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CORRECTION Open Access

Correction to: An efficient system for homology-dependent targeted gene integration in medaka (*Oryzias latipes*)

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Please note that there are two errors present in the tables of the published article [1].

Firstly, the value '3' is missing from the 5th row of the 'GFP+' column of Table 1.

Secondly, the gene sequence given for 'Candidate #28' in Additional file 6: Table S3 is incorrect. The gene sequence should be 'TCTTCGGCCTAGACTGCGAGG'.

Table 1 Comparison of integrate efficiency among each of donor plasmids

Length of homology arms	Bait sequences	Survival at 4 dpf	No GFP	GFP+	Integrate efficiency (%)
500 bp	+	70	53	17	24.3
500 bp	–	62	56	6	9.7
40 bp	+	64	61	3	4.7
20 bp	+	110	108	2	1.9

Additional file

Additional file 6: Table S3. Potential off-target sites of 7 candidates of bait sequence that selected in the first screening and previously reported bait sequences. Potential off-target sites are defined as genomic sequence harboring up to 2 bp mismatches in the total 18 bp sequences and a NGG PAM. (XLSX 10 kb)

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Reference
1. Murakami, et al. An efficient system for homology dependent targeted gene integration in medaka (*Oryzias latipes*). 2017;3:10. https://doi.org/10.1186/s40851-017-0071-x.

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