

BAIT	Sample	MiSeq			HiSeq		
		Raw Reads (single)	Percentage of valid reads	Percentage of reads mapped to the bait's chromosome	Raw Reads (paired)	Percentage of valid reads	Percentage of reads mapped to the bait's chromosome
Dbp	CD_ZT6_1	527216	81.47%	58.63%	4863932	64.95%	51.60%
	CD_ZT6_2	309974	78.27%	60.64%	2750690	70.26%	61.14%
	CD_ZT18_1	242789	79.12%	56.93%	2445516	69.98%	53.58%
	CD5_ZT18_2	265276	80.66%	60.58%	2364824	64.15%	52.76%
	HF2_ZT6_1	169290	80.71%	60.15%	1644970	73.06%	60.42%
	HF4_ZT6_2	336905	82.65%	65.92%	3977224	67.18%	59.64%
	HF5_ZT18_1	358540	81%	60%	4839496	64.03%	50.50%
	HF6_ZT18_2	455179	78.83%	59.68%	4301160	62.09%	49.79%
Pparg2	CD_ZT6_1	276220	78.12%	70.96%	2566128	72.34%	90.48%
	CD_ZT6_2	347929	70.26%	68.79%	4058268	89.87%	82.38%
	CD_ZT18_1	233898	73.22%	80.58%	2821612	90.06%	90.39%
	CD5_ZT18_2	404843	75.40%	64.90%	3434648	92.63%	80.57%
	HF2_ZT6_1	134548	75.92%	74.76%	1761798	91.57%	84.10%
	HF4_ZT6_2	194853	70.38%	67.50%	1798776	89.63%	81.88%
	HF5_ZT18_1	190469	76.31%	65.93%	2057684	92.01%	79.66%
	HF6_ZT18_2	116909	71.85%	63.89%	1388736	90.87%	81.62%
Ppara	CD_ZT6_1				55998198	60.94	48.28
	CD_ZT6_2				42724176	63.79	39.43
	CD_ZT18_1				31878820	63.24	38.15
	CD5_ZT18_2				58779518	62.75	40.29
	HF2_ZT6_1				28535284	72.66	40.86
	HF4_ZT6_2				40675704	63.85	55.24
	HF5_ZT18_1				67783622	64.83	47.87
	HF6_ZT18_2				62712786	62.78	41.33
Srebp1c	CD_ZT6_1				37296356	77.22	62
	CD_ZT6_2				22332310	73.15	62.31
	CD_ZT18_1				48289422	62.43	49.73
	CD5_ZT18_2				33443614	78.8	55.32
	HF2_ZT6_1				24107190	71.21	64.51
	HF4_ZT6_2				18151738	80.11	71.62
	HF5_ZT18_1				23262378	76.73	57.63
	HF6_ZT18_2				20166186	78.68	54.67