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| **Table S1. Primers** |
| **Primer Name**  | **Primer Sequence 5’ to 3’ and References**  |
| **Error-prone PCR** |
| ESARF-JK | CCG**GAATTC**ACCATGTTTTCTTTTTTCC |
| ESARR-JK | GC**TCTAGA**TCACTACCTGGC |
| **Site-directed mutagenesis**  |   |
| BADVF | TAACCTTTCATTCCCAGCGGTCG |
| BADRa | CTTCTCTCATCCGCCAAAAC |
| BADR500b | CCCGGCGGATTTGTCCTACTC |
| EsaA27TR | CCTTGAAAATCATACAATAACGGATACGCTTC |
| EsaA27TF | GAAGCGTATCCGTTATTGTATGATTTTCAAGG |
| EsaC76AR | GAAAGTTATCTCCGATGGGTAGTCCGG |
| EsaC76AF | CCGGACTACCCATCGGAGATAACTTTC |
| EsaG94AR | GGGTAGTCCGGATTACACTTACACTGTTG |
| EsaG94AF | CAACAGTGTAAGTGTAATCCGGACTACCC |
| EsaT220CR | CTCACGGCCCTTAAACGCACC |
| EsaT220CF | GGTGCGTTTAAGGGCCGTGAG |
| EsaT222GR | CACGGCCTTGAAACGCACCTC |
| EsaT222GF | GAGGTGCGTTTCAAGGCCGTG |
| EsaG241AR | CTTCGCCGTTTACCTGGGATG |
| EsaG241AF | CATCCCAGGTAAACGGCGAGG |
| EsaT249GR | CGTTTGCCTGGGAGGAGAATATTACGC |
| EsaT249GF | GCGTAATATTCTCCTCCCAGGCAAACG |
| EsaT281AR | GACCTGCGGTACACCAAAATTTTCTC |
| EsaT281AF | GAGAAAATTTTGGTGTACCGCAGGTC |
| EsaC302AR | CACAAAATTTTCTCTTTATACAAGCAATACAACATCG |
| EsaC302AF | CGATGTTGTATTGCTTGTATAAAGAGAAAATTTTGTG |
| EsaT310GR | CTTTATCCAAGCAAGACAACATCGTTAACGGC |
| EsaT310GF | GCCGTTACCGATGTTGTCTTGCTTGGATAAAG |
| EsaA311CR | CCAAGCAATCCAACATCGTTAACGGC |
| EsaA311CF | GCCGTTAACGATGTTGGATTGCTTGG |
| EsaA316TR | CCAAGCAATACAACTTCGTTAACGGCTTTACC |
| EsaA316TF | GGTAAAGCCGTTAACGAAGTTGTATTGCTTGG |
| EsaA398TR | GGCAACGATCTGACTGCGCTGG |
| EsaA398TF | CCAGCGCAGTCAGATCGTTGCC |
| New444R | GGGCACGATGCATATGCTGCTGATTG |
| New444F | CAATCAGCAGCATATGCATCGTGCCC |
| EsaA531CR | CAGAGCGCGGACCAAACG |
| EsaA531CF | CGTTTGGTCCGCGCTCTG |
| EsaG607AR | CCTATGCTGAGATTGCCACTATTACGGG |
| EsaG607AF | CCCGTAATAGTGGCAATCTCAGCATAGG |
| NEW613R | GCTATTGCGGGCATTTCTGTGAGTAC |
| NEW613F | GTACTCACAGAAATGCCCGCAATAGC |
| EsaG706AR | CAGGCTATCAGACTGGGTATAGAACTGGATC |
| EsaG706AF | GATCCAGTTCTATACCCAGTCTGATAGCCTG |
| EsaG728AR | GATCTTATCAGACAGGCAGCGTCAGA |
| EsaG728AF | GCTGACGCTGCCTGTCTGATAAGATC |
| EsaC728TR | CTTATCAGACTGGCAGCGTCAGCG |
| EsaC728TF | CGCTGACGCTGCCAGTCTGATAAG |
| EsaC734TR | CAGACCGGCAGTGTCAGCG |
| EsaC734TF | CGCTGACACTGCCGGTCTG |
| **HMGE variant cloning** |   |
| TEVESAR2 | GAGAACCTGTACTTCCAGGGTGGTGGTGGTGGTATGTTTTCTTTTTTCCTTGAAAATC [17] |
| ATTBR | GGGGACAACTTTGTACAAGAAAGTTGCATTACTACCTGGCCGCTGACGCTC [17] |
| ATTBTEV | GGGGACAACTTTGTACAAAAAAGTTGTGGAGAACCTGTACTTCCAG [17] |
| **Fluorescence Anisotropy**  |   |
| PesaR28 TAMRA | TAMRA-TCTTGCCTGTACTATAGTGCAGGTTAAG |
| PesaR28R | CTTAACCTGCACTATAGTACAGGCAAGA [30] |
| PesaR28 | TCTTGCCTGTACTATAGTGCAGGTTAAG [30] |
| a reverse primer for 27, 76, 94, 220, 222, 241, 249, 302, 310, 316, 398, 531 and 607 |
| b reverse primer for 311, 444, 613, 706, 728 and 734 |

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