Table S1: Examples of applications of RNAi in mosquitoes

Delivery	Mosquito Species	Target	Effect	RNAi trigger	Reference
Microinjection	*An. gambiae*, larvae	*OR7, OR40, IR76b*	Impaired olfaction	siRNA	(Liu et al. 2010)
	An. gambiae, larvae	*TRPA1*	Impaired thermosensation	siRNA	(Liu & Zwiebel 2013)
	An. gambiae, pupae	*SRPN2*	Increased hemocoel tumors by 93.5%, and 26.7% reduction in adult emergence of knockdown mosquitoes	dsRNA	(Regna et al. 2016)
	An. gambiae, adult	*SRPN2*	90% reduction in *Plasmodium berghei* but not *Plasmodium falciparum* in midgut	dsRNA	(Michel et al. 2006)
	An. gambiae, adult	*AgApy*	Unsuccessful	dsRNA	(Boisson et al. 2006)
	An. stephensi, embryo	*EGFP*	73% knockdown efficiency of EGFP	dsRNA	(Brown et al. 2003)
	Ae. aegypti, larvae	*Fez2* and *Irc*	Neuronal defects, high adult and larvae mortality	siRNA	(Hapairai et al. 2017)
	Ae. aegypti, larvae	*AeSCP-2*	Mortality in first 3 days of emergence, reduction in cholesterol, reduction in percentage of eggs hatching from treated females	siRNA	(Blitzer et al. 2005)
	Ae. aegypti, adult and pupae	*AaGr1*, *AaGr2*	74 -86% reduction of gene expression	dsRNA	(Erdelyan et al. 2012)
	Ae. aegypti, adult	*Cactus, Caspar*	Fourfold reduction in dengue virus load	dsRNA	(Xi et al. 2008)
	Ae. aegypti, adult	*AeIMUC1* and *SDR*	36.5% reduction in *Plasmodium gallinaceum* eggs in *dsSDR*-treated females and 52.3% reduction of *Plasmodium gallinaceum* eggs in *dsAeIMUC1* treated females.	dsRNA	(Berois et al. 2012)
	Ae. aegypti, adult	*EOF1*	60% non-melanized abnormal eggs, reduction in egg hatching, primary follicles undergo cell death in treated females	dsRNA	(Isoe et al. 2019)
	C. pipiens, adult	*per, tim, cry2, cyc* and *pdf*	Egg follicle length and ovarian lipid content reduced. RNAi had varied success per gene: *per* (40%), *tim* (25%), *cry2* (45%), *cyc* (15%) and *pdf* (60%) reduction in mRNA expression.	dsRNA	(Meuti et al. 2015)
Feeding/soaking	*Ae. aegypti,* larvae	*AeNAT5*	Larval growth, adult emergence	dsRNA	(Meleshkevitch et al. 2013)

	Ae. aegypti, larvae	*AaegP-gp, AaegP-gp, AaegRPS6*	Kockdown caused a significant increase in temephos toxicity (57%) and larval death	dsRNA	(Figueira-Mansur et al. 2013)
	Ae. aegypti, larvae	*CHS1, CHS2, hsp83*	Affected growth	dsRNA	(Singh et al. 2013)
Chitosan/nanop articles feeding	*Ae. aegypti,* larvae	*dopal synthase*	Affected cuticle formation and caused high mortality	dsRNA	(Chen et al. 2019)
	Ae. aegypti, larvae	*sema1*	Affected olfactory development	siRNA	(Mysore et al. 2013)
	Ae. aegypti, larvae	*vg*	Affected wing development, induced high larval and adult mortality	dsRNA	(Ramesh Kumar et al. 2016)
Chitosan/nanop articles coated in agarose gel feeding	*Ae. aegypti,* larvae	*AgCHS1* and *AgCHS2*	Reduction of *AgCHS1* (by 62.8%) and *AGCH2* (by 33.8%) in foregut, midgut, hindgut, and carcass. Increased larval mortality	dsRNA	(Zhang et al. 2010)
Bacterial delivery	*An. gambiae*, larvae	*sac1, Irc, otk*	Affected neuronal synapse formation, caused high larval mortality	siRNA	(Mysore et al. 2017)
	An. gambiae, larvae	*Agdsxf*	66% mRNA female *dsx* transcript reduction, 20.2% reduction in female progeny	dsRNA	(Taracena et al. 2019)
	Ae. aegypti, larvae	*vg*	Affected wing development, induced high larval and adult mortality	dsRNA	(Ramesh Kumar et al. 2016)
	Ae. aegypti, larvae	*gas8, bol, fzo, nht, zpg, dsxf*	92% sterility and low fertility in males	dsRNA	(Whyard et al. 2015)
	Ae. aegypti, larvae	*CHSA, CHSB*	Reduction in chitinous bristles on the abdominal segments, thinner cuticle with holes in the exoskeleton, light disruption in the intestine, overall chitin synthesis disruption. High larval mortality and low adult emergence	dsRNA	(Lopez et al. 2019)
Yeast delivery	*Ae. aegypti, Ae. albolpictus, An. gambiae, C. quinquefasciatus*	*Sem1a*	Neuronal defects, high larval mortality	shRNA	(Mysore et al. 2019)

	Ae. aegypti, Ae. albolpictus, An. gambiae, adult stages	*dop1*	Neuronal defects, high larval and adult mortality	shRNA	(Mysore et al. 2020)
	Ae. aegypti, larvae	*AeaJHAMT*	50% reduction in egg development	dsRNA	(Van Ekert et al. 2014)
	Ae. aegypti, larvae	*fez2, lrc*	Neuronal defects, high larval mortality	siRNA	(Hapairai et al. 2017)
Algal delivery	*An. stephensi*, larvae	*3-HKT*	40% increased larval mortality	dsRNA	(Kumar et al. 2013)
Viral delivery	*Ae. albopictus,* larvae	*v-ATPase subunit A*	70% reduction in gene expression, reduced survival in treated larvae	siRNA	(Gu et al. 2011)
Dehydration/ hydration	*C. pipiens,* larvae	*hsp90*	Method works for fourth instar but not first instar larvae	dsRNA	(Lopez-Martinez et al. 2012)

Table S2. Examples of mutant and transgenic lines in mosquitoes

Genetic tool	Mosquito species	Transgenic/mutant line	Reference
ZFN knockout	*Ae. aegypti*	Multiple *ORCO*$^{-}$ mutant lines. Mutant mosquitoes have impaired olfactory perception.	(Degennaro et al. 2013)
	Ae. aegypti	*GR3*$^{-}$ and *GR3*$^{pUb\text{-}ECFP}$ mutant lines. *GR3*$^{pUb\text{-}ECFP}$ has *polyubiquitin promoter-ECFP* construct inserted into the *GR3* gene, providing a visual marker for mutant individuals. Mutant mosquitoes have impaired CO_2 perception.	(McMeniman et al. 2014)
	Ae. aegypti	*TRPA1*$^{pUb\text{-}ECFP}$ and *GR19*$^{pUb\text{-}DsRed}$ mutant lines, marked with *ECFP* or *DsRed*, respectively, driven by *polyubiquitin* promoter. *TRPA1*$^{pUb\text{-}ECFP}$ mutants had impaired high temperature sensitivity. *GR19*$^{pUb\text{-}DsRed}$ mutants had no detectable defects in thermosensation.	(Corfas et al. 2015)
TALEN knockout	*Ae. aegypti*	Multiple *kmo*$^{-}$ mutant lines. Mutant mosquitoes have white eye color as larvae, pupae, and adults.	(Aryan et al. 2013)
	A. gambiae	Multiple *TEP1*$^{-}$ mutant lines. Mutant mosquitoes have increased susceptibility to *Plasmodium* infection.	(Smidler et al. 2013)
CRISPR-Cas9 knockout	*A. gambiae*	Mutants of immunity gene *FREP1*$^{-}$. Mutant mosquitoes supress *Plasmodium* infection, but also have delayed development and reduced fitness.	(Dong et al. 2018)
	A. gambiae	*AGAP009616*$^{-}$ mutant lines of a Zn- and pH-gated ion channel expressed in the mosquito midgut. Mutant mosquitoes were not viable.	(Redhai et al. 2020)
	A. stephensi	Immune gene *LRIM1*$^{-}$ mutant lines with affected microbiota, fecundity, and fertility.	(Inbar et al. 2021)
	A. funestus	*white*$^{-}$ mutants that have white eye color as adults.	(Li et al. 2018)
	A. albimanus	*white*$^{-}$ mutants that have white eye color as adults.	(Li et al. 2018)
	Ae. aegypti	Mutants in *ppk204* (AAEL010779), *ppk322* (AAEL004091), *ppk316* (AAEL000926), *ppk306* (AAEL014228), *ppk103* (AAEL002575), AAEL013647, and *wtrw* (AAAEL027478).	(Kistler et al. 2015)
	Ae. aegypti	*NPYLR7*$^{-}$ (neuropeptide Y-like receptor 7) mutants that have affected host-seeking after a blood meal.	(Duvall et al. 2019)
	Ae. aegypti	*kmo*$^{-}$ and *Met*$^{-}$ mutants, generated via transgenic expression of Cas9 and sgRNA.	(Zhu et al. 2021)
	Ae. albopictus	Multiple *kh*$^{-}$ and *yellow*$^{-}$ mutant lines that have white eye color (*kh*$^{-}$) and yellow body color (*yellow*$^{-}$).	(Liu et al. 2019)

	C. quinquefasciatus	Multiple *kmo*$^{-}$ mutant lines. Mutant mosquitoes have white eye color as larvae, pupae, and adults.	(Anderson et al. 2019)
	C. quinquefasciatus	Multiple *white*$^{-}$ mutant lines that have white eye color as adults.	(Li et al. 2020)
	C.	Video demonstration of embryo microinjection technique and production of CRISPR-Cas9 mutations by using *cycle* (*Cx.quinq, XP_001865023.1*) as an example.	(Meuti and Harrell 2020)
CRISPR-Cas9 knockout and knock-in	*A. gambiae*	*IR21a*$^{-}$ and *IR21*$^{3xP3\text{-}EYFP}$ ionotropic receptor gene mutant lines. *IR21*$^{3xP3\text{-}EYFP}$ lines is marked with *EYFP* expressed in the eyes. Mutant mosquitoes have reduced heat-seeking.	(Greppi et al. 2020)
	A. gambiae (coluzzii)	*ORCO*$^{3xP3\text{-}DsRed}$ olfactory receptor co-receptor mutant lines, marked with *DsRed* expressed in the eyes. Mutant mosquitoes have reduced olfactory perception.	(Sun et al. 2020)
	A. funestus	*white*$^{actin5c\text{-}ECFP}$ mutants that have white eye color as larvae, pupae, and adults. Mutant animals are marked with *ECFP* expressed in the midgut and gastric caecae.	(Quinn et al. 2021)
	Ae. aegypti	*IR8a*$^{pUb\text{-}DsRed}$ and *IR8a*^{attP} mutant lines in the ionotropic receptor IR8a. *IR8a*$^{pUb\text{-}DsRed}$ mosquitoes are marked with *DsRed* expression in the eyes. The mutant mosquitoes have reduced attraction to the smell of lactic acid and other volatile acids.	(Raji et al. 2019)
	Ae. aegypti	Truncated version of *fruitless* isoform, marked with *T2A-CsChrimson:tdTomato.*	(Basrur et al. 2020)
	Ae. aegypti	*op1*$^{3xP3\text{-}GFP}$, *op1*$^{3xP3\text{-}DsRed}$, *op2*$^{3xP3\text{-}GFP}$, and *op2*$^{3xP3\text{-}DsRed}$ mutants in the photoreceptors genes *op1* and *op2*. Every mutant line was labeled with GFP or DsRed expressed in the eyes. Double mutants *op1*$^{-}$*, op2*$^{-}$ have impaired vision-guided target attraction in CO_2-dependent manner.	(Zhan et al. 2021)
	C. quinquefasciatus	Generated *Vasa-Cas9* (marked with *Opie2-DsRed*) knock-in into *cardinal* (*CPIJ005949*) gene, mutating the gene and leading to an eye color phenotype. Also generated *kh*$^{-}$ knockout mutant with white eye phenotype.	(Feng et al. 2021)
	C. quinquefasciatus	*kmo*$^{Hr5/IE1\text{-}DsRed,\ 7SK\text{-}sgRNA}$ mutant lines. Mutant animals are marked with *DsRed* expression in the body. Homozygous mutant larvae have white eye color but don't survive to pupariation.	(Purusothaman et al. 2021)
CRISPR-Cas9 knockout; ReMOT Control	*A. stephensi*	Successfully targeted ECFP gene, expressed in the original transgenic line. Mutants were made by employing ReMOT Control method of injection.	(Macias et al. 2020)
	Ae. aegypti	*kmo*$^{-}$ mutants, generated with ReMOT Control method of injection. In addition, demonstrated the efficiency of P2C peptide in five other mosquito species.	(Chaverra-Rodriguez et al. 2018)
	C. pipiens	*kmo*$^{-}$ mutants, generated with ReMOT Control method of injection.	(Li et al. 2021)

Random transgenesis	*A. stephensi*	*Minos* transposon-mediated integration of *actin-EGFP* transgene.	(Catteruccia et al. 2000)
	A. gambiae	*piggyBac*-mediated integration of *Hr5/IE1-EGFP* transgene.	(Grossman et al. 2001)
	A. albimanus	*piggyBac*-mediated integration of *Dm_pUb-EGFP* transgene.	(Perera et al. 2002)
	Ae. aegypti	*Hermes*-mediated integration of *Drosophila cinnabar (cn)* gene to rescue white eye phenotype of *kh*- mutant line.	(Jasinskiene et al. 1998)
	Ae. aegypti	*Mariner*-mediated integration of *Drosophila cinnabar (cn)* gene to rescue white eye phenotype of *kh*- mutant line.	(Coates et al. 1998)
	Ae. aegypti	*piggyBac*-mediated integration of *PUb-GCamp6s* transgene marked with *OpIE2-DsRed*. Transgenic larvae were used for live Ca^{2+} imaging from muscles and neuronal tissue.	(Bui et al. 2019)
	Ae. aegypti	*piggyBac*-mediated integration of *CPA-antiZIKV_smallRNAs_array* marked with *3xP3-tdTomato*. Transgenic mosquitoes expressed Zika virus-targeting small RNAs under the control of blood-meal activated carboxypeptidase A (CPA) midgut promoter.	(Buchman et al. 2019)
	Ae. aegypti	*piggyBac*-mediated integration of *QUAS-CsChrimson::tdTomato* transgene for neuronal labeling and optogenetics when crossed with a QF2 driver.	(Sorrells et al. 2021)
	Ae. fluviatilis	*piggyBac*-mediated integration of *3xP3-EGFP* transgene.	(Rodrigues et al. 2006)
Random transgenesis; CRISPR-Cas9 knockout	*Ae. aegypti*	*Mos1*-mediated integration of *Nix_promoter-Nix* construct marked with *PUb-GFP*. Overexpression of *Nix* led to sex-conversion of females into males, and to an unexpected flightless male phenotype. To investigate this phenotype, myo-sex gene was targeted by CRISPR-Cas9.	(Aryan et al. 2020)
Random and site-directed transgenesis	*A. gambiae*	Produced an *attP* line, marked with *3xP3-ECFP*. Used it to integrate *AgCP-VIDA3* construct, marked with *3xP3-DsRed*.	(Meredith et al. 2011)
	A. gambiae	*piggyBac*-mediated integration of *nanos_promoter-modified_phiC31_intergrase-attP* transgene marked with *Hr5/IE1-DsRed2* to create a self-docking line for site-directed transgenesis. The resulting *attP* lines were subsequently used for integration of a *pattB-3xP3-ECFP* transgene.	(Meredith et al. 2013)
	Ae. aegypti	*Mos1*-mediated integration of *CPA-EGFP* transgene, marked with *3xP3-EGFP*. Transgenic mosquitoes expressed EGFP under the control of blood-meal activated carboxypeptidase A (CPA) midgut promoter.	(Franz et al. 2011)

		piggyBac-mediated integration of *attP* transgene marked with *3xP3-ECFP*. This line was later used to integrate *pattB-3xP3-DsRed, pattB-3xP3-DsRed- CPA-EGFP and pattB-3xP3-DsRed-PUb-v5B2* transgenes into a previously characterized attP26 site.	
	Ae. aegypti	*Mos1*-mediated integration of *hsp83-DsRed or hsp83-ZsGreen* transgenes, marked with *3xP3-DsRed*. Demonstrates the utility of *hsp83-FluoGeneX* construct as a new fluorescent marker.	(Webster and Scott 2021)
	Ae. albopictus	*piggyBac*-mediated integration of *3xP3-ECFP* and *attP* transgenes. The *3xP3-ECFP*,*attP* lines were subsequently successfully used for site-specific integration of *3xP3-DsRed* transgene.	(Labbé et al. 2010)
Tools for transgenesis	*A. gambiae*	This paper describes numerous plasmids, markers, etc. used by the authors for transgenesis of *A. gambiae*.	(Volohonsky et al. 2015)
TetOn/Off system; Random transgenesis	*A. stephensi*	*SRPN10-tTA* and *SRPN10-rtTA* doxycycline-sensitive driver lines, specific to midgut, hemocytes, and pericardial cells. These lines were marked with *actin5c-EGFP* and randomly integrated via *Mos1*-mediated transgenesis. *tetOP-LacZ* reporter line, marked with *actin5c-dsRed* and randomly integrated via *Mos1*-mediated transgenesis.	(Lycett et al. 2004)
GAL4/UAS system; Random transgenesis	*A. gambiae*	*CP (carboxypeptidase)-GAL4DBD::VP16* driver line, specific to midgut, marked with *3xP3-DsRed* and *UAS-Luciferase,UAS-eYFP* reporter line, marked with *3xP3-eCFP*. Both constructs were randomly integrated via *piggyBac*-mediated transgenesis.	(Lynd and Lycett 2012)
GAL4/UAS system; Site-directed transgenesis	*A. gambiae*	*HSP-GAL4* driver line, produced by enhancer-trapping and marked with *3xP3-eYFP* and *UAS-Cyp4g16_RNAi* or *UAS-Cyp4g17_RNAi* reporter lines, marked with *3xP3-eYFP*. Both constructs were integrated via *phiC31* site-directed transgenesis.	(Lynd et al. 2019)
GAL4/UAS system; Random transgenesis	*A. stephensi*	Established several driver (*PB-GAL4*, marked with *3xP3-ECFP*) and reporter (*UAS-tdTomato*, marked with *3xP3-eYFP*) lines via *piggyBac*-mediated random transgenesis. Also established *hsp70-piggyBac_transposase* marked with *3xP3-DsRed* via *Minos*-mediated random transgenesis. By crossing *GAL4* and *piggyBac_transposase* lines, re-mobilized *GAL4* and recovered several *GAL4* enhancer-trap lines with strong expression in various larval and adult tissues.	(O'Brochta et al. 2012)
GAL4/UAS system; Random transgenesis	*Ae. aegypti*	*Vg (vitellogenin)-GAL4Δ* driver line, specific to fat body, marked with *3xP3-EGFP,* and *UAS-EGFP* reporter line, marked with *3xP3-DsRed*. Both constructs were randomly integrated via *piggyBac*-mediated transgenesis.	(Kokoza and Raikhel 2011)

GAL4/UAS system; Q-system; Random transgenesis; CRISPR-Cas9 knock-in	*Ae. aegypti*	Generated *Syt1:GCaMP6s, Syt1-T2A-3XGCaMP6s*, *brp-T2A-QF2^{w}*, *Syt1-T2A-QF2-QUAS-GCaMP6s,* and *Syt1-T2A-GAL4d-UAS-GCaMP6s* by CRISPR-Cas9 knock-in for pan-neuronal live imaging. Also generated *QUAS-Syt1:tdTomato* reported line by *piggyBac* transgenesis.	(Zhao et al. 2021)
Q-system; Random transgenesis	*A. gambiae*	*piggyBac*-mediated integration of *Orco-QF2* and *QUAS-GFP* transgenes, marked with 3xP3-DsRed and 3xP3-ECFP, respectively. Animals that contain both transgenes express GFP specifically in the olfactory *Orco+* neurons.	(Riabinina et al. 2016)
Q-system; Random transgenesis	*A. gambiae*	*piggyBac*-mediated integration of *QUAS-GCamp6f* transgene that, when crossed to *Orco-QF2* line, was used for live Ca^{2+} imaging specifically from *Orco+* neurons.	(Afify et al. 2019)
Q-system; Site-directed transgenesis	*A. gambiae*	*Amt-QF2* driver line, specific to the cells that express ammonium transporter, marked with *3xP3-DsRed* and integrated in a site-directed manner.	(Ye et al. 2020)
Q-system; CRISPR-Cas9 knockout and knock-in	*A. gambiae*	QF2 driver line *IR76b-QF2* marked with *3xP3-DsRed*. *IR76b^{-}* mutant, generated by CRISPR-Cas9 insertion of *3xP3-DsRed* in the first exon.	(Ye et al. 2021)
Q-system; Random transgenesis; CRISPR-Cas9 knockout and knock-in	*Ae. aegypti*	*ppk301-T2A-QF2* driver line that expresses *QF2* under the control of endogenous ppk301 enhancer and promoter, marked with *3xP3-DsRed*. The *T2A-QF2* cassette was introduced via CRISPR-Cas9 induced break and subsequent homology-directed repair (HDR). Two reporter lines (*15x-QUAS-dTomato-T2A- GCaMP6s*, marked with *3xP3-DsRed,* and *15x-QUAS-mCD8:GFP*, marked with *3xP3-ECFP*) were generated via a *piggyBac* insertion.	(Matthews et al. 2019)
Q-system; Random and site-directed transgenesis; CRISPR-Cas9 knockout and knock-in	*Ae. aegypti*	*Mos1*-mediated integration of *QUAS-mCD8:GFP* and of *QUAS-CAMPARI2* transgenes, marked with *3xP3-ECFP*. CRISPR-Cas9 was used to produce knock-in driver lines *Orco-QF2, IR8a-QF2,* and *GR1-QF2* with and without *3xP3-DsRed* marker.	(Shankar et al. 2020)

Q-system; Random transgenesis; CRISPR-Cas9 knockout and knock-in	*Ae. aegypti*	Four driver lines *Brp-T2A-QF2, Gr4-T2A-QF2, Ir7a-T2A-QF2,* and *Ir7f-T2A-QF2* driver lines that express QF2 under the control of endogenous *Brp/GR4/IR7a/IR7f* enhancers and promoters, respectively, marked with *3xP3-DsRed*. The *T2A-QF2* cassette was introduced via CRISPR-Cas9 induced break and subsequent HDR. *15xQUAS-dTomato-T2A-TRPV1/GCaMP6s* reporter line that expresses both the dTomato fluorophore and the TRPV1 channel for chemogenetics or *GCaMP6s* for live imaging, generated via a *piggyBac* insertion. *IR7a*$^{-}$ and *IR7f*$^{-}$ mutant lines with impaired chemosensation, generated by CRISPR-Cas9 knockout.	(Jové et al. 2020)
Q-system; CRISPR-Cas9 knockout and knock-in	*Ae. aegypti*	Integrated driver+reporter line *Orco-T2A-QF2-9xQUAS-GCaMP6f*, marked with 3XP3-dsRed. This line expresses QF2, and consequently, GCaMP6f, in Orco+ olfactory neurons under the control of endogenous *Orco* enhancer and promoter. The *T2A-QF2-9xQUAS-GCaMP6f* cassette was introduced via CRISPR-Cas9 induced break and subsequent HDR.	(Zhao et al. 2020)
Q-system; split-QF; CRISPR-Cas9 knockout and knock-in	*Ae. aegypti*	QF2 driver lines *IR25a-T2A-QF2*, *IR76b-T2A-QF2*, *IR8a-T2A-QF2*, *GR3-T2A-QF2,* and *Ir25a-T2A-QF2* that express *QF2* under the control of endogenous enhancers and promoters, respectively, marked with *3xP3-DsRed*. The same approach was used to create split-QF drivers *Ir25a-T2A-QF.AD::Zip+*, marked with 3xP3-eYFP, and *Orco-T2A-Zip−::QF.DBD*, marked with *3xP3-dsRed*.	(Younger et al. 2020)
	A. gambiae	Video demonstration of embryo microinjection technique.	(Carballar-Lejarazú et al. 2021)
	C. quinquefasciatus	Video demonstration of embryo microinjection technique.	(Bui et al. 2020)

Table S3. Summary of CRISPR-Cas9 gene drives in mosquitoes

Drive Name	Species	Type	Genomic Target(s)	Construct Elements	Result	Average Drive Spread in Caged Populations	Functional Resistance?	Reference
AsMCRkh2	*A. stephensi*	Population replacement	*Kynurenine hydroxylase*	Cas9 under Vasa promoter, gRNA, DsRed fluorescent marker under *3xP3* promoter, dual anti-*Plasmodium falciparum* single-chain antibodies (m2A10 under *AsVg1* promoter, and m1C3 under *AgCPA* promoter), flanking homology regions.	Anti-*Plasmodium falciparum* single-chain antibodies were transcriptionally active upon blood feeding. Although the effects on *P. falciparum* were not tested, these antibodies have previously been shown to abolish *P. falciparum* infectivity (Isaacs et al. 2012)	~99.5% inheritance.	Yes	Gantz et al. 2015)
CRISPR^{h}	*A. gambiae*	Population suppression	*AGAP005958*	*Cas9* under *vasa2* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	Females homozygous for drive-disrupted *AGAP005958* did not lay eggs. Heterozygotes did not produce viable larvae.	94% homing rates from male parents. No larvae recovered from female parents. Costs outweigh homing rate, so expected to disappear from a population.	Yes	(Hammond et al. 2016)

CRISPR^h	*A. gambiae*	Population suppression	*AGAP007280*	*Cas9* under *vasa2* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	Females homozygous for drive-disrupted *AGAP007280* laid eggs which did not hatch. Heterozygous females' larvae production was 9.3% of wild type.	98% homing rates from both male and female parents. Starting at 50%, drive reached 75.1% frequency over four generations. When this drive was tested for 25 generations, it was found to decline to below 25% frequency by generation 25.	Yes	(Hammond et al. 2016; Hammond et al. 2017)
CRISPR^h	*A. gambiae*	Population suppression	*AGAP011377*	*Cas9* under *vasa2* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	Females homozygous for drive-disrupted *AGAP011377* did not lay eggs. Heterozygous females' larvae production was 4.6% of wild type.	Homing rates of 85% for male parents, and 69% for female parents. Costs outweigh homing rate, so expected to disappear from a population.	Yes	(Hammond et al. 2016)
Ag(QFS)1 (previously *dsxF^{CRISPRh}*)	*A. gambiae*	Population suppression	*Doublesex*	*Cas9* under *vasa* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	Heterozygous males were unaffected. Heterozygous females showed 49.8% fecundity of wild type—this was worsened when inherited from a male parent (21.7%) rather than a female (64.9%). Homozygous females replaced by non-biting, infertile, intersex phenotype. Resulting in complete population collapse, even in large cages containing age-structured populations resembling natural conditions.	Inheritance rates of 95.9% for heterozygous male parents, and 99.4% for heterozygous female parents. Drive reached 100% prevalence in caged populations.	No	(Kyrou et al. 2018; Hammond et al. 2021)

U6a-GDe exu-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6a promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *exu* promoter.	Mosquitoes carrying the drive showed the red eye marker.	Female parents: 61.3% inheritance rates. Male parents: no significant difference from Mendelian rates (*white* is sex-linked).	Yes	(Li et al. 2020)
U6b-GDe exu-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6b promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *exu* promoter.	Mosquitoes carrying the drive showed the red eye marker.	Female parents: 70.9% inheritance rates. Male parents: no significant difference from Mendelian rates (*white* is sex-linked).	Yes	(Li et al. 2020)
U6c-GDe exu-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6c promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *exu* promoter.	Mosquitoes carrying the drive showed the red eye marker. Showed low drive potential.	Female parents: 55.8% inheritance rates. Male parents: no significant difference from Mendelian rates (*white* is sex-linked).	Yes	(Li et al. 2020)
U6d-GDe exu-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6d promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *exu* promoter.	Mosquitoes carrying the drive showed the red eye marker. Showed low drive potential.	Female parents 52.5% inheritance rates. Male parents: no significant difference from Mendelian rates (*white* is sex-linked).	Yes	(Li et al. 2020)
U6b-GDe 4nitro-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6b promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *4nitro* promoter.	Mosquitoes carrying the drive showed the red eye marker.	No significant difference from Mendelian rates.	Yes	(Li et al. 2020)

U6b-GDe trunk-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6b promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *trunk* promoter.	Mosquitoes carrying the drive showed the red eye marker.	No significant difference from Mendelian rates.	Yes	(Li et al. 2020)
U6b-GDe nup50-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6b promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *nup50* promoter.	Mosquitoes carrying the drive showed the red eye marker. Female fecundity reduced by ~21.6%.	Female parents: 80.5% inheritance rates. Male parents: 66.9% inheritance rates.	Yes	(Li et al. 2020)
U6b-GDe ubiq-Cas9	*Ae. aegypti*	Population replacement	*white*	gRNA under the U6b promoter; tdTomato marker under *3xP3* promoter; homology arms. A separate construct contained *Cas9* driven by the *ubiq* promoter.	Mosquitoes carrying the drive showed the red eye marker.	Female parents: 65.5% inheritance rates. Male parents: no significant difference from Mendelian rates (*white* is sex-linked).	Yes	(Li et al. 2020)
SDGD^{011377}	*A. gambiae*	Population suppression	*AGAP011377*	*Cas9* under *vasa* promoter, gRNA under *U6* promoter, *DsRed* marker under 3xP3 promoter, I-PpoI-*eGFP* fusion under *Beta2* promoter.	Reduced fertility in females heterozygous for the drive. In a caged population, maintained a sex ratio of ~65% males, causing partial population suppression.	Average inheritance rate of 79%. When starting at 12.5% allele frequency, stable for eight generations but did not completely spread.	Not reported	(Simoni et al. 2020)
SDGD^{007280}	*A. gambiae*	Population suppression	*AGAP007280*	*Cas9* under *vasa* promoter, gRNA under *U6* promoter, *DsRed* marker under 3xP3 promoter, I-PpoI-*eGFP* fusion under *Beta2* promoter.	Heterozygotes had severely reduced fertility.	Insufficient larvae recovered to assess drive activity.	Not reported	(Simoni et al. 2020)

SDGD^{005958}	*A. gambiae*	Population suppression	*AGAP005958*	*Cas9* under *vasa* promoter, gRNA under *U6* promoter, *DsRed* marker under 3xP3 promoter, I-PpoI-*eGFP* fusion under *Beta2* promoter.	Reduced fertility in males and females heterozygous for the drive.	Average inheritance rate of 98%. High fertility costs caused drive to vanish from a caged population after two generations when starting at 12.5% allele frequency.	Not repo rted	(Simo ni et al. 2020)
SDGD^{dsx}	*A. gambiae*	Population suppression	*Doublesex*	*Cas9* under *zpg* promoter, gRNA under *U6* promoter, I-PpoI under *Beta2* promoter, *DsRed* under *3xP3* promoter.	*Doublesex* disrupted with the X-chromsome-shredding endonuclease IPpoI. No impact on fertility of male heterozygotes. Female heterozygotes had viable offspring reduced by ~30% compared to wild type. Drive led to a male-only population. Complete population collapse.	Inheritance rates of 96% from male parents and 99.9% from females. Drive prevalence reached 100% in caged populations starting at 2.5% allele prevalence (9–13 generations) and 25% allele prevalence (5–6 generations).	No	(Simo ni et al. 2020)
Rec*kh*	*A. stephensi*	Population replacement	*Kynurenine hydroxylase*	*Cas9* under *vasa* promoter, gRNA under *U6A* promoter, *GFP* under *3xP3* promoter, recoded *Kynurenine hydroxylase* sequence, *attp* sites to facilitate insertion, homology regions.	The drive disrupted *kynurenine hydroxylase* and provided a rescue sequence. Most females carrying mutated non-functional resistance alleles that did not inherit the drive lacked this rescue sequence, resulting in reduced survival, fertility, and fecundity. One functional resistance allele was reported.	~99.8% inheritance from male parents, ~57% inheritance from female parents. ≥95% (one cage had just >90%).	Yes	(Adolf i et al. 2020)

zpg-CRISPR^{h}	*A. gambiae*	Population suppression	*AGAP007280*	*Cas9* under *zpg* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	Female egg production suppressed by an average of 92% during or just after peak in drive frequency.	Females: 97.8% (paternal inheritance) and 99.1% (maternal inheritance). Males: 93.5% (paternal inheritance) and 90.6% (maternal inheritance). Reached >95% of population in 4–10 generations, then declined due to resistant alleles forming.	Yes	(Hammond et al. 2021)
nos-CRISPR^{h}	*A. gambiae*	Population suppression	*AGAP007280*	*Cas9* under *nos* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	No reported cage trial.	Females: 97.8% (paternal inheritance) and 85.2% (maternal inheritance). Males: 99.1% (paternal inheritance) and 83.6% (maternal inheritance).	Yes	(Hammond et al. 2021)
exu-CRISPR^{h}	*A. gambiae*	Population suppression	*AGAP007280*	*Cas9* under *exu* promoter, gRNA under *U6* promoter, RFP marker under *3xP3* promoter, *attp* sites to facilitate insertion, homology regions.	No reported cage trial.	No drive produced in females. For males, homing rates of 65% (paternal inheritance) and 63.1% (maternal inheritance).	Yes	(Hammond et al. 2021)

Integral gene drive	*A. gambiae*	Population replacement	*CP*	The sequence encoding the anti-*Plasmodium falciparum* peptide Scorpine was linked to the N-terminal of *CP* via a 2A autocleavage peptide. *Scorpine* was under control of the native promoter. An artificial intron encoded gRNA and *GFP* under the *3xP3* promoter. The *GFP* marker was later removed. Homology sequences flanked the construct. A separate construct contained *Cas9* driven by the *vasa* promoter, cloned into a plasmid containing *attB*, which was integrated into an *attP* docking site (E. Marois, unpublished).	Mosquitoes carrying the drive express the anti-microbial peptide Scorpine to target *P. falciparum*. The mosquito strain carrying the marker showed a reduction in *Plasmodium* prevalence, but the markerless strain showed an increased *Plasmodium* infection.	Homing rate 95.95% for marker strain. Markerless strain homing not reported.	Yes	(Hoermann et al. 2021)

Integral gene drive	*A. gambiae*	Population replacement	*APER1*	The sequence encoding the anti-*Plasmodium falciparum* peptide Scorpine was directly fused to the C-terminal of *APER1*. *Scorpine* was under control of the native promoter. An artificial intron encoded gRNA and *GFP* under the *3xP3* promoter. The *GFP* marker was later removed. Homology sequences flanked the construct. A separate construct contained *Cas9* driven by the *vasa* promoter, cloned into a plasmid containing *attB*, which was integrated into an *attP* docking site (E. Marois, unpublished).	Mosquitoes carrying the drive express the anti-microbial peptide Scorpine to target *P. falciparum*. However, Mosquitoes carrying the drive containing the marker had no significant effect on *Plasmodium* prevalence. The markerless strain showed a decrease in *Plasmodium* infectivity.	Homing rate of 95.95% for marker strain. Markerless strain homing not reported.	Yes	(Hoermann et al. 2021)

Integral gene drive	*A. gambiae*	Population replacement	*AP2*	A fusion of GFP and the sequence encoding the anti-*Plasmodium falciparum* peptide Scorpine was linked to the N-terminal of *AP2* via a 2A autocleavage peptide. *Scorpine* was under control of the native promoter. An artificial intron encoded gRNA and *cyan fluorescent protein* (*CFP*) under the *3xP3* promoter. The *CFP* marker was later removed. Homology sequences flanked the construct. A separate construct contained *Cas9* driven by the *vasa* promoter, cloned into a plasmid containing *attB*, which was integrated into an *attP* docking site (E. Marois, unpublished).	Mosquitoes carrying the drive express the anti-microbial peptide Scorpine to target *P. falciparum*. However, Mosquitoes carrying the drive containing the marker had no effect on *Plasmodium* prevalence. The markerless strain showed a decrease in *Plasmodium* infectivity.	Homing rate of 87.87% for marker strain, and 94.98% for markerless strain (difference was not statistically significant).	Yes	(Hoermann et al. 2021)
29113^{CRISPRh}	*A. gambiae*	Population suppression	*AGAP029113*	*Cas9* under *zpg* promoter, gRNA under *U6* promoter, *RFP* under *3xP3* promoter, *attp* sites to facilitate insertion homology regions.	Mosquitoes homozygous for the drive were unlikely to develop to adulthood. However, severe fitness costs to heterozygotes limited drive invasion, and the drive started to decline due to the emergence of resistant alleles.	Inheritance rates of 92.7% (maternal inheritance) and 91.3% (male paternal inheritance). Initial increase in cage population, but then a rapid decline—drive lost by generation 3.	Yes	(Fuchs et al. 2021 [preprint])