RMMG
Revista Médica de Minas Gerais

REVIEW ARTICLE

Using new generation sequencing for multiple myeloma prognosis: scoping review

Sequenciamento de nova geração para prognóstico de mieloma múltiplo: revisão de escopo

Leonardo Assad Lomonaco[1], Thereza Cristina Picado Pinheiro[1], Thainá Souza Ribeiro[1], Ildercílio Mota de Souza Lima[2], Jeniffer Dantas Ferreira[1]

ABSTRACT

Introduction: The next generation sequencing (NGS) approaches identify multiple myeloma (MM) precursor disease that will progress before major clonal expansion. **Objective:** To synthesize the scientific evidence on the use of next-generation sequencing panels for the prognosis of individuals with multiple myeloma. **Method**: This is a scoping review carried out on three databases between 2011 and 2023. Included studies met one of these criteria: (1) described the role of NGS on the genetic structure of MM; (2) delineated clonal evolution; (3) described prognostic factors and (4) revealed new treatment protocols for MM. **Results:** This search yielded 572 abstracts, with 69 studies eligible for inclusion. For MM, genetic changes involving the MAPK pathway, NAFkB pathway, DIS3, FAM46C, MYC, IRF4, TRAF3, TP53, CCND1, CYLD were the main ones identified by NGS techniques. Progression to symptomatic disease was related to changes in MYC, TP53 and copy number changes (1q+, 1q-, del 17p). As for prognosis, TP53 was identified both for mutations and losses. By expanding the identification of cytogenetic alterations, NGS can contribute to the most promising initial therapy. Studies with therapeutic protocols involving BRAF inhibitors and MAPK pathway inhibitors were identified. **Conclusion:** This scoping review offers insight into the use of next-generation sequencing for multiple myeloma prognosis. After understanding the evolution of the disease, prognosis and treatment, the NGS panel should include translocations at the IGH locus, hyperdiploidy, del(17p), accompanied by the biallelic mutation of TP53, an expression of APOBECs, MYC, N-RAS and K-RAS genes.

Keywords: Multiple myeloma; High throughput nucleotide sequencing; Prognosis; Scoping review.

[1] Centro de Ciências da Saúde e do Esporte (CCSD), Universidade Federal do Acre (UFAC), Rio Branco, Acre, Brazil.

[2] Instituto de Patologia Tropical e Saúde Pública (IPTSP), Universidade Federal de Goiás (UFG), Goiânia, Goiás, Brazil.

Associate Editor Responsible:
Geraldo Felício da Cunha Júnior
Cetus Oncologia - Unidade Belo Horizonte, CETUS, Brasil.
Belo Horizonte/MG, Brazil.

Corresponding Author:
Leonardo Assad Lomonaco
E-mail: leonardo.lomonaco@ufac.br

Supporting Sources:
This research did not receive any specific grant from funding agencies in the public, commercial or not-for-profit sectors

Conflicts of Interests:
None

RESUMO

Introdução: O uso do sequenciamento de nova geração (NGS) identifica as alterações precursoras do mieloma múltiplo (MM) e sua progressão mesmo antes da expansão clonal significativa. **Objetivo:** Sintetizar as evidências científicas do uso de painéis de sequenciamento de nova geração para o prognóstico de indivíduos com mieloma múltiplo. **Método:** Trata-se de uma revisão de escopo procedida em três bases de dados no período entre 2011 e 2023. Os estudos incluídos atenderam a um dos seguintes critérios: (1) descreveram o papel do NGS na estrutura genética do MM; (2) na evolução clonal; (3) fatores prognósticos e (4) novos protocolos de tratamento para MM. **Resultados:** Foram identificados 572 resumos, sendo 69 estudos elegíveis para a inclusão. Para o MM, as principais alterações genéticas envolvendo a via MAPK, via NAFkB, DIS3, FAM46C, MYC, IRF4, TRAF3, TP53, CCND1 e CYLD foram identificadas pelas técnicas de NGS. A progressão para doença sintomática esteve relacionada a alterações em MYC, TP53 e alterações no número de cópias (1q+, 1q-, del 17p). E, relacionada ao prognóstico estava o TP53, tanto em mutações quanto em perdas. Ao ampliar a identificação de alterações citogenéticas, o NGS pode contribuir para a terapia inicial mais promissora. Foram identificados estudos com protocolos terapêuticos inibidores de BRAF e inibidores da via MAPK. **Conclusão:** Esta revisão de escopo oferece esclarecimentos sobre o uso do sequenciamento de nova geração para o prognóstico do mieloma múltiplo. Para melhor compreender a evolução da doença, o prognóstico e o tratamento, o painel do NGS deve incluir translocações no locus IGH, hiperdiploidia, del(17p), acompanhadas pela mutação bialélica de TP53, expressão dos genes APOBECs, MYC, N-RAS e K-RAS.

Palavras-chave: Mieloma múltiplo; Sequenciamento de nucleotídeos em larga escala; Prognóstico; Revisão de escopo.

Ethics Committee:
The manuscript is based on the doctoral thesis, entitled "Epidemiological profile, molecular markers and survival analysis of individuals with multiple myeloma treated at a reference hospital in Western Amazonia", submitted to the Research Ethics Committee of the Federal University of Acre, and approved under opinion number: 7,347,230 (CAAE: 81166424.3.0000.5010)

Received on: April 25th, 2025
Approved on: August 30th, 2025
Publication Date: January 9th, 2026.

DOI: 10.5935/2238-3182.2025e35207-en

Introduction

Multiple Myeloma (MM) is a cancer of the plasma cell, resulting from the rise of malignant clonal and several subclones in the bone marrow, and the production of monoclonal immunoglobulin with lesions in target organs and lytic lesions[1,2].

Although new drugs have been introduced, the prognosis of MM is worse than that of other hematologic malignancies. Cytogenetic changes can affect disease progression and overall survival, and their identification provides an important target for more specific and effective therapies[3-7]. In this sense, Next Generation Sequencing (NGS) is a technique that has the potential to identify the precursor disease of myeloma even before expansion and clonal progression[2,6,8] due to the sequencing of millions of DNA and RNA fragments simultaneously and on a large scale, being able to detect more variants than fluorescence in situ hybridization (FISH).

However, FISH is a technique elected for Revised International Staging System (R-ISS) classification and is high risk due to the presence of del(17p) and/or translocation t(4;14) and/or translocation t(14;16), which should be performed. It should be noted that the International Myeloma Society recently recommends the genomic staging consensus in which the NGS panel was used to identify the TP53 mutation and del (1p32) as criteria for defining high-risk MM given the impact of these alterations on the prognosis of individuals[9].

Methods

Type of study

This is a scoping review which, through a systematic approach, identifies scientific evidence and summarizes the main concepts and remaining gaps on the topic[10,11]. It was conducted according to the recommendations of the international guide Preferred Reporting Items for Systematic

Reviews and Meta-Analyses Extension for Scoping Reviews (PRISMA-ScR)[12]. This protocol was registered on Open Science Framework (OSF), link: https://osf.io/d6j7h[13].

Search strategy

The Population, Concept and Context strategy was adopted to formulate the guiding question "what is the clinical relevance of using high-throughput nucleotide sequencing for the prognosis of individuals newly diagnosed with multiple myeloma?" Population - individuals newly diagnosed with multiple myeloma; Concept - high-throughput nucleotide sequencing; and Context - prognosis. The controlled vocabulary of the Medical Subject Headings (Mesh) and Health Sciences Descriptors (DeCS) databases were combined, covering all fields in the query box (Table 1).

The search for articles was carried out between January 15th and 20th, 2024, on the Medline database via PubMed, and Embase via Cochrane and Science Direct.

Eligibility and exclusion criteria

Observational, experimental and review studies were included in this investigation, published from 2011 to 2023, in English, Portuguese or Spanish, fully available. Publications that did not meet the research aim, were unrelated to the characterization of MM by NGS or were previously treated, relapses, minimal residual disease and laboratory animal studies were excluded. Book chapters, theses, dissertations, editorials and letters to the editor were excluded as well.

Screening and data extraction

The findings on the year of publication, authorship, periodical, type of study and title were cataloged and stored on spreadsheets in chronological order, by database. The selection of publications by title and abstract was carried out by pairs, separately, after excluding duplicates, following the PRISMA-ScR procedure, facilitating the extraction of the objectives, design, setting, population and outcomes of the studies.

Results

Search Procedure

The search strategy identified 572 publications and, additionally, 40 articles that were included through reference scanning (N=612) cited in the articles found. After removing the duplicate (N=1), 611 remained for evaluation of titles and abstracts. 517 failed to meet the inclusion criteria and 94 articles were selected for full reading. Of these, 24 were excluded for being out of scope, as well as 1 book chapter. Finally, 69 studies were included (Figure 1).

Description of publications

Literature mapping on NGS approaches to MM identified 69 publications, mainly carried out in multicenter institutes. It was composed of review studies (N=26), cohort study studies (N=28), cross-sectional studies (N=10), case reports (N=3) and case-control studies (N=2), published from 2011 to 2023 (Supplementary Box 2).

Table 1. Search strategy in databases according to the population, concept, context framework for scoping review.

Population	"Multiple myeloma" OR "Multiple Myelomas" OR "Myeloma, Multiple" OR "Myeloma, Plasma-Cell" OR "Myeloma, Plasma Cell" OR "Myelomas, Plasma-Cell" OR "Plasma-Cell Myeloma" OR "Plasma-Cell Myelomas" OR "Myelomatosis" OR "Myelomatoses" OR "Plasma Cell Myeloma" OR "Cell Myeloma, Plasma" OR "Myelomas, Plasma Cell" OR "Plasma Cell Myelomas" OR "Kahler Disease" OR "Myeloma-Multiple" OR "Myeloma Multiple" NOT "Neoplasm, Residual" OR "Residual Neoplasms" OR "Residual Neoplasm" OR "Minimal Residual Disease" OR "Minimal Disease, Residual" OR "Residual Minimal Disease" OR "Residual Minimal Diseases" OR "Residual Disease, Minimal" OR "Minimal Residual Diseases" OR "Residual Cancer" OR "Cancer, Residual" OR "Residual Cancers" OR "Residual Tumor" OR "Residual Tumors" OR "Residual Tumour" OR "Residual Tumours" OR "Tumour, Residual"
Concepts	"High Throughput Nucleotide Sequencing" OR "Next-Generation Sequencing" OR "Next Generation Sequencing" OR "Sequencing, Next-Generation" OR "Illumina Sequencing" OR "Sequencing, Illumina" OR "Ion Torrent Sequencing" OR "Sequencing, Ion Torrent" OR "Ion Proton Sequencing" OR "Sequencing, Ion Proton" OR "Deep Sequencing" OR "Sequencing, Deep" OR "High-Throughput RNA Sequencing" OR "High Throughput RNA Sequencing" OR "RNA Sequencing, High-Throughput" OR "Sequencing, High-Throughput RNA" OR "Massively-Parallel Sequencing" OR "Massively Parallel Sequencing" OR "Sequencing, Massively-Parallel" OR "Pyrosequencing" OR "High-Throughput Sequencing" OR "High Throughput Sequencing" OR "Sequencing, High-Throughput" OR "High-Throughput DNA Sequencing" OR "DNA Sequencing, High-Throughput" OR "High Throughput DNA Sequencing" OR "Sequencing, High-Throughput DNA"
Context	"Prognosis" OR "Prognoses" OR "Prognostic Factors" OR "Prognostic Factor" OR "Factor, Prognostic" OR "Factors, Prognostic"

Source: Health Sciences Descriptors (DeCS) and Medical Subject Headings (MeSH), 2024.

Discussion

Next Generation Sequencing

Conventional cytogenetic analysis and FISH promoted greater understanding of MM genetics, with detection of alterations being around 40%-50%. While karyotyping detects hypo- or hyperdiploidy, FISH performed on plasma cells from bone marrow samples identifies rearrangements relevant to MM. However, the plasma cell does not have a sufficient mitotic index for the test to be performed effectively[8]. The FISH technique uses specific probes for the target in question, but cannot identify other abnormalities and is not very sensitive in situations of low cellular expression[14–16]. Other sensitive techniques for identifying genetic abnormalities have emerged in recent decades, such as NGS and Gene Expression Profiles (GEP), advancing the genomics of patients with MM, identifying patients at high risk of progression to symptomatic disease and enabling new prognostic assessments and better treatment strategies[6,17–21].

It is pertinent to mention that the quality of the samples for the examination is determinative and the pre-analytical phase requires a team trained in collecting material and its appropriate interpretation[22–27]. The bone marrow samples should be collected in sodium heparin tubes, since the use of heparin does not inhibit cell growth or interfere with cell distortion, which are conditions for the correct interpretation of results in molecular analysis.

Genomic structure and clonal evolution of Multiple Myeloma

MM evolves from an indolent condition called monoclonal gammopathy of undetermined significance (MGUS), characterized by medullary infiltration below 10% of nucleated cells in the bone marrow, but already presenting primary genetic changes because of chromosomal instability acquired by plasma cells[1,7,28]. Hyperdiploidy and translocations involving the IGH gene (chromosome 14, 14p32) are the most common changes found at this stage of the disease, with hypodiploidy and pseudodiploidy being rare. Translocation t(11;14) is the most common, responsible for the increased expression of CCND1(11q13) while t(6;14) promotes overexpression of CCND3(6p21). Other recurrent translocations are t(4;14) (4p16, FGFR3/MMSET), t(14;16) (16q23, MAF), and t(14;20) (20q11, MAFB)[28].

With the evolution of the initial clonal stage of MM, secondary cytogenetic acquisitions arise[1,21,29], including changes in copy number (genomic gains or losses) and other translocations, changes in 1q+ (gain), 1p deletions, changes in MYC, 17p deletion, in a multiple-step process[3]. The cytogenetic analysis of symptomatic and asymptomatic individuals shows minimal differences. However, when people present t(14;20), del(17p) and 1p-, even in the asymptomatic stages, these changes are associated with faster progression to symptomatic myeloma, in addition to worsening overall survival and event-free survival[30–32]. Thus, the Revised Multiple Myeloma Staging System (R-ISS) score incorporated laboratory markers (Beta2-microglobulin, serum LDH and adverse cytogenetic markers like del(17p), t(4,14), t(14,16))[33,34]. A Whole Genome Sequencing associated with RNA-seq proved to be highly sensitive for the diagnosis of MM and its risk stratification[35,36].

Scales et al. (2017)[37] analyzed 513 patients with MM and 1,500 controls investigating if rare proteins and KIF18A could be related to the development of MM, with the appearance of a predominant clone and several associated and/or emerging subclones throughout the disease process[31,38–40].

Kim et al. (2021)[41] showed an overexpression of IGHV3-9, IGHV4-31 and IGHD3-3 and a decrease in IGKV4-1, different from what is seen in Western populations, suggesting that environmental factors may interfere with genomic expression. Another study compared the population of African Americans (AA) with Caucasian Americans (CA) and demonstrated that t(4;14) was common in the AA group (29%) and that mutations in TP53 were more common in CA, but there was no statistical difference between them[42]. Manojlovic et al. (2017)[43] also compared AA and CA and observed that mutations in the BCL7A, BRWD3 and AUTS2 genes were frequent among AA cases and that mutations in TP53 and IRF4 were more common in CA.

A study conducted by Jiménez et al. (2016)[15] evaluated 48 patients newly diagnosed with MM, using FISH and NGS techniques. Translocations involving the IGH gene were observed in 17 patients; three patients with t(4;14), eight patients with t(11;14), two patients with t(14;16) and four with 14q32 involvement, but without corresponding translocation. However, it was still possible to identify eight translocations not previously identified through FISH. Translocations involving chromosome 8 (MYC gene) were found in four of these samples. The analysis of NRAS, KRAS, HRAS, TP53, MYC and BRAF found changes in 33%, being 15% in NRAS, 15% in KRAS, 4% in TP53 (one case concomitantly harbored a TP53 deletion) and 2% in MYC. RAS pathway activating mutations were frequent in 29% and mutually exclusive[15].

A North American study analyzed cytogenetic abnormalities in 142 untreated patients using FISH, with 52% of patients having hyperdiploidy, 41% of patients with del(13q), 26% with t(11;14), 15% with del(17p), 10% with t(4;14) and 3% with t(14;16). Subsequently, using NGS techniques, it was observed that 75.4% of patients had at least one mutation and that approximately 61% of the genes analyzed in the panel were mutated. The main mutated genes were KRAS (24%), NRAS (17%), DIS3 (14%), TRAF3 (11%), BRAF (9%), TP53 (9%), FAM46C (8%) and CYLD (5%)[22].

Prognosis

Despite the cytogenetic complexity of MM, the mutations described above are recurrent[1,2,37] and serve as targets for the prognostic evaluation of these patients.

R-ISS is a prognostic score used in the diagnosis of multiple myeloma that includes laboratory characteristics and specific genetic alterations, including t(4;14), t(14;16), or del(17p) detected by FISH, whose presence confers a higher risk of the disease. Other laboratory evaluations, such as circulating plasma cell counts before and after treatment and minimal residual disease testing after treatment, are relevant in prognostic prospecting, as they can indicate whether the MM was sensitive to the therapy used[39,44–46]. In the literature consulted, the use of NGS techniques allowed the identification of a greater variety of genetic alterations in MM[47], but their applicability in clinical practice still requires validation.

Mutations in the MAPK pathway genes (KRAS, NRAS, BRAF) are frequently reported by NGS studies, without being important in survival or disease-free progression[28,48]. Kortuem et al. (2016)[22] observed 20% of mutation frequency in the NFkB pathway and 11% in the cyclin D1 gene (CCND1). In addition, it was suggested that the impact on disease-free time and survival was related to the STAT3 activation pathway, but in two patients there were other mutations associated with t(4;14) and del(17p)[22].

The MYC genes are frequently mutated in symptomatic patients with MM and both NGS and FISH techniques detect MYC variants, with NGS showing a higher frequency of mutational discoveries for this gene[4]. These MYC mutations imply a reduction in the time to progression to symptomatic disease as a result of the clonal evolution present in MM, which shows some similarity with the tumor growth of adenocarcinomas when associated with mutations in the K-RAS pathway[3,18,43,49]. However, their impact on survival remains unclear.

Although translocations of the Immunoglobulin (Ig) gene have a positive impact on survival[50], cases where the MYC alteration results from insertions originating from Ig genes, mainly the generation of lambda chain immunoglobulin gene, present in chromosome 22, suggest a poor prognosis[4]. Foltz et al. (2020)[51] observed that this is probably a consequence of impairment of the PVT1 generation, which is close to the MYC generation and would lead to the loss of its regulation and an impact on survival. These comments are also presented in regulatory, non-coding regions close to the PAX5 gene, but does not predict prognosis[36].

Walker et al. (2015)[48] analyzed 463 patients recently diagnosed with symptomatic MM and observed that CCND1, p53 and del(17p) mutations presented worse overall survival, as well as the ATM and ATR gene mutations. The ZFHX4 gene mutations were also associated with worse progression-free survival. However, mutations in the EGR1 and IRF4 genes showed better results in overall survival and progression-free survival[48].

NGS is also more accurate in identifying mutations in TP53 and APOBECs[5,44,45,52], which have been shown to be relevant prognostic conditions, especially for alterations in TP53. Deletions on the short arm of chromosome 17 have been linked to early relapses and a negative impact on the survival (overall or event-free) of patients due to the loss of expression of TP53[34,53]. NGS analyses demonstrate that mutations in the structure of p53 gene, or chromosomal losses at diagnosis are rare, but reflect on survival and become a point of interest in the evaluation of patients with MM[28,54–58].

Walker et al. (2019)[59] described the presence of the CKS1B amplification in patients classified as ISS stage III; while patients with a biallelic p53 mutation were classified with double-HIT MM and included in a high-risk group[59]. Corre et al. (2021)[60] compared the impact on survival of del(17p) associated or not with a biallelic mutation in the p53 gene, and the result shows that when the two are associated, survival is lower than when it is demonstrated only with del(17p).

Regarding APOBEC and the development of MM cases, it is observed that, during the initial acquisition of cytogenetic changes (hyperdiploidies and IGH translocations), pre-malignant cells are chronically exposed to AID, a cytidine-deaminase induced by activation presents in the germinal centers. This exposure leads to breaks in the DNA, mainly at the IGH locus, but which can occur in other parts of the genome. Subsequently,

the role of APOBEC emerges, especially APOBEC3B, which appears to be related to the

acquisition of several mutations in previously described genes of patients with MM, including TP53, in addition to being related to shorter survival in cases of MM[29,32,56,61].

Changes in IGLL5, when related to IGH translocation, appear to impact disease progression, but with no impact on survival[53,62]. Sequencing IGH rearrangements proved to be potential prognostic markers for patients. Hypermutation of IGH, as well as mutations in IGHV3, IGHD2 and IGHD3 suggest a satisfactory evolution in patients with MM in a multivariate analysis[62].

Laganà et al. (2018)[63] described mutations in KIF22, ORC6, ATAD5 and TSKU genes, in which the first three are linked to DNA repair processes, a condition that could constitute a high-risk disease. “Signatures” of central genes were also observed in t(4;14) (CDC42BPA CLEC11A), suggesting that they are high-risk patients[63]. Boyle et al. (2022)[54] analyzed telomeres length and showed that the shortening of telomere length in myelomatous cells is related to an adverse prognostic factor[54].

The presence of mutations in the DIS3 gene, in subclones present in MM, is associated with translocations related to IGH, causing the loss of RNA exosome functions, the loss of correct reading, disease progression through MYC overexpression and the loss of p53 regulation and is implicated in poor survival[64,65].

Mutations in KMT2C, KMT2D, EP300 and genes from the ARID family are related to poor prognosis in MM, as well as the expression of AIMP1[66,67]. Esterase gene expression changes as patients progress from newly diagnosed multiple myeloma to relapse/refractory Multiple Myeloma[68]. High expression of OVCA2, PAFAH1B3, USP4 and SIAE, and low expression of PCED1B, are markers of poor prognosis

in MM[56]. Mutation in the CDC27 gene and the PRDM1 gene are involved in the progression of the disease and a possible therapeutic target[69,70].

Therapeutic protocols

One of the possibilities with the use of NGS techniques is the identification of more specific therapeutic protocols for the treatment of patients with MM, according to the genetic alterations detected[71]. Therefore, determining the genetic alterations of disease subclones may lead to more promising initial therapy, also impacting refractory and relapsed patients . Sequencing studies have shown that the initial therapeutic protocol can promote the selection of subclones with a profile resistant to previously used drugs[72,73].

The use of MEK and MAPK pathway inhibitors as monotherapy or associated with other drugs, such as trametinib, was seen in a study with 40 patients that had an overall response rate of 40%. Cobimetinib and vemurafenib have been described in case report articles as active treatment drugs in refractory and relapsed patients, but with different results[71]. Recently, the use of ATM and ATR gene inhibitors, as well as PDL-1 inhibitors, IDH, FGFR3, PARP inhibitors, are being studied[71].

EGR1 and IRF4 mutations are susceptible to the use of immunomodulators, but resistance to bortezomib and appear to be associated with NRAS mutations in relapse[56]. KRAS inhibitors are already a reality in medical practice, being an important target in other malignant neoplasms, and can also be used in MM, as well as tyrosine kinase inhibitors[49,74].

Although NGS has increased the ability to detect genomic aberrations in MM, its validation and routine use in clinical trials has not yet been regulated. NGS and other techniques of deeper analysis of genomic sequencing in the search for therapeutic targets are promising, but several adversities in the use of these medicines are present, many of them related to the variable expression of alleles and proteins that could interfere[52]. The main obstacle to routine clinical use in MM patients is the cost and implementation of NGS techniques. Thus, several panel proposals have already been suggested to classify risk and guide patients' therapy, making them more accessible and bringing expected results.

Conclusion

NGS techniques, in the context of MM diagnosis, prognosis, and treatment, provide significant information about patients' genomic structure and oncogenesis. The ability to identify recurrent mutations was an important step toward understanding the pathways affected in MM development, revealing the complexity of the MM genome and its evolution. Among these, TP53 alterations, both biallelic mutations and associated or unassociated 17p loss, proved to be important in identifying high-risk groups in multiple myeloma patients. Translocations in the IGH locus, hyperdiploidy, and MYC expression were amplified by NGS, in terms of their structures and mutations. Other gene groups, APOBECs, N-RAS, and K-RAS, were more clearly defined in the emergence of MM. Understanding this new information is important for better classification of MM patients and, in the future, for the inclusion of NGS techniques in daily practice. The routine use of the NGS technique as a therapy definer is still imprecise and requires more robust validation.

Authors' Contributions

We describe contributions to the papers using the taxanomy (CRediT) provided above:

LAL, TCPP and TRS collected, analyzed and interpreted the data and wrote the manuscript. IMSM and JDF designed and planned the study, interpreted the data and critically reviewed the manuscript. All authors approved the final version submitted.

Copyright

Copyright© 2025 Lomonaco et al. This is an Open Access article distributed under the terms of the Creative Commons Attribution 4.0 International License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original article is properly cited.

References

1. Castaneda O, Baz R. Multiple Myeloma Genomics – A Concise Review. Acta Medica Acad [Internet]. 2019 Jun 26 [cited 2024 Feb 12];48(1):57. Available from: http://www.ama.ba/index.php/ama/article/view/358

2. Weaver CJ, Tariman JD. Multiple Myeloma Genomics: A Systematic Review. Semin Oncol Nurs [Internet]. 2017 Aug [cited 2024 Feb 12];33(3):237–53. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0749208117300360

3. Sawyer JR. The prognostic significance of cytogenetics and molecular profiling in multiple myeloma. Cancer Genet [Internet]. 2011 Jan [cited 2024 Feb 12];204(1):3–12. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0165460810005649

4. Sharma N, Smadbeck JB, Abdallah N, Zepeda-Mendoza C, Binder M, Pearce KE, et al. The Prognostic Role of *MYC* Structural Variants Identified by NGS and FISH in Multiple Myeloma. Clin Cancer Res [Internet]. 2021 Oct 1 [cited 2023 Sep 5];27(19):5430–9. Available from: https://aacrjournals.org/clincancerres/article/27/19/5430/671722/The-Prognostic-Role-of-MYC-Structural-Variants

5. Soliman AM, Das S, Teoh SL. Next-Generation Biomarkers in Multiple Myeloma: Understanding the Molecular Basis for Potential Use in Diagnosis and Prognosis. Int J Mol Sci [Internet]. 2021 Jul 13 [cited 2024 Feb 13];22(14):7470. Available from: https://www.mdpi.com/1422-0067/22/14/7470

6. Szalat R, Munshi NC. Genomic heterogeneity in multiple myeloma. Curr Opin Genet Dev [Internet]. 2015 Feb [cited 2024 Feb 12];30:56–65. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0959437X15000295

7. Furukawa Y, Kikuchi J. Molecular pathogenesis of multiple myeloma. Int J Clin Oncol [Internet]. 2015 Jun [cited 2024 Feb 12];20(3):413–22. Available from: http://link.springer.com/10.1007/s10147-015-0837-0

8. Pugh TJ, Fink JM, Lu X, Mathew S, Murata-Collins J, Willem P, 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 working group for plasma cell disorders. Cancer Genet [Internet]. 2018 Dec [cited 2024 Feb 12];228–229:184–96. Available from: https://linkinghub.elsevier.com/retrieve/pii/S2210776218300760

9. Avet-Loiseau H, Davies FE, Samur MK, Corre J, D'Agostino M, Kaiser MF, et al. International Myeloma Society/International Myeloma Working Group Consensus Recommendations on the Definition of High-Risk Multiple Myeloma. J Clin Oncol [Internet]. 2025 Jun 9 [cited 2025 Jul 18]; Available from: https://ascopubs.org/doi/10.1200/JCO-24-01893

10. Tricco AC, Lillie E, Zarin W, O'Brien K, Colquhoun H, Kastner M, et al. A scoping review on the conduct and reporting of scoping reviews. BMC Med Res Methodol [Internet]. 2016 Dec [cited 2024 Feb 19];16(1):15. Available from: http://www.biomedcentral.com/1471-2288/16/15

11. Tricco AC, Lillie E, Zarin W, O'Brien KK, Colquhoun H, Levac D, et al. PRISMA Extension for Scoping Reviews (PRISMA-ScR): Checklist and Explanation. Ann Intern Med [Internet]. 2018 Oct 2 [cited 2024 Feb 19];169(7):467–73. Available from: https://www.acpjournals.org/doi/10.7326/M18-0850

12. Peters MDJ, Marnie C, Tricco AC, Pollock D, Munn Z, Alexander L, et al. Updated methodological guidance for the conduct of scoping reviews. JBI Evid Synth [Internet]. 2020 Oct [cited 2024 Feb 19];18(10):2119–26. Available from: https://journals.lww.com/10.11124/JBIES-20-00167

13. Lomonaco LA, Pinheiro TCP, Ribeiro TS, de Souza Lima IM, Dantas Ferreira J. Using New Generation Sequencing for multiple myeloma prognosis: scoping review [Internet]. 2025 Apr 2. Available from: https://osf.io/d6j7h

14. Ikbal Atli E, Gurkan H, Onur Kirkizlar H, Atli E, Demir S, Yalcintepe S, et al. Pros and cons for fluorescent *in situ* hybridization, karyotyping and next generation sequencing for diagnosis and follow-up of multiple myeloma. Balk J Med Genet [Internet]. 2020 Mar 23 [cited 2024 Feb 12];23(2):59–64. Available from: https://www.sciendo.com/article/10.2478/bjmg-2020-0020

15. Jiménez C, Jara-Acevedo M, Corchete LA, Castillo D, Ordóñez GR, Sarasquete ME, et al. A Next-Generation Sequencing Strategy for Evaluating the Most Common Genetic Abnormalities in Multiple Myeloma. J Mol Diagn [Internet]. 2016 Jan [cited 2024 Feb 12];19(1):99–106. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1525157816301866

16. Maura F, Rustad EH, Boyle EM, Morgan GJ. Reconstructing the evolutionary history of multiple myeloma. Best Pract Res Clin Haematol [Internet]. 2020 Mar [cited 2024 Feb 12];33(1):101145. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1521692620300062

17. Lê GN, Bones J, Coyne M, Bazou D, Dowling P, O'Gorman P, et al. Current and future biomarkers for risk-stratification and treatment personalisation in multiple myeloma. Mol Omics [Internet]. 2019 [cited 2024 Feb 12];15(1):7–20. Available from: http://xlink.rsc.org/?DOI=C8MO00193F

18. Yasuda T, Sanada M, Nishijima D, Kanamori T, Iijima Y, Hattori H, et al. Clinical utility of target capture-based panel sequencing in hematological malignancies: A multicenter feasibility study. Cancer Sci [Internet]. 2020 Sep [cited 2024 Feb 12];111(9):3367–78. Available from: https://onlinelibrary.wiley.com/doi/10.1111/cas.14552

19. Corre J, Avet-Loiseau H. The Impact of Genomics on the Management of Myeloma. J Natl Compr Canc Netw [Internet]. 2011 Oct [cited 2024 Feb 12];9(10):1200–6. Available from: https://jnccn.org/view/journals/jnccn/9/10/article-p1200.xml

20. Mullighan CG. Genome sequencing of lymphoid malignancies. Blood [Internet]. 2013 Dec 5 [cited 2024 Feb 12];122(24):3899–907. Available from: https://ashpublications.org/blood/article/122/24/3899/31948/Genome-sequencing-of-lymphoid-malignancies

21. Settino M, Arbitrio M, Scionti F, Caracciolo D, Agapito G, Tassone P, et al. Identifying prognostic markers for multiple myeloma through integration and analysis of MMRF-CoMMpass data. J Comput Sci [Internet]. 2021 Apr [cited 2024 Feb 12];51:101346. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1877750321000430

22. Kortuem KM, Braggio E, Bruins L, Barrio S, Shi CS, Zhu YX, et al. Panel sequencing for clinically oriented variant screening and copy number detection in 142 untreated multiple myeloma patients. Blood Cancer J [Internet]. 2016 Feb 26 [cited 2024 Feb 12];6(2):e397–e397. Available from: https://www.nature.com/articles/bcj20161

23. Rossi A, Voigtlaender M, Janjetovic S, Thiele B, Alawi M, März M, et al. Mutational landscape reflects the biological continuum of plasma cell dyscrasias. Blood Cancer J [Internet]. 2017 Feb 24 [cited 2024 Feb 12];7(2):e537–e537. Available from: https://www.nature.com/articles/bcj201719

24. Rebmann Chigrinova E, Porret NA, Andres M, Wiedemann G, Banz Y, Legros M, et al. Correlation of plasma cell assessment by phenotypic methods and molecular profiles by NGS in patients with plasma cell dyscrasias. BMC Med Genomics [Internet]. 2022 Sep 23 [cited 2024 Feb 12];15(1):203. Available from: https://bmcmedgenomics.biomedcentral.com/articles/10.1186/s12920-022-01346-1

25. Kis O, Kaedbey R, Chow S, Danesh A, Dowar M, Li T, et al. Circulating tumour DNA sequence analysis as an alternative to multiple myeloma bone marrow aspirates. Nat Commun [Internet]. 2017 May 11 [cited 2024 Feb 12];8(1):15086. Available from: https://www.nature.com/articles/ncomms15086

26. Lin M, Lee PL, Chiu L, Chua C, Ban KHK, Lin AHF, et al. Identification of novel fusion transcripts in multiple myeloma. J Clin Pathol [Internet]. 2018 Aug [cited 2024 Feb 12];71(8):708–12. Available from: http://jcp.bmj.com/lookup/doi/10.1136/jclinpath-2017-204961

27. Sudha P, Ahsan A, Ashby C, Kausar T, Khera A, Kazeroun MH, et al. Myeloma Genome Project Panel is a Comprehensive Targeted Genomics Panel for Molecular Profiling of Patients with Multiple Myeloma. Clin Cancer Res [Internet]. 2022 Jul 1 [cited 2024 Feb 12];28(13):2854–64. Available from: https://aacrjournals.org/clincancerres/article/28/13/2854/704999/Myeloma-Genome-Project-Panel-is-a-Comprehensive

28. Robiou Du Pont S, Cleynen A, Fontan C, Attal M, Munshi N, Corre J, et al. Genomics of Multiple Myeloma. J Clin Oncol [Internet]. 2017 Mar 20 [cited 2024 Feb 12];35(9):963–7. Available from: https://ascopubs.org/doi/10.1200/JCO.2016.70.6705

29. Maura F, Bolli N, Rustad EH, Hultcrantz M, Munshi N, Landgren O. Moving From Cancer Burden to Cancer Genomics for Smoldering Myeloma: A Review. JAMA Oncol [Internet]. 2020 Mar 1 [cited 2024 Feb 12];6(3):425. Available from: https://jamanetwork.com/journals/jamaoncology/fullarticle/2757387

30. Bustoros M, Sklavenitis-Pistofidis R, Park J, Redd R, Zhitomirsky B, Dunford AJ, et al. Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. J Clin Oncol [Internet]. 2020 Jul 20 [cited 2024 Feb 12];38(21):2380–9. Available from: https://ascopubs.org/doi/10.1200/JCO.20.00437

31. Fakhri B, Vij R. Clonal Evolution in Multiple Myeloma. Clin Lymphoma Myeloma Leuk [Internet]. 2016 Aug [cited 2024 Feb 12];16:S130–4. Available from: https://linkinghub.elsevier.com/retrieve/pii/S215226501600080X

32. Maura F, Landgren O, Morgan GJ. Designing Evolutionary-based Interception Strategies to Block the Transition from Precursor Phases to Multiple Myeloma. Clin Cancer Res [Internet]. 2021 Jan 1 [cited 2024 Feb 12];27(1):15–23. Available from: https://aacrjournals.org/clincancerres/article/27/1/15/83403/Designing-Evolutionary-based-Interception

33. Bonello F, Cani L, D'Agostino M. Risk Stratification Before and During Treatment in Newly Diagnosed Multiple Myeloma: From Clinical Trials to the Real-World Setting. Front Oncol [Internet]. 2022 Mar 9 [cited 2024 Feb 12];12:830922. Available from: https://www.frontiersin.org/articles/10.3389/fonc.2022.830922/full

34. Bustoros M, Mouhieddine TH, Detappe A, Ghobrial IM. Established and Novel Prognostic Biomarkers in Multiple Myeloma. 2017;

35. Höllein A, Twardziok SO, Walter W, Hutter S, Baer C, Hernandez-Sanchez JM, et al. The combination of WGS and RNA-Seq is superior to conventional diagnostic tests in multiple myeloma: Ready for prime time? Cancer Genet [Internet]. 2020 Apr [cited 2024 Feb 12];242:15–24. Available from: https://linkinghub.elsevier.com/retrieve/pii/S2210776219305216

36. Hoang PH, Dobbins SE, Cornish AJ, Chubb D, Law PJ, Kaiser M, et al. Whole-genome sequencing of multiple myeloma reveals oncogenic pathways are targeted somatically through multiple mechanisms. Leukemia [Internet]. 2018 Nov [cited 2024 Feb 12];32(11):2459–70. Available from: https://www.nature.com/articles/s41375-018-0103-3

37. Scales M, Chubb D, Dobbins SE, Johnson DC, Li N, Sternberg MJ, et al. Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget [Internet]. 2017 May 30 [cited 2024 Feb 12];8(22):36203–10. Available from: https://www.oncotarget.com/lookup/doi/10.18632/oncotarget.15874

38. Corre J, Munshi N, Avet-Loiseau H. Genetics of multiple myeloma: another heterogeneity level? Blood [Internet]. 2015 Mar 19 [cited 2024 Feb 12];125(12):1870–6. Available from: https://ashpublications.org/blood/article/125/12/1870/33707/Genetics-of-multiple-myeloma-another-heterogeneity

39. Hultcrantz M, Yellapantula V, Rustad EH. Genomic profiling of multiple myeloma: New insights and modern technologies. Best Pract Res Clin Haematol [Internet]. 2020 Mar [cited 2024 Feb 12];33(1):101153. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1521692620300141

40. Liu R, Gao Q, Foltz SM, Fowles JS, Yao L, Wang JT, et al. Co-evolution of tumor and immune cells during progression of multiple myeloma. Nat Commun [Internet]. 2021 May 7 [cited 2024 Feb 12];12(1):2559. Available from: https://www.nature.com/articles/s41467-021-22804-x

41. Kim M, Jeon K, Hutt K, Zlotnicki AM, Kim HJ, Lee J, et al. Immunoglobulin gene rearrangement in Koreans with multiple myeloma: Clonality assessment and repertoire analysis using next-generation sequencing. Bandapalli OR, editor. PLOS ONE [Internet]. 2021 Jun 24 [cited 2024 Feb 12];16(6):e0253541. Available from: https://dx.plos.org/10.1371/journal.pone.0253541

42. Kazandjian D, Hill E, Hultcrantz M, Rustad EH, Yellapantula V, Akhlaghi T, et al. Molecular underpinnings of clinical disparity patterns in African American vs. Caucasian American multiple myeloma patients. Blood Cancer J [Internet]. 2019 Feb 4 [cited 2024 Feb 12];9(2):15. Available from: https://www.nature.com/articles/s41408-019-0177-9

43. Manojlovic Z, Christofferson A, Liang WS, Aldrich J, Washington M, Wong S, et al. Comprehensive molecular profiling of 718 Multiple Myelomas reveals significant differences in mutation frequencies between African and European descent cases. Stojanov P, editor. PLOS Genet [Internet]. 2017 Nov 22 [cited 2024 Feb 12];13(11):e1007087. Available from: https://dx.plos.org/10.1371/journal.pgen.1007087

44. Levin A, Hari P, Dhakal B. Novel biomarkers in multiple myeloma. Transl Res [Internet]. 2018 Nov [cited 2024 Feb 12];201:49–59. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1931524418300860

45. Oberle A, Brandt A, Voigtlaender M, Thiele B, Radloff J, Schulenkorf A, et al. Monitoring multiple myeloma by next-generation sequencing of V(D)J rearrangements from circulating myeloma cells and cell-free myeloma DNA. Haematologica [Internet]. 2017 Jun [cited 2024 Feb 12];102(6):1105–11. Available from: http://www.haematologica.org/lookup/doi/10.3324/haematol.2016.161414

46. Morgan GJ, Kaiser MF. How to use new biology to guide therapy in multiple myeloma. Hematology [Internet]. 2012 Dec 8 [cited 2024 Jul 16];2012(1):342–9. Available from: https://ashpublications.org/hematology/article/2012/1/342/83769/How-to-use-new-biology-to-guide-therapy-in

47. Goldsmith SR, Fiala MA, Dukeman J, Ghobadi A, Stockerl-Goldstein K, Schroeder MA, et al. Next Generation Sequencing-based Validation of the Revised International Staging System for Multiple Myeloma: An Analysis of the MMRF CoMMpass Study. Clin Lymphoma Myeloma Leuk [Internet]. 2019 May [cited 2024 Feb 12];19(5):285–9. Available from: https://linkinghub.elsevier.com/retrieve/pii/S2152265018315246

48. Walker BA, Boyle EM, Wardell CP, Murison A, Begum DB, Dahir NM, et al. Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. J Clin Oncol [Internet]. 2015 Nov 20 [cited 2024 Feb 12];33(33):3911–20. Available from: https://ascopubs.org/doi/10.1200/JCO.2014.59.1503

49. Fan G, Lou L, Song Z, Zhang X, Xiong XF. Targeting mutated GTPase KRAS in tumor therapies. Eur J Med Chem [Internet]. 2021 Dec [cited 2024 Feb 12];226:113816. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0223523421006656

50. Medina A, Jiménez C, Sarasquete ME, González M, Chillón MC, Balanzategui A, et al. Molecular profiling of immunoglobulin heavy-chain gene rearrangements unveils new potential prognostic markers for multiple myeloma patients. Blood Cancer J [Internet]. 2020 Feb 6 [cited 2024 Feb 12];10(2):14. Available from: https://www.nature.com/articles/s41408-020-0283-8

51. Foltz SM, Gao Q, Yoon CJ, Sun H, Yao L, Li Y, et al. Evolution and structure of clinically relevant gene fusions in multiple myeloma. Nat Commun [Internet]. 2020 May 29 [cited 2024 Feb 12];11(1):2666. Available from: https://www.nature.com/articles/s41467-020-16434-y

52. Szalat R, Munshi NC. Next-Generation Sequencing Informing Therapeutic Decisions and Personalized Approaches. 2016;

53. D'Agostino M, Zaccaria GM, Ziccheddu B, Rustad EH, Genuardi E, Capra A, et al. Early Relapse Risk in Patients with Newly Diagnosed Multiple Myeloma Characterized by Next-generation Sequencing. Clin Cancer Res [Internet]. 2020 Sep 15 [cited 2024 Feb 12];26(18):4832–41. Available from: https://aacrjournals.org/clincancerres/article/26/18/4832/9542/Early-Relapse-Risk-in-Patients-with-Newly

54. Boyle EM, Williams L, Blaney P, Ashby C, Bauer M, Walker BA, et al. Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. Leukemia [Internet]. 2022 Jan [cited 2024 Feb 12];36(1):221–4. Available from: https://www.nature.com/articles/s41375-021-01320-3

55. Lionetti M, Barbieri M, Manzoni M, Fabris S, Bandini C, Todoerti K, et al. Molecular spectrum of *TP53* mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. Oncotarget [Internet]. 2016 Apr 19 [cited 2024 Feb 12];7(16):21353–61. Available from: https://www.oncotarget.com/lookup/doi/10.18632/oncotarget.7241

56. Lionetti M, Neri A. Utilizing next-generation sequencing in the management of multiple myeloma. Expert Rev Mol Diagn [Internet]. 2017 Jul 3 [cited 2024 Feb 12];17(7):653–63. Available from: https://www.tandfonline.com/doi/full/10.1080/14737159.2017.1332996

57. Mishima Y, Mishima Y, Shirouchi Y, Nishimura N, Yokoyama M, Okabe T, et al. The clonal evolution during long-term clinical course of multiple myeloma. Int J Hematol [Internet]. 2021 Feb [cited 2024 Feb 12];113(2):279–84. Available from: https://link.springer.com/10.1007/s12185-020-02979-7

58. Ryland GL, Jones K, Chin M, Markham J, Aydogan E, Kankanige Y, et al. Novel genomic findings in multiple myeloma identified through routine diagnostic sequencing. J Clin Pathol [Internet]. 2018 Oct [cited 2024 Feb 12];71(10):895–9. Available from: http://jcp.bmj.com/lookup/doi/10.1136/jclinpath-2018-205195

59. Walker BA, Mavrommatis K, Wardell CP, Ashby TC, Bauer M, Davies F, et al. A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. Leukemia [Internet]. 2019 Jan [cited 2024 Feb 12];33(1):159–70. Available from: https://www.nature.com/articles/s41375-018-0196-8

60. Corre J, Perrot A, Caillot D, Belhadj K, Hulin C, Leleu X, et al. del(17p) without *TP53* mutation confers a poor prognosis in intensively treated newly diagnosed patients with multiple myeloma. Blood [Internet]. 2021 Mar 4 [cited 2024 Feb 12];137(9):1192–5. Available from: https://ashpublications.org/blood/article/137/9/1192/469702/del-17p-without-TP53-mutation-confers-a-poor

61. Yamazaki H, Shirakawa K, Matsumoto T, Hirabayashi S, Murakawa Y, Kobayashi M, et al. Endogenous APOBEC3B Overexpression Constitutively Generates DNA Substitutions and Deletions in Myeloma Cells. Sci Rep [Internet]. 2019 May 9 [cited 2024 Feb 12];9(1):7122. Available from: https://www.nature.com/articles/s41598-019-43575-y

62. White BS, Lanc I, O'Neal J, Gupta H, Fulton RS, Schmidt H, et al. A multiple myeloma-specific capture sequencing platform discovers novel translocations and frequent, risk-associated point mutations in IGLL5. Blood Cancer J [Internet]. 2018 Mar 21 [cited 2024 Feb 12];8(3):35. Available from: https://www.nature.com/articles/s41408-018-0062-y

63. Laganà A, Perumal D, Melnekoff D, Readhead B, Kidd BA, Leshchenko V, et al. Integrative network analysis identifies novel drivers of pathogenesis and progression in newly diagnosed multiple myeloma. Leukemia [Internet]. 2018 Jan [cited 2024 Feb 12];32(1):120–30. Available from: https://www.nature.com/articles/leu2017197

64. Lionetti M, Barbieri M, Todoerti K, Agnelli L, Fabris S, Tonon G, et al. A compendium of *DIS3* mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget [Internet]. 2015 Sep 22 [cited 2024 Feb 12];6(28):26129–41. Available from: https://www.oncotarget.com/lookup/doi/10.18632/oncotarget.4674

65. Weißbach S, Langer C, Puppe B, Nedeva T, Bach E, Kull M, et al. The molecular spectrum and clinical impact of *DIS 3* mutations in multiple myeloma. Br J Haematol [Internet]. 2015 Apr [cited 2024 Feb 12];169(1):57–70. Available from: https://onlinelibrary.wiley.com/doi/10.1111/bjh.13256

66. Wei R, Zhu Y, Zhang Y, Zhao W, Yu X, Wang L, et al. AIMP1 promotes multiple myeloma malignancy through interacting with ANP32A to mediate histone H3 acetylation. Cancer Commun [Internet]. 2022 Nov [cited 2024 Feb 12];42(11):1185–206. Available from: https://onlinelibrary.wiley.com/doi/10.1002/cac2.12356

67. Zhang L, Zhang R, Wang J, Chen Y, Qiao C, Shi Q, et al. Identification of clinical implications and potential prognostic models of chromatin regulator mutations in multiple myeloma. Clin Epigenetics [Internet]. 2022 Dec [cited 2024 Feb 12];14(1):93. Available from: https://clinicalepigeneticsjournal.biomedcentral.com/articles/10.1186/s13148-022-01314-7

68. Kumari R, Majumder MM, Lievonen J, Silvennoinen R, Anttila P, Nupponen NN, et al. Prognostic significance of esterase gene expression in multiple myeloma. Br J Cancer [Internet]. 2021 Apr 12 [cited 2024 Feb 12];124(8):1428–36. Available from: https://www.nature.com/articles/s41416-020-01237-1

69. Abbaspourkharyeki M, Anvekar NJ, Ramachandra NB. The Possible Role of Point Mutations and Activation of the CDC27 Gene in Progression of Multiple Myeloma. Meta Gene [Internet]. 2020 Dec [cited 2024 Feb 12];26:100761. Available from: https://linkinghub.elsevier.com/retrieve/pii/S221454002030116X

70. Bolli N, Biancon G, Moarii M, Gimondi S, Li Y, De Philippis C, et al. Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia [Internet]. 2018 Dec [cited 2024 Feb 12];32(12):2604–16. Available from: https://www.nature.com/articles/s41375-018-0037-9

71. Pawlyn C, Davies FE. Toward personalized treatment in multiple myeloma based on molecular characteristics. Blood [Internet]. 2018 Feb 14 [cited 2024 Feb 12];133(7):660–75. Available from: https://ashpublications.org/blood/article/133/7/660/260559/Toward-personalized-treatment-in-multiple-myeloma

72. Anwer F, Gee KM, Iftikhar A, Baig M, Russ AD, Saeed S, et al. Future of Personalized Therapy Targeting Aberrant Signaling Pathways in Multiple Myeloma. Clin Lymphoma Myeloma Leuk [Internet]. 2019 Jul [cited 2024 Feb 12];19(7):397–405. Available from: https://linkinghub.elsevier.com/retrieve/pii/S2152265018314630

73. Kortüm KM, Mai EK, Hanafiah NH, Shi CX, Zhu YX, Bruins L, et al. Targeted sequencing of refractory myeloma reveals a high incidence of mutations in CRBN and Ras pathway genes. Blood [Internet]. 2016 Sep 1 [cited 2024 Feb 12];128(9):1226–33. Available from: https://ashpublications.org/blood/article/128/9/1226/35773/Targeted-sequencing-of-refractory-myeloma-reveals

74. Keppler S, Weißbach S, Langer C, Knop S, Pischimarov J, Kull M, et al. Rare SNPs in receptor tyrosine kinases are negative outcome predictors in multiple myeloma. Oncotarget [Internet]. 2016 Jun 21 [cited 2024 Feb 12];7(25):38762–74. Available from: https://www.oncotarget.com/lookup/doi/10.18632/oncotarget.9607

This is an open access article distributed under the terms of the Creative Commons Attribution License.