

Table S1. Genome and exome sequencing design.

Lane #	Individuals	Library Type	Target	Sequencing
1	<i>169R 171S 172S 174S</i> <i>180R 181R 186R 187R</i> <i>189S 190S 194S 195R</i> <i>199R 201R 210R 211R</i> <i>215S 220S 221R 222S</i> <i>226S</i> (n=21)	Nextera	Whole genome	100bp PE HiSeq (KAUST)
2	<i>169R 171S 172S 174S</i> <i>180R 181R 186R 187R</i> <i>189S 190S 194S 195R</i> <i>199R 201R 210R 211R</i> <i>215S 220S 221R 222S</i> <i>226S</i> (n=21)	Nextera	Whole genome	100bp PE HiSeq (KAUST)
3	<i>21R 22R 24S 27R 30S 35R</i> <i>44S 45R 49S 52R 60R 61S</i> <i>67S 71R 90S 91S 124S</i> <i>269S 350R 370R 374R</i> <i>385S 386R 408R</i> (n=24)	Nextera	Whole genome	100bp PE HiSeq (KAUST)
4	<i>20S 23S 31R 36S 66S 74R</i> <i>76R 77S 87R 89R 119S</i> <i>127R 147S 152R 198R</i> <i>219R 225S 227R 278R</i> <i>348S 359R 361R 362S</i> <i>381S 400S</i> (n=25)	Nextera	Whole genome	100bp PE HiSeq (KAUST)
5	<i>93S 97S 99S 102R 103R</i> <i>104R 105R 112R 370R</i> <i>371S 372S 377S 379R</i> <i>380R 381S 382S 383R</i> <i>387R 398R 399S 405S</i> <i>406R 409R 411S</i> (n=24)	TruSeq	Exome	150bp PE MiSeq (Oxford)
6	<i>94S 96R 98S 100R 106R</i> <i>213R 216S 218S 233R</i> <i>235S 236S 240R 256R</i> <i>259R 260S 261S 301R</i> <i>313S 315R 316S 324S</i> <i>326R 384S 391R</i> (n=24)	TruSeq	Exome	100bp PE HiSeq (Oxford)
7	<i>101S 107S 108S 110S</i> <i>113R 114R 166S 167R</i> <i>196R 197S 200S 212R</i> <i>271S 281S 283R 288R</i> <i>292S 298R 299R 303R</i> <i>307R 308S 311S 314R</i> (n=24)	TruSeq	Exome	100bp PE HiSeq (Oxford)

Individuals in italics were sequenced twice.