

Supplementary Table S1. p-values for mutation patterns of established and novel SMGs among 65 hypermutated endometrial tumors

Gene	p-values (Fisher's Exact test §)																				Reference										
	PTEN	PIK3CA	PIK3R1	ARID1A	RPL22	KRAS	ZFHX3	ARID5B	CTCF	CSMD3	CTNNB1	GIGYF2	BCOR	CSDE1	FGRF2	CCND1	LIMCH1	RBMX	NKAP	ATR	FBXW7	PPP2R1A	HIST1H2BD	TP53	CHD4	SPOP	MECOM	METTL14	SGK1	TNFAIP6	SOX17
PTEN	---	0.5544	0.091419	0.3717	0.6283	0.4093	0.2225	0.4032	0.4032	0.5527	0.5063	0.5063	0.5921	0.3567	0.695	0.3274	0.6726	0.3274	0.2032	0.5607	0.4393	0.15513	0.49308	0.5069	0.5834	0.4166	0.33013	0.669872	0.7673	0.8769	[1, 32, 33]
PIK3CA	---	---	0.000005	0.4132	0.2315	0.0517	0.4414	0.5968	0.2819	0.3801	0.6233	0.612	0.0969	0.1663	0.4456	0.2701	0.4456	0.4122	0.4133	0.265	0.26499	0.229474	0.5742	0.2504	0.2504	0.55849	0.092949	0.7139	0.4615	[1, 32, 33]	
PIK3R1	---	---	0.519	0.3174	0.1845	0.0857	0.3863	0.6137	0.4804	0.4201	0.5799	0.276	0.6306	0.2523	0.5981	0.5981	0.2801	0.5444	0.4556	0.54436	0.069705	0.6714	0.1719	0.5276	0.6503	0.349702	0.6438	0.4	[1, 32, 33]		
ARID1A	---	---	0.1912	0.0536	0.4706	0.4966	0.5034	0.5876	0.3221	0.5694	0.6246	0.2005	0.2768	0.3278	0.1258	0.3278	0.4844	0.2722	0.6106	0.61057	0.615022	0.385	0.4725	0.1383	0.24405	0.694597	0.6058	0.6308	[1, 32, 33]		
RPL22	---	---	0.2926	0.5294	0.276	0.4966	0.1481	0.5694	0.4306	0.3754	0.5453	0.5615	0.1146	0.1258	0.3278	0.2212	0.3894	0.6106	0.12822	0.005146	0.615	0.5275	0.0157	0.6946	0.694597	0.3942	0.6308	[1, 32, 33]			
KRAS	---	---	0.5977	0.5535	0.1319	0.0564	0.2417	0.276	0.5978	0.2323	0.0139	0.4093	0.5907	0.5907	0.4788	0.0635	0.3568	0.64322	0.585338	0.5853	0.5553	0.1653	0.26282	0.262821	0.5861	0.6462	[1, 32, 33]				
ZFHX3	---	---	---	0.0354	0.4799	0.1163	0.3601	0.1566	0.5453	0.3654	0.5677	0.1949	0.2225	0.5291	0.3674	0.2628	0.3944	0.60556	0.164909	0.5087	0.0829	0.3608	0.67514	0.221841	0.476	0.3077	[1, 32, 33]				
ARID5B	---	---	0.2294	0.5903	0.344	0.6286	0.4922	0.5822	0.6584	0.5968	0.5968	0.2662	0.5141	0.4228	0.5772	0.19238	0.256512	0.6747	0.6598	0.6598	0.44872	0.448718	0.5889	0.7692	[1, 32, 33]						
CTCF	---	0.4097	0.6286	0.3714	0.4922	0.4178	0.025	0.2662	0.5968	0.4032	0.1946	0.1924	0.5772	0.19238	0.256512	0.6747	0.6598	0.6598	0.44872	0.448718	0.5889	0.7692	[1, 32, 33]								
CSMD3	---	---	0.103	0.4283	0.1787	0.367	0.2964	0.5527	0.4473	0.4473	0.4715	0.3838	0.6162	0.61619	0.707959	0.292	0.6309	0.6309	0.11458	0.523237	0.613	0.2154	[1, 32, 33]								
CTNNB1	---	---	0.2355	0.3821	0.1028	0.5789	0.4937	0.4937	0.5063	0.4277	0.0888	0.2465	0.34448	0.259265	0.259265	0.259265	0.259265	0.6001	0.3999	0.494048	0.494048	0.6375	0.2	[1, 32, 33]							
GIGYF2	---	---	0.6179	0.6445	0.5789	0.1491	0.4937	0.1917	0.1365	0.3445	0.6555	0.34448	0.259265	0.3146	0.6001	0.6001	0.49405	0.494048	0.3625	0.2	[1, 32, 33]										
BCOR	---	---	0.4605	0.4756	0.5921	0.1265	0.2061	0.0877	0.2662	0.00603	0.382876	0.3829	0.5329	0.5329	0.07177	0.432143	0.688	0.1692	[1, 32, 33]												
CSDE1	---	---	0.1345	0.6433	0.6433	0.6433	0.2921	0.2279	0.649	0.64903	0.165932	0.1659	0.1088	0.5037	0.39938	0.059409	0.7139	0.1538	[1, 32, 33]												
FGRF2	---	---	0.305	0.695	0.695	0.2471	0.6069	0.3931	0.19071	0.462454	0.5375	0.089	0.4575	0.36539	0.048077	0.7404	0.1385	[1, 32, 33]													
CCND1	---	---	0.3274	0.2536	0.2032	0.5607	0.4393	0.56067	0.110498	0.4931	0.4166	0.0048	0.66987	0.330128	0.7673	0.8769	[1, 32, 33]														
LIMCH1	---	---	0.6726	0.3798	0.5607	0.0212	0.56067	0.50692	0.5069	0.5834	0.5834	0.33013	0.330128	0.2327	0.8769	[1, 32, 33]															
RBMX	---	---	0.3798	0.5607	0.5607	0.43933	0.110498	0.1105	0.5834	0.4166	0.669872	0.0135	0.8769	[1, 32, 33]																	
NKAP	---	---	0.51	0.49	0.12166	0.554743	0.4453	0.3733	0.0543	0.29359	0.29359	0.7947	0.1077	[1, 32, 33]																	
ATR	---	---	0.4545	0.09084	0.393892	0.3939	0.3278	0.6722	0.00046	0.255746	0.8226	0.0923	[1, 32, 33]																		
FBXW7	---	---	0.5455	0.606108	0.6061	0.6722	0.6722	0.25557	0.744254	0.1774	0.9077	[1, 32, 33]																			
PPP2R1A	---	---	0.606108	0.6061	0.3278	0.0397	0.02072	0.020719	0.8226	0.0923	[1, 32, 33]																				
HIST1H2BD	---	---	0.3388	0.7202	0.2798	0.78343	0.783425	0.149	0.9231	[1, 32, 33]																					
TP53	---	---	0.7202	0.7202	0.78343	0.783425	0.149	0.9231	[1, 32, 33]																						
CHD4	---	---	0.7708	0.17605	0.176053	0.8798	0.0615	[1, 32, 33]																							
SPOP	---	---	0.82395	0.176053	0.8798	0.9385	[1, 32, 33]																								
MECOM	---	---	0.134158	0.9091	0.0462	[1, 32, 33]																									
METTL14	---	---	0.9091	0.0462	0.9692	[1, 32, 33]																									
SGK1	---	---	---	[1, 32, 33]																											
TNFAIP6	---	---	---	[1, 32, 33]																											
SOX17	---	---	---	[1, 32, 33]																											

(§) p-values <0.05, as derived via Fisher's Exact test are shown in bold text; p-values are not adjusted for FDR [32, 33]

Statistically significant (§) trend towards co-occurrence of mutations

Statistically significant (§) trend towards mutual exclusivity of mutations

No events recorded for one or both genes