

Supplementary Table 1. Primer sets designed for PCR amplicon synthesis and qASPCR

PCR amplicon synthesis	
<i>PLAGL1</i> F	TGCATGTTAGAAGAATCAGCCT
<i>PLAGL1</i> R	TGAGTCAGTTAGGTCAGTGTAGAGAGA
<i>ZNF331</i> F	CGCTCCAGAGGGAGGTATGT
<i>ZNF331</i> R	AAAGGCCTTCCCACAGTCCT
<i>ACTB</i> F	ACTGGAACGGTGAAGGTGAC
<i>ACTB</i> R	GTGGACTTGGGAGAGGACTG
qASPCR	
<i>PLAGL1</i> F	TGCATGTTAGAAGAATCAGCCT
<i>PLAGL1</i> R*	GTTCCCCAGTCTGTTTTTGGGA(C/T)
<i>ZNF331</i> F	CGCTCCAGAGGGAGGTATGT
<i>ZNF331</i> R*	GTGCCTTCTCTAGTAGCAGG(T/C)
Control oligonucleotides	
<i>PLAGL1</i>	TGCATGTTAGAAGAATCAGCCTGGCAAAGCAAAGCATTGTGA TTAGAATGAAGGGGAACCCAGGTAAAACAGACTGGGGAACC AATATGGATCTGCCTCTAGCATGCGGAAATATCTCTCTACACT GACCTAACTGACTCA
<i>ZNF331</i>	ATATGTGAAGGTACGCTTGAAAGACCACAGCGCTCCAGAGGG AGGTATGTCAATCAGATGATCATCAATTATGTCAAAAGGCTA CTAGAGAAGGCACCCCTCCTAA

* Allele-specific primers appear with the alternative allele-specific nucleotides at the 3' end in parentheses

Supplementary Table 2. Calculation of mean and standard deviation of LOI distribution of cells exhibiting LOI. 10%, 20% or 35% error cutoff were used to exclude the cells with mono-allelic expression.

cutoff error%	treatment	mean LOI%	stdev
10%	AZA 0 day	60%	6.5%
	AZA 1 day	93.5%	8.9%
	AZA 2 days	89%	6.4%
20%	AZA 0 day	73%	7.1%
	AZA 1 day	95.7%	8.3%
	AZA 2 days	97.6%	6.1%
35%	AZA 0 day	87%	7.4%
	AZA 1 day	97.2%	7.3%
	AZA 2 days	92.3%	5.8%

Supplementary Table 3. Accuracy of LOI measurements with different DNA copy numbers.

DNA concentration	LOI (%) (S.D. %)	LOI range (low, high)
20 ng	10.0 (1.0)	(9.0, 11.0)
2 ng	8.0 (3.0)	(5.0, 11.0)
200 pg	13.0 (3.0)	(10.0, 16.0)
100 pg	13.0 (4.0)	(9.0, 17.0)
50 pg	13.0 (10.0)	(3.0, 23.0)
20 pg	16.0 (10.0)	(6.0, 26.0)

Supplementary Figure 1. Simulation of all-or-none LOI and partial LOI models in single cells. **A.** Simulation of single cell LOI distribution with consideration of transcriptional pulsing efficiency as a Gaussian random variable. Left panel: all-or-none model; Right panel: alternative model. **B.** Simulation of single cell LOI distribution of cells with consideration of only the cells in the top 25% of total mRNA copies. Left panel: all-or-none model; Right panel: alternative model.