

CoReTracker report

		Clad. Val	Reassigned	Tot. count	Telford	Tot. Genes	Use. count	Trans. Val	Rea. Genes	Rea. count	Prob
MmagnB	GCG	False	False	14	0.007779	9	11	False	1	1	0
CphanA	GCT	False	False	108	-0.342692	12	71	False	2	3	0
CgallA	GCC	False	False	12	0.193408	6	8	False	1	1	0
	GCT	False	False	86	-0.375270	11	56	False	1	2	0
MmagnA	GCG	False	False	15	0.000000	9	12	False	1	1	0
CdefoA	GCA	False	False	61	-0.537943	13	38	False	1	1	0
	GCT	False	False	88	-0.356782	11	58	False	1	2	0
MingeA	GCT	False	False	88	-0.359205	12	63	False	1	1	0
MstarA	GCA	False	False	41	-0.153314	8	34	False	1	1	0
YlipoB	GCT	False	False	98	-0.335854	12	63	False	2	3	0
YlipoA	GCT	False	False	98	-0.335854	12	63	False	2	3	0
CsalmA	GCT	False	False	86	-0.371792	11	63	False	1	1	0
CjadiA	GCT	False	False	82	-0.429176	12	62	False	1	1	0
CalimA	GCA	False	False	42	-0.421418	9	27	False	1	1	0
	GCT	False	False	109	-0.467760	12	69	False	1	2	0
NbaciA	GCA	False	False	18	-0.102809	5	13	False	1	1	0
	GCT	False	False	70	-0.291934	6	56	False	1	1	0
CsuavA	GCT	False	False	71	-0.470315	11	53	False	1	1	0
SpombA	GCT	False	False	68	-0.683305	6	40	False	1	1	0
MfariB	GCT	False	False	83	-0.176966	12	78	False	1	1	0
CcastA	GCT	False	False	57	-0.220475	6	46	False	1	1	0
PcanaA	GCT	False	False	89	-0.341248	11	71	False	1	1	0
CvartA	GCT	False	False	80	-0.404328	11	64	False	1	1	0