

S1 Table. Sample quality control results

DNA								
study_name	total_reads	throughput	trim_read_ percent	duplicate_p ercent	mapped_to_ref erence_percent	ontarget_ percent	avg_frag_c verage	med_frag_c verage
XB120SBM	161,590,712	16,320,661,912	0.70	12.64	99.83	66.25	119	96
XB220SBM	170,257,736	17,196,031,336	1.22	16.78	99.85	64.58	115	93
XB320SBM	174,880,604	17,662,941,004	0.28	12.06	99.84	67.63	136	109
XB520SBM	157,417,816	15,899,199,416	0.16	12.42	99.81	64.61	117	94
XB620SBM	176,123,048	17,788,427,848	0.98	16.92	99.83	62.87	118	96
XO340SBM	165,127,008	16,677,827,808	3.47	29.46	99.86	53.29	84	69
XO540SBM	194,957,398	19,690,697,198	0.18	10.67	99.87	88.39	108	88
XP100SBM	170,317,026	17,202,019,626	1.50	20.01	99.84	62.71	108	88
XP200SBM	162,917,704	16,454,688,104	9.43	35.18	99.90	50.62	68	52
XP300SBM	199,907,096	20,190,616,696	4.33	28.80	99.84	55.76	102	67
XP500SBM	171,925,580	17,364,483,580	0.51	13.63	99.82	65.12	123	101
RNA								
study_name	Total Reads	Genes Detected	Mapping Rate	Duplicate Rate of	Unique Rate of Mapped			
RB130SBM	117,131,838	19,636	0.963	0.608	0.392			
RB230SBM	107,950,474	19,477	0.970	0.462	0.538			
RB330SBM	109,670,272	19,450	0.980	0.377	0.623			
RB530SBM	110,531,668	19,635	0.977	0.434	0.566			
RB630SBM	118,647,770	19,005	0.949	0.702	0.298			

RO250SBM	108,386,648	17,698	0.951	0.784	0.216
RO350SBM	86,090,042	16,900	0.951	0.783	0.217
RO550SBM	208,237,002	19,956	0.681	0.633	0.367
RP310SBM	101,016,678	17,860	0.958	0.699	0.301
RP510SBM	114,144,028	18,913	0.970	0.528	0.472
RP610SBM	97,070,508	19,173	0.970	0.552	0.448
