

Supplementary Table – The Pseudogenes of Barley

Table S1 : Metrics for pseudogenes and high-coverage (HC) pseudogenes, as well as template and parent genes in the barley genome. ptc: premature termination codon.

	pseudogene class	number	%	mean length (bp)	mean coverage (%)	mean identity (%)	on same chr. (%)	distance to parent <50kb (%)	with ptc (%)	transcribed
all	all pseudogenes	89,440		188	33.5	91.4	21.4	2.8	32.2	6,435
	duplicated	12,556	14.0	329	40.7	93.8	26.5	3.6	39.7	1,769
	processed	1,834	2.1	238	29.3	91.4	20.6	2.4	44.9	150
	chimeric	571	0.6	423	35.5	93.4	26.8	3.7	55.7	85
	single exon parent	38,424	43.9	190	46.4	90.3	20.1	2.4	33.5	2,150
	fragmented	36,055	40.3	130	17.4	91.7	21.0	2.9	27.1	2,281
HC	all pseudogenes	11,015		376	94.6	93.0	23.8	3.1	45.6	1,243
	duplicated	2,151	19.5	540	95.1	95.1	28.5	4.8	45.8	433
	processed	153	1.4	509	93.6	90.1	23.5	2.6	54.9	34
	chimeric	41	0.4	713	90.7	94.2	39.0	4.9	39.0	13
	single exon parent	8,224	74.7	329	94.8	92.5	22.5	2.8	45.3	717
	fragmented	446	4.1	378	89.8	93.3	24.0	1.8	47.3	46
template genes				number	%	mean length (bp,CDS)				
all genes		38,157		966						
parent genes		16,183	42.4	1,086						