Leids Universitair Medisch Centrum

B-cell Lymphoma panel version 1

Panel description

The custom Ampliseq "LYMFv1" gene panel is designed for sequencing hotspot regions frequently mutated in B-cell lymphoma. It contains 1388 amplicons and covers coding sequence in 52 oncogenes and tumor suppressor genes.

Gene	*RefSeq accession number*	*Exons*	*cDNA coordinates*	*Covered amino acids*
ATM	NM_000051	1-62	1-431, 525-977, 1008-2138, 2140-2920, 2935-3532, 3577-3674, 3693-3746, 3780-3939, 4005-4230, 4237-4611, 4640-4737, 4777-5436, 5438-6925, 6976-7097, 7200-7663, 7689-8362, 8419-8431, 8461-8527, 8536-9171	1-144, 175-326, 336-974, 979-1178, 1193-1225, 1231-1249, 1260-1313, 1335-1410, 1413-1537, 1547-1579, 1593-2309, 2326-2366, 2400-2555, 2563-2788, 2807-2811, 2821-2843, 2846-3057
B2M	NM_004048	1-3	1-360	1-120
BCL2	NM_000633	1-2	1-138, 156-272, 288-381, 461-720	1-46, 52-91, 96-127, 154-240
BCL6	NM_001706	1-8	1-591, 648-752, 804-1032, 1053-1136, 1161-1540, 1605-1834, 1840-2121	1-197, 216-251, 268-344, 351-379, 387-514, 535-612, 614-707
BCL7A	NM_001024808	1-2	1-53, 93-174	1-18, 31-58
BIRC3	NM_001165	1-6, 8	1-264, 335-1032, 1066-1579, 1622-1801	1-88, 112-344, 356-527, 541-601
BRAF	NM_004333	11, 15	1360-1432, 1742-1833	454-478, 581-611
BTG1	NM_001731	1-2	20-516	7-172
BTG2	NM_006763	1-2	1-129, 143-250, 340-477	1-43, 48-84, 114-159
BTK	NM_000061	14-15	1350-1631	450-544
CARD11	NM_032415	2-8, 14-15, 18-19, 21, 24	85-208, 221-420, 553-1341, 1822-1922, 2088-2142, 2537-2703, 2883-3006, 3368-3465	29-70, 74-140, 185-447, 608-641, 696-714, 846-901, 961-1002, 1123-1155
CD37	NM_001040031	1-6	1-564, 566-642	1-214
CD70	NM_001252	1-3	1-582	1-194
CD79A	NM_001783	5	568-652	190-218
CD79B	NM_000626	3-6	119-180, 257-377, 431-690	40-60, 86-126, 144-230
CDKN2A	NM_000077	1-3	36-146, 151-228, 246-374, 376-471	12-49, 51-76, 82-157
CREBBP	NM_004380	1-31	1-451, 478-2283, 2354-2463, 2508-2880, 2923-4068, 4134-	1-151, 160-761, 785-821, 836-960, 975-1356, 1378-1520, 1546-1630,

			4560, 4636-4890, 4912-5271, 5345-5525, 5625-5791, 5820-6321, 6341-6690, 6706-7329	1638-1757, 1782-1842, 1875-1931, 1940-2107, 2114-2230, 2236-2443
CXCR4	NM_001008540	1	950-1071	317-357
DDX3Y	NM_004660	5	381-437	127-146
EBF1	NM_024007	1-8	1-13, 201-778	1-5, 67-260
EP300	NM_001429	1-31	1-1249, 1283-2560, 2607-2922, 2998-3411, 3502-4720, 4780-5043, 5062-5411, 5472-6684, 6728-7245	1-417, 428-854, 869-974, 1000-1137, 1168-1574, 1594-1681, 1688-1804, 1824-2228, 2243-2415
ETV6	NM_001987	1-8	1-815, 841-1359	1-272, 281-453
EZH2	NM_004456	4, 17-18	382-484, 2030-2195	128-162, 677-732
GNA13	NM_006572	1-4	12-272, 275-1134	4-378
H1-4	NM_005321	1	1-181, 228-408, 507-625	1-61, 76-136, 169-209
IRF4	NM_001195286	1-2	1-184, 217-403	1-62, 73-135
IRF8	NM_002163	1-2, 6-8	1-358, 602-713, 728-1101, 1105-1204, 1227-1281	1-120, 201-238, 243-367, 369-402, 409-427
KLHL14	NM_020805	1-2	1-176, 193-646, 663-1069	1-59, 65-216, 221-357
KLHL6	NM_130446	1-7	1-516, 910-981, 1003-1147, 1183-1524, 1595-1856	1-172, 304-327, 335-383, 395-508, 532-619
KMT2D	NM_003482	1-54	1-251, 273-1112, 1122-1258, 1321-2170, 2203-2322, 2356-3427, 3454-4679, 4694-4963, 5037-5976, 5994-6274, 6295-6509, 6655-6966, 7017-7951, 8037-8068, 8088-8770, 8849-9846, 9942-10507, 10551-10673, 10752-11143, 11202-11464, 11495-11951, 11974-12355, 12391-12486, 12580-12981, 13081-13259, 13309-13839, 13911-14075, 14130-15226, 15247-15483, 15535-16546	1-84, 91-371, 374-420, 441-724, 735-774, 786-1143, 1152-1560, 1565-1655, 1679-1992, 1998-2092, 2099-2170, 2219-2322, 2339-2651, 2679-2690, 2696-2924, 2950-3282, 3314-3503, 3517-3558, 3584-3715, 3734-3822, 3832-3984, 3992-4119, 4131-4162, 4194-4327, 4361-4420, 4437-4613, 4637-4692, 4710-5076, 5083-5161, 5179-5516
BORCS8-MEF2B	NM_005919	1-5, 7	1-326, 394-665, 770-877, 1009-1098	1-109, 132-222, 257-293, 337-366
MTOR	NM_004958	1-57	4-271, 301-1622, 1652-1822, 1855-2101, 2109-7650	2-91, 101-541, 551-608, 619-701, 703-2550
MYC	NM_001354870	1-3	1-566, 585-862, 1003-1362	1-189, 195-288, 335-454
MYD88	NM_002468	1, 3-5	199-321, 505-634, 645-844	67-107, 169-212, 215-282
NOTCH1	NM_017617	25-28, 34	4417-4834, 5019-5202, 5212-5384, 6818-7072, 7190-7350, 7374-7571, 7643-7668	1473-1612, 1673-1734, 1738-1795, 2273-2358, 2397-2450, 2458-2524, 2548-2556
NOTCH2	NM_024408	11, 13, 19, 21, 23, 31-32, 34	1688-1806, 2114-2197, 2982-3075, 3358-3486, 3726-3856, 5480-5575, 5581-5709, 5782-5882, 6028-7017, 7037-7229, 7289-7416	563-602, 705-733, 994-1025, 1120-1162, 1242-1286, 1827-1859, 1861-1903, 1928-1961, 2010-2339, 2346-2410, 2430-2472
PAX5	NM_001280547	1-5	1-604	1-202

PIM1	NM_001243186	1-6	1-91, 210-328, 336-355, 365-466, 475-538, 603-1215	1-31, 70-110, 112-119, 122-156, 159-180, 201-405
PLCG2	NM_002661	15-19, 23	1468-1708, 1734-2224, 2515-2581	490-570, 578-742, 839-861
PRDM1	NM_001198	1-7	8-1097, 1136-1388, 1468-2007, 2093-2478	3-366, 379-463, 490-669, 698-826
PTEN	NM_000314	1-9	1-427, 493-625, 635-801, 824-888, 954-1114	1-143, 165-209, 212-267, 275-296, 318-372
PTPRD	NM_001040712	19-30	2841-4509	947-1503
SGK1	NM_001143676	1-14	1-1581	1-527
SOCS1	NM_003745	1	47-176, 243-447, 466-636	16-59, 81-149, 156-212
STAT6	NM_003153	2, 6-14, 16, 21	172-255, 532-599, 710-1616, 1892-1955, 2417-2504	58-85, 178-200, 237-539, 631-652, 806-835
TBL1XR1	NM_024665	1-14	43-767, 820-1122, 1145-1545	15-256, 274-374, 382-515
TMEM30A	NM_018247	1-7	1-345, 366-661, 686-1008	1-115, 122-221, 229-336
TNFAIP3	NM_001270507	1-8	1-548, 635-1320, 1338-1812, 1858-2297	1-183, 212-440, 446-604, 620-766
TNFRSF14	NM_001297605	1-6	1-555	1-185
TP53	NM_000546	1, 3-10	1-73, 97-1182	1-25, 33-394
ZEB2	NM_014795	1-9	1-257, 332-2440, 2545-3645	1-86, 111-814, 849-1215
ZFAT	NM_001029939	1-15	1-1556, 1577-3495, 3600-3696	1-519, 526-1165, 1200-1232

Panel characteristics

General: The overview table above shows genomic information of sequenced regions with an average read depth of >100 reads based on a random selected set of FFPE based samples. Variants can be detected with an allele frequency of >0.1 (10%) depending on the variant type, sequence context, sample DNA quality and quantity and amplicon read-depth. The applied technique is less suitable for detection of large exon spanning insertions/deletions. Rare variants in repetitive (homopolymer) regions can be missed. If the tumor cell percentage is < 30%, the analysis is less reliable. The intron-exon boundaries are generally covered (+/-5 bp) if a complete exon is sequenced.

For the panel-relevant genes and/or chromosomal regions copy-number variations (CNV), such as amplification/gain and deletions, and loss of heterozygosity (LOH) are determined. LOH is assessed based on informative heterozygous SNPs (if any) and/or the variant allele frequency (VAF) of the reported variant.