

Protein-Profiling of Genomic Instability in Endometrial Cancer

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SSP	Gene symbol	Normal endometrium [mean]	Diploid endometrioid [mean]	Aneuploid endometrioid [mean]	Aneuploid UPSC [mean]	Normal endometrium [standard deviation]	Diploid endometrioid [standard deviation]	Aneuploid endometrioid [standard deviation]	Aneuploid upsc [standard deviation]
210	KRT10	10.69491798	8.930775467	8.352501305	7.653597806	0.496096775	1.481574259	0.354602419	0.599118889
215	YWHAE	12.1244846	11.46739397	10.88608364	10.30571672	0.698046749	0.505712622	0.566527565	0.688661095
229	KRT9	9.769693119	6.412043732	4.677690145	5.331487051	0.62936122	1.551350676	2.4860141	0.678786907
615	KRT10	6.28447362	3.9022887	7.222503712	4.848876929	0.267529289	1.409127361	0.959018752	3.256737791
1114	ANXA5	6.660351553	7.694869977	9.264752276	9.203962513	0.817143896	1.079819899	0.619439715	0.632799957
1210	KRT9	6.932834606	7.604572282	9.891849667	9.603744554	0.678002526	1.162797704	0.59541341	1.52168342
1212	ATP5B	5.422529051	8.001186845	9.092746747	10.36141833	1.528001054	1.526797475	1.075901853	1.56393354
1222	HSPA1A	6.715617641	8.39306792	10.58480884	10.70432313	0.267635702	1.543058552	0.805803143	1.277020958
1313	ACTB	8.162118672	10.80999626	12.73376984	12.31458636	1.149931672	1.0791861	0.254589777	0.93583507
1320	ACTB	7.279755745	9.587546533	11.59591	10.8053617	0.347017072	1.36936475	0.165593028	1.762866333
1342	KRT7	5.705930221	9.578225045	8.916786723	9.729670405	1.289682416	0.99320808	0.466233841	0.842081344
1501	VIM	11.4424058	10.45489939	8.253812733	8.321507704	1.106627507	0.8552516	0.700715951	2.257871705
1607	P4HB	12.24424743	13.25131091	12.71717501	11.48008914	1.312321375	0.795526745	0.773658097	0.121736151
2003	ANXA5	8.565998305	8.57625878	11.0984855	12.35726777	0.988057616	2.144394632	0.755589533	0.913681748
2006	THEMIS	1.851060318	5.106601048	9.047669397	7.277666666	3.256857459	1.905927174	1.104853392	1.699562419
2007	ACTB	6.532626593	6.778887666	11.37296578	11.4258968	1.387418601	2.501598917	0.901454134	0.412202907
2111	HSP90AB1	6.304058339	8.123903941	10.63305859	10.70076023	2.186708747	0.743602007	0.066134338	0.43505199
2117	ARHGODIA	11.03561344	8.418801737	8.546820569	9.510270297	0.689863694	0.695276556	2.323355621	1.016741766
2120	ACTB	5.610163533	6.516219273	9.665187718	8.822246387	0.980519735	1.884848078	0.365764963	0.13854893
2302	ANXA5	13.41036345	12.97408715	11.00370659	11.0368081	0.214680425	0.641447169	1.166291707	0.603709291
2327	TXNL1	9.161100441	8.031325571	7.134664214	7.485405554	0.288498105	0.620522118	1.183175023	0.314930189
2509	HSPD1	7.67424627	9.858847064	10.8991931	11.7213198	0.839063469	1.46049328	0.826355851	0.836483228
2621	VIM	12.09706197	9.40252999	7.910754763	7.807234956	0.851139088	1.602076181	1.805836394	0.434939248
2623	ATP5B	12.52055935	12.71165998	13.91401126	12.74774898	0.653023983	0.585308188	0.344516483	0.755567002
2811	HSP90AB1	8.244513826	6.841394461	3.716791384	3.608917453	1.059070478	1.391152487	1.175704513	1.645908756
3009	RAB18	8.444744317	9.263324951	8.618864242	7.417257533	0.409491584	0.727552123	0.376697161	0.572171573
3020	KRT9	5.234139311	7.025241901	10.21450839	10.23953677	3.11213062	2.58706767	0.907771908	0.741144897
3220	KRT10	6.731319176	8.984364622	10.76290302	10.41355731	0.654441993	1.317574911	0.525478319	0.674361006
3221	CLIC1	11.60509539	9.452271737	10.08589437	9.805047477	0.662937765	0.816079755	1.001781772	1.049928333
3230	ACTB	10.34509991	9.471759241	11.88067819	11.89427511	0.497340908	1.423509673	0.403010082	0.190337934
3301	ATP5B	7.551873756	9.765061109	10.9089822	10.77712987	1.167456956	0.686873685	0.779796284	0.886399707
3314	ATP5B	6.943126221	5.987765725	8.490992995	7.42796489	0.977185243	0.723791686	0.610478571	1.993557294
3503	ACTB	11.269091301	12.72620161	12.16427416	12.45044682	0.639940308	0.318283604	0.926214654	0.593651225
3505	ATP5B	10.31089276	9.196759243	11.35409859	10.41167854	0.283474855	1.014872815	0.502007049	1.066071519
3602	VIM	11.81106205	8.479059745	7.287239905	9.288019244	0.773036462	0.981060517	0.56561406	0.660462166
3806	HSPA5	7.880644648	8.114226216	10.70272697	9.79475924	1.963108597	0.73691011	0.730864235	1.362706893
4005	RBPA	8.444795588	11.86412834	11.03158331	11.73206422	0.546736554	1.032843561	2.23547514	0.821502249
4006	ACTG1	7.305868529	8.502768027	11.2157152	11.39464495	1.107663124	0.835287208	0.676917351	0.434945765
4011	RAB18	7.022352833	9.598298552	9.63583781	9.799328895	0.289571838	0.527346304	1.003011225	1.138005855
4107	HSPB1	10.85909759	9.826428809	11.85168406	11.53967955	1.050294329	0.994445732	0.469199111	0.576450156
4207	ATP5B	10.74758184	11.70292621	11.78828936	11.86947925	0.280993172	0.33810114	1.017294342	0.28251772
4315	PDIA6	7.32061478	8.417131369	10.79171959	11.61301807	1.462874897	1.544338015	1.334678784	0.511935875
4419	ALB	8.233056859	7.69504237	10.45541231	10.19765688	1.158252751	1.122425567	0.270300003	0.801248954
4611	HSPD1	7.37525475	9.265381323	9.653972293	10.71425747	0.367270151	0.586979188	0.950181906	0.533678435
4621	DES	11.9760606	6.714837672	7.87900241	8.514678041	0.824331498	1.099020783	1.589549643	1.064858881
5009	HSPA5	5.74070882	7.902160969	11.01397678	10.87260203	2.026378159	2.245957595	0.674667233	0.892694441
5104	ACTB	9.660372795	11.13266062	13.49462679	13.54290014	0.35408547	1.175570783	0.573502952	0.310259962
5107	PRDX4	8.032453224	7.827400823	9.296505502	9.745442578	0.785558236	1.123862197	0.473163467	0.139780011
5217	DDAH2	11.01753609	7.920203358	8.56483195	7.760243682	0.446778496	1.148071743	1.767096197	0.339138673
5230	ANXA2	6.40213434	9.212778434	11.32290059	11.92627534	1.363616013	1.187099566	0.461131545	0.080705222
5304	CAPZA1	10.88618347	9.592566746	10.20716138	10.48651485	0.411744276	0.461175336	0.664105219	0.923829796
5322	RPLPO	12.04747568	10.86761443	9.500988321	9.997651671	0.554547688	0.677422033	0.636561187	1.128830877
5424	KRT10	9.433656855	13.2153308	12.88033418	11.65882141	0.978162521	0.384456424	0.752806995	0.803840676
5703	HNRNPK	10.04949355	4.330024758	8.103743384	9.428027307	1.406542114	2.520656206	1.497123609	0.248701653
5711	PLCB4	6.492656697	7.982812049	9.270616892	9.805913016	0.849688699	1.002503062	1.635688063	1.110461038
6113	HSPB1	7.775841818	10.12438069	11.16413436	10.40097019	1.311353676	0.446198205	0.891901134	0.634304597
6304	ANXA4	12.60606169	10.65757825	9.931631615	9.627734099	0.34123027	0.941861576	1.167219292	0.892844818
7123	GRB2	9.051477505	7.989420197	9.679025075	8.742993249	0.21090828	0.612105086	0.328108316	0.338890542
7451	MPST	9.07058622	5.164444036	5.81800863	6.996736454	0.398583798	1.359398627	2.32931764	0.881041687
7519	PDIA3	5.972321986	7.876068972	9.877160743	9.615991248	0.835462821	1.525812007	1.071829759	1.155949218
7537	CRKL	8.363557499	4.383253299	7.35109702	6.527724448	0.26830816	1.353383785	1.397681199	1.243151109
7815	LMNA	7.002936524	6.385021252	2.34721191	4.161427706	2.074134023	1.990774134	1.06878881	1.470203776
8101	PARK7	12.09809183	9.202281661	9.887018692	9.659607191	0.448337206	0.429607049	1.24943817	1.627404188
8308	ANXA4	5.528110632	7.558309025	9.332571101	9.496158212	1.941900243	1.126466428	1.437368858	2.969607041
8507	GDI2	10.64028503	8.773605565	10.02296634	9.314665449	0.446822695	0.723808327	1.166229135	0.879235697
8514	SEPT2	10.83494874	6.403196642	7.196757259	5.51510625	0.485801531	1.195793547	0.183252686	0.710461959
8609	CCT2	11.02677387	7.629357742	7.761979251	7.650095199	0.885398734	0.683553685	0.923713399	1.30267949
8620	PDIA3	9.661991183	6.170676585	9.368637878	7.649228103	0.946379152	1.836306665	0.211435401	1.157001302
9301	AKR7A2	10.0794443	7.035073421	7.992612189	10.22717138	0.41859352	1.911601517	2.196019451	0.591620085