

Mouse 1 chronic

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 10917 | 40.573 | TGTGCTAGCTCTGCTGGGGGAGACTATGCTGAGCAGTCTTTC | ASSAGGDYAEQF | TRBV17 | TRBJ2-1 |
| 6198 | 23.035 | TGTGCTAGCAGGCTACAGGAAACCAAGACACCCAGTACTTT | ASRLQGNQDTQY | TRBV17 | TRBJ2-5 |
| 1829 | 6.797 | TGTGCCAGCAGAAAGTAGGGGGCTGGACCAAGACACCCAGTACTTT | ASRSRGLDQDTQY | TRBV13-3 | TRBJ2-5 |
| 1022 | 3.798 | TGTGCCAGCAGTCCGGGACACGCAAAACACAGAAGTCTTCTTT | ASSPGHANTEVF | TRBV13-3 | TRBJ1-1 |
| 1003 | 3.728 | TGTGCCAGCGGGGACGGCAACTATGCTGAGCAGTCTTTC | ASGDGNYAEQF | TRBV13-3 | TRBJ2-1 |
| 694 | 2.579 | TGTGCTAGCAGTAGAGCGGTCAGGGGGAACACAGAAGTCTTCTTT | ASSRAVRGNTEVF | TRBV17 | TRBJ1-1 |
| 581 | 2.159 | TGTGCCAGCAGTGATGGGGGTTCCACACAGAAGTCTTCTTT | ASSDGGFHTEVF | TRBV13-1 | TRBJ1-1 |
| 507 | 1.884 | TGTGCCAGCAGTGATGGGGGAGTCAAAACACCTTGACTTT | ASSDGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 424 | 1.576 | TGTGCCAGCGGTGATGAGGCAGGGGCTCAAACCTCCGACTACACCTTC | ASGDEAGGSNSDYT | TRBV13-2 | TRBJ1-2 |
| 387 | 1.438 | TGTGCTAGCAGTAGAGGTGATGAAACAGTACTTC | ASSRQYEQY | TRBV17 | TRBJ2-7 |
| 321 | 1.193 | TGTGCCAGCAGGACAGGGGTTGCAAAACACAGAAGTCTTCTTT | ASRTGGANTEVF | TRBV13-1 | TRBJ1-1 |
| 283 | 1.052 | TGTGCCAGCAGCCAAGAGACAAACGCAAACTCCGACTACACCTTC | ASSQEETNANSDYT | TRBV2 | TRBJ1-2 |
| 277 | 1.029 | TGTGCTAGCAGTCTACAGGAAACAACCAAGACACCCAGTACTTT | ASSPTGNNQDTQY | TRBV17 | TRBJ2-5 |
| 183 | 0.680 | TGTGCCAGCAGTATAGCTCTGCGTAGTCAAAACACCTTGACTTT | ASSIALRSQNTLY | TRBV19 | TRBJ2-4 |
| 174 | 0.647 | TGTGCCAGCAGGTGGGGGAATAGTCAAAACACCTTGACTTT | ASRWGNSQNTLY | TRBV13-3 | TRBJ2-4 |
| 146 | 0.543 | TGTGCCAGCAGTTTGGGGGGTTTTCCAACGAAAGATTATTTTTTC | ASSLGGFSNERLF | TRBV14 | TRBJ1-4 |
| 122 | 0.453 | TGTGCCAGCAGTAGGGGGGTTAACCAAGACACCCAGTACTTT | ASSDRGVNQDTQY | TRBV13-3 | TRBJ2-5 |
| 111 | 0.413 | TGTGCTAGCAGTTAAGGGGGGCTGAACAGTACTTC | ASSLRGAEQY | TRBV29 | TRBJ2-7 |
| 97 | 0.361 | TGTGCCAGCAGTGATGGACAAAATAACAACCAAGGCTCCGCTTTTT | ASSDQNNNQAPL | TRBV13-3 | TRBJ1-5 |
| 95 | 0.353 | TGTGCCAGCGGTGATGGCCGGGGCAAAAGATTATTTTTTC | ASGDGPGERLF | TRBV13-2 | TRBJ1-4 |
| 93 | 0.346 | TGTGCTAGCAGTAGAGCTGGGGGAAACTATGCTGAGCAGTCTTTC | ASSRAGGNYAEQF | TRBV17 | TRBJ2-1 |
| 90 | 0.334 | TGTGCCAGCAGTGATGGGGGAGGAATTCGCCCTCTACTTT | ASSDGGGRNSPLY | TRBV13-3 | TRBJ1-6 |
| 82 | 0.305 | TGTGCTAGCAGTAGAAGTGGACTGGGGGGGATTCAAAACACCTTGACTTT | ASSRSLGGIQNTLY | TRBV17 | TRBJ2-4 |
| 81 | 0.301 | TGTGCTAGCAGTCCAGGGAATAACAACCAAGGCTCCGCTTTTT | ASSPGNNNQAPL | TRBV17 | TRBJ1-5 |
| 78 | 0.290 | TGTGCCAGCAGTGATGGGGGGCGCTGCTGAGCAGTCTTTC | ASSDGGARAEQF | TRBV13-3 | TRBJ2-1 |
| 78 | 0.290 | TGTGCCAGCAGTGATGGGGGACACAACGAAAGATTATTTTTTC | ASSDGGHNERLF | TRBV13-1 | TRBJ1-4 |
| 77 | 0.286 | TGTGCCAGCAGTGTGGGCAATGCAAACTCCGACTACACCTTC | ASSVGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 68 | 0.253 | TGTGCCAGCAGTCCAGGGGGCGCAACCAAGGCTCCGCTTTTT | ASSPGGNQAPL | TRBV13-3 | TRBJ1-5 |
| 63 | 0.234 | TGTGCTAGCAGTAGGAGTCAAAACAAGCTCAACGAAAGATTATTTTTTC | GARDQTRLNERLF | TRBV20 | TRBJ1-4 |
| 59 | 0.219 | TGTGCTAGCAGTTACGGGGTGCTGAGCAGTCTTTC | ASSLRGAEQF | TRBV29 | TRBJ2-1 |
| 53 | 0.197 | TGTGCCAGCAGTGATAGGAAACGGTAATTCGCCCTCTACTTT | ASSVGNNSPLY | TRBV13-3 | TRBJ1-6 |
| 52 | 0.193 | TGTGCCAGCAGTGACAGGGGTTCTGAAATACGCTCTATTTT | ASSDRGSGNTLY | TRBV13-3 | TRBJ1-3 |
| 50 | 0.186 | TGTGCTAGCAGTACCGCCGGGACAGCAAAACACAGAAGTCTTCTTT | ASSTAGTANTEVF | TRBV17 | TRBJ1-1 |
| 50 | 0.186 | TGTGCCAGCAGTCCCGGGGTTAGTCAAAACACCTTGACTTT | ASSPGGSQNTLY | TRBV19 | TRBJ2-4 |
| 50 | 0.186 | TGTGCCAGCAGTCCAGGGGAGCTATAATTCGCCCTCTACTTT | ASSPGSYNSPLY | TRBV14 | TRBJ1-6 |
| 49 | 0.182 | TGTGCCAGCAGCTTAAGCCAGTATGCTGAGCAGTCTTTC | ASSLSQYAEQF | TRBV3 | TRBJ2-1 |
| 48 | 0.178 | TGTGCCAGCAGCCGGGACACAGTCAAAACACCTTGACTTT | ASSPGHSQNTLY | TRBV19 | TRBJ2-4 |
| 47 | 0.175 | TGTGCCAGCAGCTAAAGGGAAACTCCGACTACACCTTC | ASSLKGNSDYT | TRBV3 | TRBJ1-2 |
| 46 | 0.171 | TGTGCCAGCAGCTCGACAGGGGAAGGGGTTGAACAGTACTTC | ASSSTGEGVEQY | TRBV4 | TRBJ2-7 |
| 45 | 0.167 | TGTGCCAGCGGTGATGCACTGGGTAGTGCAGAAACGCTGATTTT | ASGDALGSAETLY | TRBV13-2 | TRBJ2-3 |
| 43 | 0.160 | TGTGCCAGCTCTCGAGGGGAACCAAGACACCCAGTACTTT | ASSLEGNQDTQY | TRBV12-2 | TRBJ2-5 |
| 42 | 0.156 | TGTGCTAGCAGTAGAGACCGGGGACAGGGGGAACACCCAGTACTTT | ASSRDRDRGNTQY | TRBV17 | TRBJ2-5 |
| 40 | 0.149 | TGTGCCAGCGGTGATAGAGGACAGGATTCTGAAAATACGCTCTATTTT | ASGDRGQDSGNTLY | TRBV13-2 | TRBJ1-3 |
| 40 | 0.149 | TGTGCCAGCAGCTCACATCTAGTCAAAACACCTTGACTTT | ASSFTSSQNTLY | TRBV3 | TRBJ2-4 |
| 38 | 0.141 | TGTGCCAGCAGTATGGGAATAGTCAAAACACCTTGACTTT | ASSYGNNSQNTLY | TRBV4 | TRBJ2-4 |
| 37 | 0.138 | TGTGCCAGCAGTGGGGACAGGGGAGGGCCACGGGACGCTACTTT | ASSWGQGRATGQLY | TRBV4 | TRBJ2-2 |
| 37 | 0.138 | TGTGCAAGCAGCTTATGGGGGACTATGCTGAGCAGTCTTTC | ASSLWGYAEQF | TRBV16 | TRBJ2-1 |

Mouse 2 chronic

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|-------------------|------------|------------|
| 2781 | 10.974 | TGTGCCAGCAGTATGGGGGACGGCTATGCTGAGCAGTCTTC | ASSMGDGYAEQF | TRBV13-3 | TRBJ2-1 |
| 2587 | 10.209 | TGTGCCAGCGGTGGGGACAATGCAAACCTCCGACTACACCTTC | ASGGDNANSDYT | TRBV13-2 | TRBJ1-2 |
| 2389 | 9.427 | TGTGCCGGGTGGACAGGGAATTCTGAAATACGCTCTATTTT | AGWTGNSGNTLY | TRBV13-3 | TRBJ1-3 |
| 2223 | 8.772 | TGTGCCAGCAGTGATTGGGGTAACTATGCTGAGCAGTCTTC | ASSDWGNVYAEQF | TRBV13-1 | TRBJ2-1 |
| 2111 | 8.330 | TGTGCCAGCAGTCCCGGTAATAGTCAAAACACCTTGACTTT | ASSPGNSQNTLY | TRBV14 | TRBJ2-4 |
| 2098 | 8.279 | TGTGCCAGCAGTCCCGGGAATAACAACAGGCTCCGCTTTT | ASSPGNNQAPL | TRBV14 | TRBJ1-5 |
| 1528 | 6.030 | TGTGCCAGCAGTATAGGACAAAATAATCGCCCTCTACTTT | ASSIGQNSPLY | TRBV19 | TRBJ1-6 |
| 1007 | 3.974 | TGTGCCAGCAGTGACGGTTCCTATAATCGCCCTCTACTTT | ASSDGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 910 | 3.591 | TGTGCTAGCAGTCCCGGGGGGACACCCCGGGCAGCTACTTT | ASSPAGDHPGQLY | TRBV17 | TRBJ2-2 |
| 856 | 3.378 | TGTGCCAGCAGTGATGACTGGGGGGGCGGGGAGCTGAGCAGTCTTC | ASSDDWGGAGAEQF | TRBV13-3 | TRBJ2-1 |
| 653 | 2.577 | TGTGCCAGCGGTGATGAGGGGACAAAACCTCCGACTACACCTTC | ASGDEGQNSDYT | TRBV13-2 | TRBJ1-2 |
| 550 | 2.170 | TGTGCCAGCGGACCGGGGGGGTCAAGACACCCAGTACTTT | ASATGGGQDTQY | TRBV13-3 | TRBJ2-5 |
| 500 | 1.973 | TGTGCCAGCAGTGATGGGACATTTAACAGGCTCCGCTTTT | ASSDGTFNQAPL | TRBV13-3 | TRBJ1-5 |
| 388 | 1.531 | TGTGCCAGCAGTCCGGGAATAATCGCCCTCTACTTT | ASSSGNYNSPLY | TRBV14 | TRBJ1-6 |
| 373 | 1.472 | TGTGCTAGCAGCTGGGGGGGACTATGCTGAGCAGTCTTC | ASSLGGDYAEQF | TRBV17 | TRBJ2-1 |
| 351 | 1.385 | TGTGCCAGCAGTGAAGGGAACCTCCGACTACACCTTC | ASSEGNSDYT | TRBV13-3 | TRBJ1-2 |
| 336 | 1.326 | TGTGCAAGCAGCTTAGTGGGACAGGGGGGAGCAGTACTTC | ASSLDQGSGQY | TRBV16 | TRBJ2-7 |
| 288 | 1.136 | TGTGGTGTAGGGATCAGGACAATTCACAGAAAAGATTATTTTTC | GARDQDNSNERLF | TRBV20 | TRBJ1-4 |
| 276 | 1.089 | TGTGCCAGCAGGACGGTTCCTATAATCGCCCTCTACTTT | ASRDGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 263 | 1.038 | TGTGCCAGCAGTCCGGACAAGCAAACACAGAAGTCTTCTTT | ASSSGQANTEVF | TRBV3 | TRBJ1-1 |
| 167 | 0.659 | TGTGCTAGCAGTACAGGGGGCTCAAACACAGAAGTCTTCTTT | ASSTGGSNTEVF | TRBV17 | TRBJ1-1 |
| 159 | 0.627 | TGTGCAAGCAGCCCTTGACTTT | ASSPLY | TRBV16 | TRBJ2-4 |
| 158 | 0.623 | TGCACCTGCAGTGACGGCCGGGACTGGGGAACTCCTATGAACAGTACTTC | TCSAGRDRWGNVSYEQY | TRBV1 | TRBJ2-7 |
| 154 | 0.608 | TGTGCCAGCAGTGAGTGGGGGGGGATGCTGAGCAGTCTTC | ASSEWGGDAEQF | TRBV13-3 | TRBJ2-1 |
| 146 | 0.576 | TGTGCTAGCAGTAGATGGAGTGGGGGGGCTGACACCTTGACTTT | ASSRWSGGADTLY | TRBV17 | TRBJ2-4 |
| 137 | 0.541 | TGTGCCAGCGGTGATGGGGGGGGCCTCCGACTACACCTTC | ASGDGGGAHSDYT | TRBV13-2 | TRBJ1-2 |
| 129 | 0.509 | TGTGCTAGCAGTCCGACTGGGGTCTAGTGCAGAAACGCTGATTTT | ASSFGLGSSAETLY | TRBV17 | TRBJ2-3 |
| 123 | 0.485 | TGTGCCAGCAGTGAAGGCAATGCAAACCTCCGACTACACCTTC | ASSEGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 116 | 0.458 | TGTGCCAGCGGTGGGGACAATGCAAACCTCCGACTACGCTTC | ASGGDNANSDYA | TRBV13-2 | TRBJ1-2 |
| 113 | 0.446 | TGTGCCAGCAGTATTGGACAGGCAAACCTCCGACTACACCTTC | ASSIGQANSDYT | TRBV13-3 | TRBJ1-2 |
| 102 | 0.403 | TGTGCCAGCAGTGTGGGACAGGGAAACAGGCTCCGCTTTT | ASSVGQGNQAPL | TRBV13-3 | TRBJ1-5 |
| 99 | 0.391 | TGTGCCAGCAGGACAGGGACCTCCAAGACACCCAGTACTTT | ASRRDRDLQDTQY | TRBV19 | TRBJ2-5 |
| 96 | 0.379 | TGTGCCAGCGGTGATCGAGGGACAGCAAACACAGAAGTCTTCTTT | ASGDRGTANTEVF | TRBV13-2 | TRBJ1-1 |
| 96 | 0.379 | TGTGCCAGCAGTGAATCAGCTGAGCAGTCTTC | ASSESAEQF | TRBV13-1 | TRBJ2-1 |
| 95 | 0.375 | TGTGCCAGCGCCCTGGGGGGGCGGAGAACAGTACTTC | ASAPWGGGEQY | TRBV13-3 | TRBJ2-7 |
| 89 | 0.351 | TGTGCCAGCAGTGGGGTCTTTCCAACGAAAGATTATTTTTC | ASSGGLSNERLF | TRBV13-3 | TRBJ1-4 |
| 83 | 0.328 | TGTGGTGTAGGGATCAAACAAATGCAAACCTCCGACTACACCTTC | GARDQTNANSDYT | TRBV20 | TRBJ1-2 |
| 83 | 0.328 | TGTGCTAGCAGTGTCCCGGGGAACTATGCTGAGCAGTCTTC | ASSVPGNYAEQF | TRBV17 | TRBJ2-1 |
| 76 | 0.300 | TGTGCCAGCAGGACAGGGGGAGCAAACACAGAAGTCTTCTTT | ASRTGGANTEVF | TRBV13-1 | TRBJ1-1 |
| 76 | 0.300 | TGTGCTAGCAGTCCGGGACAATATGAACAGTACTTC | ASSPGQYEQY | TRBV17 | TRBJ2-7 |
| 73 | 0.288 | TGTGCCAGCAACCAAGGCAATAGTCAAACACCTTGACTTT | ASNQGNSQNTLY | TRBV14 | TRBJ2-4 |
| 72 | 0.284 | TGTGCCAGCAGTGGCCGGGGCCGAAACACCGGGCAGCTCTACTTT | ASSGRGRNTGQLY | TRBV13-1 | TRBJ2-2 |
| 66 | 0.260 | TGTGCCAGCGGTGATAGGACTGGGGATAGTGCAGAAACGCTGATTTT | ASGDRTGDSAEPLY | TRBV13-2 | TRBJ2-3 |
| 59 | 0.233 | TGTGGTGTAGGGACAGTCAAACACCTTGACTTT | GARDSQNTLY | TRBV20 | TRBJ2-4 |
| 58 | 0.229 | TGTGCCAGCAGCCGGGACAGTGCAGAAACGCTGTATTTT | ASSRDSAETLY | TRBV3 | TRBJ2-3 |
| 55 | 0.217 | TGTGCCAGCAACAGTAACAACAGGCTCCGCTTTT | ASNSNNQAPL | TRBV13-1 | TRBJ1-5 |
| 51 | 0.201 | TGTGCCACACGACTGGGGCTTAAACACCGGGCAGCTCTACTTT | ATTDWGLNTGQLY | TRBV19 | TRBJ2-2 |
| 50 | 0.197 | TGTGCTAGCAGACCGAACTGGGGGGACTATGCTGAGCAGTCTTC | ASRPNWGDYAEQF | TRBV17 | TRBJ2-1 |
| 48 | 0.189 | TGTGGTGTATACAGGGTCAAACACAGAAGTCTTCTTT | GAIQGTNTEVF | TRBV20 | TRBJ1-1 |
| 44 | 0.174 | TGTGCCAGCAGTACCTGGGGAGACACCGGGCAGCTCTACTTT | ASSTWGDGTQLY | TRBV13-3 | TRBJ2-2 |

Mouse 3 chronic Part I

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 3880 | 19.220 | TGTGCCAGCGGTGATGGTAATCCAACGAAAGATTATTTTC | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 2339 | 11.587 | TGTGCCAGCTCTCTCGTGGGACAGACAACTCCGACTACACCTTC | ASSLVGQTNSDYT | TRBV12-1 | TRBJ1-2 |
| 2144 | 10.621 | TGTGCTAGCAGTAGAGAGGGACAGAAGTATGCTGAGCAGTCTTC | ASSREGQNYAEQF | TRBV17 | TRBJ2-1 |
| 1932 | 9.571 | TGTGGTGCTTTGGACAGGGAGGGTCCAAACGAAAGATTATTTTC | GALDREGSNERLF | TRBV20 | TRBJ1-4 |
| 548 | 2.715 | TGTGCCAGCGGTGATCGGGCTGGGGATAACTATGCTGAGCAGTCTTC | ASGDRAEDNYAEQF | TRBV13-2 | TRBJ2-1 |
| 548 | 2.715 | TGTGCTAGCAGTAGAGGGGATAACTATGCTGAGCAGTCTTC | ASSRGNVYAEQF | TRBV17 | TRBJ2-1 |
| 494 | 2.447 | TGTGCCAGCAGTATAGGGCAGGCAACACAGAAGTCTCTTT | ASSIGQANTEVF | TRBV19 | TRBJ1-1 |
| 491 | 2.432 | TGTGCCAGCAGTATAGGGGATAACTATGCTGAGCAGTCTTC | ASSVGNQAPL | TRBV13-3 | TRBJ1-5 |
| 449 | 2.224 | TGTGCTAGCAGTAGAGGACAATATGAACAGTACTTC | ASSRQYEQY | TRBV17 | TRBJ2-7 |
| 440 | 2.180 | TGTGCCAGCAGTGGGGACTGGGGGCTAGTCTCTATGAACAGTACTTC | ASSRGLGSSSYEQY | TRBV26 | TRBJ2-7 |
| 367 | 1.818 | TGTGGTGCTAGGGATCAAACATTTTCCAACGAAAGATTATTTTC | GARDQTFNSNERLF | TRBV20 | TRBJ1-4 |
| 360 | 1.783 | TGTGCCAGCAGTATCGGCCAGATTTCCAACGAAAGATTATTTTC | ASSIGQISNERLF | TRBV19 | TRBJ1-4 |
| 297 | 1.471 | TGTGCCAGCAGTATAGAGGGACTGGGGGTTATGCTGAGCAGTCTTC | ASSIEGLGGYAEQF | TRBV19 | TRBJ2-1 |
| 246 | 1.219 | TGTGCCAGCGGTGATAGGGGGTGGCTAGTGACAGAAACGCTGATTTT | ASGDRGVASAETLY | TRBV13-2 | TRBJ2-3 |
| 244 | 1.209 | TGTGCCAGCGGTGATCGACAGGGTCTAGTGACAGAAACGCTGATTTT | ASGDRQSSAETLY | TRBV13-2 | TRBJ2-3 |
| 218 | 1.080 | TGTGCCAGCGGGGGACACATGCAAACTCCGACTACACCTTC | ASGGTHANSDYT | TRBV13-2 | TRBJ1-2 |
| 215 | 1.065 | TGTGCCAGCAGTCCGACAGGGAGTGGGGAACTATGCTGAGCAGTCTTC | ASSSDREWGNVYAEQF | TRBV3 | TRBJ2-1 |
| 174 | 0.862 | TGTGCCAGCAGTATGGCAATAGTCAAACACCTTGTACTTT | ASSDGNQNTLY | TRBV13-3 | TRBJ2-4 |
| 158 | 0.783 | TGTGCCAGCAGTACTGGGGCTACCAAGACACCCAGTACTTT | ASSTGGYQDTQY | TRBV19 | TRBJ2-5 |
| 124 | 0.614 | TGTGGTGCTAGGGATCGGACAAATGCAAAACAGAAAGTCTCTTT | GARDRTNANTEVF | TRBV20 | TRBJ1-1 |
| 108 | 0.535 | TGTGCCAGCAGTGCAGGGGGTCAAACACCTTGTACTTT | ASSAGGQNTLY | TRBV13-3 | TRBJ2-4 |
| 99 | 0.490 | TGTGCTAGCAGTAGAGATGGGGTAACTATGCTGAGCAGTCTTC | ASSRDGGNYAEQF | TRBV17 | TRBJ2-1 |
| 97 | 0.481 | TGTGCTAGCAGTAGAGGAGGAACTATGCTGAGCAGTCTTC | ASSRGGNYAEQF | TRBV17 | TRBJ2-1 |
| 92 | 0.456 | TGTGCCAGCTCTCTCGGCGGGGTTAAATTCGCCCTACTTTT | ASSLGGGLNSPLY | TRBV12-1 | TRBJ1-6 |
| 92 | 0.456 | TGTGCCAGCAGTATGACACAGACAAACAGAAAGTCTCTTT | ASSDAQNTNEVF | TRBV13-3 | TRBJ1-1 |
| 92 | 0.456 | TGTGCCAGCAGTACAAGATAACAAACAGGCTCCGCTTTT | ASSYKNNQAPL | TRBV13-3 | TRBJ1-5 |
| 90 | 0.446 | TGTGCCAGCTCTACTGGGGGAGTCTCTATGAACAGTACTTC | ASSYWGSSYEQY | TRBV12-1 | TRBJ2-7 |
| 89 | 0.441 | TGTGCCAGCAGACGGGACAGGGATCAAACACCTTGTACTTT | ASRRDRDQNTLY | TRBV14 | TRBJ2-4 |
| 86 | 0.426 | TGCACCTGCAGTGCAGATCGGCGCTGGGGAACTATGCTGAGCAGTCTTC | TCSADRRWGNVYAEQF | TRBV1 | TRBJ2-1 |
| 84 | 0.416 | TGTGCTGGAGTCTCAGTAGGGGGACAGTAACTATGCTGAGCAGTCTTC | AWLSLRRDSNYAEQF | TRBV31 | TRBJ2-1 |
| 82 | 0.406 | TGTGCCAGCAGTGCAGGGGAAACGCAAACTCCGACTACACCTTC | ASSAGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 80 | 0.396 | TGTGCTAGCAGTAGAGCTCCGGACATCAACTCCGACTACACCTTC | ASSRAPDINSYD | TRBV17 | TRBJ1-2 |
| 79 | 0.391 | TGTGCCAGCGGTGATGGGACTGGGGGGAGGTGACACCCAGTACTTT | ASGDGTGGVEDTQY | TRBV13-2 | TRBJ2-5 |
| 78 | 0.386 | TGTGCTAGCAGTCCCGGGGGGACCAAGACACCCAGTACTTT | ASSPGGDQDTQY | TRBV17 | TRBJ2-5 |
| 76 | 0.376 | TGTGGTGCTAGGGATCAGGACAGTGCACAAACAGAAAGTCTCTTT | GARDQDSANTEVF | TRBV20 | TRBJ1-1 |
| 74 | 0.367 | TGTGCCAGCGGTGATCGGGGACAGGGGAACTATGCTGAGCAGTCTTC | ASGDRGQGNVYAEQF | TRBV13-2 | TRBJ2-1 |
| 72 | 0.357 | TGTGCCAGCAGCCAGGGGGCGGCAACAGGCTCCGCTTTT | ASSPGGNQAPL | TRBV13-3 | TRBJ1-5 |
| 71 | 0.352 | TGTGCCAGCGGTGATAGGGGACTGGCTAGTGACAGAAACGCTGATTTT | ASGDRGLASAETLY | TRBV13-2 | TRBJ2-3 |
| 69 | 0.342 | TGTGCCAGCGTCTGGGGGTAGTCAAACACCTTGTACTTT | ASRLGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 69 | 0.342 | TGTGCCAGCAGTATGGCAATGCAAACTCCGACTACACCTTC | ASSDGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 66 | 0.327 | TGTGCCAGCGGTGATAGGGGGAGGGAGTCAAACACCTTGTACTTT | ASGDRGEGSQNTLY | TRBV13-2 | TRBJ2-4 |
| 62 | 0.307 | TGTGCCAGCGGTGGGCTAAATGCAAACTCCGACTACACCTTC | ASGGLNANSDYT | TRBV13-2 | TRBJ1-2 |
| 59 | 0.292 | TGTGCCAGCAGTATCTGGGGGGGTACTTT | ASSIWGGY | TRBV19 | TRBJ2-4 |
| 54 | 0.267 | TGTGCTAGCAGTCCACCCGGGACTCTGAATGGTGGAAATACGCTCTATTTT | ASSSPRDLNNGNTLY | TRBV29 | TRBJ1-3 |
| 54 | 0.267 | TGTGCTAGCAGTCCCGGGGGACCAAGACACCCAGTACTTT | ASSPAGDQDTQY | TRBV17 | TRBJ2-5 |
| 53 | 0.263 | TGTGCCAGCAGTGGGGGGCGGCAATTCGCCCTACTTTT | ASSAGGANSPLY | TRBV13-3 | TRBJ1-6 |
| 52 | 0.258 | TGTGGTGCTAGGGATCAGACAGGGACAAACACAGAAGTCTCTTT | GARDQGTNTEVF | TRBV20 | TRBJ1-1 |
| 52 | 0.258 | TGTGCCAGCAGTATGCGTGGTATGCTGAGCAGTCTTC | ASSDAWYAEQF | TRBV13-3 | TRBJ2-1 |
| 50 | 0.248 | TGTGCCAGCGGTGACGGCAATGCAAACTCCGACTACACCTTC | ASGDGNANSDYT | TRBV13-2 | TRBJ1-2 |
| 46 | 0.228 | TGTGCCAGCGGTGATGGGGACAGGGGGCGGCTGAGCAGTCTTC | ASGDGDRGPVYAEQF | TRBV13-2 | TRBJ2-1 |
| 45 | 0.223 | TGTGGTGCTAGGGATCAACAGGGATCAAACCTCCGACTACACCTTC | GARDQGSNSDYT | TRBV20 | TRBJ1-2 |
| 45 | 0.223 | TGTGGTGACAGGGACAGGGGAGGGGAAACACCCAGTACTTT | GARDRGGEDTQY | TRBV20 | TRBJ2-5 |
| 41 | 0.203 | TGTGCCAGCGGTGGGGACAGGGCAGACACCCAGTACTTT | ASGGDRADTQY | TRBV13-2 | TRBJ2-5 |
| 41 | 0.203 | TGTGCTAGCAGCCTGGGGGGGAAACAGTACTTC | ASSRLGGEQY | TRBV17 | TRBJ2-7 |
| 40 | 0.198 | TGTGCTAGCAGTTCTGGGGGGGATACTTAACACCCGGCAGCTACTTTT | ASSFWGILNTGQLY | TRBV29 | TRBJ2-2 |
| 40 | 0.198 | TGTGCCAGCAGTCCGACTGGGGGTTAACTATGCTGAGCAGTCTTC | ASSPDWGVNYAEQF | TRBV15 | TRBJ2-1 |
| 40 | 0.198 | TGTGCCAGCAGTGCAGGGGACACCTTGTACTTT | ASSDRDLY | TRBV13-3 | TRBJ2-4 |
| 38 | 0.188 | TGTGCTAGCAGCCGGGACAACTAAACACAGAAGTCTCTTT | ASSPQLNTEVF | TRBV29 | TRBJ1-1 |
| 37 | 0.183 | TGTGCCAGCGGTGATAACAGGCAAACTCCGACTACACCTTC | ASGDNQANSDYT | TRBV13-2 | TRBJ1-2 |
| 36 | 0.178 | TGTGCCAGCAGCCAGGGACAGGGGAGGAAACACAGAAGTCTCTTT | ASSQGGRNTEVF | TRBV4 | TRBJ1-1 |
| 36 | 0.178 | TGTGCCAGCTCTCCGGGACAGGGACAGAAAGTCTCTTT | ASSLRDRDTEVF | TRBV12-1 | TRBJ1-1 |
| 36 | 0.178 | TGTGCCAGCAGTACAGCGGCGCAACACAGAAGTCTCTTT | ASSYSGANTEVF | TRBV4 | TRBJ1-1 |
| 36 | 0.178 | TGTGGTGCTAGACAGGGGGCAGGCTCCGACTACACCTTC | GARQAGGSDYT | TRBV20 | TRBJ1-2 |
| 35 | 0.173 | TGTGCCAGCAGTTAAACTACCGGGACAATCTATGGCTACACCTTC | ASSLNLPGQSYGYT | TRBV29 | TRBJ1-2 |
| 35 | 0.173 | TGTGCTAGCAGTCAACTCTTAACCAAGACACCCAGTACTTT | ASSTNLNQDTQY | TRBV17 | TRBJ2-5 |
| 35 | 0.173 | TGTGCCAGCAGTTCGGCATCTATGCTGAGCAGTCTTC | ASSSASYAEQF | TRBV14 | TRBJ2-1 |
| 34 | 0.168 | TGTGCCAGCAGTGCAGGGGACATAACTATGCTGAGCAGTCTTC | ASSEGHNYAEQF | TRBV19 | TRBJ2-1 |
| 33 | 0.163 | TGTGCCAGCAGCCTGACAGGGGGGCAACAGAAGTCTCTTT | ASSPDRGRTEVF | TRBV5 | TRBJ1-1 |
| 33 | 0.163 | TGTGCCAGCAGTATGGACCGCTGTATTTT | ASSDGLY | TRBV13-1 | TRBJ2-3 |
| 33 | 0.163 | TGTGCCAGCGGTGATCGGGGGTAAACCAAGACACCCAGTACTTT | ASGDAGGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 32 | 0.159 | TGTGCCAGCAGTCCGGGACAGGGGAAACGGCAGCTACTTTT | ASSVRDRNGQLY | TRBV13-1 | TRBJ2-2 |
| 32 | 0.159 | TGTGCCAGCAGTAGAGGGGTAACCTATGCTGAGCAGTCTTC | ASSEEGNYAEQF | TRBV13-3 | TRBJ2-1 |
| 32 | 0.159 | TGCACCTGCAGTGCAGACAGCAGAAAGTCTCTTT | TCSADSTEVF | TRBV1 | TRBJ1-1 |
| 32 | 0.159 | TGTGCCAGCAGCCTGGGGTGTGCAAAACACCTTGTACTTT | ASSPGGSQNTLY | TRBV19 | TRBJ2-4 |

Mouse 3 chronic Part II

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 31 | 0.154 | TGTGCCAGCTCTCTCGGGACAGGGGGCCGGAATAACGCTCTATTTT | ASSLGTGAGNTLY | TRBV12-2 | TRBJ1-3 |
| 31 | 0.154 | TGTGGTGTAGGGATCGGGACAATTCACACGAAAGATTATTTTTC | GARDRDINSNERLF | TRBV20 | TRBJ1-4 |
| 31 | 0.154 | TGTAGTTCTAGACCACATAAATATGCTGAGCAGTTCTTC | SSRPHNYAEQF | TRBV30 | TRBJ2-1 |
| 30 | 0.149 | TGTGCCAGCAGTGACCGGGACTGGGCAAAACACCGGGCAGCTCTACTTT | ASSDRDWANTGQLY | TRBV13-1 | TRBJ2-2 |
| 30 | 0.149 | TGTGCCAGCAGCTCAACCACTTCAAACACCGGGCAGCTCTACTTT | ASSSTTSNTGQLY | TRBV4 | TRBJ2-2 |
| 30 | 0.149 | TGTGCCAGCAGCTCTGGGGGAACTATGCTGAGCAGTTCTTC | ASSPGGNVYAEQF | TRBV14 | TRBJ2-1 |
| 30 | 0.149 | TGTGCCAGCAGTGCAGGTTCTATAATTGCCCCCTCTACTTT | ASSAGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 29 | 0.144 | TGTGCCAGCAGCTTAGAGGGGGGGGCGACTAGTGCAGAAACGCTGTATTTT | ASSLEGGATSLETLY | TRBV3 | TRBJ2-3 |
| 29 | 0.144 | TGTGCCAGCTCTCGGACTGGGGGGCAGGTGCTGAGCAGTTCTTC | ASSRTGGAGAEQF | TRBV12-1 | TRBJ2-1 |
| 28 | 0.139 | TGTGCCAGCAGTCCAGGGAATAACAACACAGGCTCCGCTTTTT | ASSPGNNNQAPL | TRBV14 | TRBJ1-5 |
| 28 | 0.139 | TGTGCCAGCAGCAAGAACCAGTCAACGAAAGATTATTTTTC | ASSQEPVNERLF | TRBV5 | TRBJ1-4 |
| 27 | 0.134 | TGTGCTAGCAGTAGGGGGACAGGGGGATTAATTCGCCCTCTACTTT | ASSRGDRGINSPLY | TRBV17 | TRBJ1-6 |
| 27 | 0.134 | TGTGCCAGCGGTGACCGGGACAGGGGACTATGCTGAGCAGTTCTTC | ASGDRTGDYAEQF | TRBV13-2 | TRBJ2-1 |
| 27 | 0.134 | TGTGGTGTAGTGAACAGGGCACCCAGTACTTT | GASEQGTQY | TRBV20 | TRBJ2-5 |
| 27 | 0.134 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 26 | 0.129 | TGTGGTGTAGGGATCGGGACAGGGGTAATGGAATAACGCTCTATTTT | GARDRDRGNGNTLY | TRBV20 | TRBJ1-3 |
| 26 | 0.129 | TGTGGTGTAGGGTGGACAGTAGTCAAACACCTTGTACTTT | GARVDSSQNTLY | TRBV20 | TRBJ2-4 |
| 26 | 0.129 | TGCACCTGCAGTCTCGAACTGGGTATGCTGAGCAGTTCTTC | TCSARTGYAEQF | TRBV1 | TRBJ2-1 |
| 26 | 0.129 | TGTGCCAGCATGAGGTTCTCTATGAACAGTACTTC | ASMRFVYEQY | TRBV19 | TRBJ2-7 |
| 25 | 0.124 | TGTGCCAGCGGTGATGCTCTTCTAGTGCAGAAACGCTGTATTTT | ASGDALPSAETLY | TRBV13-2 | TRBJ2-3 |
| 25 | 0.124 | TGTGCAAGCAGCTCTCTCGGGGACCAAGACACCCAGTACTTT | ASSSSWGDQDTQY | TRBV16 | TRBJ2-5 |
| 25 | 0.124 | TGTGCTAGCAGTAGTGGGGGCGACTATGCTGAGCAGTTCTTC | ASSSGDYAEQF | TRBV17 | TRBJ2-1 |
| 25 | 0.124 | TGTGCCAGCAGCTCGGGACTGGGGATGAACAGTACTTC | ASSSGLGDEQY | TRBV4 | TRBJ2-7 |
| 24 | 0.119 | TGTGCCAGCAGTACTGGGGACAAACACCTTGTACTTT | ASSDWGQNTLY | TRBV13-3 | TRBJ2-4 |
| 24 | 0.119 | TGTGCCAGCAGCCCTGGGGGGCGCGGAACAGTACTTC | ASSPWGGAEQY | TRBV13-3 | TRBJ2-7 |
| 24 | 0.119 | TGTGCCAGCAGTCCCTCTATGAACAGTACTTC | ASSASYEQY | TRBV13-1 | TRBJ2-7 |
| 23 | 0.114 | TGTGCCAGCAGTATTCCACTGGGGGGAGCAACTATGCTGAGCAGTTCTTC | ASSDSTGGSNYAEQF | TRBV13-1 | TRBJ2-1 |
| 23 | 0.114 | TGTGCCAGCAGTCCGGGAGCTATAATTCGCCCTCTACTTT | ASSSGSYNSPLY | TRBV14 | TRBJ1-6 |
| 22 | 0.109 | TGTGCTAGCAGTAGAGATGGGTCTAACTATGCTGAGCAGTTCTTC | ASSRDRGSNYAEQF | TRBV17 | TRBJ2-1 |
| 22 | 0.109 | TGTGCCAGCTCTCCGGACTGGGCAGTCAAACACCTTGTACTTT | ASSSGLGSQNTLY | TRBV12-1 | TRBJ2-4 |
| 22 | 0.109 | TGTGGTGTAGGGATCAAGACACATCAAACACAGAAGTCTCTTTT | GARDQDTSNTEVF | TRBV20 | TRBJ1-1 |
| 22 | 0.109 | TGTGCTGAGTTTCCGGGACAACTATGCTGAGCAGTTCTTC | AWFRDNYAEQF | TRBV31 | TRBJ2-1 |
| 21 | 0.104 | TGTGCCAGCAGTTTACTGGGGGGCTGGCTGAGCAGTTCTTC | ASSLLGLAEQF | TRBV15 | TRBJ2-1 |
| 21 | 0.104 | TGTGCCAGCAGTGTGGGACAGGGGACTCCGACTACACCTTC | ASSVGGQTSQDYT | TRBV13-3 | TRBJ1-2 |
| 21 | 0.104 | TGTGCCAGCAGCCCTGGGGTTTCTATGCTGAGCAGTTCTTC | ASSPWGFYAEQF | TRBV3 | TRBJ2-1 |
| 20 | 0.099 | TGTGCCAGCAGCGAAGGACTGGGGGGAGGAGACCCAGTACTTT | ASSEGLGGDQY | TRBV3 | TRBJ2-5 |
| 20 | 0.099 | TGTGCTAGCAGTTCCGGGACAGGGGAGACACCCAGTACTTT | ASSSGQDQY | TRBV29 | TRBJ2-5 |
| 19 | 0.094 | TGTGCCAGCGGTGATGAGGGGGGGCTCAAACACCTTGTACTTT | ASGDEGGGQNTLY | TRBV13-2 | TRBJ2-4 |
| 19 | 0.094 | TGTGCCAGCAGTTTACGACAGACTTCTGGAATAACGCTCTATTTT | ASSLRQTSQNTLY | TRBV15 | TRBJ1-3 |
| 17 | 0.084 | TGTGCTAGCAGACTGGGGGAACTATGCTGAGCAGTTCTTC | ASTTGGNYAEQF | TRBV17 | TRBJ2-1 |
| 17 | 0.084 | TGTGCCAGCAGCAAGAGGACTGGGGGGTGAACAGTACTTC | ASSQEDWGGEQY | TRBV5 | TRBJ2-7 |
| 17 | 0.084 | TGTGCCAGCAGCCAGGGGACTGGAATAACGCTCTATTTT | ASSQGTGNTLY | TRBV5 | TRBJ1-3 |
| 17 | 0.084 | TGCACCTGCAGCCTGGGGGGCTGACACCTTGTACTTT | TCSAGGADTLY | TRBV1 | TRBJ2-4 |
| 16 | 0.079 | TGTGCTAGCAGTTTAGGGACCCCTAGTGCAGAAACGCTGTATTTT | ASSLGTPSAETLY | TRBV29 | TRBJ2-3 |
| 16 | 0.079 | TGTGCTAGCAGTCTGGGGGGGATAACTATGCTGAGCAGTTCTTC | ASSLGGDNYAEQF | TRBV17 | TRBJ2-1 |
| 15 | 0.074 | TGTGCCAGCGGTGAGTCCCGGGACTATAACCAAGACACCCAGTACTTT | ASGESRDYNDQDTQY | TRBV13-2 | TRBJ2-5 |
| 15 | 0.074 | TGTGCTAGCAGTAGAGCCGGGACAGCAAAACAGAAAGTCTTCTTT | ASSRAGTANTEVF | TRBV17 | TRBJ1-1 |
| 15 | 0.074 | TGTGCCAGTAGGGGTAGAGGGACGGCCACAGTACGCAATTTT | ASRRGTATDQY | TRBV19 | TRBJ2-3 |
| 15 | 0.074 | TGTGCCAGCAGTTGGACAGGGTCTTCTGGAATAACGCTCTATTTT | ASSWTGSSGNTLY | TRBV13-3 | TRBJ1-3 |
| 15 | 0.074 | TGTGGTGTAGGGATCTGGCAAATTCACGAAAGATTATTTTTC | GARDLANSNERLF | TRBV20 | TRBJ1-4 |
| 15 | 0.074 | TGTGCTAGCAGTTTAAAGGGGACAGAAACAGTACTTC | ASSLRGREQY | TRBV29 | TRBJ2-7 |
| 14 | 0.069 | TGTGCTAGCAGTTACGCCGGGACCAACTATGCTGAGCAGTTCTTC | ASSRRDNTYAEQF | TRBV29 | TRBJ2-1 |
| 14 | 0.069 | TGTGCCACAGTATTTGGGACTAGCGGGAAGAATGAGCAGTTCTTC | ATSDFGTSGKNEQF | TRBV29 | TRBJ2-1 |
| 14 | 0.069 | TGTGCTAGCAGACTGGGACTGGCTAGTGCAGAAACGCTGTATTTT | ASRLGLASAETLY | TRBV17 | TRBJ2-3 |
| 14 | 0.069 | TGTGCCAGCAGTATAGCGAGACAAACAATTCGCCCTCTACTTT | ASSIARQNNNSPLY | TRBV19 | TRBJ1-6 |
| 14 | 0.069 | TGTGCTAGCAGTATGGGGGGCTCAAACACAGAAGTCTTCTTT | ASSMGGSNTEVF | TRBV17 | TRBJ1-1 |
| 14 | 0.069 | TGTGCCAGCAGTGAAGGCAATGCAAACCTCGGACTACACCTTC | ASSEGNANSQDYT | TRBV13-3 | TRBJ1-2 |
| 14 | 0.069 | TGTGCCAGCAGTATAGGGGGCGCTGAGCAGTTCTTC | ASSIGGAEQF | TRBV19 | TRBJ2-1 |
| 13 | 0.064 | TGTGCTAGCAGTAGAGAATGGGGGGCCACACCGGGCAGCTCTACTTT | ASSREWGHTGQLY | TRBV17 | TRBJ2-2 |
| 13 | 0.064 | TGTGCTAGCACTGGGGGGGTAACATGCTGAGCAGTTCTTC | ASTGGGNYAEQF | TRBV17 | TRBJ2-1 |
| 13 | 0.064 | TGTGCCAGCAGTCTGCTGGGGGGGAAAGACACCCAGTACTTT | ASSLLGGEDTQY | TRBV26 | TRBJ2-5 |
| 13 | 0.064 | TGTGCCAGCAGCTTACGGGGGATACCGGGCAGCTCTACTTT | ASSLRGITGQLY | TRBV3 | TRBJ2-2 |
| 13 | 0.064 | TGTGCTAGCAGTAGGGACAGAAACAGAAAGTCTTCTTT | ASSRDRNTEVF | TRBV17 | TRBJ1-1 |
| 13 | 0.064 | TGTGCCAGCTCTCTCGAGGGGCAAAACACCTTGTACTTT | ASSLEGQNTLY | TRBV12-2 | TRBJ2-4 |
| 13 | 0.064 | TGTGCCAGCAGTATGATTGGACAACCGACTACACCTTC | ASSDDWTTDYT | TRBV13-1 | TRBJ1-2 |
| 13 | 0.064 | TGTGCCAGCAGCAAGAGCTGGGGGCCGAAGTCTTCTTT | ASSQELGAEVF | TRBV5 | TRBJ1-1 |
| 13 | 0.064 | TGCACCTGCAGTGCAGCATCTATGAACAGTACTTC | TCSAAIYEQY | TRBV1 | TRBJ2-7 |
| 12 | 0.059 | TGTGCCAGCAGTATACCTCGACAGGCAAAACAGAAAGTCTTCTTT | ASSIPRQANTEVF | TRBV19 | TRBJ1-1 |
| 12 | 0.059 | TGTGCCAGCAGCTTATCAGGGGAGGACTCCGACTACACCTTC | ASSLSGEDSDYT | TRBV3 | TRBJ1-2 |

Mouse 4 chronic

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 7972 | 30.855 | TGTGCCAGCGGTGATGCTGGGGGAGTGCAGAAACGCTGTATTTT | ASGDAWGS AETLY | TRBV13-2 | TRBJ2-3 |
| 5250 | 20.320 | TGTGCTAGCAGTAGTGGAGGGGACTATGCTGAGCAGTTCCTC | ASSGGDYAEQF | TRBV17 | TRBJ2-1 |
| 2405 | 9.308 | TGTGCCAGCGGTGATCGACAAAATGCAAACACAGAAGTCTTCTTT | ASGDRQNANTEVF | TRBV13-2 | TRBJ1-1 |
| 2001 | 7.745 | TGTGCCAGCAGCAACACAGAAACACAGAAGTCTTCTTT | ASSQHRNTEVF | TRBV5 | TRBJ1-1 |
| 1158 | 4.482 | TGTGCCAGCGGTGATTGGGGGGAAGTGAATCAAACACCTTGACTTT | ASGDWGEVNQNTLY | TRBV13-2 | TRBJ2-4 |
| 914 | 3.538 | TGTGCCAGCAGTGGGGGACTGGGGGGGCGCCATGCTGAGCAGTTCCTC | ASSGDWGGADAEQF | TRBV13-3 | TRBJ2-1 |
| 464 | 1.796 | TGTGGTGTAGTGACAGAAATAGTCTCTATGAACAGTACTTC | GASDRNSSYEYQ | TRBV20 | TRBJ2-7 |
| 462 | 1.788 | TGTGCCAGCAGTGCCTGGGGGGGCGAGCTGAGCAGTTCCTC | ASSAWGGDAEQF | TRBV13-1 | TRBJ2-1 |
| 420 | 1.626 | TGTGCCAGCAGTGTCCCGGGGGATCCCAAGACACCCAGTACTTT | ASSVPGGSQDTQY | TRBV13-3 | TRBJ2-5 |
| 418 | 1.618 | TGTGCCAGCAGTGGTGTGGGACAGGGGTCCAACGAAAGATTATTTTTT | ASSVGGQGSNERLF | TRBV13-3 | TRBJ1-4 |
| 393 | 1.521 | TGTGCCAGCTCATCCGACAGGGGAGAAGGAGAACACCCGGCAGCTACTTT | ASSSDREKENTGQLY | TRBV12-2 | TRBJ2-4 |
| 332 | 1.285 | TGTGCCAGCAAGACTGGGGGGGCGCATGACACCCAGTACTTT | ASKTGGAHDTQY | TRBV13-3 | TRBJ2-5 |
| 308 | 1.192 | TGTGCCAGCGGTGACGGGAATTCACGAAAGATTATTTTTT | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 295 | 1.142 | TGTGCCAGCAGTATGGGGGCTATAATTGCCCCCTCTACTTT | ASSDGGYNSPLY | TRBV13-3 | TRBJ1-6 |
| 178 | 0.689 | TGTGCCAGCAGTCCGGGACAGGGAGGGGGGTACTTC | ASSPGQGGGY | TRBV14 | TRBJ2-7 |
| 177 | 0.685 | TGTGCTAGCACCCCGGACAGGGGACCAAGACACCCAGTACTTT | ASTPAGDQDTQY | TRBV17 | TRBJ2-5 |
| 149 | 0.577 | TGTGCCAGCAGTACAGGGAACCGTCAAACACCTTGACTTT | ASSTGNRQNTLY | TRBV19 | TRBJ2-4 |
| 140 | 0.542 | TGTGCCAGCAGTGTCCGGGACAGGGGGTATGAACAGTACTTC | ASSLGTGGYEYQ | TRBV14 | TRBJ2-7 |
| 114 | 0.441 | TGTGCCAGCAGCACAGGGGCGTCCACCTACGAGCAGTACTTC | ASSTGASTYEYQ | TRBV29 | TRBJ2-7 |
| 110 | 0.426 | TGTGCCAGCAGCTTAGATGGGGGACTGGGAGTGCAGAAACGCTGTATTTT | ASSLDGGTGS AETLY | TRBV3 | TRBJ2-3 |
| 109 | 0.422 | TGTGCCAGCAGCCAGGGACTGGGGGATACTATGAACAGTACTTC | ASSPGTGGYYEYQ | TRBV15 | TRBJ2-7 |
| 107 | 0.414 | TGTGCCAGCAGTATGGGACAAAAGAAGTCTTCTTT | ASSDGTKEVF | TRBV13-1 | TRBJ1-1 |
| 102 | 0.395 | TGCACCTGCACTGGACAAATAAATTCGCCCTCTACTTT | TCSGQYNSPLY | TRBV1 | TRBJ1-6 |
| 95 | 0.368 | TGTGCCAGCAGTCCGGGACATTTTTCCAACGAAAGATTATTTTTT | ASSPGHFSNERLF | TRBV15 | TRBJ1-4 |
| 93 | 0.360 | TGTGCCAGCAGTATTGGCTGGGGGACTAGTCAAACACCTTGACTTT | ASSIGWGT SQNTLY | TRBV19 | TRBJ2-4 |
| 93 | 0.360 | TGCACCTGCACTGCCGGACAGGGAGTGCAGAAACGCTGTATTTT | TCSARTGSAETLY | TRBV1 | TRBJ2-3 |
| 85 | 0.329 | TGTGCCAGCAGTACGGCAATGCAAACACAGAAGTCTTCTTT | ASSDGNANTEVF | TRBV13-3 | TRBJ1-1 |
| 82 | 0.317 | TGTGCCAGCAGTACCCGGGACTGGGAGCAGAAACGCTGTATTTT | ASSDPGLGAETLY | TRBV13-1 | TRBJ2-3 |
| 81 | 0.314 | TGTGCCAGCAGTGTGGGACAGTCAAACACAGAAGTCTTCTTT | ASSVGGQSNTEVF | TRBV13-3 | TRBJ1-1 |
| 76 | 0.294 | TGTGCCAGCAGTGAAGGGGGTGGTAATTCGCCCTCTACTTT | ASSEGGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 73 | 0.283 | TGTGCCAGCAGCTCGACAGCTCCAACCAGGCTCCGCTTTTT | ASSSTASNQAPL | TRBV4 | TRBJ1-5 |
| 73 | 0.283 | TGTGCAAGCAGCTTGGGACAGGGTCTATGAACAGTACTTC | ASSLGTGSYEYQ | TRBV16 | TRBJ2-7 |
| 72 | 0.279 | TGTGCCAGCGGGTCAAACACCGGGCAGCTACTTT | ASGSNTGQLY | TRBV13-3 | TRBJ2-2 |
| 70 | 0.271 | TGTGCCAGCAGTATGCACGCTTT | ASSDAR | TRBV13-3 | TRBJ1-6 |
| 68 | 0.263 | TGTGCCAGCAGTTTTCCCGGACAGGGGGATGAACAGTACTTC | ASSFPDRGDEYQ | TRBV15 | TRBJ2-7 |
| 68 | 0.263 | TGTGCCAGCAGTGGGGACAGGGGACAACCAGGCTCCGCTTTTT | ASSGDRDNQAPL | TRBV13-1 | TRBJ1-5 |
| 67 | 0.259 | TGTGCCAGCAGCAAGATTACTGGGGGGGATGAACAGTACTTC | ASSQDYWGGYEYQ | TRBV5 | TRBJ2-7 |
| 63 | 0.244 | TGTGCCAGCAGCCACTGGGGGGGCGCGGAAACGCTGTATTTT | ASSPLGGRAETLY | TRBV26 | TRBJ2-3 |
| 59 | 0.228 | TGTGCCAGCAGTATGGCAATAAGAATTCGCCCTCTACTTT | ASSDGNKNSPLY | TRBV13-3 | TRBJ1-6 |
| 56 | 0.217 | TGTGCTAGCAGTAGTAGGGACTGGGGTAAGTATGCTGAGCAGTTCCTC | ASSSRDWGN YAEQF | TRBV17 | TRBJ2-1 |
| 56 | 0.217 | TGCACCTGCACTGGGACTGGGGGGGCTCTTCAAACACCTTGACTTT | TCSGTGGALQNTLY | TRBV1 | TRBJ2-4 |
| 56 | 0.217 | TGTGCAACGACACCTACAATGAGCAGTTCCTC | ANDTYNEQF | TRBV13-2 | TRBJ2-1 |
| 53 | 0.205 | TGTGCCAGCAGTGAAGGGCAGGGACAGGCTCCGCTTTTT | ASSEGGQOAPL | TRBV13-3 | TRBJ1-5 |
| 52 | 0.201 | TGTGCTAGCAGTAGAGATGGCAGCTCTATGAACAGTACTTC | ASSRDGSSYEYQ | TRBV17 | TRBJ2-7 |
| 52 | 0.201 | TGTGCCAGCAGTGCAGTGTCTATGCTGAGCAGTTCCTC | ASSATVYAEQF | TRBV13-1 | TRBJ2-1 |
| 51 | 0.197 | TGTGCCAGCAGTATGGGACAGGGAGCAACGAAAGATTATTTTTT | ASSDGTGSNERLF | TRBV13-1 | TRBJ1-4 |
| 51 | 0.197 | TGTGCCAGCAGCCCTCTATGAACAGTACTTC | ASSPSYEYQ | TRBV13-3 | TRBJ2-7 |
| 46 | 0.178 | TGTGCCAGCAGTGTGGGACAGAATTCCTATAATTCGCCCTCTACTTT | ASSVGGQNSYNSPLY | TRBV19 | TRBJ1-6 |
| 45 | 0.174 | TGTGCCAGCAGTACTCGAGGGGCGAGAGGCAATCAGCCCCAGCATTTT | ASSYSRARGNQ PQH | TRBV8 | TRBJ1-5 |
| 43 | 0.166 | TGTGCCAGCAGCCAGGGGGCCGAGAACAGTACTTC | ASSPGGREYQ | TRBV13-3 | TRBJ2-7 |
| 42 | 0.163 | TGTGCTAGCAGTATACAGGGAAACTATGCTGAGCAGTTCCTC | ASSIQGN YAEQF | TRBV17 | TRBJ2-1 |
| 38 | 0.147 | TGTGCAAGCAGCTTAGAAAAGGGACTGGGGGGTCAAACACCTTGACTTT | ASSLEKLG GQNTLY | TRBV16 | TRBJ2-4 |

Mouse 5 chronic

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 2168 | 64.256 | TGTGCTAGCAGTAGAGCCGGGGACAACATGAACAGTACTTC | ASSRAGDNYEQY | TRBV17 | TRBJ2-7 |
| 329 | 9.751 | TGTGCTAGCAGTTTTACGGGTTTATGTCAGAAAACGCTGATTTT | ASSFTGFSAETLY | TRBV29 | TRBJ2-3 |
| 104 | 3.082 | TGTGCTAGCAGTAGACCAGGGAACTATGCTGAGCAGTCTCTC | ASSRPGNYAEQF | TRBV17 | TRBJ2-1 |
| 98 | 2.905 | TGCACCTGCAGTGCAGATCGGCAGAAATCTAACTATGCTGAGCAGTCTCTC | TCSADRRQNSNYAEQF | TRBV1 | TRBJ2-1 |
| 62 | 1.838 | TGTAGTTCTAGAGACAACACAGAAGTCTTCTTT | SSRDNTEVF | TRBV30 | TRBJ1-1 |
| 54 | 1.600 | TGTGCCAGCGGTGACCCCTGACTGGGACTCCTATGAACAGTACTTC | ASGDPDWDSYEQY | TRBV13-2 | TRBJ2-7 |
| 49 | 1.452 | TGTGCCAGCGGTGATGGCGGGGGGACACTCCGACTACACCTTC | ASGDGGGAHSDYT | TRBV13-2 | TRBJ1-2 |
| 35 | 1.037 | TGTGCCAGCGGGACAGGGGGCTATAATTCGCCCTCTACTTT | ASGTGGYNSPLY | TRBV19 | TRBJ1-6 |
| 34 | 1.008 | TGTGCTAGCAGTAGGGGGGACAACATGCTGAGCAGTCTCTC | ASSRGNDAEQF | TRBV17 | TRBJ2-1 |
| 33 | 0.978 | TGTGCCAGCAGCAAGACAACGGCAGGGGAATGCAGAAACGCTGATTTT | ASSQDKRQNAETLY | TRBV5 | TRBJ2-3 |
| 31 | 0.919 | TGTGCCAGCAGTGTTCCTGGGGGGATGAACAGTACTTC | ASSVSWGDEQY | TRBV13-3 | TRBJ2-7 |
| 24 | 0.711 | TGTGCCAGCAGTTTTCGGGGATTTTCCAACGAAAGATTATTTTC | ASSFGGISNERLF | TRBV14 | TRBJ1-4 |
| 24 | 0.711 | TGTGGTGTAGGGATCGCACAGGGGAAACACAGAAGTCTTCTTT | GARDRTGGNTEVF | TRBV20 | TRBJ1-1 |
| 23 | 0.682 | TGTGCTAGCACACAGGGGTAACATGCTGAGCAGTCTCTC | ASTTGGNYAEQF | TRBV17 | TRBJ2-1 |
| 21 | 0.622 | TGTGCCTGGAGTCTAAGGGACTGGGGTAACCAAGACACCCAGTACTTT | AWSLRDWGNQDTQY | TRBV31 | TRBJ2-5 |
| 18 | 0.533 | TGTGCCAGCAGCATAGGACAGAAACACAGGCTCCGCTTTTT | ASSIGQNNQAPL | TRBV19 | TRBJ1-5 |
| 17 | 0.504 | TGTGCCAGCGGTGACAGGACTGGGGGGCCGACAGAAACGCTGATTTT | ASGDRTGGAAETLY | TRBV13-2 | TRBJ2-3 |
| 17 | 0.504 | TGTGCCAGCAGTCTGGGGGGAGTCAAAACACCTGTACTTT | ASSPGGSQNTLY | TRBV19 | TRBJ2-4 |
| 17 | 0.504 | TGTGCCAGCAGTGCCGGGGGACAGGGGGAGTCTTCTTT | ASSAAGTGGVF | TRBV13-1 | TRBJ1-1 |
| 13 | 0.385 | TGTGCCAGCGGTGATCGGACTGGGGGCCATGCTGAGCAGTCTCTC | ASGDRTGGHYAEQF | TRBV13-2 | TRBJ2-1 |
| 12 | 0.356 | TGTGCCAGCTGGGCTGGGGGTAGTCAAAACACCTGTACTTT | ASWAGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 12 | 0.356 | TGTGCCAGCAGTATAACAACATAATTCGCCCTCTACTTT | ASSINNYNSPLY | TRBV19 | TRBJ1-6 |
| 11 | 0.326 | TGTGCCAGCAGTAGTACAGGGCAGGTAAACTCCGACTACACCTTC | ASSDAGQVNSDYT | TRBV13-3 | TRBJ1-2 |
| 10 | 0.296 | TGTGGTGTAGAGACGATGCAAAACACAGAAGTCTTCTTT | GARDANTEVF | TRBV20 | TRBJ1-1 |
| 9 | 0.267 | TGTGCCAGCAGTATACCCTGGGGTCTAGTCAAAACACCTGTACTTT | ASSIPWGSQNTLY | TRBV19 | TRBJ2-4 |
| 9 | 0.267 | TGTGCCTGGAGTCTAGGAGGTAACAACACAGGCTCCGCTTTTT | AWSLGGNNQAPL | TRBV31 | TRBJ1-5 |
| 9 | 0.267 | TGTGCCAGCAGTAGAGGGAATGCAAACTCCGACTACACCTTC | ASSEGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 9 | 0.267 | TGTGCCAGCAGTATAGCCAACATGAACAGTACTTC | ASSIANYEQY | TRBV19 | TRBJ2-7 |
| 8 | 0.237 | TGTGCTAGCAGTAGTTCCTCAACTATAATTCGCCCTCTACTTT | ASSSSNYNSPLY | TRBV17 | TRBJ1-6 |
| 8 | 0.237 | TGTGCTAGCAGGACAGGGGACAGTCCAAAGACACCCAGTACTTT | ASRQGTVQDTQY | TRBV29 | TRBJ2-5 |
| 7 | 0.207 | TGTGCTAGCAGTGGGGACAGGGCTGCAAAACACAGAAGTCTTCTTT | ASSGDRAANTEVF | TRBV29 | TRBJ1-1 |
| 7 | 0.207 | TGTGCCAGCACCGACTGGGGGGCAACACCGGGCAGCTCTACTTT | ASTDWGGNTGQLY | TRBV26 | TRBJ2-2 |
| 7 | 0.207 | TGTGCCAGCAGTCCAGGGAATAACAACACAGGCTCCGCTTTTT | ASSPGNNNQAPL | TRBV14 | TRBJ1-5 |
| 7 | 0.207 | TGTGCCAGCAGGGACAGGCATTCTGGAAATACGCTCTATTTT | ASDRDRHSGNTLY | TRBV13-3 | TRBJ1-3 |
| 7 | 0.207 | TGGGCCAGCGGTGACGGGGGGCTGAGCCAGGCTCCGCTTTTT | ASGDGGLSQAPL | TRBV13-2 | TRBJ1-5 |
| 7 | 0.207 | TGTGCCAGCAGTACTGGGGGGCTATGAACAGTACTTC | ASSDWGGYEQY | TRBV13-3 | TRBJ2-7 |
| 6 | 0.178 | TGCACCTGCAGTGCAGACCGGGACAGGGGTAACATGCTGAGCAGTCTCTC | TCSADRRDRGNYAEQF | TRBV1 | TRBJ2-1 |
| 6 | 0.178 | TGTGCCAGCGGTGATCGGGGACAACAACTCCGACTACACCTTC | ASGDRGQTNDSYT | TRBV13-2 | TRBJ1-2 |
| 6 | 0.178 | TGTGCTAGCATTACTGGGGGGACCAAGACACCCAGTACTTT | ASITGGDQDTQY | TRBV17 | TRBJ2-5 |
| 6 | 0.178 | TGTGCCAGCAGTTCAGGGAACATAATTCGCCCTCTACTTT | ASSSGNYNSPLY | TRBV19 | TRBJ1-6 |
| 6 | 0.178 | TGTGCCAGCAGTGTGGCAATGCAAACTCCGACTACACCTTC | ASSDGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 5 | 0.148 | TGTGCTAGCAGTAGAGCCGGGGACAACATGAAAAGTACGTC | ASSRAGDNYEY | TRBV17 | TRBJ2-7 |
| 5 | 0.148 | TGTGCCAGCGCAGGGGGGGCTTCAAAACACCTGTACTTT | ASAGGGFQNTLY | TRBV19 | TRBJ2-4 |
| 4 | 0.119 | TGTGCCAGCAGCTTAGAGGACAGGGAGGGCTCCGACTACACCTTC | ASSLEDREGSDYT | TRBV3 | TRBJ1-2 |
| 4 | 0.119 | TGTGGTGTAGGGATCTAACAGAAACAACTCCGACTACACCTTC | GARDLTETNSDYT | TRBV20 | TRBJ1-2 |
| 4 | 0.119 | TGCACCTGCAGTGCAGGGGGGGCTAGTCAAAACACCTGTACTTT | TCSAGGASQNTLY | TRBV1 | TRBJ2-4 |
| 4 | 0.119 | TGTGCTAGCACCACTGGGGGGGACTATGCTGAGCAGTCTCTC | ASTTGGDYAEQF | TRBV17 | TRBJ2-1 |
| 4 | 0.119 | TGTGCTAGCAGTCTCCTCAGGGTCAAAACACAGAAGTCTTCTTT | ASSSSGSNTEVF | TRBV17 | TRBJ1-1 |
| 4 | 0.119 | TGTGCCAGCAGTGCAGGGGGGGCAACAGGCTCCGCTTTTT | ASSAGGNQAPL | TRBV13-3 | TRBJ1-5 |

Mouse 6 chronic Part I

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 8514 | 53.083 | TGTGCCAGCAGTGAGGACAGGGGGCTCCGACTACACCTTC | ASSEDRLSDYT | TRBV13-3 | TRBJ1-2 |
| 2060 | 12.844 | TGTGGTGTAGGGGACAGAGTATTTCCAACGAAAGATTATTTTT | GARGQISNERLF | TRBV20 | TRBJ1-4 |
| 1120 | 6.983 | TGTGCTAGCAGTTTACAGGGGACAGGCTCCGCTTTTT | ASSLQGGQAPL | TRBV17 | TRBJ1-5 |
| 836 | 5.212 | TGTGGTGTAGGGATCAGGACAATTTCCAACGAAAGATTATTTTT | GARDQDNSNERLF | TRBV20 | TRBJ1-4 |
| 396 | 2.469 | TGCACCTGCAGTGACAATTCCTATAATTCGCCCTCTACTTT | TCSDNSYNSPLY | TRBV1 | TRBJ1-6 |
| 315 | 1.964 | TGTGCCAGCGGTGATGCGCTGGGGTATGCAGAAACGCTGATTTT | ASGDALGYAETLY | TRBV13-2 | TRBJ2-3 |
| 307 | 1.914 | TGTGCTAGCAGCTGCACAGGATTTAGTGCAAAACGCTGTATTTT | ASSSTGFAETLY | TRBV29 | TRBJ2-3 |
| 249 | 1.552 | TGTGCCAGCGGTGATAGGGCTGGGGATACTATGCTGAGCAGTCTTTC | ASGDRAGDNYAEQF | TRBV13-2 | TRBJ2-1 |
| 134 | 0.835 | TGTGCTAGCAGTATTGGGGGGGATTATGCTGAGCAGTCTTTC | ASSIGGDYAEQF | TRBV17 | TRBJ2-1 |
| 83 | 0.517 | TGTGCCAGCAGCAGCGCGGGGGTGCAACTCCGACTACACCTTC | ASSSAGGANSDYT | TRBV4 | TRBJ1-2 |
| 73 | 0.455 | TGTGCCAGCGGTGATCGGGACAGGTGGAACACCGGGCAGCTACTTT | ASGDRDRWNTGQLY | TRBV13-2 | TRBJ2-2 |
| 72 | 0.449 | TGTGCCAGCAGTATCCAGGGACGCAACCAAGCTCCGCTTTTT | ASSIQGRNQAPL | TRBV19 | TRBJ1-5 |
| 65 | 0.405 | TGTGGTGTAGGGATCGGACAGGGGGTTCGGAATACGCTCTATTTT | GARDRTGGSGNTLY | TRBV20 | TRBJ1-3 |
| 62 | 0.387 | TGTGCTAGCAGTAGAGCCGGGACAGCAACACAGAAGTCTTCTTT | ASSRAGTANTEVF | TRBV17 | TRBJ1-1 |
| 58 | 0.362 | TGTGCTAGCAGTTCCAGGGACAGAAACAACCGGGCAGCTCTACTTT | ASSSRDRNTGQLY | TRBV29 | TRBJ2-2 |
| 58 | 0.362 | TGTGCCAGCAGTATAGAGGGAACTATAATTCGCCCTCTACTTT | ASSIEGNYNSPLY | TRBV19 | TRBJ1-6 |
| 54 | 0.337 | TGTGCCAGCAGCAAGATCTCGGGACAGAAGTCTTCTTT | ASSQDLGTEVF | TRBV5 | TRBJ1-1 |
| 51 | 0.318 | TGTGCTGGAGTGGGACAGGGGGCAGGAATTCGCCCTCTACTTT | AWSGTGGRNPLY | TRBV31 | TRBJ1-6 |
| 50 | 0.312 | TGTGCCAGCGGTGATGCAGGACTGGGGGTAGTCAAAACACCTGTACTTT | ASGDAGLGGSQNTLY | TRBV13-2 | TRBJ2-4 |
| 48 | 0.299 | TGTGCCAGCAGACTGGGGAGTAGTCAAAACACCTGTACTTT | ASRLGSSQNTLY | TRBV19 | TRBJ2-4 |
| 45 | 0.281 | TGTGCAAGCTCTACTGGGGTCTATGCTGAGCAGTCTTTC | ASSYWGLYAEQF | TRBV16 | TRBJ2-1 |
| 40 | 0.249 | TGTGCCAGCGGTGATCGGACAGGGAGTAATGCTGAGCAGTCTTTC | ASGDRTGSNYAEQF | TRBV13-2 | TRBJ2-1 |
| 40 | 0.249 | TGTGCCAGCAGTCCCGACTGGGGGGGAACTATGCTGAGCAGTCTTTC | ASSPDWGGNYAEQF | TRBV15 | TRBJ2-1 |
| 40 | 0.249 | TGTGCTAGCAGAGTGGGGGGGACCAAGACACCCAGTACTTT | ASRVGGDQDTQY | TRBV17 | TRBJ2-5 |
| 40 | 0.249 | TGTGCCAGCAGACTGGGGGGAAGTCAAAACACCTGTACTTT | ASRLGSSQNTLY | TRBV13-3 | TRBJ2-4 |
| 38 | 0.237 | TGTGCCAGCAGACACGCAAACTCCGACTACACCTTC | ASRHANSDYT | TRBV13-3 | TRBJ1-2 |
| 35 | 0.218 | TGTGCCAGCAGTGACAGGGGTAGTCAAAACACCTGTACTTT | ASSDRGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 34 | 0.212 | TGTGGTGTAGGGACCATGACAGGGAGAATGCAGAAACGCTGATTTT | GARDHDRENAETLY | TRBV20 | TRBJ2-3 |
| 34 | 0.212 | TGTGCCAGCAGCAAACTGGGTAGTCAAAACACCTGTACTTT | ASSQNWVVSQNTLY | TRBV5 | TRBJ2-4 |
| 34 | 0.212 | TGTGCTAGCAGTAGGGCAGATAACTATGCTGAGCAGTCTTTC | ASSRADNYAEQF | TRBV17 | TRBJ2-1 |
| 34 | 0.212 | TGTGCCAGCAGTGAGGGGGGAGGGAATTCGCCCTCTACTTT | ASSEGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 32 | 0.200 | TGTGCTAGCAGTGACAGGGGGCACAACCAAGGCTCCGCTTTTT | ASSAGGDNQAPL | TRBV17 | TRBJ1-5 |
| 32 | 0.200 | TGTGCCAGCAGGGCAGGGGGCGCAAAACACAGAAGTCTTCTTT | ASRAGGANTEVF | TRBV13-3 | TRBJ1-1 |
| 30 | 0.187 | TGTGCCAGCAGAACAGGGGGCTATAATTCGCCCTCTACTTT | ASRTGGYNSPLY | TRBV19 | TRBJ1-6 |
| 29 | 0.181 | TGTGCCAGCGGTGATCGGACAGGCTCTAGTGCAAAACGCTGATTTT | ASGDRTGSSAETLY | TRBV13-2 | TRBJ2-3 |
| 28 | 0.175 | TGTGCTGGAGTCTACGGGACTGGGAGAACCAAGACCCAGTACTTT | AWSLRDWENQDTQY | TRBV31 | TRBJ2-5 |
| 28 | 0.175 | TGTGCTAGCAGTAGAGACGGGACTGGGGCTATGAACAGTACTTC | ASSRDGTGGYEYQ | TRBV17 | TRBJ2-7 |
| 26 | 0.162 | TGTGCCAGCGGTGATAGGGGACTGGGGAATGCTGAGCAGTCTTTC | ASGDRGLGNYAEQF | TRBV13-2 | TRBJ2-1 |
| 24 | 0.150 | TGTGCCAGCAGTATGGCAATGCAAACTCCGACTACACCTTC | ASSDGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 24 | 0.150 | TGTGCAAGCAGGAGGGACAGGGACTATGAACAGTACTTC | ASRRDRDYEQY | TRBV16 | TRBJ2-7 |
| 23 | 0.143 | TGTGCTAGCAGTAGTGGGGTTCAAAACACCGAGCTCTACTTT | ASSSRGSNTGQLY | TRBV17 | TRBJ2-2 |
| 23 | 0.143 | TGTGCCAGCAGTATGGGGTTCAAAACACAGAAGTCTTCTTT | ASSDGGSNTEVF | TRBV13-3 | TRBJ1-1 |
| 23 | 0.143 | TGTGCCAGCAGTATCAGGGGGCAAACTCCGACTACACCTTC | ASSYQGANSDYT | TRBV4 | TRBJ1-2 |
| 23 | 0.143 | TGTGCTAGCCTGAGGGGGATGAACAGTACTTC | ASLEGDEQY | TRBV29 | TRBJ2-7 |
| 22 | 0.137 | TGCACCTGCAGTGCCCACTGGGGGGGCGCGGTGCAGAAACGCTGATTTT | TCSAHWGGAGAETLY | TRBV1 | TRBJ2-3 |
| 22 | 0.137 | TGTGGTGTAGGGATACGACCTTTTCCAACGAAAGATTATTTTT | GARDTTFISNERLF | TRBV20 | TRBJ1-4 |
| 22 | 0.137 | TGTGCCAGCAGAACTAGTGCAAAACGCTGATTTT | ASRTSAETLY | TRBV13-1 | TRBJ2-3 |
| 21 | 0.131 | TGTGCTAGCAGTTTAGCGCAAAACCAAGACACCCAGTACTTT | ASSLATNQDTQY | TRBV29 | TRBJ2-5 |
| 20 | 0.125 | TGTGCTAGCAGTTCAGGGGACAAAACAGTGCAGAAACGCTGATTTT | ASSSRDKTSAETLY | TRBV29 | TRBJ2-3 |
| 20 | 0.125 | TGCACCTGCAGTCCGACTGGGGGGGAGTGCAGAAACGCTGATTTT | TCSPTGGGSAETLY | TRBV1 | TRBJ2-3 |
| 20 | 0.125 | TGTGCCAGCGGTGATGGGAATTTCCAACGAAAGATTATTTTT | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 19 | 0.118 | TGTGCCAGCAGTTTAGGACTGGGGTCTAGTCAAAACACCTGTACTTT | ASSLGLSSQNTLY | TRBV15 | TRBJ2-4 |
| 19 | 0.118 | TGTGCAAGCAGCCGACTGGGGGGGCGCAACCGGGCAGCTCTACTTT | ASSPTGGARTGQLY | TRBV16 | TRBJ2-2 |
| 19 | 0.118 | TGTGCTAGCAGTAGGGGGGATAACTATGCTGAGCAGTCTTTC | ASSRGNDAEQF | TRBV17 | TRBJ2-1 |
| 19 | 0.118 | TGTGCCAGCGCCCGGGACAATAATTCGCCCTCTACTTT | ASGPGTNSPLY | TRBV13-2 | TRBJ1-6 |
| 18 | 0.112 | TGTGCCAGCAGTATAGGACTGGGGGGGCGCAACCAAGACCCAGTACTTT | ASSDRDTGGADQDTQY | TRBV13-3 | TRBJ2-5 |
| 18 | 0.112 | TGTGCCAGCAGTGACAGGGGGGCAACACCGGGCAGCTCTACTTT | ASSDQGANTGQLY | TRBV13-3 | TRBJ2-2 |
| 18 | 0.112 | TATGCTGAGCAGTCTTTC | AEQF | TRBV21 | TRBJ2-1 |
| 17 | 0.106 | TGTGCCAGCAGCGGATCGGGGAATTCACCCCTCACCTTT | ASSRSGNSPLH | TRBV14 | TRBJ1-6 |
| 17 | 0.106 | TGTGCAAGCAGCTTAGCCTGGGGGGATGAACAGTACTTC | ASSLAWGDEQY | TRBV16 | TRBJ2-7 |
| 17 | 0.106 | GGGGAAACGCTGATTTT | ETLY | TRBV5 | TRBJ2-3 |
| 16 | 0.100 | TGTGCCAGTCCCCAGGGGGCATTTCCAACGAAAGATTATTTTT | ASSPGGISNERLF | TRBV12-1 | TRBJ1-4 |
| 16 | 0.100 | TGTGCCAGCGGTGATGGGCTGGTTAGTGCAAAACGCTGATTTT | ASGDGLVSAETLY | TRBV13-2 | TRBJ2-3 |
| 16 | 0.100 | TGTGGTGTAGGGATAGAGACAATAGTCAAAACACCTGTACTTT | GARDRDNQNTLY | TRBV20 | TRBJ2-4 |
| 16 | 0.100 | TGTGCTAGCAGTAGAGTTTGGGGGGAGAAAACGCTGATTTT | ASSRVWGEKTLY | TRBV17 | TRBJ2-3 |
| 16 | 0.100 | TGTGCCAGCAGTATCTGGGGGTTATGAACAGTACTTC | ASSDLGGYEYQY | TRBV13-3 | TRBJ2-7 |
| 16 | 0.100 | TGTGCCAGCAGCCCGGGGGGCGGGACACCCAGTACTTT | ASSPGRDQY | TRBV4 | TRBJ2-5 |

Mouse 6 chronic Part II

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| | | | | | |
| 15 | 0.094 | TGTGCCAGCGGTGCCTGGGGGGCGCCGGCAGCTCTACTTT | ASGAWGGAGQLY | TRBV13-2 | TRBJ2-2 |
| 15 | 0.094 | TGTGCCAGCGGTGGGGACAATGCAAACCTCCGACTACACCTTC | ASGGDNANSDYT | TRBV13-2 | TRBJ1-2 |
| 15 | 0.094 | TGTGCCAGCAGTTTCAGGGGGCCCAAGACACCCAGTACTTT | ASSFRGPQDTQY | TRBV14 | TRBJ2-5 |
| 15 | 0.094 | TGTGCCAGCAGTGAGCGAGGAAACACAGAAGTCTTCTTT | ASSERGNTEVF | TRBV13-3 | TRBJ1-1 |
| 15 | 0.094 | TGTGCCAGCTCTCCGGGGGAGGAGATTATTTTTT | ASSLRGRRLF | TRBV12-1 | TRBJ1-4 |
| 14 | 0.087 | TGTGCTAGCAGTAGAAGCGATAACTATGCTGAGCAGTTCTTC | ASSRSDNYAEQF | TRBV17 | TRBJ2-1 |
| 14 | 0.087 | TGTGCTAGCAGTAAAGGGCAGTATGAACAGTACTTC | ASSKGQYEQY | TRBV17 | TRBJ2-7 |
| 13 | 0.081 | TGTGCCAGCAGCTTAAGAAGGACTGGGGGGTTTCAAACACCTTGACTTT | ASSLRRTGGFQNTLY | TRBV3 | TRBJ2-4 |
| 13 | 0.081 | TGTGCCAGCGGTGATAGGGCTGGGGGGAATGCAGAAACGCTGTATTTT | ASGDRAGGNAETLY | TRBV13-2 | TRBJ2-3 |
| 13 | 0.081 | TGTGGTGTAGGGATCTGGACAATGCAAACACAGAAGTCTTCTTT | GARDLDNANTEVF | TRBV20 | TRBJ1-1 |
| 13 | 0.081 | TGCACCTGCAGTGTCTGGGGGCCAAGTCAAAACACCTTGACTTT | TCSVWGPSQNTLY | TRBV1 | TRBJ2-4 |
| 13 | 0.081 | TGTGCCAGCAGTCCGGGACATAGTCAAACACCTTGACTTT | ASSPGHSQNTLY | TRBV19 | TRBJ2-4 |
| 13 | 0.081 | TGTGCCAGCAGTAAAGGGACTGGGGGGCCCTTGACTTT | ASSERDWGGPLY | TRBV13-3 | TRBJ2-4 |
| 13 | 0.081 | TGTGCCAGCTCTCGATGCTGGGGCCGAACAGTACTTC | ASSLDAGAEQY | TRBV12-1 | TRBJ2-7 |
| 13 | 0.081 | TGTGCCAGCGGTGATGGGTTTGAGAAACGCTGTATTTT | ASGDGFAETLY | TRBV13-2 | TRBJ2-3 |
| 11 | 0.069 | TGTGCCAGCAGCCAAGATGGTGCTGCGGGGGCCCGAGAGACCCAGTACTTC | ASSQDGAAGARETQY | TRBV5 | TRBJ2-5 |
| 11 | 0.069 | TGTGCCAGCTCTCGACTGGGGGTATAACTATGCTGAGCAGTTCTTC | ASSLDWGYNYAEQF | TRBV12-1 | TRBJ2-1 |
| 11 | 0.069 | TGTGCCAGCAGTAAAGACAGGGGGCGGGGAAATACGCTCTATTTT | ASSERQGARGNTLY | TRBV13-1 | TRBJ1-3 |
| 11 | 0.069 | TGTGCAAGCAGCTTAGATTGGACTGGGGGTCAAACACCTTGACTTT | ASSLDWTGGQNTLY | TRBV16 | TRBJ2-4 |

Mouse 7 chronic

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|-------------------|------------|------------|
| 5379 | 23.245 | TGTGCCAGCAGTGATGGGGGTTCAAACACAGAAGTCTTCTTT | CASSDGGSNTEVFF | TRBV13-3 | TRBJ1-1 |
| 4821 | 20.834 | GGGAAACGCTGTATTTT | GETLYF | TRBV5 | TRBJ2-3 |
| 1822 | 7.874 | TGTGGTGCTAGGGACAGGGGGCATAATTCGCCCTCTACTTT | CGARDRGHNSPLYF | TRBV20 | TRBJ1-6 |
| 1627 | 7.031 | TGTGCCAGCGGTGACTGGGGGAAAAGAATCAAACACCTTGTACTTT | CASGDWGEKNQNTLYF | TRBV13-2 | TRBJ2-4 |
| 949 | 4.101 | TGTGCTAGCAGTTTATCGAGGCATAACCAAGACACCCAGTACTTT | CASSLSRHNQDTQYF | TRBV29 | TRBJ2-5 |
| 930 | 4.019 | TGTGCCAGCGGTGATCGCGGCAAAAATAGTGCGAAACGCTGTATTTT | CASGDRGKNSAETLYF | TRBV13-2 | TRBJ2-3 |
| 643 | 2.779 | TGTGCTAGCAGTAGACTGGACAGGGGGCCTCTATGAACAGTACTTC | CASSRLDRGRSYEQYF | TRBV17 | TRBJ2-7 |
| 506 | 2.187 | TGTGCCAGCGGTACCAGGACTGGGGTAGTGCAAAACGCTGTATTTT | CASGDRTGGSAETLYF | TRBV13-2 | TRBJ2-3 |
| 502 | 2.169 | TGTGGTGCTCTGGACAGGACCTTTTCCAACGAAAGATTATTTTTT | CGALDRTFNSERLFF | TRBV20 | TRBJ1-4 |
| 433 | 1.871 | TGTGCCAGCAGCTCGGACAGGGCCTTTGCAACACCCGGCAGCTACTTT | CASSSDRAFANTGQLYF | TRBV3 | TRBJ2-2 |
| 298 | 1.288 | TGTGCTAGCGGGACACATGCTGAGCAGTTCTTC | CASGTHAEQFF | TRBV17 | TRBJ2-1 |
| 271 | 1.171 | TGTGCCAGCGGTGATCGCGGGGGGCGCATGCTGAGCAGTTCTTC | CASGDAGGAHAEQFF | TRBV13-2 | TRBJ2-1 |
| 239 | 1.033 | TGTGCCAGCAGTATACGTTTTGACAATAGTGCAAAACGCTGTATTTT | CASSIRFDNSAETLYF | TRBV19 | TRBJ2-3 |
| 227 | 0.981 | TGTGCCAGCGGTGATAGGGCTGGGGGAATCAAACACCTTGTACTTT | CASGDRAGGNQNTLYF | TRBV13-2 | TRBJ2-4 |
| 210 | 0.908 | TGTGCCAGCAGGGACCGTTCTATAATTCGCCCTCTACTTT | CASRDRSYNSPLYF | TRBV19 | TRBJ1-6 |
| 201 | 0.869 | TGTGCCAGCGGTGATGCTGGGGGGCGAAACGCTGTATTTT | CASGDWGGGETLYF | TRBV13-2 | TRBJ2-3 |
| 200 | 0.864 | TGTGCCAGCAGTACAGGGTTCCAAGACACCCAGTACTTT | CASSTGFQDTQYF | TRBV13-3 | TRBJ2-5 |
| 194 | 0.838 | TGTGCCAGCGGTGATGGGACAGGGGTTGAACAGTACTTC | CASGDGTGVEQYF | TRBV13-2 | TRBJ2-7 |
| 194 | 0.838 | TGCAGCGTCTGACAGTTTACGACGAGCAGTACTTC | CSVLTVYDEQYF | TRBV30 | TRBJ2-7 |
| 184 | 0.795 | TGTGCTAGCAGTAGAACGGGGGATAACTATGCTGAGCAGTTCTTC | CASSRTGDNIAEQFF | TRBV17 | TRBJ2-1 |
| 179 | 0.774 | TGTGCTAGCAGTAGCCGGGGGAGGGACACCCGGCAGCTACTTT | CASSSRGRDTGQLYF | TRBV17 | TRBJ2-2 |
| 175 | 0.756 | TGTGCCAGCAGTCCGGGACACGCAAAACACAGAAGTCTTCTTT | CASSPGHANTEVFF | TRBV13-3 | TRBJ1-1 |
| 175 | 0.756 | TGCGCCAGCAGTTCAGGACAGGGGACCACGAGCAGTACTTC | CASSFRDGDHEQYF | TRBV12-2 | TRBJ2-7 |
| 168 | 0.726 | TGTGCTAGCAGTAGGGGACAGGGGGGACAGTACTTC | CASSRQGGQYF | TRBV17 | TRBJ2-7 |
| 157 | 0.678 | TGTGCCAGCTCTCTCGACACTATGAACAGTACTTC | CASSPRHYEQYF | TRBV12-2 | TRBJ2-7 |
| 136 | 0.588 | TGTGCCAGCGGTGATCGGGGGCAGATTCTGAAATACGCTCTATTTT | CASGDRGADSGNTLYF | TRBV13-2 | TRBJ1-3 |
| 128 | 0.553 | TGTGCCAGCAGTACAGGGAATAAATTCGCCCTCTACTTT | CASSTGNYNSPLYF | TRBV19 | TRBJ1-6 |
| 117 | 0.506 | TGTGCCAGCAGGTGGGGGGCGGTCAAACACCTTGTACTTT | CASRWGGGQNTLYF | TRBV13-3 | TRBJ2-4 |
| 115 | 0.497 | TGTGCTGGAGTCTAGGGGACTGGGGGGCAGAAACGCTGTATTTT | CAWSLGDWGAETLYF | TRBV31 | TRBJ2-3 |
| 108 | 0.467 | TGTGCCAGCAGTCCCGGACTGGGGGGGAGTACTTC | CASSPGTGGYF | TRBV13-3 | TRBJ2-7 |
| 107 | 0.462 | TGTGCTAGCAGTAGAGCCGGGGACAACATGAACAGTACTTC | CASSRAGDNYEQYF | TRBV17 | TRBJ2-7 |
| 104 | 0.449 | TGTGCCAGCAGTACTGGGGGGGAAGCACCTTGTACTTT | CASSDWGGSTLYF | TRBV13-3 | TRBJ2-4 |
| 99 | 0.428 | TGTGCCAGCAGTATGCCGACAGATAAACACAGAAGTCTTCTTT | CASSDARQINTEVFF | TRBV13-1 | TRBJ1-1 |
| 95 | 0.411 | TGTGCCAGCGGTGATGCACTGGGGGGGCTTTTGAACAGTACTTC | CASGDALGGAFEQYF | TRBV13-2 | TRBJ2-7 |
| 95 | 0.411 | TGTGCCAGCAGTCCAGGGGTAACCAAGACACCCAGTACTTT | CASSPGGNQDTQYF | TRBV19 | TRBJ2-5 |
| 95 | 0.411 | TGTGCCAGCAGGGAGGAAATCTGAAATACGCTCTATTTT | CASREGNSGNTLYF | TRBV13-3 | TRBJ1-3 |
| 91 | 0.393 | TGTGCTAGCAGTAGGGCAGGGGACCAAGACACCCAGTACTTT | CASSRAGDQDTQYF | TRBV17 | TRBJ2-5 |
| 88 | 0.380 | TGTGCCAGCAGTATGGCGGGTTTCAAACACCTTGTACTTT | CASSDGGFQNTLYF | TRBV13-3 | TRBJ2-4 |
| 87 | 0.376 | TGTGCCAGCGGTGATGGCAATGCAAACCTCCGACTACACCTTC | CASGDGNANSDYTF | TRBV13-2 | TRBJ1-2 |
| 83 | 0.359 | TGTGCCAGCGGTGATCGCGTGGGGGAACTATGCTGAGCAGTTCTTC | CASGDRAGGNIAEQFF | TRBV13-2 | TRBJ2-1 |
| 81 | 0.350 | TGTGCCAGCAGTCTGGGACAGAATGCAAACACAGAAGTCTTCTTT | CASSLGQNAANTEVFF | TRBV15 | TRBJ1-1 |
| 81 | 0.350 | TGTGCTGGAGTATGGGATTAACCAAGACACCCAGTACTTT | CAWSDGINQDTQYF | TRBV31 | TRBJ2-5 |
| 74 | 0.320 | TGTGCCAGCAGCCGCGAGGGGGCCGGTAGCCAGCCACAGCATTTT | CASRPQAGSQPHF | TRBV29 | TRBJ1-5 |
| 73 | 0.315 | TGTGCCAGCAGTATTGGACAGTTTCTATAATTCGCCCTCTACTTT | CASSIGQFSYNSPLYF | TRBV19 | TRBJ1-6 |
| 67 | 0.290 | TGTGCCAGCAGCTTAGATGCGGGTAGTCAGCCCCAGCATTTT | CASSLDAGSQPHF | TRBV14 | TRBJ1-5 |
| 65 | 0.281 | TGTGGTGCTAGGGATCAGCAGGCTAGTGCAAAACGCTGTATTTT | CGARDQQAETLYF | TRBV20 | TRBJ2-3 |
| 63 | 0.272 | TGTGCTAGCAGTAGAGATGGCGGGGGAATGCTGAGCAGTTCTTT | CASSRDGGGNYAEQFF | TRBV17 | TRBJ2-1 |
| 61 | 0.264 | TGTGCCAGCAGTCCCGGACAGGGAGGTCCGACTACACCTTC | CASSPGTGRSDYTF | TRBV26 | TRBJ1-2 |
| 61 | 0.264 | TGTGCCAGCAGTTAGACAGGGGAAAAACACCTTGTACTTT | CASSLDRGNKNTLYF | TRBV3 | TRBJ2-4 |
| 59 | 0.255 | TGTGCCAGCAGTCTGGGGGGGCAAGACACCCAGTACTTT | CASSPGGGQDTQYF | TRBV19 | TRBJ2-5 |
| 59 | 0.255 | TGTGCCAGCAGTATTGGGGGGGAAAAACACCTTGTACTTT | CASSDLGENTLYF | TRBV13-1 | TRBJ2-4 |
| 58 | 0.251 | TGTGCCAGCAGCAGGGTAACCAAGACACCCAGTACTTT | CASSTGNQDTQYF | TRBV13-3 | TRBJ2-5 |
| 57 | 0.246 | TGTCCAGCGGTGATCGCGGCAAAAATAGTGCAAAACGCTGTATTTT | CPSGDRGKNSAETLYF | TRBV13-2 | TRBJ2-3 |
| 49 | 0.212 | TGTGCCAGCGGTGATGGGGAGGGACTGGGGGTATCTGAACAGTACTTC | CASGDGEGLVSEQYF | TRBV13-2 | TRBJ2-7 |

Mouse 1 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 7702 | 47.225 | TGTGCCAGCAGTGTGGGACAGGGACCCAACGAAAGATTATTTTTT | ASSVGQGPNERLF | TRBV13-3 | TRBJ1-4 |
| 5371 | 32.933 | TGTGCCAGCAGCACAGGGAATAACAACCAGGCTCCGCTTTTT | ASSTGNNNQAPL | TRBV13-3 | TRBJ1-5 |
| 558 | 3.421 | TGTGCTAGCAGTTTAGGGGACTGGGGGTTCAAAACACCTTGACTTT | ASSLGDWGVQNTLY | TRBV29 | TRBJ2-4 |
| 334 | 2.048 | TGTGCCAGCAGTCCAGGGAATTCTGAAATACGCTCTATTTT | ASSPGNSGNTLY | TRBV14 | TRBJ1-3 |
| 316 | 1.938 | TGTGCTAGCAGTTCCTCGCCGGGACACAACTATGCTGAGCAGTCTTTC | ASSRRDTNYAEQF | TRBV29 | TRBJ2-1 |
| 292 | 1.790 | TGTGGTGTAGGGTAGAAAACCTCCGACTACACCTTC | GARVENS DYT | TRBV20 | TRBJ1-2 |
| 178 | 1.091 | TGTGCTAGCAGTTTTGGGGGTTTGTGTCAGAAACGCTGTATTTT | ASSFGGFS AETLY | TRBV29 | TRBJ2-3 |
| 157 | 0.963 | TGTGCCAGCAGTGTCCGACAGGGCAACTCCGACTACACCTTC | ASSVGQGN S DYT | TRBV13-3 | TRBJ1-2 |
| 135 | 0.828 | TGTGCCAGCAGTGATGGGGGAGGGAATTCGCCCTCTACTTT | ASSDGGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 124 | 0.760 | TGTGCCAGCAGGGACAGACATTCTGAAATACGCTCTATTTT | ASRDRHSGNTLY | TRBV13-3 | TRBJ1-3 |
| 120 | 0.736 | TGTGCCAGCAGTCAACAGGGGAGGGGAAGTGCAGAAACGCTGTATTTT | ASSQQGRGSAETLY | TRBV13-3 | TRBJ2-3 |
| 112 | 0.687 | TGTGGTGTAGGGATCGGGACAGGGAGAATGGAAATACGCTCTATTTT | GARDRDRENGNTLY | TRBV20 | TRBJ1-3 |
| 108 | 0.662 | TGTGCTAGCAGTAGAGTGCAAACTATGCTGAGCAGTCTTTC | ASSRVQNYAEQF | TRBV17 | TRBJ2-1 |
| 95 | 0.583 | TGTGCTAGCAGTCCCTCGGGTAAACCAAGACACCCAGTACTTT | ASSSPGVNQDTQY | TRBV17 | TRBJ2-5 |
| 93 | 0.570 | TGTGCCAGCAGTCACTGGGGGGCGATGCTGAGCAGTCTTTC | ASSHWGGDAEQF | TRBV13-3 | TRBJ2-1 |
| 71 | 0.435 | TGTGCCAGCGGTGATAGGTCAGGGGAAACACAGAAGTCTTCTTT | ASGDRSGGNT E V F | TRBV13-2 | TRBJ1-1 |
| 68 | 0.417 | TGTGCCAGCAGGACAGGGACCTATAATTCGCCCTCTACTTT | ASRTGTYN S PLY | TRBV13-3 | TRBJ1-6 |
| 67 | 0.411 | TGTGCCAGCAGGACACATAAGTGCAGAAACGCTGTATTTT | ASRTHSAETLY | TRBV13-3 | TRBJ2-3 |
| 60 | 0.368 | TGTGCCAGCAGTGATTGGGGGCCAAACACCGGGCAGCTCTACTTT | ASSDWGPNTGQLY | TRBV13-1 | TRBJ2-2 |
| 54 | 0.331 | TGTGCCAGCAGAACAGGGAATGTTAATTCGCCCTCTACTTT | ASRTGNVNSPLY | TRBV14 | TRBJ1-6 |
| 51 | 0.313 | TGTGCTAGCAGTAGTGGGGGACTATGCTGAGCAGTCTTTC | ASSSGGDYAEQF | TRBV17 | TRBJ2-1 |
| 45 | 0.276 | TGTGCCAGCAGTGCGGGACAAAATAATTCGCCCTCTACTTT | ASSAGQNN S PLY | TRBV13-3 | TRBJ1-6 |
| 45 | 0.276 | TGTGCCAGCAGGTCAGGGAATTATAATTCGCCCTCTACTTT | ASRSGNYN S PLY | TRBV14 | TRBJ1-6 |
| 43 | 0.264 | TGTGCCAGCAGGACAGGGGTTAATTCGCCCTCTACTTT | ASRTGVNSPLY | TRBV13-3 | TRBJ1-6 |
| 39 | 0.239 | TGCACCTGCAGTGCAGATGTGGGTCTAGTGCAGAAACGCTGTATTTT | TCSADV GSSAETLY | TRBV1 | TRBJ2-3 |
| 38 | 0.233 | TGTGCCAGCGGGCGGGACAGGGGCTTAGTGCAGAAACGCTGTATTTT | ASGRDRGLSAETLY | TRBV13-3 | TRBJ2-3 |
| 33 | 0.202 | TGCTCCAGCAGTCAAGGCAGGGGGAGGTCCGACTACACCTTC | SSSQGRGRSDYT | TRBV23 | TRBJ1-2 |

Mouse 2 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 12113 | 70.502 | TGTGCCAGCGGTGATAGGGCAGGGGCTAGTGCAGAAACGCTGTATTTT | ASGDRAGASAETLY | TRBV13-2 | TRBJ2-3 |
| 2968 | 17.275 | TGTGCCAGCAGTGCCTGGGGGGCGATGCTGAGCAGTTCTTC | ASSAWGGDAEQF | TRBV13-1 | TRBJ2-1 |
| 925 | 5.384 | TGTGCTAGCACTGCTGGGGGAACTATGCTGAGCAGTTCTTC | ASTAGGNVYAEQF | TRBV17 | TRBJ2-1 |
| 314 | 1.828 | TGTGCCAGCAGTATAGGAAATCTGGAATACGCTCTATTTT | ASSIGNSGNTLY | TRBV19 | TRBJ1-3 |
| 180 | 1.048 | TGTGCTAGCAGTAGACGGGTAACTATGCTGAGCAGTTCTTC | ASSRPGNYAEQF | TRBV17 | TRBJ2-1 |
| 114 | 0.664 | TGTGCCAGCGGTGAGAGACAAGTAAACACAGAAGTCTTCTTT | ASGERQVNEVVF | TRBV13-2 | TRBJ1-1 |
| 74 | 0.431 | TGTGCCAGCAGTTTGGGCAATAGTCAAACACCTTGACTTT | ASSLGNSQNTLY | TRBV14 | TRBJ2-4 |
| 73 | 0.425 | TGTGCCAGCGGTGATGGCAATCCAACGAAAGATTATTTTTC | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 64 | 0.373 | TGTGCCAGCAGTCTGGGGGGATGCAAAACACCTTGACTTT | ASSPGGMQNTLY | TRBV19 | TRBJ2-4 |
| 60 | 0.349 | TGTGCCAGCAGTGTGGGGGGCACATGCTGAGCAGTTCTTC | ASSAGGAHAEQF | TRBV13-3 | TRBJ2-1 |
| 58 | 0.338 | TGTGCCAGCAGTGGCCAGACAGGAATCAAACACCTTGACTTT | ASSGQTGIQNTLY | TRBV13-3 | TRBJ2-4 |
| 54 | 0.314 | TGTGCCAGCGGTGAGTGGGACAGGGGGCAGTTTCTGGAATACGCTCTATTTT | ASGEWDRGQFSGNTLY | TRBV13-2 | TRBJ1-3 |
| 51 | 0.297 | TGTGCCAGCAGTACTGGGGGACAGGGGACACCGGGCAGCTCTACTTT | ASSDWGTGDTGQLY | TRBV13-3 | TRBJ2-2 |
| 46 | 0.268 | TGTGCTAGCAGTAGAGCCGGGACAACATGAACAGTACTTC | ASSRAGDNVYEQY | TRBV17 | TRBJ2-7 |
| 45 | 0.262 | TGTGCCAGCGGTGGCAGCAATGCAAACCTCCGACTACACCTTC | ASGGSNANSDYT | TRBV13-2 | TRBJ1-2 |
| 42 | 0.244 | TGTGCCAGCCGAGGGACAGAAGACCCAGTACTTT | ASRGTEDTQY | TRBV13-3 | TRBJ2-5 |

Mouse 3 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 7134 | 38.164 | TGTGCTAGCAGTAGTGGGGGGGACTATGCTGAGCAGTTCTTC | ASSSGGDYAEQF | TRBV17 | TRBJ2-1 |
| 2100 | 11.234 | TGTGCCAGCGGTGATGCACTGGGGGTTGACACCCAGTACTTT | ASGDALGVDTQY | TRBV13-2 | TRBJ2-5 |
| 1084 | 5.799 | TGCACCTGCAGTGACAGATAGACACAGGGGTAACCTATGCTGAGCAGTTCTTC | TCSADRHGRNYAEQF | TRBV1 | TRBJ2-1 |
| 1058 | 5.660 | TGTGCCAGCAGCCGACTGGGGGGGATCTCCAAGACACCCAGTACTTT | ASSRTGGDLQDTQY | TRBV5 | TRBJ2-5 |
| 708 | 3.788 | TGTGCTAGCAGGATACAGGGTAACCAAGACACCCAGTACTTT | ASRIQGNQDTQY | TRBV17 | TRBJ2-5 |
| 691 | 3.697 | TGTGCCAGCAGCCAGGGTTCCTATAATTCCGCCCTCTACTTT | ASSQGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 530 | 2.835 | TGTGCCAGCAGCTCTACCGGACAGGACAGGATGGCTACACCTTC | ASSSYRTGQDGYT | TRBV16 | TRBJ1-2 |
| 525 | 2.809 | TGCACCTGCAGTGACTGGGGGGTAAACACCGGGCAGCTCTACTTT | TCSDWGVNTGQLY | TRBV1 | TRBJ2-2 |
| 483 | 2.584 | TGTGCTAGCAGTCCCGGACACTCTAGTCAAAACACCTTGTACTTT | ASSPGHSSQNTLY | TRBV29 | TRBJ2-4 |
| 478 | 2.557 | TGTGCCAGCAGTGACTGGGGGGTGAACAGTACTTC | ASSDWGVEQY | TRBV13-3 | TRBJ2-7 |
| 368 | 1.969 | TGTGCTAGCAGTAGACCCGGGACAGCAAACACAGAAGTCTTCTTT | ASSRAGTANTEVF | TRBV17 | TRBJ1-1 |
| 343 | 1.835 | TGTGCCAGCAGTCAGGGTTATGGCTACACCTTC | ASSQGYGYT | TRBV8 | TRBJ1-2 |
| 323 | 1.728 | TGTGCTAGCAGTTTAAAGCGGGACTGGGGGTAGTCAAAACACCTTGTACTTT | ASSLSGTGGSQNTLY | TRBV29 | TRBJ2-4 |
| 321 | 1.717 | TGCGCCAGCAGCCAAGATATAGCAGGGGGGACTGAAGCTTTCTTT | ASSQDIAGGTEAF | TRBV5 | TRBJ1-1 |
| 317 | 1.696 | TGCGCTAGCAGCCAAGAACAGGGATTTAATTCACCCCTCCACTTT | ASSQEQQGFNSPLH | TRBV5 | TRBJ1-6 |
| 235 | 1.257 | TGTGCCAGCGGTGATAGGGGGGATCTAGTGCAAAACGCTGTATTTT | ASGDRGGSSAETLY | TRBV13-2 | TRBJ2-3 |
| 214 | 1.145 | TGTGCCAGCAGGAAATCAGGGGGCACTGAAGCTTTCTTT | ASRKS GGTEAF | TRBV16 | TRBJ1-1 |
| 198 | 1.059 | TGTGGTGCTAGGGCCAGCATTAACCAAGACACCCAGTACTTT | GARASINQDTQY | TRBV20 | TRBJ2-5 |
| 192 | 1.027 | TGTGCCAGCAGCTCTCGAGACTGGGGGCAAAACACCTTGTACTTT | ASSSRDWGQNTLY | TRBV3 | TRBJ2-4 |
| 185 | 0.990 | TGTGCCAGCAGCTTCTATTACAGATACGCAGTATTTT | ASSFLFTDTQY | TRBV16 | TRBJ2-3 |
| 165 | 0.883 | TGTGCTGGAGTTCCTGGGACAGGGAAAACACCGGGCAGCTCTACTTT | AWSSRDRENTGQLY | TRBV31 | TRBJ2-2 |
| 162 | 0.867 | TGTGCTAGCAGTAGTTGGGGGTACCAAGACACCCAGTACTTT | ASSSWGYQDTQY | TRBV17 | TRBJ2-5 |
| 143 | 0.765 | TGTGCCAGCAGTTCGAGAGGATTAGCGCACACAGATACGCAGTATTTT | ASSSRGLAHTDTQY | TRBV16 | TRBJ2-3 |
| 136 | 0.728 | TGTGCCTGGACCTTTAGTACCAACACTGAAGCTTTCTTT | AWTFSTNTEAF | TRBV31 | TRBJ1-1 |
| 129 | 0.690 | TGTGCCAGCAGCTCCCGGGACAGGAATAACTATGCTGAGCAGTTCTTC | ASSSRDRNNYAEQF | TRBV3 | TRBJ2-1 |
| 129 | 0.690 | TGTGCTGGCAGGATACAGGGTAACCAAGACACCCAGTACTTT | AGRIQGNQDTQY | TRBV17 | TRBJ2-5 |
| 108 | 0.578 | TGTGCCAGCGGTGAGGGTTATGGCTACACCTTC | ASGQGYGYT | TRBV13-2 | TRBJ1-2 |
| 103 | 0.551 | TGTGCCAGCAGCCCGGGGGGACTAGCAAATGAGCAGTTCTTC | ASSPGGLANEQF | TRBV12-2 | TRBJ2-1 |
| 67 | 0.358 | TGTGCCAGCAGCTTATTAGGACAGTTCAATGAAAACTGTTTTTT | ASSLLGQFNEKLF | TRBV15 | TRBJ1-4 |
| 64 | 0.342 | TGCACCTGCAGTGACAGATCCAACAACACCCGGGACGCTCTACTTT | TCSADPTNTGQLY | TRBV1 | TRBJ2-2 |

Mouse 4 αPD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 5440 | 25.473 | TGTGCCAGCGGTGATAGGGCTGGGGGTAGTGCAGAAACGCTGATTTT | ASGDRAGGSAETLY | TRBV13-2 | TRBJ2-3 |
| 2884 | 13.504 | TGTGCCAGCAGTCCCGGGAATAGTCAAAACACCTTGACTTT | ASSPGNSQNTLY | TRBV14 | TRBJ2-4 |
| 1661 | 7.778 | TGTGCCAGCAGTGAGGGAAACTCAAACCTCCGACTACACCTTC | ASSEGNSNSDYT | TRBV13-3 | TRBJ1-2 |
| 1449 | 6.785 | TGTGCCAGCGGTGATGCAGGCAGGTTAAACACCGGGCAGCTCTACTTT | ASGDAGRINTGQLY | TRBV13-2 | TRBJ2-2 |
| 1344 | 6.293 | TGTGGTGCTAGGGATCAACAGGGATCAAACCTCCGACTACACCTTC | GARDQQGNSDYT | TRBV20 | TRBJ1-2 |
| 1069 | 5.006 | TGTGCCAGCAGGACTGGGGGGCGCAGGCTGAGCAGTTCTTC | ASRTGGAQAEQF | TRBV13-3 | TRBJ2-1 |
| 850 | 3.980 | TGTGCTAGCAGTAGAGCGGGGGACAACATGAACAGTACTTC | ASSRAGDNYEQY | TRBV17 | TRBJ2-7 |
| 741 | 3.470 | TGTGCCAGCAGTTCACAGGGAATTCTGAAATACGCTCTATTTT | ASSFPNGSNTLY | TRBV3 | TRBJ1-3 |
| 527 | 2.468 | TGTGCTAGCAGTCTGGGGGGGACTATGCTGAGCAGTTCTTC | ASSLGGDYAEQF | TRBV17 | TRBJ2-1 |
| 484 | 2.266 | TGTGCCAGCAGCATTAGCGGGGATCCTTCTACGAGCAGTACTTC | ASSISGDPSYEQY | TRBV16 | TRBJ2-7 |
| 397 | 1.859 | TGCTCCAGCAGTCCCGGGACTGGGGGGCGAGGGCACCGGGCAGCTCTACTTT | SSSPRDWGGEGTGQLY | TRBV23 | TRBJ2-2 |
| 397 | 1.859 | TGTGCCTGGAGTCTTTGGGGGAGTCAAAACACCTTGACTTT | AWSLWGSQNTLY | TRBV31 | TRBJ2-4 |
| 361 | 1.690 | TGTGCCAGCAGTGCAGGGGGCGGAACTCCGACTACACCTTC | ASSAGGNSDYT | TRBV13-3 | TRBJ1-2 |
| 361 | 1.690 | TGTGCCAGCAGTGATTGGGGGGTTGAGCAGTTCTTC | ASSDWGVEQF | TRBV13-3 | TRBJ2-1 |
| 327 | 1.531 | TGTGCCAGCGTTTCTATGGGGTACAATGAGCAGTTCTTC | ASVSMGYNEQF | TRBV13-2 | TRBJ2-1 |
| 317 | 1.484 | TGTGCTAGCAGTTACGGAGGTTTAGTGCAGAAACGCTGTATTTT | ASSYGGFSAETLY | TRBV29 | TRBJ2-3 |
| 306 | 1.433 | TGTGCCAGCAGTGACTGGGGGGCAACACCGGGCAGCTCTACTTT | ASSDWGANTGQLY | TRBV26 | TRBJ2-2 |
| 302 | 1.414 | TGTGCCAGCAGTCGAGGAAGGGATTGGAATGAGCAGTTCTTC | ASSRGRDWNEQF | TRBV3 | TRBJ2-1 |
| 279 | 1.306 | TGTGCCAGCAGTGAACAGAAAGAGACCCAGTACTTC | ASSGTEETQY | TRBV29 | TRBJ2-5 |
| 263 | 1.232 | TGTGGTGCTAGGGTGAACACAGAAGTCTTCTTT | GARVNTEVF | TRBV20 | TRBJ1-1 |
| 244 | 1.143 | TGTGCCAGCAGCAAGAAGATTGGGGGGGAGAAACAGTACTTC | ASSQEDWGGGEQY | TRBV5 | TRBJ2-7 |
| 230 | 1.077 | TGTGCCAGCGGTGATTGGCTGGGGGGTCAAGACACCCAGTACTTT | ASGDWLGGQDTQY | TRBV13-2 | TRBJ2-5 |
| 219 | 1.025 | TGTGCCAGCAGTTTCGGCAATAGTCAAAACACCTTGACTTT | ASSFGNSQNTLY | TRBV14 | TRBJ2-4 |
| 206 | 0.965 | TGTGCCAGCAAGATAACAAAATAAATTCACCCCTCACTTT | ASKITNNNSPLH | TRBV13-2 | TRBJ1-6 |
| 198 | 0.927 | TGTGCCAGCAGTCCGGCAACTCTACGAGCAGTACTTC | ASSSGNSYEQY | TRBV29 | TRBJ2-7 |
| 160 | 0.749 | TGTGCAAGCAGCCCTCCGGACAGATTTCAAAACACCTTGACTTT | ASSPPDRFQNTLY | TRBV16 | TRBJ2-4 |
| 122 | 0.571 | TGTGCCAGCGGTGATGCGGGGGTAACCAAGACACCCAGTACTTT | ASGDAGGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 109 | 0.510 | TGTGCCAGCAGCCTCCGGGACAACCTCTATGAACAGTACTTC | ASSLRDNSYEQY | TRBV15 | TRBJ2-7 |
| 109 | 0.510 | TGTAGTTCTAGAAGTGATAGTGCAGAAACGCTGTATTTT | SSRSDSAETLY | TRBV30 | TRBJ2-3 |

Mouse 5 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 15993 | 60.543 | TGTGCCAGCAGTGCAGGTTCTATAATTCGCCCTCTACTTT | ASSAGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 2122 | 8.033 | TGTGCCAGCAGCTCCCGGGACTGGGGAAACTATGCTGAGCAGTTCTTC | ASSSRDWGNIAEQF | TRBV4 | TRBJ2-1 |
| 1501 | 5.682 | TGTGCCAGCAGTGAAGGGGGCTATAATTCGCCCTCTACTTT | ASSEGGYNSPLY | TRBV13-3 | TRBJ1-6 |
| 756 | 2.862 | TGTGCCAGCAGCGCAGGCAATGCAAATCCGACTACACCTTC | ASSAGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 725 | 2.745 | TGTGCCAGCGGTGACCCGGGACTGGGGTAACCAAGACACCCAGTACTTT | ASGDRDWGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 676 | 2.559 | TGTGCCAGCTCCCTGGGTAACCAAGACACCCAGTACTTT | ASSLGNQDTQY | TRBV13-3 | TRBJ2-5 |
| 343 | 1.298 | TGTGCCAGCACTGGGTCTAGTGCAGAAACGCTGTATTTT | ASTGSSAETLY | TRBV13-3 | TRBJ2-3 |
| 295 | 1.117 | TGTGCTAGCAGTCCCGGGCTGGGGAAACTATGCTGAGCAGTTCTTC | ASSSRDWGNIAEQF | TRBV29 | TRBJ2-1 |
| 278 | 1.052 | TGTGCCAGCGGTGATCGGACTGGGGATAACCAAGACACCCAGTACTTT | ASGDRTDGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 267 | 1.011 | TGTGCTAGCAGTTCAGGGAATAACAACAGGCTCCGCTTTTT | ASSSGNINQAPL | TRBV17 | TRBJ1-5 |
| 257 | 0.973 | TGTGCCAGCAGTGATCAGGGACTGGCTAACTATGCTGAGCAGTTCTTC | ASSDQGLANIAEQF | TRBV13-1 | TRBJ2-1 |
| 239 | 0.905 | TGTGCCAGCAGCACAGGGAATAACAACAGGCTCCGCTTTTT | ASSTGNINQAPL | TRBV13-3 | TRBJ1-5 |
| 207 | 0.784 | TGTGCCAGCACTCCCGGAAATAGTCAAAACACCTTGACTTT | ASSSGNSQNTLY | TRBV14 | TRBJ2-4 |
| 204 | 0.772 | TGTGCTAGCCGGACAGGGGTCTATGAACAGTACTTC | ASRTGVVYEQY | TRBV17 | TRBJ2-7 |
| 152 | 0.575 | TGTGCCAGCAGTCCCGGGACAGGGAGAGGAAATACGCTCTATTTT | ASSPGTGRNNTLY | TRBV13-3 | TRBJ1-3 |
| 125 | 0.473 | TGTGCCAGCGGTGATGGGGGGGCGCCACACAGAAGTCTTCTTT | ASGDDGGGHATEVF | TRBV13-2 | TRBJ1-1 |
| 116 | 0.439 | TGTGCCAGCAGTTTTGGCAGCTCTATGAACAGTACTTC | ASSFGSSYEQY | TRBV14 | TRBJ2-7 |
| 115 | 0.435 | TGTGCCAGCAGTGATACAGGGCTGAGCAGTTCTTC | ASSEYRAEQF | TRBV13-1 | TRBJ2-1 |
| 110 | 0.416 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 103 | 0.390 | TGTGCTAGCAGTTGAAAACAACTCCGACTACACCTTC | ASSWKTNSDYT | TRBV29 | TRBJ1-2 |
| 95 | 0.360 | TGTGCTAGCAGTTCAGTCTACTCCGACTACACCTTC | ASSVYSYDYL | TRBV29 | TRBJ1-2 |
| 94 | 0.356 | TGTGCCAGCTCTACTGGGGTAGTCAAAACACCTTGACTTT | ASSTGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 82 | 0.310 | TGTGCCAGCAGTGAAGCACAGGGGTTCAAAACACCTTGACTTT | ASSEAQGVQNTLY | TRBV13-3 | TRBJ2-4 |
| 74 | 0.280 | TGTGGTGCTAGGGATGCACAGGGGGACACAGAAGTCTTCTTT | GARDAQGDTEVF | TRBV20 | TRBJ1-1 |
| 70 | 0.265 | TGTGCCAGCAGTGATGGGACATATAATTCGCCCTCTACTTT | ASSDGTYSPLY | TRBV13-3 | TRBJ1-6 |
| 69 | 0.261 | TGTGCCAGCAGCTTCAAGGAGGCAACAGGCTCCGCTTTTT | ASSFQGGNQAPL | TRBV3 | TRBJ1-5 |
| 69 | 0.261 | TGTGCCAGCAGCCCAATAATCTGAAAATACGCTCTATTTT | ASSPNNNSGNTLY | TRBV5 | TRBJ1-3 |
| 68 | 0.257 | TGTGCCAGCAGTCCACAGGGGGCAAACACGGGCGAGCTCTACTTT | ASSPQGANTGQLY | TRBV13-3 | TRBJ2-2 |
| 66 | 0.250 | TGCAGTGCTAGTGGGGCGCTCAGGGCGAGACCCAGTACTTC | SASGAAQGETQY | TRBV30 | TRBJ2-5 |
| 64 | 0.242 | TGTGCTAGCGGGGGACAGGGCGTACAATGAGCAGTTCTTC | ASGGTGPYNEQF | TRBV19 | TRBJ2-1 |
| 64 | 0.242 | TGTGCTAGCAGTAGTTACAGGGGTGCAGAAACGCTGTATTTT | ASSSYRGAETLY | TRBV17 | TRBJ2-3 |
| 64 | 0.242 | TGTGCCAGCAGTGATGGGTTCTATAATTCGCCCTCTACTTT | ASSDGFYNSPLY | TRBV13-1 | TRBJ1-6 |
| 62 | 0.235 | TGTGCCAGCAGCAAGAGGGGGGGGATATGAACAGTACTTC | ASSQEGGGYEQY | TRBV5 | TRBJ2-7 |
| 61 | 0.231 | TGTGCTAGCAGTCCGACAGGGGAGGAACAGTACTTC | ASSPTGEEQY | TRBV29 | TRBJ2-7 |
| 58 | 0.220 | TGTGCCAGCAGCTACGGGACAAACACCTTGACTTT | ASSYGTNTLY | TRBV4 | TRBJ2-4 |
| 57 | 0.216 | TGCGCCAGCAGCTTAACCGGACCTAGGGGATGAGCAGTTCTTC | ASSLTGTLGDEQF | TRBV12-2 | TRBJ2-1 |
| 57 | 0.216 | TGTGCCAGCAGTGAAGGCAATCAAACCTCCGACTACACCTTC | ASSEGNNSDYT | TRBV13-3 | TRBJ1-2 |
| 55 | 0.208 | TGTGGTGCTAGGGATCAACAGGGGGAAACACAGAAGTCTTCTTT | GARDQQGGNTEVF | TRBV20 | TRBJ1-1 |
| 53 | 0.201 | TGTGCAAGCAGCCGGGACTGGGGGGAAAGTGCAGAAACGCTGTATTTT | ASSSRDWGSAETLY | TRBV16 | TRBJ2-3 |
| 52 | 0.197 | TGTGCCAGCTCTCCGACTGGGGGGCCAGTCAAAACACCTTGACTTT | ASSPTGGPSQNTLY | TRBV12-1 | TRBJ2-4 |
| 50 | 0.189 | TGTGCCAGCAGCGTAGGGGGGGCCGACAAGAGACCCAGTACTTC | ASSVGGARQETQY | TRBV12-2 | TRBJ2-5 |
| 50 | 0.189 | TGTGCTAGCAACCCCGCCAGGCCTATGAACAGTACTTC | ASNPRQAYEQY | TRBV29 | TRBJ2-7 |
| 49 | 0.185 | TGTGCCAGCAGTGCAGGGGGCGCAAACACAGAAGTCTTCTTT | ASSAGGANTEVF | TRBV13-3 | TRBJ1-1 |
| 49 | 0.185 | TGTGCCAGCAGCTTAGAGGGGACCTGGGACGAGCAGTACTTC | ASSLEGTWDEQY | TRBV16 | TRBJ2-7 |
| 46 | 0.174 | TGTGCCAGCAGATGGGGGGTAGTCAAAACACCTTGACTTT | ASRWGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 45 | 0.170 | TGTGCTAGCAGTAGAAGGGGGCGGAACCCGGGCGAGCTCTACTTT | ASSRRGRNTGQLY | TRBV17 | TRBJ2-2 |
| 44 | 0.167 | TGTGCCAGCGGTGATCGGGACAATAACAACCCGGGCGAGCTCTACTTT | ASGDRDKSNTGQLY | TRBV13-2 | TRBJ2-2 |
| 43 | 0.163 | TGTGCCAGCAGTATAGGGTCTATAATTCGCCCTCTACTTT | ASSIGSYNSPLY | TRBV19 | TRBJ1-6 |
| 42 | 0.159 | TGTGCCAGCAGCCCGGGACAAGCAAACACAGAAGTCTTCTTT | ASSPGQANTEVF | TRBV5 | TRBJ1-1 |
| 41 | 0.155 | TGTGCCAGCAGTCCCTGGGGGGCGCATGCTGAGCAGTTCTTC | ASSPWGAHAEQF | TRBV3 | TRBJ2-1 |
| 39 | 0.148 | TGTGCCAGCACCGGACTGGGGATAACTATGCTGAGCAGTTCTTC | ASTGLDNYAEQF | TRBV13-3 | TRBJ2-1 |

Mouse 6 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 5458 | 27.330 | TGTGCCAGCAGCAACAGCCATAACAACACAGGCTCCGCTTTT | ASSNSHNNQAPL | TRBV13-3 | TRBJ1-5 |
| 3076 | 15.402 | TGTGCTAGCAGTCCAGGGGGCGGGGTAGTCAAACACCTTGACTTT | ASSPGGGGQNTLY | TRBV29 | TRBJ2-4 |
| 2891 | 14.476 | TGTGCCAGCAGTGGGGACTGGGGGGCGCAGATGCTGAGCAGTCTTC | ASSGDWGGADAEQF | TRBV13-3 | TRBJ2-1 |
| 2051 | 10.270 | TGTGCCAGCGGTGGCCTCAATGCAAACCTCCGACTACACCTTC | ASGGLNANSDYT | TRBV13-2 | TRBJ1-2 |
| 1013 | 5.072 | TGTGCCAGCAGTGATTACTGGGGAAACACCTTGACTTT | ASSDYWGNTLY | TRBV13-3 | TRBJ2-4 |
| 746 | 3.735 | TGTGCCAGCGGTGATGCTGGGGGGCTCATGCTGAGCAGTCTTC | ASGDAGGAHAEQF | TRBV13-2 | TRBJ2-1 |
| 485 | 2.429 | TGTGCCAGCAGTATGGGTGGGGTCTAGTCAAACACCTTGACTTT | ASSMGWSSQNTLY | TRBV19 | TRBJ2-4 |
| 290 | 1.452 | TGTGCCAGCAGCTCAGGGACTAGCGGAAACAATGAGCAGTCTTC | ASSSGTSGNNEQF | TRBV14 | TRBJ2-1 |
| 275 | 1.377 | TGTGCCAGCAGCTGGGGGAATGGTCAAACACCTTGACTTT | ASTWGNQNTLY | TRBV19 | TRBJ2-4 |
| 252 | 1.262 | TGTGCCAGCAGTGATGGTAACAGTAACACAGAAAGTCTCTTT | ASSDGNSTEVF | TRBV13-3 | TRBJ1-1 |
| 205 | 1.026 | TGTGCCAGCAGCTATCCCGGACTGGGGGAACCAAGACACCCAGTACTTT | ASSYPRDWGNQDTQY | TRBV4 | TRBJ2-5 |
| 199 | 0.996 | TGTGCCATCGGGGACCTCTCGAACACCGGGGAGCTGTTTTT | AIGDLSNTGELF | TRBV13-2 | TRBJ2-2 |
| 186 | 0.931 | TGTGCCAGCAGTATAGGAAACAGTAATTCGCCCTCTACTTT | ASSIGNSNSPLY | TRBV19 | TRBJ1-6 |
| 148 | 0.741 | TATGCCAGCAGCCCTGGACAGGGCGTGGACGAGCAGTACTTC | ASSPGQGVDEQY | TRBV8 | TRBJ2-7 |
| 130 | 0.651 | TGTGCCAGCGGTGATAGAGCTGGGGTAAACCAAGACACCCAGTACTTT | ASGDRAGGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 128 | 0.641 | TGTGCCAGCGGTGACCGGGACAGGGGAAGTCAAACACCTTGACTTT | ASGDRDRGSQNTLY | TRBV13-2 | TRBJ2-4 |
| 103 | 0.516 | TGTGCTAGCAGTAGCCCCGGGACAGGGGGCGATGAACAGTACTTC | ASSSPGTGGDEQY | TRBV17 | TRBJ2-7 |
| 99 | 0.496 | TGTGCAAGCAGCCCTGGACTGGGGCGAGGTATGCTGAGCAGTCTTC | ASSPGLGARYAEQF | TRBV16 | TRBJ2-1 |
| 96 | 0.481 | TGTGCCAGCCAGGGACAGGTGGAAGAAGGCAGTACTTC | ASQGTGRRQY | TRBV13-2 | TRBJ2-7 |
| 94 | 0.471 | TGTGCCAGCAGCTCTACCGGACAGGACAGGATGGCTACACCTTC | ASSYRTGQDGYT | TRBV16 | TRBJ1-2 |
| 92 | 0.461 | TGTGCCAGCAGCCCAAGGGCCGGGACAGGGTCTTGAGGGAGCAGTACTTC | ASSQAGTGSLEQY | TRBV14 | TRBJ2-7 |
| 91 | 0.456 | TGTGCAAGCAGCTTAGAGGACAAGGGGGCTGAGCAGTCTTC | ASLEDKGAEQF | TRBV16 | TRBJ2-1 |
| 88 | 0.441 | TGTGCCAGCAGCGAGGGGACAGGGCGAACACTGAAGCTTTCTTT | ASSEGTGANTEAF | TRBV12-2 | TRBJ1-1 |
| 87 | 0.436 | TGTGCCAGCAGTGATGAAGGGGTGTCCAACGAAGATTATTTTT | ASSDEGVSNERLF | TRBV13-3 | TRBJ1-4 |
| 87 | 0.436 | TGTGCCAGCGGTGGCCTCAATGCAAACCTCCGACTACGCCTTC | ASGGLNANSDYA | TRBV13-2 | TRBJ1-2 |
| 86 | 0.431 | TGTGCCAGCAACCCCTGGACTAGCGGGGCTACGAGCAGTACTTC | ASNPWTSGAYEQY | TRBV12-2 | TRBJ2-7 |
| 80 | 0.401 | TGTGCTAGCAGTTCCTCCAGGGGAGGCACAGAAGTCTCTTT | ASSSPRGGTEVF | TRBV29 | TRBJ1-1 |
| 78 | 0.391 | TGCAGTGCTAGAGATCTGGACAGGGTGGCATCGATGAGCAGTCTTC | SARDLDRVGIDEQF | TRBV30 | TRBJ2-1 |
| 76 | 0.381 | TGTGCTGGAGTGGGGCCCTAAGGGGGCTACGAGCAGTACTTC | AWSGGPKGAYEQY | TRBV31 | TRBJ2-7 |
| 75 | 0.376 | TGTGCCAGCAGGAATACAGGGGGCACTGAAGCTTTCTTT | ASRNTGGTEAF | TRBV16 | TRBJ1-1 |
| 74 | 0.371 | TGTGCTAGCAGCGGACTGGAGGAGACACCTTGACTTT | ASSGTGGDTLY | TRBV17 | TRBJ2-4 |
| 74 | 0.371 | TGCGCCAGCAAGGGGACTACTATGGCTACACCTTC | ASKGDYYGYT | TRBV16 | TRBJ1-2 |
| 71 | 0.356 | TGTGCCAGCAGACAAGGACAGGGTAACACCTACAATGAGCAGTCTTC | ASRQQGNTYNEQF | TRBV8 | TRBJ2-1 |
| 68 | 0.340 | TGTGCCAGCAGTGCTCACACATTCTGGAATACGCTCTATTTT | ASSASHHSGNTLY | TRBV13-3 | TRBJ1-3 |
| 66 | 0.330 | TGTGCCAGCAGTTTAAGCCCCCTAGCGCTTTGGTTCAGTTCTTC | ASSLPPSALGQF | TRBV29 | TRBJ2-1 |
| 64 | 0.320 | TGTGCCACCCGGACAGGGGGACAAACACAGAAGTCTCTTT | ATRTGGTNTTEVF | TRBV13-3 | TRBJ1-1 |
| 64 | 0.320 | TGTGCCAGCAGTGATGGTAACAGTAACACAAAAGTCTCTTT | ASSDGNSTKVF | TRBV13-3 | TRBJ1-1 |
| 58 | 0.290 | TGTGCCAGCAGTGATGGGAGAACACAGAAGTCTCTTT | ASSDWENTEVF | TRBV13-1 | TRBJ1-1 |
| 56 | 0.280 | TGTGCCAGCTCTCTGGACTGGGGCCCCAAGACACCCAGTACTTT | ASSLDWGPQDTQY | TRBV12-2 | TRBJ2-5 |
| 56 | 0.280 | TATGCCAGCAGTAGCCCCGGATGATGACACTGAAGCTTTCTTT | ASSPPDDDEAF | TRBV13-1 | TRBJ1-1 |
| 54 | 0.270 | TGTGCCAGCAGCTTGGGGACAAAAGACACCCAGTACTTT | ASSLGTKDTQY | TRBV3 | TRBJ2-5 |
| 54 | 0.270 | TATGCTGAGCAGTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 53 | 0.265 | TGCAGTGCTACACAGCAGCTAAGTGGCTACACCTTC | SATRQLSGYT | TRBV30 | TRBJ1-2 |
| 51 | 0.255 | TGTGCCAGCGGACAGGGGGATGGCTACACCTTC | ASGQGDGYT | TRBV16 | TRBJ1-2 |
| 47 | 0.235 | TGCAGTGCTAGAGATCTAGCGGGCCCCGGCAGATACGAGTATTTT | SARDLAGPGTDTQY | TRBV30 | TRBJ2-3 |
| 47 | 0.235 | TGTGCCAGCAGCTTAGGGACTGGGGTCTATGAACAGTACTTC | ASSLGTGVYEQY | TRBV3 | TRBJ2-7 |
| 47 | 0.235 | TGTGCCAGCAGTTGGGCGAACACAGATACGAGTATTTT | ASSWANTDTQY | TRBV8 | TRBJ2-3 |
| 43 | 0.215 | TGTGCCAGCAGTGAAGGCAATGCAAACCTCCGACTACACCTTC | ASSEGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 41 | 0.205 | TGCAGTGCCACACCGACTAGCGGCGACCAAGAGACCCAGTACTTC | SATPTSGDQETQY | TRBV30 | TRBJ2-5 |
| 40 | 0.200 | TGTGCCAGCGGTGATGGCAATGCAAACCTCCGACTACACCTTC | ASGDGNANSDYT | TRBV13-2 | TRBJ1-2 |
| 39 | 0.195 | TGTGGTGTAGGGACTTGACAGGGTCAAACGAAGATTATTTTT | GARDLTGSNERLF | TRBV20 | TRBJ1-4 |
| 39 | 0.195 | TGTGCTGGGGGTAACACCCGGGACAGTCTACTTT | AWGVNTGQLY | TRBV17 | TRBJ2-2 |

Mouse 7 αPD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|------------|---|------------------|------------|------------|
| 1715 | 91.4179104 | TGTGCCAGCAGCTTAGAGGACAGGGAGGGCTCCGACTACACCTTC | ASSLEDREGSDYT | TRBV3 | TRBJ1-2 |
| 78 | 4.15778252 | TGTGCTAGCAGTCTGGGGGGGACTATGCTGAGCAGTTCTTC | ASSLGGDYAEQF | TRBV17 | TRBJ2-1 |
| 25 | 1.3326226 | TGTGCCAGCAGTCCCACTGGGAATAACCAAGACACCCAGTACTTT | ASSPTGNNQDTQY | TRBV13-3 | TRBJ2-5 |
| 19 | 1.01279318 | TGTGCCAGCAGTCCGGGGGGTAGTCAAAACACCTTGACTTT | ASSPGGSQNTLY | TRBV19 | TRBJ2-4 |
| 17 | 0.90618337 | TGTGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 14 | 0.74626866 | TGTGCTAGCAGTGGGGACTGGGGGGCAGGGGAACAGTACTTC | ASSGDWGAGEQY | TRBV29 | TRBJ2-7 |
| 8 | 0.42643923 | TGTGCCAGCGGTGATGCAGGGGGGGCTATGCTGAGCAGTTCTTC | ASGDAGGGYAEQF | TRBV13-2 | TRBJ2-1 |

Mouse 8 α PD-L1

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|---|------------------|------------|------------|
| 4465 | 38.819 | TGTGCCAGCAGGCCCTACAATAGTCAAAACACCTTGTACTTT | ASRPYNSQNTLY | TRBV19 | TRBJ2-4 |
| 1200 | 10.433 | TGTGCCAGCGGTGATCGGGACAGGGGAAACACCGGGCAGCTACTTT | ASGDRDRGNTGQLY | TRBV13-2 | TRBJ2-2 |
| 1192 | 10.363 | TGTGCAAGCAGCTTATGGGGGCTCTATGCTGAGCAGTTCTTC | ASSLWGLYAEQF | TRBV16 | TRBJ2-1 |
| 635 | 5.521 | TGTGCTAGCAAGTTTCAGGGGACTATGCTGAGCAGTTCTTC | ASKVQGDYAEQF | TRBV17 | TRBJ2-1 |
| 504 | 4.382 | TGTGGTGCTAGGGATCAGGACAATTCACGAAAGATTATTTTT | GARDQDNSNERLF | TRBV20 | TRBJ1-4 |
| 500 | 4.347 | TGTGCCAGCAGCTTAGGAAGGGGACTGGGGAACTCCTATGAACAGTACTTC | ASSLGRDWGNSYEQY | TRBV3 | TRBJ2-7 |
| 472 | 4.104 | TGTGCCAGCAGTATAGTCAAAACACAGGCTCCGCTTTTT | ASSIGQNNQAPL | TRBV19 | TRBJ1-5 |
| 341 | 2.965 | TGTGCCAGCAGTATAGGGCAGAATAATTCGCCCTCTACTTT | ASSIGQNNSPLY | TRBV19 | TRBJ1-6 |
| 268 | 2.330 | TGTGCCAGCAGTGATGGAGGGGGTAATTCGCCCTCTACTTT | ASSDGGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 266 | 2.313 | TGTGCTAGCAGTAGAGGGGACAACCTATGCTGAGCAGTTCTTC | ASSRGDNYAEQF | TRBV17 | TRBJ2-1 |
| 247 | 2.147 | TGTGGTGCTAGGGATCGGGACAATTCACGAAAGATTATTTTT | GARDRDNNSNERLF | TRBV20 | TRBJ1-4 |
| 240 | 2.087 | TGTGCCAGCGGTGATCGAGGGGCTCAAACCTATGCTGAGCAGTTCTTC | ASGDRGASNYAEQF | TRBV13-2 | TRBJ2-1 |
| 85 | 0.739 | TGTGCCAGCGGTGGGGACAATGCAAACCTCCGACTACACCTTC | ASGGDNANSDYT | TRBV13-2 | TRBJ1-2 |
| 78 | 0.678 | TGTGCCAGCAGTGACGGGGTTCACGAAAGATTATTTTT | ASSDGGNSNERLF | TRBV13-3 | TRBJ1-4 |
| 69 | 0.600 | TGTGCCAGCGGTGATCTTGGGAACCAAGACACCCAGTACTTC | ASGDLGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 64 | 0.556 | TGTGCCAGCGGTGATGACGGGGGCGCCATGCTGAGCAGTTCTTC | ASGDAGGAHAEQF | TRBV13-2 | TRBJ2-1 |
| 62 | 0.539 | TGTGCCAGCAGTGATGGCAATGCAAACCTCCGACTACACCTTC | ASSDGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 56 | 0.487 | TGTGCCAGCGGTGACCGGACTGGGGGCACTATGCTGAGCAGTTCTTC | ASGDRTGGHYAEQF | TRBV13-2 | TRBJ2-1 |
| 54 | 0.469 | TGTGCCAGCAGTGACTGGGGGGCGCCGAACAGTACTTC | ASSDWGGAEQY | TRBV13-3 | TRBJ2-7 |
| 50 | 0.435 | TGTGCCAGCAGCGGGGACTGGGGGGGAACTATGCTGAGCAGTTCTTC | ASSGDWGGNYAEQF | TRBV13-3 | TRBJ2-1 |
| 48 | 0.417 | TGTGGTGCTCCAGGGCGAGACAACAGGCTCCGCTTTTT | GAPGRDNQAPL | TRBV20 | TRBJ1-5 |
| 44 | 0.383 | TGTGCCAGCAGTATAGGGGCTAATAATTCGCCCTCTACTTT | ASSIGANNSPLY | TRBV19 | TRBJ1-6 |
| 43 | 0.374 | TGTGCCAGCAGTGCCGGGGGTGTAACCTCCGACTACACCTTC | ASSAGGANSDYT | TRBV13-3 | TRBJ1-2 |
| 39 | 0.339 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 33 | 0.287 | TGTGCCAGCAGCGCCGGGAATTCGGAATACGCTCTATTTT | ASSAGNSGNTLY | TRBV14 | TRBJ1-3 |
| 32 | 0.278 | TGTGCCAGCAGTATAGCTCGACAGGGGAACACAGAAGTCTCTTT | ASSIARQGNTVEF | TRBV19 | TRBJ1-1 |
| 31 | 0.270 | TGTGCCAGCGGTGATGGCAATGCAAACCTCCGACTACACCTTC | ASGDGNANSDYT | TRBV13-2 | TRBJ1-2 |
| 30 | 0.261 | TGTGCCAGCGGTGATGCCTGGGGGGCGAAACGCTGTATTTT | ASGDAWGGETLY | TRBV13-2 | TRBJ2-3 |
| 30 | 0.261 | TGTGCCAGCGGTGATGCGGACAGGGGGGTTGAACAGTACTTC | ASGDAAGGVEQY | TRBV13-2 | TRBJ2-7 |
| 30 | 0.261 | TGCTCCAGCAGTCAATGGGGACAGTATGCTGAGCAGTTCTTC | SSSQWQQYAEQF | TRBV23 | TRBJ2-1 |
| 23 | 0.200 | TGTGCCAGCAGCTTAGATGGGGGGGCGCCTGCAGAAACGCTGATTTT | ASSLDGGAPAETLY | TRBV3 | TRBJ2-3 |
| 23 | 0.200 | TGTGCCAGCAGTATCGGACAGGGGAACACAGAAGTCTCTTT | ASSIGQGNTVEF | TRBV19 | TRBJ1-1 |
| 22 | 0.191 | TGTGCCAGCAGCCCCGGTGGGGGTTAACCAAGACACCCAGTACTTT | ASSPGWGVNQDTQY | TRBV5 | TRBJ2-5 |
| 22 | 0.191 | TGTGCTAGCAGTCAATCCTGGGGGCAAGACCCAGTACTTT | ASSQSWGQDTQY | TRBV21 | TRBJ2-5 |
| 21 | 0.183 | TGTGCCAGCGGTGGGGGTAATTCGGAATACGCTCTATTTT | ASGGGNSGNTLY | TRBV13-2 | TRBJ1-3 |
| 20 | 0.174 | TGTGCCAGCAGTACTGGGGGGGCTATGCTGAGCAGTTCTTC | ASSDWGGYAEQF | TRBV19 | TRBJ2-1 |
| 19 | 0.165 | TGTGCTAGCAGTCCCGGGACAGGGGTAACACCGGGCAGCTACTTT | ASSSRDRGNTGQLY | TRBV29 | TRBJ2-2 |
| 18 | 0.156 | TGTGCCAGCAGTCCCGGACAATCAACGAAAGATTATTTTT | ASSPGTINERLF | TRBV14 | TRBJ1-4 |
| 17 | 0.148 | TGTGCTAGCAGGGGGACAATAACCAAGACACCCAGTACTTT | ASRGTNNQDTQY | TRBV17 | TRBJ2-5 |
| 17 | 0.148 | TGTGCCAGCAGTCTGGGGGAACTATGCTGAGCAGTTCTTC | ASSPGGNYAEQF | TRBV14 | TRBJ2-1 |
| 17 | 0.148 | TGTGCCAGCAGTTACAGGGGAACTCCGACTACACCTTC | ASSYRGNSDYT | TRBV19 | TRBJ1-2 |
| 16 | 0.139 | TGTGCCAGCAGTGACGGGGGGGCAACACAGAAGTCTCTTT | ASSDGGANTEVF | TRBV13-3 | TRBJ1-1 |
| 15 | 0.130 | TGTGCCAGCAGTCCGGGCCCTATAATTCGCCCTCTACTTT | ASSPGPYNSPLY | TRBV19 | TRBJ1-6 |
| 15 | 0.130 | TGTGCCAGCAGTGAGGACAGGGGGCTCCGACTACACCTTC | ASSDRGLSDYT | TRBV13-3 | TRBJ1-2 |
| 15 | 0.130 | TGTGCCAGCAGTCCCGGACATGGTGAACAGTACTTC | ASSPGHGEQY | TRBV19 | TRBJ2-7 |
| 14 | 0.122 | TGTGCCAGCAGTGATGCTGGAATTCGCCCTCTACTTT | ASSDAWNSPLY | TRBV13-3 | TRBJ1-6 |

Mouse 1 Immune Part I

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 2815 | 13.633 | TGTGCCAGCAGTGCAGGACACTTTAACACAGAAGTCTTCTTT | ASSAGHFNTEVF | TRBV13-3 | TRBJ1-1 |
| 2420 | 11.720 | TGTGCTAGCACACTGGGGGGACTATGCTGAGCAGTTCTTC | ASTTGGDYAEQF | TRBV17 | TRBJ2-1 |
| 1113 | 5.390 | TGTGCCAGCAGTGAAGGCAACTATAATTCCGCCCTCTACTTT | ASSEGNYSPLY | TRBV13-3 | TRBJ1-6 |
| 930 | 4.504 | TGTGCCAGCAGTCCGGCAATGCAAACTCCGACTACACCTTC | ASSFGNANSDYT | TRBV3 | TRBJ1-2 |
| 915 | 4.431 | TGTGCCAGCAGTGATGGTCTATAATTCCGCCCTCTACTTT | ASSDGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 808 | 3.913 | TGTGCTAGCAGTTTGGGGGGTTAGTGCAGAAACGCTGTATTTT | ASSLGGFSAETLY | TRBV29 | TRBJ2-3 |
| 702 | 3.400 | TGTGCCAGCGGTGATCGGGACACCGCTAGTGCAGAAACGCTGTATTT | ASGDRDTASAETLY | TRBV13-2 | TRBJ2-3 |
| 689 | 3.337 | TGTGCCAGCAGCCCCGGGAATAGTCAAAACACCTTGTACTTT | ASSPGNSQNTLY | TRBV14 | TRBJ2-4 |
| 664 | 3.216 | TGTGCTAGCAGTAGAGGGGATAACTATGCTGAGCAGTCTCTC | ASSRGDNYAEQF | TRBV17 | TRBJ2-1 |
| 656 | 3.177 | TGTGCTGGAGTCTCCGGGACAGGATAACCAAGACACCCAGTACTTT | AWSLRDRDNQDTQY | TRBV31 | TRBJ2-5 |
| 641 | 3.104 | TGTGCCAGCAGTGATGCAAGACAAATTAACACAGAAGTCTTCTTT | ASSDARQINTEVF | TRBV13-1 | TRBJ1-1 |
| 598 | 2.896 | TGTGCTAGCAGTTTAGCGGGTATAGTGCAGAAACGCTGTATTTT | ASSLGGYSAETLY | TRBV29 | TRBJ2-3 |
| 587 | 2.843 | TGTGCCAGCTCTCGCCGGACAGATAAATTCGCCCTCTACTTT | ASSLAGQYNSPLY | TRBV12-1 | TRBJ1-6 |
| 363 | 1.758 | TGTGCTGGAGTCCGGACTGGGGGTATGAACAGTACTTC | AWSRDWGYEQY | TRBV31 | TRBJ2-7 |
| 348 | 1.685 | TGTGCCAGCAGTAGTGTGACTGGGGGATTGAACAGTACTTC | ASSELTGGIEQY | TRBV13-1 | TRBJ2-7 |
| 343 | 1.661 | TGTGGTGCTAGGGATCGCACAAATTCACAGAAAGATTATTTTTT | GARDRTNSNERLF | TRBV20 | TRBJ1-4 |
| 302 | 1.463 | TGTGCCAGCAGCGCGGGACCGGGCAGCTCTACTTT | ASSGGTGQLY | TRBV13-3 | TRBJ2-2 |
| 255 | 1.235 | TGTGCCAGCGGTGATAGGGGACAACTAGTGCAGAAACGCTGTATTTT | ASGDRGQSSAETLY | TRBV13-2 | TRBJ2-3 |
| 232 | 1.124 | TGTGCCAGCAGTGATAGGGGCGGGAGCTCTATGAACAGTACTTC | ASSDRGGSSYEQY | TRBV13-3 | TRBJ2-7 |
| 218 | 1.056 | TGTGCTAGCAGTAGCCGTTCTGGGGGAAACTATGCTGAGCAGTTCTTC | ASSRSGGNYAEQF | TRBV17 | TRBJ2-1 |
| 208 | 1.007 | TGTGCTAGCAGTCTACTGGGGACTATGCTGAGCAGTTCTTC | ASSLLGDYAEQF | TRBV17 | TRBJ2-1 |
| 170 | 0.823 | TGTGCCAGCGGTGATAGGGCTGGGTCTAGTGCAGAAACGCTGTATTTT | ASGDRAGSSAETLY | TRBV13-2 | TRBJ2-3 |
| 162 | 0.785 | TGTGCCAGCAGGACAGGGAACATAAATTCGCCCTCTACTTT | ASRTGNHNSPLY | TRBV13-3 | TRBJ1-6 |
| 155 | 0.751 | TGTGCTAGCAGTAGCCCGGTGCAAAACACAGAAGTCTTCTTT | ASSAGANTEVF | TRBV17 | TRBJ1-1 |
| 146 | 0.707 | TGTGCCAGCAGCGAAGGGGGTGGGAATTCGCCCTCTACTTT | ASSEGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 138 | 0.668 | TGTGCCAGCGGGACAGGCATTCTGAAATACGCTCTACTTT | ASRRDRHSGNTLY | TRBV13-3 | TRBJ1-3 |
| 137 | 0.664 | TGTGGTGCTAGGGATCAAGACAGGGGGCAGGGTGAACAGTACTTC | GARDQDRGQGEQY | TRBV20 | TRBJ2-7 |
| 136 | 0.659 | TGTGCTGGAGTCCCTCCCGGGTGGACACAGAAGTCTTCTTT | AWSPLPRVDTEVF | TRBV31 | TRBJ1-1 |
| 135 | 0.654 | TGTGCTAGCAGTCCCGCCGGACAGTAACTATGCTGAGCAGTCTTC | ASSRRDNSYAEQF | TRBV29 | TRBJ2-1 |
| 128 | 0.620 | TGTGCCAGCAGGACAGGGGGTAGTCAAAACACCTTGTACTTT | ASRTGGSQNTLY | TRBV19 | TRBJ2-4 |
| 119 | 0.576 | TGTGCCAGCAGCTTAGATGGGGGGCCCCCGCAGAAACGCTGTATTTT | ASSLDGGPPAETLY | TRBV3 | TRBJ2-3 |
| 111 | 0.538 | TGTGCCAGCAGTATAGGGACATAACACAGGCTCCGCTTTTTT | ASSIGTYNQAPL | TRBV19 | TRBJ1-5 |
| 109 | 0.528 | TGTGCTAGCAGTCTGGGGGGACTATGCTGAGCAGTCTTCTTC | ASSLGGDYAEQF | TRBV17 | TRBJ2-1 |
| 96 | 0.465 | TGTGCCAGCAGTATAAGTTGGACAGGGGGCTATGAACAGTACTTC | ASSISWTGGYEQY | TRBV19 | TRBJ2-7 |
| 96 | 0.465 | TGTGCCAGCAGTGATGGGAACAGAACTCCGACTACACCTTC | ASSDGNRNSDYT | TRBV13-3 | TRBJ1-2 |
| 96 | 0.465 | TGTGGTGCTAGGGCCCTCAAGCAACACAGAAAGTCTTCTTT | GARAPQANTEVF | TRBV20 | TRBJ1-1 |
| 96 | 0.465 | TGTAGTTCTAGATCGGACTTCTCAGAAACGCTGTATTTT | SSRSDFSETLY | TRBV30 | TRBJ2-3 |
| 93 | 0.450 | TGTGCTAGCAGTTCGACGGGGTTAGTGCAGAAACGCTGTATTTT | ASSSTGFSAETLY | TRBV29 | TRBJ2-3 |
| 93 | 0.450 | TGTGCTGGAGTGGGGACTGGGGTTATGAACAGTACTTC | AWSGDWGYEQY | TRBV31 | TRBJ2-7 |
| 85 | 0.412 | TGTGCCAGCAGTGGAGACTGGGGGGGAACTATGCTGAGCAGTCTTC | ASSGDWGGNYAEQF | TRBV13-3 | TRBJ2-1 |
| 76 | 0.368 | TGTGCTAGCAGTAGCAACACCGGGCAGCTCTACTTT | ASSNTGQLY | TRBV17 | TRBJ2-2 |
| 72 | 0.349 | TGTGCCAGCGGTGATCCGGGGGTAACCAAGACACCCAGTACTTT | ASGDAGGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 70 | 0.339 | TGTGCCAGCAGTCCGGGACATGCAAAACACAGAAGTCTTCTTT | ASSPGHANTEVF | TRBV13-3 | TRBJ1-1 |
| 68 | 0.329 | TGTGGTGCTAGCAGGGGCACAGAAGTCTTCTTT | GASRGTEVF | TRBV20 | TRBJ1-1 |
| 67 | 0.324 | TGTGCCAGCAGCCCTTGACACCTAGTGCAGAAACGCTGTATTTT | ASSPLTPSAETLY | TRBV5 | TRBJ2-3 |
| 67 | 0.324 | TGTGCTAGCAAAACAGGGGGCCTATGCTGAGCAGTCTTCTTC | ASKTGGAYAEQF | TRBV29 | TRBJ2-1 |
| 66 | 0.320 | TGTGCTGGAGTCAACCGGGACAGGGGATCTGGAAATACGCTCTATTTT | AWSHRDRGSGNTLY | TRBV31 | TRBJ1-3 |
| 66 | 0.320 | TGTGCCAGCGGTGATCGGACCGTCTCTAGTGCAGAAACGCTGTATTTT | ASGDRTVSSAETLY | TRBV13-2 | TRBJ2-3 |
| 65 | 0.315 | TGTGCCAGCAGGGACTGGTATGCTGAGCAGTCTTCTTC | ASRDWYAEQF | TRBV13-3 | TRBJ2-1 |
| 62 | 0.300 | TGTGCTGGAGTCTAAGGGACTGGGAGAACCAAGACACCCAGTACTTT | AWSLRDWENQDTQY | TRBV31 | TRBJ2-5 |
| 61 | 0.295 | TGTGGTGCTAGGGATCGCGACAATCAAACTCCGACTACACCTTC | GARDRDNNSNSDYT | TRBV20 | TRBJ1-2 |
| 61 | 0.295 | TGTGCCAGCAGTGACGGCAATGCAAACTCCGACTACACCTTC | ASSDGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 61 | 0.295 | TGTGCCAGCAGTACAGGGGGTCTTCAAAACACCTTGTACTTT | ASSTGGFQNTLY | TRBV19 | TRBJ2-4 |
| 60 | 0.291 | TGTGCTAGCAGTAGGGCAGGGAACTATGCTGAGCAGTCTTCTTC | ASSRAGNYAEQF | TRBV17 | TRBJ2-1 |
| 60 | 0.291 | TGTGCCAGCGGGACTGGGAATAGTCAAAACACCTTGTACTTT | ASGTGNSQNTLY | TRBV13-3 | TRBJ2-4 |
| 58 | 0.281 | TGTGCCATAGGGACTGGGGGGCTCAAGACACCCAGTACTTT | AIGTGGQLQDTQY | TRBV13-3 | TRBJ2-5 |
| 58 | 0.281 | TGTGCCAGCAGTGTCCGACAGGGTAATTCGCCCTCTACTTT | ASSVQGNSPLY | TRBV13-1 | TRBJ1-6 |
| 56 | 0.271 | TGTGCTAGCAGTCCCGAGGGACAACAACTATGCTGAGCAGTCTTCTTC | ASSSRGTTNYAEQF | TRBV29 | TRBJ2-1 |
| 56 | 0.271 | TGTGCCAGCAGTGATAACCCCTATAATTCGCCCTCTACTTT | ASSDNPYNSPLY | TRBV13-1 | TRBJ1-6 |
| 53 | 0.257 | TGTGCCAGCGGTGACCCGGGACAAAACACAGAAGTCTTCTTT | ASGDPGQNTTEVF | TRBV13-2 | TRBJ1-1 |
| 53 | 0.257 | TGTGCCAGCAGTGTGGGGGACGGCACCGGGCAGCTCTACTTT | ASSVGDGTGQLY | TRBV13-3 | TRBJ2-2 |
| 51 | 0.247 | TGTGCTAGCACCTTGGGGGGGACCAAGACACCCAGTACTTT | ASTLGGDQDTQY | TRBV17 | TRBJ2-5 |
| 50 | 0.242 | TGTGCTAGCAGTATAGGGGGGACTATGCTGAGCAGTCTTCTTC | ASSIGGDYAEQF | TRBV17 | TRBJ2-1 |
| 49 | 0.237 | TGTGCTGGAGTCTCCGGACTGGGTAACACCGGGCAGCTCTACTTT | AWSLRDWWNTGQLY | TRBV31 | TRBJ2-2 |
| 48 | 0.232 | TGTGGTGCTAGGGATCAGACAGGGGGCAACACAGAAGTCTTCTTT | GARDQDTGGNTEVF | TRBV20 | TRBJ1-1 |
| 47 | 0.228 | TGTGCCAGCAGTCCGGGACAGGGGGCGGACGCTGTATTTT | ASSRDRGRTLY | TRBV4 | TRBJ2-3 |
| 40 | 0.194 | TGTGCTAGCAGTCCCGGGACAGGAAACACCGGGCAGCTCTACTTT | ASSRDRRENTGQLY | TRBV29 | TRBJ2-2 |
| 39 | 0.189 | TGTGCCAGCAGCAAGATGACAGTAACTCCGACTACACCTTC | ASSQDDNSNSDYT | TRBV5 | TRBJ1-2 |
| 36 | 0.174 | TGTGGTGCTAGGGATCAGCAGTTTTCAACAGAAAGATTATTTTTT | GARDQQFSNERLF | TRBV20 | TRBJ1-4 |
| 36 | 0.174 | TGTGCCAGCAAAACAGGGAATTCGAAATACGCTCTATTTT | ASKTGNNGNTLY | TRBV13-3 | TRBJ1-3 |
| 35 | 0.170 | TGTGCCAGCAGATTCAGGGGGCAACACAGAAGTCTTCTTT | ASRFQGANTEVF | TRBV19 | TRBJ1-1 |

Mouse 1 Immune Part II

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| | | | | | |
| 34 | 0.165 | TGTGCCAGCAGTACAGGGAACCAAGACACCCAGTACTTT | ASSTGNQDTQY | TRBV13-3 | TRBJ2-5 |
| 33 | 0.160 | TGTGCCAGCAGTGACTGGGGCGGGGATGCTGAGCAGTTCTTC | ASSDWGGDAEQF | TRBV13-3 | TRBJ2-1 |
| 33 | 0.160 | TGTGCCAGCGGTGATGGGACAGGGGTTGAACAGTACTTC | ASGDGTGVEQY | TRBV13-2 | TRBJ2-7 |
| 32 | 0.155 | TGTGCCAGCAGCTGGAACGGGGCGCAAACTCCGACTACACCTTC | ASSWNGGANSDYT | TRBV4 | TRBJ1-2 |
| 32 | 0.155 | TGTGCCAGCGGTGCCGGACTGGGGGTTATGAACAGTACTTC | ASGAGLGGYEQY | TRBV13-2 | TRBJ2-7 |
| 31 | 0.150 | TGTGCCAGCGGTGATGGAATTCACAAAGAAAGATTATTTTT | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 30 | 0.145 | TGTGGTGCTAGGGATAGGACAGGGTCTCTGGAAATACGCTCTATTTT | GARDRTGSSGNTLY | TRBV20 | TRBJ1-3 |
| 30 | 0.145 | TGTGCCAGCGGTGATCTCGTTTCAACGAAAGATTATTTTT | ASGDLVSNERLF | TRBV13-2 | TRBJ1-4 |
| 30 | 0.145 | TGTGCCAGCACCCCGGAATAGTCAAACGCCTTGACTTTT | ASSPGNSQNALY | TRBV14 | TRBJ2-4 |
| 30 | 0.145 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 29 | 0.140 | TGTGGTGCTAGGGACCGGACAGGGGCGAGGAAATACGCTCTATTTT | GARDRDRGQNTLY | TRBV20 | TRBJ1-3 |
| 29 | 0.140 | TGTGCCAGCGGGGACAGAAATGCAAACTCCGACTACACCTTC | ASGGQNANSDYT | TRBV13-2 | TRBJ1-2 |
| 28 | 0.136 | TGTGCCAGCTCACCTGGGGGGGCGCGCACTCCGACTACACCTTC | ASSPGGGAHSDYT | TRBV12-1 | TRBJ1-2 |
| 28 | 0.136 | TGTGCCAGCAGACTGGGGGGTAGTCAAACACCTTGACTTTT | ASRLGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 28 | 0.136 | TGTGCCAGCAGAACCAGGACAGGGACCCAGGCTCCGCTTTT | ASRTGTGTQAPL | TRBV19 | TRBJ1-5 |
| 27 | 0.131 | TGTGCCAGCAGTGTCCCTGGGGGCGCAGACACCTTGACTTTT | ASSVPGGADTLY | TRBV13-3 | TRBJ2-4 |
| 27 | 0.131 | TGTGCCAGCAGTGCTGGACATAACTATGCTGAGCAGTTCTTC | ASSAGHNYAEQF | TRBV13-3 | TRBJ2-1 |
| 26 | 0.126 | TGTGGTGCTAGGGATCGGGACAGTTCCAACGAAAGATTATTTTT | GARDRDSNERLF | TRBV20 | TRBJ1-4 |
| 26 | 0.126 | TGTGCCAGCAGTTCAAGGAATTCTGAAATACGCTCTATTTT | ASSSGNSGNTLY | TRBV14 | TRBJ1-3 |
| 24 | 0.116 | TGTGCCAGCGGTGATAGACAGGACAATAACTATGCTGAGCAGTTCTTC | ASGDRQDNNYAEQF | TRBV13-2 | TRBJ2-1 |
| 24 | 0.116 | TGTGGTGCTAGGGATCAGACCAATGCAAACACAGAAGTCTTCTTT | GARDQTNANTEVF | TRBV20 | TRBJ1-1 |
| 22 | 0.107 | TGTGCCAGCAGCTACTCTATGAACAGTACTTC | ASSYSYEQY | TRBV4 | TRBJ2-7 |
| 21 | 0.102 | TGTGCCAGCGGTGACCGGGTCCGGATGAACTATGCTGAGCAGTTCTTC | ASGDRGRMNYAEQF | TRBV13-2 | TRBJ2-1 |
| 21 | 0.102 | TGTGCCAGCGGTGATGCTGGGGGGGAGAAACGCTGTATTTT | ASGDAWGGETLY | TRBV13-2 | TRBJ2-3 |
| 21 | 0.102 | TGTGCCAGCAGTCTGGGGGGTCCAAGACACCCAGTACTTT | ASSPGGVQDTQY | TRBV19 | TRBJ2-5 |
| 20 | 0.097 | TGTGCCAGCAGTGAGGGCAATGCAAACCTCCGACTACACCTTC | ASSEGNANSDYT | TRBV13-3 | TRBJ1-2 |
| 20 | 0.097 | TGTGCCAGCAGCGTGGGACAGGGGAACACAGAAGTCTTCTTT | ASSVGQGNTEVF | TRBV13-3 | TRBJ1-1 |
| 19 | 0.092 | TGTGCAAGCAGCTTAGAGGGGGACTGGGGTATGAACAGTACTTC | ASSLEGDWGYEQY | TRBV16 | TRBJ2-7 |
| 19 | 0.092 | TGTGCCAGCGGTGATGGGAATGCAAACCTCCGACTACACCTTC | ASGDGNANSDYT | TRBV13-2 | TRBJ1-2 |
| 19 | 0.092 | TGTGCCAGCAGTGATGGACAGGGGAATGCTGAGCAGTTCTTC | ASSDGQNAEQF | TRBV13-3 | TRBJ2-1 |

Mouse 2 Immune Part I

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 1996 | 8.549 | TGTGCTAGCAGCGCAGGGGGGACTATGCTGAGCAGTTCTTC | ASSAGGDYAEQF | TRBV17 | TRBJ2-1 |
| 1366 | 5.851 | TGTGCCAGCTGGGACAGGGGGCATGAACAGTACTTC | ASWDRGHEQY | TRBV13-1 | TRBJ2-7 |
| 1233 | 5.281 | TGTGCCAGCGGTGACCGGGACTGGGGTCTATGAACAGTACTTC | ASGDRDWGSYEQY | TRBV13-2 | TRBJ2-7 |
| 990 | 4.240 | TGTGCCAGCAGGCTGGGGGAAGTCAAAACACCTTGACTTT | ASRLGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 823 | 3.525 | TGTGCCAGCAGTGAAGGCAACTATAATTCCGCCCTCTACTTT | ASSEGNYSPLY | TRBV13-3 | TRBJ1-6 |
| 799 | 3.422 | TGTGCCAGCAACTGGGGCAACCAAGACCCAGTACTTT | ASNWGNQDTQY | TRBV13-3 | TRBJ2-5 |
| 719 | 3.079 | TGTGCTAGCAGTAGAGCCGGGACAACATGAACAGTACTTC | ASSRAGDNYEQY | TRBV17 | TRBJ2-7 |
| 629 | 2.694 | TGTGCTAGCAGTCCCCGACATTCTCTATAATTCCGCCCTCTACTTT | ASSPRHSSYSPLY | TRBV29 | TRBJ1-6 |
| 552 | 2.364 | TGTGCTAGCAGTCTGGGGGGACTATGCTGAGCAGTTCTTC | ASSPGGDYAEQF | TRBV17 | TRBJ2-1 |
| 500 | 2.142 | TGTGCCAGCAGAACTATGCTGAGCAGTTCTTC | ASRNAYEQF | TRBV19 | TRBJ2-1 |
| 496 | 2.124 | TGTGCCAGCAGTCCGGGACACGCAACACAGAAGTCTCTTT | ASSPGHANTEVF | TRBV13-3 | TRBJ1-1 |
| 481 | 2.060 | TGTGCCAGCAGCTTACCAGAATAAATTCGCCCTCTACTTT | ASSLPEYNSPLY | TRBV3 | TRBJ1-6 |
| 477 | 2.043 | TGTGCCAGCAGTACAGGGTCTCTATAATTCCGCCCTCTACTTT | ASSQGSYSPLY | TRBV13-3 | TRBJ1-6 |
| 443 | 1.897 | TGTGCTAGCACCCGGACTGGGGTAACACCGGGCAGCTCTACTTT | ASTPDWGN TGQLY | TRBV29 | TRBJ2-2 |
| 386 | 1.653 | TGTGCCAGCAACTGGGGGGCGGTGCTGAGCAGTTCTTC | ASNWGGGAEQF | TRBV4 | TRBJ2-1 |
| 359 | 1.538 | TGTGGTGCTCAGGGGGTATGCTGAGCAGTTCTTC | GASGGYAEQF | TRBV20 | TRBJ2-1 |
| 357 | 1.529 | TGTGCCAGCAGTCTGGGGGGCCCAAGACCCAGTACTTT | ASSPGGAQDTQY | TRBV19 | TRBJ2-5 |
| 352 | 1.508 | TGTGCCAGCAGCGCCAGGCTCTGGAAATACGCTCTATTTT | ASSAQASGNTLY | TRBV13-3 | TRBJ1-3 |
| 300 | 1.285 | TGTAGTTCTAGCATGGGACAGGGGAAACAGTACTTC | SSSMGQKQY | TRBV30 | TRBJ2-7 |
| 297 | 1.272 | TGTGCCAGCAGTCCAGGGGTAACCAAGACCCAGTACTTT | ASSPGNQDTQY | TRBV19 | TRBJ2-5 |
| 293 | 1.255 | TGTGCCAGCAGTCCGGGGGAAGTCAAAACACCTTGACTTT | ASSPGGSQNTLY | TRBV19 | TRBJ2-4 |
| 268 | 1.148 | TGTGCTAGCATACAGGGGGTAACCAAGACCCAGTACTTT | ASIQGGNQDTQY | TRBV17 | TRBJ2-5 |
| 256 | 1.096 | TGTGCCAGCAGGACAGGGGGACAACACAGAAGTCTCTTT | ASRTGNTNEVF | TRBV13-3 | TRBJ1-1 |
| 256 | 1.096 | TGTGCCAGCGGTGACGGAATTCACAAAGAAAGATTATTTTC | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 247 | 1.058 | TGTGCTAGCAGTTTCTCAAATGCAACACAGAAGTCTCTTT | ASSFSNANTEVF | TRBV29 | TRBJ1-1 |
| 236 | 1.011 | TGTGGTGCTAGGGATCTTACAGATTCCAACGAAAGATTATTTTC | GARDLTDNSNERLF | TRBV20 | TRBJ1-4 |
| 230 | 0.985 | TGTGGTGCTAGGGATCAGACAGGGGGAAACGAAAGATTATTTTC | GARDQTGGNERLF | TRBV20 | TRBJ1-4 |
| 221 | 0.947 | TGTGCCAGCAGCGCGGGGACTGGGGGGCGCCGACCCAGTACTTT | ASSAGTGGAPDTQY | TRBV3 | TRBJ2-5 |
| 205 | 0.878 | TGTGCCAGCTCTCTGGCTGGGATATGCTGAGCAGTTCTTC | ASSLWLGYAEQF | TRBV12-1 | TRBJ2-1 |
| 203 | 0.869 | TGTGCCAGCAGCAAGCCTGGGGGGCTCTATGAACAGTACTTC | ASSQAWGGSYEQY | TRBV5 | TRBJ2-7 |
| 201 | 0.861 | TGTGCTGGAGTCTCCGGGACTGGGGGAACCAAGACCCAGTACTTT | AWSLRDWGNQDTQY | TRBV31 | TRBJ2-5 |
| 201 | 0.861 | TGTGCCAGCAGTTTAGGCAACTATAATTCCGCCCTCTACTTT | ASSLGNYSPLY | TRBV14 | TRBJ1-6 |
| 187 | 0.801 | TGTGCTGGAGTACCCGGGACTGGGGGAATAACTATGCTGAGCAGTTCTTC | AWSTRDWGN NYAEQF | TRBV31 | TRBJ2-1 |
| 183 | 0.784 | TGTGCAAGCAGCTCTTCGGACAGAGGGACACCCAGTACTTT | ASSSFGQRDTQY | TRBV16 | TRBJ2-5 |
| 166 | 0.711 | TGTGGTGCTAGGGATCTGGACAATGCAAACTCCGACTACACCTTC | GARDLDNANSDYT | TRBV20 | TRBJ1-2 |
| 162 | 0.694 | TGTGCCAGCAGTCCGGGACATAGTCAAAACACCTTGACTTT | ASSPGHSQNTLY | TRBV19 | TRBJ2-4 |
| 160 | 0.685 | TGTAGTTCTAGAGAGCATAACTATGCTGAGCAGTTCTTC | SSREHNYAEQF | TRBV30 | TRBJ2-1 |
| 159 | 0.681 | TGTGCCAGCAGTACAGGGAATAACAACAGGCTCCGCTTTT | ASSTGNNNQAPL | TRBV13-3 | TRBJ1-5 |
| 153 | 0.655 | TGTGCTAGCAGTAGAGCGCAGAACTATGCTGAGCAGTTCTTC | ASSRAQNYAEQF | TRBV17 | TRBJ2-1 |
| 153 | 0.655 | TGTGCTAGCAGTAGAGGGGACAACATGCTGAGCAGTTCTTC | ASSRGN NYAEQF | TRBV17 | TRBJ2-1 |
| 146 | 0.625 | TGTGCCAGCAGCGGGGTTCTCTATAATTCCGCCCTCTACTTT | ASTGGSYSPLY | TRBV19 | TRBJ1-6 |
| 144 | 0.617 | TGTGGTGCTAGGGTTGACAACCTCTATGAACAGTACTTC | GARVDNSYEQY | TRBV20 | TRBJ2-7 |
| 136 | 0.582 | TGTGCCAGCAGCCTCAGGGGAGTCCGCACCCAGTACTTT | ASSLRVGTQY | TRBV14 | TRBJ2-5 |
| 133 | 0.570 | TGTGCAAGCTCCGGGACAGGGGCGAACTATGCTGAGCAGTTCTTC | ASSGTGANYAEQF | TRBV16 | TRBJ2-1 |
| 130 | 0.557 | TGTGCCAGCGGTGATCGGGCTGGGGTAGTGCAAAACGCTGTATTTT | ASGDRAGGSAETLY | TRBV13-2 | TRBJ2-3 |
| 130 | 0.557 | TGTGCCAGCAGCCGCTGGGACAGGGGACCACTGAAGCTTTCTTT | ASSRLGQTTEAF | TRBV4 | TRBJ1-1 |
| 128 | 0.548 | TGTGGTGCGAGGGCCCCACAGGGGAACACAGAAGTCTCTTT | GARPPQGNTEVF | TRBV20 | TRBJ1-1 |
| 127 | 0.544 | TGTGCCAGCAGTGATAGGGCAGGGTGGAAATTCGCCCTCTACTTT | ASSDRAGWNSPLY | TRBV13-3 | TRBJ1-6 |
| 124 | 0.531 | TGTGCTAGCAGTTTGGGGGGTTAGTGCAAAACGCTGTATTTT | ASSLGGFSAETLY | TRBV29 | TRBJ2-3 |
| 113 | 0.484 | TGTGCCAGCAAAATGGGGGGCAGTCAAAACACCTTGACTTT | ASKMGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 112 | 0.480 | TGTGCCAGCAGCCGTACGGACAGGAAACAAACCCGGGCGCTCTACTTT | ASSPYQETNTGQLY | TRBV3 | TRBJ2-2 |
| 111 | 0.475 | TGTGGTGCTAGGGATGGGGCGCTATAATTCCGCCCTCTACTTT | GARDGGAYNSPLY | TRBV20 | TRBJ1-6 |
| 109 | 0.467 | TGTGCTAGCAGTTACACAGTTTTAGTGCAAAACGCTGTATTTT | ASSYTGFSAETLY | TRBV29 | TRBJ2-3 |
| 107 | 0.458 | TGTGGTGCTCTCGACAGGGAAGGCTCAACAGAAAGATTATTTTC | GALDREGSNERLF | TRBV20 | TRBJ1-4 |
| 106 | 0.454 | TGTGCCAGCGGTGAGGGTTGGGGGGATCAGAAACGCTGTATTTT | ASGEGWGGSETLY | TRBV13-2 | TRBJ2-3 |
| 105 | 0.450 | TGTGCCAGCGGTGATCGGGGAGATTATAACTATGCTGAGCAGTTCTTC | ASGDRGDYNYAEQF | TRBV13-2 | TRBJ2-1 |
| 99 | 0.424 | TGTGCCAGCGGAGGGACACATGCAAACTCCGACTACACCTTC | ASSGTHANSDYT | TRBV13-2 | TRBJ1-2 |
| 93 | 0.398 | TGTGCCAGCAGTGACAGGGGGGGAACTCCGACTACACCTTC | ASSAGGGNSDYT | TRBV13-3 | TRBJ1-2 |
| 88 | 0.377 | TGTGCCAGCAGGTACAGGAACTCCGACTACACCTTC | ASRSGNSDYT | TRBV13-3 | TRBJ1-2 |
| 86 | 0.368 | TGTCCCGCAGGACAGGGCCCAACAGGCTCCGCTTTT | AARTGPNQAPL | TRBV13-3 | TRBJ1-5 |
| 85 | 0.364 | TGTGCCAGCAGCCCTGGGGGGGAAAGACACCCAGTACTTT | ASSPWGGKDTQY | TRBV5 | TRBJ2-5 |
| 80 | 0.343 | TGTGCAAGCAGCCGACAGGGGACAGGGTCCAACGAAAGATTATTTTC | ASSPTGQGSNERLF | TRBV16 | TRBJ1-4 |
| 74 | 0.317 | TGTGCTGGAGTCTAGAGGGACTGTCAAAACCGGGCAGCTCTACTTT | AWSLEGLSNTGQLY | TRBV31 | TRBJ2-2 |
| 74 | 0.317 | TGTGCTAGCACCCGGACTGGGGTAACACCGGGCAGCTCTGCTTT | ASTPDWGN TGQLC | TRBV29 | TRBJ2-2 |
| 74 | 0.317 | TGTGCCAGCAGTATATGGGGAACAGTGCAAAACGCTGTATTTT | ASSIWGTS AETLY | TRBV19 | TRBJ2-3 |
| 73 | 0.313 | TGTGCTAGCACCTGGGGGGAACTATGCTGAGCAGTTCTTC | ASTLGGNYAEQF | TRBV17 | TRBJ2-1 |
| 73 | 0.313 | TGTGCCAGCAGGATGGGAAATCTGGAATACGCTATTTT | ASRMGNSGNTLY | TRBV19 | TRBJ1-3 |
| 70 | 0.300 | TGTGCCAGCGGTGATCGACAGGGGGGAGTGCAAAACGCTGTATTTT | ASGDRQGGSAETLY | TRBV13-2 | TRBJ2-3 |
| 69 | 0.296 | TGTGCCAGCAGTACCGGACAAACAAACAGGCTCCGCTTTT | ASSTGQNNQAPL | TRBV13-3 | TRBJ1-5 |
| 69 | 0.296 | TGTGCCAGCAGTGAACACCGGGCAGCTCTACTTT | ASRWNTGQLY | TRBV13-3 | TRBJ2-2 |

Mouse 2 Immune Part II

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 68 | 0.291 | TGTGCCAGCAGTACTGGGGGGCGCACCAAGACACCCAGTACTTT | ASSTGGAHQDTQY | TRBV13-3 | TRBJ2-5 |
| 64 | 0.274 | TGTGCTAGCAGTACTCGGACTGGGGGCAACTATGCTGAGCAGTTCTTC | ASSTRTGGNYAEQF | TRBV29 | TRBJ2-1 |
| 64 | 0.274 | TGTGCCAGCAGCAAGATCTGGGGTTCTCTATGAACAGTACTTC | ASSQDLGFSYEYQ | TRBV5 | TRBJ2-7 |
| 64 | 0.274 | TGTGCCAGCAGTCTGGGGGGCGTCAAAACACCTTGACTTTT | ASSPGGRQNTLY | TRBV19 | TRBJ2-4 |
| 64 | 0.274 | TGTGCCAGCGGTGATCGGACTGGGGGAACTATGCTGAGCAGTTCTTC | ASGDRTGGNYAEQF | TRBV13-2 | TRBJ2-1 |
| 63 | 0.270 | TGTGCCAGCAGTATGGGTTCTATAATTCGCCCTCTACTTT | ASSMGSYNSPLY | TRBV19 | TRBJ1-6 |
| 62 | 0.266 | TGTGCTAGCAGTAGAGATGACGGATCGTCTGCTGAGCAGTTCTTC | ASSRDDGSSAEQF | TRBV17 | TRBJ2-1 |
| 61 | 0.261 | TGTGCCAGCAGCCCCGGGGGGTTCAAAACACCTTGACTTT | ASSPGGVQNTLY | TRBV19 | TRBJ2-4 |
| 58 | 0.248 | TGTGCTAGCAGTAGTCCAGGGTTAAACCAAGACACCCAGTACTTT | ASSSPGVNQDTQY | TRBV17 | TRBJ2-5 |
| 58 | 0.248 | TGTGCCAGCAGTACTGGGGGCTGCTGAGCAGTTCTTC | ASSYWGPAEQF | TRBV4 | TRBJ2-1 |
| 58 | 0.248 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 56 | 0.240 | TGTGCCAGCAGTCCGGGGTCTATAATTCGCCCTCTACTTT | ASSPGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 56 | 0.240 | TGTGCCAGCAGCCCCGGACCTAGTGACAGAAACGCTGTATTTT | ASSPGPSAETLY | TRBV13-3 | TRBJ2-3 |
| 54 | 0.231 | TGTGCCAGCAGTGACAGATTTAACTATGCTGAGCAGTTCTTC | ASSDRFNIAEQF | TRBV13-1 | TRBJ2-1 |
| 53 | 0.227 | TGTGCCAGCAGTGATTGGGGGAGTCAAAACACCTTGACTTT | ASSDWGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 52 | 0.223 | TGTGCCAGCGGGGACAGAATGCAAACCTCCGACTACACCTTC | ASGGQNANSYDT | TRBV13-2 | TRBJ1-2 |
| 51 | 0.218 | TGTGCCAGCAGTGACAGGAATGCAAACCTCCGACTACACCTTC | ASSDRNANSYDT | TRBV13-3 | TRBJ1-2 |
| 49 | 0.210 | TGTGCCAGCAGTCCGGGACAGGGGAACAGGCTCCGCTTTTT | ASSPGQGNQAPL | TRBV13-3 | TRBJ1-5 |
| 48 | 0.206 | TGTGCCAGCAGCCCCGACAGGGTCTTAATAACTATGCTGAGCAGTTCTTC | ASSPDRVLNNAEQF | TRBV3 | TRBJ2-1 |
| 48 | 0.206 | TGTGCCAGCAGTGATGGGACAGGGGCAAAACACAGAAGTCTTCTTT | ASSDGTGANTEVF | TRBV13-3 | TRBJ1-1 |
| 47 | 0.201 | TGTGCCAGCAGTGATGCAGACACCTTGACTTT | ASSDADTLY | TRBV13-3 | TRBJ2-4 |
| 46 | 0.197 | TGTGCCAGCGGTGAGGGGAATAGTCAAAACACCTTGACTTT | ASGEGNSQNTLY | TRBV13-2 | TRBJ2-4 |
| 45 | 0.193 | TGTGCTAGCAGTCCGACTGGGATTAACCAAGACACCCAGTACTTT | ASSRTGINQDTQY | TRBV17 | TRBJ2-5 |
| 45 | 0.193 | TGTGGTCTAGGGATCAGGACAATCCAACGAAAGATTATTTTT | GARDQDNSNERLF | TRBV20 | TRBJ1-4 |
| 45 | 0.193 | TGCCAGCAACCAAGAACAGGGATTAACTACCCCTCCACTTT | ASNQEQGFNSPLH | TRBV5 | TRBJ1-6 |
| 43 | 0.184 | TGTGCTAGCAGTAGTGGGGGACTGGAAATACGCTCTATTTT | ASSSGGTGNTLY | TRBV17 | TRBJ1-3 |
| 43 | 0.184 | TGTGCCAGCAGCTTACACAACTATGCTGAGCAGTTCTTC | ASSLHNYAEQF | TRBV3 | TRBJ2-1 |
| 42 | 0.180 | TGTGCCAGCGGGGACTGGGGGGCACTCTATGAACAGTACTTC | ASGGLGGHSYEYQ | TRBV13-2 | TRBJ2-7 |
| 42 | 0.180 | TGTGGTCTAGGGATCAGGACAGTCCAACGAAAGATTATTTTT | GARDQDSSNERLF | TRBV20 | TRBJ1-4 |
| 42 | 0.180 | TGTGGTCTAGGGATCAGGACAATGCAAACACAGAAGTCTTCTTT | GARDQDNANTEVF | TRBV20 | TRBJ1-1 |
| 42 | 0.180 | TGTGCTAGCAGTTGGGGGCAAACTCCGACTACACCTTC | ASSWGANSYDT | TRBV29 | TRBJ1-2 |
| 41 | 0.176 | TGTGCCAGCAGCGGGACTGGGGGTTCCAAGACACCCAGTACTTT | ASSGTGGFQDTQY | TRBV26 | TRBJ2-5 |
| 39 | 0.167 | TGTGCTAGCAGTAGACTCCCCGGGACTGGGGGCAAGACACCCAGTACTTT | ASSRPGTGGQDQY | TRBV17 | TRBJ2-5 |
| 39 | 0.167 | TGTGCTAGCAGTCTCAGGGAATTGACACAGAAGTCTTCTTT | ASSLQGDTEVF | TRBV17 | TRBJ1-1 |
| 39 | 0.167 | TGTGGTCTAGGGGCGACTATGCTGAGCAGTTCTTC | GARDGYAEQF | TRBV20 | TRBJ2-1 |
| 37 | 0.158 | TGTGCCAGCAGTATAGGACAGGGGTACACAGAAGTCTTCTTT | ASSIGQGYTEVF | TRBV19 | TRBJ1-1 |
| 37 | 0.158 | TGTGCCAGCAGCCAGGAGGGGGACAACAGGCTCCGCTTTTT | ASSQEGDNQAPL | TRBV13-1 | TRBJ1-5 |
| 36 | 0.154 | TGCAGTGCAGAAACAGGGACTCGGAGCTCTACGAGCAGTACTTC | SAETGTRSSYEYQ | TRBV30 | TRBJ2-7 |
| 36 | 0.154 | TGTGCCAGCAGCCCCGGGGGGGCAACAGGCTCCGCTTTTT | ASSPGGGNQAPL | TRBV13-3 | TRBJ1-5 |
| 34 | 0.146 | TGTGCCAGCAGTGGCCGGGACAGGGACAATGACAGAAACGCTGATTTT | ASSGRDRDNAETLY | TRBV13-3 | TRBJ2-3 |
| 34 | 0.146 | TGTGCCAGCAGTCTGGGGGGCGCATGCTGAGCAGTTCTTC | ASRSGGAHAEQF | TRBV13-3 | TRBJ2-1 |
| 33 | 0.141 | TGTGCCAGCGGTGATCGGGGGGGTCTAGTGCAGAAACGCTGATTTT | ASGDRGGSSAETLY | TRBV13-2 | TRBJ2-3 |
| 33 | 0.141 | TGTGGTCTAGGGATATGGACAATCCAACGAAAGATTATTTTT | GARDMDNSNERLF | TRBV20 | TRBJ1-4 |
| 33 | 0.141 | TGTGCCAGCAGCTCCACTGGGGTTGAACAGTACTTC | ASSSTGVEYQ | TRBV4 | TRBJ2-7 |
| 31 | 0.133 | TGTGCTAGCAGCGGGGACTGGGGGATTCAAAACACCTTGACTTT | ASSGDWGIQNTLY | TRBV17 | TRBJ2-4 |
| 31 | 0.133 | TGTGCCAGCAGTGTGGGACAGTCAAACCTCCGACTACACCTTC | ASSVGQSNSDYT | TRBV13-3 | TRBJ1-2 |
| 31 | 0.133 | TGTGCCAGCAGCTCCGGGAATAATTCGCCCTCTACTTT | ASSSGNYNSPLY | TRBV14 | TRBJ1-6 |
| 30 | 0.128 | TGTGCTAGCAGCTACAGGGTAACAACAGGCTCCGCTTTTT | ASSLQGNQAPL | TRBV17 | TRBJ1-5 |
| 29 | 0.124 | TGTGCCAGCAAGAAGACTGGGACAGGGCACCTACGAGCAGTACTTC | ASKELQGTYEQY | TRBV3 | TRBJ2-7 |
| 27 | 0.116 | TGTGCCAGCAGCTTATTACAGTCTCTCTATGAACAGTACTTC | ASSSYYSFSYEYQ | TRBV4 | TRBJ2-7 |
| 26 | 0.111 | TGTGGTCTAGGGACCGGACAATTCAAACCTCCGACTACACCTTC | GARDRDNSNSDYT | TRBV20 | TRBJ1-2 |
| 24 | 0.103 | TGTGCAAGCAGCTTAGATTGGACTGGGGGCAAAACACCTTGACTTT | ASSLDWTGGQNTLY | TRBV16 | TRBJ2-4 |
| 24 | 0.103 | TGTGCCAGCTCTCGAACAGGGGCGGTTATGAACAGTACTTC | ASSLEQGARYEQY | TRBV12-2 | TRBJ2-7 |
| 24 | 0.103 | TGTGCCAGCGGTGATGCTGGGGGGCCCATGCTGAGCAGTTCTTC | ASGDAGGAHAEQF | TRBV13-2 | TRBJ2-1 |
| 24 | 0.103 | TGTGGTCTGTAGACCGGGACACCGCAAACCTCCGACTACACCTTC | GAVDRDTANSYDT | TRBV20 | TRBJ1-2 |
| 24 | 0.103 | TGTGCCAGCAAGACAGGGGCTTCCAAGACACCCAGTACTTT | ASKTGGFQDTQY | TRBV19 | TRBJ2-5 |
| 23 | 0.099 | TGTGCTAGCAGTAGGGGACAATTTCTGGAATACGCTCTATTTT | ASSRQYSGNTLY | TRBV17 | TRBJ1-3 |
| 23 | 0.099 | TGTGCCAGCCGGGACAGGCATTCTGGAATACGCTCTATTTT | ASRRDRHSNTLY | TRBV13-3 | TRBJ1-3 |
| 23 | 0.099 | TGTAGTTCTAGCGACGGGACTGGGTATGAACAGTACTTC | SSSDGTGYEQY | TRBV30 | TRBJ2-7 |
| 22 | 0.094 | TGTGCCAGCGGTGATAGAGGACAATCTAGTGCAGAAACGCTGATTTT | ASGDRGQSSAETLY | TRBV13-2 | TRBJ2-3 |
| 22 | 0.094 | TGTGGTCTAGGGATCGATACAGGGAATCTGGAATACGCTCTATTTT | GARDRYRESGNTLY | TRBV20 | TRBJ1-3 |
| 22 | 0.094 | TGTGCCAGCAGTCCAGGGAACAACAGGCTCCGCTTTTT | ASSPGNNQAPL | TRBV13-3 | TRBJ1-5 |
| 21 | 0.090 | TGTGCTAGCAGTATCGGGGGCGACCAAGACACCCAGTACTTT | ASSIGGDQDTQY | TRBV17 | TRBJ2-5 |

Mouse 3 Immune Part I

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 2489 | 11.094 | TGTGCTAGCAGTATACAGGGGAACATGCTGAGCAGTTCTTC | ASSIQGNVYAEQF | TRBV17 | TRBJ2-1 |
| 1733 | 7.725 | TGTGCTAGCAAGACAGGGGGGACCAAGACCCAGTACTTT | ASKTGGDQDTQY | TRBV17 | TRBJ2-5 |
| 968 | 4.315 | TGTGCCAGCGGTGATAGGGGGCCTCTAGTGCAGAAACGCTGTATTTT | ASGDRGASSAETLY | TRBV13-2 | TRBJ2-3 |
| 893 | 3.980 | TGCACCTGCAGTGCAGGGATTACAGAAAGTCTTCTT | TCSAGFEVVF | TRBV1 | TRBJ1-1 |
| 829 | 3.695 | TGTGGTGTAGGGACTGGGGGATGCTGAGCAGTTCTTC | GARDWGDVYAEQF | TRBV20 | TRBJ2-1 |
| 717 | 3.196 | TGTGCTAGCAGTTATGGGGTTTTAGTGCAGAAACGCTGTATTTT | ASSYGGFSAETLY | TRBV29 | TRBJ2-3 |
| 699 | 3.116 | TGTGCCAGCAGCGGAGGGAATTTTGAAATACGCTCTATTTT | ASTAGNFGNTLY | TRBV13-3 | TRBJ1-3 |
| 615 | 2.741 | TGTGCCAGCAGCGGAGGGAATTTGAAATACGCTCTATTTT | ASSAGNSGNTLY | TRBV13-3 | TRBJ1-3 |
| 602 | 2.683 | TGTGCCAGCGGTGATCGGGCTGGGAGTAGTGCAGAAACGCTGTATTTT | ASGDRAGSSAETLY | TRBV13-2 | TRBJ2-3 |
| 567 | 2.527 | TGTGCCAGCGGTGACCGGGACTTTTCTAGTGCAGAAACGCTGTATTTT | ASGDRDFSSAETLY | TRBV13-2 | TRBJ2-3 |
| 535 | 2.385 | TGTGCCAGCAGTTCTGGAAATCCAAACGAAAGATTATTTTTC | ASSSGNSNERLF | TRBV13-3 | TRBJ1-4 |
| 508 | 2.264 | TGTGCCAGCAGCGCGGGAACTATAATTCGCCCTCTACTTT | ASSAGNYSPLY | TRBV14 | TRBJ1-6 |
| 503 | 2.242 | TGTGCCAGCGGTGACCGGGACAGGGGGAGTCAAAACACCTTGACTTT | ASGDRDRGSQNTLY | TRBV13-2 | TRBJ2-4 |
| 473 | 2.108 | TGTGCCAGCAGTCCAGGGGGAGCCCAAGACACCCAGTACTTT | ASSPGGAQDTQY | TRBV19 | TRBJ2-5 |
| 408 | 1.819 | TGTGCTAGCAGCAGAGGGGGGACTATGCTGAGCAGTTCTTC | ASTRGGDYAEQF | TRBV17 | TRBJ2-1 |
| 390 | 1.738 | TGTGCCAGCGGGACAATTTCTATAATTCGCCCTCTACTTT | ASGTNSYNSPLY | TRBV19 | TRBJ1-6 |
| 383 | 1.707 | TGTGCTAGCAGTAGAGGAGACAACTATGCTGAGCAGTTCTTC | ASSRGNVYAEQF | TRBV17 | TRBJ2-1 |
| 374 | 1.667 | TGTGCCAGCGGTGACCGGGACAGGGGAGTGCAGAAACGCTGTATTTT | ASGDRTEGSAETLY | TRBV13-2 | TRBJ2-3 |
| 356 | 1.587 | TGCACCTGCACCGACAACATGAACAGTACTTC | TCTDNYEQY | TRBV1 | TRBJ2-7 |
| 352 | 1.569 | TGTGCCAGCAGTTAGAGGGGAGGACTAGTCAAAACACCTTGACTTT | ASSLEGGTSQNTLY | TRBV3 | TRBJ2-4 |
| 323 | 1.440 | TGTGCCAGCAGTATTGGGGGGGGCGGTGCAGAAACGCTGTATTTT | ASSIGGGGAEPLY | TRBV19 | TRBJ2-3 |
| 304 | 1.355 | TGTGGTGTAGGGATCGGACAGGGGCAAACTCCGACTACACCTTC | GARDRTGANSQNTLY | TRBV20 | TRBJ1-2 |
| 274 | 1.221 | TGTGCCAGCAGGAAACGGGAATAACAACCCAGCTCCGCTTTT | ASRNGNNQAPL | TRBV13-3 | TRBJ1-5 |
| 244 | 1.088 | TGTGCCAGCAGTGAAGGCAACTATAATTCGCCCTCTACTTT | ASSEGNYSPLY | TRBV13-3 | TRBJ1-6 |
| 240 | 1.070 | TGTGCCAGCGGTGACCGGGACAGGGGAACTATGCTGAGCAGTTCTTC | ASGDRDRGNVYAEQF | TRBV13-2 | TRBJ2-1 |
| 227 | 1.012 | TGTGCTAGCAGTTCCCGGGACTGGGATAACAAGACACCCAGTACTTT | ASSSRDWDNQDTQY | TRBV29 | TRBJ2-5 |
| 214 | 0.954 | TGTGCCAGCACAACAGGGAATAATTCGCCCTCTACTTT | ASTTGNYSPLY | TRBV19 | TRBJ1-6 |
| 195 | 0.869 | TGTGCCAGCAGTATAAAACAGAAACCAACCGCTCCGCTTTT | ASSIKQNNQAPL | TRBV19 | TRBJ1-5 |
| 195 | 0.869 | TGTGCCAGCAGACAGGGGAATAACAAGACACCCAGTACTTT | ASRQGNNDQDTQY | TRBV13-3 | TRBJ2-5 |
| 184 | 0.820 | TGTGCCAGCAGTCCAGGGGGGGTAATTCGCCCTCTACTTT | ASSPGGGNSPLY | TRBV13-3 | TRBJ1-6 |
| 179 | 0.798 | TGTGCCAGCAGTGTGACGGGGGACATCTATGCTGAGCAGTTCTTC | ASSDAGRDIYAEQF | TRBV13-3 | TRBJ2-1 |
| 177 | 0.789 | TGTGCCAGCAGTATGGGACAGAGGTAGAAGTCTTCTTT | ASSYGTVEVVF | TRBV4 | TRBJ1-1 |
| 170 | 0.758 | TGTGCCAGCAGTTTTGGACAGGGGAGGGCACCGGGCAGCTCTACTTT | ASSFWTGRGTGQLY | TRBV14 | TRBJ2-2 |
| 169 | 0.753 | TGTGCCAGCGGTGACGGCAATTCACGAAAGATTATTTTTC | ASGDGNSNERLF | TRBV13-2 | TRBJ1-4 |
| 165 | 0.735 | TGTGCTAGCAGTTTTGAGGGTATAGTGCAGAAACGCTGTATTTT | ASSFEGYSAETLY | TRBV29 | TRBJ2-3 |
| 159 | 0.709 | TGTGCCAGCAGCGGGACAATAATGCTGAGCAGTTCTTC | ASSRDNYAEQF | TRBV13-3 | TRBJ2-1 |
| 156 | 0.695 | TGTGCCAGCAGTCTGGGGTAACTATGCTGAGCAGTTCTTC | ASSPGGNVYAEQF | TRBV14 | TRBJ2-1 |
| 143 | 0.637 | TGTGCTAGCAAGAGATCTGGGGACCAAGACACCCAGTACTTT | ASKRSGDQDTQY | TRBV17 | TRBJ2-5 |
| 138 | 0.615 | TGTGCTAGCAGTAGACTGGGCGTCAAGACACCCAGTACTTT | ASSRPRQDTQY | TRBV17 | TRBJ2-5 |
| 133 | 0.593 | TGTGCCAGTCCGACAGGGGGGCAAAACAGAAAGTCTTCTTT | ASRTGGANTEVVF | TRBV13-1 | TRBJ1-1 |
| 129 | 0.575 | TGTGCCAGCAGCAAGCCTGGGGGTTAAACAAGACACCCAGTACTTT | ASSQAWGVNQDTQY | TRBV5 | TRBJ2-5 |
| 119 | 0.530 | TGTGCCAGCAGTGAACGGGACAGGGGGCTCCGACTACACCTTC | ASSDWTGGSDYT | TRBV13-3 | TRBJ1-2 |
| 104 | 0.464 | TGTGCCAGCGGTGAGATCAGGGGGAGGAATTCGCCCTCTACTTT | ASGEIRGRNSPLY | TRBV13-2 | TRBJ1-6 |
| 101 | 0.450 | TGTGCTGGAGGGACAGGGGATATAATTCGCCCTCTACTTT | AWRDRGYSPLY | TRBV31 | TRBJ1-6 |
| 99 | 0.441 | TGTGCCAGCAGTACGGCAACTATAATTCGCCCTCTACTTT | ASSDGNYSPLY | TRBV13-3 | TRBJ1-6 |
| 98 | 0.437 | TGTGCCAGCGGTGACCGGGGGGGCGCTAGTGCAGAAACGCTGTATTTT | ASGDRGGASAETLY | TRBV13-2 | TRBJ2-3 |
| 98 | 0.437 | TGTGCCACCGCCACAGGGGGGCGGAATTCGCCCTCTACTTT | ATATGGRNSPLY | TRBV13-3 | TRBJ1-6 |
| 95 | 0.423 | TGTGCTAGCAGTAGAGACAAAATGCTGAGCAGTTCTTC | ASSRAQNYAEQF | TRBV17 | TRBJ2-1 |
| 94 | 0.419 | TGTGCCAGCAGCAGGGGAATAACTATGCTGAGCAGTTCTTC | ASTTGNVYAEQF | TRBV13-3 | TRBJ2-1 |
| 94 | 0.419 | TGTGCCAGCAGTCCCGGGAATGCAAACTCCGACTACACCTTC | ASSPGNANSQNTLY | TRBV13-1 | TRBJ1-2 |
| 93 | 0.415 | TGTGCCAGCAGTGGGGGGAGTCAAAACACCTTGACTTTT | ASSEGGSQNTLY | TRBV13-3 | TRBJ2-4 |
| 82 | 0.366 | TGTGCTAGCAGCTTGGATCTATAATTCGCCCTCTACTTT | ASSLGSYSPLY | TRBV29 | TRBJ1-6 |
| 79 | 0.352 | TGTGCCAGCTCTCTGAGGGACTGGGGAATGCTGAGCAGTTCTTC | ASSLEGLGNAEQF | TRBV12-1 | TRBJ2-1 |
| 77 | 0.343 | TGTGCCAGCGGTGATGCACTGGGGGGACTAGTGCAGAAACGCTGTATTTT | ASGDALGGTSAETLY | TRBV13-2 | TRBJ2-3 |
| 77 | 0.343 | TGTGCTAGCAGTACGGGAAACACCGGGCAGCTCTACTTT | ASSTGNTGQLY | TRBV17 | TRBJ2-2 |
| 75 | 0.334 | TGTGCTAGCAGTCTACAGGGAGGGAACCAAGACACCCAGTACTTT | ASSLQGGNQDTQY | TRBV17 | TRBJ2-5 |
| 74 | 0.330 | TGTGCCACCGGGACAGGGAATAATTCGCCCTCTACTTT | ATGTGNNSPLY | TRBV13-3 | TRBJ1-6 |
| 73 | 0.325 | TGTGCCAGCAGCAAGTCTGGGGGGCAAAAGTCAAAACACCTTGACTTT | ASSQVLGGQSQNTLY | TRBV5 | TRBJ2-4 |
| 71 | 0.316 | TGTGCCAGCGGTGATGCTGGGGTAAACAAGACACCCAGTACTTT | ASGDAGGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 68 | 0.303 | TATGCTGAGCAGTTCTTC | AEQF | TRBV21 | TRBJ2-1 |
| 67 | 0.299 | TGTGCCAGCAGAGAGGGTTCTATAATTCGCCCTCTACTTT | ASREGYSNSPLY | TRBV13-3 | TRBJ1-6 |
| 66 | 0.294 | TGTGCCAGCTCTCTGCTGGGGGGCGCGGAAACACCCAGTACTTT | ASSLAGGARNTQY | TRBV12-1 | TRBJ2-5 |
| 66 | 0.294 | TGTGCCAGCAGTGTGGGAATAACAACAGGCTCCGCTTTT | ASSDGNNNQAPL | TRBV13-3 | TRBJ1-5 |
| 66 | 0.294 | TGTGCCAGCAGACAGGGGACTATAATTCGCCCTCTACTTT | ASRQGTYSNSPLY | TRBV13-3 | TRBJ1-6 |
| 64 | 0.285 | TGTGCCAGCAGTCCAGGTAATTCGAAATACGCTCTATTTT | ASDPGNSGNTLY | TRBV13-3 | TRBJ1-3 |
| 63 | 0.281 | TGTGCCAGCAGTATGCGCCAGCGTCAAGTCTTGGCAGTTTTC | ASSLAPASGLEQF | TRBV15 | TRBJ2-1 |
| 63 | 0.281 | TGTGCCAGCAGTGATGGGGGGCGATGCTGAGCAGTTCTTC | ASSDWGGDAEQF | TRBV13-3 | TRBJ2-1 |
| 63 | 0.281 | TGTGCCAGCAGTACTGGGGGCAAAACACCTTGACTTT | ASSDWGQNTLY | TRBV13-3 | TRBJ2-4 |
| 62 | 0.276 | TGTGGTGTAGGGATCTAGACAGGGGAACTCCGACTACACCTTC | GARDLDRGNSQNTLY | TRBV20 | TRBJ1-2 |
| 58 | 0.259 | TGTGCCAGCAGCCCGCGGGCGCAGCTCTGGAACACCATATATTTT | ASSPRGASSGNTLY | TRBV8 | TRBJ1-3 |
| 57 | 0.254 | TGCACCTGCAGTCCGACAGGGGACTGGGTAATGCTGAGCAGTTCTTC | TCSADRGLGNVYAEQF | TRBV1 | TRBJ2-1 |
| 54 | 0.241 | TGTGCCAGCAGTGTGGGGGGGGAGTGCAGAAACGCTGTATTTT | ASSAGGSSAETLY | TRBV19 | TRBJ2-3 |

Mouse 3 Immune Part II

| Reads | Frequency | CDR3 Nucleotide sequence | CDR3 AA sequence | V segments | J segments |
|-------|-----------|--|------------------|------------|------------|
| 52 | 0.232 | TGTGCCAGCAGTATAGAACGGAAATGCAAACACAGAAGTCTTCTTT | ASSIERNANTEVF | TRBV19 | TRBJ1-1 |
| 52 | 0.232 | TGTGCCAGCAGCTTAGACCGGGTTCCTACAATGAGCAGTTCTTC | ASSLDGGSYNEQF | TRBV16 | TRBJ2-1 |
| 51 | 0.227 | TGTGCCTGGAGAGACTGGGGAGAAGACACCCAGTACTTT | AWRDWGEDTQY | TRBV31 | TRBJ2-5 |
| 49 | 0.218 | TGTGCAAGCAGCCCCGCGGGGGGACCAAGACACCCAGTACTTT | ASSPRGGDQDTQY | TRBV16 | TRBJ2-5 |
| 47 | 0.209 | TGTGCCAGCACGGCAGGGAATTTTGGAAATGCGCTCTATTTT | ASTAGNFGNALY | TRBV13-3 | TRBJ1-3 |
| 47 | 0.209 | TGTGGTGTAGCCTGGGACAGGCAAACACAGAAGTCTTCTTT | GASLGQANTEVF | TRBV20 | TRBJ1-1 |
| 44 | 0.196 | TGTGCCAGCGGTGGGACAGAACTCCGACTACACCTTC | ASGGQNANSDYT | TRBV13-2 | TRBJ1-2 |
| 44 | 0.196 | TGTGCCAGCAGCCGGACTGGGGGGACTATGAACAGTACTTC | ASSRDWGDYEQY | TRBV4 | TRBJ2-7 |
| 43 | 0.192 | TGTGCCAGCGGTGATAGGACTGGGGGAACTATGCTGAGCAGTTCTTC | ASGDRTGGNIAEQF | TRBV13-2 | TRBJ2-1 |
| 42 | 0.187 | TGTGCCAGCGGTGACCGGGACAGAGCAAACACAGAAGTCTTCTTT | ASGDRDRANTEVF | TRBV13-2 | TRBJ1-1 |
| 41 | 0.183 | TGTGCTAGCAGTTCGGGACAAAAGTGTGAGAAACGCTGTATTTT | ASSSRDKTSAETLY | TRBV29 | TRBJ2-3 |
| 39 | 0.174 | TGCAGTGTAGATAGGACTAGCGGGAGCTATGAGCAGTCTTTC | SARDRTSGSYEQF | TRBV30 | TRBJ2-1 |
| 39 | 0.174 | TGTGCCAGCAGTCCGGGACAGAAATGAACAGTACTTC | ASSPGQNEQY | TRBV19 | TRBJ2-7 |
| 36 | 0.160 | TGTGCTAGCAAAGTGGGGGAGACCAAGACACCCAGTACTTT | ASKLGGDQDTQY | TRBV17 | TRBJ2-5 |
| 34 | 0.152 | TGTGCCAGCAGCAAGACGAGGGACACGCAAAGTCCGACTACACCTTC | ASSQDEGHANSDYT | TRBV2 | TRBJ1-2 |
| 34 | 0.152 | TGTGGTGTACTAAACCGGGACAATCCAACGAAAGATTATTTTTC | GVLNDRDNSNERLF | TRBV20 | TRBJ1-4 |
| 34 | 0.152 | TGTGCCAGCAGTGCAGGGGCGCACTGAAGCTTCTTT | ASSARGGTEAF | TRBV13-1 | TRBJ1-1 |
| 33 | 0.147 | TGTGCTAGCAGTTCGCGGGACAATAACCAAGACACCCAGTACTTT | ASSSRGTTNQDTQY | TRBV29 | TRBJ2-5 |
| 33 | 0.147 | TGTGCCAGCAGTCTGGGGGGGCTATGCTGAGCAGTTCTTC | ASSPGGGYAEQF | TRBV13-3 | TRBJ2-1 |
| 33 | 0.147 | TGTGCCAGCGGTGATGGGGGGTCCCAAGAAGTCTTCTTT | ASGDGGSPEVF | TRBV13-2 | TRBJ1-1 |
| 32 | 0.143 | TGTGCCAGCAGTTTTAACTCGGGCTACAATGAGCAGTCTTTC | ASSFNISGYNEQF | TRBV15 | TRBJ2-1 |
| 31 | 0.138 | TGTGCCAGCAGCCCCGACTGGGGGGTCAAGACACCCAGTACTTT | ASSPDWGGQDTQY | TRBV3 | TRBJ2-5 |
| 31 | 0.138 | TGTGCCAGCACGGCAGGGAATTTTGGAAATGAGTCTATTTT | ASTAGNFGSTLY | TRBV13-3 | TRBJ1-3 |
| 30 | 0.134 | TGTGCCAGCGGTAACGGAGGAGTAGCGGGATTCCTGCAATGAGCAGTTCTTC | ASNGGGASGISCNEQF | TRBV13-2 | TRBJ2-1 |
| 29 | 0.129 | TGTGCCAGCGGTGACCGGGACAGGGGTAACCAAGACACCCAGTACTTT | ASGDRDRGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 28 | 0.125 | TGTGCCAGCGGAACAGGGGGCTATAATTCGCCCTCTACTTT | ASGTGGYNSPLY | TRBV19 | TRBJ1-6 |
| 27 | 0.120 | TGTGCCAGCGGACAGGGTCTATAATTCGCCCTCTACTTT | ASGTGSYNSPLY | TRBV13-3 | TRBJ1-6 |
| 27 | 0.120 | TGTGCCAGCAGTCCGGGACATGCAAACACAGAAGTCTTCTTT | ASSPGHANTEVF | TRBV13-3 | TRBJ1-1 |
| 27 | 0.120 | TGTGCCAGCAGGACCGGGACACCAACAGGCTCCGCTTTT | ASRTGTPNQAPL | TRBV13-3 | TRBJ1-5 |
| 27 | 0.120 | TGTGCTAGCAGTGTGGGACAGTATGAACAGTACTTC | ASSVQYEQY | TRBV17 | TRBJ2-7 |
| 26 | 0.116 | TGTGCCAGCGGTGATGACAGTGGGGGACCTCAAACACCTTGTACTTT | ASGDAVGGPQNTLY | TRBV13-2 | TRBJ2-4 |
| 25 | 0.111 | TGTGCCAGCGGTGATGCCGGACAGGGGATTCTGAAATACGCTCTATTTT | ASGDAGQGDSGNTLY | TRBV13-2 | TRBJ1-3 |
| 25 | 0.111 | TGTGCCAGCGGTGATCGTGGGGAGGAAACCAAGACACCCAGTACTTT | ASGDRGEGNQDTQY | TRBV13-2 | TRBJ2-5 |
| 25 | 0.111 | TGTGCCAGCGGTGAAGGGACTGACTCCTATGAACAGTACTTC | ASGEGTDSYEQY | TRBV13-2 | TRBJ2-7 |
| 25 | 0.111 | TGTGCCAGCAGTGTGGGGTTCCAACGAAAGATTATTTTTC | ASSDGGSNERLF | TRBV13-1 | TRBJ1-4 |
| 24 | 0.107 | TGTGCCAGCAGTCTCGGAGGGTCCAACACTGAAGCTTCTTT | ASSLGGSNTEAF | TRBV16 | TRBJ1-1 |
| 24 | 0.107 | TGTGCCAGCAGTACCGGGACAGGGGGCATAGCTTCTTT | ASSTGTGGIAF | TRBV16 | TRBJ1-1 |
| 23 | 0.103 | TGTGCAAGCAGCTTAGCTGGGGGGAAACACCGGGCAGCTCTACTTT | ASSLGGWGGNTGQLY | TRBV16 | TRBJ2-2 |
| 22 | 0.098 | TGTGCCAGCAGTCCGGGGGGCTTTCAAACACCTTGTACTTT | ASSPGGFQNTLY | TRBV19 | TRBJ2-4 |
| 22 | 0.098 | TGCACCTGACAGTGTGGTGTAGTCAAACACCTTGTACTTT | TCSAGSQNTLY | TRBV1 | TRBJ2-4 |
| 22 | 0.098 | TGTGCCAGCAGCGGGACCGCCTTGGCTACACCTTC | ASSGDRLGYT | TRBV12-1 | TRBJ1-2 |
| 21 | 0.094 | TGTGCCAGCGGAACTGGGGGATAACTATGCTGAGCAGTCTTTC | ASGNWGDNYAEQF | TRBV13-2 | TRBJ2-1 |
| 21 | 0.094 | TGTGGTGTAGGGACTGGGAGAGCTCCTATGAACAGTACTTC | GARDWESSYEQY | TRBV20 | TRBJ2-7 |
| 21 | 0.094 | TGTGCCAGCAGCTTAGCGGGAGTAGAGACCCAGTACTTC | ATALAGVETQY | TRBV13-2 | TRBJ2-5 |
| 21 | 0.094 | TGTGGTGTCCAGACAGCCGAAACACAGAAGTCTTCTTT | GVPDSRNEVF | TRBV20 | TRBJ1-1 |
| 20 | 0.089 | TGTGCCAGCGGGATAGGGACAGGGCTAGTGCAGAAACGCTGTATTTT | ASGDRDRASAEPLY | TRBV13-2 | TRBJ2-3 |
| 20 | 0.089 | TGTGCCAGCAGTCTGACATTTAAACCAAGACACCCAGTACTTT | ASSLTFNQDTQY | TRBV13-3 | TRBJ2-5 |