EuroClonality Standard Operating Procedure (SOP) for

One-step IG/TR NGS-based MRD detection

Version 1.0 (July 2024)

This SOP is based on the following publication of the EuroClonality-NGS Working Group, with some modifications to optimize the library preparation for MRD quantitation.

Brüggemann et al., Standardized next-generation sequencing of immunoglobulin and T-cell receptor gene recombinations for MRD marker identification in acute lymphoblastic leukaemia; a EuroClonality-NGS validation study. *Leukemia 2019;33:2241-2253. doi: 10.1038/s41375-019-0496-7.*

For complementary information or questions, please go to www.EuroClonality.org or contact Eva Froňková (eva.fronkova@lfmotol.cuni.cz)

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- Primers for one-step IG/TR NGS-based MRD detection
- Index sequences

1. Introduction

This SOP provides detailed instructions how to prepare amplicon sequencing libraries for **MRD detection using EuroClonality-NGS IGH-VJ-FR1, IGH-DJ, IGK-VJ, intron-Kde, TRB-VJ, TRB-DJ, TRG and TRD primer sets**, on the Illumina MiSeq platform. This SOP is also suitable for **marker screening with only 100 ng of DNA** input used.

2. Equipment and reagents

2.1 Equipment required:

- Thermocycler
- 1 full set of pipettes comprising: P10µl, P20µl, P100µl, P200µl and P1000µl
- HeatBlock
- Gel electrophoresis chamber
- UV lamp
- Vortex
- Microfuge
- Light Cycler LC480/Qubit Fluorometer
- Laminar flow hood
- Illumina MiSeq sequencer

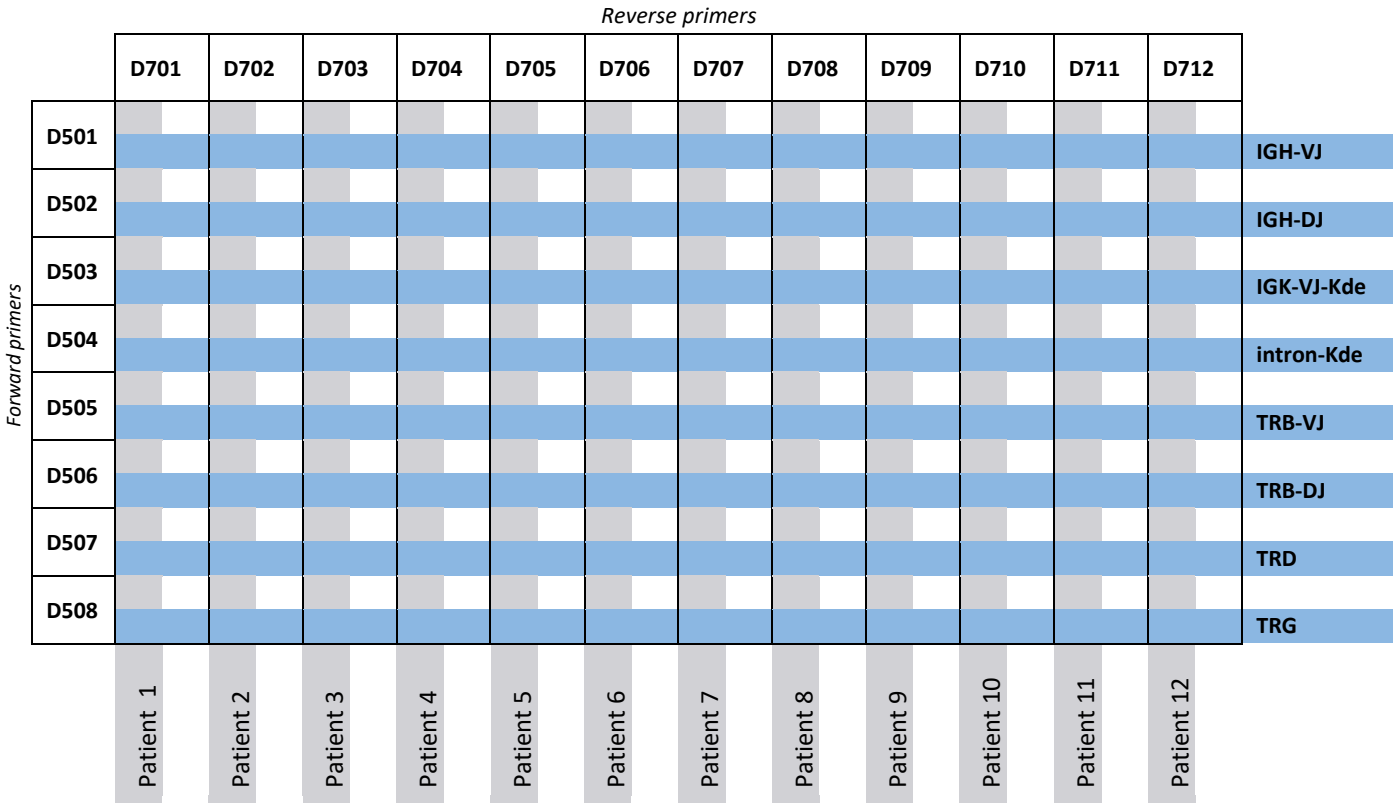
2.2 Reagents & Consumables:

- Product purification kit (Agencourt SPRISelect, Agencourt AMPure XP, MinElute Gel)
- Fast Start HiFi Polymerase/EagleTaq DNA Polymerase/AmpliTaq Gold DNA Polymerase
- 10x PCR buffer II, dNTPs (10mM), MgCl2 (25mM)
- ddH2O
- EuroClonality-NGS Primers (Brüggemann et al., 2019)
- PCR tubes
- Pipette tips
- Gel Red
- Gel loading dye

- Scalpel, Agarose, TBE (or TAE) Buffer (for Gel Purification)
- 10M NaOH
- 1,5 ml Low Binding Tubes
- Ice block
- Qubit® dsDNA HS Assay Kit/QuantiT PicoGreen dsDNA Assay Kit
- Illumina PhiX spike in control v3 (Illumina: FC1103001)
- MiSeq Reagent Kit v2, 2×250bp (Illumina, order no. MS1022003)
- Tween 20 (SigmaAldrich: P13791L)

3. Primer mix preparation

Suggested primer design follows this scheme, so that each system shares a unique barcode in the Forward primer and the Reverse primers can be used to barcode individual samples. This can be used for Marker screening using all 8 primer sets per patient or with selected systems for NGS MRD quantitation in follow-up samples.



The concentration of individual primers in the final PCR reaction mix is specified in the Primer e c ed s S nd c cu ed s e c e se e s e c n e added to the final reaction mix.

4. PCR Library preparation

4.1 **Prepare your samples:** DNA samples should have a concentration of at least 100 ng/µl. (Adjust the final volume of H2O and DNA, so that **2 µg** of DNA is used in each PCR; this protocol was tested with DNA volume of up to **20 µl**, please be aware that increasing the amount of DNA can inhibit PCR).

4.2 **Prepare the master mixes:** Prepare the individual master mix for each target-specific PCR (see table below).
Primer mixes should be prepared with respective concentrations from the Primer Table.

	Stock concentration	IGH-VJ-FR1		IGH-DJ		IGK-VJ-Kde		Intron-Kde	
		Final concentration	µl/sample	Final concentration	µl/sample	Final concentration	µl/sample	Final concentration	µl/sample
PCR Buffer II	10x	1x	10 µl	1x	10 µl	1x	10 µl	1x	10 µl
$MgCl_2$	25 mM	1.5 mM	6 µl	**3 mM**	**12 µl**	1.5 mM	6 µl	1.5 mM	6 µl
dNTP-MIX	10mM	0.2 mM	2 µl	0.2 mM	2 µl	0.2 mM	2 µl	0.2 mM	2 µl
Forward Primer MIX			4 µl		4 µl		4 µl		4 µl
H_2O			51.5 µl		45.5 µl		51.5 µl		51.5 µl
Roche HF/ AmpliTaq Gold	5U/µl	2.5U/rxn	0.5 µl	2.5U/rxn	0.5 µl	2.5U/rxn	0.5 µl	2.5/rxn	0.5 µl
Total			**74.0 µl**		**74.0 µl**		**74.0 µl**		**74.0 µl**

	Stock concentration	TRB-VJ		TRB-DJ		TRD		TRG	
		Final concentration	µl/sample	Final concentration	µl/sample	Final concentration	µl/sample	Final concentration	µl/sample
PCR Buffer II	10x	1x	10 µl	1x	10 µl	1x	10 µl	1x	10 µl
$MgCl_2$	25 mM	4 mM	16 µl	4 mM	16 µl	**2 mM**	**8 µl**	4 mM	16 µl
dNTP-MIX	10mM	0.2 mM	2 µl	0.2 mM	2 µl	0.2 mM	2 µl	0.2 mM	2 µl
Forward Primer MIX			4 µl		4 µl		4 µl		4 µl
H_2O			41.5 µl		41.5 µl		49.5 µl		41.5 µl
Roche HF/ AmpliTaq Gold	5U/µl	2.5U/rxn	0.5 µl	2.5U/rxn	0.5 µl	2.5U/rxn	0.5 µl	2.5U/rxn	0.5 µl
Total			**74.0 µl**		**74.0 µl**		**74.0 µl**		**74.0 µl**

4.3 Pipette the master mix into PCR tubes.
4.4 Into all tubes add:
4 µl of reverse primer mix.
2 µl of cIT-QC (spike-ins)
up to 20 µl of DNA sample (2 µg).
4.5 Final volume of each PCR reaction is 100 µl.
4.6. Place the strips into a thermocycler and select the correct program to run.

PCR conditions are NOT the same for all systems (see below).

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

* For the **TRB-VJ** system, an annealing temperature of **65°C** should be used.

Once the run has finished, either store the products at 4°C, or continue with **gel electrophoresis** to check the successful PCR amplification of all tubes. If you identify positive bands, move forward to the next steps, otherwise repeat.

Expected size range of the specific library for each system:

System	Size (bp)
IGH-VJ-FR1	440 - 640
IGH-DJ	220 - 320
IGK-VJ-Kde	250 - 350
intron-Kde	270 - 340
TRB-VJ	270 - 370
TRB-DJ	260 - 370
TRG	210 - 320
TRD	270 - 410

4.7 **Perform the purification of the libraries**:

You can use a commercial kit of your preference (Agencourt SPRISelect, Agencourt AMPure XP beads, MinElute Gel extraction kit). We recommend the Agencourt SPRISelect, because it allows precise selection of fragment lengths validated for each lot. Recommended ratios of PCR product and SPRISelect beads are:

- **1:1** for **IGK-VJ-Kde**, **intron-Kde**, **TRG** and **TRD** systems (30 µl PCR sample + 30 µl beads);

- **1:0.9** for **IGH-DJ** and **TRB-DJ** (30 µl PCR sample + 27 µl beads);
- **1:0.7 for IGH-VJ-FR1** and **TRB-VJ** (30 µl PCR sample + 21 µl beads).

4.8 **Quantify all purified products** using either Qubit® dsDNA HS Assay Kit, or QuantiT PicoGreen dsDNA Assay Kit, according to the manufacturer's instructions.

4.9 **Pool the products** in equimolar ratios into **1 final pool with the concentration of 4 nM** based on the median size of the libraries and concentrations.

5. Sequencing on MiSeq

5. 1 **Perform the sequencing run** according to the MiSeq System Guide and Library preparation instructions. Use **2 x 250 bp v2 chemistry** and add **10-15 % PhiX** control library to avoid low-complexity library issues. We recommend a final concentration of **7 pM** for the amplicon library (this can be adjusted if you get optimal results with a different concentration on your MiSeq instrument, but please be cautious to avoid overclustering).

5.2 **For clarity, consistency, and simplified analysis:**

a. Use **Sample name (CODE)**, and the relevant EuroClonality-NGS **primer set names** (IGH-VJ-FR1, IGH-DJ, IGK-VJ-Kde, intron-Kde, TRB-VJ, TRB-DJ, TRD, TRG) for sample names of the respective tubes, bookended by underscores:
e.g. 1234-FU1_**IGH-DJ** or 3456-FU2_**TRD**

b. If using a polyclonal run control, add **"runQC"** to the **polyclonal** sample name, since these will serve as run quality controls and will not be analysed for spike-ins:
e.g. 220130_**runQC**_IGH-VJ-FR1

6. Data analysis

We recommend to use **ARResT/Interrogate (http://arrest.tools/interrogate-latest)** to analyze your NGS data. Please follow the instructions on the website.

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Primers for one-step IG/TR NGS-based MRD detection

Tube	Primer nomenclature	Direction	Primer-specific part	Adapter1	Index	Index sequence	Adapter2	merged name	merged sequence	Stock Concentration	PCR Vol	Primer concentration	No. of primers in mix	Dilution	Dilution Factor	Dilution volume	ul of Primer	ul of H2O	Final Volume	Aqua
IGH-V	IGH-V-FR1-B	5'	GCAGTCTGGAGCAGAGGTGAAAA	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-B_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCAGTCTGGAGCAGAGGTGAAAA	500	25	0.10	15	13.333	0.075	40	3.00	37.00	600	537.00
IGH-V	IGH-V-FR1-E	5'	GAGGTGCAGCTGTTGGAGTC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-E_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGGTGCAGCTGTTGGAGTC	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-G	5'	CAGTGGGGCGCAGGACTGTT	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-G_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGTGGGGCGCAGGACTGTT	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-H	5'	CCAGGACTGGTGAAGCCTCC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-H_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCAGGACTGGTGAAGCCTCC	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-K	5'	CCTCAGTGAAGGTTTCCTGCAAGG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-K_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTCAGTGAAGGTTTCCTGCAAGG	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-L	5'	AAACCCACAGAGACCCTCACGCTGAC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-L_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAAACCCACAGAGACCCTCACGCTGAC	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-M	5'	CTGGGGGGTCCCTGAGACTCTCCTG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-M_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGGGGGGTCCCTGAGACTCTCCTG	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-N	5'	CTTCACAGACCCTGTCCCTCACCTG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-N_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTTCACAGACCCTGTCCCTCACCTG	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-O	5'	TCGCAGACCCTCTCACTCACCTGTG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-O_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTCGCAGACCCTCTCACTCACCTGTG	500	25	0.10	15	13.333	0.075	40	3.00	37.00		
IGH-V	IGH-V-FR1-A	5'	CTGGGGCTGAGGTGAAGAAG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-A_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGGGGCTGAGGTGAAGAAG	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-V	IGH-V-FR1-C	5'	TCACCTTGAAGGAGTCTGGTCC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-C_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTCACCTTGAAGGAGTCTGGTCC	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-V	IGH-V-FR1-D	5'	AGGTGCAGCTGGTGGAGTC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-D_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGTGCAGCTGGTGGAGTC	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-V	IGH-V-FR1-F	5'	CCAGGACTGGTGAAGCCTTC	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-F_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCAGGACTGGTGAAGCCTTC	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-V	IGH-V-FR1-I	5'	GTACAGCTGCAGCAGTCAGG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-I_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACAGCTGCAGCAGTCAGG	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-V	IGH-V-FR1-J	5'	GCTGGTGCAATCTGGGTCTG	AATGATACGGCGACCACCGAGATCTACAC	D501	TATAGCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-V-FR1-J_D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCTGGTGCAATCTGGGTCTG	500	25	0.20	15	6.667	0.15	40	6.00	34.00		
IGH-D	IGH-D-A	5'	GATTCYGAACAGCCCCGAGTCA	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-A_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGATTCYGAACAGCCCCGAGTCA	500	25	0.20	8	12.500	0.08	75	6.00	69.00	600	552
IGH-D	IGH-D-B	5'	GATTTTGTGGGGGYTCGTGTC	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-B_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGATTTTGTGGGGGYTCGTGTC	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-C	5'	GTTTGRRGTGAGGTCTGTGTCA	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-C_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTTGRRGTGAGGTCTGTGTCA	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-D	5'	GTTTRGRRTGAGGTCTGTGTCACT	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-D_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTTRGRRTGAGGTCTGTGTCACT	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-E	5'	CTTTTTGTGAAGGSCCCTCCTR	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-E_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTCTTTTTGTGAAGGSCCCTCCTR	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-F	5'	GTTATTGTCAGGSGRTGTCAGAC	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-F_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTATTGTCAGGSGRTGTCAGAC	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-G	5'	GTTATTGTCAGGGGGTGYCAGRC	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-G_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTATTGTCAGGGGGTGYCAGRC	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGH-D	IGH-D-H	5'	GTTTCTGAAGSTGTCTGTRTCAC	AATGATACGGCGACCACCGAGATCTACAC	D502	ATAGAGGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGH-D-H_D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTTCTGAAGSTGTCTGTRTCAC	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
IGK-V	IGK-V-A	5'	AAGTGGGGTCCCATCAAGGTTCAG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-A_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAAGTGGGGTCCCATCAAGGTTCAG	500	25	0.10	11	18.182	0.055	50	2.75	47.25	550	519.75
IGK-V	IGK-V-B	5'	AGTCCCATCTCGGTTCAGTGGCAG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-B_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGTCCCATCTCGGTTCAGTGGCAG	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-C	5'	GAAACAGGGGTCCCATCAAGGTTC	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-C_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGAAACAGGGGTCCCATCAAGGTTC	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-D	5'	TCCCAGACAGATTCAGTGGCAGTG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-D_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTCCCAGACAGATTCAGTGGCAGTG	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-E	5'	CTGGAGTGCCAGATAGGTTCAGTG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-E_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGGAGTGCCAGATAGGTTCAGTG	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-F	5'	CCCTGGAGTCCCAGACAGGTTCAG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-F_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCTGGAGTCCCAGACAGGTTCAG	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-G	5'	GCATCCCAGCCAGGTTCAGTG	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-G_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCATCCCAGCCAGGTTCAGTG	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-H	5'	GTCCCTGACCGATTCAGTGGCA	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-H_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTCCCTGACCGATTCAGTGGCA	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-I	5'	AATCCCACCTCGATTCAGTGGC	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-I_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAATCCCACCTCGATTCAGTGGC	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-J	5'	CTCAGGGGTCCCCTCGAGGTT	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-J_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCAGGGGTCCCCTCGAGGTT	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-V	IGK-V-K	5'	AGACACTGGGGTCCCAGCCA	AATGATACGGCGACCACCGAGATCTACAC	D503	CCTATCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-V-K_D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGACACTGGGGTCCCAGCCA	500	25	0.10	11	18.182	0.055	50	2.75	47.25		
IGK-Intron	IGK-INTR-A	5'	GAGTGGCTTTGGTGGCCATGC	AATGATACGGCGACCACCGAGATCTACAC	D504	GGCTCTGA	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	IGK-INTR-A_D504	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGTGGCTTTGGTGGCCATGC	100	25	0.10	1	40.000	0.025	550	13.75	536.25	550.00	536.25
TRB-V	TRB-V-C	5'	TCGCTTCTCACCTGAATGCCC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-C_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTCGCTTCTCACCTGAATGCCC	100	25	0.01	38	16.842	0.059375	16	0.950	15.05	608	499.89
TRB-V	TRB-V-A	5'	CTCAGTTGAAAGGCCTGATGGA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-A_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCAGTTGAAAGGCCTGATGGA	100	25	0.01	38	8.421	0.11875	16	1.900	14.10		
TRB-V	TRB-V-X	5'	GGAAGCATCCCTGATCGATTCT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-X_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGGAAGCATCCCTGATCGATTCT	100	25	0.01	38	8.421	0.11875	16	1.900	14.10		
TRB-V	TRB-V-AA	5'	TCAGCTAAGTGCCTCCCAAATT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AA_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTCAGCTAAGTGCCTCCCAAATT	100	25	0.01	38	8.421	0.11875	16	1.900	14.10		
TRB-V	TRB-V-B	5'	AGTTCCAAATCGCTTCTCACCT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-B_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTAGTTCCAAATCGCTTCTCACCT	100	25	0.01	38	8.421	0.11875	16	1.900	14.10		
TRB-V	TRB-V-F	5'	TTCCCTAATCGATTCTCAGGGC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-F_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTTCCCTAATCGATTCTCAGGGC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-J	5'	TACAACTGCCAAAGGAGAGGTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-J_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTACAACTGCCAAAGGAGAGGTC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-L	5'	TAAAGGAGAAGTCCCGAATGGC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-L_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTAAAGGAGAAGTCCCGAATGGC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-M	5'	GGAGAAGTTCCCAATGGCTACA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-M_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGGAGAAGTTCCCAATGGCTACA	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-S	5'	ATAAAGGAGAAGTCCCCGATGG	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-S_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTATAAAGGAGAAGTCCCCGATGG	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-W	5'	CTCTAGATGATTCGGGGATGCC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-W_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCTAGATGATTCGGGGATGCC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-Z	5'	TGAAGCAGACACCCCTGATAAC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-Z_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTGAAGCAGACACCCCTGATAAC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-AE	5'	TGAGCGATTTTTAGCCCAATGC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AE_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTGAGCGATTTTTAGCCCAATGC	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-AG	5'	ACAAAGGAGAGATCTCTGATGGA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AG_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTACAAAGGAGAGATCTCTGATGGA	100	25	0.03	38	4.211	0.2375	16	3.800	12.20		
TRB-V	TRB-V-D	5'	GGAAACTTCCCTGGTCGATTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-D_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGGAAACTTCCCTGGTCGATTC	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-N	5'	CAACGATCGGTTCTTTGCAGTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-N_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCAACGATCGGTTCTTTGCAGTC	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-O	5'	TAAATCAGGGCTGCTCAGTGAT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-O_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTAAATCAGGGCTGCTCAGTGAT	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-P	5'	CAGTGATCGGTTCTCTGCAGAG	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-P_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGTGATCGGTTCTCTGCAGAG	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-R	5'	CTTGAACGATTCTCCGCACAAC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-R_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTTGAACGATTCTCCGCACAAC	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-V	5'	CCGAGGATCGATTCTCAGCTAA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-V_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCCGAGGATCGATTCTCAGCTAA	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-AB	5'	GCCAAAGGAACGATTTTCTGCT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AB_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGCCAAAGGAACGATTTTCTGCT	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-AI	5'	AGGGAGATGTTCCTGAAGGGTA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AI_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGGAGATGTTCCTGAAGGGTA	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-AJ	5'	CCTGAGGGGTACAGTGTCTCTA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AJ_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTGAGGGGTACAGTGTCTCTA	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-AL	5'	CAGAATCTCTCAGCCTCCAGAC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AL_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGAATCTCTCAGCCTCCAGAC	500	25	0.05	38	10.526	0.095	16	1.520	14.48		
TRB-V	TRB-V-E	5'	ACTTCCCTGATCGATTCTCAGC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-E_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTACTTCCCTGATCGATTCTCAGC	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-H	5'	CTCAGGTCACCAGTTCCCTAAC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-H_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCAGGTCACCAGTTCCCTAAC	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-I	5'	CCTAGATTTTCAGGTCGCCAGT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-I_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTAGATTTTCAGGTCGCCAGT	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-Q	5'	CTCAACTAGACAAATCGGGGCT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-Q_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCAACTAGACAAATCGGGGCT	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-U	5'	ATCGATTTTCTGCAGAGAGGCT	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-U_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTATCGATTTTCTGCAGAGAGGCT	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-Y	5'	CGGTATGCCCAACAATCGATTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-Y_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCGGTATGCCCAACAATCGATTC	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-AC	5'	CTGAAGGGTACAGCGTCTCTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AC_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGAAGGGTACAGCGTCTCTC	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-AH	5'	TCCTCTGAGTCAACAGTCTCCA	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AH_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTCCTCTGAGTCAACAGTCTCCA	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-AK	5'	CTGAGGCCACATATGAGAGTGG	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AK_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGAGGCCACATATGAGAGTGG	500	25	0.10	38	5.263	0.19	16	3.040	12.96		
TRB-V	TRB-V-G	5'	GATTCTCAGGTCTCCAGTTCCC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-G_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGATTCTCAGGTCTCCAGTTCCC	500	25	0.15	38	3.509	0.285	16	4.560	11.44		
TRB-V	TRB-V-K	5'	TACCACTGGCAAAGGAGAAGTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-K_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTACCACTGGCAAAGGAGAAGTC	500	25	0.15	38	3.509	0.285	16	4.560	11.44		
TRB-V	TRB-V-T	5'	CAAAGGAGAAGTCTCAGATGGC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-T_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAAGGAGAAGTCTCAGATGGC	500	25	0.15	38	3.509	0.285	16	4.560	11.44		
TRB-V	TRB-V-AD	5'	TTTCTCATCAACCATGCAAGCC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AD_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTTTTCTCATCAACCATGCAAGCC	500	25	0.15	38	3.509	0.285	16	4.560	11.44		
TRB-V	TRB-V-AF	5'	GGAGATGCACAAGAAGCGATTC	AATGATACGGCGACCACCGAGATCTACAC	D505	AGGCGAAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-V-AF_D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCTGGAGATGCACAAGAAGCGATTC	500	25	0.15	38	3.509	0.285	16	4.560	11.44		
TRB-D	TRB-D-A	5'	CCTCCACTCCCCTCAAAGGA	AATGATACGGCGACCACCGAGATCTACAC	D506	TAATCTTA	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-D-A_D506	AATGATACGGCGACCACCGAGATCTACACTAATCTTAACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTCCACTCCCCTCAAAGGA	500	25	0.10	2	100.000	0.01	275	2.75	272.25	550	544.50
TRB-D	TRB-D-B	5'	CAGACTAACCTCTGCCACCTG	AATGATACGGCGACCACCGAGATCTACAC	D506	TAATCTTA	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRB-D-B_D506	AATGATACGGCGACCACCGAGATCTACACTAATCTTAACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGACTAACCTCTGCCACCTG	500	25	0.10	2	100.000	0.01	275	2.75	272.25		
TRG-V	TRG-V-E	5'	CAAGCATGAGGAGGAGCTGGAAATTG	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-E_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAGCATGAGGAGGAGCTGGAAATTG	100	25	0.05	8	10.000	0.1	75	7.50	67.50	600	564.00
TRG-V	TRG-V-F	5'	ACGTCTACATCCACTCTCACC	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-F_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTACGTCTACATCCACTCTCACC	100	25	0.05	8	10.000	0.1	75	7.50	67.50		
TRG-V	TRG-V-A	5'	GCACAAGGAACAACTTGAGATTG	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-A_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCACAAGGAACAACTTGAGATTG	500	25	0.10	8	25.000	0.04	75	3.00	72.00		
TRG-V	TRG-V-B	5'	TGGAAGCACAAGGAAGAACTTGAGAA	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-B_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTTGGAAGCACAAGGAAGAACTTGAGAA	500	25	0.10	8	25.000	0.04	75	3.00	72.00		
TRG-V	TRG-V-C	5'	GCACAGGGAAGAGCCTTAAATT	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-C_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCACAGGGAAGAGCCTTAAATT	500	25	0.10	8	25.000	0.04	75	3.00	72.00		
TRG-V	TRG-V-D	5'	CAGGAGGTGGAGCTGGATATT	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-D_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGGAGGTGGAGCTGGATATT	500	25	0.10	8	25.000	0.04	75	3.00	72.00		
TRG-V	TRG-V-G	5'	CTCTCACTTCAATCCTTACCATCAA	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-G_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCTCACTTCAATCCTTACCATCAA	500	25	0.10	8	25.000	0.04	75	3.00	72.00		
TRG-V	TRG-V-H	5'	GCTCACACTTCCACTTCCACTTTGAAAATAAAGT	AATGATACGGCGACCACCGAGATCTACAC	D507	CAGGACGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRG-V-H_D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCTCACACTTCCACTTCCACTTTGAAAATAAAGT	500	25	0.20	8	12.500	0.08	75	6.00	69.00		
TRD-F	TRD-V-A	5'	GAATGCAAAAAGTGGTCGCTATTC	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-A_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTGAATGCAAAAAGTGGTCGCTATTC	500	25	0.20	9	11.111	0.09	50	4.50	45.50	450	409.50
TRD-F	TRD-V-B	5'	TGCAAAGAACCTGGCTGTACT	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-B_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCAAAGAACCTGGCTGTACT	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-C	5'	TGCAGATTTTACTCAAGGACGG	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-C_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCAGATTTTACTCAAGGACGG	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-D	5'	GCAAAATGCAACAGAAGGTCG	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-D_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTGCAAAATGCAACAGAAGGTCG	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-E	5'	GATAAAAATGAAGATGGAAGATTCACTGT	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-E_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTGATAAAAATGAAGATGGAAGATTCACTGT	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-F	5'	CTCCTTCAATAAAAGTGCCAAGC	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-F_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCCTTCAATAAAAGTGCCAAGC	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-G	5'	ATTGAAAAGAAGTCAGGAAGACTAAGT	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-G_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTATTGAAAAGAAGTCAGGAAGACTAAGT	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-V-H	5'	TCCAGAAAGCAGCCAAATCC	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-V-H_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTTCCAGAAAGCAGCCAAATCC	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
TRD-F	TRD-D-A	5'	AGGGGTATTGTGGATGGCAG	AATGATACGGCGACCACCGAGATCTACAC	D508	GTACTGAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	TRD-D-A_D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGGGTATTGTGGATGGCAG	500	25	0.20	9	11.111	0.09	50	4.50	45.50		
IGH-DJ	IGH-J-FR1-A	3'	CTTACCTGAGGAGACGGTGACC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGH-J-FR1-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTACCTGAGGAGACGGTGACC	200	25	0.40	1	20.000	0.05	150	7.50	142.50	150	142.50
IGH-VJ	IGH-J-FR1-A	3'	CTTACCTGAGGAGACGGTGACC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGH-J-FR1-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTACCTGAGGAGACGGTGACC	200	25	0.10	2	40.000	0.025	75	1.88	73.13	150	146.25
IGH-VJ	IGH-J-FR1-B	3'	CTCACCTGAGGAGACGGTGACC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGH-J-FR1-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTCACCTGAGGAGACGGTGACC	200	25	0.10	2	40.000	0.025	75	1.88	73.13		
IGK-Kde	IGK-DE-A	3'	GCAGCTGCAGACTCATGAGGAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGK-DE-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGCTGCAGACTCATGAGGAG	200	25	0.10	1	80.000	0.0125	150	1.88	148.13	150	148.13
IGK-J	IGK-DE-A	3'	GCAGCTGCAGACTCATGAGGAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGK-DE-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGCTGCAGACTCATGAGGAG	200	25	0.10	4	20.000	0.05	40	2.00	38.00	160	152.00
IGK-J	IGK-J-A	3'	ACGTTTGATCTCCACCTTGGTCCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGK-J-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACGTTTGATCTCCACCTTGGTCCC	200	25	0.10	4	20.000	0.05	40	2.00	38.00		
IGK-J	IGK-J-B	3'	ACGTTTGATATCCACTTTGGTCCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGK-J-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACGTTTGATATCCACTTTGGTCCC	200	25	0.10	4	20.000	0.05	40	2.00	38.00		
IGK-J	IGK-J-C	3'	ACGTTTAATCTCCAGTCGTGTCCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	IGK-J-C_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACGTTTAATCTCCAGTCGTGTCCC	200	25	0.10	4	20.000	0.05	40	2.00	38.00		
TRB-J	TRB-J-A	3'	CTACAACTGTGAGTCTGGTGCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTACAACTGTGAGTCTGGTGCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48	168	157.5
TRB-J	TRB-J-B	3'	CTACAACGGTTAACCTGGTCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTACAACGGTTAACCTGGTCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-C	3'	TACAACAGTGAGCCAACTTCCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-C_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTACAACAGTGAGCCAACTTCCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-D	3'	CAAGACAGAGAGCTGGGTTCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-D_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGACAGAGAGCTGGGTTCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-E	3'	CTAGGATGGAGAGTCGAGTCCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-E_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTAGGATGGAGAGTCGAGTCCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-F	3'	CTGTCACAGTGAGCCTGGTC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-F_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGTCACAGTGAGCCTGGTC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-G	3'	CCTTCTTACCTAGCACGGTGAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-G_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCTTCTTACCTAGCACGGTGAG	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-H	3'	TTACCCAGTACGGTCAGCCTAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-H_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTACCCAGTACGGTCAGCCTAG	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-I	3'	CTTACCGAGCACTGTCAGCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-I_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTACCGAGCACTGTCAGCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-J	3'	CTTACCCAGCACTGAGAGCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-J_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTACCCAGCACTGAGAGCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-K	3'	TCACCGAGCACCAGGAGCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-K_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCACCGAGCACCAGGAGCC	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-N	3'	GAATCTCACCTGTGACCGTGAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-N_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAATCTCACCTGTGACCGTGAG	200	25	0.03	14	22.857	0.04375	12	0.53	11.48		
TRB-J	TRB-J-L	3'	GAAAACTCACCCAGCACGGTC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-L_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAAAACTCACCCAGCACGGTC	200	25	0.10	14	5.714	0.175	12	2.10	9.90		
TRB-J	TRB-J-M	3'	TCACCCAGCACGGTCAGCC	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRB-J-M_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCACCCAGCACGGTCAGCC	200	25	0.10	14	5.714	0.175	12	2.10	9.90		
TRG-J	TRG-J-A	3'	AGTGTTGTTCCACTGCCAAAG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRG-J-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGTTGTTCCACTGCCAAAG	200	25	0.20	4	10.000	0.1	40	4.00	36.00	160	144.00
TRG-J	TRG-J-B	3'	GTTCCGGGACCAAATACCTTG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRG-J-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTCCGGGACCAAATACCTTG	200	25	0.20	4	10.000	0.1	40	4.00	36.00		
TRG-J	TRG-J-C	3'	GAGCTTAGTCCCTTCAGCAAATA	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRG-J-C_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGCTTAGTCCCTTCAGCAAATA	200	25	0.20	4	10.000	0.1	40	4.00	36.00		
TRG-J	TRG-J-D	3'	CCTAGTCCCTTTTGCAAACG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRG-J-D_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCTAGTCCCTTTTGCAAACG	200	25	0.20	4	10.000	0.1	40	4.00	36.00		
TRD-R	TRD-J-A	3'	TTCCACAGTCACACGGGT	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-J-A_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTCCACAGTCACACGGGT	200	25	0.20	6	6.667	0.15	25	3.75	21.25	150	127.50
TRD-R	TRD-J-B	3'	GGTTCCACGATGAGTTGTGTT	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-J-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGTTCCACGATGAGTTGTGTT	200	25	0.20	6	6.667	0.15	25	3.75	21.25		
TRD-R	TRD-J-C	3'	CACGAAGAGTTTGATGCCAGT	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-J-C_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACGAAGAGTTTGATGCCAGT	200	25	0.20	6	6.667	0.15	25	3.75	21.25		
TRD-R	TRD-J-D	3'	GTTGTTGTACCTCCAGATAGGTT	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-J-D_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTGTTGTACCTCCAGATAGGTT	200	25	0.20	6	6.667	0.15	25	3.75	21.25		
TRD-R	TRD-J-E	3'	TGGCTAGAAACACTTACTTGCA	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-J-E_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGGCTAGAAACACTTACTTGCA	200	25	0.20	6	6.667	0.15	25	3.75	21.25		
TRD-R	TRD-D-B	3'	CCCAGGGAAATGGCACTTTTG	CAAGCAGAAGACGGCATACGAGAT	D701	CGAGTAAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TRD-D-B_D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCCAGGGAAATGGCACTTTTG	200	25	0.20	6	6.667	0.15	25	3.75	21.25		

EuroClonality

Index sequences

D501	TATAGCCT
D502	ATAGAGGC
D503	CCTATCCT
D504	GGCTCTGA
D505	AGGCGAAG
D506	TAATCTTA
D507	CAGGACGT
D508	GTACTGAC
D701	CGAGTAAT
D702	TCTCCGGA
D703	AATGAGCG
D704	GGAATCTC
D705	TTCTGAAT
D706	ACGAATTC
D707	AGCTTCAG
D708	GCGCATTA
D709	CATAGCCG
D710	TTCGCGGA
D711	GCGCGAGA
D712	CTATCGCT

A501	TGAACCTT
A502	TGCTAAGT
A503	TGTTCTCT
A504	TAAGACAC
A505	CTAATCGA
A506	CTAGAACA
A507	TAAGTTCC
A508	TAGACCTA
A701	ATCACGAC
A702	ACAGTGGT
A703	CAGATCCA
A704	ACAAACGG
A705	ACCCAGCA
A706	AACCCCTC
A707	CCCAACCT
A708	CACCACAC
A709	GAAACCCA
A710	TGTGACCA
A711	AGGGTCAA
A712	AGGAGTGG