Auflistung der 210 Genbereiche, des Custom Actionable Solid Tumor Panel CDHS-36709Z-1345 (Qiagen) mit insgesamt 19.472 Basen kodierende Sequenz

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
AKT1	chr14	NM_005163.2	AKT1 Exon 3	105.246.541	105.246.562	16 - 20	22	9	COSM33765: c.49G>A (E17K)
							22	**13**	Basen kodierende Sequenz gesamt
ALK	chr2	NM_004304.4	ALK Exon 5	29.606.669	29.606.689	398 - 404	21		COSM20713: c.1201C>T (R401*)
			ALK Exon 8	29.541.181	29.541.201	539 - 545	21		COSM48230: c.1625C>G (P542R)
			ALK Exon 15	29.455.257	29.455.277	842 - 848	21		COSM148825: c.2535T>C (G845G)
			ALK Exon 18	29.449.809	29.449.829	1009 - 1015	21		COSM148824: c.3036G>A (T1012T)
			ALK Exon 19	29.448.400	29.448.420	1027 - 1033	21		COSM4133807: c.3089A>C (H1030P)
			ALK Exon 20	29.446.286	29.446.306	1088 - 1094	21		COSM28502: c.3271G>A (D1091N)
			ALK Exon 22	29.445.246	29.445.283	1151 - 1160	38	9	COSM98478: c.3452C>T (T1151M)
			ALK Exon 22	29.445.182	29.445.223	1168 - 1172	42	28	COSM28498: c.3512T>A (I1171N)
			ALK Exon 23	29.443.684	29.443.707	1172 - 1178	24	6	COSM28055: c.3522C>A (F1174L)
			ALK Exon 23	29.443.597	29.443.641	1193 - 1207	45		COSM99137: c.3586C>A (L1196M)
			ALK Exon 24	29.436.848	29.436.870	1242 - 1248	23	2	COSM28499: c.3733T>G(F1245V)
			ALK Exon 25	29.432.645	29.432.693	1266 - 1279	49	7	COSM28056: c.3824G>A (R1275Q)
			ALK Exon 29	29.416.605	29.416.625	1443 - 1449	21		COSM5019786: c.4338C>T (T1446T)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			ALK Exon 29	29.416.471	29.416.491	1488 - 1494	21		COSM1130802: c.4472A>G (K1491R)
							389	**337**	Basen kodierende Sequenz gesamt
BRAF	chr7	NM_004333.4	BRAF Exon 7	140.500.155	140.500.175	323 - 327	21		COSM33964: c.977T>C (I326T)
			BRAF Exon 11*	140.481.376	140.481.503	439 - 477	128	10	COSM460: c.1406G>C (G469A)
			BRAF Exon 12*	140.477.781	140.477.885	478 - 506	105	20	COSM243226: c.1514T>A (L505H)
			BRAF Exon 15*	140.453.065	140.453.203	581 - 620	139	20	COSM476: c.1799T>A (V600E)
			BRAF Exon 16	140.449.140	140.449.180	634 - 646	41		COSM4161857: c.1929A>G (G643G)
							434	**384**	Basen kodierende Sequenz gesamt
CALR	chr19	NM_004343.3	CALR Exon 9*	13.054.527	13.054.727	352 - 418	201		COSM1738055: c.1099_1150del (L367Tfs*46)
							201	**201**	Basen kodierende Sequenz gesamt
CTNNB1	chr3	NM_001098209.1	CTNNB1 Exon 3*	41.266.007	41.266.254	5 - 81	248	20	COSM5664: c.121A>G (T41A); COSM5667: c.134C>T (S45F)
							248	**228**	Basen kodierende Sequenz gesamt
EGFR	chr7	NM_005228.3	EGFR Exon 2	55.210.065	55.210.087	59 - 66	23		COSM35602: c.185T>G (L62R)
			EGFR Exon 3	55.211.070	55.211.107	105 - 117	38		COSM21683: c.323G>A (R108K)
			EGFR Exon 4	55.214.338	55.214.358	155 - 161	21		COSM42978: c.474C>T (N158N)
			EGFR Exon 6	55.220.264	55.220.284	219 - 225	21		COSM35508: c.664C>T (R222C)

Gen	Lage (hg19)	Transkript	**Amplifikat (Covered target region)**						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			EGFR Exon 7	55.221.700	55.221.720	250 - 255	21	4	COSM35752: c.754C>T (R252C)
			EGFR Exon 7	55.221.733	55.221.753	260 - 266	21		COSM21684: c.787A>C (T263P)
			EGFR Exon 7	55.221.811	55.221.832	286 - 292	22		COSM21687: c.866C>T (A289V)
			EGFR Exon 8	55.223.533	55.223.553	301 - 307	21		COSM2149971: c.910C>T (H304Y)
			EGFR Exon 12	55.227.997	55.228.019	489 - 495	23		COSM236670: c.1476C>A (S492R)
			EGFR Exon 13	55.229.245	55.229.265	518 - 524	21		COSM3721608: c.1562G>A (R521K)
			EGFR Exon 14*	55.231.426	55.231.516	544 - 574	91		ClinVar376211: c.1636C>T (p.Pro546Ser)
			EGFR Exon 15	55.233.027	55.233.053	593 - 601	27		COSM21690: c.1793G>T (G598V)
			EGFR Exon 15	55.233.099	55.233.119	617 - 623	21		COSM35825: c.1859G>A (C620Y)
		NM_201284	*EGFR Exon 16*	55.238.077	55.238.097	653 - 659	21		COSM54529: c.1957A>T (S653C)
		NM_201284	*EGFR Exon 16*	55.238.102	55.238.122	662 - 668	21		COSM3942265: c.1993G>T (E665*)
			EGFR Exon 17	55.240.697	55.240.717	648 - 654	21		COSM35840: c.1951G>A (V651M)
			EGFR Exon 17	55.240.776	55.240.816	674 - 687	41		COSM22555: c.2030G>A (R677H)
			EGFR Exon 18*	55.241.617	55.241.637	689 - 695	21		COSM13178: c.2081C>T (P694L)
			EGFR Exon 18*	55.241.646	55.241.736	699 - 728	91		COSM6239: c.2156G>C (G719A)
			Intron 18-19	55.241.745	55.241.765		21	21	
			EGFR Exon 19*	55.242.405	55.242.523	729 - 761	119	20	COSM6223: c.2235_2249del15 (E746_A750del)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			EGFR Exon 20*	55.248.976	55.249.181	762 - 823	206	20	COSM6240: c.2369C>T (T790M)
			EGFR Exon 21*	55.259.402	55.259.577	824 - 875	176	20	COSM6224: c.2573T>G (L858R)
			EGFR Exon 22	55.260.473	55.260.493	881 - 887	21		COSM28575: c.2650G>A (E884K)
			EGFR Exon 23	55.266.459	55.266.481	918 - 924	23		COSM28515: c.2763C>A (S921R)
			EGFR Exon 25	55.268.906	55.268.926	991 - 997	21		COSM3762773: c.2982C>T (D994D)
							1205	**1120**	Basen kodierende Sequenz gesamt
ERBB2	chr17	NM_004448.2	*Intron*	37.855.803	37.855.850		48	48	
			ERBB2 Exon 8*	37.868.171	37.868.310	301 - 341	140	20	COSM48358: c.929C>T (S310F)
			ERBB2 Exon 17*	37.879.562	37.879.720	649 - 695	159	20	COSM436498: c.2033G>A (R678Q); COSM4000121: c.1963A>G (I655V)
			ERBB2 Exon 19*	37.880.155	37.880.273	737 - 769	119	20	COSM14060: c.2264T>C (L755S); COSM1251412: c.2305G>T (D769Y)
			ERBB2 Exon 20*	37.880.969	37.881.174	770 - 831	206	20	COSM14062: c.2329G>T (V777L); COSM20959: c.2324_2325ins12
			ERBB2 Exon 21*	37.881.292	37.881.467	832 - 883	176	20	COSM14065: c.2524G>A (V842I)
			ERBB2 Exon 22*	37.881.570	37.881.665	884 - 909	96	20	COSM978678: c.2690G>A (R897Q)
			ERBB2 Exon 23*	37.881.950	37.882.116	909 - 958	167	20	COSM6005645: c.2790G>T (E930D)
							1111	**923**	Basen kodierende Sequenz gesamt
ESR1	chr6	NM_000125.3	ESR1 Exon 1	152.129.067	152.129.087	7 - 13	21		COSM3761554: c.30T>C (S10S)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			ESR1 Exon 4	152.265.445	152.265.465	300 - 306	21		COSM4745827: c.908A>G (K303R)
			Intron	152.396.026	152.396.046		21	21	
			ESR1 Exon 8	152.419.912	152.419.936	534 - 541	25		COSM94250: c.1613A>G (D538G); COSM1074639: c.1610A>C (Y537S)
			ESR1 Exon 8	152.420.085	152.420.105	591 - 596*	21	4	COSM3761556: c.1782G>A (T594T)
							109	**84**	Basen kodierende Sequenz gesamt
FGFR1	chr8	NM_023110.2	FGFR1 Exon 11*	38.275.509	38.275.388	477 - 518	122		41 Mutationen in COSMIC, aber keine Hotspots
			FGFR1 Exon 12*	38.274.934	38.274.824	518 - 555	101		26 Mutationen in COSMIC, aber keine Hotspots
			FGFR1 Exon 13*	38.273.578	38.273.388	555 - 618	191		COSM19176: c.1731C>A (N577K)
			FGFR1 Exon 14*	38.272.419	38.272.297	619 - 659	123		34 Mutationen in COSMIC, aber keine Hotspots
			FGFR1 Exon 15*	38.272.147	38.272.077	660 - 683	71		22 Mutationen in COSMIC, aber keine Hotspots
			FGFR1 Exon 16*	38.271.807	38.271.670	683 - 729	138		COSM35673: c.2059A>G (K687E)
							746	**746**	Basen kodierende Sequenz gesamt
FGFR2	chr10	NM_022970.3	FGFR2 Exon 7*	123.279.683	123.279.493	250 - 313	191		COSM36903: c.755C>G (S252W)
			FGFR2 Exon 8*	123.278.343	123.278.196	314 - 363	148		29 Mutationen in COSMIC, aber keine Hotspots
			FGFR2 Exon 9*	123.274.833	123.274.631	363 - 430	203		COSM36904: c.1127A>G (Y376C) COSM36906: c.1147T>C (C383R)
			FGFR2 Exon 12*	123.258.119	123.258.009	522 -559	111		COSM36912: c.1650T>A (N550K)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			FGFR2 Exon 13*	123.256.236	123.256.046	559 - 622	191		53 Mutationen in COSMIC, aber keine Hotspots
			FGFR2 Exon 14*	123.247.627	123.247.505	623 - 663	123		COSM36909: c.1978A>G (K660E) COSM683053: c.1980G>C (K660N)
			FGFR2 Exon 15*	123.246.938	123.246.868	664 - 687	71		21 Mutationen in COSMIC, aber keine Hotspots
			FGFR2 Exon 16*	123.245.046	123.244.909	687 - 733	138		COSM6854598: c.2183A>G (N728S)
			FGFR2 Exon 17*	123.243.317	123.243.212	733 - 768	106		28 Mutationen in COSMIC, aber keine Hotspots
							1282	**1282**	Basen kodierende Sequenz gesamt
FGFR3	chr8	NM_023110.2	FGFR3 Exon 7*	1803562	1803752	247 - 310	191		
			FGFR3 Intron 8*	1805447	1805546		100	100	
			FGFR3 Exon 9*	1806057	1806247	361 - 424	191		
			FGFR3 Exon 14*	1807778	1807900	615 - 655	123		
			FGFR3 Exon 15*	1807984	1808054	656 - 678	71		
			FGFR3 Exon 16*	1808273	1808410	679 - 725	138		
							814	**714**	Basen kodierende Sequenz gesamt
FOXL2	chr3	NM_023067.3	FOXL2 Exon 1	138.665.153	138.665.174	131 - 137	22		COSM33661: c.402C>G (C134W)
							22	**22**	Basen kodierende Sequenz gesamt

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
GNA11	chr19	NM_002067.2	GNA11 Exon 5	3.118.932	3.118.953	206 - 212	22		COSM52969: c.626A>T (Q209L)
							22	**22**	Basen kodierende Sequenz gesamt
GNAQ	chr9	NM_002072.4	GNAQ Exon 5	80.409.478	80.409.500	205 - 212	23		COSM28757: c.626A>T (Q209L); COSM28758: c.626A>C (Q209P)
							23	**23**	Basen kodierende Sequenz gesamt
GNAS	chr20	NM_080425.3	GNAS Exon 8*	57.484.405	57.484.478	839 - 863	74		COSM27895: c.2531G>A (R844H) COSM27887: c.2530C>T (R844C)
			GNAS Exon 9*	57.484.576	57.484.634	863 - 883	59		COSM27888: c.2609A>T (Q870L) + weitere Q870
							133	**133**	Basen kodierende Sequenz gesamt
H3F3A	chr1	NM_002107.4	H3F3A Exon 2*	226.252.053	226.252.180	1 - 43	128		COSM327928: c.83A>T (K28M) + weitere K28 COSM1732355: c.103G>T (G35W) + weitere G35
							128	**128**	Basen kodierende Sequenz gesamt
HFE	chr6	NM_000410.3	HFE Exon 4*	26.092.903	26.093.198	206 - 298	296		50 Mutationen in COSMIC, aber keine Hotspots
							296	**296**	Basen kodierende Sequenz gesamt
HRAS	chr11	NM_005343.4	HRAS Exon 2*	534.322	534.212	1 - 37	111		COSM483: c.35G>T (G12V) + weitere G12 COSM486: c.37G>C (G13R) + weitere G13
			HRAS Exon 3*	533.944	533.766	38 - 97	179		COSM499: c.182A>G (Q61R)
			HRAS Exon 4*	533.612	533.453	97 - 150	160		COSM254733: c.351G>C (K117N) + weitere K117 COSM99642: c.355G>A (D119N) +weitere D119
							450	**450**	Basen kodierende Sequenz gesamt
IDH1	chr2	NM_005896.3	IDH1 Exon 4	209.113.103	209.113.124	128 - 135	22		COSM28746: c.395G>A (R132H); COSM28747: c.394C>T (R132C)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
							22	**22**	Basen kodierende Sequenz gesamt
IDH2	chr15	NM_002168.2	IDH2 Exon 4	90.631.828	90.631.849	169 - 175	22		COSM33733: c.515G>A (R172K)
			IDH2 Exon 4	90.631.924	90.631.945	137 - 143	22		COSM41590: c.419G>A (R140Q)
							44	**44**	Basen kodierende Sequenz gesamt
JAK2	chr9	NM_004972.3	JAK2 Exon 12*	5069925	5070052	505 - 547	128		COSM24439: c.1615_1616inv (K539L) + weitere K539
			JAK2 Exon 13*	5072492	5072626	548 - 592	135		83 Mutationen in COSMIC, aber keine Hotspots
			JAK2 Exon 14*	5073698	5073785	593 - 622	88		COSM12600: c.1849G>T (V617F)
			JAK2 Exon 16*	5078306	5078444	665 - 711	139		COSM29300: c.2047A>G (R683G)
			JAK2 Exon 20*	5089674	5089863	858 - 921	190		183 Mutationen in COSMIC, aber keine Hotspots
							680	**680**	Basen kodierende Sequenz gesamt
KIT	chr4	NM_000222.2	KIT Exon 2	55.561.748	55.561.775	47 - 55	28		COSM1146: c.154G>A (D52N)
			KIT Exon 8	55.589.758	55.589.788	414 - 423	31		COSM29014: c.1255_1257delGAC (D419del)
			KIT Exon 9*	55.592.013	55.592.226	449 - 514	214	20	COSM1326: c.1509_1510insGCCTAT (Y503_F504insAY)
			KIT Exon 10	55.593.454	55.593.491	538 - 549	38	1	COSM28026: c.1621A>C (M541L)
			KIT Exon 11*	55.593.572	55.593.718	550 - 592	147	20	COSM1217: c.1669_1674del6 (W557_K558del)
			KIT Exon 13*	55.594.167	55.594.297	627 - 664	131	20	COSM1304: c.1924A>G (K642E), COSM12706: c.1961T>C (V654A)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			KIT Exon 14*	55.595.491	55.595.661	664 - 714	171	20	COSM12708: c.2009C>T (T670I)
			KIT Exon 15	55.597.485	55.597.507	714 - 718	23	9	COSM1306: c.2143_2145delAGC (S715del)
			Intron	55.599.149	55.599.169		21	21	
			KIT Exon 17*	55.599.226	55.599.368	788 - 828	143	20	COSM1314: c.2447A>T (D816V)
			Intron	55.599.391	55.599.411		21	21	
			KIT Exon 18*	55.602.654	55.602.674	829 - 832	21	10	COSM13172: c.2485G>C (A829P)
			KIT Exon 18*	55.602.684	55.602.704	836 - 842	21		COSM1324: c.2515G>A (E839K)
			KIT Exon 18*	55.602.753	55.602.775	859 - 865	23		COSM1325: c.2586G>C (L862L)
			KIT Exon 20	55.603.362	55.603.382	907 - 913	21		COSM5609257: c.2732C>T (P911L)
			KIT Exon 21	55.604.649	55.604.669	953 - 959	21		COSM71350: c.2867G>A (R956Q)
							1075	**913**	Basen kodierende Sequenz gesamt
KRAS	chr12	NM_004985.3	KRAS 3'UTR	25.360.214	25.360.234		21	21	
			KRAS Exon 5	25.362.795	25.362.815	161 - 167	21		COSM41307: c.491G>A (p.R164Q)
			KRAS Exon 4*	25.378.538	25.378.717	97 - 150	180	20	COSM19404: c.436G>A (A146T)
			KRAS Exon 3*	25.380.158	25.380.356	38 - 97	199	20	COSM554: c.183A>C (Q61H)
			KRAS Exon 2*	25.398.198	25.398.339	1 - 37	142	20	COSM521: c.35G>A (G12D)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
							563	**482**	Basen kodierende Sequenz gesamt
MET	chr7	NM_001127500.2	MET Exon 16*	116.417.443	116.417.523	1105 - 1132	81		47 Mutationen in COSMIC, aber keine Hotspots
			MET Exon 17	116.418.875	116.418.884	1147 - 1152	10		18 Mutationen in COSMIC, aber keine Hotspots
			MET Exon 17	116.419.101	116.419.016	1190 - 1192	16		5 Mutationen in COSMIC, aber keine Hotspots
			MET Exon 18*	116.422.042	116.422.151	1193 - 1229	110		34 Mutationen in COSMIC, aber keine Hotspots
			MET Exon 19	116.423.397	116.423.418	1243 - 1249	22		COSM699: c.3743A>G (Y1248C)
			MET Exon 19	116.423.464	116.423.485	1265 - 1271	22		COSM700: c.3757T>G (Y1253D) COSM691: c.3803T>C (M1268T)
							261	**261**	Basen kodierende Sequenz gesamt
MPL	chr1	NM_5373.2	MPL Exon 10*	43.814.934	43.815.030	490 - 522	97		COSM18918: c.1544G>T (W515L)
							97	**97**	Basen kodierende Sequenz gesamt
MYD88	chr3	NM_002468.4	MYD88 Exon 5*	38.182.623	38.182.777	259 - 310	155		COSM85940: c.818T>C (L273P)
							155	**155**	Basen kodierende Sequenz gesamt
NPM1	chr5	NM_002520.6	NPM1 Exon 11*	170.837.531	170.837.569	283 - 295	39		3.608 Mutationen in COSMIC, davon 3.442 frameshift insertions an Position c.859
							39	**39**	Basen kodierende Sequenz gesamt
NTRK1	chr1	NM_002529.3	NTRK1 Exon 15*	156.845.872	156.846.002	501 - 544	131		55 Mutationen in COSMIC, aber keine Hotspots
			NTRK1 Exon 16*	156.846.192	156.846.364	545 - 602	173		86 Mutationen in COSMIC, aber keine Hotspots

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			NTRK1 Exon 17*	156.848.914	156.849.154	602 - 682	241		109 Mutationen in COSMIC, aber keine Hotspots
							545	**545**	Basen kodierende Sequenz gesamt
NTRK2	chr9	NM_006180.4	NTRK2 Exon 19*	87.570.198	87.570.432	646 - 724	235		99 Mutationen in COSMIC, aber keine Hotspots
			NTRK2 Exon 20*	87.635.111	87.635.279	725 - 777	169		58 Mutationen in COSMIC, aber keine Hotspots
							404	**404**	Basen kodierende Sequenz gesamt
NTRK3	chr15	NM_002530.3	NTRK3 Exon 15*	88.483.984	88.483.854	529 - 572	131		76 Mutationen in COSMIC, aber keine Hotspots
			NTRK3 Exon 16*	88.476.415	88.476.243	573 - 630	173		127 Mutationen in COSMIC, aber keine Hotspots
			NTRK3 Exon 17*	88.472.675	88.472.412	630 - 711	264		134 Mutationen in COSMIC, aber keine Hotspots
							568	**568**	Basen kodierende Sequenz gesamt
NRAS	chr1	NM_002524.4	NRAS Exon 4*	115.252.180	115.252.359	97 - 150	180	20	COSM4170228: c.437C>T (A146V)
			NRAS Exon 3*	115.256.411	115.256.609	38 - 97	199	20	COSM584: c.182A>G (Q61R)
			NRAS Exon 2*	115.258.661	115.258.808	1 - 37	148	20	COSM564: c.35G>A (G12D)
							527	**467**	Basen kodierende Sequenz gesamt
PDGFRa	chr4	NM_006206.4	PDGFRA Exon 3	55.127.438	55.127.458	76 - 82	21		COSM5019287:c.236G>A (G79D)
			PDGFRA Exon 4	55.130.068	55.130.088	201 - 207	21		COSM4416371:c.612T>C (N204N)
			PDGFRA Exon 5	55.131.108	55.131.128	218 - 224	21		COSM6438148: c.661C>T (L221F)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			PDGFRA Exon 5	55.131.132	55.131.171	226 - 238	40		COSM42897: c.704G>A (C235Y)
			PDGFRA Exon 7	55.133.716	55.133.736	311 - 316	21	3	COSM1666925: c.939T>G (G313G)
			PDGFRA Exon 10	55.139.761	55.139.781	475 - 481	21		COSM5008347: c.1432T>C (S478P)
			PDGFRA Exon 12*	55.140.998	55.141.150	552 - 596	153	20	COSM12418: c.1698_1712del15; COSM739: c.1682T>A (V561D)
			PDGFRA Exon 13	55.143.567	55.143.587	600 - 606	21		COSM4417622: c.1809G>A (A603A)
			PDGFRA Exon 14*	55.144.053	55.144.183	631 - 668	131	20	COSM22414: c.1977C>G (N659K)
			PDGFRA Exon 15	55.144.537	55.144.557	671 - 677	21		COSM743: c.2021C>T (T674I)
			PDGFRA Exon 18*	55.151.998	55.152.140	814 - 854	143	20	COSM736: c.2525A>T (D842V); COSM22413: c.2472C>T (V824V)
			Intron	55.153.537	55.153.558		22	22	
			PDGFRA Exon 23	55.161.370	55.161.390	1068 - 1074	21		COSM12893: c.3211G>A (D1071N)
							657	**572**	Basen kodierende Sequenz gesamt
PIK3CA	chr3	NM_006218.2	**PIK3CA Exon 2***	178.916.604	178.916.975	1 - 118	372	20	COSM746: c.263G>A (R88Q)
			PIK3CA Exon 3*	178.917.468	178.917.697	118 - 188	230	20	COSM751: c.353G>A (G118D)
			PIK3CA Exon 4*	178.919.068	178.919.338	188 - 271	271	20	COSM86047: c.665C>T (A222V)
			PIK3CA Exon 5*	178.921.322	178.921.587	272 - 353	266	20	COSM754: c.1035T>A (N345K)
			PIK3CA Exon 6*	178.922.281	178.922.386	354 - 382	106	20	COSM86044: c.1093G>A (E365K)

Gen	Lage (hg19)	Transkript	**Amplifikat (Covered target region)**						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
			PIK3CA Exon 7*	178.927.373	178.927.498	382 - 417	126	20	COSM328028: c.1173A>G (I391M)
			PIK3CA Exon 8*	178.927.964	178.928.136	418 - 468	173	20	COSM757: c.1258T>C (C420R)
			PIK3CA Exon 9*	178.928.209	178.928.363	469 - 513	155	20	COSM136387: c.1412C>T (P471L)
			PIK3CA Exon 10*	178.935.988	178.936.132	514 - 555	145	20	COSM763: c.1633G>A (E545K); COSM760: c.1624G>A (E542K)
			PIK3CA Exon 11*	178.936.974	178.937.075	555 - 582	102	20	COSM30790: c.1700A>G (K567R)
			PIK3CA Exon 12*	178.937.349	178.937.533	583 - 637	185	20	COSM1041500: c.1810T>C (C604R)
			PIK3CA Exon 13*	178.937.727	178.937.850	638 - 672	124	20	COSM250052: c.1913T>C (V638A)
			PIK3CA Exon 14*	178.938.764	178.938.955	672 - 729	192	20	COSM87306: c.2176G>A (E726K)
			PIK3CA Exon 15*	178.941.859	178.941.985	730 - 765	127	20	COSM6148: c.2198A>G (K733R)
			PIK3CA Exon 16*	178.942.478	178.942.619	765 - 806	142	20	COSM4598858: c.2352G>C (E784D)
			PIK3CA Exon 17*	178.943.740	178.943.838	806 - 832	99	20	COSM1041508: c.2452C>T (R818C)
			PIK3CA Exon 18*	178.947.050	178.947.240	832 - 889	191	20	COSM4481256: c.2494C>T (R832*)
			PIK3CA Exon 19*	178.947.782	178.947.919	889 - 928	138	20	COSM769: c.2702G>T (C901F)
			PIK3CA Exon 20*	178.948.003	178.948.174	929 - 979	172	20	COSM94980: c. 2908G>A (E970K)
			PIK3CA Exon 21*	178.951.872	178.952.162	979 - 1069*	291	20	COSM775: c.3140A>G (H1047R)
							3607	**3207**	Basen kodierende Sequenz gesamt

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
POLE	chr12	NM_006231.2	POLE Exon 9*	133.253.239	133.253.132	268 - 303	108		COSM937332: c.857C>G (P286R) + weitere P286
			POLE Exon 11*	133.252.406	133.252.321	341 - 369	86		71 Mutationen in COSMIC, aber keine Hotspots
			POLE Exon 13*	133.250.293	133.250.161	409 - 453	133		COSM204094: c.1231G>T (V411L) + weitere V411
			POLE Exon 14*	133.249.863	133.249.750	454 - 491	114		COSM937318: c.1366G>C (A456P)
							441	**441**	Basen kodierende Sequenz gesamt
RAF1	chr3	NM_002880.3	RAF1 Exon 17	12.626.113	12.626.133	610 - 616	21		COSM97875: c.1837C>G (L613V)
			RAF1 Exon 7	12.645.689	12.645.709	254 - 260	21		COSM181063: c.770C>T (S257L)
							42	**42**	Basen kodierende Sequenz gesamt
RET	chr10	NM_020975.5	RET Exon 10	43.609.061	43.609.082	606 - 613	22		COSM95656: c.1827C>A (C609*)
			RET Exon 10	43.609.086	43.609.114	615 - 623	29		COSM29804: c.1858T>C (C620R)
			RET Exon 11	43.609.926	43.609.961	627 - 638	36	2	COSM966: c.1900T>C (C634R)
			RET Exon 13	43.613.830	43.613.851	765 - 772	22		COSM4418405: c.2307G>T (L796L)
			RET Exon 13	43.613.895	43.613.919	787 - 794	25		COSM1159820: c.2372A>T (Y791F)
			RET Exon 15	43.615.558	43.615.579	880 - 886	22		COSM1570338: c. 2651A>T (E884V)
			RET Exon 15	43.615.583	43.615.604	888 - 894	22		COSM918124: c.2672C>T (S891L)
			RET Exon 16	43.617.406	43.617.427	915 - 921	22		COSM965: c.2753T>C (M918T)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
							200	**198**	Basen kodierende Sequenz gesamt
SRSF2	chr17	NM_003016.4	SRSF2 Exon 1*	74.733.242	74.732.881	1 - 121	640		COSM211504: c.284C>A (P95H) + weitere P95
							640	**640**	Basen kodierende Sequenz gesamt
STK11	chr19	NM_000455.4	STK11 Exon 1*	1.206.913	1.207.202	1 - 97	289		COSM12925: c.109C>T (Q37*) + weitere Q37
			STK11 Exon 2*	1.218.416	1.218.499	97 - 125	84		50 Mutationen in COSMIC, aber keine Hotspots
			STK11 Exon 3*	1.219.323	1.219.412	125 - 155	90		60 Mutationen in COSMIC, aber keine Hotspots
			STK11 Exon 4*	1.220.372	1.220.504	155 - 199	133		COSM20944: c.580G>T (D194Y) + weitere D194
			STK11 Exon 5*	1.220.580	1.220.716	200 - 245	137		175 Mutationen in COSMIC, aber keine Hotspots
			STK11 Exon 6*	1.221.212	1.221.339	245 - 288	128		163 Mutationen in COSMIC, aber keine Hotspots
			STK11 Exon 7*	1.221.948	1.222.005	288 - 307	58		46 Mutationen in COSMIC, aber keine Hotspots
			STK11 Exon 8*	1.222.984	1.223.171	307 - 370	188		COSM21360: c.1062C>G (F354L) + weitere F354
							1107	**1107**	Basen kodierende Sequenz gesamt
TERT	chr5	NM_198253.2	TERT Promoter + Exon 1*	1.295.364	1.294.886	c.-255 - c.219	523	304	Chr5:1295228: c.-124C>T (C228T) Chr5:1295250: c.-146C>T (C250T)
							523	**219**	Basen kodierende Sequenz gesamt
TP53	chr17	NM_000546.5	TP53 Exon 11*	7.572.917	7.573.018	367 - 394*	102	20	COSM13747: c.1146delA (K382fs)
			TP53 Exon 10*	7.573.917	7.574.043	332 - 367	127	20	COSM11073: c.1024C>T (R342*)

Gen	Lage (hg19)	Transkript	Amplifikat (Covered target region)						Wichtige Mutationen (nach COSMIC)
			Name	Start	Stopp	Aminosäuren	Größe target region	Größe nicht-kodierende Sequenz	
		NM_001276699	TP53 Exon 6*	7.576.527	7.576.594	173 - 188*	68	20	
		NM_001126116	TP53 Exon 6*	7.576.615	7.576.667	200 - 210*	53	20	
			TP53 Exon 9*	7.576.843	7.576.936	307 - 331	94	20	COSM10786: c.949C>T (Q317*)
			TP53 Exon 8*	7.577.009	7.577.165	261 - 307	157	20	COSM10660: c.818G>A (R273H)
			TP53 Exon 7*	7.577.489	7.577.618	225 - 261	130	20	COSM10662: c.743G>A (R248Q); COSM10656: c.742C>T (R248W)
			TP53 Exon 6*	7.578.167	7.578.299	187 - 224	133	20	COSM10654: c.637C>T (R213*); COSM10758: c.659A>G (Y220C)
			TP53 Exon 5*	7.578.361	7.578.564	126 - 187	204	20	COSM10648: c.524G>A (R175H); COSM10670: c.469G>T (V157F)
			TP53 Exon 4*	7.579.302	7.579.600	33 - 125	299	20	COSM250061: c.215C>G (P72R); COSM44492: c.273G>A (W91*)
			TP53 Exon 3*	7.579.690	7.579.731	25 - 32	42	20	COSM85573: c.80delC (P27fs)
			TP53 Exon 2*	7.579.829	7.579.922	1 - 25	94	20	COSM11606: c.31G>C (E11Q)
							1503	**1263**	Basen kodierende Sequenz gesamt

Erklärung: vollständig untersuchte Exone sind mit * markiert, fett hervorgehoben wichtige Hotspotmutationen