Gen	*Chromosoom regio*	*Type afwijking**	*Startpositie*	*Eindpositie*	*Bron**	*Ziekte**	*Evidence**
FAF1	1p32.3	loss	50906935	51425936	1,2	MM	1
CDKN2C	1p32.3	loss	51434366	51440309	1,2	MM	1
BCL10	1p22.3	t(1;14)	85731459	85742587	5	Ly, MALT	1
MTF2	1p22.1	loss	93544792	93604638	1,2	MM	2
TMED5	1p22.1	loss	93615299	93646246	1,2	MM	2
FAM46C	1p12	loss	118148604	118171011	1,2	MM	1
CKS1B	1q21.3	gain	154947118	154951725	1,2	MM	1
MYCN	2p24.3	gain	16080559	16087129	2,7	CLL	1
ALK	2p23.2	t(2;17), t(2;5)	29415639	30144477	4,5	LY, ALK+DLBCL, ALCL	1
REL	2p16.1	gain	61108629	61155291	2,7	CLL	2
XPO1	2p15	mutation	61705070	61765418	7	CLL	2
CXCR4	2q22.1	mutation	136871918	136875725	5	LPL	1
SF3B1	2q33.1	mutation	198256700	198299771	7	CLL	1
MYD88	3p22.2	mutation	38179969	38184510	7	CLL,LPL	1
SETD2	3p21.31	loss, cth	47057897	47205467	6,7	CLL	1
FOXP1	3p13	t(3;14)	71003864	71633140	5	Ly, MALT	1
BCL6	3q27.3	t(3;14),t(2;3),t(3;22), 3q27rearrangement	187439164	187463513	4,5	Ly, FL,DLBCL	1
TP63	3q28	rearrangement	189349215	189615068	10	ALK-ALCL	1
FGFR3	4p16.3	t(4;14)	1795039	1810599	1,3,4	MM	1
WHSC1	4p16.3	t(4;14)	1873123	1983934	1,5	MM	1
NPM1	5q35.1	t(2;5)	170814707	170837888	4,5	LY, ALK+DLBCL, ALCL	1
DUSP22	6p25.3	t(6;7)	292056	351355	4	ALCL	1

Gen	*Chromosoom regio*	*Type afwijking**	*Startpositie*	*Eindpositie*	*Bron**	*Ziekte**	*Evidence**
IRF4	6p25.3	t(6;7)	391738	411443	4	ALCL	1
CCND3	6p21.1	t(6;14)	41902671	42016610	1,3,5	MM	1
FOXO3	6q21	loss	108881025	109005971	7	CLL	2
POT1	7q31.33	mutation	124462439	124570037	7	CLL	2
BRAF	7q34	mutation	140433812	140624564	5	HCL	1
TRIM35	8p21.2	loss	27142402	27168836	7	CLL	2
MYC	8q24.21	Focal gain, t(8;14), t(2;8),t(8;22)	128748314	128753680	1,2,3,4,5,7	CLL, MM,Ly,BL,DLBCL,FL	2
PVT1	8q24.21	focal gain	128806778	129113499	1,2	MM	2
MAFA	8q24.3	t(8;14)	144510229	144512602	5	MM	1
NOTCH1	9q34.3	mutation	139388884	139440238	7	CLL	1
PTEN	10q23.31	loss	89623194	89731687	3	MM	1
PIK3A	10q24.1	gain	98353068	98480279	2	CLL	2
CCND1	11q13.3	t(11;14), t(2;11),t(11;22)	69455873	69469242	1,3,4,5	MM,Ly,MCL	1
MRE11A	11q21	loss	94150468	94227040	7	CLL	2
BIRC3	11q22.2	loss, CNLOH, t(11;18)	102188193	102210135	2,5,7	CLL,Ly,MZL	1
ATM	11q22.3	loss, CNLOH	108093558	108239826	2,7	CLL	1
H2AFX	11q23.3	loss	118964584	118966177	7	CLL	2
CCND2	12p13.32	t(12;14)	4382901	4414522	5	MM,Ly,MCL	1
RB1	13q14.2	loss	48877883	49056026	1,2,3,5,7	MM, CLL	1
DLEU regio	13q14.2q14.3	loss	50456688	51417885	2,7	CLL	1
TGDS	13q32.1	loss	95226307	95248529	3	MM	1

Gen	*Chromosoom regio*	*Type afwijking**	*Startpositie*	*Eindpositie*	*Bron**	*Ziekte**	*Evidence**
TCL1A	14q32.13	rearrangement	96176305	96180533	5	T-PLL	1
TCL1B	14q32.13	rearrangement	96152755	96158980	5	T-PLL	1
MGA	15q15.1	loss	41952610	42062141	2,7	CLL	2
MAF	16q23.2	loss,t(14;16)	79627744	79634622	1,3,4,5	MM	1
TP53	17p13.1	loss/CNLOH, mutatie	7571719	7590868	1,2,4,5,7,8,9	MM, CLL, HCL,LPL,FL	1
CLTC	17q23.1	t(2;17)	57697049	57774317	4,5	LY, ALK+DLBCL	1
MALT1	18q21.32	t(11;18), t(14;18)	56338617	56417371	5	LY, MZL	1
BCL2	18q21.33	t(14;18),t(2;18),t(18;22)	60790578	60986613	4,5	LY, FL, DLBCL	1
MAFB	20q12	t(14;20)	39314516	39317876	1,3,4,5	MM	1
PRAME	22q11.22	gain	22890117	22901768	3	MM	1

Type afwijking:

Bij genen waarbij als type afwijking “CNLOH” of “mutatie” staat kan je ook “deletie” lezen en het betreffende gen in de brief opnemen.

Bron:
1= genenlijst **WHGD** landelijk 2017
2 = artikel **Schoumans** et al., Guidelines for genomic array analysis in acquired haematological neoplastic disorders, **Genes, Chromosomes&Cancer 2016**
3= artikel **Pugh** et al., Assessing genome-wide copy number aberrations and copy-neutral loss-of-heterozygosity as best practice: An evidence-based review from the Cancer Genomics Consortium (CGC) working group for plasma cell disorders, **cancer genetics 2018**
4= artikel **Rack** et al., European recommandations and quality assurance for cytogenomic analysis of haematological neoplasm, **Leukemia 2019**
5= WHO Classification of tumours of haematopoietic and lymphoid tissues, Swerdlow et al., revised 4th edition 2017
6= artikel **Parker** et al., Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia, **Leukemia** 2016
7= artikel **Chun** et al., Assessing copy number aberrations and copy-neutral loss-of-heterozygosity across the genome as best practice: An evidence-based review from the Cancer Genomics Consortium (CGC) working group for chronic lymphocytic leukemia, **cancer genetics 2018**
8= Advani et al; doi: 10.1016/j.hemonc.2019.05.002
9= Poulain et al; doi: 10.1158/1078-0432.CCR-17-0007)
10= Genomic Quality Assessment (GenQA)

Ziekte: **MM** = plasma cell neoplasm; **CLL** = chronische lymphocytische Leukemie; **HCL** = Hairy cell leukemie; **LPL** = lymoplasmacytair lymfoom; **LY** = Lymfoom. **MCL**= mantel cel lymfoom, **BL**= Burkitt lymfoom, **FL**= folliculair lymfoom, **DLBCL**= diffuus grootcellig B-cel lymfoom, **ALCL**= anaplastisch large cell lymfoma, **MZL**= marginale zone lymfoma, **MALT=** Extranodaal marginale zone lymfoma

Evidence: 1)present in WHO classification 2)recurrent (>5 cases for CNV en >2 for CNLOH in well-powered studies with expert consensus)