extract (ME, 20 μ g) by comparison with whole mitochondria fraction (WM, 20 μ g), nuclear extract (NE, 10 μ g), and cytoplasmic extract (CE, 10 μ g) of *xrs5* cell line using Control 1 (ds-oligo with single AP site lesion). SSB – single strand break (AP site cleavage resulting from endonucleolytic activity of ME, NE, and CE), SSB+1 - cleaved strand with 1 nucleotide incorporated (resulting from polymerase activity of ME, NE, and CE); SSB-1/SSB-2 - cleaved strand with 1 or 2 nucleotides cleaved (resulting from exonucleolytic activity of CE). Original scans of X-ray films are presented on the right, and annotated, graphically processed radiograms are presented on the left.