**Supplementary material 2. Primers used for NGS, PCR, Sanger sequencing, and analysis of V(D)J recombination**

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|  | **Sequence** | **Amplicon size, bp** |
| ***ARID1A* (27,100,914)** | Forward | 5'-GGCACATATGGCCCTCCTG-3' | 195 |
| Reverse | 5'-GGCAGTGGCAGGATAGGC-3' |
| ***ARID1A* (27,105,550)** | Forward | 5'-GCAGAGAGCACATGGGC-3' | 201 |
| Reverse | 5'-CCCAGGATCCAGTAGCGTTC-3' |
| ***CXCR4* (136,872,465-136,872,543)** | Forward | 5'-AGGCCCTAGCTTTCTTCCAC-3' | 205 |
| Reverse | 5'-CATCTGTGTTAGCTGGAGTGAA-3' |
| ***MYD88* (38,182,626)** | Forward | 5'-CGGATGGTGGTGGTTGTCTC-3' | 198 |
| Reverse | 5'-AGATTTGGTGCAGGGGTTGG-3' |
| ***MYD88* (38,182,641)** | Forward | 5'-GTTGAAGACTGGGCTTGTCC-3' | 136 |
| Reverse | 5'-AGGATGCTGGGGAACTCTTT-3' |
| ***MYD88* (38,182,641) for ASO-PCR** | Forward | 5'-TGCCAGGGGTACTTAGATGG-3' | 150 |
| Mut. R\* | 5'-TTGTACTTGATGGGGA**G**CG-3' |
| ***KMT2D* (49,420,078)** | Forward | 5'-GAGAACGGCTGCACATGTTC-3' | 216 |
| Reverse | 5'-TGATTACAAACTCCGGCCGC-3' |
| **PNA** | - | N term-GGTGGACATTCATCTGTT | - |
| **Framework region 3** | - | 5'-GACACGGC(C,T)(A,G)TGTATTACTG-3' | - |
| **JHC** | - | 5'-ACCTGAGGAGACGGTGACC-3' |

Covering positions of each gene are shown in parentheses. JHC, joining region of the immunoglobulin heavy chain gene. \*Mut. R, mutant-specific reverse primer, has a substitutional base that matches the variant nucleotide at the 3' terminal (underlined) and a mismatch base at the third from the 3' terminal (bold).