

Table S1 Sequence counts for each sample showing total reads and mapping rate.

Sample ID	mRNA + lncRNA			circRNA			miRNA	
	Total reads	Q30 (%)	Mapping rate	Total reads	Q30 (%)	Mapping rate	Total reads	Match rate (%)
DUGL-1	90944754	91.523	0.9451	89185916	93.109	0.9998	10049366	67.83
DUGL-2	89202446	91.943	0.959	107753740	93.221	0.9998	11331648	64.7
DUGL-3	83859136	90.869	0.9521	97322210	93.459	0.9997	11399364	68.75
AGL-1	94825328	93.197	0.9578	101882260	93.348	0.9997	10452382	69.28
AGL-2	56705944	88.656	0.9393	111828624	93.539	0.9997	8459156	64.8
AGL-3	83597374	91.569	0.9458	90009586	93.612	0.9997	8375536	63.72

DUGL, deep underground laboratory; AGL, above ground laboratory; Q30, phred quality score 30.