

No.	Abbrev.	Plant	Tissue	Illumina GA / HiSeq				Unigenes	Predicted full-length CDS
				SRA accession number	Number of raw reads	Number of cleaned reads	Average transcript read depth (reads/bp)		
3	CMA	<i>Chelidonium majus</i>	Stem	SRX096034	62,362,786	50,819,736	32.3	45,005	32,416
3a	CMA_RT	<i>Chelidonium majus</i>	Root	SRX096036	60,969,004	53,233,416	35.0	24,292	34,955