

Information on the microsatellite panel used for EAS

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Legend

- 1) CoM = code of marker
- 2) chromStart corresponding to the UCSC freeze May 2004
- 3) chromEnd corresponding to the UCSC freeze May 2004
- 4) dist = Distance to previous marker
- 5) name = repetitive sequence
- 6) count = number of repetitions recommended
- 7) the tail CATCGCTGATTGCACAT was added to the 5'-end of each forward Primer
- 8) reverse primer in 5' to 3' direction
- 9) length of PCR amplicon includes 18 bp tail

CoM	chromStart	chromEnd	dist	name	count	forwardPrimer	reversePrimer	PCR(length)
#1.0.0.0	31257596	31257623	0	AT	17,5	CATCGCTGATTTCGCACATGCCACCATACCCCACTAATT	CCGTCAAACCTTGACTGTTC	189
#1.0.0.1	31312162	31312237	54539	TTTC	10,0	CATCGCTGATTTCGCACATCCCCACAAAAACCCCTGT	CACTCCAGACGCGGCAAC	259
#1.0.0.2	31367133	31367187	54896	GT	21,0	CATCGCTGATTTCGCACATCAAGCATATCTGCCATTTGG	ATCTACCAGGGCCCAGTAGT	223
#1.0.0.2.1	31417350	31417376	50163	TTTG	8,8	CATCGCTGATTTCGCACATTCCCTTAATTTTTCTTTTTGCC	ACCATTGCACTCCAGCCT	195
#1.0.0.3	31457383	31457414	40007	GT	23,0	CATCGCTGATTTCGCACATACCACAGTCTCTATCAGTCCA	TTTCTGCGTTTTTCAGCCT	168
#1.0.0.4	31465639	31465733	8225	TC	15,5	CATCGCTGATTTCGCACATCTGGCCTGGACCTACTGTATC	AAGGGTGTCTGACACCTGAC	248
#1.0.0.5	31518185	31518230	52452	GT	11,0	CATCGCTGATTTCGCACATGTCAGGGAGGAGAGAAAAGTG	GCTGGACTCTGCTAGGACAC	220
#1.0.0.6	31562618	31562648	44388	TC	16,5	CATCGCTGATTTCGCACATCTGGCCTGGACCTACTGTATC	GCAAGAAAGGGTGTCTGAC/	190
#1.0.0.7	31579706	31579743	17058	TG	23,0	CATCGCTGATTTCGCACATAGTGTTCATTGCAGGC	CAAATCCAAACCACAATGAG	208
#1.0.0.7.1	31628000	31628046	48257	TTTTG	8,6	CATCGCTGATTTCGCACATACCTCAAGTGATCCACCCA	TGGGCGACAGAATGAGACT	173
#1.0.0.8	31685399	31685441	57353	GT	14,0	CATCGCTGATTTCGCACATGGATAACAGAACGAGACCCTG	TCAGTTGTGGTTGAAAAGAG	218
#1.0.0.9	31728077	31728116	42636	AC	18,0	CATCGCTGATTTCGCACATCTCCCACGGTGTTCAG	GAGACCGGAAGTGACGGT	155
#1.0.1.0	31787584	31787634	59468	AC	20,0	CATCGCTGATTTCGCACATCCAAGCAGCTACAGTTTGCT	GAACTCAGGATGGAGGGCT	186
#1.0.1.1	31791707	31791746	4073	GT	18,0	CATCGCTGATTTCGCACATAGTTAAGGACCAGGGAGG	AGAAAAACAGAACTGGCACA	273
#1.0.1.2	31811564	31811606	19818	CA	21,5	CATCGCTGATTTCGCACATTGCTCTCACTCTCAGGCCT	CAGCAGGGTTTAGAAGGGA	202
#1.0.1.3	31814868	31814906	3262	AC	22,5	CATCGCTGATTTCGCACATCTTTCTCCCTCATAACCCCA	GGACTCAAAGCGGTGAACA	148
#1.0.1.4	31821837	31821870	6931	TG	22,0	CATCGCTGATTTCGCACATTGGCCAGTTGTGTCCAGT	AGGCAGAGGTTGCATTGAG	152
#1.0.1.5	31885313	31885351	63443	AC	21,5	CATCGCTGATTTCGCACATTGACAGGGCGAGACTGTCT	GGAGAGTTCATGGAGAGAGC	185
#1.0.1.5.1	31949675	31949703	64324	ATTT	9	CATCGCTGATTTCGCACATCACTTACTGCCATCCTTGCA	CCTGGGTGACAGAGCAAGA	133
#1.0.1.5.2	32014195	32014255	64492	TA	33,5	CATCGCTGATTTCGCACATGGTGCCTGGAATGTAGAACAT	CGAGTTTCGCACCACTGTAGT	183
#1.0.1.6	32142832	32142941	128577	AAGA	16,5	CATCGCTGATTTCGCACATTACACTCTAGCCCAGGCGA	CCACCCACTTCCTCCACTA	217
#1.0.1.7	32153778	32153908	10837	AGAA	18,3	CATCGCTGATTTCGCACATCCTGGGCAACAGAGCTCA	CACCACGCCTGACCACAA	210
#1.0.1.7.1	32211745	32211783	57837	AAAAC	7,8	CATCGCTGATTTCGCACATGGTTGCAGTGAGCCAAGAT	CTCCTACCTTGTGCTGCTTC	179
#1.0.1.8	32287350	32287399	75567	AAAT	12,5	CATCGCTGATTTCGCACATCAGACTGGGACTCCATCTCA	TGTTAGTGGTCCCCAAGGTA	167
#1.0.1.9	32352070	32352121	64671	AT	27,0	CATCGCTGATTTCGCACATAGGTTTCATCCATGTTGTACA	GGCAAAGTCAAGAACTTCC	237
#1.0.2.0	32362237	32362251	10116	TA	13,5	CATCGCTGATTTCGCACATGAACATATGAACGCACGTGTC	CTGTGGAAAGCAGTTTGGAT	168
#1.0.2.1	32377724	32377750	15473	AAT	14,3	CATCGCTGATTTCGCACATGGACATGCTATTTTTGCATGT	CACAACACTCAACCCTGCT	262
#1.0.2.2	32442808	32442833	65058	GT	12,0	CATCGCTGATTTCGCACATTCTTTCTCAACTCTCAGGGA	ACCTCTCATTCTTGCTGGAA	178
#1.0.2.3	32442999	32443033	166	AG	26,5	CATCGCTGATTTCGCACATCTCCAGCAAGAATGAGAGGT	AGTATCCACTCACCAGGGCT	201
#1.0.2.4	32446163	32446199	3130	TA	10,5	CATCGCTGATTTCGCACATAGGGAATCAGTGGTCTACGAA	TGTTTTGAGTATGCATTGCC	201
#1.0.2.5	32449996	32450040	3797	TG	14,5	CATCGCTGATTTCGCACATGCTAGTCTGTGCCAAGGAACT	GAAGAAGGTGACCTGGACCT	164
#1.0.2.6	32505535	32505566	55495	AC	12,5	CATCGCTGATTTCGCACATCAGCTCAAGGACAAGAGAGGA	CCACATCCCAAAGACATGC	187
#1.0.2.7	32511353	32511396	5787	AC	16,0	CATCGCTGATTTCGCACATCCTCCTTCAACACACAGACAC	TGGAATCTCATCAAGGTCAG	125
#1.0.2.7.2	32663146	32663179	151750	TAAA		CATCGCTGATTTCGCACATCAACAAAGCGAGACTCCATC	GGAAATGGAGAGGCAGAAG/	195
#1.0.2.8	32721614	32721644	58435	GT	16,0	CATCGCTGATTTCGCACATCATTGAGTTGTGTGCATT	GACTGAGTCTGAGTTGGGCA	157

CoM	chromStart	chromEnd	dist	name	count	forwardPrimer	reversePrimer	PCR(length)
#1.0.2.9	32722622	32722639	978	AG	12,5	CATCGCTGATTTCGCACATCAGGGATGAAACCAACAAGAT	CAGTCGGTGTCAATTTTTCTC	227
#1.0.3.0	32778135	32778163	55496	GT	11,5	CATCGCTGATTTCGCACATTGCCCTGAGGTCTATGCTG	CAGCTCTTCTTAACCTGCCA	161
#1.0.3.1	32825101	32825141	46938	TG	10,0	CATCGCTGATTTCGCACATTCAATGATTCATGAGCCAAGA	TGCCATTCAATGTAAGCCTT/	119
#1.0.3.1.2	32949071	32949113	123930	TATT	8	CATCGCTGATTTCGCACATCCACCATGCCTGGCTAAT	GTTTGAGACCAGCCTGATCA	123
#1.0.3.2	32961966	32962013	12853	GATA	12,0	CATCGCTGATTTCGCACATGGAGTCCATTGTGGTTGGA	TCATGGTTGCTTTTCCTTCA	207
#1.0.3.3	33008385	33008409	46372	CA	11,5	CATCGCTGATTTCGCACATTCTTTCTCCCACTCCACTTCT	ATGGATGCTGCATGAGGA	207
#1.0.3.4	33074791	33074851	66382	TA	25,5	CATCGCTGATTTCGCACATGGCAACATCTCAAGTCTCTC	CTGCACAATGGAGTAATGCA	213
#1.0.3.4.2	33160605	33160661	85754	AAGG	14,2	CATCGCTGATTTCGCACATAGAGCGAGATTATGTCTCAA	GGCTGGACTAGGAGCGT	149
#1.0.3.5	33218303	33218333	57642	AT	15,5	CATCGCTGATTTCGCACATGAGTTTGAGACCAGCCTAGGA	TCCTGGGTAACCTGGGACTAC	149
#1.0.3.6	33232070	33232096	13737	AC	13,5	CATCGCTGATTTCGCACATCCATCAGCTTTATTTGGATCA	GCCCTCCTTGTGTCTTTGTT/	218
#1.0.3.7	33281727	33281753	49631	AG	13,5	CATCGCTGATTTCGCACATGGTGGAGGGCAGAATCATT	AATGTTTGCCAGGAACCTGTG	119
#1.0.3.8	33316475	33316533	34722	TG	17,5	CATCGCTGATTTCGCACATAAGGAAGTCTCAAAGGCTCTG	TTGGTATGCCACTGCACAC	140
#1.0.3.9	33321669	33321709	5136	CA	20,5	CATCGCTGATTTCGCACATTGGGCAGGACAAAAGTATTTTC	GCCACTGGAGAAGAATCAAC	142
#1.0.4.0	33410343	33410371	88634	AC	15,5	CATCGCTGATTTCGCACATCAGAGCAAGATTCCGTCTCA	GGCAGGGTTGGTTCTTTCT	157
#1.0.4.1	33453896	33453965	43525	AAAT	12,5	CATCGCTGATTTCGCACATAGAGCGAGACTCCGTCTCA	GCACAGTGATCTCGTCAGTG	173
#1.0.4.2	33485461	33485509	31496	TG	24,5	CATCGCTGATTTCGCACATGGAAGTGAAGACGGATCCA	GATAGCCCTGGGACATGGT	175
#1.0.4.3	33516845	33516900	31336	TG	13,5	CATCGCTGATTTCGCACATGTCTCCTGAGTCCCCAGAGAT	CCTAGCCAAGAATGCAGAAG	149
#1.0.4.4	33558564	33558650	41664	TATC	11,5	CATCGCTGATTTCGCACATTTGTTTGTCTTTTGGCTGTTG	AGGTTGCAGTGAGCCAAGT	201
#1.0.4.5	33570645	33570680	11995	GT	11,0	CATCGCTGATTTCGCACATGCTAACAGCTCTGATCCACG	AGGCAGAGGTTGCAGTGAG	153
#1.0.4.6	33578171	33578205	7491	TG	13,5	CATCGCTGATTTCGCACATTTATTCTCCTGCCTCAGCCT	TCCAGCATTGTGAAACCTCT	153
#1.0.4.6.1	33638415	33638451	60210	TTTA	9,2	CATCGCTGATTTCGCACATACCTCTGCTTCTGGGCT	TGAGCTGAGATCGCACCA	205
#1.0.4.7	33662781	33662810	24330	AC	15,0	CATCGCTGATTTCGCACATCCCCTGAGTGAGTGCACA	CAGATGAGGAAACTGAGGCT	216
#1.0.4.8	33689516	33689545	26706	GT	15,0	CATCGCTGATTTCGCACATGGTGTGCCAGTGTGTCTGA	ACAGCCAGGGAGAGTGTAC/	169
#1.0.4.8.2	33790633	33790667	101088	TCAT	8,8	CATCGCTGATTTCGCACATGACCTGTTTGGAAATGTAGGCT	TGGGCCCCAGAAAATTATA	133
#1.0.4.9	33827239	33827274	36572	GT	18,0	CATCGCTGATTTCGCACATGGGACAGACAACCTCTGCA	TGCCCCCTAACCTGCTTCTA	157
#1.0.5.0	33842742	33842787	15468	CA	14,5	CATCGCTGATTTCGCACATCCCCCAAACCTTAGTAGCTTCA	AACTTAGGTGCAGGCCGTA	146
#1.0.5.1	33901448	33901504	58661	ATA	13,7	CATCGCTGATTTCGCACATGAGACATTTTTGCGGCAAT	CTTCTGGGAATCATCCTGC	171
#1.0.5.2	33950685	33950725	49181	GT	18,0	CATCGCTGATTTCGCACATATGTGTGGGCATGTGAGTG	GTGTTTCTAACCTAGGACTGC	126
#1.0.5.3	34026337	34026378	75612	GT	16,5	CATCGCTGATTTCGCACATAGTCTGTGGGTCTGTATGCCT	GAACTTCCCTGGGTGAGGT	129
#1.0.5.4	34065262	34065304	38884	TC	12,0	CATCGCTGATTTCGCACATCTATGTGGCCATGGAAGTGT	ACTGCACTCTAGCCTGGGA	160
#1.0.5.5	34089739	34089759	24435	AC	10,5	CATCGCTGATTTCGCACATTGCGGAGTAGCTGGGACTA	TGCGGAGTAGCTGGGACTA	142
#1.0.5.6	34107725	34107755	17966	AC	19,0	CATCGCTGATTTCGCACATTGCGGAGTAGCTGGGACTA	GGCTTTGGAAGTCAGAAGG/	128
#1.0.5.7	34145403	34145443	37648	GT	20,5	CATCGCTGATTTCGCACATACACACTCCCGGCTTTACA	CCAAATTCCTGGGTGCAT	154
#1.0.5.8	34163555	34163596	18112	AC	21,0	CATCGCTGATTTCGCACATAGACATGCACCCCTACACAC	GCTAGCCTGGTTCTTAGGGT	154
#1.0.5.9	34173157	34173221	9561	TG	11,0	CATCGCTGATTTCGCACATCAGTGCAAAGGCCATGTG	GCAGATCCAGGCACTAAGC	205

CoM	chromStart	chromEnd	dist	name	count	forwardPrimer	reversePrimer	PCR(length)
#1.0.6.0	34186865	34186909	13644	AC	20,0	CATCGCTGATTTCGCACATCGTCTCATGCATTTGGATATC	AGTGTTCTTGCCTGTCTGAC,	188
#1.0.6.1	34187144	34187179	235	CA	12,0	CATCGCTGATTTCGCACATACTCACAGGCTCTTGGT	CACTGTTAATGCTGCCTCCA	129
#1.0.6.2	34212319	34212360	25140	AC	21,0	CATCGCTGATTTCGCACATGCTTCCAGATCCTTCGTGA	GGTGTTCCTTTCTCCTCT	203
#1.0.6.3	34230346	34230383	17986	AC	19,0	CATCGCTGATTTCGCACATAAGATGGGAGGTTAGATGGA	CTGCTTTTTGTCCCGCAT	137
#1.0.6.4	34256743	34256786	26360	AAT	14,7	CATCGCTGATTTCGCACATGTGAGCCGAGATAGTGCCA	GACTTCAGTGATCTGCCTGC	204
#1.0.6.5	34296689	34296712	39903	CA	12,0	CATCGCTGATTTCGCACATTGGTGCTTTTGCCAACTTA	AGCCTCCTGAGTAACTGGGA	195
#1.0.6.5.1	34372332	34372370	75620	ATAC	9,8	CATCGCTGATTTCGCACATCCAGACCCTGTTCGGTAAATAC	CATCGCTGGCACATATACTG	157
#1.0.6.6	34430150	34430191	57780	AC	17,5	CATCGCTGATTTCGCACATCCTATGAACAGCCATTGCAC	GATTACAGGCGTGAGCCAC	146
#1.0.6.7	34434014	34434047	3823	AC	17,0	CATCGCTGATTTCGCACATCCTCCAAGGTTTCTTACCCA	TGGGAAGTTTCAACATCCTG	178
#1.0.6.8	34472071	34472095	38024	AC	25,0	CATCGCTGATTTCGCACATGGACCCTGTCTCAAAACACAC	CACTGTCCCTGGCCTAGAAT	174
#1.0.6.9	34480476	34480525	8381	AC	12,0	CATCGCTGATTTCGCACATTACTGATACATCCCGGACA	CATGTGGAGAGGAGCAGGT	122
#1.0.7.0	34526036	34526070	45511	AAT	11,7	CATCGCTGATTTCGCACATGCCAAGATCATGCCATTGT	GGCCTCTCAAAGTGTGGA	161
#1.0.7.1	34538170	34538215	12100	GT	23,0	CATCGCTGATTTCGCACATGGAAGCATGGAAGTTGTGTC	GCTTCCCTAAAGCTGAATTC,	187
#1.0.7.2	34539237	34539268	1022	CAT	10,7	CATCGCTGATTTCGCACATTTGCAATAACCCTATGAGGC	ATGGCAACAGCACCTACCT	155
#1.0.7.2.1	34573794	34573834	34526	TGTT	10,2	CATCGCTGATTTCGCACATGAATCACCTGGAGAACCCTGA	GACAGAGGGAGACCACGTC	158
#1.0.7.2.2	34688972	34689003	115138	AAC	10,7	CATCGCTGATTTCGCACATGGGTGACAGAGTGAGACCCT	TGGATGTGAGCTCCAACCTA	159
#1.0.7.3	34749583	34749613	60580	AC	16,0	CATCGCTGATTTCGCACATGGGTGACAGAGAGATCCTGTC	CTCACCCATTTCTGTTCT	152
#1.0.7.3.1	34782160	34782193	32547	AAAAC	9	CATCGCTGATTTCGCACATTGGCAACAGTGCAAGACTCT	GGAGTCTCTCTGTTGCCAT	173
#1.0.7.3.2	34841161	34841209	58968	ATTT	11,8	CATCGCTGATTTCGCACATTCCCTTTCTCCTTCCTGGA	GCAATGGAGCAAGACTCAAT	150
#1.0.7.3.3	34877452	34877491	36243	TTTA	9,8	CATCGCTGATTTCGCACATGAAGCATTGTCCCTTGTCT	GAGACAGAGCGAGACTCCG	208
#1.0.7.3.4	34928289	34928337	50798	CCTCT	9,8	CATCGCTGATTTCGCACATGCAAGACAAAGTCCCCTGTAT	TGGGATAGCCAAAGGAATG	183
#1.0.7.4	34989375	34989406	61038	TTG	10,7	CATCGCTGATTTCGCACATGTTACCATGCCTGGCCTAA	CGGAGTTATGAGCCAAGAT	148
#1.0.7.5	34999846	34999883	10440	GT	19,0	CATCGCTGATTTCGCACATATGGCCTCCAGGATCTAT	GTCACAGACCTGGCTGGAT	167