cancers

Supplementary Materials: The Dynamics of Nucleotide Variants in the Progression from Low–Intermediate Myeloma Precursor Conditions to Multiple Myeloma: Studying Serial Samples with a Targeted Sequencing Approach

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Table S1. Percentage of PCs in the precursor BM smears. For each patient, the start precursor phase, the total number of serial precursor samples and the percentage of PCs in the BM smears chronologically ordered were indicated.

Patient	Precursor Stage	Number of Serial Precursor Samples	% PCs in BM Smear, Chronologically over Time
			Precursor Phase
1	MGUS	1	6
2	SMM	1	12
3	MGUS	2	3–1
4	MGUS	1	5
5	MGUS	1	5
6	SMM	1	12
7	MGUS	1	3
8	MGUS	2	4–2
9	MGUS	1	4
10	MGUS	2	6–9
11	MGUS	1	3
12	MGUS*	5	6–9–17–8–12
13	MGUS	1	5
14	MGUS*	6	6–6–10–12–17–16
15	MGUS*	5	12–12–8–13–19
16	MGUS*	3	7–12–30
17	MGUS	4	5–8–7–12
18	MGUS*	2	9–19
19	MGUS	1	5
20	MGUS*	5	6–3–3–4–10
21	MGUS	1	1

US: Variant PC: plasma cells; BM: bone marrow.

Table S2. Detailed overview of the 29 identified variants. A total of 29 variants were detected in 20 different genes. Each identified somatic variant was annotated and classified as Pathogenic, Likely Pathogenic or Variant of Unknown Significance, according to the Belgian guidelines[1]. For each variant, the location (chromosome and coordinate) and HGVS coding and protein sequence name was showed.

Gene	Classification	HGVSc	HGVSp	Chr	Coordinate
ARID2	LIKELYPATHOGENIC	NM_152641.2:c.3410C > A	NP_689854.2:p.Ser1137Ter	12	46245316
BCL7A	US	NM_020993.3:c.36C > A	NP_066273.1:p.Ser12Arg	12	122460033
BCL7A	US	NM_020993.3:c.74T > C	NP_066273.1:p.Ile25Thr	12	122460071
BRAF	LIKELYPATHOGENIC	NM_004333.4:c.1780G > A	NP_004324.2:p.Asp594Asn	7	140453155
DIS3	US	NM_014953.3:c.1663_1668delGTGGAC	NP_055768.3:p.Val555_Asp556del	13	73345220
DNMT3A	LIKELYPATHOGENIC	NM_175629.2:c.939G > A	NP_783328.1:p.Trp313Ter	2	25470535
FAM46C	US	NM_017709.3:c.275A > G	NP_060179.2:p.Asp92Gly	1	118165765
FAM46C	LIKELYPATHOGENIC	NM_017709.3:c.584_585delAT	NP_060179.2:p.Tyr195Ter	1	118166072
HIST1H1D	LIKELYPATHOGENIC	NM_005320.2:c.556G > A	NP_005311.1:p.Ala186Thr	6	26234606
HIST1H1E	US	NM_005321.2:c.139G > A	NP_005312.1:p.Ala47Thr	6	26156757
IDH1	US	NM_005896.2:c.940C > T	NP_005887.2:p.Arg314Cys	2	209104638
IKBKB	US	NM_001556.2:c.2033C > G	NP_001547.1:p.Ala678Gly	8	42183534
IRF4	US	NM_002460.3:c.316G > T	NP_002451.2:p.Asp106Tyr	6	394920
KRAS	PATHOGENIC	NM_033360.2:c.38G > A	NP_203524.1:p.Gly13Asp	12	25398281
KRAS	PATHOGENIC	NM_033360.2:c.35G > A	NP_203524.1:p.Gly12Asp	12	25398284
KRAS	PATHOGENIC	NM_033360.2:c.436G > A	NP_203524.1:p.Ala146Thr	12	25378562
KRAS	LIKELYPATHOGENIC	NM_033360.2:c.176C > A	NP_203524.1:p.Ala59Glu	12	25380282
KRAS	PATHOGENIC	NM_033360.2:c.38G > A	NP_203524.1:p.Gly13Asp	12	25398281
KRAS	PATHOGENIC	NM_033360.2:c.35G > A	NP_203524.1:p.Gly12Asp	12	25398284
MAX	US	NM_002382.4:c.312G > T	NP_002373.3:p.Lys104Asn	14	65543365
NRAS	PATHOGENIC	NM_002524.4:c.35G > C	NP_002515.1:p.Gly12Ala	1	115258747
NRAS	PATHOGENIC	NM_002524.4:c.181C > A	NP_002515.1:p.Gln61Lys	1	115256530
PTPN11	LIKELYPATHOGENIC	NM_002834.3:c.1520C > A	NP_002825.3:p.Thr507Lys	12	112926900
PTPN11	LIKELYPATHOGENIC	NM_002834.3:c.181G > A	NP_002825.3:p.Asp61Asn	12	112888165
RASA2	US	NM_006506.2:c.622_626delAAGAA	NP_006497.2:p.Lys208AspfsTer13	3	141274689
SETD2	LIKELYPATHOGENIC	NM_014159.6:c.4667_4670delTCAC	NP_054878.5:p.Leu1556GlnfsTer8	3	47155410
SP140	US	NM_007237.4:c.265G > A	NP_009168.4:p.Val89Ile	2	231102955
TP53	LIKELYPATHOGENIC	NM_000546.5:c.574C > T	NP_000537.3:p.Gln192Ter	17	7578275
XBP1	US	NM_001079539.1:c.11T > C	NP_001073007.1:p.Val4Ala	22	29196502

US: Variant of Unknown Significance; HGVSc: Human Genome Variation Society coding; HGVSp: Human Genome Variation Society protein; Chr: Chromosome.

References

1. Froyen, G.; Le Mercier, M.; Lierman, E.; Vandepoele, K.; Nollet, F.; Boone, E.; Van der Meulen, J.; Jacobs, K.; Lambin, S.; Vander Borght, S.; et al. Standardization of Somatic Variant Classifications in Solid and Haematological Tumours by a Two-Level Approach of Biological and Clinical Classes: An Initiative of the Belgian ComPerMed Expert Panel. *Cancers* **2019**, *11*, 2030, doi:10.3390/cancers11122030.