**Table S1**. Primer sequences for isoform variants.

| Primer name | Sequence | n | GC % | Tm | Location | Details | Type |
|---|---|---|---|---|---|---|---|
| AGER-F | GACTCTTAGCTGGCACTTGGA | 21 | 52.4 | 59.7 | exon 5 | For all variants | |
| AGER-R | GCTGGGGTCACCATTAGCTC | 20 | 60 | 60.5 | exon 6 | | |
| AGERvs-F | AGCATCATCGAACCAGGCGA | 20 | 55 | 59.8 | exon 8/9 | 183bp amplicon including exon coding for transmembrane; | 1 |
| AGERvs-R | TCCTGGTTTTCTGGGGCCTT | 20 | 55 | 59.1 | exon 11 | 139bp amplicon for soluble AGER. | 1 |
| IFI27-F | CTTCACTGCGGCGGGAATC | 19 | 63.2 | 59 | exon 4 | 118bp amplicon for all variants. | |
| IFI27-R | CAGGATGAACTTGGTCAATCCG | 22 | 50 | 57.9 | exon 5 | | |
| IFI27V-F | CACATTCTCAGGAACTCTCCTTC | 23 | 47.8 | 57.4 | exon 1 | Different sizes amplicons when used with IFI27-R. | 1 |
| IFNGR1-F | GTCAGAGTTAAAGCCAGGGTTG | 22 | 50 | 57.8 | exon 3 | 122bp amplicon for all variants. | |
| IFNGR1-R | GCTTCTCCTCCTTTCTGATATCCA | 24 | 25.8 | 58.8 | exon 4 | | |
| IFNGR1v1-F | CAGGGTGTGAGCAGGGCTG | 19 | 68.4 | 60.3 | exon 1 | For use with IFNGR1v-R | 2 |
| IFNGR1v2-F | GAAGTCACCAGAAAATAGTCTTCTC | 25 | 40 | 56.8 | exon 1 | For use with IFNGR1v-R | 2 |
| IFNGR1v3-F | GGACATTTCTCCATTTCTCAGAAC | 24 | 41.7 | 57 | exon 1 | For use with IFNGR1v-R | 2 |
| IFNGR1v-R | GTTGGTGCAACTTAGCTGATCT | 22 | 45.5 | 57.5 | exon 7 | | 2 |
| IFNGR2-F | CTACGCCTTCGAGCTGAGCT | 20 | 60 | 59.9 | exon 3 | 144bp amplicon for all variants. | |
| IFNGR2-R | GTCAAAGGGAGAGGAGAACCTG | 22 | 54.5 | 58.6 | exon 4 | | |
| IFNGR2v-F | CATGCGACCGACGCTGCT | 18 | 66.7 | 60.5 | exon 1 | Use with IFNGR2-R. Variant 1 is 57bp longer (547bp) than variant 2 | 1 |
| IFNGR2v1-R | GAGTAGCTGCTGAATCATTGC | 21 | 47.6 | 55.7 | exon 2 | Variant-specific primer for extra exon 2. Use with IFNGR2-R. | 2 |
| IL13RA1-F | GCCACCTGTGACAAATTTGAGT | 22 | 45 | 59.6 | exon 3 | 155bp amplicon for all variants. | |
| IL13RA1-R | CGACGAGTTTCCGGAGCTAT | 20 | 55 | 59.6 | exon 4 | | |
| | Primers for variants were not synthesized because only one Refseq sequence for this gene was available. | | | | | | |
| IL13RA2-F | TGCTCAGATGACGGAATTTGGA | 22 | 45 | 60 | exon 8 | 150bp amplicon for all variants. | |
| IL13RA2-R | CTTACGCAAAAGCAGACCGG | 20 | 55 | 59.8 | exon 9 | | |
| | Only one IL13RA2 Refseq was reported and no primers for variants were synthesized. | | | | | | |
| IL17RA-F | CAACATCACCGTGGAGACCC | 20 | 60 | 60.67 | exon 7 | 199bp amplicon for all variants. | |
| IL17RA-R | TGCGTAGAGTGAGTGTGACG | 20 | 55 | 59.76 | exon 8 | | |
| IL17RAv-F | CACTCCGCGACTGTTTCCTG | 20 | 60 | 59.2 | exon 9 | To differentiate between variants with alternative exon. The | 1 |
| IL17RAv-R | GAGTAGATGATCCAGACCTTCCTG | 24 | 50 | 58.9 | exon 13 | amplicon sizes were 266bp for v1 and 171 bp for v2 with no exon | 1 |
| IL17RC-F | GACGAACATCTGCCCCTTCA | 20 | 55 | 60.04 | exon 10 | 199bp amplicon for all variants. | |
| IL17RC-R | TGACGTTCTCCCAGGAAAGC | 20 | 55 | 59.97 | exon 11 | | |
| IL17RCv-F | AGAAGGAGACCGACTGTGAC | 20 | 55 | 58.7 | exon 3 | Exons 6 and 7 could be variable. Expected amplicons were 270bp, | 1 |
| IL17RCv-R | GCTGTGTGTGGTTGAGTTCC | 20 | 55 | 59.3 | exon 8 | 276bp and 345bp. | 1 |
| IL4R-Fn | GTGCGTGTGCCACCTGCT | 18 | 66.7 | 60.6 | exon 5 | 149bp amplicon for all variants. | |
| IL4R-Rn | GTGAACTGTCAGGTTTCCTGGG | 22 | 54.5 | 59.6 | exon 6 | | |
| IL4Rv-F | ATGGGGTGGCTTTGCTCTGG | 20 | 60 | 60.6 | exon 3 | Maximal amplicon size of 1kb. | 1 |
| IL4Re10v-R | ACCGCTTCTCCCACTGTGAC | 20 | 60 | 60 | exon 10 | | 1 |
| MYD88-F | CCGGATGGTGGTGGTTGT | 18 | 61 | 59.6 | exon 4 | For all variants | |
| MYD88-R | ATGCTGGGGAACTCTTTCTTCA | 22 | 45 | 59.6 | exon 5 | | |
| MYD88v-F | TGCTGGAGCTGGGACCCAG | 19 | 68.4 | 63.89 | exon 1 | Variants amplicons differ in size from 50 to 390bps. | 1 |
| MYD88v-R | AGACAACCACCACCATCCGG | 20 | 60 | 62.12 | exon 4 | | 1 |
| PDGFRA-F | AGAGATCATTGGAGGCCGTG | 20 | 55 | 57.4 | exon 2 | 151bp amplicon for all variants. Only recognize 3 of 5 Refseq | |
| PDGFRA-R | TTAGGCTCAGCCCTGTGAGA | 20 | 55 | 58 | exon 3 | reported variants. | |
| PDGFRA-Fn | GAACATTGTAAACTTGCTGGGAG | 23 | 43.5 | 57.1 | exon 14 | Recognize all variants. 152bp amplicon for all variants. | |
| PDGFRA-Rn | CAGCTCTTTCTTTGGCTTCTCTG | 23 | 47.8 | 58.7 | exon 15 | | |
| PDGFRAv1-R | CTGAGTTATCATCTGAAAGGAGGT | 24 | 41.7 | 56.9 | exon 17 | 400bp amplicon with PDGFRA-Fn. | 2 |
| PDGFRAv2-R | GCTTGGGCCTGAGCATGAC | 19 | 63.2 | 58.9 | exon 17 | 420bp amplicon with PDGFRA-Fn. | 2 |
| PDGFRB-F | CAACTTCGAGTGGACATACCC | 21 | 2.4 | 56.6 | exon 5 | 92bp amplicon for all variants. | |
| PDGFRB-R | AGCGGATGTGGTAAGGCATA | 20 | 50 | 56.7 | exon 6 | | |
| PDGFRBv-F | CTGGGAGAGGGCAGTAAGGA | 20 | 60 | 58.1 | exon 1 | 960bp amplicon for v1, 880bp for v2 y 954bp for v3. All using PDGF | 1 |
| TGFBR1-Fn | GATTATCATGAGCATGGATCCCT | 23 | 46.5 | 56.7 | exon 5 | 155bp amplicon for all variants. | |
| TGFBR1-R | TCTCTATGAGCAATGGCTGGC | 21 | 52 | 58.4 | exon 6 | | |
| TGFBR1v-F | CGAGATAGGCCGTTTGTATGTG | 22 | 50 | 57.8 | exon 2 | Using with TGFBR1-R: 773bp amplicon for v3, 762bp for v1, and 5 | 1 |
| TGFBR2-F | GATGTGAGATTTTCCACCTGTGAC | 24 | 46 | 59 | exon 2/3 | 172bp amplicon for all variants. | |
| TGFBR2-R | TTGGGGTCATGGCAAACTGT | 20 | 50 | 60.11 | exon 3/4 | | |
| TGFBR2v-F | CCGCTGCACATCGTCCTGT | 19 | 63.2 | 60.4 | Exón 1 | Used with TGFBR2-R: 359bp for v1 and 283bp for v2. | 1 |
| TGFBR3-F | GAGCTGACGCTGTGTACGAAGA | 22 | 55 | 62.6 | exon 13 | 165bp amplicon for all variants. | |
| TGFBR3-R | TTCTGCTTCATGGTGGATCACAG | 23 | 48 | 60.9 | exon 14 | | |
| | The only difference among reported TGFBR3 variants was a single aminoacid that was not tested in this study. | | | | | | |
| TNC-F | GGACAATGCGTCTCGGGC | 18 | 66.7 | 58.3 | exon 3 | For all TNC variants. 150bp amplicon. | |
| TNC-R | CTCTGTGACCCGCATCTCAT | 20 | 55 | 57.4 | exon 4 | | |
| TNCv-F | GCAAGCCCGCACGTGTGAA | 19 | 63.2 | 61.8 | exon 10 | For amplification of variable zone including exons 11 to 17/18. | 1 |
| TNCv-R | CCTCCAGCTGACAGTAGCCGA | 21 | 61.9 | 61.8 | exon 19 | The amplicon ranges from 60bp up to 2kb. | 1 |
| HPRTe-F | CCTGGCGTCGTGATTAGTGAT | 21 | 52.4 | 58.4 | | Endogenous control: houskeeping gene | |
| HPRTe-R | GAGCACACAGAGGGCTACAA | 20 | 55 | 57.5 | | | |