

# **Protein-Profiling of Genomic Instability in Endometrial Cancer**

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**S7: Identifications of the normal endometrium versus diploid endometrioid-carcinoma analysis**

SSP	Gene symbol	Protein name	Accession number	Sequence coverage (%)	Matched/ searched peptides	Score	N vs. De	De vs. Ae	Ae vs. Au	De vs. Au	Trend (N-De-Ae-Au)	Fold change (logarithmized)
<b>Lower expression in diploid endometrioid cancer</b>												
2117	ARHGDI2	Rho GDP dissociation inhibitor (GDI) alpha	NP_004300	35	8/54	4.2x10 <sup>-3</sup>	↓					0.77
3221	CLIC1	Chloride intracellular channel protein 1	NP_001279	40	8/41	2.3x10 <sup>-3</sup>	↓					0.79
3602	VIM	Vimentin	NP_003371	39	17/58	3.9x10 <sup>-5</sup>	↓					0.75
4621	DES	Desmin	NP_001918	39	14/66	1.1x10 <sup>-3</sup>	↓					0.58
5217	DDAH2	Dimethylarginine dimethylaminohydrolase 2	NP_039268	27	9/50	3.5x10 <sup>-3</sup>	↓					0.72
5304	CAPZA1	F-actin-capping protein subunit alpha-1	NP_006126	35	6/56	0.23	↓					0.88
7451	MPST	Mercaptopyruvate sulfurtransferase isoform 2	NP_001013454	23	5/31	0.018	↓					0.61
7537	CRKL	Crk-like protein	NP_005198	32	8/38	8.2x10 <sup>-4</sup>	↓					0.58
8101	PARK7	Parkinson disease protein 7	NP_009193	61	10/59	1.4x10 <sup>-4</sup>	↓					0.76
8507	GDI2	Rab GDP dissociation inhibitor beta isoform 1	NP_001485	39	14/60	2.5x10 <sup>-3</sup>	↓					0.80
8514	SEPT2	Septin-2	NP_004395	32	10/50	4.3x10 <sup>-4</sup>	↓					0.67
8609	CCT2	Chaperonin containing TCP1, subunit 2	NP_006422	30	12/41	1.8x10 <sup>-5</sup>	↓					0.77
<b>Higher expression in diploid endometrioid cancer</b>												
1342	KRT7	Keratin 7	AAH02700	16	7/39	0.080	↑					1.62
3503	ACTB	β-actin	AAH12854	28	7/33	9.7x10 <sup>-3</sup>	↑					1.13
4005	RBP4	Retinol binding protein 4	AAH20633	36	5/60	0.12	↑					1.41
4011	RAB1B	RAB IB	NP_112243	28	5/33	7.0x10 <sup>-5</sup>	↑					1.34
4207	ATP5B	ATP-Synthase 5B	NP_001677	15	5/43	0.073	↑					1.11
4611	HSPD1	HSP60	AAA36022	21	8/75	0.65	↑				↑	1.28
5424	KRT10	Keratin 10 <sup>a</sup>	AAH34697	15	6/47	0.23	↑					1.35

<sup>a</sup> One protein (KRT10) was identified out of at least two protein spots and showed non homogenous up- or down regulation between groups due to possible post-translational modification and was thus excluded from pathway analysis.

SSP, Individual identification number for protein spots analysis software; N, normal ; De, diploid endometrioid ; Ae, aneuploid endometrioid ; Au, aneuploid UPSC