

Supplementary File 1. Mapping statistics of RRBS sequencing

Group	Sample	Batch	Sex	# raw reads	# uniquely mapped	mappability	Coverage (X)	Bisulfite Conversion Rate	CHH methylation level (Phage)
AGA	C1	I	M	61,245,798	26,149,105	42.70%	13.80	97.8%	0.58%
AGA	C14	I	F	60,628,986	26,138,791	43.11%	13.80	97.8%	0.79%
AGA	C16	II	M	35,194,500	21,533,106	61.18%	11.36	97.3%	0.56%
AGA	C25	II	F	35,804,510	21,315,575	59.53%	11.25	97.2%	0.55%
AGA	C4	II	M	36,724,538	22,271,211	60.64%	11.75	97.1%	0.78%
AGA	C7	I	F	36,724,538	19,617,804	42.95%	10.35	97.7%	0.80%
LGA	L1	I	M	58,915,794	34,345,336	58.30%	18.13	97.1%	0.72%
LGA	L2	I	M	53,518,376	31,751,105	59.33%	16.76	97.1%	0.67%
LGA	L4	I	F	57,641,385	34,250,660	59.42%	18.08	97.0%	0.72%
LGA	L6	II	F	32,523,318	19,716,676	60.62%	10.41	97.1%	0.83%
LGA	L7	II	M	30,076,719	18,526,448	61.60%	9.78	96.9%	0.81%
IUGR	U2	I	F	63,283,725	31,744,721	50.16%	16.75	97.6%	0.65%
IUGR	U4	I	M	55,009,840	28,131,913	51.14%	14.85	97.4%	0.63%
IUGR	U8	I	M	59,103,335	30,938,586	52.35%	16.33	97.5%	0.60%
IUGR	U10	II	F	28,982,758	18,244,986	62.95%	9.63	97.1%	0.75%
IUGR	U3	II	M	37,911,450	22,849,190	60.27%	12.06	97.3%	0.81%
IUGR	U5	II	F	31,465,006	19,540,179	62.10%	10.31	96.8%	0.75%

1. read length: 100 bp

2. fragment size (*in silico* mapping): 40-500bp