

EuroClonality-NGS Working group
Standard Operating Procedure (SOP) for
Two-step IG/TR NGS-based marker
identification for the Illumina MiSeq platform

Version 1.0 (11 June 2019)

Updated in Version 1.0

- Not applicable (new SOP).

For complementary information or questions,
please go to www.euroclonalityngs.org
or contact Michaela Kotrová at m.kotrova@med2.uni-kiel.de

EuroClonality-NGS Working group SOP for Two-step IG/TR NGS-based marker identification for the Illumina MiSeq platform

Content

1.	Working definitions, material references and general remarks	3
2.	1 st step PCR	5
3.	Purification of TRB (VJ, DJ) PCR products by gel extraction	6
4.	2 nd step PCR	7
5.	Appendix	11

1. Working definitions, material references and general remarks

- This SOP provides detailed instructions on how to prepare amplicon sequencing libraries for **target screening using EuroClonality-NGS primer sets** for IGH (VJ + DJ), IGK (VJ-Kde + intron-Kde), TRB (VJ + DJ), TRG and TRD on Illumina MiSeq.
- Besides patient samples it is highly recommended to include **negative control** (water) and **positive control** (buffy coat) libraries in each run.
- Please comply with all recommendations. Even small deviations will impact the results.

Equipment:

- Thermocycler
- 1 full set of pipettes comprising P10 μ l, P20 μ l, P100 μ l, P200 μ l and P1000 μ l
- Heat Block
- Gel electrophoresis chamber
- UV lamp
- Vortex
- Microfuge
- Plate centrifuge
- Light Cycler LC480/Qubit Fluorometer
- Laminar flow hood
- Illumina MiSeq sequencer

Reagents & Consumables:

- dNTPs (ROTH, Cat No: L785.3)
- EagleTaq DNA Polymerase (Roche, Cat No: 05206952190) **or** AmpliTaq Gold DNA Polymerase with Buffer II and MgCl₂ (ThermoFisher Scientific, Cat No: N8080241)
- In combination with Eagle Taq DNA Polymerase: FastStart PCR Buffer (Roche, Cat No: 05917166103) and MgCl₂ (Roche, Cat No:11600770103)
- Fast Start High Fidelity PCR System (Roche, Cat No: 04738292001)
- HPLC-H₂O (Merck, Cat No: 1153331000, or other)
- Gel Red (VWR, Cat No: 41003-1)

- Gel loading dye (self-made)
- Agarose
- TBE (or TAE) Buffer
- TE Buffer
- 10M NaOH
- Scalpel
- PCR plate caps
- Pipette tips
- 1,5 ml Low Binding Tubes
- 0.2 ml PCR tubes
- Ice block
- MinElute Gel extraction kit (Qiagen, Cat No: 28606, or other)
- Qubit® dsDNA HS Assay Kit (ThermoFisher Scientific, Cat No: Q32854) **or**
QuantiT PicoGreen dsDNA Assay Kit (ThermoFisher Scientific, Cat No: 50107677)
- Illumina PhiX spike in control v3 (Illumina, Cat No: FC1103001)
- MiSeq Reagent Kit v2, 2×251bp (Illumina, Cat No: MS1022003)
- Tween 20 (ROTH, Cat No: 9127.1, or other)
- Buffy coat DNA
- Spike-in DNA (described in Knecht et al., Leukemia, accepted)
- 1st and 2nd step primers (see Appendix)

2. 1st step PCR

2.1. Prepare your samples:

- 2.1.1. Normalize patients' diagnostic DNA to 100 ng/μl (dilute with TE buffer).
- 2.1.2. Dilute buffy coat (BC) DNA to 100 and 10 ng/μl (dilute with TE buffer).

Note: Pipetting BC into each PCR serves as control of the PCR concerning detection of a band after gel electrophoresis and can be skipped if a user is experienced with the technique. Preparing the BC control library serves as the quality control of run performance.

- 2.2. Prepare the master mixes: prepare the individual master mix for each target-specific PCR (see Table 1 below). For IGK and TRB, prepare the double amount.
- 2.3. Vortex and centrifuge the master mixes.

Note: IGK and TRB targets are amplified in two separate reactions (TRB-VJ and DJ and IGK-VJ-Kde and intron-Kde).

Table 1. Composition of 1st step PCR master mixes.

	1 st PCR													
	Stock concentration	IGH-VJ		IGH-DJ		IGK-VJ-Kde, intron-Kde		TRB-VJ, TRB-DJ		TRG		TRD		
		Final concentration	μl/library	Final concentration	μl/library	Final concentration	μl/library	Final concentration	μl/library	Final concentration	μl/library	Final concentration	μl/library	
PCR Buffer II	10x	1x	5	1x	5	1x	5	1x	5	1x	5	1x	5	
MgCl ₂	25 mM	2.5 mM	5	3 mM	6	1.5 mM	3	4 mM	8	4 mM	8	2 mM	4	
dNTP-Mix	10 mM	0.2 mM	1	0.4 mM	2.0	0.2 mM	1	0.2 mM	1	0.2 mM	1	0.2 mM	1	
EagleTaq/Amplicon Gold	5 U/μl	1U/rxn	0.2	1.5U/rxn	0.3	1U/rxn	0.2	1U/rxn	0.2	1U/rxn	0.2	1 U/rxn	0.2	

reaction volume: 50μl

- 2.4. Pipette the master mix into the PCR tubes.
- 2.5. Pipette the 1st step primers into all tubes.
- 2.6. Add 1 μl of patient DNA (100 ng) into the appropriate tube(s).
- 2.7. Add 1 μl of HPLC-H₂O or 1 μl of buffy coat (100 ng) into the appropriate tubes.
- 2.8. Add 1 μl of buffy coat (10 ng) DNA and 720 copies of spike-in DNA into all tubes containing patient's DNA.

- 2.9. Add the appropriate amount of HPLC-H₂O into all tubes to a total reaction volume of 50 µl.
- 2.10. Vortex and centrifuge the PCR strips.
- 2.11. Place the strips into a thermocycler and select the correct program to run (see Table 2 below).

Note: PCR conditions are the same for all target-specific PCRs.

Table 2. 1st step PCR program.

1 cycle	Initial denaturation	94°C	10 min
	Denaturation	94°C	1 min
35 cycles	Annealing	63°C	1 min
	Extension	72°C	30 sec
1 cycle	Final extension	72°C	30 min
		12°C	∞

- 2.12. Once the run has finished, either store the products at 20°C, or continue with gel electrophoresis to check the successful PCR amplification of all targets (IGH-VJ, IGH-DJ, IGK-VJ-Kde, intron-Kde, TRG and TRD). If you identify positive bands, move forward to the next steps, otherwise repeat the 1st PCR.

3. Purification of TRB (VJ, DJ) PCR products by gel extraction

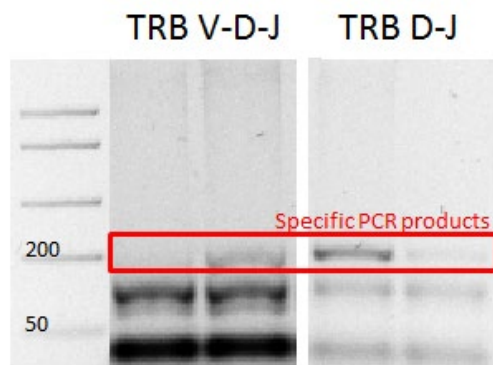
Note: As the TRB PCR (both VJ and DJ) leads to unspecific products (for instance TRB-VJ around 188-190bp), a gel extraction prior to the 2nd round PCR is necessary for TRB PCR products. You can use any commercial kit. We prefer the MinElute Gel extraction kit.

- 3.1. For the gel electrophoresis, use 21 µl of the TRB PCR product + 9 µl gel loading dye and mix it.
- 3.2. Pipette the mix (30 µl) into a big-sized gel (2% agarose).
- 3.3. Run the gel at 130V for 55 minutes.
- 3.4. Purify the bands according to the manufacturer's instructions for your commercial kit.

Table 3. Expected fragment lengths of TRB target products and unspecific products.

	Fragment length	Unspecific product
TRB-VJ	200 bp	180 bp
TRB-DJ	210 bp	190 bp

Figure 1. Example of TRB PCR products after gel electrophoresis.



4. 2nd step PCR

- 4.1. Dilute the 1st round PCR products (TRG, TRD, IGH-VJ, IGH-DJ, IGK-VJ-Kde and intron-Kde) 1:50. If the band on the gel is too weak (for example as the first and the fourth sample in Figure 1), do not dilute the PCR product before the 2nd round. TRB (both VJ and DJ) PCR products should never be diluted after the gel extraction.
- 4.2. Prepare the master mix for the 2nd round PCR (see Table 4 below).
- 4.3. Vortex and centrifuge the master mix.

Note: Keep the polymerase and the master mix on ice.

Table 4. Composition of 2nd step PCR master mixes.

	Stock concentration	all genes	
		Final concentration	µl/library
PCR Buffer with MgCl ₂	10x	1x	5
dNTP-Mix	18 mM	1.8 mM	0
	10 mM	0.2 mM	1
see the central primer table for concentrations			
Fast Start High Fidelity polymerase	5 U/µl	2.5U/rxn	0.5

reaction volume: 50µl

- 4.4. Pipette the master mix into the PCR tubes.
- 4.5. Into each tube, add the unique combination of the barcoded forward and reverse primers (see Table 5 below, primer concentrations in the central primer table).

Table 5. Barcodes of forward and reverse primers.

reverse barcodes

	D701	D702	D703	D704	D705	D706	D707	D708	D709	D710	D711	D712	
D501	█	█	█	█	█	█	█	█	█	█	█	█	IGH-VJ
D502	█	█	█	█	█	█	█	█	█	█	█	█	IGH-DJ
D503	█	█	█	█	█	█	█	█	█	█	█	█	IGK-VJ-Kde
D504	█	█	█	█	█	█	█	█	█	█	█	█	intron-Kde
D505	█	█	█	█	█	█	█	█	█	█	█	█	TRB-VJ
D506	█	█	█	█	█	█	█	█	█	█	█	█	TRB-DJ
D507	█	█	█	█	█	█	█	█	█	█	█	█	TRD
D508	█	█	█	█	█	█	█	█	█	█	█	█	TRG
	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7	Patient 8	Patient 9	Patient 10	cPTC	water	

96 combinations

forward barcodes

- 4.6. Add the 1st round PCR products into the PCR tubes: 1 µl of 1:50 diluted TRG, TRD, IGH-VJ, IGH-DJ, IGK-VJ-Kde and intron-Kde products (unless the band was too weak, see 4.1) and 3 µl of undiluted TRB products.

- 4.7. Vortex the PCR tubes.
- 4.8. Place the plate into a thermocycler and select the correct program to run (see Table 6 below).

Table 6. 2nd step PCR program.

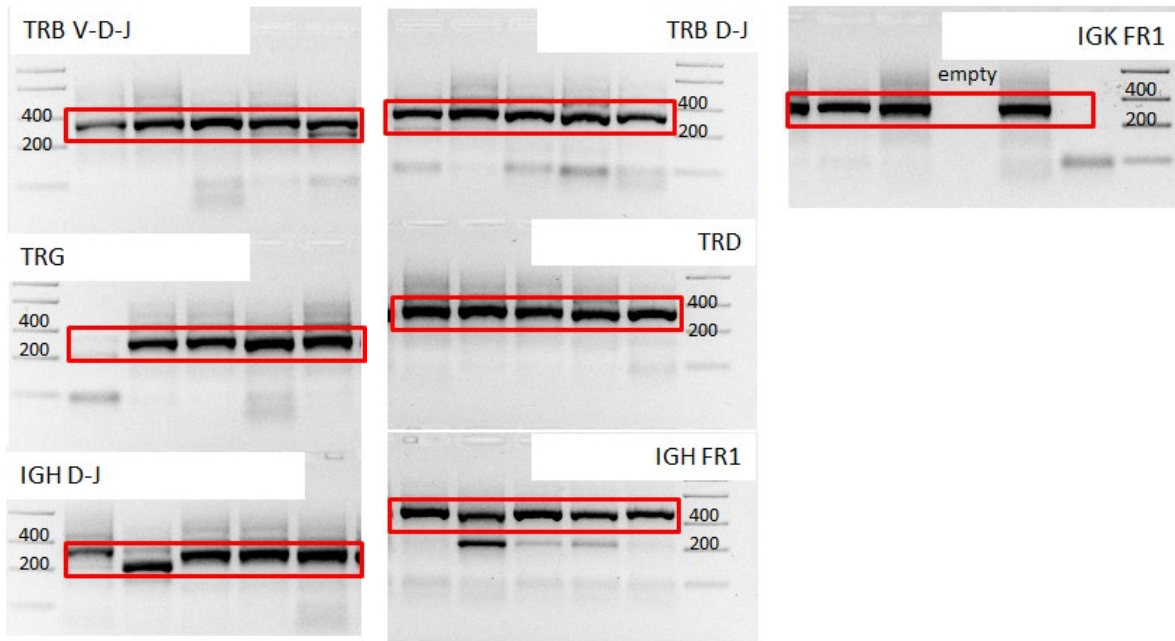
1 cycle	Initial denaturation	95°C	2 min
20 cycles	Denaturation	94°C	30 sec
	Annealing	63°C	30 sec
	Extension	72°C	30 sec
1 cycle	Final extension	72°C	5 min
		12°C	∞

- 4.9. Check the length of all the 2nd round PCR products by gel electrophoresis (see Figure 2).
- 4.10. Quantify all 2nd round PCR products using either Qubit® dsDNA HS Assay Kit or QuantiT PicoGreen dsDNA Assay Kit, according to the manufacturer's instructions.
- 4.11. Create targetwise subpools by pooling all libraries covering the same target gene.

Note: This will result in 8 subpools, each containing libraries created by the same mix of 1st round PCR primers.

- 4.12. Perform the gel extraction of the 8 subpools with 21 µl of the PCR product mixed with 9 µl gel loading dye (see also the instructions in Section 3).

Figure 2. Example of 2nd step PCR products after gel electrophoresis.



- 4.13. Quantify all subpools using either Qubit® dsDNA HS Assay Kit, or QuantiT PicoGreen dsDNA Assay Kit, according to the manufacturer's instructions.
- 4.14. Pool the subpools in equimolar ratios into one final pool.
- 4.15. Perform sequencing on the MiSeq instrument employing the 2×250 MiSeq reagent Kit, according to the manufacturer's instructions.

5. Appendix

Table 7. 1st step primers.

1 st step PCR	Primer nomenclature	µM in PCR	Primer direction	Primer sequence with M13 adapter (<i>forward/reverse</i>) 5' to 3'
TRB V-J	TRB-V-C-1	0.00625µM	5'	GTAAAACGACGGCCAGTTCGCTTCTCACCTGAATGCC
	TRB-V-A-1	0.0125µM	5'	GTAAAACGACGGCCAGTCTCAGTTGAAAGGCCTGATGGA
	TRB-V-X-1	0.0125µM	5'	GTAAAACGACGGCCAGTGAAGCATCCCTGATCGATTCT
	TRB-V-AA-1	0.0125µM	5'	GTAAAACGACGGCCAGTTCAGCTAAGTGCCCTCCCAAAT
	TRB-V-B-1	0.025µM	5'	GTAAAACGACGGCCAGTAGTTCCAAATCGCTTCTCACCT
	TRB-V-F-1	0.025µM	5'	GTAAAACGACGGCCAGTTCCCTAATCGATTCTCAGGGC
	TRB-V-J-1	0.025µM	5'	GTAAAACGACGGCCAGTTACAACGCAAAGGAGAGGTC
	TRB-V-L-1	0.025µM	5'	GTAAAACGACGGCCAGTTAAAGGAGAAGTCCCGAATGGC
	TRB-V-M-1	0.025µM	5'	GTAAAACGACGGCCAGTGGAGAAGTTCCTCAATGGCTACA
	TRB-V-S-1	0.025µM	5'	GTAAAACGACGGCCAGTATAAAGGAGAAGTCCCGATGG
	TRB-V-W-1	0.025µM	5'	GTAAAACGACGGCCAGTCTCTAGATGATTCGGGGATGCC
	TRB-V-Z-1	0.025µM	5'	GTAAAACGACGGCCAGTTGAAGCAGACACCCCTGATAAC
	TRB-V-AE-1	0.025µM	5'	GTAAAACGACGGCCAGTTGAGCGATTTTTAGCCCAATGC
	TRB-V-AG-1	0.025µM	5'	GTAAAACGACGGCCAGTACAAAGGAGAGATCTCTGATGGA
	TRB-J-A-1	0.025µM	3'	TAATACGACTCACTATAGGGCTACAACGTGAGTCTGGTGCC
	TRB-J-B-1	0.025µM	3'	TAATACGACTCACTATAGGGCTACAACGGTTAACCTGGTCC
	TRB-J-C-1	0.025µM	3'	TAATACGACTCACTATAGGGTACAACAGTGAGCCAACTTCCC
	TRB-J-D-1	0.025µM	3'	TAATACGACTCACTATAGGGCAAGACAGAGAGCTGGGTCC
	TRB-J-E-1	0.025µM	3'	TAATACGACTCACTATAGGGCTAGGATGGAGAGTCGAGTCCC
	TRB-J-F-1	0.025µM	3'	TAATACGACTCACTATAGGGCTGTCACAGTGAGCCTGGTC
TRB-J-G-1	0.025µM	3'	TAATACGACTCACTATAGGGCCTTCTTACCTAGCACGGTGAG	
TRB-J-H-1	0.025µM	3'	TAATACGACTCACTATAGGGTTACCCAGTACGGTCAGCCTAG	
TRB-J-I-1	0.025µM	3'	TAATACGACTCACTATAGGGCTTACCGAGCACTGTCAGCC	

EuroClonality-NGS SOP for two-step marker identification (MiSeq)
Version 1.0 (updated: 11 June 2019)

TRB-J-J-1	0.025µM	3'	TAATACGACTCACTATAGGGCTTACCCAGCACTGAGAGCC
TRB-J-K-1	0.025µM	3'	TAATACGACTCACTATAGGGTCACCCAGCACCAGGAGCC
TRB-J-N-1	0.025µM	3'	TAATACGACTCACTATAGGGGAATCTCACCTGTGACCGTGAG
TRB-V-D-1	0.05µM	5'	GTAAAACGACGGCCAGTGGAAACTTCCCTGGTCGATTC
TRB-V-N-1	0.05µM	5'	GTAAAACGACGGCCAGTCAACGATCGGTTCTTTGCAGTC
TRB-V-O-1	0.05µM	5'	GTAAAACGACGGCCAGTTAAATCAGGGCTGCTCAGTGAT
TRB-V-P-1	0.05µM	5'	GTAAAACGACGGCCAGTCAGTGATCGGTTCTCTGCAGAG
TRB-V-R-1	0.05µM	5'	GTAAAACGACGGCCAGTCTTGAACGATTCTCCGCACAAC
TRB-V-V-1	0.05µM	5'	GTAAAACGACGGCCAGTCCGAGGATCGATTCTCAGCTAA
TRB-V-AB-1	0.05µM	5'	GTAAAACGACGGCCAGTGCCAAAGGAACGATTTTCTGCT
TRB-V-AI-1	0.05µM	5'	GTAAAACGACGGCCAGTAGGGAGATGTTCCCTGAAGGGTA
TRB-V-AJ-1	0.05µM	5'	GTAAAACGACGGCCAGTCTGAGGGGTACAGTGTCTCTA
TRB-V-AL-1	0.05µM	5'	GTAAAACGACGGCCAGTCAGAATCTCTCAGCCTCCAGAC
TRB-V-E-1	0.1µM	5'	GTAAAACGACGGCCAGTACTTCCCTGATCGATTCTCAGC
TRB-V-H-1	0.1µM	5'	GTAAAACGACGGCCAGTCTCAGGTCACCAGTTCCCTAAC
TRB-V-I-1	0.1µM	5'	GTAAAACGACGGCCAGTCTAGATTTTCAGGTCGCCAGT
TRB-V-Q-1	0.1µM	5'	GTAAAACGACGGCCAGTCTCAACTAGACAAATCGGGGCT
TRB-V-U-1	0.1µM	5'	GTAAAACGACGGCCAGTATCGATTTTCTGCAGAGAGGCT
TRB-V-Y-1	0.1µM	5'	GTAAAACGACGGCCAGTCGGTATGCCCAACAATCGATTC
TRB-V-AC-1	0.1µM	5'	GTAAAACGACGGCCAGTCTGAAGGGTACAGCGTCTCTC
TRB-V-AH-1	0.1µM	5'	GTAAAACGACGGCCAGTTCCTCTGAGTCAACAGTCTCCA
TRB-V-AK-1	0.1µM	5'	GTAAAACGACGGCCAGTCTGAGGCCACATATGAGAGTGG
TRB-J-L-1	0.1µM	3'	TAATACGACTCACTATAGGGGAAAACCTACCCAGCACGGTC
TRB-J-M-1	0.1µM	3'	TAATACGACTCACTATAGGGTCACCCAGCACGGTCAGCC
TRB-V-G-1	0.15µM	5'	GTAAAACGACGGCCAGTGATTCTCAGGTCTCCAGTTCCC
TRB-V-K-1	0.15µM	5'	GTAAAACGACGGCCAGTTACCACTGGCAAAGGAGAAGTC
TRB-V-T-1	0.15µM	5'	GTAAAACGACGGCCAGTCAAAGGAGAAGTCTCAGATGGC
TRB-V-AD-1	0.15µM	5'	GTAAAACGACGGCCAGTTTCTCATCAACCATGCAAGCC
TRB-V-AF-1	0.15µM	5'	GTAAAACGACGGCCAGTGGAGATGCACAAGAAGCGATTC

EuroClonality-NGS SOP for two-step marker identification (MiSeq)
Version 1.0 (updated: 11 June 2019)

TRB D-J	TRB-J-A-1	0.025µM	3'	TAATACGACTCACTATAGGGCTACAACGTGAGTCTGGTGCC
	TRB-J-B-1	0.025µM	3'	TAATACGACTCACTATAGGGCTACAACGGTTAACCTGGTCC
	TRB-J-C-1	0.025µM	3'	TAATACGACTCACTATAGGGTACAACAGTGAGCCAACCTCCC
	TRB-J-D-1	0.025µM	3'	TAATACGACTCACTATAGGGCAAGACAGAGAGCTGGGGTCC
	TRB-J-E-1	0.025µM	3'	TAATACGACTCACTATAGGGCTAGGATGGAGAGTCGAGTCCC
	TRB-J-F-1	0.025µM	3'	TAATACGACTCACTATAGGGCTGTCACAGTGAGCCTGGTC
	TRB-J-G-1	0.025µM	3'	TAATACGACTCACTATAGGGCCTTCTTACCTAGCACGGTGAG
	TRB-J-H-1	0.025µM	3'	TAATACGACTCACTATAGGGTTACCCAGTACGGTCAGCCTAG
	TRB-J-I-1	0.025µM	3'	TAATACGACTCACTATAGGGCTTACCGAGCACTGTCAGCC
	TRB-J-J-1	0.025µM	3'	TAATACGACTCACTATAGGGCTTACCCAGCACTGAGAGCC
	TRB-J-K-1	0.025µM	3'	TAATACGACTCACTATAGGGTCACCGAGCACCAGGAGCC
	TRB-J-N-1	0.025µM	3'	TAATACGACTCACTATAGGGGAATCTCACCTGTGACCGTGAG
	TRB-D-A-1	0.1µM	5'	GTAAAACGACGGCCAGTCCTCCACTCCCCTCAAAGGA
	TRB-D-B-1	0.1µM	5'	GTAAAACGACGGCCAGTCAGACTAACCTCTGCCACCTG
	TRB-J-L-1	0.1µM	3'	TAATACGACTCACTATAGGGGAAAACCTCACCCAGCACGGTC
TRB-J-M-1	0.1µM	3'	TAATACGACTCACTATAGGGTCACCCAGCACGGTCAGCC	
TRG	TRG-V-E-1	0.05µM	5'	GTAAAACGACGGCCAGTCAAGCATGAGGAGGAGCTGGAAATTG
	TRG-V-F-1	0.05µM	5'	GTAAAACGACGGCCAGTACGTCTACATCCACTCTCACC
	TRG-V-A-1	0.1µM	5'	GTAAAACGACGGCCAGTGCACAAGGAACAACCTTGAGATTG
	TRG-V-B-1	0.1µM	5'	GTAAAACGACGGCCAGTTGGAAGCACAAAGGAAGAACTTGAGAA
	TRG-V-C-1	0.1µM	5'	GTAAAACGACGGCCAGTGCACAGGGAAGAGCCTTAAATTT
	TRG-V-D-1	0.1µM	5'	GTAAAACGACGGCCAGTCAGGAGGTGGAGCTGGATATT
	TRG-V-G-1	0.1µM	5'	GTAAAACGACGGCCAGTCTCTCACTTCAATCCTTACCATCAA
	TRG-V-H-1	0.2µM	5'	GTAAAACGACGGCCAGTGCTCACACTTCCACTTCCACTTTGAAAATAAAGT
	TRG-J-A-1	0.2µM	3'	TAATACGACTCACTATAGGGAGTGTGTGTTCCACTGCCAAAAG
	TRG-J-B-1	0.2µM	3'	TAATACGACTCACTATAGGGGTTCCGGGACCAAATACCTTG
	TRG-J-C-1	0.2µM	3'	TAATACGACTCACTATAGGGGAGCTTAGTCCCTTCAGCAAATA
TRG-J-D-1	0.2µM	3'	TAATACGACTCACTATAGGGCCTAGTCCCTTTTGCAAACG	
TRD	TRD-V-A-1	0.2µM	5'	GTAAAACGACGGCCAGTGAATGCAAAAAGTGGTCGCTATTC

EuroClonality-NGS SOP for two-step marker identification (MiSeq)
Version 1.0 (updated: 11 June 2019)

	TRD-V-B-1	0.2µM	5'	GTAAAACGACGGCCAGT TGCAAAGAACCTGGCTGTACT
	TRD-V-C-1	0.2µM	5'	GTAAAACGACGGCCAGT TG CAGATTTTACTCAAGGACGG
	TRD-V-D-1	0.2µM	5'	GTAAAACGACGGCCAGT GCAAAATGCAACAGAAGGTCG
	TRD-V-E-1	0.2µM	5'	GTAAAACGACGGCCAGT GATAAAAAATGAAGATGGGAAGATTCACTGT
	TRD-V-F-1	0.2µM	5'	GTAAAACGACGGCCAGT CTCTTCAATAAAAAGTGCCAAGC
	TRD-V-G-1	0.2µM	5'	GTAAAACGACGGCCAGT ATTGAAAAGAAGTCAGGAAGACTAAGT
	TRD-V-H-1	0.2µM	5'	GTAAAACGACGGCCAGT TCCAGAAAAGCAGCCAAATCC
	TRD-D-A-1	0.2µM	5'	GTAAAACGACGGCCAGT AGGGGTATTGTGGATGGCAG
	TRD-J-A-1	0.2µM	3'	TAATACGACTCACTATAGGG TTCCACAGTCACACGGGT
	TRD-J-B-1	0.2µM	3'	TAATACGACTCACTATAGGG GTTCCACGATGAGTTGTGTT
	TRD-J-C-1	0.2µM	3'	TAATACGACTCACTATAGGG CACGAAGAGTTTGATGCCAGT
	TRD-J-D-1	0.2µM	3'	TAATACGACTCACTATAGGG GTTGTGTACCTCCAGATAGGTT
	TRD-J-E-1	0.2µM	3'	TAATACGACTCACTATAGGG TGGCTAGAAACACTTACTTGCA
	TRD-D-B-1	0.2µM	3'	TAATACGACTCACTATAGGG CCCAGGGAAATGGCACTTTTG
IGH D-J	IGH-D-A-1	0.2µM	5'	GTAAAACGACGGCCAGT GATTCYGAACAGCCCCGAGTCA
	IGH-D-B-1	0.2µM	5'	GTAAAACGACGGCCAGT GATTTTGTGGGGGYTCGTGTC
	IGH-D-C-1	0.2µM	5'	GTAAAACGACGGCCAGT GTTTGRRTGAGGTCTGTGTCA
	IGH-D-D-1	0.2µM	5'	GTAAAACGACGGCCAGT GTTTRRRTGAGGTCTGTGTCACT
	IGH-D-E-1	0.2µM	5'	GTAAAACGACGGCCAGT CTTTTTGTGAAGGSCCTCCTR
	IGH-D-F-1	0.2µM	5'	GTAAAACGACGGCCAGT GTTATTGTCAGGSGRTGTCAGAC
	IGH-D-G-1	0.2µM	5'	GTAAAACGACGGCCAGT GTTATTGTCAGGGGGTGYCAGRC
	IGH-D-H-1	0.2µM	5'	GTAAAACGACGGCCAGT GTTCTGAAGSTGTCTGTRTCAC
	IGH-J-A-1	0.4µM	3'	TAATACGACTCACTATAGGG CTTACCTGAGGAGACGGTGACC
IGH V-J	IGH-V-FR1-B-1	0.1µM	5'	GTAAAACGACGGCCAGT GCAGTCTGGAGCAGAGGTGAAAA
	IGH-V-FR1-E-1	0.1µM	5'	GTAAAACGACGGCCAGT GAGGTGCAGCTGTTGGAGTC
	IGH-V-FR1-G-1	0.1µM	5'	GTAAAACGACGGCCAGT CAGTGGGGCGCAGGACTGTT
	IGH-V-FR1-H-1	0.1µM	5'	GTAAAACGACGGCCAGT CCAGGACTGGTGAAGCCTCC
	IGH-V-FR1-K-1	0.1µM	5'	GTAAAACGACGGCCAGT CCTCAGTGAAGGTTTCTGCAAGG
	IGH-V-FR1-L-1	0.1µM	5'	GTAAAACGACGGCCAGT AAACCCACAGAGACCCTCACGCTGAC

EuroClonality-NGS SOP for two-step marker identification (MiSeq)
Version 1.0 (updated: 11 June 2019)



	IGH-V-FR1-M-1	0.1µM	5'	GTAAAACGACGGCCAGTCTGGGGGGTCCCTGAGACTCTCCTG
	IGH-V-FR1-N-1	0.1µM	5'	GTAAAACGACGGCCAGTCTTCACAGACCCTGTCCCTCACCTG
	IGH-V-FR1-O-1	0.1µM	5'	GTAAAACGACGGCCAGTTCGCAGACCCTCTACTCACCTGTG
	IGH-J-A-1	0.1µM	3'	TAATACGACTCACTATAGGGCTTACCTGAGGAGACGGTGACC
	IGH-J-B-1	0.1µM	3'	TAATACGACTCACTATAGGGCTCACCTGAGGAGACGGTGACC
	IGH-V-FR1-A-1	0.2µM	5'	GTAAAACGACGGCCAGTCTGGGGCTGAGGTGAAGAAG
	IGH-V-FR1-C-1	0.2µM	5'	GTAAAACGACGGCCAGTTCACCTTGAAGGAGTCTGGTCC
	IGH-V-FR1-D-1	0.2µM	5'	GTAAAACGACGGCCAGTAGGTGCAGCTGGTGGAGTC
	IGH-V-FR1-F-1	0.2µM	5'	GTAAAACGACGGCCAGTCCAGGACTGGTGAAGCCTTC
	IGH-V-FR1-I-1	0.2µM	5'	GTAAAACGACGGCCAGTGTACAGCTGCAGCAGTCAGG
	IGH-V-FR1-J-1	0.2µM	5'	GTAAAACGACGGCCAGTGCTGGTGCAATCTGGGTCTG
IGK-A	IGK-V-A-1	0.1µM	5'	GTAAAACGACGGCCAGTAAGTGGGGTCCCATCAAGGTTTCAG
	IGK-V-B-1	0.1µM	5'	GTAAAACGACGGCCAGTAGTCCCATCTCGGTTTCAGTGGCAG
	IGK-V-C-1	0.1µM	5'	GTAAAACGACGGCCAGTGAAACAGGGGTCCCATCAAGGTTTC
	IGK-V-D-1	0.1µM	5'	GTAAAACGACGGCCAGTTCCCAGACAGATTCAGTGGCAGTG
	IGK-V-E-1	0.1µM	5'	GTAAAACGACGGCCAGTCTGGAGTGCCAGATAGGTTTCAGTG
	IGK-V-F-1	0.1µM	5'	GTAAAACGACGGCCAGTCCCTGGAGTCCCAGACAGGTTTCAG
	IGK-V-G-1	0.1µM	5'	GTAAAACGACGGCCAGTGCATCCCAGCCAGGTTTCAGTG
	IGK-V-H-1	0.1µM	5'	GTAAAACGACGGCCAGTGTCCCTGACCGATTCAGTGGCA
	IGK-V-I-1	0.1µM	5'	GTAAAACGACGGCCAGTAATCCCACCTCGATTCAGTGGC
	IGK-V-J-1	0.1µM	5'	GTAAAACGACGGCCAGTCTCAGGGGTCCCCTCGAGGTT
	IGK-V-K-1	0.1µM	5'	GTAAAACGACGGCCAGTAGACACTGGGGTCCCAGCCA
	IGK-DE-A-1	0.1µM	3'	TAATACGACTCACTATAGGGGCAGCTGCAGACTCATGAGGAG
	IGk-J-A-1	0.1µM	3'	TAATACGACTCACTATAGGGACGTTTGATCTCCACCTTGGTCCC
	IGK-J-B-1	0.1µM	3'	TAATACGACTCACTATAGGGACGTTTGATATCCACTTTGGTCCC
IGK-J-C-1	0.1µM	3'	TAATACGACTCACTATAGGGACGTTTAATCTCCAGTCGTGTCCC	
IGK-B	IGK-INTR-A-1	0.1µM	5'	GTAAAACGACGGCCAGTGAGTGGCTTTGGTGGCCATGC
	IGK-DE-A-1	0.1µM	3'	TAATACGACTCACTATAGGGGCAGCTGCAGACTCATGAGGAG

Table 8. 2nd step primers.

2 nd step PCR	Primer nomenclature	µM in PCR	Primer direction	Barcoded primer sequence with M13 adapter (forward/reverse) 5' to 3'
forward	I11-D501-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D502-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D503-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D504-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D505-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACAGGGGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D506-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACTAATCTTAACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D507-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
	I11-D508-F	0.2µM	5'	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTGTAAAACGACGGCCAGT
reverse	I11-D701-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D702-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATTTCTCCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D703-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATAATGAGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D704-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATGGAATCTCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D705-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATTTCTGAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D706-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATACGAATTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D707-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATAGCTTCAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D708-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATGCGCATTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D709-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATCATAGCCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D710-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATTTCCGGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D711-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATGCGCGAGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG
	I11-D712-R	0.2µM	3'	CAAGCAGAAGACGGCATAACGAGATCTATCGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAATACGACTCACTATAGGG