

Model ID	Somatic mutation (amino acid change)					Somatic copy number alteration (log2 copy number ratio) [1]				
	VHL	PBRM1	PIK3CA	KDM5C	ARID1A	Chr. 3p	Chr. 5q	Chr. 14q	Chr. 7	Chr. 17
RESL3	L89H			R68Efs*5		-1.00	0.98	0.00	-2.01	0.00
RESL4			D350G		Q594*	-0.64	0.70	0.65	1.08	1.32
RESL5						-0.70	0.16	-0.95	2.18	-0.01
RESL10	H125Qfs*7		H1047R			-0.76	0.38	-0.72	1.64	0.63
RESL11						0.00	0.00	0.00	0.00	0.99
RESL12	V166D	Q779*				0.02	0.03	-0.98	1.62	-0.23

[1] include CNV because otherwise RESL5 has no mutation detected, and it would be weird