

1 **SUPPLEMENTARY FILES**

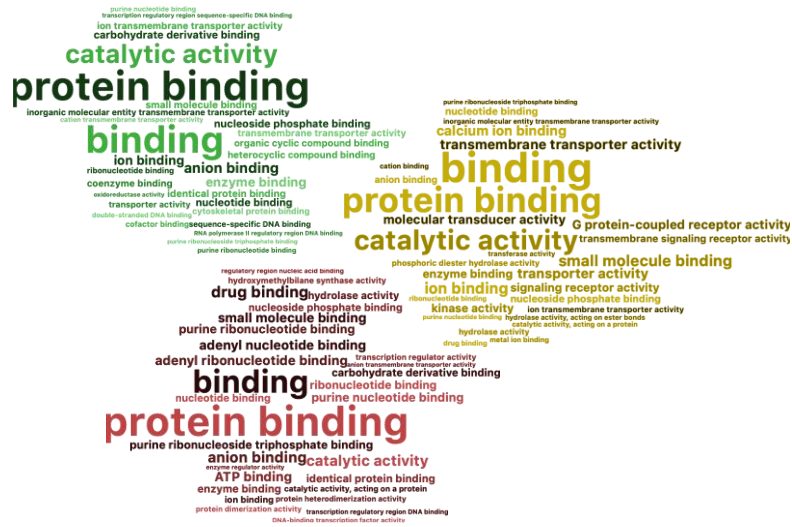
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3 **File S01 A, B and C: Annotated VCF files of all color associated SNPs obtained**
4 **through SNPEff.**

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6 **File S2:** Enrichment analysis of all color-associated SNPs with high, moderate and
7 modifier impact – actual colors corresponding to the color phenotype: bottom for red, left
8 for green and right for yellow.

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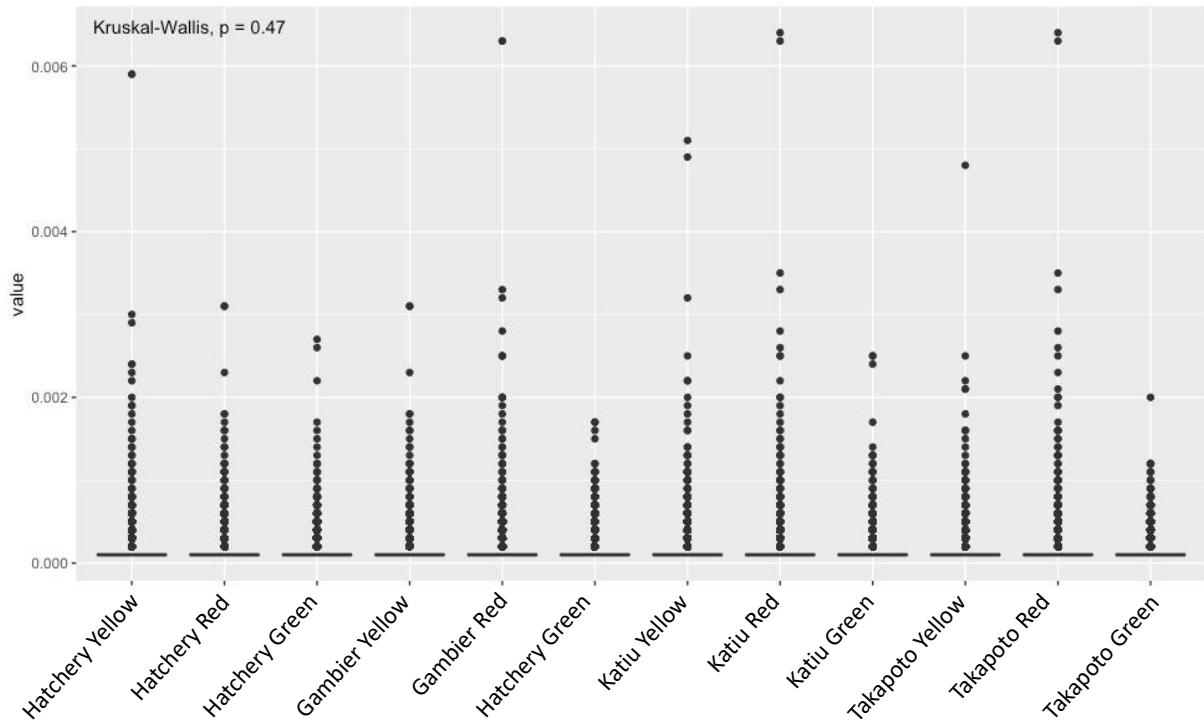
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14 **File S3:**

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16 **A:** Box plot of Pi diversity values by pool.



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B: Matrix of a pairwise Wilcoxon rank sum test. Legend: HY (Hatchery Yellow), HR (Hatchery Red), HG (Hatchery Green), GY (Gambier Yellow), GR (Gambier Red), GG (Gambier Green), KY (Katiu Yellow), KR (Katiu Red), KG (Katiu Green), TY (Takapoto Yellow), TR (Takapoto Red), TG (Takapoto Green)

	HY	HR	HG	GY	GR	GG	KY	KR	KG	TY	TR
HR	1	-	-	-	-	-	-	-	-	-	-
HG	0.91	0.91	-	-	-	-	-	-	-	-	-
GY	1	1	0.91	-	-	-	-	-	-	-	-
GR	1	1	0.91	1	-	-	-	-	-	-	-
GG	0.91	0.91	0.98	0.91	0.91	-	-	-	-	-	-
KY	0.87	0.87	0.83	0.87	0.87	0.83	-	-	-	-	-
KR	0.91	0.91	0.91	0.91	0.91	0.91	0.91	-	-	-	-
KG	0.91	0.91	0.91	0.91	0.91	0.98	0.8	0.91	-	-	-
TY	0.92	0.91	1	0.91	0.92	0.92	0.83	0.91	0.91	-	-
TR	0.91	0.91	0.91	0.91	0.91	0.91	0.91	1	0.91	0.91	-
TG	0.91	0.91	0.91	0.91	0.91	0.91	0.47	0.83	0.91	0.91	0.83

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File S4:

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A - List of all red specific SNPs, from left to right: with the transcripts code; the proteins that are encoding by genes related to pigmentation impacted by the SNPs; the SNP place corresponding to the number of base (after the underscore) in the scaffold code; reference allele; alternative allele; impact of the SNP; and allelic frequencies for red, yellow and green phenotype.

transcripts	Gene name	SNP position	R	A	Impact	Red's AF	Yellow's AF	Green's AF
scaffold605 size17310.14	Beta,beta-carotene 15,15'-dioxygenase	scaffold605 size17310.14 50152	A	T	Upstream gene	0.515715817	0.599040831	0.484628734
scaffold8173 size41510.14	Bifunctional purine biosynthesis protein PURH	scaffold8173 size41510.14 50121	G	C	Upstream gene	0.952082147	0.92797657	0.85322908
scaffold6003 size54905.10	Cytochrome P450 26A1-like	scaffold6003 size54905.10 3122	A	C	Intergenic	0.708563225	0.751351468	0.812912089
scaffold417 size388363.34	Cytochrome P450 2C8	scaffold417 size388363.34 29087	A	T	Intergenic region	0.969551485	0.900485424	0.823202804
scaffold417 size388363.34	Cytochrome P450 2C8	scaffold417 size388363.34 29355	G	T	Intergenic region	0.9649712	0.933456183	0.925194938
scaffold4234 size70448.7	Cytochrome P450 2C8	scaffold4234 size70448.7 48281	C	T	upstream_gene_variant	0.695819849	0.739572216	0.81726452
scaffold353 size151707.13	Cytochrome P450 2C8	scaffold353 size151707.13 73590	A	T	intron_variant	0.736388464	0.722691234	0.594777918
scaffold2294 size169326.2	Cytochrome P450 3A2	scaffold2294 size169326.2 2277	C	T	missense_variant	0.80854452	0.931637807	0.815174306
scaffold1969 size103037.16	Cytochrome P450 3A4	scaffold1969 size103037.16 48966	T	C	Intron	0.985897047	0.835895166	0.889425998
scaffold655 size199117.17	Cytochrome P450 4F8-like	scaffold655 size199117.17 14782	C	A	Upstream gene	0.90864899	0.841163952	0.811255693
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 130621	A	G	Intergenic region	0.828496277	0.71108361	0.581735272
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 127821	A	G	Intergenic region	0.964370267	0.866413342	0.656325175
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 107033	T	G	intron_variant	0.665903999	0.583019936	0.479498978
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 107148	A	T	intron_variant	0.700719915	0.55800332	0.422491024
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 106662	C	T	intron_variant	0.666528787	0.597087144	0.444504022
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 111879	T	C	intron_variant	0.842650282	0.748955171	0.579734848
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 104040	T	G	intron_variant	0.906324618	0.783969050	0.612682063
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 113739	C	T	intron_variant	0.857869778	0.678095861	0.498014845
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 116741	C	T	upstream_gene_variant	0.31729625	0.38986536	0.558645328
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 100892	T	C	intron_variant	0.891666667	0.756257796	0.542574586
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 116689	A	G	upstream_gene_variant	0.806575354	0.783480933	0.613256095
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 112462	T	A	intron_variant	0.964691527	0.912632539	0.825923728
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 122017	A	G	Intergenic region	0.91012863	0.756422675	0.595193177
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121550	G	T	Intergenic region	0.916733835	0.737264279	0.534016888
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 124355	G	A	Intergenic region	0.957396215	0.80659816	0.56655844
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121774	G	C	Intergenic region	0.947950646	0.804084492	0.57681704
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 123137	T	G	Intergenic region	0.804626267	0.586279246	0.449769317
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 126279	G	A	Intergenic region	0.96442361	0.842211312	0.55275763
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121759	A	T	Intergenic region	0.915761005	0.788619596	0.56212386
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 122869	A	T	Intergenic region	0.984394652	0.884359552	0.805171981
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121746	A	T	Intergenic region	0.891050505	0.752344321	0.547415527
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 124468	C	A	Intergenic region	0.985685232	0.962953617	0.905022316
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 128208	T	C	Intergenic region	0.943561984	0.760253008	0.560228902
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 128105	G	A	Intergenic region	0.985428128	0.918620935	0.873672315
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 124550	G	A	Intergenic region	0.719086399	0.504498877	0.33742903
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 123772	T	A	Intergenic region	0.945785398	0.795710513	0.584338768
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121985	A	G	Intergenic region	0.925352096	0.778086831	0.568765436
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 121822	A	T	Intergenic region	0.962972596	0.814359642	0.577639917
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 123216	A	T	Intergenic region	0.898595669	0.72984596	0.508126284
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 126338	T	C	Intergenic region	0.662421209	0.522709285	0.378684748
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 126540	A	G	Intergenic region	0.961392154	0.89636238	0.732063623
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 126540	G	A	Intergenic region	0.952428511	0.829947177	0.5693004
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 127498	A	T	Intergenic region	0.954684449	0.854040044	0.656436531
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 127334	T	C	Intergenic region	0.936801671	0.802443484	0.580567227
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 128552	A	C	Intergenic region	0.954336333	0.767631209	0.572462259
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 137696	G	A	Intergenic region	0.914337682	0.82155796	0.534197249
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140942	G	A	Intergenic region	0.961392154	0.89636238	0.732063623
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 129755	G	A	Intergenic region	0.984824511	0.835174142	0.655804647
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 130159	A	T	Intergenic region	0.863986847	0.801534235	0.63085451
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138489	G	T	Intergenic region	0.954599455	0.867370466	0.740896144
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138484	T	C	Intergenic region	0.957600393	0.865104403	0.750117283
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 136001	A	T	Intergenic region	0.98751398	0.943900539	0.768852161
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140782	T	C	Intergenic region	0.909830586	0.952312734	0.955888678
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140942	G	A	Intergenic region	0.944625038	0.897870275	0.704351157
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138391	C	T	Intergenic region	0.95385089	0.871794872	0.732637253
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141495	A	T	Intergenic region	0.981827201	0.879357452	0.740940695
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140776	T	C	Intergenic region	0.912393556	0.952485768	0.959038388
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138208	C	T	Intergenic region	0.947437442	0.886201173	0.695264776
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138828	T	C	Intergenic region	0.97053901	0.916774015	0.762742365
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 139902	A	G	Intergenic region	0.978493137	0.929313066	0.762269349
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141184	A	A	Intergenic region	0.884573413	0.755815644	0.41824383
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 143102	A	C	Intergenic region	0.822060277	0.61527692	0.347017045
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138868	A	G	Intergenic region	0.930386406	0.890933517	0.72861607
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138383	A	G	Intergenic region	0.960714286	0.875744048	0.731063134
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138396	G	T	Intergenic region	0.958122037	0.871428571	0.737155022
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138974	A	G	Intergenic region	0.910337376	0.824505609	0.498773367
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141958	T	A	Intergenic region	0.913669163	0.63682443	0.26643238
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 138639	T	T	Intergenic region	0.95542955	0.935051155	0.737635928
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140864	A	T	Intergenic region	0.963915298	0.880784103	0.764850816
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141468	A	C	Intergenic region	0.973639456	0.901566185	0.748913935
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 140816	T	C	Intergenic region	0.903081568	0.943751575	0.957636662
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 136302	G	T	Intergenic region	0.96432788	0.821428571	0.565551411
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 144298	A	T	Intergenic region	0.931163004	0.89300436	0.738821086
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141482	A	T	Intergenic region	0.974188312	0.88938406	0.44139915
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 143161	G	T	Intergenic region	0.790453964	0.6125	0.282024325
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 136367	G	A	Intergenic region	0.974725275	0.834783208	0.55027039
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 141978	C	G	Intergenic region	0.700897436	0.592152894	0.250250518
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 60430	A	T	upstream_gene_variant	0.946500247	0.864542129	0.719184464
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 61312	C	T	upstream_gene_variant	0.959698882	0.828636929	0.668843401
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 60777	A	G	upstream_gene_variant	0.614753175	0.521562778	0.447071389
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 62416	T	A	upstream_gene_variant	0.953589053	0.860411723	0.715812867
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 61305	C	T	upstream_gene_variant	0.930114796	0.811417526	0.650907236
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 63095	C	T	upstream_gene_variant	0.930512516	0.819547256	0.676493156
scaffold2460 size144317.18	porphobilinogen deaminase	scaffold2460 size144317.18 60471	T	C	upstream_gene_variant	0.724529572	0.671141008	0.519

B - List of all yellow specific SNPs, from left to right: with the transcripts code; the proteins that are encoding by genes related to pigmentation impacted by the SNPs; the SNP place corresponding to the number of base (after the underscore) in the scaffold code; reference allele; alternative allele; impact of the SNP; and allelic frequencies for red, yellow and green phenotypes.

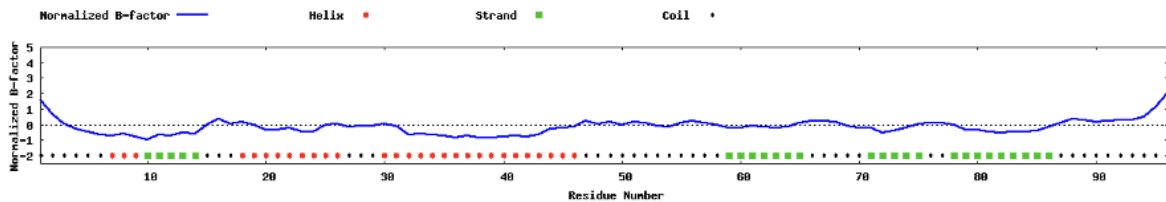
transcripts	Gene name	SNP position	R	A	impact	Red's AF	Yellow's AF	Green's AF
scaffold1219 size14984.2	amorphous calcium carbonate binding protein 1	scaffold1219 size14984.2 11628	T	G	upstream gene variant	0.925084502	0.911592087	0.962188279
scaffold1219 size14984.2	amorphous calcium carbonate binding protein 1	scaffold1219 size14984.2 11660	A	T	upstream gene variant	0.637810449	0.69471917	0.799332873
scaffold1219 size14984.2	amorphous calcium carbonate binding protein 1	scaffold1219 size14984.2 7885	T	G	downstream gene variant	0.692837846	0.655041066	0.718970047
scaffold97 size234723.4	amorphous calcium carbonate binding protein 1	scaffold97 size234723.4 13738	T	A	upstream gene variant	0.224785692	0.137438155	0.277067131
scaffold5945 size55440.1	cadherin-23 isoform X1	scaffold5945 size55440.1 53306	C	G	upstream gene variant	0.876784634	0.845343003	0.94691629
scaffold5945 size55440.1	cadherin-23 isoform X1	scaffold5945 size55440.1 49639	C	A	intron variant	0.755842297	0.760117913	0.77655209
scaffold5945 size55440.1	cadherin-23 isoform X1	scaffold5945 size55440.1 48952	T	C	missense variant	0.652283534	0.618162393	0.732375248
scaffold5945 size55440.1	cadherin-23 isoform X1	scaffold5945 size55440.1 49073	T	A	intron variant	0.873202614	0.831136468	0.914658754
scaffold7897 size43079.5	cadherin-23 isoform X1	scaffold7897 size43079.5 25046	C	A	intron variant	0.367920331	0.406697665	0.348014031
scaffold2505 size92724.2	cadherin-23 isoform X2	scaffold2505 size92724.2 60662	G	T	intron variant	0.933719291	0.934110171	0.960124105
scaffold234 size272526.38	cadherin-23-like isoform X3	scaffold234 size272526.38 207359	C	T	intergenic region	0.91686437	0.9018175	0.869123872
scaffold2505 size92724.1	cadherin-23-like isoform X3	scaffold2505 size92724.1 18810	C	T	intron variant	0.86537074	0.865843672	0.90107426
scaffold2505 size92724.1	cadherin-23-like isoform X3	scaffold2505 size92724.1 29819	A	G	intron variant	0.896043358	0.89219733	0.912491856
scaffold562 size200826.1	copper/zinc superoxide dismutase	scaffold562 size200826.1 43820	G	A	intergenic region	0.595933805	0.605798082	0.647571709
scaffold109 size389597.14	copper/zinc superoxide dismutase	scaffold109 size389597.14 223108	A	G	downstream gene variant	0.899460837	0.887365591	0.957576697
scaffold1092 size179208.14	copper/zinc superoxide dismutase	scaffold1092 size179208.14 121855	T	A	upstream gene variant	0.871486974	0.778905593	0.848507304
scaffold1092 size179208.10	copper/zinc superoxide dismutase	scaffold1092 size179208.10 89636	A	T	upstream gene variant	0.849744467	0.881638999	0.914382412
scaffold11014 size28661.2	copper/zinc superoxide dismutase	scaffold11014 size28661.2 2549	C	A	downstream gene variant	0.921393449	0.940526911	0.974760527
scaffold11014 size28661.2	copper/zinc superoxide dismutase	scaffold11014 size28661.2 2991	T	G	downstream gene variant	0.940681445	0.935659364	0.997368421
scaffold112 size675390.132	copper/zinc superoxide dismutase	scaffold112 size675390.132 51926	A	G	intergenic region	0.844551182	0.809749212	0.797894725
scaffold112 size675390.132	copper/zinc superoxide dismutase	scaffold112 size675390.132 51058	A	G	intergenic region	0.853862476	0.847902204	0.785847777
scaffold1183 size219875.2	copper/zinc superoxide dismutase	scaffold1183 size219875.2 24681	A	G	upstream gene variant	0.851810894	0.81789658	0.875464
scaffold12 size329199.6	copper/zinc superoxide dismutase	scaffold12 size329199.6 22276	C	T	upstream gene variant	0.783948928	0.793279368	0.924104344
scaffold1320 size225772.17	copper/zinc superoxide dismutase	scaffold1320 size225772.17 59142	G	T	upstream gene variant	0.937065972	0.943277367	0.92148927
scaffold1335 size119901.13	copper/zinc superoxide dismutase	scaffold1335 size119901.13 82315	A	T	intron variant	0.222696102	0.163904526	0.240279752
scaffold1412 size117757.9	copper/zinc superoxide dismutase	scaffold1412 size117757.9 38094	C	T	upstream gene variant	0.327205662	0.382240027	0.253706423
scaffold1440 size256764.20	copper/zinc superoxide dismutase	scaffold1440 size256764.20 174679	G	T	upstream gene variant	0.929672108	0.933864469	0.908771556
scaffold1440 size256764.20	copper/zinc superoxide dismutase	scaffold1440 size256764.20 175328	C	T	upstream gene variant	0.806374384	0.804032921	0.84868088
scaffold1460 size244210.17	copper/zinc superoxide dismutase	scaffold1460 size244210.17 8734	C	G	upstream gene variant	0.82466041	0.897521802	0.895020522
scaffold1498 size160682.4	copper/zinc superoxide dismutase	scaffold1498 size160682.4 53036	T	C	intron variant	0.806381844	0.823703836	0.89682858
scaffold1520 size200124.32	copper/zinc superoxide dismutase	scaffold1520 size200124.32 111755	A	T	upstream gene variant	0.880139191	0.881022192	0.939095606
scaffold1574 size113249.4	copper/zinc superoxide dismutase	scaffold1574 size113249.4 51961	T	C	intron variant	0.872314458	0.868005479	0.942884199
scaffold1890 size140805.17	copper/zinc superoxide dismutase	scaffold1890 size140805.17 92739	A	C	upstream gene variant	0.789841644	0.726411819	0.692082823
scaffold1903 size152924.21	copper/zinc superoxide dismutase	scaffold1903 size152924.21 69697	T	C	intergenic region	0.328205611	0.350407864	0.321598295
scaffold1928 size104068.10	copper/zinc superoxide dismutase	scaffold1928 size104068.10 42051	C	G	upstream gene variant	0.893775297	0.916398416	0.814064774
scaffold2390 size226504.12	copper/zinc superoxide dismutase	scaffold2390 size226504.12 57764	G	A	upstream gene variant	0.770950144	0.741096693	0.933031945
scaffold2390 size226504.12	copper/zinc superoxide dismutase	scaffold2390 size226504.12 60328	T	A	downstream gene variant	0.442775744	0.473117974	0.618027007
scaffold2456 size156049.1	copper/zinc superoxide dismutase	scaffold2456 size156049.1 24185	C	T	intergenic region	0.579226447	0.521491013	0.487870629
scaffold316 size347727.2	copper/zinc superoxide dismutase	scaffold316 size347727.2 5832	G	A	intergenic region	0.801346801	0.784443924	0.906230512
scaffold3323 size193577.9	copper/zinc superoxide dismutase	scaffold3323 size193577.9 31887	A	G	upstream gene variant	0.233744403	0.180342571	0.133627451
scaffold3858 size411225.12	copper/zinc superoxide dismutase	scaffold3858 size411225.12 59795	G	T	intergenic region	0.941745718	0.919595568	0.975282738
scaffold386 size423945.19	copper/zinc superoxide dismutase	scaffold386 size423945.19 260985	A	G	intergenic region	0.90688248	0.906473041	0.924262145
scaffold386 size423945.19	copper/zinc superoxide dismutase	scaffold386 size423945.19 385248	C	T	intergenic region	0.774021528	0.752785615	0.84186905
scaffold4103 size91226.4	copper/zinc superoxide dismutase	scaffold4103 size91226.4 37732	G	T	intergenic region	0.933780319	0.882075481	0.929166667
scaffold4160 size113367.7	copper/zinc superoxide dismutase	scaffold4160 size113367.7 7518	G	T	intron variant	0.819940106	0.82228505	0.743310553
scaffold417 size388363.30	copper/zinc superoxide dismutase	scaffold417 size388363.30 187193	C	T	intergenic region	0.614294589	0.556605471	0.714697965
scaffold4324 size150199.11	copper/zinc superoxide dismutase	scaffold4324 size150199.11 84106	G	A	downstream gene variant	0.612625475	0.644326545	0.545435123
scaffold4324 size150199.11	copper/zinc superoxide dismutase	scaffold4324 size150199.11 92727	T	A	upstream gene variant	0.325857598	0.349778653	0.5234441
scaffold4485 size144309.11	copper/zinc superoxide dismutase	scaffold4485 size144309.11 78782	C	A	downstream gene variant	0.757525178	0.765239871	0.726021411
scaffold523 size284731.6	copper/zinc superoxide dismutase	scaffold523 size284731.6 54936	T	A	intergenic region	0.86629141	0.891232175	0.966918348
scaffold5416 size239699.13	copper/zinc superoxide dismutase	scaffold5416 size239699.13 125178	T	C	upstream gene variant	0.49920093	0.496768713	0.435925209
scaffold562 size200826.1	copper/zinc superoxide dismutase	scaffold562 size200826.1 31587	G	C	intergenic region	0.895978238	0.864448384	0.861020181
scaffold626 size237541.24	copper/zinc superoxide dismutase	scaffold626 size237541.24 124713	A	G	downstream gene variant	0.94443659	0.931910584	0.911318256
scaffold719 size199701.38	copper/zinc superoxide dismutase	scaffold719 size199701.38 125384	T	G	downstream gene variant	0.94597908	0.928118624	0.975097344
scaffold770 size231676.6	copper/zinc superoxide dismutase	scaffold770 size231676.6 26081	A	T	stop gained	0.886541996	0.879853271	0.949438259
scaffold770 size231676.6	copper/zinc superoxide dismutase	scaffold770 size231676.6 26087	G	A	downstream gene variant	0.834662589	0.863033463	0.933245573
scaffold770 size231676.6	copper/zinc superoxide dismutase	scaffold770 size231676.6 47169	C	A	intergenic region	0.839739719	0.847572362	0.901160720
scaffold770 size231676.6	copper/zinc superoxide dismutase	scaffold770 size231676.6 54689	G	C	intergenic region	0.92232598	0.924161255	0.958811309
scaffold818 size379131.4	copper/zinc superoxide dismutase	scaffold818 size379131.4 13952	G	A	downstream gene variant	0.925645701	0.924290077	0.981148217
scaffold937 size181198.13	copper/zinc superoxide dismutase	scaffold937 size181198.13 131636	T	C	intron variant	0.95094511	0.936696668	0.982189522
scaffold3263 size165871.16	cytochrome b5 reductase 4-like isoform X3	scaffold3263 size165871.16 73814	T	A	intergenic region	0.695305632	0.729963288	0.608682439
scaffold417 size388363.26	cytochrome P450 2C8-like	scaffold417 size388363.26 126041	T	G	upstream gene variant	0.840381663	0.849121604	0.894167564
scaffold3435 size139597.33	cytochrome P450 3A11-like isoform X1	scaffold3435 size139597.33 105262	T	C	intron variant	0.938724385	0.936388268	0.971267534
scaffold9123 size36889.1	cytochrome P450 3A11-like isoform X1	scaffold9123 size36889.1 30428	G	A	intron variant	0.95271618	0.922247958	0.955017597
scaffold5925 size155237.27	cytochrome P450 4F8-like	scaffold5925 size155237.27 135045	C	T	intergenic region	0.207410521	0.213662287	0.311173346
scaffold1749 size108746.29	hypoxanthine-guanine phosphoribosyltransferase	scaffold1749 size108746.29 82049	C	T	intron variant	0.59450892	0.631951765	0.565311005
scaffold1749 size108746.29	hypoxanthine-guanine phosphoribosyltransferase	scaffold1749 size108746.29 74624	C	T	upstream gene variant	0.496719307	0.538671197	0.599848237
scaffold337 size296661.9	laccase-4 like isoform X1	scaffold337 size296661.9 26903	T	C	upstream gene variant	0.365793187	0.359614338	0.445983161
scaffold4044 size72409.3	Laccase-6	scaffold4044 size72409.3 7801	T	G	upstream gene variant	0.89961108	0.894926839	0.801538897
scaffold2334 size95770.2	tyrosinase B3.2	scaffold2334 size95770.2 50948	A	T	intergenic region	0.928754309	0.916319428	0.870859528
scaffold2426 size145584.3	tyrosinase B4	scaffold2426 size145584.3 113288	C	T	intergenic region	0.723050765	0.674079207	0.759529895
scaffold6020 size75420.4	tyrosinase B4	scaffold6020 size75420.4 14397	C	T	downstream gene variant	0.547817696	0.554753935	0.509860859
scaffold5775 size102228.1	tyrosinase B Pmax1	scaffold5775 size102228.1 18945	G	A	intergenic region	0.927516234	0.929495074	1
scaffold5775 size102228.1	tyrosinase B Pmax1	scaffold5775 size102228.1 21643	G	A	intergenic region	0.936159694	0.947860963	1
scaffold1797 size279199.10	tyrosinase-like protein 1	scaffold1797 size279199.10 140999	C	A	intergenic region	0.276081974	0.357726257	0.443553626
scaffold1797 size279199.10	tyrosinase-like protein 1	scaffold1797 size279199.10 75418	A	G	intergenic region	0.678819444	0.674577482	0.572349629
scaffold1797 size279199.10	tyrosinase-like protein 1	scaffold1797 size279199.10 8228	A	G	intergenic region	0.2434133	0.240490548	0.17905931
scaffold9953 size33018.5	tyrosinase-like protein 1	scaffold9953 size33018.5 3342	G	A	intergenic region	0.718320118	0.796330694	0.801337166
scaffold10826 size62665.3	tyrosine-protein kinase PR2 isoform X1	scaffold10826 size62665.3 1539	A	G	downstream gene variant	0.241963947	0.208215498	0.39748847
scaffold10826 size62665.3	tyrosine-protein kinase PR2 isoform X1	scaffold10826 size62665.3 1608	G	A	downstream gene variant	0.214041975	0.19375126	0.305384199
scaffold1018 size15965.26	tyrosine-protein kinase transmembrane receptor Ror	scaffold1018 size15965.26 123029	A	T	intron variant	0.772203314	0.789272234	0.879810161
scaffold6110 size41108.10	tyrosine-protein phosphatase non-receptor type 1	scaffold6110 size41108.10 21921	C	T	downstream gene variant	0.744289773	0.748952037	0.752568394
scaffold5286 size98312.12	tyrosine-protein phosphatase non-receptor type 11 isoform X1	scaffold5286 size98312.12 75622	T	A	intron variant	0.93797954	0.909285714	0.976388889
scaffold4726 size85232.4	tyrosine-protein phosphatase non-receptor type 23	scaffold4726 size85232.4 2882	C	T	intergenic region	0.880592385	0.890455305	0.885397942
scaffold4726 size85232.4	tyrosine-protein phosphatase non-receptor type 23	scaffold4726 size85232.4 63146	T	G	intergenic region	0.825057296	0.829744542	0.849187874
scaffold1490 size115539.4	visual pigment-like receptor peropsin	scaffold1490 size115539.4 64221	A					

C - List of all green specific SNPs, from left to right: with the transcripts code; the proteins that are encoding by genes related to pigmentation impacted by the SNPs; the SNP place corresponding to the number of base (after the underscore) in the scaffold code; reference allele; alternative allele; impact of the SNP; and allelic frequencies for red, yellow and green phenotypes.

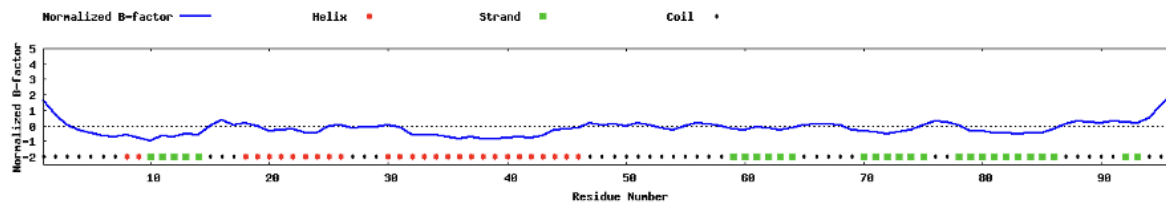
transcripts	Gene name	SNP	R	A	impact	Red's AF	Yellow's AF	Green's AF
scaffold605 size173110.34	Cadherin EGF LAG seven-pass G-type receptor 2	scaffold605 size173110_154272	G	A	downstream_gene_variant	0.805907087	0.777020225	0.789821316
scaffold910 size252188.4	Cadherin-23	scaffold910 size252188_14555	T	C	intron_variant	0.936815709	0.954407794	0.95638941
scaffold234 size272526.38	cadherin-23-like isoform X3	scaffold234 size272526_211612	C	T	intergenic_region	0.852221135	0.850536729	0.82749144
scaffold2505 size92724.1	cadherin-23-like isoform X3	scaffold2505 size92724_18810	T	C	intron_variant	0.86537074	0.865843672	0.90107426
scaffold14161 size18149.1	calcium-binding protein LPS1-alpha-like	scaffold14161 size18149_12593	A	T	intron_variant	0.836027236	0.824552687	0.817016807
scaffold791 size153329.12	Cytochrome P450 20A1	scaffold791 size153329_87835	T	C	intron_variant	0.691928077	0.698565283	0.712101868
scaffold791 size153329.12	Cytochrome P450 20A1	scaffold791 size153329_88867	G	T	intron_variant	0.805654401	0.840786398	0.81093886
scaffold1310 size120650.23	cytochrome P450 2C8	scaffold1310 size120650_80870	C	A	intron_variant	0.77810725	0.740362147	0.754549077
scaffold49 size265340.7	cytochrome P450 2C8	scaffold49 size265340_51856	C	A	upstream_gene_variant	0.670114386	0.750633017	0.753257132
scaffold49 size265340.7	cytochrome P450 2C8	scaffold49 size265340_61554	C	T	intron_variant	0.888403396	0.898256154	0.89336054
scaffold49 size265340.6	cytochrome P450 2C8-like	scaffold49 size265340_38705	A	C	intron_variant	0.889979989	0.952203486	0.966111111
scaffold1341 size119781.4	Cytochrome P450 4A25	scaffold1341 size119781_6168	C	T	downstream_gene_variant	0.918895657	0.949343501	0.957331175
scaffold1676 size364098.104	cytochrome P450 4F12-like	scaffold1676 size364098_330215	A	T	intergenic_region	0.920481336	0.934329138	0.906390929
scaffold1676 size364098.104	cytochrome P450 4F12-like	scaffold1676 size364098_331860	C	A	intergenic_region	0.943708073	0.95677454	0.944662023
scaffold551 size158850.4	ferritin 1	scaffold551 size158850_20422	A	C	upstream_gene_variant	0.940316116	0.969825621	0.951635209
scaffold5249 size131904.15	ferrochelatase, mitochondrial	scaffold5249 size131904_104547	G	A	intergenic_region	0.926883141	0.934336563	0.9367971
scaffold2158 size160354.18	flavin reductase (NADPH)	scaffold2158 size160354_118513	T	C	intergenic_region	0.9193817	0.898537274	0.890424598
scaffold1115 size353168.19	glutathione S-transferase 1-like	scaffold1115 size353168_63863	A	T	intron_variant	0.270505546	0.250070173	0.228927432
scaffold12296 size49253.2	multidrug resistance-associated protein 1	scaffold12296 size49253_11119	A	G	downstream_gene_variant	0.800833126	0.742559479	0.771122548
scaffold915 size243652.70	Multidrug resistance-associated protein 1	scaffold915 size243652_171213	C	G	upstream_gene_variant	0.868952339	0.898203015	0.912329655
scaffold2357 size95418.10	multidrug resistance-associated protein 1 isoform X1	scaffold2357 size95418_83886	C	A	intergenic_region	0.830724746	0.887748418	0.85921053
scaffold7087 size47719.1	multidrug resistance-associated protein 1-like isoform X1	scaffold7087 size47719_1109	A	C	intergenic_region	0.934650909	0.979166667	0.972170686
scaffold7087 size47719.1	multidrug resistance-associated protein 1-like isoform X1	scaffold7087 size47719_1241	A	T	intergenic_region	0.860992851	0.870014153	0.866125601
scaffold11594 size1006.5	perlucin-like protein	scaffold11594 size1006_34205	A	T	upstream_gene_variant	0.841733661	0.897606122	0.923381611
scaffold3547 size129194.18	perlucin-like protein	scaffold3547 size129194_105367	A	T	downstream_gene_variant	0.457122894	0.492490287	0.557910277
scaffold3547 size129194.18	perlucin-like protein	scaffold3547 size129194_105379	A	T	downstream_gene_variant	0.48554368	0.510598158	0.50144815
scaffold1567 size137386.7	perlucin-like protein isoform X1	scaffold1567 size137386_22342	G	T	upstream_gene_variant	0.275866069	0.259850464	0.32703608
scaffold454 size172198.10	Tyrosinase 1	scaffold454 size172198_160132	T	C	intergenic_region	0.78410398	0.867416285	0.870616152
scaffold454 size172198.10	Tyrosinase 1	scaffold454 size172198_56577	C	A	intergenic_region	0.919871795	0.926869472	0.936012748
scaffold1980 size291657.3	tyrosinase B2.1	scaffold1980 size291657_59414	C	G	intron_variant	0.950615033	0.967797443	0.946989114
scaffold101 size233448.23	urease subunit alpha-like	scaffold101 size233448_106064	A	G	intron_variant	0.359974162	0.359209226	0.429068463
scaffold101 size233448.23	urease subunit alpha-like	scaffold101 size233448_148567	G	A	intergenic_region	0.877671023	0.910906695	0.914858458
scaffold2909 size388074.62	visual pigment-like receptor peropsin	scaffold2909 size388074_257210	T	A	downstream_gene_variant	0.861870445	0.848308763	0.900331821

File S5:

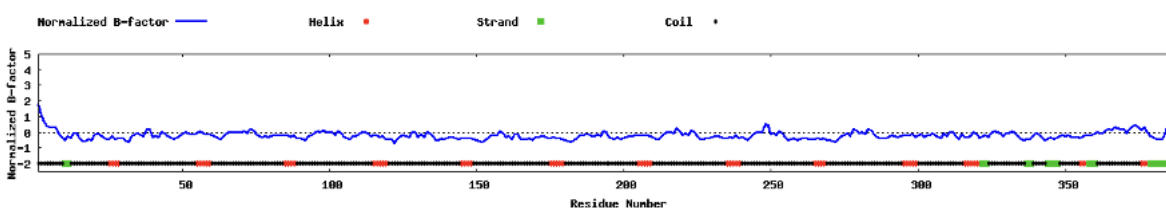
A – Secondary structure prediction by I-Tasser for the PBGD reference sequence.



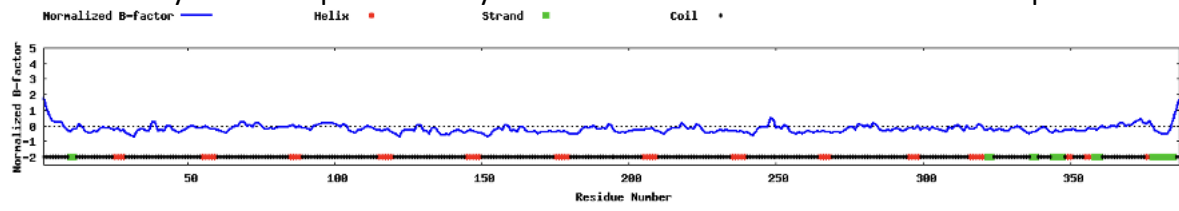
B – Secondary structure prediction by I-Tasser for the PBGD alternative sequence.



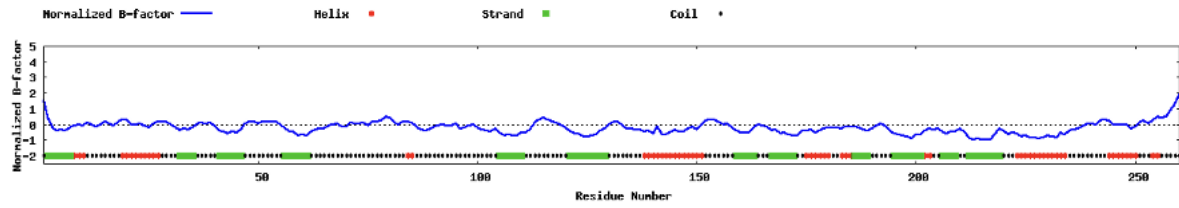
C – Secondary structure prediction by I-Tasser for the Shematin reference sequence.



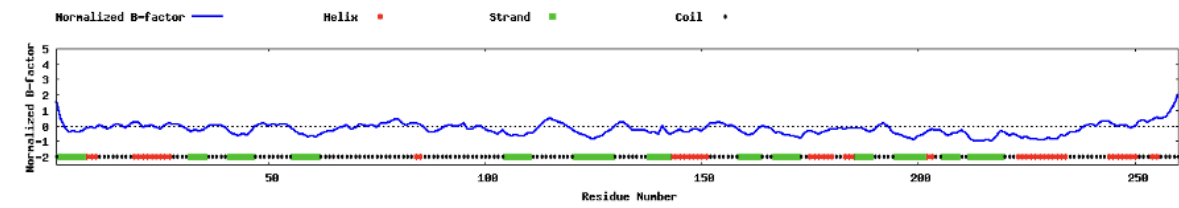
D – Secondary structure prediction by I-Tasser for the Shematin alternative sequence.



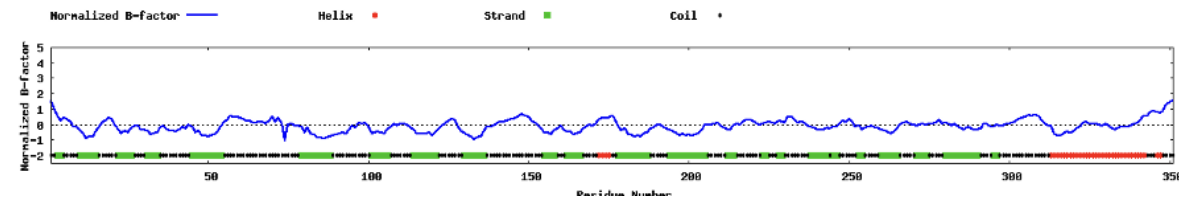
E – Secondary structure prediction by I-Tasser for the Cytochrome P450 3A29 reference sequence.



F – Secondary structure prediction by I-Tasser for the Cytochrome P450 3A29 alternative sequence.



G – Secondary structure prediction by I-Tasser for the Cadherin reference sequence.



H – Secondary structure prediction by I-Tasser for the Cadherin alternative sequence.

