

**Table S1.** Descriptive statistics for alignment parameter using HITSAT2.

GENETIC GROUP 1			
SEQUENCE ID	Raw reads	Clean Reads (Mb)	Overall alignment rate (%)
1	23,225,642	19,014,864	81.87013302
2	20,051,086	17,212,955	85.84549984
3	18,988,306	15,889,039	83.67802267
4	20,205,500	17,574,112	86.97687263
5	18,829,397	16,264,153	86.37638794
6	20,146,026	17,381,814	86.27912026
7	18,249,944	16,186,137	88.69143379
8	19,573,711	16,880,873	86.24257812
9	17,903,628	15,736,760	87.89704522
10	19,769,426	17,087,279	86.43285344
11	17,534,365	15,482,048	88.29545866
12	21,066,221	15,814,760	75.07165144
13	22,230,830	18,936,800	85.18260452
14	20,087,642	17,272,061	85.98351663
15	17,484,201	15,082,220	86.26199161
16	20,735,282	18,109,819	87.33818522
17	18,991,037	15,699,968	82.6704092
18	16,449,275	14,561,444	88.5233179
19	20,211,361	17,472,382	86.44831983
20	20,560,712	17,973,022	87.41439499
21	17,944,043	15,322,488	85.39038833
22	17,679,765	15,634,492	88.43156003
23	17,659,388	15,043,701	85.18812203
24	19,262,155	16,550,940	85.92465381
MEAN	19,368,289	16,591,005	85.66066527
GENETIC GROUP 2			
SEQUENCE ID	Reads raw	Reads cleaned (Mb)	Overall alignment rate (%)
1	8,205,798	7,254,724	88.40973175
2	12,342,938	10,774,148	87.2899791
3	11,174,277	9,899,320	88.59025063
4	9,411,232	8,328,025	88.49027417
5	10,210,766	9,017,716	88.31576397
6	10,441,025	9,227,088	88.37339246
7	10,691,977	9,361,547	87.55674465
8	8,200,461	7,328,352	89.36512228
9	10,407,413	9,191,569	88.31751945
10	9,680,276	8,322,409	85.97284829
11	10,977,085	9,747,828	88.80160808
12	9,609,337	8,581,017	89.29874142
13	9,711,313	8,588,163	88.43462259
14	8,758,872	7,734,901	88.30932796
15	10,250,216	8,932,195	87.14152951
16	9,346,752	8,236,241	88.1187497
17	12,612,367	11,168,260	88.55007153
18	8,100,136	7,143,194	88.18609959
19	9,168,261	8,114,508	88.50651176
20	9,867,034	8,820,733	89.39599276
MEAN	19,916,754	17,577,194	88.25330751