

## Corrigendum

## ExoCET: exonuclease in vitro assembly combined with RecET recombination for highly efficient direct DNA cloning from complex genomes

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Nucleic Acids Research (2017) gkx1249, <https://doi.org/10.1093/nar/gkx1249>The authors wish to make the corrections highlighted in **bold** to Table 1 of their article. The corrections have also been made in the published article and do not affect the results and overall conclusions of the work.**Table 1.** Large genomic segments directly cloned from bacteria, mammalian cells and human blood with ExoCET

Target	Source	Genome (Mb)	Digestion enzymes	Fragment (kb)	Vector	c.f.u. (/ml)	Correct/checked
<i>plu3535-3532</i>	<i>P. luminescens</i> DSM15139	5.69	XbaI	38	pBAC2015	1815±132	12/12
<i>plu2670</i>	<i>P. luminescens</i> DSM15139	5.69	XbaI+XmaI	53	p15A	787±194	10/12
salinomycin cluster	<i>S. albus</i> DSM41398	8.38	EcoRV	106	pBeloBAC11	425±91	2/24
salinomycin cluster	<i>S. albus</i> DSM41398	8.38	Cas9	106	pBeloBAC11	260±14	1/24
<i>Wnt4</i>	Mouse melanoma B16 cell	2800.06	<b>SwaI</b>	45	p15A	76±16	8/25
<i>Lmbr11-Tuba1a</i>	Mouse melanoma B16 cell	2800.06	<b>SwaI</b>	53	p15A	52±6	1/12
<i>Prkar1a</i>	Mouse melanoma B16 cell	2800.06	<b>HpaI</b>	8	p15A	205±17	10/12
<i>IGFLR1-ARHGAP33</i>	Human blood	3221.49	BstZ17I	41	p15A	275±76	5/48
<i>ZBTB32-LIN37</i>	Human blood	3221.49	NdeI	45	p15A	115±35	2/48
<i>Dpy30</i>	Mouse melanoma B16 cell	2800.06	<b>BamHI+KpnI</b>	8.7	p15A	273±18	9/12
<i>DPY30</i>	HEK 293T cell	<b>3221.49</b>	SpeI	9.1	p15A	40±10	17/24
<i>DPY30</i>	Human blood	3221.49	SpeI	9.1	p15A	45±2	5/24
<i>Oct4-Venus</i>	Mouse R1 ES cells	2800.06	EcoRV+PacI	9.6	p15A	34±1	9/36
<i>Nanog-Cherry</i>	Mouse R1 ES cells	2800.06	NdeI	13	p15A	49±12	17/54
<i>Gata2-Venus</i>	Mouse GM8 ES cells	2800.06	BstZ17I	16.8	p15A	212±27	5/45
<i>MLL4</i> (1)	Mouse R1 ES cells	2800.06	SspI+SpeI	17.1	p15A	127±38	7+3/24
<i>MLL4</i> (2)						323±65	2+2/36
<i>MLL4</i> (3)						142±27	6+9/72
<i>MLL4</i> (4)						483±91	3+5/36

All experiments were done in triplicate; c.f.u. includes standard deviation and fidelity was monitored by restriction analysis of the indicated number of colonies. For the MLL4 experiments, fidelity shows the targeted allele + wt allele/colonies examined. DNA analyses are shown in Supplementary Figure S6.

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