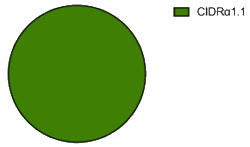
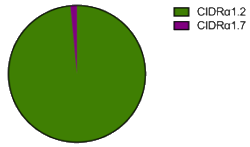
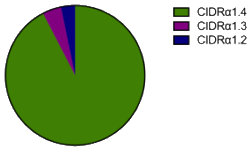
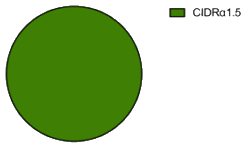
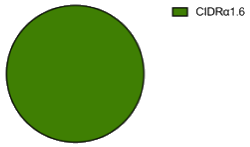
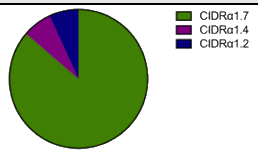
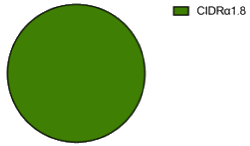
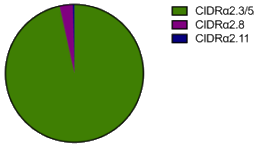
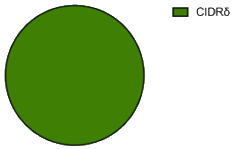
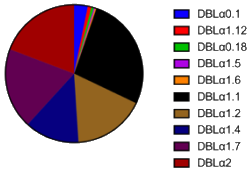
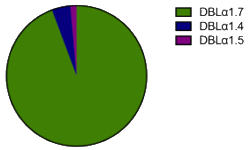
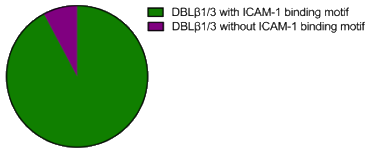
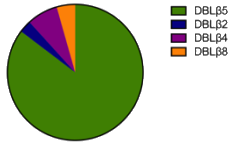
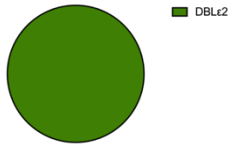
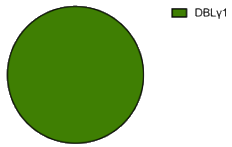
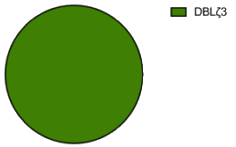
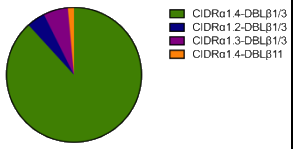
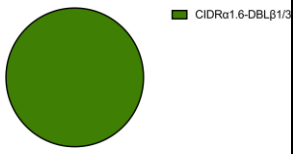
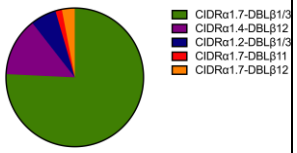
Primer Name (Domains target)	Forward Primers (5' → 3')	Reverse Primers (5' → 3')	Amplicon size bp Exact Or Min - Max	Coverage CIVIC dataset Number of sequences amplified with intended domain class / number of sequences with intended domain class (%)	Specificity CIVIC dataset Number of sequences amplified with intended domain class / number of domain sequences amplified (%)	Specificity graphic	Coverage ----- Specificity Pf3K dataset
CIDRα1.1	TAGATGCCCTAAAATGGGAACATSAACT TAGACAYCATAARGTGGGAACATSAACT TAGACASCATAARGTGGGAATATGAACT TAGACACCATAAAATGGGAACATCAACT	ACAATMHGTSACATTAGTATTATTTATGCAA ACAATYGGTGYCATAATTATTATTTATGCAA ACAATCCGTGACATTAGTATTATTTATACAA	65	105/117 (90%)	105/105 (100%)		716/797 (89%) ------- 716/717 (100%)
CIDRα1.2	TAAGGGATACTATTAAGTGGAATGA TAAMGGATACTATATTGTGGAATGA	CTTCATTTTTGTCTAGTTTATCCATAAC CTTCTCCTTGGTTAAGATCATTCAGAAC CTTCATCKTGRTTAAGCTTATCCATAACGTG	252-255	64/90 (71%)	64/65 (98%)		240/275 (87%) ------- 240/300 (80%)
CIDRα1.4	AATAGACAGTATAAAGTGG AATAGACACTATAWADTGGG AATGGATACTATAAGTTGGG	KGTTTCRTCTTGKTTAAACT TGCTTCTCCTTCGTTAAACT KKYTTCATCTTKGTTAAGCT	253-256	85/111 (77%)	85/92 (92%)		582/564 (61%) ------- 582/584 (99%)
CIDRα1.5	GAGATAMTATARWTTGGAAAAATGAMCT GGGATACTATAAATTGGAAAAGCG TAGACACTATAAATTGGGAAWATAAACT TGGATACTACAGATTGGGATCGTA ACGATACTATAGACTGGAAATACG	AAGCCAACTTTGAAAACATTTACA AACCCATTKDTMAAARCATTTACA AACCCATTTATCAAAACACGTACA	110-113	45/54 (83%)	45/45 (100%)		325/452 (72%) ------- 325/332 (98%)
CIDRα1.6	AAWCTATSAAAWATGGMAATGYTATTA CAGCTATGAGAACTGGTTATGCTATTA	TTATTTATACAATTTGTAAGTTCGTTTTTCCA ATTATTTATACAAYCCTTAAGTTCBRTTTCCCA ATTATTTATACAATTCATAAGGTCATTTTT	189	32/42 (76%)	32/32 (100%)		192/328 (59%) ------- 192/192 (100%)

Primer Name (Domains target)	**Forward Primers (5' → 3')**	**Reverse Primers (5' → 3')**	**Amplicon size bp** Exact Or Min - Max	**Coverage** **CIVIC dataset** Number of sequences amplified with intended domain class / number of sequences with intended domain class (%)	**Specificity** **CIVIC dataset** Number of sequences amplified with intended domain class / number of domain sequences amplified (%)	Specificity graphic	**Coverage** **-----** **Specificity** **Pf3K dataset**
CIDRα1.7	CGGAAACTATAAGGTGGAACGATAA CGGAAACTATAACGTGGAAMGATAA AGGATACTATAWTGTGGAATGATAA	AATAGTTCCTTTATACTATTCCATTC AATAGTTTCTTTATACTACTCCATTC AATAGTTTCTTTATACTATTCCATTC AATARTTYCTTTATATTATTCCATTC	138 - 141	63/74 (84%)	63/73 (86%)		474/636 (75%) ------- 474/474 (100%)
CIDRα1.8	TATTAATAGACAYCATAAARTGGGAA TATTAATAGACAGTATAATGTGGGAA TAATAAAGGATACTATAAAGTGGGAA	ACAATTSTTGTTACATTYATTATMACAAT ACAATTTTCGTTACAGCCATTRTYACAAT	95	44/50 (88%)	44/44 (100%)		248/305 (81%) ------- 248/253 (98%)
CIDRα2.3/5/6/ 7/9/10	TTYTTTTGGRATKGGGTACATGATATGTTAM TTTTTTTGGRAKTGGGTWTATSRTATGTTAC TTTTTTTGGAAGTGGGTTACCGAAATGTTAA	AAGTTSTSTCTTCCACTCTACAGAATC AAGTTSBTTTCTCCAMTCTAMAGAATC AAGTTCTTTCCTCCAATMYATAGAATC AWGTTCGTTTCTCCATTTAATAGAATS	60	251/460 (55%)	251/260 (97%)		1603/3084 (52%) ------- 1603/1630 (98%)
CIDRδ-Nter	TAAATGTAACTTACATGTATGTGAAC TAAATGTWACTTAGAYGTATGTGAAC TAAATGTAAGTTAGATGTGTGTGAAC TAAATGTAAYATAAATGTATGTGAAY TAAATGTAATTTASATGTATGTGAAC	AATACTTTAACCAACGYTTARTCAATAC AATATTCTAACCACCGTTTAAATAGTAC AATACATCAACCAACGCTTAATCAATAC AATACTGYAACCAACGTTTAATCAATAC AAKRCTCTAWCCAACGTTTAATRAATAC	104	124/157 (78%)	124/124 (100%)		398/555 (72%) ------- 398/403 (99%)
DBLα2/1.1/1.2/ 1.4/1.7	GAYTATGTYCCTCAATWTTTACGTTGGT GATTACGTNCCTCAATWTTTACGBTGGT GATTACGTHCCTCAATWTTTAAGATGGT GACTAYGTYCCTCAAYWTTTAMGWTGGT	NTACAATCATATCCATYATGWCWACAA GTACAATCAWATCCATTCTGACTACAA KTACARTCAWATCCATTAARACTACAA	122	325/599 (54%)	325/343 (95%)		1976/3641 (54%) ------- 1976/2009 (98%)

Primer Name (Domains target)	Forward Primers (5' → 3')	Reverse Primers (5' → 3')	Amplicon size bp Exact Or Min - Max	Coverage CIVIC dataset Number of sequences amplified with intended domain class / number of sequences with intended domain class (%)	Specificity CIVIC dataset Number of sequences amplified with intended domain class / number of domain sequences amplified (%)	Specificity graphic	Coverage ----- Specificity Pf3K dataset
DBLα1.7	AATATAGACATCCTTGTGCTCG AGGATAGACATCCTTGTCGTTT MATATAGRCATCCTTGYGCTGG GTGAAAGAGATCCTTGTTATCG	ACATACAGCTCCTTCCAAATTAAACA ACATATTGCATCTCCTTTATCTGAAAA ACATTCTGCTTCACYTTCRTWTGAAAA TACATACTGCTCCTTCCAAATTCGGATT	64 - 65	66/116 (58%)	67/70 (96%)		311/746 (42%) ------- 311/327 (95%)
DBLβ1/3	TACAAAVAMGCAGAARTTTATGCTS TACGCAAAAGCACGAATTRYTGCTA	TTATAATACCCAGWACCRCCATT	50	71/81 (87% of DBLβ1 or DBLβ3 with ICAM-1 binding motif)	71/77 (92%)		489/595 (82%) ------- 489/595 (82%)
DBLβ5	TGGATGAMNGAATGGGHCGAATGGT TAAGATGGATGAATGAATGGGCWGAATG TGGATGTCCGAATGGGCAGAATGGT TGGTTAACMGAATGGKCCGAATGGTTC	TAATTBTTGTAAGAAAGCTACCAC TATTGGGGTCAAAAAATCTACCAC GGAGTAATTCTTGTAAAAATTTAACCAC	325 - 346	58/223 (26%)	58/68 (85%)		314/3403 (9%) ------- 314/357 (88%)
DBLε2	WAATTTAATAGGTTTGGAAGCAYAY AAMWTTAATWGGTTTGGGAGCAC ARATTTRATWGGTTTAAATGCAYAC AAAATTAATAGGTTTAGAAGCACAC	GRCATAATTGTYGTACTCTAGGWGRMA GRCATAAYTGMTBATCTCTAGGAGAAA AAYATAATTGTTGTACTCTAGGAGAAA GACATAATTGTTGCACTCTAGGAGRMA	86 - 92	40/64 (63%)	40/40 (100%)		325/595 (55%) ------- 325/327 (99%)
DBLγ1	AGCTTTYATCAAATCTGCAGCAGCAGAAACA AGCATTCATCSAATGTKCWGCAGCAGAAACT	AAAAAATCTCTATAATCTCCAAAYGTGTAGAACAT CATAAATCTCTATAATCACCAAATGTGTAGAACAT	153 - 228	51/112 (46%)	51/51 (100%)		62/335 (78%) ------- 62/65 (95%)

Primer Name (Domains target)	Forward Primers (5' → 3')	Reverse Primers (5' → 3')	Amplicon size bp Exact Or Min - Max	Coverage CIVIC dataset Number of sequences amplified with intended domain class / number of sequences with intended domain class (%)	Specificity CIVIC dataset Number of sequences amplified with intended domain class / number of domain sequences amplified (%)	Specificity graphic	Coverage ----- Specificity Pf3K dataset
DBLξ3	AYCCCCCYGTTGWTGAYTATATYCCWCA ATCCACCTGATAATGATTACATTCCACA DTCCTCCTTAYGATGATTATATWCCWCA AACCTCCTTATGWYGAYTAYATTCCWCA	TTCTGACCATTCAGTCATCCATCT YTCTCCCCATTCCTTCATCCATCT TTCMCTCCATTCAGTYAWCCAACG TTCACTCCATTCTTGCATCCAWCG	59	65/97 (67%)	65/65 (100%)		387/621 (62%) ------- 387/391 (99%)
CIDRα1.4-DBLβ1/3	TGGAATAAACTTAAGGAAAATTTAAAARAAAAAAT AACTTAAAGAAAATTTAAAAAAGCAAATTGCG TGGAWGAACTTAAACAAAAWTTARAARAAAAAAT	CGTTTATAATATTGTGCKATTTGTTTYAC CGTTTAAGGTATTGTGCTATTTGTTTYAC CKTTTAAARTATTGTGCTATTTGTTTYAC	238 - 266	60/99 (61%) 28/40 (70%) DBLβ1/3 with ICAM-1-binding motif 32/59 (54%) DBLβ1/3 without ICAM-1-binding motif	60/68 (88%)		337/ 826 (41%) ------- 337/368 (92%)
CIDRα1.6-DBLβ1/3	AAAAGATATAGCTGAAAGATGCATAGACAATAA AAAAGAAACTGCAACAATATGCAAAGATAATAA	CGTTTATAATATTGTGCTATTTGTTTYAC TKTTGCATATSTTCHGCTARTTGTTTTAC	144 - 156	21/26 (81%) 6/8 (75%) DBLβ1/3 with ICAM-1-binding motif 15/18 (83%) DBLβ1/3 without ICAM-1-binding motif	21/21 (100%)		146/258 (57%) ------- 146/163 (90%)
CIDRα1.7-DBLβ1/3	GAATGGAATAGTATAAAGGAACTATT GAATGGAGTAGTATAAAGAAACTATT GAATGGAATAGTATAAAGAAACTATT GAATGGAATAATATAAAGRAAYTATT	CKTTTATAATATTGTGCKAYTTGTTTTAC CKTTTAAAGTATTGTGCTATTTGTTTYAC CGTTTATAATATTGTGCKATTTGTTTCAC	377 - 401	50/64 (78%) 10/15 (67%) DBLβ1/3 with ICAM-1-binding motif 40/49 (82%) DBLβ1/3 without ICAM-1-binding motif	50/69 (72%)		316/495 (64%) ------- 316/382 (83%)

Supplemental table S1a - *In silico* newly designed RT-qPCR *var* gene primers based on CIVIC dataset
Coverage and specificity values were calculated on CIVIC and Pf3K (African countries) datasets

Name	Primer
F1-primer	5’-AAACAAATMGCACAATAYYWTAAA-3’
F2-primer	5’-GCAMGMAGTTTYGCNGATATWGG-3’
R1-primer	5’-TGTAYATATCCTTCAGCAGTACTATA-3’
R2-primer	5’-TGTATATATCCTTCAGGAGTACTATA-3’

Supplemental table S1b - *In silico* designed primers used in Sanger sequencing