

Supplementary Materials: Development Implementation and Assessment of Molecular Diagnostics by Next Generation Sequencing in Personalized Treatment of Cancer: Experience of a Public Reference Healthcare Hospital.

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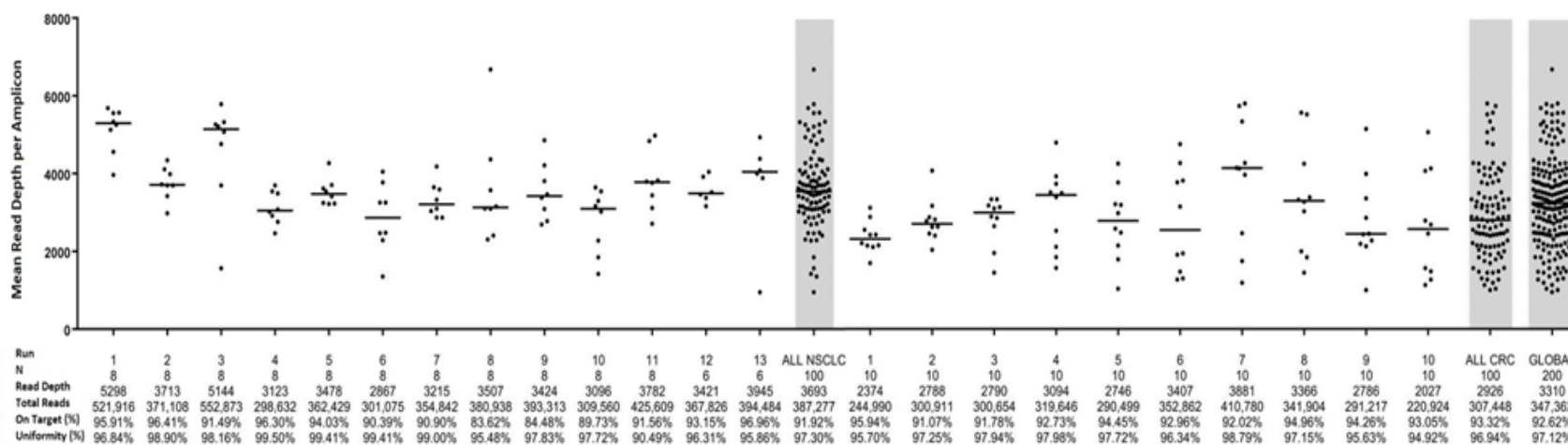


Figure S1. NGS quality metrics. N- Number of samples analyzed per run; Read Depth- Represents the mean value of reads of each amplicon; Total Reads-Represent mean total reads per samples; "On target"-Represents the mean % of reads over the sequences of interest; Uniformity-Represents the mean % of uniformity coverage.

Table S1. Pathogenic variants detected in NSCLC patients.

Patient	Chr Position	Gene	NG/NM	Fusion	Mutation Type	Exon	Amino Acid Change	CDS	Total Coverage	Variant Coverage	VAF
NSCLC1	chr3:178952090	<i>PIK3CA</i>	NM_006218.2		missense	21	p.Gly1049Arg	c.3145G>C	3995	773	19 %
	chr7:55259515	<i>EGFR</i>	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	3959	800	20 %
NSCLC2	chr7:55242462	<i>EGFR</i>	NM_005228.3		nonframeshift deletion	19	p.Glu746_Thr751delinsVA	c.2237_2253delinsTGCT	3996	2318	58 %
NSCLC3	chr7:55242464	<i>EGFR</i>	NM_005228.3		nonframeshift deletion	19	p.Glu746_Ala750del	c.2235_2249del	3535	107	3 %
NSCLC4	chr7:55259515	<i>EGFR</i>	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	3523	390	11 %
NSCLC5	chr3:178952085	<i>PIK3CA</i>	NM_006218.2		missense	21	p.His1047Leu	c.3140A>T	3994	3052	76 %
	chr17:7578190	<i>TP53</i>	NM_000546.5		missense	6	p.Tyr220Cys	c.659A>G	3999	2653	66 %
NSCLC7	chr2:42522656	<i>ALK</i>	NG_009445.1	EML4 - ALK		6 20					-
NSCLC8	chr17:7577094	<i>TP53</i>	NM_000546.5		missense	8	p.Arg282Trp	c.844C>T	1396	237	17 %
NSCLC9	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3993	1375	34 %
	chr17:7578442	<i>TP53</i>	NM_000546.5		missense	5	p.Tyr163Cys	c.488A>G	1128	668	59 %
NSCLC10	chr17:7578457	<i>TP53</i>	NM_000546.5		missense	5	p.Arg158Pro	c.473G>C	1657	1365	82 %
NSCLC11	chr12:25380275	<i>KRAS</i>	NM_033360.3		missense	3	p.Gln61His	c.183A>T	3996	1568	39 %
NSCLC12	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3329	788	24 %
NSCLC13	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Asp	c.35G>A	3996	1738	43 %
	chr17:7578530	<i>TP53</i>	NM_000546.5		missense	5	p.Phe134Val	c.400T>G	2745	743	27 %
NSCLC14	chr17:7577534	<i>TP53</i>	NM_000546.5		missense	7	p.Arg249Ser	c.747G>T	3215	535	17 %
	chr17:7578406	<i>TP53</i>	NM_000546.5		missense	5	p.Arg175Leu	c.524G>T	2127	211	10 %
NSCLC15	chr12:25398281	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly13Asp	c.38G>A	3998	1275	32 %
	chr17:7578468	<i>TP53</i>	NM_000546.5		frameshift deletion	5	p.Gly154fs	c.461_461del	1119	228	20 %
NSCLC16	chr2:42522656	<i>ALK</i>	NG_009445.1	EML4 - ALK		6 20					-
NSCLC17	chr3:41266113	<i>CTNNB1</i>	NM_001904.3		missense	3	p.Ser37Cys	c.110C>G	1781	298	17 %
	chr7:55241677	<i>EGFR</i>	NM_005228.3		missense	18	p.Glu709Lys	c.2125G>A	2721	1101	40 %
NSCLC18	chr7:55241707	<i>EGFR</i>	NM_005228.3		missense	18	p.Gly719Cys	c.2155G>T	2709	1100	41 %
	chr17:7577535	<i>TP53</i>	NM_000546.5		missense	7	p.Arg249Thr	c.746G>C	3997	1583	40 %
NSCLC19	chr7:55259515	<i>EGFR</i>	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	3637	248	7 %
	chr17:7578269	<i>TP53</i>	NM_000546.5		missense	6	p.Leu194Phe	c.580C>T	2652	228	9 %
NSCLC20	chr12:25398281	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly13Asp	c.38G>A	3513	599	17 %
	chr17:7578461	<i>TP53</i>	NM_000546.5		missense	5	p.Val157Phe	c.469G>T	3379	849	25 %
NSCLC22	chr6:117645578	<i>ROS1</i>	NG_033929.1	EZR - ROS1		10 34					-
NSCLC23	chr7:140453136	<i>BRAF</i>	NM_004333.4		missense	15	p.Val600Glu	c.1799T>A	3997	128	3 %
NSCLC24	chr7:140453136	<i>BRAF</i>	NM_004333.4		missense	15	p.Val600Glu	c.1799T>A	3993	205	5 %
	chr12:25380275	<i>KRAS</i>	NM_033360.3		missense	3	p.Gln61His	c.183A>C	3996	525	13 %
NSCLC25	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3994	248	6 %
	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3988	305	8 %
NSCLC26	chr17:7578535	<i>TP53</i>	NM_000546.5		missense	5	p.Lys132Arg	c.395A>G	3098	176	6 %
	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3880	504	13 %
NSCLC28	chr7:140481402	<i>BRAF</i>	NM_004333.4		missense	11	p.Gly469Val	c.1406G>T	3956	1038	26 %
NSCLC29	chr17:7577538	<i>TP53</i>	NM_000546.5		missense	7	p.Arg248Leu	c.743G>T	3958	669	17 %
NSCLC30	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	2386	357	15 %
NSCLC31	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	2688	738	27 %
	chr17:7577538	<i>TP53</i>	NM_000546.5		missense	7	p.Arg248Leu	c.743G>T	3878	629	16 %

	chr19:1221313	<i>STK11</i>	NM_000455.4		frameshift deletion	6	p.Pro281fs	c.837_837del	1984	567	29 %
NSCLC32	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3905	976	25 %
NSCLC33	chr17:7578469	<i>TP53</i>	NM_000546.5		missense	5	p.Gly154Val	c.461G>T	1336	469	35 %
NSCLC34	chr17:7574003	<i>TP53</i>	NM_000546.5		nonsense	10	p.Arg342Ter	c.1024C>T	3695	763	21 %
	chr17:7577114	<i>TP53</i>	NM_000546.5		frameshift insertion	8	p.Cys275fs	c.823_824insT	2190	87	4 %
NSCLC35	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3999	2387	60 %
	chr17:7577120	<i>TP53</i>	NM_000546.5		missense	8	p.Arg273Leu	c.818G>T	1726	900	52 %
NSCLC36	chr17:7578403	<i>TP53</i>	NM_000546.5		missense	5	p.Cys176Tyr	c.527G>A	2573	1840	72 %
NSCLC38	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	2941	254	9 %
NSCLC39	chr3:41266134	<i>CTNNB1</i>	NM_001904.3		missense	3	p.Pro44Leu	c.131C>T	2260	789	35 %
	chr3:178936091	<i>PIK3CA</i>	NM_006218.2		missense	10	p.Glu545Lys	c.1633G>A	3887	550	14 %
NSCLC40	chr17:7579355	<i>TP53</i>	NM_000546.5		missense	4	p.Leu111Arg	c.332T>G	2014	785	39 %
	chr7:140453134	<i>BRAF</i>	NM_004333.4		missense	15	p.Lys601Glu	c.1801A>G	1452	397	27 %
NSCLC41	chr17:7577046	<i>TP53</i>	NM_000546.5		nonsense	8	p.Glu298Ter	c.892G>T	1550	145	9 %
NSCLC42	chr17:7579358	<i>TP53</i>	NM_000546.5		missense	4	p.Arg110Leu	c.329G>T	552	130	24 %
NSCLC43	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	2833	170	6 %
NSCLC44	chr17:7578526	<i>TP53</i>	NM_000546.5		missense	5	p.Cys135Tyr	c.404G>A	1405	638	45 %
NSCLC45	chr17:7578208	<i>TP53</i>	NM_000546.5		missense	6	p.His214Arg	c.641A>G	3215	1476	46 %
NSCLC46	chr12:25398284	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3996	896	22 %
NSCLC48	chr3:178936082	<i>PIK3CA</i>	NM_006218.2		missense	10	p.Glu542Gln	c.1624G>C	3664	282	8 %
	chr17:7578461	<i>TP53</i>	NM_000546.5		missense	5	p.Val157Phe	c.469G>T	2290	225	10 %
NSCLC49	chr17:7578395	<i>TP53</i>	NM_000546.5		missense	5	p.His179Tyr	c.535C>T	3965	845	21 %
NSCLC50	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3991	1456	36 %
	chr17:7577528	<i>TP53</i>	NM_000546.5		nonframeshift deletion	7	p.Arg249del	c.745_747delAGG	3912	1240	32 %
NSCLC51	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3728	888	24 %
	chr17:7578517	<i>TP53</i>	NM_000546.5		missense	5	p.Ala138Val	c.413C>T	2464	486	20 %
NSCLC52	chr7:140453154	<i>BRAF</i>	NM_004333.4		missense	15	p.Asp594Val	c.1781A>T	1493	64	4 %
	chr12:25398281	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly13Asp	c.38G>A	1946	98	5 %
NSCLC53	chr10:89717712	<i>PTEN</i>	NM_000314.4		missense	7	p.Pro246Leu	c.737C>T	3977	422	11 %
	chr17:37880981	<i>ERBB2</i>	NM_004448.3		duplication	20	p.Ala771_Met774dup	c.2311_2322dup	2146	556	26 %
NSCLC55	chr17:7577022	<i>TP53</i>	NM_000546.5		nonsense	8	p.Arg306Ter	c.916C>T	1091	300	28 %
NSCLC56	chr4:153247289	<i>FBXW7</i>	NM_033632.3		missense	10	p.Arg505Ser	c.1513C>A	3996	121	3 %
NSCLC57	chr7:55242478	<i>EGFR</i>	NM_005228.3		frameshift deletion		p.Glu747_Ala750delinsP	c.2238_2248delinsGC	3559	172	5 %
	chr12:25398285	<i>KRAS</i>	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3438	2740	80 %
NSCLC58	chr7:140481411	<i>BRAF</i>	NM_004333.4		missense	11	p.Gly466Val	c.1397G>T	2459	453	18 %
	chr17:7579882	<i>TP53</i>	NM_000546.5		nonsense	2	p.Glu11Ter	c.31G>T	3442	630	18 %
NSCLC59	chr7:55242468	<i>EGFR</i>	NM_005228.3		nonframeshift deletion	19	p.Glu746_Arg748del	c.2236_2244del	1647	1101	67 %
	chr17:7577105	<i>TP53</i>	NM_000546.5		missense	8	p.Pro278Arg	c.833C>G	524	84	16 %
NSCLC60	chr2:42522656	<i>ALK</i>	NG_009445.1	EML4 ALK		13 20					-
NSCLC61	chr7:140453136	<i>BRAF</i>	NM_004333.4		missense	15	p.Val600Glu	c.1799T>A	3920	227	6 %
	chr17:7577517	<i>TP53</i>	NM_000546.5		missense	7	p.Ile255Asn	c.764T>A	1850	104	6 %
NSCLC64	chr1:115256529	<i>NRAS</i>	NM_002524.4		missense	3	p.Gln61Leu	c.182A>T	3987	500	13 %
	chr17:7577035	<i>TP53</i>	NM_000546.5		frameshift deletion	8	p.Pro301fs	c.902_902delC	1416	89	6 %
NSCLC65	chr3:178952146	<i>PIK3CA</i>	NM_006218.2		missense	21	p.Leu1067Phe	c.3201G>C	3997	365	9 %
	chr4:153249460	<i>FBXW7</i>	NM_033632.3		missense	9	p.Asp440His	c.1318G>C	3996	263	7 %
	chr7:140481411	<i>BRAF</i>	NM_004333.4		missense	11	p.Gly466Ala	c.1397G>C	2599	651	25 %

	chr17:7578441	TP53	NM_000546.5		nonsense	5	p.Tyr163Ter	c.489C>A	1795	444	25 %
NSCLC66	chr2:42522656	ALK	NG_009445.1	EML4 - ALK		6120					-
NSCLC67	chr17:7578452	TP53	NM_000546.5		frameshift deletion	5	p.Met160fs	c.477_477delC	3261	579	18 %
NSCLC68	chr7:55259515	EGFR	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	3973	113	3 %
	chr17:7578430	TP53	NM_000546.5		frameshift deletion	5	p.Gln167fs	c.499_499delC	3289	170	5 %
NSCLC69	chr17:7578280	TP53	NM_000546.5		missense	6	p.Pro190Leu	c.569C>T	1334	114	9 %
NSCLC70	chr12:25398280	KRAS	NM_033360.3		missense	2	p.Gly13Glu	c.38_39delinsAA	3982	1797	45 %
NSCLC71	chr17:7577099	TP53	NM_000546.5		missense	8	p.Arg280Thr	c.839G>C	1332	461	35 %
NSCLC72	chr17:7577539	TP53	NM_000546.5		missense	7	p.Arg248Trp	c.742C>T	1676	616	37 %
NSCLC73	chr17:7577108	TP53	NM_000546.5		missense	8	p.Cys277Phe	c.830G>T	1465	473	32 %
NSCLC74	chr7:55259515	EGFR	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	523	167	32 %
NSCLC75	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3998	641	16 %
NSCLC76	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3994	2031	51 %
	chr17:7577534	TP53	NM_000546.5		missense	7	p.Arg249Ser	c.747G>C	1786	642	36 %
NSCLC78	chr12:25380285	KRAS	NM_033360.3		missense	3	p.Thr58Ile	c.173C>T	4000	98	2 %
	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3994	1132	28 %
NSCLC79	chr7:140481411	BRAF	NM_004333.4		missense	11	p.Gly466Val	c.1397G>T	3999	1994	50 %
	chr17:7577103	TP53	NM_000546.5		frameshift insertion	8	p.Gly279fs	c.834_835insT	2670	1151	43 %
NSCLC80	chr2:212578301	ERBB4	NM_005235.2		missense	8	p.Gly319Val	c.956G>T	2793	1008	36 %
	chr17:7578457	TP53	NM_000546.5		missense	5	p.Arg158Leu	c.473G>T	1036	784	76 %
NSCLC81	chr17:37880981	ERBB2	NM_004448.3		duplication	20	p.Ala771_Met774dup	c.2311_2322dup	1467	200	14 %
NSCLC82	chr7:140481411	BRAF	NM_004333.4		missense	11	p.Gly466Val	c.1397G>T	3993	343	9 %
	chr17:7578442	TP53	NM_000546.5		missense	5	p.Tyr163Cys	c.488A>G	3860	238	6 %
NSCLC83	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Arg	c.34G>C	3993	777	19 %
NSCLC84	chr17:7578469	TP53	NM_000546.5		missense	5	p.Gly154Val	c.461G>T	1480	351	24 %
NSCLC85	chr17:7578392	TP53	NM_000546.5		nonsense	5	p.Glu180Ter	c.538G>T	1666	534	32 %
	chr19:1220487	STK11	NM_000455.4		missense	4	p.Asp194Tyr	c.580G>T	749	209	28 %
NSCLC86	chr17:7577090	TP53	NM_000546.5		missense	8	p.Arg283Pro	c.848G>C	1148	51	4 %
NSCLC87	chr17:7578431	TP53	NM_000546.5		nonsense	5	p.Gln167Ter	c.499C>T	1896	880	46 %
NSCLC88	chr3:41266098	CTNNB1	NM_001904.3		missense	3	p.Asp32Val	c.95A>T	513	20	4 %
	chr7:140453155	BRAF	NM_004333.4		missense	15	p.Asp594Asn	c.1780G>A	798	187	23 %
NSCLC89	chr3:178936082	PIK3CA	NM_006218.2		missense	10	p.Glu542Lys	c.1624 G>A	710	16	2 %
	chr7:55242464	EGFR	NM_005228.3		nonframeshift deletion	19	p.Glu746_Ala750del	c.2235_2249del	1283	242	19 %
NSCLC90	chr12:25398284	KRAS	NM_033360.3		missense	2	p.Gly12Val	c.35G>T	3993	589	15 %
NSCLC91	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3996	157	4 %
	chr17:37881022	ERBB2	NM_004448.3		missense	20	p.Arg784His	c.2351G>A	4000	147	4 %
NSCLC92	chr7:55259515	EGFR	NM_005228.3		missense	21	p.Leu858Arg	c.2573T>G	3989	409	10 %
	chr17:7578469	TP53	NM_000546.5		missense	5	p.Gly154Val	c.461G>T	2903	199	7 %
NSCLC93	chr7:55248998	EGFR	NM_005228.3		duplication	20	p.Ala767_Val769dup	c.2300_2308dup	2758	1009	37 %
NSCLC94	chr12:25380276	KRAS	NM_033360.3		missense	3	p.Gln61Leu	c.182A>T	3998	535	13 %
NSCLC96	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Ser	c.34G>A	1552	287	18 %
NSCLC97	chr2:42522656	ALK	NG_009445.1	ALK Fusion							-
	chr3:178936082	PIK3CA	NM_006218.2		missense	9	p.Glu542Lys	c.1624G>A	1994	136	7 %
NSCLC98	chr17:7578394	TP53	NM_000546.5		missense	5	p.His179Arg	c.536A>G	1769	198	11 %
NSCLC99	chr12:25398285	KRAS	NM_033360.3		missense	2	p.Gly12Cys	c.34G>T	3659	509	14 %
NSCLC100	chr17:7578457	TP53	NM_000546.5		missense	5	p.Arg158Leu	c.473G>T	3835	2682	70 %

CDS- Coding sequence nomenclature; Total Coverage- Total reads in the genomic region; Variant Coverage- Total variant reads; VAF- Variant allele frequency (%).

Table S2. Pathogenic variants detected in mCRC patients.

Patient	Chr Position	Gene	NG/NM	Mutation Type	Exon	Amino Acid Change	CDS	Total Coverage	Variant Coverage	VAF
CRC1	chr17:7577547	TP53	NM_000546.5	Missense	7	p.Gly245Val	c.734G>T	1686	166	10 %
CRC3	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	4777	1603	34 %
	chr18:48591826	SMAD4	NM_005359.5	Missense	9	p.Glu330Gly	c.989A>G	3709	1556	42 %
CRC4	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Cys	c.34G>T	2505	547	22 %
	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3142	705	22 %
CRC5	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Cys	c.34G>T	3997	1126	28 %
	chr17:7578382	TP53	NM_000546.5	Nonsense	5	p.Ser183Ter	c.548C>G	2085	993	48 %
CRC6	chr17:7578392	TP53	NM_000546.5	Deletion	5	p. Arg174_His179del	c.520_537del	1490	730	49 %
	chr17:7578269	TP53	NM_000546.5	Missense	6	p.Leu194Phe	c.580C>T	1846	49	3 %
CRC7	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	1544	236	15 %
CRC8	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3994	1.358	34 %
CRC9	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	2733	1.613	59 %
CRC10	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3689	165	4 %
	chr17:7577120	TP53	NM_000546.5	Missense	8	p.Arg273His	c.818G>A	1433	166	12 %
CRC11	chr17:7578212	TP53	NM_000546.5	Nonsense	6	p.Arg213Ter	c.637C>T	2045	382	19 %
	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Cys	c.34G>T	3997	1.126	28 %
CRC12	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	2268	58	3 %
	chr17:7577121	TP53	NM_000546.5	Missense	8	p.Arg273Cys	c.817C>T	2150	163	8 %
CRC13	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Ala	c.35G>C	2938	762	26 %
	chr17:7578395	TP53	NM_000546.5	Missense	5	p.His179Tyr	c.535C>T	2444	1.040	43 %
CRC14	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	2870	207	7 %
	chr3:178952090	PIK3CA	NM_006218.2	Missense	20	p.His1049Arg	c.3145G>C	3123	226	7 %
CRC15	chr17:7578406	TP53	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	2765	144	5 %
	chr1:115256529	NRAS	NM_002524.4	Missense	3	p.Gln61Arg	c.182A>G	1773	105	6 %
CRC16	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	1847	107	6 %
CRC18	chr7:140453136	BRAF	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	2154	356	17 %
CRC19	chr12:25378647	KRAS	NM_033360.3	Missense	4	p.Lys117Asn	c.351A>T	3897	1.888	48 %
CRC20	chr17:7577538	TP53	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	3984	330	8 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3993	710	18 %
CRC21	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3930	100	3 %
	chr17:7577538	TP53	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	3974	923	23 %
CRC22	chr7:140453136	BRAF	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	3987	1.237	31 %
	chr17:7577022	TP53	NM_000546.5	Nonsense	8	p.Arg306Ter	c.916C>T	1148	515	45 %
CRC23	chr3:178936095	PIK3CA	NM_006218.2	Missense	9	p.Gln546Arg	c.1637A>G	3410	310	9 %
	chr18:48603032	SMAD4	NM_005359.5	Nonsense	11	p.Arg445Ter	c.1333C>T	2530	169	7 %
CRC24	chr17:7578403	TP53	NM_000546.5	Missense	5	p.Cys176Tyr	c.527G>A	553	110	20 %
	chr3:178952085	PIK3CA	NM_006218.2	Missense	20	p.His1047Arg	c.3140A>G	1384	286	21 %
CRC25	chr17:7577539	TP53	NM_000546.5	Missense	7	p.Arg248Trp	c.742C>T	1811	260	14 %
	chr7:140453136	BRAF	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	2192	314	14 %
CRC26	chr4:153249348	FBXW7	NM_033632.3	Missense	8	p.Arg465His	c.1394G>A	3283	765	23 %

	chr17:7577547	TP53	NM_000546.5	Missense	7	p.Gly245Asp	c.734G>A	1304	252	19 %
	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Ser	c.34G>A	3997	1.822	46 %
CRC27	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3934	334	8 %
	chr17:7577551	TP53	NM_000546.5	Missense	7	p.Gly244Ser	c.730G>A	4000	1.632	41 %
CRC28	chr17:7577559	TP53	NM_000546.5	Missense	7	p.Ser241Phe	c.722C>T	2123	587	28 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	3486	346	10 %
CRC30	chr17:7577094	TP53	NM_000546.5	Missense	8	p.Arg282Trp	c.844C>T	580	220	38 %
	chr12:25378562	KRAS	NM_033360.3	Missense	4	p.Ala146Thr	c.436G>A	4000	1.003	25 %
CRC31	chr12:25398262	KRAS	NM_033360.3	Missense	2	p.Leu19Phe	c.57G>T	3175	683	22 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	2595	994	38 %
CRC32	chr3:178936091	PIK3CA	NM_006218.2	Missense	9	p.Glu545Lys	c.1633G>A	2186	514	24 %
	chr17:7578388	TP53	NM_000546.5	Missense	5	p.Arg181His	c.542G>A	1668	541	32 %
	chr17:7578461	TP53	NM_000546.5	Missense	5	p.Val157Leu	c.469G>C	1665	1.038	62 %
CRC33	chr12:25398282	KRAS	NM_033360.3	Missense	2	p.Gly13Cys	c.37G>T	3997	1.037	26 %
CRC34	chr17:7577022	TP53	NM_000546.5	Nonsense	8	p.Arg306Ter	c.916C>T	926	279	30 %
CRC35	chr17:7577120	TP53	NM_000546.5	Missense	8	p.Arg273His	c.818G>A	520	260	50 %
CRC36	chr17:7577538	TP53	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	1240	567	45 %
	chr12:25378561	KRAS	NM_033360.3	Missense	4	p.Ala146Val	c.437C>T	3100	352	11 %
CRC38	chr17:7577538	TP53	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	1387	201	14 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	3088	429	14 %
CRC39	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3759	218	6 %
	chr7:140453148	BRAF	NM_004333.4	Missense	15	p.Gly596Val	c.1787G>T	3915	647	17 %
CRC40	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3979	606	15 %
	chr17:7578406	TP53	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	820	220	27 %
CRC41	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3309	756	23 %
	chr4:153249348	FBXW7	NM_033632.3	Missense	8	p.Arg465His	c.1394G>A	2213	624	28 %
CRC42	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Ser	c.34G>A	2981	246	8 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	3972	1.210	30 %
CRC43	chr18:48591892	SMAD4	NM_005359.5	Missense	9	p.Gly352Val	c.1055G>T	3997	377	9 %
	chr12:25398285	KRAS	NM_033360.3	Missense	2	p.Gly12Ser	c.34G>A	5555	2.817	51 %
CRC44	chr3:178936082	PIK3CA	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3813	790	21 %
CRC45	chr17:7577081	TP53	NM_000546.5	Missense	8	p.Glu286Gly	c.857A>G	1722	843	49 %
	chr14:105246551	AKT	NM_0001014431.1	Missense	4	p.Glu17Lys	c.49G>A	700	21	3 %
CRC46	chr12:25399291	KRAS	NM_033360.3	Missense	2	p.Gly13Asp	c.38G>A	4000	243	6 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	5059	476	9 %
CRC47	chr3:178936095	PIK3CA	NM_006218.2	Missense	9	p.Gln546Arg	c.1637A>G	4078	623	15 %
	chr18:48591918	SMAD4	NM_005359.5	Missense	9	p.Arg361Cys	c.1081C>T	3348	551	16 %
CRC49	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	2185	1.198	55 %
	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Phe	c.34_35delGGinsTT	3707	1.380	37 %
CRC51	chr7:116411923	MET	NM_001127500.1	Missense	14	p.Arg988Cys	c.2962C>T	2473	893	36 %
	chr17:7578406	TP53	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	2473	893	36 %
CRC53	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	3972	1.210	30 %
	chr3:178952085	PIK3CA	NM_006218.2	Missense	20	p.His1047Arg	c.3140A>G	3270	1.921	59 %
CRC54	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	4000	1.985	50 %
	chr17:7577539	TP53	NM_000546.5	Missense	7	p.Arg248Trp	c.742C>T	1219	352	29 %
CRC55	chr12:25398284	KRAS	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	2713	447	16 %

CRC57	chr3:178936091	<i>PIK3CA</i>	NM_006218.2	Missense	9	p.Glu545Lys	c.1633G>A	3519	557	16 %
	chr17:7577094	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg282Trp	c.844C>T	2827	2,227	79 %
CRC58	chr4:153249446	<i>FBXW7</i>	NM_033632.3	Missense	11	p.Ser582Leu	c.1745C>T	6903	1,631	24 %
	chr12:25378562	<i>KRAS</i>	NM_033360.3	Missense	4	p.Ala146Val	c.437C>T	3503	1,575	45 %
CRC59	chr17:7578263	<i>TP53</i>	NM_000546.5	Nonsense	6	p.Arg196Ter	c.586C>T	2290	771	34 %
	chr17:7577538	<i>TP53</i>	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	2905	652	22 %
CRC60	chr4:153249348	<i>FBXW7</i>	NM_033632.3	Missense	8	p.Arg465His	c.1394G>A	4444	1,148	26 %
	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	5064	1,715	34 %
	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361Cys	c.1081C>T	5582	313	6 %
CRC61	chr17:7578406	<i>TP53</i>	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	2198	1,071	49 %
	chr3:41266136	<i>CTNNB1</i>	NM_001904.3	Missense	3	p.Ser45Pro	c.133T>C	1961	812	41 %
	chr12:25378562	<i>KRAS</i>	NM_033360.3	Missense	4	p.Ala146Thr	c.436G>A	3232	653	20 %
	chr10:89717769	<i>PTEN</i>	NM_000314.4	Deletion	7	p.Lys267fs	c.795del	3202	917	29 %
CRC62	chr10:89720852	<i>PTEN</i>	NM_000314.4	Missense	8	p.Arg335Ter	c.1003C>T	1932	505	26 %
	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	6260	908	15 %
CRC63	chr17:7578406	<i>TP53</i>	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	2317	710	31 %
CRC64	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	7456	2,076	28 %
CRC65	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	8743	3,635	42 %
	chr17:7577509	<i>TP53</i>	NM_000546.5	Missense	7	p.Glu258Lys	c.772G>A	2227	1,475	66 %
CRC67	chr12:25399291	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly13Asp	c.38G>A	1043	120	12 %
CRC68	chr17:7578550	<i>TP53</i>	NM_000546.5	Missense	5	p.Ser127Phe	c.380C>T	893	444	50 %
CRC69	chr17:7577120	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg273His	c.818G>A	512	236	46 %
CRC70	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	4342	1,861	43 %
	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361Cys	c.1081C>T	2151	455	21 %
CRC71	chr17:7574018	<i>TP53</i>	NM_000546.5	Missense	10	p.Arg337Cys	c.1009C>T	503	65	13 %
	chr17:7578437	<i>TP53</i>	NM_000546.5	Nonsense	5	p.Gln165Ter	c.493C>T	503	65	13 %
CRC72	chr12:25378561	<i>KRAS</i>	NM_033360.3	Missense	4	p.Ala146Val	c.437C>T	3852	1,551	40 %
	chr17:7578406	<i>TP53</i>	NM_000546.5	Missense	5	p.Arg175His	c.524G>A	900	219	24 %
CRC73	chr7:140453136	<i>BRAF</i>	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	1926	572	30 %
	chr10:89711907	<i>PTEN</i>	NM_000314.4	Missense	6	p.Tyr177His	c.529T>C	1756	556	32 %
CRC75	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3670	1,084	30 %
	chr17:577548	<i>TP53</i>	NM_000546.5	Missense	7	p.Gly245Ser	c.733G>A	3999	523	13 %
CRC76	chr7:140453136	<i>BRAF</i>	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	2207	619	28 %
	chr17:7577580	<i>TP53</i>	NM_000546.5	Missense	7	p.Tyr234Cys	c.701A>G	3916	1,013	26 %
	chr17:7578388	<i>TP53</i>	NM_000546.5	Missense	5	p.Arg181Pro	c.542G>C	2798	493	18 %
CRC79	chr3:41266137	<i>CTNNB1</i>	NM_001904.3	Missense	3	p.Ser45Phe	c.134C>T	2738	1,684	62 %
	chr12:25399291	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly13Asp	c.38G>A	5040	1,716	34 %
CRC80	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361His	c.1082G>A	5362	1,763	33 %
	chr17:7577538	<i>TP53</i>	NM_000546.5	Missense	7	p.Arg248Gln	c.743G>A	10196	3,395	33 %
CRC81	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	3843	656	17 %
	chr18:48591901	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Asp355Val	c.1064A>T	2709	266	10 %
	chr17:7578212	<i>TP53</i>	NM_000546.5	Nonsense	6	p.Arg213Ter	c.637C>T	2974	272	9 %
CRC84	chr7:140453132	<i>BRAF</i>	NM_004333.4	Missense	15	p.Lys601Asn	c.1803A>C	1289	161	12 %
	chr1:115256529	<i>NRAS</i>	NM_002524.4	Missense	3	p.Gln61Arg	c.182A>G	2955	327	11 %
CRC82	chr17:7577124	<i>TP53</i>	NM_000546.5	Missense	8	p.Val272Leu	c.814G>T	1156	147	13 %
	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	2514	1,051	42 %

CRC85	chr7:140453136	<i>BRAF</i>	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	2078	291	14 %
	chr3:178936082	<i>PIK3CA</i>	NM_006218.2	Missense	9	p.Gly542Lys	c.1624 G>A	3964	849	21 %
CRC86	chr15:66727455	<i>MAP2K1</i>	NM_002755.3	Missense	2	p.Lys57Asn	c.171G>C	1408	169	12 %
	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361His	c.1082G>A	3722	599	16 %
CRC87	chr12:25399291	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly13Asp	c.38G>A	4564	500	11 %
	chr17:7577094	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg282Trp	c.844C>T	876	134	15 %
CRC88	chr4:153258983	<i>FBXW7</i>	NM_033632.3	Nonsense	4	p.Arg278Ter	c.832C>T	5498	547	10 %
	chr12:25398285	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Ser	c.34G>A	6281	1.442	23 %
	chr17:7577563	<i>TP53</i>	NM_000546.5	Missense	7	p.Asn239Ile	c.716A>T	3477	557	16 %
	chr17:7577563	<i>TP53</i>	NM_000546.5	Missense	7	p.Ser240Gly	c.718A>G	3477	557	16 %
CRC89	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Ser	c.34G>A	8221	1.366	17 %
CRC90	chr17:7578272	<i>TP53</i>	NM_000546.5	Missense	6	p.His193Tyr	c.577C>T	1911	233	12 %
CRC91	chr7:140453136	<i>BRAF</i>	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	3104	686	22 %
	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361Cys	c.1081C>T	2253	460	20 %
CRC92	chr7:140453136	<i>BRAF</i>	NM_004333.4	Missense	15	p.Val600Glu	c.1799T>A	2077	142	7 %
	chr17:7577120	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg273His	c.818G>A	2077	142	7 %
CRC94	chr17:7578529	<i>TP53</i>	NM_000546.5	Missense	5	p.Phe134Cys	c.401T>G	3395	1.329	39 %
CRC95	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Asp	c.35G>A	1386	495	36 %
	chr17:7577094	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg282Trp	c.844C>T	821	226	28 %
CRC97	chr9:139399362	<i>NOTCH</i>	NM_017617.3	Missense	26	p.Arg1594Gln	c.4781G>A	560	252	45 %
CRC98	chr17:7577140	<i>TP53</i>	NM_000546.5	Frameshift	8	p.Gly266fs	c.797delG	905	445	49 %
CRC99	chr12:25398284	<i>KRAS</i>	NM_033360.3	Missense	2	p.Gly12Val	c.35G>T	3984	1.423	36 %
	chr17:7577094	<i>TP53</i>	NM_000546.5	Missense	8	p.Arg282Trp	c.844C>T	1758	875	50 %
CRC100	chr18:48591918	<i>SMAD4</i>	NM_005359.5	Missense	9	p.Arg361His	c.1082G>A	2325	745	32 %
	chr17:7578266	<i>TP53</i>	NM_000546.5	Missense	6	p.Ile195Phe	c.583A>T	689	219	32 %

CDS- Coding sequence nomenclature; Total Coverage- Total reads in the genomic region; Variant Coverage- Total variant reads; VAF- Variant allele frequency (%).



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