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COMPREHENSIVE ANALYSIS OF BASELINE OUTCOME BIOPREDICTORS IN YOUNGER PATIENTS WITH MANTLE CELL LYMPHOMA: THE ANCILLARY BIOLOGICAL STUDIES OF FONDAZIONE ITALIANA LINFOMI (FIL) MCL0208 CLINICAL TRIAL



Simone Ferrero* 1, 2, Gian Maria Zaccaria¹, Daniela Barbero¹, Andrea Evangelista³, Alice Di Rocco⁴, Alessandro Re⁵, Vittorio Stefoni⁶, Federica Cavallo^{1, 2}, Umberto Vitolo⁷, Monica Balzarotti⁸, Chiara Rusconi⁹, Maria Gomes da Silva¹⁰, Marco Ghislieri¹¹, Paola Omedè², Alberto Zamò¹², Giovannino Ciccone³, Valter Gattei¹³, Gianluca Gaidano¹⁴, Sergio Cortelazzo¹⁵, Marco Ladetto¹⁶

¹Molecular Biotechnologies and Health Sciences - Hematology Division, Università di Torino, ²SC Ematologia I, AOU Città della Salute e della Scienza di Torino, ³Unit of Clinical Epidemiology, CPO, Città della Salute e della Scienza, Hospital of Turin, Torino, ⁴Department of Cellular Biotechnologies and Hematology, Sapienza University, Roma, ⁵Division of Hematology, Spedali Civili, Brescia, ⁶Institute of Hematology "L. e A. Seràgnoli" University of Bologna, Bologna, ⁷SC Ematologia II, AOU Città della Salute e della Scienza di Torino, Torino, ⁸Division of Hematology, Humanitas Cancer Center, ⁹Division of Haematology, Department of Haematology and Oncology, Niguarda Cancer Center, ASST Grande Ospedale Metropolitano Niguarda, Milano, Italy, ¹⁰Departamento de Hematologia, Instituto Português de Oncologia, Lisboa, Portugal, ¹¹Department of Electronics and Telecommunications of Politecnico di Torino, ¹²Department of Oncology, Pathology, University of Turin, Torino, ¹³Clinical and Experimental Onco-Hematology Unit, IRCCS CRO Aviano-National Cancer Institute, Aviano, ¹⁴Division of Hematology, Department of Translational Medicine, Novara, ¹⁵Humanitas/Gavazzeni Cancer Center, Bergamo, ¹⁶Hematology Division, A.O. SS Antonio e Biagio and Cesare Arrigo, Alessandria, Italy



1. INTRODUCTION

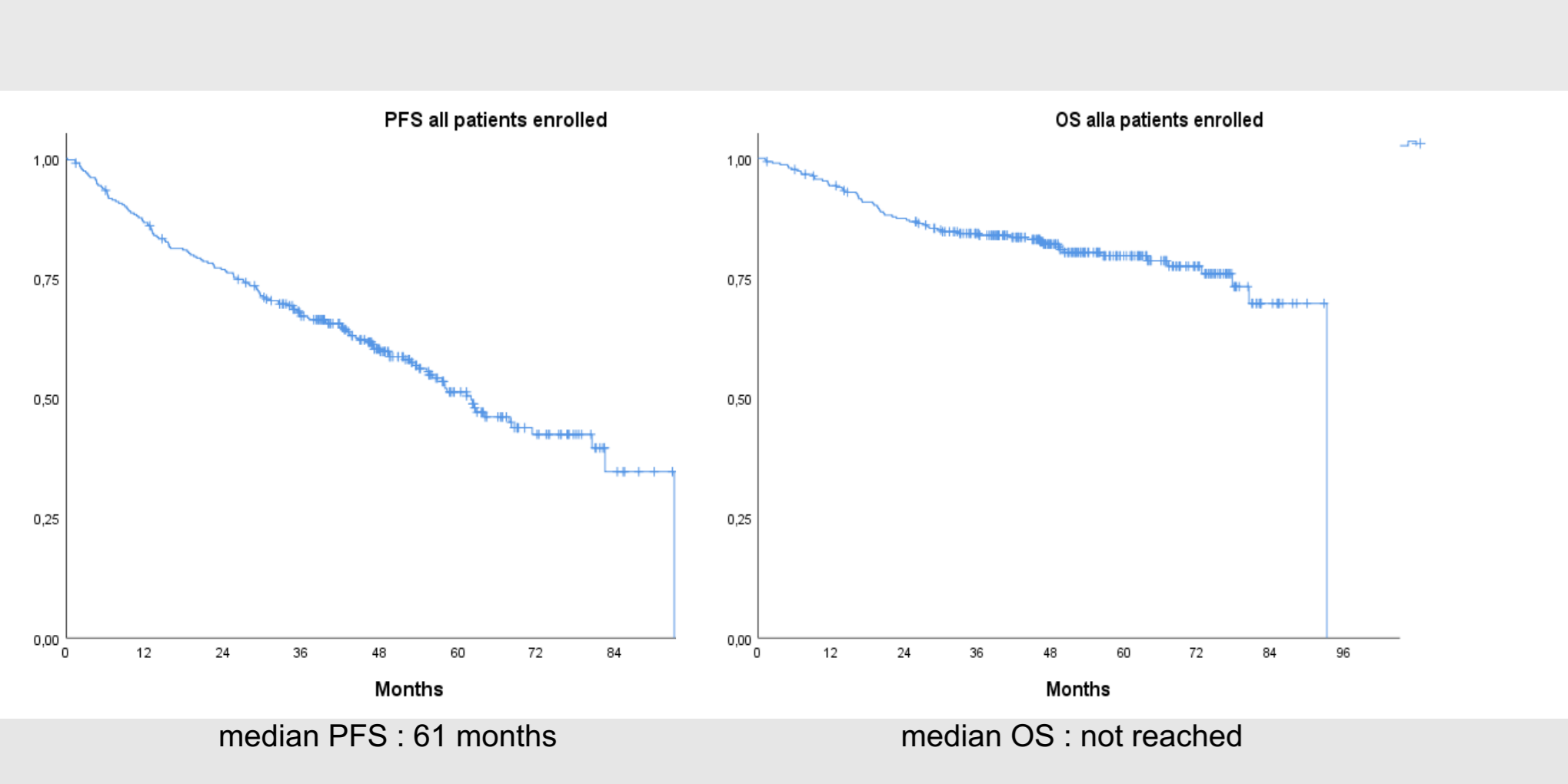
Despite the improvement in therapeutic schedules, a relevant fraction of mantle cell lymphoma (MCL) patients still experience primary treatment failure. This is due to a deep biological heterogeneity, not adequately dissected by the clinical predictors alone, as the MIPI

2. OBJECTIVE

The Fondazione Italiana Linfomi (FIL) MCL0208 trial is a prospective, randomized phase III trial comparing lenalidomide maintenance vs observation after an intensive citarabine containing chemo-immunotherapy followed by autologous transplantation in frontline MCL patients <66 years. Several biological ancillary studies were planned upfront, prospectively investigating the prognostic impact of putative biomarkers. Here we present a comprehensive analysis of the clinical impact of all the identified biopredictors.

3. METHODS

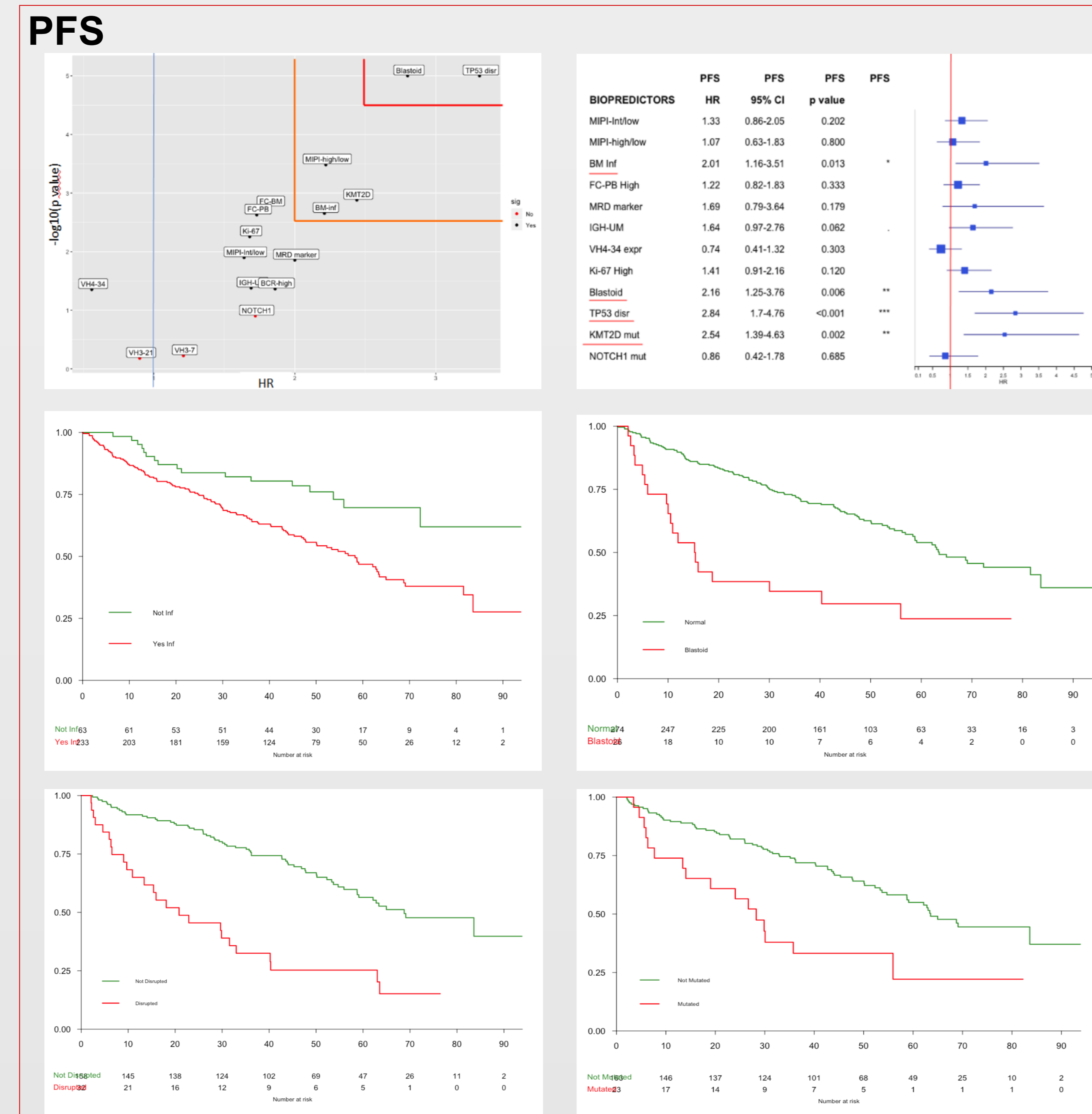
Trial details, as well as methods for immunohistochemistry, flow cytometry (FC), immunoglobulin heavy chain (IGH) gene sequencing and minimal residual disease (MRD) analysis have been presented.[Ferrero, ASH 2018] The "BCR-high" gene expression signature was tested by RT-PCR [Bomben, Haematologica 2018], somatic mutations by high-throughput targeted resequencing.[Ferrero, EHA 2017]. The optimal cut-off value for FC was determined by applying receiver operating curve (ROC) analysis. Survival analyses were performed by both univariate (UV) and multivariate (MV) Cox modeling via R (v.3.5.2): the variables showing a p<0.2 after UV were selected for the MV, including cases with missing values.



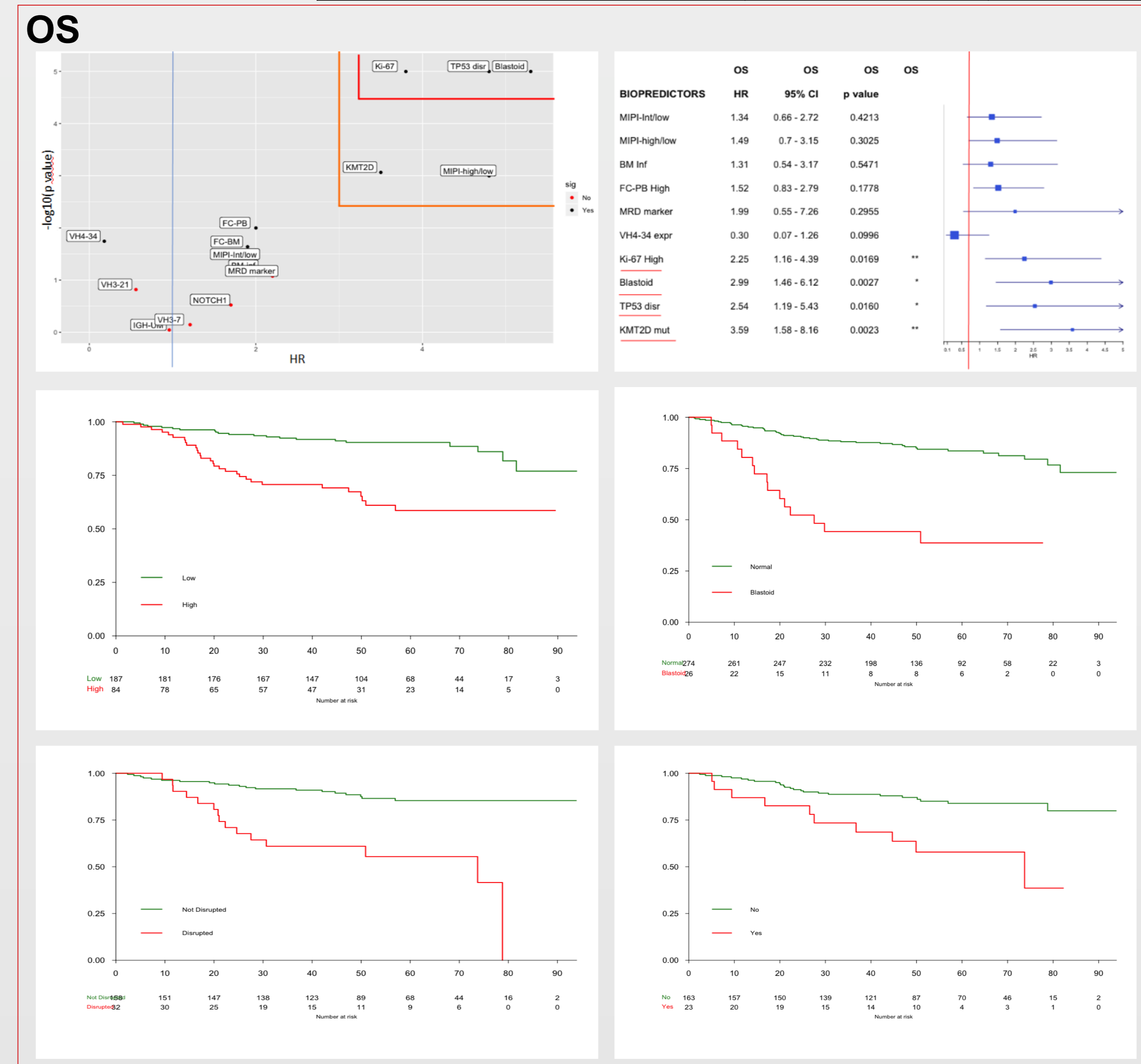
4. RESULTS

| PREDICTORS | RESULTS |
|-----------------------------------|--|
| MIPI score | 60% low risk 24% intermediate risk 16% high risk |
| Baseline bone marrow infiltration | 233/296 (79%) |
| Baseline median FC value | BM 7% (0.01-93) PB 4% (0.02-92) |
| Molecular marker for MRD | 250/300 (83%) |
| Available IGH sequence | 211/250 (84%) |
| IGH rearrangements | IGHV3-21 (21%) IGHV4-34 (16%) IGHV3-7 (8%) |
| Median IGH homology | 99.2% (89.9-100) |
| IGH unmutated (above 98% cut-off) | 163/211(77%) |
| Ki-67≥30% | 84/271 (31%) |
| SOX11+ | 167/183 (92%) |
| Blastoid histology | 26/300 (9%) |
| TP53 disruption | 32/190 (16%) |
| KMT2D mutation | 23/186 (12%) |
| NOTCH1 mutations | 14/186 (8%) |
| "BCR-high" signature | 40/83 (48%) |

PFS impact in univariate and multivariate. After a median follow-up of 51 months, several baseline biopredictors negatively impacted PFS in UV: BMinf, high FC-BM/PB, MRD marker+, IGH-UM, Ki-67≥30%, B-hist, TP53 and KMT2D mut, "BCR-high" signature. No significant outcome discrimination could be made on the basis of stereotyped IGH or SOX11 staining. After MV BMinf, IGH-UM, B-hist, TP53/KMT2D mut remained significant, as opposed to MIPI. Similar results were reported for OS by UV, indicating FC-BM/PB, Ki-67≥30%, B-hist, TP53/KMT2D mut as significant predictors. Finally, after MV, Ki-67≥30%, Bhist and KMT2D mut remained significant for OS, as opposed to MIPI.



| | PFS | | | | | | OS | | | | | | |
|------------------------------|------------|-----------|----------|------------------|-----------|---------|------------|-------------|-------------|------------------|-------------|-------------|--------|
| | Univariate | | | Multivariate Cox | | | Univariate | | | Multivariate Cox | | | |
| | HR | 95% CI | p_value | HR | 95% CI | p_value | HR | 95% CI | p_value | HR | 95% CI | p_value | |
| MIPI (Intermediate vs low) | 1.64 | 1.11-2.43 | 0.01267 | 1.33 | 0.86-2.05 | 0.202 | 2 | 1.03 - 3.75 | 0.04 | 1.34 | 0.66 - 2.72 | 0.4213 | |
| MIPIst (high vs. low) | 2.22 | 1.44-3.43 | 0.00033 | 1.07 | 0.63-1.83 | 0.800 | 4.8 | 2.66 - 8.7 | <0.001 | 1.49 | 0.7 - 3.15 | 0.3025 | |
| BM Infiltration (yes vs. no) | 2.21 | 1.33-3.68 | 0.00222 | 2.01 | 1.16-3.51 | 0.013 | * | 2.1 | 0.95 - 4.61 | 0.066 | 1.31 | 0.54 - 3.17 | 0.5471 |
| FC-BM (high vs. low) | 1.82 | 1.25-2.65 | 0.00172 | - | - | - | 1.9 | 1.1 - 3.46 | 0.023 | - | - | - | |
| FC-PB (high vs. low) | 1.73 | 1.21-2.45 | 0.00236 | 1.22 | 0.82-1.83 | 0.333 | 2 | 1.18 - 3.37 | 0.01 | 1.52 | 0.83 - 2.79 | 0.1778 | |
| MRD marker (yes vs. no) | 2 | 1.15-3.48 | 0.01395 | 1.69 | 0.79-3.64 | 0.179 | 2.2 | 0.9 - 5.62 | 0.084 | 1.99 | 0.55 - 7.26 | 0.2955 | |
| IGH-UM | 1.69 | 1.02-2.81 | 0.04176 | 1.64 | 0.97-2.76 | 0.062 | * | 0.96 | 0.5 - 1.84 | 0.905 | - | - | |
| VH3-21 | 0.9 | 0.57-1.4 | 0.66222 | - | - | - | 0.56 | 0.25 - 1.24 | 0.152 | - | - | - | |
| VH3-7 | 1.21 | 0.59-2.5 | 0.5964 | - | - | - | 1.21 | 0.43 - 3.37 | 0.716 | - | - | - | |
| VH4-34 | 0.56 | 0.32-0.99 | 0.04426 | 0.74 | 0.41-1.32 | 0.303 | 0.18 | 0.04 - 0.75 | 0.018 | 0.30 | 0.07 - 1.26 | 0.0996 | |
| Ki-67 ≥ 30% | 1.68 | 1.16-2.43 | 0.00555 | 1.41 | 0.91-2.16 | 0.120 | 3.8 | 2.19 - 6.68 | <0.00001 | 2.25 | 1.16 - 4.39 | 0.0169 | |
| Blastoid histology | 2.8 | 1.72-4.55 | <0.00001 | 2.16 | 1.25-3.76 | 0.006 | ** | 5.3 | 2.95 - 9.65 | <0.00001 | 2.99 | 1.46 - 6.12 | 0.0027 |
| TP53 disruption | 3.31 | 2.08-5.26 | <0.00001 | 2.84 | 1.7-4.76 | <0.001 | *** | 4.8 | 2.45 - 9.45 | <0.00001 | 2.54 | 1.19 - 5.43 | 0.0160 |
| KMT2D mutation | 2.44 | 1.42-4.22 | 0.00132 | 2.54 | 1.39-4.63 | 0.002 | ** | 3.5 | 1.68 - 7.37 | 0.00086 | 3.59 | 1.58 - 8.16 | 0.0023 |
| NOTCH1 mutation | 1.72 | 0.86-3.42 | 0.12563 | 0.86 | 0.42-1.78 | 0.685 | - | 1.7 | 0.61 - 4.95 | 0.30 | - | - | |
| BCR-high | 1.86 | 1.02-3.4 | 0.04326 | - | - | - | - | - | - | - | - | - | |
| TOT | 16 | | | 12 | | | 15 | | | 10 | | | |



5. CONCLUSION

→First comprehensive analysis of the clinical impact of a composite panel of easily implementable biopredictors in a multicenter, prospective, clinical trial for MCL patients
→Several known variables maintain their independent prognostic value, underlining the biological complexity of MCL. Notably, all these biomarkers are of relative simple and applicable determination.
→Interestingly, the biological predictors emerged over clinical predictors, such as MIPI, suggesting that biological features might be the key drivers of outcome in MCL.

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