

Table S3. Potential posttranslational modifications of PCNA_V3 and PCNA_V4.

Site modification	Description	PCNA_V3	PCNA_V4
14	N ⁶ -Acety-L-lysine	Lys14	Gln13
77	N ⁶ -Acety-L-lysine	-	Lys77
80	N ⁶ -Acety-L-lysine	-	Lys80
164	Isopeptide glycylisn (Lys-Gly) (binding with G-Cter on SUMO2) (binding with G-Cter in ubiquitin)	-	Lys164
211	Phosphotyrosine	-	Tyr211
248	N ⁶ -Acety-L-lysine	-	Lys240
254	Isopeptide glycylisn (Lys-Gly) (binding with G-Cter on SUMO2)	-	Lys246

Table S4. Domains found in the new PCNA transcript variants.

Domain	Site	PCNA_V3	PCNA_V4
Domain I	1-123	1-49, 88-94, 103-105	1-55, 63-123
Domain II	132-258	133-143, 180-186, 228-231	132-261
IDCL	118-134	133-134	118-134
DNA-binding site	60-80	-	63-80
Loop J, Asp113, Gly178	105-110, 113, 178	-	105-110, 113, 178

Table S5. Homology analysis of the novel PCNA transcript variants.

Model	Robetta		Ramachandran (PROCHECK ²⁴)		
	Aling reliability	Template structure (PDB)	Favored	Allowed	No Allowed
PCNA_V3	0.9771	PCNA <i>A. thaliana</i> (2ZVW)	85.1%	14.4%	0.5%
PCNA_V4	0.7951	PCNA <i>S. cerevisiae</i> (3K4X)	87.5%	12.5%	0.0%