SUPPLEMENTARY DATA FOR

DNA motifs determining the accuracy of repeat duplication during CRISPR adaptation in *Haloarcula hispanica*

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SUPPLEMENTARY FIGURES

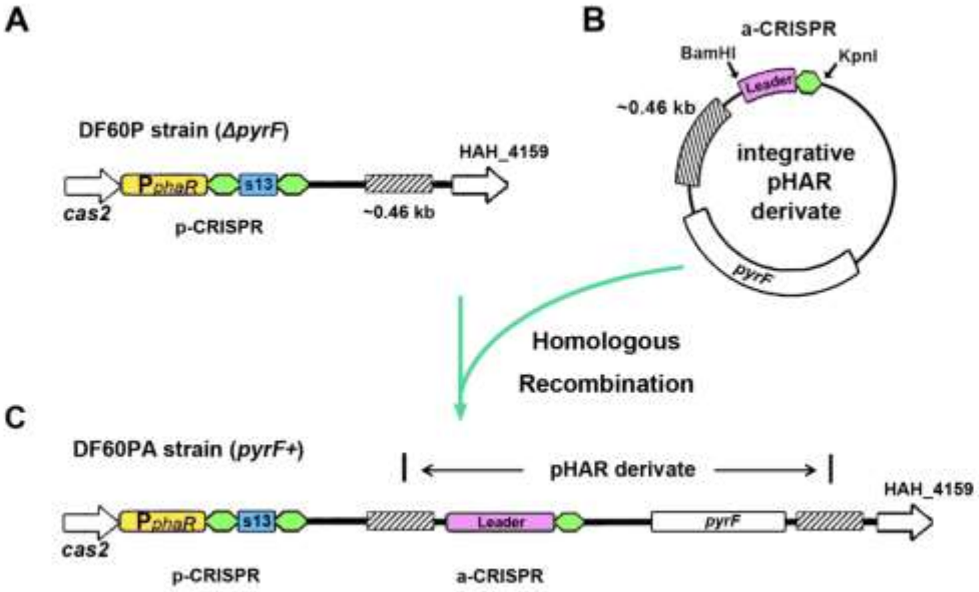

Figure S1. A diagram showing the construction of the DF60PA strain. (A) The wild-type CRISPR of the *H. hispanica* auxotrophic strain DF60 (Δ*pyrF*) was substituted by the priming-CRISPR (p-CRISPR), generating the DF60P strain. **(B)** The adaptation-CRISPR (a-CRISPR) construct (the leader and one repeat) was cloned into the pHAR-derived integrative vector, which carries a selection marker (*pyrF*) and a ~460-bp chromosomal sequence (shadowed) for homologous recombination. **(C)** Transformed into the DF60P strain and cultured under selective pressure (in AS168 medium devoid of yeast extract), the modified pHAR derivate integrates into the chromosome, resulting in the linear coexistence of p-CRISPR and a-CRISPR in DF60PA cells.

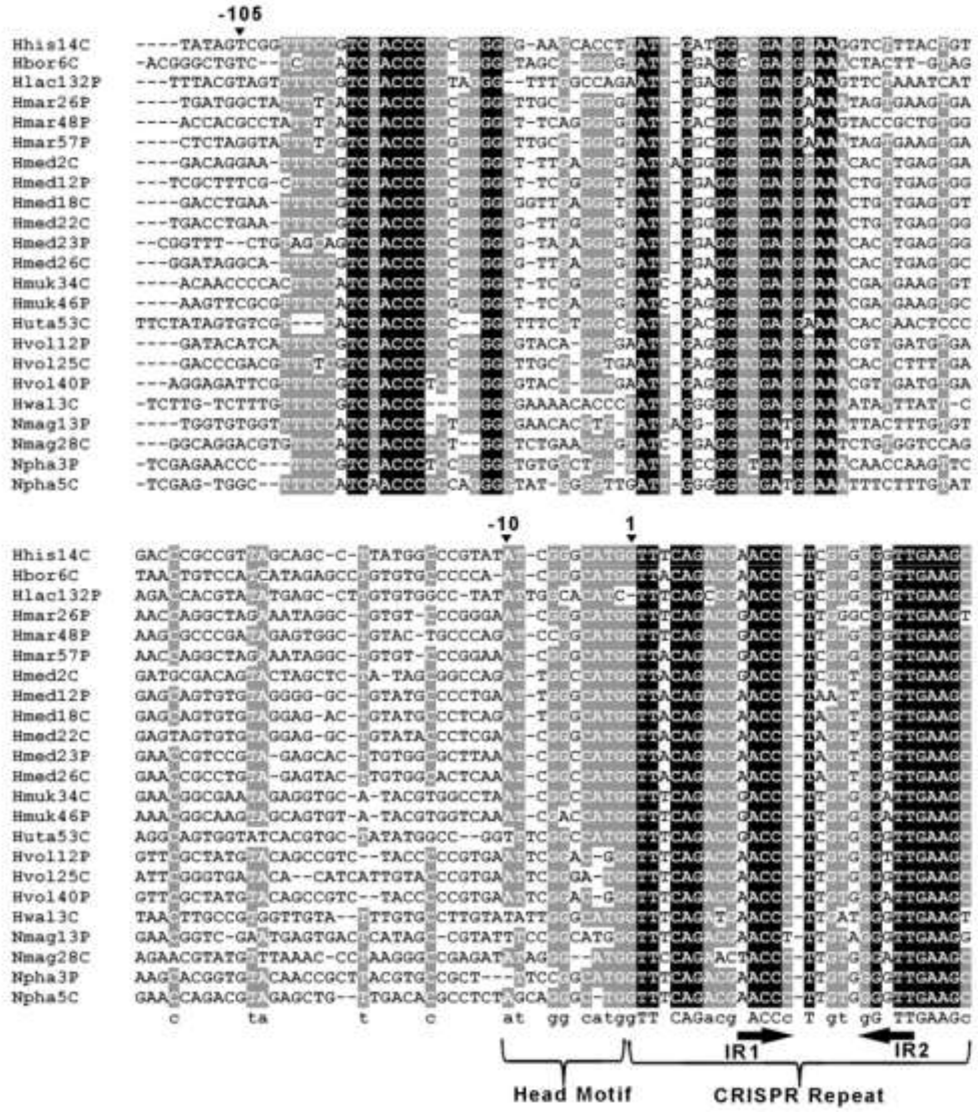

Figure S2. Multi-alignment of the leader and repeat sequences of haloarchaeal CRISPRs that share similar repeats. For each CRISPR, the first repeat and its upstream ~110-bp sequence (which contains the leader) were retrieved and aligned together. The first repeat-nucleotide is labeled by the number ‘1’, and the relative positions of some leader-nucleotides are also labeled. Nucleotides with high or medium conservation are shown in white against black or grey. The CRISPR repeat carries a pair of inverted repeats (designated IR1 and IR2). Each CRISPR is designated with four letters (which represent organisms), the repeat number, and a “C” or “P” letter to indicate its location (on the chromosome or a plasmid). The analyzed CRISPRs are from: *Halogeometricum borinquense* (Hbor) DSM 11551, *Haloarcula hispanica* (Hhis) ATCC 33960, *Halorubrum lacusprofundi* (Hlac) ATCC 49239, *Haloarcula marismortui* (Hmar) ATCC 43049, *Haloferax mediterranei* (Hmed) ATCC 33500, *Halomicrobium mukohataei* (Hmuk) DSM 12286, *Halorhabdus utahensis* (Huta) DSM 12940, *Haloferax volcanii* (Hvol) DS2, *Haloquadratum walsbyi* (Hwal) DSM 16790, *Natrialba magadii* (Nmag) ATCC 43099 and *Natronomonas pharaonis* (Npha) DSM 2160. ***Note that*** the repeat length is conservatively 30 bp, with the exception of the 31-bp repeat from Hlac132P.

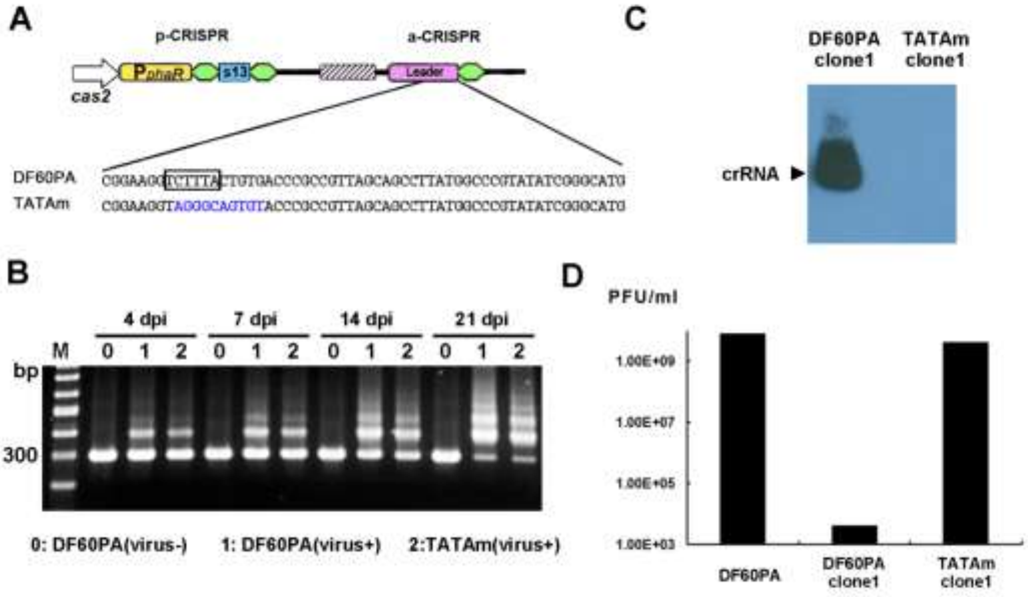

Figure S3. The different immunity effects of a-CRISPRs with a new spacer. (A) A mutant (TATAm) lacking the TATA box of the a-CRISPR was constructed. **(B)** Expansion of the a-CRISPRs in DF60PA and TATAm at 4, 7, 14, 21 days post HHPV-2 infection (dpi). The uninfected culture of DF60PA was used as the negative control. The gel shows a representative result of three replicates. Lane M, dsDNA size marker. **(C)** Northern blotting analysis of the crRNA in DF60PA_clone1 and TATAm_clone1 (Supplementary Data S1). A biotin-labeled repeat-specific DNA probe was used for hybridization, and was detected using the Chemiluminescent Nucleic Acid Detection Module Kit (Thermo Fisher Scientific). **(D)** During the plaque assay, the new spacer of DF60PA_clone1 caused a ~10^6-fold drop in PFU/ml compared to its parental strain DF60PA. In contrast, the new spacer in TATAm did not provide evident immunity. Three replicates were performed for each strain to get an average PFU value. ***Note that*** the virus-free DF60PA_clone1 was directly isolated from the virus-infected DF60PA culture, but from the infected culture of TATAm, virus-free clones could hardly be isolated, so we amplified the expanded a-CRISPR from TATAm_clone1, re-constructed it in the virus-free DF60P strain (using pHAR-in), and then performed the plaque assay.

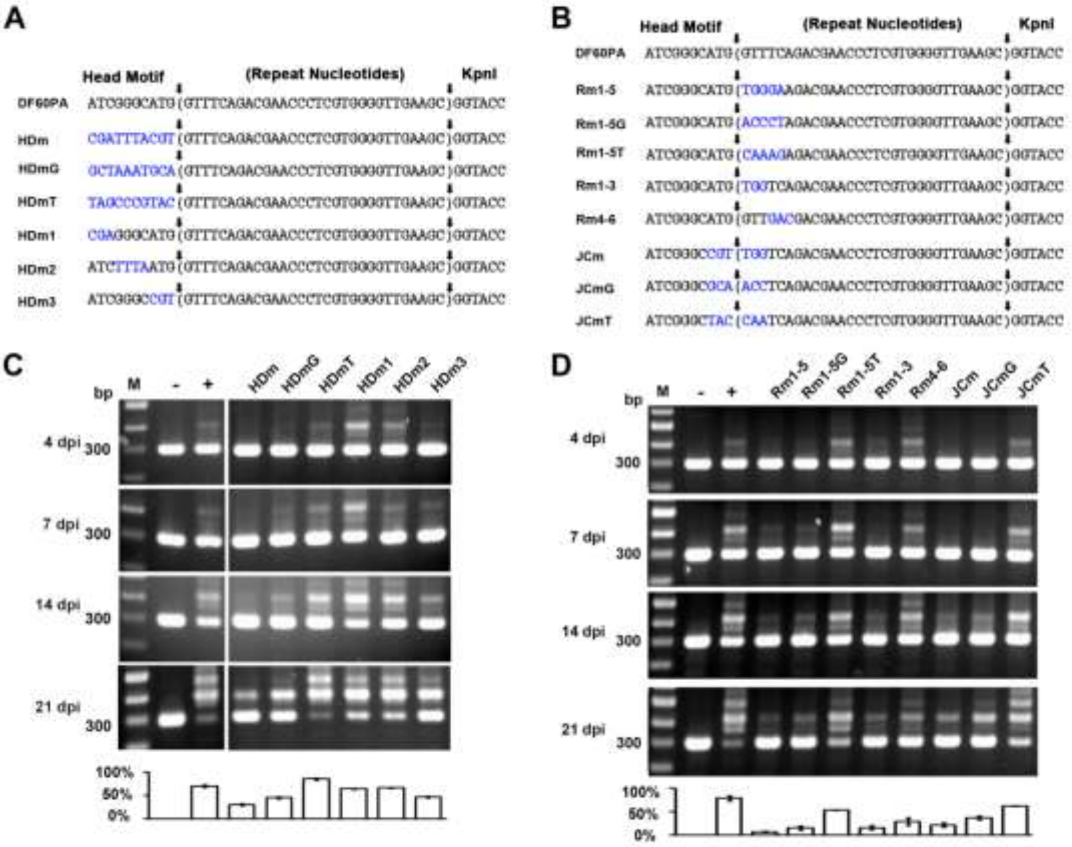

Figure S4. Mutations surrounding the leader-repeat junction differently impaired a-CRISPR expansion. Various mutations (in blue) were introduced into the head motif **(A)**, the first repeat-nucleotides, or both **(B)**. Sequences between vertical arrows were duplicated during spacer integration. **(C)** and **(D)** respectively show the expansion of the a-CRISPRs in panels **A** and **B** at 4, 7, 14, 21 days post HHPV-2 infection (dpi). DNA from the infected (+) or uninfected (-) DF60PA cells was used as the positive or negative control. Three replicates were tested for each mutant, and each gel shows a representative result. The ~300-bp (parental) and larger (expanded) bands of the 21-dpi samples were relatively quantified, and the percentage of expanded PCR products in each lane is shown in the histogram. Lane Ms, dsDNA size markers.

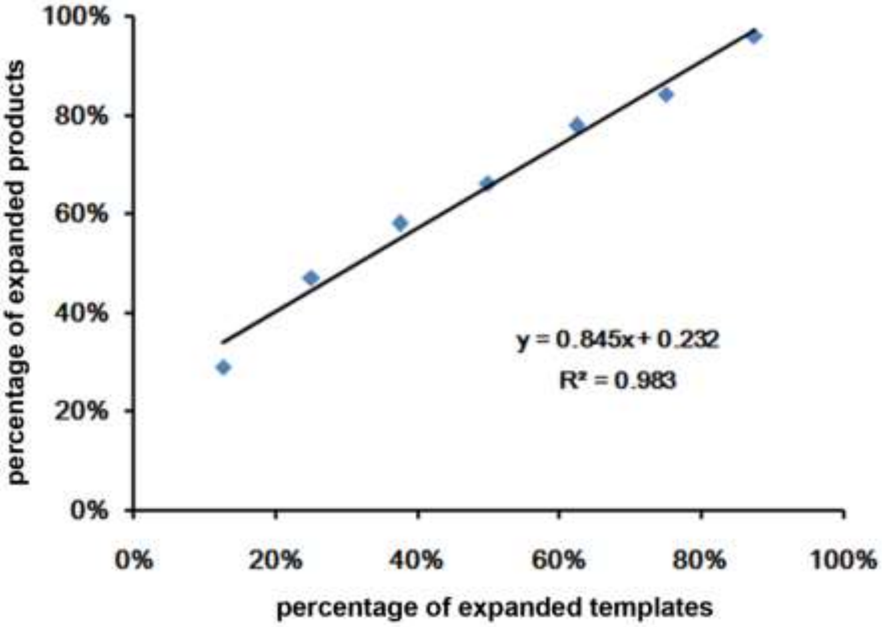

Figure S5. A standard curve of PCR on cultures with varying amounts of expanded samples. The DF60PA (containing the parental a-CRISPR) and DF60PA_clone1 (containing the a-CRISPR expanded by one new spacer) exponential cultures of the same OD were mixed in different ratios (7:1, 6:2, 5:3, 4:4, 3:5, 2:6 and 1:7), and the mixtures were immediately subjected to the PCR procedure applied in our adaptation assays. As described in the main text, the parental and expanded PCR products were relatively quantified. Three replications were performed to get an average percentage of expanded PCR products for each of the seven samples. The observed percentage of expanded PCR products and the theoretical percentage of expanded templates are shown on this scatter plot, and their linear correlation coefficient is given.

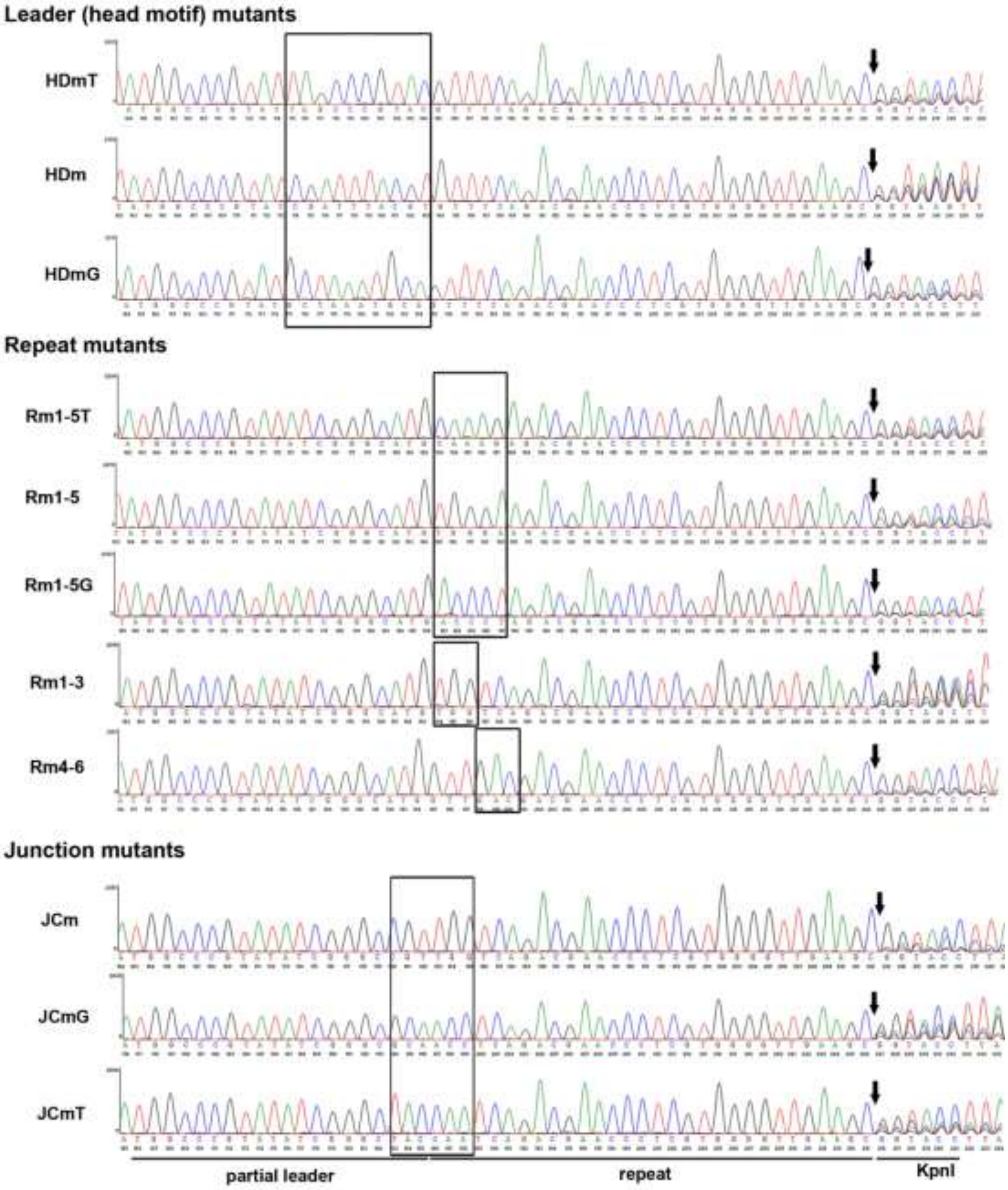

Figure S6. The sequencing chromatograph of the expanded a-CRISPRs containing different mutations adjacent to the leader-repeat junction. Primer Exp-Fa (**Table S2**) was used for DNA sequencing. Mutated nucleotides are framed. Multiple nucleotide signals were detected for positions downstream of each vertical arrow. The leader and repeat sequences, as well as the KpnI restriction site are respectively indicated at the bottom.

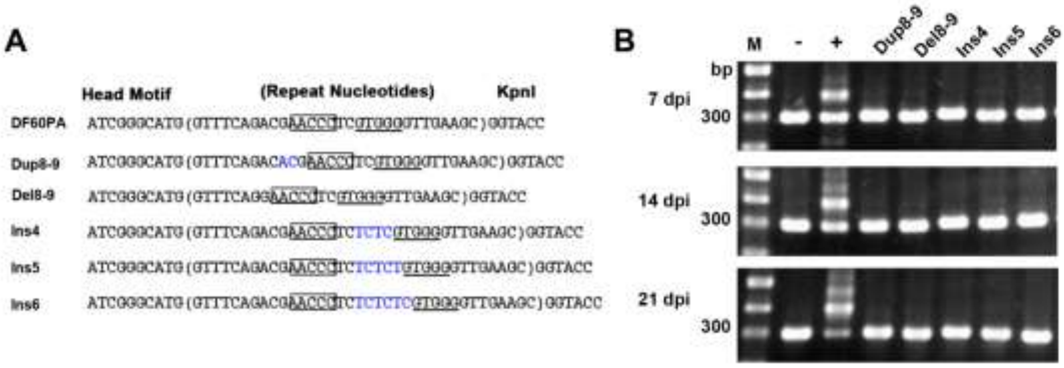

Figure S7. Some a-CRISPR mutants that failed to acquire new spacers. (A) Schematic representation of the mutants. In Dup8-9 and Del8-9, the nucleotides 8-9 of the a-CRISPR repeat (in brackets) were duplicated and deleted, respectively. In Ins4, Ins5 and Ins6, four to six extra nucleotides were inserted between the AACCC (boxed) and GTGGG (underlined) motifs. Extra nucleotides are in blue. **(B)** No expansion was observed for any of the mutants listed in panel **A** at 7, 14 or 21 days post HHPV-2 infection (dpi). DNA from the infected (+) or uninfected (-) DF60PA cells was used as the positive or negative control. Three replicates were tested for each mutant, and each gel shows a representative result. Lane Ms, dsDNA size markers.

SUPPLEMENTARY TABLES

Table S1. Strains and plasmids used in this study

Strains/Plasmids	Description	Source or reference
***H. hispanica* strains**		
DF60	*pyrF*-deleted strain of *H. hispanica* ATCC 33960	(1)
DF60P	DF60 with its wild-type CRISPR substituted by p-CRISPR	This study
DF60PA	DF60P transformed by the integrative plasmid pCR-A	This study
ΔCR	DF60 with its only CRISPR deleted	This study
ΔCR-A	ΔCR transformed by the integrative plasmid pCR-A	This study
TATAm	DF60P transformed by the integrative plasmid pTATAm	This study
HDm	DF60P transformed by the integrative plasmid pHDm	This study
HDmG	DF60P transformed by the integrative plasmid pHDmG	This study
HDmT	DF60P transformed by the integrative plasmid pHDmT	This study
HDm1	DF60P transformed by the integrative plasmid pHDm1	This study
HDm2	DF60P transformed by the integrative plasmid pHDm2	This study
HDm3	DF60P transformed by the integrative plasmid pHDm3	This study
Rm1-5T	DF60P transformed by the integrative plasmid pRm1-5T	This study
Rm1-5	DF60P transformed by the integrative plasmid pRm1-5	This study
Rm1-5G	DF60P transformed by the integrative plasmid pRm1-5G	This study
Rm1-3	DF60P transformed by the integrative plasmid pRm1-3	This study
Rm4-6	DF60P transformed by the integrative plasmid pRm4-6	This study
JCmT	DF60P transformed by the integrative plasmid pJCmT	This study
JCm	DF60P transformed by the integrative plasmid pJCm	This study
JCmG	DF60P transformed by the integrative plasmid pJCmG	This study
Rm6-10	DF60P transformed by the integrative plasmid pRm6-10	This study
Rm11-15	DF60P transformed by the integrative plasmid pRm11-15	This study
Rm16-30	DF60P transformed by the integrative plasmid pRm16-30	This study
Rm10-12	DF60P transformed by the integrative plasmid pRm10-12	This study
Rm13-15	DF60P transformed by the integrative plasmid pRm13-15	This study
Rm18-22	DF60P transformed by the integrative plasmid pRm18-22	This study
Rm23-30	DF60P transformed by the integrative plasmid pRm23-30	This study
Rm26-30	DF60P transformed by the integrative plasmid pRm26-30	This study
Rm21-25	DF60P transformed by the integrative plasmid pRm21-25	This study
Rm16-20	DF60P transformed by the integrative plasmid pRm16-20	This study
Rm16-17	DF60P transformed by the integrative plasmid pRm16-17	This study
Rm-GT	DF60P transformed by the integrative plasmid pRm-GT	This study
Dup6	DF60P transformed by the integrative plasmid pDup6	This study
Del6	DF60P transformed by the integrative plasmid pDel6	This study
Dup6-7	DF60P transformed by the integrative plasmid pDup6-7	This study

Del6-7	DF60P transformed by the integrative plasmid pDel6-7	This study
Dup8-9	DF60P transformed by the integrative plasmid pDup8-9	This study
Del8-9	DF60P transformed by the integrative plasmid pDel8-9	This study
Dup16	DF60P transformed by the integrative plasmid pDup16	This study
Del16	DF60P transformed by the integrative plasmid pDel16	This study
Dup16-17	DF60P transformed by the integrative plasmid pDup16-17	This study
Dup18	DF60P transformed by the integrative plasmid pDup18	This study
Dup19	DF60P transformed by the integrative plasmid pDup19	This study
Dup20	DF60P transformed by the integrative plasmid pDup20	This study
Dup21-25	DF60P transformed by the integrative plasmid pDup21-25	This study
Del21-25	DF60P transformed by the integrative plasmid pDel21-25	This study
Ins3	DF60P transformed by the integrative plasmid pIns3	This study
Ins4	DF60P transformed by the integrative plasmid pIns4	This study
Ins5	DF60P transformed by the integrative plasmid pIns5	This study
Ins6	DF60P transformed by the integrative plasmid pIns6	This study
Plasmids		
pHAR	4.0 kb; suicide vector containing *pyrF* and its native promoter	(1)
pCR-P	5.3 kb; modified pHAR to replace the wild-type CRISPR with p-CRISPR	This study
pΔCR	4.8 kb; modified pHAR to knock out the only CRISPR	This study
pHAR-in	4.4 kb; modified pHAR with a 460-bp chromosomal sequence	This study
pCR-A	4.6 kb; modified pHAR-in with an a-CRISPR structure containing the complete 105-bp leader and a single repeat	This study
pTATAm	4.6 kb; modified pCR-A with the TATA box mutated	This study
pHDm	4.6 kb; modified pCR-A with the head motif mutated	This study
pHDmG	4.6 kb; modified pCR-A with the head motif mutated	This study
pHDmT	4.6 kb; modified pCR-A with the head motif mutated	This study
pHDm1	4.6 kb; modified pCR-A with the head motif partially mutated	This study
pHDm2	4.6 kb; modified pCR-A with the head motif partially mutated	This study
pHDm3	4.6 kb; modified pCR-A with the head motif partially mutated	This study
pRm1-5	4.6 kb; modified pCR-A with the repeat nucleotides 1-5 mutated	This study
pRm1-5T	4.6 kb; modified pCR-A with the repeat nucleotides 1-5 mutated	This study
pRm1-5G	4.6 kb; modified pCR-A with the repeat nucleotides 1-5 mutated	This study
pRm1-3	4.6 kb; modified pCR-A with the repeat nucleotides 1-3 mutated	This study
pRm4-6	4.6 kb; modified pCR-A with the repeat nucleotides 4-6 mutated	This study
pJCm	4.6 kb; modified pCR-A with the 6 bp at the leader-repeat junction mutated	This study
pJCmT	4.6 kb; modified pCR-A with the 6 bp at the leader-repeat junction mutated	This study
pJCmG	4.6 kb; modified pCR-A with the 6 bp at the leader-repeat junction mutated	This study
pRm6-10	4.6 kb; modified pCR-A with the repeat nucleotides 6-10 mutated	This study
pRm11-15	4.6 kb; modified pCR-A with the repeat nucleotides 11-15 mutated	This study
pRm16-30	4.6 kb; modified pCR-A with the repeat nucleotides 16-30 mutated	This study
pRm10-12	4.6 kb; modified pCR-A with the repeat nucleotides 10-12 mutated	This study
pRm13-15	4.6 kb; modified pCR-A with the repeat nucleotides 13-15 mutated	This study
pRm18-22	4.6 kb; modified pCR-A with the repeat nucleotides 18-22 mutated	This study
pRm23-30	4.6 kb; modified pCR-A with the repeat nucleotides 23-30 mutated	This study

pRm26-30	4.6 kb; modified pCR-A with the repeat nucleotides 26-30 mutated	This study
pRm21-25	4.6 kb; modified pCR-A with the repeat nucleotides 21-25 mutated	This study
pRm16-20	4.6 kb; modified pCR-A with the repeat nucleotides 16-20 mutated	This study
pRm16-17	4.6 kb; modified pCR-A with the repeat nucleotides 16-17 mutated	This study
pRm-GT	4.6 kb; modified pCR-A with the repeat nucleotides 16, 17, 20 mutated	This study
pDup6	4.6 kb; modified pCR-A with the repeat nucleotide 6 duplicated	This study
pDel6	4.6 kb; modified pCR-A with the repeat nucleotide 6 deleted	This study
pDup6-7	4.6 kb; modified pCR-A with the repeat nucleotides 6-7 duplicated	This study
pDel6-7	4.6 kb; modified pCR-A with the repeat nucleotides 6-7 deleted	This study
pDup8-9	4.6 kb; modified pCR-A with the repeat nucleotides 8-9 duplicated	This study
pDel8-9	4.6 kb; modified pCR-A with the repeat nucleotides 8-9 deleted	This study
pDup16	4.6 kb; modified pCR-A with the repeat nucleotide 16 duplicated	This study
pDel16	4.6 kb; modified pCR-A with the repeat nucleotide 16 deleted	This study
pDup16-17	4.6 kb; modified pCR-A with the repeat nucleotides 16-17 duplicated	This study
pDup18	4.6 kb; modified pCR-A with the repeat nucleotide 18 duplicated	This study
pDup19	4.6 kb; modified pCR-A with the repeat nucleotides 19 duplicated	This study
pDup20	4.6 kb; modified pCR-A with the repeat nucleotide 20 duplicated	This study
pDup21-25	4.6 kb; modified pCR-A with the repeat nucleotides 21-25 duplicated	This study
pDel21-25	4.6 kb; modified pCR-A with the repeat nucleotides 21-25 deleted	This study
pIns3	4.6 kb; modified pCR-A with 3 extra repeat nucleotides	This study
pIns4	4.6 kb; modified pCR-A with 4 extra repeat nucleotides	This study
pIns5	4.6 kb; modified pCR-A with 5 extra repeat nucleotides	This study
pIns6	4.6 kb; modified pCR-A with 6 extra repeat nucleotides	This study

Table S2. Oligonucleotides used in this study

Primer[a]	**5'–3' sequence**[b]
For spacer acquisition assay	
Exp-Fp	TACGGCGACGATCCAACTGA
Exp-Rp	CGACCAGCGCGAAGTAA
Exp-Fa	CGGGGTCATCCTCGTCTC
Exp-Ra	CCGCGAAACAGCTCAAACAG
For DF60P and ΔCR construction	
P-UF	CGCGGATCCCTCGCAGACCGGGTACTAT
P-UR	CTAGTCTAGACGACTATAGAAACCG
phaR-bridge2	CTAGTCTAGACGAAGGGAACATATATGTTACTGCAGGTACAA
phaR-bridge1	TTACTGCAGGTACAACACCGAGTTAGGAGATGGTTTCAGACGAACCC
P-DF	TTACGGACTGGTCGA
P-DR	ATAGGGTACCGGGCTTGCCGACTGAA
ΔCR-UF	CGCGGATCCCTCGCAGACCGGGTACTAT
ΔCR-UR	GAGGTGCGGTTTATAAACGGCGGGTCACAGTA
ΔCR-DF	CTGTGACCCGCCGTTTATAAACCGCACCTCCTCAT

ΔCR-DR	ATAGGGTACCGGGCTTGCCGACTGAA
For modification of pHAR (to be an integrative vector)	
ChrSeq-F	CCCAAGCTTTGGGCTATCGTATTATGGGCACTA
ChrSeq-R	CGCGGATCCTGGGCAATAGCAAGAAACCGTGAT
For a-CRISPR construction and modification	
A-F	CGCGGATCCTCGGTTTCCGTCGAC
A-R	CGGGGTACCGCTTCAACCCCACGA
TATAm-DF	AAGGT***AGGGCAGTGT***ACCCGCCGTTAGCAG
TATAm-UR	CGGGT***ACACTGCCCT***ACCTTCCGTCGAC
HDm-DF	CGTAT***CGATTTACGT***GTTTCAGACGAACCC
HDm-UR	GAAAC***ACGTAAATCG***ATACGGGCCATAAGG
HDmT-DF	CGTAT***TAGCCCGTAC***GTTTCAGACGAACCC
HDmT-UR	GAAAC***GTACGGGCTA***ATACGGGCCATAAGG
HDmG-DF	CGTAT***GCTAAATGCA***GTTTCAGACGAACCC
HDmG-UR	GAAAC***TGCATTTAGC***ATACGGGCCATAAGG
HDm1-DF	CCTTATGGCCCGTAT***CGA***GGGCATGGTTTCAGA
HDm1-UR	TCTGAAACCATGCCC***TCG***ATACGGGCCATAAGG
HDm2-DF	TATGGCCCGTATATC***TTTA***ATGGTTTCAGACGAA
HDm2-UR	TTCGTCTGAAACCAT***TAAA***GATATACGGGCCATA
HDm3-DF	GCCCGTATATCGGGC***CGT***GTTTCAGACGAACCC
HDm3-UR	GGGTTCGTCTGAAAC***ACG***GCCCGATATACGGGC
Rm1-5-DF	GCATG***TGGGA***AGACGAACCCTCGTG
Rm1-5-UR	CGTCT***TCCCA***CATGCCCGATATACG
Rm1-5T-DF	GCATG***CAAAG***AGACGAACCCTCGTG
Rm1-5T-UR	CGTCT***CTTTG***CATGCCCGATATACG
Rm1-5G-DF	GCATG***ACCCT***AGACGAACCCTCGTG
Rm1-5G-UR	CGTCT***AGGGT***CATGCCCGATATACG
Rm1-3-DF	CGTATATCGGGCATG***TGG***TCAGACGAACCCTCG
Rm1-3-UR	CGAGGGTTCGTCTGA***CCA***CATGCCCGATATACG
Rm4-6-DF	ATATCGGGCATGGTT***GAC***GACGAACCCTCGTGG
Rm4-6-UR	CCACGAGGGTTCGTC***GTC***AACCATGCCCGATAT
JCm-DF	GCCCGTATATCGGGC***CGTTGG***TCAGACGAACCC
JCm-UR	GGGTTCGTCTGA***CCAACG***GCCCGATATACGGGC
JCmT-DF	GCCCGTATATCGGGC***TACCAA***TCAGACGAACCC
JCmT-UR	GGGTTCGTCTGA***TTGGTA***GCCCGATATACGGGC
JCmG-DF	GCCCGTATATCGGGC***GCAACC***TCAGACGAACCC
JCmG-UR	GGGTTCGTCTGA***GGTTGC***GCCCGATATACGGGC
Rm6-10-DF	GTTTC***CTCAT***AACCCTCGTG
Rm6-10-UR	GGGTT***ATGAG***GAAACCATGC
Rm11-15-DF	AGACG***CCAAA***TCGTGGGGTT
Rm11-15-UR	CACGA***TTTGG***CGTCTGAAAC
Rm10-12-DF	GGCATGGTTTCAGAC***TCC***CCCTCGTGGGGTTGA
Rm10-12-UR	TCAACCCCACGAGGG***GGA***GTCTGAAACCATGCC
Rm13-15-DF	ATGGTTTCAGACGAA***AAA***TCGTGGGGTTGAAGC

Rm13-15-UR	GCTTCAACCCCACGA***TTT***TTCGTCTGAAACCAT
Rm16-30-R	CGGGGTACC***TAGGACCAAAACATC***GGGTTCGTCTGAAAC
Rm18-22-R	CGGGGTACCGCTTCAAC***GGAGA***GAGGGTTCGTCTGAAAC
Rm23-30-R	CGGGGTACC***ATCCTGGT***CCCACGAGGGTTCGTCTGAAAC
Rm26-30-R	CGGGGTACC***TAGGA***AACCCCACGAGGGTTCGTCTGAAAC
Rm21-25-R	CGGGGTACCGCTTC***CCAAA***CACGAGGGTTCGTCTGAAAC
Rm16-20-R	CGGGGTACCGCTTCAACCC***ACATC***GGGTTCGTCTGAAAC
Rm16-17-R	CGGGGTACCGCTTCAACCCCAC***TC***GGGTTCGTCTGAAAC
Rm-GT-R	CGGGGTACCGCTTCAACCC***AA***CT***C***GGGTTCGTCTGAAAC
Dup6-R	CGGGGTACCGCTTCAACCCCACGAGGGTTCGTC***T***TGAAAC
Del6-R	CGGGGTACCGCTTCAACCCCACGAGGGTTCGTCGAAAC
Dup6-7-R	CGGGGTACCGCTTCAACCCCACGAGGGTTCGT***CT***CTGAAAC
Del6-7-R	CGGGGTACCGCTTCAACCCCACGAGGGTTCGTGAAAC
Del8-9-R	CGGGGTACCGCTTCAACCCCACGAGGGTTCCTGAAAC
Dup8-9-R	CGGGGTACCGCTTCAACCCCACGAGGGTTC***GT***GTCTGAAAC
Dup16-R	CGGGGTACCGCTTCAACCCCACG***A***AGGGTTCGTCTGAAAC
Del16-R	CGGGGTACCGCTTCAACCCCACGGGGTTCGTCTGAAAC
Dup16-17-R	CGGGGTACCGCTTCAACCCCAC***GA***GAGGGTTCGTCTGAAAC
Dup18-R	CGGGGTACCGCTTCAACCCCA***C***CGAGGGTTCGTCT
Dup19-R	CGGGGTACCGCTTCAACCCC***A***ACGAGGGTTCGTCT
Dup20-R	CGGGGTACCGCTTCAACCC***C***CACGAGGGTTCGTCT
Dup21-25-R	CGGGGTACCGCTTC***AACCC***AACCCCACGAGGGTTCGTCT
Del21-25-R	CGGGGTACCGCTTCCACGAGGGTTCGTCT
Ins3-R	CGGGGTACCGCTTCAACCCCAC***GGA***GAGGGTTCGTCTGAAAC
Ins4-R	CGGGGTACCGCTTCAACCCCAC***GAGA***GAGGGTTCGTCTGAAAC
Ins5-R	CGGGGTACCGCTTCAACCCCAC***AGAGA***GAGGGTTCGTCTGAAAC
Ins6-R	CGGGGTACCGCTTCAACCCCAC***GAGAGA***GAGGGTTCGTCTGAAAC

[a] Forward and reverse primers are indicated with letters F and R, respectively. During the bridge PCR procedure, the UF (upstream forward)/UR (upstream reverse) and DF (downstream forward)/DR (downstream reverse) primer pairs were used to amplify the upstream and downstream fragments, respectively.

[b] Designed restriction sequences are underlined. Mutated (or inserted) nucleotides are shown in bold and italic.

Table S3. Spacers that were acquired from the HHPV-2 genome by different a-CRISPR constructs

Spacer ID[a]	**Spacer sequences (5'–3')**	**Positions**[b]	**Strand**[c]	**PAM 5'–3'**
DF60PA_1.1	TTCGGATCGTGGAATGAAGATGAGTCGTTCCCTGAA	7014-7049	+	TTC
DF60PA_2.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6451-6486	+	TTC
DF60PA_3.1	AGGGAACGACTCATCTTCATTCCACGATCCGAAGA	7046-7012	-	TTC

DF60PA_3.2	CTTTTTGCGTATTGGACGCCCACATGGTAGCCGCC	1162-1128	-	TTC
DF60PA_3.3	AGACGAGGCGAACGCAGCGAGGAACGTACCCATCGA	2841-2806	-	TTC
DF60PA_4.1	TCATCCATCACGTAGCGCAGCGAACGACCAGCACCA	737-702	-	TTC
DF60PA_5.1	ATCGAGATCCGCAGCGAACTCATCATCTTGCAGCTC	6066-6031	-	TTC
DF60PA_5.2	CCAGTGGGGAATTGACCAGTCATCTCCTGCGCGA	1359-1392	+	TTC
DF60PA_5.3	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
DF60PA_6.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
DF60PA_6.2	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACG	6873-6906	+	TTC
DF60PA_7.1	ATACACAAGCACAGGACACCTCCCGCGGACCCACAG	7458-7423	-	TTC
DF60PA_7.2	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCG	6171-6206	+	TTC
DF60PA_8.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGA	672-639	-	TTC
DF60PA_8.2	GGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCTG	7982-8018	+	TTC
TATAm_6.3	CCTCGGTCAGAATAGGCTGCGTTCGCTGCTCTGGT	7297-7331	+	TTC
TATAm_7.1	AGCGAACAGACCAGCTCGCAGGTTCCACGACCACGG	7157-7122	-	TTC
TATAm_7.2	CTTTTTGCGTATTGGACGCCCACATGGTAGCCGCCC	1162-1127	-	TTC
TATAm_7.3	CACGACCACGGCGCAGAATCATCAGGATCATACGC	7132-7098	-	TTC
TATAm_1.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
TATAm_2.1	GCTGAATTACAGTGAGCGTCGTAAGATGTTCGCTG	2470-2504	+	TTC
TATAm_2.2	GTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCGC	7237-7272	+	TTC
TATAm_2.3	AATACATCGGTCCTGTGCTGCTGATCGTTGGCTG	6171-6204	+	TTC
TATAm_2.4	TTTCGCAGACCACGACGGGGGCCGGGTATAGCGAACG	1698-1662	-	TTC
TATAm_3.1	GAACTTCAGACCCGAGCGCAGTATCAGCGAACGT	6450-6417	-	TTC
TATAm_3.2	CTGATTCGTACGTGCTGCCGTCTTGCGACGTGTTG	3753-3719	-	TTC
TATAm_3.3	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGA	672-639	-	TTC
TATAm_4.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
TATAm_5.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6453-6486	+	TTC
TATAm_5.2	TTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGG	6984-7018	+	TTC
TATAm_5.3	AACATATTCACGGACCCGATCAACGACCGACTCAGG	2088-2053	-	TTC
TATAm_6.1	CGCTCGCACTGGCCGGTGTCGCTCTGGCCGGTGCTG	3181-3216	+	TTC
TATAm_6.2	TCATCCATCACGTAGCGCAGCGAACGACCAGCACCA	737-702	-	TTC
JCm_1.1	GACCCGCGCCAACGGGTATGAGTTTGCGGCGTTCAA	7714-7749	+	TTC
JCm_2.1	AGGTGACGAATCAGTACCGCCACCATCAGCAGCAA	1446-1412	-	TTC
JCm_3.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
JCmT_1.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
JCmT_1.2	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7782	+	TTC
JCmT_2.1	TTCGGATCGTGGAATGAAGATGAGTCGTTCCCTGA	7014-7048	+	TTC
JCmT_3.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7782	+	TTC
JCmT_4.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCGT	408-373	-	TTC
JCmT_5.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7782	+	TTC
JCmG_1.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC

JCmG_2.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCAC	796-762	-	TTC
Rm1-5T_1.1	ACTATCGAAACACAGGCGTTTACGATTATTCGGTCT	5866-5901	+	TTC
Rm1-5T_2.1	GTCGAGAATGCGATTGCTGATGCTGATTCTGGTCCGG	6378-6414	+	TTC
Rm1-5T_3.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm1-5T_4.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGC	7481-7514	+	TTC
Rm1-5T_5.1	GCTGTCTTTCGTCGAGAATGCGATTGCTGATGCTG	6368-6402	+	TTC
Rm1-5T_6.1	GTCGAGAATGCGATTGCTGATGCTGATTCTGGTCCGG	6378-6414	+	TTC
Rm1-5T_7.1	ACTATCGAAACACAGGCGTTTACGATTATTCGGTCT	5866-5901	+	TTC
Rm1-5_1.1	GCCAAACACAGCTCGAGCTGCAAGAAGAGTCTCAAT	4483-4518	+	TTC
Rm1-5_2.1	AGGTGACGAATCAGTACCGCCACCATCAGCAGCAA	1446-1412	-	TTC
Rm1-5_3.1	GCTGATACTGCGCTCGGGTCTGAAGTTCGGAAAA	6423-6456	+	TTC
Rm1-5_4.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Rm1-5G_1.1	GCAGACCACGACGGGGGCCGGGTATAGCGAACGG	1694-1661	-	TTC
Rm1-5G_2.1	GCGCTCTAAAGCCTTCAGCCGCGCTCGCTCTTTATC	498-463	-	TTC
Rm1-5G_3.1	AAGCGATTGGCTACGTTGCCTTTCTTTAAGAGCGA	6960-6994	+	TTC
Rm1-5G_4.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Rm1-3_1.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACTG	796-760	-	TTC
Rm1-3_2.1	CCTCGGTCAGAATAGGCTGCGTTCGCTGCTCTGGTT	7297-7332	+	TTC
Rm1-3_3.1	GACTTGTCCGGTCTGTCGCTCGGTGGCATACCCGG	4536-4570	+	TTC
Rm4-6_1.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGCGT	7782-7816	+	TTC
Rm4-6_2.1	TTCGGATCGTGGAATGAAGATGAGTCGTTCCCTG	7014-7047	+	TTC
Rm4-6_2.2	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm4-6_2.3	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTG	6873-6908	+	TTC
Rm4-6_3.1	TCAGTCGCATCAGTCCCATCAACCAGAGACAGAGAC	3703-3668	-	TTC
Rm4-6_3.2	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7782	+	TTC
Rm4-6_3.3	AGCGAATACGGACGCTCTTTTTCGCCCAGCTCAACA	2472-2437	-	TTC
Rm6-10_1.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm6-10_2.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCGTG	408-372	-	TTC
Rm6-10_3.1	AGCTCGTCTCGAAGGTGATGAGGCTGTGCTGGTGCTT	4951-4987	+	TTC
Rm6-10_4.1	GCTGATACTGCGCTCGGGTCTGAAGTTCGGAAAACG	6423-6458	+	TTC
Rm6-10_5.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTG	6873-6908	+	TTC
Rm6-10_6.1	TTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGG	6984-7018	+	TTC
Rm6-10_7.1	AGCCGCGCTCGCTCTTTATCCTGATACGCAGCCATC	482-447	-	TTC
Rm6-10_8.1	GCTGATACTGCGCTCGGGTCTGAAGTTCGGAAAA	6423-6456	+	TTC
Rm6-10_9.1	CTTTTTGCGTATTGGACGCCCACATGGTAGCCGCCC	1162-1127	-	TTC
Rm6-10_10.1	CTCAATCACCTCCTCACCGGCATCCGGGTTTATCCAC	2395-2359	-	TTC
Rm6-10_11.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7782	+	TTC
Rm6-10_11.2	GTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCG	7237-7271	+	TTC
Rm10-12_1.1	GCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTA	5191-5225	+	TTC
Rm10-12_2.1	CTTTCGATTGTTGCTGTCGTCTTGATCGGGTCCG	5407-5440	+	TTC

Rm10-12_3.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6451-6486	+	TTC
Rm10-12_4.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Rm10-12_5.1	TCAGTCGCATCAGTCCCATCAACCAGAGACAGAG	3703-3670	-	TTC
Rm10-12_6.1	AGAAAGGTACGACGTACGGCCCGACGACGTGGGATG	4195-4230	+	TTC
Rm10-12_7.1	GGTAAATAGAGGTATCCAAAATGCAATTTTTTAAAAT	4617-4653	+	TTC
Rm10-12_8.1	GACTTGTCCGGTCTGTCGCTCGGTGGCATACCCGG	4536-4570	+	TTC
Rm10-12_9.1	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCG	6171-6206	+	TTC
Rm10-12_10.1	ATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAG	234-199	-	TTC
Rm16-30_1.1	GACGAGGCGAACGCAGCGAGGAACGTACCCATCG	2840-2807	-	TTCA
Rm16-30_2.1	CGACTGAGGATATTGTTGATCCGATCACGGCGG	3976-4008	+	TTC
Rm16-30_3.1	CTGTTGGTGAGGGTTCCCACCCACAAACCCACCCA	7361-7395	+	TTC
Rm16-30_4.1	TCGATCACCGTGCGAAACGTCGCCGCGCTCGCCT	920-887	-	TTC
Rm16-30_4.2	TCATCCATCACGTAGCGCAGCGAACGACCAGCACC	737-703	-	TTC
Rm16-30_5.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACC	672-637	-	TTC
Rm16-30_5.2	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGG	5286-5321	+	TTC
Rm16-30_6.1	GGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCT	7982-8017	+	TTC
Rm16-30_7.1	GGTCTGTGTCTCTACTGCTACGTTTCTGAAACTGA	7883-7917	+	TTC
Rm16-30_8.1	CAGCTGGGTATTGTAATGAGTCAGAATGTTCTGCTG	3551-3516	-	TTC
Rm16-30_9.1	CCACCCACAAACCCACCCACCCACAGGACACCGGA	7377-7411	+	TTC
Rm18-22_1.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
Rm18-22_2.1	AGTGGTGAGTTGACTGCGCTCGAGGAAACACAGTCG	7062-7097	+	TTC
Rm18-22_3.1	TGAAACTGAATCGTCGTCTGTTCGGGAGTGGTCTGA	7909-7944	+	TTC
Rm18-22_4.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6451-6486	+	TTC
Rm18-22_5.1	GCTGAAGATATGAGTTGGTCGGAGCTGCTCGAAGA	7155-7189	+	TTC
Rm18-22_6.1	CGGCAGCGGGTGGATAAACCCGGATGCCGGTGAGGA	2350-2385	+	TTC
Rm18-22_6.2	GGTCTGCTGCTCGGTCCTGTGTGATGTCCGTCGTGC	5897-5932	+	TTC
Rm18-22_7.1	CGCTTGATAACAGTTGGATGGCTGCGTATCAGGAT	431-465	+	TTC
Rm18-22_8.1	TGACTCATTACAATACCCAGCTGGAACAGGTGAAA	3529-3563	+	TTC
Rm23-30_1.1	GAAGAGGGCACGCTGCCTGATCACGGTGAGTCGCTG	5941-5976	+	TTC
Rm23-30_2.1	GAAGAGGGCACGCTGCCTGATCACGGTGAGTCGCT	5941-5975	+	TTC
Rm23-30_3.1	GTGCTGATCGATGAGGGCAGCACGCACTTCGATGCT	6804-6839	+	TTC
Rm23-30_4.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCG	408-374	-	TTC
Rm23-30_5.1	CAGTCAGACGCCGGTTTGTCGAGATCATGTGCATCA	989-954	-	TTC
Rm23-30_5.2	TGCTGAATAGCAGCGAAATACTCATTTATCGATGA	3520-3486	-	TTC
Rm23-30_6.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGCGTT	7782-7817	+	TTC
Rm23-30_7.1	GGTAAATAGAGGTATCCAAAATGCAATTTTTTAAAATA	4617-4654	+	TTC
Rm23-30_8.1	CGCTCGCACTGGCCGGTGTCGCTCTGGCCGGTGCTG	3181-3216	+	TTC
Rm23-30_9.1	GTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCGC	7237-7272	+	TTC
Rm23-30_10.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGA	672-639	-	TTC
Rm23-30_11.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGCGT	7782-7816	+	TTC

Rm23-30_12.1	CGACTGAGGATATTGTTGATCCGATCACGGCGG	3976-4008	+	TTC
Rm26-30_1.1	CCACCCACAAACCCACCCACCCACAGGACACCGGA	7377-7411	+	TTC
Rm26-30_2.1	GCTGTCTTTCGTCGAGAATGCGATTGCTGATGCTG	6368-6402	+	TTC
Rm26-30_3.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Rm26-30_3.2	GCTGATACTGCGCTCGGGTCTGAAGTTCGGAAAACG	6423-6458	+	TTC
Rm26-30_4.1	TCATCCATCACGTAGCGCAGCGAACGACCAGCACCA	737-702	-	TTC
Rm26-30_5.1	AGGGGCAACAGCAGAATCAGGTATCGGAACGTCAC	1641-1607	-	TTC
Rm26-30_6.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCGT	7748-7783	+	TTC
Rm26-30_7.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGA	7481-7512	+	TTC
Rm26-30_8.1	GCGCTTTTCTGTCGAGCCAGACGAATCTTCAACAGT	288-253	-	TTC
Rm26-30_9.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACCG	672-636	-	TTC
Rm21-25_1.1	GTTCTCGCTTAGTAGCGGAGCATACGCTGACTACTC	3803-3838	+	TTC
Rm21-25_2.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
Rm21-25_3.1	GTTACCCCGGGGGCTATCGCTTATAAGGTAGTA	2226-2258	+	TTC
Rm21-25_4.1	GCGCTTTTCTGTCGAGCCAGACGAATCTTCAACAGTG	288-252	-	TTC
Rm21-25_4.2	GCCTCGTCTGAAACTCGGTCGTTTGACCGGTACGA	2833-2867	+	TTC
Rm21-25_5.1	TCTGCTGGCTGCGTTGATCGTCGTGTTACCTCTGCGC	6720-6756	+	TTC
Rm21-25_6.1	AACATATTCACGGACCCGATCAACGACCGACTCAGG	2088-2053	-	TTC
Rm21-25_6.2	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCT	6451-6485	+	TTC
Rm21-25_7.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACC	672-637	-	TTC
Rm21-25_7.2	GATTGTTGCTGTCGTCTTGATCGGGTCCGGTCTGAT	5412-5447	+	TTC
Rm21-25_8.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGCGTTG	7782-7818	+	TTC
Rm21-25_9.1	CCTGAAGATCGCCTTTTCAGTGGTGAGTTGACTGC	7044-7078	+	TTC
Rm16-20_1.1	CCCACTGGGAACCGCAGGCAGTACACACGACATTGA	1366-1331	-	TTC
Rm16-20_2.1	ACGAATAAGAAGATTACTGATGGCAGTGGTAATG	4149-4182	+	TTC
Rm16-20_3.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGC	7782-7814	+	TTC
Rm16-20_4.1	TTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGGAT	6984-7020	+	TTC
Rm16-20_5.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm16-20_6.1	GTGGGACGCTTGATCCTGATGCTGATGAACAGC	7782-7814	+	TTC
Rm16-20_7.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm16-20_7.2	AGGATGAGCTGGGCGAGCTGCAAGATGATGAGTTCGC	6017-6053	+	TTC
Rm16-20_8.1	GCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTA	5191-5225	+	TTC
Rm16-20_9.1	TGCTACCCGCTCCGGATCAACCGTACGGCCAGCC	5326-5293	-	TTCA
Rm16-20_10.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCGTG	408-372	-	TTC
Rm16-17_1.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGG	5286-5321	+	TTC
Rm16-17_2.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Rm16-17_3.1	CTTTCGATTGTTGCTGTCGTCTTGATCGGGTCCGG	5407-5441	+	TTC
Rm16-17_4.1	TGAAACTGAATCGTCGTCTGTTCGGGAGTGGTCTG	7909-7943	+	TTC
Rm16-17_5.1	ATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCA	234-200	-	TTC
Rm16-17_6.1	ATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAG	234-199	-	TTC

Rm16-17_7.1	GATTGTTGCTGTCGTCTTGATCGGGTCCGGTCTG	5412-5445	+	TTC
Rm16-17_8.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Rm16-17_9.1	CCCACTGGGAACCGCAGGCAGTACACACGACATTG	1366-1332	-	TTC
Rm16-17_10.1	TCATCCATCACGTAGCGCAGCGAACGACCAGCAC	737-704	-	TTC
Rm16-17_11.1	CTCAAGGTTGGCAAGAACATGCAGTTAGAAGAGAT	5719-5753	+	TTC
Rm-GT_1.1	CGACTGAGGATATTGTTGATCCGATCACGGCGGCG	3976-4010	+	TTC
Rm-GT_2.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGG	5286-5321	+	TTC
Rm-GT_3.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACTG	796-760	-	TTC
Rm-GT_4.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCAG	7481-7516	+	TTC
Rm-GT_5.1	GTGAGACACTTGATCCTGATGCTGATGAACAGCGT	7782-7816	+	TTC
Rm-GT_6.1	CGGCAGCGGGTGGATAAACCCGGATGCCGGTGAGG	2350-2384	+	TTC
Rm-GT_7.1	GCTGAAGATATGAGTTGGTCGGAGCTGCTCGAAGA	7155-7189	+	TTC
Rm-GT_8.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCGT	408-373	-	TTC
Rm-GT_9.1	CTGTTGGTGAGGGTTCCCACCCACAAACCCACCCA	7361-7395	+	TTC
Rm-GT_10.1	GTGCTGATCGATGAGGGCAGCACGCACTTCGATGCTC	6804-6840	+	TTC
Rm-GT_11.1	GCTATACCCGGCCCCCGTCGTGGTCTGCGAAAGAAG	1667-1702	+	TTC
Dup6_1.1	CGTCGCGCAAAGCGGACAGGTATCAGGCTCAGTG	1575-1542	-	TTC
Dup6_2.1	TGAAACTGAATCGTCGTCTGTTCGGGAGTGGTCTG	7909-7943	+	TTC
Dup6_3.1	ACGCCGATTAGTCCGAGCATCGAAGTGCGTGCTG	6854-6821	-	TTC
Dup6_4.1	CGAGCAGGACTGTCAGTCGCAGGCAACCAAGCAAC	1934-1900	-	TTC
Dup6_5.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCG	5286-5319	+	TTC
Dup6_6.1	CTTGTGCAGCGACAGGGGCAACGCCGCCGATCAG	4715-4682	-	TTC
Dup6_7.1	AGGTGACGAATCAGTACCGCCACCATCAGCAGCAACA	1446-1410	-	TTC
Dup6_8.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACG	6873-6906	+	TTC
Dup6_9.1	GACTTGTCCGGTCTGTCGCTCGGTGGCATACCCGG	4536-4570	+	TTC
Dup6_10.1	TCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTC	920-886	-	TTC
Del6_1.1	TTTCGCAGACCACGACGGGGGCCGGGTATAGCGA	1698-1665	-	TTC
Del6_2.1	CGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACC	672-637	-	TTC
Del6_3.1	ATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAG	234-199	-	TTC
Del6_4.1	AGGTGACGAATCAGTACCGCCACCATCAGCAGCAA	1446-1412	-	TTC
Del6_5.1	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCGT	6171-6207	+	TTC
Del6_6.1	GCTGATACTGCGCTCGGGTCTGAAGTTCGGAAAA	6423-6456	+	TTC
Del6_7.1	ATACAGTTTTTTGGAGAACACATTTACGCGCTCTT	324-290	-	TTC
Del6_8.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6453-6486	+	TTC
Del6_9.1	GGATAGTTGAGCACGTTGGTAATGATGTGTCTGCC	7982-8016	+	TTC
Del6_10.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACT	796-761	-	TTC
Del6_11.1	GCAGACCACGACGGGGGCCGGGTATAGCGAACGGA	1694-1660	-	TTC
Del6_12.1	TGGTCCGGCGACGTTCGCTGATACTGCGCTCGGGT	6407-6441	+	TTC
Dup16_1.1	TTTGGGATTGTACGTGATCTCTTCGCCGTCGTCGT	2599-2565	-	TTC
Dup16_2.1	TCGAGCAGGACTGTCAGTCGCAGGCAACCAAGCAAC	1935-1900	-	TTC
Dup16_3.1	ACACCAGCAGCAGCGCCAGCAGTCACACCAACGG	3124-3091	-	TTC

Dup16_4.1	CTTTTTGCGTATTGGACGCCCACATGGTAGCCG	1162-1130	-	TTC
Dup16_5.1	TCTGCTGGCTGCGTTGATCGTCGTGTTACCTCTG	6720-6753	+	TTC
Dup16_6.1	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTG	6171-6204	+	TTC
Dup16_7.1	ACTTGTATTCCCTCGGTCAGAATAGGCTGCGTTCGCTG	7287-7324	+	TTC
Dup16_8.1	GCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTA	5191-5225	+	TTC
Dup16_9.1	ACTAAGCGAGTGACGTTGACTGATGCTGGTGCGT	5000-5033	+	TTC
Dup16_10.1	CGCTCGCACTGGCCGGTGTCGCTCTGGCCGGTGCTG	3181-3216	+	TTC
Dup16_11.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Dup16_12.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACT	796-761	-	TTC
Del16_1.1	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTGC	6171-6205	+	TTC
Del16_2.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Del16_3.1	TCTTGTGCAGCGACAGGGGCAACGCCGCCGATCAGC	4716-4681	-	TTC
Del16_4.1	GCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTA	5191-5225	+	TTC
Del16_5.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTG	6873-6908	+	TTC
Del16_6.1	GTGCTGATCGATGAGGGCAGCACGCACTTCGATGCT	6804-6839	+	TTC
Del16_7.1	GTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCGC	7237-7272	+	TTC
Del16_8.1	GCTGAAGATATGAGTTGGTCGGAGCTGCTCGAAGA	7155-7189	+	TTC
Del16_9.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGT	6873-6907	+	TTC
Del16_10.1	GCTATATGGCTGGCCGTACGGTTGATCCGGGGCGG	5286-5320	+	TTC
Dup16-17_1.1	CTGGTGCTCGCCAGATTCATCGAGATCCGCAGCG	6084-6051	-	TTC
Dup16-17_2.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGG	5286-5320	+	TTC
Dup16-17_3.1	GGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTA	6451-6486	+	TTC
Dup16-17_4.1	ATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAG	234-199	-	TTC
Dup16-17_5.1	GGGAGCTGTCGGTAACTGGTCCTAACGGTAATCCG	5648-5682	+	TTC
Dup16-17_6.1	GCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGG	5286-5321	+	TTC
Dup16-17_7.1	CGTCGCGCAAAGCGGACAGGTATCAGGCTCAGCGT	1575-1541	-	TTC
Dup16-17_8.1	GCGCTCTAAAGCCTTCAGCCGCGCTCGCTCTTTATC	498-463	-	TTC
Dup16-17_9.1	TCATCAGCCACTTTCATCGACGTAGCACCCTCTT	3355-3322	-	TTC
Dup16-17_10.1	CGTCGCGCAAAGCGGACAGGTATCAGGCTCAGCG	1575-1542	-	TTC
Dup18_1.1	CTCAAGGTTGGCAAGAACATGCAGTTAGAAGAGATG	5719-5754	+	TTC
Dup18_2.1	GGTCTGTGTCTCTACTGCTACGTTTCTGAAACTG	7883-7916	+	TTC
Dup18_3.1	CTTTTTGCGTATTGGACGCCCACATGGTATCCGC	1162-1129	-	TTC
Dup18_4.1	ATACAGTTTTTTGGAGAACACATTTACGCGCTCTT	324-290	-	TTC
Dup18_5.1	GTGCTGATCGATGAGGGCAGCACGCACTTCGATG	6804-6837	+	TTC
Dup18_6.1	AGGATGAGCTGGGCGAGCTGCAAGATAATGAGTTCGC	6017-6053	+	TTC
Dup18_7.1	CGGTTTCCGTCTGATGACTTTCGGGAGCTGTCGGTA	5626-5661	+	TTC
Dup18_8.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCGT	7748-7783	+	TTC
Dup18_9.1	AGTGGTGAGTTGACTGCGCTCGAGGAAACACAGTCG	7062-7097	+	TTC
Dup18_10.1	GATTGTTGCTGTCGTCTTGATCAGGTCCGGTCGGATC	5412-5448	+	TTC
Dup19_1.1	GCTGAAGATATGAGTTGGTCGGAGCTGCTCGAAG	7155-7188	+	TTC
Dup19_2.1	TGACTCATTACAATACCCAGCTGGAACAGGTGAAA	3529-3563	+	TTC
Dup19_2.2	GTGGGACGCTTGATCCTGATGCTGATGAACAGCGT	7782-7816	+	TTC
Dup19_3.1	AGGATCAGACCGCATACCATACTCGAGACGCAGCGT	408-373	-	TTC

Dup19_4.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACTG	796-760	-	TTC
Dup19_5.1	TTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGG	7481-7516	+	TTC
Dup19_6.1	GAACGTACGCACGACGGACATCACACAGGACCGAGC	5940-5905	-	TTC
Dup19_7.1	ATCGACGTAGCACCCTCTTGGATTGCAGACTTAAGG	3340-3305	-	TTC
Dup19_8.1	CTACAAACCGTTGGTGTGACTGCTGGCGCTGCTG	3084-3117	+	TTC
Dup19_9.1	AGAAAGGTACGACGTACGACCCGACGACGTGGGAT	4195-4229	+	TTC
Dup20_1.1	CTACAAACCGTTGGTGTGACTGCTGGCGCTGCTGCT	3084-3119	+	TTC
Dup20_2.1	CCACCCACAAACCCACCCACCCACAGGACACCGGA	7377-7411	+	TTC
Dup20_3.1	GACTTGTCCGGTCTGTCGCTCGGTGGCATACCCG	4536-4569	+	TTC
Dup20_4.1	TCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTCG	920-885	-	TTC
Dup20_5.1	TCTGCTGGCTGCGTTGATCGTCGTGTTACCTCTG	6720-6753	+	TTC
Dup20_6.1	GTACACGTTGACCGGGCAGCATGCCGTTGTCGCGTCGA	2772-2809	+	TTC
Dup20_7.1	GAATCATTAGCGAGATATGCAGCAGCATACGAAGC	1088-1054	-	TTC
Dup20_8.1	ACTAATAAGAGGATTACTGATGGCTGTGGTAATGA	4149-4183	+	TTC
Dup20_9.1	CTAGTGCTCGCCAGATTCAACGAGCAACCGATCAGG	2010-1975	-	TTC
Dup20_10.1	TTTAACACCGAGCCTAAAGGTGCTGAGTTCTTCGG	6984-7018	+	TTC
Dup21-25_1.1	AGTGGTGAGTTGACTGCGCTCGAGGAAACACAGTCGG	7062-7098	+	TTC
Dup21-25_2.1	TCATCCATCACGTAGCGCAGCGAACGACCAGCACC	737-703	-	TTC
Dup21-25_3.1	TCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTCGA	920-884	-	TTC
Dup21-25_4.1	TTTCGCAGACCACGACGGGGGCCGGGTATAGCGAAC	1698-1663	-	TTC
Dup21-25_5.1	GCGCTTTTCTGTCGAGCCAGACGAATCTTCAACAGT	288-253	-	TTC
Dup21-25_6.1	GCGCTCTTGTTCAGGTGACGAATCAGTACCGCCACC	1458-1423	-	TTC
Dup21-25_7.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCACT	796-761	-	TTC
Dup21-25_8.1	GACCCGCGCCAACGGGTATGAGTTTGCGGCGTTCAAGC	7714-7751	+	TTC
Dup21-25_9.1	CGACTGAGGATATTGTTGATCCGATCACGGCGGC	3976-4009	+	TTC
Dup21-25_10.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTG	6873-6908	+	TTC
Dup21-25_11.1	AGGGGCAACAGCAGAATCAGGTATCGGAACGTCACC	1641-1606	-	TTC
Del21-25_1.1	GAAGAGGGCACGCTGCCTGATCACGGTGAGTCGCTG	5941-5976	+	TTC
Del21-25_2.1	GTCGAGAATGCGATTGCTGATGCTGATTCTGGTCC	6378-6412	+	TTC
Del21-25_3.1	GGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCTG	7982-8018	+	TTC
Del21-25_4.1	GGATAGTTGAGCACGTTGGTAATGATGTGTCTG	7982-8014	+	TTC
Del21-25_5.1	GTCTTGCGGTGATTGCTGCTGAGTCTGACTGCGGTA	8137-8172	+	TTC
Del21-25_6.1	GGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCT	7982-8017	+	TTC
Del21-25_7.1	AGCAGAACATTCTGACTCATTACAATACCCAGCTG	3517-3551	+	TTC
Del21-25_8.1	GCCAAACACAGCTCGAGCTGCAAGAAGAGTCTCAA	4483-4517	+	TTC
Del21-25_8.2	CGTACCCGCCGACTTGCCGACGCTTTCCGGTATG	823-790	-	TTC
Del21-25_9.1	TTGCGCGAGCGCGAGGTTCGCTGTAATGCGATTGTCC	7562-7598	+	TTC
Del21-25_10.1	AGTGGTGAGTTGACTGCGCTCGAGGAAACACAGTCG	7062-7097	+	TTC
Del21-25_11.1	GCAGACCACGACGGGGGCCGGGTATAGCGAACGGACA	1694-1658	-	TTC
Ins3_1.1	CGGTATGTGGCTCACCTTGAGTCCACCGGACCCA	796-763	-	TTC
Ins3_2.1	GCTGTCTTTCGTCGAGAATGCGATTGCTGATGCTG	6368-6402	+	TTC
Ins3_3.1	CGTACCCGCCGACTTGCCGACGCTTTCCGGTATGTG	823-788	-	TTC
Ins3_4.1	AAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCG	7748-7779	+	TTC

Ins3_5.1	GAATCATTAGCGAGATATGCAGCAGCATACGAAG	1088-1055	-	TTC
Ins3_6.1	GTGCTGATCGATGAGGGCAGCACGCACTTCGATG	6804-6837	+	TTC
Ins3_7.1	CCTCGGTCAGAATAGGCTGCGTTCGCTGCTCTGGTT	7297-7332	+	TTC
Ins3_8.1	ACTCCGTTAGCAAAACGCTTTGCGAAACTGAACG	6873-6906	+	TTC
Ins3_9.1	AATACATCGGTCCTGCGCTGCTGATCGTTGGCTGC	6171-6205	+	TTC
Ins3_10.1	TTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGG	6984-7018	+	TTC

[a] Each spacer is designated with the mutant name followed by two numbers (separated by a dot). The first is the clone number, and the second indicates its location within the expanded array according to the leader (e.g. “DF60PA_1.1” is the most recently acquired spacer in clone1 of DF60PA).

[b] The positions of protospacers (from which a spacer was derived) on the HHPV-2 genome.

[c] “+” and “-” correspond respectively to the coding strand and the template strand of the *rep* gene (ORF1).

SUPPLEMENTARY DATA

Data S1. Sequencing results of different a-CRISPR constructs with spacer insertions.

Note: The mutated or inserted nucleotide(s) are in red, and the designed restriction sites (BamH1 and KpnI) are underlined. The sequences duplicated during spacer integration are framed, and duplication size may be normal (30 bp) or aberrant (29, 31, 32 or 33 bp) in different a-CRISPRs. The viral sequences from which new spacers derived are summarized in **Table S3**.

<The wild-type a-CRISPR>

(1) DF60PA clones (30-bp normal duplication)

DF60PA_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTTCGGATC
GTGGAATGAAGATGAGTCGTTCCCTGAAGTTTCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGGA

DF60PA_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGAAAAC
GTTAGATACTGACGTTGCGTCTGAAGCTAGTTTCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTTGTTTCGCGG

DF60PA_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCAGGGAAC

GACTCATCTTCATTCCACGATCCGAAGAGTTTCAGACGAACCCTCGTGGGGTTGAAGCCTTTTTGCGTATTGGACGCCCACATGGTAGCCGCCGTTTCAGACGAACCCTCGTGGGGTTGAAGCAGACGAGGCGAACGCAGCGAGGAACGTACCCATCGAGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGTTTCGCGGA

DF60PA_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTCATCCATCACGTAGCGCAGCGAACGACCAGCACCAGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCG

DF60PA_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCATCGAGATCCGCAGCGAACTCATCATCTTGCAGCTCGTTTCAGACGAACCCTCGTGGGGTTGAAGCCCAGTGGGGAATTGACCAGTCATCTCCTGCGCGAGTTTCAGACGAACCCTCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGCTGG

DF60PA_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCGGA

DF60PA_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCATACACAAGCACAGGACACCTCCCGCGGACCCACAGGTTTCAGACGAACCCTCGTGGGGTTGAAGCAATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGG

DF60PA_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCCGCGATCTCCCGAGCGTGATCAACTGGGGGCCGAGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCTGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGG

<The TATA-lacking mutant>

(2) TATAm clones (30-bp normal duplication)

TATAm_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTTGTTTCGCGGA

TATAm_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGCTGAATTACAGTGAGCGTCGTAAGATGTTCGCTGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCGCGTTTCAGACGAACCCTCGTGGGGTTGAAGCAATACATCGGTCCTGTGCTGCTGATCGTTGGCTGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTTTCGCAGACCACGACGGGGGCCGGGTATAGCGAACGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGCTGGTTTCGCGGAC

TATAm_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGAACTTCAGACCCGAGCGCAGTATCAGCGAACGTGTTTCAGACGAACCCTCGTGGGGTTGAAGCCTGATTCGTACGTGCTGCCGTCTTGCGACGTGTTGGTTTCAGACGAACCCTCGTGGGGTTGAAGCCGCGATCTCCCGAGCGTGATCAACTGGGGGCCGAGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGTGGGTTTTCGCGGA

TATAm_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

TATAm_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGAAAACGTTAGATACTGACGTTGCGTCTGAAGCTAGTTTCAGACGAACCCTCGTGGGGTTGAAGCTTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCAACATATTCACGGACCCGATCAACGACCGACTCAGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCGG

TATAm_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCCGCTCG

CACTGGCCGGTGTCGCTCTGGCCGGTGCTGGTTTCAGACGAACCCTCGTGGGGTTGAAGCTCATCCATCACGTAGCGCAGCGAACGACCAGCACCAGTTTCAGACGAACCCTCGTGGGGTTGAAGCCCTCGGTCAGAATAGGCTGCGTTCGCTGCTCTGGTGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGGTTTCGCGGA

TATAm_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTAGGGCAGTGTACCCGCCGTTGGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGAAGCAGCGAACAGACCAGCTCGCAGGTTCCACGACCACGGGTTTCAGACGAACCCTCGTGGGGTTGAAGCCTTTTTGCGTATTGGACGCCCACATGGTAGCCGCCCGTTTCAGACGAACCCTCGTGGGGTTGAAGCCACGACCACGGCGCAGAATCATCAGGATCATACGCGTTTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGTGGTTTTCGCGGA

<Leader-Repeat Junction mutants>

(3) JCm clones (30-bp normal duplication size)

JCm_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCCGTTGGTCAGACGAACCCTCGTGGGGTTGAAGCGACCCGCGCCAACGGGTATGAGTTTGCGGCGTTCAATGGTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

JCm_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCCGTTGGTCAGACGAACCCTCGTGGGGTTGAAGCAGGTGACGAATCAGTACCGCCACCATCAGCAGCAATGGTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCGG

JCm_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCCGTTGGTCAGACGAACCCTCGTGGGGTTGAAGCTTGATGCGGTTTCACTACTGTCCGATGCGCGAGCGGTGGTCAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGTTTCGCGG

(4) JCmT clones (30-bp normal duplication size)

JCmT_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCTACCAATCAGACGAACCCTCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTCAATCAGACGAACCCTCGTGGGGTTGAAGCAAGCATAAAGGCAATGACCGCGTTTCTGAAGTGCGCAATCAGACGAACCCTCGTGG

GGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTTGGTTTCGCGGA

JCmT_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCTACCAATCAGACGAACCCTCGTGGGGTTGAAGCTTCGGAT
CGTGGAATGAAGATGAGTCGTTCCCTGACAATCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

JCmT_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCTACCAATCAGACGAACCCTCGTGGGGTTGAAGCAAGCATA
AAGGCAATGACCGCGTTTCTGAAGTGCGCAATCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCGG

JCmT_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCTACCAATCAGACGAACCCTCGTGGGGTTGAAGCAGGATCA
GACCGCATACCATACTCGAGACGCAGCGTCAATCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

JCmT_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCTACCAATCAGACGAACCCTCGTGGGGTTGAAGCAAGCATA
AAGGCAATGACCGCGTTTCTGAAGTGCGCAATCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGT

(5) JCmG clones (30-bp normal duplication size)

JCmG_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCGCAACCTCAGACGAACCCTCGTGGGGTTGAAGCACTCCGT
TAGCAAAACGCTTTGCGAAACTGAACGTACCTCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTTGTTTCGCGG

JCmG_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCGCAACCTCAGACGAACCCTCGTGGGGTTGAAGCCGGTATG
TGGCTCACCTTGAGTCCACCGGACCCACACCTCAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGTTGGTTTCGCGGA

<Important repeat mutants >

(6) Rm16-30 clones (31-bp aberrant duplication)

Rm16-30_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGACGAGGCGAACGCAGCGAGGAACGTACCCATCGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

Rm16-30_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGCGACTGAGGATATTGTTGATCCGATCACGGCGGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

Rm16-30_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGCTGTTGGTGAGGGTTCCCACCCACAAACCCACCCAGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGCTGTTTCGCGG

Rm16-30_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGTCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTGTTTCAGACGAACCCGATGTTTTGGTCCTAGTCATCCATCACGTAGCGCAGCGAACGACCAGCACCGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCGG

Rm16-30_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGCGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACCGTTTCAGACGAACCCGATGTTTTGGTCCTAGGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGGTTTCGCG

Rm16-30_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCTGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTCGCGG

Rm16-30_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGGGTCTGTGTCTCTACTGCTACGTTTCTGAAACTGAGTTTCAGACGAACCCGATGTTTTGGTCCTAGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTCGCGGAGA

Rm16-30_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGCAGCTGG
GTATTGTAATGAGTCAGAATGTTCTGCTGGTTTCAGACGAACCCGATGTTTTGGTCCTA
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTCGCGG

Rm16-30_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTTTTGGTCCTAGCCACCCA
CAAACCCACCCACCCACAGGACACCGGAGTTTCAGACGAACCCGATGTTTTGGTCCTA
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGAG

(7) Rm18-22 clones (31-bp aberrant size with one exception)

Rm18-22_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGTTGATGCG
GTTTCACTACTGTCCGATGCGCGAGCGGGTTTCAGACGAACCTCTCTCCGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGGTGTTTTCGCGG

Rm18-22_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGAGTGGTG
AGTTGACTGCGCTCGAGGAAACACAGTCGGTTTCAGACGAACCTCTCTCCGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGGTTTCGCGGA

Rm18-22_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGTGAAACT
GAATCGTCGTCTGTTCGGGAGTGGTCTGAGTTTCAGACGAACCTCTCTCCGTTGAAGC
GGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTTGTTTCGCGG

Rm18-22_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGGGAAAAC
GTTAGATACTGACGTTGCGTCTGAAGCTAGTTTCAGACGAACCTCTCTCCGTTGAAGC
GGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGA

Rm18-22_clone5 (exceptional)

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGCTGAAGAT
ATGAGTTGGTCGGAGCTGCTCGAAGAGTTTCAGACGAACCTCTCTCCGTTGAAGCGGT
ACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTGTTTCGCGG

Rm18-22_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGCGGCAGC
GGGTGGATAAACCCGGATGCCGGTGAGGAGTTTCAGACGAACCTCTCTCCGTTGAAG
CGGGTCTGCTGCTCGGTCCTGTGTGATGTCCGTCGTGCGTTTCAGACGAACCTCTCTC
CGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGGTTTCGCGGA

Rm18-22_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATTGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGCGCTTGAT
AACAGTTGGATGGCTGCGTATCAGGATGTTTCAGACGAACCTCTCTCCGTTGAAGCGG
TACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGG

Rm18-22_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCTCTCTCCGTTGAAGCGTGACTCAT
TACAATACCCAGCTGGAACAGGTGAAAGTTTCAGACGAACCTCTCTCCGTTGAAGCGG
TACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGGA

(8) Rm23-30 clones (30-bp normal duplication size)

Rm23-30_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGAAGAGG
GCACGCTGCCTGATCACGGTGAGTCGCTGGTTTCAGACGAACCCTCGTGGGACCAGG
ATGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTTGTTTCGCGG

Rm23-30_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGAAGAGG
GCACGCTGCCTGATCACGGTGAGTCGCTGTTTCAGACGAACCCTCGTGGGACCAGGAT
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGG

Rm23-30_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGTGCTGAT
CGATGAGGGCAGCACGCACTTCGATGCTGTTTCAGACGAACCCTCGTGGGACCAGGAT
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

Rm23-30_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATAGGATCA
GACCGCATACCATACTCGAGACGCAGCGGTTTCAGACGAACCCTCGTGGGACCAGGAT
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGG

Rm23-30_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATCAGTCAG
ACGCCGGTTTGTCGAGATCATGTGCATCAGTTTCAGACGAACCCTCGTGGGACCAGGA
TTGCTGAATAGCAGCGAAATACTCATTTATCGATGAGTTTCAGACGAACCCTCGTGGG
ACCAGGATGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGG

Rm23-30_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGTGGGAC
GCTTGATCCTGATGCTGATGAACAGCGTTGTTTCAGACGAACCCTCGTGGGACCAGGA
TGGTACCTTAGCGGAACTGATTCATTCGCTGTTTGACTGTTTTCGCGG

Rm23-30_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGGTAAAT
AGAGGTATCCAAAATGCAATTTTTTAAAATAGTTTCAGACGAACCCTCGTGGGACCAG
GATGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGGA

Rm23-30_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATCGCTCGC
ACTGGCCGGTGTCGCTCTGGCCGGTGCTGGTTTCAGACGAACCCTCGTGGGACCAGG
ATGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGGA

Rm23-30_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCTTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGTCTGCT
GCGGTGGTGATCGGCGTGGATACCGTCGCGTTTCAGACGAACCCTCGTGGGACCAGGA
TGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTTTCGCGG

Rm23-30_clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATCGCGATCT
CCCGAGCGTGATCAACTGGGGGCCGAGTTTCAGACGAACCCTCGTGGGACCAGGATG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Rm23-30_clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATGTGGGAC
GCTTGATCCTGATGCTGATGAACAGCGTGTTTCAGACGAACCCTCGTGGGACCAGGAT
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGGA

Rm23-30_clone12

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGACCAGGATCGACTGA
GGATATTGTTGATCCGATCACGGCGGGTTTCAGACGAACCCTCGTGGGACCAGGATGG
TACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGG

(9) Rm16-20 clones (31-bp aberrant size with one exception)

Rm16-20_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGCCCACT
GGGAACCGCAGGCAGTACACACGACATTGAGTTTCAGACGAACCCGATGTGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGGA

Rm16-20_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGACGAAT
AAGAAGATTACTGATGGCAGTGGTAATGGTTTCAGACGAACCCGATGTGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGG

Rm16-20_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTGGGA
CGCTTGATCCTGATGCTGATGAACAGCGTTTCAGACGAACCCGATGTGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Rm16-20_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGTTTAAG
AGCGAGCCTGAGGTTGCTGAGTTCTTCGGATGTTTCAGACGAACCCGATGTGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTCGCGGA

Rm16-20_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGACTCCG
TTAGCAAAACGCTTTGCGAAACTGAACGTGTTTCAGACGAACCCGATGTGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Rm16-20_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTGGGA
CGCTTGATCCTGATGCTGATGAACAGCGTTTCAGACGAACCCGATGTGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Rm16-20_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTGTTTCAGACGAACCCGATGTGGGTTGAAGCGAGGATGAGCTGGGCGAGCTGCAAGATGATGAGTTCGCGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCG

Rm16-20_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGGCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTAGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Rm16-20_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCGTGCTACCCGCTCCGGATCAACCGTACGGCCAGCCGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Rm16-20_clone10 (exceptional)

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGATGTGGGTTGAAGCAGGATCAGACCGCATACCATACTCGAGACGCAGCGTGGTTTCAGACGAACCCGATGTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

(10)Rm-GT clones (30-bp normal duplication size)

Rm-GT_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCCGACTGAGGATATTGTTGATCCGATCACGGCGGCGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGT

Rm-GT_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGT

Rm-GT_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCCGGTATGTGGCTCACCTTGAGTCCACCGGACCCACTGGTTTCAGACGAACCCGAGTTGGGTTGA

AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGA

Rm-GT_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCTTGATGC
GGTTTCACTACTGTCCGATGCGCGAGCAGGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGG

Rm-GT_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGTGAGAC
ACTTGATCCTGATGCTGATGAACAGCGTGTTTCAGACGAACCCGAGTTGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Rm-GT_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCCGGCAGC
GGGTGGATAAACCCGGATGCCGGTGAGGGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGG

Rm-GT_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGCTGAAG
ATATGAGTTGGTCGGAGCTGCTCGAAGAGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGG

Rm-GT_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCAGGATCA
GACCGCATACCATACTCGAGACGCAGCGTGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Rm-GT_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCCTGTTGG
TGAGGGTTCCCACCCACAAACCCACCCAGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Rm-GT_clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGTGCTGA
TCGATGAGGGCAGCACGCACTTCGATGCTCGTTTCAGACGAACCCGAGTTGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Rm-GT_clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCGAGTTGGGTTGAAGCGCTATACC
CGGCCCCCGTCGTGGTCTGCGAAAGAAGGTTTCAGACGAACCCGAGTTGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

(11)Dup6 clones (31-bp aberrant duplication)

Dup6 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCCGTCGC
GCAAAGCGGACAGGTATCAGGCTCAGTGGTTTCAAGACGAACCCTCGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Dup6 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCTGAAAC
TGAATCGTCGTCTGTTCGGGAGTGGTCTGGTTTCAAGACGAACCCTCGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup6 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCACGCCG
ATTAGTCCGAGCATCGAAGTGCGTGCTGGTTTCAAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Dup6 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCTCGAGC
AGGACTGTCAGTCGCAGGCAACCAAGCAACGTTTCAAGACGAACCCTCGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup6 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGCTATAT
GGCTGGCCGTACGGTTGATCCGGAGCGGTTTCAAGACGAACCCTCGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGTTTCGCGG

Dup6 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCTCTTGT
GCAGCGACAGGGGCAACGCCGCCGATCAGGTTTCAAGACGAACCCTCGTGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCG

Dup6 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCAGGTGACGAATCAGTACCGCCACCATCAGCAGCAACAGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGGTTTCGCGG

Dup6 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCG

Dup6 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGACTTGTCCGGTCTGTCGCTCGGTGGCATACCCGGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup6 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAAGACGAACCCTCGTGGGGTTGAAGCTCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTCGTTTCAAGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

(12)Del6 clones (29-bp aberrant duplication size)

Del6 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCTTTCGCAGACCACGACGGGGGCCGGGTATAGCGAGTTTCGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del6 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCCGCGATCTCCCGAGCGTGATCAACTGGGGGCCGACCGTTTCGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del6 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAGGTTTCGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGG

Del6 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCAGGTGACG
AATCAGTACCGCCACCATCAGCAGCAAGTTTCGACGAACCCTCGTGGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del6 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCAATACATCG
GTCCTGCGCTGCTGATCGTTGGCTGCGTGTTTCGACGAACCCTCGTGGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del6 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCGCTGATACT
GCGCTCGGGTCTGAAGTTCGGAAAAGTTTCGACGAACCCTCGTGGGGTTGAAGCGGT
ACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del6 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCATACAGTTT
TTTGGAGAACACATTTACGCGCTCTTGTTTCGACGAACCCTCGTGGGGTTGAAGCGGT
ACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGG

Del6 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCGGAAAACG
TTAGATACTGACGTTGCGTCTGAAGCTAGTTTCGACGAACCCTCGTGGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGG

Del6 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCGGATAGTT
GAGCACGTTGGTAATGATGTGTCTGCCGTTTCGACGAACCCTCGTGGGGTTGAAGCGG
TACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Del6 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCCGGTATGTG
GCTCACCTTGAGTCCACCGGACCCACTGTTTCGACGAACCCTCGTGGGGTTGAAGCG
GTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGG

Del6 _clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT

ATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCGCAGACCACGACGGGGGCCGGGTATAGCGAACGGAGTTTCGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Del6 _clone12

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCGACGAACCCTCGTGGGGTTGAAGCTGGTCCGGCGACGTTCGCTGATACTGCGCTCGGGTGTTTCGACGAACCCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

(13)Dup16 clones (31-bp aberrant duplication)

Dup16 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCTTTGGGATTGTACGTGATCTCTTCGCCGTCGTCGTGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Dup16 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCTCGAGCAGGACTGTCAGTCGCAGGCAACCAAGCAACGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGAA

Dup16 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCACACCAGCAGCAGCGCCAGCAGTCACACCAACGGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGAC

Dup16 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCCTTTTTGCGTATTGGACGCCCACATGGTAGCCGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGA

Dup16 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCTCTGCTGGCTGCGTTGATCGTCGTGTTACCTCTGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGGT

Dup16 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC

TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCAATAC
ATCGGTCCTGCGCTGCTGATCGTTGGCTGGTTTCAGACGAACCCTTCGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTTGTTTCGCGGA

Dup16 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCACTTG
TATTCCCTCGGTCAGAATAGGCTGCGTTCGCTGGTTTCAGACGAACCCTTCGTGGGGTT
GAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTTGTTTCGCGG

Dup16 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGCTGA
TCGGTGGTCCGTGGTCGTCTGGTGACGCTAGTTTCAGACGAACCCTTCGTGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup16 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCACTAA
GCGAGTGACGTTGACTGATGCTGGTGCGTGTTTCAGACGAACCCTTCGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

Dup16 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCCGCTC
GCACTGGCCGGTGTCGCTCTGGCCGGTGCTGGTTTCAGACGAACCCTTCGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGATTCTTGC
CAGTGCTC

Dup16 _clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCGCTAT
ATGGCTGGCCGTACGGTTGATCCGGAGCGGGTTTCAGACGAACCCTTCGTGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Dup16 _clone12

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GGAGGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCC
TTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTTCGTGGGGTTGAAGCCGGTA
TGTGGCTCACCTTGAGTCCACCGGACCCACTGTTTCAGACGAACCCTTCGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTTGTTTCGCGG

(14)Del16 clones (29-bp aberrant duplication size)

Del16_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG

GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCAATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGAT

Del16_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGGA

Del16_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCTCTTGTGCAGCGACAGGGGCAACGCCGCCGATCAGCGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTT

Del16_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGCTGATCGGTGGTCCGTGGTCGTCTGGTGACGCTAGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

Del16_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTGGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGAA

Del16_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGTGCTGATCGATGAGGGCAGCACGCACTTCGATGCTGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Del16_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGTCTGCTGCGGTGGTGATCGGCGTGGATACCGTCGCGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Del16_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGCTGAAGA

TATGAGTTGGTCGGAGCTGCTCGAAGAGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGG

Del16_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Del16_clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCATAAGGCCCGTATATCGGGCATGGTTTCAGACGAACCCCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGGGCGGGTTTCAGACGAACCCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGA

(15)Dup16-17 clones (32-bp aberrant duplication size)

Dup16 -17_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCCTGGTGCTCGCCAGATTCATCGAGATCCGCAGCGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGG

Dup16 -17_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTTGTTTCGCGG

Dup16 -17_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGAAAACGTTAGATACTGACGTTGCGACTGAAGCTAGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTTCGCGG

Dup16 -17_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCATTACAACAGTCGCGCCGCAGCGTGCGACCGTGCAGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCGGG

Dup16 -17_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGGAG

CTGTCGGTAACTGGTCCTAACGGTAATCCGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTTCGCGG

Dup16 -17_clone6

CGAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGCTATATGGCTGGCCGTACGGTTGATCCGGAGCGGGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup16 -17_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCCGTCGCGCAAAGCGGACAGGTATCAGGCTCAGCGTGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGG

Dup16 -17_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGCGCTCTAAAGCCTTCAGCCGCGCTCGCTCTTTATCGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGTTTCGCGG

Dup16 -17_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCTCATCAGCCACTTTCATCGACGTAGCACCCTCTTGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGGTTTCGCGG

Dup16 -17_clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCCGTCGCGCAAAGCGGACAGGTATCAGGCTCAGCGGTTTCAGACGAACCCTCTCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGG

(16)Dup18 clones (31-bp aberrant duplication)

Dup18_clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCCTCAAGGTTGGCAAGAACATGCAGTTAGAAGAGATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGGTGTTTTTCGCGGA

Dup18_clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCATCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCGGTCTG

TGTCTCTACTGCTACGTTTCTGAAACTGGTTTCAGACGAACCCTCGGTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGCCGTGTTTCGCGG

Dup18_clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCCTTTTTG
CGTATTGGACGCCCACATGGTATCCGCGTTTCAGACGAACCCTCGGTGGGGTTGAAGC
GGTACCTTATCGGAACTGATTCACTCGCTGTTTGACTGGTTCTCGGG

Dup18_clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCATACAG
TTTTTTGGAGAACACATTTACGCGCTCTTGTTTCAGACGAACCCTCGGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTT

Dup18_clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCGTGCTG
ATCGATGAGGGCAGCACGCACTTCGATGGTTTCAGACGAACCCTCGGTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTG

Dup18_clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCAGGATG
AGCTGGGCGAGCTGCAAGATAATGAGTTCGCGTTTCAGACGAACCCTCGGTGGGGTT
GAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGG

Dup18_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCCGGTTT
CCGTCTGATGACTTTCGGGAGCTGTCGGTAGTTTCAGACGAACCCTCGGTGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTG

Dup18_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCAAGCAT
AAAGGCAATGACCGCGTTTCTGAAGTGCGTGTTTCAGACGAACCCTCGGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTG

Dup18_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCAGTGGT
GAGTTGACTGCGCTCGAGGAAACACAGTCGGTTTCAGACGAACCCTCGGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTT

Dup18_clone10
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGGTGGGGTTGAAGCGATTGTT
GCTGTCGTCTTGATCAGGTCCGGTCGGATCGTTTCAGACGAACCCTCGGTGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAC

(17)Dup19 clones (30-bp normal duplication size)

Dup19_clone1
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGGCTGAAG
ATATGAGTTGGTCGGAGCTGCTCGAAGGTTTCAGACGAACCCTCGTTGGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTTTCGCGG

Dup19_clone2
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGTGACTCAT
TACAATACCCAGCTGGAACAGGTGAAAGTTTCAGACGAACCCTCGTTGGGGTTGAAG
GTGGGACGCTTGATCCTGATGCTGATGAACAGCGTGTTTCAGACGAACCCTCGTTGGG
GTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGATTGG

Dup19_clone3
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGAGGATCA
GACCGCATACCATACTCGAGACGCAGCGTGTTTCAGACGAACCCTCGTTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTG

Dup19_clone4
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGCGGTATGT
GGCTCACCTTGAGTCCACCGGACCCACTGGTTTCAGACGAACCCTCGTTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGA

Dup19_clone5
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGTTGATGCG
GTTTCACTACTGTCCGATGCGCGAGCGGGTTTCAGACGAACCCTCGTTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTT

Dup19_clone6
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGGAACGTA
CGCACGACGGACATCACACAGGACCGAGCGTTTCAGACGAACCCTCGTTGGGGTTGA

AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTG

Dup19_clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGATCGACGT
AGCACCCTCTTGGATTGCAGACTTAAGGGTTTCAGACGAACCCTCGTTGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTTGTTTCGCGG

Dup19_clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGCTACAAA
CCGTTGGTGTGACTGCTGGCGCTGCTGGTTTCAGACGAACCCTCGTTGGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTTGTTTCGCGGA

Dup19_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTTGGGGTTGAAGAGAAAGG
TACGACGTACGACCCGACGACGTGGGATGTTTCAGACGAACCCTCGTTGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGGG

(18)Dup20 clones (30-bp normal duplication size)

Dup20 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGCTACAAA
CCGTTGGTGTGACTGCTGGCGCTGCTGCTGTTTCAGACGAACCCTCGTGGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

Dup20 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGCCACCCA
CAAACCCACCCACCCACAGGACACCGGAGTTTCAGACGAACCCTCGTGGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAG

Dup20 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGGACTTGT
CCGGTCTGTCGCTCGGTGGCATACCCGGTTTCAGACGAACCCTCGTGGGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGG

Dup20 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGTCGATCA
CCGTGCGAAACGTCGCCGCGCTCGCCTCGGTTTCAGACGAACCCTCGTGGGGGTTGA

AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGATTTCGCGG

Dup20 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGTCTGCTG
GCTGCGTTGATCGTCGTGTTACCTCTGGTTTCAGACGAACCCTCGTGGGGGTTGAAGC
GGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTG

Dup20 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGGTACACG
TTGACCGGGCAGCATGCCGTTGTCGCGTCGAGTTTCAGACGAACCCTCGTGGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGG

Dup20 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGGAATCATT
AGCGAGATATGCAGCAGCATACGAAGCGTTTCAGACGAACCCTCGTGGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup20 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGACTAATA
AGAGGATTACTGATGGCTGTGGTAATGAGTTTCAGACGAACCCTCGTGGGGGTTGAAG
CGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGCTTTTCTTCGGGG

Dup20 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGCTAGTGC
TCGCCAGATTCAACGAGCAACCGATCAGGGTTTCAGACGAACCCTCGTGGGGGTTGA
AGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGG

Dup20 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGGTTGAAGTTTAACA
CCGAGCCTAAAGGTGCTGAGTTCTTCGGGTTTCAGACGAACCCTCGTGGGGGTTGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

(19)Dup21-25 clones (30-bp normal duplication size)

Dup21-25 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTAGTGGTG
AGTTGACTGCGCTCGAGGAAACACAGTCGGGTTTCAGACGAACCCTCGTGGGGTTGG

GTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTTCATCCATCACGTAGCGCAGCGAACGACCAGCACCGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTTCGATCACCGTGCGAAACGTCGCCGCGCTCGCCTCGAGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTTTTCGCAGACCACGACGGGGGCCGGGTATAGCGAACGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAACGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTGCGCTTTTCTGTCGAGCCAGACGAATCTTCAACAGTGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTANCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTGCGCTCTTGTTCAGGTGACGAATCAGTACCGCCACCGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGTTTCGCGGA

Dup21-25 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTCGGTATGTGGCTCACCTTGAGTCCACCGGACCCACTGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Dup21-25 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGGTGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTGACCCGCGCCAACGGGTATGAGTTTGCGGCGTTCAAGCGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGTTTCGCGGA

Dup21-25 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTCGACTGAGGATATTGTTGATCCGATCACGGCGGCGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

Dup21-25 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGTGGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGG.

Dup21-25 _clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGGGTTGGGTTAGGGGCAACAGCAGAATCAGGTATCGGAACGTCACCGTTTCAGACGAACCCTCGTGGGGTTGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGG

(20)Del21-25 clones (30-bp normal duplication size)

Del21-25 _clone1

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGAAGAGGGCACGCTGCCTGATCACGGTGAGTCGCTGGTTTCAGACGAACCCTCGTGGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTTGTTTCGCGG

Del21-25 _clone2

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGTCGAGAATGCGATTGCTGATGCTGATTCTGGTCCGTTTCAGACGAACCCTCGTGGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGA

Del21-25 _clone3

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGGATAGTTGAGCACGTTGGTAATGATGTGTCTGCCTGGTTTCAGACGAACCCTCGTGGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del21-25 _clone4

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGGATAGTTGAGCACGTTGGTAATGATGTGTCTGGTTTCAGACGAACCCTCGTGGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGG

Del21-25 _clone5

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGTCTTGC
GGTGATTGCTGCTGAGTCTGACTGCGGTAGTTTCAGACGAACCCTCGTGGAAGCGGTA
CCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGTTTCGCGG

Del21-25 _clone6

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGGATAGT
TGAGCACGTTGGTAATGATGTGTCTGCCTGTTTCAGACGAACCCTCGTGGAAGCGGTA
CCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGTTTCGCGGA

Del21-25 _clone7

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACAGCAGAA
CATTCTGACTCATTACAATACCCAGCTGGTTTCAGACGAACCCTCGTGGAAGCGGTAC
CTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGGA

Del21-25 _clone8

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGCCAAAC
ACAGCTCGAGCTGCAAGAAGAGTCTCAAGTTTCAGACGAACCCTCGTGGAAGCGGTA
CCGTACCCGCCGACTTGCCGACGCTTTCCGGTATGGTTTCAGACGAACCCTCGTGGAA
GCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

Del21-25 _clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACTTGCGCG
AGCGCGAGGTTCGCTGTAATGCGATTGTCCGTTTCAGACGAACCCTCGTGGAAGCGGT
ACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGG

Del21-25 _clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCGTGGTTTCAGACGAACCCTCGTGGAAGCGGTACAGTGGTG
AGTTGACTGCGCTCGAGGAAACACAGTCGGTTTCAGACGAACCCTCGTGGAAGCGGT
ACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGA

Del21-25 _clone11

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCGTGGAAGCGGTACGCAGACC
ACGACGGGGGCCGGGTATAGCGAACGGACAGTTTCAGACGAACCCTCGTGGAAGCGG
TACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTTGGTTTCGCGG

(21) Ins3_clones (33-bp normal duplication size)

Ins3_clone1
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCCGGTA
TGTGGCTCACCTTGAGTCCACCGGACCCAGTTTCAGACGAACCCTCTCCGTGGGGTTG
AAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGA

Ins3_clone2
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGCTG
TCTTTCGTCGAGAATGCGATTGCTGATGCTGGTTTCAGACGAACCCTCTCCGTGGGGTT
GAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGAGG

Ins3_clone3
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCCGTA
CCCGCCGACTTGCCGACGCTTTCCGGTATGTGGTTTCAGACGAACCCTCTCCGTGGGG
TTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGA

Ins3_clone4
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCAAGC
ATAAAGGCAATGACCGCGTTTCTGAAGTGCGGTTTCAGACGAACCCTCTCCGTGGGGT
TGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGTTA

Ins3_clone5
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGAAT
CATTAGCGAGATATGCAGCAGCATACGAAGGTTTCAGACGAACCCTCTCCGTGGGGTT
GAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGGA

Ins3_clone6
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGTGC
TGATCGATGAGGGCAGCACGCACTTCGATGGTTTCAGACGAACCCTCTCCGTGGGGTT
GAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTTGTTTCGCGGAA

Ins3_clone7
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG
GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTT
ATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCCCTC
GGTCAGAATAGGCTGCGTTCGCTGCTCTGGTTGTTTCAGACGAACCCTCTCCGTGGGG
TTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGCTGTTTCGCGGGA

Ins3_clone8
GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGG

GAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCACTCCGTTAGCAAAACGCTTTGCGAAACTGAACGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGG

Ins3_clone9

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCAATACATCGGTCCTGCGCTGCTGATCGTTGGCTGCGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGACTGGTTTCGCGGGAA

Ins3_clone10

GAAAATCACGGTTTCTTGCTATTGCCCAGGATCCTCGGTTTCCGTCGACCCCCCGGGGGGAAGCACCTTATTGATGGTCGACGGAAGGTCTTTACTGTGACCCGCCGTTAGCAGCCTTATGGCCCGTATATCGGGCATGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCTTTAAGAGCGAGCCTGAGGTTGCTGAGTTCTTCGGGTTTCAGACGAACCCTCTCCGTGGGGTTGAAGCGGTACCTTAGCGGAACTGATTCAGTCGCTGTTTGAGTGGTTTCGCGGA

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