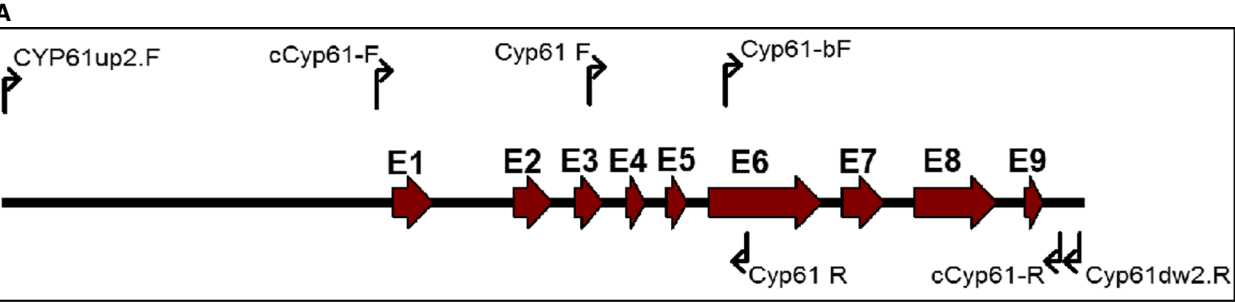




Exon (E) or Intron (I)	E-1										I-1										E-2					I-2					E-3		I-3					E-4		I-4...																					
Position (pb)	34 *	79 *	93	99	135	144	150	159	182	189	200	232	233	253	256	290	292	318	325	334	361	365	376/377	415	423	454	461	470	482	506	545	590	593	628	645	648	651	662	670	671	672	723	732	825	835	845	846	867	870	893	894/895	904	909/910	945	963	994	995	996			
UCD67-385	A	G	T	C	G	G	C	C	A	T	T	G	A	T	A	G	T	A	T	A	C	T	C	-	-	A	G	A	C	A	T	T	T	T	C	G	G	T	C	T	C	A	T	C	T	A	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A
CBS6938	A	G	T	C	G	G	C	C	A	T	T	G	G	T	A	G	T	A	T	A	C	T	C	-	-	A	G	A	C	A	T	T	T	T	C	G	G	T	C	T	C	A	T	C	T	A	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A
VKMY2786	A	G	T	C	G	G	C	C	A	T	T	G	G	T	A	G	T	A	T	A	C	T	C	-	-	A	G	A	C	A	T	T	T	T	C	G	G	T	C	T	C	A	T	C	T	A	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A
UCD67-210	A	G	T	C	G	G	C	C	A	T	T	G	A	T	A	G	T	A	T	A	C	T	C	-	-	A	G	A	C	A	T	T	T	T	C	G	G	T	C	T	C	A	T	C	T	A	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A
AVHN2	G	A	C	T	A	A	T	T	G	T	C	T	A	C	G	T	G	C	C	C	C	C	C	C	-	-	A	G	T	A	T	C	C	T	A	A	G	T	C	T	C	A	T	C	T	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A	
ANCH03	G	A	C	T	A	A	T	T	G	T	C	T	A	C	G	T	G	C	C	C	C	C	C	C	-	-	A	G	T	C	T	G	C	T	T	C	G	C	G	T	T	C	T	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A			
ANCH07	G	A	C	T	A	A	T	T	G	T	C	T	A	C	G	T	G	C	C	C	C	C	C	C	-	-	A	G	T	C	T	G	C	T	T	C	G	C	G	T	T	C	T	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A			
ANCH10	G	A	C	T	A	A	T	T	G	T	C	T	A	C	G	T	G	C	C	C	C	C	C	C	-	-	A	G	T	C	T	G	C	T	T	C	G	C	G	T	T	C	T	A	A	A	C	A	T	-	-	-	-	T	T	C	T	A			

Exon (E) or Intron (I)	...I-4			E-5			I-5						E-6			I-6		E-7		I-7			E-8					I-8					E-9																									
Position (pb)	1012	1031	1062	1094	1100	1103	1139	1145	1154	1150	1159	1178	1086	1192	1193	1204	1206	1216	1221	1224/1225	1226	1262	1295	1322	1361	1457	1573*	1683	1687	1702	1744	1800	1824	1923	1937	1943	1960	1968	1969	1970	1978	2076*	2138	2147	2207	2216	2231	2306	2368/2369	2381	2382	2443	2445	2454	2467	2468	2516	2537
UCD67-385	T	C	C	G	T	T	C	C	C	G	C	C	C	C	T	T	A	T	G	T	C	T	A	C	A	T	G	T	T	T	G	C	C	T	C	C	G	A	T	A	C	C	T	A	A	T	G	---	T	A	T	C	G	G	T	T	C	
CBS6938	T	C	C	G	T	T	C	C	C	G	C	C	A	T	T	A	T	G	T	T	C	T	A	C	A	T	G	T	T	T	T	G	C	C	T	C	C	G	A	T	A	C	C	T	A	A	T	G	---	T	A	T	C	G	G	T	T	C
VKMY2786	T	C	C	G	T	T	C	C	C	G	C	C	A	T	T	A	T	G	T	T	C	T	A	C	A	T	G	T	T	T	T	G	C	C	T	C	C	G	A	T	A	C	C	T	A	A	T	G	---	T	A	T	C	G	G	T	T	C
UCD67-210	C	C	C	G	T	T	C	C	C	G	C	C	A	T	T	A	T	G	T	T	C	T	A	C	A	T	G	T	T	T	T	G	C	C	T	C	C	G	A	T	A	C	C	T	A	A	T	G	---	T	A	T	C	G	G	T	T	C
AVHN2	C	C	T	A	C	A	T	T	G	T	-	-	C	C	T	A	G	C	A	C	T	T	C	G	T	A	A	A	C	A	C	C	T	C	T	-	-	C	T	T	C	G	G	C	A	CCT	G	G	C	T	A	A	C	C	T			
ANCH03	C	T	T	A	C	A	T	T	G	T	-	-	C	C	A	G	C	A	C	T	T	C	G	T	A	A	A	A	C	A	C	C	T	C	T	T	T	-	-	C	T	T	C	G	G	C	A	CCT	G	G	C	T	A	A	C	C	T	
ANCH07	C	T	T	A	C	A	T	T	G	T	-	-	C	C	A	G	C	A	C	T	T	C	G	T	A	A	A	A	C	A	C	C	T	T	T	T	-	-	C	T	T	C	G	G	C	A	CCT	G	G	C	T	A	A	C	C	T		
ANCH10	C	T	T	A	C	A	T	T	G	T	-	-	C	C	A	G	C	A	C	T	T	C	G	T	A	A	A	A	C	A	C	C	T	T	T	T	-	-	C	T	T	C	G	G	C	A	CCT	G	G	C	T	A	A	C	C	T		